

Figure S1. Multidimensional scaling analysis of the RNA-seq experiments.

Samples are projected on the two first dimensions according to their gene expression profiles. Closeness between samples on the grid indicates a strong similarity.

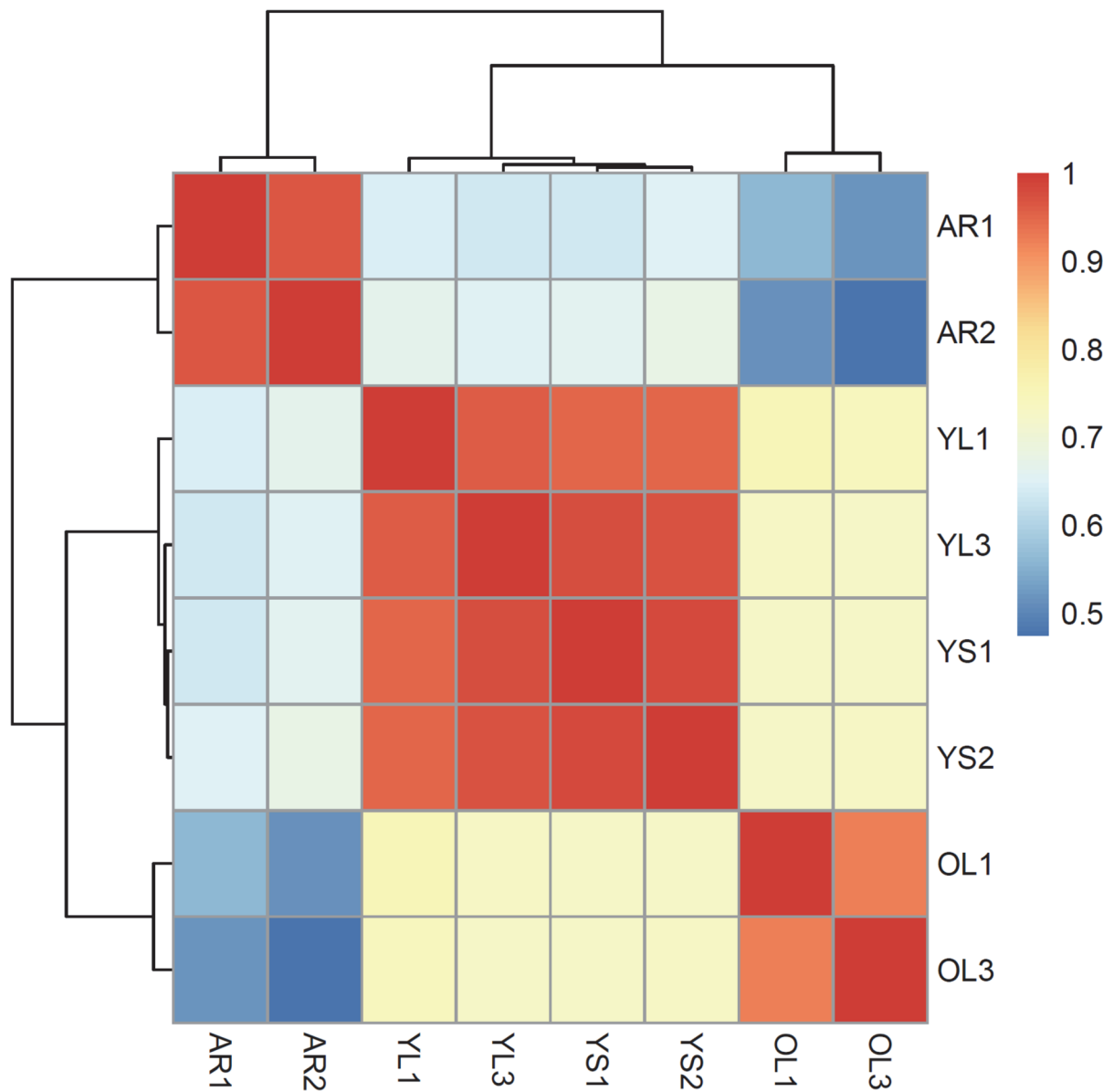


Figure S2. Similar tissue type are strongly correlated. Spearman's rho correlation was measured to check biological replicate homogeneity. Higher rho values indicate stronger similarities between pairs of samples.

$-\log_{10}(Pval)$ ● 5 ● 10 ● 15 ● 20

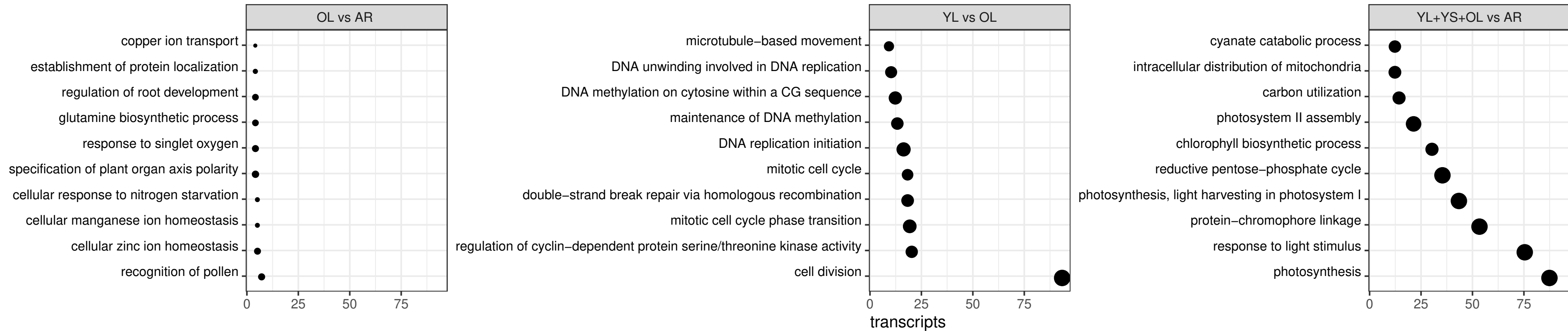


Figure S3. DEG with $\log_{2}FC > 2$ mapped to GO biological pathways that are significantly enriched ($p < 0.05$)

$-\log_{10}(Pval)$ • 4 ● 8 ● 12 ● 16 ● 20

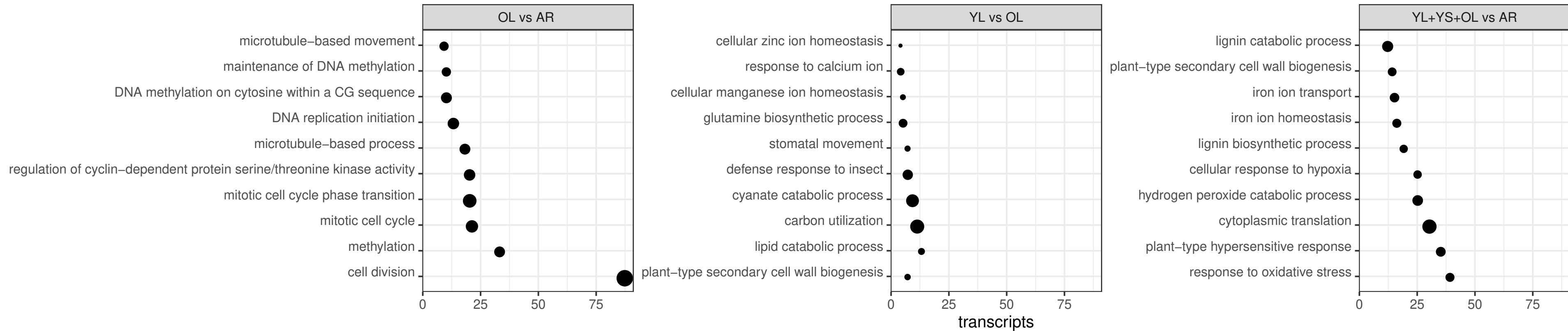


Figure S4. DEG with $\log_{2}FC < 2$ mapped GO biological pathways that are significantly enriched ($p < 0.05$).

YLvsOL 4527 DEG

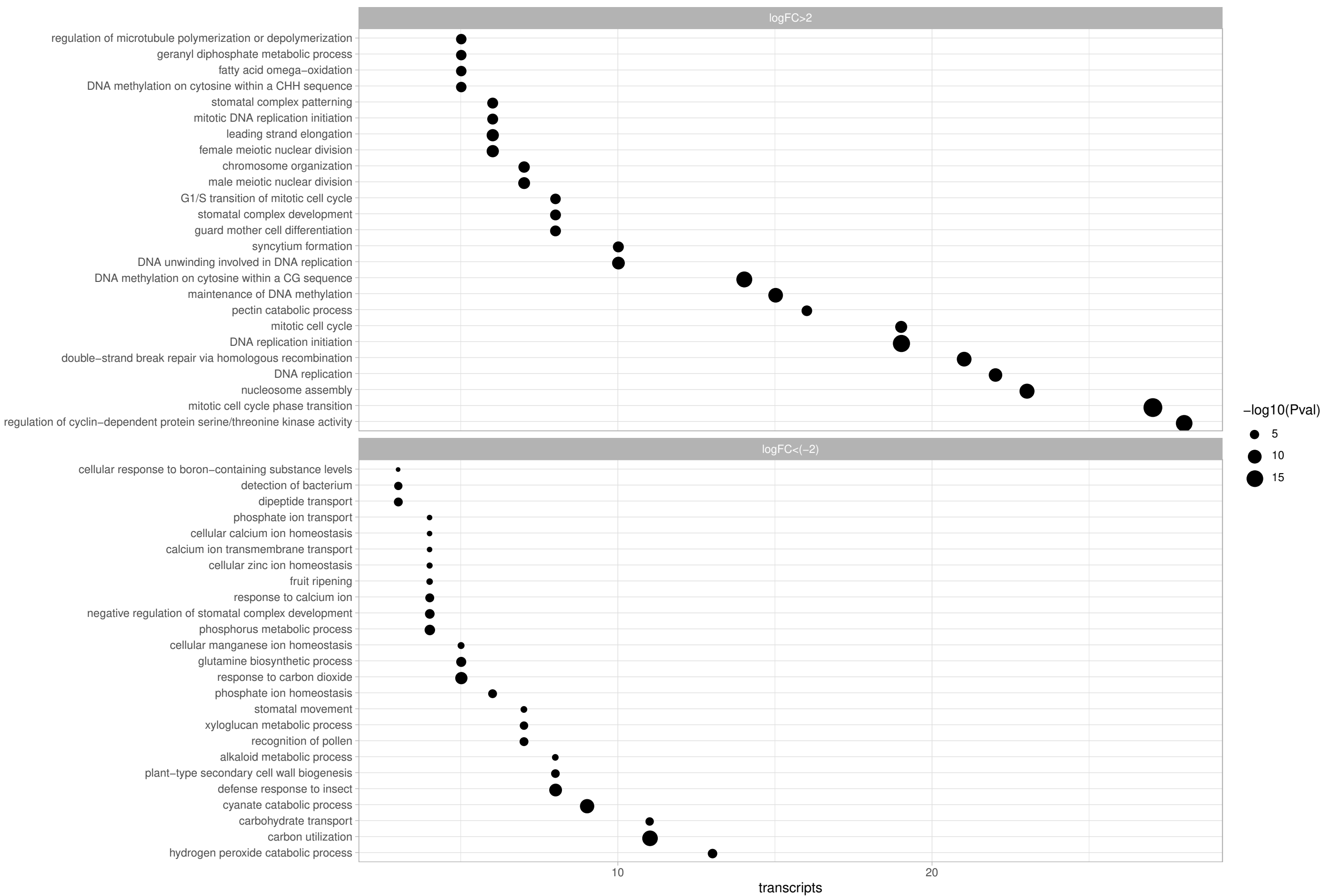


Figure S5. Significantly enriched GO biological pathways ($p < 0.05$) in the upregulated (log fold change > 2) and downregulated (log fold change < -2) YLvsOL DEG comparison.

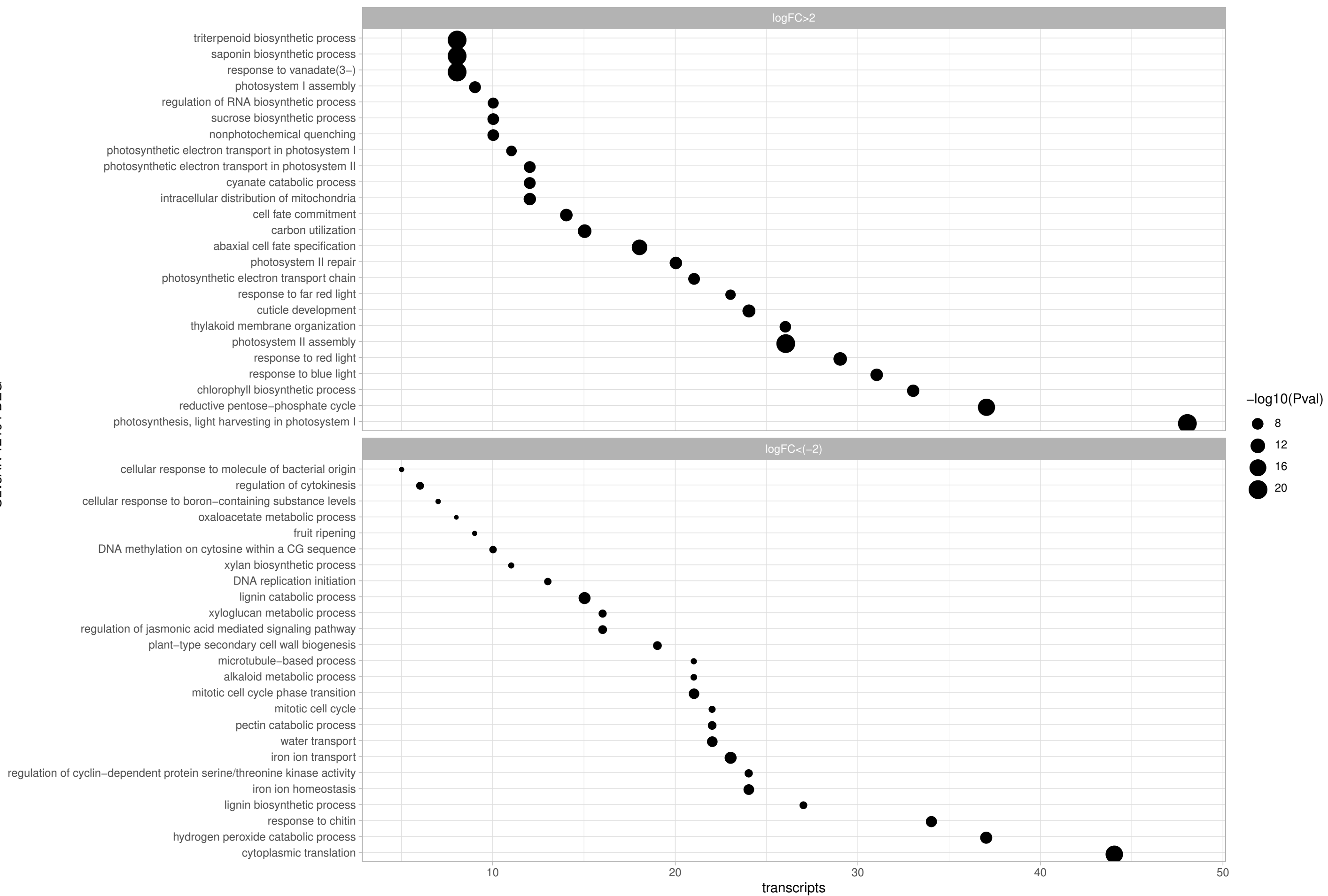


Figure S6. Significantly enriched GO biological pathways ($p < 0.05$) in the upregulated (log fold change > 2) and downregulated (log fold change < -2) OLvsAR DGE comparison.

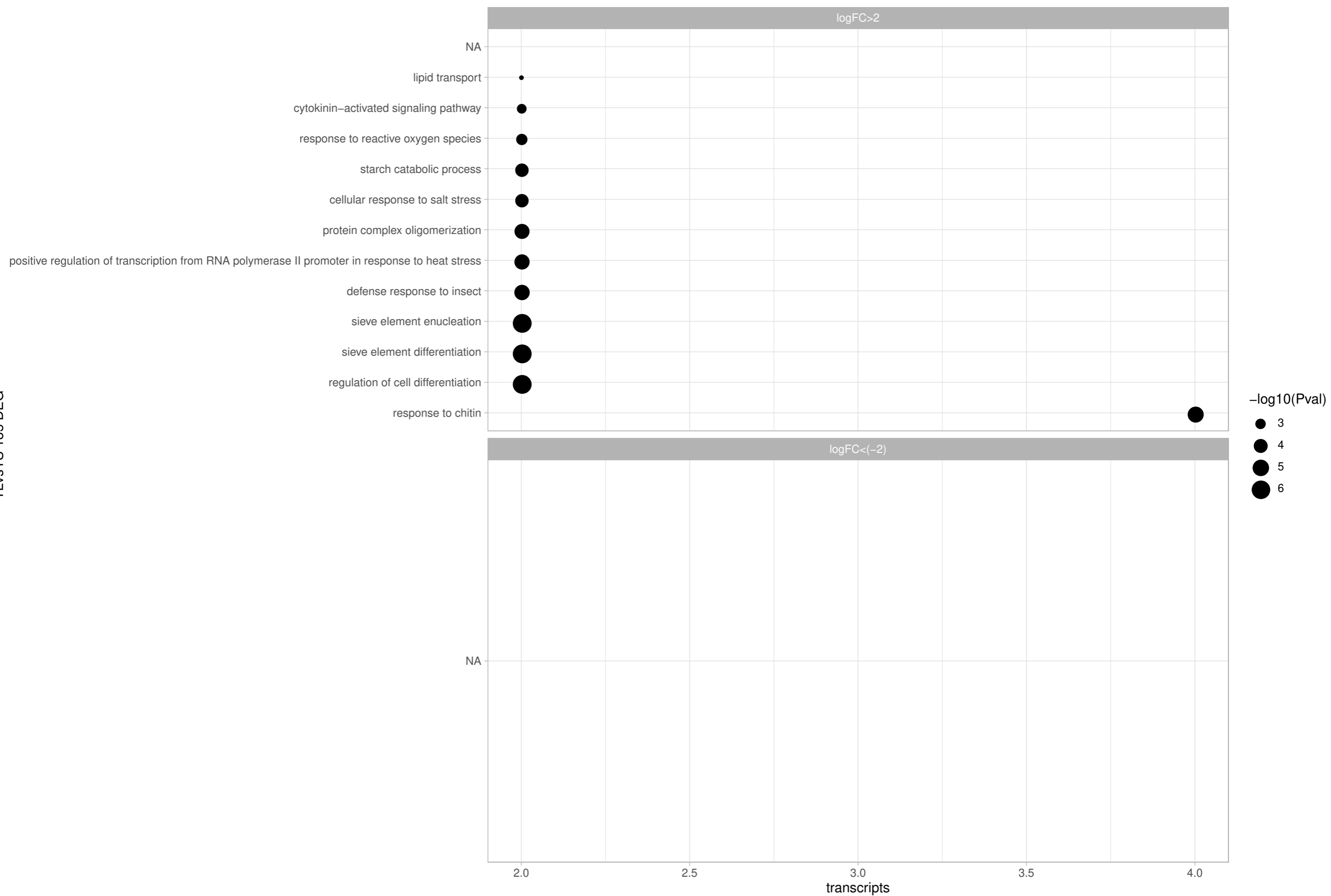


Figure S7. Significantly enriched GO biological pathways ($p < 0.05$) in the upregulated (log fold change > 2) and downregulated (log fold change < -2) YLvsYS DEG comparison.

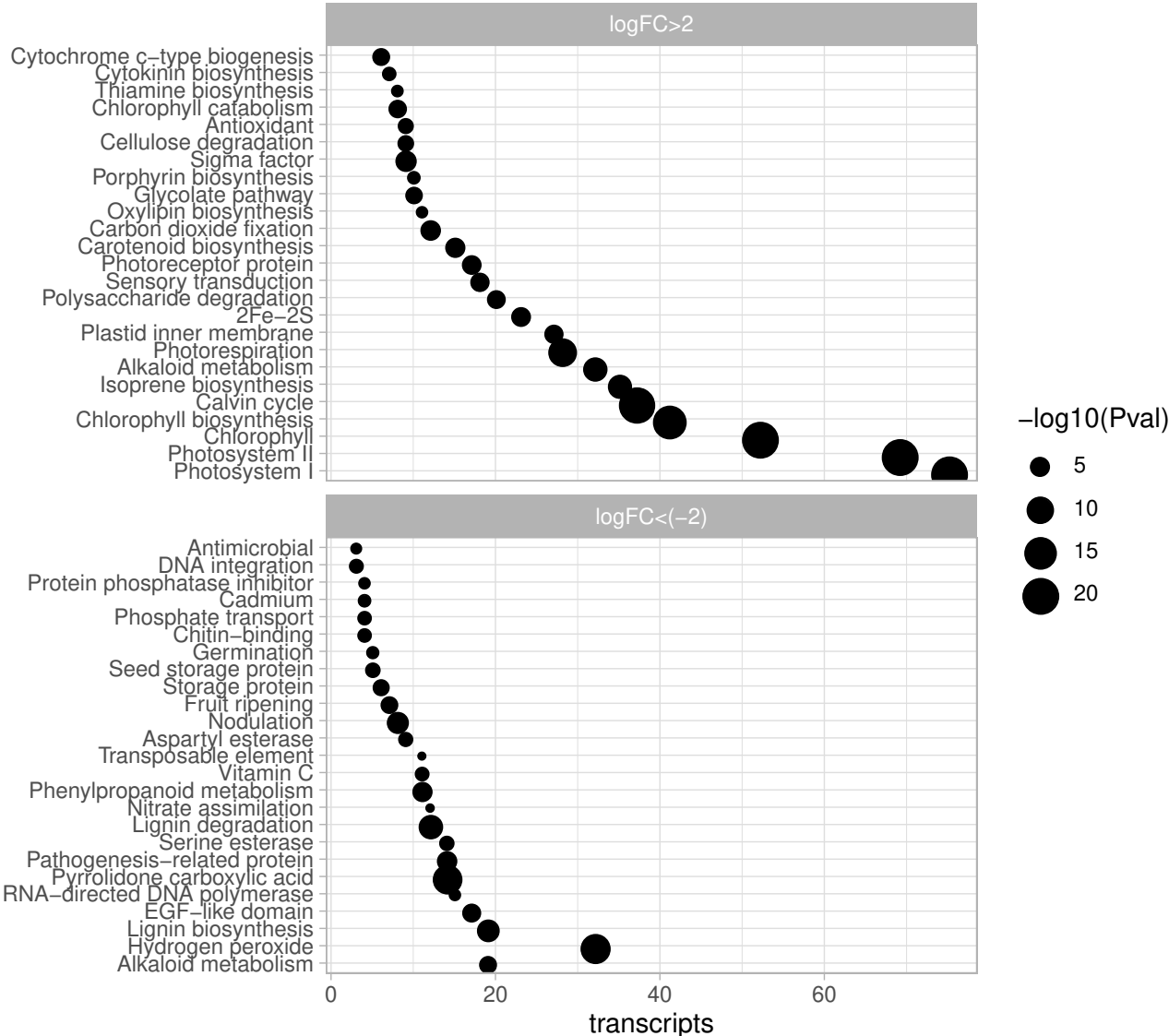


Figure S8. Significantly enriched GO biological pathways ($p < 0.05$) in the upregulated (log fold change > 2) and downregulated (log fold change < 2) YLvsAR

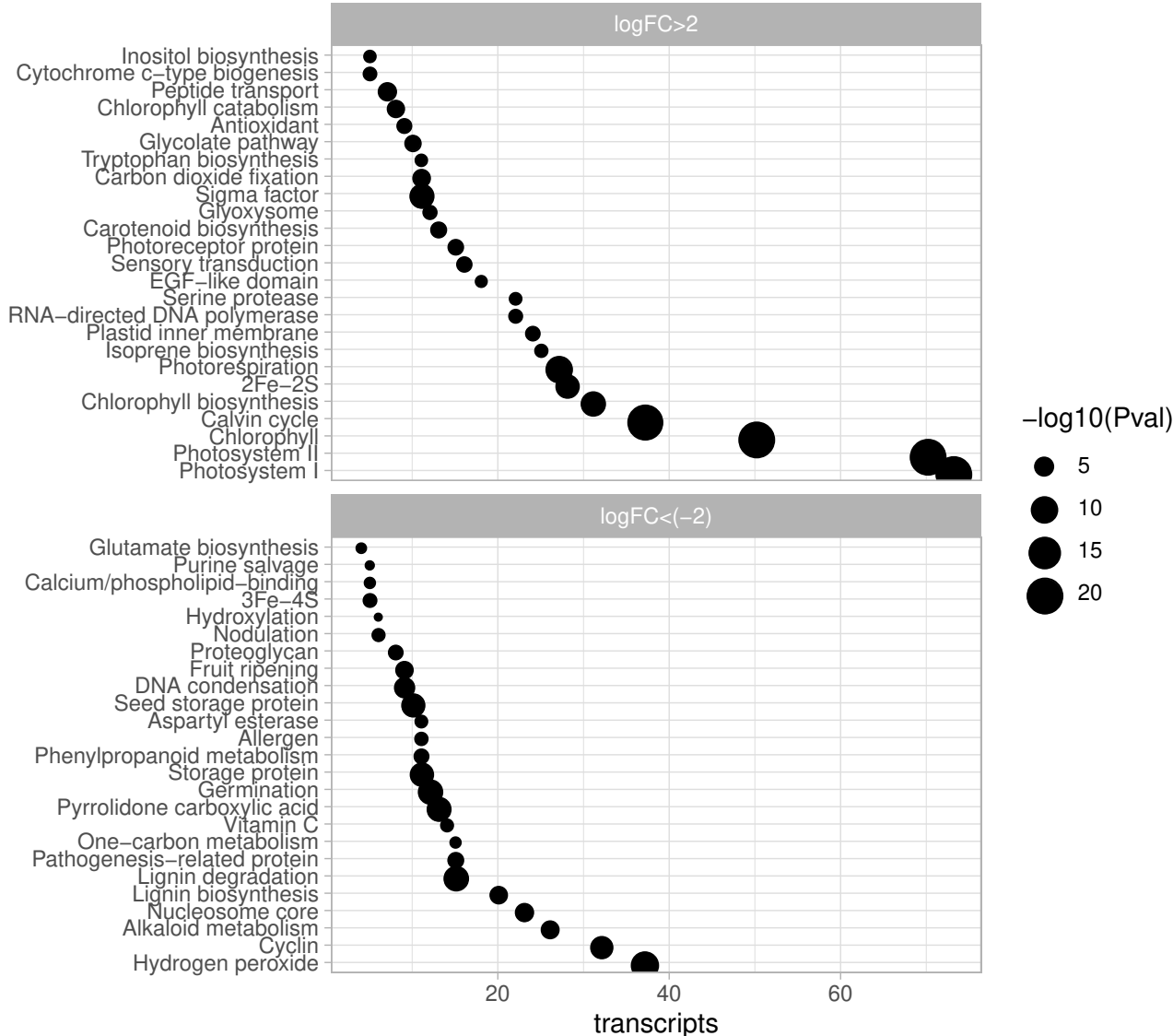


Figure S9. Significantly enriched GO Keywords ($p < 0.05$) in the upregulated (\log fold change > 2) and downregulated (\log fold change > 2) OLvsAR DEG comparison.

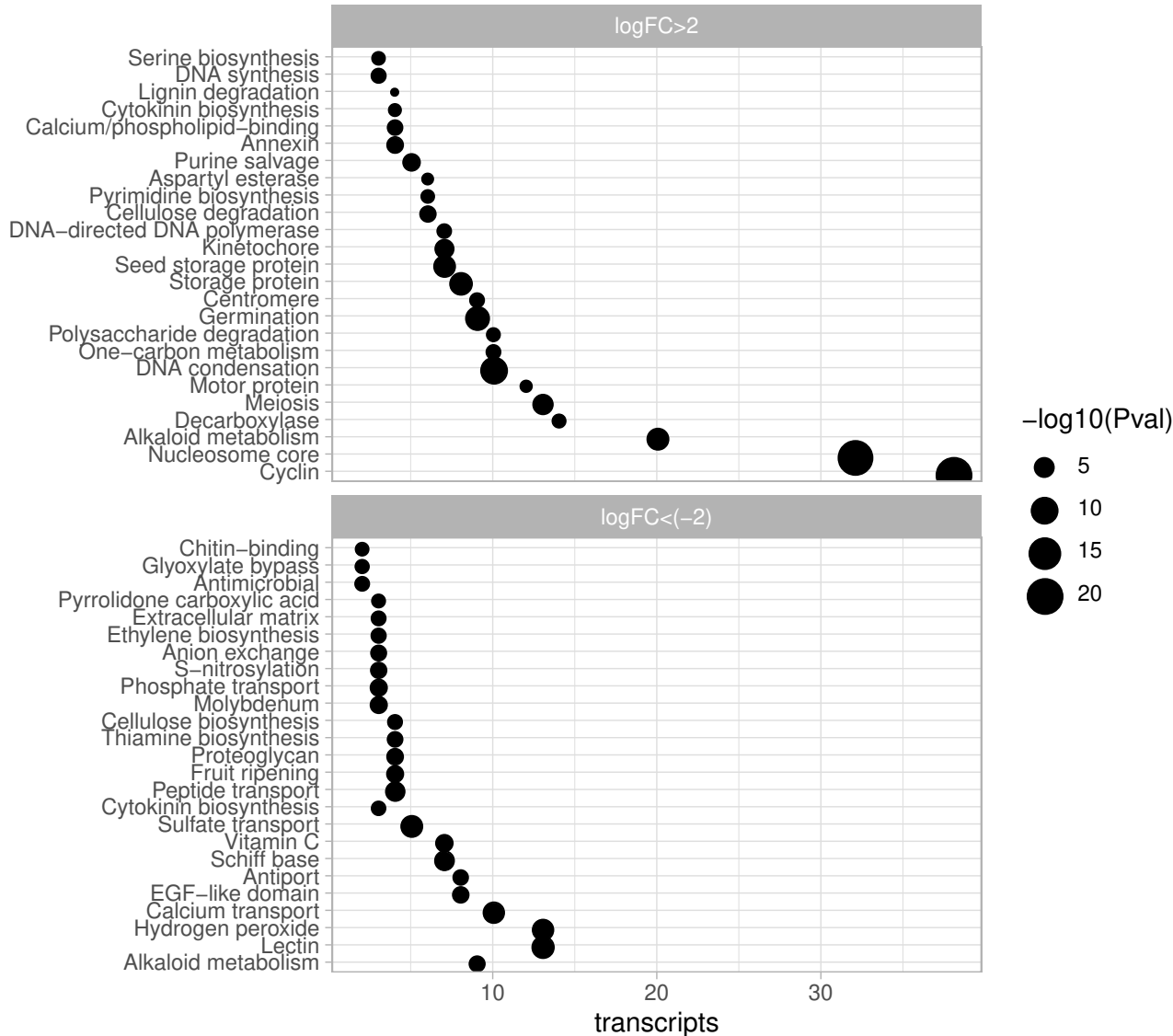
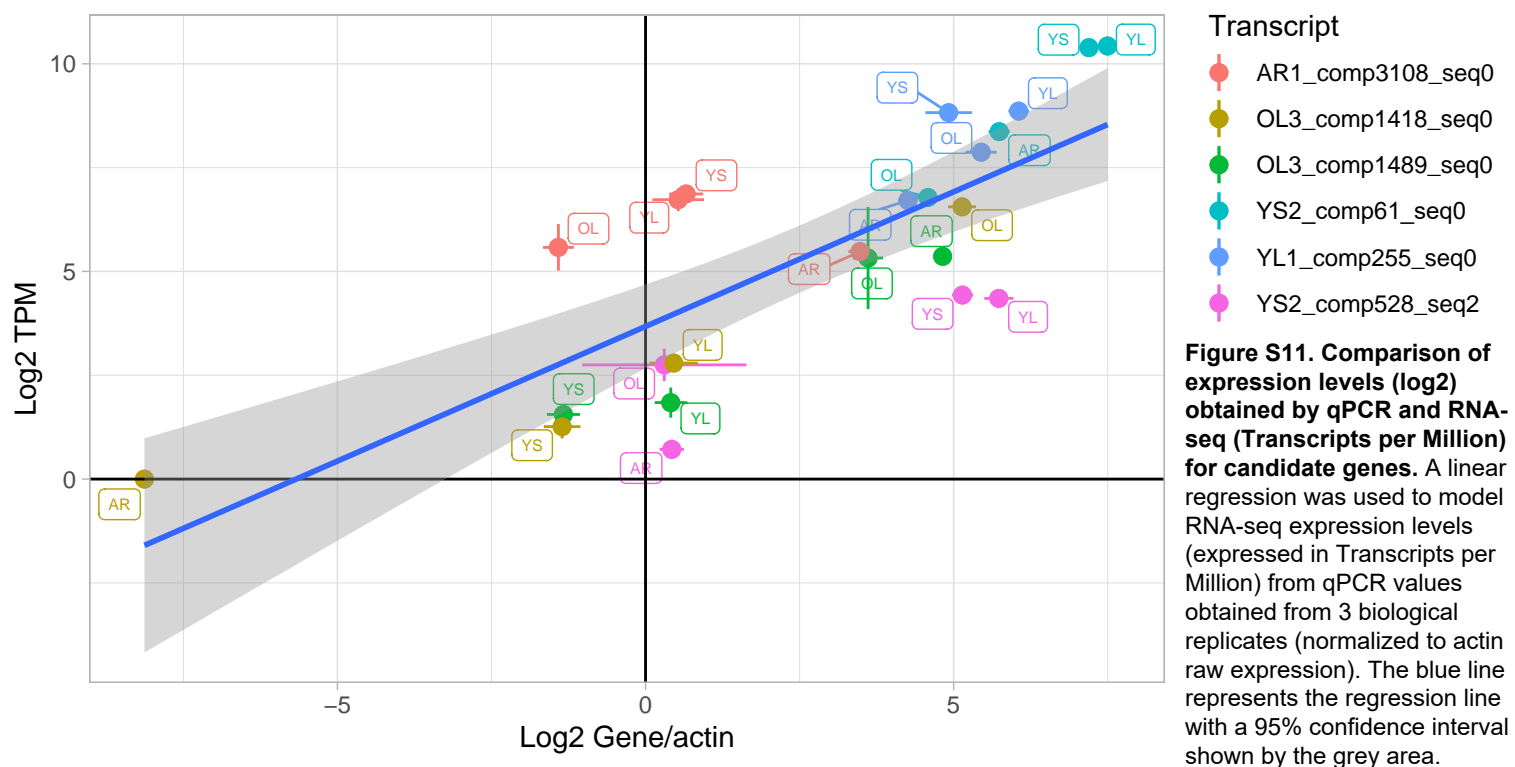


Figure S10. Significantly enriched GO Keywords ($p < 0.05$) in the upregulated (\log fold change > 2) and downregulated (\log fold change < 2) YLvsOL DEG comparison.



Dimerization domain

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Cr16OMT      1 MDVQSEEFRGAQAQIWSQSCSFITSASLSKCAVKLGIPDTIDNHGKPITLSELTNALVPPV
Vm16OMT     1 MDVQSDEFSKAQAHIWSQVLCHIPTATIKCAIELGLGIPDAIDNHGKAMTLAELTNSL-PLI
AR_comp35   1 MDVQSEEFRKAQAHIWRHASCLIPTACLICAVELGIADAIHSHGKPMPLSDLTNSL-PS-
AR_comp1185 1 MDVQSEEFRKAQAHIWRHASCLIPTACLICAVELGIADAIHSHGKPMPLSDLTNSL-PS-
YS1_comp1836 1 MDLEASEIIRKAQAKFLSCSFSFSTSGASLKCAVOLGIPDAIHNHGKPMSISELTNSL--LI

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Cr16OMT     61 HPSKAPFIYRLRMRVLAKNGFCSEEQLDGETEPLYSLTPSSRILLKKEPLNRGIVLTMAD
Vm16OMT     60 NPSKAPFVRRLMRILVKNGFFSEQOITND-HIAYGLTPSSRILLKNEPLNRGLVLANLD
AR_comp35   59 NPSRAPHIHRVMRVLVKDGFFTEEQS----NVYALTPSSRLLLKNEPLNRGLVLANLD
AR_comp1185 59 NPSRAPHIHRVMRVLVKDGFFTEEQS----NVYALTPSSRLLLKNEPLNRGLVLPMLE
YS1_comp1836 59 NPSKAPYIHRLMRILVISGYFSEEEP-----NVYSLNSLSRLLLKNOPLSLRAFVLYTLE

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O-methyltransferase domain

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Cr16OMT     121 PVQLKAWESLSDWYQNEDDS-STAFETA-HGKNFWGYSSSEHMEHAEFFNEAMASDSQLIS
Vm16OMT     119 PSHMKSWVVALSEWFQNDNEEAKTAFEIAHNGKNFDYSAEDTEHAEIFNEAMASDSKLVS
AR_comp35   114 PSHMKSWVVALSEWFQNDNEEAKTAFEIAHNGKNFDYSAEDTEHAEIFNEAMASDSKLVS
AR_comp1185 114 TANVKALDALGRWFQTED---QTSFEIAHDGKTFDYSVEQTKHAQNENENMASDSKFVA
YS1_comp1836 114 IAEMKAWNSLSDWFKNED---PTAFETA-HGKNYWDYCVEDK-LGKGFDEIMATDSSLVS

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Cr16OMT     179 KLL-IGEYKFLFEGLASLVDIGGGTGTIAKAIAKNFPOLKCTVFDLPHVVANLES--KEN
Vm16OMT     179 ELLINTEYKLFEGLTSMVDVGGGTGTIAKAIAKTFPNLNCTVFDLPHVVANLES--MGN
AR_comp35   174 ELLINTEYKLFEGLTSMVDVGGGTGTIAKAIAKTFPNLNCTVFDLPHVVANLES--MGN
AR_comp1185 171 KL-LTTEYKLFKGLDSIVDVGGGTGTIAKAIAKAFPYLRCTVFDOPHVANLES--TEN
YS1_comp1836 169 KLL-IPDYKFLFEGLSSMVDVGGGTGTVAKAIAKSFPSSLKCTVFDLPRVVADLKPTTEEN

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Cr16OMT     236 VEFVAGDMFEKIPSANAIFLKWILHDWNDEDCVKILKSCKKAIPA--KGGKVIIDMVM-
Vm16OMT     237 LEFVAGDMFVKIPPANAIFLKWILHDWNDEDCVKILKACKKAIPEKEKGGKVIVIDTVI-
AR_comp35   232 LEFVAGDMFVKIPPANAIFLKWILHDWNDEDCVKILKACKKAIPEKEKGGKVIVIDTVI-
AR_comp1185 228 LEFVGGDMFDRIPSADAIILKIVLHDWNDEDCVKILKNCKKSIPEKEKGGKLILIENVM-
YS1_comp1836 228 LEFVAGDMFDKIPPANAIFLKWVLHDWKDEDCVKILKNCKKSIPEKEKGGKVIIDTVLM

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Cr16OMT     293 YSDKKDDDHLVKTQTSMDMAMLVNFAAKERCEKEWAFLFKEAGFSDYKIFPKLDFTRSLIE
Vm16OMT     296 GSKINDDESIKAQLSMDMGMMVDFASKERDEKEWASLFKEAGFSNYKIFPKLDFTRSVIE
AR_comp35   291 GSKINDDESIKAQLSMDMGMMVDFASKERDEKEWASLFKEAGFSNYKIFPKLDFTRSVIE
AR_comp1185 287 FSKKDDNESVKIQMAWDIDMLTLFGAKERTEDEWATLIROAGFSGYKIFPNMDFVRSIIE
YS1_comp1836 288 DSQKHDNELVKTQISSDMDMMVLFCAKERNEKEWAKLFKEAGFSGYKIFPMLDER-CPIE

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Cr16OMT     353 VYP
Vm16OMT     356 VYP
AR_comp35   351 VYP
AR_comp1185 347 VYP
YS1_comp1836 347 VYP

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Figure S12. Alignment of the amino-acid sequences of 16-O-tabersonine methyltransferase candidates. Sequence identity and similarity are highlighted by black and grey shading, respectively. The dimerization domain is highlighted in red and the O-methyltransferase domain is highlighted in blue.

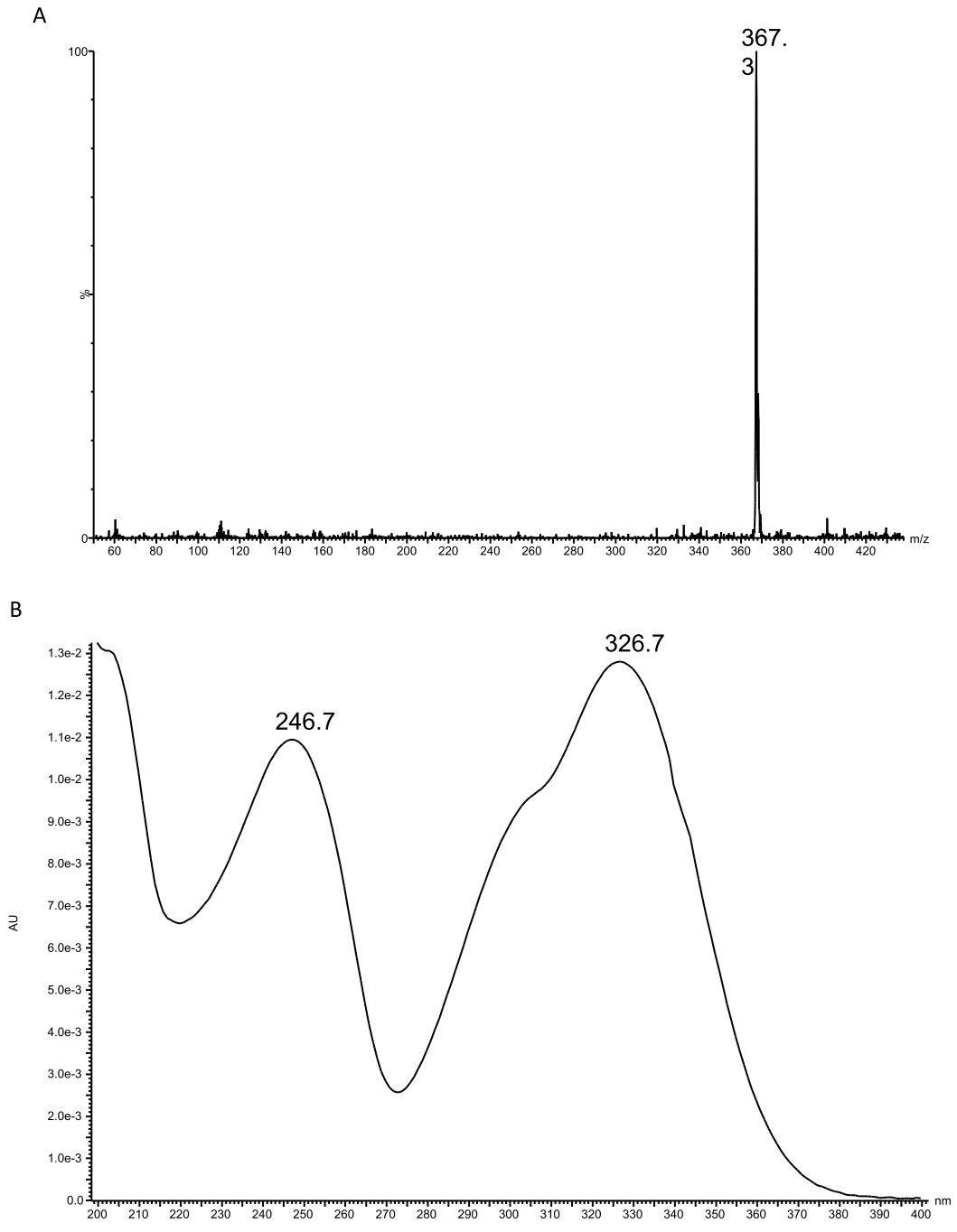


Figure S13. UPLC-DAD-MS analysis of 16-methoxytabersonine. (A) MS spectrum and (B) UV spectrum

TableS1

MIA	Transcript	% ID	Alignment length	Mismatch	Gapopen	MIA start	MIA end	Transcript start	Transcript end	E-value	Bitscore
	YS2_GAGATTCC-ATAGAGGC_comp2127_seq1	85.856	2326	280	9	132	2453	273	2553	0	2715
	YL3_CGCTCATT-ATAGAGGC_comp1779_seq8	86.735	2141	244	7	132	2268	247	2351	0	2585
	YL3_CGCTCATT-ATAGAGGC_comp1779_seq8	81.771	192	26	2	2262	2453	2431	2613	2.94E-46	188
	YL3_CGCTCATT-ATAGAGGC_comp1779_seq5	86.933	1852	199	9	138	1985	398	2210	0	2248
	YL3_CGCTCATT-ATAGAGGC_comp1779_seq5	85.614	285	41	0	1984	2268	2294	2578	1.33E-88	329
	YL3_CGCTCATT-ATAGAGGC_comp1779_seq5	81.771	192	26	2	2262	2453	2658	2840	2.94E-46	188
	AR1_GAGATTCC-CCTATCCT_comp8926_seq1	81.237	1956	367	0	468	2423	1115	3070	0	1873
	OL3_CGCTCATT-GGCTCTGA_comp1793_seq1	85.478	1267	144	7	132	1394	226	1456	0	1460
	OL3_CGCTCATT-GGCTCTGA_comp1793_seq1	87.184	593	74	2	1393	1985	1593	2183	0	720
DXS1 (KC625536.1)	OL3_CGCTCATT-GGCTCTGA_comp1793_seq1	84.12	466	65	2	1984	2449	2267	2723	8.38E-142	506
	YL1_CGCTCATT-TATAGCCT_comp1491_seq4	73.777	1922	496	4	444	2358	295	2215	0	1184
	AR1_GAGATTCC-CCTATCCT_comp8926_seq1	72.282	1959	536	6	444	2397	1099	3055	0	1065
	YS2_GAGATTCC-ATAGAGGC_comp2127_seq1	71.252	1941	541	14	467	2397	584	2517	0	937
	YS1_GAGATTCC-TATAGCCT_comp16391_seq0	74.211	1489	371	7	878	2358	1717	3200	0	935
	YL1_CGCTCATT-TATAGCCT_comp3571_seq0	84.672	822	126	0	871	1692	1	822	0	915
	YL1_CGCTCATT-TATAGCCT_comp3571_seq0	87.847	288	35	0	1970	2257	2335	2622	2.21E-98	361
	YL1_CGCTCATT-TATAGCCT_comp3571_seq0	87.943	282	34	0	1684	1965	1564	1845	9.42E-97	356
DXS2 (DQ848672.1)	YL1_CGCTCATT-TATAGCCT_comp3571_seq0	86.792	159	21	0	2256	2414	3195	3353	2.37E-47	192
	YL1_CGCTCATT-TATAGCCT_comp1491_seq4	87.967	2169	243	5	32	2185	94	2259	0	2729
	YS1_GAGATTCC-TATAGCCT_comp16391_seq0	88.066	1525	182	0	661	2185	1720	3244	0	1930
	AR1_GAGATTCC-CCTATCCT_comp8926_seq1	77.923	1993	430	4	127	2114	1002	2989	0	1602
	YS2_GAGATTCC-ATAGAGGC_comp2127_seq1	70.629	1859	540	4	259	2114	596	2451	0	879
	YS2_GAGATTCC-ATAGAGGC_comp28794_seq0	85.752	751	92	4	34	772	50	797	0	868
	YS1_GAGATTCC-TATAGCCT_comp445_seq2	88.005	1634	157	14	1	1613	352	1967	0	2037
	YL3_CGCTCATT-ATAGAGGC_comp492_seq0	87.636	1561	155	14	96	1629	728	2277	0	1918
	YL3_CGCTCATT-ATAGAGGC_comp492_seq0	90.816	98	9	0	1	98	300	397	1.00E-30	136
	YL1_CGCTCATT-TATAGCCT_comp16369_seq2	87.627	1382	133	14	275	1629	849	2219	0	1694
YL3_CGCTCATT-ATAGAGGC_comp434_seq2	92.004	1113	86	1	1	1110	213	1325	0	1606	
YL3_CGCTCATT-ATAGAGGC_comp434_seq2	79.89	547	72	14	1110	1629	1472	2007	5.51E-129	462	
	YS1_GAGATTCC-TATAGCCT_comp445_seq3	91.982	1110	89	0	1	1110	352	1461	0	1602
	YS1_GAGATTCC-TATAGCCT_comp445_seq3	75.75	400	59	14	1257	1629	1892	2280	1.48E-66	255
	YS1_GAGATTCC-TATAGCCT_comp445_seq3	91.156	147	13	0	1110	1256	1620	1766	6.74E-52	206
	YS2_GAGATTCC-ATAGAGGC_comp2915_seq1	84.587	1077	120	13	38	1075	1351	2420	0	1177
	YL1_CGCTCATT-TATAGCCT_comp25159_seq0	74.118	85	10	2	949	1024	1	82	6.35E-07	57.2
	YS2_GAGATTCC-ATAGAGGC_comp22987_seq0	95.652	23	1	0	384	406	1	23	0.6	37.4
	OL1_CGCTCATT-CCTATCCT_comp6333_seq2	89.286	28	3	0	662	689	477	450	0.6	37.4
	AR2_GAGATTCC-GGCTCTGA_comp22244_seq0	92.593	27	0	1	1336	1362	25	1	0.6	37.4
	YS1_GAGATTCC-TATAGCCT_comp1496_seq2	84.572	1426	186	12	90	1504	245	1647	0	1557
	AR1_GAGATTCC-CCTATCCT_comp2159_seq1	84.561	1425	187	12	90	1504	281	1682	0	1553
	YL3_CGCTCATT-ATAGAGGC_comp1768_seq0	88.545	969	111	0	90	1058	234	1202	0	1247
	YL3_CGCTCATT-ATAGAGGC_comp1768_seq0	88.136	59	7	0	1227	1285	1719	1777	2.99E-12	75.2

TableS1

CMK (DQ848671.1)	YL3_CGCTCATT-ATAGAGGC_comp1768_seq0	85.417	48	7	0	1169	1216	1199	1246	2.80E-06	55.4
	AR1_GAGATTCC-CCTATCCT_comp2159_seq2	92.323	495	38	0	638	1132	941	1435	0	722
	AR1_GAGATTCC-CCTATCCT_comp2159_seq2	85.278	557	82	0	90	646	281	837	0	636
	AR1_GAGATTCC-CCTATCCT_comp2159_seq2	73.438	384	69	12	1131	1504	1675	2035	2.01E-52	208
	YL3_CGCTCATT-ATAGAGGC_comp18_seq9	76.907	485	78	12	1031	1504	1869	2330	3.18E-94	347
	YS1_GAGATTCC-TATAGCCT_comp2048_seq1	85.405	740	78	7	1	719	179	909	0	843
	AR2_GAGATTCC-GGCTCTGA_comp29267_seq0	92.722	371	27	0	346	716	1002	1372	9.27E-155	547
	YL3_CGCTCATT-ATAGAGGC_comp2559_seq2	82.318	509	60	7	1	488	87	586	8.13E-143	508
	YL3_CGCTCATT-ATAGAGGC_comp2559_seq2	90.431	209	20	0	478	686	1498	1706	1.38E-76	288
MECS (AF250236.1)	AR2_GAGATTCC-GGCTCTGA_comp5554_seq2	85.676	377	42	3	124	488	197	573	1.47E-120	434
	AR2_GAGATTCC-GGCTCTGA_comp5554_seq2	92.975	242	17	0	478	719	1539	1780	2.66E-98	360
	AR2_GAGATTCC-GGCTCTGA_comp5554_seq2	87.805	41	5	0	1	41	89	129	1.80E-05	51.8
	AR1_GAGATTCC-CCTATCCT_comp4429_seq6	81.579	38	7	0	845	882	202	165	0.4	37.4
	YS2_GAGATTCC-ATAGAGGC_comp287_seq1	89.876	2331	220	6	42	2364	139	2461	0	3128
	AR1_GAGATTCC-CCTATCCT_comp972_seq1	89.79	2331	222	6	42	2364	135	2457	0	3119
	AR1_GAGATTCC-CCTATCCT_comp972_seq2	89.79	2331	222	6	42	2364	135	2457	0	3119
	AR1_GAGATTCC-CCTATCCT_comp972_seq6	89.79	2331	222	6	42	2364	135	2457	0	3119
	OL1_CGCTCATT-CCTATCCT_comp301_seq2	90.707	2249	209	0	116	2364	398	2646	0	3113
HDS (AY184810.2)	OL1_CGCTCATT-CCTATCCT_comp301_seq2	92.308	26	2	0	52	77	206	231	0.3	39.2
	YS1_GAGATTCC-TATAGCCT_comp439_seq2	88.865	1419	122	3	1	1392	147	1556	0	1865
	AR2_GAGATTCC-GGCTCTGA_comp1917_seq2	89.177	1349	113	2	1	1325	88	1427	0	1795
	AR2_GAGATTCC-GGCTCTGA_comp1917_seq2	86.486	74	7	1	1322	1392	1580	1653	3.82E-16	87.8
	YS1_GAGATTCC-TATAGCCT_comp439_seq0	92.056	1133	87	1	263	1392	882	2014	0	1636
	YS1_GAGATTCC-TATAGCCT_comp439_seq0	79.508	244	33	5	40	267	3	245	1.62E-52	208
	OL3_CGCTCATT-GGCTCTGA_comp26094_seq0	91.56	936	76	1	460	1392	934	1869	0	1330
	OL3_CGCTCATT-GGCTCTGA_comp26094_seq0	93.939	198	12	0	265	462	3	200	2.74E-81	304
	YL3_CGCTCATT-ATAGAGGC_comp21618_seq1	91.799	756	59	1	640	1392	410	1165	0	1083
HDR (DQ848676.1)	YL3_CGCTCATT-ATAGAGGC_comp21618_seq1	93.145	248	17	0	397	644	1	248	2.25E-101	370
	AR1_GAGATTCC-CCTATCCT_comp1158_seq0	81.466	1187	145	25	36	1206	120	1247	0	1104
	YS2_GAGATTCC-ATAGAGGC_comp566_seq2	84.258	775	89	10	388	1156	1384	2131	0	832
	YS2_GAGATTCC-ATAGAGGC_comp566_seq2	77.344	256	28	7	137	389	19	247	9.33E-49	196
	AR2_GAGATTCC-GGCTCTGA_comp16125_seq3	83.484	775	95	10	388	1156	3012	3759	0	805
	AR2_GAGATTCC-GGCTCTGA_comp16125_seq3	79.31	58	1	1	332	389	1829	1875	5.90E-07	57.2
	YS2_GAGATTCC-ATAGAGGC_comp29331_seq0	92.727	165	12	0	315	479	1	165	2.05E-63	244
	YS2_GAGATTCC-ATAGAGGC_comp29331_seq0	92.391	92	7	0	477	568	1003	1094	2.68E-30	134
	YS1_GAGATTCC-TATAGCCT_comp15918_seq0	96.552	58	2	0	332	389	1203	1260	6.72E-19	96.9
IDI1 (EU135981.1)	AR1_GAGATTCC-CCTATCCT_comp8039_seq0	87.905	1265	147	2	2	1263	301	1562	0	1588
	AR1_GAGATTCC-CCTATCCT_comp30038_seq0	89.655	29	3	0	1196	1224	30	2	0.16	39.2
	YL3_CGCTCATT-ATAGAGGC_comp1244_seq0	95.455	22	1	0	39	60	3610	3589	1.9	35.6
	AR2_GAGATTCC-GGCTCTGA_comp5097_seq2	91.667	24	2	0	691	714	2295	2318	1.9	35.6
	YL3_CGCTCATT-ATAGAGGC_comp1244_seq6	95.455	22	1	0	39	60	3498	3477	1.9	35.6
GPPS (KF561462.1)											

TableS1

	YL1_CGCTCATT-TATAGCCT_comp695_seq0	85.882	1615	215	6	153	1762	323	1929	0	1869
	YL1_CGCTCATT-TATAGCCT_comp695_seq0	89.189	37	4	0	91	127	285	321	1.23E-04	50
	YS1_GAGATTCC-TATAGCCT_comp841_seq0	87.888	677	77	2	1090	1762	1649	2324	0	847
	OL3_CGCTCATT-GGCTCTGA_comp6736_seq2	80.46	783	121	5	93	874	185	936	0	729
	YL3_CGCTCATT-ATAGAGGC_comp13409_seq0	86.965	537	65	2	1230	1762	874	1409	0	648
	YL3_CGCTCATT-ATAGAGGC_comp13409_seq0	95.833	24	1	0	1090	1113	390	413	0.22	39.2
	YS1_GAGATTCC-TATAGCCT_comp19336_seq1	87.847	288	35	0	943	1230	2	289	1.49E-98	361
	YS1_GAGATTCC-TATAGCCT_comp19336_seq1	88.764	89	10	0	1481	1569	1169	1257	1.01E-24	116
GES (JN882024.1)	YS1_GAGATTCC-TATAGCCT_comp19336_seq1	95.833	24	1	0	1230	1253	726	749	0.22	39.2
	AR1_GAGATTCC-CCTATCCT_comp589_seq7	79.961	1537	300	2	23	1551	1306	2842	0	1382
	AR1_GAGATTCC-CCTATCCT_comp2452_seq0	81.882	861	156	0	316	1176	1	861	0	850
	AR1_GAGATTCC-CCTATCCT_comp2452_seq0	79.191	173	26	2	1385	1555	866	1030	4.58E-35	150
	YL3_CGCTCATT-ATAGAGGC_comp1775_seq0	80.248	805	149	2	753	1555	2	798	0	735
	YS1_GAGATTCC-TATAGCCT_comp8154_seq1	80.863	371	61	2	1187	1555	5	367	8.82E-95	349
G10H (AJ251269.1)	AR1_GAGATTCC-CCTATCCT_comp7341_seq0	73.913	184	48	0	1164	1347	1434	1617	9.45E-25	116
	YL3_CGCTCATT-ATAGAGGC_comp70_seq0	87.871	1113	135	0	129	1241	146	1258	0	1398
	OL3_CGCTCATT-GGCTCTGA_comp191_seq2	86.667	600	80	0	642	1241	1622	2221	0	722
	AR1_GAGATTCC-CCTATCCT_comp635_seq0	68.704	949	280	9	298	1233	2061	3005	2.28E-94	347
	AR1_GAGATTCC-CCTATCCT_comp635_seq0	72.185	151	36	2	136	283	1792	1939	5.04E-14	80.6
	YS1_GAGATTCC-TATAGCCT_comp6458_seq0	82.158	241	43	0	732	972	1	241	2.44E-62	241
10HGO (KF302069.1)	YS2_GAGATTCC-ATAGAGGC_comp2835_seq1	82.553	235	41	0	738	972	1	235	8.52E-62	239
	YL3_CGCTCATT-ATAGAGGC_comp477_seq1	84.9	1053	159	0	115	1167	409	1461	0	1182
	YL3_CGCTCATT-ATAGAGGC_comp477_seq1	86.667	120	16	0	1	120	199	318	1.36E-33	145
	YS1_GAGATTCC-TATAGCCT_comp296_seq0	69.685	1049	292	11	78	1106	302	1344	6.55E-120	432
	OL1_CGCTCATT-CCTATCCT_comp26_seq0	65.448	1094	340	15	82	1153	195	1272	9.75E-61	235
	OL1_CGCTCATT-CCTATCCT_comp11291_seq2	66.289	353	97	9	758	1099	1363	1704	4.74E-14	80.6
	OL1_CGCTCATT-CCTATCCT_comp11291_seq2	95.652	23	0	1	871	893	1552	1573	6.2	33.7
IS (JX974564.1)	AR2_GAGATTCC-GGCTCTGA_comp6919_seq0	84.211	38	5	1	37	74	234	270	0.15	39.2
	OL1_CGCTCATT-CCTATCCT_comp520_seq1	83.735	1537	246	2	14	1548	261	1795	0	1640
	AR2_GAGATTCC-GGCTCTGA_comp3144_seq0	85.755	351	50	0	1198	1548	431	781	9.97E-113	408
	OL3_CGCTCATT-GGCTCTGA_comp13994_seq0	89.416	274	29	0	661	934	3	276	3.72E-99	363
	YS1_GAGATTCC-TATAGCCT_comp11762_seq0	89.286	252	27	0	683	934	1	252	6.30E-90	333
	YS1_GAGATTCC-TATAGCCT_comp11762_seq0	80.682	88	17	0	1206	1293	1686	1773	1.81E-14	82.4
	YS1_GAGATTCC-TATAGCCT_comp17871_seq1	90.244	205	20	0	730	934	1	205	3.49E-74	280
IO (KF302066.1)	YS1_GAGATTCC-TATAGCCT_comp17871_seq1	86.869	99	13	0	933	1031	1040	1138	7.21E-26	120
	YS2_GAGATTCC-ATAGAGGC_comp558_seq3	84.855	1446	219	0	75	1520	832	2277	0	1620
	OL3_CGCTCATT-GGCTCTGA_comp2126_seq0	84.165	1162	184	0	70	1231	72	1233	0	1267
	YS2_GAGATTCC-ATAGAGGC_comp8577_seq0	67.845	1415	415	20	98	1492	162	1556	4.50E-124	446
	YL3_CGCTCATT-ATAGAGGC_comp1412_seq1	83.74	369	60	0	1160	1528	1388	1756	7.13E-109	396
7DLGT (AB733667.1)	YS1_GAGATTCC-TATAGCCT_comp607_seq1	84.928	345	52	0	1184	1528	1063	1407	1.06E-106	389
	YL1_CGCTCATT-TATAGCCT_comp444_seq0	85.597	1222	156	7	662	1874	835	2045	0	1397

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7DLH (KF415115.1)	YL1_CGCTCATT-TATAGCCT_comp444_seq0	86.364	506	66	1	165	667	236	741	3.58E-170	600
	OL1_CGCTCATT-CCTATCCT_comp2662_seq1	68.421	1121	329	13	614	1726	783	1886	3.36E-107	390
	OL1_CGCTCATT-CCTATCCT_comp2662_seq1	73.469	98	26	0	233	330	408	505	7.44E-08	60.8
	AR2_GAGATTCC-GGCTCTGA_comp35_seq9	66.021	1498	477	14	233	1717	742	2220	9.02E-102	372
	OL3_CGCTCATT-GGCTCTGA_comp1360_seq3	68.489	1006	280	16	735	1726	1112	2094	3.59E-94	347
	AR2_GAGATTCC-GGCTCTGA_comp17345_seq0	67.033	1183	349	16	569	1735	494	1651	5.33E-92	340
	YS2_GAGATTCC-ATAGAGGC_comp88_seq3	85.714	1078	151	1	39	1116	385	1459	0	1249
	YS2_GAGATTCC-ATAGAGGC_comp1328_seq0	86.269	1005	135	1	112	1116	5289	6290	0	1189
	YL1_CGCTCATT-TATAGCCT_comp5423_seq0	84.903	828	122	1	39	866	2873	3697	0	928
	YL1_CGCTCATT-TATAGCCT_comp5423_seq0	89.535	344	36	0	773	1116	2120	2463	4.50E-128	459
LAMT (EU057974.1)	YL1_CGCTCATT-TATAGCCT_comp5423_seq0	83.871	31	5	0	551	581	878	908	5.9	33.7
	OL3_CGCTCATT-GGCTCTGA_comp1728_seq2	83.862	756	116	2	24	779	238	987	0	810
	OL3_CGCTCATT-GGCTCTGA_comp1728_seq2	88.663	344	39	0	773	1116	2169	2512	9.91E-124	444
	YS1_GAGATTCC-TATAGCCT_comp18495_seq0	88.53	558	64	0	559	1116	2842	3399	0	719
	AR2_GAGATTCC-GGCTCTGA_comp35_seq9	86.951	1617	203	2	15	1630	631	2240	0	1963
	YS1_GAGATTCC-TATAGCCT_comp24972_seq0	87.259	1295	165	0	342	1636	1436	2730	0	1591
	YS1_GAGATTCC-TATAGCCT_comp24972_seq0	86.722	241	32	0	105	345	3	243	2.32E-77	291
	YS1_GAGATTCC-TATAGCCT_comp24972_seq0	72.973	74	5	3	1661	1732	2785	2845	0.005	44.6
	YL1_CGCTCATT-TATAGCCT_comp7664_seq0	86.38	1138	155	0	499	1636	317	1454	0	1353
	YL1_CGCTCATT-TATAGCCT_comp7664_seq0	83.929	168	27	0	63	230	150	317	3.02E-44	181
SLS1 (L10081.1)	YL1_CGCTCATT-TATAGCCT_comp7664_seq0	72.973	74	5	3	1661	1732	1509	1569	0.005	44.6
	YL1_CGCTCATT-TATAGCCT_comp14816_seq0	86.883	831	109	0	806	1636	424	1254	0	1007
	YL1_CGCTCATT-TATAGCCT_comp14816_seq0	89.6	250	26	0	565	814	1	250	2.17E-90	334
	YL1_CGCTCATT-TATAGCCT_comp14816_seq0	72.973	74	5	3	1661	1732	1309	1369	0.005	44.6
	YS2_GAGATTCC-ATAGAGGC_comp2723_seq0	86.845	821	108	0	816	1636	478	1298	0	994
	YS2_GAGATTCC-ATAGAGGC_comp2723_seq0	86.264	182	25	0	52	233	101	282	1.46E-54	215
	YS2_GAGATTCC-ATAGAGGC_comp2723_seq0	72.973	74	5	3	1661	1732	1353	1413	0.005	44.6
	AR2_GAGATTCC-GGCTCTGA_comp35_seq9	87.626	1584	196	0	1	1584	667	2250	0	1974
	YS1_GAGATTCC-TATAGCCT_comp24972_seq0	87.792	1286	157	0	286	1571	1436	2721	0	1611
	YS1_GAGATTCC-TATAGCCT_comp24972_seq0	86.307	241	33	0	49	289	3	243	8.40E-76	286
SLS2 (KF309242.1)	YL1_CGCTCATT-TATAGCCT_comp7664_seq0	86.714	1129	150	0	443	1571	317	1445	0	1361
	YL1_CGCTCATT-TATAGCCT_comp7664_seq0	82.738	168	29	0	7	174	150	317	1.33E-41	172
	YL1_CGCTCATT-TATAGCCT_comp14816_seq0	87.698	821	101	0	751	1571	425	1245	0	1025
	YL1_CGCTCATT-TATAGCCT_comp14816_seq0	86.8	250	33	0	509	758	1	250	1.09E-80	302
	YS2_GAGATTCC-ATAGAGGC_comp2723_seq0	87.562	812	101	0	760	1571	478	1289	0	1009
	YS2_GAGATTCC-ATAGAGGC_comp2723_seq0	84.746	177	27	0	1	177	106	282	3.35E-49	197
	YS2_GAGATTCC-ATAGAGGC_comp2723_seq0	90	30	3	0	503	532	454	483	0.057	41
	known MIA genes from <i>C. roseu</i>	78.534	955	195	4	44	991	102	1053	0	789
	YS2_GAGATTCC-ATAGAGGC_comp2161_seq0	82.051	39	7	0	815	853	8327	8365	0.15	39.2
	YL3_CGCTCATT-ATAGAGGC_comp4991_seq1	82.051	39	7	0	815	853	2791	2829	0.15	39.2
OL1_CGCTCATT-CCTATCCT_comp1693_seq1	92.308	26	2	0	904	929	1163	1188	0.15	39.2	

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STR (X53602.1)	YL3_CGCTCATT-ATAGAGGC_comp10885_seq1	95.652	23	1	0	1045	1067	1410	1388	0.51	37.4
	YS2_GAGATTCC-ATAGAGGC_comp324_seq0	80.227	1057	201	4	1	1050	661	1716	0	953
	YS2_GAGATTCC-ATAGAGGC_comp324_seq0	75.844	385	88	2	1050	1433	1786	2166	1.67E-71	271
	YL3_CGCTCATT-ATAGAGGC_comp4131_seq0	70.44	159	45	2	824	981	1727	1884	3.69E-10	68
	YS1_GAGATTCC-TATAGCCT_comp9626_seq1	84.211	38	5	1	831	868	668	632	0.18	39.2
	AR1_GAGATTCC-CCTATCCT_comp8861_seq1	100	21	0	0	437	457	1687	1667	0.18	39.2
TDC (MG748691.1)	YL3_CGCTCATT-ATAGAGGC_comp9172_seq1	84.211	38	5	1	831	868	659	623	0.18	39.2
	YL1_CGCTCATT-TATAGCCT_comp255_seq0	79.31	1537	265	11	133	1662	1595	3085	0	1337
	OL1_CGCTCATT-CCTATCCT_comp1264_seq0	77.739	867	184	5	417	1277	391	1254	0	679
	OL1_CGCTCATT-CCTATCCT_comp1264_seq0	85.256	156	23	0	1430	1585	1251	1406	3.30E-43	178
	OL1_CGCTCATT-CCTATCCT_comp1264_seq0	86.429	140	19	0	263	402	76	215	5.97E-40	167
	OL3_CGCTCATT-GGCTCTGA_comp686_seq1	83.443	610	98	2	478	1084	958	1567	0	639
	OL3_CGCTCATT-GGCTCTGA_comp686_seq1	87.931	348	40	2	133	479	517	863	9.43E-120	432
	OL3_CGCTCATT-GGCTCTGA_comp686_seq1	73.469	490	100	3	1173	1662	1838	2297	2.22E-83	311
	YL3_CGCTCATT-ATAGAGGC_comp1113_seq0	71.298	655	152	8	931	1580	2	625	2.37E-89	331
	AR2_GAGATTCC-GGCTCTGA_comp5833_seq1	67.018	949	282	8	142	1082	378	1303	5.96E-78	293
SGD (EU072423.1)	AR2_GAGATTCC-GGCTCTGA_comp5833_seq1	67.974	153	46	1	1417	1566	1608	1760	9.48E-06	53.6
	OL1_CGCTCATT-CCTATCCT_comp374_seq0	86.575	1095	147	0	1	1095	176	1270	0	1312
	AR2_GAGATTCC-GGCTCTGA_comp706_seq1	86.066	1098	150	1	1	1095	61	1158	0	1288
	AR2_GAGATTCC-GGCTCTGA_comp706_seq3	86.066	1098	150	1	1	1095	61	1158	0	1288
	AR2_GAGATTCC-GGCTCTGA_comp706_seq4	86.066	1098	150	1	1	1095	61	1158	0	1288
GS1 (KF302079.1)	YL3_CGCTCATT-ATAGAGGC_comp123_seq0	85.845	1095	155	0	1	1095	2080	3174	0	1276
	OL1_CGCTCATT-CCTATCCT_comp374_seq0	84.081	1093	168	1	1	1087	176	1268	0	1187
	YL3_CGCTCATT-ATAGAGGC_comp123_seq0	83.715	1093	172	1	1	1087	2080	3172	0	1169
	AR2_GAGATTCC-GGCTCTGA_comp706_seq1	83.212	1096	175	2	1	1087	61	1156	0	1146
	AR2_GAGATTCC-GGCTCTGA_comp706_seq3	83.212	1096	175	2	1	1087	61	1156	0	1146
GS2 (KF302078.1)	AR2_GAGATTCC-GGCTCTGA_comp706_seq4	83.212	1096	175	2	1	1087	61	1156	0	1146
	AR1_GAGATTCC-CCTATCCT_comp3108_seq0	81.699	1071	181	2	6	1064	157	1224	0	1052
	OL1_CGCTCATT-CCTATCCT_comp14114_seq0	74.637	757	160	7	325	1062	501	1244	1.72E-139	497
	YL3_CGCTCATT-ATAGAGGC_comp42_seq0	69.436	1047	276	11	40	1052	177	1213	4.92E-121	435
	AR1_GAGATTCC-CCTATCCT_comp80_seq0	67.739	1057	305	10	38	1064	287	1337	3.79E-97	356
THAS1 (KM524258.1)	AR1_GAGATTCC-CCTATCCT_comp3050_seq0	67.739	1057	305	10	38	1064	281	1331	3.79E-97	356
	OL1_CGCTCATT-CCTATCCT_comp3640_seq0	75.909	1100	260	3	18	1116	210	1305	0	780
	YS2_GAGATTCC-ATAGAGGC_comp697_seq4	78.672	783	162	3	11	792	98	876	0	650
	YS2_GAGATTCC-ATAGAGGC_comp697_seq4	72.566	113	31	0	949	1061	1033	1145	3.48E-09	64.4
	OL3_CGCTCATT-GGCTCTGA_comp1793_seq1	73.4	1094	284	5	25	1116	2866	3954	0	645
	YS2_GAGATTCC-ATAGAGGC_comp4098_seq3	73.4	1094	284	5	25	1116	4818	5906	0	645
THAS2 (KU865323.1)	YL1_CGCTCATT-TATAGCCT_comp13612_seq0	75.938	906	213	3	206	1110	847	1748	0	643
	OL1_CGCTCATT-CCTATCCT_comp3640_seq0	81.088	1121	192	6	18	1134	201	1305	0	1058
	OL3_CGCTCATT-GGCTCTGA_comp1793_seq1	80.454	926	161	6	213	1134	3045	3954	0	845
	YS2_GAGATTCC-ATAGAGGC_comp4098_seq3	80.454	926	161	6	213	1134	4997	5906	0	845

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	YL1_CGCTCATT-TATAGCCT_comp13612_seq0	79.563	915	173	4	215	1128	847	1748	0	801
THAS3 (KU865322.1)	YS2_GAGATTCC-ATAGAGGC_comp697_seq4	70.31	1098	302	9	18	1109	96	1175	7.74E-138	491
	AR1_GAGATTCC-CCTATCCT_comp3108_seq0	81.648	1068	194	2	1	1067	158	1224	0	1036
	OL1_CGCTCATT-CCTATCCT_comp14114_seq0	76.923	767	159	7	305	1065	490	1244	9.57E-162	571
	AR1_GAGATTCC-CCTATCCT_comp80_seq0	68.587	1076	320	9	7	1067	265	1337	5.31E-108	392
	OL1_CGCTCATT-CCTATCCT_comp1134_seq1	68.03	1076	326	9	7	1067	141	1213	7.38E-100	365
THAS4 (KU865324.1)	AR1_GAGATTCC-CCTATCCT_comp3050_seq0	67.844	1076	328	9	7	1067	259	1331	3.82E-97	356
	AR1_GAGATTCC-CCTATCCT_comp3108_seq0	82.303	1068	187	2	1	1067	158	1224	0	1067
	OL1_CGCTCATT-CCTATCCT_comp14114_seq0	77.004	761	159	6	310	1065	495	1244	9.57E-162	571
	AR1_GAGATTCC-CCTATCCT_comp80_seq0	69.274	1074	316	6	7	1067	265	1337	4.96E-121	435
	OL1_CGCTCATT-CCTATCCT_comp1134_seq1	68.715	1074	322	6	7	1067	141	1213	6.90E-113	408
HYS (KU865325.1)	AR1_GAGATTCC-CCTATCCT_comp3050_seq0	68.063	1074	329	6	7	1067	259	1331	4.08E-103	376
	YL1_CGCTCATT-TATAGCCT_comp32_seq1	82.626	1508	256	2	1	1505	244	1748	0	1535
	YL1_CGCTCATT-TATAGCCT_comp32_seq4	82.626	1508	256	2	1	1505	244	1748	0	1535
	YL3_CGCTCATT-ATAGAGGC_comp58_seq1	82.56	1508	257	2	1	1505	201	1705	0	1530
	YS2_GAGATTCC-ATAGAGGC_comp3760_seq0	84.491	619	96	0	887	1505	992	1610	0	684
GO (MF770508.1)	AR2_GAGATTCC-GGCTCTGA_comp139_seq0	67.253	1478	432	21	7	1461	173	1621	6.98E-121	435
	OL3_CGCTCATT-GGCTCTGA_comp6787_seq2	85.747	863	123	0	1	863	37	899	0	1002
	YL1_CGCTCATT-TATAGCCT_comp16622_seq1	85.315	858	126	0	194	1051	1429	2286	0	980
	YS2_GAGATTCC-ATAGAGGC_comp697_seq1	85.315	858	126	0	194	1051	1531	2388	0	980
	YL3_CGCTCATT-ATAGAGGC_comp42_seq0	81.526	996	184	0	56	1051	223	1218	0	967
redox1 (MF770509.1)	AR1_GAGATTCC-CCTATCCT_comp530_seq0	77.333	975	210	4	84	1051	371	1341	0	755
	YL3_CGCTCATT-ATAGAGGC_comp101_seq3	82.613	972	169	0	1	972	133	1104	0	991
	AR2_GAGATTCC-GGCTCTGA_comp687_seq0	80.844	569	109	0	1	569	98	666	6.19E-151	535
	AR2_GAGATTCC-GGCTCTGA_comp687_seq0	85.217	230	34	0	743	972	1832	2061	5.82E-69	262
	AR2_GAGATTCC-GGCTCTGA_comp687_seq0	87.634	186	23	0	564	749	1009	1194	9.85E-60	232
	YL3_CGCTCATT-ATAGAGGC_comp101_seq2	80.316	569	112	0	1	569	133	701	3.91E-147	522
	YL3_CGCTCATT-ATAGAGGC_comp101_seq2	86.308	409	56	0	564	972	1044	1452	2.81E-136	486
	YS1_GAGATTCC-TATAGCCT_comp65_seq1	80.316	569	112	0	1	569	94	662	3.91E-147	522
	YS1_GAGATTCC-TATAGCCT_comp65_seq1	86.308	409	56	0	564	972	1005	1413	2.81E-136	486
	AR2_GAGATTCC-GGCTCTGA_comp12013_seq0	73.893	858	210	7	37	887	199	1049	4.76E-146	518
redox2 (MF770510.1)	AR2_GAGATTCC-GGCTCTGA_comp12013_seq0	91.667	24	2	0	949	972	1078	1101	1.5	35.6
	YL3_CGCTCATT-ATAGAGGC_comp1258_seq0	79.013	1277	242	7	1	1261	163	1429	0	1086
	AR2_GAGATTCC-GGCTCTGA_comp10632_seq0	71.654	254	61	5	122	368	178	427	1.68E-26	122
	AR2_GAGATTCC-GGCTCTGA_comp10632_seq0	70.588	119	33	2	740	857	835	952	8.72E-05	50
	YL1_CGCTCATT-TATAGCCT_comp10318_seq0	63.83	799	238	18	11	782	67	841	4.51E-21	104
	YL1_CGCTCATT-TATAGCCT_comp10318_seq0	71.895	153	43	0	1089	1241	1184	1336	1.48E-14	82.4
	YS2_GAGATTCC-ATAGAGGC_comp4073_seq1	81.034	58	11	0	1048	1105	1174	1231	2.05E-06	55.4
SAT (MF770511.1)	YS1_GAGATTCC-TATAGCCT_comp9325_seq0	93.75	32	2	0	1073	1104	1188	1219	8.72E-05	50
	YS2_GAGATTCC-ATAGAGGC_comp776_seq0	76.106	1582	344	7	16	1579	126	1691	0	1148
	AR2_GAGATTCC-GGCTCTGA_comp14833_seq0	67.846	1583	453	21	11	1568	4	1555	2.75E-145	517

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	AR2_GAGATTCC-GGCTCTGA_comp21526_seq0	71.014	414	120	0	397	810	539	952	6.49E-52	206
	AR2_GAGATTCC-GGCTCTGA_comp21526_seq0	71.823	181	45	3	143	317	217	397	1.25E-16	89.7
	AR2_GAGATTCC-GGCTCTGA_comp21526_seq0	72.794	136	36	1	1445	1579	1569	1704	2.76E-12	75.2
PAS	AR1_GAGATTCC-CCTATCCT_comp1722_seq0	70.36	361	107	0	432	792	500	860	1.63E-40	168
	YL1_CGCTCATT-TATAGCCT_comp1884_seq0	67.778	450	145	0	252	701	597	1046	2.95E-37	158
	YL1_CGCTCATT-TATAGCCT_comp695_seq0	85.882	1615	215	6	153	1762	323	1929	0	1869
	YL1_CGCTCATT-TATAGCCT_comp695_seq0	89.189	37	4	0	91	127	285	321	0.000123	50
	YS1_GAGATTCC-TATAGCCT_comp841_seq0	87.888	677	77	2	1090	1762	1649	2324	0	847
	OL3_CGCTCATT-GGCTCTGA_comp6736_seq2	80.46	783	121	5	93	874	185	936	0	729
	YL3_CGCTCATT-ATAGAGGC_comp13409_seq0	86.965	537	65	2	1230	1762	874	1409	0	648
	YL3_CGCTCATT-ATAGAGGC_comp13409_seq0	95.833	24	1	0	1090	1113	390	413	0.22	39.2
	YS1_GAGATTCC-TATAGCCT_comp19336_seq1	87.847	288	35	0	943	1230	2	289	1.49E-98	361
	YS1_GAGATTCC-TATAGCCT_comp19336_seq1	88.764	89	10	0	1481	1569	1169	1257	1.01E-24	116
DPAS (KU865331)	YS1_GAGATTCC-TATAGCCT_comp19336_seq1	95.833	24	1	0	1230	1253	726	749	0.22	39.2
	YL3_CGCTCATT-ATAGAGGC_comp166_seq2	74.669	983	216	9	10	983	284	1242	0	639
	AR1_GAGATTCC-CCTATCCT_comp606_seq1	73.333	510	116	4	475	983	381	871	1.59E-82	307
	AR2_GAGATTCC-GGCTCTGA_comp17902_seq0	72.757	301	64	2	684	984	207	489	1.60E-44	181
	YL1_CGCTCATT-TATAGCCT_comp661_seq0	66.612	614	174	7	25	621	149	748	5.58E-44	179
CS (MF770512.1)	AR1_GAGATTCC-CCTATCCT_comp5172_seq0	78.417	139	30	0	845	983	13	151	5.58E-25	116
	YL3_CGCTCATT-ATAGAGGC_comp166_seq2	80.234	941	177	3	25	962	311	1245	0	854
	AR1_GAGATTCC-CCTATCCT_comp606_seq1	80	485	94	1	478	962	393	874	4.42E-121	435
	YL1_CGCTCATT-TATAGCCT_comp661_seq0	67.885	903	238	16	8	881	147	1026	2.79E-79	297
	AR2_GAGATTCC-GGCTCTGA_comp17902_seq0	80.351	285	56	0	678	962	207	491	5.76E-69	262
TS (MF770513.1)	YS1_GAGATTCC-TATAGCCT_comp13751_seq2	66.332	597	145	17	28	604	1364	1924	1.11E-33	145
	YL3_CGCTCATT-ATAGAGGC_comp166_seq2	79.277	941	189	3	25	965	311	1245	0	810
	AR1_GAGATTCC-CCTATCCT_comp606_seq1	78.745	494	105	0	472	965	381	874	1.19E-115	417
	YL1_CGCTCATT-TATAGCCT_comp661_seq0	67.037	901	256	12	8	886	147	1028	3.90E-71	269
	AR2_GAGATTCC-GGCTCTGA_comp17902_seq0	79.649	285	58	0	681	965	207	491	3.00E-66	253
VS1 (MF770514.1)	OL1_CGCTCATT-CCTATCCT_comp1318_seq1	66.534	502	135	7	28	523	84	558	3.20E-34	147
	YL3_CGCTCATT-ATAGAGGC_comp166_seq2	80.293	888	171	2	49	935	352	1236	0	807
	AR1_GAGATTCC-CCTATCCT_comp606_seq1	80.206	485	96	0	451	935	381	865	2.92E-123	443
	AR2_GAGATTCC-GGCTCTGA_comp17902_seq0	80.42	286	56	0	660	945	207	492	1.62E-69	264
	YL1_CGCTCATT-TATAGCCT_comp661_seq0	66.469	844	250	8	71	891	227	1060	1.85E-62	241
	YL1_CGCTCATT-TATAGCCT_comp661_seq0	79.487	39	8	0	8	46	147	185	1.4	35.6
VS2 (MF770515.1)	AR1_GAGATTCC-CCTATCCT_comp5172_seq0	81.119	143	27	0	793	935	3	145	5.66E-31	136
	YS2_GAGATTCC-ATAGAGGC_comp528_seq2	77.958	1538	304	6	1	1513	2107	3634	0	1251
	YL1_CGCTCATT-TATAGCCT_comp104_seq6	77.893	1538	305	6	1	1513	2274	3801	0	1245
	YS1_GAGATTCC-TATAGCCT_comp15820_seq1	74.339	1438	334	8	107	1513	305	1738	0	926
	YS2_GAGATTCC-ATAGAGGC_comp37475_seq2	79.321	619	113	1	910	1513	998	1616	4.44E-155	549
T16H1 (FJ647194.1)	OL3_CGCTCATT-GGCTCTGA_comp1489_seq0	68.279	1406	400	17	133	1512	943	2328	3.65E-137	489
	YS2_GAGATTCC-ATAGAGGC_comp528_seq2	78.335	1574	314	9	3	1559	2077	3640	0	1285

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T16H2 (JF742645.1)	YL1_CGCTCATT-TATAGCCT_comp104_seq6	78.272	1574	315	9	3	1559	2244	3807	0	1281	
	YS1_GAGATTCC-TATAGCCT_comp15820_seq1	74.054	1453	366	4	113	1558	295	1743	0	913	
	YS2_GAGATTCC-ATAGAGGC_comp37475_seq2	81.28	625	117	0	935	1559	998	1622	3.13E-170	600	
	OL3_CGCTCATT-GGCTCTGA_comp1489_seq0	68.355	1441	410	21	143	1569	937	2345	4.08E-137	489	
16OMT (EF444544.1)	AR2_GAGATTCC-GGCTCTGA_comp35_seq0	75.923	1084	225	6	60	1128	583	1645	0	783	
	YS2_GAGATTCC-ATAGAGGC_comp61_seq0	75.668	1085	241	9	60	1128	2794	3871	0	747	
	AR1_GAGATTCC-CCTATCCT_comp1185_seq0	72.913	1078	256	6	60	1128	581	1631	1.15E-180	634	
	YS1_GAGATTCC-TATAGCCT_comp1836_seq0	72.146	1095	257	9	49	1128	126	1187	1.94E-171	603	
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq1	72.628	917	200	10	1	913	3643	2774	1.77E-147	524	
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq1	82.008	239	43	0	913	1151	2478	2240	3.66E-61	237	
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq1	90	110	11	0	1325	1434	2237	2128	1.46E-34	149	
	YL3_CGCTCATT-ATAGAGGC_comp5333_seq0	75.795	723	163	4	192	913	3124	2413	1.36E-142	508	
	YL3_CGCTCATT-ATAGAGGC_comp5333_seq0	79.949	394	63	4	1078	1464	2062	1678	2.31E-95	351	
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq2	74.412	723	158	5	192	913	2711	2015	9.79E-132	471	
T3O (LN831958.1)	YS2_GAGATTCC-ATAGAGGC_comp8318_seq2	86.765	204	20	1	1325	1521	1588	1385	2.02E-64	248	
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq2	79.73	74	15	0	1078	1151	1664	1591	1.37E-09	66.2	
	AR1_GAGATTCC-CCTATCCT_comp629_seq5	67.134	1354	379	26	168	1488	192	1512	1.66E-103	378	
	AR1_GAGATTCC-CCTATCCT_comp5822_seq1	65.632	1385	433	16	112	1485	237	1589	1.36E-85	318	
	T3R (KP122966.1)	AR1_GAGATTCC-CCTATCCT_comp3108_seq0	77.788	1049	226	6	22	1068	189	1232	0	821
		OL1_CGCTCATT-CCTATCCT_comp14114_seq0	74.009	681	158	6	396	1071	591	1257	1.37E-116	421
		AR1_GAGATTCC-CCTATCCT_comp80_seq0	67.191	1018	309	12	67	1067	335	1344	1.13E-79	298
		OL1_CGCTCATT-CCTATCCT_comp1134_seq1	66.437	1016	320	10	67	1067	211	1220	5.48E-71	269
		YL3_CGCTCATT-ATAGAGGC_comp42_seq0	78.71	310	63	1	7	313	160	469	2.84E-68	260
		YL3_CGCTCATT-ATAGAGGC_comp42_seq0	66.914	538	170	6	515	1048	680	1213	1.29E-34	149
NMT (HM584929.1)		YL1_CGCTCATT-TATAGCCT_comp302_seq2	77.549	971	192	15	25	978	211	1172	0	724
		YL1_CGCTCATT-TATAGCCT_comp302_seq2	75.8	781	178	7	25	798	1692	2468	7.06E-151	535
		AR2_GAGATTCC-GGCTCTGA_comp630_seq4	76.369	986	207	15	10	978	1276	2252	0	684
		YS1_GAGATTCC-TATAGCCT_comp198_seq4	75.628	796	183	7	10	798	2351	3142	1.66E-152	540
	OL3_CGCTCATT-GGCTCTGA_comp6929_seq0	73.598	856	217	6	20	869	213	1065	3.43E-142	506	
	YL1_CGCTCATT-TATAGCCT_comp938_seq4	75.173	721	170	4	153	867	47	764	1.12E-135	484	
	D4H (U71604.1)	AR1_GAGATTCC-CCTATCCT_comp12530_seq0	78.772	1140	229	7	68	1202	54	1185	0	946
		YL3_CGCTCATT-ATAGAGGC_comp5037_seq1	71.826	827	212	10	321	1141	2325	3136	5.21E-115	416
		YL3_CGCTCATT-ATAGAGGC_comp5037_seq1	82	50	9	0	139	188	2143	2192	8.30E-05	50
		YS1_GAGATTCC-TATAGCCT_comp5438_seq0	71.814	816	210	9	332	1141	2238	3039	6.34E-114	412
YS1_GAGATTCC-TATAGCCT_comp5438_seq0		82	50	9	0	139	188	2046	2095	8.30E-05	50	
AR1_GAGATTCC-CCTATCCT_comp2987_seq0		69.652	804	222	9	332	1127	359	1148	5.95E-89	329	
D4H (U71604.1)		OL1_CGCTCATT-CCTATCCT_comp614_seq1	69.406	791	227	7	332	1119	5056	5834	1.08E-85	318
		AR1_GAGATTCC-CCTATCCT_comp10689_seq2	69.337	1298	322	24	31	1314	19	1254	1.18E-142	508
		AR2_GAGATTCC-GGCTCTGA_comp333_seq6	66.023	1295	364	23	31	1314	142	1371	4.12E-85	316
		AR2_GAGATTCC-GGCTCTGA_comp333_seq4	66.023	1295	364	23	31	1314	142	1371	4.12E-85	316
	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	66.486	555	168	7	202	753	575	1114	4.41E-34	147	

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DAT (AF053307.1)	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	69.082	207	52	3	1108	1314	1415	1609	1.54E-14	82.4
	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	82.857	35	6	0	41	75	54	88	0.57	37.4
	AR2_GAGATTCC-GGCTCTGA_comp1084_seq0	63.105	1301	353	34	31	1314	402	1592	5.37E-33	143
TEX1 (MG873080.1)	YS2_GAGATTCC-ATAGAGGC_comp528_seq2	69.342	1383	373	21	92	1438	2198	3565	9.78E-151	535
	YS1_GAGATTCC-TATAGCCT_comp15820_seq1	69.136	1377	388	15	94	1438	298	1669	3.41E-150	533
	YL1_CGCTCATT-TATAGCCT_comp104_seq6	69.27	1383	374	21	92	1438	2365	3732	4.16E-149	529
	OL3_CGCTCATT-GGCTCTGA_comp1489_seq0	66.935	1367	413	18	103	1446	919	2269	1.36E-104	381
	AR2_GAGATTCC-GGCTCTGA_comp863_seq0	66.012	1324	427	12	124	1431	314	1630	9.18E-88	325
	YS2_GAGATTCC-ATAGAGGC_comp528_seq2	69.192	1373	394	15	103	1462	2209	3565	1.48E-148	527
	YL1_CGCTCATT-TATAGCCT_comp104_seq6	69.119	1373	395	15	103	1462	2376	3732	1.80E-147	524
	YS1_GAGATTCC-TATAGCCT_comp15820_seq1	67.632	1347	409	15	124	1455	328	1662	1.58E-116	421
	OL3_CGCTCATT-GGCTCTGA_comp1489_seq0	65.852	1391	412	17	103	1470	919	2269	2.86E-94	347
TEX2 (MG873081.1)	AR2_GAGATTCC-GGCTCTGA_comp863_seq0	65.799	1345	429	9	124	1460	314	1635	4.24E-92	340
	OL3_CGCTCATT-GGCTCTGA_comp1418_seq0	72.105	1520	382	16	1	1505	452	1944	0	796
T19H (HQ901597.1)	OL3_CGCTCATT-GGCTCTGA_comp12875_seq0	65.649	1278	401	21	97	1361	301	1553	7.56E-70	266
	AR1_GAGATTCC-CCTATCCT_comp10373_seq0	68.027	294	92	2	1054	1346	1064	1356	6.64E-20	100
	AR2_GAGATTCC-GGCTCTGA_comp863_seq0	73.81	168	39	3	1207	1370	1388	1554	8.09E-19	96.9
	OL1_CGCTCATT-CCTATCCT_comp520_seq1	70.918	196	56	1	1162	1357	1433	1627	9.86E-18	93.3
	AR1_GAGATTCC-CCTATCCT_comp10689_seq2	69.219	1293	330	19	1	1259	4	1262	2.75E-144	513
TAT (KU821123.1)	AR2_GAGATTCC-GGCTCTGA_comp333_seq6	69.438	1263	329	22	14	1249	137	1369	3.13E-137	489
	AR2_GAGATTCC-GGCTCTGA_comp333_seq4	69.438	1263	329	22	14	1249	137	1369	3.13E-137	489
	AR2_GAGATTCC-GGCTCTGA_comp1084_seq0	64.969	1276	351	31	13	1261	396	1602	3.83E-60	233
	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	65.961	1087	317	26	190	1263	575	1621	6.93E-57	223
	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	96.154	26	1	0	418	443	464	489	0.013	42.8
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq1	74.058	902	186	12	19	916	3631	2774	7.04E-159	562
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq1	81.435	237	44	0	916	1152	2478	2242	5.43E-59	230
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq1	88.889	108	12	0	1327	1434	2235	2128	2.17E-32	141
	YL3_CGCTCATT-ATAGAGGC_comp5333_seq0	77.317	723	152	4	195	916	3124	2413	8.57E-158	558
	YL3_CGCTCATT-ATAGAGGC_comp5333_seq0	79.032	372	65	3	1097	1461	2046	1681	1.36E-85	318
	YL3_CGCTCATT-ATAGAGGC_comp5333_seq0	81.356	59	11	0	916	974	2117	2059	7.09E-07	57.2
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq2	75.657	723	149	5	195	916	2711	2015	3.20E-144	513
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq2	85.149	202	23	1	1327	1521	1586	1385	1.56E-59	232
	YS2_GAGATTCC-ATAGAGGC_comp8318_seq2	81.356	59	11	0	916	974	1719	1661	7.09E-07	57.2
V19H (MK050464.10)	YS2_GAGATTCC-ATAGAGGC_comp8318_seq2	78.571	56	12	0	1097	1152	1648	1593	0.000367	48.2
	AR1_GAGATTCC-CCTATCCT_comp5822_seq1	71.865	622	161	7	868	1485	978	1589	1.66E-84	315
	YS1_GAGATTCC-TATAGCCT_comp6764_seq2	69.771	698	183	10	805	1488	2776	3459	2.31E-76	288
	AR1_GAGATTCC-CCTATCCT_comp10689_seq2	68.261	1317	321	24	27	1326	18	1254	2.98E-131	470
	AR2_GAGATTCC-GGCTCTGA_comp333_seq6	66.412	1307	354	18	28	1326	142	1371	1.77E-102	374
	AR2_GAGATTCC-GGCTCTGA_comp333_seq4	66.412	1307	354	18	28	1326	142	1371	1.77E-102	374
	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	68.467	574	163	7	190	760	566	1124	1.89E-51	205
	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	72.596	208	43	6	1120	1326	1415	1609	4.75E-21	104

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MAT (AF253415.1)	YS2_GAGATTCC-ATAGAGGC_comp13380_seq0	82.857	35	6	0	38	72	54	88	0.58	37.4
	AR2_GAGATTCC-GGCTCTGA_comp1084_seq0	66.725	568	147	12	28	592	402	930	8.59E-37	156
	AR2_GAGATTCC-GGCTCTGA_comp1084_seq0	68.722	227	58	4	1102	1326	1377	1592	4.45E-15	84.2
	YL1_CGCTCATT-TATAGCCT_comp302_seq2	98.046	921	18	0	49	969	157	1077	0	1581
	YL1_CGCTCATT-TATAGCCT_comp302_seq2	83.488	969	160	0	1	969	1590	2558	0	1027
	AR2_GAGATTCC-GGCTCTGA_comp630_seq4	97.001	867	26	0	103	969	1291	2157	0	1447
	YS1_GAGATTCC-TATAGCCT_comp198_seq4	80.997	863	161	1	107	969	2373	3232	0	816
	AR1_GAGATTCC-CCTATCCT_comp3145_seq1	84.248	711	97	3	159	866	1	699	0	778
	AR1_GAGATTCC-CCTATCCT_comp3145_seq1	79.048	105	22	0	865	969	815	919	2.17E-17	91.5
VmPiNMT (KC708450)	OL3_CGCTCATT-GGCTCTGA_comp6929_seq0	77.855	867	192	0	103	969	218	1084	0	699
Transporters (TPs):											
TP	transcript	% ID	Alignment length	Mismatch	Gapopen	TP start	TP end	Transcript start	Transcript end	E-value	Bitscore
NPF2.1 (KR054375.1)	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	77.333	1725	381	6	192	1914	713	2429	0	1330
	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	87.179	156	20	0	239	394	401	556	1.73E-47	192
	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	78.431	51	11	0	192	242	160	210	0.02	42.8
	OL1_CGCTCATT-CCTATCCT_comp26741_seq0	76.236	1456	337	3	459	1914	1472	2918	0	1061
	YL1_CGCTCATT-TATAGCCT_comp4178_seq2	75.326	1459	351	3	459	1914	1452	2904	0	1003
	YL1_CGCTCATT-TATAGCCT_comp3070_seq2	77.114	887	200	1	1031	1914	2041	2927	0	682
	YL1_CGCTCATT-TATAGCCT_comp3070_seq2	76.014	838	195	2	202	1039	288	1119	1.01E-170	601
YS2_GAGATTCC-ATAGAGGC_comp11749_seq1	75.369	881	214	1	1034	1914	1179	2056	6.83E-173	609	
NPF2.2 (KR054376.1)	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	77.493	1755	377	10	96	1844	683	2425	0	1355
	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	83.117	154	26	0	173	326	401	554	2.82E-38	161
	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	79.012	81	17	0	96	176	130	210	1.37E-10	69.8
	OL1_CGCTCATT-CCTATCCT_comp26741_seq0	76.823	1454	328	4	393	1846	1472	2916	0	1094
	YL1_CGCTCATT-TATAGCCT_comp4178_seq2	75.585	1454	352	2	393	1846	1452	2902	0	1016
	YL1_CGCTCATT-TATAGCCT_comp3070_seq2	75.312	960	214	7	18	973	179	1119	0	652
	YL1_CGCTCATT-TATAGCCT_comp3070_seq2	76.303	844	200	0	965	1808	2041	2884	1.04E-176	621
YS2_GAGATTCC-ATAGAGGC_comp11749_seq1	76.109	879	207	2	968	1846	1179	2054	5.77E-180	632	
NPF2.3 (KR054377.1)	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	77.803	1784	366	6	128	1908	673	2429	0	1433
	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	84.416	154	24	0	218	371	401	554	5.62E-41	170
	OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	72.165	97	18	3	128	221	120	210	0.000462	48.2
	YL1_CGCTCATT-TATAGCCT_comp4178_seq2	79.691	1423	277	2	438	1854	1452	2868	0	1265
	OL1_CGCTCATT-CCTATCCT_comp26741_seq0	79.534	1417	284	1	438	1854	1472	2882	0	1249
	YL1_CGCTCATT-TATAGCCT_comp3070_seq2	81.758	899	152	3	1010	1908	2041	2927	0	879
	YL1_CGCTCATT-TATAGCCT_comp3070_seq2	81.229	911	156	4	111	1018	221	1119	0	868
YS2_GAGATTCC-ATAGAGGC_comp11749_seq1	80.048	842	168	0	1013	1854	1179	2020	0	762	
	OL3_CGCTCATT-GGCTCTGA_comp8789_seq0	82.886	1788	291	6	1	1788	109	1881	0	1831
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	69.693	1630	418	20	106	1717	519	2090	0	691
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	78.218	303	66	0	79	381	185	487	6.84E-65	250
	YS2_GAGATTCC-ATAGAGGC_comp3442_seq2	68.611	1663	499	11	64	1716	335	1984	1.23E-175	618
	AR2_GAGATTCC-GGCTCTGA_comp6824_seq0	68.163	1671	492	11	55	1717	156	1794	9.46E-171	601

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NPF2.4 (KR054378.1)	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	71.411	829	225	5	58	880	289	1111	7.78E-115	416
	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	66.026	833	277	4	887	1716	1636	2465	4.92E-54	214
NPF2.5 (KR054379.1)	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	79.799	1688	286	9	86	1767	517	2155	0	1516
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	87.047	386	47	1	6	391	133	515	3.98E-131	470
	OL3_CGCTCATT-GGCTCTGA_comp8789_seq0	70.662	1677	456	12	40	1701	163	1818	0	785
	YS2_GAGATTCC-ATAGAGGC_comp3442_seq2	69.952	1674	469	13	46	1705	335	1988	0	724
	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	76.761	809	183	3	6	813	258	1062	2.68E-171	603
	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	66.627	851	267	7	865	1705	1626	2469	1.22E-61	239
	AR2_GAGATTCC-GGCTCTGA_comp6824_seq0	68.378	1714	487	22	40	1736	159	1834	1.14E-169	598
	AR2_GAGATTCC-GGCTCTGA_comp6824_seq0	86.18	1780	231	2	1	1780	93	1857	0	2105
	OL3_CGCTCATT-GGCTCTGA_comp8789_seq0	68.645	1668	503	14	64	1718	160	1820	7.74E-172	605
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	68.741	1398	393	12	113	1499	517	1881	3.29E-151	536
NPF2.6 (KR054380.1)	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	74.32	331	83	2	56	385	153	482	7.28E-52	206
	YS2_GAGATTCC-ATAGAGGC_comp3442_seq2	67.629	1662	511	16	72	1717	334	1984	2.08E-147	524
NPF2.7 (KR054381.1)	YL1_CGCTCATT-TATAGCCT_comp5423_seq0	85.583	326	47	0	1	326	74	399	6.80E-103	376
	YS2_GAGATTCC-ATAGAGGC_comp3442_seq2	86.403	1743	234	1	37	1779	308	2047	0	2073
	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	84.802	908	135	1	872	1779	1624	2528	0	1014
	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	84.54	815	123	2	64	875	295	1109	0	895
	OL3_CGCTCATT-GGCTCTGA_comp8789_seq0	69.424	1668	469	16	64	1712	169	1814	0	673
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	68.54	1548	425	12	104	1640	517	2013	1.15E-169	598
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	78.246	285	62	0	64	348	170	454	1.50E-60	235
NPF2.8 (KR054382.1)	AR2_GAGATTCC-GGCTCTGA_comp6824_seq0	67.351	1657	503	12	63	1712	164	1789	4.88E-149	529
	YS2_GAGATTCC-ATAGAGGC_comp3442_seq2	79.965	1727	330	6	76	1797	332	2047	0	1543
	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	77.133	914	197	4	887	1797	1624	2528	0	699
	YL3_CGCTCATT-ATAGAGGC_comp3976_seq4	79.075	822	161	5	79	893	295	1112	0	695
	OL3_CGCTCATT-GGCTCTGA_comp8789_seq0	66.707	1670	515	19	79	1729	169	1816	2.55E-127	457
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	66.338	1625	479	18	119	1729	517	2087	1.61E-123	444
	YL3_CGCTCATT-ATAGAGGC_comp13973_seq0	75.09	277	67	2	88	363	179	454	2.93E-44	181
	AR2_GAGATTCC-GGCTCTGA_comp6824_seq0	69.159	963	265	19	78	1027	164	1107	1.42E-92	342
	AR2_GAGATTCC-GGCTCTGA_comp6824_seq0	63.089	382	126	3	1387	1768	1464	1830	1.02E-05	53.6
	YL3_CGCTCATT-ATAGAGGC_comp2760_seq1	78.218	1717	351	5	1	1716	254	1948	0	1409
NPF2.9 (KX372303.1)	YL1_CGCTCATT-TATAGCCT_comp789_seq5	74.941	850	198	2	867	1716	3127	3961	1.03E-163	578
	YL1_CGCTCATT-TATAGCCT_comp789_seq6	74.706	850	200	2	867	1716	3966	4800	5.36E-161	569
	YL1_CGCTCATT-TATAGCCT_comp789_seq0	74.706	850	200	2	867	1716	3922	4756	5.36E-161	569
	YL1_CGCTCATT-TATAGCCT_comp28142_seq0	74.441	313	80	0	1404	1716	158	470	2.45E-51	205
	YL1_CGCTCATT-TATAGCCT_comp28142_seq0	83.803	142	23	0	829	970	15	156	1.35E-35	152
	YL1_CGCTCATT-TATAGCCT_comp28142_seq0	76	75	18	0	1642	1716	495	569	2.80E-06	55.4
	AR1_GAGATTCC-CCTATCCT_comp18788_seq0	82.497	1554	260	3	1	1554	192	1733	0	1573
	OL1_CGCTCATT-CCTATCCT_comp74_seq2	81.778	1575	275	3	1	1575	2257	3819	0	1544
	YS1_GAGATTCC-TATAGCCT_comp122_seq0	81.651	1575	277	3	1	1575	1509	3071	0	1535
	OL3_CGCTCATT-GGCTCTGA_comp1979_seq2	81.587	1575	278	3	1	1575	936	2498	0	1530

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MATE1 (KX372304.1)	OL1_CGCTCATT-CCTATCCT_comp7876_seq0	83.482	1235	204	0	320	1554	3127	4361	0	1308
	YS2_GAGATTCC-ATAGAGGC_comp3345_seq1	82.43	1383	237	3	112	1491	308	1687	0	1391
	YS2_GAGATTCC-ATAGAGGC_comp3345_seq1	85.714	35	5	0	9	43	229	263	0.053	41
	YS1_GAGATTCC-TATAGCCT_comp124_seq0	82.43	1383	237	3	112	1491	2469	3848	0	1391
	YS1_GAGATTCC-TATAGCCT_comp124_seq0	84.615	39	6	0	5	43	2386	2424	0.004	44.6
	YL3_CGCTCATT-ATAGAGGC_comp598_seq6	82.357	1383	238	3	112	1491	2895	4274	0	1386
	YL3_CGCTCATT-ATAGAGGC_comp598_seq6	84.615	39	6	0	5	43	2812	2850	0.004	44.6
	YS2_GAGATTCC-ATAGAGGC_comp3345_seq7	82.357	1383	238	3	112	1491	311	1690	0	1386
	YS2_GAGATTCC-ATAGAGGC_comp3345_seq7	85.714	35	5	0	9	43	229	263	0.053	41
	AR1_GAGATTCC-CCTATCCT_comp14782_seq0	76.637	672	154	1	820	1491	941	1609	5.66E-141	502
MATE2 (KX372305.1)	AR1_GAGATTCC-CCTATCCT_comp14782_seq0	80	40	8	0	320	359	441	480	0.65	37.4
	OL3_CGCTCATT-GGCTCTGA_comp2267_seq1	99.184	4044	32	1	1	4044	1547	5589	0	7142
	YL1_CGCTCATT-TATAGCCT_comp818_seq3	78.995	1771	372	0	2274	4044	2892	4662	0	1517
	YL1_CGCTCATT-TATAGCCT_comp818_seq3	70.379	2245	628	17	40	2270	593	2814	0	1009
	YS2_GAGATTCC-ATAGAGGC_comp1760_seq0	71.981	2873	768	17	40	2898	579	3428	0	1510
	YS2_GAGATTCC-ATAGAGGC_comp1760_seq0	75.32	859	212	0	2908	3766	3815	4673	3.20E-168	594
	YS2_GAGATTCC-ATAGAGGC_comp1760_seq0	82.927	82	14	0	3771	3852	4935	5016	3.93E-15	86
	YS1_GAGATTCC-TATAGCCT_comp1672_seq3	71.911	2873	770	17	40	2898	608	3457	0	1501
	YS1_GAGATTCC-TATAGCCT_comp1672_seq3	75.661	945	230	0	2908	3852	3901	4845	0	668
	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	71.536	2252	613	12	655	2898	181	2412	0	1144
	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	75.443	790	194	0	2977	3766	3027	3816	3.42E-155	551
	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	81.707	82	15	0	3771	3852	4078	4159	1.67E-13	80.6
VmTPT2 (KC511773.1)	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	80.263	76	15	0	2908	2983	2853	2928	3.02E-10	69.8
	OL3_CGCTCATT-GGCTCTGA_comp2267_seq1	87.305	4230	534	1	37	4266	1363	5589	0	5205
	YS2_GAGATTCC-ATAGAGGC_comp1760_seq0	71.399	2867	780	17	268	3120	588	3428	0	1433
	YS2_GAGATTCC-ATAGAGGC_comp1760_seq0	75.086	871	215	2	3119	3988	3804	4673	1.75E-165	585
	YS2_GAGATTCC-ATAGAGGC_comp1760_seq0	81.053	95	18	0	3993	4087	4935	5029	9.75E-17	91.5
	YS1_GAGATTCC-TATAGCCT_comp1672_seq3	71.259	2867	784	17	268	3120	617	3457	0	1415
	YS1_GAGATTCC-TATAGCCT_comp1672_seq3	75.67	970	234	2	3119	4087	3890	4858	0	679
	YL1_CGCTCATT-TATAGCCT_comp818_seq3	77.314	1772	400	2	2496	4266	2892	4662	0	1377
	YL1_CGCTCATT-TATAGCCT_comp818_seq3	71.251	2014	562	9	268	2270	602	2609	0	996
	YL1_CGCTCATT-TATAGCCT_comp818_seq3	75	68	17	0	2425	2492	2747	2814	0.004	46.4
	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	71.188	2256	617	15	874	3120	181	2412	0	1101
	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	75.601	791	191	2	3199	3988	3027	3816	1.26E-154	549
	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	88.06	67	8	0	3993	4059	4078	4144	4.14E-15	86
CrTPT2 (KC511771.1)	OL1_CGCTCATT-CCTATCCT_comp1940_seq1	77.011	87	20	0	3119	3205	2842	2928	1.11E-09	68
Transcription Factors (TFs):											
TF	transcript	% ID	Alignment length	Mismatch	Gapopen	TF start	TF end	Transcript start	Transcript end	E-value	Bitscore
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	78.509	228	49	0	365	592	662	889	1.93E-47	190
	YL1_CGCTCATT-TATAGCCT_comp6621_seq0	74.308	253	59	2	365	611	688	940	3.27E-38	159

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ORCA2 (AJ238740.1)	YS2_GAGATTCC-ATAGAGGC_comp27339_seq0	74.336	226	45	1	367	592	422	634	1.39E-36	154
	YS2_GAGATTCC-ATAGAGGC_comp27339_seq0	91.429	35	3	0	76	110	134	168	4.27E-05	50
	AR2_GAGATTCC-GGCTCTGA_comp3513_seq0	75.568	176	43	0	376	551	496	671	2.36E-27	123
	YS1_GAGATTCC-TATAGCCT_comp5858_seq0	73.988	173	45	0	379	551	616	788	5.19E-23	109
	YL1_CGCTCATT-TATAGCCT_comp6621_seq0	80.669	269	49	1	1085	1353	666	931	6.95E-65	250
	YL1_CGCTCATT-TATAGCCT_comp6621_seq0	76.316	76	18	0	837	912	124	199	8.49E-07	57.2
	AR2_GAGATTCC-GGCTCTGA_comp3513_seq0	84.615	182	28	0	1122	1303	497	678	9.05E-51	203
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	78.947	209	44	0	1104	1312	656	864	1.03E-43	179
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	78.481	79	14	2	823	898	33	111	6.97E-08	60.8
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	75	48	12	0	991	1038	345	392	9.7	33.7
ORCA3 (AJ251250.1)	AR1_GAGATTCC-CCTATCCT_comp14477_seq0	83.333	138	23	0	1112	1249	458	595	2.13E-33	145
	AR1_GAGATTCC-CCTATCCT_comp11153_seq4	73.14	242	62	1	1145	1386	435	673	2.59E-32	141
ORCA4 (KR703577.1)	YL1_CGCTCATT-TATAGCCT_comp6621_seq0	78.516	256	55	0	340	595	675	930	1.80E-54	214
	YL1_CGCTCATT-TATAGCCT_comp6621_seq0	81.928	83	10	3	16	95	126	206	3.98E-12	73.4
	AR2_GAGATTCC-GGCTCTGA_comp3513_seq0	84.066	182	29	0	365	546	497	678	1.39E-49	197
	AR1_GAGATTCC-CCTATCCT_comp11153_seq4	77.542	236	51	2	361	595	408	642	3.72E-44	179
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	74.429	219	55	1	337	554	645	863	3.26E-32	140
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	86.667	60	8	0	19	78	55	114	3.98E-12	73.4
ORCA5 (KR703578.1)	AR1_GAGATTCC-CCTATCCT_comp14477_seq0	80.142	141	28	0	355	495	458	598	5.90E-29	129
	AR2_GAGATTCC-GGCTCTGA_comp3513_seq0	81.191	319	51	2	614	932	488	797	1.83E-81	304
	AR2_GAGATTCC-GGCTCTGA_comp3513_seq0	78.75	80	14	1	25	101	178	257	8.33E-10	66.2
	AR1_GAGATTCC-CCTATCCT_comp14477_seq0	81.503	173	29	1	584	753	426	598	3.31E-40	167
	AR1_GAGATTCC-CCTATCCT_comp14477_seq0	80.723	83	10	1	25	101	146	228	1.32E-13	78.8
	YL1_CGCTCATT-TATAGCCT_comp6621_seq0	81.437	167	31	0	631	797	708	874	1.41E-38	161
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	81.679	131	24	0	631	761	682	812	8.32E-29	129
ORCA6 (MN614455.1)	YL1_CGCTCATT-TATAGCCT_comp10613_seq0	72.989	174	47	0	624	797	554	727	1.16E-20	102
	AR2_GAGATTCC-GGCTCTGA_comp3513_seq0	82.162	185	33	0	271	455	487	671	7.12E-46	185
	AR1_GAGATTCC-CCTATCCT_comp14477_seq0	80.952	147	28	0	271	417	458	604	2.66E-32	140
	OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	74.869	191	48	0	281	471	674	864	4.80E-29	129
	YS1_GAGATTCC-TATAGCCT_comp5858_seq0	74.566	173	44	0	283	455	616	788	1.06E-24	114
	YS2_GAGATTCC-ATAGAGGC_comp27339_seq0	70.244	205	48	2	267	471	418	609	8.13E-20	98.7
	YS2_GAGATTCC-ATAGAGGC_comp27339_seq0	85.714	28	4	0	126	153	235	262	2.8	33.7
BIS1 (KM409646.2)	YL3_CGCTCATT-ATAGAGGC_comp4742_seq3	73.982	1130	199	22	3	1101	269	1334	0	699
	AR1_GAGATTCC-CCTATCCT_comp8525_seq2	74.291	564	133	4	511	1071	750	1304	3.90E-97	356
	AR1_GAGATTCC-CCTATCCT_comp8525_seq2	78.947	114	19	2	7	116	285	397	7.07E-18	93.3
	OL1_CGCTCATT-CCTATCCT_comp6055_seq0	65.82	433	128	7	622	1038	880	1308	4.76E-20	100
	AR2_GAGATTCC-GGCTCTGA_comp1597_seq3	78.947	114	19	2	7	116	300	412	7.07E-18	93.3
	YL1_CGCTCATT-TATAGCCT_comp10816_seq0	93.548	31	1	1	859	888	1680	1650	0.003	44.6
	AR1_GAGATTCC-CCTATCCT_comp8525_seq2	70.934	867	152	15	372	1230	551	1325	2.60E-125	450
	AR1_GAGATTCC-CCTATCCT_comp8525_seq2	69.811	159	24	4	1	159	282	416	2.15E-12	75.2
	YL3_CGCTCATT-ATAGAGGC_comp4742_seq3	71.575	584	142	5	631	1214	750	1309	2.44E-81	304

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	YL3_CGCTCATT-ATAGAGGC_comp4742_seq3	72.857	70	7	3	9	78	275	332	0.15	39.2
	OL1_CGCTCATT-CCTATCCT_comp6055_seq0	71.171	222	64	0	662	883	809	1030	8.54E-24	113
	OL1_CGCTCATT-CCTATCCT_comp6055_seq0	67.485	163	53	0	1013	1175	1145	1307	2.01E-06	55.4
	AR2_GAGATTCC-GGCTCTGA_comp1597_seq3	69.811	159	24	4	1	159	297	431	2.15E-12	75.2
	AR2_GAGATTCC-GGCTCTGA_comp1597_seq3	76	100	15	3	372	468	566	659	3.19E-10	68
	AR2_GAGATTCC-GGCTCTGA_comp1597_seq3	83.871	31	5	0	215	245	466	496	6.6	33.7
BIS2 (KM409645.1)	AR2_GAGATTCC-GGCTCTGA_comp1660_seq1	80.952	63	12	0	757	819	891	953	4.73E-08	60.8
	OL3_CGCTCATT-GGCTCTGA_comp2316_seq0	80	1415	181	27	1158	2552	1441	2773	0	1247
	OL1_CGCTCATT-CCTATCCT_comp4812_seq0	80.783	1353	191	24	1185	2501	1078	2397	0	1222
	OL1_CGCTCATT-CCTATCCT_comp4812_seq0	70.926	1080	191	21	77	1076	8	1044	7.71E-155	549
	OL1_CGCTCATT-CCTATCCT_comp2168_seq4	74.927	1029	181	18	77	1079	107	1084	0	681
	YS1_GAGATTCC-TATAGCCT_comp2461_seq6	74.636	1029	184	18	77	1079	204	1181	0	668
	YS1_GAGATTCC-TATAGCCT_comp14327_seq2	80.18	666	91	18	1895	2540	3	647	1.22E-158	562
	YS1_GAGATTCC-TATAGCCT_comp14327_seq2	76.087	92	8	5	2261	2350	655	734	1.23E-06	57.2
MYC2 (AF283507.2)	YS1_GAGATTCC-TATAGCCT_comp14327_seq2	73.529	102	16	5	2450	2547	735	829	0.000183	50
	AR1_GAGATTCC-CCTATCCT_comp24292_seq0	77.204	329	51	6	322	632	542	864	2.93E-65	250
	YS1_GAGATTCC-TATAGCCT_comp87_seq4	71.498	414	85	8	30	425	154	552	8.96E-53	208
	YS1_GAGATTCC-TATAGCCT_comp87_seq3	71.294	425	83	10	30	427	154	566	3.13E-52	206
	AR1_GAGATTCC-CCTATCCT_comp16215_seq2	77.533	227	30	7	424	632	808	1031	2.74E-40	167
WRKY1 (HQ646368.1)	AR2_GAGATTCC-GGCTCTGA_comp1658_seq0	75.771	227	31	6	424	632	3831	4051	4.96E-37	156
	AR1_GAGATTCC-CCTATCCT_comp737_seq2	72.233	533	94	14	104	600	328	842	1.76E-74	280
	AR1_GAGATTCC-CCTATCCT_comp737_seq2	96.97	33	1	0	70	102	267	299	1.27E-06	55.4
	YL1_CGCTCATT-TATAGCCT_comp10081_seq1	69.458	203	56	2	206	405	179	378	2.62E-15	84.2
	AR2_GAGATTCC-GGCTCTGA_comp7502_seq0	70.408	196	53	4	203	397	261	452	1.11E-13	78.8
	AR2_GAGATTCC-GGCTCTGA_comp7502_seq2	68.837	215	52	5	194	396	240	451	3.89E-13	77
ZCT1 (AJ632082.1)	AR1_GAGATTCC-CCTATCCT_comp6246_seq5	78.75	80	15	2	200	278	527	605	2.99E-08	60.8
	AR2_GAGATTCC-GGCTCTGA_comp7502_seq0	69.737	608	124	15	80	657	90	667	3.09E-66	253
	AR2_GAGATTCC-GGCTCTGA_comp7502_seq0	73.75	160	29	9	805	958	840	992	2.09E-11	71.6
	AR2_GAGATTCC-GGCTCTGA_comp7502_seq2	66.026	624	111	19	64	657	76	628	6.82E-43	176
	AR2_GAGATTCC-GGCTCTGA_comp7502_seq2	71.519	158	27	9	808	958	802	948	1.32E-07	59
	AR1_GAGATTCC-CCTATCCT_comp737_seq2	71.689	219	51	5	236	447	409	623	3.54E-21	104
	AR2_GAGATTCC-GGCTCTGA_comp5665_seq0	80.556	72	14	0	379	450	1288	1359	2.55E-10	68
	AR2_GAGATTCC-GGCTCTGA_comp5665_seq0	71.053	76	22	0	238	313	1096	1171	0.12	39.2
ZCT2 (AJ632083.1)	YL1_CGCTCATT-TATAGCCT_comp10081_seq1	73.737	99	26	0	214	312	145	243	1.08E-08	62.6
	AR1_GAGATTCC-CCTATCCT_comp521_seq0	72.048	991	174	23	61	1023	171	1086	9.68E-149	527
	AR2_GAGATTCC-GGCTCTGA_comp1098_seq4	71.287	1010	166	28	61	1019	1556	2492	1.35E-140	500
	OL3_CGCTCATT-GGCTCTGA_comp7752_seq4	71.125	987	179	25	57	998	186	1111	4.40E-134	479
	OL1_CGCTCATT-CCTATCCT_comp2136_seq4	69.679	343	63	13	676	1005	926	1240	9.12E-29	129
ZCT3 (AJ632084.1)	AR2_GAGATTCC-GGCTCTGA_comp10369_seq0	75.862	87	15	1	679	765	481	401	3.19E-09	64.4
	YL1_CGCTCATT-TATAGCCT_comp1354_seq1	68.293	1066	143	29	1	1042	103	997	9.27E-124	444
	YS2_GAGATTCC-ATAGAGGC_comp2064_seq8	67.864	1058	146	26	1	1042	2965	3844	1.68E-120	434

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GATA1 (MK801106.1)	OL3_CGCTCATT-GGCTCTGA_comp8246_seq1	67.628	1075	149	31	1	1044	49	955	1.91E-113	410	
	YS1_GAGATTCC-TATAGCCT_comp2284_seq2	68.045	1064	149	35	1	1042	119	1013	9.91E-111	401	
	YS2_GAGATTCC-ATAGAGGC_comp4735_seq0	73.786	515	81	9	539	1044	326	795	5.14E-89	329	
	YS2_GAGATTCC-ATAGAGGC_comp4735_seq0	91.304	23	2	0	83	105	181	203	5.5	33.7	
	YS1_GAGATTCC-TATAGCCT_comp3725_seq0	77.524	1882	300	38	5	1858	186	1972	0	1427	
	YS1_GAGATTCC-TATAGCCT_comp3725_seq0	100	19	0	0	1	19	168	186	2.9	35.6	
	YL1_CGCTCATT-TATAGCCT_comp4560_seq1	80.074	1345	215	17	5	1320	130	1450	0	1189	
	YL1_CGCTCATT-TATAGCCT_comp4560_seq1	72.176	478	66	20	1386	1858	1716	2131	5.51E-60	233	
	YL1_CGCTCATT-TATAGCCT_comp4560_seq1	100	19	0	0	1	19	112	130	2.9	35.6	
	YL1_CGCTCATT-TATAGCCT_comp4560_seq0	78.753	1219	199	12	6	1205	112	1289	0	1031	
	YL1_CGCTCATT-TATAGCCT_comp4560_seq0	71.084	664	107	22	1203	1858	1393	1979	8.73E-83	309	
	OL1_CGCTCATT-CCTATCCT_comp4376_seq4	81.124	694	116	2	621	1314	849	1527	0	666	
	OL1_CGCTCATT-CCTATCCT_comp4376_seq4	77.671	627	98	10	6	613	125	728	3.70E-138	493	
	OL1_CGCTCATT-CCTATCCT_comp4376_seq4	69.933	449	78	17	1380	1825	1668	2062	1.30E-42	176	
GBF1 (AF084971.1)	YL1_CGCTCATT-TATAGCCT_comp4162_seq2	75.269	93	23	0	1118	1210	1082	1174	5.90E-09	64.4	
GBF2 (AF084972.1)	OL3_CGCTCATT-GGCTCTGA_comp5631_seq2	81.358	1797	232	28	22	1786	124	1849	0	1698	
	AR1_GAGATTCC-CCTATCCT_comp6026_seq0	83.374	1215	146	18	574	1769	706	1883	0	1251	
	AR1_GAGATTCC-CCTATCCT_comp6026_seq0	85.985	264	32	2	355	618	398	656	1.08E-81	306	
	AR1_GAGATTCC-CCTATCCT_comp6026_seq0	69.424	278	48	10	22	289	138	388	5.61E-22	107	
	AR2_GAGATTCC-GGCTCTGA_comp6592_seq4	82.512	1258	152	21	574	1803	761	1978	0	1243	
	AR2_GAGATTCC-GGCTCTGA_comp6592_seq4	77.758	571	78	14	22	582	146	677	7.27E-122	439	
	YS1_GAGATTCC-TATAGCCT_comp5460_seq5	84.724	995	119	8	188	1163	234	1214	0	1103	
	YS1_GAGATTCC-TATAGCCT_comp5460_seq5	80.787	635	79	15	1160	1786	2377	2976	2.08E-160	567	
	YS1_GAGATTCC-TATAGCCT_comp5460_seq5	73.196	97	23	2	5	100	83	177	3.79E-05	51.8	
	YS1_GAGATTCC-TATAGCCT_comp5460_seq5	81.818	44	8	0	82	125	180	223	0.006	44.6	
	AR1_GAGATTCC-CCTATCCT_comp11579_seq0	82.381	840	109	15	866	1686	1895	2714	0	816	
	AR1_GAGATTCC-CCTATCCT_comp11579_seq0	92.069	290	23	0	574	863	738	1027	6.81E-116	419	
	GBF2 (AF084972.1)	AR1_GAGATTCC-CCTATCCT_comp11579_seq0	75.207	605	81	16	18	582	78	653	1.50E-111	405
	AR2_GAGATTCC-GGCTCTGA_comp630_seq3	78.341	651	78	11	385	1026	424	1020	3.62E-154	545	
AR2_GAGATTCC-GGCTCTGA_comp630_seq3	82.692	104	15	1	1	101	157	260	1.04E-21	105		
AR2_GAGATTCC-GGCTCTGA_comp630_seq3	82.051	78	14	0	236	313	323	400	1.45E-13	78.8		
AR2_GAGATTCC-GGCTCTGA_comp630_seq4	78.341	651	78	11	385	1026	424	1020	3.62E-154	545		
AR2_GAGATTCC-GGCTCTGA_comp630_seq4	82.692	104	15	1	1	101	157	260	1.04E-21	105		
AR2_GAGATTCC-GGCTCTGA_comp630_seq4	82.051	78	14	0	236	313	323	400	1.45E-13	78.8		
AR2_GAGATTCC-GGCTCTGA_comp630_seq1	78.221	652	79	11	384	1026	420	1017	1.26E-153	544		
AR2_GAGATTCC-GGCTCTGA_comp630_seq1	82.692	104	15	1	1	101	157	260	1.04E-21	105		
AR2_GAGATTCC-GGCTCTGA_comp630_seq1	80	95	19	0	236	330	323	417	9.77E-16	86		
OL1_CGCTCATT-CCTATCCT_comp1173_seq1	78.034	651	80	11	385	1026	483	1079	1.88E-151	536		
OL1_CGCTCATT-CCTATCCT_comp1173_seq1	82.692	104	15	1	1	101	219	322	1.04E-21	105		
OL1_CGCTCATT-CCTATCCT_comp1173_seq1	79.487	78	16	0	236	313	382	459	7.51E-11	69.8		
YL3_CGCTCATT-ATAGAGGC_comp915_seq2	77.914	652	81	11	384	1026	630	1227	6.55E-151	535		

TableS1

CtERF5 (MK862158.1)	YL3_CGCTCATT-ATAGAGGC_comp915_seq2	80.769	78	15	0	253	330	550	627	6.17E-12	73.4
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TableS2

Transcript ID	MIA	Communities	sprot_Top_BLASTX_hit
YS2_GAGATTCC-ATAGAGGC_comp13351_seq1	NA	1	Y3037_ARATH^Y3037_ARATH^Q:412-2247,H:43-639^42.86%ID^E:4e-128^RecName: Full=Probable inactive leucine-rich repeat receptor-like protein kinase At3g03770
OL3_CGCTCATT-GGCTCTGA_comp10301_seq0	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp2586_seq1	NA	1	.
YL3_CGCTCATT-ATAGAGGC_comp19793_seq1	NA	1	C86A2_ARATH^C86A2_ARATH^Q:2-346,H:409-523^75.65%ID^E:2e-53^RecName: Full=Cytochrome P450 86A2
YS2_GAGATTCC-ATAGAGGC_comp1135_seq0	NA	1	RL212_ARATH^RL212_ARATH^Q:27-518,H:1-164^84.76%ID^E:7e-100^RecName: Full=60S ribosomal protein L21-2
AR1_GAGATTCC-CCTATCCT_comp8017_seq0	NA	1	DST1_DICDI^DST1_DICDI^Q:863-1696,H:15-283^57.55%ID^E:2e-97^RecName: Full=Serine/threonine-protein kinase dst1 {ECO:0000250 UniProtKB:O61125}
YL3_CGCTCATT-ATAGAGGC_comp3883_seq1	NA	1	F135B_XENLA^F135B_XENLA^Q:2876-3694,H:1102-1362^41.09%ID^E:5e-51^RecName: Full=Protein FAM135B
OL1_CGCTCATT-CCTATCCT_comp1577_seq4	NA	1	GLGL1_SOLTU^GLGL1_SOLTU^Q:941-2191,H:2-417^81.29%ID^E:0^RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 1
YS2_GAGATTCC-ATAGAGGC_comp561_seq1	NA	1	C81F1_ARATH^C81F1_ARATH^Q:172-1560,H:39-499^40.88%ID^E:3e-118^RecName: Full=Cytochrome P450 81F1 {ECO:0000305}
YS1_GAGATTCC-TATAGCCT_comp8849_seq1	NA	1	FDL1_ARATH^FDL1_ARATH^Q:168-1520,H:3-415^28.14%ID^E:1e-29^RecName: Full=F-box/FBD/LRR-repeat protein At1g13570
YL3_CGCTCATT-ATAGAGGC_comp188_seq0	NA	1	BGL17_ARATH^BGL17_ARATH^Q:1932-3023,H:33-395^56.87%ID^E:4e-135^RecName: Full=Beta-glucosidase 17
YS1_GAGATTCC-TATAGCCT_comp2178_seq1	NA	1	.
OL1_CGCTCATT-CCTATCCT_comp2611_seq3	NA	1	.
YL3_CGCTCATT-ATAGAGGC_comp7990_seq0	NA	1	EDL17_ARATH^EDL17_ARATH^Q:114-1505,H:10-467^48.08%ID^E:1e-128^RecName: Full=Sugar transporter ERD6-like 17
YL1_CGCTCATT-TATAGCCT_comp6895_seq1	NA	1	EAAC_ARATH^EAAC_ARATH^Q:83-1255,H:1-379^69.57%ID^E:1e-172^RecName: Full=Probable envelope ADP,ATP carrier protein, chloroplastic
AR2_GAGATTCC-GGCTCTGA_comp2954_seq0	NA	1	C71DC_CATRO^C71DC_CATRO^Q:267-1745,H:2-492^50.2%ID^E:1e-166^RecName: Full=Tabersonine 16-hydroxylase
YL1_CGCTCATT-TATAGCCT_comp3031_seq4	NA	1	.
YL3_CGCTCATT-ATAGAGGC_comp22491_seq0	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp15661_seq0	NA	1	.
YS1_GAGATTCC-TATAGCCT_comp3802_seq2	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp5672_seq0	NA	1	BH048_ARATH^BH048_ARATH^Q:632-1372,H:27-270^50.2%ID^E:3e-51^RecName: Full=Transcription factor bHLH48
YL1_CGCTCATT-TATAGCCT_comp3021_seq0	NA	1	.
YS2_GAGATTCC-ATAGAGGC_comp776_seq0	PAS	1	THCAS_CANSA^THCAS_CANSA^Q:197-1681,H:32-540^44.92%ID^E:1e-133^RecName: Full=Tetrahydrocannabinolic acid synthase
YS2_GAGATTCC-ATAGAGGC_comp1760_seq0	CrTPT2	1	AB32G_ARATH^AB32G_ARATH^Q:318-3440,H:1-1043^75.84%ID^E:0^RecName: Full=ABC transporter G family member 32 {ECO:0000303 PubMed:18299247}
YL3_CGCTCATT-ATAGAGGC_comp16614_seq0	NA	1	.
OL1_CGCTCATT-CCTATCCT_comp3680_seq3	NA	1	GLGL2_SOLTU^GLGL2_SOLTU^Q:3403-5007,H:1-519^73.83%ID^E:0^RecName: Full=Glucose-1-phosphate adenylyltransferase large subunit 2, chloroplastic/amyloplastic
YL1_CGCTCATT-TATAGCCT_comp12228_seq3	NA	1	.
YS2_GAGATTCC-ATAGAGGC_comp16202_seq0	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp2644_seq3	NA	1	GPDH2_ORYSJ^GPDH2_ORYSJ^Q:731-2029,H:16-382^68.13%ID^E:0^RecName: Full=Probable glycerol-3-phosphate dehydrogenase [NAD(+)] 2, cytosolic
YS2_GAGATTCC-ATAGAGGC_comp8501_seq0	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp33140_seq0	NA	1	AAE13_ARATH^AAE13_ARATH^Q:2119-3087,H:222-540^73.37%ID^E:2e-159^RecName: Full=Malonate--CoA ligase
OL1_CGCTCATT-CCTATCCT_comp517_seq13	NA	1	ECR_ARATH^ECR_ARATH^Q:4949-5878,H:1-310^81.29%ID^E:7e-174^.
AR2_GAGATTCC-GGCTCTGA_comp2244_seq1	STR	1	STSY_RAUSE^STSY_RAUSE^Q:58-1059,H:1-333^77.61%ID^E:3e-171^RecName: Full=Strictosidine synthase
YL1_CGCTCATT-TATAGCCT_comp2609_seq5	NA	1	.
OL1_CGCTCATT-CCTATCCT_comp3318_seq1	NA	1	CER1_ARATH^CER1_ARATH^Q:892-2229,H:171-620^59.87%ID^E:3e-159^RecName: Full=Protein ECERIFERUM 1
YL3_CGCTCATT-ATAGAGGC_comp6907_seq0	NA	1	Y1491_ARATH^Y1491_ARATH^Q:219-1655,H:21-499^78.29%ID^E:0^RecName: Full=Uncharacterized protein At1g04910
YS1_GAGATTCC-TATAGCCT_comp65_seq1	NA	1	MER_ERYCB^MER_ERYCB^Q:109-663,H:4-194^56.25%ID^E:7e-61^RecName: Full=Methylecgonone reductase
YL3_CGCTCATT-ATAGAGGC_comp3908_seq3	NA	1	CSE_ARATH^CSE_ARATH^Q:258-1172,H:23-323^31.7%ID^E:1e-41^RecName: Full=Caffeoylshikimate esterase
YL3_CGCTCATT-ATAGAGGC_comp1258_seq0	SAT	1	VINSY_RAUSE^VINSY_RAUSE^Q:163-1392,H:1-408^65.06%ID^E:0^RecName: Full=Vinorine synthase
YS2_GAGATTCC-ATAGAGGC_comp32416_seq0	NA	1	CADH6_ORYSJ^CADH6_ORYSJ^Q:13-246,H:70-147^75.64%ID^E:5e-34^RecName: Full=Probable cinnamyl alcohol dehydrogenase 6
YL3_CGCTCATT-ATAGAGGC_comp13569_seq0	NA	1	.
YS2_GAGATTCC-ATAGAGGC_comp3900_seq3	NA	1	FH3_ORYSJ^FH3_ORYSJ^Q:2023-3180,H:809-1205^77.58%ID^E:0^RecName: Full=Formin-like protein 3
YL1_CGCTCATT-TATAGCCT_comp193_seq6	NA	1	RL362_ARATH^RL362_ARATH^Q:123-452,H:1-112^80.36%ID^E:9e-49^RecName: Full=60S ribosomal protein L36-2

TableS2

YS2_GAGATTCC-ATAGAGGC_comp2915_seq1	CMS	1	ISPD_ARATH^ISPD_ARATH^Q:1565-2311,H:56-299^77.51%ID^E:1e-121^RecName: Full=2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, chloroplastic
YS2_GAGATTCC-ATAGAGGC_comp5426_seq0	NA	1	TRY_ARATH^TRY_ARATH^Q:78-326,H:7-87^68.67%ID^E:1e-28^RecName: Full=Transcription factor TRY
YL1_CGCTCATT-TATAGCCT_comp6500_seq0	NA	1	SHN2_ARATH^SHN2_ARATH^Q:172-756,H:1-189^57.36%ID^E:2e-48^RecName: Full=Ethylene-responsive transcription factor SHINE 2
YL1_CGCTCATT-TATAGCCT_comp621_seq0	NA	1	.
YS1_GAGATTCC-TATAGCCT_comp445_seq2	DXR	1	DXR_MENPI^DXR_MENPI^Q:367-1776,H:1-470^86.86%ID^E:0^RecName: Full=1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic
YS1_GAGATTCC-TATAGCCT_comp24972_seq0	SLS1	1	C72A1_CATRO^C72A1_CATRO^Q:1427-2701,H:93-517^91.29%ID^E:0^RecName: Full=Secologanin synthase
YL1_CGCTCATT-TATAGCCT_comp14134_seq1	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp15133_seq0	NA	1	GDL17_ARATH^GDL17_ARATH^Q:182-1192,H:34-370^70.21%ID^E:4e-171^RecName: Full=GDSL esterase/lipase At1g33811
YL1_CGCTCATT-TATAGCCT_comp2275_seq4	NA	1	UBP1_NICPL^UBP1_NICPL^Q:1100-2194,H:21-384^86.89%ID^E:0^RecName: Full=Oligouridylate-binding protein 1
YS2_GAGATTCC-ATAGAGGC_comp2920_seq0	NA	1	PPR39_ARATH^PPR39_ARATH^Q:245-658,H:69-204^39.13%ID^E:1e-35^RecName: Full=Pentatricopeptide repeat-containing protein At1g12775, mitochondrial
YS2_GAGATTCC-ATAGAGGC_comp10625_seq1	NA	1	Y2921_ARATH^Y2921_ARATH^Q:31-1602,H:4-502^32%ID^E:9e-60^RecName: Full=Putative leucine-rich repeat receptor-like protein kinase At2g19210
YL1_CGCTCATT-TATAGCCT_comp29020_seq2	NA	1	.
YS1_GAGATTCC-TATAGCCT_comp22171_seq0	NA	1	C81F1_ARATH^C81F1_ARATH^Q:852-1457,H:300-499^50%ID^E:1e-43^RecName: Full=Cytochrome P450 81F1 {ECO:0000305}
YL1_CGCTCATT-TATAGCCT_comp4005_seq1	NA	1	WSD1_ARATH^WSD1_ARATH^Q:319-1278,H:61-386^27.03%ID^E:1e-26^RecName: Full=O-acyltransferase WSD1
YS2_GAGATTCC-ATAGAGGC_comp3651_seq3	NA	1	FHYRK_ARATH^FHYRK_ARATH^Q:1731-2336,H:178-379^81.19%ID^E:6e-110^RecName: Full=Bifunctional riboflavin kinase/FMN phosphatase
YS2_GAGATTCC-ATAGAGGC_comp3692_seq0	NA	1	SCRK6_ARATH^SCRK6_ARATH^Q:420-1502,H:28-384^81.16%ID^E:1e-177^RecName: Full=Probable fructokinase-6, chloroplastic
YS1_GAGATTCC-TATAGCCT_comp18331_seq0	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp1075_seq1	NA	1	.
YL1_CGCTCATT-TATAGCCT_comp444_seq0	DL7H	1	C72A1_CATRO^C72A1_CATRO^Q:232-1896,H:1-522^51.17%ID^E:0^RecName: Full=Secologanin synthase
YL3_CGCTCATT-ATAGAGGC_comp9604_seq2	NA	1	KGLT_PETHY^KGLT_PETHY^Q:231-1583,H:5-448^64.46%ID^E:0^RecName: Full=Kaempferol 3-O-beta-D-galactosyltransferase
YL3_CGCTCATT-ATAGAGGC_comp1778_seq0	NA	1	BGAL5_ARATH^BGAL5_ARATH^Q:538-2550,H:61-731^71.83%ID^E:0^RecName: Full=Beta-galactosidase 5
YL3_CGCTCATT-ATAGAGGC_comp412_seq0	NA	1	RNFT2_MOUSE^RNFT2_MOUSE^Q:1847-2782,H:129-439^28.25%ID^E:1e-33^RecName: Full=RING finger and transmembrane domain-containing protein 2
YS2_GAGATTCC-ATAGAGGC_comp10747_seq0	NA	1	.
YL3_CGCTCATT-ATAGAGGC_comp10883_seq2	NA	1	DOF53_ARATH^DOF53_ARATH^Q:332-622,H:59-168^58.18%ID^E:6e-30^RecName: Full=Dof zinc finger protein DOF5.3
YL3_CGCTCATT-ATAGAGGC_comp22283_seq0	NA	1	SMT1_ARATH^SMT1_ARATH^Q:458-1018,H:149-335^78.07%ID^E:2e-106^RecName: Full=Cycloartenol-C-24-methyltransferase
OL1_CGCTCATT-CCTATCCT_comp35745_seq0	NA	1	.
YS2_GAGATTCC-ATAGAGGC_comp1818_seq4	NA	1	IDD9_ARATH^IDD9_ARATH^Q:401-1399,H:39-365^59%ID^E:2e-95^RecName: Full=Protein indeterminate-domain 9 {ECO:0000303 PubMed:16784536}
YL1_CGCTCATT-TATAGCCT_comp2414_seq3	NA	2	CCD53_ORYSJ^CCD53_ORYSJ^Q:2149-2952,H:59-328^33.09%ID^E:8e-34^RecName: Full=Cyclin-D5-3
YL3_CGCTCATT-ATAGAGGC_comp25903_seq0	NA	2	.
YL1_CGCTCATT-TATAGCCT_comp5995_seq1	NA	2	RH52A_ORYSJ^RH52A_ORYSJ^Q:509-1651,H:80-474^47.73%ID^E:1e-100^RecName: Full=DEAD-box ATP-dependent RNA helicase 52A
YS1_GAGATTCC-TATAGCCT_comp17005_seq0	NA	2	PID_ARATH^PID_ARATH^Q:220-1452,H:37-438^63.55%ID^E:3e-177^RecName: Full=Protein kinase PINOID
YS2_GAGATTCC-ATAGAGGC_comp4578_seq8	NA	2	DPOLA_ORYSJ^DPOLA_ORYSJ^Q:1194-2783,H:295-831^67.04%ID^E:0^RecName: Full=DNA polymerase alpha catalytic subunit
YS2_GAGATTCC-ATAGAGGC_comp7927_seq0	NA	2	.
YL3_CGCTCATT-ATAGAGGC_comp7058_seq2	NA	2	Y2182_ARATH^Y2182_ARATH^Q:931-3513,H:27-888^73.15%ID^E:0^.
YS1_GAGATTCC-TATAGCCT_comp204_seq5	NA	2	ABP20_PRUPE^ABP20_PRUPE^Q:2853-3449,H:4-202^66%ID^E:6e-77^RecName: Full=Auxin-binding protein ABP20
YS2_GAGATTCC-ATAGAGGC_comp11930_seq0	NA	2	H1_MAIZE^H1_MAIZE^Q:289-492,H:52-119^64.71%ID^E:5e-21^RecName: Full=Histone H1
YL3_CGCTCATT-ATAGAGGC_comp12994_seq0	NA	2	BGAL8_ARATH^BGAL8_ARATH^Q:171-2483,H:37-851^54.45%ID^E:0^RecName: Full=Beta-galactosidase 8
YS1_GAGATTCC-TATAGCCT_comp13633_seq0	NA	2	INVB_ARATH^INVB_ARATH^Q:188-1858,H:13-570^78.25%ID^E:0^RecName: Full=Probable alkaline/neutral invertase B {ECO:0000305}
YS1_GAGATTCC-TATAGCCT_comp1212_seq3	NA	2	GRF6_ORYSJ^GRF6_ORYSJ^Q:1117-1470,H:157-271^70.34%ID^E:1e-45^RecName: Full=Growth-regulating factor 6
YS1_GAGATTCC-TATAGCCT_comp767_seq6	NA	2	.
YL3_CGCTCATT-ATAGAGGC_comp3939_seq2	NA	2	Y4374_ARATH^Y4374_ARATH^Q:908-2677,H:29-622^61.27%ID^E:0^RecName: Full=Probable inactive receptor kinase At4g23740
OL3_CGCTCATT-GGCTCTGA_comp6787_seq2	redox1	2	NU155_ARATH^NU155_ARATH^Q:1019-5659,H:1-1464^65.74%ID^E:0^RecName: Full=Nuclear pore complex protein NUP155 {ECO:0000303 PubMed:12034489}
YS1_GAGATTCC-TATAGCCT_comp10834_seq2	NA	2	XYNF1_ASPOR^XYNF1_ASPOR^Q:1037-1792,H:42-293^29.77%ID^E:2e-28^RecName: Full=Endo-1,4-beta-xylanase F1
YS1_GAGATTCC-TATAGCCT_comp124_seq0	NA	2	LAL5_ARATH^LAL5_ARATH^Q:2436-3797,H:11-464^60.79%ID^E:8e-167^.

TableS2

YL1_CGCTCATT-TATAGCCT_comp14048_seq1	NA	2 DPB_ARATH^DPB_ARATH^Q:259-624,H:104-226^53.23%ID^E:2e-32^RecName: Full=Transcription factor-like protein DPB
YS2_GAGATTCC-ATAGAGGC_comp48_seq0	NA	2 CIPKC_ARATH^CIPKC_ARATH^Q:329-1636,H:20-459^78.64%ID^E:0^RecName: Full=CBL-interacting serine/threonine-protein kinase 12
YL3_CGCTCATT-ATAGAGGC_comp662_seq3	NA	2 CADH6_ORYSJ^CADH6_ORYSJ^Q:95-1162,H:2-358^72.83%ID^E:1e-177^RecName: Full=Probable cinnamyl alcohol dehydrogenase 6
YS2_GAGATTCC-ATAGAGGC_comp369_seq0	NA	2 RL74_ARATH^RL74_ARATH^Q:286-1023,H:1-244^79.27%ID^E:2e-130^RecName: Full=60S ribosomal protein L7-4
YS2_GAGATTCC-ATAGAGGC_comp705_seq0	NA	2 21KD_DAUCA^21KD_DAUCA^Q:736-1218,H:28-188^55.28%ID^E:1e-58^RecName: Full=21 kDa protein
YS1_GAGATTCC-TATAGCCT_comp11479_seq0	NA	2 CMT2_ARATH^CMT2_ARATH^Q:127-813,H:726-950^53.68%ID^E:7e-116^RecName: Full=DNA (cytosine-5)-methyltransferase CMT2
YL1_CGCTCATT-TATAGCCT_comp8260_seq1	NA	2 GTOMC_ORYSJ^GTOMC_ORYSJ^Q:1-264,H:136-223^55.68%ID^E:4e-24^RecName: Full=Probable tocopherol O-methyltransferase, chloroplastic
YS1_GAGATTCC-TATAGCCT_comp17_seq1	NA	2 TET3_ARATH^TET3_ARATH^Q:1322-2176,H:1-285^68.42%ID^E:5e-125^RecName: Full=Tetraspanin-3
YS2_GAGATTCC-ATAGAGGC_comp2803_seq0	NA	2 Y3228_ARATH^Y3228_ARATH^Q:1273-1671,H:13-147^52.59%ID^E:3e-39^RecName: Full=PHD finger protein At3g20280
YL1_CGCTCATT-TATAGCCT_comp616_seq1	NA	2 CADH6_ORYSJ^CADH6_ORYSJ^Q:536-1603,H:2-358^72.83%ID^E:0^RecName: Full=Probable cinnamyl alcohol dehydrogenase 6
YL1_CGCTCATT-TATAGCCT_comp11114_seq0	NA	2 IAA17_ARATH^IAA17_ARATH^Q:84-659,H:2-219^46.33%ID^E:3e-55^RecName: Full=Auxin-responsive protein IAA17
AR2_GAGATTCC-GGCTCTGA_comp969_seq0	NA	2 H4_SOYBN^H4_SOYBN^Q:220-453,H:22-99^100%ID^E:5e-45^RecName: Full=Histone H4
YL1_CGCTCATT-TATAGCCT_comp3917_seq0	NA	2 Y5720_ARATH^Y5720_ARATH^Q:381-2264,H:30-666^52.15%ID^E:0^RecName: Full=Probable inactive receptor kinase At5g67200
YL1_CGCTCATT-TATAGCCT_comp3285_seq0	NA	2 VIL2_ARATH^VIL2_ARATH^Q:460-2259,H:2-714^36.29%ID^E:1e-94^RecName: Full=VIN3-like protein 2
YL3_CGCTCATT-ATAGAGGC_comp15965_seq1	NA	2 .
YL1_CGCTCATT-TATAGCCT_comp302_seq2	NMT	2 GTOMC_ORYSJ^GTOMC_ORYSJ^Q:1698-2549,H:75-357^48.24%ID^E:3e-88^RecName: Full=Probable tocopherol O-methyltransferase, chloroplastic
YS2_GAGATTCC-ATAGAGGC_comp12704_seq0	NA	2 NAT1_ARATH^NAT1_ARATH^Q:327-1883,H:2-520^86.71%ID^E:0^RecName: Full=Nucleobase-ascorbate transporter 1
YS2_GAGATTCC-ATAGAGGC_comp61_seq0	Vm16OMT	2 HTOMT_CATRO^HTOMT_CATRO^Q:2794-3867,H:1-355^70.28%ID^E:8e-156^RecName: Full=Tabersonine 16-O-methyltransferase
YS1_GAGATTCC-TATAGCCT_comp8503_seq3	NA	2 ROGF1_ARATH^ROGF1_ARATH^Q:764-2506,H:1-548^66.55%ID^E:0^RecName: Full=Rop guanine nucleotide exchange factor 1
YL3_CGCTCATT-ATAGAGGC_comp9464_seq1	NA	2 .
YS2_GAGATTCC-ATAGAGGC_comp5812_seq2	NA	2 LTL1_ARATH^LTL1_ARATH^Q:1690-1920,H:289-365^76.62%ID^E:8e-35^RecName: Full=GDSL esterase/lipase LTL1
YS2_GAGATTCC-ATAGAGGC_comp21866_seq0	NA	2 .
AR1_GAGATTCC-CCTATCCT_comp3145_seq1	VmPINMT	2 GTOMC_ORYSJ^GTOMC_ORYSJ^Q:2-916,H:92-359^41.23%ID^E:4e-80^RecName: Full=Probable tocopherol O-methyltransferase, chloroplastic
AR2_GAGATTCC-GGCTCTGA_comp2837_seq1	NA	2 PPO1_IPOBA^PPO1_IPOBA^Q:341-1708,H:1-457^63.83%ID^E:0^RecName: Full=Polyphenol oxidase I, chloroplastic
YS2_GAGATTCC-ATAGAGGC_comp8982_seq1	NA	2 .
YL3_CGCTCATT-ATAGAGGC_comp2768_seq1	NA	2 .
AR1_GAGATTCC-CCTATCCT_comp1782_seq4	NA	2 KC1D_PONAB^KC1D_PONAB^Q:1149-2012,H:3-278^38.51%ID^E:6e-55^RecName: Full=Casein kinase I isoform delta
YS1_GAGATTCC-TATAGCCT_comp10782_seq1	NA	2 SMC5_ARATH^SMC5_ARATH^Q:281-3400,H:3-1042^62.21%ID^E:0^RecName: Full=Structural maintenance of chromosomes protein 5
YL1_CGCTCATT-TATAGCCT_comp17245_seq0	NA	2 .
YS2_GAGATTCC-ATAGAGGC_comp324_seq0	TDC	2 DDC_CATRO^DDC_CATRO^Q:661-2163,H:1-500^88.45%ID^E:0^RecName: Full=Aromatic-L-amino-acid decarboxylase
YL3_CGCTCATT-ATAGAGGC_comp11681_seq0	NA	2 ANXD3_ARATH^ANXD3_ARATH^Q:22-975,H:1-321^57.63%ID^E:1e-129^RecName: Full=Annexin D3
AR1_GAGATTCC-CCTATCCT_comp386_seq2	NA	2 MLO6_ARATH^MLO6_ARATH^Q:748-2376,H:5-581^59.66%ID^E:0^RecName: Full=MLO-like protein 6
YL1_CGCTCATT-TATAGCCT_comp12249_seq2	NA	2 WAXS4_ARATH^WAXS4_ARATH^Q:215-1186,H:21-337^39.2%ID^E:6e-60^RecName: Full=Probable long-chain-alcohol O-fatty-acyltransferase 4
OL1_CGCTCATT-CCTATCCT_comp6039_seq0	NA	2 .
YL1_CGCTCATT-TATAGCCT_comp202_seq1	NA	3 RUBA_PEA^RUBA_PEA^Q:1424-3199,H:1-587^86.99%ID^E:0^RecName: Full=RuBisCO large subunit-binding protein subunit alpha, chloroplastic
YS2_GAGATTCC-ATAGAGGC_comp28794_seq0	DXS3	3 DXS2_ORYSJ^DXS2_ORYSJ^Q:101-811,H:12-247^75.21%ID^E:2e-115^RecName: Full=Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic
YL3_CGCTCATT-ATAGAGGC_comp22045_seq0	NA	3 .
YS2_GAGATTCC-ATAGAGGC_comp2791_seq1	NA	3 FLS2_ARATH^FLS2_ARATH^Q:110-1351,H:8-477^28.54%ID^E:2e-29^RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2
YL3_CGCTCATT-ATAGAGGC_comp3100_seq5	NA	3 PII2_ARATH^PII2_ARATH^Q:2363-3541,H:30-423^61.06%ID^E:2e-132^RecName: Full=Piriformospora indica-insensitive protein 2
AR1_GAGATTCC-CCTATCCT_comp25230_seq0	NA	3 .
YL3_CGCTCATT-ATAGAGGC_comp2756_seq3	NA	3 CELF3_BOVIN^CELF3_BOVIN^Q:830-2026,H:5-439^36.61%ID^E:1e-68^RecName: Full=CUGBP Elav-like family member 3
YL3_CGCTCATT-ATAGAGGC_comp477_seq1	IS	3 IRIS_CATRO^IRIS_CATRO^Q:199-1458,H:1-388^83.33%ID^E:0^RecName: Full=Iridoid synthase
YS2_GAGATTCC-ATAGAGGC_comp37355_seq0	NA	3 RAC1_BETVU^RAC1_BETVU^Q:900-1328,H:54-197^92.36%ID^E:5e-75^RecName: Full=Rac-like GTP-binding protein RHO1
YL3_CGCTCATT-ATAGAGGC_comp10649_seq0	NA	3 ARAK_ARATH^ARAK_ARATH^Q:617-3511,H:66-1034^72.38%ID^E:0^RecName: Full=L-arabinokinase

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YS2_GAGATTCC-ATAGAGGC_comp2711_seq8	NA	3	LVSG_DICDI^LVSG_DICDI^Q:1856-2908,H:384-772^38.39%ID^E:4e-71^RecName: Full=Probable inactive serine/threonine-protein kinase lvsG
YL1_CGCTCATT-TATAGCCT_comp5166_seq0	NA	3	.
YL3_CGCTCATT-ATAGAGGC_comp3314_seq1	NA	3	Y3565_ARATH^Y3565_ARATH^Q:1642-2610,H:164-498^61.83%ID^E:1e-129^RecName: Full=Probable inactive receptor-like protein kinase At3g56050
YS1_GAGATTCC-TATAGCCT_comp1665_seq2	NA	3	BLH6_ARATH^BLH6_ARATH^Q:1000-2730,H:3-494^42.76%ID^E:3e-115^RecName: Full=BEL1-like homeodomain protein 6
YL3_CGCTCATT-ATAGAGGC_comp7757_seq0	NA	3	Y5656_ARATH^Y5656_ARATH^Q:312-2372,H:1-667^56.05%ID^E:0^RecName: Full=BTB/POZ domain-containing protein At5g66560
YL1_CGCTCATT-TATAGCCT_comp9867_seq0	NA	3	CIPK1_ORYSJ^CIPK1_ORYSJ^Q:1-276,H:148-239^76.09%ID^E:7e-75^RecName: Full=CBL-interacting protein kinase 1
AR1_GAGATTCC-CCTATCCT_comp22848_seq1	NA	3	MSI4_ARATH^MSI4_ARATH^Q:65-220,H:66-117^82.69%ID^E:3e-23^RecName: Full=WD-40 repeat-containing protein MSI4
YL1_CGCTCATT-TATAGCCT_comp7173_seq1	NA	3	RABA3_ARATH^RABA3_ARATH^Q:189-842,H:23-237^71.3%ID^E:5e-103^RecName: Full=Ras-related protein RABA3
YL1_CGCTCATT-TATAGCCT_comp6388_seq3	NA	3	PMA4_NICPL^PMA4_NICPL^Q:4708-3239,H:390-801^71.02%ID^E:0^RecName: Full=Plasma membrane ATPase 4
YL1_CGCTCATT-TATAGCCT_comp643_seq0	NA	3	RAN3_ARATH^RAN3_ARATH^Q:79-717,H:1-213^98.12%ID^E:7e-142^RecName: Full=GTP-binding nuclear protein Ran-3
YS1_GAGATTCC-TATAGCCT_comp264_seq2	NA	3	.
AR1_GAGATTCC-CCTATCCT_comp1758_seq2	NA	3	SYT_MIMIV^SYT_MIMIV^Q:868-1755,H:57-342^44.15%ID^E:1e-72^RecName: Full=Tyrosine--tRNA ligase
YS2_GAGATTCC-ATAGAGGC_comp6671_seq1	NA	3	NLTL2_ARATH^NLTL2_ARATH^Q:303-716,H:26-162^53.62%ID^E:2e-40^RecName: Full=Non-specific lipid-transfer protein-like protein At2g13820
YS1_GAGATTCC-TATAGCCT_comp14492_seq0	NA	3	RL15_PETHY^RL15_PETHY^Q:1380-1991,H:1-204^94.61%ID^E:2e-112^RecName: Full=60S ribosomal protein L15
AR2_GAGATTCC-GGCTCTGA_comp9401_seq0	NA	3	.
YL3_CGCTCATT-ATAGAGGC_comp4742_seq3	BIS1	3	BBR_ARATH^BBR_ARATH^Q:2045-2518,H:180-335^67.09%ID^E:3e-53^RecName: Full=E3 ubiquitin ligase BIG BROTHER-related
YS2_GAGATTCC-ATAGAGGC_comp5910_seq2	NA	3	VSR1_ARATH^VSR1_ARATH^Q:2339-4132,H:22-623^77.24%ID^E:0^RecName: Full=Vacuolar-sorting receptor 1
YL1_CGCTCATT-TATAGCCT_comp5093_seq2	NA	3	IAA14_ARATH^IAA14_ARATH^Q:352-843,H:4-151^48.8%ID^E:7e-32^RecName: Full=Auxin-responsive protein IAA14
AR1_GAGATTCC-CCTATCCT_comp589_seq7	G10H	3	C76B6_CATRO^C76B6_CATRO^Q:1306-2784,H:1-493^86%ID^E:0^RecName: Full=Geraniol 8-hydroxylase
AR1_GAGATTCC-CCTATCCT_comp20069_seq0	NA	3	CB4_SPIOL^CB4_SPIOL^Q:1590-1081,H:80-249^90%ID^E:1e-94^RecName: Full=Chlorophyll a-b binding protein CP24, chloroplastic
YS2_GAGATTCC-ATAGAGGC_comp10055_seq1	NA	3	.
OL3_CGCTCATT-GGCTCTGA_comp7833_seq1	NA	3	POL4_DROME^POL4_DROME^Q:611-1714,H:876-1234^25.88%ID^E:6e-29^RecName: Full=Retrovirus-related Pol polyprotein from transposon 412
YS2_GAGATTCC-ATAGAGGC_comp558_seq3	DL7GT	3	UGT8_CATRO^UGT8_CATRO^Q:834-2273,H:3-482^88.12%ID^E:0^RecName: Full=7-deoxyloganic acid glucosyltransferase
YL1_CGCTCATT-TATAGCCT_comp20383_seq0	NA	3	.
YL1_CGCTCATT-TATAGCCT_comp5868_seq1	NA	3	VAP21_ARATH^VAP21_ARATH^Q:498-1160,H:1-220^64.29%ID^E:2e-81^RecName: Full=Vesicle-associated protein 2-1
YL1_CGCTCATT-TATAGCCT_comp7706_seq0	NA	3	.
YS1_GAGATTCC-TATAGCCT_comp5831_seq1	NA	3	.
YS1_GAGATTCC-TATAGCCT_comp10376_seq0	NA	3	.
AR1_GAGATTCC-CCTATCCT_comp4243_seq0	NA	3	.
YS2_GAGATTCC-ATAGAGGC_comp1901_seq0	NA	3	ASPG1_ARATH^ASPG1_ARATH^Q:217-1569,H:45-500^58.42%ID^E:2e-169^RecName: Full=Protein ASPARTIC PROTEASE IN GUARD CELL 1
AR1_GAGATTCC-CCTATCCT_comp3050_seq0	THAS1	4	10HGO_CATRO^10HGO_CATRO^Q:256-1335,H:1-360^86.94%ID^E:0^RecName: Full=8-hydroxygeraniol dehydrogenase
OL1_CGCTCATT-CCTATCCT_comp1163_seq6	NA	4	GATP3_SOLL^GATP3_SOLL^Q:1986-2429,H:370-516^80.41%ID^E:6e-74^RecName: Full=Gamma aminobutyrate transaminase 3, chloroplastic
AR1_GAGATTCC-CCTATCCT_comp8371_seq0	NA	4	HIS2_ARATH^HIS2_ARATH^Q:186-1004,H:23-279^68.5%ID^E:9e-121^RecName: Full=Histidine biosynthesis bifunctional protein hisI, chloroplastic
AR1_GAGATTCC-CCTATCCT_comp28_seq3	NA	4	.
YL3_CGCTCATT-ATAGAGGC_comp3627_seq0	NA	4	CYC6_ARATH^CYC6_ARATH^Q:474-698,H:100-174^88%ID^E:7e-45^RecName: Full=Cytochrome c6, chloroplastic {ECO:0000303 PubMed:12037572}
YS1_GAGATTCC-TATAGCCT_comp8635_seq3	NA	4	.
YS2_GAGATTCC-ATAGAGGC_comp8318_seq1	T3O	4	C71D7_SOLCH^C71D7_SOLCH^Q:3390-3109,H:82-182^46.53%ID^E:2e-49^RecName: Full=Cytochrome P450 71D7
YS1_GAGATTCC-TATAGCCT_comp6764_seq2	V19H	4	HACL_ARATH^HACL_ARATH^Q:229-1950,H:1-572^79.62%ID^E:0^RecName: Full=2-hydroxyacyl-CoA lyase
YL3_CGCTCATT-ATAGAGGC_comp14054_seq2	NA	4	.
YS1_GAGATTCC-TATAGCCT_comp11712_seq2	NA	4	.
AR1_GAGATTCC-CCTATCCT_comp2271_seq1	NA	4	.
YL3_CGCTCATT-ATAGAGGC_comp70_seq0	8HG0	4	ADHX_ORYSI^ADHX_ORYSI^Q:149-1249,H:8-377^44.89%ID^E:1e-92^RecName: Full=Alcohol dehydrogenase class-3
YL3_CGCTCATT-ATAGAGGC_comp4424_seq2	NA	4	RGLG2_ARATH^RGLG2_ARATH^Q:675-1517,H:184-468^71.23%ID^E:5e-146^RecName: Full=E3 ubiquitin-protein ligase RGLG2
YS2_GAGATTCC-ATAGAGGC_comp6211_seq1	NA	4	KPRS4_SPIOL^KPRS4_SPIOL^Q:220-1173,H:1-318^87.74%ID^E:0^RecName: Full=Ribose-phosphate pyrophosphokinase 4

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YL3_CGCTCATT-ATAGAGGC_comp25807_seq0	NA	4 .
YS2_GAGATTCC-ATAGAGGC_comp1127_seq1	NA	4 STIP1_ARATH^STIP1_ARATH^Q:1314-3857,H:1-841^53.51%ID^E:0^RecName: Full=Septin and tuftelin-interacting protein 1 homolog 1
YS1_GAGATTCC-TATAGCCT_comp72982_seq0	NA	4 .
YL1_CGCTCATT-TATAGCCT_comp13722_seq1	NA	4 PDPK2_ARATH^PDPK2_ARATH^Q:848-1456,H:32-234^91.13%ID^E:0^RecName: Full=3-phosphoinositide-dependent protein kinase 2
YS2_GAGATTCC-ATAGAGGC_comp13836_seq1	NA	4 MCM9_ARATH^MCM9_ARATH^Q:917-2809,H:12-640^75.63%ID^E:0^RecName: Full=Probable DNA helicase MCM9
YL1_CGCTCATT-TATAGCCT_comp1306_seq0	NA	4 THO4A_ARATH^THO4A_ARATH^Q:205-741,H:1-172^59.67%ID^E:5e-44^RecName: Full=THO complex subunit 4A
OL3_CGCTCATT-GGCTCTGA_comp9667_seq1	NA	4 CBSX3_ARATH^CBSX3_ARATH^Q:421-885,H:16-206^51.31%ID^E:1e-51^RecName: Full=CBS domain-containing protein CBSX3, mitochondrial
YL3_CGCTCATT-ATAGAGGC_comp14103_seq1	NA	4 .
AR1_GAGATTCC-CCTATCCT_comp4362_seq3	NA	4 RP8L2_ARATH^RP8L2_ARATH^Q:996-2741,H:345-901^31.18%ID^E:1e-68^RecName: Full=Probable disease resistance RPP8-like protein 2
OL1_CGCTCATT-CCTATCCT_comp5736_seq1	NA	5 2A5B_ARATH^2A5B_ARATH^Q:711-2147,H:1-485^70.43%ID^E:0^RecName: Full=Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform
OL3_CGCTCATT-GGCTCTGA_comp87_seq0	NA	5 GLNA2_VITVI^GLNA2_VITVI^Q:1-246,H:225-306^95.12%ID^E:2e-44^RecName: Full=Glutamine synthetase cytosolic isozyme 2
OL3_CGCTCATT-GGCTCTGA_comp166_seq3	NA	5 .
OL3_CGCTCATT-GGCTCTGA_comp8049_seq3	NA	5 .
OL3_CGCTCATT-GGCTCTGA_comp5964_seq3	NA	5 .
OL3_CGCTCATT-GGCTCTGA_comp3166_seq0	NA	5 C71DC_CATRO^C71DC_CATRO^Q:276-1646,H:38-492^59.04%ID^E:0^RecName: Full=Tabersonine 16-hydroxylase
OL3_CGCTCATT-GGCTCTGA_comp6046_seq2	NA	5 .
OL3_CGCTCATT-GGCTCTGA_comp3275_seq3	NA	5 LENG8_XENLA^LENG8_XENLA^Q:1359-2120,H:515-765^47.86%ID^E:4e-66^RecName: Full=Leukocyte receptor cluster member 8 homolog
OL1_CGCTCATT-CCTATCCT_comp1318_seq1	VS	5 HIDM_GLYEC^HIDM_GLYEC^Q:72-566,H:12-178^52.07%ID^E:2e-43^RecName: Full=2-hydroxyisoflavanone dehydratase
YS1_GAGATTCC-TATAGCCT_comp1103_seq2	NA	6 .
YS1_GAGATTCC-TATAGCCT_comp6148_seq1	NA	6 IDD2_ARATH^IDD2_ARATH^Q:253-624,H:1-122^76.61%ID^E:1e-62^RecName: Full=Protein indeterminate-domain 2 {ECO:0000303 PubMed:16784536}
YL1_CGCTCATT-TATAGCCT_comp20633_seq0	NA	6 Y1174_SYNP6^Y1174_SYNP6^Q:188-1219,H:2-339^55.36%ID^E:5e-100^RecName: Full=Uncharacterized lipoprotein syc1174_c
OL3_CGCTCATT-GGCTCTGA_comp4608_seq0	NA	6 ARID5_ARATH^ARID5_ARATH^Q:1224-2120,H:131-434^66.23%ID^E:2e-121^RecName: Full=AT-rich interactive domain-containing protein 5
AR2_GAGATTCC-GGCTCTGA_comp1085_seq1	NA	6 RAB7_VIGAC^RAB7_VIGAC^Q:2089-2649,H:19-206^90.96%ID^E:5e-117^RecName: Full=Ras-related protein Rab7
YS2_GAGATTCC-ATAGAGGC_comp11931_seq1	NA	6 YNB1_YEAST^YNB1_YEAST^Q:499-1446,H:51-417^31.84%ID^E:2e-47^RecName: Full=Uncharacterized protein YNL011C
OL3_CGCTCATT-GGCTCTGA_comp5315_seq0	NA	6 TOC34_PEA^TOC34_PEA^Q:691-1266,H:111-301^65.1%ID^E:6e-79^RecName: Full=Translocase of chloroplast 34
AR1_GAGATTCC-CCTATCCT_comp2374_seq0	NA	6 CLPP6_ARATH^CLPP6_ARATH^Q:485-1204,H:38-271^77.92%ID^E:1e-120^RecName: Full=ATP-dependent Clp protease proteolytic subunit 6, chloroplastic {ECO:0000303 PubMed:11299370}
OL3_CGCTCATT-GGCTCTGA_comp8459_seq0	NA	6 ARFH_ARATH^ARFH_ARATH^Q:582-2246,H:185-773^61.59%ID^E:0^RecName: Full=Auxin response factor 8
YS2_GAGATTCC-ATAGAGGC_comp3776_seq2	NA	6 CSP1_ARATH^CSP1_ARATH^Q:331-1200,H:6-299^43.56%ID^E:9e-32^RecName: Full=Cold shock protein 1
OL1_CGCTCATT-CCTATCCT_comp4311_seq2	NA	6 .
OL3_CGCTCATT-GGCTCTGA_comp9977_seq1	ORCA2	6 ERF99_ARATH^ERF99_ARATH^Q:673-903,H:91-168^73.08%ID^E:2e-33^RecName: Full=Ethylene-responsive transcription factor 13
AR1_GAGATTCC-CCTATCCT_comp3443_seq0	NA	7 F3PH_ARATH^F3PH_ARATH^Q:174-1706,H:1-508^39.96%ID^E:4e-121^RecName: Full=Flavonoid 3'-monooxygenase
AR1_GAGATTCC-CCTATCCT_comp76_seq2	NA	7 E13B_WHEAT^E13B_WHEAT^Q:367-1611,H:26-453^45.92%ID^E:9e-123^RecName: Full=Glucan endo-1,3-beta-glucosidase
AR2_GAGATTCC-GGCTCTGA_comp7052_seq0	NA	7 ANX4_FRAAN^ANX4_FRAAN^Q:82-1017,H:1-314^64.97%ID^E:9e-146^RecName: Full=Annexin-like protein RJ4
AR2_GAGATTCC-GGCTCTGA_comp35_seq9	NA	7 C72A1_CATRO^C72A1_CATRO^Q:667-2238,H:1-524^90.84%ID^E:0^RecName: Full=Secologanin synthase
YS1_GAGATTCC-TATAGCCT_comp9360_seq0	NA	7 LHTL6_ARATH^LHTL6_ARATH^Q:336-1577,H:19-432^72.95%ID^E:0^RecName: Full=Lysine histidine transporter-like 6
AR1_GAGATTCC-CCTATCCT_comp15336_seq0	NA	7 AKT1_ARATH^AKT1_ARATH^Q:195-2792,H:7-857^67.97%ID^E:0^RecName: Full=Potassium channel AKT1
AR1_GAGATTCC-CCTATCCT_comp902_seq1	NA	7 AL3H1_ARATH^AL3H1_ARATH^Q:3199-3702,H:191-358^72.02%ID^E:2e-74^RecName: Full=Aldehyde dehydrogenase family 3 member H1
AR1_GAGATTCC-CCTATCCT_comp7406_seq5	NA	7 IDD2_ARATH^IDD2_ARATH^Q:585-2090,H:1-447^52.38%ID^E:5e-124^RecName: Full=Protein indeterminate-domain 2 {ECO:0000303 PubMed:16784536}
YL1_CGCTCATT-TATAGCCT_comp695_seq0	GES	7 GERS_OCIBA^GERS_OCIBA^Q:288-1925,H:31-566^63.39%ID^E:0^RecName: Full=Geraniol synthase, chloroplastic
YL3_CGCTCATT-ATAGAGGC_comp24426_seq0	NA	8 NCPR_CATRO^NCPR_CATRO^Q:239-880,H:501-714^91.59%ID^E:2e-138^RecName: Full=NADPH--cytochrome P450 reductase {ECO:0000255 HAMAP-Rule:MF_03212}
OL3_CGCTCATT-GGCTCTGA_comp2316_seq0	MYC2	8 SYY_PARUW^SYY_PARUW^Q:1-1062,H:70-422^52.82%ID^E:1e-120^RecName: Full=Tyrosine--tRNA ligase {ECO:0000255 HAMAP-Rule:MF_02006}
YL1_CGCTCATT-TATAGCCT_comp28191_seq0	NA	8 .
YL1_CGCTCATT-TATAGCCT_comp5601_seq1	NA	8 .
YL1_CGCTCATT-TATAGCCT_comp19800_seq0	NA	8 .

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YL1_CGCTCATT-TATAGCCT_comp1884_seq0	NA	8	RETOL_ARATH^RETOL_ARATH^Q:403-1920,H:32-536^59.33%ID^E:0^RecName: Full=Reticuline oxidase-like protein
AR1_GAGATTCC-CCTATCCT_comp34936_seq0	NA	8	.
YL1_CGCTCATT-TATAGCCT_comp10398_seq1	NA	8	.
OL1_CGCTCATT-CCTATCCT_comp10937_seq0	NA	8	CIPKB_ARATH^CIPKB_ARATH^Q:302-1267,H:95-421^57.88%ID^E:2e-118^RecName: Full=CBL-interacting serine/threonine-protein kinase 11
OL3_CGCTCATT-GGCTCTGA_comp34446_seq0	NA	8	.
YS2_GAGATTCC-ATAGAGGC_comp4455_seq0	NA	9	.
YS1_GAGATTCC-TATAGCCT_comp18356_seq0	NA	9	.
YL1_CGCTCATT-TATAGCCT_comp10613_seq0	ORCA5	9	EF106_ARATH^EF106_ARATH^Q:111-797,H:1-190^38.43%ID^E:8e-26^RecName: Full=Ethylene-responsive transcription factor ERF106
YS1_GAGATTCC-TATAGCCT_comp14430_seq1	NA	9	.
YS1_GAGATTCC-TATAGCCT_comp9517_seq0	NA	9	EB1C_ARATH^EB1C_ARATH^Q:515-898,H:215-328^49.62%ID^E:2e-26^RecName: Full=Microtubule-associated protein RP/EB family member 1C
YS1_GAGATTCC-TATAGCCT_comp9328_seq0	NA	9	TBL34_ARATH^TBL34_ARATH^Q:661-1365,H:171-405^53.62%ID^E:1e-107^RecName: Full=Protein trichome birefringence-like 34
YL1_CGCTCATT-TATAGCCT_comp6908_seq3	NA	9	.
YS2_GAGATTCC-ATAGAGGC_comp6201_seq1	NA	9	.
YS2_GAGATTCC-ATAGAGGC_comp92_seq2	NA	9	MYO2_ARATH^MYO2_ARATH^Q:4807-6198,H:647-1116^53.24%ID^E:5e-150^RecName: Full=Myosin-2
YS2_GAGATTCC-ATAGAGGC_comp1198_seq1	NA	9	.
YL1_CGCTCATT-TATAGCCT_comp9896_seq0	NA	9	.
YL3_CGCTCATT-ATAGAGGC_comp2341_seq2	NA	9	MTDH_FRAAN^MTDH_FRAAN^Q:2520-3485,H:35-356^67.7%ID^E:5e-139^RecName: Full=Probable mannitol dehydrogenase
YL3_CGCTCATT-ATAGAGGC_comp166_seq2	CS	9	HIDH_SOYBN^HIDH_SOYBN^Q:302-1240,H:4-318^48.91%ID^E:3e-93^RecName: Full=2-hydroxyisoflavanone dehydratase
YL1_CGCTCATT-TATAGCCT_comp27681_seq0	NA	9	.
AR1_GAGATTCC-CCTATCCT_comp1435_seq3	NA	9	RAC5_ORYSJ^RAC5_ORYSJ^Q:234-755,H:1-174^94.25%ID^E:5e-117^RecName: Full=Rac-like GTP-binding protein 5
YL1_CGCTCATT-TATAGCCT_comp11923_seq3	NA	9	ASPM_SHEEP^ASPM_SHEEP^Q:867-3644,H:702-1662^24.78%ID^E:7e-52^RecName: Full=Abnormal spindle-like microcephaly-associated protein homolog
YL3_CGCTCATT-ATAGAGGC_comp4884_seq0	NA	9	.
YS1_GAGATTCC-TATAGCCT_comp37971_seq0	NA	9	.
YS1_GAGATTCC-TATAGCCT_comp15581_seq0	NA	9	.
YL1_CGCTCATT-TATAGCCT_comp6685_seq0	NA	9	.
YL3_CGCTCATT-ATAGAGGC_comp55552_seq0	NA	9	.
OL1_CGCTCATT-CCTATCCT_comp11695_seq0	NA	10	.
YS2_GAGATTCC-ATAGAGGC_comp15556_seq7	NA	10	CASTO_LOTJA^CASTO_LOTJA^Q:660-2075,H:90-565^75.68%ID^E:0^RecName: Full=Ion channel CASTOR
AR2_GAGATTCC-GGCTCTGA_comp1876_seq1	NA	10	ARP9_ORYSI^ARP9_ORYSI^Q:6424-8193,H:1-586^62.86%ID^E:0^RecName: Full=Actin-related protein 9
OL1_CGCTCATT-CCTATCCT_comp55598_seq0	NA	10	PP2A2_ARATH^PP2A2_ARATH^Q:425-973,H:124-306^96.72%ID^E:3e-129^RecName: Full=Serine/threonine-protein phosphatase PP2A-2 catalytic subunit
OL1_CGCTCATT-CCTATCCT_comp58112_seq0	NA	10	.
YL1_CGCTCATT-TATAGCCT_comp32410_seq0	NA	10	.
YS2_GAGATTCC-ATAGAGGC_comp14565_seq0	NA	10	.
AR1_GAGATTCC-CCTATCCT_comp331_seq0	NA	10	.
YL3_CGCTCATT-ATAGAGGC_comp13576_seq1	NA	10	C3H3_ARATH^C3H3_ARATH^Q:242-1228,H:23-338^45.72%ID^E:1e-77^RecName: Full=Zinc finger CCCH domain-containing protein 3
YS2_GAGATTCC-ATAGAGGC_comp805_seq0	NA	10	GGAP1_ARATH^GGAP1_ARATH^Q:704-1879,H:1-387^76.53%ID^E:0^RecName: Full=GDP-L-galactose phosphorylase 1
YS1_GAGATTCC-TATAGCCT_comp7766_seq6	NA	10	CMBL_HUMAN^CMBL_HUMAN^Q:655-1227,H:28-217^30.96%ID^E:1e-22^RecName: Full=Carboxymethylenebutenolidase homolog
YS2_GAGATTCC-ATAGAGGC_comp38970_seq0	NA	10	.
AR1_GAGATTCC-CCTATCCT_comp1158_seq0	IDI1	10	IDI1_CAMAC^IDI1_CAMAC^Q:315-1016,H:1-234^89.32%ID^E:4e-153^RecName: Full=Isopentenyl-diphosphate Delta-isomerase I
YL3_CGCTCATT-ATAGAGGC_comp6028_seq1	NA	10	.
YL3_CGCTCATT-ATAGAGGC_comp4093_seq1	NA	10	.
YS2_GAGATTCC-ATAGAGGC_comp38763_seq0	NA	10	.
OL1_CGCTCATT-CCTATCCT_comp3640_seq0	THAS2	10	10HGO_CATRO^10HGO_CATRO^Q:196-1302,H:4-360^58.54%ID^E:8e-134^RecName: Full=8-hydroxygeraniol dehydrogenase
YS2_GAGATTCC-ATAGAGGC_comp48268_seq0	NA	10	.

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YS2_GAGATTCC-ATAGAGGC_comp2162_seq0	NA	10 .
YS1_GAGATTCC-TATAGCCT_comp57747_seq0	NA	10 CID9_ARATH^CID9_ARATH^Q:5-406,H:118-251^79.85%ID^E:3e-79^RecName: Full=Polyadenylate-binding protein-interacting protein 9
YS2_GAGATTCC-ATAGAGGC_comp39036_seq0	NA	10 .
YS2_GAGATTCC-ATAGAGGC_comp12232_seq0	NA	10 .
YL3_CGCTCATT-ATAGAGGC_comp33457_seq0	NA	10 .
AR1_GAGATTCC-CCTATCCT_comp4203_seq9	NA	10 UGPA_HORVU^UGPA_HORVU^Q:2-268,H:104-192^87.64%ID^E:1e-44^RecName: Full=UTP--glucose-1-phosphate uridylyltransferase
YS2_GAGATTCC-ATAGAGGC_comp1795_seq5	NA	10 .
YS2_GAGATTCC-ATAGAGGC_comp33887_seq0	NA	10 .
YS2_GAGATTCC-ATAGAGGC_comp5239_seq2	NA	10 .
OL1_CGCTCATT-CCTATCCT_comp2934_seq3	NA	11 P2C52_ARATH^P2C52_ARATH^Q:1685-3094,H:1-467^73.68%ID^E:0^RecName: Full=Probable protein phosphatase 2C 52
YS2_GAGATTCC-ATAGAGGC_comp1245_seq0	NA	11 GAI_SOLLC^GAI_SOLLC^Q:423-2090,H:26-588^67.47%ID^E:0^RecName: Full=DELLA protein GAI
YL1_CGCTCATT-TATAGCCT_comp2035_seq0	NA	11 SDC1_ORYSJ^SDC1_ORYSJ^Q:1806-2429,H:274-481^62.02%ID^E:4e-88^RecName: Full=Serine decarboxylase 1
YS2_GAGATTCC-ATAGAGGC_comp6216_seq0	NA	11 PAS1_ARATH^PAS1_ARATH^Q:289-1812,H:1-460^65.94%ID^E:0^RecName: Full=Peptidyl-prolyl cis-trans isomerase PASTICCINO1
YS1_GAGATTCC-TATAGCCT_comp8724_seq0	NA	11 YQK1_SCHPO^YQK1_SCHPO^Q:82-999,H:3-303^33.23%ID^E:4e-35^RecName: Full=UPF0676 protein C1494.01
YS1_GAGATTCC-TATAGCCT_comp6147_seq0	NA	11 .
YL3_CGCTCATT-ATAGAGGC_comp3510_seq4	NA	11 Y1461_ARATH^Y1461_ARATH^Q:849-2270,H:88-565^69.85%ID^E:0^RecName: Full=Probable serine/threonine-protein kinase At1g54610
YL3_CGCTCATT-ATAGAGGC_comp5404_seq1	NA	11 BP73_ORYSJ^BP73_ORYSJ^Q:359-1318,H:30-372^40.23%ID^E:1e-50^RecName: Full=SAP-like protein BP-73
YL1_CGCTCATT-TATAGCCT_comp11035_seq1	NA	11 Y1491_ARATH^Y1491_ARATH^Q:480-1850,H:44-483^35.64%ID^E:6e-73^RecName: Full=Uncharacterized protein At1g04910
YL1_CGCTCATT-TATAGCCT_comp24563_seq0	NA	11 .
OL1_CGCTCATT-CCTATCCT_comp1051_seq1	NA	11 LGUL_CICAR^LGUL_CICAR^Q:878-1276,H:54-186^80.45%ID^E:3e-73^RecName: Full=Lactoylglutathione lyase
YL1_CGCTCATT-TATAGCCT_comp9848_seq1	NA	11 .
YL3_CGCTCATT-ATAGAGGC_comp2061_seq2	NA	11 ICE1_ARATH^ICE1_ARATH^Q:966-2189,H:115-494^51.91%ID^E:5e-102^RecName: Full=Transcription factor ICE1
YL3_CGCTCATT-ATAGAGGC_comp16753_seq0	NA	11 .
YS1_GAGATTCC-TATAGCCT_comp5053_seq1	NA	11 .
YL1_CGCTCATT-TATAGCCT_comp3439_seq2	NA	11 Y5133_ARATH^Y5133_ARATH^Q:1686-3032,H:10-458^60.84%ID^E:0^RecName: Full=BTB/POZ domain-containing protein At5g41330
OL1_CGCTCATT-CCTATCCT_comp2674_seq2	NA	11 SUBL_ARATH^SUBL_ARATH^Q:289-2580,H:22-755^52.8%ID^E:0^.
YL1_CGCTCATT-TATAGCCT_comp12940_seq0	NA	11 CDA7L_HUMAN^CDA7L_HUMAN^Q:639-935,H:343-443^50.5%ID^E:5e-26^RecName: Full=Cell division cycle-associated 7-like protein
YS1_GAGATTCC-TATAGCCT_comp15918_seq0	NA	11 .
OL3_CGCTCATT-GGCTCTGA_comp157_seq6	NA	11 COL2_ARATH^COL2_ARATH^Q:3619-4866,H:1-347^47.49%ID^E:2e-91^RecName: Full=Zinc finger protein CONSTANS-LIKE 2
YS2_GAGATTCC-ATAGAGGC_comp20_seq11	NA	11 URH2_ARATH^URH2_ARATH^Q:394-1278,H:6-282^72.88%ID^E:6e-143^RecName: Full=Probable uridine nucleosidase 2
YL1_CGCTCATT-TATAGCCT_comp255_seq0	SGD	11 SG1_RAUSE^SG1_RAUSE^Q:1583-3088,H:32-532^82.7%ID^E:0^RecName: Full=Strictosidine-O-beta-D-glucosidase
YS2_GAGATTCC-ATAGAGGC_comp528_seq2	T16H1	11 C71DC_CATRO^C71DC_CATRO^Q:2140-3633,H:1-493^74.8%ID^E:0^RecName: Full=Tabersonine 16-hydroxylase
YS1_GAGATTCC-TATAGCCT_comp5427_seq0	NA	11 .
OL3_CGCTCATT-GGCTCTGA_comp2293_seq2	NA	12 IPPK_ARATH^IPPK_ARATH^Q:1032-2057,H:104-441^56.43%ID^E:8e-113^RecName: Full=Inositol-pentakisphosphate 2-kinase
YS1_GAGATTCC-TATAGCCT_comp5896_seq1	NA	12 .
YL3_CGCTCATT-ATAGAGGC_comp3968_seq5	NA	12 PDS5B_MOUSE^PDS5B_MOUSE^Q:708-3425,H:161-1075^23.32%ID^E:1e-48^RecName: Full=Sister chromatid cohesion protein PDS5 homolog B
YL1_CGCTCATT-TATAGCCT_comp53601_seq0	NA	12 RUXG_ARATH^RUXG_ARATH^Q:150-386,H:1-79^94.94%ID^E:1e-45^RecName: Full=Probable small nuclear ribonucleoprotein G
YS2_GAGATTCC-ATAGAGGC_comp1805_seq0	NA	12 PLSP1_ARATH^PLSP1_ARATH^Q:457-1044,H:96-291^77.04%ID^E:4e-106^RecName: Full=Chloroplast processing peptidase
YL1_CGCTCATT-TATAGCCT_comp1491_seq4	DXS2	12 DXS2_ORYSJ^DXS2_ORYSJ^Q:147-2255,H:12-712^81.56%ID^E:0^RecName: Full=Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic
YL1_CGCTCATT-TATAGCCT_comp20888_seq0	NA	12 .
YL1_CGCTCATT-TATAGCCT_comp3346_seq5	NA	12 PUB6_ARATH^PUB6_ARATH^Q:588-1658,H:7-381^38.32%ID^E:7e-71^RecName: Full=U-box domain-containing protein 6
YL1_CGCTCATT-TATAGCCT_comp13745_seq0	NA	12 .
YS2_GAGATTCC-ATAGAGGC_comp75153_seq0	NA	13 .
YL1_CGCTCATT-TATAGCCT_comp5567_seq1	NA	13 SIPL1_ARATH^SIPL1_ARATH^Q:240-1358,H:1-372^76.68%ID^E:0^RecName: Full=Signal peptide peptidase-like 1

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YL3_CGCTCATT-ATAGAGGC_comp2760_seq1	NPF2.9	13 PTR37_ARATH^PTR37_ARATH^Q:293-1912,H:22-548^43.38%ID^E:9e-167^RecName: Full=Protein NRT1/ PTR FAMILY 2.7
YS2_GAGATTCC-ATAGAGGC_comp150_seq7	NA	13 Y1745_ARATH^Y1745_ARATH^Q:750-1634,H:8-285^35.64%ID^E:7e-32^RecName: Full=Uncharacterized protein At1g51745
OL1_CGCTCATT-CCTATCCT_comp6197_seq0	NA	13 ARFA_ARATH^ARFA_ARATH^Q:2-556,H:308-497^48.24%ID^E:8e-37^RecName: Full=Auxin response factor 1
YS2_GAGATTCC-ATAGAGGC_comp6043_seq1	NA	13 SKIP5_ARATH^SKIP5_ARATH^Q:2142-2537,H:130-273^61.81%ID^E:2e-50^RecName: Full=F-box protein SKIP5
YS2_GAGATTCC-ATAGAGGC_comp9205_seq0	NA	13 .
YS2_GAGATTCC-ATAGAGGC_comp14379_seq0	NA	13 H2AV3_ORYSJ^H2AV3_ORYSJ^Q:123-533,H:1-137^83.21%ID^E:1e-60^RecName: Full=Probable histone H2A variant 3
YL1_CGCTCATT-TATAGCCT_comp60629_seq0	NA	13 .
YS2_GAGATTCC-ATAGAGGC_comp1021_seq4	NA	13 PAS2A_ORYSJ^PAS2A_ORYSJ^Q:2278-2910,H:1-211^73.93%ID^E:2e-95^.
YS1_GAGATTCC-TATAGCCT_comp17484_seq0	NA	13 SILD_FORIN^SILD_FORIN^Q:1010-1288,H:9-101^61.29%ID^E:8e-23^RecName: Full=Secoisolaricresinol dehydrogenase
OL3_CGCTCATT-GGCTCTGA_comp24855_seq0	NA	14 .
YS1_GAGATTCC-TATAGCCT_comp8170_seq2	NA	14 RSH3C_ARATH^RSH3C_ARATH^Q:1477-1905,H:215-345^47.55%ID^E:1e-24^RecName: Full=Probable GTP diphosphokinase RSH3, chloroplastic
OL1_CGCTCATT-CCTATCCT_comp31_seq2	NA	14 SFH6_ARATH^SFH6_ARATH^Q:1951-2721,H:37-295^62.5%ID^E:9e-115^RecName: Full=Phosphatidylinositol/phosphatidylcholine transfer protein SFH6
OL3_CGCTCATT-GGCTCTGA_comp21501_seq0	NA	14 .
YL1_CGCTCATT-TATAGCCT_comp1669_seq5	NA	14 INO1_TOBAC^INO1_TOBAC^Q:1075-2211,H:132-510^94.2%ID^E:0^RecName: Full=Inositol-3-phosphate synthase
YL1_CGCTCATT-TATAGCCT_comp18714_seq1	NA	14 .
YL1_CGCTCATT-TATAGCCT_comp1354_seq1	GATA1	14 P2C09_ORYSJ^P2C09_ORYSJ^Q:1416-1853,H:252-413^67.28%ID^E:5e-55^RecName: Full=Probable protein phosphatase 2C 9
YL1_CGCTCATT-TATAGCCT_comp20874_seq0	NA	14 .
OL3_CGCTCATT-GGCTCTGA_comp4703_seq4	NA	14 APG3_ARATH^APG3_ARATH^Q:408-1211,H:50-317^83.58%ID^E:3e-149^RecName: Full=Peptide chain release factor APG3, chloroplastic {ECO:0000305}
YL1_CGCTCATT-TATAGCCT_comp15844_seq2	NA	14 .
AR1_GAGATTCC-CCTATCCT_comp303_seq2	NA	15 .
AR1_GAGATTCC-CCTATCCT_comp521_seq0	ZCT3	15 ZAT10_ARATH^ZAT10_ARATH^Q:199-912,H:1-223^49.8%ID^E:8e-57^RecName: Full=Zinc finger protein ZAT10
AR1_GAGATTCC-CCTATCCT_comp814_seq11	NA	15 PGLR_VITVI^PGLR_VITVI^Q:2138-3325,H:59-455^51.39%ID^E:5e-124^RecName: Full=Probable polygalacturonase
AR1_GAGATTCC-CCTATCCT_comp1653_seq0	NA	15 PLA2A_ARATH^PLA2A_ARATH^Q:172-600,H:3-145^55.17%ID^E:3e-50^RecName: Full=Phospholipase A2-alpha {ECO:0000303 PubMed:16140037}
AR1_GAGATTCC-CCTATCCT_comp2186_seq5	NA	15 B3GT7_ARATH^B3GT7_ARATH^Q:740-1732,H:88-308^52.11%ID^E:1e-79^RecName: Full=Beta-1,3-galactosyltransferase 7
AR1_GAGATTCC-CCTATCCT_comp737_seq2	ZCT1	15 ZAT12_ARATH^ZAT12_ARATH^Q:298-639,H:5-109^57.39%ID^E:2e-29^RecName: Full=Zinc finger protein ZAT12
YL3_CGCTCATT-ATAGAGGC_comp1769_seq0	NA	15 PUMP5_ARATH^PUMP5_ARATH^Q:384-1355,H:1-311^73.39%ID^E:4e-146^RecName: Full=Mitochondrial uncoupling protein 5
AR1_GAGATTCC-CCTATCCT_comp3339_seq0	NA	15 .
AR1_GAGATTCC-CCTATCCT_comp20837_seq1	NA	15 WRK33_ARATH^WRK33_ARATH^Q:514-909,H:194-328^56.74%ID^E:8e-26^RecName: Full=Probable WRKY transcription factor 33
YS1_GAGATTCC-TATAGCCT_comp11393_seq0	NA	15 .
AR2_GAGATTCC-GGCTCTGA_comp5642_seq3	NA	15 E70A1_ARATH^E70A1_ARATH^Q:306-2003,H:66-627^29.11%ID^E:4e-77^RecName: Full=Exocyst complex component EXO70A1
AR1_GAGATTCC-CCTATCCT_comp19692_seq0	NA	15 .
YL1_CGCTCATT-TATAGCCT_comp1138_seq1	NA	15 XTH2_SOYBN^XTH2_SOYBN^Q:154-936,H:30-283^66.28%ID^E:6e-117^RecName: Full=Xyloglucan endotransglucosylase/hydrolase 2 {ECO:0000250 UniProtKB:Q38857}
YL1_CGCTCATT-TATAGCCT_comp2433_seq0	NA	15 CML31_ORYSJ^CML31_ORYSJ^Q:354-752,H:15-150^49.26%ID^E:5e-32^RecName: Full=Probable calcium-binding protein CML31
AR1_GAGATTCC-CCTATCCT_comp15923_seq0	NA	15 .
AR1_GAGATTCC-CCTATCCT_comp15349_seq0	NA	15 .
AR2_GAGATTCC-GGCTCTGA_comp25525_seq0	NA	15 .
YL1_CGCTCATT-TATAGCCT_comp1591_seq0	NA	15 RAP24_ARATH^RAP24_ARATH^Q:953-1651,H:76-329^56.03%ID^E:7e-60^RecName: Full=Ethylene-responsive transcription factor RAP2-4
AR1_GAGATTCC-CCTATCCT_comp3391_seq0	NA	15 .
AR1_GAGATTCC-CCTATCCT_comp19574_seq0	NA	15 .
YL1_CGCTCATT-TATAGCCT_comp8028_seq1	NA	15 NAC81_ARATH^NAC81_ARATH^Q:626-901,H:54-147^90.43%ID^E:2e-39^RecName: Full=Protein ATAF2
AR1_GAGATTCC-CCTATCCT_comp21765_seq0	NA	15 .
AR2_GAGATTCC-GGCTCTGA_comp3473_seq2	NA	15 WRK40_ARATH^WRK40_ARATH^Q:1211-1579,H:183-302^48.82%ID^E:3e-24^RecName: Full=Probable WRKY transcription factor 40
YL1_CGCTCATT-TATAGCCT_comp20940_seq0	NA	15 .
AR2_GAGATTCC-GGCTCTGA_comp1098_seq4	NA	15 RTNLQ_ARATH^RTNLQ_ARATH^Q:222-1385,H:4-373^50%ID^E:1e-91^RecName: Full=Reticulon-like protein B17

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AR1_GAGATTCC-CCTATCCT_comp26846_seq1	NA	15 .
YL1_CGCTCATT-TATAGCCT_comp34042_seq0	NA	15 .
OL3_CGCTCATT-GGCTCTGA_comp30250_seq0	NA	15 RS13_SOYBN^ARS13_SOYBN^Q:100-519,H:1-140^92.86%ID^E:5e-86^RecName: Full=40S ribosomal protein S13
AR2_GAGATTCC-GGCTCTGA_comp2596_seq1	NA	15 RING1_GOSHI^RING1_GOSHI^Q:682-1068,H:163-287^46.15%ID^E:1e-31^RecName: Full=E3 ubiquitin-protein ligase RING1
AR1_GAGATTCC-CCTATCCT_comp21983_seq0	NA	15 .
OL3_CGCTCATT-GGCTCTGA_comp62954_seq0	NA	15 ARFF_ORYSJ^ARFF_ORYSJ^Q:192-365,H:164-221^89.66%ID^E:3e-51^RecName: Full=Auxin response factor 6
YL1_CGCTCATT-TATAGCCT_comp2206_seq7	NA	15 WRK40_ARATH^WRK40_ARATH^Q:1321-1728,H:165-302^44.59%ID^E:1e-21^RecName: Full=Probable WRKY transcription factor 40
AR2_GAGATTCC-GGCTCTGA_comp656_seq7	NA	15 COBRA_ARATH^COBRA_ARATH^Q:469-1668,H:35-435^83.79%ID^E:0^RecName: Full=Protein COBRA
AR1_GAGATTCC-CCTATCCT_comp2897_seq1	NA	15 .
AR2_GAGATTCC-GGCTCTGA_comp630_seq3	CrERF5	15 ERF5_NICSY^ERF5_NICSY^Q:157-1017,H:1-282^46.28%ID^E:6e-47^RecName: Full=Ethylene-responsive transcription factor 5
YL1_CGCTCATT-TATAGCCT_comp1014_seq1	NA	16 QCR72_ARATH^QCR72_ARATH^Q:416-775,H:3-122^73.33%ID^E:2e-53^RecName: Full=Cytochrome b-c1 complex subunit 7-2
AR2_GAGATTCC-GGCTCTGA_comp36070_seq0	NA	16 VAP12_ARATH^VAP12_ARATH^Q:1450-2037,H:40-221^62.63%ID^E:1e-71^RecName: Full=Vesicle-associated protein 1-2
AR2_GAGATTCC-GGCTCTGA_comp10915_seq2	NA	16 .
AR1_GAGATTCC-CCTATCCT_comp4311_seq2	NA	16 .
YL1_CGCTCATT-TATAGCCT_comp32_seq1	GO	16 C7BL3_CICIN^C7BL3_CICIN^Q:361-1737,H:37-488^38.7%ID^E:9e-111^RecName: Full=Costunolide synthase
YS2_GAGATTCC-ATAGAGGC_comp7642_seq3	NA	16 HCS2_ARATH^HCS2_ARATH^Q:280-1245,H:9-329^65.02%ID^E:1e-143^RecName: Full=Biotin--protein ligase 2
OL1_CGCTCATT-CCTATCCT_comp6428_seq0	NA	16 M2K9_ARATH^M2K9_ARATH^Q:288-1262,H:1-308^60.43%ID^E:2e-114^RecName: Full=Mitogen-activated protein kinase kinase 9
YL1_CGCTCATT-TATAGCCT_comp32588_seq0	NA	16 .
OL3_CGCTCATT-GGCTCTGA_comp1418_seq0	T19H	17 C71A2_SOLME^C71A2_SOLME^Q:587-1945,H:46-503^50.33%ID^E:6e-151^RecName: Full=Cytochrome P450 71A2
OL3_CGCTCATT-GGCTCTGA_comp132_seq7	NA	17 FRO6_ARATH^FRO6_ARATH^Q:3030-4742,H:189-738^57.9%ID^E:0^RecName: Full=Ferric reduction oxidase 6
OL3_CGCTCATT-GGCTCTGA_comp15162_seq0	NA	17 .
YL1_CGCTCATT-TATAGCCT_comp12179_seq1	NA	17 BOR4_ARATH^BOR4_ARATH^Q:168-2138,H:6-669^69.66%ID^E:0^RecName: Full=Boron transporter 4
OL3_CGCTCATT-GGCTCTGA_comp7365_seq1	NA	17 RNHX1_ARATH^RNHX1_ARATH^Q:783-2540,H:1-584^25.62%ID^E:5e-41^RecName: Full=Putative ribonuclease H protein At1g65750
OL3_CGCTCATT-GGCTCTGA_comp1249_seq0	NA	17 .
OL1_CGCTCATT-CCTATCCT_comp119_seq1	NA	17 .
OL1_CGCTCATT-CCTATCCT_comp368_seq0	NA	18 METE_CATRO^METE_CATRO^Q:156-2450,H:1-765^95.16%ID^E:0^RecName: Full=5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
AR2_GAGATTCC-GGCTCTGA_comp3587_seq0	NA	18 IDH1_ARATH^IDH1_ARATH^Q:613-1503,H:67-367^87.71%ID^E:8e-171^RecName: Full=Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial
YL3_CGCTCATT-ATAGAGGC_comp5981_seq5	NA	18 APY2_ARATH^APY2_ARATH^Q:2126-2938,H:201-471^71.59%ID^E:1e-120^RecName: Full=Apyrase 2
YS2_GAGATTCC-ATAGAGGC_comp1097_seq5	NA	18 .
AR1_GAGATTCC-CCTATCCT_comp6659_seq0	NA	18 .
AR2_GAGATTCC-GGCTCTGA_comp7061_seq1	NA	18 PXL1_ARATH^PXL1_ARATH^Q:167-3247,H:1-1029^63.89%ID^E:0^RecName: Full=Leucine-rich repeat receptor-like protein kinase PXL1
YL1_CGCTCATT-TATAGCCT_comp13796_seq1	NA	18 S61G2_ARATH^S61G2_ARATH^Q:3-206,H:2-69^89.71%ID^E:9e-23^RecName: Full=Protein transport protein Sec61 subunit gamma-2
AR1_GAGATTCC-CCTATCCT_comp2488_seq0	NA	18 ACS_ARATH^ACS_ARATH^Q:1426-1989,H:540-727^87.77%ID^E:8e-94^RecName: Full=Acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal
AR2_GAGATTCC-GGCTCTGA_comp5665_seq0	ZCT2	18 PI3K_ARATH^PI3K_ARATH^Q:1-309,H:712-814^95.15%ID^E:4e-57^RecName: Full=Phosphatidylinositol 3-kinase VPS34
AR1_GAGATTCC-CCTATCCT_comp7698_seq2	NA	18 BIG1_ARATH^BIG1_ARATH^Q:1905-7001,H:2-1685^66.3%ID^E:0^RecName: Full=Brefeldin A-inhibited guanine nucleotide-exchange protein 1
AR1_GAGATTCC-CCTATCCT_comp2717_seq1	NA	18 TMCO1_RAT^TMCO1_RAT^Q:195-743,H:5-184^44.15%ID^E:5e-40^RecName: Full=Transmembrane and coiled-coil domains protein 1
YL3_CGCTCATT-ATAGAGGC_comp3830_seq1	NA	18 .
AR1_GAGATTCC-CCTATCCT_comp8039_seq0	GPPS	18 SPS3_ARATH^SPS3_ARATH^Q:300-1559,H:1-422^66.59%ID^E:0^RecName: Full=Solaneyl diphosphate synthase 3, chloroplastic/mitochondrial
AR1_GAGATTCC-CCTATCCT_comp17606_seq0	NA	18 .
YS2_GAGATTCC-ATAGAGGC_comp287_seq1	HDS	18 ISPG_ARATH^ISPG_ARATH^Q:239-2449,H:1-737^86.02%ID^E:0^RecName: Full=4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic
AR2_GAGATTCC-GGCTCTGA_comp1042_seq4	NA	18 .
AR1_GAGATTCC-CCTATCCT_comp1722_seq0	NA	18 THCAS_CANSA^THCAS_CANSA^Q:162-1625,H:46-540^45.96%ID^E:2e-130^RecName: Full=Tetrahydrocannabinolic acid synthase
OL3_CGCTCATT-GGCTCTGA_comp4392_seq1	NA	18 CYC_ABUTH^CYC_ABUTH^Q:140-472,H:1-111^94.59%ID^E:2e-70^RecName: Full=Cytochrome c
YL1_CGCTCATT-TATAGCCT_comp6904_seq2	NA	18 INVA_VICFA^INVA_VICFA^Q:6713-8377,H:71-630^70%ID^E:0^RecName: Full=Acid beta-fructofuranosidase

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YL3_CGCTCATT-ATAGAGGC_comp826_seq0	NA	18 14334_SOLLC^14334_SOLLC^Q:652-1428,H:4-260^79.15%ID^E:9e-140^RecName: Full=14-3-3 protein 4
YL3_CGCTCATT-ATAGAGGC_comp116_seq0	NA	18 RL9_PEA^RL9_PEA^Q:447-815,H:1-123^82.11%ID^E:7e-67^RecName: Full=60S ribosomal protein L9
YL3_CGCTCATT-ATAGAGGC_comp3473_seq0	NA	18 METK1_CATRO^METK1_CATRO^Q:99-1277,H:1-393^96.95%ID^E:0^RecName: Full=S-adenosylmethionine synthase 1
AR1_GAGATTCC-CCTATCCT_comp1014_seq2	NA	18 NOTUM_MOUSE^NOTUM_MOUSE^Q:2970-3719,H:106-368^29.7%ID^E:3e-23^RecName: Full=Palmitoleoyl-protein carboxylesterase NOTUM [ECO:0000250 UniProtKB:Q6P988]
YL3_CGCTCATT-ATAGAGGC_comp56582_seq0	NA	18 PKHA8_RAT^PKHA8_RAT^Q:531-965,H:327-471^34.93%ID^E:6e-21^RecName: Full=Pleckstrin homology domain-containing family A member 8
AR1_GAGATTCC-CCTATCCT_comp46_seq0	NA	18 SAHH_CATRO^SAHH_CATRO^Q:259-1713,H:1-485^94.85%ID^E:0^RecName: Full=Adenosylhomocysteinase
AR1_GAGATTCC-CCTATCCT_comp12098_seq0	NA	18 UBP1_ARATH^UBP1_ARATH^Q:934-1974,H:785-1083^40.17%ID^E:2e-56^RecName: Full=Ubiquitin carboxyl-terminal hydrolase 1
OL1_CGCTCATT-CCTATCCT_comp1720_seq1	NA	19 FLS_PETHY^FLS_PETHY^Q:113-1117,H:13-348^75%ID^E:2e-157^RecName: Full=Flavonol synthase/flavanone 3-hydroxylase
YS2_GAGATTCC-ATAGAGGC_comp9582_seq0	NA	19 HYES_HUMAN^HYES_HUMAN^Q:110-1027,H:237-544^33.02%ID^E:4e-36^RecName: Full=Bifunctional epoxide hydrolase 2
OL1_CGCTCATT-CCTATCCT_comp520_seq1	IO	19 C76A2_SOLME^C76A2_SOLME^Q:383-1777,H:43-503^50.97%ID^E:6e-168^RecName: Full=Cytochrome P450 76A2
YS1_GAGATTCC-TATAGCCT_comp5894_seq4	NA	19 PERK1_ARATH^PERK1_ARATH^Q:1022-2218,H:252-651^79.25%ID^E:0^RecName: Full=Proline-rich receptor-like protein kinase PERK1
AR1_GAGATTCC-CCTATCCT_comp37384_seq0	NA	19 .
YL1_CGCTCATT-TATAGCCT_comp24385_seq0	NA	19 TRBP2_ARATH^TRBP2_ARATH^Q:3-227,H:165-239^98.67%ID^E:2e-39^RecName: Full=Tryptophan synthase beta chain 2, chloroplastic
YL3_CGCTCATT-ATAGAGGC_comp17087_seq0	NA	19 .
YS2_GAGATTCC-ATAGAGGC_comp5954_seq0	NA	20 E70B1_ARATH^E70B1_ARATH^Q:239-2152,H:1-620^64.75%ID^E:0^RecName: Full=Exocyst complex component EXO70B1
YL3_CGCTCATT-ATAGAGGC_comp11008_seq1	NA	20 .
OL3_CGCTCATT-GGCTCTGA_comp13259_seq1	NA	20 CLPX_SPHWW^CLPX_SPHWW^Q:642-1646,H:65-404^54.55%ID^E:4e-118^RecName: Full=ATP-dependent Clp protease ATP-binding subunit ClpX [ECO:0000255 HAMAP-Rule:MF_00175]
YL3_CGCTCATT-ATAGAGGC_comp32910_seq0	NA	20 .
YS2_GAGATTCC-ATAGAGGC_comp6479_seq1	NA	20 ADT1_GOSHI^ADT1_GOSHI^Q:155-1318,H:1-386^83.76%ID^E:0^RecName: Full=ADP,ATP carrier protein 1, mitochondrial
AR1_GAGATTCC-CCTATCCT_comp3108_seq0	T3R	20 10HGO_CATRO^10HGO_CATRO^Q:164-1228,H:2-360^63.51%ID^E:1e-145^RecName: Full=8-hydroxygeraniol dehydrogenase
OL1_CGCTCATT-CCTATCCT_comp209_seq10	NA	20 .
YS1_GAGATTCC-TATAGCCT_comp6840_seq0	NA	20 .
YL3_CGCTCATT-ATAGAGGC_comp30598_seq0	NA	20 .
AR2_GAGATTCC-GGCTCTGA_comp29260_seq0	NA	21 .
AR1_GAGATTCC-CCTATCCT_comp14477_seq0	ORCA3	21 ERF99_ARATH^ERF99_ARATH^Q:401-604,H:70-136^72.06%ID^E:6e-25^RecName: Full=Ethylene-responsive transcription factor 13
AR1_GAGATTCC-CCTATCCT_comp6627_seq1	NA	21 .
AR1_GAGATTCC-CCTATCCT_comp18379_seq1	NA	21 .
AR1_GAGATTCC-CCTATCCT_comp2945_seq0	NA	21 RA51B_ARATH^RA51B_ARATH^Q:6971-8011,H:26-370^66.57%ID^E:4e-122^RecName: Full=DNA repair protein RAD51 homolog 2
YS2_GAGATTCC-ATAGAGGC_comp9578_seq1	NA	21 Y4374_ARATH^Y4374_ARATH^Q:320-2167,H:18-635^56.05%ID^E:0^RecName: Full=Probable inactive receptor kinase At4g23740
OL3_CGCTCATT-GGCTCTGA_comp25748_seq0	NA	22 .
YS1_GAGATTCC-TATAGCCT_comp40843_seq0	NA	22 .
YS1_GAGATTCC-TATAGCCT_comp8051_seq0	NA	22 .
OL3_CGCTCATT-GGCTCTGA_comp21659_seq0	NA	22 .
AR2_GAGATTCC-GGCTCTGA_comp12782_seq0	NA	22 .
OL3_CGCTCATT-GGCTCTGA_comp34622_seq0	NA	22 .
OL3_CGCTCATT-GGCTCTGA_comp2285_seq1	NPF2.1	22 PTR21_ARATH^PTR21_ARATH^Q:684-2408,H:44-609^54.43%ID^E:0^RecName: Full=Protein NRT1/ PTR FAMILY 2.13
YS1_GAGATTCC-TATAGCCT_comp64350_seq0	NA	22 .
YL1_CGCTCATT-TATAGCCT_comp16103_seq0	NA	22 PEX13_ARATH^PEX13_ARATH^Q:451-735,H:202-304^66.02%ID^E:1e-27^RecName: Full=Peroxisomal membrane protein 13
YS2_GAGATTCC-ATAGAGGC_comp11235_seq0	NA	23 CX32_ARATH^CX32_ARATH^Q:640-1569,H:63-369^69.03%ID^E:2e-150^RecName: Full=Probable serine/threonine-protein kinase Cx32, chloroplastic
OL3_CGCTCATT-GGCTCTGA_comp18596_seq0	NA	23 .
OL1_CGCTCATT-CCTATCCT_comp22262_seq0	NA	23 BPS1_ARATH^BPS1_ARATH^Q:994-1986,H:1-326^56.12%ID^E:4e-123^RecName: Full=Protein BPS1, chloroplastic
OL3_CGCTCATT-GGCTCTGA_comp2267_seq1	VmTPT2	23 AB32G_ARATH^AB32G_ARATH^Q:1321-5580,H:1-1418^70.34%ID^E:0^RecName: Full=ABC transporter G family member 32 [ECO:0000303 PubMed:18299247]
YL1_CGCTCATT-TATAGCCT_comp12043_seq2	NA	23 BCS1_SCHPO^BCS1_SCHPO^Q:1059-1733,H:195-423^29.05%ID^E:1e-24^RecName: Full=Probable mitochondrial chaperone bcs1
OL1_CGCTCATT-CCTATCCT_comp671_seq2	NA	23 SEC8_ARATH^SEC8_ARATH^Q:2372-5161,H:143-1053^68.17%ID^E:0^RecName: Full=Exocyst complex component SEC8

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OL1_CGCTCATT-CCTATCCT_comp13536_seq1	NA	23 .
YS1_GAGATTCC-TATAGCCT_comp17664_seq1	NA	23 P2C51_ARATH^P2C51_ARATH^Q:134-1405,H:30-447^54.55%ID^E:1e-139^RecName: Full=Probable protein phosphatase 2C 51
OL3_CGCTCATT-GGCTCTGA_comp2330_seq3	NA	24 .
YL3_CGCTCATT-ATAGAGGC_comp15500_seq0	NA	24 Y1680_ARATH^Y1680_ARATH^Q:2339-4210,H:30-648^42.17%ID^E:9e-86^RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At1g68400
YL1_CGCTCATT-TATAGCCT_comp8450_seq0	NA	24 YERG_SCHPO^YERG_SCHPO^Q:37-378,H:204-320^42.74%ID^E:8e-23^RecName: Full=Uncharacterized RING finger protein C2F3.16
YS1_GAGATTCC-TATAGCCT_comp15900_seq1	NA	24 SIGD_ARATH^SIGD_ARATH^Q:957-1427,H:258-414^54.78%ID^E:9e-82^RecName: Full=RNA polymerase sigma factor sigD, chloroplastic
OL3_CGCTCATT-GGCTCTGA_comp3385_seq1	NA	24 .
YS2_GAGATTCC-ATAGAGGC_comp1361_seq4	NA	24 CYB5E_ARATH^CYB5E_ARATH^Q:2054-2449,H:2-133^81.82%ID^E:2e-70^RecName: Full=Cytochrome b5 isoform E {ECO:0000303 PubMed:19054355}
OL3_CGCTCATT-GGCTCTGA_comp8789_seq0	NPF2.4	24 PTR53_ARATH^PTR53_ARATH^Q:121-1830,H:27-597^57.62%ID^E:0^RecName: Full=Protein NRT1/ PTR FAMILY 2.11
OL3_CGCTCATT-GGCTCTGA_comp35783_seq0	NA	24 .
OL3_CGCTCATT-GGCTCTGA_comp19373_seq0	NA	24 .
AR2_GAGATTCC-GGCTCTGA_comp2182_seq0	NA	25 XCP1_ARATH^XCP1_ARATH^Q:155-1150,H:26-353^72.59%ID^E:0^RecName: Full=Xylem cysteine proteinase 1
YS1_GAGATTCC-TATAGCCT_comp17355_seq0	NA	25 .
YL3_CGCTCATT-ATAGAGGC_comp25012_seq1	NA	25 CSLCC_ARATH^CSLCC_ARATH^Q:1254-3374,H:1-699^78.22%ID^E:0^RecName: Full=Probable xyloglucan glycosyltransferase 12
YS2_GAGATTCC-ATAGAGGC_comp3345_seq1	MATE2	25 ALIS3_ARATH^ALIS3_ARATH^Q:2756-3742,H:22-349^75.99%ID^E:8e-171^RecName: Full=ALA-interacting subunit 3
AR2_GAGATTCC-GGCTCTGA_comp901_seq0	NA	25 .
AR1_GAGATTCC-CCTATCCT_comp2521_seq4	NA	25 UPL3_ARATH^UPL3_ARATH^Q:848-6109,H:151-1888^71.65%ID^E:0^RecName: Full=E3 ubiquitin-protein ligase UPL3
YS1_GAGATTCC-TATAGCCT_comp1496_seq2	CMK	26 ISPE_SOLLC^ISPE_SOLLC^Q:362-1471,H:31-399^75.95%ID^E:2e-175^RecName: Full=4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic
AR2_GAGATTCC-GGCTCTGA_comp7989_seq1	NA	26 .
AR1_GAGATTCC-CCTATCCT_comp4372_seq0	NA	26 .
YS2_GAGATTCC-ATAGAGGC_comp147_seq0	NA	26 RS33_ARATH^RS33_ARATH^Q:169-834,H:1-222^87.84%ID^E:3e-142^RecName: Full=40S ribosomal protein S3-3
YL1_CGCTCATT-TATAGCCT_comp29003_seq0	NA	26 .
AR1_GAGATTCC-CCTATCCT_comp1690_seq3	NA	26 PMT2_ARATH^PMT2_ARATH^Q:374-2215,H:1-616^76.45%ID^E:0^RecName: Full=Probable methyltransferase PMT2
YS2_GAGATTCC-ATAGAGGC_comp21925_seq0	NA	26 .
AR1_GAGATTCC-CCTATCCT_comp3686_seq1	NA	27 .
AR1_GAGATTCC-CCTATCCT_comp15754_seq0	NA	27 .
AR1_GAGATTCC-CCTATCCT_comp10689_seq2	DAT	27 DAT_CATRO^DAT_CATRO^Q:1-1251,H:5-437^54.71%ID^E:5e-150^RecName: Full=Deacetylvinidoline O-acetyltransferase
AR2_GAGATTCC-GGCTCTGA_comp216_seq0	NA	27 .
AR2_GAGATTCC-GGCTCTGA_comp22743_seq0	NA	27 .
OL3_CGCTCATT-GGCTCTGA_comp5631_seq2	GBF2	28 HBP1A_WHEAT^HBP1A_WHEAT^Q:439-1467,H:18-319^45.3%ID^E:4e-54^RecName: Full=Transcription factor HBP-1a
AR2_GAGATTCC-GGCTCTGA_comp2924_seq0	NA	28 .
AR1_GAGATTCC-CCTATCCT_comp4693_seq1	NA	28 .
YL3_CGCTCATT-ATAGAGGC_comp15371_seq1	NA	28 RDR5_ARATH^RDR5_ARATH^Q:546-3176,H:114-975^48.45%ID^E:0^RecName: Full=Probable RNA-dependent RNA polymerase 5
YL3_CGCTCATT-ATAGAGGC_comp4673_seq1	NA	28 NSA2_HUMAN^NSA2_HUMAN^Q:2-265,H:149-236^78.41%ID^E:1e-42^RecName: Full=Ribosome biogenesis protein NSA2 homolog
AR2_GAGATTCC-GGCTCTGA_comp9703_seq0	NA	28 INVB_DAUCA^INVB_DAUCA^Q:1146-3059,H:4-656^67.48%ID^E:0^RecName: Full=Beta-fructofuranosidase, soluble isoenzyme I
YS2_GAGATTCC-ATAGAGGC_comp6465_seq1	NA	29 Y283_BACHD^Y283_BACHD^Q:829-1725,H:1-265^39.33%ID^E:1e-58^RecName: Full=Uncharacterized isomerase BH0283
YL3_CGCTCATT-ATAGAGGC_comp37282_seq0	NA	29 .
AR1_GAGATTCC-CCTATCCT_comp12730_seq0	NA	29 .
YL3_CGCTCATT-ATAGAGGC_comp1199_seq2	NA	29 GSTX4_TOBAC^GSTX4_TOBAC^Q:401-1045,H:5-220^68.52%ID^E:6e-101^RecName: Full=Probable glutathione S-transferase
YL3_CGCTCATT-ATAGAGGC_comp3815_seq0	NA	29 CSK2C_ARATH^CSK2C_ARATH^Q:57-521,H:96-250^80%ID^E:2e-89^RecName: Full=Casein kinase II subunit beta'
YS2_GAGATTCC-ATAGAGGC_comp88_seq3	LAMT	29 MT878_ARATH^MT878_ARATH^Q:389-1450,H:3-361^41.1%ID^E:4e-79^RecName: Full=Probable S-adenosylmethionine-dependent methyltransferase At5g38780
YS1_GAGATTCC-TATAGCCT_comp3264_seq4	NA	29 LOR12_ARATH^LOR12_ARATH^Q:1818-2432,H:9-205^50%ID^E:5e-54^RecName: Full=Protein LURP-one-related 12
AR2_GAGATTCC-GGCTCTGA_comp32417_seq0	NA	29 .
AR1_GAGATTCC-CCTATCCT_comp19025_seq0	NA	29 C2D61_ARATH^C2D61_ARATH^Q:2-235,H:285-362^79.49%ID^E:4e-34^RecName: Full=C2 domain-containing protein At1g53590

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AR1_GAGATTCC-CCTATCCT_comp4621_seq0	NA	29 BB_ARATH^BB_ARATH^Q:1423-1734,H:138-241^66.67%ID^E:5e-39^RecName: Full=E3 ubiquitin ligase BIG BROTHER
AR1_GAGATTCC-CCTATCCT_comp2309_seq1	NA	29 HHP2_ARATH^HHP2_ARATH^Q:519-1337,H:75-356^60.07%ID^E:4e-79^RecName: Full=Heptahelical transmembrane protein 2
YS1_GAGATTCC-TATAGCCT_comp9272_seq0	NA	29 KPYC_SOLTU^KPYC_SOLTU^Q:840-1322,H:347-506^41.61%ID^E:6e-31^RecName: Full=Pyruvate kinase, cytosolic isozyme
YS1_GAGATTCC-TATAGCCT_comp439_seq2	HDR	30 ISPH_ARATH^ISPH_ARATH^Q:147-1547,H:1-466^78.09%ID^E:0^RecName: Full=4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic
OL1_CGCTCATT-CCTATCCT_comp161_seq5	NA	30 FRO7_ARATH^FRO7_ARATH^Q:3155-5278,H:32-747^59.58%ID^E:0^RecName: Full=Ferric reduction oxidase 7, chloroplastic
OL1_CGCTCATT-CCTATCCT_comp991_seq7	NA	30 .
OL1_CGCTCATT-CCTATCCT_comp5868_seq2	NA	30 MOC2B_ARATH^MOC2B_ARATH^Q:1951-2445,H:18-183^66.87%ID^E:7e-57^RecName: Full=Molybdopterin synthase catalytic subunit {ECO:0000255 HAMAP-Rule:MF_03052}
YS2_GAGATTCC-ATAGAGGC_comp6690_seq0	NA	30 PERR_RAUSE^PERR_RAUSE^Q:232-1107,H:1-289^74.66%ID^E:2e-154^RecName: Full=Perakine reductase
OL1_CGCTCATT-CCTATCCT_comp9509_seq1	NA	30 Y4885_ARATH^Y4885_ARATH^Q:309-2498,H:312-1041^42.57%ID^E:2e-172^RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g08850
YL1_CGCTCATT-TATAGCCT_comp615_seq1	NA	30 STR4_ARATH^STR4_ARATH^Q:734-1729,H:1-321^62.46%ID^E:5e-87^RecName: Full=Rhodanese-like domain-containing protein 4, chloroplastic
YS2_GAGATTCC-ATAGAGGC_comp9283_seq0	NA	30 Y1480_ARATH^Y1480_ARATH^Q:312-1265,H:55-357^39.69%ID^E:3e-59^RecName: Full=Uncharacterized protein At1g18480
YL1_CGCTCATT-TATAGCCT_comp4903_seq0	NA	30 NIFU1_ARATH^NIFU1_ARATH^Q:212-703,H:66-230^79.39%ID^E:3e-63^RecName: Full=NifU-like protein 1, chloroplastic
OL1_CGCTCATT-CCTATCCT_comp7103_seq2	NA	30 RH41_ARATH^RH41_ARATH^Q:768-2225,H:12-490^59.8%ID^E:0^RecName: Full=DEAD-box ATP-dependent RNA helicase 41
YL3_CGCTCATT-ATAGAGGC_comp1376_seq3	NA	30 RVE8_ARATH^RVE8_ARATH^Q:203-565,H:31-151^82.64%ID^E:6e-47^RecName: Full=Protein REVEILLE 8
YL1_CGCTCATT-TATAGCCT_comp3675_seq3	NA	30 SIGE_ARATH^SIGE_ARATH^Q:721-2280,H:1-516^62.93%ID^E:0^RecName: Full=RNA polymerase sigma factor sigE, chloroplastic/mitochondrial
YL1_CGCTCATT-TATAGCCT_comp12033_seq1	NA	31 C90A1_ARATH^C90A1_ARATH^Q:285-1586,H:41-468^75.86%ID^E:0^RecName: Full=Cytochrome P450 90A1
YS2_GAGATTCC-ATAGAGGC_comp2127_seq1	DXS1	31 PWD_ARATH^PWD_ARATH^Q:2912-6307,H:48-1196^63.9%ID^E:0^RecName: Full=Phosphoglucan, water dikinase, chloroplastic
YL3_CGCTCATT-ATAGAGGC_comp4506_seq1	NA	31 .
YS2_GAGATTCC-ATAGAGGC_comp11659_seq0	NA	31 .
YS2_GAGATTCC-ATAGAGGC_comp8026_seq0	NA	31 .
YL1_CGCTCATT-TATAGCCT_comp11163_seq2	NA	31 .
YL3_CGCTCATT-ATAGAGGC_comp38593_seq0	NA	31 SYE_ARATH^SYE_ARATH^Q:709-1746,H:223-568^76.37%ID^E:0^.
AR2_GAGATTCC-GGCTCTGA_comp894_seq1	NA	32 .
AR1_GAGATTCC-CCTATCCT_comp8273_seq2	NA	32 S38A7_DANRE^S38A7_DANRE^Q:251-1336,H:56-409^25.33%ID^E:2e-25^RecName: Full=Putative sodium-coupled neutral amino acid transporter 7
YS1_GAGATTCC-TATAGCCT_comp13751_seq2	TS	32 LAX3_MEDTR^LAX3_MEDTR^Q:2-1273,H:42-465^89.15%ID^E:0^RecName: Full=Auxin transporter-like protein 3
AR2_GAGATTCC-GGCTCTGA_comp3252_seq1	NA	32 CTR1_ARATH^CTR1_ARATH^Q:2705-3418,H:562-805^49.59%ID^E:2e-69^RecName: Full=Serine/threonine-protein kinase CTR1 {ECO:0000303 PubMed:8431946}
YS2_GAGATTCC-ATAGAGGC_comp2275_seq1	NA	32 PPME1_MOUSE^PPME1_MOUSE^Q:263-1162,H:13-372^43.61%ID^E:2e-93^RecName: Full=Protein phosphatase methylesterase 1
YL1_CGCTCATT-TATAGCCT_comp13794_seq0	NA	33 .
YS1_GAGATTCC-TATAGCCT_comp3725_seq0	GBF1	33 CPRF1_PETCR^CPRF1_PETCR^Q:479-1702,H:1-406^54.33%ID^E:8e-136^RecName: Full=Common plant regulatory factor 1
YS1_GAGATTCC-TATAGCCT_comp19403_seq0	NA	33 .
YS1_GAGATTCC-TATAGCCT_comp15574_seq0	NA	33 CFI_CAMSI^CFI_CAMSI^Q:122-673,H:37-219^70.65%ID^E:2e-89^RecName: Full=Chalcone--flavonone isomerase
YL1_CGCTCATT-TATAGCCT_comp11427_seq0	NA	33 DCP1_ARATH^DCP1_ARATH^Q:257-907,H:1-211^77.52%ID^E:2e-108^RecName: Full=mRNA-decapping enzyme-like protein
AR2_GAGATTCC-GGCTCTGA_comp24852_seq0	NA	34 .
AR1_GAGATTCC-CCTATCCT_comp13415_seq0	NA	34 HFA6B_ARATH^HFA6B_ARATH^Q:459-1457,H:47-402^50.68%ID^E:5e-106^RecName: Full=Heat stress transcription factor A-6b
AR1_GAGATTCC-CCTATCCT_comp31298_seq0	NA	34 .
AR1_GAGATTCC-CCTATCCT_comp42375_seq0	NA	34 .
AR1_GAGATTCC-CCTATCCT_comp25166_seq0	NA	34 .
AR1_GAGATTCC-CCTATCCT_comp821_seq3	NA	34 PER5_VITVI^PER5_VITVI^Q:296-1213,H:26-328^55.56%ID^E:8e-105^RecName: Full=Peroxidase 5 {ECO:0000250 UniProtKB:P22195}
AR2_GAGATTCC-GGCTCTGA_comp15931_seq0	NA	34 PHT17_ORYSJ^PHT17_ORYSJ^Q:3-218,H:211-284^67.57%ID^E:9e-24^RecName: Full=Probable inorganic phosphate transporter 1-7
AR2_GAGATTCC-GGCTCTGA_comp370_seq0	NA	34 14KD_DAUCA^14KD_DAUCA^Q:321-569,H:54-136^67.47%ID^E:2e-28^RecName: Full=14 kDa proline-rich protein DC2.15
YL3_CGCTCATT-ATAGAGGC_comp101_seq3	redox2	34 MER_ERYCB^MER_ERYCB^Q:148-1101,H:4-327^54.77%ID^E:6e-114^RecName: Full=Methylecgonone reductase
AR1_GAGATTCC-CCTATCCT_comp1106_seq0	NA	34 CERK1_ARATH^CERK1_ARATH^Q:244-2034,H:22-617^59.74%ID^E:0^RecName: Full=Chitin elicitor receptor kinase 1
AR2_GAGATTCC-GGCTCTGA_comp12553_seq0	NA	34 LORF2_MOUSE^LORF2_MOUSE^Q:1716-3227,H:397-895^27.41%ID^E:2e-42^RecName: Full=LINE-1 retrotransposable element ORF2 protein
AR1_GAGATTCC-CCTATCCT_comp16225_seq0	NA	34 ACCH1_ARATH^ACCH1_ARATH^Q:118-960,H:12-288^50.18%ID^E:4e-73^RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1

TableS2

AR1_GAGATTCC-CCTATCCT_comp30027_seq0	NA	34 .
AR2_GAGATTCC-GGCTCTGA_comp22761_seq0	NA	34 .
YL3_CGCTCATT-ATAGAGGC_comp5165_seq0	NA	35 Y5102_ARATH^Y5102_ARATH^Q:1752-3065,H:1-410^75.8%ID^E:0^RecName: Full=Serine/threonine-protein kinase At5g01020
OL1_CGCTCATT-CCTATCCT_comp374_seq0	GS1	35 MTDH_FRAAN^MTDH_FRAAN^Q:212-1258,H:10-356^57.02%ID^E:1e-115^RecName: Full=Probable mannitol dehydrogenase
AR2_GAGATTCC-GGCTCTGA_comp10111_seq1	NA	35 PYRD2_RAT^PYRD2_RAT^Q:122-1753,H:34-581^51.72%ID^E:0^RecName: Full=Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2
AR1_GAGATTCC-CCTATCCT_comp696_seq16	NA	35 BGH3B_BACO1^BGH3B_BACO1^Q:1249-2835,H:107-658^31.05%ID^E:4e-72^RecName: Full=Beta-glucosidase BoGH3B
YS2_GAGATTCC-ATAGAGGC_comp6183_seq2	NA	35 YIF1B_MOUSE^YIF1B_MOUSE^Q:488-1138,H:83-305^32.61%ID^E:5e-28^RecName: Full=Protein YIF1B
YL1_CGCTCATT-TATAGCCT_comp10608_seq0	NA	35 SFT2B_HUMAN^SFT2B_HUMAN^Q:233-616,H:27-158^39.39%ID^E:4e-23^RecName: Full=Vesicle transport protein SFT2B
AR1_GAGATTCC-CCTATCCT_comp977_seq0	NA	35 SF3BA_ARATH^SF3BA_ARATH^Q:186-446,H:1-87^94.25%ID^E:8e-51^RecName: Full=Uncharacterized protein At3g23325
AR1_GAGATTCC-CCTATCCT_comp6_seq2	NA	36 .
AR1_GAGATTCC-CCTATCCT_comp24292_seq0	CrWRKY1	36 WRK70_ARATH^WRK70_ARATH^Q:551-766,H:109-180^62.5%ID^E:2e-21^RecName: Full=Probable WRKY transcription factor 70
AR1_GAGATTCC-CCTATCCT_comp3465_seq0	NA	36 Y3272_ARATH^Y3272_ARATH^Q:414-1277,H:85-371^69.79%ID^E:4e-151^RecName: Full=Kelch repeat-containing protein At3g27220
AR1_GAGATTCC-CCTATCCT_comp572_seq0	NA	36 .
AR2_GAGATTCC-GGCTCTGA_comp1660_seq1	BIS2	37 BH093_ARATH^BH093_ARATH^Q:717-1313,H:146-351^66.02%ID^E:2e-66^RecName: Full=Transcription factor bHLH93
YS2_GAGATTCC-ATAGAGGC_comp11524_seq0	NA	37 FBK9_ARATH^FBK9_ARATH^Q:114-1199,H:15-383^41.98%ID^E:4e-74^RecName: Full=F-box/kelch-repeat protein At1g23390
OL3_CGCTCATT-GGCTCTGA_comp23128_seq0	NA	37 .
OL3_CGCTCATT-GGCTCTGA_comp28247_seq0	NA	37 .
OL3_CGCTCATT-GGCTCTGA_comp55923_seq0	NA	37 .
OL3_CGCTCATT-GGCTCTGA_comp21836_seq0	NA	37 .
AR1_GAGATTCC-CCTATCCT_comp8890_seq1	NA	38 AGL8_SOLTU^AGL8_SOLTU^Q:160-879,H:1-250^68.9%ID^E:2e-113^RecName: Full=Agamous-like MADS-box protein AGL8 homolog
AR1_GAGATTCC-CCTATCCT_comp12530_seq0	D4H	38 DV4H_CATRO^DV4H_CATRO^Q:56-1183,H:24-400^67.72%ID^E:0^RecName: Full=Deacetoxyvindoline 4-hydroxylase
AR1_GAGATTCC-CCTATCCT_comp13728_seq0	NA	38 .
AR2_GAGATTCC-GGCTCTGA_comp26468_seq0	NA	39 .
AR1_GAGATTCC-CCTATCCT_comp18788_seq0	MATE1	39 TT12_ARATH^TT12_ARATH^Q:204-1712,H:3-492^47.34%ID^E:5e-141^.

Table S3

Primers	Sequence (5' - 3')	Application
vm16OMT1like-for vm16OMT1like-rev yYS1_comp1836_seq0-for yYS1_comp1836_seq0-rev	CTGAGAAGATCTATGGATGCGAAAGTGGATGAGTTAG CTGAGAAGATCTTTAAGGATAAACCTCAATGACACTTCTAATG CTGAGAGGATCCATGGATCTTGAAGCTTCTGAGATTCGT CTGAGAGGATCCAGGATATACCTCAATAGGACACCTGAAATCTA	Heterologous expression of tabersonine 16-O-methyltransferase candidates in yeast
vm16OMTYFP-for vm16OMTYFP-rev	CTGAGAAGTATGATGGATGCGAAAGTGGATGAGTTAG CTGAGAAGTATGATGGATGCGAAAGTGGATGAGTTAG	Subcellular localization studies
qVmActin-for qVmActin-rev qVm16OMT-for - (YS2_comp61_seq0) qVm16OMT-rev - (YS2_comp61_seq0) qVmYL1_comp255_seq0-for qVmYL1_comp255_seq0-rev qVmOL3_comp1418_seq0-for qVmOL3_comp1418_seq0-rev qVmOL3_comp1489_seq0-for qVmOL3_comp1489_seq0-rev qVmAR1_comp3108_seq0-for qVmAR1_comp3108_seq0-rev qVmYS2_comp528_seq2-for qVmYS2_comp528_seq2-rev	GGAGCTGAGAGATCCGTTG GAATTCCTGCAGCTTCCATC CAGTTATCTATGGACATGGGCATGA TTAGAAATTGAATTAGTACATTGTCCCT CTACTACACTTCCTCTTAAGAGACGT ACTTTGGGGCAAAATATATCCACTAA TGTAGAAGTGCATTGGCAAAATTTGAT TCGTCTCGTTTGTGTTCCACTAT GATATGACAGAGAAATTTGGGTTGACA ACGCTTTCGCCTGGAATAATAAGTG CAGAACACAATATAGTTGCAGACGTT ACATAGGAACACTCTAAAATCTGCAT TTCCATTTGATGGAAACTTTATGGT AGGCATGTGCAAAATGTGCAATCC	qPCR analysis