SNP	Gene	CHR	Chromosomal Position	Residue WT > NS	Amino Acid Position	Minor Allele	Cases MAF	Controls MAF	Major Allele	SIFT	Poly Phen prediction
rs10018786	POLN	4	2162255	M/L	310	G	0.055	0.1073	T	no prediction	benign
rs1042714	ADRB2	5	148186666	Q/E	27	G	0.4949	0.4031	C	Tolerated	benign
rs1044141	STK17A	7	43437520	K/E	361	A	0.298	0.2266	G	Tolerated	benign
rs10516782/rs2230600	PTPN13	4	88048177	I/M	1331/1503/1522/1527	G	0.1134	0.2042	A	no prediction	benign
rs1061472	ATP7B	13	51422489	K/R	669/831	A	0.5	0.4339	G	Tolerated	possibly damaging/benign
rs12022378	DCLRE1B	1	114160431	H/Y	60	T	0.2323	0.1536	C	no prediction	benign
rs13815	MT	22	41853812	A/G	302	C	0.2576	0.3679	G	Tolerated	benign
rs16879334	MTRR	5	7944506	P/R	449/476	G	0	0.02835	C	no prediction	probably damaging
rs17112809	MMS19L	10	99215836	V/I	525	T	0.025	0.002604	C	no prediction	benign
rs17572019	PPARGC1B	5	149192664	V/I	278	A	0.06111	0.1278	G	no prediction	benign
rs1799999	PPP1R3A	7	113112385	D/Y	904	T	0.06	0.1289	G	damaging	probably damaging
rs1801249	ATP7B	13	51413355	V/A	932/1139	T	0.5213	0.4317	C	Tolerated	benign
rs1866389	THBS4	5	79397021	A/P	386	G	0.26	0.1958	C	Tolerated	benign
rs2108622	CYP4F2	19	15851431	M/V	433	T	0.31	0.2345	C	damaging	benign
rs2140516	SLC13A1	7	122403185	N/S	173	C	0.3586	0.2708	T	Tolerated	benign
rs216321	VWF	12	6014245	Q/R	851	T	0.07732	0.1383	C	Tolerated	benign
rs2229113	IL10RA	11	117374880	G/R	351	A	0.275	0.3516	G	no prediction	probably damaging
rs2269429	TNXB	6	32137161	G/S	2554	A	0.1263	0.075	G	damaging	benign
rs2281891	CYP2C18	10	96483048	T/M	384	A	0.095	0.1605	G	damaging	probably damaging
rs2287622	ABCB11	2	169655835	A/V	444	T	0.3367	0.4197	C	Tolerated	benign
rs2302524	PLAUR	19	48848312	K/R	174/219	C	0.234	0.1603	T	Tolerated	benign
rs2304821	PTPRB	12	69249886	M/T	939	A	0.1421	0.08639	G	Tolerated	benign
rs299295	HMMR	5	162842294	A/V	468/483	T	0.28	0.1979	C	Tolerated	benign
rs3130618	BAT4	6	31740113	R/L	40	A	0.148	0.2266	C	Tolerated	probably damaging
rs3736265	PPARGC1A	4	23490976	T/M	611	A	0.025	0.09585	G	damaging	benign
rs3803036	PTPRR	12	69425931	R/K	314	A	0.18	0.2539	G	Tolerated	benign
rs4151060	BTRC	10	103288089	A/S	506/542	T	0.1	0.04922	G	Tolerated	benign
rs4253211	ERCC6	10	50348323	R/P	1229	C	0.1616	0.09896	G	Tolerated	benign
rs4647201	EPM2AIP1	3	37008495	A/S	359	A	0.03571	0.005263	C	no prediction	benign
rs506504	CHEK1	11	125030405	I/V	470	T	0.06633	0.02865	C	Tolerated	benign
rs527221	DMPK	19	50967816	L/V	422	C	0.06122	0.1263	G	Tolerated	benign
rs5760	TBXAS1	7	139160106	V/G	390	T	0.005682	0.03141	G	Tolerated	probably damaging
rs578430	MUSK	9	110642698	L/V	829	T	0.06061	0.02577	G	Tolerated	benign
rs5882	CETP	16	55573593	E/A	209	C	0.07576	0.03665	A	Tolerated	benign
rs628031	SLC22A1	6	160531256	V/M	408	A	0.4583	0.3729	G	Tolerated	benign
rs679899	APOB	2	21162566	V/A	618	A	0.3939	0.4895	G	Tolerated	benign
rs7011	CINP	14	101884795	H/R	164	T	0.3081	0.2266	C	Tolerated	benign
rs732774	ATP7B	13	51421809	R/K	951	G	0.5155	0.4339	A	Tolerated	benign
rs753381	PLCG1	20	39230879	Q/E	337	C	0.399	0.3237	G	Tolerated	benign
rs7732671	PPARGC1B	5	149192436	A/P	202	C	0.075	0.1392	G	no prediction	benign
rs8191613	NEIL2	8	11674685	R/Q	102	A	0	0.03109	G	no prediction	benign
rs8191664	NEIL2	8	11680962	R/L	256	T	0	0.02332	G	no prediction	benign
rs882709	SETX	9	132234560	A/G	659	G	0.035	0.07772	C	Tolerated	benign
rs956868	WNK1	12	861173	T/P	1055	A	0.08081	0.1492	C	Tolerated	benign
rs9808232	ROCK2	2	11309718	T/N	430	G	0.5	0.4404	T	no prediction	benign
rs9890721	MYCBPAP	17	45958502	R/W	688	C	0.5	0.4136	T	no prediction	probably damaging