

Table S3. The list of variants that have a minor allele frequency less than 5% in 1000 Genomes or ESP-6500

CHR	Start	End	REF	ALT	Filter	QUAL	Gene	Impact	Father	Motchr	Son	Daughter	gnomAD	1K Genomes	ExAC	ESP 6500	SIFT	CADD	DANN	Polyphen2	FATHMM-MKL	M-CAP	
chr1	69885	69986	G	C	VQSRTrancheSNP99.90to100.00	69.02999878	OR4F5	missense_variant	G/G	G/C	G/G	G/G	NA	NA	NA	NA	Tolerated	19.21	Tolerated	Damaging	Tolerated	Tolerated	
chr1	1333636	1333637	C	T	None	6468.899902	CNNL2	missense_variant	C/C	C/T	C/C	C/T	NA	NA	NA	NA	Tolerated	22.7	Tolerated	Tolerated	NA	Damaging	
chr1	2303346	2303348	CA	CAA	None	1079.900024	MORRN1	splice_region_variant	CA/	CA/	CA/CAA	CA/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr1	11718659	11718660	C	T	None	1701.329956	FBXO44	missense_variant	C/C	C/C	C/C	C/T	3.2423E-05	NA	0.00004119	NA	Damaging	25.3	Damaging	Damaging	NA	Tolerated	
chr1	13036586	13036587	C	T	None	37993.39844	PRAMEF22	missense_variant	/	T/T	T/T	T/T	NA	NA	NA	NA	NA	0.291	NA	NA	NA	NA	
chr1	13330477	13330478	A	T	None	69.47000122	PRAMEF3	missense_variant	/	/	T/T	T/T	NA	NA	NA	NA	Tolerated	7.534	NA	Tolerated	NA	NA	
chr1	13368671	13368672	G	A	None	79.79000092	PRAMEF5	missense_variant	G/G	/	G/G	A/A	NA	NA	NA	NA	Tolerated	4.253	Tolerated	Tolerated	Tolerated	Tolerated	
chr1	16259470	16259471	G	T	None	10773.90039	SPEN	missense_variant	G/G	G/T	G/T	G/G	NA	NA	NA	NA	Damaging_low_confidence	16.55	Tolerated	Tolerated	Damaging	Tolerated	
chr1	20209062	20209063	G	T	None	2583.899902	OTUD3	missense_variant	G/G	G/T	G/T	G/G	3.2319E-05	NA	NA	NA	Tolerated	22	Tolerated	Tolerated	Damaging	Damaging	
chr1	23279828	23279829	C	T	None	6414.899902	LACTBL1	missense_variant	C/T	C/C	C/T	C/C	3.247E-05	NA	NA	NA	Tolerated	25.7	Tolerated	Damaging	Damaging	Damaging	
chr1	27176839	27176840	G	A	None	8833.900391	ZDHHCH8	missense_variant	G/A	G/G	G/A	G/G	3.231E-05	NA	NA	NA	Damaging	32	Damaging	Damaging	NA	Damaging	
chr1	28817531	28817532	T	C	None	8433.900391	PHACTR4	splice_region_variant	T/C	T/C	T/T	T/C	NA	NA	NA	NA	NA	4.175	NA	NA	NA	NA	
chr1	33992839	33992840	C	T	None	3562.330078	CSMD2	missense_variant	C/C	C/C	C/C	C/T	NA	NA	NA	NA	Tolerated	22.7	Tolerated	Tolerated	NA	Damaging	
chr1	52729424	52729425	T	TC	None	2067.899902	ZFYVE9	splice_region_variant	T/	T/TC	T/TC	T/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr1	119427452	119427453	G	A	None	5630.330078	TBX15	missense_variant	G/G	G/G	G/G	G/A	NA	NA	NA	NA	Tolerated_low_confidence	20.7	Tolerated	Tolerated	NA	Damaging	
chr1	145522713	145522714	T	C	None	8450.900391	PBX11B	missense_variant	T/T	T/C	T/C	T/C	NA	NA	NA	NA	Tolerated	13.54	NA	Tolerated	NA	Tolerated	
chr1	146418520	146418521	G	A	VQSRTrancheSNP99.90to100.00	270.3900146	NBPFI2	missense_variant	G/A	G/A	G/A	G/A	NA	NA	NA	NA	NA	0.002	NA	NA	NA	NA	
chr1	151811308	151811312	TA	T	None	6351.859863	C2CD4D	nservative_inframe_deleti	TA/GA	TA/GA	TA/GA	TA/GA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr1	162824892	162824893	G	T	None	12980.90039	C1orf110	missense_variant	G/T	G/G	G/G	G/T	NA	NA	NA	NA	Tolerated	3.795	Tolerated	Tolerated	Tolerated	Tolerated	
chr1	214826809	214826812	CTT	C	None	11838.40039	CENPF	splice_region_variant	C/	/	/	C/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr1	218696796	218696797	G	A	None	2889.899902	C1orf143	splice_region_variant	G/G	G/A	G/A	G/G	NA	NA	NA	NA	NA	0.128	NA	NA	NA	NA	
chr1	225569248	225569249	T	A	None	3684.899902	DNAH14	missense_variant	T/T	T/A	T/A	T/T	NA	NA	NA	NA	Tolerated	11.36	Tolerated	Tolerated	NA	Tolerated	
chr1	234601455	234601457	TA	TAA	None	1547.939941	TARBP1	splice_region_variant	TA/TAA	TA/TAA	TA/TAA	TA/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr1	235659620	235659622	GA	GAA	None	1783.939941	B3GALNT2	splice_region_variant	GA/GAA	GA/	GA/GAA	GA/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr2	33749622	33749623	A	G	None	4374.899902	RASGRP3	splice_region_variant	A/G	A/A	A/G	A/A	NA	NA	NA	NA	NA	1.177	NA	NA	NA	NA	
chr2	44078721	44078722	G	C	None	7801.899902	ABCG8	splice_acceptor_variant	G/G	G/C	G/G	G/C	NA	NA	NA	NA	NA	33	NA	NA	NA	NA	
chr2	44545233	44545235	GT	GTT	None	4163.859863	SLC3A1	splice_region_variant	GT/GTT	/GTT	/GTT	GT/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr2	67630540	67630541	A	C	None	5467.899902	ETAA1	missense_variant	A/G	A/A	A/A	A/C	NA	NA	NA	NA	Tolerated	0.095	Tolerated	Tolerated	Tolerated	Tolerated	
chr2	90458537	90458538	T	C	VQSRTrancheSNP99.90to100.00	68621.89844	CH17-132F21.1	missense_variant	T/C	T/C	T/C	T/C	NA	NA	NA	NA	NA	15.3	NA	NA	NA	NA	
chr2	97851072	97851074	GC	G	VQSRTrancheINDEL99.00to99.9C	4557.899902	ANKRD36	frameshift_variant	GC/G	GC/G	GC/G	GC/G	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr2	97851077	97851078	A	AG	VQSRTrancheINDEL99.00to99.9C	4452.899902	ANKRD36	frameshift_variant	A/AG	A/AG	A/AG	A/AG	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr2	97851081	97851086	GTAAT	G	VQSRTrancheINDEL99.00to99.9C	4538.899902	ANKRD36	splice_region_variant	GTAAT/G	GTAAT/G	GTAAT/G	GTAAT/G	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr2	97909718	97909719	A	G	VQSRTrancheSNP99.90to100.00	11142.90039	ANKRD36	missense_variant	A/G	A/G	A/G	A/G	NA	NA	NA	NA	Tolerated	2.083	Tolerated	Tolerated	NA	Tolerated	
chr2	99634755	99634756	A	G	None	5426.899902	TSGA10	missense_variant	A/A	A/G	A/G	A/A	NA	NA	NA	NA	Tolerated	17.71	Tolerated	Tolerated	NA	Damaging	
chr2	105472229	105472230	G	A	None	3826.899902	POU3F3	missense_variant	G/G	G/A	G/A	G/G	NA	NA	NA	NA	Tolerated_low_confidence	21.3	Tolerated	Damaging	Damaging	Damaging	
chr2	111886179	111886182	CTT	CT	None	2349.899902	BCL2L11	splice_region_variant	CTT/	CTT/CT	CTT/CT	CTT/CT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr2	113996646	113996647	C	CTT	None	13315.2998	PAX8-AS1	splice_region_variant	/CTT	/CTT	/CTT	C/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr2	128615661	128615662	C	T	None	8881.900391	POLR2D	missense_variant	C/T	C/C	C/C	C/T	NA	NA	NA	NA	NA	14.91	NA	NA	NA	NA	
chr2	160884741	160884742	A	T	None	2970.899902	PLA2R1	missense_variant	A/T	A/A	A/T	A/A	NA	NA	NA	NA	Tolerated	13.13	Tolerated	Tolerated	NA	Tolerated	
chr2	165657062	165657063	T	C	None	3164.899902	COBLL1	missense_variant	T/C	T/T	T/C	T/T	NA	NA	NA	NA	Tolerated_low_confidence	10.43	Tolerated	Tolerated	Tolerated	Tolerated	
chr2	202139641	202139642	C	T	None	2281.330078	CASP8	missense_variant	C/C	C/C	C/T	C/C	NA	NA	NA	NA	Tolerated	9.429	Tolerated	Tolerated	NA	Tolerated	
chr2	202359264	202359265	G	T	None	5776.899902	ALS2CR11	missense_variant	G/T	G/T	G/G	G/T	NA	NA	NA	NA	NA	0.005	NA	NA	NA	NA	
chr2	210560008	210560009	G	A	None	3897.330078	MAP2	missense_variant	G/G	G/G	G/G	G/A	NA	NA	NA	NA	NA	27	NA	NA	NA	NA	
chr2	230377592	230377593	A	C	None	7202.899902	DNER	missense_variant	A/C	A/A	A/A	A/C	NA	NA	NA	NA	Damaging	22.2	Tolerated	Tolerated	Damaging	Damaging	
chr2	233998683	233998684	G	A	None	7427.899902	INPP5D	splice_region_variant	G/A	G/G	G/A	G/G	NA	NA	NA	NA	NA	1.768	NA	NA	NA	NA	
chr3	4358087	4358088	C	T	None	2550.899902	SETMAR	missense_variant	C/T	C/C	C/C	C/T	NA	NA	NA	NA	Tolerated	20.6	Tolerated	Tolerated	NA	Tolerated	
chr3	35763277	35763278	G	T	None	3526.330078	ARPP21	missense_variant	G/G	G/G	G/T	G/G	NA	NA	NA	NA	Damaging	31	Damaging	Damaging	NA	Damaging	
chr3	50313047	50313048	T	C	None	34624.89844	SEMA3B	splice_donor_variant	T/C	T/C	T/T	T/C	NA	NA	NA	NA	NA	26.7	NA	NA	NA	NA	
chr3	52474424	52474425	C	T	None	11603.90039	SEMA3G	missense_variant	C/T	C/C	C/C	C/T	NA	NA	NA	NA	Damaging	15.68	Tolerated	Tolerated	Damaging	Tolerated	
chr3	63898303	63898304	G	C	None	1007.900024	ATXN7	missense_variant	G/G	G/C	G/C	G/G	NA	NA	NA	NA	Damaging_low_confidence	22.3	Tolerated	Tolerated	NA	Damaging	
chr3	123332874	123332875	GTAAT	G	VQSRTrancheSNP99.90to100.00	11142.90039	ANKRD36	missense_variant	A/G	A/G	A/G	A/G	NA	NA	NA	NA	Tolerated	2.083	Tolerated	Tolerated	NA	Tolerated	
chr3	130308809	130308810	T	A	None	1948.329956	COL6A6	splice_region_variant	T/T	T/T	T/A	T/T	NA	NA	NA	NA	NA	7.894	NA	NA	NA	NA	
chr3	143708519	143708520	C	T	None	10628.90039	C3orf58	missense_variant	C/T	C/T	C/C	C/T	3.2283E-05	NA	NA	NA	NA	Tolerated	23.4	Tolerated	Tolerated	NA	Damaging
chr3	176752010	176752011	G	T	None	1656.900024	TBL1XR1	missense_variant	G/T	G/G	G/G	G/T	NA	NA	NA	NA	Damaging	26.9	Damaging	Damaging	NA	Damaging	
chr3	184542692	184542694	AT	ATT	VQSRTrancheSNP99.90to100.00	1439.900024	VP58	splice_region_variant	AT/ATT	AT/ATT	AT/ATT	AT/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr4	9245670	9245671	T	C	None	8843.94043	USP17L17	missense_variant	T/C	T/C	T/C	T/C	NA	NA	NA	NA	Tolerated	13.93	Tolerated	Damaging	NA	Tolerated	
chr4	37448269	37448270	T	G	None	4915.899902	KIAA1239	missense_variant	T/G	T/T	T/T	T/G	3.23E-05	NA	NA	NA	Tolerated	21.7	Tolerated	Tolerated	Damaging	Tolerated	
chr4	48502241	48502242	A	G	None	2566.899902	FRYL	splice_region_variant	A/G	A/A	A/A	A/G	NA	NA	NA	NA	NA	16.54	NA	NA	NA	NA	
chr4	77662895	77662896	C	A	None	4588.330078	SHROOM3	missense_variant	C/C	C/C	C/A	C/C	NA	NA	NA	NA	Tolerated	0.242	Tolerated	Tolerated	Tolerated	Tolerated	
chr4	90170407	90170408	G	A	None	6036.330078	GPRIN3	missense_variant	G/G	G/G	G/A	G/G	NA	NA	NA	NA	Tolerated	0.001	Tolerated	Tolerated	NA	Tolerated	
chr4	100571948	100571949	A	G	None	14784.90039	RP11-766F14.2	missense_variant	A/G	A/A	A/A	A/G	NA	NA	NA	NA	NA	0.807	Tolerated	NA	Tolerated	Tolerated	
chr4	103826756	103826757	T	C	None	2212.939941	SLC9B1	missense_variant	T/C	T/C	T/C	T/C	NA	NA	NA	NA	Tolerated	15.06	Tolerated	Tolerated	NA	Damaging	
chr4	106682152	106682155	ATT	AT	None	1005.070007	GSTCD	splice_region_variant	ATT/	/AT	ATT/	ATT/	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr4	154624270	154624271	A	G	None	8120.899902	TLR2	missense_variant	A/G	A/G	A/G	A/A	NA	NA	NA	NA	Damaging	26.3	Damaging	Damaging	Damaging	Damaging	
chr4	159573033	159573034	C	A	None	2301.330078	RFXP1	missense_variant	C/C	C/C	C/A	C/C	NA	NA	NA	NA	Tolerated	23.1	Tolerated	Tolerated	NA	Damaging	
chr4	183717897	183717898	G	C	None	3965.899902	TENM3	missense_variant	G/C	G/G	G/C	G/G	NA	NA	NA	NA	Tolerated	17.64	Tolerated	Tolerated	NA	Damaging	
chr4	184114861	184114862	G	C	None	1606.900024	VWVC2	splice_donor_variant	G/G	G/C	G/C	G/G	NA	NA	NA	NA	NA	34	NA	NA	NA	NA	
chr5	140557	140																					

chr8	11163694	11163695	C	T	None	3375.899902	MTMR9	splice_region_variant	C/T	C/T	C/T	C/C	NA	NA	NA	NA	NA	9.274	NA	NA	NA	NA	
chr8	11970340	11970341	A	G	VQSRTrancheSNP99.90to100.00	359.1700134	ZNF705D	missense_variant	A/A	G/G	A/A	A/G	NA	NA	NA	NA	Tolerated	14.35	Tolerated	Tolerated	NA	Tolerated	
chr8	11995836	11995837	G	A	None	6194.899902	USP17L2	missense_variant	G/G	G/A	G/G	G/A	NA	NA	NA	NA	NA	14.93	NA	NA	NA	NA	
chr8	21956447	21956452	TCCTC	T	None	24560.90039	FAM160B2	splice_region_variant	TCCTC/TCCTC	TCCTC/T	TCCTC/TCCTC	TCCTC/T	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr8	37418148	37418149	G	T	None	6593.899902	RP11-150012.5	splice_region_variant	G/T	G/T	G/T	G/G	NA	NA	NA	NA	NA	5.817	NA	NA	NA	NA	
chr8	38964656	38964657	C	G	None	1166.900024	ADAM32	missense_variant	C/C	C/G	C/C	C/G	NA	NA	NA	NA	NA	0.957	NA	NA	NA	NA	
chr8	43046661	43046662	C	T	None	13731.90039	HGSNAT	stop_gained	C/T	C/T	C/T	C/C	NA	NA	NA	NA	NA	37	Damaging	NA	Damaging	NA	
chr8	48875546	48875547	C	T	None	3116.899902	MCM4	missense_variant	C/T	C/C	C/C	C/T	NA	NA	NA	NA	NA	25.2	NA	NA	NA	NA	
chr8	86376346	86376347	G	A	None	6730.899902	CA2	splice_region_variant	G/G	G/A	G/G	G/A	NA	NA	NA	NA	NA	20.7	NA	NA	NA	NA	
chr8	86575123	86575124	G	C	VQSRTrancheSNP99.90to100.00	3226.899902	REXO1L1P	missense_variant	G/C	C/C	G/C	G/C	NA	NA	NA	NA	Damaging	8.256	NA	Tolerated	NA	NA	
chr8	86575184	86575185	C	T	None	1348.900024	REXO1L1P	missense_variant	C/T	C/T	C/T	C/C	NA	NA	NA	NA	Tolerated_low_confidence	0.002	NA	Tolerated	NA	NA	
chr8	93898862	93898863	T	C	None	2411.330078	TRIQR	missense_variant	T/T	T/T	T/C	T/T	NA	NA	NA	NA	Tolerated_low_confidence	12	Tolerated	Tolerated	Tolerated	Tolerated	
chr8	95835357	95835358	G	A	None	16825.90039	INTS8	missense_variant	G/A	G/G	G/G	G/A	NA	NA	NA	NA	NA	11.73	NA	NA	NA	NA	
chr8	104337664	104337665	C	A	None	4960.899902	FZD6	missense_variant	C/A	C/C	C/C	C/A	NA	NA	NA	NA	Tolerated	19.92	Tolerated	Tolerated	NA	Damaging	
chr8	126443358	126443359	C	A	None	1822.900024	TRIB1	missense_variant	C/A	C/C	C/C	C/A	NA	NA	NA	NA	NA	15.96	NA	NA	NA	NA	
chr8	144801558	144801559	G	A	None	3255.330078	MAPK15	missense_variant	G/G	G/G	G/A	G/G	3.2333E-05	NA	NA	NA	NA	Damaging	28	Damaging	Damaging	NA	Damaging
chr9	17858	17859	A	G	None	838	XXYac-YRM2039.2	splice_region_variant	G/G	G/G	A/A	G/G	NA	NA	NA	NA	NA	7.455	NA	NA	NA	NA	
chr9	5968218	5968219	C	T	None	3935.899902	KIAA2026	missense_variant	C/C	C/T	C/T	C/C	NA	NA	NA	NA	Tolerated	16.21	Tolerated	Tolerated	Tolerated	Tolerated	
chr9	35313929	35313930	C	T	None	2759.899902	UNC13B	stop_gained	C/C	C/T	C/T	C/T	NA	NA	NA	NA	NA	37	Damaging	NA	Damaging	NA	
chr9	36263172	36263174	CT	CTT	None	2256.899902	CLTA	splice_region_variant	CT/.	CT/CTT	CT/CTT	CT/CTT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr9	40704071	40704072	C	A	VQSRTrancheSNP99.90to100.00	889.3300171	SPATA31A3	missense_variant	C/C	C/C	C/C	C/A	NA	NA	NA	NA	Damaging	13.31	Tolerated	Damaging	Tolerated	Tolerated	
chr9	43816629	43816630	C	CT	VQSRTrancheINDEL99.00to99.99	901.8599854	CNTNAP3B	splice_region_variant	C/CT	C/CT	C/CT	C/C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr9	43905762	43905763	C	T	None	38.34000015	CNTNAP3B	missense_variant	C/C	C/C	C/T	C/C	NA	NA	NA	NA	Damaging	22.7	NA	Damaging	NA	NA	
chr9	43915532	43915533	G	T	VQSRTrancheSNP99.90to100.00	44.91999817	CNTNAP3B	missense_variant	G/G	G/T	G/G	G/T	NA	NA	NA	NA	Damaging	16.69	NA	Damaging	NA	NA	
chr9	43915556	43915557	C	T	VQSRTrancheSNP99.90to100.00	736.9000244	CNTNAP3B	missense_variant	C/T	C/T	C/C	C/T	NA	NA	NA	NA	Damaging	13.68	NA	Tolerated	NA	NA	
chr9	65505910	65505911	C	T	None	60.54000092	SPATA31A7	missense_variant	C/C	C/T	C/T	C/C	NA	NA	NA	NA	Tolerated	0.194	NA	Tolerated	NA	NA	
chr9	69421982	69421983	G	C	VQSRTrancheSNP99.90to100.00	111.7699966	ANKRD20A4	missense_variant	G/G	G/C	G/G	G/C	NA	NA	NA	NA	Tolerated	0.268	Tolerated	Tolerated	Tolerated	Tolerated	
chr9	79928966	79928967	A	T	None	4093.899902	VPS13A	missense_variant	A/T	A/T	A/A	A/T	NA	NA	NA	NA	Tolerated	21.4	Damaging	Damaging	Damaging	Tolerated	
chr9	79936559	79936560	A	G	None	5788.899902	VPS13A	missense_variant	A/A	A/G	A/G	A/A	NA	NA	NA	NA	Tolerated	15.3	Damaging	Tolerated	Damaging	Tolerated	
chr9	80043849	80043850	G	T	None	2286.899902	GNA14	missense_variant	G/G	G/T	G/T	G/G	NA	NA	NA	NA	Damaging	25.9	Damaging	Damaging	Damaging	Damaging	
chr9	87342672	87342673	A	G	None	7871.899902	NTRK2	missense_variant	A/G	A/G	A/A	A/G	NA	NA	NA	NA	Tolerated	22.1	Tolerated	Tolerated	NA	Damaging	
chr9	95526791	95526792	T	C	None	9749.900391	BICD2	missense_variant	T/C	T/C	T/T	T/C	NA	NA	NA	NA	Damaging	24.6	Tolerated	Tolerated	NA	Damaging	
chr9	135117355	135117356	T	A	None	1968.329956	NTNG2	missense_variant	T/T	T/T	T/T	T/A	NA	NA	NA	NA	Damaging	23	Tolerated	Damaging	Damaging	Damaging	
chr9	139342612	139342613	C	T	None	4701.330078	SEC16A	missense_variant	C/C	C/C	C/T	C/C	NA	NA	NA	NA	Tolerated	10.76	Tolerated	Tolerated	NA	Tolerated	
chr10	64136379	64136380	G	A	None	4924.899902	ZNF365	missense_variant	G/G	G/A	G/G	G/A	NA	NA	NA	NA	Tolerated	11.83	Tolerated	Tolerated	NA	Tolerated	
chr10	75435024	75435025	T	C	None	7633.330078	AGAP5	missense_variant	T/T	T/C	T/T	T/T	NA	NA	NA	NA	Tolerated	6.509	Tolerated	Damaging	Tolerated	Tolerated	
chr10	79745663	79745664	A	G	None	3520.899902	POLR3A	missense_variant	A/A	A/G	A/G	A/A	NA	NA	NA	NA	Tolerated	22.4	Tolerated	Tolerated	Damaging	Damaging	
chr10	81609751	81609752	C	T	VQSRTrancheSNP99.90to100.00	2731.879883	NUTM2E	missense_variant	T/T	T/T	C/C	T/T	NA	NA	NA	NA	NA	0.033	NA	NA	NA	NA	
chr10	88822543	88822544	C	T	None	3509.899902	GLUD1	missense_variant	C/C	C/T	C/C	C/T	NA	NA	NA	NA	Damaging	32	Damaging	Damaging	Damaging	Damaging	
chr10	97098992	97098993	G	C	None	6618.899902	SORBS1	missense_variant	G/C	G/G	G/G	G/C	NA	NA	NA	NA	Tolerated	22.5	Damaging	Tolerated	Damaging	Damaging	
chr10	97101437	97101438	G	A	None	3425.899902	SORBS1	splice_region_variant	G/A	G/G	G/G	G/A	NA	NA	NA	NA	NA	18.97	NA	NA	NA	NA	
chr10	98155060	98155061	G	A	None	5952.899902	TLL2	missense_variant	G/A	G/A	G/A	G/G	NA	NA	NA	NA	Damaging	23.5	Damaging	Damaging	Damaging	Tolerated	
chr10	98273330	98273331	C	G	None	5968.899902	TLL2	missense_variant	C/G	C/C	C/C	C/G	NA	NA	NA	NA	Tolerated_low_confidence	14.77	Damaging	Tolerated	Damaging	Damaging	
chr10	101594151	101594152	G	C	None	3087.330078	ABCC2	missense_variant	G/G	G/G	G/C	G/G	NA	NA	NA	NA	Damaging	28.2	Tolerated	Damaging	Damaging	Damaging	
chr10	134740132	134740133	C	T	None	2946.330078	TTC40	missense_variant	C/C	C/C	C/T	C/C	NA	NA	NA	NA	Tolerated	14.87	Tolerated	Tolerated	Tolerated	Damaging	
chr11	2797255	2797256	A	C	VQSRTrancheSNP99.90to100.00	79.33000183	KCNQ1	missense_variant	A/C	A/A	A/A	A/A	NA	NA	NA	NA	Tolerated	21.6	Tolerated	Tolerated	NA	Damaging	
chr11	3723692	3723693	G	C	None	1658.329956	NUP98	missense_variant	G/G	G/G	G/G	G/C	NA	NA	NA	NA	Tolerated	21.4	Tolerated	Tolerated	Damaging	Tolerated	
chr11	4881399	4881400	A	C	None	2571.330078	OR51H1P	stop_gained	A/A	A/A	A/A	A/C	NA	NA	NA	NA	NA	38	NA	NA	NA	NA	
chr11	6637738	6637741	ATT	AT	None	6554.350098	TPP1	splice_region_variant	/AT	/AT	/AT	/AT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr11	46342941	46342943	CA	C	None	84.95999908	CREB3L1	splice_region_variant	C/C	CA/CA	CA/CA	CA/C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr11	46404339	46404342	GCC	GC	None	12951.90039	MDK	frameshift_variant	GCC/GC	GCC/.	GCC/GC	GCC/GC	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr11	58377799	58377800	G	T	None	6138.899902	ZFP91	missense_variant	G/T	G/G	G/G	G/T	NA	NA	NA	NA	Damaging_low_confidence	26.3	Tolerated	Damaging	Damaging	Tolerated	
chr11	61546307	61546309	CG	C	None	7809.859863	MYRF	frameshift_variant	CG/C	CG/CG	CG/C	CG/CG	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr11	61546310	61546311	C	CTTACCT	None	7931.859863	MYRF	frameshift_variant	C/CTTACCT	C/C	C/CTTACCT	C/C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr11	64875082	64875083	G	A	None	10791.90039	VP551	missense_variant	G/G	G/A	G/A	G/G	NA	NA	NA	NA	NA	23	NA	NA	NA	NA	
chr11	86158199	86158200	C	T	None	3630.330078	ME3	missense_variant	C/C	C/C	C/C	C/T	NA	NA	NA	NA	Damaging	25.2	Tolerated	Damaging	NA	Damaging	
chr11	111742117	111742118	G	C	None	3344.899902	ALG9	missense_variant	G/G	G/C	G/G	G/C	NA	NA	NA	NA	Tolerated_low_confidence	15.65	Tolerated	Tolerated	Tolerated	NA	
chr11	116744743	116744744	G	A	None	8344.900391	SIK3	missense_variant	G/A	G/G	G/G	G/A	NA	NA	NA	NA	Damaging	24.8	Damaging	Damaging	NA	Damaging	
chr11	116744744	116744745	C	A	None	8344.900391	SIK3	missense_variant	C/A	C/C	C/C	C/A	NA	NA	NA	NA	Damaging	24.6	Damaging	Damaging	NA	Damaging	
chr11	118981619	118981620	C	T	None	9148.900391	C2CD2L	missense_variant	C/T	C/C	C/T	C/C	NA	NA	NA	NA	Tolerated	22.4	Tolerated	Tolerated	Damaging	Tolerated	
chr11	134026978	134026979	T	A	None	3435.330078	NCAPD3	missense_variant	T/T	T/T	T/A	T/A	NA	NA	NA	NA	Damaging	23.5	Tolerated	Damaging	Damaging	Tolerated	
chr12	68519	68520	C	T	VQSRTrancheSNP99.90to100.00	3852.919922	RP11-598F7.1	splice_region_variant	C/T	C/T	C/C	T/T	NA	NA	NA	NA	NA	2.297	NA	NA	NA	NA	
chr12	9020901	9020902	G	C	None	5826.899902	A2ML1	missense_variant	G/C	G/G	G/G	G/C	NA	NA	NA	NA	Tolerated	7.168	Tolerated	Tolerated	NA	Tolerated	
chr12	21602493	21602494	C	T	None	6743.899902	PYROXD1	splice_region_variant	C/T	C/A	C/T	C/C	NA	NA	NA	NA	NA	21.8	NA	NA	NA	NA	
chr12	48144916	48144917	A	C	VQSRTrancheSNP99.90to100.00	499.3299866	RAPGEF3	missense_variant	A/C	A/A	A/A	A/A	NA	NA	NA	NA	Tolerated	10.2	Tolerated	Tolerated	NA	Tolerated	
chr12	49075782	49075783	G	A	None	12068.90039	KANS12	missense_variant	G/A	G/G	G/A	G/G	NA	NA	NA	NA	NA	11.71	NA	NA	NA	NA	
chr12	49315299	49315301	AT	A	None	932.9000244	FKBP11	splice_region_variant	AT/.	AT/.	AT/.	AT/A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
chr12	49444483	49444484	C	T	None	6950.899902	KMT2D	missense_variant	C/T	C/C	C/T	C/C	NA	NA	NA	NA	Damaging_low_confidence	23.2	Tolerated	Tolerated	Damaging	Damaging	
chr12	50589673	50589675	CA	CAA	None	2239.899902	UMA1	splice_region_variant	CA/.	CA/.	CA/.												

chr15	80736695	80736702	GGTGTGT	G	None	12368.90039	RP11-210M15.1	frameshift_variant	GGTGTGT/.	GGTGTGT/.	GGTGTGT/.	G/.	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr15	80736695	80736702	GGTGTGT	GGT	None	12368.90039	RP11-210M15.1	splice_acceptor_variant	GGTGTGT/GGT	GGTGTGT/.	GGTGTGT/.	/GGT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr15	81637321	81637322	A	G	None	2747.330078	TMC3	missense_variant	A/A	A/A	A/G	A/A	NA	NA	NA	NA	NA	Damaging	13.99	Tolerated	Tolerated	NA	NA	Damaging	NA	NA
chr16	64454	64455	C	T	VQSRTrancheSNP99.90to100.00	119.3300018	WASH4P	missense_variant	C/C	C/C	C/T	C/C	NA	NA	NA	NA	NA	NA	11.99	NA	NA	NA	NA	NA	NA	NA
chr16	779017	779018	G	A	None	4386.330078	HAGHL	missense_variant	G/G	G/G	G/G	G/A	NA	NA	NA	NA	NA	NA	19.94	NA	NA	NA	NA	NA	NA	NA
chr16	2079747	2079748	C	T	None	2909.330078	SLC9A3R2	missense_variant	C/C	C/C	C/C	C/T	NA	NA	NA	NA	NA	Damaging	13.37	Tolerated	Tolerated	NA	NA	Tolerated	NA	NA
chr16	3487141	3487142	C	G	None	3267.330078	ZNF597	missense_variant	C/C	C/C	C/G	C/C	NA	NA	NA	NA	NA	Damaging	24.9	Tolerated	Damaging	Damaging	Damaging	Damaging	NA	NA
chr16	4546126	4546129	CTT	CT	None	2467.310059	HMOX2	splice_region_variant	/CT	/CT	/.	/CT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr16	10631837	10631838	C	T	None	6705.899902	EMP2	missense_variant	C/T	C/C	C/C	C/T	3.231E-05	NA	NA	NA	NA	Tolerated	23.4	Damaging	Tolerated	NA	NA	Damaging	NA	NA
chr16	11554891	11554892	G	A	None	6004.899902	CTD-3088G3.8	missense_variant	G/A	G/G	G/G	G/A	NA	NA	NA	NA	NA	NA	16.66	NA	NA	NA	NA	NA	NA	NA
chr16	19869066	19869068	TA	T	None	341.1900024	GPCR5B	splice_region_variant	TA/T	TA/TA	TA/T	TA/T	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr16	20839760	20839761	G	C	None	6130.899902	AC004381.6	missense_variant	G/G	G/C	G/G	G/C	NA	NA	NA	NA	NA	Damaging	22.7	Tolerated	Damaging	NA	NA	Damaging	NA	NA
chr16	21747678	21747679	G	A	None	9012.900391	OTOA	missense_variant	G/G	G/A	G/G	G/A	NA	NA	NA	NA	NA	Tolerated	15.67	Tolerated	Tolerated	NA	NA	Tolerated	NA	NA
chr16	29495805	29495806	C	A	VQSRTrancheSNP99.90to100.00	32.61000061	RP11-231C14.4	missense_variant	C/A	C/C	C/C	C/C	NA	NA	NA	NA	NA	NA	9.805	NA	NA	NA	NA	NA	NA	NA
chr16	29495857	29495858	G	A	VQSRTrancheSNP99.90to100.00	112.8799973	RP11-231C14.4	missense_variant	G/G	G/G	G/A	G/G	NA	NA	NA	NA	NA	NA	10.97	NA	NA	NA	NA	NA	NA	NA
chr16	29496710	29496711	C	CTGAGGGTG	None	10382	RP11-231C14.4	isruptive_inframe_insertio	C/CGCTGAGGGTGGA	GCTGAGGGTG	C/C	/CGCTGAGGGTGG.	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr16	31926498	31926499	T	G	None	3198.330078	ZNF267	missense_variant	T/T	T/T	T/G	T/T	NA	NA	NA	NA	NA	Damaging	17.01	Tolerated	Damaging	Tolerated	Tolerated	Tolerated	NA	NA
chr16	48210995	48210996	A	G	None	2185.330078	ABCC11	missense_variant	A/A	A/A	A/G	A/A	NA	NA	NA	NA	NA	Tolerated	13.33	Tolerated	Tolerated	NA	NA	Tolerated	NA	NA
chr16	53721783	53721784	A	G	None	5267.899902	RPGRIPL1	missense_variant	A/G	A/G	A/G	A/A	NA	NA	NA	NA	NA	Tolerated	24.5	Damaging	Damaging	NA	NA	Damaging	NA	NA
chr16	56876466	56876469	CTT	CT	None	8620.860352	NPUP3	splice_region_variant	CT/CT	CTT/CT	CTT/CT	/CT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr16	66757486	66757487	G	GT	None	1581.939941	DYNC1L2	splice_region_variant	G/GT	G/GT	G/GT	G/GT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr16	88497181	88497182	G	A	None	8717.900391	RNF469	missense_variant	G/A	G/A	G/A	G/G	NA	NA	NA	NA	NA	Tolerated	11.04	Tolerated	Tolerated	NA	NA	Damaging	NA	NA
chr16	89017634	89017635	G	A	None	27685.90039	RP11-830F9.6	missense_variant	G/A	G/A	G/G	G/A	NA	NA	NA	NA	NA	Damaging_low_confidence	14.33	NA	unknown	NA	NA	NA	NA	NA
chr16	89920927	89920928	C	T	None	5050.330078	SPIRE2	missense_variant	C/C	C/C	C/T	C/C	6.4645E-05	NA	NA	NA	NA	Damaging	28.5	Damaging	Damaging	NA	NA	Damaging	NA	NA
chr16	90228997	90228998	C	T	None	704.4699707	FAM157C	splice_region_variant	C/C	C/C	C/C	C/T	NA	NA	NA	NA	NA	NA	6.252	NA	NA	NA	NA	NA	NA	NA
chr17	17039560	17039567	CCAGCAG	CCAG	None	37256.30078	MPRIIP	isruptive_inframe_deletio	/CCAG	CCAG/CCAG	/CCAG	CCAG/CCAG	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr17	20946964	20946965	C	T	None	1318.900024	USP22	missense_variant	C/C	C/T	C/C	C/C	NA	NA	NA	NA	NA	NA	9.871	NA	NA	NA	NA	NA	NA	NA
chr17	34495989	34495990	C	G	VQSRTrancheSNP99.90to100.00	1547.939941	TBC1D3B	missense_variant	C/G	C/G	C/G	C/G	NA	NA	NA	NA	NA	Tolerated	10.06	Tolerated	Damaging	Tolerated	Tolerated	Tolerated	NA	NA
chr17	37676270	37676271	G	A	None	4731.899902	CDK12	missense_variant	G/G	G/A	G/G	G/A	NA	NA	NA	NA	NA	Damaging	31	Tolerated	Damaging	NA	NA	Damaging	NA	NA
chr17	39925848	39925849	C	T	None	10923.90039	JUP	missense_variant	C/T	C/C	C/C	C/T	NA	NA	NA	NA	NA	Tolerated	23	Tolerated	Tolerated	NA	NA	Damaging	NA	NA
chr17	40275063	40275064	G	T	None	14786.2998	HSPB9	stop_gained	G/G	G/G	G/T	G/G	NA	NA	NA	NA	NA	NA	35	NA	NA	NA	NA	NA	NA	NA
chr17	40275064	40275065	A	T	None	14786.2998	HSPB9	missense_variant	A/A	A/A	A/T	A/A	NA	NA	NA	NA	NA	NA	23.9	NA	NA	NA	NA	NA	NA	NA
chr17	42477070	42477071	G	A	None	20730.90039	GPATCH8	missense_variant	G/A	G/A	G/A	G/G	NA	NA	NA	NA	NA	Tolerated_low_confidence	0.001	Tolerated	Tolerated	Tolerated	Tolerated	Tolerated	NA	NA
chr17	47779287	47779289	CA	CAA	None	2143.899902	SLC35B1	splice_region_variant	CA/.	CA/.	CA/CAA	CA/.	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr17	56280590	56280591	G	A	None	10563.90039	EPX	missense_variant	G/A	G/G	G/G	G/A	6.4566E-05	NA	NA	NA	NA	Damaging	24.5	Damaging	Damaging	Damaging	Damaging	Damaging	NA	NA
chr17	58093261	58093262	G	A	VQSRTrancheSNP99.90to100.00	1326.050049	BC1D3P1-DHX40P	splice_region_variant	G/A	G/A	G/A	G/G	NA	NA	NA	NA	NA	NA	7.226	NA	NA	NA	NA	NA	NA	NA
chr17	60345507	60345508	A	G	None	5024.350098	TBC1D3P2	splice_region_variant	G/G	/.	G/G	G/G	NA	NA	NA	NA	NA	NA	7.189	NA	NA	NA	NA	NA	NA	NA
chr17	60349878	60349879	G	A	VQSRTrancheSNP99.90to100.00	2479.939941	TBC1D3P2	splice_region_variant	G/A	G/A	G/A	G/A	NA	NA	NA	NA	NA	NA	5.948	NA	NA	NA	NA	NA	NA	NA
chr17	72838757	72838758	C	T	None	8094.899902	GRIN2C	missense_variant	C/T	C/C	C/C	C/T	3.2316E-05	NA	NA	NA	NA	Tolerated_low_confidence	14.38	Tolerated	Tolerated	Tolerated	Tolerated	Tolerated	Damaging	NA
chr17	72839346	72839347	G	A	None	1064.900024	GRIN2C	missense_variant	G/G	G/A	G/G	G/A	3.3176E-05	NA	NA	NA	NA	Tolerated_low_confidence	18.02	Damaging	Tolerated	Tolerated	Tolerated	Damaging	NA	NA
chr17	72843670	72843671	C	T	None	6050.899902	GRIN2C	missense_variant	C/T	C/C	C/C	C/T	NA	NA	NA	NA	NA	Damaging	25.5	Tolerated	Damaging	NA	NA	Damaging	NA	NA
chr17	73723565	73723566	A	G	None	7454.899902	ITGB4	missense_variant	A/G	A/A	A/A	A/G	NA	NA	NA	NA	NA	NA	20.3	Tolerated	Tolerated	NA	NA	Damaging	NA	NA
chr18	14772185	14772186	C	T	None	8187.899902	ANKRD30B	stop_gained	C/T	C/T	C/T	C/C	NA	NA	NA	NA	NA	NA	26.4	Tolerated	NA	Tolerated	NA	NA	NA	NA
chr18	19119973	19119978	GATAT	GAT	None	11987.2998	ESCO1	splice_region_variant	/GAT	/GAT	/GAT	GAT/GAT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr18	21123535	21123538	TAA	TA	None	6238.310059	NPC1	splice_region_variant	/TA	/TA	/TA	/TA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr18	44109210	44109211	C	T	None	5164.330078	LOXHD1	missense_variant	C/C	C/C	C/T	C/C	0.00012923	NA	NA	NA	NA	Damaging	29.3	Tolerated	Damaging	NA	NA	Damaging	NA	NA
chr18	48447467	48447468	A	T	None	7488.899902	ME2	missense_variant	A/T	A/T	A/T	A/A	NA	NA	NA	NA	NA	Tolerated	22.1	Tolerated	Tolerated	NA	NA	Damaging	NA	NA
chr18	77798529	77798530	C	G	None	2762.330078	RBFA	missense_variant	C/C	C/C	C/C	C/G	NA	NA	NA	NA	NA	Damaging	24.2	Damaging	Damaging	NA	NA	Damaging	NA	NA
chr19	111436	111437	G	A	VQSRTrancheSNP99.90to100.00	189.9100037	OR4F17	stop_gained	G/A	G/G	G/A	G/G	NA	NA	NA	NA	NA	NA	35	Tolerated	NA	Tolerated	NA	NA	NA	NA
chr19	1229349	1229350	C	T	None	4226.899902	C19orf26	missense_variant	C/C	C/T	C/T	C/C	NA	NA	NA	NA	NA	NA	15.72	NA	NA	NA	NA	NA	NA	NA
chr19	1371269	1371270	G	A	None	25025.90039	MUM1	missense_variant	G/A	G/A	G/G	G/A	NA	NA	NA	NA	NA	NA	0.208	NA	NA	NA	NA	NA	NA	NA
chr19	2037629	2037630	G	GT	None	2919.860107	MKNK2	splice_region_variant	G/.	G/.	G/GT	/GT	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr19	3852617	3852618	A	G	None	3127.330078	ZFR2	splice_region_variant	A/A	A/A	A/A	A/G	NA	NA	NA	NA	NA	NA	4.9	NA	NA	NA	NA	NA	NA	NA
chr19	7440747	7440748	C	T	None	9621.900391	CTB-133G6.1	missense_variant	C/T	C/T	C/C	C/T	NA	NA	NA	NA	NA	NA	0.368	Tolerated	NA	Tolerated	Tolerated	Tolerated	NA	NA
chr19	9000186	9000187	C	T	VQSRTrancheSNP99.90to100.00	8427.94043	MUC16	missense_variant	C/T	C/T	C/T	C/T	NA	NA	NA	NA	NA	NA	12.97	Tolerated	Damaging	NA	NA	Tolerated	NA	NA
chr19	9000204	9000205	C	A	VQSRTrancheSNP99.90to100.00	3203.899902	MUC16	missense_variant	C/A	C/A	C/C	C/C	0.00724722	NA	NA	NA	NA	NA	7.02	Tolerated	Damaging	Tolerated	Tolerated	Tolerated	NA	NA
chr19	10398787	10398789	TG	T	None	7883.859863	ICAM4	frameshift_variant	TG/T	TG/TG	TG/T	TG/TG	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr19	11666070	11666073	CAA	CA	None	2548.330078	ELOF1	splice_region_variant	/CA	/CA	/CA	CAA/CA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
chr19	14627589	14627590	T	G	None	8596.900391	DNAJB1	missense_variant	T/T	T/T	T/T	T/G	NA	NA	NA	NA	NA	Damaging	23.6	Tolerated	Damaging	NA	NA	Damaging	NA	NA
chr19	17015033	17015034	G	T	None	3131.899902	CPAMD8	splice_donor_variant	G/T	G/G	G/T	G/G	NA	NA	NA	NA	NA	NA	14.97	NA	NA	NA	NA	NA	NA	NA
chr19</																										