Global human frequencies of predicted nuclear pathogenic variants and the role played by protein hydrophobicity in pathogenicity potential

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Results

1- Correlations for the averages of MutPred and hydrophobicity values per protein

We checked the correlations for the averages of MutPred and hydrophobicity values per protein both in mtDNA and nDNA coded proteins (Figures S1-S7). The values of r2 were: 0.177 (positive correlation) with all proteins together; 0.085 (negative correlation) for mtDNA; 0.088 (positive) for nDNA; 0.433 (negative) for mtDNA without ATP8; 0.132 for nDNA (positive) without values of hydrophobicity higher than 0.377; 0.797 (negative) for nDNA highly hydrophobic; and 0.010 (slightly negative) for nDNA and mtDNA highly hydrophobic.

It seems that there is a tendency for a positive correlation between MutPred and hydrophobicity when values of the hydrophobicity are not extremely high, and then an inversion in the tendency. As the number of proteins in this upper extreme of the hydrophobicity scale is low (the 12 mtDNA and five nDNA – ATP5G1, ATP5G2, ATP5G3, SDHC and SDHD), this inversion must be taken with caution. Especially so because even for the low hydrophobic range of the dataset, the variation of values is very high, rendering the correlation to be low.

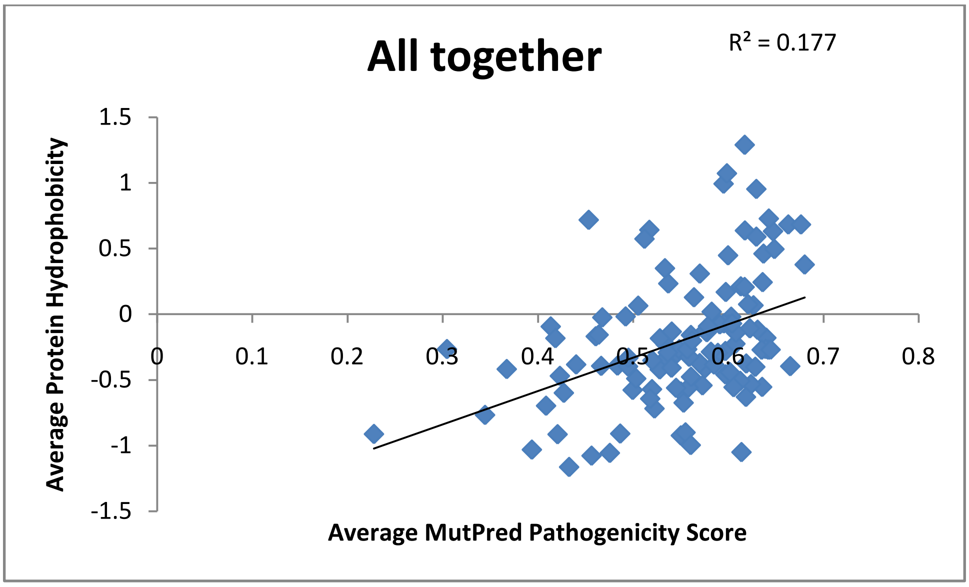

Figure S1. Correlation for the averages of MutPred and hydrophobicity values per protein in nDNA and mtDNA coded proteins.

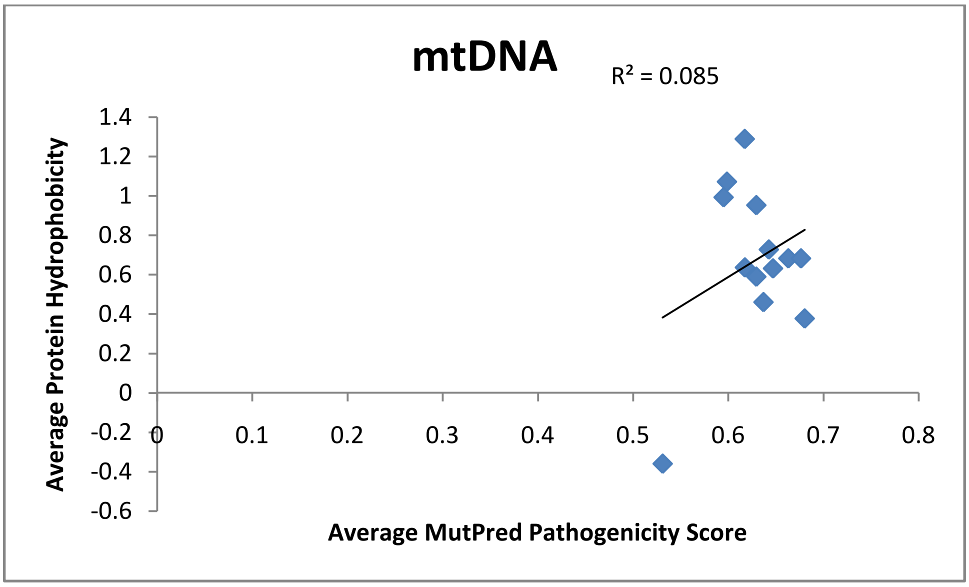

Figure S2. Correlation for the averages of MutPred and hydrophobicity values per protein in mtDNA coded proteins.

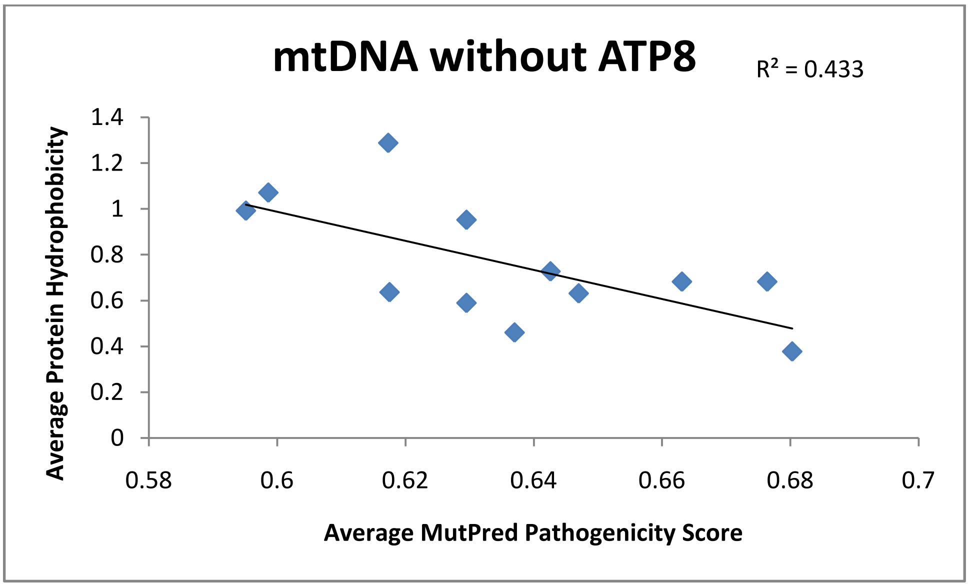

Figure S3. Correlation for the averages of MutPred and hydrophobicity values per protein in mtDNA coded proteins except ATP8.

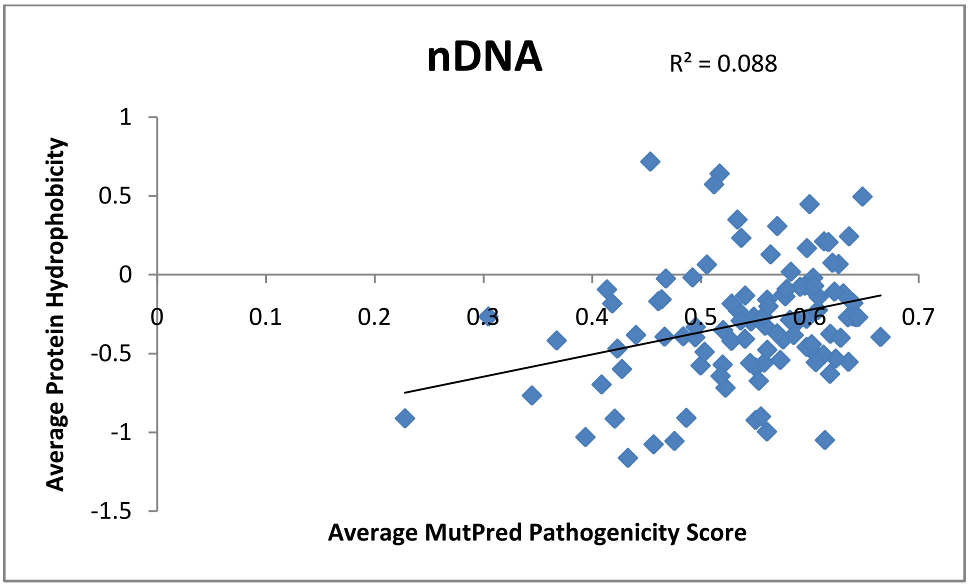

Figure S4. Correlation for the averages of MutPred and hydrophobicity values per protein in nDNA coded proteins.

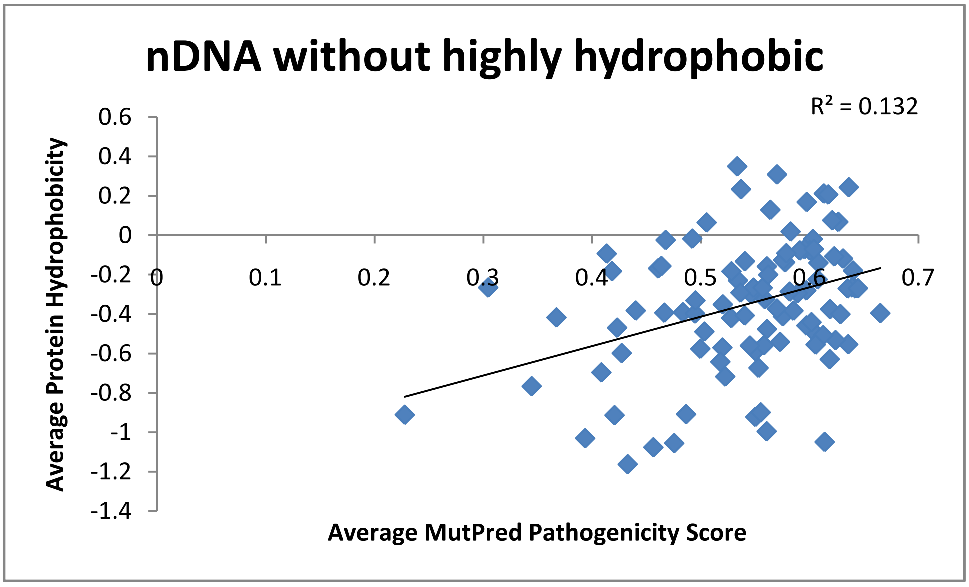

Figure S5. Correlation for the averages of MutPred and hydrophobicity values per protein in nDNA coded proteins without highly hydrophobic.

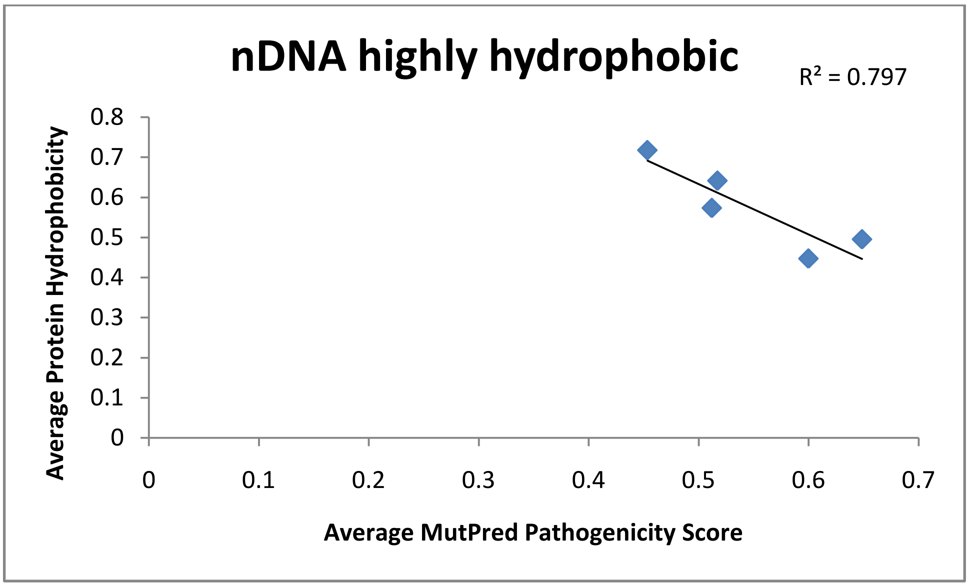

Figure S6. Correlation for the averages of MutPred and hydrophobicity values per protein in highly hydrophobic nDNA coded proteins.

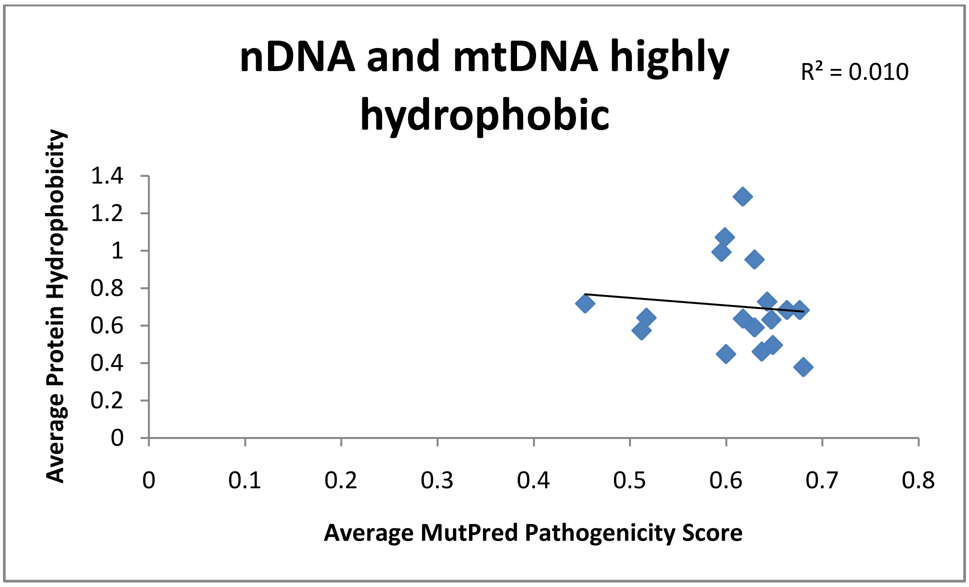

Figure S7. Correlation for the averages of MutPred and hydrophobicity values per protein in highly hydrophobic nDNA and mtDNA coded proteins.

2- Comparison between pathogenicity predictors

We compared results from MutPred, PolyPhen and SIFT scores in the observed dataset of non-synonymous mutations, in order to ascertain about its concordance. As can be seen in Figures S8 and S9, there is a good correlation between MutPred and the other two pathogenecity scores, especially so with SIFT. The bigger discrepancies are for the way mutations occurring in the first codon of the proteins are interpreted, being considered deleterious in MutPred and SIFT and benign in Polyphen.

But as even so, for some SNVs there are discrepancies between the predictors, in the comparison between the distributions of potential pathogenic SNVs in these nuclear genes across global human populations, for which we wanted to be conservative, we decided for a major vote between the three classifiers, MutPred, SIFT and PolyPhen (reported in Table S2).

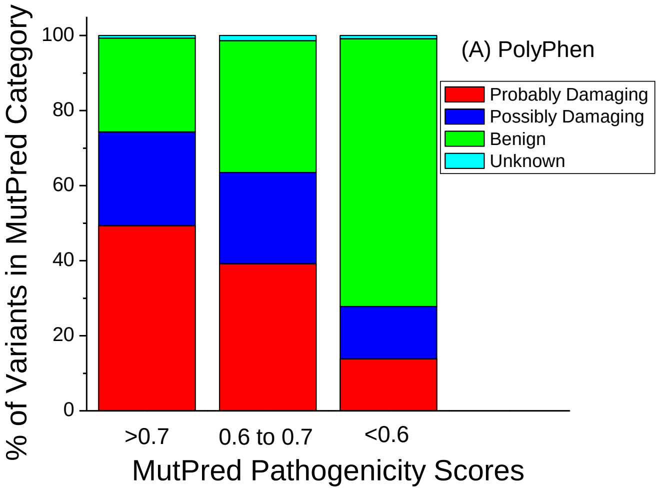

Figure S8. Comparison between MutPred and PolyPhen pathogenicity scores.

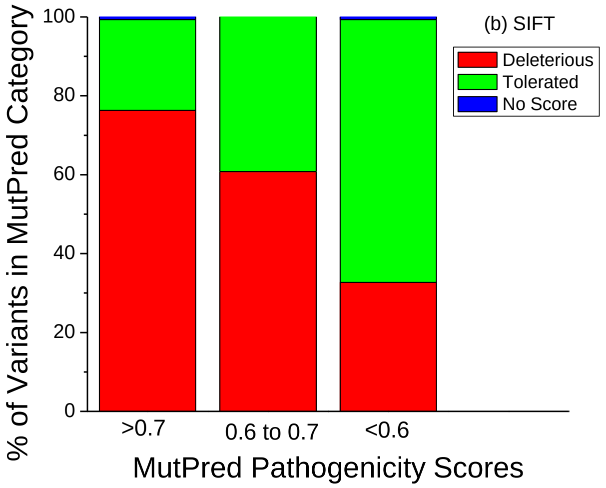

Figure S9. Comparison between MutPred and SIFT pathogenicity scores.

We also ascertained if the MutPred prediction for all theoretical values in the nDNA and mtDNA coded proteins is correlated (R^2=0.143) with the values predicted by SIFT (Figure S10). Of course the correlation is negative, as in MutPred the highest pathogenic values are close to 1, while in SIFT are closer to 0.

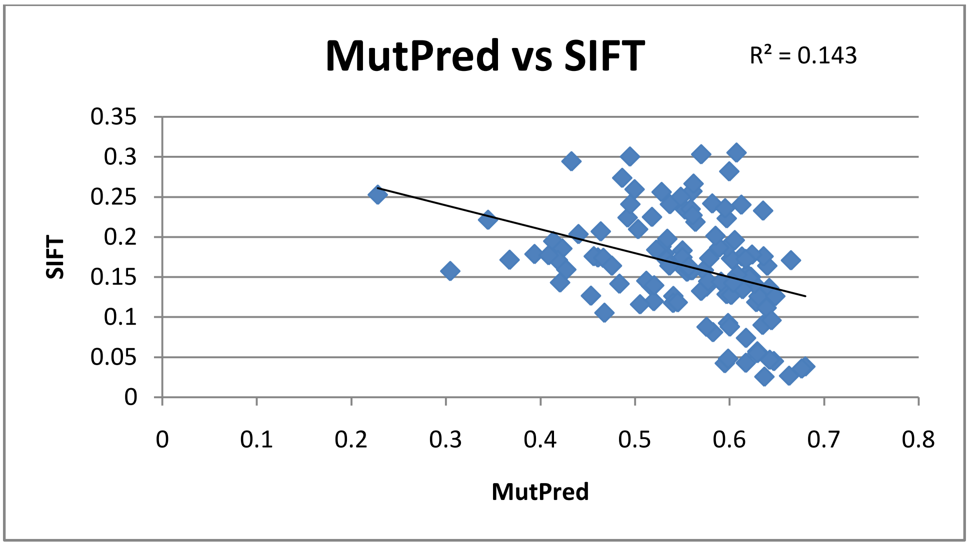

Figure S10. Correlation between MutPred and SIFT pathogenicity average scores per protein based on all possible non-synonymous mutations.

3- Comparison between hydrophobicity measures

We tested several measures of hydrophobicity and several scales, and confirmed that results follow always the same pattern (Figures S11-S13).

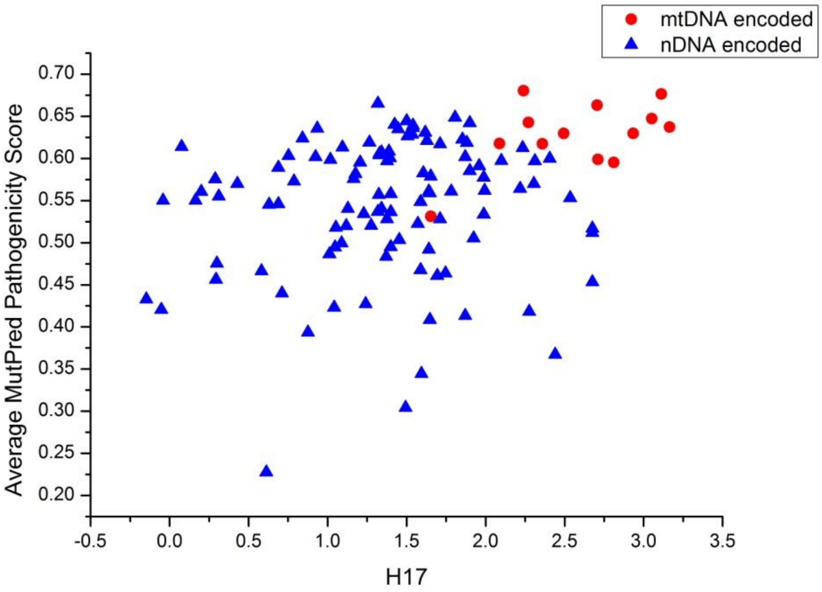

Figure S11. Assessing hydrophobicity influence at the protein and amino acid level, using H17 measure (the maximal local hydrophobicity of a segment)
Average pathogenicity score per nDNA and mtDNA coded proteins.

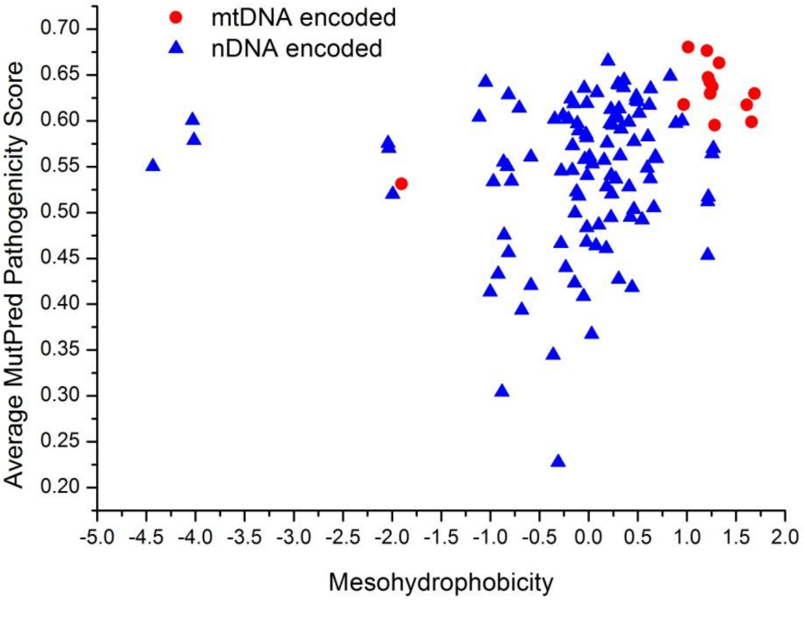

Figure S12. Assessing hydrophobicity influence at the protein and amino acid level, using mesohydrophobicity measure (the average regional hydrophobicity over an extended region of the sequence) and KD scale
Average pathogenicity score per nDNA and mtDNA coded proteins.

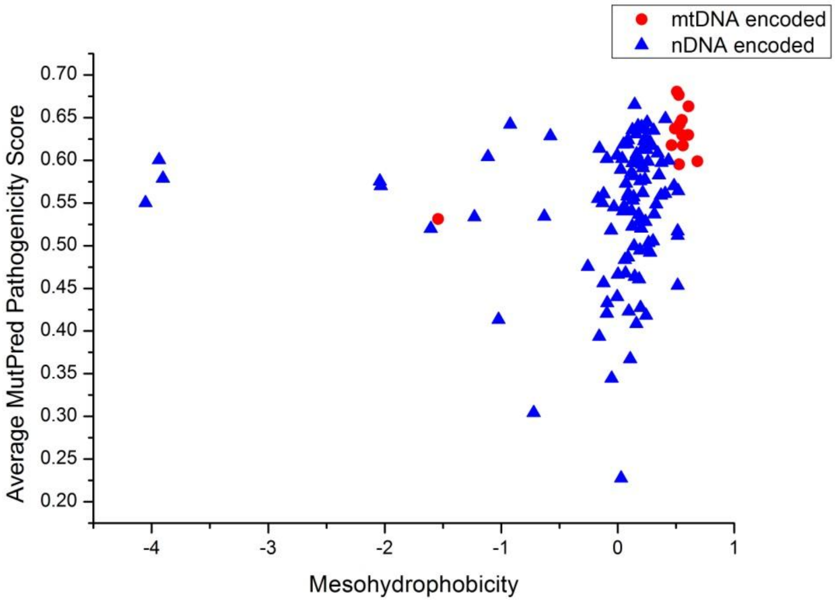

Figure S13. Assessing hydrophobicity influence at the protein and amino acid level, using mesohydrophobicity measure (the average regional hydrophobicity over an extended region of the sequence) and ECS scale
Average pathogenicity score per nDNA and mtDNA coded proteins.

4- Evaluating hydrophobicity influence at amino acid level

The differences between the genetic codes mean that tryptophan and methionine are coded by two codons in mtDNA compared with one in nDNA, isoleucine by two in mtDNA and three in nDNA, and arginine by four in mtDNA and six in nDNA. When comparing the proportion of amino acids between the two sets of proteins (Figure S14A) it shows higher proportions of mtDNA tryptophan and methionine, and lower ones of arginine, but isoleucine is more frequent (double) in mtDNA – no direct relation between frequency and number of codons.

When analysing the MutPred scores of all the non-synonymous substitutions per amino acid in the two sets of proteins (Figure S14B), pathogenicity values are higher for all mtDNA coded in basically all amino acids, meaning that the risk of a non-synonymous mutation in the mtDNA is higher than the respective mutation in the nDNA coded genes for mt proteins, irrespectively of the different amino acid genetic codes. There is a tendency for the difference in MutPred scores per amino acid, between nDNA and mtDNA coded mt-proteins, being higher for the less hydrophobic amino acids and more identical for the more hydrophobic ones.

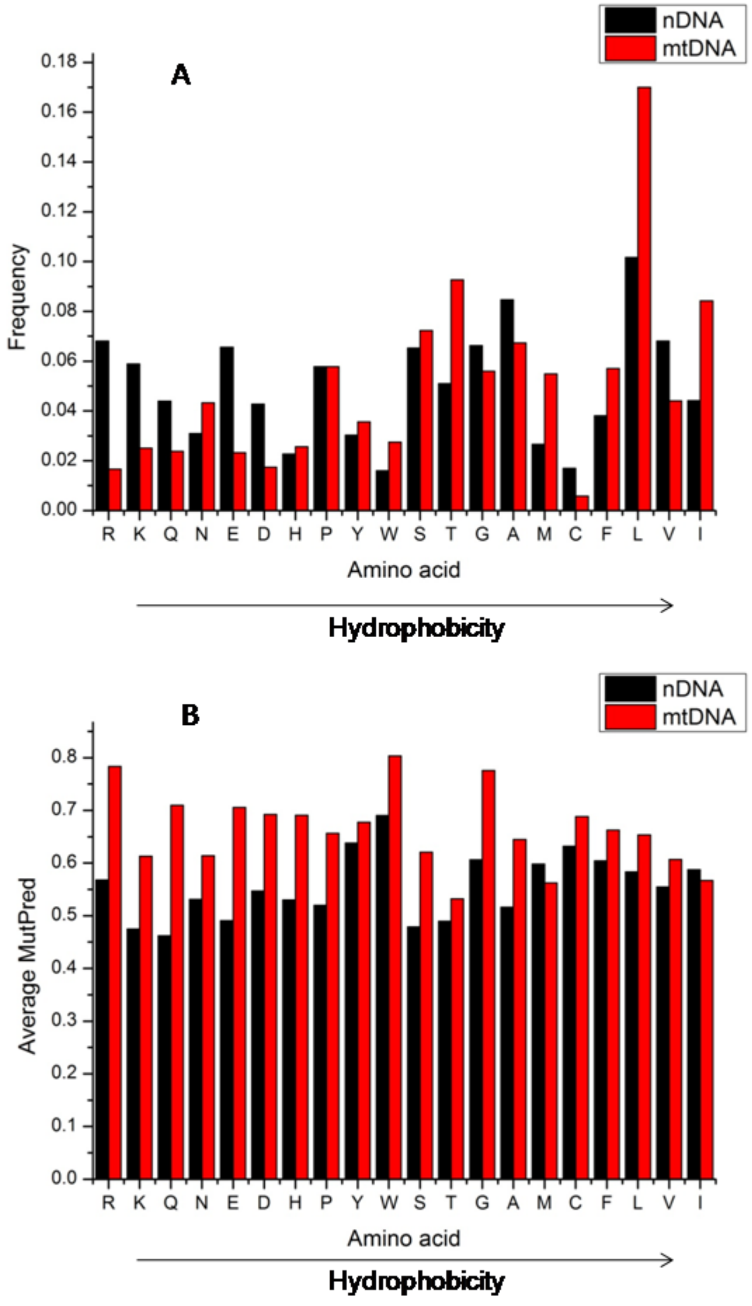

Figure S14. Assessing hydrophobicity influence at the amino acid level
(A) Frequency of amino acids.
(B) Average pathogenicity score across amino acids in the nDNA encoded proteins. Amino acids ordered from lower to higher hydrophobicity.

Table S1- The 104 nuclear genes encoding mitochondrial proteins, their function, location in the genome and information on the transcript used.

Gene	Function	chr	Range	Size	Sense	Transcript	No. of transcripts	Exons	Length (bp)	Length (aa)	CCDS
AK2	catalytic	1	33473585-33546597	73013	reverse	ENST00000354858	14	6	1021	239	CCDS374
AK3	catalytic	9	4711155-4742043	30889	reverse	ENST00000359883	4	5	1536	157	CCDS56561
AK4	catalytic	1	65613232-65697828	84597	forward	ENST00000327299	8	5	6836	223	CCDS629
ATP5A1	complex V	18	43664110-43684300	20191	reverse	ENST00000398752	10	12	1916	553	CCDS11927
ATP5B	complex V	12	57031959-57039798	7840	reverse	ENST00000262030	13	10	1789	529	CCDS8924
ATP5C1	complex V	10	7830092-7849778	19687	forward	ENST00000356708	11	10	1163	298	CCDS31142
ATP5D	complex V	19	1241749-1244823	3075	forward	ENST00000215375	2	4	995	168	CCDS12058
ATP5E	complex V	20	57600522-57607437	6916	reverse	ENST00000243997	3	3	3665	51	CCDS13476
ATP5EP2	complex V	13	28519343-28519727	385	forward	ENST00000381026	1	1	385	51	
ATP5F1	complex V	1	111991486-112005395	13910	forward	ENST00000369722	6	7	3156	256	CCDS836
ATP5G1	complex V	17	46970127-46973233	3107	forward	ENST00000355938	11	5	598	136	CCDS11539
ATP5G2	complex V	12	54026510-54071192	44683	reverse	ENST00000338662	8	5	1792	157	CCDS31812
ATP5G3	complex V	2	176040986-176049335	8350	reverse	ENST00000284727	5	5	5484	142	CCDS2263
ATP5H	complex V	17	73032145-73043074	10930	reverse	ENST00000301587	3	6	622	161	CCDS11712
ATP5I	complex V	4	666225-668127	1903	reverse	ENST00000304312	5	4	365	69	CCDS3337
ATP5J	complex V	21	27088815-27107984	19170	reverse	ENST00000284971	8	4	614	108	CCDS13574
ATP5J2	complex V	7	99046098-99063954	17857	reverse	ENST00000292475	13	4	607	94	CCDS5665
ATP5L	complex V	11	118271869-118302211	30343	forward	ENST00000300688	8	3	1571	103	CCDS8397
ATP5L2	complex V	22	43035809-43036607	799	reverse	ENST00000505920	1	1	799	100	CCDS54534
ATP5O	complex V	21	35275757-35288284	12528	reverse	ENST00000290299	10	7	932	213	CCDS13634
ATP5S	complex V	14	50779044-50802276	23233	forward	ENST00000245448	11	4	1671	127	CCDS32076
COX10	complex IV	17	13972846-14111994	139149	forward	ENST00000261643	4	7	2873	443	CCDS11166
COX11	complex IV	17	53038568-53046064	7497	reverse	ENST00000299335	1	4	2414	276	CCDS11583

COX15	complex IV	10	101471601-101491866	20266	reverse	ENST00000370483	4	9	2356	410	CCDS7482
COX16	complex IV	14	70792102-70826448	34347	reverse	ENST00000389912	4	4	1413	106	CCDS9802
COX17	complex IV	3	119373360-119396301	22942	reverse	ENST00000261070	7	3	684	63	CCDS2993
COX18	complex IV	4	73921797-73935472	13676	reverse	ENST00000295890	5	6	3128	333	CCDS3554
COX4I1	complex IV	16	85833290-85840608	7319	forward	ENST00000253452	1	5	708	169	CCDS10955
COX4I2	complex IV	20	30225691-30232809	7119	forward	ENST00000376075	2	5	693	171	CCDS13187
COX5A	complex IV	15	75212132-75230509	18378	reverse	ENST00000322347	1	5	1268	150	CCDS10273
COX5B	complex IV	2	98262503-98264846	2344	forward	ENST00000258424	4	4	712	129	CCDS2032
COX6A1	complex IV	12	120875893-120878545	2653	forward	ENST00000229379	3	3	572	109	CCDS9197
COX6A2	complex IV	16	31439055-31439731	677	reverse	ENST00000287490	1	3	419	97	CCDS10712
COX6B1	complex IV	19	36139125-36149686	10562	forward	ENST00000392201	2	4	435	103	
COX6B2	complex IV	19	55861076-55866182	5107	reverse	ENST00000326529	1	5	1657	88	CCDS42630
COX6C	complex IV	8	100885428-100906290	20863	reverse	ENST00000520468	10	4	828	75	CCDS6284
COX7A1	complex IV	19	36641824-36643771	1948	reverse	ENST00000292907	3	4	762	79	CCDS12490
COX7A2	complex IV	6	75947391-75960039	12649	reverse	ENST00000370081	9	5	914	115	CCDS34486
COX7A2L	complex IV	2	42560686-42596150	35465	reverse	ENST00000378669	6	4	3056	114	CCDS1808
COX7B	complex IV	X	77154935-77162870	7936	forward	ENST00000481445	3	3	2471	80	CCDS14437
COX7B2	complex IV	4	46736844-46911252	174409	reverse	ENST00000355591	5	3	542	81	CCDS3472
COX7C	complex IV	5	85913721-85916779	3059	forward	ENST00000247655	7	3	666	63	CCDS4063
COX8A	complex IV	11	63742079-63744015	1937	forward	ENST00000314133	1	2	507	69	CCDS8054
COX8C	complex IV	14	93813537-93814702	1166	forward	ENST00000342144	1	2	533	72	CCDS9910
CYC1	complex III	8	145149930-145152428	2499	forward	ENST00000318911	4	7	1240	325	CCDS6415
DGUOK	Fission	2	74153953-74186088	32136	forward	ENST00000264093	9	7	1144	277	CCDS1931
MFF	Fission	2	228189867-228222550	32684	forward	ENST00000353339	27	11	2186	342	CCDS2465
MFN1	Fusion	3	179065480-179112719	47240	forward	ENST00000471841	11	18	5224	741	CCDS3228
MFN2	Fusion	1	12040238-12073571	33334	forward	ENST00000235329	8	19	4539	757	CCDS30587

MTERF	Transcription termination factor	7	91500243-91510034	9792	reverse	ENST00000419292	7	2	3882	379	
MTFR1	Fission	8	66556124-66683496	127373	forward	ENST00000518609	16	9	1166	317	
NDUFAF2	complex I	5	60240956-60448853	207898	forward	ENST00000296597	4	4	708	169	CCDS3979
NDUFAF3	complex I	3	49057892-49060905	3014	forward	ENST00000326925	6	5	1989	184	CCDS2784
NDUFAF4	complex I	6	97337189-97345757	8569	reverse	ENST00000316149	3	3	2399	175	CCDS5037
NDUFB1	complex I	14	92582466-92588261	5796	reverse	ENST00000329559	6	3	528	105	CCDS9901
NDUFB10	complex I	16	2009519-2011976	2458	forward	ENST00000268668	2	4	695	172	CCDS10451
NDUFB11	complex I	X	47001615-47004903	3289	reverse	ENST00000377811	3	3	1388	153	CCDS48100
NDUFB2	complex I	7	140390577-140422590	32014	forward	ENST00000247866	17	4	504	105	CCDS5862
NDUFB3	complex I	2	201936156-201950473	14318	forward	ENST00000237889	4	3	755	98	CCDS2336
NDUFB4	complex I	3	120315156-120321347	6192	forward	ENST00000184266	6	3	671	129	CCDS2999
NDUFB5	complex I	3	179322478-179345435	22958	forward	ENST00000259037	15	6	1141	189	CCDS3234
NDUFB6	complex I	9	32552997-32573160	20164	reverse	ENST00000379847	2	4	1366	128	CCDS6528
NDUFB7	complex I	19	14676892-14682886	5995	reverse	ENST00000215565	1	3	541	137	CCDS12314
NDUFB8	complex I	10	102267203-102289757	22555	reverse	ENST00000370320	11	5	684	172	
NDUFB9	complex I	8	125551344-125580751	29408	forward	ENST00000276689	7	4	711	179	CCDS6352
NDUFC1	complex I	4	140188034-140223705	35672	reverse	ENST00000394228	12	6	761	76	CCDS3746
NDUFC2	complex I	11	77779350-77791265	11916	reverse	ENST00000281031	6	3	2518	119	CCDS8257
NDUFS1	complex I	2	206986149-207024327	38179	reverse	ENST00000233190	10	19	5211	727	CCDS2366
NDUFS2	complex I	1	161166894-161184185	17292	forward	ENST00000367993	17	15	2042	463	CCDS1224
NDUFS3	complex I	11	47586888-47606114	19227	forward	ENST00000263774	14	7	958	264	CCDS7941
NDUFS4	complex I	5	52856463-52979168	122706	forward	ENST00000296684	6	5	673	175	CCDS3960
NDUFS5	complex I	1	39491990-39500308	8319	forward	ENST00000372969	2	3	548	106	CCDS434
NDUFS6	complex I	5	1801514-1816719	15206	forward	ENST00000274137	3	4	1082	124	CCDS3866
NDUFS7	complex I	19	1383526-1395587	12062	forward	ENST00000546283	18	8	1060	206	
NDUFS8	complex I	11	67798084-67804111	6028	forward	ENST00000313468	15	7	791	210	CCDS8176

NDUFV1	complex I	11	67374323-67380006	5684	forward	ENST00000322776	29	10	1596	464	CCDS8173
NDUFV2	complex I	18	9102628-9134343	31716	forward	ENST00000318388	7	8	930	249	CCDS11842
NDUFV3	complex I	21	44299754-44329783	30030	forward	ENST00000354250	5	4	1575	473	CCDS33572
NT5M	Fission	17	17206649-17250977	44329	forward	ENST00000446264	6	5	1615	239	
OPA1	Fusion	3	193310933-193415612	104680	forward	ENST00000361908	19	30	6439	997	CCDS33917
OPA3	Role in mitochondrial processes	19	46030685-46105470	74786	reverse	ENST00000263275	3	2	7871	179	CCDS12668
PEO1	TWINLKE helicase	10	102747124-102754158	7035	forward	ENST00000311916	5	5	3131	684	CCDS7506
PINK1	Cellular stress	1	20959948-20978004	18057	forward	ENST00000321556	3	8	2660	581	CCDS211
POLG	Polimerase	15	89859534-89878092	18559	reverse	ENST00000268124	13	23	4502	1239	CCDS10350
POLG2	Polimerase	17	62473904-62493184	19281	reverse	ENST00000539111	1	8	1592	485	CCDS32706
POLRMT	Transcription	19	617223-633568	16346	reverse	ENST00000215591	1	21	3800	1230	CCDS12036
SDHA	complex II	5	218356-256815	38460	forward	ENST00000264932	22	15	2390	664	CCDS3853
SDHB	complex II	1	17345217-17380665	35449	reverse	ENST00000375499	8	8	1153	280	CCDS176
SDHC	complex II	1	161284047-161332984	48938	forward	ENST00000367975	9	5	1127	169	CCDS1230
SDHD	complex II	11	111957497-111990353	32857	forward	ENST00000375549	8	4	1439	159	CCDS31678
SSBP1	Replication	7	141438121-141487722	49602	forward	ENST00000265304	14	7	687	148	CCDS5866
TFAM	Transcription	10	60144782-60158981	14200	forward	ENST00000487519	4	6	5414	246	
TK2	DNA synthesis	16	66541906-66584315	42410	reverse	ENST00000451102	8	10	3738	265	CCDS10805
UCP1	mitochondrial transporter protein	4	141480588-141489959	9372	reverse	ENST00000262999	1	6	1462	307	CCDS3753
UCP2	mitochondrial transporter protein	11	73685712-73694352	8641	reverse	ENST00000310473	10	8	2113	309	CCDS8228

UCP3	mitochondrial transporter protein	11	73711326-73720480	9155	reverse	ENST00000314032	5	7	2623	312	CCDS8229
UQCRB	complex III	8	97238148-97247862	9715	reverse	ENST00000287022	9	4	5575	111	CCDS6269
UQCRC1	complex III	3	48636435-48648409	11975	reverse	ENST00000203407	10	13	1985	480	CCDS2774
UQCRC2	complex III	16	21963981-21994981	31001	forward	ENST00000268379	1	14	2615	453	CCDS10601
UQCRFS1	complex III	19	29698167-29704136	5970	reverse	ENST00000304863	1	2	1224	274	CCDS12415
UQCRH	complex III	1	46769303-46782448	13146	forward	ENST00000311672	5	4	604	91	CCDS30704
UQCRQ	complex III	5	132202252-132203723	1472	forward	ENST00000378670	6	3	839	82	CCDS34237
UQCR10	complex III	22	30163352-30166402	3051	forward	ENST00000330029	4	2	916	63	CCDS46680
UQCR11	complex III	19	1597154-1605483	8330	reverse	ENST00000262946	1	3	1335	56	CCDS12073

Table S2- Observed non-synonymous mutations in 1,092 individuals (246 are from Africans including Afro-Americans, 379 Europeans, 286 Asians and 181 Americans) from the 1000 Genomes dataset and MutPred, PolyPhen and SIFT pathogenicity scores (and the majority vote).

Gene	**Uploaded Variation**	**Position in cDNA**	**Position in CDS**	**Position in protein**	**Amino acid change**	**Codon change**	**Co-located Variation**	**MutPred**	**MutPred Prediction**	**PolyPhen Score**	**PolyPhen Prediction**	**SIFT Score**	**SIFT Prediction**	**Pathogenic Vote**
AK2	1_33487277_T/C	411	247	83	I/V	Att/Gtt	rs184683619	0.577	Neutral	0.212	benign	0.270	tolerated	0
AK2	1_33487007_C/T	550	386	129	S/N	aGc/aAc	rs61750965	0.297	Neutral	0.001	benign	0.560	tolerated	0
AK2	1_33486974_G/A	583	419	140	T/I	aCa/aTa	rs192209857	0.589	Neutral	0.880	possibly damaging	0.040	deleterious	1
AK2	1_33480172_C/T	613	449	150	R/H	cGt/cAt	rs149227118	0.561	Neutral	0.639	possibly damaging	0.000	deleterious	1
AK2	1_33480161_C/T	624	460	154	E/K	Gag/Aag	rs148421308	0.483	Neutral	0.854	possibly damaging	0.820	tolerated	0
AK2	1_33478891_C/T	775	611	204	R/Q	cGg/cAg	rs200179721	0.544	Neutral	0.008	benign	0.200	tolerated	0
AK2	1_33478877_C/T	789	625	209	A/T	Gcc/Acc	rs12116440	0.095	Neutral	0.056	benign	0.390	tolerated	0
AK2	1_33478853_C/G	813	649	217	D/H	Gat/Cat	rs185081372	0.341	Neutral	0.024	benign	0.050	tolerated	0

AK3	9_4719182_C/A	318	187	63	A/S	Gcc/Tcc	rs188377589	0.359	Neutral	0.006	benign	0.410	tolerated	0
AK3	9_4719161_T/A	339	208	70	I/F	Att/Ttt	rs141090350	0.365	Neutral	0.374	benign	0.010	deleterious	1
AK3	9_4718440_T/G	463	332	111	K/T	aAg/aCg	rs151087607	0.436	Neutral	0.250	benign	0.030	deleterious	1
AK3	9_4713058_G/A	523	392	131	T/I	aCc/aTc	rs140003401	0.382	Neutral	0.912	probably damaging	0.000	deleterious	2
AK4	1_65614154_T/A	269	64	22	C/S	Tgc/Agc	rs17853973	0.752	Pathogenic	0.006	benign	1.000	tolerated	1
AK4	1_65684463_G/A	497	292	98	E/K	Gaa/Aaa	rs200696544	0.591	Neutral	0.030	benign	0.170	tolerated	0
AK4	1_65684545_G/A	579	374	125	R/H	cGc/cAc	rs142956995	0.642	Possibly Pathogenic	0.002	benign	0.200	tolerated	0
AK4	1_65690489_G/A	698	493	165	E/K	Gaa/Aaa	rs185251178	0.722	Pathogenic	0.671	possibly damaging	0.010	deleterious	2
AK4	1_65691837_A/G	854	649	217	I/V	Att/Gtt	rs201234545	0.220	Neutral	0.000	benign	0.640	tolerated	0
ATP5A1	18_43678173_C/T	147	25	9	A/T	Gcc/Acc	rs141639003	0.352	Neutral	0.000	unknown	0.080	tolerated	0
ATP5A1	18_43678172_G/A	148	26	9	A/V	gCc/gTc	rs200039737	0.330	Neutral	0.000	unknown	0.080	tolerated	0
ATP5A1	18_43675064_C/A	216	94	32	A/S	Gct/Tct	rs79011243	0.173	Neutral	0.005	benign	0.150	tolerated	0
ATP5A1	18_43675046_C/T	234	112	38	A/T	Gcc/Acc	rs189208584	0.167	Neutral	0.001	benign	0.730	tolerated	0
ATP5A1	18_43669662_G/C	642	520	174	L/V	Ctg/Gtg	rs11541929	0.299	Neutral	0.001	benign	1.000	tolerated	0
ATP5A1	18_43668207_T/C	789	667	223	I/V	Att/Gtt	rs77958705	0.197	Neutral	0.059	benign	0.110	tolerated	0
ATP5B	12_57039713_G/A	86	35	12	P/L	cCg/cTg	rs200568028	0.303	Neutral	0.000	benign	0.010	deleterious	1
ATP5B	12_57039675_A/G	124	73	25	S/P	Tcg/Ccg	rs144845797	0.177	Neutral	0.009	benign	0.080	tolerated	0
ATP5B	12_57039674_G/A	125	74	25	S/L	tCg/tTg	rs2293450	0.263	Neutral	0.000	benign	0.110	tolerated	0
ATP5B	12_57039080_C/T	236	185	62	R/H	cGc/cAc	rs41291993	0.338	Neutral	0.001	benign	0.050	deleterious	1
ATP5B	12_57037309_C/T	721	670	224	A/T	Gcc/Acc	rs200966693	0.668	Possibly Pathogenic	0.967	probably damaging	0.000	deleterious	2
ATP5B	12_57037209_T/C	821	770	257	N/S	aAc/aGc	rs142007312	0.257	Neutral	0.002	benign	0.520	tolerated	0

ATP5B	12_57032995_G/A	1435	1384	462	R/C	Cgt/Tgt	rs200610844	0.709	Pathogenic	0.993	probably damaging	0.000	deleterious	3
ATP5B	12_57032900_C/A	1530	1479	493	Q/H	caG/caT	rs145015204	0.336	Neutral	0.391	benign	0.050	tolerated	0
ATP5C1	10_7838106_A/G	158	79	27	T/A	Act/Gct	rs199602842	0.468	Neutral	0.724	possibly damaging	0.000	deleterious	1
ATP5C1	10_7840983_C/T	333	254	85	P/L	cCt/cTt	rs146307767	0.528	Neutral	0.046	benign	0.310	tolerated	0
ATP5C1	10_7841811_A/G	584	505	169	I/V	Att/Gtt	rs139967528	0.689	Possibly Pathogenic	0.037	benign	0.240	tolerated	0
ATP5C1	10_7844268_G/A	752	673	225	V/M	Gtg/Atg	rs199960374	0.770	Pathogenic	0.820	possibly damaging	0.030	deleterious	2
ATP5C1	10_7844756_C/T	908	829	277	R/C	Cgt/Tgt	rs137988284	0.908	Pathogenic	0.692	possibly damaging	0.030	deleterious	2
ATP5D	19_1241932_C/T	184	83	28	A/V	gCc/gTc	rs199988557	0.285	Neutral	0.000	unknown	0.520	tolerated	0
ATP5D	19_1244170_A/G	471	370	124	M/V	Atg/Gtg	rs200344400	0.393	Neutral	0.051	benign	0.210	tolerated	0
ATP5D	19_1244401_G/A	573	472	158	E/K	Gag/Aag	rs200593395	0.664	Possibly Pathogenic	0.987	probably damaging	0.020	deleterious	2
ATP5E	20_57605431_G/T	217	86	29	T/K	aCa/aAa	rs146230809	0.464	Neutral	0.010	benign	0.080	tolerated	0
ATP5EP2	13_28519416_A/G	74	20	7	Q/R	cAg/cGg	rs7334094	0.459	Neutral	0.989	probably damaging	0.000	deleterious	2
ATP5F1	1_111998734_A/G	856	250	84	I/V	Atc/Gtc	rs151112830	0.355	Neutral	0.029	benign	0.410	tolerated	0
ATP5F1	1_111999312_A/G	1054	448	150	I/V	Att/Gtt	rs150276317	0.702	Pathogenic	0.003	benign	0.060	tolerated	1
ATP5F1	1_111999319_C/T	1061	455	152	T/M	aCg/aTg	rs1264895	0.118	Neutral	0.007	benign	0.170	tolerated	0
ATP5F1	1_112002094_G/A	1135	529	177	A/T	Gct/Act	rs144377157	0.531	Neutral	0.035	benign	0.450	tolerated	0
ATP5F1	1_112002202_G/C	1243	637	213	E/Q	Gaa/Caa	rs182170395	0.465	Neutral	0.077	benign	0.030	deleterious	1
ATP5F1	1_112002232_G/A	1273	667	223	V/M	Gtg/Atg	rs146878380	0.909	Pathogenic	0.999	probably damaging	0.000	deleterious	3
ATP5G1	17_46970783_C/G	89	4	2	Q/E	Cag/Gag	rs201139259	0.240	Neutral	0.154	benign	0.090	tolerated	0
ATP5G2	12_54069975_A/G	1208	2	1	M/T	aTg/aCg	rs201675029	0.761	Pathogenic	0.000	unknown	0.010	deleterious	2
ATP5G2	12_54063677_C/T	1349	143	48	R/Q	cGa/cAa	rs140613495	0.211	Neutral	0.008	benign	0.250	tolerated	0
ATP5G2	12_54063056_C/T	1441	235	79	A/T	Gcc/Acc	rs145981161	0.209	Neutral	0.016	benign	0.130	tolerated	0

ATP5G3	2_176046090_G/A	3057	32	11	P/L	cCc/cTc	rs142182201	0.472	Neutral	0.800	possibly damaging	0.010	deleterious	1
ATP5G3	2_176044863_G/A	3108	83	28	S/L	tCa/tTa	rs144490355	0.365	Neutral	0.002	benign	0.220	tolerated	0
ATP5G3	2_176043906_T/C	3218	193	65	I/V	Atc/Gtc	rs36089250	0.244	Neutral	0.000	benign	1.000	tolerated	0
ATP5H	17_73038667_T/G	143	79	27	I/L	Att/Ctt	rs200410651	0.321	Neutral	0.107	benign	0.740	tolerated	0
ATP5H	17_73038316_T/C	243	179	60	N/S	aAt/aGt	rs143915019	0.468	Neutral	0.008	benign	0.770	tolerated	0
ATP5I	4_668015_A/G	113	22	8	S/P	Tct/Cct	rs143075692	0.715	Pathogenic	0.665	possibly damaging	0.010	deleterious	2
ATP5I	4_668009_G/A	119	28	10	L/F	Ctc/Ttc	rs76028807	0.739	Pathogenic	0.818	possibly damaging	0.010	deleterious	2
ATP5I	4_667134_T/G	239	148	50	K/Q	Aag/Cag	rs147287885	0.536	Neutral	0.021	benign	0.170	tolerated	0
ATP5I	4_667115_C/T	258	167	56	R/Q	cGg/cAg	rs181881252	0.500	Neutral	0.048	benign	0.120	tolerated	0
ATP5J	21_27102014_G/C	219	92	31	A/G	gCa/gGa	rs73338261	0.798	Pathogenic	0.985	probably damaging	0.050	deleterious	3
ATP5J	21_27097641_T/G	312	185	62	D/A	gAt/gCt	rs182225698	0.897	Pathogenic	0.959	probably damaging	0.000	deleterious	3
ATP5J2	7_99063760_G/A	195	5	2	A/V	gCg/gTg	rs201512015	0.170	Neutral	0.718	possibly damaging	0.000	deleterious	1
ATP5J2	7_99063739_G/C	216	26	9	A/G	gCc/gGc	rs117298057	0.201	Neutral	0.002	benign	0.370	tolerated	0
ATP5J2	7_99056770_T/G	446	256	86	K/Q	Aag/Cag	rs146584377	0.497	Neutral	0.892	possibly damaging	0.010	deleterious	1
ATP5J2	7_99055969_C/T	456	266	89	R/Q	cGg/cAg	rs144185727	0.504	Neutral	0.066	benign	0.060	tolerated	0
ATP5L	11_118277742_G/C	655	143	48	R/T	aGa/aCa	rs181465227	0.385	Neutral	0.002	benign	0.690	tolerated	0
ATP5L	11_118279769_G/A	780	268	90	G/R	Gga/Aga	rs200472961	0.873	Pathogenic	0.460	possibly damaging	0.030	deleterious	2
ATP5L2	22_43036264_C/T	344	17	6	R/H	cGt/cAt	rs148856876	0.452	Neutral	0.005	benign	0.190	tolerated	0
ATP5L2	22_43035994_C/G	614	287	96	R/P	cGt/cCt	rs145437748	0.794	Pathogenic	0.668	possibly damaging	0.040	deleterious	2
ATP5O	21_35288061_C/T	224	7	3	A/T	Gcc/Acc	rs202191698	0.207	Neutral	0.062	benign	0.040	deleterious	1
ATP5O	21_35288049_A/G	236	19	7	S/P	Tcc/Ccc	rs201852944	0.291	Neutral	0.233	benign	0.180	tolerated	0

ATP5O	21_35286801_G/C	257	40	14	R/G	Cga/Gga	rs190343471	0.686	Possibly Pathogenic	0.831	possibly damaging	0.000	deleterious	1
ATP5O	21_35281496_T/C	435	218	73	K/R	aAa/aGa	rs140827929	0.372	Neutral	0.103	benign	0.160	tolerated	0
ATP5O	21_35281461_G/A	470	253	85	R/C	Cgt/Tgt	rs150994121	0.493	Neutral	0.819	possibly damaging	0.000	deleterious	1
ATP5O	21_35281421_T/C	510	293	98	K/R	aAa/aGa	rs4842	0.174	Neutral	0.032	benign	0.140	tolerated	0
ATP5O	21_35279713_C/T	590	373	125	V/I	Gtt/Att	rs190233927	0.531	Neutral	0.013	benign	1.000	tolerated	0
ATP5O	21_35275939_T/C	750	533	178	D/G	gAt/gGt	rs182975028	0.780	Pathogenic	0.232	benign	0.020	deleterious	2
ATP5O	21_35275936_G/A	753	536	179	P/L	cCg/cTg	rs191960490	0.816	Pathogenic	0.013	benign	0.080	tolerated	1
ATP5O	21_35275931_T/C	758	541	181	I/V	Atc/Gtc	rs141125740	0.831	Pathogenic	0.482	possibly damaging	0.040	deleterious	2
ATP5O	21_35275914_A/C	775	558	186	I/M	atT/atG	rs11552279	0.812	Pathogenic	0.950	probably damaging	0.000	deleterious	3
ATP5O	21_35275907_T/C	782	565	189	I/V	Att/Gtt	rs75701641	0.713	Pathogenic	0.482	possibly damaging	0.100	tolerated	1
ATP5O	21_35275835_C/A	854	637	213	V/F	Gtc/Ttc	rs142550850	0.428	Neutral	0.064	benign	0.000	deleterious	1
ATP5S	14_50779764_G/A	718	26	9	R/Q	cGa/cAa	rs192355817	0.281	Neutral	0.059	benign	0.360	tolerated	0
ATP5S	14_50788213_C/T	745	53	18	P/L	cCg/cTg	rs2275592	0.305	Neutral	0.000	benign	1.000	tolerated	0
ATP5S	14_50788240_G/A	772	80	27	C/Y	tGt/tAt	rs201427439	0.324	Neutral	0.002	benign	1.000	tolerated	0
ATP5S	14_50789309_G/A	925	233	78	R/H	cGc/cAc	rs185659761	0.556	Neutral	0.966	probably damaging	0.000	deleterious	2
ATP5S	14_50789387_C/T	1003	311	104	A/V	gCg/gTg	rs142828913	0.306	Neutral	0.977	probably damaging	0.240	tolerated	1
ATP5S	14_50789401_G/A	1017	325	109	D/N	Gac/Aac	rs140662926	0.464	Neutral	0.078	benign	0.380	tolerated	0
ATP5S	14_50789426_T/C	1042	350	117	F/S	tTt/tCt	rs192482233	0.611	Possibly Pathogenic	0.985	probably damaging	0.000	deleterious	2
COX10	17_13972938_C/T	93	16	6	H/Y	Cac/Tac	rs199881731	0.350	Neutral	0.933	probably damaging	0.000	deleterious	2
COX10	17_13977679_C/T	160	83	28	T/I	aCt/aTt	rs16948978	0.184	Neutral	0.006	benign	0.080	tolerated	0
COX10	17_13977689_C/A	170	93	31	D/E	gaC/gaA	rs141481210	0.458	Neutral	0.000	benign	1.000	tolerated	0

COX10	17_13980058_A/T	261	184	62	T/S	Aca/Tca	rs2230351	0.156	Neutral	0.024	benign	0.040	deleterious	1
COX10	17_13980134_C/T	337	260	87	T/I	aCa/aTa	rs144000161	0.265	Neutral	0.003	benign	0.110	tolerated	0
COX10	17_13980164_A/G	367	290	97	Y/C	tAt/tGt	rs16948986	0.113	Neutral	0.001	benign	0.190	tolerated	0
COX10	17_13980176_C/T	379	302	101	P/L	cCt/cTt	rs145948285	0.374	Neutral	0.177	benign	0.050	deleterious	1
COX10	17_13980185_C/T	388	311	104	P/L	cCg/cTg	rs202207627	0.298	Neutral	0.003	benign	0.210	tolerated	0
COX10	17_13980254_T/C	457	380	127	I/T	aTt/aCt	rs201424119	0.393	Neutral	0.001	benign	0.350	tolerated	0
COX10	17_13980350_G/A	553	476	159	R/Q	cGa/cAa	rs8077302	0.587	Neutral	0.056	benign	0.250	tolerated	0
COX10	17_14005467_G/T	609	532	178	A/S	Gca/Tca	rs200373790	0.703	Pathogenic	0.903	possibly damaging	0.040	deleterious	2
COX10	17_14005498_G/A	640	563	188	C/Y	tGt/tAt	rs200827701	0.520	Neutral	0.854	possibly damaging	0.070	tolerated	0
COX10	17_14063243_C/T	751	674	225	P/L	cCg/cTg	rs104894556	0.948	Pathogenic	0.462	possibly damaging	0.290	tolerated	1
COX10	17_14063251_C/T	759	682	228	R/C	Cgt/Tgt	rs114521946	0.653	Possibly Pathogenic	0.638	possibly damaging	0.020	deleterious	1
COX10	17_14110129_G/A	1008	931	311	A/T	Gca/Aca	rs200472593	0.683	Possibly Pathogenic	0.970	probably damaging	0.000	deleterious	2
COX10	17_14110267_G/T	1146	1069	357	A/S	Gcg/Tcg	rs188087012	0.567	Neutral	0.877	possibly damaging	0.220	tolerated	0
COX10	17_14110294_G/T	1173	1096	366	V/L	Gtg/Ttg	rs111541535	0.723	Pathogenic	0.000	benign	0.820	tolerated	1
COX10	17_14110397_A/G	1276	1199	400	Y/C	tAc/tGc	rs200260465	0.747	Pathogenic	0.995	probably damaging	0.000	deleterious	3
COX10	17_14110489_C/T	1368	1291	431	R/W	Cgg/Tgg	rs113058506	0.380	Neutral	0.500	possibly damaging	0.000	deleterious	1
COX11	17_53045947_G/A	118	61	21	H/Y	Cac/Tac	rs73990239	0.260	Neutral	0.034	benign	0.010	deleterious	1
COX11	17_53045787_G/A	278	221	74	P/L	cCt/cTt	rs34080917	0.117	Neutral	0.000	benign	0.110	tolerated	0
COX11	17_53040677_T/C	695	638	213	N/S	aAt/aGt	rs199579556	0.628	Possibly Pathogenic	0.999	probably damaging	0.420	tolerated	1
COX11	17_53040119_T/A	863	806	269	K/M	aAg/aTg	rs200586356	0.406	Neutral	0.370	benign	0.150	tolerated	0
COX15	10_101487264_G/A	380	329	110	P/L	cCa/cTa	rs144644373	0.817	Pathogenic	0.372	benign	0.060	tolerated	1

COX15	10_101486775_G/A	583	532	178	R/C	Cgt/Tgt	rs192078749	0.510	Neutral	0.868	possibly damaging	0.010	deleterious	1
COX15	10_101486759_C/T	599	548	183	R/H	cGt/cAt	rs35483721	0.704	Pathogenic	0.355	benign	0.030	deleterious	2
COX15	10_101486736_C/T	622	571	191	V/I	Gtc/Atc	rs187284527	0.529	Neutral	0.077	benign	1.000	tolerated	0
COX15	10_101483799_G/A	715	664	222	R/C	Cgc/Tgc	rs2231682	0.894	Pathogenic	0.997	probably damaging	0.000	deleterious	3
COX15	10_101483721_G/C	793	742	248	P/A	Ccg/Gcg	rs183558471	0.437	Neutral	0.003	benign	1.000	tolerated	0
COX15	10_101480782_T/C	845	794	265	H/R	cAt/cGt	rs200876059	0.536	Neutral	0.458	possibly damaging	0.250	tolerated	0
COX15	10_101478249_C/T	892	841	281	V/M	Gtg/Atg	rs201703572	0.904	Pathogenic	1.000	probably damaging	0.000	deleterious	3
COX15	10_101478110_C/T	1031	980	327	R/Q	cGg/cAg	rs199761049	0.942	Pathogenic	0.986	probably damaging	0.000	deleterious	3
COX15	10_101476166_A/G	1091	1040	347	I/T	aTt/aCt	rs144580290	0.438	Neutral	0.018	benign	0.400	tolerated	0
COX16	14_70826303_A/G	146	2	1	M/T	aTg/aCg	rs188182259	0.996	Pathogenic	0.057	benign	0.030	deleterious	2
COX16	14_70826238_A/C	211	67	23	L/V	Ttg/Gtg	rs182316587	0.451	Neutral	0.210	benign	0.020	deleterious	1
COX16	14_70809397_C/T	263	119	40	R/Q	cGa/cAa	rs139410596	0.543	Neutral	0.999	probably damaging	0.000	deleterious	2
COX18	4_73935357_G/A	102	10	4	R/W	Cgg/Tgg	rs187930178	0.477	Neutral	0.888	possibly damaging	0.000	deleterious	1
COX18	4_73931077_T/C	580	488	163	D/G	gAt/gGt	rs141592190	0.741	Pathogenic	0.723	possibly damaging	0.000	deleterious	2
COX18	4_73931056_G/C	601	509	170	A/G	gCc/gGc	rs148370240	0.666	Possibly Pathogenic	0.077	benign	0.010	deleterious	1
COX18	4_73931009_A/T	648	556	186	F/I	Ttt/Att	rs193287733	0.570	Neutral	0.006	benign	0.220	tolerated	0
COX18	4_73927613_T/C	837	745	249	M/V	Atg/Gtg	rs189709178	0.304	Neutral	0.002	benign	0.300	tolerated	0
COX18	4_73927571_T/C	879	787	263	M/V	Atg/Gtg	rs115487882	0.697	Possibly Pathogenic	0.003	benign	0.930	tolerated	0
COX18	4_73927549_A/G	901	809	270	I/T	aTt/aCt	rs181365781	0.744	Pathogenic	0.092	benign	0.010	deleterious	2

COX18	4_73927540_G/A	910	818	273	T/M	aCg/aTg	rs138323566	0.706	Pathogenic	0.684	possibly damaging	0.010	deleterious	2
COX18	4_73923943_C/T	982	890	297	R/H	cGt/cAt	rs186168799	0.502	Neutral	0.616	possibly damaging	0.010	deleterious	1
COX18	4_73923937_G/A	988	896	299	P/L	cCt/cTt	rs200107314	0.669	Possibly Pathogenic	0.995	probably damaging	0.000	deleterious	2
COX4I1	16_85838545_A/G	146	76	26	S/G	Agt/Ggt	rs147346083	0.464	Neutral	0.007	benign	1.000	tolerated	0
COX4I1	16_85838594_G/A	195	125	42	R/H	cGt/cAt	rs201313443	0.613	Possibly Pathogenic	0.997	probably damaging	0.050	tolerated	1
COX4I2	20_30226848_G/A	103	28	10	V/M	Gtg/Atg	rs199601484	0.411	Neutral	0.003	benign	0.060	tolerated	0
COX4I2	20_30227741_G/C	163	88	30	G/R	Ggt/Cgt	rs148327783	0.391	Neutral	0.038	benign	0.080	tolerated	0
COX4I2	20_30227828_G/C	250	175	59	A/P	Gct/Cct	rs147223483	0.457	Neutral	0.009	benign	0.500	tolerated	0
COX4I2	20_30231292_C/G	408	333	111	F/L	ttC/ttG	rs145481393	0.607	Possibly Pathogenic	0.592	possibly damaging	0.170	tolerated	0
COX4I2	20_30232598_C/T	482	407	136	T/M	aCg/aTg	rs201685557	0.490	Neutral	0.949	probably damaging	0.010	deleterious	2
COX4I2	20_30232603_G/A	487	412	138	E/K	Gag/Aag	rs119455950	0.902	Pathogenic	0.433	benign	0.010	deleterious	2
COX4I2	20_30232673_G/A	557	482	161	R/H	cGc/cAc	rs11907253	0.183	Neutral	0.010	benign	0.220	tolerated	0
COX5A	15_75230282_G/C	228	74	25	S/C	tCc/tGc	rs200367305	0.324	Neutral	0.189	benign	0.090	tolerated	0
COX5A	15_75221559_G/A	269	115	39	R/C	Cgc/Tgc	rs200811470	0.684	Possibly Pathogenic	0.953	probably damaging	0.000	deleterious	2
COX5A	15_75221462_C/T	366	212	71	R/H	cGt/cAt	rs150174803	0.831	Pathogenic	0.194	benign	0.010	deleterious	2
COX5A	15_75219196_G/C	404	250	84	P/A	Cca/Gca	rs199907556	0.910	Pathogenic	1.000	probably damaging	0.020	deleterious	3
COX5A	15_75219190_G/A	410	256	86	P/S	Ccc/Tcc	rs200875315	0.709	Pathogenic	0.901	possibly damaging	0.000	deleterious	2
COX5B	2_98263883_A/G	301	254	85	N/S	aAc/aGc	rs75630766	0.458	Neutral	0.344	benign	0.040	deleterious	1
COX6A1	12_120875934_C/T	42	5	2	A/V	gCg/gTg	rs200221639	0.306	Neutral	0.000	unknown	0.030	deleterious	missing
COX6A1	12_120876205_T/C	164	127	43	F/L	Ttc/Ctc	rs201293121	0.709	Pathogenic	0.020	benign	0.100	tolerated	1
COX6A1	12_120876304_C/A	263	226	76	H/N	Cat/Aat	rs140243339	0.724	Pathogenic	0.993	probably damaging	0.000	deleterious	3

COX6A1	12_120878320_A/G	347	310	104	T/A	Act/Gct	rs200936136	0.390	Neutral	0.096	benign	0.340	tolerated	0
COX6A2	16_31439613_A/C	119	34	12	L/V	Ttg/Gtg	rs140129800	0.230	Neutral	0.214	benign	0.040	deleterious	1
COX6B1	19_36145481_C/T	210	166	56	R/C	Cgc/Tgc	rs149686147	0.758	Pathogenic	0.113	benign	0.060	tolerated	1
COX6B2	19_55865795_C/A	278	95	32	C/F	tGc/tTc	rs149294692	0.903	Pathogenic	0.998	probably damaging	0.000	deleterious	3
COX6C	8_100904243_G/A	462	7	3	P/S	Ccc/Tcc	rs149663441	0.397	Neutral	0.004	benign	1.000	tolerated	0
COX6C	8_100904215_C/T	490	35	12	R/H	cGt/cAt	rs200470517	0.838	Pathogenic	0.048	benign	0.150	tolerated	1
COX7A1	19_36642421_T/G	592	130	44	K/Q	Aag/Cag	rs17882491	0.868	Pathogenic	0.998	probably damaging	0.000	deleterious	3
COX7A1	19_36642390_C/T	623	161	54	R/Q	cGa/cAa	rs150190766	0.720	Pathogenic	0.788	possibly damaging	0.020	deleterious	2
COX7A2	6_75953516_C/G	342	31	11	V/L	Gtt/Ctt	rs113123058	0.269	Neutral	0.008	benign	0.000	deleterious	1
COX7A2	6_75953470_C/T	388	77	26	C/Y	tGc/tAc	rs190629998	0.388	Neutral	0.002	benign	0.120	tolerated	0
COX7A2	6_75950056_C/T	561	250	84	A/T	Gcc/Acc	rs115820973	0.255	Neutral	0.052	benign	0.090	tolerated	0
COX7A2L	2_42580456_C/G	930	100	34	A/P	Gca/Cca	rs150177100	0.292	Neutral	0.037	benign	0.340	tolerated	0
COX7A2L	2_42580380_T/C	1006	176	59	K/R	aAa/aGa	rs200309743	0.533	Neutral	0.058	benign	0.430	tolerated	0
COX7A2L	2_42578481_C/T	1053	223	75	V/I	Gtc/Atc	rs185444762	0.517	Neutral	0.024	benign	0.410	tolerated	0
COX7A2L	2_42578409_T/C	1125	295	99	I/V	Atc/Gtc	rs150597431	0.259	Neutral	0.026	benign	0.690	tolerated	0
COX7A2L	2_42578367_T/G	1167	337	113	N/H	Aac/Cac	rs199682193	0.395	Neutral	0.726	possibly damaging	0.060	tolerated	0
COX7B	X_77158147_C/A	164	48	16	S/R	agC/agA	rs61752458	0.643	Possibly Pathogenic	0.821	possibly damaging	0.010	deleterious	1
COX7B2	4_46737193_G/A	193	17	6	A/V	gCc/gTc	rs200964160	0.670	Possibly Pathogenic	0.052	benign	0.410	tolerated	0
COX7B2	4_46737163_T/C	223	47	16	Q/R	cAa/cGa	rs111699375	0.411	Neutral	0.000	benign	1.000	tolerated	0
COX7B2	4_46737129_A/T	257	81	27	H/Q	caT/caA	rs201505906	0.396	Neutral	0.664	possibly damaging	0.010	deleterious	1
COX7B2	4_46737040_G/A	346	170	57	T/I	aCa/aTa	rs140822119	0.432	Neutral	0.004	benign	0.200	tolerated	0
COX8A	11_63742157_C/T	79	5	2	S/F	tCc/tTc	rs148986341	0.468	Neutral	0.008	benign	0.010	deleterious	1

COX8A	11_63742183_G/A	105	31	11	G/S	Ggc/Agc	rs199919249	0.196	Neutral	0.951	probably damaging	0.070	tolerated	1
COX8A	11_63742219_C/T	141	67	23	R/C	Cgc/Tgc	rs144339685	0.352	Neutral	0.909	probably damaging	0.060	tolerated	1
COX8C	14_93813619_C/G	83	5	2	P/R	cCt/cGt	rs201659311	0.277	Neutral	0.954	probably damaging			missing
COX8C	14_93813724_G/T	188	110	37	R/L	cGg/cTg	rs199879752	0.363	Neutral	0.972	probably damaging			missing
COX8C	14_93813726_C/T	190	112	38	P/S	Ccc/Tcc	rs114399408	0.435	Neutral	0.739	possibly damaging			0
COX8C	14_93814387_G/C	218	140	47	G/A	gGa/gCa	rs201893758	0.741	Pathogenic	0.033	benign			missing
CYC1	8_145150832_A/G	299	226	76	M/V	Atg/Gtg	rs7820984	0.376	Neutral	0.000	benign	0.660	tolerated	0
CYC1	8_145150833_T/C	300	227	76	M/T	aTg/aCg	rs144257411	0.365	Neutral	0.000	benign	0.320	tolerated	0
CYC1	8_145150929_C/A	396	323	108	T/N	aCc/aAc	rs145609083	0.378	Neutral	0.230	benign	0.010	deleterious	1
CYC1	8_145151126_G/T	499	426	142	E/D	gaG/gaT	rs201814058	0.512	Neutral	0.952	probably damaging	0.050	tolerated	1
CYC1	8_145151364_T/C	651	578	193	L/S	tTg/tCg	rs201129717	0.485	Neutral	0.786	possibly damaging	0.080	tolerated	0
CYC1	8_145151366_C/G	653	580	194	P/A	Ccc/Gcc	rs199884423	0.852	Pathogenic	1.000	probably damaging	0.000	deleterious	3
CYC1	8_145151545_G/A	743	670	224	G/R	Ggg/Agg	rs148021370	0.661	Possibly Pathogenic	0.685	possibly damaging	0.010	deleterious	1
CYC1	8_145152023_C/T	932	859	287	R/C	Cgc/Tgc	rs74494160	0.611	Possibly Pathogenic	0.974	probably damaging	0.010	deleterious	2

DGUOK	2_74154041_G/T	89	4	2	A/S	Gcc/Tcc	rs147551003	0.237	Neutral	0.041	benign	0.050	deleterious	1
DGUOK	2_74166092_C/A	283	198	66	H/Q	caC/caA	rs138034585	0.478	Neutral	0.005	benign	0.150	tolerated	0
DGUOK	2_74166093_G/A	284	199	67	V/I	Gta/Ata	rs62641679	0.624	Possibly Pathogenic	0.004	benign	0.360	tolerated	0
DGUOK	2_74166105_C/G	296	211	71	P/A	Cct/Gct	rs184770596	0.848	Pathogenic	0.437	possibly damaging	0.000	deleterious	2
DGUOK	2_74173927_T/C	422	337	113	F/L	Ttt/Ctt	rs141810774	0.767	Pathogenic	0.075	benign	0.080	tolerated	1
DGUOK	2_74177730_T/A	547	462	154	N/K	aaT/aaA	rs144181978	0.809	Pathogenic	0.992	probably damaging	0.010	deleterious	3
DGUOK	2_74177777_A/G	594	509	170	Q/R	cAg/cGg	rs74874677	0.792	Pathogenic	0.793	possibly damaging	0.080	tolerated	1
MFF	2_228194472_G/C	452	11	4	G/A	gGa/gCa	rs145010660	0.077	Neutral	0.005	benign	0.370	tolerated	0
MFF	2_228194480_A/T	460	19	7	S/C	Agt/Tgt	rs3211097	0.095	Neutral	0.418	benign	0.140	tolerated	0
MFF	2_228194481_G/T	461	20	7	S/I	aGt/aTt	rs3211098	0.089	Neutral	0.182	benign	0.260	tolerated	0
MFF	2_228194483_G/T	463	22	8	D/Y	Gac/Tac	rs78872053	0.241	Neutral	0.232	benign	0.000	deleterious	1
MFF	2_228195407_A/G	545	104	35	Y/C	tAc/tGc	rs200132653	0.738	Pathogenic	0.997	probably damaging	0.000	deleterious	3
MFF	2_228195455_A/G	593	152	51	E/G	gAa/gGa	rs182099421	0.659	Possibly Pathogenic	0.982	probably damaging	0.000	deleterious	2
MFF	2_228195473_C/T	611	170	57	P/L	cCg/cTg	rs149692814	0.534	Neutral	0.997	probably damaging	0.000	deleterious	2
MFF	2_228195496_G/A	634	193	65	G/R	Gga/Aga	rs201993285	0.413	Neutral	0.426	benign	0.220	tolerated	0
MFF	2_228197177_A/C	743	302	101	D/A	gAc/gCc	rs143374639	0.847	Pathogenic	0.288	benign	0.000	deleterious	2
MFF	2_228205039_G/A	902	461	154	R/Q	cGg/cAg	rs140493973	0.543	Neutral	0.982	probably damaging	0.120	tolerated	1
MFF	2_228212070_A/G	1163	722	241	Q/R	cAg/cGg	rs200608831	0.517	Neutral	0.937	probably damaging	0.030	deleterious	2
MFF	2_228220422_T/C	1283	842	281	I/T	aTt/aCt	rs145321987	0.769	Pathogenic	0.097	benign	0.020	deleterious	2
MFF	2_228220451_G/A	1312	871	291	V/I	Gta/Ata	rs191608569	0.603	Possibly Pathogenic	0.120	benign	0.020	deleterious	1
MFN1	3_179066700_A/G	187	61	21	I/V	Atc/Gtc	rs193215263	0.549	Neutral	0.052	benign	0.050	deleterious	1

MFN1	3_179069715_G/A	266	140	47	R/Q	cGa/cAa	rs187323205	0.379	Neutral	0.001	benign	0.600	tolerated	0
MFN1	3_179069717_A/C	268	142	48	I/L	Ata/Cta	rs142787699	0.401	Neutral	0.006	benign	0.280	tolerated	0
MFN1	3_179082937_G/A	803	677	226	R/Q	cGg/cAg	rs143476739	0.485	Neutral	0.919	probably damaging	0.000	deleterious	2
MFN1	3_179093011_T/C	1105	979	327	C/R	Tgt/Cgt	rs149864152	0.638	Possibly Pathogenic	0.864	possibly damaging	0.000	deleterious	1
MFN1	3_179093015_T/A	1109	983	328	I/N	aTc/aAc	rs200775244	0.609	Possibly Pathogenic	1.000	probably damaging	0.000	deleterious	2
MFN1	3_179093053_A/C	1147	1021	341	T/P	Act/Cct	rs200339629	0.498	Neutral	0.090	benign	0.020	deleterious	1
MFN1	3_179094898_T/C	1292	1166	389	L/P	cTt/cCt	rs200247518	0.591	Neutral	0.940	probably damaging	0.040	deleterious	2
MFN1	3_179094919_A/G	1313	1187	396	K/R	aAa/aGa	rs199736732	0.336	Neutral	0.003	benign	0.450	tolerated	0
MFN1	3_179095227_A/G	1446	1320	440	I/M	atA/atG	rs186155706	0.338	Neutral	0.003	benign	0.030	deleterious	1
MFN1	3_179096187_A/T	1514	1388	463	D/V	gAt/gTt	rs141885014	0.257	Neutral	0.018	benign	0.050	deleterious	1
MFN1	3_179096584_A/C	1770	1644	548	L/F	ttA/ttC	rs200881774	0.296	Neutral	0.010	benign	0.400	tolerated	0
MFN1	3_179104270_A/G	1991	1865	622	Y/C	tAt/tGt	rs186960036	0.875	Pathogenic	1.000	probably damaging	0.000	deleterious	3
MFN1	3_179107886_G/A	2233	2107	703	D/N	Gat/Aat	rs200188689	0.568	Neutral	0.080	benign	0.650	tolerated	0
MFN2	1_12052615_C/T	501	179	60	T/M	aCg/aTg	rs138345244	0.354	Neutral	0.831	possibly damaging	0.090	tolerated	0
MFN2	1_12052675_G/T	561	239	80	G/V	gGt/gTt	rs139827903	0.420	Neutral	0.030	benign	0.010	deleterious	1
MFN2	1_12061533_G/A	1214	892	298	G/R	Ggg/Agg	rs41278630	0.682	Possibly Pathogenic	0.001	benign	0.480	tolerated	0
MFN2	1_12062112_C/T	1434	1112	371	A/V	gCg/gTg	rs201675158	0.308	Neutral	0.002	benign	0.280	tolerated	0
MFN2	1_12062145_C/T	1467	1145	382	A/V	gCg/gTg	rs201165591	0.471	Neutral	0.379	benign	0.090	tolerated	0
MFN2	1_12064068_C/T	1502	1180	394	R/C	Cgt/Tgt	rs186448929	0.527	Neutral	0.079	benign	0.040	deleterious	1
MFN2	1_12064087_G/A	1521	1199	400	R/Q	cGa/cAa	rs138072432	0.484	Neutral	0.919	probably damaging	0.040	deleterious	2
MFN2	1_12064645_C/T	1689	1367	456	P/L	cCa/cTa	rs78658090	0.835	Pathogenic	0.018	benign	0.050	deleterious	2

MFN2	1_12065879_A/C	1929	1607	536	D/A	gAc/gCc	rs190705310	0.783	Pathogenic	0.990	probably damaging	0.000	deleterious	3
MFN2	1_12069692_G/A	2435	2113	705	V/I	Gtc/Atc	rs142271930	0.756	Pathogenic	0.018	benign	0.380	tolerated	1
MFN2	1_12069698_C/T	2441	2119	707	R/W	Cgg/Tgg	rs119103267	0.836	Pathogenic	0.978	probably damaging	0.010	deleterious	3
MFN2	1_12069725_G/A	2468	2146	716	A/T	Gcc/Acc	rs144860227	0.726	Pathogenic	0.178	benign	0.630	tolerated	1
MTERF	7_91503980_C/T	145	68	23	R/Q	cGa/cAa	rs190837494	0.283	Neutral	0.001	benign	0.800	tolerated	0
MTERF	7_91503951_C/T	174	97	33	V/I	Gtt/Att	rs201580782	0.296	Neutral	0.003	benign	0.670	tolerated	0
MTERF	7_91503914_G/A	211	134	45	T/I	aCa/aTa	rs144315661	0.270	Neutral	0.000	benign	0.030	deleterious	1
MTERF	7_91503846_T/G	279	202	68	M/L	Atg/Ctg	rs199603020	0.559	Neutral	0.002	benign	0.130	tolerated	0
MTERF	7_91503759_T/C	366	289	97	S/G	Agc/Ggc	rs148655332	0.519	Neutral	0.007	benign	0.260	tolerated	0
MTERF	7_91503744_C/T	381	304	102	A/T	Gct/Act	rs201335490	0.622	Possibly Pathogenic	0.960	probably damaging	0.000	deleterious	2
MTERF	7_91503699_C/T	426	349	117	E/K	Gag/Aag	rs202031297	0.502	Neutral	0.085	benign	0.270	tolerated	0
MTERF	7_91503687_T/C	438	361	121	K/E	Aaa/Gaa	rs181549251	0.474	Neutral	0.003	benign	0.720	tolerated	0
MTERF	7_91503524_C/T	601	524	175	R/Q	cGa/cAa	rs200438840	0.847	Pathogenic	0.190	benign	0.080	tolerated	1
MTERF	7_91503417_C/T	708	631	211	A/T	Gca/Aca	rs17856025	0.136	Neutral	0.001	benign	0.520	tolerated	0
MTERF	7_91503384_G/C	741	664	222	P/A	Cct/Gct	rs143980432	0.726	Pathogenic	0.251	benign	0.090	tolerated	1
MTERF	7_91503356_C/T	769	692	231	R/Q	cGg/cAg	rs78445151	0.840	Pathogenic	0.674	possibly damaging	0.190	tolerated	1
MTERF	7_91503317_T/C	808	731	244	N/S	aAt/aGt	rs149530545	0.423	Neutral	0.001	benign	0.510	tolerated	0
MTERF	7_91503235_T/G	890	813	271	R/S	agA/agC	rs139218723	0.577	Neutral	0.515	possibly damaging	0.040	deleterious	1
MTERF	7_91503228_C/T	897	820	274	A/T	Gca/Aca	rs10266424	0.128	Neutral	0.000	benign	1.000	tolerated	0
MTERF	7_91503114_T/C	1011	934	312	I/V	Ata/Gta	rs139119978	0.563	Neutral	0.022	benign	0.100	tolerated	0

MTERF	7_91502930_T/C	1195	1118	373	K/R	aAa/aGa	rs199652694	0.553	Neutral	0.005	benign	0.400	tolerated	0
MTFR1	8_66582195_G/C	176	8	3	G/A	gGc/gCc	rs201019084	0.264	Neutral	0.090	benign	0.220	tolerated	0
MTFR1	8_66594600_A/G	247	79	27	R/G	Agg/Ggg	rs144584935	0.396	Neutral	0.000	benign	1.000	tolerated	0
MTFR1	8_66617012_A/G	485	317	106	D/G	gAc/gGc	rs141941459	0.333	Neutral	0.044	benign	0.310	tolerated	0
MTFR1	8_66617076_G/T	549	381	127	K/N	aaG/aaT	rs201556776	0.648	Possibly Pathogenic	1.000	probably damaging	0.000	deleterious	2
MTFR1	8_66619338_G/A	731	563	188	S/N	aGt/aAt	rs200811406	0.475	Neutral	0.062	benign	0.080	tolerated	0
MTFR1	8_66620091_G/A	898	730	244	V/M	Gtg/Atg	rs150962565	0.168	Neutral	0.137	benign	0.110	tolerated	0
MTFR1	8_66620167_G/A	974	806	269	R/Q	cGg/cAg	rs184253762	0.300	Neutral	0.999	probably damaging	0.060	tolerated	1
NDUFAF2	5_60448675_G/A	530	403	135	A/T	Gct/Act	rs201187582	0.303	Neutral	0.738	possibly damaging	0.080	tolerated	0
NDUFAF2	5_60448723_G/A	578	451	151	G/S	Ggt/Agt	rs9885480	0.328	Neutral	0.738	possibly damaging	0.200	tolerated	0
NDUFAF3	3_49059639_C/T	1196	62	21	P/L	cCc/cTc	rs199568117	0.305	Neutral	0.001	benign	0.670	tolerated	0
NDUFAF4	6_97345638_G/T	120	40	14	L/I	Cta/Ata	rs145392673	0.500	Neutral	0.416	benign	0.060	tolerated	0
NDUFAF4	6_97344663_T/C	277	197	66	K/R	aAa/aGa	rs148667964	0.514	Neutral	0.172	benign	0.290	tolerated	0
NDUFAF4	6_97339133_A/T	455	375	125	N/K	aaT/aaA	rs200279216	0.783	Pathogenic	0.999	probably damaging	0.140	tolerated	2
NDUFAF4	6_97339017_A/T	571	491	164	F/Y	tTc/tAc	rs201754378	0.579	Neutral	0.738	possibly damaging	0.020	deleterious	1
NDUFB1	14_92588049_G/C	213	73	25	L/V	Ctg/Gtg	rs138437079	0.157	Neutral	0.037	benign	0.280	tolerated	0
NDUFB1	14_92583974_T/C	289	149	50	N/S	aAc/aGc	rs201547910	0.685	Possibly Pathogenic	0.649	possibly damaging	0.010	deleterious	1
NDUFB1	14_92583956_C/T	307	167	56	R/Q	cGg/cAg	rs190083501	0.757	Pathogenic	0.807	possibly damaging	0.020	deleterious	2

NDUFB1	14_92583927_T/A	336	196	66	M/L	Atg/Ttg	rs149760197	0.603	Possibly Pathogenic	0.002	benign	0.270	tolerated	0
NDUFB1	14_92583867_G/A	396	256	86	R/W	Cgg/Tgg	rs151054506	0.792	Pathogenic	0.025	benign	0.110	tolerated	1
NDUFB10	16_2009733_C/G	215	108	36	D/E	gaC/gaG	rs200975991	0.785	Pathogenic	0.999	probably damaging	0.010	deleterious	3
NDUFB10	16_2011596_T/C	475	368	123	V/A	gTg/gCg	rs201663429	0.343	Neutral	0.158	benign	0.360	tolerated	0
NDUFB2	7_140396561_G/T	90	17	6	R/L	cGg/cTg	rs200087759	0.585	Neutral	0.193	benign	0.010	deleterious	1
NDUFB3	2_201943624_C/T	342	19	7	H/Y	Cat/Tat	rs144513268	0.234	Neutral	0.000	benign	0.020	deleterious	1
NDUFB3	2_201943639_C/T	357	34	12	H/Y	Cat/Tat	rs182420107	0.255	Neutral	0.000	benign	0.040	deleterious	1
NDUFB3	2_201943669_T/C	387	64	22	W/R	Tgg/Cgg	rs142609245	0.729	Pathogenic	0.996	probably damaging	0.000	deleterious	3
NDUFB3	2_201950223_T/C	505	182	61	V/A	gTt/gCt	rs139936993	0.454	Neutral	0.022	benign	0.920	tolerated	0
NDUFB4	3_120315283_C/T	128	77	26	S/F	tCt/tTt	rs150031407	0.575	Neutral	0.997	probably damaging	0.000	deleterious	2
NDUFB4	3_120315384_A/T	229	178	60	I/F	Atc/Ttc	rs142688627	0.773	Pathogenic	0.936	probably damaging	0.100	tolerated	2
NDUFB4	3_120321071_T/G	395	344	115	L/R	cTt/cGt	rs149224531	0.716	Pathogenic	0.937	probably damaging	0.590	tolerated	2
NDUFB4	3_120321095_G/A	419	368	123	R/Q	cGa/cAa	rs201413691	0.815	Pathogenic	0.115	benign	0.030	deleterious	2
NDUFB5	3_179322703_A/C	214	100	34	T/P	Act/Cct	rs35399127	0.304	Neutral	0.986	probably damaging	0.040	deleterious	2
NDUFB5	3_179332803_A/T	283	169	57	I/F	Atc/Ttc	rs148532160	0.354	Neutral	0.910	probably damaging	0.000	deleterious	2
NDUFB5	3_179336257_T/C	511	397	133	Y/H	Tat/Cat	rs4147793	0.317	Neutral	1.000	probably damaging	0.000	deleterious	2
NDUFB5	3_179336264_G/A	518	404	135	R/K	aGa/aAa	rs145089839	0.373	Neutral	0.005	benign	1.000	tolerated	0
NDUFB6	9_32573054_G/C	107	5	2	T/R	aCg/aGg	rs138358975	0.253	Neutral	0.798	possibly damaging	0.000	deleterious	1
NDUFB6	9_32572983_G/C	178	76	26	Q/E	Cag/Gag	rs199895242	0.330	Neutral	0.987	probably damaging	0.000	deleterious	2
NDUFB6	9_32572939_C/T	222	120	40	M/I	atG/atA	rs190070706	0.251	Neutral	0.059	benign	0.570	tolerated	0

NDUFB6	9_32572932_T/C	229	127	43	M/V	Atg/Gtg	rs142741532	0.171	Neutral	0.005	benign	1.000	tolerated	0
NDUFB6	9_32571013_G/A	320	218	73	T/I	aCt/aTt	rs200723755	0.347	Neutral	0.274	benign	0.330	tolerated	0
NDUFB6	9_32570989_A/G	344	242	81	I/T	aTt/aCt	rs148891049	0.448	Neutral	0.870	possibly damaging	0.010	deleterious	1
NDUFB6	9_32553935_G/A	428	326	109	T/I	aCa/aTa	rs143339409	0.349	Neutral	0.009	benign	0.110	tolerated	0
NDUFB6	9_32553915_C/T	448	346	116	V/I	Gta/Ata	rs190587227	0.362	Neutral	0.994	probably damaging	0.350	tolerated	1
NDUFB7	19_14682809_C/A	78	4	2	G/W	Ggg/Tgg	rs189994454	0.528	Neutral	0.999	probably damaging	0.000	deleterious	2
NDUFB7	19_14682725_C/A	162	88	30	G/C	Ggc/Tgc	rs201675767	0.742	Pathogenic	1.000	probably damaging	0.000	deleterious	3
NDUFB7	19_14682721_A/C	166	92	31	F/C	tTc/tGc	rs200041574	0.866	Pathogenic	0.742	possibly damaging	0.000	deleterious	2
NDUFB7	19_14677608_G/A	324	250	84	R/W	Cgg/Tgg	rs200757972	0.700	Pathogenic	0.895	possibly damaging	0.000	deleterious	2
NDUFB7	19_14677049_G/A	384	310	104	R/W	Cgg/Tgg	rs200292442	0.614	Possibly Pathogenic	0.937	probably damaging	0.020	deleterious	2
NDUFB7	19_14677043_G/C	390	316	106	R/G	Cgg/Ggg	rs3752220	0.270	Neutral	0.004	benign	0.060	tolerated	0
NDUFB7	19_14677022_T/G	411	337	113	K/Q	Aag/Cag	rs202223254	0.444	Neutral	0.002	benign	0.360	tolerated	0
NDUFB8	10_102289587_C/G	35	22	8	V/L	Gtc/Ctc	rs139827718	0.625	Possibly Pathogenic	0.010	benign	0.360	tolerated	0
NDUFB8	10_102289572_A/C	50	37	13	W/G	Tgg/Ggg	rs201604335	0.692	Possibly Pathogenic	0.398	benign	0.020	deleterious	1
NDUFB8	10_102289263_G/T	99	86	29	A/D	gCc/gAc	rs200405716	0.718	Pathogenic	0.998	probably damaging	0.080	tolerated	2
NDUFB8	10_102286733_G/A	324	311	104	P/L	cCg/cTg	rs185514139	0.625	Possibly Pathogenic	0.294	benign	0.010	deleterious	1
NDUFB8	10_102286256_G/C	381	368	123	P/R	cCt/cGt	rs74154666	0.519	Neutral	0.850	possibly damaging	0.220	tolerated	0
NDUFB8	10_102286251_A/T	386	373	125	S/T	Tct/Act	rs1802224	0.515	Neutral	0.042	benign	0.230	tolerated	0
NDUFB8	10_102286179_C/T	458	445	149	V/M	Gtg/Atg	rs141801241	0.329	Neutral	0.020	benign	0.170	tolerated	0

NDUFB9	8_125555335_T/C	193	109	37	Y/H	Tac/Cac	rs140417066	0.581	Neutral	0.953	probably damaging	0.030	deleterious	2
NDUFB9	8_125555366_G/T	224	140	47	R/L	cGg/cTg	rs142723791	0.598	Neutral	0.885	possibly damaging	0.000	deleterious	1
NDUFB9	8_125555387_A/T	245	161	54	E/V	gAa/gTa	rs138066988	0.579	Neutral	0.040	benign	1.000	tolerated	0
NDUFB9	8_125555426_C/G	284	200	67	A/G	gCc/gGc	rs200765174	0.578	Neutral	0.006	benign	1.000	tolerated	0
NDUFB9	8_125555446_C/T	304	220	74	R/C	Cgt/Tgt	rs199940282	0.393	Neutral	0.002	benign	0.230	tolerated	0
NDUFB9	8_125562029_C/T	520	436	146	P/S	Cct/Tct	rs10195	0.124	Neutral	0.009	benign	0.140	tolerated	0
NDUFB9	8_125562065_C/G	556	472	158	R/G	Cga/Gga	rs148402231	0.301	Neutral	0.662	possibly damaging	0.000	deleterious	1
NDUFC1	4_140216277_C/T	425	91	31	V/M	Gtg/Atg	rs201811659	0.297	Neutral	0.840	possibly damaging	0.020	deleterious	1
NDUFC1	4_140216214_C/T	488	154	52	V/I	Gtc/Atc	rs200399570	0.223	Neutral	0.021	benign	0.220	tolerated	0
NDUFC1	4_140216203_C/A	499	165	55	W/C	tgG/tgT	rs201035643	0.674	Possibly Pathogenic	0.997	probably damaging	0.000	deleterious	2
NDUFC1	4_140213733_C/G	536	202	68	E/Q	Gag/Cag	rs72939460	0.274	Neutral	0.991	probably damaging	0.010	deleterious	2
NDUFC2	11_77790655_G/C	611	136	46	L/V	Cta/Gta	rs8875	0.172	Neutral	0.010	benign	0.500	tolerated	0
NDUFC2	11_77781037_C/T	831	356	119	R/H	cGt/cAt	rs183610034	0.799	Pathogenic	0.999	probably damaging	0.000	deleterious	3
NDUFS1	2_207018354_G/C	316	49	17	P/A	Cct/Gct	rs201997807	0.365	Neutral	0.000	benign	0.330	tolerated	0
NDUFS1	2_207012277_T/C	796	529	177	I/V	Ata/Gta	rs140126185	0.794	Pathogenic	0.996	probably damaging	0.000	deleterious	3
NDUFS1	2_207011753_A/G	878	611	204	M/T	aTg/aCg	rs148544177	0.334	Neutral	0.065	benign	0.090	tolerated	0
NDUFS1	2_207008821_G/C	1175	908	303	T/S	aCc/aGc	rs75666426	0.364	Neutral	0.346	benign	0.270	tolerated	0
NDUFS1	2_207007550_C/A	1260	993	331	Q/H	caG/caT	rs145401558	0.441	Neutral	0.038	benign	0.170	tolerated	0
NDUFS1	2_207007482_A/T	1328	1061	354	L/H	cTc/cAc	rs139690694	0.727	Pathogenic	0.933	probably damaging	0.000	deleterious	3
NDUFS1	2_207006704_C/T	1490	1223	408	R/H	cGt/cAt	rs151279101	0.873	Pathogenic	1.000	probably damaging	0.000	deleterious	3
NDUFS1	2_207003310_G/C	1558	1291	431	L/V	Ctt/Gtt	rs78042826	0.446	Neutral	0.013	benign	0.630	tolerated	0

NDUFS1	2_207003221_A/C	1647	1380	460	H/Q	caT/caG	rs202214721	0.634	Possibly Pathogenic	0.987	probably damaging	0.020	deleterious	2
NDUFS1	2_206997706_C/T	1783	1516	506	V/I	Gtt/Att	rs137889316	0.538	Neutral	0.072	benign	0.400	tolerated	0
NDUFS1	2_206994857_T/C	1930	1663	555	I/V	Atc/Gtc	rs200131601	0.523	Neutral	0.010	benign	0.610	tolerated	0
NDUFS1	2_206994821_T/C	1966	1699	567	I/V	Att/Gtt	rs147685849	0.465	Neutral	0.005	benign	1.000	tolerated	0
NDUFS1	2_206991540_G/C	2180	1913	638	T/S	aCt/aGt	rs200782941	0.330	Neutral	0.002	benign	1.000	tolerated	0
NDUFS1	2_206991498_T/C	2222	1955	652	N/S	aAt/aGt	rs201644320	0.266	Neutral	0.048	benign	0.410	tolerated	0
NDUFS1	2_206991447_T/C	2273	2006	669	N/S	aAt/aGt	rs142716964	0.339	Neutral	0.001	benign	0.880	tolerated	0
NDUFS2	1_161172233_C/A	506	58	20	P/T	Cct/Act	rs11538340	0.257	Neutral	0.009	benign	0.060	tolerated	0
NDUFS2	1_161180473_T/C	1407	959	320	V/A	gTt/gCt	rs144937332	0.710	Pathogenic	0.780	possibly damaging	0.000	deleterious	2
NDUFS2	1_161180482_G/A	1416	968	323	R/Q	cGa/cAa	rs35086265	0.314	Neutral	0.051	benign	0.120	tolerated	0
NDUFS2	1_161182208_C/G	1502	1054	352	P/A	Cct/Gct	rs11576415	0.316	Neutral	0.916	probably damaging	0.000	deleterious	2
NDUFS2	1_161182232_G/T	1526	1078	360	D/Y	Gat/Tat	rs145577083	0.570	Neutral	1.000	probably damaging	0.000	deleterious	2
NDUFS2	1_161182259_G/A	1553	1105	369	A/T	Gca/Aca	rs200509897	0.418	Neutral	0.037	benign	0.180	tolerated	0
NDUFS2	1_161183502_G/T	1724	1276	426	A/S	Gct/Tct	rs186476170	0.745	Pathogenic	0.843	possibly damaging	0.080	tolerated	1
NDUFS2	1_161183958_T/C	1815	1367	456	I/T	aTt/aCt	rs140731056	0.817	Pathogenic	0.816	possibly damaging	0.000	deleterious	2
NDUFS3	11_47600677_C/T	116	34	12	R/C	Cgc/Tgc	rs201457989	0.556	Neutral	0.397	benign	0.030	deleterious	1
NDUFS3	11_47603733_G/C	557	475	159	V/L	Gtg/Ctg	rs148331180	0.683	Possibly Pathogenic	0.289	benign	0.810	tolerated	0
NDUFS3	11_47605878_G/A	722	640	214	D/N	Gat/Aat	rs201626967	0.389	Neutral	0.123	benign	0.020	deleterious	1
NDUFS3	11_47605891_G/A	735	653	218	R/Q	cGg/cAg	rs78121716	0.576	Neutral	0.987	probably damaging	0.000	deleterious	2
NDUFS3	11_47605987_A/G	831	749	250	E/G	gAg/gGg	rs201167810	0.263	Neutral	0.005	benign	0.000	deleterious	1
NDUFS4	5_52856497_C/A	33	5	2	A/E	gCg/gAg	rs148595893	0.282	Neutral	0.112	benign	0.000	deleterious	1
NDUFS4	5_52856502_G/C	38	10	4	V/L	Gtg/Ctg	rs185711494	0.297	Neutral	0.000	benign	0.120	tolerated	0

NDUFS4	5_52856539_G/A	75	47	16	R/Q	cGg/cAg	rs188911977	0.340	Neutral	0.008	benign	0.380	tolerated	0
NDUFS4	5_52856563_C/A	99	71	24	A/D	gCc/gAc	rs146259362	0.401	Neutral	0.255	benign	0.040	deleterious	1
NDUFS4	5_52856572_T/A	108	80	27	V/D	gTt/gAt	rs145347909	0.293	Neutral	0.064	benign	0.020	deleterious	1
NDUFS4	5_52899282_G/T	127	99	33	R/S	agG/agT	rs200926524	0.293	Neutral	0.024	benign	0.020	deleterious	1
NDUFS4	5_52942135_C/T	278	250	84	R/C	Cgc/Tgc	rs184765529	0.777	Pathogenic	0.994	probably damaging	0.000	deleterious	3
NDUFS4	5_52954401_T/G	399	371	124	M/R	aTg/aGg	rs199541993	0.735	Pathogenic	0.535	possibly damaging	0.000	deleterious	2
NDUFS4	5_52978992_T/A	497	469	157	S/T	Tcc/Acc	rs149482195	0.329	Neutral	0.074	benign	0.210	tolerated	0
NDUFS4	5_52979034_A/G	539	511	171	R/G	Aga/Gga	rs200758718	0.605	Possibly Pathogenic	0.999	probably damaging	0.000	deleterious	2
NDUFS5	1_39494611_C/T	302	215	72	T/M	aCg/aTg	rs201757086	0.343	Neutral	0.188	benign	0.040	deleterious	1
NDUFS5	1_39500125_C/T	365	278	93	T/I	aCc/aTc	rs200515387	0.282	Neutral	0.999	probably damaging	0.000	deleterious	2
NDUFS5	1_39500140_A/C	380	293	98	H/P	cAc/cCc	rs192512172	0.199	Neutral	0.847	possibly damaging	0.000	deleterious	1
NDUFS5	1_39500141_C/A	381	294	98	H/Q	caC/caA	rs146279654	0.260	Neutral	0.847	possibly damaging	0.060	tolerated	0
NDUFS6	5_1802445_A/T	161	143	48	D/V	gAt/gTt	rs199652659	0.287	Neutral	0.003	benign	0.070	tolerated	0
NDUFS6	5_1814495_G/A	247	229	77	V/M	Gtg/Atg	rs187737486	0.414	Neutral	0.941	probably damaging	0.060	tolerated	1
NDUFS6	5_1814523_C/T	275	257	86	A/V	gCg/gTg	rs192286856	0.313	Neutral	0.674	possibly damaging	0.500	tolerated	0
NDUFS6	5_1815992_G/A	355	337	113	G/S	Ggt/Agt	rs200109710	0.685	Possibly Pathogenic	0.974	probably damaging	0.080	tolerated	1
NDUFS7	19_1387824_G/A	332	31	11	G/S	Ggc/Agc	rs201112782	0.323	Neutral	0.002	benign	0.590	tolerated	0
NDUFS7	19_1388538_C/T	369	68	23	P/L	cCg/cTg	rs1142530	0.186	Neutral	0.000	benign	0.350	tolerated	0
NDUFS7	19_1388855_C/G	447	146	49	A/G	gCc/gGc	rs11551666	0.251	Neutral	0.004	benign	0.120	tolerated	0
NDUFS7	19_1393344_G/A	860	559	187	A/T	Gca/Aca	rs201420030	0.717	Pathogenic	0.111	benign	0.000	deleterious	2
NDUFS8	11_67799622_C/T	111	4	2	R/C	Cgc/Tgc	rs150278938	0.371	Neutral	0.000	benign	0.130	tolerated	0

NDUFS8	11_67799637_C/A	126	19	7	P/T	Cct/Act	rs142658611	0.257	Neutral	0.005	benign	0.260	tolerated	0
NDUFS8	11_67799649_C/T	138	31	11	R/W	Cgg/Tgg	rs201990988	0.493	Neutral	0.059	benign	0.000	deleterious	1
NDUFS8	11_67799671_G/A	160	53	18	R/H	cGt/cAt	rs201017561	0.411	Neutral	0.041	benign	0.170	tolerated	0
NDUFS8	11_67803759_C/A	519	412	138	R/S	Cgc/Agc	rs201484242	0.595	Neutral	1.000	probably damaging	0.000	deleterious	2
NDUFS8	11_67803929_G/A	609	502	168	G/S	Ggc/Agc	rs147344724	0.496	Neutral	0.098	benign	0.140	tolerated	0
NDUFV1	11_67376023_G/T	309	156	52	R/S	agG/agT	rs199609729	0.392	Neutral	0.012	benign	0.500	tolerated	0
NDUFV1	11_67376936_G/T	493	340	114	V/L	Gtg/Ttg	rs200365831	0.693	Possibly Pathogenic	0.165	benign	0.030	deleterious	1
NDUFV1	11_67376982_A/G	539	386	129	E/G	gAg/gGg	rs144291845	0.441	Neutral	0.242	benign	0.030	deleterious	1
NDUFV1	11_67377036_G/A	593	440	147	R/Q	cGg/cAg	rs199972110	0.674	Possibly Pathogenic	0.511	possibly damaging	0.300	tolerated	0
NDUFV1	11_67377050_C/T	607	454	152	R/C	Cgc/Tgc	rs151144350	0.567	Neutral	0.038	benign	0.080	tolerated	0
NDUFV1	11_67377870_T/C	682	529	177	Y/H	Tat/Cat	rs180950242	0.645	Possibly Pathogenic	0.995	probably damaging	0.000	deleterious	2
NDUFV1	11_67377904_G/A	716	563	188	G/D	gGc/gAc	rs142982022	0.899	Pathogenic	0.488	possibly damaging	0.030	deleterious	2
NDUFV1	11_67377936_C/T	748	595	199	R/C	Cgc/Tgc	rs201289242	0.557	Neutral	0.466	possibly damaging	0.020	deleterious	1
NDUFV1	11_67378498_G/A	886	733	245	V/M	Gtg/Atg	rs200829846	0.854	Pathogenic	0.818	possibly damaging	0.020	deleterious	2
NDUFV1	11_67378525_A/G	913	760	254	I/V	Atc/Gtc	rs201908937	0.872	Pathogenic	0.435	possibly damaging	0.000	deleterious	2
NDUFV1	11_67378876_G/T	1069	916	306	G/C	Ggt/Tgt	rs201382784	0.968	Pathogenic	0.998	probably damaging	0.000	deleterious	3
NDUFV1	11_67378883_C/T	1076	923	308	T/M	aCg/aTg	rs200925993	0.381	Neutral	0.268	benign	0.010	deleterious	1
NDUFV1	11_67379374_A/G	1240	1087	363	I/V	Atc/Gtc	rs200270653	0.472	Neutral	0.003	benign	0.680	tolerated	0
NDUFV1	11_67379608_A/C	1333	1180	394	K/Q	Aag/Cag	rs145679247	0.410	Neutral	0.045	benign	0.340	tolerated	0
NDUFV1	11_67379615_T/C	1340	1187	396	M/T	aTg/aCg	rs200627507	0.662	Possibly Pathogenic	0.068	benign	0.010	deleterious	1
NDUFV1	11_67379853_G/A	1472	1319	440	R/H	cGc/cAc	rs146910804	0.440	Neutral	0.083	benign	0.020	deleterious	1

NDUFV2	18_9117855_T/C	188	74	25	L/S	tTg/tCg	rs199997775	0.478	Neutral	0.223	benign	0.010	deleterious	1
NDUFV2	18_9117867_T/C	200	86	29	V/A	gTt/gCt	rs906807	0.160	Neutral	0.000	benign	1.000	tolerated	0
NDUFV2	18_9117899_G/A	232	118	40	V/M	Gtg/Atg	rs75362221	0.478	Neutral	0.181	benign	0.010	deleterious	1
NDUFV2	18_9119324_C/T	235	121	41	H/Y	Cac/Tac	rs202166758	0.687	Possibly Pathogenic	0.991	probably damaging	0.000	deleterious	2
NDUFV2	18_9119355_C/A	266	152	51	T/N	aCt/aAt	rs142405606	0.285	Neutral	0.809	possibly damaging	0.050	deleterious	1
NDUFV2	18_9122573_G/A	477	363	121	M/I	atG/atA	rs200422010	0.768	Pathogenic	1.000	probably damaging	0.000	deleterious	3
NDUFV2	18_9122586_C/A	490	376	126	P/T	Cca/Aca	rs199560855	0.865	Pathogenic	0.993	probably damaging	0.000	deleterious	3
NDUFV2	18_9124909_C/G	621	507	169	F/L	ttC/ttG	rs201708711	0.835	Pathogenic	0.992	probably damaging	0.000	deleterious	3
NDUFV2	18_9124974_A/G	686	572	191	N/S	aAt/aGt	rs200691654	0.560	Neutral	0.113	benign	0.010	deleterious	1
NDUFV3	21_44313454_C/G	80	11	4	P/R	cCg/cGg	rs77606940	0.328	Neutral	0.031	benign	0.120	tolerated	0
NDUFV3	21_44317073_G/T	154	85	29	A/S	Gct/Tct	rs78214542	0.143	Neutral	0.217	benign	0.080	tolerated	0
NDUFV3	21_44317080_C/T	161	92	31	T/M	aCg/aTg	rs148054698	0.199	Neutral	0.913	probably damaging	0.000	deleterious	2
NDUFV3	21_44317112_G/A	193	124	42	E/K	Gaa/Aaa	rs201455116	0.215	Neutral	0.060	benign	0.280	tolerated	0
NDUFV3	21_44317156_A/C	237	168	56	K/N	aaA/aaC	rs141922962	0.208	Neutral	0.998	probably damaging	0.000	deleterious	2
NDUFV3	21_44323388_C/T	335	266	89	A/V	gCt/gTt	rs200656693	0.079	Neutral	0.006	benign	1.000	tolerated	0
NDUFV3	21_44323412_C/T	359	290	97	A/V	gCt/gTt	rs35064727	0.160	Neutral	0.996	probably damaging	0.160	tolerated	1
NDUFV3	21_44323430_G/T	377	308	103	G/V	gGc/gTc	rs201597963	0.112	Neutral	0.263	benign	0.020	deleterious	1
NDUFV3	21_44323667_G/C	614	545	182	R/T	aGa/aCa	rs201154517	0.320	Neutral	0.139	benign	0.010	deleterious	1
NDUFV3	21_44323948_G/A	895	826	276	E/K	Gaa/Aaa	rs202060146	0.289	Neutral	0.011	benign	0.610	tolerated	0
NDUFV3	21_44323957_A/G	904	835	279	K/E	Aaa/Gaa	rs141329399	0.182	Neutral	0.978	probably damaging	0.010	deleterious	2
NDUFV3	21_44324329_G/A	1276	1207	403	E/K	Gag/Aag	rs61746238	0.267	Neutral	0.000	benign	0.940	tolerated	0

NDUFV3	21_44324365_G/A	1312	1243	415	D/N	Gac/Aac	rs10595	0.155	Neutral	0.182	benign	0.410	tolerated	0
NDUFV3	21_44324372_G/A	1319	1250	417	R/Q	cGa/cAa	rs114225578	0.201	Neutral	0.001	benign	1.000	tolerated	0
NDUFV3	21_44324377_G/A	1324	1255	419	G/S	Ggc/Agc	rs183648098	0.159	Neutral	0.005	benign	0.790	tolerated	0
NT5M	17_17209862_G/C	489	273	91	K/N	aaG/aaC	rs199941205	0.724	Pathogenic	0.993	probably damaging	0.030	deleterious	3
NT5M	17_17248203_C/A	741	525	175	D/E	gaC/gaA	rs201242235	0.940	Pathogenic	0.991	probably damaging	0.000	deleterious	3
NT5M	17_17250159_C/T	797	581	194	P/L	cCg/cTg	rs2240876	0.430	Neutral	0.000	benign	0.520	tolerated	0
NT5M	17_17250197_G/A	835	619	207	A/T	Gcc/Acc	rs145194793	0.254	Neutral	0.718	possibly damaging	0.160	tolerated	0
OPA1	3_193332522_C/A	277	43	15	Q/K	Cag/Aag	rs75414918	0.210	Neutral	0.000	benign	0.160	tolerated	0
OPA1	3_193332564_C/G	319	85	29	P/A	Cca/Gca	rs145565705	0.389	Neutral	0.023	benign	0.020	deleterious	1
OPA1	3_193332718_A/G	473	239	80	Y/C	tAt/tGt	rs151103940	0.436	Neutral	0.456	possibly damaging	0.030	deleterious	1
OPA1	3_193332823_C/T	578	344	115	A/V	gCc/gTc	rs200983556	0.371	Neutral	0.134	benign	0.520	tolerated	0
OPA1	3_193334991_G/A	707	473	158	S/N	aGt/aAt	rs7624750	0.168	Neutral	0.001	benign	0.810	tolerated	0
OPA1	3_193336676_C/T	809	575	192	A/V	gCg/gTg	rs34307082	0.119	Neutral	0.235	benign	0.040	deleterious	1
OPA1	3_193343987_G/A	965	731	244	R/H	cGc/cAc	rs201202646	0.189	Neutral	0.830	possibly damaging	0.010	deleterious	1
OPA1	3_193349441_T/C	1010	776	259	L/P	cTt/cCt	rs200223621	0.486	Neutral	0.108	benign	0.030	deleterious	1

OPA1	3_193360767_G/A	1414	1180	394	A/T	Gca/Aca	rs190223702	0.657	Possibly Pathogenic	0.911	probably damaging	0.030	deleterious	2
OPA1	3_193361167_A/G	1491	1257	419	I/M	atA/atG	rs143319805	0.920	Pathogenic	0.998	probably damaging	0.000	deleterious	3
OPA1	3_193363363_A/G	1810	1576	526	K/E	Aag/Gag	rs201301622	0.465	Neutral	0.434	benign	0.130	tolerated	0
OPA1	3_193364870_G/A	1951	1717	573	A/T	Gca/Aca	rs182251953	0.342	Neutral	0.111	benign	0.590	tolerated	0
OPA1	3_193366644_G/A	2176	1942	648	V/I	Gtt/Att	rs200756304	0.290	Neutral	0.169	benign	0.470	tolerated	0
OPA1	3_193372737_A/G	2279	2045	682	N/S	aAt/aGt	rs142694017	0.344	Neutral	0.016	benign	0.790	tolerated	0
OPA1	3_193375011_A/G	2501	2267	756	E/G	gAg/gGg	rs199925668	0.444	Neutral	0.049	benign	0.380	tolerated	0
OPA1	3_193377336_C/T	2686	2452	818	R/W	Cgg/Tgg	rs190235251	0.559	Neutral	0.954	probably damaging	0.010	deleterious	2
OPA1	3_193380621_A/G	2711	2477	826	N/S	aAt/aGt	rs200428940	0.197	Neutral	0.037	benign	0.420	tolerated	0
OPA1	3_193380726_G/A	2816	2582	861	R/Q	cGa/cAa	rs200412464	0.314	Neutral	0.012	benign	0.350	tolerated	0
OPA1	3_193409895_A/C	3207	2973	991	E/D	gaA/gaC	rs189036094	0.149	Neutral	0.006	benign	0.190	tolerated	0
OPA3	19_46087989_G/C	134	34	12	L/V	Cta/Gta	rs200742525	0.403	Neutral	0.086	benign	0.470	tolerated	0
OPA3	19_46057071_C/T	341	241	81	A/T	Gca/Aca	rs186796646	0.889	Pathogenic	1.000	probably damaging	0.000	deleterious	3
OPA3	19_46056900_C/T	512	412	138	A/T	Gcg/Acg	rs142402590	0.496	Neutral	0.013	benign	0.390	tolerated	0
PEO1	10_102748430_C/T	648	463	155	R/W	Cgg/Tgg	rs200405447	0.466	Neutral	0.608	possibly damaging	0.010	deleterious	1
PEO1	10_102748493_G/A	711	526	176	A/T	Gct/Act	rs199810842	0.454	Neutral	0.008	benign	0.540	tolerated	0
PEO1	10_102748601_G/A	819	634	212	G/R	Ggg/Agg	rs117140867	0.320	Neutral	0.001	benign	0.620	tolerated	0
PEO1	10_102748644_G/T	862	677	226	C/F	tGc/tTc	rs187291192	0.266	Neutral	0.045	benign	0.190	tolerated	0
PEO1	10_102749069_G/A	1287	1102	368	V/I	Gta/Ata	rs17113613	0.713	Pathogenic	0.035	benign	0.610	tolerated	1

PEO1	10_102749079_G/A	1297	1112	371	R/Q	cGg/cAg	rs143309797	0.417	Neutral	0.501	possibly damaging	0.590	tolerated	0
PEO1	10_102750648_A/T	1800	1615	539	I/F	Atc/Ttc	rs200192223	0.635	Possibly Pathogenic	0.466	possibly damaging	0.000	deleterious	1
PEO1	10_102750730_A/G	1882	1697	566	K/R	aAg/aGg	rs116046810	0.348	Neutral	0.080	benign	0.340	tolerated	0
PEO1	10_102753154_G/C	2127	1942	648	V/L	Gtg/Ctg	rs190487176	0.207	Neutral	0.008	benign	0.260	tolerated	0
PEO1	10_102753257_G/A	2230	2045	682	R/H	cGt/cAt	rs182559752	0.116	Neutral	0.002	benign	0.200	tolerated	0
PINK1	1_20960385_A/T	438	344	115	Q/L	cAg/cTg	rs148871409	0.130	Neutral	0.037	benign	0.220	tolerated	0
PINK1	1_20964401_C/T	548	454	152	R/W	Cgg/Tgg	rs45608139	0.494	Neutral	0.734	possibly damaging	0.000	deleterious	1
PINK1	1_20964533_C/T	680	586	196	P/S	Cca/Tca	rs35802484	0.267	Neutral	0.019	benign	0.010	deleterious	1
PINK1	1_20964546_C/T	693	599	200	A/V	gCa/gTa	rs149822257	0.224	Neutral	0.062	benign	1.000	tolerated	0
PINK1	1_20964573_C/T	720	626	209	P/L	cCg/cTg	rs34677717	0.700	Pathogenic	0.001	benign	0.290	tolerated	1
PINK1	1_20966389_G/T	774	680	227	G/V	gGt/gTt	rs138018628	0.540	Neutral	0.934	probably damaging	0.020	deleterious	2
PINK1	1_20966404_C/T	789	695	232	A/V	gCc/gTc	rs144071530	0.528	Neutral	0.988	probably damaging	0.010	deleterious	2
PINK1	1_20971050_A/T	938	844	282	T/S	Acc/Tcc	rs200036561	0.361	Neutral	0.963	probably damaging	0.010	deleterious	2
PINK1	1_20971057_C/A	945	851	284	S/Y	tCc/tAc	rs113092523	0.526	Neutral	0.872	possibly damaging	0.010	deleterious	1
PINK1	1_20971063_C/T	951	857	286	P/L	cCg/cTg	rs146691996	0.541	Neutral	0.989	probably damaging	0.010	deleterious	2
PINK1	1_20971075_G/A	963	869	290	G/E	gGg/gAg	rs181675228	0.596	Neutral	0.998	probably damaging	0.030	deleterious	2
PINK1	1_20971111_G/A	999	905	302	R/H	cGc/cAc	rs201940147	0.576	Neutral	0.054	benign	0.080	tolerated	0
PINK1	1_20971119_C/G	1007	913	305	P/A	Cct/Gct	rs112600292	0.361	Neutral	0.975	probably damaging	0.000	deleterious	2
PINK1	1_20971141_G/A	1029	935	312	R/Q	cGg/cAg	rs202128685	0.600	Possibly Pathogenic	0.899	possibly damaging	0.070	tolerated	0
PINK1	1_20971155_G/A	1043	949	317	V/I	Gtt/Att	rs200949139	0.835	Pathogenic	0.827	possibly damaging	0.030	deleterious	2

PINK1	1_20972103_G/A	1104	1010	337	R/H	cGc/cAc	rs184043309	0.453	Neutral	0.191	benign	0.050	deleterious	1
PINK1	1_20972108_G/A	1109	1015	339	A/T	Gcc/Acc	rs55831733	0.879	Pathogenic	0.720	possibly damaging	0.050	tolerated	1
PINK1	1_20972111_G/A	1112	1018	340	A/T	Gcc/Acc	rs3738136	0.187	Neutral	0.004	benign	1.000	tolerated	0
PINK1	1_20972168_G/A	1169	1075	359	A/T	Gcg/Acg	rs76753586	0.596	Neutral	1.000	probably damaging	0.000	deleterious	2
PINK1	1_20975079_G/A	1299	1205	402	S/N	aGc/aAc	rs200728364	0.532	Neutral	0.979	probably damaging	0.020	deleterious	2
PINK1	1_20975105_G/A	1325	1231	411	G/S	Ggc/Agc	rs45478900	0.815	Pathogenic	0.027	benign	1.000	tolerated	1
PINK1	1_20975111_C/G	1331	1237	413	L/V	Ctg/Gtg	rs202130946	0.611	Possibly Pathogenic	0.999	probably damaging	0.000	deleterious	2
PINK1	1_20975549_C/T	1407	1313	438	A/V	gCa/gTa	rs183454580	0.811	Pathogenic	0.916	probably damaging	0.000	deleterious	3
PINK1	1_20975662_G/A	1520	1426	476	E/K	Gag/Aag	rs115477764	0.727	Pathogenic	0.014	benign	0.350	tolerated	1
PINK1	1_20976940_G/A	1596	1502	501	R/Q	cGa/cAa	rs61744200	0.453	Neutral	0.998	probably damaging	0.120	tolerated	1
PINK1	1_20977000_A/C	1656	1562	521	N/T	aAt/aCt	rs1043424	0.233	Neutral	0.007	benign	0.020	deleterious	1
PINK1	1_20977042_C/T	1698	1604	535	S/L	tCg/tTg	rs146126901	0.377	Neutral	0.999	probably damaging	0.000	deleterious	2
POLG	15_89876985_T/C	335	1	1	M/V	Atg/Gtg	rs201786897	0.915	Pathogenic	0.026	benign	0.000	deleterious	2
POLG	15_89876858_T/C	462	128	43	Q/R	cAg/cGg	rs28567406	0.130	Neutral	0.077	benign	0.560	tolerated	0
POLG	15_89876578_G/C	742	408	136	D/E	gaC/gaG	rs115109291	0.409	Neutral	0.033	benign	1.000	tolerated	0
POLG	15_89876408_C/T	912	578	193	R/Q	cGg/cAg	rs3176162	0.164	Neutral	0.003	benign	0.370	tolerated	0
POLG	15_89873415_G/A	1086	752	251	T/I	aCt/aTt	rs113994094	0.602	Possibly Pathogenic	0.001	benign	0.210	tolerated	0
POLG	15_89873364_C/G	1137	803	268	G/A	gGg/gCg	rs61752784	0.938	Pathogenic	0.995	probably damaging	0.000	deleterious	3

POLG	15_89871763_G/C	1508	1174	392	L/V	Ctg/Gtg	rs145289229	0.555	Neutral	0.992	probably damaging	0.030	deleterious	2
POLG	15_89870557_G/T	1608	1274	425	A/D	gCc/gAc	rs200399546	0.633	Possibly Pathogenic	0.775	possibly damaging	0.000	deleterious	1
POLG	15_89870432_C/T	1733	1399	467	A/T	Gcc/Acc	rs113994095	0.751	Pathogenic	0.997	probably damaging	0.000	deleterious	3
POLG	15_89870429_T/C	1736	1402	468	N/D	Aat/Gat	rs145843073	0.724	Pathogenic	0.007	benign	0.890	tolerated	1
POLG	15_89870178_C/A	1884	1550	517	G/V	gGg/gTg	rs61752783	0.586	Neutral	0.018	benign	0.390	tolerated	0
POLG	15_89869955_T/C	1934	1600	534	S/G	Agt/Ggt	rs201097813	0.135	Neutral	0.238	benign	0.310	tolerated	0
POLG	15_89869919_G/A	1970	1636	546	R/C	Cgc/Tgc	rs2307447	0.190	Neutral	0.418	benign	0.020	deleterious	1
POLG	15_89868870_G/A	2094	1760	587	P/L	cCg/cTg	rs113994096	0.667	Possibly Pathogenic	0.661	possibly damaging	0.000	deleterious	1
POLG	15_89868793_G/A	2171	1837	613	H/Y	Cac/Tac	rs147407423	0.358	Neutral	0.204	benign	0.180	tolerated	0
POLG	15_89867424_C/T	2318	1984	662	E/K	Gaa/Aaa	rs2307450	0.206	Neutral	0.002	benign	0.130	tolerated	0
POLG	15_89867351_G/A	2391	2057	686	A/V	gCc/gTc	rs201481404	0.272	Neutral	0.028	benign	0.310	tolerated	0
POLG	15_89866735_C/T	2499	2165	722	R/H	cGt/cAt	rs185645212	0.670	Possibly Pathogenic	0.001	benign	0.170	tolerated	0
POLG	15_89866699_T/C	2535	2201	734	H/R	cAt/cGt	rs56119329	0.485	Neutral	0.136	benign	0.310	tolerated	0
POLG	15_89866691_C/G	2543	2209	737	G/R	Gga/Cga	rs121918054	0.807	Pathogenic	0.963	probably damaging	0.000	deleterious	3
POLG	15_89866682_T/C	2552	2218	740	N/D	Aac/Gac	rs78347903	0.533	Neutral	0.453	possibly damaging	0.550	tolerated	0
POLG	15_89866676_C/T	2558	2224	742	V/M	Gtg/Atg	rs147827654	0.538	Neutral	1.000	probably damaging	0.000	deleterious	2
POLG	15_89866654_A/G	2580	2246	749	F/S	tTt/tCt	rs202037973	0.860	Pathogenic	1.000	probably damaging	0.000	deleterious	3
POLG	15_89866030_C/T	2703	2369	790	R/H	cGt/cAt	rs191490663	0.613	Possibly Pathogenic	0.939	probably damaging	0.050	deleterious	2
POLG	15_89865073_T/C	2826	2492	831	Y/C	tAt/tGt	rs41549716	0.680	Possibly Pathogenic	0.948	probably damaging	0.070	tolerated	1
POLG	15_89864211_C/G	3101	2767	923	G/R	Ggc/Cgc	rs60636456	0.902	Pathogenic	0.997	probably damaging	0.000	deleterious	3

POLG	15_89864088_G/A	3224	2890	964	R/C	Cgc/Tgc	rs201477273	0.846	Pathogenic	0.998	probably damaging	0.000	deleterious	3
POLG	15_89864081_A/C	3231	2897	966	L/R	cTa/cGa	rs142347031	0.975	Pathogenic	1.000	probably damaging	0.000	deleterious	3
POLG	15_89864019_C/T	3293	2959	987	A/T	Gct/Act	rs200258601	0.416	Neutral	0.910	probably damaging	0.120	tolerated	1
POLG	15_89862462_C/T	3435	3101	1034	R/K	aGg/aAg	rs201014720	0.423	Neutral	0.004	benign	0.550	tolerated	0
POLG	15_89862296_G/A	3473	3139	1047	R/W	Cgg/Tgg	rs181860632	0.860	Pathogenic	0.991	probably damaging	0.020	deleterious	3
POLG	15_89862193_C/T	3576	3242	1081	R/Q	cGa/cAa	rs140079523	0.520	Neutral	0.986	probably damaging	0.060	tolerated	1
POLG	15_89861978_A/C	3610	3276	1092	F/L	ttT/ttG	rs74034411	0.873	Pathogenic	0.963	probably damaging	0.000	deleterious	3
POLG	15_89861826_T/C	3762	3428	1143	E/G	gAg/gGg	rs2307441	0.533	Neutral	0.202	benign	0.060	tolerated	0
POLG	15_89861818_G/A	3770	3436	1146	R/C	Cgc/Tgc	rs2307440	0.792	Pathogenic	0.993	probably damaging	0.000	deleterious	3
POLG	15_89861812_G/A	3776	3442	1148	R/C	Cgc/Tgc	rs149099318	0.687	Possibly Pathogenic	0.951	probably damaging	0.000	deleterious	2
POLG	15_89860726_T/C	3858	3524	1175	Q/R	cAg/cGg	rs188348569	0.700	Pathogenic	0.985	probably damaging	0.020	deleterious	3
POLG	15_89859994_C/A	4042	3708	1236	Q/H	caG/caT	rs3087374	0.043	Neutral	0.009	benign	0.060	tolerated	0
POLG	15_89859992_G/A	4044	3710	1237	P/L	cCt/cTt	rs200788482	0.184	Neutral	0.492	possibly damaging	0.010	deleterious	1

POLG2	17_62493007_G/A	178	80	27	A/V	gCg/gTg	rs117792639	0.177	Neutral	0.078	benign	0.010	deleterious	1
POLG2	17_62492965_C/T	220	122	41	G/E	gGa/gAa	rs146504115	0.116	Neutral	0.697	possibly damaging	0.030	deleterious	1
POLG2	17_62492962_C/T	223	125	42	G/E	gGg/gAg	rs201278573	0.118	Neutral	0.000	benign	0.790	tolerated	0
POLG2	17_62492780_C/T	405	307	103	G/S	Ggc/Agc	rs200118378	0.866	Pathogenic	0.999	probably damaging	0.000	deleterious	3
POLG2	17_62492690_G/A	495	397	133	H/Y	Cac/Tac	rs112984118	0.288	Neutral	0.189	benign	0.140	tolerated	0
POLG2	17_62492582_C/T	603	505	169	A/T	Gca/Aca	rs1427463	0.173	Neutral	0.001	benign	0.620	tolerated	0
POLG2	17_62492552_C/A	633	535	179	G/W	Ggg/Tgg	rs200880373	0.503	Neutral	0.994	probably damaging	0.000	deleterious	2
POLG2	17_62489138_C/T	661	563	188	G/D	gGt/gAt	rs191057592	0.805	Pathogenic	1.000	probably damaging	0.010	deleterious	3
POLG2	17_62489027_C/T	772	674	225	R/Q	cGa/cAa	rs148101254	0.521	Neutral	0.000	benign	0.380	tolerated	0
POLG2	17_62488876_T/C	801	703	235	T/A	Act/Gct	rs148941150	0.668	Possibly Pathogenic	0.776	possibly damaging	0.140	tolerated	0
POLG2	17_62479069_A/C	1256	1158	386	D/E	gaT/gaG	rs61751983	0.647	Possibly Pathogenic	0.706	possibly damaging	0.530	tolerated	0
POLG2	17_62476451_C/G	1345	1247	416	G/A	gGt/gCt	rs17850455	0.349	Neutral	0.999	probably damaging	0.380	tolerated	1
POLG2	17_62474079_G/A	1417	1319	440	T/I	aCa/aTa	rs200118292	0.597	Neutral	0.918	probably damaging	0.030	deleterious	2
POLRMT	19_633500_A/G	69	13	5	C/R	Tgc/Cgc	rs200921997	0.275	Neutral	0.000	benign	0.890	tolerated	0
POLRMT	19_632915_G/A	168	112	38	P/S	Ccc/Tcc	rs12610885	0.197	Neutral	0.008	benign	1.000	tolerated	0
POLRMT	19_630130_C/T	288	232	78	V/M	Gtg/Atg	rs140649984	0.182	Neutral	0.029	benign	0.090	tolerated	0
POLRMT	19_630075_C/T	343	287	96	S/N	aGt/aAt	rs189184481	0.178	Neutral	0.023	benign	0.190	tolerated	0
POLRMT	19_630035_C/T	383	327	109	M/I	atG/atA	rs77466198	0.245	Neutral	0.000	benign	0.390	tolerated	0
POLRMT	19_629970_C/T	448	392	131	R/Q	cGg/cAg	rs113148837	0.230	Neutral	0.000	benign	0.510	tolerated	0

POLRMT	19_629887_G/A	531	475	159	R/C	Cgc/Tgc	rs149933500	0.317	Neutral	0.241	benign	0.050	tolerated	0
POLRMT	19_629841_C/A	577	521	174	C/F	tGc/tTc	rs146345748	0.188	Neutral	0.001	benign	0.700	tolerated	0
POLRMT	19_629739_T/C	679	623	208	Q/R	cAg/cGg	rs199600661	0.099	Neutral	0.001	benign	0.310	tolerated	0
POLRMT	19_629733_G/A	685	629	210	P/L	cCg/cTg	rs182390676	0.218	Neutral	0.002	benign	0.890	tolerated	0
POLRMT	19_629605_G/A	813	757	253	R/W	Cgg/Tgg	rs145312875	0.390	Neutral	0.488	possibly damaging	0.050	deleterious	1
POLRMT	19_625131_T/C	1002	946	316	I/V	Atc/Gtc	rs115263594	0.374	Neutral	0.284	benign	0.090	tolerated	0
POLRMT	19_624894_T/A	1021	965	322	Q/L	cAg/cTg	rs138732981	0.370	Neutral	0.292	benign	0.010	deleterious	1
POLRMT	19_624890_C/T	1025	969	323	M/I	atG/atA	rs143022703	0.508	Neutral	0.497	possibly damaging	0.120	tolerated	0
POLRMT	19_624850_C/T	1065	1009	337	V/I	Gtt/Att	rs201346718	0.281	Neutral	0.058	benign	0.400	tolerated	0
POLRMT	19_624763_G/A	1152	1096	366	P/S	Ccc/Tcc	rs201473800	0.259	Neutral	0.005	benign	0.300	tolerated	0
POLRMT	19_623576_G/A	1224	1168	390	H/Y	Cac/Tac	rs199567642	0.464	Neutral	0.674	possibly damaging	1.000	tolerated	0
POLRMT	19_623546_A/G	1254	1198	400	F/L	Ttt/Ctt	rs41553913	0.683	Possibly Pathogenic	0.153	benign	0.120	tolerated	0
POLRMT	19_623505_G/C	1295	1239	413	C/W	tgC/tgG	rs201389191	0.496	Neutral	0.723	possibly damaging	0.030	deleterious	1
POLRMT	19_622830_C/G	1502	1446	482	M/I	atG/atC	rs138594532	0.561	Neutral	0.001	benign	1.000	tolerated	0
POLRMT	19_622587_C/A	1677	1621	541	A/S	Gcc/Tcc	rs56226067	0.236	Neutral	0.002	benign	0.570	tolerated	0

POLRMT	19_622583_T/A	1681	1625	542	E/V	gAg/gTg	rs200807835	0.478	Neutral	0.014	benign	0.050	deleterious	1
POLRMT	19_622367_C/T	1689	1633	545	E/K	Gag/Aag	rs115950441	0.457	Neutral	0.000	benign	0.750	tolerated	0
POLRMT	19_622336_T/G	1720	1664	555	E/A	gAg/gCg	rs2238549	0.189	Neutral	0.000	benign	0.880	tolerated	0
POLRMT	19_622207_C/T	1849	1793	598	R/H	cGt/cAt	rs61745193	0.417	Neutral	0.001	benign	0.240	tolerated	0
POLRMT	19_621561_C/A	2193	2137	713	V/L	Gtg/Ttg	rs10421235	0.474	Neutral	0.035	benign	0.720	tolerated	0
POLRMT	19_621090_C/T	2664	2608	870	D/N	Gac/Aac	rs139383492	0.527	Neutral	0.398	benign	0.000	deleterious	1
POLRMT	19_620005_C/T	2895	2839	947	E/K	Gag/Aag	rs151235528	0.509	Neutral	0.208	benign	0.550	tolerated	0
POLRMT	19_619982_G/C	2918	2862	954	D/E	gaC/gaG	rs200607630	0.885	Pathogenic	0.999	probably damaging	0.000	deleterious	3
POLRMT	19_619719_G/A	2989	2933	978	A/V	gCa/gTa	rs201811276	0.814	Pathogenic	0.999	probably damaging	0.000	deleterious	3
POLRMT	19_617838_G/A	3490	3434	1145	T/I	aCc/aTc	rs201558272	0.538	Neutral	0.570	possibly damaging	0.080	tolerated	0
POLRMT	19_617634_G/A	3573	3517	1173	R/C	Cgc/Tgc	rs147740567	0.714	Pathogenic	0.737	possibly damaging	0.020	deleterious	2
POLRMT	19_617582_C/T	3625	3569	1190	R/Q	cGg/cAg	rs150648879	0.631	Possibly Pathogenic	0.642	possibly damaging	0.070	tolerated	0
POLRMT	19_617573_G/A	3634	3578	1193	S/F	tCt/tTt	rs142850300	0.544	Neutral	0.048	benign	0.760	tolerated	0
POLRMT	19_617470_T/G	3648	3592	1198	I/L	Atc/Ctc	rs138715064	0.645	Possibly Pathogenic	0.006	benign	0.690	tolerated	0
POLRMT	19_617466_A/G	3652	3596	1199	L/S	tTg/tCg	rs151287767	0.612	Possibly Pathogenic	0.016	benign	0.220	tolerated	0
POLRMT	19_617297_G/A	3726	3670	1224	R/C	Cgt/Tgt	rs199982300	0.620	Possibly Pathogenic	0.658	possibly damaging	0.030	deleterious	1
SDHA	5_218487_G/A	132	17	6	G/D	gGc/gAc	rs187964306	0.339	Neutral	0.031	benign	0.280	tolerated	0
SDHA	5_223646_A/T	228	113	38	D/V	gAt/gTt	rs34635677	0.325	Neutral	0.001	benign	0.560	tolerated	0
SDHA	5_223666_G/A	248	133	45	A/T	Gct/Act	rs140736646	0.301	Neutral	0.004	benign	0.110	tolerated	0
SDHA	5_223679_A/G	261	146	49	D/G	gAt/gGt	rs80207011	0.343	Neutral	0.002	benign	0.330	tolerated	0
SDHA	5_224487_T/C	278	163	55	Y/H	Tat/Cat	rs142926807	0.496	Neutral	0.546	possibly damaging	0.010	deleterious	1

SDHA	5_226091_G/A	665	550	184	G/R	Ggg/Agg	rs148246073	0.565	Neutral	0.975	probably damaging	0.000	deleterious	2
SDHA	5_233598_A/G	1017	902	301	Y/C	tAt/tGt	rs182055219	0.616	Possibly Pathogenic	0.972	probably damaging	0.000	deleterious	2
SDHA	5_233687_G/A	1106	991	331	A/T	Gcc/Acc	rs200526913	0.736	Pathogenic	0.974	probably damaging	0.000	deleterious	3
SDHA	5_233748_T/G	1167	1052	351	I/S	aTc/aGc	rs200103530	0.766	Pathogenic	0.930	probably damaging	0.000	deleterious	3
SDHA	5_235416_T/C	1337	1222	408	Y/H	Tat/Cat	rs201826964	0.891	Pathogenic	1.000	probably damaging	0.000	deleterious	3
SDHA	5_236676_G/A	1509	1394	465	R/Q	cGg/cAg	rs138277996	0.707	Pathogenic	0.525	possibly damaging	0.020	deleterious	2
SDHA	5_240563_C/T	1638	1523	508	T/I	aCa/aTa	rs151266052	0.356	Neutral	0.367	benign	0.010	deleterious	1
SDHA	5_240575_G/A	1650	1535	512	R/Q	cGa/cAa	rs192818312	0.738	Pathogenic	0.996	probably damaging	0.000	deleterious	3
SDHA	5_251207_C/T	1767	1652	551	T/M	aCg/aTg	rs181238392	0.543	Neutral	0.722	possibly damaging	0.030	deleterious	1
SDHA	5_254512_G/A	1914	1799	600	R/Q	cGg/cAg	rs1126568	0.885	Pathogenic	0.998	probably damaging	0.000	deleterious	3
SDHA	5_256500_T/G	2075	1960	654	C/G	Tgt/Ggt	rs60587941	0.547	Neutral	0.969	probably damaging	0.000	deleterious	2
SDHA	5_256509_G/A	2084	1969	657	V/I	Gtc/Atc	rs6962	0.293	Neutral	0.034	benign	0.450	tolerated	0
SDHA	5_256519_C/G	2094	1979	660	A/G	gCc/gGc	rs191412461	0.497	Neutral	0.075	benign	0.130	tolerated	0
SDHB	1_17380507_G/C	159	8	3	A/G	gCg/gGg	rs11203289	0.675	Possibly Pathogenic	0.114	benign	0.020	deleterious	1
SDHB	1_17380483_C/T	183	32	11	R/H	cGc/cAc	rs111430410	0.714	Pathogenic	0.291	benign	0.100	tolerated	1
SDHB	1_17371286_T/C	321	170	57	H/R	cAt/cGt	rs35962811	0.396	Neutral	0.000	benign	1.000	tolerated	0
SDHB	1_17354297_A/G	638	487	163	S/P	Tct/Cct	rs33927012	0.196	Neutral	0.000	benign	0.650	tolerated	0

SDHB	1_17349180_G/A	839	688	230	R/C	Cgc/Tgc	rs138996609	0.924	Pathogenic	0.998	probably damaging	0.000	deleterious	3
SDHB	1_17349159_G/A	860	709	237	P/S	Cca/Tca	rs186768244	0.287	Neutral	0.064	benign	0.410	tolerated	0
SDHC	1_161293437_T/G	203	54	18	F/L	ttT/ttG	rs200761743	0.395	Neutral	0.000	benign	0.940	tolerated	0
SDHC	1_161298206_C/T	247	98	33	T/M	aCg/aTg	rs148566767	0.268	Neutral	0.482	possibly damaging	0.070	tolerated	0
SDHC	1_161326496_T/G	420	271	91	L/V	Tta/Gta	rs144532303	0.376	Neutral	0.003	benign	0.870	tolerated	0
SDHD	11_111958581_C/T	188	53	18	A/V	gCt/gTt	rs192332761	0.644	Possibly Pathogenic	0.007	benign	0.350	tolerated	0
SDHD	11_111958677_A/G	284	149	50	H/R	cAc/cGc	rs11214077	0.260	Neutral	0.797	possibly damaging	0.090	tolerated	0
SDHD	11_111959668_G/C	382	247	83	A/P	Gct/Cct	rs202239399	0.739	Pathogenic	0.955	probably damaging	0.010	deleterious	3
SDHD	11_111965636_A/G	557	422	141	Y/C	tAt/tGt	rs199772639	0.733	Pathogenic	0.885	possibly damaging	0.060	tolerated	1
SSBP1	7_141438979_C/T	146	13	5	P/S	Cct/Tct	rs148887629	0.445	Neutral	0.060	benign	0.170	tolerated	0
SSBP1	7_141441981_T/C	170	37	13	F/L	Ttt/Ctt	rs192517454	0.259	Neutral	0.001	benign	0.560	tolerated	0
SSBP1	7_141443490_T/C	348	215	72	V/A	gTt/gCt	rs200664859	0.427	Neutral	0.001	benign	0.450	tolerated	0
SSBP1	7_141443499_T/C	357	224	75	L/P	cTg/cCg	rs78598246	0.401	Neutral	0.000	benign	0.280	tolerated	0
SSBP1	7_141443764_G/A	422	289	97	V/M	Gtg/Atg	rs148271472	0.569	Neutral	0.819	possibly damaging	0.030	deleterious	1
TFAM	10_60145327_T/C	546	20	7	M/T	aTg/aCg	rs200473819	0.376	Neutral	0.042	benign	0.260	tolerated	0
TFAM	10_60145342_G/C	561	35	12	S/T	aGt/aCt	rs1937	0.162	Neutral	0.019	benign	0.510	tolerated	0
TFAM	10_60145390_G/T	609	83	28	R/L	cGa/cTa	rs199678369	0.598	Neutral	0.993	probably damaging	0.180	tolerated	1
TFAM	10_60146077_A/G	725	199	67	I/V	Ata/Gta	rs138243284	0.506	Neutral	0.034	benign	1.000	tolerated	0

TK2	16_66583885_G/A	431	80	27	S/L	tCa/tTa	rs191573607	0.256	Neutral	0.897	possibly damaging	0.020	deleterious	1
TK2	16_66565357_C/T	652	301	101	D/N	Gat/Aat	rs148450491	0.593	Neutral	0.131	benign	0.050	tolerated	0
TK2	16_66565297_G/T	712	361	121	H/N	Cat/Aat	rs137854429	0.687	Possibly Pathogenic	0.457	possibly damaging	0.000	deleterious	1
TK2	16_66562931_C/T	766	415	139	A/T	Gca/Aca	rs138479499	0.722	Pathogenic	0.937	probably damaging	0.010	deleterious	3
TK2	16_66551710_C/T	871	520	174	V/M	Gtg/Atg	rs149036717	0.561	Neutral	0.360	benign	0.010	deleterious	1
TK2	16_66545906_T/C	1114	763	255	I/V	Ata/Gta	rs144419486	0.665	Possibly Pathogenic	0.686	possibly damaging	0.060	tolerated	0
UCP1	4_141489766_G/A	194	118	40	R/W	Cgg/Tgg	rs150067245	0.912	Pathogenic	0.999	probably damaging	0.000	deleterious	3
UCP1	4_141489068_C/T	266	190	64	A/T	Gct/Act	rs45539933	0.139	Neutral	0.000	benign	1.000	tolerated	0
UCP1	4_141484519_G/C	555	479	160	A/G	gCg/gGg	rs200389729	0.765	Pathogenic	0.995	probably damaging	0.000	deleterious	3
UCP1	4_141484292_C/A	676	600	200	E/D	gaG/gaT	rs138611550	0.364	Neutral	0.009	benign	0.680	tolerated	0
UCP1	4_141483471_T/A	761	685	229	M/L	Atg/Ttg	rs2270565	0.174	Neutral	0.001	benign	0.290	tolerated	0
UCP1	4_141483389_A/G	843	767	256	M/T	aTg/aCg	rs140138182	0.557	Neutral	0.006	benign	0.130	tolerated	0
UCP1	4_141481151_A/G	899	823	275	F/L	Ttc/Ctc	rs146114327	0.603	Possibly Pathogenic	0.975	probably damaging	0.000	deleterious	2
UCP2	11_73689309_C/T	958	115	39	V/I	Gtc/Atc	rs148253207	0.751	Pathogenic	0.127	benign	0.040	deleterious	2
UCP2	11_73689131_T/C	980	137	46	E/G	gAa/gGa	rs201348391	0.459	Neutral	0.493	possibly damaging	0.010	deleterious	1
UCP2	11_73689128_C/T	983	140	47	S/N	aGt/aAt	rs144018051	0.344	Neutral	0.001	benign	0.520	tolerated	0
UCP2	11_73689104_G/A	1007	164	55	A/V	gCc/gTc	rs660339	0.174	Neutral	0.002	benign	0.080	tolerated	0
UCP2	11_73689099_C/T	1012	169	57	A/T	Gcc/Acc	rs145662569	0.254	Neutral	0.002	benign	0.280	tolerated	0
UCP2	11_73689056_C/T	1055	212	71	R/H	cGt/cAt	rs182694614	0.701	Pathogenic	0.264	benign	0.000	deleterious	2
UCP2	11_73689051_C/G	1060	217	73	E/Q	Gag/Cag	rs200489709	0.783	Pathogenic	0.720	possibly damaging	0.010	deleterious	2
UCP2	11_73689041_C/T	1070	227	76	R/Q	cGa/cAa	rs45541732	0.276	Neutral	0.068	benign	0.400	tolerated	0

UCP2	11_73687922_C/G	1321	478	160	V/L	Gtc/Ctc	rs144885917	0.411	Neutral	0.002	benign	0.840	tolerated	0
UCP2	11_73686657_C/T	1537	694	232	A/T	Gcc/Acc	rs200027152	0.535	Neutral	0.214	benign	0.000	deleterious	1
UCP2	11_73686632_G/A	1562	719	240	T/M	aCg/aTg	rs201373362	0.829	Pathogenic	1.000	probably damaging	0.000	deleterious	3
UCP2	11_73686622_C/G	1572	729	243	M/I	atG/atC	rs139945658	0.741	Pathogenic	0.300	benign	0.130	tolerated	1
UCP2	11_73686548_G/C	1646	803	268	A/G	gCc/gGc	rs45490393	0.87	Pathogenic	0.199	benign	0.020	deleterious	2
UCP2	11_73686137_G/C	1688	845	282	S/C	tCc/tGc	rs45596837	0.316	Neutral	0.968	probably damaging	0.000	deleterious	2
UCP3	11_73718077_A/C	564	11	4	L/R	cTg/cGg	rs141482270	0.376	Neutral	0.625	possibly damaging	0.190	tolerated	0
UCP3	11_73718030_C/T	611	58	20	A/T	Gca/Aca	rs199679366	0.773	Pathogenic	0.980	probably damaging	0.000	deleterious	3
UCP3	11_73717417_C/T	687	134	45	G/E	gGg/gAg	rs147631608	0.589	Neutral	0.998	probably damaging	0.000	deleterious	2
UCP3	11_73717396_G/A	708	155	52	T/M	aCg/aTg	rs17848367	0.426	Neutral	0.038	benign	0.060	tolerated	0
UCP3	11_73717342_C/T	762	209	70	R/Q	cGg/cAg	rs58614015	0.769	Pathogenic	0.506	possibly damaging	0.130	tolerated	1
UCP3	11_73717340_T/G	764	211	71	T/P	Act/Cct	rs143786748	0.507	Neutral	0.648	possibly damaging	0.040	deleterious	1
UCP3	11_73717301_C/T	803	250	84	G/S	Ggc/Agc	rs183714776	0.713	Pathogenic	0.997	probably damaging	0.000	deleterious	3
UCP3	11_73717277_C/T	827	274	92	A/T	Gcc/Acc	rs192655642	0.732	Pathogenic	0.718	possibly damaging	0.020	deleterious	2
UCP3	11_73717219_G/A	885	332	111	A/V	gCg/gTg	rs74907838	0.290	Neutral	0.002	benign	0.440	tolerated	0
UCP3	11_73716960_C/T	909	356	119	R/Q	cGg/cAg	rs17848372	0.552	Neutral	0.996	probably damaging	0.000	deleterious	2
UCP3	11_73716835_C/T	1034	481	161	G/R	Ggg/Agg	rs201405748	0.737	Pathogenic	0.990	probably damaging	0.000	deleterious	3
UCP3	11_73716829_T/C	1040	487	163	M/V	Atg/Gtg	rs201679589	0.372	Neutral	0.005	benign	0.900	tolerated	0
UCP3	11_73715571_C/T	1154	601	201	D/N	Gac/Aac	rs201993988	0.742	Pathogenic	0.998	probably damaging	0.000	deleterious	3

UCP3	11_73714978_C/T	1271	718	240	V/M	Gtg/Atg	rs138705669	0.723	Pathogenic	0.999	probably damaging	0.010	deleterious	3
UCP3	11_73714927_G/T	1322	769	257	L/I	Ctc/Atc	rs145884716	0.489	Neutral	0.009	benign	0.470	tolerated	0
UCP3	11_73712501_G/A	1448	895	299	R/W	Cgg/Tgg	rs142927779	0.590	Neutral	0.988	probably damaging	0.000	deleterious	2
UCP3	11_73712478_C/A	1471	918	306	M/I	atG/atT	rs199959534	0.448	Neutral	0.000	benign	0.200	tolerated	0
UCP3	11_73712465_G/A	1484	931	311	P/S	Ccg/Tcg	rs200773036	0.351	Neutral	0.084	benign	0.070	tolerated	0
UCP3	11_73712464_G/A	1485	932	311	P/L	cCg/cTg	rs76629964	0.375	Neutral	0.884	possibly damaging	0.000	deleterious	1
UQCR10	22_30163526_A/G	169	139	47	I/V	Atc/Gtc	rs76013375	0.196	Neutral	0.013	benign	0.350	tolerated	0
UQCR10	22_30165686_A/G	200	170	57	K/R	aAg/aGg	rs199810262	0.714	Pathogenic	0.860	possibly damaging	0.200	tolerated	1
UQCR11	19_1599448_C/A	237	162	54	K/N	aaG/aaT	rs181112176	0.508	Neutral	0.793	possibly damaging	0.280	tolerated	0
UQCRB	8_97247742_G/A	121	17	6	A/V	gCc/gTc	rs200758329	0.411	Neutral	0.013	benign	0.120	tolerated	0
UQCRB	8_97244082_T/A	282	178	60	M/L	Atg/Ttg	rs145974195	0.438	Neutral	0.005	benign	0.290	tolerated	0
UQCRB	8_97244060_A/T	304	200	67	L/Q	cTg/cAg	rs139283183	0.645	Possibly Pathogenic	0.926	probably damaging	0.040	deleterious	2
UQCRB	8_97244011_T/G	353	249	83	K/N	aaA/aaC	rs145828292	0.566	Neutral	0.485	possibly damaging	0.000	deleterious	1
UQCRB	8_97243321_G/A	402	298	100	R/W	Cgg/Tgg	rs199583530	0.606	Possibly Pathogenic	0.000	unknown	0.080	tolerated	0
UQCRC1	3_48646654_T/C	568	151	51	S/G	Agc/Ggc	rs117171524	0.648	Possibly Pathogenic	0.276	benign	0.000	deleterious	1
UQCRC1	3_48643235_C/A	682	265	89	A/S	Gca/Tca	rs201250580	0.678	Possibly Pathogenic	0.270	benign	0.030	deleterious	1
UQCRC1	3_48641799_G/T	910	493	165	R/S	Cgt/Agt	rs191821836	0.768	Pathogenic	1.000	probably damaging	0.000	deleterious	3

UQCRC1	3_48641060_C/G	1060	643	215	D/H	Gac/Cac	rs17080284	0.251	Neutral	0.997	probably damaging	0.090	tolerated	1
UQCRC1	3_48638807_G/C	1217	800	267	P/R	cCa/cGa	rs149245457	0.492	Neutral	0.060	benign	0.050	deleterious	1
UQCRC1	3_48638801_C/T	1223	806	269	R/H	cGc/cAc	rs62618742	0.389	Neutral	0.395	benign	0.160	tolerated	0
UQCRC1	3_48638548_G/A	1243	826	276	R/C	Cgc/Tgc	rs201911056	0.549	Neutral	0.172	benign	0.010	deleterious	1
UQCRC1	3_48638472_T/C	1319	902	301	N/S	aAt/aGt	rs144710790	0.198	Neutral	0.274	benign	0.430	tolerated	0
UQCRC1	3_48638451_T/C	1340	923	308	N/S	aAt/aGt	rs187641562	0.667	Possibly Pathogenic	0.117	benign	0.230	tolerated	0
UQCRC1	3_48638440_C/T	1351	934	312	G/S	Ggc/Agc	rs145869559	0.917	Pathogenic	1.000	probably damaging	0.000	deleterious	3
UQCRC1	3_48637996_G/A	1549	1132	378	R/C	Cgc/Tgc	rs200354059	0.625	Possibly Pathogenic	0.996	probably damaging	0.000	deleterious	2
UQCRC1	3_48637143_C/T	1720	1303	435	E/K	Gag/Aag	rs139999010	0.432	Neutral	0.002	benign	0.050	tolerated	0
UQCRC1	3_48637071_A/T	1792	1375	459	Y/N	Tat/Aat	rs202030377	0.596	Neutral	0.047	benign	0.000	deleterious	1
UQCRC2	16_21968584_A/G	826	62	21	K/R	aAa/aGa	rs188964091	0.380	Neutral	0.012	benign	0.050	deleterious	1
UQCRC2	16_21974117_C/G	1189	425	142	T/R	aCa/aGa	rs139500759	0.846	Pathogenic	0.314	benign	0.030	deleterious	2
UQCRC2	16_21974134_C/A	1206	442	148	R/S	Cgt/Agt	rs2228473	0.190	Neutral	0.295	benign	0.540	tolerated	0
UQCRC2	16_21974204_C/T	1276	512	171	T/I	aCt/aTt	rs202168192	0.340	Neutral	0.002	benign	1.000	tolerated	0
UQCRC2	16_21976762_G/A	1312	548	183	R/Q	cGg/cAg	rs4850	0.232	Neutral	0.085	benign	0.070	tolerated	0
UQCRC2	16_21982936_G/A	1525	761	254	R/H	cGt/cAt	rs11863893	0.219	Neutral	0.008	benign	0.650	tolerated	0
UQCRC2	16_21983430_A/C	1717	953	318	Q/P	cAg/cCg	rs146974535	0.675	Possibly Pathogenic	0.007	benign	0.290	tolerated	0

UQCRC2	16_21991888_A/G	1909	1145	382	Y/C	tAc/tGc	rs139312246	0.569	Neutral	0.972	probably damaging	0.010	deleterious	2
UQCRC2	16_21991927_A/T	1948	1184	395	E/V	gAa/gTa	rs190027776	0.531	Neutral	0.701	possibly damaging	0.070	tolerated	0
UQCRC2	16_21991953_G/T	1974	1210	404	G/C	Ggt/Tgt	rs181040575	0.809	Pathogenic	0.992	probably damaging	0.000	deleterious	3
UQCRFS1	19_29704010_A/C	127	16	6	S/A	Tcc/Gcc	rs8100724	0.169	Neutral	0.001	benign	1.000	tolerated	0
UQCRFS1	19_29699006_G/A	385	274	92	R/C	Cgc/Tgc	rs185606879	0.866	Pathogenic	0.822	possibly damaging	0.010	deleterious	2
UQCRFS1	19_29698816_T/G	575	464	155	K/T	aAg/aCg	rs201719321	0.545	Neutral	0.816	possibly damaging	0.010	deleterious	1
UQCRH	1_46774783_A/G	201	65	22	E/G	gAa/gGa	rs41292543	0.168	Neutral	0.746	possibly damaging	0.030	deleterious	1
UQCRH	1_46775905_G/A	296	160	54	D/N	Gat/Aat	rs189114560	0.359	Neutral	0.030	benign	1.000	tolerated	0
UQCRH	1_46775975_C/A	366	230	77	A/E	gCg/gAg	rs181971906	0.826	Pathogenic	0.998	probably damaging	0.240	tolerated	2
UQCRQ	5_132202583_G/A	151	10	4	E/K	Gag/Aag	rs137995316	0.420	Neutral	0.014	benign	0.110	tolerated	0

Table S3- Observed non-synonymous mutations in 1,092 individuals (246 are from Africans including Afro-Americans, 379 Europeans, 286 Asians and 181 Americans) from the 1000 Genomes dataset and frequencies and p-values of Hardy-Weinberg equilibrium test (overall and per population group when overall was significant).

			Frequencies											
Gene	**Uploaded Variation**	**Co-located Variation**	**All**		**AFR**		**AMR**		**ASN**		**EUR**		**HW (p-value)**	**HW per groups (p-value)**
AK2	1_33487277_T/C	rs184683619	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
AK2	1_33487007_C/T	rs61750965	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	0.995	0.005	1.00000	

AK2	1_33486974_G/A	rs192209857	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
AK2	1_33480172_C/T	rs149227118	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
AK2	1_33480161_C/T	rs148421308	0.995	0.005	0.988	0.012	0.989	0.011	1.000	0.000	1.000	0.000	1.00000	
AK2	1_33478891_C/T	rs200179721	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
AK2	1_33478877_C/T	rs12116440	0.994	0.006	1.000	0.000	0.989	0.011	1.000	0.000	0.988	0.012	1.00000	
AK2	1_33478853_C/G	rs185081372	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
AK3	9_4719182_C/A	rs188377589	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
AK3	9_4719161_T/A	rs141090350	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
AK3	9_4718440_T/G	rs151087607	0.002	0.998	0.006	0.994	0.006	0.994	0.000	1.000	0.000	1.000	1.00000	
AK3	9_4713058_G/A	rs140003401	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
AK4	1_65614154_T/A	rs17853973	0.207	0.793	0.520	0.480	0.066	0.934	0.274	0.726	0.020	0.980	0.00000	AFR-0.70376; AMR-1.00000; ASN-0.05546; EUR-1.00000
AK4	1_65684463_G/A	rs200696544	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
AK4	1_65684545_G/A	rs142956995	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
AK4	1_65690489_G/A	rs185251178	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
AK4	1_65691837_A/G	rs201234545	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
ATP5A1	18_43678173_C/T	rs141639003	0.996	0.004	1.000	0.000	0.986	0.014	0.995	0.005	1.000	0.000	1.00000	
ATP5A1	18_43678172_G/A	rs200039737	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
ATP5A1	18_43675064_C/A	rs79011243	0.019	0.981	0.077	0.923	0.008	0.992	0.000	1.000	0.000	1.000	1.00000	
ATP5A1	18_43675046_C/T	rs189208584	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5A1	18_43669662_G/C	rs11541929	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5A1	18_43668207_T/C	rs77958705	0.007	0.993	0.014	0.986	0.000	1.000	0.000	1.000	0.012	0.988	1.00000	
ATP5B	12_57039713_G/A	rs200568028	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5B	12_57039675_A/G	rs144845797	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5B	12_57039674_G/A	rs2293450	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
ATP5B	12_57039080_C/T	rs41291993	0.967	0.033	0.998	0.002	0.981	0.019	0.897	0.103	0.992	0.008	0.33934	
ATP5B	12_57037309_C/T	rs200966693	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	

ATP5B	12_57037209_T/C	rs142007312	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
ATP5B	12_57032995_G/A	rs200610844	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
ATP5B	12_57032900_C/A	rs145015204	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
ATP5C1	10_7838106_A/G	rs199602842	0.999	0.001	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.00000	
ATP5C1	10_7840983_C/T	rs146307767	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5C1	10_7841811_A/G	rs139967528	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5C1	10_7844268_G/A	rs199960374	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5C1	10_7844756_C/T	rs137988284	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
ATP5D	19_1241932_C/T	rs199988557	0.999	0.001	0.994	0.006	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5D	19_1244170_A/G	rs200344400	0.998	0.002	1.000	0.000	1.000	0.000	0.993	0.007	1.000	0.000	1.00000	
ATP5D	19_1244401_G/A	rs200593395	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5E	20_57605431_G/T	rs146230809	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5EP2	13_28519416_A/G	rs7334094	0.992	0.008	0.967	0.033	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
ATP5F1	1_111998734_A/G	rs151112830	0.997	0.003	1.000	0.000	0.994	0.006	1.000	0.000	0.993	0.007	1.00000	
ATP5F1	1_111999312_A/G	rs150276317	0.996	0.004	1.000	0.000	1.000	0.000	0.986	0.014	1.000	0.000	1.00000	
ATP5F1	1_111999319_C/T	rs1264895	0.998	0.002	0.994	0.006	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
ATP5F1	1_112002094_G/A	rs144377157	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
ATP5F1	1_112002202_G/C	rs182170395	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
ATP5F1	1_112002232_G/A	rs146878380	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5G1	17_46970783_C/G	rs201139259	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
ATP5G2	12_54069975_A/G	rs201675029	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
ATP5G2	12_54063677_C/T	rs140613495	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5G2	12_54063056_C/T	rs145981161	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
ATP5G3	2_176046090_G/A	rs142182201	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	
ATP5G3	2_176044863_G/A	rs144490355	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
ATP5G3	2_176043906_T/C	rs36089250	0.002	0.998	0.000	1.000	0.000	1.000	0.007	0.993	0.001	0.999	1.00000	
ATP5H	17_73038667_T/G	rs200410651	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5H	17_73038316_T/C	rs143915019	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5I	4_668015_A/G	rs143075692	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	

ATP5I	4_668009_G/A	rs76028807	0.007	0.993	0.000	1.000	0.003	0.997	0.000	1.000	0.020	0.980	1.00000	
ATP5I	4_667134_T/G	rs147287885	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5I	4_667115_C/T	rs181881252	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5J	21_27102014_G/C	rs73338261	0.008	0.992	0.035	0.965	0.000	1.000	0.000	1.000	0.000	1.000	0.06084	
ATP5J	21_27097641_T/G	rs182225698	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5J2	7_99063760_G/A	rs201512015	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5J2	7_99063739_G/C	rs117298057	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	0.011	0.989	1.00000	
ATP5J2	7_99056770_T/G	rs146584377	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
ATP5J2	7_99055969_C/T	rs144185727	0.999	0.001	1.000	0.000	0.997	0.003	1.000	0.000	0.997	0.003	1.00000	
ATP5L	11_118277742_G/C	rs181465227	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5L	11_118279769_G/A	rs200472961	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5L2	22_43036264_C/T	rs148856876	0.996	0.004	0.986	0.014	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
ATP5L2	22_43035994_C/G	rs145437748	0.999	0.001	1.000	0.000	0.994	0.006	1.000	0.000	1.000	0.000	1.00000	
ATP5O	21_35288061_C/T	rs202191698	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
ATP5O	21_35288049_A/G	rs201852944	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
ATP5O	21_35286801_G/C	rs190343471	0.001	0.999	0.000	1.000	0.008	0.992	0.000	1.000	0.000	1.000	1.00000	
ATP5O	21_35281496_T/C	rs140827929	0.005	0.995	0.000	1.000	0.008	0.992	0.000	1.000	0.009	0.991	1.00000	
ATP5O	21_35281461_G/A	rs150994121	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
ATP5O	21_35281421_T/C	rs4842	0.071	0.929	0.120	0.880	0.058	0.942	0.014	0.986	0.090	0.910	0.81887	
ATP5O	21_35279713_C/T	rs190233927	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5O	21_35275939_T/C	rs182975028	0.001	0.999	0.000	1.000	0.006	0.994	0.000	1.000	0.000	1.000	1.00000	
ATP5O	21_35275936_G/A	rs191960490	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
ATP5O	21_35275931_T/C	rs141125740	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
ATP5O	21_35275914_A/C	rs11552279	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
ATP5O	21_35275907_T/C	rs75701641	0.004	0.996	0.018	0.982	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
ATP5O	21_35275835_C/A	rs142550850	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
ATP5S	14_50779764_G/A	rs192355817	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5S	14_50788213_C/T	rs2275592	0.435	0.565	0.463	0.537	0.442	0.558	0.399	0.601	0.439	0.561	0.53751	
ATP5S	14_50788240_G/A	rs201427439	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	

ATP5S	14_50789309_G/A	rs185659761	0.002	0.998	0.008	0.992	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
ATP5S	14_50789387_C/T	rs142828913	0.997	0.003	0.990	0.010	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
ATP5S	14_50789401_G/A	rs140662926	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
ATP5S	14_50789426_T/C	rs192482233	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX10	17_13972938_C/T	rs199881731	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX10	17_13977679_C/T	rs16948978	0.978	0.022	0.904	0.096	0.994	0.006	1.000	0.000	1.000	0.000	0.42405	
COX10	17_13977689_C/A	rs141481210	0.001	0.999	0.000	1.000	0.003	0.997	0.000	1.000	0.001	0.999	1.00000	
COX10	17_13980058_A/T	rs2230351	0.929	0.071	0.994	0.006	0.909	0.091	0.878	0.122	0.934	0.066	0.25426	
COX10	17_13980134_C/T	rs144000161	0.998	0.002	1.000	0.000	1.000	0.000	0.991	0.009	1.000	0.000	1.00000	
COX10	17_13980164_A/G	rs16948986	0.978	0.022	0.904	0.096	0.994	0.006	1.000	0.000	1.000	0.000	0.42282	
COX10	17_13980176_C/T	rs145948285	0.997	0.003	0.998	0.002	1.000	0.000	0.991	0.009	1.000	0.000	1.00000	
COX10	17_13980185_C/T	rs202207627	0.999	0.001	1.000	0.000	1.000	0.000	0.998	0.002	0.999	0.001	1.00000	
COX10	17_13980254_T/C	rs201424119	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
COX10	17_13980350_G/A	rs8077302	0.488	0.512	0.465	0.535	0.506	0.494	0.453	0.547	0.520	0.480	0.20325	
COX10	17_14005467_G/T	rs200373790	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX10	17_14005498_G/A	rs200827701	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX10	17_14063243_C/T	rs104894556	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX10	17_14063251_C/T	rs114521946	0.993	0.007	0.972	0.028	0.997	0.003	0.998	0.002	1.000	0.000	1.00000	
COX10	17_14110129_G/A	rs200472593	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
COX10	17_14110267_G/T	rs188087012	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX10	17_14110294_G/T	rs111541535	0.997	0.003	0.998	0.002	1.000	0.000	1.000	0.000	0.992	0.008	1.00000	
COX10	17_14110397_A/G	rs200260465	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
COX10	17_14110489_C/T	rs113058506	0.998	0.002	0.996	0.004	1.000	0.000	1.000	0.000	0.997	0.003	1.00000	
COX11	17_53045947_G/A	rs73990239	0.002	0.998	0.008	0.992	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX11	17_53045787_G/A	rs34080917	0.005	0.995	0.022	0.978	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX11	17_53040677_T/C	rs199579556	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX11	17_53040119_T/A	rs200586356	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
COX15	10_101487264_G/A	rs144644373	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX15	10_101486775_G/A	rs192078749	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	

COX15	10_101486759_C/T	rs35483721	0.993	0.007	0.976	0.024	0.992	0.008	1.000	0.000	0.999	0.001	1.00000	
COX15	10_101486736_C/T	rs187284527	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX15	10_101483799_G/A	rs2231682	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
COX15	10_101483721_G/C	rs183558471	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX15	10_101480782_T/C	rs200876059	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX15	10_101478249_C/T	rs201703572	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX15	10_101478110_C/T	rs199761049	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX15	10_101476166_A/G	rs144580290	0.998	0.002	0.992	0.008	1.000	0.000	1.000	0.000	1.000	0.000	0.00366	AFR-1.00000; Other monomorphic
COX16	14_70826303_A/G	rs188182259	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX16	14_70826238_A/C	rs182316587	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX16	14_70809397_C/T	rs139410596	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX18	4_73935357_G/A	rs187930178	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	0.011	0.989	1.00000	
COX18	4_73931077_T/C	rs141592190	0.002	0.998	0.000	1.000	0.000	1.000	0.007	0.993	0.000	1.000	1.00000	
COX18	4_73931056_G/C	rs148370240	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX18	4_73931009_A/T	rs193287733	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX18	4_73927613_T/C	rs189709178	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
COX18	4_73927571_T/C	rs115487882	0.010	0.990	0.039	0.961	0.000	1.000	0.000	1.000	0.003	0.997	0.09246	
COX18	4_73927549_A/G	rs181365781	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX18	4_73927540_G/A	rs138323566	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
COX18	4_73923943_C/T	rs186168799	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX18	4_73923937_G/A	rs200107314	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX4I1	16_85838545_A/G	rs147346083	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX4I1	16_85838594_G/A	rs201313443	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX4I2	20_30226848_G/A	rs199601484	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX4I2	20_30227741_G/C	rs148327783	0.002	0.998	0.004	0.996	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	
COX4I2	20_30227828_G/C	rs147223483	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX4I2	20_30231292_C/G	rs145481393	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX4I2	20_30232598_C/T	rs201685557	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	

COX4I2	20_30232603_G/A	rs119455950	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX4I2	20_30232673_G/A	rs11907253	0.075	0.925	0.112	0.888	0.113	0.887	0.002	0.998	0.088	0.912	0.38690	
COX5A	15_75230282_G/C	rs200367305	0.002	0.998	0.004	0.996	0.000	1.000	0.002	0.998	0.003	0.997	1.00000	
COX5A	15_75221559_G/A	rs200811470	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX5A	15_75221462_C/T	rs150174803	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX5A	15_75219196_G/C	rs199907556	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX5A	15_75219190_G/A	rs200875315	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX5B	2_98263883_A/G	rs75630766	0.994	0.006	0.974	0.026	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX6A1	12_120875934_C/T	rs200221639	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX6A1	12_120876205_T/C	rs201293121	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX6A1	12_120876304_C/A	rs140243339	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
COX6A1	12_120878320_A/G	rs200936136	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
COX6A2	16_31439613_A/C	rs140129800	0.997	0.003	1.000	0.000	0.994	0.006	0.998	0.002	0.996	0.004	1.00000	
COX6B1	19_36145481_C/T	rs149686147	0.999	0.001	1.000	0.000	0.994	0.006	1.000	0.000	1.000	0.000	1.00000	
COX6B2	19_55865795_C/A	rs149294692	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX6C	8_100904243_G/A	rs149663441	0.002	0.998	0.002	0.998	0.000	1.000	0.000	1.000	0.004	0.996	1.00000	
COX6C	8_100904215_C/T	rs200470517	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX7A1	19_36642421_T/G	rs17882491	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
COX7A1	19_36642390_C/T	rs150190766	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
COX7A2	6_75953516_C/G	rs113123058	0.995	0.005	0.980	0.020	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX7A2	6_75953470_C/T	rs190629998	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX7A2	6_75950056_C/T	rs115820973	0.999	0.001	1.000	0.000	1.000	0.000	0.995	0.005	1.000	0.000	1.00000	
COX7A2L	2_42580456_C/G	rs150177100	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX7A2L	2_42580380_T/C	rs200309743	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX7A2L	2_42578481_C/T	rs185444762	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX7A2L	2_42578409_T/C	rs150597431	0.007	0.993	0.000	1.000	0.000	1.000	0.028	0.972	0.000	1.000	1.00000	
COX7A2L	2_42578367_T/G	rs199682193	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX7B	X_77158147_C/A	rs61752458	0.007	0.993	0.024	0.976	0.007	0.993	0.000	1.000	0.000	1.000	1.00000	
COX7B2	4_46737193_G/A	rs200964160	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	

COX7B2	4_46737163_T/C	rs111699375	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX7B2	4_46737129_A/T	rs201505906	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
COX7B2	4_46737040_G/A	rs140822119	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
COX8A	11_63742157_C/T	rs148986341	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
COX8A	11_63742183_G/A	rs199919249	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
COX8A	11_63742219_C/T	rs144339685	0.997	0.003	0.986	0.014	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX8C	14_93813619_C/G	rs201659311	0.999	0.001	0.994	0.006	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
COX8C	14_93813724_G/T	rs199879752	0.994	0.006	0.986	0.014	0.997	0.003	0.990	0.010	1.000	0.000	1.00000	
COX8C	14_93813726_C/T	rs114399408	0.955	0.045	0.856	0.144	0.950	0.050	1.000	0.000	0.988	0.012	0.01770	AFR-1.00000; AMR-0.35910; ASN-Monomorphic; EUR-1.00000
COX8C	14_93814387_G/C	rs201893758	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
CYC1	8_145150832_A/G	rs7820984	0.030	0.970	0.126	0.874	0.006	0.994	0.000	1.000	0.001	0.999	0.00189	AFR-0.56077; AMR-1.00000; ASN-Monomorphic; EUR-1.00000
CYC1	8_145150833_T/C	rs144257411	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	0.005	0.995	1.00000	
CYC1	8_145150929_C/A	rs145609083	0.001	0.999	0.004	0.996	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
CYC1	8_145151126_G/T	rs201814058	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
CYC1	8_145151364_T/C	rs201129717	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
CYC1	8_145151366_C/G	rs199884423	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
CYC1	8_145151545_G/A	rs148021370	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
CYC1	8_145152023_C/T	rs74494160	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
DGUOK	2_74154041_G/T	rs147551003	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	0.995	0.005	1.00000	
DGUOK	2_74166092_C/A	rs138034585	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
DGUOK	2_74166093_G/A	rs62641679	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
DGUOK	2_74166105_C/G	rs184770596	0.996	0.004	1.000	0.000	0.981	0.019	1.000	0.000	0.999	0.001	1.00000	
DGUOK	2_74173927_T/C	rs141810774	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	

DGUOK	2_74177730_T/A	rs144181978	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
DGUOK	2_74177777_A/G	rs74874677	0.988	0.012	1.000	0.000	0.981	0.019	1.000	0.000	0.974	0.026	1.00000	
MFF	2_228194472_G/C	rs145010660	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
MFF	2_228194480_A/T	rs3211097	0.804	0.196	0.935	0.065	0.757	0.243	0.813	0.187	0.734	0.266	0.10505	
MFF	2_228194481_G/T	rs3211098	0.804	0.196	0.935	0.065	0.757	0.243	0.815	0.185	0.734	0.266	0.08412	
MFF	2_228194483_G/T	rs78872053	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MFF	2_228195407_A/G	rs200132653	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MFF	2_228195455_A/G	rs182099421	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
MFF	2_228195473_C/T	rs149692814	0.998	0.002	0.992	0.008	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
MFF	2_228195496_G/A	rs201993285	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
MFF	2_228197177_A/C	rs143374639	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MFF	2_228205039_G/A	rs140493973	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
MFF	2_228212070_A/G	rs200608831	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFF	2_228220422_T/C	rs145321987	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
MFF	2_228220451_G/A	rs191608569	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
MFN1	3_179066700_A/G	rs193215263	0.999	0.001	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.00000	
MFN1	3_179069715_G/A	rs187323205	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
MFN1	3_179069717_A/C	rs142787699	0.998	0.002	0.990	0.010	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MFN1	3_179082937_G/A	rs143476739	0.003	0.997	0.000	1.000	0.011	0.989	0.000	1.000	0.003	0.997	1.00000	
MFN1	3_179093011_T/C	rs149864152	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
MFN1	3_179093015_T/A	rs200775244	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
MFN1	3_179093053_A/C	rs200339629	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MFN1	3_179094898_T/C	rs200247518	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
MFN1	3_179094919_A/G	rs199736732	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MFN1	3_179095227_A/G	rs186155706	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFN1	3_179096187_A/T	rs141885014	0.998	0.002	1.000	0.000	1.000	0.000	0.991	0.009	1.000	0.000	1.00000	
MFN1	3_179096584_A/C	rs200881774	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MFN1	3_179104270_A/G	rs186960036	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFN1	3_179107886_G/A	rs200188689	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	

MFN2	1_12052615_C/T	rs138345244	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFN2	1_12052675_G/T	rs139827903	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MFN2	1_12061533_G/A	rs41278630	0.002	0.998	0.000	1.000	0.003	0.997	0.000	1.000	0.004	0.996	1.00000	
MFN2	1_12062112_C/T	rs201675158	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFN2	1_12062145_C/T	rs201165591	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFN2	1_12064068_C/T	rs186448929	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
MFN2	1_12064087_G/A	rs138072432	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
MFN2	1_12064645_C/T	rs78658090	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFN2	1_12065879_A/C	rs190705310	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MFN2	1_12069692_G/A	rs142271930	0.003	0.997	0.000	1.000	0.000	1.000	0.000	1.000	0.008	0.992	1.00000	
MFN2	1_12069698_C/T	rs119103267	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MFN2	1_12069725_G/A	rs144860227	0.003	0.997	0.006	0.994	0.000	1.000	0.000	1.000	0.004	0.996	1.00000	
MTERF	7_91503980_C/T	rs190837494	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MTERF	7_91503951_C/T	rs201580782	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
MTERF	7_91503914_G/A	rs144315661	0.002	0.998	0.000	1.000	0.003	0.997	0.000	1.000	0.004	0.996	1.00000	
MTERF	7_91503846_T/G	rs199603020	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
MTERF	7_91503759_T/C	rs148655332	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
MTERF	7_91503744_C/T	rs201335490	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
MTERF	7_91503699_C/T	rs202031297	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MTERF	7_91503687_T/C	rs181549251	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	
MTERF	7_91503524_C/T	rs200438840	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MTERF	7_91503417_C/T	rs17856025	0.981	0.019	0.917	0.083	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
MTERF	7_91503384_G/C	rs143980432	0.002	0.998	0.004	0.996	0.006	0.994	0.002	0.998	0.000	1.000	1.00000	
MTERF	7_91503356_C/T	rs78445151	0.997	0.003	0.988	0.012	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MTERF	7_91503317_T/C	rs149530545	0.001	0.999	0.000	1.000	0.000	1.000	0.005	0.995	0.000	1.000	1.00000	
MTERF	7_91503235_T/G	rs139218723	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	

MTERF	7_91503228_C/T	rs10266424	0.587	0.413	0.823	0.177	0.522	0.478	0.563	0.437	0.483	0.517	0.00014	AFR-0.18563; AMR-0.17979; ASN-0.63233; EUR-0.75546
MTERF	7_91503114_T/C	rs139119978	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
MTERF	7_91502930_T/C	rs199652694	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
MTFR1	8_66582195_G/C	rs201019084	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
MTFR1	8_66594600_A/G	rs144584935	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MTFR1	8_66617012_A/G	rs141941459	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
MTFR1	8_66617076_G/T	rs201556776	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
MTFR1	8_66619338_G/A	rs200811406	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
MTFR1	8_66620091_G/A	rs150962565	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
MTFR1	8_66620167_G/A	rs184253762	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFAF2	5_60448675_G/A	rs201187582	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFAF2	5_60448723_G/A	rs9885480	0.001	0.999	0.000	1.000	0.006	0.994	0.000	1.000	0.001	0.999	1.00000	
NDUFAF3	3_49059639_C/T	rs199568117	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFAF4	6_97345638_G/T	rs145392673	0.996	0.004	0.984	0.016	1.000	0.000	1.000	0.000	0.999	0.001	0.01605	AFR-0.05613; AMR, ASN-Monomorphic; EUR-1.00000
NDUFAF4	6_97344663_T/C	rs148667964	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFAF4	6_97339133_A/T	rs200279216	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFAF4	6_97339017_A/T	rs201754378	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFB1	14_92588049_G/C	rs138437079	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFB1	14_92583974_T/C	rs201547910	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFB1	14_92583956_C/T	rs190083501	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFB1	14_92583927_T/A	rs149760197	0.002	0.998	0.000	1.000	0.003	0.997	0.000	1.000	0.004	0.996	1.00000	
NDUFB1	14_92583867_G/A	rs151054506	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFB10	16_2009733_C/G	rs200975991	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFB10	16_2011596_T/C	rs201663429	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	

NDUFB2	7_140396561_G/T	rs200087759	0.999	0.001	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.00000	
NDUFB3	2_201943624_C/T	rs144513268	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFB3	2_201943639_C/T	rs182420107	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFB3	2_201943669_T/C	rs142609245	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFB3	2_201950223_T/C	rs139936993	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFB4	3_120315283_C/T	rs150031407	0.998	0.002	1.000	0.000	1.000	0.000	0.993	0.007	1.000	0.000	1.00000	
NDUFB4	3_120315384_A/T	rs142688627	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFB4	3_120321071_T/G	rs149224531	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFB4	3_120321095_G/A	rs201413691	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFB5	3_179322703_A/C	rs35399127	0.993	0.007	1.000	0.000	0.989	0.011	1.000	0.000	0.984	0.016	1.00000	
NDUFB5	3_179332803_A/T	rs148532160	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFB5	3_179336257_T/C	rs4147793	0.001	0.999	0.000	1.000	0.000	1.000	0.005	0.995	0.000	1.000	1.00000	
NDUFB5	3_179336264_G/A	rs145089839	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFB6	9_32573054_G/C	rs138358975	0.001	0.999	0.006	0.994	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFB6	9_32572983_G/C	rs199895242	0.001	0.999	0.000	1.000	0.006	0.994	0.000	1.000	0.000	1.000	1.00000	
NDUFB6	9_32572939_C/T	rs190070706	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFB6	9_32572932_T/C	rs142741532	0.001	0.999	0.006	0.994	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFB6	9_32571013_G/A	rs200723755	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFB6	9_32570989_A/G	rs148891049	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFB6	9_32553935_G/A	rs143339409	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFB6	9_32553915_C/T	rs190587227	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFB7	19_14682809_C/A	rs189994454	0.001	0.999	0.000	1.000	0.008	0.992	0.000	1.000	0.000	1.000	1.00000	
NDUFB7	19_14682725_C/A	rs201675767	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
NDUFB7	19_14682721_A/C	rs200041574	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFB7	19_14677608_G/A	rs200757972	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFB7	19_14677049_G/A	rs200292442	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFB7	19_14677043_G/C	rs3752220	0.002	0.998	0.000	1.000	0.000	1.000	0.007	0.993	0.000	1.000	1.00000	
NDUFB7	19_14677022_T/G	rs202223254	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFB8	10_102289587_C/G	rs139827718	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	

NDUFB8	10_102289572_A/C	rs201604335	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFB8	10_102289263_G/T	rs200405716	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFB8	10_102286733_G/A	rs185514139	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFB8	10_102286256_G/C	rs74154666	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFB8	10_102286251_A/T	rs1802224	0.997	0.003	0.988	0.012	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFB8	10_102286179_C/T	rs141801241	0.996	0.004	1.000	0.000	1.000	0.000	0.984	0.016	1.000	0.000	1.00000	
NDUFB9	8_125555335_T/C	rs140417066	0.001	0.999	0.006	0.994	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFB9	8_125555366_G/T	rs142723791	0.993	0.007	0.972	0.028	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFB9	8_125555387_A/T	rs138066988	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFB9	8_125555426_C/G	rs200765174	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFB9	8_125555446_C/T	rs199940282	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFB9	8_125562029_C/T	rs10195	0.888	0.112	0.843	0.157	0.948	0.052	0.860	0.140	0.909	0.091	1.00000	
NDUFB9	8_125562065_C/G	rs148402231	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFC1	4_140216277_C/T	rs201811659	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFC1	4_140216214_C/T	rs200399570	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFC1	4_140216203_C/A	rs201035643	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFC1	4_140213733_C/G	rs72939460	0.998	0.002	0.992	0.008	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFC2	11_77790655_G/C	rs8875	0.149	0.851	0.045	0.955	0.221	0.779	0.082	0.918	0.232	0.768	0.12107	
NDUFC2	11_77781037_C/T	rs183610034	0.998	0.002	1.000	0.000	1.000	0.000	0.993	0.007	1.000	0.000	1.00000	
NDUFS1	2_207018354_G/C	rs201997807	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS1	2_207012277_T/C	rs140126185	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFS1	2_207011753_A/G	rs148544177	0.997	0.003	0.986	0.014	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFS1	2_207008821_G/C	rs75666426	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFS1	2_207007550_C/A	rs145401558	0.002	0.998	0.008	0.992	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS1	2_207007482_A/T	rs139690694	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFS1	2_207006704_C/T	rs151279101	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFS1	2_207003310_G/C	rs78042826	0.002	0.998	0.000	1.000	0.003	0.997	0.000	1.000	0.005	0.995	1.00000	
NDUFS1	2_207003221_A/C	rs202214721	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFS1	2_206997706_C/T	rs137889316	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	

NDUFS1	2_206994857_T/C	rs200131601	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFS1	2_206994821_T/C	rs147685849	0.001	0.999	0.006	0.994	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS1	2_206991540_G/C	rs200782941	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFS1	2_206991498_T/C	rs201644320	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFS1	2_206991447_T/C	rs142716964	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFS2	1_161172233_C/A	rs11538340	0.072	0.928	0.085	0.915	0.047	0.953	0.079	0.921	0.070	0.930	0.16608	
NDUFS2	1_161180473_T/C	rs144937332	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS2	1_161180482_G/A	rs35086265	0.003	0.997	0.002	0.998	0.000	1.000	0.000	1.000	0.008	0.992	1.00000	
NDUFS2	1_161182208_C/G	rs11576415	0.949	0.051	0.988	0.012	0.961	0.039	0.990	0.010	0.887	0.113	0.52399	
NDUFS2	1_161182232_G/T	rs145577083	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFS2	1_161182259_G/A	rs200509897	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFS2	1_161183502_G/T	rs186476170	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFS2	1_161183958_T/C	rs140731056	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFS3	11_47600677_C/T	rs201457989	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFS3	11_47603733_G/C	rs148331180	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFS3	11_47605878_G/A	rs201626967	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS3	11_47605891_G/A	rs78121716	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFS3	11_47605987_A/G	rs201167810	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFS4	5_52856497_C/A	rs148595893	0.001	0.999	0.000	1.000	0.003	0.997	0.000	1.000	0.001	0.999	1.00000	
NDUFS4	5_52856502_G/C	rs185711494	0.001	0.999	1.000	0.000	1.000	0.000	0.003	0.997	1.000	0.000	1.00000	
NDUFS4	5_52856539_G/A	rs188911977	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFS4	5_52856563_C/A	rs146259362	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
NDUFS4	5_52856572_T/A	rs145347909	0.001	0.999	0.006	0.994	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS4	5_52899282_G/T	rs200926524	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFS4	5_52942135_C/T	rs184765529	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFS4	5_52954401_T/G	rs199541993	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFS4	5_52978992_T/A	rs149482195	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS4	5_52979034_A/G	rs200758718	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFS5	1_39494611_C/T	rs201757086	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	

NDUFS5	1_39500125_C/T	rs200515387	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFS5	1_39500140_A/C	rs192512172	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFS5	1_39500141_C/A	rs146279654	0.002	0.998	0.006	0.994	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	
NDUFS6	5_1802445_A/T	rs199652659	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFS6	5_1814495_G/A	rs187737486	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFS6	5_1814523_C/T	rs192286856	0.999	0.001	1.000	0.000	1.000	0.000	1.000	0.000	0.997	0.003	1.00000	
NDUFS6	5_1815992_G/A	rs200109710	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS7	19_1387824_G/A	rs201112782	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS7	19_1388538_C/T	rs1142530	0.556	0.444	0.709	0.291	0.525	0.475	0.670	0.330	0.387	0.613	0.17663	
NDUFS7	19_1388855_C/G	rs11551666	0.999	0.001	0.994	0.006	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFS7	19_1393344_G/A	rs201420030	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
NDUFS8	11_67799622_C/T	rs150278938	0.999	0.001	1.000	0.000	1.000	0.000	1.000	0.000	0.997	0.003	1.00000	
NDUFS8	11_67799637_C/A	rs142658611	0.001	0.999	0.006	0.994	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS8	11_67799649_C/T	rs201990988	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFS8	11_67799671_G/A	rs201017561	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFS8	11_67803759_C/A	rs201484242	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFS8	11_67803929_G/A	rs147344724	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFV1	11_67376023_G/T	rs199609729	0.999	0.001	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.00000	
NDUFV1	11_67376936_G/T	rs200365831	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFV1	11_67376982_A/G	rs144291845	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFV1	11_67377036_G/A	rs199972110	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFV1	11_67377050_C/T	rs151144350	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFV1	11_67377870_T/C	rs180950242	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFV1	11_67377904_G/A	rs142982022	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFV1	11_67377936_C/T	rs201289242	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFV1	11_67378498_G/A	rs200829846	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFV1	11_67378525_A/G	rs201908937	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFV1	11_67378876_G/T	rs201382784	0.999	0.001	0.998	0.002	1.000	0.000	1.000	0.000	0.997	0.003	1.00000	
NDUFV1	11_67378883_C/T	rs200925993	0.999	0.001	1.000	0.000	0.997	0.003	0.998	0.002	1.000	0.000	1.00000	

NDUFV1	11_67379374_A/G	rs200270653	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFV1	11_67379608_A/C	rs145679247	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFV1	11_67379615_T/C	rs200627507	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFV1	11_67379853_G/A	rs146910804	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFV2	18_9117855_T/C	rs199997775	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFV2	18_9117867_T/C	rs906807	0.760	0.240	0.799	0.201	0.820	0.180	0.783	0.217	0.843	0.157	0.56374	
NDUFV2	18_9117899_G/A	rs75362221	0.004	0.996	0.018	0.982	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFV2	18_9119324_C/T	rs202166758	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFV2	18_9119355_C/A	rs142405606	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFV2	18_9122573_G/A	rs200422010	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NDUFV2	18_9122586_C/A	rs199560855	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFV2	18_9124909_C/G	rs201708711	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFV2	18_9124974_A/G	rs200691654	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
NDUFV3	21_44313454_C/G	rs77606940	0.999	0.001	1.000	0.000	1.000	0.000	1.000	0.000	0.997	0.003	1.00000	
NDUFV3	21_44317073_G/T	rs78214542	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFV3	21_44317080_C/T	rs148054698	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFV3	21_44317112_G/A	rs201455116	1.000	0.000	0.002	0.998	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFV3	21_44317156_A/C	rs141922962	0.996	0.004	0.998	0.002	0.994	0.006	1.000	0.000	0.993	0.007	1.00000	
NDUFV3	21_44323388_C/T	rs200656693	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFV3	21_44323412_C/T	rs35064727	0.998	0.002	0.992	0.008	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
NDUFV3	21_44323430_G/T	rs201597963	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
NDUFV3	21_44323667_G/C	rs201154517	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NDUFV3	21_44323948_G/A	rs202060146	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFV3	21_44323957_A/G	rs141329399	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
NDUFV3	21_44324329_G/A	rs61746238	0.008	0.992	0.000	1.000	0.014	0.986	0.000	1.000	0.017	0.983	1.00000	
NDUFV3	21_44324365_G/A	rs10595	0.522	0.478	0.726	0.274	0.392	0.608	0.336	0.664	0.594	0.406	0.02177	AFR-0.74814; AMR-0.43484; ASN-0.79154; EUR-1.00000

NDUFV3	21_44324372_G/A	rs114225578	0.002	0.998	0.008	0.992	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
NDUFV3	21_44324377_G/A	rs183648098	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
NT5M	17_17209862_G/C	rs199941205	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
NT5M	17_17248203_C/A	rs201242235	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
NT5M	17_17250159_C/T	rs2240876	0.865	0.135	0.990	0.010	0.859	0.141	0.643	0.357	0.955	0.045	0.00000	AFR-1.00000; AMR-0.13128; ASN-0.25085; EUR-1.00000
NT5M	17_17250197_G/A	rs145194793	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	0.007	0.993	1.00000	
OPA1	3_193332522_C/A	rs75414918	0.011	0.989	0.000	1.000	0.011	0.989	0.028	0.972	0.005	0.995	1.00000	
OPA1	3_193332564_C/G	rs145565705	0.998	0.002	0.992	0.008	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
OPA1	3_193332718_A/G	rs151103940	0.998	0.002	0.992	0.008	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
OPA1	3_193332823_C/T	rs200983556	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
OPA1	3_193334991_G/A	rs7624750	0.457	0.543	0.604	0.396	0.434	0.566	0.339	0.661	0.460	0.540	0.02382	AFR-1.00000; AMR-0.76448; ASN-0.18845; EUR-0.60482
OPA1	3_193336676_C/T	rs34307082	0.976	0.024	0.984	0.016	0.975	0.025	0.972	0.028	0.975	0.025	0.46223	
OPA1	3_193343987_G/A	rs201202646	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
OPA1	3_193349441_T/C	rs200223621	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
OPA1	3_193360767_G/A	rs190223702	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
OPA1	3_193361167_A/G	rs143319805	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
OPA1	3_193363363_A/G	rs201301622	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
OPA1	3_193364870_G/A	rs182251953	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
OPA1	3_193366644_G/A	rs200756304	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
OPA1	3_193372737_A/G	rs142694017	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
OPA1	3_193375011_A/G	rs199925668	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
OPA1	3_193377336_C/T	rs190235251	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
OPA1	3_193380621_A/G	rs200428940	1.000	0.000	1.000	9.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	

OPA1	3_193380726_G/A	rs200412464	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
OPA1	3_193409895_A/C	rs189036094	0.999	0.001	1.000	0.000	0.994	0.006	1.000	0.000	1.000	0.000	1.00000	
OPA3	19_46087989_G/C	rs200742525	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
OPA3	19_46057071_C/T	rs186796646	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
OPA3	19_46056900_C/T	rs142402590	0.998	0.002	0.990	0.010	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
PEO1	10_102748430_C/T	rs200405447	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
PEO1	10_102748493_G/A	rs199810842	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
PEO1	10_102748601_G/A	rs117140867	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
PEO1	10_102748644_G/T	rs187291192	0.999	0.001	1.000	0.000	0.994	0.006	1.000	0.000	1.000	0.000	1.00000	
PEO1	10_102749069_G/A	rs17113613	0.039	0.961	0.128	0.872	0.041	0.959	0.000	1.000	0.011	0.989	0.02260	AFR-1.00000; AMR-0.26005; ASN-Monomorphic; EUR-1.00000
PEO1	10_102749079_G/A	rs143309797	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
PEO1	10_102750648_A/T	rs200192223	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
PEO1	10_102750730_A/G	rs116046810	0.999	0.001	0.994	0.006	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
PEO1	10_102753154_G/C	rs190487176	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
PEO1	10_102753257_G/A	rs182559752	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
PINK1	1_20960385_A/T	rs148871409	0.976	0.024	0.994	0.006	0.959	0.041	1.000	0.000	0.955	0.045	0.46290	
PINK1	1_20964401_C/T	rs45608139	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
PINK1	1_20964533_C/T	rs35802484	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
PINK1	1_20964546_C/T	rs149822257	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
PINK1	1_20964573_C/T	rs34677717	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
PINK1	1_20966389_G/T	rs138018628	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
PINK1	1_20966404_C/T	rs144071530	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
PINK1	1_20971050_A/T	rs200036561	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
PINK1	1_20971057_C/A	rs113092523	0.003	0.997	0.012	0.988	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
PINK1	1_20971063_C/T	rs146691996	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
PINK1	1_20971075_G/A	rs181675228	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	

PINK1	1_20971111_G/A	rs201940147	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
PINK1	1_20971119_C/G	rs112600292	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
PINK1	1_20971141_G/A	rs202128685	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
PINK1	1_20971155_G/A	rs200949139	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
PINK1	1_20972103_G/A	rs184043309	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
PINK1	1_20972108_G/A	rs55831733	0.001	0.999	0.000	1.000	0.000	1.000	0.002	0.998	0.001	0.999	1.00000	
PINK1	1_20972111_G/A	rs3738136	0.101	0.899	0.020	0.980	0.058	0.942	0.274	0.726	0.042	0.958	0.00000	AFR-0.08949; AMR-0.46087; ASN-0.10486; EUR-1.00000
PINK1	1_20972168_G/A	rs76753586	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
PINK1	1_20975079_G/A	rs200728364	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
PINK1	1_20975105_G/A	rs45478900	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
PINK1	1_20975111_C/G	rs202130946	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
PINK1	1_20975549_C/T	rs183454580	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
PINK1	1_20975662_G/A	rs115477764	0.009	0.991	0.035	0.965	0.006	0.994	0.000	1.000	0.000	1.000	1.00000	
PINK1	1_20976940_G/A	rs61744200	0.010	0.990	0.039	0.961	0.006	0.994	0.000	1.000	0.000	1.000	1.00000	
PINK1	1_20977000_A/C	rs1043424	0.719	0.281	0.778	0.222	0.779	0.221	0.636	0.364	0.714	0.286	0.88235	
PINK1	1_20977042_C/T	rs146126901	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89876985_T/C	rs201786897	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
POLG	15_89876858_T/C	rs28567406	0.037	0.963	0.081	0.919	0.030	0.970	0.016	0.984	0.028	0.972	1.00000	
POLG	15_89876578_G/C	rs115109291	0.002	0.998	0.008	0.992	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLG	15_89876408_C/T	rs3176162	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89873415_G/A	rs113994094	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	
POLG	15_89873364_C/G	rs61752784	0.996	0.004	1.000	0.000	0.992	0.008	1.000	0.000	0.993	0.007	1.00000	
POLG	15_89871763_G/C	rs145289229	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	
POLG	15_89870557_G/T	rs200399546	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89870432_C/T	rs113994095	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
POLG	15_89870429_T/C	rs145843073	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	

POLG	15_89870178_C/A	rs61752783	0.005	0.995	0.002	0.998	0.011	0.989	0.000	1.000	0.008	0.992	1.00000	
POLG	15_89869955_T/C	rs201097813	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLG	15_89869919_G/A	rs2307447	0.003	0.997	0.012	0.988	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLG	15_89868870_G/A	rs113994096	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.003	0.997	1.00000	
POLG	15_89868793_G/A	rs147407423	0.001	0.999	0.002	0.998	0.006	0.994	0.000	1.000	0.000	1.000	1.00000	
POLG	15_89867424_C/T	rs2307450	0.993	0.007	1.000	0.000	0.959	0.041	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89867351_G/A	rs201481404	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLG	15_89866735_C/T	rs185645212	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
POLG	15_89866699_T/C	rs56119329	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLG	15_89866691_C/G	rs121918054	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
POLG	15_89866682_T/C	rs78347903	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLG	15_89866676_C/T	rs147827654	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
POLG	15_89866654_A/G	rs202037973	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89866030_C/T	rs191490663	0.999	0.001	1.000	0.000	0.994	0.006	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89865073_T/C	rs41549716	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	0.005	0.995	1.00000	
POLG	15_89864211_C/G	rs60636456	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89864088_G/A	rs201477273	0.002	0.998	0.000	1.000	0.000	1.000	0.007	0.993	0.000	1.000	1.00000	
POLG	15_89864081_A/C	rs142347031	0.999	0.001	1.000	0.000	1.000	0.000	1.000	0.000	0.997	0.003	1.00000	
POLG	15_89864019_C/T	rs200258601	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
POLG	15_89862462_C/T	rs201014720	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89862296_G/A	rs181860632	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLG	15_89862193_C/T	rs140079523	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
POLG	15_89861978_A/C	rs74034411	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLG	15_89861826_T/C	rs2307441	0.017	0.983	0.002	0.998	0.008	0.992	0.000	1.000	0.044	0.956	0.03559	AFR-1.00000; AMR-1.00000; ASN-Monomorphic; EUR-0.15094
POLG	15_89861818_G/A	rs2307440	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLG	15_89861812_G/A	rs149099318	0.005	0.995	0.010	0.990	0.014	0.986	0.002	0.998	0.001	0.999	1.00000	

POLG	15_89860726_T/C	rs188348569	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLG	15_89859994_C/A	rs3087374	0.038	0.962	0.006	0.994	0.055	0.945	0.000	1.000	0.079	0.921	0.00323	AFR-1.00000; AMR-0.08897; ASN-Monomorphic; EUR-0.27384
POLG	15_89859992_G/A	rs200788482	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLG2	17_62493007_G/A	rs117792639	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLG2	17_62492965_C/T	rs146504115	0.999	0.001	0.994	0.006	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLG2	17_62492962_C/T	rs201278573	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
POLG2	17_62492780_C/T	rs200118378	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
POLG2	17_62492690_G/A	rs112984118	0.005	0.995	0.022	0.978	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLG2	17_62492582_C/T	rs1427463	0.750	0.250	0.260	0.740	0.804	0.196	0.963	0.037	0.881	0.119	0.00000	AFR-0.06938; AMR-0.15698; ASN-1.00000; EUR-0.45712
POLG2	17_62492552_C/A	rs200880373	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLG2	17_62489138_C/T	rs191057592	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
POLG2	17_62489027_C/T	rs148101254	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLG2	17_62488876_T/C	rs148941150	0.001	0.999	0.002	0.998	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
POLG2	17_62479069_A/C	rs61751983	0.997	0.003	0.998	0.002	0.983	0.017	1.000	0.000	1.000	0.000	1.00000	
POLG2	17_62476451_C/G	rs17850455	0.994	0.006	0.998	0.002	1.000	0.000	1.000	0.000	0.984	0.016	1.00000	
POLG2	17_62474079_G/A	rs200118292	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
POLRMT	19_633500_A/G	rs200921997	0.995	0.005	0.980	0.020	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLRMT	19_632915_G/A	rs12610885	0.137	0.863	0.055	0.945	0.108	0.892	0.240	0.760	0.127	0.873	0.24233	
POLRMT	19_630130_C/T	rs140649984	0.998	0.002	0.992	0.008	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLRMT	19_630075_C/T	rs189184481	0.991	0.009	1.000	0.000	1.000	0.000	0.965	0.035	1.000	0.000	1.00000	
POLRMT	19_630035_C/T	rs77466198	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
POLRMT	19_629970_C/T	rs113148837	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	

POLRMT	19_629887_G/A	rs149933500	0.017	0.983	0.073	0.927	0.003	0.997	0.000	1.000	0.000	1.000	0.00297	AFR-0.12568; AMR-1.00000; ASN, EUR-Monomorphic
POLRMT	19_629841_C/A	rs146345748	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
POLRMT	19_629739_T/C	rs199600661	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLRMT	19_629733_G/A	rs182390676	0.005	0.995	0.020	0.980	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_629605_G/A	rs145312875	0.003	0.997	0.012	0.988	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_625131_T/C	rs115263594	0.004	0.996	0.018	0.982	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_624894_T/A	rs138732981	0.009	0.991	0.018	0.982	0.014	0.986	0.000	1.000	0.008	0.992	1.00000	
POLRMT	19_624890_C/T	rs143022703	0.989	0.011	0.951	0.049	0.997	0.003	1.000	0.000	1.000	0.000	0.00740	AFR-0.10236; AMR-1.00000; ASN, EUR-Monomorphic
POLRMT	19_624850_C/T	rs201346718	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLRMT	19_624763_G/A	rs201473800	0.000	1.000	0.005	0.995	0.000	1.000	0.017	0.983	0.000	1.000	1.00000	
POLRMT	19_623576_G/A	rs199567642	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_623546_A/G	rs41553913	0.957	0.043	0.829	0.171	0.986	0.014	1.000	0.000	0.992	0.008	0.00070	AFR-0.65568; AMR-1.00000; ASN-Monomorphic; EUR-1.00000
POLRMT	19_623505_G/C	rs201389191	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_622830_C/G	rs138594532	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
POLRMT	19_622587_C/A	rs56226067	0.003	0.997	0.004	0.996	0.000	1.000	0.007	0.993	0.000	1.000	1.00000	
POLRMT	19_622583_T/A	rs200807835	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
POLRMT	19_622367_C/T	rs115950441	0.986	0.014	0.939	0.061	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLRMT	19_622336_T/G	rs2238549	0.552	0.448	0.722	0.278	0.434	0.566	0.544	0.456	0.505	0.495	0.17957	
POLRMT	19_622207_C/T	rs61745193	0.993	0.007	1.000	0.000	0.994	0.006	1.000	0.000	0.982	0.018	0.05344	
POLRMT	19_621561_C/A	rs10421235	0.082	0.918	0.199	0.801	0.064	0.936	0.072	0.928	0.022	0.978	0.54177	
POLRMT	19_621090_C/T	rs139383492	0.989	0.011	0.976	0.024	0.978	0.022	0.998	0.002	0.997	0.003	1.00000	
POLRMT	19_620005_C/T	rs151235528	0.992	0.008	0.963	0.037	1.000	0.000	1.000	0.000	1.000	0.000	0.06799	

POLRMT	19_619982_G/C	rs200607630	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
POLRMT	19_619719_G/A	rs201811276	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
POLRMT	19_617838_G/A	rs201558272	0.001	0.999	0.000	1.000	0.000	1.000	0.002	0.998	0.001	0.999	1.00000	
POLRMT	19_617634_G/A	rs147740567	0.002	0.998	0.010	0.990	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_617582_C/T	rs150648879	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
POLRMT	19_617573_G/A	rs142850300	0.002	0.998	0.008	0.992	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_617470_T/G	rs138715064	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
POLRMT	19_617466_A/G	rs151287767	0.996	0.004	0.998	0.002	0.994	0.006	1.000	0.000	0.993	0.007	1.00000	
POLRMT	19_617297_G/A	rs199982300	0.001	0.999	0.000	1.000	0.008	0.992	0.000	1.000	0.000	1.000	1.00000	
SDHA	5_218487_G/A	rs187964306	0.004	0.996	0.016	0.984	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
SDHA	5_223646_A/T	rs34635677	0.988	0.012	1.000	0.000	0.986	0.014	1.000	0.000	0.972	0.028	1.00000	
SDHA	5_223666_G/A	rs140736646	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
SDHA	5_223679_A/G	rs80207011	0.999	0.001	0.994	0.006	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
SDHA	5_224487_T/C	rs142926807	0.006	0.994	0.000	1.000	0.000	1.000	0.023	0.977	0.000	1.000	1.00000	
SDHA	5_226091_G/A	rs148246073	0.006	0.994	0.000	1.000	0.000	1.000	0.023	0.977	0.000	1.000	1.00000	
SDHA	5_233598_A/G	rs182055219	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
SDHA	5_233687_G/A	rs200526913	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
SDHA	5_233748_T/G	rs200103530	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
SDHA	5_235416_T/C	rs201826964	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
SDHA	5_236676_G/A	rs138277996	0.068	0.932	0.063	0.937	0.108	0.892	0.084	0.916	0.041	0.959	0.00769	AFR-0.60736; AMR-0.23072; ASN-0.23760; EUR-1.00000
SDHA	5_240563_C/T	rs151266052	0.997	0.003	0.986	0.014	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
SDHA	5_240575_G/A	rs192818312	0.001	0.999	0.006	0.994	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
SDHA	5_251207_C/T	rs181238392	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
SDHA	5_254512_G/A	rs1126568	0.014	0.986	0.006	0.994	0.006	0.994	0.005	0.995	0.030	0.970	1.00000	
SDHA	5_256500_T/G	rs60587941	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
SDHA	5_256509_G/A	rs6962	0.161	0.839	0.346	0.654	0.202	0.798	0.042	0.958	0.112	0.888	0.14551	

SDHA	5_256519_C/G	rs191412461	0.998	0.002	1.000	0.000	0.989	0.011	1.000	0.000	1.000	0.000	1.00000	
SDHB	1_17380507_G/C	rs11203289	0.009	0.991	0.037	0.963	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
SDHB	1_17380483_C/T	rs111430410	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
SDHB	1_17371286_T/C	rs35962811	0.001	0.999	0.002	0.998	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
SDHB	1_17354297_A/G	rs33927012	0.992	0.008	0.998	0.002	0.994	0.006	1.000	0.000	0.982	0.018	1.00000	
SDHB	1_17349180_G/A	rs138996609	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
SDHB	1_17349159_G/A	rs186768244	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
SDHC	1_161293437_T/G	rs200761743	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
SDHC	1_161298206_C/T	rs148566767	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
SDHC	1_161326496_T/G	rs144532303	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
SDHD	11_111958581_C/T	rs192332761	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
SDHD	11_111958677_A/G	rs11214077	0.991	0.009	1.000	0.000	0.975	0.025	1.000	0.000	0.985	0.015	1.00000	
SDHD	11_111959668_G/C	rs202239399	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
SDHD	11_111965636_A/G	rs199772639	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
SSBP1	7_141438979_C/T	rs148887629	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
SSBP1	7_141441981_T/C	rs192517454	0.001	0.999	0.000	1.000	0.000	1.000	0.005	0.995	0.000	1.000	1.00000	
SSBP1	7_141443490_T/C	rs200664859	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
SSBP1	7_141443499_T/C	rs78598246	0.005	0.995	0.000	1.000	0.000	1.000	0.019	0.981	0.000	1.000	1.00000	
SSBP1	7_141443764_G/A	rs148271472	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
TFAM	10_60145327_T/C	rs200473819	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
TFAM	10_60145342_G/C	rs1937	0.094	0.906	0.008	0.992	0.091	0.909	0.171	0.829	0.092	0.908	0.00626	AFR-1.00000; AMR-0.16640; ASN-0.05974; EUR-0.75673
TFAM	10_60145390_G/T	rs199678369	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
TFAM	10_60146077_A/G	rs138243284	0.999	0.001	1.000	0.000	1.000	0.000	0.995	0.005	1.000	0.000	1.00000	
TK2	16_66583885_G/A	rs191573607	0.003	0.997	0.006	0.994	0.006	0.994	0.000	1.000	0.001	0.999	1.00000	
TK2	16_66565357_C/T	rs148450491	0.999	0.001	1.000	0.000	1.000	0.000	0.995	0.005	1.000	0.000	1.00000	
TK2	16_66565297_G/T	rs137854429	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	

TK2	16_66562931_C/T	rs138479499	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
TK2	16_66551710_C/T	rs149036717	0.999	0.001	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.00000	
TK2	16_66545906_T/C	rs144419486	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
UCP1	4_141489766_G/A	rs150067245	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.004	0.996	1.00000	
UCP1	4_141489068_C/T	rs45539933	0.910	0.090	0.093	0.907	0.075	0.925	0.075	0.925	0.074	0.926	0.70593	
UCP1	4_141484519_G/C	rs200389729	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UCP1	4_141484292_C/A	rs138611550	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UCP1	4_141483471_T/A	rs2270565	0.070	0.930	0.045	0.955	1.000	0.000	1.000	0.000	1.000	0.000	0.36830	
UCP1	4_141483389_A/G	rs140138182	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UCP1	4_141481151_A/G	rs146114327	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UCP2	11_73689309_C/T	rs148253207	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	0.995	0.005	1.00000	
UCP2	11_73689131_T/C	rs201348391	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UCP2	11_73689128_C/T	rs144018051	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UCP2	11_73689104_G/A	rs660339	0.432	0.568	0.423	0.577	0.442	0.558	0.451	0.549	0.418	0.582	0.53680	
UCP2	11_73689099_C/T	rs145662569	0.997	0.003	0.988	0.012	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UCP2	11_73689056_C/T	rs182694614	0.999	0.001	0.996	0.004	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UCP2	11_73689051_C/G	rs200489709	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
UCP2	11_73689041_C/T	rs45541732	0.996	0.004	0.986	0.014	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UCP2	11_73687922_C/G	rs144885917	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
UCP2	11_73686657_C/T	rs200027152	0.999	0.001	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.00000	
UCP2	11_73686632_G/A	rs201373362	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UCP2	11_73686622_C/G	rs139945658	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UCP2	11_73686548_G/C	rs45490393	0.004	0.996	0.014	0.986	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
UCP2	11_73686137_G/C	rs45596837	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UCP3	11_73718077_A/C	rs141482270	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UCP3	11_73718030_C/T	rs199679366	0.989	0.011	0.986	0.014	0.989	0.011	0.988	0.012	0.991	0.009	1.00000	
UCP3	11_73717417_C/T	rs147631608	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
UCP3	11_73717396_G/A	rs17848367	0.001	0.999	0.002	0.998	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UCP3	11_73717342_C/T	rs58614015	0.999	0.001	0.998	0.002	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	

UCP3	11_73717340_T/G	rs143786748	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UCP3	11_73717301_C/T	rs183714776	0.998	0.002	0.992	0.008	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UCP3	11_73717277_C/T	rs192655642	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
UCP3	11_73717219_G/A	rs74907838	0.003	0.997	0.014	0.986	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UCP3	11_73716960_C/T	rs17848372	0.998	0.002	0.996	0.004	1.000	0.000	0.997	0.003	1.000	0.000	1.00000	
UCP3	11_73716835_C/T	rs201405748	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UCP3	11_73716829_T/C	rs201679589	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
UCP3	11_73715571_C/T	rs201993988	1.000	0.000	1.000	0.000	0.997	0.003	1.000	0.000	1.000	0.000	1.00000	
UCP3	11_73714978_C/T	rs138705669	0.999	0.001	1.000	0.000	1.000	0.000	1.000	0.000	0.997	0.003	1.00000	
UCP3	11_73714927_G/T	rs145884716	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
UCP3	11_73712501_G/A	rs142927779	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UCP3	11_73712478_C/A	rs199959534	0.001	0.999	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	1.00000	
UCP3	11_73712465_G/A	rs200773036	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UCP3	11_73712464_G/A	rs76629964	0.001	0.999	0.000	1.000	0.003	0.997	0.002	0.998	0.000	1.000	1.00000	
UQCR10	22_30163526_A/G	rs76013375	0.868	0.132	0.667	0.333	0.923	0.077	0.902	0.098	0.947	0.053	0.00001	AFR-0.19684; AMR-1.00000; ASN-1.00000; EUR-0.27504
UQCR10	22_30165686_A/G	rs199810262	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UQCR11	19_1599448_C/A	rs181112176	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UQCRB	8_97247742_G/A	rs200758329	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UQCRB	8_97244082_T/A	rs145974195	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
UQCRB	8_97244060_A/T	rs139283183	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UQCRB	8_97244011_T/G	rs145828292	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UQCRB	8_97243321_G/A	rs199583530	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
UQCRC1	3_48646654_T/C	rs117171524	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UQCRC1	3_48643235_C/A	rs201250580	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UQCRC1	3_48641799_G/T	rs191821836	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UQCRC1	3_48641060_C/G	rs17080284	0.993	0.007	1.000	0.000	1.000	0.000	0.974	0.026	1.000	0.000	1.00000	

UQCRC1	3_48638807_G/C	rs149245457	0.005	0.995	0.000	1.000	0.000	1.000	0.019	0.981	0.000	1.000	1.00000	
UQCRC1	3_48638801_C/T	rs62618742	0.987	0.013	0.998	0.002	0.983	0.017	1.000	0.000	0.972	0.028	0.16127	
UQCRC1	3_48638548_G/A	rs201911056	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.001	0.999	1.00000	
UQCRC1	3_48638472_T/C	rs144710790	0.001	0.999	0.000	1.000	0.000	1.000	0.000	1.000	0.004	0.996	1.00000	
UQCRC1	3_48638451_T/C	rs187641562	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UQCRC1	3_48638440_C/T	rs145869559	0.999	0.001	1.000	0.000	0.997	0.003	1.000	0.000	0.999	0.001	1.00000	
UQCRC1	3_48637996_G/A	rs200354059	0.001	0.999	0.004	0.996	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	
UQCRC1	3_48637143_C/T	rs139999010	0.999	0.001	1.000	0.000	1.000	0.000	1.000	0.000	0.996	0.004	1.00000	
UQCRC1	3_48637071_A/T	rs202030377	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UQCRC2	16_21968584_A/G	rs188964091	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UQCRC2	16_21974117_C/G	rs139500759	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
UQCRC2	16_21974134_C/A	rs2228473	0.017	0.983	0.069	0.931	0.011	0.989	0.000	1.000	0.000	1.000	0.03959	AFR-0.31932; AMR-1.00000; ASN, EUR-Monomorphic
UQCRC2	16_21974204_C/T	rs202168192	1.000	0.000	0.998	0.002	1.000	0.000	1.000	0.000	1.000	0.000	1.00000	
UQCRC2	16_21976762_G/A	rs4850	0.021	0.979	0.010	0.990	0.017	0.983	0.000	1.000	0.046	0.954	0.38436	
UQCRC2	16_21982936_G/A	rs11863893	0.056	0.944	0.234	0.766	0.019	0.981	0.000	1.000	0.000	1.000	0.00000	AFR-1.00000; AMR-1.00000; ASN, EUR-Monomorphic
UQCRC2	16_21983430_A/C	rs146974535	0.998	0.002	1.000	0.000	0.997	0.003	1.000	0.000	0.995	0.005	1.00000	
UQCRC2	16_21991888_A/G	rs139312246	0.999	0.001	1.000	0.000	1.000	0.000	0.995	0.005	1.000	0.000	1.00000	
UQCRC2	16_21991927_A/T	rs190027776	1.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	0.999	0.001	1.00000	
UQCRC2	16_21991953_G/T	rs181040575	1.000	0.000	1.000	0.000	1.000	0.000	0.998	0.002	1.000	0.000	1.00000	
UQCRFS1	19_29704010_A/C	rs8100724	0.064	0.936	0.063	0.937	0.099	0.901	0.005	0.995	0.092	0.908	0.31140	
UQCRFS1	19_29699006_G/A	rs185606879	0.001	0.999	0.000	1.000	0.006	0.994	0.000	1.000	0.000	1.000	1.00000	
UQCRFS1	19_29698816_T/G	rs201719321	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	

UQCRH	1_46774783_A/G	rs41292543	0.951	0.049	0.992	0.008	0.923	0.077	1.000	0.000	0.900	0.100	0.00342	AFR-1.00000; AMR-0.28155; ASN-Monomorphic; EUR-0.24299
UQCRH	1_46775905_G/A	rs189114560	0.000	1.000	0.000	1.000	0.003	0.997	0.000	1.000	0.000	1.000	1.00000	
UQCRH	1_46775975_C/A	rs181971906	0.000	1.000	0.000	1.000	0.000	1.000	0.002	0.998	0.000	1.000	1.00000	
UQCRQ	5_132202583_G/A	rs137995316	0.000	1.000	0.002	0.998	0.000	1.000	0.000	1.000	0.000	1.000	1.00000	

Table S4- GeneBank accession numbers of mtDNA sequences used.

AF346963	AY339422	DQ137403	EF153813	EU095236	EU849091	FJ383594	FJ951574	GU733823	HM771160	HQ681883	JN857049	JQ324761	JQ702300	JQ703003	JQ703703	JQ704403	JQ705103	JQ705803
AF346964	AY339423	DQ137404	EF153814	EU095238	EU855118	FJ383595	FJ951575	GU733824	HM771161	HQ681884	JN857050	JQ324762	JQ702301	JQ703004	JQ703704	JQ704404	JQ705104	JQ705804
AF346965	AY339424	DQ137405	EF153815	EU095239	EU862197	FJ383596	FJ951576	GU733825	HM771162	HQ686079	JN857051	JQ324763	JQ702302	JQ703005	JQ703705	JQ704405	JQ705105	JQ705805
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AF346968	AY339427	DQ137408	EF153818	EU095242	EU882063	FJ383599	FJ951579	GU797137	HM771165	HQ696459	JN857054	JQ324766	JQ702305	JQ703008	JQ703708	JQ704408	JQ705108	JQ705808
AF346969	AY339428	DQ137409	EF153819	EU095243	EU884127	FJ383600	FJ951580	GU797476	HM771166	HQ696491	JN857055	JQ324767	JQ702306	JQ703009	JQ703709	JQ704409	JQ705109	JQ705809
AF346970	AY339429	DQ137410	EF153820	EU095244	EU910091	FJ383601	FJ951581	GU797785	HM771167	HQ698266	JN857056	JQ324768	JQ702307	JQ703010	JQ703710	JQ704410	JQ705110	JQ705810
AF346971	AY339430	DQ137411	EF153821	EU095245	EU914954	FJ383602	FJ951582	GU797829	HM771168	HQ698894	JN857057	JQ324769	JQ702308	JQ703011	JQ703711	JQ704411	JQ705111	JQ705811
AF346972	AY339431	DQ149511	EF153822	EU095246	EU919746	FJ383603	FJ951583	GU799583	HM771169	HQ699438	JN857058	JQ324770	JQ702309	JQ703012	JQ703712	JQ704412	JQ705112	JQ705812
AF346973	AY339432	DQ149512	EF153823	EU095247	EU926147	FJ383604	FJ951584	GU808335	HM771170	HQ699439	JN857059	JQ324771	JQ702310	JQ703013	JQ703713	JQ704413	JQ705113	JQ705813
AF346974	AY339433	DQ149513	EF153824	EU095248	EU926618	FJ383605	FJ951585	GU810005	HM771171	HQ700378	JN857060	JQ324772	JQ702311	JQ703014	JQ703714	JQ704414	JQ705114	JQ705814
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AF346986	AY339445	DQ200803	EF177427	EU095534	EU935441	FJ383618	FJ951597	GU810017	HM771183	HQ729918	JN899290	JQ324784	JQ702323	JQ703026	JQ703726	JQ704426	JQ705126	JQ705826
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AF346993	AY339452	DQ272111	EF177434	EU095541	EU935448	FJ383625	FJ951604	GU810024	HM771190	HQ840516	JN969087	JQ324791	JQ702330	JQ703033	JQ703733	JQ704433	JQ705133	JQ705833
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AF346997	AY339456	DQ272115	EF177438	EU095545	EU935452	FJ383629	FJ951608	GU810028	HM771194	HQ843088	JN990448	JQ324795	JQ702334	JQ703037	JQ703737	JQ704437	JQ705137	JQ705837
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AF347001	AY339460	DQ272119	EF177442	EU095549	EU935456	FJ383633	FJ951612	GU810032	HM771198	HQ844516	JQ025225	JQ324799	JQ702338	JQ703041	JQ703741	JQ704441	JQ705141	JQ705841
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AF347007	AY339466	DQ272125	EF185793	EU130562	EU935462	FJ383639	FJ951618	GU810038	HM771204	HQ873489	JQ044794	JQ324805	JQ702344	JQ703047	JQ703747	JQ704447	JQ705147	JQ705847
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AF347009	AY339468	DQ282387	EF185795	EU130575	EU935464	FJ383641	FJ966912	GU810040	HM771206	HQ873491	JQ044796	JQ324807	JQ702346	JQ703049	JQ703749	JQ704449	JQ705149	JQ705849
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AF347011	AY339470	DQ282389	EF185797	EU130942	EU935466	FJ383643	FJ968773	GU810042	HM771208	HQ873493	JQ044798	JQ324809	JQ702348	JQ703051	JQ703751	JQ704451	JQ705151	JQ705851
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AY339416	AY972053	EF153807	EU095230	EU787451	FJ383588	FJ951568	GU733815	HM771154	HQ676806	JN857043	JQ324755	JQ702294	JQ702997	JQ703697	JQ704397	JQ705097	JQ705797	
AY339417	DQ137398	EF153808	EU095231	EU795361	FJ383589	FJ951569	GU733816	HM771155	HQ676807	JN857044	JQ324756	JQ702295	JQ702998	JQ703698	JQ704398	JQ705098	JQ705798	
AY339418	DQ137399	EF153809	EU095232	EU825946	FJ383590	FJ951570	GU733817	HM771156	HQ677568	JN857045	JQ324757	JQ702296	JQ702999	JQ703699	JQ704399	JQ705099	JQ705799	
AY339419	DQ137400	EF153810	EU095233	EU828638	FJ383591	FJ951571	GU733818	HM771157	HQ677712	JN857046	JQ324758	JQ702297	JQ703000	JQ703700	JQ704400	JQ705100	JQ705800	
AY339420	DQ137401	EF153811	EU095234	EU828774	FJ383592	FJ951572	GU733819	HM771158	HQ677908	JN857047	JQ324759	JQ702298	JQ703001	JQ703701	JQ704401	JQ705101	JQ705801	
AY339421	DQ137402	EF153812	EU095235	EU849002	FJ383593	FJ951573	GU733820	HM771159	HQ678685	JN857048	JQ324760	JQ702299	JQ703002	JQ703702	JQ704402	JQ705102	JQ705802	

Table S5- ProtParam data (from ExPASy) in the mtDNA and nDNA coded genes.

	Grand average of hydropathicity (GRAVY)	Mean MutPred	Number aa	Molecular weight	Theoretical PI	Number of negatively charged residues (Asp + Glu)	Number of positively charged residues (Arg + Lys)	Extinction coefficient (M^{-1} cm^{-1}, at 280 nm measured in water)	Abs 0.1% (=1 g/l)	Instability index	Aliphatic index
ATP6	0.952	0.6295	226	24817.2	10.09	4	10	20970	0.845	34.74 (stable)	144.65
ATP8	-0.36	0.5311	68	7991.6	9.92	1	7	19480	2.438	51.4 (unstable)	78.82
COX1	0.682	0.6631	513	57041.3	6.19	25	18	120780	2.117	28.97 (stable)	104.17
COX2	0.46	0.637	227	25565	4.67	22	10	35535	1.39	37.11 (stable)	117.27
COX3	0.377	0.6803	261	29950.7	6.78	10	8	82390	2.751	22.96 (stable)	91.92
CYTB	0.631	0.647	380	42717.5	7.83	15	16	91455	2.141	41.02 (unsatble)	118.89
ND1	0.682	0.6764	318	35660.5	6.11	15	14	70360	1.973	41.94 (unstable)	123.08
ND2	0.636	0.6175	347	38960.9	9.84	6	16	75400	1.935	34.35 (stable)	119.22
ND3	0.992	0.5951	115	13186	4.33	8	4	26470	2.007	50.62 (unstable)	140
ND4	0.727	0.6426	459	51580.9	9.4	12	20	90995	1.764	35.98 (stable)	128.58
ND4L	1.288	0.6173	98	10741.1	5.73	3	1	6085	0.567	46 (unstable)	146.33
ND5	0.589	0.6295	603	67026.5	9.14	20	20	90215	1.346	33.95 (stable)	116.7
ND6	1.071	0.5986	174	18622.1	4.18	13	5	43890	2.357	29.48 (stable)	125.75
AK2	-0.281	0.597	239	26477.7	7.67	33	34	7700	0.291	37.38 (stable)	88.62
AK3	-0.542	0.5729	157	18191.8	8.73	19	21	28420	1.562	39.01 (stable)	88.15
AK4	-0.376	0.6189	223	25268	8.47	26	28	27055	1.071	41.42 (unstable)	92.65
ATP5A1	-0.067	0.5985	553	59750.6	9.16	60	68	23965	0.401	30.82 (stable)	99.49
ATP5B	0.018	0.5826	529	56559.9	5.26	64	49	19370	0.342	37.51 (stable)	98.85
ATP5C1	-0.18	0.64	298	32996	9.23	34	41	27390	0.83	32.38 (stable)	93.72
ATP5D	0.233	0.537	168	17489.9	5.34	17	13	2980	0.17	37.59 (stable)	102.98
ATP5E	-0.412	0.5755	51	5779.7	9.93	4	11	9970	1.725	6.32 (stable)	80.39
ATP5EP2	-0.373	0.57	51	5806.8	10.15	3	12	9970	1.717	2.99 (stable)	84.12
ATP5F1	-0.159	0.5608	256	28908.6	9.37	23	31	24870	0.86	36.65 (stable)	96.76
ATP5G1	0.641	0.5171	136	14276.7	9.81	4	10	4595	0.322	44.74 (unstable)	101.25
ATP5G2	0.717	0.4534	157	16334.2	9.22	7	11	3105	0.19	54.96 (unstable)	110.06
ATP5G3	0.573	0.512	142	14693	9.57	6	11	4595	0.313	32.82 (stable)	97.75
ATP5H	-0.554	0.6356	161	18491.2	5.21	27	23	36440	1.971	34.21 (stable)	81.3

ATP5I	-0.571	0.5199	69	7933.2	9.34	11	14	5960	0.751	52.32 (unstable)	96.23
ATP5J	-0.478	0.6017	108	12587.5	9.52	14	18	2980	0.237	50.47 (unstable)	77.59
ATP5J2	-0.169	0.4608	94	10917.8	9.7	6	15	19035	1.743	37.56 (stable)	83.94
ATP5L	0.243	0.6361	103	11428.4	9.65	7	12	18450	1.614	29.07 (stable)	107.86
ATP5L2	0.211	0.6132	100	11036.9	9.91	6	12	16960	1.537	29.46 (stable)	105.3
ATP5O	-0.02	0.6031	213	23277.3	9.97	17	31	7575	0.325	34.34 (stable)	101.55
ATP5S	-0.383	0.4402	127	14666.8	6.79	15	15	35450	2.417	45.43 (unstable)	66.06
COX10	0.128	0.564	443	48910.1	9.36	29	44	73630	1.505	53 (unstable)	95.35
COX11	-0.421	0.528	276	31429.9	9.22	27	35	60765	1.933	59.63 (unstable)	69.64
COX15	0.168	0.5974	410	46030.2	9.85	26	44	81735	1.776	44.72 (unstable)	103.24
COX16	-0.767	0.3445	106	12293.2	9.49	16	21	15470	1.258	39.77 (stable)	73.58
COX17	-0.589	0.5503	63	6915.1	6.8	10	10	375	0.054	77.97 (unstable)	63.65
COX18	0.308	0.5701	333	37062.6	9.86	18	32	79660	2.149	53.22 (unstable)	110.45
COX4I1	-0.459	0.5971	169	19576.7	9.52	20	28	40450	2.066	26.91 (stable)	72.66
COX4I2	-0.674	0.5531	171	20010	9.65	17	27	49055	2.452	56.36 (unstable)	58.77
COX5A	-0.295	0.5891	150	16762.1	6.3	21	20	18575	1.108	46.17 (unstable)	91.73
COX5B	-0.298	0.546	129	13695.6	9.07	12	16	14230	1.039	43.06 (unstable)	78.06
COX6A1	-0.384	0.5852	109	12154.8	9.3	9	11	15470	1.273	38.23 (stable)	72.39
COX6A2	-0.442	0.6018	97	10815.4	10.91	3	11	16960	1.568	30.39 (stable)	73.51
COX6B1	-0.923	0.5502	103	12035.4	6.81	12	12	28210	2.344	33.61 (stable)	40.78
COX6B2	-0.9	0.5551	88	10528.9	9.21	8	13	24200	2.298	35.59 (stable)	52.05
COX6C	-0.271	0.6421	75	8781.4	10.38	7	16	5960	0.679	41.77 (unstable)	82
COX7A1	-0.23	0.5342	79	9117.5	10.12	5	11	11460	1.257	34.25 (stable)	92.53
COX7A2	-0.025	0.4677	115	12843.9	9.23	10	14	17085	1.33	63.34 (unstable)	92.43
COX7A2L	-0.157	0.4638	114	12614.6	9.43	7	13	18910	1.499	48.93 (unstable)	75.35
COX7B	-0.401	0.6284	80	9160.5	10.28	4	10	19480	2.127	31.65 (stable)	75.5
COX7B2	-0.119	0.6308	81	9077.4	9.74	4	8	17990	1.982	37 (stable)	79.51
COX7C	-0.078	0.6004	63	7245.5	10.29	3	9	8480	1.17	74.45 (unstable)	83.49
COX8A	0.349	0.5335	69	7579.1	10.26	4	8	6990	0.922	62.48 (unstable)	118.7
COX8C	-0.094	0.4135	72	8128.6	12.08	1	12	2980	0.367	76.93 (unstable)	88.19
CYC1	-0.138	0.5775	325	35421.9	9.15	29	37	37735	1.065	37.61 (stable)	81.14
DGUOK	-0.287	0.5818	277	32055.8	8.76	30	33	52035	1.623	59.11 (unstable)	88.05
MFF	-0.559	0.5581	342	38464.5	9.01	42	45	30940	0.804	63.61 (unstable)	82.43
MFN1	-0.267	0.5485	741	84100.4	5.87	102	88	62755	0.746	41.93 (unstable)	92.23
MFN2	-0.325	0.5589	757	86402	6.52	97	92	72600	0.84	47.67 (unstable)	86.13
MTERF	-0.225	0.6075	379	43641.6	9.46	41	56	36940	0.846	55.87 (unstable)	96.99

MTFR1	-0.577	0.4996	317	35324.6	9.4	37	46	21095	0.597	58.95 (unstable)	82.49
NDUFAF2	-1.163	0.4328	169	19856.3	8.94	26	29	43430	2.187	51.29 (unstable)	54.26
NDUFAF3	-0.184	0.5282	184	20350.2	8.48	16	18	22710	1.116	49.02 (unstable)	90.16
NDUFAF4	-0.533	0.6239	175	20266.4	8.85	26	29	11460	0.565	32.63 (stable)	90.23
NDUFB1	0.064	0.5054	105	11912	9.02	10	13	23615	1.982	40.2 (unstable)	97.43
NDUFB10	-1.031	0.3937	172	20776.6	8.72	26	30	30620	1.474	59.38 (unstable)	59.59
NDUFB11	-0.418	0.3673	153	17316.6	5.13	23	19	29450	1.701	52.47 (unstable)	76.54
NDUFB2	-0.47	0.4231	105	12058.4	5.44	14	10	30480	2.528	68.89 (unstable)	60.38
NDUFB3	-0.718	0.5225	98	11401.9	9.1	12	15	27960	2.452	19.73 (stable)	55.82
NDUFB4	-0.63	0.6186	129	15208.6	9.85	13	22	18910	1.243	55.66 (unstable)	84.81
NDUFB5	-0.183	0.4184	189	21750.2	9.62	21	28	31400	1.444	56.04 (unstable)	92.91
NDUFB6	-0.697	0.4086	128	15489.1	9.63	15	22	30940	1.998	66.98 (unstable)	74.45
NDUFB7	-0.996	0.5606	137	16401.9	9.1	23	28	13200	0.805	50.96 (unstable)	62.7
NDUFB8	-0.508	0.6126	172	20038.9	7.05	17	17	55015	2.745	42.71 (unstable)	56.69
NDUFB9	-1.077	0.4564	179	21830.9	8.57	28	31	62130	2.846	61.65 (unstable)	54.02
NDUFC1	-0.266	0.3045	76	8734.2	10.2	6	12	15470	1.771	71.92 (unstable)	98.82
NDUFC2	-0.396	0.6651	119	14187.5	9.04	16	19	13410	0.945	57.58 (unstable)	86.13
NDUFS1	-0.108	0.6227	727	79467.5	5.89	88	81	63465	0.799	42.85 (unstable)	92.02
NDUFS2	-0.266	0.6393	463	52545.6	7.21	55	55	72685	1.383	39.74 (stable)	85.08
NDUFS3	-0.292	0.5365	264	30241.5	6.98	35	35	41035	1.357	37.57 (stable)	87.5
NDUFS4	-0.643	0.518	175	20107.9	10.3	18	30	41480	2.063	50.27 (unstable)	69.6
NDUFS5	-0.914	0.4207	106	12517.5	9.27	15	21	17210	1.375	75.14 (unstable)	62.64
NDUFS6	-0.394	0.4665	124	13711.6	8.58	14	17	6335	0.462	30.91 (stable)	72.34
NDUFS7	-0.133	0.5406	206	22202.7	9.91	14	25	24660	1.111	62.3 (unstable)	75.29
NDUFS8	-0.392	0.4836	210	23705	6	28	26	26400	1.114	43.09 (unstable)	72.19
NDUFV1	-0.271	0.6351	464	50817	8.51	54	59	70650	1.39	39.73 (stable)	79.27
NDUFV2	-0.267	0.5569	249	27391.5	8.22	26	28	23170	0.846	44.28 (unstable)	81.89
NDUFV3	-0.912	0.2278	473	50984	9.18	61	69	5960	0.117	60.23 (unstable)	59.43
NT5M	-0.126	0.5758	239	25903.6	8.1	26	28	35450	1.369	49.01 (unstable)	73.14
OPA1	-0.599	0.4273	997	115884.4	7.87	150	152	136875	1.181	45.82 (unstable)	86.24
OPA3	-0.201	0.562	179	19996.2	9.07	19	23	22585	1.129	46.42 (unstable)	93.35
PEO1	-0.398	0.4947	684	77154.2	9.13	79	91	87360	1.132	47.58 (unstable)	83.55
PINK1	-0.018	0.4922	581	62769	9.43	46	66	69870	1.113	48.3 (unstable)	95.46
POLG	-0.49	0.5033	1239	139562	6.46	148	140	253920	1.819	51.96 (unstable)	77.81
POLG2	-0.352	0.5203	485	54911	8.64	55	61	72015	1.311	41.49 (unstable)	88.99
POLRMT	-0.332	0.4951	1230	138620.3	9.19	125	157	145115	1.047	50.18 (unstable)	87.68

SDHA	-0.27	0.6445	664	72691.5	7.06	74	73	71375	0.982	37.04 (stable)	79.34
SDHB	-0.408	0.5404	280	31629.7	9.03	30	42	43735	1.383	60.13 (unstable)	76.39
SDHC	0.447	0.5998	169	18610.2	9.74	6	14	28210	1.516	47.79 (unstable)	110.83
SDHD	0.495	0.6485	159	17043	8.92	7	11	35200	2.065	33.2 (stable)	114.21
SSBP1	-0.561	0.5452	148	17259.6	9.59	18	23	19940	1.155	47.44 (unstable)	87.43
TFAM	-0.909	0.4865	246	29096.6	9.74	33	52	48150	1.655	61.03 (unstable)	67.44
TK2	-0.477	0.5609	265	31004.7	8.71	34	38	56295	1.816	49.74 (unstable)	84.19
UCP1	0.206	0.6172	307	33004.5	9.26	20	30	23420	0.71	37.97 (stable)	95.57
UCP2	0.067	0.6265	309	33229.3	9.74	19	34	27765	0.836	41.95 (unstable)	82.46
UCP3	0.075	0.6209	312	34215.8	9.31	22	33	29380	0.859	39.31 (stable)	84.97
UQCRB	-1.05	0.6139	111	13530.4	8.73	21	23	32430	2.397	35.97 (stable)	74.77
UQCRC1	-0.141	0.6082	480	52645.8	5.94	54	46	57590	1.094	45.67 (unstable)	87.04
UQCRC2	-0.071	0.5954	453	48443	8.74	37	41	26485	0.547	36.05 (stable)	87.73
UQCRFS1	-0.078	0.5911	274	29667.9	8.55	28	31	23170	0.781	47.23 (unstable)	90
UQCRH	-1.056	0.4756	91	10738.7	4.39	29	11	250	0.023	80.06 (unstable)	66.37
UQCRQ	-0.556	0.6056	82	9906.3	10.07	8	14	12950	1.307	49.38 (unstable)	66.46
UQCR10	-0.092	0.5787	63	7308.4	9.45	6	9	9970	1.364	41.82 (unstable)	88.41
UQCR11	-0.071	0.604	56	6569.6	9.87	4	8	31970	4.866	-14.17 (stable)	92.14

Table S6- List of individuals from 1000 Genomes dataset bearing non-synonymous mutations in the 104 nDNA genes, when using a conservative classification (putative pathogenic according to the major voting system of the three pathogenicity scores, in HW equilibrium, and a global frequency higher than 0.5%).

Individual	Population	Subpopulation	Hits	Genes	rs	MutPreds
NA12889	EUR	CEU	2	POLG-NDUFS2	rs113994095-rs145577083	0.751-0.57
NA20503	EUR	TSI	2	SDHA-MFN1	rs201826964-rs143476739	0.891-0.485
NA20828	EUR	TSI	2	NDUFV2-POLG	rs201708711-rs147827654	0.835-0.538
HG00097	EUR	GBR	1	NDUFS4	rs184765529	0.777
HG00101	EUR	GBR	1	UCP1	rs150067245	0.912
HG00114	EUR	GBR	1	UCP3	rs201405748	0.737
HG00117	EUR	GBR	1	UCP1	rs150067245	0.912
HG00119	EUR	GBR	1	UCP3	rs138705669	0.723
HG00124	EUR	GBR	1	UCP3	rs138705669	0.723
HG00126	EUR	GBR	1	UQCRC1	rs145869559	0.917

HG00129	EUR	GBR	1	POLG	rs121918054	0.807
HG00141	EUR	GBR	1	NDUFV3	rs141922962	0.208
HG00146	EUR	GBR	1	NDUFV3	rs141922962	0.208
HG00156	EUR	GBR	1	COX5A	rs150174803	0.831
HG00173	EUR	FIN	1	POLG	rs61752784	0.938
HG00176	EUR	FIN	1	COX18	rs181365781	0.744
HG00177	EUR	FIN	1	POLG	rs145289229	0.555
HG00182	EUR	FIN	1	COX18	rs138323566	0.706
HG00187	EUR	FIN	1	UCP1	rs150067245	0.912
HG00188	EUR	FIN	1	OPA3	rs186796646	0.889
HG00249	EUR	GBR	1	MFN2	rs119103267	0.836
HG00250	EUR	GBR	1	DGUOK	rs144181978	0.809
HG00252	EUR	GBR	1	POLG	rs142347031	0.975
HG00258	EUR	GBR	1	NDUFB7	rs200292442	0.614
HG00259	EUR	GBR	1	POLG2	rs200118292	0.597
HG00264	EUR	GBR	1	POLG	rs142347031	0.975
HG00265	EUR	GBR	1	COX10	rs199881731	0.350
HG00271	EUR	FIN	1	POLG	rs61752784	0.938
HG00275	EUR	FIN	1	UCP2	rs148253207	0.751
HG00326	EUR	FIN	1	UCP2	rs148253207	0.751
HG00331	EUR	FIN	1	POLG	rs145289229	0.555
HG00349	EUR	FIN	1	ATP5B	rs200610844	0.709
HG00375	EUR	FIN	1	POLG	rs61752784	0.938
HG00378	EUR	FIN	1	UCP2	rs148253207	0.751
HG00384	EUR	FIN	1	UCP2	rs148253207	0.751
HG01334	EUR	GBR	1	POLRMT	rs200607630	0.885
HG01617	EUR	IBS	1	NDUFV1	rs201382784	0.968
HG01620	EUR	IBS	1	DGUOK	rs184770596	0.848
NA11994	EUR	CEU	1	UCP2	rs45490393	0.87
NA12044	EUR	CEU	1	CYC1	rs199884423	0.852
NA12347	EUR	CEU	1	AK4	rs185251178	0.722
NA12718	EUR	CEU	1	NDUFS1	rs151279101	0.873
NA12751	EUR	CEU	1	MTFR1	rs201556776	0.648
NA12842	EUR	CEU	1	NDUFV3	rs141922962	0.208
NA12873	EUR	CEU	1	COX4I2	rs201685557	0.490
NA12874	EUR	CEU	1	NDUFV3	rs141922962	0.208

NA20506	EUR	TSI	1	COX10	rs200472593	0.683
NA20508	EUR	TSI	1	POLG2	rs200118378	0.866
NA20519	EUR	TSI	1	ATP5B	rs200966693	0.668
NA20530	EUR	TSI	1	POLG	rs61752784	0.938
NA20531	EUR	TSI	1	NDUFV3	rs141922962	0.208
NA20539	EUR	TSI	1	COX16	rs139410596	0.543
NA20581	EUR	TSI	1	NDUFB4	rs142688627	0.773
NA20752	EUR	TSI	1	PINK1	rs200949139	0.835
NA20754	EUR	TSI	1	POLRMT	rs201811276	0.814
NA20758	EUR	TSI	1	POLG	rs61752784	0.938
NA20759	EUR	TSI	1	COX6A1	rs140243339	0.724
NA20775	EUR	TSI	1	NDUFV1	rs201382784	0.968
NA20799	EUR	TSI	1	MFN1	rs143476739	0.485
NA20811	EUR	TSI	1	UQCRB	rs139283183	0.645
NA20814	EUR	TSI	1	MFF	rs200132653	0.738
HG00701	ASN	CHS	3	NDUFS7-ATP5L-MTERF	rs201420030-rs200472961-rs201335490	0.717-0.873-0.622
HG00443	ASN	CHS	2	SDHA-NT5M	rs200103530-rs201242235	0.766-0.94
HG00448	ASN	CHS	2	POLG-NDUFS8	rs201477273-rs201484242	0.846-0.595
HG00475	ASN	CHS	2	NDUFC2-COX15	rs183610034-rs199761049	0.799-0.942
HG00530	ASN	CHS	2	COX18-NDUFV1	rs141592190-rs180950242	0.741-0.645
HG00565	ASN	CHS	2	NDUFB8-UCP3	rs200405716-rs17848372	0.718-0.552
NA18557	ASN	CHB	2	NDUFB4-NDUFS1	rs150031407-rs202214721	0.575-0.634
NA18617	ASN	CHB	2	COX18-UQCRC2	rs141592190-rs181040575	0.741-0.809
NA18626	ASN	CHB	2	POLG-UCP3	rs201477273-rs17848372	0.846-0.552
NA18636	ASN	CHB	2	NDUFAF4-NDUFC1	rs200279216-rs201035643	0.783-0.674
NA18964	ASN	JPT	2	ATP5G2-UQCRC2	rs201675029-rs139312246	0.761-0.569
HG00421	ASN	CHS	1	MFN1	rs186960036	0.875
HG00422	ASN	CHS	1	POLG	rs2307440	0.792
HG00436	ASN	CHS	1	NDUFB7	rs201675767	0.742
HG00445	ASN	CHS	1	UQCRC2	rs139500759	0.846
HG00449	ASN	CHS	1	COX15	rs2231682	0.894
HG00542	ASN	CHS	1	NDUFC2	rs183610034	0.799
HG00557	ASN	CHS	1	COX18	rs141592190	0.741
HG00559	ASN	CHS	1	NT5M	rs199941205	0.724
HG00581	ASN	CHS	1	OPA1	rs190223702	0.657
HG00583	ASN	CHS	1	COX18	rs141592190	0.741

HG00589	ASN	CHS	1	NDUFS7	rs201420030	0.717
HG00590	ASN	CHS	1	SDHA	rs200526913	0.736
HG00593	ASN	CHS	1	NT5M	rs199941205	0.724
HG00595	ASN	CHS	1	NDUFB5	rs4147793	0.317
HG00653	ASN	CHS	1	OPA1	rs190223702	0.657
HG00662	ASN	CHS	1	NDUFB4	rs150031407	0.575
HG00672	ASN	CHS	1	POLG	rs181860632	0.86
HG00684	ASN	CHS	1	NDUFB4	rs150031407	0.575
HG00692	ASN	CHS	1	UQCRH	rs181971906	0.826
HG00704	ASN	CHS	1	POLG2	rs191057592	0.805
HG00707	ASN	CHS	1	NDUFC2	rs183610034	0.799
HG01113	ASN	CLM	1	NDUFS5	rs200515387	0.282
NA18527	ASN	CHB	1	ATP5S	rs192482233	0.611
NA18530	ASN	CHB	1	UCP3	rs192655642	0.732
NA18536	ASN	CHB	1	NDUFS4	rs200758718	0.605
NA18542	ASN	CHB	1	NDUFS4	rs199541993	0.735
NA18544	ASN	CHB	1	MFF	rs200608831	0.517
NA18546	ASN	CHB	1	POLG	rs201477273	0.846
NA18550	ASN	CHB	1	NDUFB7	rs201675767	0.742
NA18555	ASN	CHB	1	SDHA	rs60587941	0.547
NA18564	ASN	CHB	1	NDUFB4	rs150031407	0.575
NA18567	ASN	CHB	1	ATP5C1	rs137988284	0.908
NA18572	ASN	CHB	1	NDUFB10	rs200975991	0.785
NA18573	ASN	CHB	1	SDHB	rs138996609	0.924
NA18592	ASN	CHB	1	ATP5D	rs200593395	0.664
NA18597	ASN	CHB	1	PINK1	rs200036561	0.361
NA18603	ASN	CHB	1	NDUFS3	rs78121716	0.576
NA18605	ASN	CHB	1	NDUFB4	rs201413691	0.815
NA18608	ASN	CHB	1	POLG	rs201477273	0.846
NA18613	ASN	CHB	1	ATP5J	rs182225698	0.897
NA18615	ASN	CHB	1	UCP2	rs200489709	0.783
NA18620	ASN	CHB	1	PINK1	rs146691996	0.541
NA18627	ASN	CHB	1	NDUFB7	rs200757972	0.7
NA18633	ASN	CHB	1	PINK1	rs200728364	0.532
NA18639	ASN	CHB	1	NDUFC2	rs183610034	0.799
NA18640	ASN	CHB	1	MFN2	rs190705310	0.783

NA18647	ASN	CHB	1	PINK1	rs200728364	0.532
NA18942	ASN	JPT	1	COX5A	rs200875315	0.709
NA18943	ASN	JPT	1	ATP5F1	rs146878380	0.909
NA18945	ASN	JPT	1	COX15	rs2231682	0.894
NA18956	ASN	JPT	1	MFN2	rs78658090	0.835
NA18959	ASN	JPT	1	ATP5C1	rs199960374	0.77
NA18961	ASN	JPT	1	UCP2	rs45596837	0.316
NA18968	ASN	JPT	1	SDHD	rs202239399	0.739
NA18974	ASN	JPT	1	NDUFB5	rs4147793	0.317
NA18984	ASN	JPT	1	COX6B2	rs149294692	0.903
NA18985	ASN	JPT	1	NDUFS2	rs140731056	0.817
NA18988	ASN	JPT	1	UCP3	rs147631608	0.589
NA18998	ASN	JPT	1	ATP5S	rs185659761	0.556
NA19003	ASN	JPT	1	PINK1	rs202130946	0.611
NA19005	ASN	JPT	1	CYC1	rs74494160	0.611
NA19009	ASN	JPT	1	COX15	rs201703572	0.904
NA19012	ASN	JPT	1	PINK1	rs138018628	0.540
NA19056	ASN	JPT	1	COX16	rs188182259	0.996
NA19062	ASN	JPT	1	UQCRC2	rs139312246	0.569
NA19063	ASN	JPT	1	UQCRC2	rs139312246	0.569
NA19066	ASN	JPT	1	NDUFB5	rs4147793	0.317
NA19075	ASN	JPT	1	UCP2	rs201373362	0.829
NA19079	ASN	JPT	1	PINK1	rs181675228	0.596
NA19081	ASN	JPT	1	NDUFV2	rs202166758	0.687
NA19373	AFR	LWK	3	UCP3-UCP1-PINK1	rs183714776-rs200389729-rs112600292	0.713-0.765-0.361
NA18507	AFR	YRI	2	POLG-POLG	rs74034411-rs60636456	0.873-0.902
NA18909	AFR	YRI	2	PINK1-NDUFC1	rs76753586-rs72939460	0.596-0.274
NA19346	AFR	LWK	2	UCP3-UQCRC1	rs142927779-rs200354059	0.59-0.625
NA19380	AFR	LWK	2	UQCRC1-NDUFV2	rs191821836-rs199560855	0.768-0.865
NA18487	AFR	YRI	1	NDUFV1	rs142982022	0.899
NA18511	AFR	YRI	1	COX5A	rs200811470	0.684
NA18516	AFR	YRI	1	NDUFC1	rs72939460	0.274
NA18519	AFR	YRI	1	NDUFB7	rs200041574	0.866
NA18520	AFR	YRI	1	ATP5O	rs141125740	0.831
NA18858	AFR	YRI	1	NDUFB9	rs140417066	0.581
NA18871	AFR	YRI	1	SDHA	rs192818312	0.738

NA18908	AFR	YRI	1	NDUFC1	rs72939460	0.274
NA18933	AFR	YRI	1	COX10	rs200373790	0.703
NA19028	AFR	LWK	1	POLG	rs202037973	0.86
NA19036	AFR	LWK	1	NDUFV3	rs141922962	0.208
NA19108	AFR	YRI	1	NDUFS1	rs139690694	0.727
NA19114	AFR	YRI	1	NDUFV1	rs142982022	0.899
NA19118	AFR	YRI	1	NDUFS1	rs139690694	0.727
NA19130	AFR	YRI	1	NDUFV1	rs200829846	0.854
NA19147	AFR	YRI	1	NDUFB5	rs148532160	0.354
NA19149	AFR	YRI	1	POLRMT	rs147740567	0.714
NA19171	AFR	YRI	1	POLRMT	rs147740567	0.714
NA19185	AFR	YRI	1	ATP5S	rs185659761	0.556
NA19198	AFR	YRI	1	NDUFB4	rs149224531	0.716
NA19200	AFR	YRI	1	MFF	rs149692814	0.534
NA19204	AFR	YRI	1	POLG2	rs200880373	0.503
NA19222	AFR	YRI	1	MFF	rs149692814	0.534
NA19235	AFR	YRI	1	TK2	rs138479499	0.722
NA19248	AFR	YRI	1	POLRMT	rs147740567	0.714
NA19256	AFR	YRI	1	PINK1	rs144071530	0.528
NA19310	AFR	LWK	1	UCP2	rs45490393	0.87
NA19311	AFR	LWK	1	AK3	rs140003401	0.382
NA19312	AFR	LWK	1	UCP2	rs182694614	0.701
NA19315	AFR	LWK	1	POLRMT	rs147740567	0.714
NA19318	AFR	LWK	1	NDUFC1	rs72939460	0.274
NA19324	AFR	LWK	1	UCP2	rs182694614	0.701
NA19327	AFR	LWK	1	POLG	rs188348569	0.7
NA19328	AFR	LWK	1	PINK1	rs183454580	0.811
NA19332	AFR	LWK	1	COX4I2	rs119455950	0.902
NA19338	AFR	LWK	1	COX4I2	rs119455950	0.902
NA19347	AFR	LWK	1	UCP3	rs17848372	0.552
NA19352	AFR	LWK	1	UCP3	rs183714776	0.713
NA19372	AFR	LWK	1	NDUFV3	rs148054698	0.199
NA19374	AFR	LWK	1	UCP3	rs183714776	0.713
NA19376	AFR	LWK	1	UCP3	rs17848372	0.552
NA19377	AFR	LWK	1	UCP1	rs146114327	0.603
NA19382	AFR	LWK	1	NDUFV2	rs199560855	0.865

NA19436	AFR	LWK	1	UCP2	rs45490393	0.87
NA19444	AFR	LWK	1	UCP3	rs183714776	0.713
NA19446	AFR	LWK	1	MFF	rs143374639	0.847
NA19448	AFR	LWK	1	UQCRC1	rs200354059	0.625
NA19449	AFR	LWK	1	UCP2	rs45490393	0.870
NA19453	AFR	LWK	1	COX5A	rs199907556	0.91
NA19456	AFR	LWK	1	NDUFB5	rs148532160	0.354
NA19463	AFR	LWK	1	UCP2	rs45490393	0.87
NA19468	AFR	LWK	1	UCP3	rs142927779	0.59
NA19469	AFR	LWK	1	SDHA	rs192818312	0.738
NA19470	AFR	LWK	1	SDHA	rs192818312	0.738
NA19472	AFR	LWK	1	AK3	rs140003401	0.382

Table S7- Mutations in the 104 nDNA genes reported in OMIM dataset.

Gene	Mutation	Mutation abbreviated	Base substitution	MutPred	Presence in 1000 genomes	Geographical Origin in 1000 genomes (population code)	State	Patients	Disease
AK2	ARG103TRP	R103W	C307T	0.982	NO		Homozygous	1 patient from Portugal	Reticular dysgenesis
AK2	ARG186CYS	R186C	C556T	0.958	NO		Homozygous	1 patient from France	Reticular dysgenesis
AK2	MET1VAL	M1V	A1G	0.872	NO		Heterozygous	German male	Reticular dysgenesis
AK2	ASP165GLY	D165G	A546G	0.808	NO		Homozygous	2 separate consanguineous pedigrees from Cape Verde (Western Africa)	Reticular dysgenesis
ATP5A1	ARG329CYS	R329C	C985T	0.805	NO		Heterozygous	2 siblings born of unrelated Dutch parents	Mitochondrial complex v (atp synthase) deficiency, nuclear type 4 (1 family); death early in infancy
ATP5E	TYR12CYS	Y12C	A35G	0.787	NO		Homozygous	1 Austrian	Mitochondrial complex V (atp synthase) deficiency, nuclear type 3
COX10	PRO225LEU	P225L	C878T	0.948	YES	1 Asian heterozygous (CHB)	Heterozygous	1 white male	Mitochondrial complex IV deficiency
COX10	ASN204LYS	N204K	C612A	0.915	NO		Homozygous	1 born to first-cousin parents - large African consanguineous family	Mitochondrial complex IV deficiency; encephalopathy, progressive mitochondrial, with proximal renal tubulopathy due to mitochondrial complex IV deficiency
COX10	THR196LYS	T196K	C791A	0.912	NO		Heterozygous	1 white male	Mitochondrial complex IV deficiency

COX10	ASP336GLY	D336G	A1211G	0.876	NO		Heterozygous	1 child from health non-consanguineous German parents	Leigh syndrome
COX10	ASP336VAL	D336V	A1211T	0.863	NO		Heterozygous	1 child from health non-consanguineous German parents	Leigh syndrome
COX15	ARG217TRP	R217W	C700T	0.766	NO		Heterozygous and homozygous	1 child of white couple	Cardioencephalomyopathy, fatal infantile, due to cytochrome c oxidase deficiency 2; leigh syndrome due to mitochondrial complex iv deficiency
COX4I2	GLU138LYS	E138K	G412A	0.902	YES	2 African heterozygous (LWK)	Homozygous	5 Arab Muslim patients	Exocrine pancreatic insufficiency, dyserythropoietic anemia, and calvarial hyperostosis
COX6B1	ARG37HIS	R37H	G221A	0.944	NO		Homozygous	2 siblings born of consanguineous Saudi Arabian parents	Cytochrome c oxidase deficiency
DGUOK	GLU227LYS	E227K	G679A	0.955	NO		Heterozygous	1 (no population information)	Hepatocerebral type of mitochondrial dna depletion syndrome-3
DGUOK	ARG142LYS	R142K	G425A	0.931	NO		Heterozygous	1 (no population information)	Hepatocerebral type of mitochondrial dna depletion syndrome-3
DGUOK	ASP255TYR	D255Y	G255T	0.839	NO		Homozygous	3 from 2 unrelated Old Colony Mennonite families	Hepatocerebral type of mitochondrial dna depletion syndrome-3 associated with cystathioninuria
MFN2	ARG280HIS	R280H	G839A	0.909	NO		Homozygous; heterozygous	affected members of a family; a large multigenerational Korean family	Charcot-marie-tooth disease-2a2
MFN2	PHE216SER	F216S	T647C	0.885	NO		Heterozygous	2 British sibs	Charcot-marie-tooth disease, axonal, type 2a2, autosomal recessive
MFN2	HIS165ASP	H165D	C493G	0.882	NO		Homozygous	11 members from a family	Charcot-marie-tooth disease-2a2
MFN2	GLN276ARG	Q276R	A827G	0.881	NO		Heterozygous	1 patient	Hereditary motor and sensory neuropathy VI
MFN2	ARG364TRP	R364W	C1090T	0.865	NO		Heterozygous	1 father and 2 sons; 7 Korean families	Hereditary motor and sensory neuropathy VI; charcot-marie-tooth disease, axonal, type 2a2, included
MFN2	TRP740SER	W740S	G2219C	0.863	NO		Homozygous	affected members of a family	Charcot-marie-tooth disease-2a2
MFN2	LYS357ASN	K357N	G1071C	0.837	NO		Homozygous	Japanese patient	Charcot-marie-tooth disease-2a2
MFN2	ARG707TRP	R707W	C2119T	0.836	YES	1 European heterozygous (GBR)	Homozygous	1 patient	Charcot-marie-tooth disease, axonal, type 2a2
MFN2	ARG104TRP	R104W	C310T	0.810	NO		Heterozygous	Italian father and 2 sons	Hereditary motor and sensory neuropathy VI; charcot-marie-tooth disease, axonal, type 2a2, included
MFN2	ARG94TRP	R94W	C280T	0.807	NO		Homozygous; heterozygous	1 patient; African American mother and daughter; 2 Korean families	Charcot-marie-tooth disease-2a2; hereditary motor and sensory neuropathy with optic atrophy
MFN2	THR206ILE	T206I	C617T	0.806	NO		heterozygous	father and son	Hereditary motor and sensory neuropathy VI

MFN2	PRO251ALA	P251A	C751G	0.775	NO		Homozygous	affected members of an Italian family	Charcot-marie-tooth disease-2a2
MFN2	THR362MET	T362M	C1085T	0.760	NO		Heterozygous	Korean mother and daughter; 2 Italian sibs	Charcot-marie-tooth disease, axonal, type 2a2
MFN2	ARG94GLN	R94Q	G281A	0.736	NO		Homozygous	Japanese family; and Russian; one Spanish	Charcot-marie-tooth disease-2a2
MFN2	LEU76PRO	L76P	T227C	0.730	NO		Homozygous	affected members of a family	Charcot-marie-tooth disease-2a2
MFN2	ARG468HIS	R468H	G1403A	0.687	YES	1 European homozygous (GBR); 1 European heterozygous (CEU); 1 African heterozygous (ASW); 2 American heterozygous (CLM, PUR)	Heterozygous	6 unrelated Spanish families	Charcot-marie-tooth disease, axonal, type 2a2
MFN2	VAL69PHE	V69F	G205T	0.423	NO		Homozygous	affected members of a Turkish family	Charcot-marie-tooth disease-2a2
NDUFAF3	MET1THR	M1T	T2C	0.980	NO		Heterozygous	1 daughter of unrelated parents of Jewish origin	Mitochondrial complex I deficiency
NDUFAF3	GLY77ARG	G77R	G229C	0.912	NO		Homozygous	3 Muslim sibs	Mitochondrial complex I deficiency; dead by 3 month
NDUFAF3	ARG122PRO	R122P	G365C	0.803	NO		Homozygous	1 born of consanguineous Arab Muslim parents	Mitochondrial complex I deficiency; died at age 4 months
NDUFAF4	LEU65PRO	L65P	T194C	0.967	NO		Homozygous	5 members of a consanguineous family; 1 unrelated	Mitochondrial complex i deficiency
NDUFB3	TRP22ARG	W22R	T64C	0.729	YES	1 American heterozygous (CLM)	Homozygous	1 born of unrelated parents of British and Dutch descent	Mitochondrial complex I deficiency
NDUFS1	ASP619ASN	D619N	G1855A	0.937	NO		Heterozygous	1 patient	Mitochondrial complex I deficiency; died at age 12 years
NDUFS1	LEU231VAL	L231V	C691G	0.923	NO		Homozygous	1 Spanish child	Mitochondrial complex I deficiency
NDUFS1	ARG241TRP	R241W	C721T	0.885	NO		Homozygous	1 patient	Mitochondrial complex I deficiency; died at age 5 months
NDUFS1	ARG408CYS	R408C	C1222T	0.865	NO		Homozygous	1 born of consanguineous parents	Mitochondrial complex i deficiency; death at age 8 months
NDUFS1	ASP252GLY	D252G	A755G	0.838	NO		Heterozygous	1 patient	Mitochondrial complex I deficiency
NDUFS1	THR595ALA	T595A	A1783G	0.643	NO		Homozygous	2 sibs born of consanguineous parents	Mitochondrial complex I deficiency
NDUFS2	ARG228GLN	R228Q	G683A	0.943	NO		Homozygous	2 sibs of a consanguineous family	Mitochondrial complex I deficiency
NDUFS2	SER413PRO	S413P	T1237C	0.922	NO		Homozygous	3 sibs of a consanguineous family	Mitochondrial complex I deficiency
NDUFS2	PRO229GLN	P229Q	C686A	0.799	NO		Homozygous	1 patient	Mitochondrial complex I deficiency

NDUFS3	ARG199TRP	R199W	C595T	0.970	NO		Heterozygous; homozygous	1 boy from Reunion Island; 1	Leigh syndrome due to mitochondrial complex I deficiency
NDUFS3	THR145ILE	T145I	C434T	0.779	NO		Heterozygous	1 boy from Reunion Island	Leigh syndrome due to mitochondrial complex I deficiency
NDUFS6	CYS115TYR	C115Y	G344A	0.950	NO		Homozygous	2 unrelated infants, both of Jewish Caucasus descent	Mitochondrial complex i deficiency with fatal infantile lactic acidosis
NDUFS7	VAL122MET	V122M		0.813	NO			2 male sibs	Leigh syndrome due to mitochondrial complex I deficiency; died at 3.5 years and 5 years
NDUFS7	ARG145HIS	R145H	G434A	0.733	NO		Homozygous	1 patient born to consanguineous Tunisian parents	Leigh syndrome due to mitochondrial complex I deficiency
NDUFS8	PRO85LEU	P85L	C254T	0.926	NO		Heterozygous	1 patient	Leigh syndrome due to mitochondrial complex I deficiency
NDUFS8	ARG138HIS	R138H	G413A	0.758	NO		Heterozygous	1 patient	Leigh syndrome due to mitochondrial complex I deficiency
NDUFS8	PRO79LEU	P79L	C236T	0.750	NO		Heterozygous	1 patient	Leigh syndrome due to mitochondrial complex I deficiency; death at the age of 11 weeks
NDUFS8	ALA159ASP	A159D	C476A	0.739	NO		Heterozygous	1 patient	Mitochondrial complex I deficiency
NDUFS8	ARG102HIS	R102H	G305A	0.729	NO		Heterozygous	1 patient	Leigh syndrome due to mitochondrial complex I deficiency; death at the age of 11 weeks
NDUFS8	ARG77TRP	R77W	C229T	0.570	NO		Heterozygous	1 patient	Mitochondrial complex I deficiency
NDUFS8	GLU63GLN	E63Q	G187C	0.507	NO		Homozygous	1 patient	Leigh syndrome due to mitochondrial complex I deficiency
NDUFV1	THR423MET	T423M	C1268T	0.877	NO		Heterozygous	2 sibs	Mitochondrial complex I deficiency
NDUFV1	GLU214LYS	E214K	G640A	0.849	NO		Heterozygous	1 patient	Mitochondrial complex I deficiency
NDUFV1	ALA341VAL	A341V	C1022T	0.815	NO		Homozygous	1 patient	Mitochondrial complex I deficiency
OPA1	GLY337GLU	G337E	G899A	0.926	NO			affected members of a family	Optic atrophy 1
OPA1	ILE419MET	I419M	A1146G	0.920	YES	1 American heterozygous (PUR)	Heterozygous	1; 2 sibs	Optic atrophy with or without deafness, ophthalmoplegia, myopathy, ataxia, and neuropathy, included
OPA1	GLY476VAL	G476V	G1316T	0.866	NO		Heterozygous	1 Italian and daughter	Optic atrophy with or without deafness, ophthalmoplegia, myopathy, ataxia, and neuropathy
OPA1	ILE469VAL	I469V	A1294G	0.858	NO		Heterozygous	2 sibs	Optic atrophy with or without deafness, ophthalmoplegia, myopathy, ataxia, and neuropathy
OPA1	SER582ARG	S582R	C1635G	0.834	NO		Heterozygous	7 affected members of a 3-generation family; 3 affected	Optic atrophy with or without deafness, ophthalmoplegia, myopathy, ataxia, and neuropathy

								members of an Austrian family	
OPA1	ARG327GLN	R327Q	G869A	0.790	NO			1 family from Cuba	Optic atrophy 1
OPA1	ARG482HIS	R482H	G1334A	0.734	NO			1 Japanese; Utah; Belgian; 6 other family, one Spanish	Optic atrophy with or without deafness, ophthalmoplegia, myopathy, ataxia, and neuropathy
OPA1	TYR619CYS	Y619C	A1741G	0.602	NO		Heterozygous	1 patient	Optic atrophy with or without deafness, ophthalmoplegia, myopathy, ataxia, and neuropathy
OPA1	VAL947ASP	V947D	T2729A	0.597	NO			1 Italian and 6 other members of the family were affected	Optic atrophy with or without deafness, ophthalmoplegia, myopathy, ataxia, and neuropathy
OPA3	GLY93SER	G93S	G277A	0.830	NO		Heterozygous	affected members of a French family	Optic atrophy and cataract, autosomal dominant
OPA3	GLN105GLU	Q105E	C313G	0.651	NO		Heterozygous	affected members of a family	Optic atrophy and cataract, autosomal dominant
PEO1	LEU381PRO	L381P	T1442C	0.925	NO			affected members of an Italian family	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	ALA475PRO	A475P	G1423C	0.895	NO		Heterozygous	affected members of a Pakistani family	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	ARG303GLN	R303Q	G908A	0.864	NO		Heterozygous	1 patient	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	TRP474CYS	W474C		0.860	NO			affected members of a pedigree	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	ARG374TRP	R374W	C1120T	0.854	NO		Heterozygous	5 patients from 2 unrelated French families	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	TRP315LEU	W315L		0.825	NO			affected members of a pedigree	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	ALA318THR	A318T	G952A	0.815	NO		Heterozygous	2 Finnish sibs	Mitochondrial dna depletion syndrome 7 (hepatocerebral type)
PEO1	ALA359THR	A359T		0.786	NO		Homozygous	affected members of a large, consanguineous Italian family	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	THR457ILE	T457I	C1370T	0.786	NO		Homozygous	2 Algerian sibs and a first cousin	Mitochondrial dna depletion syndrome 7 (hepatocerebral type); died by age 3 years
PEO1	LYS319GLU	K319E	A955G	0.769	NO		Heterozygous	2 sibs	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PEO1	ARG354PRO	R354P	G1061C	0.766	NO			affected members of an Italian family	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3

PEO1	TYR508CYS	Y508C	A1708G	0.766	NO		Homozygous; heterozygous	Finnish patients	Mitochondrial dna depletion syndrome 7 (hepatocerebral type)
PEO1	ARG334GLN	R334Q	G1031A	0.741	NO		Heterozygous	sporadic case	Progressive external ophthalmoplegia with mitochondrial dna deletions, digenic
PEO1	SER369TYR	S369Y	C1106A	0.698	NO		Heterozygous	2 families from Tasmania	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 3
PINK1	LEU347PRO	L347P	T1040C	0.938	NO		Homozygous	3 affected members of a Filipino family; another Filipino and 2 affected sibs	Parkinson disease 6, autosomal recessive early-onset
PINK1	HIS271GLN	H271Q	C813A	0.921	NO		Homozygous	Japanese patient	Parkinson disease 6, autosomal recessive early-onset
PINK1	TYR431HIS	Y431H		0.845	NO		Heterozygous	1 sporadic patient	Parkinson disease 6, late-onset, susceptibility to
PINK1	ALA217ASP	A217D	C650A	0.840	NO		Homozygous	5 affected members of a large consanguineous Sudanese family	Parkinson disease 6, autosomal recessive early-onset
PINK1	THR313MET	T313M	C1032T	0.821	NO		Homozygous	2 affected members of a large consanguineous Saudi Arabian family; 2 additional members affected	Parkinson disease 6, autosomal recessive early-onset
PINK1	ARG279HIS	R279H	G836A	0.784	NO		Heterozygous	1 Italian; 1 Korean	Parkinson disease 6, early-onset
PINK1	GLY309ASP	G309D	G11185A	0.749	NO		Homozygous	consanguineous Spanish family	Parkinson disease 6, autosomal recessive early-onset
PINK1	PRO399LEU	P399L	C1196T	0.731	NO		Heterozygous	2 Chinese sibs	Parkinson disease, autosomal recessive early-onset, digenic, pink1/dj1
POLG	ARG853TRP	R853W	C2839T	0.989	NO		Heterozygous	2 Italian sisters	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal recessive
POLG	GLY848SER	G848S		0.973	NO		Heterozygous	2 sibs	Alpers syndrome
POLG	TYR955CYS	Y955C	A2864G	0.971	NO		?; heterozygous	affected members of a 3-generation Belgian pedigree; 4 Italian and 1 Greek; 4 adPEO families, including the Swedish family	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 1
POLG	ALA957SER	A957S	G2869T	0.964	NO		Heterozygous; homozygous	2 families from a small village in northwest Sicily	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 1
POLG	PRO1073LEU	P1073L	C3218T	0.960	NO		Heterozygous	4 patients	Mitochondrial dna depletion syndrome 4a (alpers type)
POLG	HIS932TYR	H932Y	C2794T	0.957	NO		Heterozygous	2 Italian sibs	Sensory ataxic neuropathy, dysarthria, and ophthalmoparesis

POLG	GLY1051ARG	G1051R	G3151C	0.922	NO		Heterozygous	2 Italian sibs	Sensory ataxic neuropathy, dysarthria, and ophthalmoparesis
POLG	LEU304ARG	L304R	T911G	0.874	NO		Heterozygous	3 affected sibs	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal recessive
POLG	ARG227TRP	R227W	C697T	0.859	NO		Heterozygous	1 patient	Mitochondrial dna depletion syndrome 4b (mngie type)
POLG	TRP748SER	W748S	G2243C	0.838	NO		Heterozygous; homozygous	British patient; 3 Finnish sibs; another Finnish; 4 children	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal recessive
POLG	GLY737ARG	G737R	G2491C	0.807	YES	1 European heterozygous (GBR)	Heterozygous	2 Italian sisters	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal recessive
POLG	ASN864SER	N864S	A2591T	0.788	NO		Heterozygous	2 sisters	Mitochondrial dna depletion syndrome 4b (mngie type)
POLG	ALA467THR	A467T	G1399A	0.751	YES	1 European heterozygous (CEU)	Heterozygous; homozygous	3 affected sibs; 1 patient; 3 sibs; 1 Belgian	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal recessive
POLG	GLN497HIS	Q497H	G1491C	0.713	NO		Heterozygous; homozygous	2 families	Spinocerebellar ataxia with epilepsy
POLG	TYR831CYS	Y831C	A2492G	0.680	YES	4 European heterozygous (3 FIN, TSI)	Heterozygous	2 sibs	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 1
POLG	ARG627TRP	R627W		0.676	NO		Heterozygous	sporadic case	Sensory ataxic neuropathy, dysarthria, and ophthalmoparesis
POLG	PRO587LEU	P587L	C1760T	0.667	YES	2 European heterozygous (FIN, GBR)	Heterozygous	2 sisters; 3 families; 2 sibs, another patient	Mitochondrial dna depletion syndrome 4b (mngie type)
POLG	ARG3PRO	R3P	G8C	0.658	NO		Heterozygous	2 affected individuals in another family	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal recessive
POLG	THR251ILE	T251I		0.602	YES	2 European heterozygous (FIN, GBR)	Heterozygous	1 patient	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal recessive
POLG		E1143G	A3428G	0.533	YES	1 African heterozygous (ASW); 3 American heterozygous (CLM, 2 PUR); 2 European homozygous (GBR, TSI); 29 European heterozygous (2 CEU, 4 FIN, 13 GBR, IBS, 9 TSI)	Heterozygous	5 patients	Sensory ataxic neuropathy, dysarthria, and ophthalmoparesis
POLG	SER511ASN	S511N	G1532A	0.480	NO		Heterozygous	6 affected members of a large family	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 1
POLG2	GLY451GLU	G451E	G1352A	0.950	NO		Heterozygous	1 patient	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 4

POLG2	PRO205ARG	P205R	C614G	0.823	NO		Heterozygous	1 patient	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 4
POLG2	ARG369GLY	R369G	A1105G	0.783	NO		Heterozygous	1 patient	Progressive external ophthalmoplegia with mitochondrial dna deletions, autosomal dominant, 4
SDHA	MET1LEU	M1L	A-to-C	0.977	NO		Heterozygous	1 patient	Leigh syndrome due to mitochondrial complex II deficiency
SDHA	ARG589TRP	R589W	C1765T	0.916	NO		Heterozygous germline	1 patient	Paragangliomas 5
SDHA	ARG554TRP	R554W	C1684T	0.903	NO		Heterozygous	2 sibs	Leigh syndrome due to mitochondrial complex II deficiency
SDHA	ALA524VAL	A524V	C-to-T	0.901	NO		Heterozygous	1 patient	Leigh syndrome due to mitochondrial complex II deficiency
SDHA	GLY555GLU	G555E	G1664A	0.851	NO		Homozygous	1; 1 Palestinian; 15 Bedouin patients from a single tribe with neonatal dilated cardiomyopathy, including 13 patients from 2 consanguineous families and 2 sporadic patients	Mitochondrial complex II deficiency, leigh syndrome, included, cardiomyopathy, dilated, 1gg, included
SDHA	SER509LEU	S509L	C1526T	0.468	NO		Heterozygous	1 patient	Mitochondrial complex II deficiency
SDHA	THR508ILE	T508I	C1523T	0.356	YES	7 African heterozygous (ASW, 5 LWK, YRI)	Heterozygous	1 patient	Mitochondrial complex II deficiency
SDHB	PRO197ARG	P197R	C724G	0.949	NO		Heterozygous	3 individuals from a family	Paragangliomas 4
SDHB	ARG46GLY	R46G	C270G	0.925	NO		Heterozygous	2 unrelated patients	Pheochromocytoma
SDHB	ARG242HIS	R242H	G725A	0.922	NO		Heterozygous	man and son; 1 patient; 1 patient	Paragangliomas 4; sporadic pheochromocytoma; sporadic gastrointestinal stromal tumor
SDHB	CYS101TYR	C101Y	G436A	0.920	NO		Heterozygous	2 unrelated patients	Pheochromocytoma
SDHB	SER100PHE	S100F	C299T	0.872	NO		Heterozygous	1 patient	Pheochromocytoma
SDHB	HIS132PRO	H132P	A-to-C	0.862	NO		Heterozygous	2 brothers and their mother	Paragangliomas 4
SDHB	VAL140PHE	V140F	G418T	0.724	NO		Heterozygous	2 sibs	Paragangliomas 4
SDHB	ALA3GLY	A3G	C-to-G	0.675	YES	18 African heterozygous (4 ASW, 2 LWK, 12 YRI); 1 European heterozygous (TSI)		1 patient	Cowden disease 2
SDHB	SER163PRO	S163P		0.196	YES	1 African heterozygous (ASW); 2 American heterozygous (CLM, MXL); 14 European heterozygous (2 CEU, 4 FIN, 3 GBR, IBS, 4 TSI)		2 patients	Cowden disease 2

SDHD	HIS102LEU	H102L	A-to-T	0.985	NO			affected members of a family	Paragangliomas 1
SDHD	TYR114CYS	Y114C		0.984	NO			affected members of a German family	Paragangliomas 1
SDHD	MET1VAL	M1V	A1G	0.977	NO			3 unrelated patients	Paraganglioma, carotid body, somatic
SDHD	MET1ILE	M1I	G-to-C	0.972	NO			father and his 2 sons	Paragangliomas 1
SDHD	ASP92TYR	D92Y	G-to-T	0.960	NO			Dutch founder mutation; 1 patient	Paragangliomas 1; sporadic pheochromocytoma
SDHD	PRO81LEU	P81L	C-to-T	0.931	NO		Heterozygous	5 families; 3 families; 1 individual; 4 individuals from a family; 14 families	Paragangliomas 1; pheochromocytoma; sensorineural deafness in association with paragangliomas
SDHD	LEU139PRO	L139P		0.920	NO			7 Dutch families	Paragangliomas 1
SDHD	HIS145ASN	H145N	C-to-A	0.760	NO			1 patient	Cowden disease 3
SDHD	HIS50ARG	H50R	A149G	0.260	YES	18 American heterozygous (2 CLM, 10 MXL, 6 PUR); 22 European heterozygous (10 CEU, 4 FIN, 2 IBS, 6 TSI)		1 patient; 1 patient; 2 unrelated patient	Carcinoid tumors, intestinal; pheochromocytoma; merkel cell carcinoma, somatic; cowden disease 3
SDHD	GLY12SER	G12S		0.158	YES	2 African heterozygous (ASW); 2 American homozygous (CLM); 8 American heterozygous (2 CLM, 6 PUR); 12 European heterozygous (2 CEU, 10 TSI)		several patients	Cowden disease 3; paragangliomas 1; carcinoid tumors, intestinal; pheochromocytoma
TK2	ILE212ASN	I212N	T542A	0.848	NO			3 Muslim-Arab infants	Mitochondrial dna depletion syndrome 2 (myopathic type)
TK2	HIS121ASN	H121N		0.687	YES	1 American heterozygous (MXL)	Homozygous	Ashkenazi Jewish patient	Mitochondrial dna depletion syndrome 2 (myopathic type)
TK2	THR108MET	T108M		0.644	NO		Heterozygous; homozygous	2 sibs; 3 sibs; 2 unrelated patients	Mitochondrial dna depletion syndrome 2 (myopathic type)
TK2	ILE53MET	I53M		0.580	NO		Homozygous	brother and sister from Hispanic family	Mitochondrial dna depletion syndrome 2 (myopathic type)
TK2	ARG90CYS	R90C	C268T	0.556	NO		Heterozygous	1 patient	Mitochondrial dna depletion syndrome 2 (myopathic type)
UCP3	ARG70TRP	R70W		0.868	NO			15-year-old male of Chinese descent	Obesity, severe, and type II diabetes
UCP3	VAL102ILE	V102I		0.742	YES	1 American heterozygous (MXL)	Heterozygous; homozygous	1 Gullah-speaking African American woman and 4 children	Obesity, severe, and type II diabetes
UQCRC2	ARG183TRP	R183W	C547T	0.638	NO		Homozygous	3 affected individuals from a large consanguineous Mexican kindred	Mitochondrial complex III deficiency, nuclear type 5

UQCRQ	SER45PHE	S45F	C208T	0.760	NO		Homozygous	affected members of a large Israeli Bedouin kindred	Mitochondrial complex III deficiency, nuclear type 4

Table S8- Mutations in the 104 nDNA genes reported in COSMIC dataset.

Gene	Position	Mutation (CDS)	Mutation (Amino Acid)	Mutation (Amino Acid) Our Transcript	Mutation ID (COSM)	Count	Confirmed somatic	MutPred	Presence in 1000 genomes	Population
AK2	108	c.323C>A	p.A108E		COSM464459	1	YES	0.909	No	
AK2	112	c.334G>A	p.D112N		COSM1182333	2	YES	0.577	No	
AK2	145	c.434A>T	p.H145L		COSM534886	1	YES	0.612	No	
AK2	150	c.448C>A	p.R150S		COSM534888	1	YES	0.553	No	
AK2	170	c.508G>A	p.E170K		COSM534890	1	YES	0.583	No	
AK3	71	c.213G>C	p.M71I	M1I	COSM69597	1	YES	0.589	No	
AK3	76	c.226C>T	p.L76F	L5F	COSM304405	1	YES	0.348	No	
AK3	152	c.456C>G	p.D152E		COSM293356	1	YES	0.857	No	
AK3	179	c.535C>G	p.Q179E		COSM69596	1	YES	0.533	No	
AK3	211	c.633C>A	p.F211L		COSM324684	1	YES	0.444	No	
AK4	76	c.226G>A	p.E76K		COSM83910	1	YES	0.659	No	
AK4	150	c.449A>G	p.D150G		COSM464868	1	YES	0.781	No	
AK4	197	c.589A>G	p.T197A		COSM1235262	1	YES	0.281	No	
AK4	209	c.626T>C	p.L209P		COSM25652	1	YES	0.682	No	
ATP5A1	78	c.233G>A	p.G78D		COSM279065	1	YES	0.578	No	
ATP5A1	83	c.248G>A	p.R83H		COSM563874	1	YES	0.619	No	
ATP5A1	85	c.254A>G	p.H85R		COSM265290	1	YES	0.534	No	
ATP5A1	106	c.317C>A	p.S106Y		COSM1184103	2	YES	0.515	No	
ATP5A1	120	c.359G>A	p.G120E		COSM188279	1	YES	0.660	No	
ATP5A1	144	c.430G>A	p.E144K		COSM417836	1	YES	0.299	No	
ATP5A1	182	c.545G>A	p.R182Q		COSM259569	1	YES	0.813	No	
ATP5A1	212	c.635G>C	p.G212A		COSM563875	1	YES	0.859	No	
ATP5A1	224	c.670G>T	p.D224Y		COSM473854	1	YES	0.870	No	
ATP5A1	306	c.917A>G	p.H306R		COSM171586	1	YES	0.752	No	
ATP5A1	382	c.1144C>G	p.P382A		COSM709481	1	YES	0.801	No	
ATP5A1	441	c.1321C>A	p.R441S		COSM709482	1	YES	0.861	No	
ATP5A1	454	c.1360G>A	p.D454N		COSM1136052	1	YES	0.643	No	

ATP5A1	519	c.1556A>T	p.H519L		COSM709483	1	YES	0.720	No	
ATP5B	30	c.88C>G	p.Q30E		COSM416140	1	YES	0.210	No	
ATP5B	41	c.121C>T	p.H41Y		COSM135597	1	YES	0.266	No	
ATP5B	80	c.239C>A	p.P80Q		COSM694428	1	YES	0.791	No	
ATP5B	151	c.452C>A	p.P151H		COSM212211	1	YES	0.539	No	
ATP5B	155	c.464G>C	p.R155T		COSM941795	1	YES	0.277	No	
ATP5B	160	c.479C>A	p.T160N		COSM941794	1	YES	0.248	No	
ATP5B	252	c.754G>A	p.E252K		COSM549343	1	YES	0.540	No	
ATP5B	284	c.850C>G	p.L284V		COSM1188529	1	YES	0.743	No	
ATP5B	365	c.1094A>G	p.D365G		COSM468685	1	YES	0.789	No	
ATP5B	403	c.1208C>A	p.S403Y		COSM694429	1	YES	0.850	No	
ATP5B	419	c.1255G>A	p.D419N		COSM192044	1	YES	0.343	No	
ATP5B	459	c.1376A>C	p.K459T		COSM292368	1	YES	0.746	No	
ATP5C1	1	c.3G>T	p.M1I		COSM1171725	1	YES	0.993	No	
ATP5C1	9	c.25G>T	p.G9W		COSM539727	1	YES	0.562	No	
ATP5C1	12	c.34G>C	p.A12P		COSM685287	1	YES	0.512	No	
ATP5C1	26	c.76G>A	p.A26T		COSM175286	1	YES	0.762	No	
ATP5C1	58	c.173G>T	p.R58L		COSM465992	1	YES	0.716	No	
ATP5C1	81	c.241G>A	p.D81N		COSM159280	1	YES	0.416	No	
ATP5C1	95	c.284G>T	p.G95V		COSM268730	1	YES	0.515	No	
ATP5C1	182	c.544G>A	p.E182K		COSM254558	1	YES	0.661	No	
ATP5C1	198	c.592A>T	p.T198S		COSM539724	1	YES	0.529	No	
ATP5C1	222	c.664G>T	p.D222Y		COSM685285	1	YES	0.567	No	
ATP5C1	273	c.819G>C	p.L273F		COSM685284	1	YES	0.867	No	
ATP5D	139	c.416C>T	p.A139V		COSM178124	1	YES	0.390	No	
ATP5EP2	46	c.136G>T	p.V46L		COSM86282	1	YES	0.517	No	
ATP5F1	20	c.59C>T	p.A20V		COSM1127480	1	YES	0.353	No	
ATP5F1	111	c.332A>G	p.Y111C		COSM527394	1	YES	0.579	No	
ATP5F1	161	c.482A>G	p.Q161R		COSM423449	1	YES	0.471	No	
ATP5F1	206	c.618G>A	p.M206I		COSM458710	1	YES	0.510	No	
ATP5F1	208	c.622C>T	p.R208C		COSM201242	1	YES	0.816	No	
ATP5G1	2	c.5A>T	p.Q2L		COSM328764	1	YES	0.348	No	
ATP5G2	85	c.253G>T	p.D85Y		COSM468597	1	YES	0.458	No	
ATP5G2	132	c.394G>A	p.A132T		COSM69764	1	YES	0.533	No	
ATP5G2	140	c.418G>C	p.E140Q		COSM694066	1	YES	0.742	No	
ATP5G2	157	c.469A>G	p.M157V		COSM694067	1	YES	0.453	No	

ATP5G3	41	c.121G>C	p.G41R		COSM77318	1	YES	0.202	No	
ATP5G3	74	c.221A>C	p.K74T		COSM279067	1	YES	0.526	No	
ATP5G3	97	c.290G>T	p.G97V		COSM717675	1	YES	0.786	No	
ATP5G3	135	c.403G>C	p.A135P		COSM571286	1	YES	0.761	No	
ATP5H	135	c.403G>A	p.D135N		COSM140802	1	YES	0.901	No	
ATP5I	63	c.187G>A	p.E63K		COSM138420	1	YES	0.501	No	
ATP5J	1	c.2T>C	p.M1T		COSM248869	1	YES	0.921	No	
ATP5J	31	c.91G>A	p.A31T		COSM1029617	1	YES	0.789	No	
ATP5J2	29	c.87G>C	p.W29C		COSM69765	1	YES	0.798	No	
ATP5J2	92	c.275A>C	p.K92T		COSM199229	1	YES	0.529	No	
ATP5L	1	c.2T>C	p.M1T		COSM686171	1	YES	0.692	No	
ATP5L	23	c.68C>T	p.S23L		COSM259571	1	YES	0.527	No	
ATP5L	34	c.100G>A	p.A34T		COSM159281	1	YES	0.658	No	
ATP5L	44	c.131C>T	p.A44V		COSM923566	1	YES	0.644	No	
ATP5L	84	c.252G>T	p.L84F		COSM541014	1	YES	0.415	No	
ATP5L	85	c.253A>T	p.M85L		COSM170485	1	YES	0.635	No	
ATP5L2	29	c.85G>A	p.A29T		COSM479030	1	YES	0.402	No	
ATP5L2	76	c.226A>G	p.N76D		COSM1154031	1	YES	0.804	No	
ATP5O	64	c.190A>G	p.R64G		COSM73778	1	YES	0.597	No	
ATP5O	139	c.416T>C	p.V139A		COSM186094	1	YES	0.699	No	
ATP5O	156	c.467A>T	p.E156V		COSM419247	1	YES	0.589	No	
ATP5O	172	c.515A>C	p.K172T		COSM279068	1	YES	0.618	No	
ATP5S	33	c.98C>A	p.P33Q		COSM698448	1	YES	0.497	No	
ATP5S	34	c.102G>C	p.W34C		COSM212304	1	YES	0.483	No	
ATP5S	85	c.254G>T	p.W85L		COSM698447	1	YES	0.485	No	
ATP5S	91	c.273C>G	p.H91Q		COSM159282	1	YES	0.176	No	
ATP5S	106	c.316G>A	p.D106N		COSM329053	1	YES	0.464	No	
COX10	118	c.354G>C	p.L118F		COSM704963	2	YES	0.242	No	
COX10	142	c.425G>A	p.R142Q		COSM1202102	1	YES	0.477	No	
COX10	199	c.595G>T	p.A199S		COSM1202103	1	YES	0.728	No	
COX10	249	c.746C>T	p.A249V		COSM272527	1	YES	0.667	No	
COX10	259	c.776C>T	p.T259I		COSM975654	1	YES	0.679	No	
COX10	275	c.824C>T	p.T275I		COSM266298	1	YES	0.869	No	
COX10	436	c.1307G>T	p.G436V		COSM704960	1	YES	0.189	No	
COX11	6	c.16C>G	p.R6G		COSM1165723	1	YES	0.329	No	
COX11	6	c.17G>T	p.R6L		COSM70282	1	YES	0.304	No	

COX11	10	c.28A>G	p.R10G		COSM190825	1	YES	0.431	No	
COX11	101	c.302C>A	p.A101D		COSM561681	1	YES	0.547	No	
COX11	207	c.619G>C	p.E207Q		COSM706793	1	YES	0.493	No	
COX11	258	c.772T>C	p.S258P		COSM473065	1	YES	0.870	No	
COX15	36	c.107G>A	p.R36H		COSM168044	1	YES	0.224	No	
COX15	44	c.131G>A	p.S44N		COSM131094	1	YES	0.241	No	
COX15	49	c.146T>C	p.V49A		COSM1202105	1	YES	0.188	No	
COX15	57	c.169A>G	p.T57A		COSM913783	1	YES	0.231	No	
COX15	67	c.200G>T	p.R67L		COSM536872	1	YES	0.574	No	
COX15	86	c.256C>A	p.L86I		COSM167910	2	YES	0.447	No	
COX15	115	c.343G>A	p.E115K		COSM70283	1	YES	0.479	No	
COX15	282	c.844G>A	p.A282T		COSM465166	1	YES	0.918	No	
COX15	310	c.928C>A	p.P310T		COSM1202104	1	YES	0.355	No	
COX15	345	c.1034G>T	p.R345L		COSM536873	1	YES	0.629	No	
COX16	16	c.47T>A	p.L16H		COSM698824	1	YES	0.657	No	
COX16	60	c.179A>C	p.K60T		COSM195030	1	YES	0.241	No	
COX16	85	c.254G>T	p.R85M		COSM1202106	1	YES	0.526	No	
COX17	8	c.23A>C	p.N8T		COSM295010	1	YES	0.197	No	
COX18	84	c.251G>A	p.G84D		COSM1202107	1	YES	0.705	No	
COX18	133	c.397C>T	p.R133C		COSM280089	1	YES	0.584	No	
COX18	148	c.443A>T	p.Y148F		COSM588170	1	YES	0.624	No	
COX18	150	c.450G>T	p.K150N		COSM260263	1	YES	0.486	No	
COX18	162	c.485G>A	p.R162Q		COSM196003	1	YES	0.766	No	
COX18	264	c.791C>T	p.S264L		COSM317176	1	YES	0.814	No	
COX4I1	39	c.117G>A	p.M39I		COSM23302	1	YES	0.247	No	
COX4I1	53	c.159G>C	p.K53N		COSM559445	1	YES	0.408	No	
COX4I1	93	c.279G>A	p.M93I		COSM139027	1	YES	0.815	No	
COX4I1	115	c.343G>A	p.A115T		COSM265687	1	YES	0.698	No	
COX4I1	115	c.344C>T	p.A115V		COSM197384	1	YES	0.636	No	
COX4I1	162	c.485A>T	p.Y162F		COSM704511	1	YES	0.906	No	
COX4I2	8	c.23G>A	p.S8N		COSM184859	1	YES	0.363	No	
COX4I2	45	c.133T>C	p.Y45H		COSM1179513	1	YES	0.443	No	
COX4I2	116	c.346G>A	p.A116T		COSM170860	1	YES	0.646	No	
COX4I2	146	c.437G>A	p.R146H		COSM184861	1	YES	0.675	No	
COX4I2	164	c.490T>A	p.Y164N		COSM328778	1	YES	0.799	No	
COX5A	130	c.389T>G	p.L130R		COSM248923	1	YES	0.892	No	

COX5A	142	c.425C>T	p.P142L		COSM964939	1	YES	0.532	No	
COX5B	73	c.217A>T	p.T73S		COSM576613	1	YES	0.803	No	
COX5B	73	c.218C>T	p.T73I		COSM1024095	1	YES	0.820	No	
COX6A2	58	c.172G>A	p.E58K		COSM970271	1	YES	0.566	No	
COX6A2	87	c.259G>A	p.V87M		COSM297106	2	YES	0.543	No	
COX6B1	5	c.15G>T	p.M5I	M22I	COSM711942	1	YES	0.253	No	
COX6B1	20	c.58C>T	p.R20C	R37C	COSM239429	1	YES	0.939	No	
COX6B1	59	c.175C>T	p.R59C	R76C	COSM566200	2	YES	0.524	No	
COX6B1	69	c.206G>T	p.W69L	W86L	COSM711940	1	YES	0.941	No	
COX6B2	8	c.24G>T	p.E8D		COSM568066	2	YES	0.189	No	
COX6B2	36	c.106T>G	p.F36V		COSM475301	1	YES	0.807	No	
COX6B2	70	c.210C>A	p.S70R		COSM248863	1	YES	0.440	No	
COX6C	7	c.20C>T	p.P7L		COSM748140	1	YES	0.429	No	
COX6C	23	c.67A>G	p.M23V		COSM131392	1	YES	0.521	No	
COX7A1	9	c.26C>A	p.A9E		COSM995393	1	YES	0.230	No	
COX7A1	48	c.142G>A	p.V48I		COSM995390	1	YES	0.283	No	
COX7A1	54	c.161G>A	p.R54Q		COSM268939	1	YES	0.720	Yes	1 AMR
COX7A2	23	c.69T>G	p.H23Q	H55Q	COSM484359	1	YES	0.281	No	
COX7A2	40	c.120A>C	p.E40D	E72D	COSM1202110	1	YES	0.484	No	
COX7A2L	17	c.50C>A	p.A17D		COSM721854	1	YES	0.338	No	
COX7A2L	75	c.223G>A	p.V75I		COSM721855	1	YES	0.517	Yes	1 ASN
COX7A2L	90	c.268A>T	p.T90S		COSM575315	2	YES	0.687	No	
COX7B	40	c.119C>T	p.A40V		COSM1125532	1	YES	0.449	No	
COX7B	71	c.211A>G	p.R71G		COSM1125534	1	YES	0.627	No	
COX7B2	15	c.43A>T	p.I15F		COSM734343	1	YES	0.451	No	
COX7B2	26	c.78C>G	p.S26R		COSM734344	1	YES	0.444	No	
COX7B2	69	c.205C>A	p.P69T		COSM189549	1	YES	0.848	No	
COX7B2	72	c.215G>T	p.R72I		COSM734345	1	YES	0.714	No	
COX7B2	75	c.223C>A	p.P75T		COSM734346	1	YES	0.832	No	
COX7C	42	c.124T>G	p.C42G		COSM1070996	1	YES	0.372	No	
COX8A	16	c.46G>A	p.A16T		COSM1202112	1	YES	0.271	No	
COX8C	25	c.73G>A	p.A25T		COSM292558	1	YES	0.092	No	
CYC1	51	c.152C>G	p.S51C		COSM1173390	1	YES	0.305	No	
CYC1	78	c.232C>G	p.L78V		COSM604563	1	YES	0.359	No	
CYC1	93	c.278G>C	p.S93T		COSM239500	1	YES	0.278	No	
CYC1	95	c.283C>G	p.P95A		COSM1173391	1	YES	0.491	No	

CYC1	100	c.298G>A	p.G100S		COSM1202775	1	YES	0.813	No	
CYC1	103	c.308C>G	p.S103C		COSM1173392	1	YES	0.593	No	
CYC1	136	c.406G>A	p.V136M		COSM1202776	1	YES	0.589	No	
CYC1	157	c.469G>A	p.G157S		COSM604562	1	YES	0.539	No	
CYC1	188	c.562G>A	p.A188T		COSM300950	1	YES	0.850	No	
CYC1	210	c.629A>T	p.Y210F		COSM749638	1	YES	0.875	No	
CYC1	222	c.664C>G	p.P222A		COSM749636	1	YES	0.618	No	
CYC1	238	c.712C>A	p.P238T		COSM1097184	1	YES	0.710	No	
CYC1	265	c.795G>C	p.Q265H		COSM749635	1	YES	0.924	No	
DGUOK	197	c.589C>A	p.Q197K		COSM576056	1	YES	0.630	No	
MFF	29	c.85G>A	p.E29K		COSM32965	1	YES	0.628	No	
MFF	48	c.144G>T	p.R48S		COSM325800	2	YES	0.832	No	
MFF	149	c.446G>C	p.R149T		COSM212816	1	YES	0.626	No	
MFF	162	c.484C>T	p.R162C		COSM170118	2	YES	0.666	No	
MFF	216	c.646G>A	p.E216K		COSM442425	1	YES	0.438	No	
MFF	216	c.647A>G	p.E216G		COSM1214964	1	YES	0.413	No	
MFF	236	c.706C>A	p.R236S		COSM574011	1	YES	0.559	No	
MFF	250	c.748C>T	p.R250C		COSM282778	1	YES	0.484	No	
MFF	261	c.781G>A	p.A261T		COSM1214963	1	YES	0.369	No	
MFF	306	c.917G>T	p.R306L		COSM1017385	1	YES	0.780	No	
MFF	312	c.936G>C	p.E312D		COSM211864	1	YES	0.409	No	
MFF	342	c.1024C>T	p.R342C		COSM1017387	1	YES	0.613	No	
MFN1	12	c.35T>C	p.V12A		COSM1163333	1	YES	0.407	No	
MFN1	35	c.104T>A	p.F35Y		COSM71629	1	YES	0.550	No	
MFN1	53	c.157G>T	p.D53Y		COSM582508	1	YES	0.457	No	
MFN1	102	c.305C>T	p.P102L		COSM325802	1	YES	0.942	No	
MFN1	137	c.411G>T	p.K137N		COSM729800	1	YES	0.613	No	
MFN1	193	c.577G>C	p.D193H		COSM419698	1	YES	0.620	No	
MFN1	209	c.625G>A	p.E209K		COSM78080	1	YES	0.620	No	
MFN1	238	c.713G>A	p.R238H		COSM1041543	1	YES	0.619	No	
MFN1	262	c.784C>T	p.H262Y		COSM1214976	1	YES	0.448	No	
MFN1	279	c.835C>A	p.R279S		COSM729799	1	YES	0.727	No	
MFN1	301	c.902A>T	p.E301V		COSM582507	1	YES	0.634	No	
MFN1	357	c.1070C>T	p.S357L		COSM240660	1	YES	0.460	No	
MFN1	378	c.1132G>C	p.D378H		COSM446032	1	YES	0.420	No	
MFN1	400	c.1198G>A	p.E400K		COSM1166064	1	YES	0.271	No	

MFN1	415	c.1243G>C	p.D415H		COSM32336	1	YES	0.433	No	
MFN1	450	c.1350G>T	p.E450D		COSM1214975	1	YES	0.555	No	
MFN1	480	c.1438T>G	p.L480V		COSM171385	1	YES	0.433	No	
MFN1	484	c.1451T>C	p.L484P		COSM119854	1	YES	0.712	No	
MFN1	563	c.1687C>T	p.P563S		COSM208809	1	YES	0.188	No	
MFN1	574	c.1721A>T	p.N574I		COSM145623	1	YES	0.490	No	
MFN1	620	c.1859C>T	p.T620I		COSM582505	1	YES	0.697	No	
MFN1	622	c.1865A>G	p.Y622C		COSM582504	1	YES	0.875	Yes	1 ASN
MFN2	7	c.20G>T	p.R7L		COSM894744	1	YES	0.567	No	
MFN2	78	c.232G>A	p.V78I		COSM1214979	1	YES	0.313	No	
MFN2	202	c.604G>T	p.G202C		COSM462754	1	YES	0.888	No	
MFN2	294	c.881G>T	p.R294L		COSM325803	1	YES	0.495	No	
MFN2	397	c.1189C>T	p.R397W		COSM894763	1	YES	0.394	No	
MFN2	468	c.1402C>T	p.R468C		COSM1214977	1	YES	0.505	No	
MFN2	479	c.1436C>G	p.S479C		COSM527753	1	YES	0.418	No	
MFN2	510	c.1528C>T	p.R510W		COSM139268	1	YES	0.482	No	
MFN2	523	c.1568C>T	p.S523F		COSM136092	1	YES	0.456	No	
MFN2	564	c.1690C>T	p.R564W		COSM75405	1	YES	0.500	No	
MFN2	628	c.1882G>A	p.A628T		COSM180956	1	YES	0.769	No	
MFN2	646	c.1936G>A	p.V646I		COSM180958	1	YES	0.437	No	
MFN2	659	c.1976G>T	p.R659M		COSM180960	1	YES	0.751	No	
MFN2	684	c.2051G>A	p.C684Y		COSM894773	1	YES	0.862	No	
MFN2	710	c.2129T>C	p.L710P		COSM894775	1	YES	0.943	No	
MFN2	739	c.2215G>A	p.G739S		COSM248808	1	YES	0.455	No	
MTERF	61	c.182A>C	p.K61T	K41T	COSM485704	1	YES	0.410	No	
MTERF	148	c.443A>T	p.K148M	K128T	COSM220426	1	YES	0.421	No	
MTERF	187	c.560G>C	p.G187A	G167A	COSM747602	1	YES	0.929	No	
MTERF	212	c.634A>G	p.K212E	K192E	COSM162594	1	YES	0.633	No	
MTERF	222	c.665G>A	p.G222D	G202D	COSM1092853	1	YES	0.555	No	
MTERF	238	c.714T>G	p.I238M	I218M	COSM167657	1	YES	0.773	No	
MTERF	260	c.778C>T	p.R260W	R240W	COSM262076	1	YES	0.635	No	
MTERF	274	c.820A>G	p.I274V	I254V	COSM220606	1	YES	0.468	No	
MTERF	303	c.908T>G	p.L303R	L283R	COSM485703	1	YES	0.870	No	
MTERF	347	c.1039G>A	p.E347K	E327K	COSM1092851	1	YES	0.568	No	
MTERF	362	c.1085G>A	p.R362Q	R342Q	COSM282905	1	YES	0.729	No	
MTFR1	91	c.271G>T	p.A91S	A75S	COSM1101030	1	YES	0.633	No	

MTFR1	146	c.436G>A	p.A146T	A130T	COSM194527	1	YES	0.671	No	
MTFR1	177	c.530C>G	p.S177C	S161C	COSM461411	1	YES	0.548	No	
MTFR1	251	c.751C>T	p.R251W	R235W	COSM257442	1	YES	0.710	No	
MTFR1	287	c.860G>A	p.R287Q	R271Q	COSM276137	1	YES	0.323	No	
MTFR1	311	c.933G>T	p.L311F	L295F	COSM295475	1	YES	0.281	No	
MTFR1	313	c.937G>T	p.G313W	G297W	COSM605999	1	YES	0.655	No	
NDUFAF2	1	c.1A>G	p.M1V		COSM1069220	1	YES	0.999	No	
NDUFAF2	6	c.16G>T	p.D6Y		COSM132735	1	YES	0.332	No	
NDUFAF2	43	c.128G>A	p.G43E		COSM296315	1	YES	0.568	No	
NDUFAF2	81	c.241A>G	p.T81A		COSM482937	1	YES	0.326	No	
NDUFAF3	62	c.184A>G	p.S62G		COSM480222	1	YES	0.600	No	
NDUFAF3	88	c.262C>A	p.Q88K		COSM480223	1	YES	0.448	No	
NDUFAF3	98	c.292A>G	p.T98A		COSM584043	2	YES	0.529	No	
NDUFAF3	100	c.300C>G	p.D100E		COSM291592	1	YES	0.562	No	
NDUFAF4	27	c.80C>T	p.P27L		COSM136556	1	YES	0.844	No	
NDUFAF4	72	c.215C>G	p.S72C		COSM175640	1	YES	0.872	No	
NDUFAF4	83	c.247G>C	p.A83P		COSM199016	1	YES	0.618	No	
NDUFAF4	89	c.265G>A	p.E89K		COSM1216919	1	YES	0.574	No	
NDUFAF4	98	c.292G>A	p.D98N		COSM265725	1	YES	0.376	No	
NDUFAF4	112	c.335G>A	p.G112D		COSM88608	1	YES	0.855	No	
NDUFAF4	116	c.346A>T	p.I116F		COSM743775	1	YES	0.581	No	
NDUFAF4	129	c.386T>C	p.F129S		COSM199015	1	YES	0.317	No	
NDUFAF4	162	c.484G>A	p.E162K		COSM276287	1	YES	0.533	No	
NDUFAF4	173	c.518G>T	p.R173L		COSM597678	1	YES	0.409	No	
NDUFB1	8	c.23C>T	p.S8F		COSM699087	1	YES	0.280	No	
NDUFB1	26	c.77C>T	p.A26V		COSM267011	1	YES	0.204	No	
NDUFB10	16	c.46C>T	p.R16C		COSM1216920	1	YES	0.496	No	
NDUFB10	58	c.172T>C	p.Y58H		COSM1189137	1	YES	0.739	No	
NDUFB10	62	c.185A>G	p.Y62C		COSM1216921	1	YES	0.493	No	
NDUFB11	49	c.145C>A	p.P49T		COSM116227	1	YES	0.167	No	
NDUFB11	75	c.223G>T	p.G75C		COSM488389	1	YES	0.419	No	
NDUFB11	131	c.391G>A	p.E131K	E121K	COSM612906	1	YES	0.609	No	
NDUFB11	147	c.440T>C	p.M147T	M137T	COSM1121707	1	YES	0.364	No	
NDUFB2	41	c.121G>C	p.E41Q		COSM599342	1	YES	0.384	No	
NDUFB2	43	c.127C>T	p.R43W		COSM39205	1	YES	0.431	No	
NDUFB2	44	c.130T>C	p.Y44H		COSM205025	1	YES	0.764	No	

NDUFB2	49	c.145C>A	p.Q49K		COSM599340	1	YES	0.318	No	
NDUFB2	75	c.223C>T	p.H75Y		COSM599338	1	YES	0.747	No	
NDUFB2	99	c.295A>G	p.I99V		COSM71804	1	YES	0.350	No	
NDUFB3	61	c.182T>C	p.V61A		COSM418914	1	YES	0.454	Yes	1 EUR
NDUFB3	67	c.201C>A	p.F67L		COSM283157	1	YES	0.303	No	
NDUFB4	12	c.35G>A	p.R12H		COSM1216922	1	YES	0.381	No	
NDUFB4	27	c.80C>T	p.P27L		COSM445374	1	YES	0.417	No	
NDUFB4	67	c.199C>T	p.R67C		COSM202670	1	YES	0.878	No	
NDUFB5	9	c.26G>C	p.R9P		COSM729784	1	YES	0.381	No	
NDUFB5	19	c.56C>G	p.S19C		COSM729783	1	YES	0.294	No	
NDUFB5	30	c.88G>T	p.G30W		COSM729782	1	YES	0.503	No	
NDUFB5	51	c.152G>T	p.G51V		COSM582499	1	YES	0.690	No	
NDUFB5	91	c.272T>G	p.V91G		COSM1216924	1	YES	0.434	No	
NDUFB5	121	c.362T>G	p.I121S		COSM1216925	1	YES	0.615	No	
NDUFB5	122	c.364G>T	p.A122S		COSM1041566	1	YES	0.462	No	
NDUFB5	186	c.556A>G	p.T186A		COSM110199	1	YES	0.274	No	
NDUFB6	16	c.46C>G	p.R16G		COSM753653	1	YES	0.276	No	
NDUFB6	31	c.91C>G	p.R31G		COSM422385	1	YES	0.332	No	
NDUFB6	32	c.95A>T	p.E32V		COSM291159	1	YES	0.408	No	
NDUFB6	75	c.223G>T	p.V75L		COSM487365	1	YES	0.422	No	
NDUFB7	39	c.115A>T	p.M39L		COSM1172580	1	YES	0.724	No	
NDUFB7	56	c.167G>A	p.R56Q		COSM1216926	1	YES	0.949	No	
NDUFB7	65	c.193C>G	p.R65G		COSM991923	1	YES	0.449	No	
NDUFB7	83	c.248A>C	p.E83A		COSM991921	1	YES	0.635	No	
NDUFB7	101	c.301G>A	p.E101K		COSM71805	1	YES	0.728	No	
NDUFB7	131	c.392T>C	p.V131A		COSM709778	1	YES	0.147	No	
NDUFB8	36	c.108G>T	p.M36I		COSM682494	1	YES	0.584	No	
NDUFB8	81	c.241C>T	p.R81C		COSM913950	1	YES	0.347	No	
NDUFB8	148	c.443A>G	p.D148G		COSM913948	1	YES	0.524	No	
NDUFB8	148	c.443A>T	p.D148V		COSM682495	1	YES	0.541	No	
NDUFB9	32	c.94G>T	p.V32F		COSM71806	1	YES	0.336	No	
NDUFB9	57	c.171G>A	p.M57I		COSM604216	1	YES	0.569	No	
NDUFB9	129	c.385C>T	p.R129W		COSM203218	1	YES	0.337	No	
NDUFB9	169	c.506A>G	p.Y169C		COSM289298	1	YES	0.436	No	
NDUFB9	175	c.523C>T	p.R175W		COSM749441	1	YES	0.334	No	
NDUFC2	16	c.46G>A	p.E16K		COSM545424	1	YES	0.860	No	

NDUFC2	59	c.175C>T	p.R59C		COSM932235	1	YES	0.935	No	
NDUFC2	119	c.355C>T	p.R119C		COSM325934	1	YES	0.796	No	
NDUFS1	45	c.133C>G	p.P45A		COSM719648	1	YES	0.449	No	
NDUFS1	52	c.155C>A	p.A52D		COSM209716	1	YES	0.877	No	
NDUFS1	80	c.239T>C	p.V80A		COSM1015302	1	YES	0.786	No	
NDUFS1	133	c.399G>T	p.Q133H		COSM719649	1	YES	0.606	No	
NDUFS1	244	c.730G>A	p.E244K		COSM719650	1	YES	0.632	No	
NDUFS1	257	c.770T>G	p.V257G		COSM418893	1	YES	0.705	No	
NDUFS1	261	c.782T>G	p.I261S		COSM209715	1	YES	0.776	No	
NDUFS1	270	c.808G>A	p.V270M		COSM209714	1	YES	0.768	No	
NDUFS1	274	c.822G>T	p.L274F		COSM168726	1	YES	0.471	No	
NDUFS1	285	c.854G>T	p.W285L		COSM1015299	1	YES	0.771	No	
NDUFS1	304	c.912G>T	p.E304D		COSM476798	1	YES	0.387	No	
NDUFS1	320	c.959A>T	p.E320V		COSM719651	1	YES	0.614	No	
NDUFS1	325	c.973C>A	p.R325S		COSM573224	1	YES	0.607	No	
NDUFS1	408	c.1223G>A	p.R408H		COSM1216928	1	YES	0.873	Yes	1 EUR
NDUFS1	438	c.1313T>G	p.L438R		COSM75584	1	YES	0.784	No	
NDUFS1	473	c.1417A>C	p.M473L		COSM573227	1	YES	0.537	No	
NDUFS1	483	c.1448G>T	p.R483I		COSM476797	1	YES	0.733	No	
NDUFS1	501	c.1502G>A	p.R501Q		COSM176567	1	YES	0.468	No	
NDUFS1	538	c.1613G>A	p.R538Q		COSM1216927	1	YES	0.516	No	
NDUFS1	560	c.1678T>A	p.L560M		COSM1015291	1	YES	0.601	No	
NDUFS1	609	c.1826C>A	p.A609E		COSM573230	1	YES	0.893	No	
NDUFS1	623	c.1868T>G	p.I623R		COSM215852	3	YES	0.891	No	
NDUFS1	696	c.2088G>T	p.M696I		COSM573231	1	YES	0.722	No	
NDUFS1	727	c.2181C>G	p.C727W		COSM719652	1	YES	0.429	No	
NDUFS2	158	c.474G>T	p.L158F		COSM463273	1	YES	0.777	No	
NDUFS2	179	c.536G>A	p.R179H		COSM174960	1	YES	0.834	No	
NDUFS2	246	c.737A>C	p.Q246P		COSM1159812	1	YES	0.424	No	
NDUFS2	256	c.766G>C	p.D256H		COSM211966	1	YES	0.605	No	
NDUFS2	269	c.806G>A	p.R269Q		COSM175692	1	YES	0.636	No	
NDUFS2	276	c.826G>T	p.G276W		COSM530173	1	YES	0.845	No	
NDUFS2	276	c.827G>T	p.G276V		COSM530172	1	YES	0.927	No	
NDUFS2	294	c.881G>T	p.R294L		COSM530171	1	YES	0.917	No	
NDUFS2	321	c.961G>T	p.G321C		COSM530170	1	YES	0.763	No	
NDUFS2	345	c.1033G>A	p.A345T		COSM898530	1	YES	0.403	No	

NDUFS2	393	c.1177C>T	p.P393S		COSM530169	1	YES	0.317	No	
NDUFS2	455	c.1363G>A	p.D455N		COSM424374	1	YES	0.947	No	
NDUFS3	63	c.188A>G	p.E63G		COSM1135189	1	YES	0.340	No	
NDUFS3	88	c.263T>A	p.I88N		COSM189979	1	YES	0.672	No	
NDUFS3	141	c.421A>G	p.I141V		COSM542634	1	YES	0.566	No	
NDUFS3	142	c.424C>T	p.R142C		COSM189980	1	YES	0.631	No	
NDUFS3	151	c.452C>T	p.T151M		COSM1177712	1	YES	0.515	No	
NDUFS4	52	c.155T>C	p.L52P		COSM482874	1	YES	0.435	No	
NDUFS4	83	c.247G>T	p.A83S		COSM1068700	1	YES	0.741	No	
NDUFS4	141	c.422A>C	p.N141T		COSM482875	1	YES	0.573	No	
NDUFS4	165	c.494C>A	p.S165Y		COSM172461	1	YES	0.507	No	
NDUFS4	172	c.514G>T	p.V172L		COSM1132150	3	YES	0.484	No	
NDUFS5	16	c.47G>A	p.R16Q		COSM1216929	1	YES	0.380	No	
NDUFS5	23	c.67G>T	p.G23C		COSM464575	1	YES	0.289	No	
NDUFS5	62	c.184G>T	p.D62Y		COSM262345	1	YES	0.799	No	
NDUFS5	75	c.223C>T	p.R75C		COSM171773	1	YES	0.690	No	
NDUFS6	83	c.247C>T	p.R83W		COSM178268	1	YES	0.582	No	
NDUFS6	93	c.277G>T	p.A93S		COSM1066947	1	YES	0.490	No	
NDUFS6	97	c.290C>A	p.P97Q		COSM591595	1	YES	0.927	No	
NDUFS6	109	c.325A>G	p.T109A		COSM301194	1	YES	0.260	No	
NDUFS6	121	c.362A>G	p.Q121R		COSM737416	1	YES	0.338	No	
NDUFS8	11	c.32G>A	p.R11Q		COSM690326	1	YES	0.281	No	
NDUFS8	13	c.38T>A	p.L13Q		COSM467314	1	YES	0.382	No	
NDUFS8	57	c.170G>T	p.R57L		COSM544996	2	YES	0.464	No	
NDUFS8	104	c.311A>G	p.Y104C		COSM1216930	1	YES	0.535	No	
NDUFS8	171	c.513T>G	p.F171L		COSM931176	1	YES	0.496	No	
NDUFV1	151	c.451G>A	p.A151T		COSM429726	1	YES	0.874	No	
NDUFV1	152	c.454C>A	p.R152S		COSM544667	1	YES	0.530	No	
NDUFV1	224	c.671G>T	p.R224L		COSM1127663	1	YES	0.703	No	
NDUFV1	237	c.709G>T	p.G237C		COSM140661	1	YES	0.886	No	
NDUFV1	256	c.767G>A	p.R256H		COSM545005	1	YES	0.650	No	
NDUFV1	269	c.806G>A	p.R269H		COSM194563	1	YES	0.412	No	
NDUFV1	307	c.919G>A	p.V307I		COSM931138	1	YES	0.534	No	
NDUFV1	321	c.961G>A	p.G321S		COSM931139	1	YES	0.823	No	
NDUFV1	368	c.1102G>A	p.A368T		COSM267012	1	YES	0.412	No	
NDUFV1	369	c.1106G>A	p.R369H		COSM690337	1	YES	0.592	No	

NDUFV1	449	c.1346G>A	p.R449Q		COSM1216931	1	YES	0.531	No	
NDUFV1	454	c.1361C>T	p.A454V		COSM690335	1	YES	0.366	No	
NDUFV2	120	c.359C>T	p.T120I		COSM710333	1	YES	0.700	No	
NDUFV2	131	c.391C>G	p.H131D		COSM438420	1	YES	0.791	No	
NDUFV2	134	c.401T>C	p.V134A		COSM710331	1	YES	0.826	No	
NDUFV2	214	c.640C>A	p.P214T		COSM710330	1	YES	0.346	No	
NDUFV3	105	c.313G>A	p.V105M		COSM725056	1	YES	0.118	No	
NDUFV3	120	c.358A>G	p.T120A		COSM71807	1	YES	0.201	No	
NDUFV3	337	c.1010C>T	p.P337L		COSM162861	1	YES	0.202	No	
NDUFV3	407	c.1219A>T	p.M407L		COSM1216933	1	YES	0.299	No	
NT5M	96	c.287G>T	p.W96L		COSM560001	1	YES	0.756	No	
NT5M	129	c.386G>T	p.C129F		COSM300617	1	YES	0.812	No	
NT5M	132	c.395C>G	p.P132R		COSM976105	1	YES	0.902	No	
OPA1	37	c.110C>T	p.S37L		COSM729922	1	YES	0.219	No	
OPA1	38	c.113G>A	p.R38Q		COSM276444	1	YES	0.430	No	
OPA1	71	c.211C>T	p.R71C		COSM1186478	1	YES	0.466	No	
OPA1	127	c.380C>T	p.P127L		COSM729921	1	YES	0.572	No	
OPA1	240	c.718C>G	p.Q240E	Q222E	COSM729919	1	YES	0.158	No	
OPA1	254	c.762C>G	p.S254R	S236R	COSM163086	1	YES	0.298	No	
OPA1	255	c.764C>T	p.T255M	T237M	COSM1042645	1	YES	0.199	No	
OPA1	289	c.865G>A	p.E289K	E271K	COSM420082	1	YES	0.351	No	
OPA1	404	c.1211A>T	p.D404V	D386V	COSM583133	1	YES	0.483	No	
OPA1	482	c.1446G>C	p.Q482H	Q464H	COSM729916	1	YES	0.408	No	
OPA1	513	c.1538A>G	p.H513R	H495R	COSM209289	1	YES	0.429	No	
OPA1	613	c.1837G>C	p.E613Q	E595Q	COSM420081	2	YES	0.254	No	
OPA1	663	c.1988T>C	p.L663P	L645P	COSM479865	1	YES	0.822	No	
OPA1	736	c.2208T>G	p.F736L	F718L	COSM257602	1	YES	0.449	No	
OPA1	774	c.2320G>A	p.E774K	E756K	COSM460826	1	YES	0.462	No	
OPA1	857	c.2569A>G	p.N857D	N839D	COSM269765	1	YES	0.473	No	
OPA1	938	c.2813T>C	p.I938T	I920T	COSM1218454	1	YES	0.462	No	
OPA1	952	c.2854C>A	p.Q952K	Q934K	COSM325999	1	YES	0.506	No	
OPA1	974	c.2920G>A	p.E974K	E956K	COSM1042655	1	YES	0.406	No	
OPA3	9	c.26C>T	p.A9V		COSM190928	1	YES	0.721	No	
PEO1	104	c.310A>T	p.I104F		COSM73879	1	YES	0.669	No	
PEO1	109	c.326G>A	p.G109D		COSM173465	1	YES	0.784	No	
PEO1	153	c.457G>A	p.E153K		COSM1159509	2	YES	0.547	No	

PEO1	229	c.685G>C	p.D229H		COSM213236	1	YES	0.440	No	
PEO1	233	c.698A>G	p.Y233C		COSM144796	1	YES	0.417	No	
PEO1	243	c.727G>A	p.A243T		COSM200073	1	YES	0.340	No	
PEO1	341	c.1022G>T	p.R341L		COSM536792	1	YES	0.393	No	
PEO1	343	c.1028T>C	p.L343P		COSM913997	1	YES	0.623	No	
PEO1	357	c.1070G>A	p.R357H		COSM1157856	1	YES	0.483	No	
PEO1	438	c.1314C>A	p.N438K		COSM159448	1	YES	0.577	No	
PEO1	473	c.1417C>T	p.H473Y		COSM465179	1	YES	0.333	No	
PEO1	488	c.1462T>C	p.F488L		COSM914001	1	YES	0.721	No	
PEO1	491	c.1471C>G	p.Q491E		COSM1188026	1	YES	0.466	No	
PEO1	495	c.1484G>T	p.R495M		COSM682483	1	YES	0.404	No	
PEO1	499	c.1495G>T	p.D499Y		COSM1188027	1	YES	0.516	No	
PEO1	540	c.1618G>T	p.G540W		COSM536791	1	YES	0.478	No	
PEO1	553	c.1657G>C	p.V553L		COSM301783	1	YES	0.474	No	
PEO1	615	c.1843G>A	p.G615S		COSM536790	1	YES	0.810	No	
PINK1	209	c.625C>T	p.P209S		COSM284026	1	YES	0.278	No	
PINK1	215	c.644C>T	p.P215L		COSM13351	1	YES	0.449	No	
PINK1	359	c.1076C>T	p.A359V		COSM276758	1	YES	0.489	No	
PINK1	394	c.1181T>A	p.I394N		COSM299977	1	YES	0.391	No	
PINK1	407	c.1219C>T	p.R407W		COSM903279	1	YES	0.686	No	
PINK1	409	c.1225G>C	p.G409R		COSM678819	1	YES	0.980	No	
PINK1	482	c.1444G>A	p.V482M		COSM72183	1	YES	0.632	No	
PINK1	504	c.1510G>A	p.A504T		COSM463872	1	YES	0.546	No	
POLG	241	c.722C>T	p.P241L		COSM241212	1	YES	0.357	No	
POLG	327	c.979A>C	p.K327Q		COSM288244	1	YES	0.214	No	
POLG	427	c.1281G>A	p.M427I		COSM197746	1	YES	0.603	No	
POLG	443	c.1328G>T	p.R443L		COSM702186	1	YES	0.331	No	
POLG	457	c.1370G>T	p.R457L		COSM556359	1	YES	0.396	No	
POLG	496	c.1488G>T	p.K496N		COSM434512	1	YES	0.377	No	
POLG	523	c.1569T>A	p.D523E		COSM1163104	1	YES	0.222	No	
POLG	546	c.1637G>A	p.R546H		COSM471216	1	YES	0.276	No	
POLG	661	c.1981C>G	p.L661V		COSM966307	1	YES	0.286	No	
POLG	676	c.2027C>T	p.A676V		COSM292274	1	YES	0.323	No	
POLG	709	c.2126G>T	p.R709L		COSM556360	1	YES	0.410	No	
POLG	797	c.2391G>C	p.M797I		COSM556361	1	YES	0.624	No	
POLG	807	c.2419C>T	p.R807C		COSM1221462	1	YES	0.931	No	

POLG	823	c.2467C>A	p.R823S		COSM556362	1	YES	0.456	No	
POLG	825	c.2473G>A	p.V825M		COSM72244	1	YES	0.312	No	
POLG	840	c.2519T>C	p.I840T		COSM556363	1	YES	0.758	No	
POLG	944	c.2830G>C	p.E944Q		COSM471215	1	YES	0.554	No	
POLG	1000	c.2998G>A	p.E1000K		COSM13897	1	YES	0.559	No	
POLG	1026	c.3076C>T	p.R1026C		COSM197744	1	YES	0.562	No	
POLG	1039	c.3117G>C	p.K1039N		COSM556364	1	YES	0.459	No	
POLG	1047	c.3140G>T	p.R1047L		COSM556365	1	YES	0.701	No	
POLG	1071	c.3211C>T	p.R1071C		COSM556366	2	YES	0.584	No	
POLG	1086	c.3257C>T	p.S1086L		COSM458937	1	YES	0.349	No	
POLG	1148	c.3443G>A	p.R1148H		COSM1162068	1	YES	0.767	No	
POLG	1217	c.3650C>T	p.A1217V		COSM284133	1	YES	0.297	No	
POLG2	6	c.16G>T	p.A6S		COSM707635	1	YES	0.229	No	
POLG2	12	c.36G>T	p.K12N		COSM296513	1	YES	0.335	No	
POLG2	26	c.76G>C	p.D26H		COSM417399	1	YES	0.220	No	
POLG2	34	c.101C>T	p.T34M		COSM40849	1	YES	0.183	No	
POLG2	272	c.814A>C	p.N272H		COSM707636	1	YES	0.409	No	
POLG2	283	c.848G>A	p.G283D		COSM982895	1	YES	0.407	No	
POLG2	314	c.942G>A	p.M314I		COSM982894	2	YES	0.580	No	
POLG2	328	c.983G>A	p.R328Q		COSM473201	1	YES	0.735	No	
POLG2	368	c.1103A>C	p.H368P		COSM1162024	1	YES	0.509	No	
POLG2	381	c.1141A>G	p.I381V		COSM473200	1	YES	0.468	No	
POLG2	442	c.1324T>A	p.L442M		COSM473199	1	YES	0.582	No	
POLRMT	89	c.266C>T	p.A89V		COSM267228	1	YES	0.285	No	
POLRMT	108	c.324G>C	p.Q108H		COSM459830	1	YES	0.226	No	
POLRMT	147	c.439C>A	p.P147T		COSM1002860	1	YES	0.191	No	
POLRMT	294	c.881C>T	p.P294L		COSM1221533	1	YES	0.663	No	
POLRMT	458	c.1372C>T	p.R458C		COSM1221532	1	YES	0.475	No	
POLRMT	786	c.2356G>A	p.A786T		COSM714021	1	YES	0.669	No	
POLRMT	826	c.2476G>C	p.E826Q		COSM88643	1	YES	0.331	No	
POLRMT	848	c.2542C>G	p.L848V		COSM459831	1	YES	0.801	No	
POLRMT	875	c.2623G>A	p.A875T		COSM1221531	1	YES	0.782	No	
POLRMT	958	c.2872G>A	p.G958S		COSM568191	1	YES	0.505	No	
POLRMT	971	c.2911G>A	p.A971T		COSM1002846	1	YES	0.514	No	
POLRMT	1029	c.3086C>T	p.S1029F		COSM714023	1	YES	0.853	No	
POLRMT	1136	c.3406G>A	p.A1136T		COSM1002837	1	YES	0.799	No	

SDHA	110	c.328G>T	p.A110S		COSM737284	1	YES	0.710	No	
SDHA	126	c.376A>C	p.T126P		COSM1067040	1	YES	0.914	No	
SDHA	176	c.528G>C	p.Q176H		COSM737283	1	YES	0.577	No	
SDHA	208	c.622T>C	p.S208P		COSM1067046	1	YES	0.756	No	
SDHA	229	c.686G>A	p.G229E		COSM1067048	1	YES	0.662	No	
SDHA	236	c.706G>A	p.A236T		COSM277194	1	YES	0.667	No	
SDHA	240	c.718G>C	p.E240Q		COSM247233	2	YES	0.255	No	
SDHA	248	c.743G>C	p.R248T		COSM290530	1	YES	0.622	No	
SDHA	331	c.991G>A	p.A331T		COSM284843	1	YES	0.736	Yes	1 ASN
SDHA	379	c.1135C>T	p.R379C		COSM267390	1	YES	0.769	No	
SDHA	379	c.1136G>T	p.R379L		COSM591868	1	YES	0.714	No	
SDHA	469	c.1405C>A	p.L469M		COSM591867	1	YES	0.366	No	
SDHA	554	c.1661G>A	p.R554Q		COSM738214	1	YES	0.642	No	
SDHA	583	c.1747G>C	p.E583Q		COSM591819	1	YES	0.464	No	
SDHA	584	c.1750G>A	p.A584T		COSM1067145	1	YES	0.469	No	
SDHA	585	c.1754G>A	p.R585Q		COSM1067147	1	YES	0.917	No	
SDHA	593	c.1778C>T	p.A593V		COSM177948	1	YES	0.665	No	
SDHA	658	c.1973C>A	p.P658Q		COSM591818	1	YES	0.740	No	
SDHB	33	c.98C>T	p.A33V		COSM899772	1	YES	0.369	No	
SDHB	63	c.187G>A	p.V63I		COSM530928	1	YES	0.472	No	
SDHB	94	c.281G>C	p.R94T		COSM677085	1	YES	0.733	No	
SDHB	163	c.488C>A	p.S163Y		COSM284844	1	YES	0.352	No	
SDHB	198	c.593G>A	p.S198N		COSM95234	1	YES	0.625	No	
SDHB	209	c.626C>A	p.P209H		COSM181960	1	YES	0.839	No	
SDHB	211	c.632T>C	p.V211A		COSM463435	1	YES	0.585	No	
SDHB	265	c.793G>C	p.E265Q		COSM458393	1	YES	0.320	No	
SDHC	11	c.31C>T	p.R11C		COSM414371	1	YES	0.691	No	
SDHD	45	c.134G>A	p.G45E		COSM540695	1	YES	0.732	No	
SDHD	76	c.227T>A	p.L76H		COSM466328	1	YES	0.811	No	
SDHD	117	c.350G>T	p.G117V		COSM284845	1	YES	0.903	No	
SDHD	120	c.359T>C	p.L120S		COSM1127911	1	YES	0.557	No	
SDHD	126	c.376G>T	p.A126S		COSM140674	1	YES	0.435	No	
SSBP1	50	c.149G>A	p.G50E		COSM137952	1	YES	0.403	No	
SSBP1	56	c.167T>G	p.I56R		COSM76594	1	YES	0.575	No	
SSBP1	58	c.172T>G	p.S58A		COSM1227625	1	YES	0.711	No	
SSBP1	74	c.221A>T	p.Q74L		COSM745329	1	YES	0.481	No	

SSBP1	84	c.250T>C	p.W84R		COSM205318	1	YES	0.875	No	
SSBP1	107	c.320G>A	p.R107Q		COSM205319	1	YES	0.536	No	
TFAM	105	c.314C>T	p.A105V		COSM271556	1	YES	0.699	No	
TFAM	114	c.341T>G	p.I114R		COSM684830	1	YES	0.814	No	
TFAM	130	c.388G>A	p.E130K		COSM1187945	1	YES	0.402	No	
TFAM	143	c.429G>A	p.M143I		COSM1128029	1	YES	0.263	No	
TFAM	173	c.517G>T	p.A173S		COSM684829	1	YES	0.466	No	
TFAM	178	c.533C>A	p.P178Q		COSM465787	1	YES	0.699	No	
TK2	84	c.251A>G	p.D84G	D42G	COSM1229330	1	YES	0.208	No	
TK2	240	c.719G>T	p.R240M	R198M	COSM703937	1	YES	0.668	No	
TK2	243	c.729G>T	p.E243D	E201D	COSM174046	1	YES	0.853	No	
UCP1	7	c.20C>T	p.S7L		COSM732534	1	YES	0.319	No	
UCP1	68	c.203C>A	p.T68K		COSM326812	1	YES	0.421	No	
UCP1	74	c.221T>A	p.L74H		COSM732535	1	YES	0.794	No	
UCP1	92	c.274A>G	p.R92G		COSM291092	1	YES	0.878	No	
UCP1	122	c.365C>T	p.T122M		COSM447414	1	YES	0.544	No	
UCP1	208	c.622T>A	p.L208I		COSM480899	1	YES	0.530	No	
UCP1	289	c.865T>C	p.F289L		COSM76940	1	YES	0.663	No	
UCP2	27	c.79G>A	p.A27T		COSM195855	1	YES	0.840	No	
UCP2	71	c.212G>A	p.R71H		COSM1231655	1	YES	0.701	Yes	1 AFR 1 ASN
UCP2	133	c.397G>T	p.V133L		COSM690738	1	YES	0.619	No	
UCP2	285	c.853G>A	p.V285M		COSM1231654	1	YES	0.717	No	
UCP2	289	c.865G>A	p.V289I		COSM1231656	1	YES	0.628	No	
UCP3	70	c.209G>A	p.R70Q		COSM690735	1	YES	0.769	Yes	1 AFR 1 ASN
UCP3	87	c.260G>A	p.R87H		COSM1231658	1	YES	0.868	No	
UCP3	89	c.267G>A	p.M89I		COSM690736	1	YES	0.535	No	
UCP3	144	c.431T>G	p.F144C		COSM690737	1	YES	0.791	No	
UCP3	152	c.455C>T	p.P152L		COSM136851	1	YES	0.394	No	
UCP3	161	c.481G>T	p.G161W		COSM303512	1	YES	0.737	No	
UCP3	201	c.602A>G	p.D201G		COSM221548	2	YES	0.737	No	
UCP3	299	c.896G>T	p.R299L		COSM545046	1	YES	0.592	No	
UQCR10	5	c.14C>A	p.T5K		COSM166873	1	YES	0.251	No	
UQCR11	35	c.103G>A	p.A35T		COSM564985	1	YES	0.531	No	
UQCR11	38	c.113G>T	p.W38L		COSM564986	1	YES	0.686	No	
UQCR11	55	c.163G>C	p.D55H		COSM78749	1	YES	0.537	No	
UQCRB	3	c.8G>T	p.G3V		COSM606751	1	YES	0.177	No	

UQCRB	5	c.14A>G	p.Q5R		COSM606752	1	YES	0.380	No	
UQCRB	6	c.17C>G	p.A6G		COSM78750	1	YES	0.456	No	
UQCRB	100	c.298C>T	p.R100W		COSM752431	1	YES	0.606	Yes	1 EUR
UQCRB	111	c.332A>C	p.K111T		COSM198997	1	YES	0.300	No	
UQCRC1	82	c.244G>A	p.E82K		COSM300211	1	YES	0.904	No	
UQCRC1	94	c.282G>T	p.E94D		COSM1045890	1	YES	0.934	No	
UQCRC1	152	c.456G>T	p.Q152H		COSM1186285	1	YES	0.602	No	
UQCRC1	175	c.525T>G	p.N175K		COSM1231860	1	YES	0.533	No	
UQCRC1	179	c.537G>T	p.M179I		COSM140449	1	YES	0.540	No	
UQCRC1	343	c.1028C>T	p.T343I		COSM1231859	1	YES	0.775	No	
UQCRC1	363	c.1089G>A	p.M363I		COSM1131417	1	YES	0.298	No	
UQCRC1	380	c.1139G>T	p.C380F		COSM1179517	1	YES	0.702	No	
UQCRC1	422	c.1265G>A	p.R422H		COSM242183	2	YES	0.622	No	
UQCRC1	472	c.1414C>T	p.R472C		COSM1045886	1	YES	0.739	No	
UQCRC1	479	c.1435C>T	p.R479C		COSM294933	1	YES	0.711	No	
UQCRC2	101	c.301C>A	p.R101S		COSM557207	1	YES	0.715	No	
UQCRC2	143	c.427G>A	p.A143T		COSM1231862	1	YES	0.455	No	
UQCRC2	147	c.439C>T	p.R147C		COSM167876	1	YES	0.662	No	
UQCRC2	208	c.623T>A	p.F208Y		COSM32283	1	YES	0.743	No	
UQCRC2	230	c.689T>C	p.L230P		COSM242184	1	YES	0.907	No	
UQCRC2	248	c.742G>T	p.G248C		COSM968516	1	YES	0.540	No	
UQCRC2	303	c.908G>A	p.S303N		COSM702316	1	YES	0.381	No	
UQCRC2	353	c.1057G>T	p.A353S		COSM286363	1	YES	0.675	No	
UQCRC2	448	c.1343C>A	p.P448H		COSM557206	1	YES	0.781	No	
UQCRFS1	83	c.247A>G	p.I83V		COSM474494	4	YES	0.544	No	
UQCRFS1	92	c.275G>A	p.R92H		COSM1231863	1	YES	0.796	No	
UQCRFS1	108	c.322G>A	p.E108K		COSM710562	1	YES	0.633	No	
UQCRFS1	157	c.470C>G	p.S157C		COSM565706	1	YES	0.586	No	
UQCRFS1	169	c.506G>T	p.W169L		COSM565707	1	YES	0.825	No	
UQCRFS1	198	c.593C>A	p.P198Q		COSM418347	1	YES	0.616	No	
UQCRFS1	249	c.747C>G	p.I249M		COSM710563	1	YES	0.707	No	
UQCRFS1	265	c.793T>C	p.F265L		COSM994352	1	YES	0.605	No	
UQCRFS1	272	c.815T>C	p.I272T		COSM286364	1	YES	0.454	No	
UQCRH	29	c.86C>T	p.P29L		COSM139285	1	YES	0.587	No	
UQCRH	68	c.203C>T	p.T68M		COSM298165	1	YES	0.482	No	
UQCRQ	65	c.193G>C	p.E65Q		COSM589264	2	YES	0.272	No	