Supplementary Table 1. Information on the 174 single nucleotide variants identified by whole-exome sequencing

Chr	Position	Major/ Minor allele	Gene	Variant Type	UW AF	UW exomes	Database	Family ID	polyPhen	Grantham	SIFT	GERP score	Likelihood Ratio Test	BLOSUM62	PhyloP	Linkage	No of UA carriers	No of families with variant	Filter	Removed from PedGenie Analysis
1	10163148	A/G	UBE4B	missense	0.000326	1534		2		98	1	4.44	Damaging	-2	2.30705	0	0	1	2	<85% MIP data
1	31437727	C/G	PUM1	missense	0.011416	1533		8	possibly-damaging	103	1	5.19	Damaging	-2	6.08836	0	0	5	1	<85% MIP data
1	39341749	C/T	GJA9	missense	0.002932	1535	dbSNP	3	probably-damaging	125	1	4.77	Damaging	-2	5.638	0	0	2	2	<85% MIP data
1	45806798	G/A	TOE1	missense	0.000977	1535		9		29	0.995	5.44	Damaging	3	5.70556	0	0	1	2	
1	55166892	C/T	C1orf175	missense	0	1531		7		64	0.952	4.42	Damaging	0	2.82372	0	1	1	4	
1	89730473	G/A	GBP5	nonsense	0	1535		17		NA	0.749	2.58	No alignment	NA	0.890488	0	0	1	2	
1	94107885	A/G	BCAR3	missense	0	1534		4		98	0.986	4.08	Damaging	-3	1.33124	0	1	1	4	<85% MIP data
1	144814705	C/T	NBPF9	nonsense	0.00607	659		8		NA	0.003	0.839	No alignment	NA	1.27788	0	0	2	1	<85% MIP data
1	156928890	C/T	ARHGEF11	missense	0	1535		10		56	0.425	4.16	Damaging	1	3.80677	0	0	1	2	
1	156941538	C/A	ARHGEF11	missense	0	1535		10		102	1	5.11	Damaging	-2	3.988	0	0	1	2	
1	179078052	T/A	ABL2	missense	0.004235	1535	dbSNP	8		58	1	5.31	Damaging	1	4.55258	0	1	2	3	
1	208206836	G/A	PLXNA2	missense	0	1535		10		81	0.998	5.07	Damaging	-1	6.01487	0	0	1	2	
1	208391027	C/A	PLXNA2	missense	0.003909	1535	dbSNP	4		32	1	5.35	Damaging	1	3.18605	0	0	1	2	
1	211263989	G/C	KCNH1	missense	0	1534		3		94	0.988	-2.48	Damaging	0	-0.01494	1	0	1	2	
1	247320105	G/T	ZNF124	nonsense	0.004889	1534	dbSNP	7		NA	0	-1.06	No alignment	NA	-3.08882	0	0	1	1	<85% MIP data
2	15359049	G/T	NBAS	missense	0.000326	1534		10		38	1	5.22	Damaging	-1	5.62072	0	0	1	2	
2	15701332	G/A	NBAS	missense	0	1535		2		74	1	4.47	Damaging	-1	3.494	0	0	1	2	
2	20840823	G/A	HS1BP3	missense	0.005537	1535	dbSNP	7		101	1	4.3	Damaging	-3	1.75357	1	0	1	1	
2	27883899	T/G	SUPT7L	missense	0.003592	1531		1		65	0.871	0.539	Damaging	0	0.343543	1	0	1	2	
2	27887160	C/T	SLC4A1AP	missense	0.012378	1535	dbSNP_ 1000Genomes	8	possibly-damaging	180	0.032	0.435	Damaging	-3	0.592717	0	0	2	1	
2	53943803	C/T	ASB3	missense	0.004563	1534		4		21	1	5.21	Damaging	1	3.93676	0	1	2	4	
2	53943868	T/C	ASB3	missense	0.001304	1534		10		46	1	5.1	Damaging	1	3.03365	0	0	1	2	
2	68613681	C/T	PLEK	missense	0.000977	1535		8		180	1	5.03	Damaging	-3	3.93259	0	0	1	1	
2	68740759	T/C	APLF	missense	0	1532		9		81	1	5.82	Damaging	-1	2.94007	0	0	1	2	<85% MIP data
2	74763247	C/T	LOXL3	missense	0.019218	1535	dbSNP_ 1000Genomes	7	probably-damaging	29	0.748	3.62	Damaging	0	2.23035	0	0	1	1	
2	74883750	G/A	SEMA4F	missense	0.006515	1535		6		29	0.996	2.01	Damaging	3	0.892189	1	0	2	2	<85% MIP data
2	86255108	G/T	POLR1A	nonsense	0.008818	1531	1000Genomes	11		NA	1	3.01	No alignment	NA	0.891843	0	0	6	2	Artifact

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2	101638972	C/T	TBC1D8	missense	0	1531		4		10	1	4.91	Damaging	1	0.589386	0	1	1	4	
2	113089980	A/T	ZC3H6	missense	0	1522		5		152	0.003	0.554	Not damaging	-3	0.961079	0	0	1	1	
2	158157377	G/A	GALNT5	missense	0	1535		8		23	0.987	4.07	Not damaging	1	2.20207	0	1	1	3	
2	196728886	A/G	DNAH7	missense	0.005552	1531	1000Genomes	7	probably-damaging	89	0.993	4.85	Damaging	-1	4.8451	0	0	2	1	
2	217012977	G/T	XRCC5	missense	0.002608	1534	dbSNP	5	benign	99	1	5.27	Damaging	1	3.26874	0	0	1	2	<85% MIP data
3	436384	A/T	CHL1	missense	0.009452	1534		8	probably-damaging	58	0.996	5.12	Damaging	1	4.65036	0	0	2	1	
3	43618737	G/T	ANO10	nonsense	0.001306	1531		8		NA	1	5.54	No alignment	NA	4.58971	0	0	2	2	
3	44776091	C/T	ZNF501	missense	0.015033	1530	dbSNP_ 1000Genomes	8	probably-damaging	180	0.978	0.475	No alignment	-3	-0.11771	0	0	2	1	
3	45046811	G/A	EXOSC7	missense	0.000326	1534		9		56	1	5.63	Damaging	1	6.326	0	0	1	2	
3	46479430	C/T	LTF	splice-5	0	1535		8		NA	0.983	4.38	No alignment	NA	3.14637	0	0	1	2	<85% MIP data
3	46939588	G/T	PTH1R	missense	0	1535	dbSNP_ 1000Genomes	15	possibly-damaging	102	1	4.7	No alignment	-2	1.06822	1	0	1	1	
3	47286320	T/C	KIF9	missense	0.008795	1535	1000Genomes	15		26	1	4.52	Damaging	2	1.54337	1	0	1	1	
3	49848475	G/A	UBA7	missense	0	1535		10		64	0.999	5.2	Damaging	0	6.177	0	0	1	2	<85% MIP data
3	51994306	T/A	PCBP4	missense	0.00456	1535		14		143	0.956	4.7	Damaging	-2	2.51633	0	0	1	2	
3	69087804	G/A	TMF1	missense	0.004248	1530	dbSNP_ 1000Genomes	9	possibly-damaging	180	0.971	5.37	Damaging	-3	1.93776	0	0	1	2	<85% MIP data
3	87018099	T/A	VGLL3	missense	0.005879	1531	dbSNP_ 1000Genomes	10		99	1	5.34	Damaging	-3	4.43385	0	0	2	2	
3	113729839	C/T	KIAA1407	missense	0.007166	1535		13		43	1	4.71	Damaging	1	1.85858	1	0	1	1	
3	130449216	C/T	PIK3R4	missense	0	1532		2		10	1	4.82	Damaging	1	1.57966	0	0	1	2	<85% MIP data
3	192973579	G/A	HRASLS	splice-5	0.002606	1535	1000Genomes	10		NA	1	5.07	No alignment	NA	5.486	0	0	1	2	
4	17844980	G/A	NCAPG,LCORL	missense	0.001631	1533		5		58	1	5.71	Damaging	0	5.308	0	1	2	3	<85% MIP data
4	87728733	C/G	PTPN13	missense	0	1530		3		32	0.997	4.92	Damaging	1	4.4084	0	0	1	2	
4	113303632	A/G	ALPK1	missense	0.008469	1535	dbSNP	10	probably-damaging	43	1	5.19	Damaging	1	4.20712	0	0	1	2	
4	113352745	G/A	ALPK1	missense	0.013355	1535	dbSNP	11	benign	94	0	-1.66	Not damaging	-1	-0.28995	1	0	2	2	
4	113359801	T/C	ALPK1	missense	0.009452	1534	dbSNP_ 1000Genomes	8	probably-damaging	98	0.975	4.9	Damaging	-3	4.58809	0	0	2	2	
4	143045853	A/G	INPP4B	missense	0.004235	1535	dbSNP	17	possibly-damaging	64	1	5.32	Damaging	0	4.6712	1	0	2	1	

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4	169305816	G/A	DDX60L	nonsense	0.00098	1531		8		NA	0.344	-2.96	No alignment	NA	-0.10859	0	0	1	1	
5	41150035	A/G	C6	splice-5	0.002934	1534	dbSNP_ 1000Genomes	11		NA	0.995	4.51	No alignment	NA	3.24573	0	0	2	2	
5	54593201	T/G	DHX29	missense	0.003588	1533		4		76	1	5.18	Damaging	-1	4.60019	0	0	1	2	
5	73981299	C/T	HEXB	missense	0.006845	1534		18	probably-damaging	22	0	-4.23	Damaging	0	-0.04597	0	0	1	2	
5	75886262	G/A	IQGAP2	missense	0.000326	1534		5		58	0.999	5.57	Damaging	0	6.298	1	0	1	1	
5	83362312	C/G	EDIL3	missense	0.006845	1534		5		94	0.998	1.96	Damaging	0	0.56163	1	0	1	1	<85% MIP data
5	115151969	G/T	CDO1	missense	0.000977	1535		16	probably-damaging	110	1	1.89	Damaging	-1	2.95975	0	0	1	2	
5	125880710	C/T	ALDH7A1	missense	0.00684	1535	dbSNP_ 1000Genomes	16	probably-damaging	58	0.978	4.73	Damaging	0	4.35541	0	0	1	2	
5	139908868	G/T	ANKHD1,ANKHD1-EIF4EBP3	missense	0	1535		5		50	1	5	Damaging	-1	3.93485	0	0	1	2	
5	141309743	G/T	KIAA0141	nonsense	0	1535		2		NA	1	4.38	No alignment	NA	2.77691	0	0	1	2	<85% MIP data
6	2768965	A/G	WRNIP1, LOC100288968	missense	0.00456	1535	dbSNP_ 1000Genomes	12	benign	29	0.996	5.32	Damaging	0	2.33964	0	0	2	2	<85% MIP data
6	17764896	G/C	KIF13A	missense	0.006532	1531	dbSNP_ 1000Genomes	19		45	0.342	-7.57	Damaging	2	-0.608	1	0	1	1	
6	17781508	T/G	KIF13A	missense	0.002286	1531		4		76	1	5.09	Damaging	-1	3.16512	0	0	1	2	
6	20546697	G/A	CDKAL1	missense	0.009452	1534		19	probably-damaging	43	0.997	5.15	Damaging	1	4.772	1	0	1	1	
6	31939898	C/T	DOM3Z,STK19	missense	0.003932	1526		19		64	0	-4.13	No alignment	0	-0.13722	1	1	2	4	
6	32157473	T/C	PBX2	missense	0	872		19		56	1	3.22	Damaging	1	3.63076	1	0	1	1	
6	32362521	C/A	BTNL2	missense	0.006515	1535	1000Genomes	11	probably-damaging	159	0.97	1.02	Damaging	-3	0.402992	1	0	2	1	
6	32363888	C/T	BTNL2	missense	0.006881	872	1000Genomes	11	possibly-damaging	23	0.956	2.61	Not damaging	1	0.298732	1	0	2	1	
6	36099050	C/T	MAPK13	missense	0.01272	1533	dbSNP	11		145	0.896	2.66	Damaging	-2	3.89725	1	0	1	2	
6	109308747	T/C	SESN1	nonsense	0	1534		18		NA	1	5.57	No alignment	NA	4.8611	0	0	1	2	<85% MIP data
6	132271464	T/C	CTGF, LOC100131774	missense	0	1534		9		26	1	5.22	Damaging	2	1.62817	1	0	1	2	
6	159667972	C/T	FNDC1	missense	0.004899	1531	dbSNP	12		81	0.765	5.07	Damaging	-1	3.754	1	0	1	1	<85% MIP data
7	4900991	C/G	RADIL,PAPOLB	missense	0.005225	1531	dbSNP_ 1000Genomes	11	possibly-damaging	29	1	4.31	No alignment	NA	3.18541	0	0	2	2	
7	12376626	G/A	VWDE	nonsense	0	663		4		NA	0.008	-0.682	No alignment	NA	-0.12796	0	0	1	1	
7	27183182	A/T	HOXA5, LOC100133311	missense	0	1535		5		94	1	5.1	Damaging	0	3.0688	0	0	1	2	<85% MIP data

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7	42007201	T/C	GLI3	missense	0.000651	1535	dbSNP	15		10	1	3.87	Damaging	1	1.37369	1	0	1	1	
7	47849070	C/A	C7orf69,PKD1L1	splice-5	0.000326	1535		8		NA	1	4.7	No alignment	NA	3.44242	0	0	4	2	<85% MIP data
7	76111831	T/C	DTX2	missense	0.006193	1534		4		81	1	5.05	Damaging	-1	1.99788	0	0	1	2	<85% MIP data
7	86800364	G/C	DMTF1	missense	0.013364	1534	1000Genomes	17		27	1	4.3	Damaging	-1	2.14525	0	0	4	1	
7	92085763	C/T	GATAD1	missense	0.007818	1535	dbSNP_ 1000Genomes	19	probably-damaging	101	0.998	3.99	Damaging	-3	1.53702	1	0	3	1	<85% MIP data
7	92764419	A/G	SAMD9L	missense	0.009132	1533	dbSNP_ 1000Genomes	19	possibly-damaging	155	1	4.6	Damaging	-2	4.70036	1	0	2	1	
7	93106966	G/A	CALCR	missense	0	1534		8		180	1	3.68	No alignment	NA	4.89444	0	0	1	1	
7	97861243	T/C	TECPR1	missense	0	1531		6		43	1	5.03	Damaging	1	2.23546	0	0	1	2	<85% MIP data
7	114298247	A/C	FOXP2	missense	0	1527		17		38	1	5.66	Damaging	-1	1.7362	1	0	3	1	Artifact
8	18080115	C/T	NAT1	nonsense	0.001629	1535	dbSNP	11		NA	0	-0.095	No alignment	NA	0.109417	0	0	1	2	
8	41574488	C/T	ANK1	missense	0.000651	1535		16		29	1	5.26	Damaging	3	4.27555	0	0	1	2	
8	70515476	A/G	SULF1	missense	0.003909	1535	1000Genomes	2		29	0.986	5.82	Damaging	3	5.29408	0	0	1	2	
8	95390840	T/C	RAD54B	missense	0	1532		8		94	1	4.21	Damaging	-1	3.48591	0	1	1	3	
9	34255988	A/C	KIF24	missense	0.008795	1535	dbSNP	17		102	0.003	2.08	Not damaging	-2	-0.00211	1	0	2	1	
9	116155807	G/T	ALAD	nonsense	0	1535		8		NA	1	4.02	No alignment	NA	1.11768	0	0	1	2	
9	127982839	C/A	RABEPK	missense	0.003583	1535	dbSNP_ 1000Genomes	19	probably-damaging	76	0.997	5.35	Damaging	-1	3.1325	1	0	1	2	
10	31137481	C/T	ZNF438	missense	0.00228	1535		15		94	0	1.14	Damaging	-1	0.268079	1	0	1	1	
10	32311866	G/C	KIF5B	missense	0	1534		17		215	1	2.88	Damaging	-2	3.40883	0	1	1	3	
10	34558715	C/T	PARD3	missense	0.003909	1535		15		125	0.994	4.75	Not damaging	-2	3.36695	1	0	1	1	
10	52005095	G/A	ASAH2	nonsense	0.005212	1535	1000Genomes	15		NA	0.002	1.28	No alignment	NA	0.484417	1	0	1	1	
10	61830704	G/A	ANK3	missense	0	1535		17		64	0.909	5.02	Damaging	0	3.23403	0	0	1	2	<85% MIP data
10	61836157	G/T	ANK3	nonsense	0.001303	1535		17		NA	1	5.25	No alignment	NA	5.74583	0	0	2	2	Artifact
10	115485285	T/C	CASP7	missense	0.003259	1534		8		22	1	5.01	Damaging	0	4.97518	0	1	2	3	
10	127693479	A/G	FANK1	missense	0.019544	1535	dbSNP	13		29	0.966	5.44	Damaging	0	3.81412	0	0	3	1	
10	134579287	T/C	INPP5A	missense	0	1535		2		155	1	3.9	Damaging	-2	2.82196	0	0	1	2	<85% MIP data
11	803401	G/A	LRDD	missense	0.016612	1535	dbSNP	4	possibly-damaging	155	0.843	1.27	Damaging	-2	0.641402	0	0	1	2	
11	64883000	G/C	TM7SF2	missense	0	1531		8		215	1	4.52	Damaging	-2	5.26654	0	0	1	1	

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11	65147013	C/T	SLC25A45	missense	0.004572	1531	dbSNP_ 1000Genomes	1		98	0.998	4.31	Damaging	-2	3.9278	0	0	1	2	
11	65294543	G/A	SCYL1	missense	0.00098	1531		16		10	0.999	4.41	Damaging	1	1.51232	1	0	1	1	
12	2968078	G/A	FOXM1	missense	0.008149	1534	dbSNP	8	probably-damaging	98	1	4.37	Damaging	-3	5.03644	0	0	2	1	
12	49434409	G/A	MLL2	missense	0.005229	1530	dbSNP_ 1000Genomes	8		74	0.998	4.86	Damaging	-1	3.8459	0	1	2	3	
12	56087092	G/C	ITGA7	missense	0.000326	1535		3		29	1	4.4	Damaging	2	1.57569	0	0	1	2	
12	113565637	G/A	RASAL1	missense	0.005212	1535		13		64	0.62	1.38	Damaging	0	0.612724	1	0	2	1	
12	120635224	G/T	RPLP0	nonsense	0.000326	1535		8		NA	0.99	1.88	No alignment	NA	0.971441	0	0	5	2	Artifact
12	122404946	C/T	WDR66	missense	0.005879	1531		13		180	0.999	4.26	Damaging	-3	1.52732	1	0	1	1	
12	132238953	G/A	SFRS8	missense	0.000986	1521		6	possibly-damaging	23	0.96	5.3	Damaging	1	6.14929	0	0	1	2	<85% MIP data
13	53617309	C/T	OLFM4	nonsense	0.013355	1535	dbSNP_ 1000Genomes	17		NA	0.817	4.93	No alignment	NA	2.92478	0	0	4	1	
13	73333935	A/G	DIS3	nonsense	0.002934	1534		7		NA	0.998	5.71	No alignment	NA	3.16557	0	0	1	1	<85% MIP data
13	77754330	C/T	MYCBP2	missense	0.002932	1535	dbSNP_ 1000Genomes	14		29	0.976	5.56	Damaging	3	5.76391	0	0	2	2	
14	20850171	G/A	TEP1	missense	0.003909	1535		2		98	0.603	5.17	Damaging	-3	3.66893	0	0	2	2	
14	20872834	C/T	TEP1	missense	0.001954	1535		18		43	1	5.12	Damaging	1	3.73325	0	0		2	
14	55458040	A/G	WDHD1	missense	0.014658	1535	dbSNP_ 1000Genomes	6	possibly-damaging	98	0.169	3.44	Damaging	-3	1.49805	1	0	1	2	
14	56145134	T/C	KTN1	missense	0.002609	1533	1000Genomes	6	probably-damaging	89	1	3.89	Not damaging	-1	2.12348	1	0	1	2	
14	57747123	T/C	MUDENG	missense	0	1535		6		180	0.998	5.53	Damaging	-3	4.80139	1	0	1	2	<85% MIP data
15	66813452	C/T	ZWILCH	missense	0.000651	1535		17		89	0	0.225	Not damaging	-1	0.298559	1	1	1	3	
15	72192205	C/G	MYO9A	missense	0.001629	1535		9	probably-damaging	103	0.081	4.47	No alignment	-2	2.1152	0	0	1	2	
15	78921343	G/A	CHRNB4	missense	0.001629	1535	dbSNP	16	probably-damaging	64	0.839	4.82	Damaging	0	5.831	0	0	1	1	
15	90347148	G/C	ANPEP	missense	0.001954	1535		10	probably-damaging	60	0.996	3.15	Damaging	0	2.45393	0	0	1	1	<85% MIP data
15	99454613	G/A	IGF1R	missense	0.001303	1535	dbSNP	7	possibly-damaging	43	0.987	5.62	Damaging	1	2.55654	0	1	1	3	
16	2153765	G/A	PKD1	missense	0.00689	1524		10		180	1	3.32	Damaging	-3	2.28561	0	0	1	1	
16	3642722	C/G	BTBD12	missense	0.00228	1535		2		29	0.056	4.03	Damaging	2	1.15498	0	0	2	2	
16	14339497	T/C	MKL2	missense	0.006845	1534	1000Genomes	4, 10	benign	74	0.973	2.21	Not damaging	-1	0.488669	1	1	2	4	
16	17292204	G/A	XYLT1	missense	0.003909	1535	dbSNP	10	probably-damaging	98	1	5	Damaging	-3	5.73831	0	0	1	2	

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16	23635348	A/C	PALB2	missense	0.001956	1534	dbSNP	8		61	1	5.46	Damaging	-2	2.82349	0	1	2	3	
16	30958481	G/A	FBXL19	missense	0.008887	1519	dbSNP	9	possibly-damaging	43	1	4.92	Damaging	1	2.09863	0	0	1	2	<85% MIP data
16	50655597	C/A	NKD1	missense	0	1535		3		144	1	4.81	Damaging	-2	2.40839	0	0	1	2	<85% MIP data
16	78420806	G/A	WWOX	missense	0	1531		7		46	1	5.17	Damaging	1	4.777	0	1	1	4	<85% MIP data
16	89704543	C/A	DPEP1	nonsense	0.000651	1535		8		NA	0.995	3.45	No alignment	NA	1.76557	0	0	2	2	<85% MIP data
17	4620564	C/T	ARRB2	missense	0	1534		19		89	0.976	4.97	Damaging	-1	5.513	0	0	1	2	<85% MIP data
17	9497560	C/T	WDR16	missense	0.004886	1535	dbSNP	8		64	0.141	5.14	Damaging	0	3.77412	0	1	2	3	<85% MIP data
17	18149133	A/T	FLII	missense	0.001954	1535		12		22	1	5.25	Damaging	3	4.88419	1	0	1	2	<85% MIP data
17	26940279	C/T	SGK494	splice-5	0.000977	1535		12		NA	1	4.63	No alignment	NA	5.07087	1	0	1	2	
17	27068436	G/A	NEK8	missense	0.000651	1535		6	possibly-damaging	56	0.96	5.08	Damaging	1	2.88275	0	0	1	2	
17	27075334	G/A	TRAF4	missense	0.00684	1535	dbSNP_ 1000Genomes	13	probably-damaging	58	1	4.04	Damaging	0	3.76061	0	0	2	2	
17	76200907	A/G	AFMID	splice-3	0.002932	1535		17		NA	0.962	4.54	No alignment	NA	4.09151	0	0	1	1	
18	7013926	A/G	LAMA1	missense	0	1535		1		155	1	4.55	Damaging	-2	1.21707	0	0	1	2	
18	28983529	C/T	DSG4	missense	0.00684	1535	dbSNP	15	probably-damaging	98	1	5.66	Damaging	-3	4.417	0	0	2	2	<85% MIP data
18	31263416	G/A	ASXL3	missense	0	1530		11		125	1	4.01	No alignment	NA	5.47443	1	0	1	1	
18	33689570	G/A	SLC39A6	missense	0.000327	1530		4		180	1	4.73	Damaging	-3	1.72635	0	0	1	1	
19	2827722	C/A	ZNF554	nonsense	0	1531		5		NA	0.001	-1.62	No alignment	NA	-0.58836	0	1	1	3	<85% MIP data
19	7688165	G/C	XAB2	missense	0.000326	1535		13		58	0.944	4.52	Damaging	1	5.29333	1	0	1	1	<85% MIP data
19	13869786	G/T	CCDC130	missense	0.002283	1533		12	probably-damaging	102	1	4.62	Damaging	-2	4.925	0	0	2	1	
19	15164634	G/A	CASP14	missense	0.000326	1535		13		125	0.177	4.14	Damaging	-2	3.088	1	0	1	2	
19	35757755	C/A	LSR	nonsense	0	1535		17		NA	1	1.73	No alignment	NA	0.500323	0	0	2	2	<85% MIP data
19	36302863	C/A	PRODH2	splice-5	0	1535		7		NA	0.994	4.48	No alignment	NA	3.86735	0	0	1	2	<85% MIP data
19	40748535	C/G	AKT2	missense	0.000977	1535		7		60	0.208	5.55	Damaging	0	1.67877	0	1	1	3	<85% MIP data
19	45593547	C/T	GEMIN7	nonsense	0	1535		19		NA	0.97	4.71	No alignment	NA	4.778	1	0	1	2	
19	49448116	A/T	DHDH	missense	0	1535		16		112	0.963	4.24	Damaging	-1	1.96897	1	0	1	1	<85% MIP data

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19	49703651	A/T	TRPM4	nonsense	0.001956	1534		7		NA	0.998	3.86	No alignment	NA	4.29214	0	1	2	3	
19	50368466	C/T	PNKP	missense	0.003257	1535	dbSNP	9	probably-damaging	29	0.042	3.03	Damaging	0	1.02412	0	0	1	2	<85% MIP data
19	50949163	G/A	MYBPC2	missense	0.011757	1531	dbSNP_ 1000Genomes	16	probably-damaging	43	0.859	2.68	Damaging	1	1.90665	1	0	1	1	
19	53384826	C/T	ZNF320	missense	0.004563	1534		18	probably-damaging	125	0.002	0.759	No alignment	-2	1.66921	0	0	1	2	<85% MIP data
19	54802701	C/T	LILRA3	missense	0.009221	1464		9	probably-damaging	94	0	-5.13	Not damaging	-1	-1.55596	0	0	2	2	<85% MIP data
19	54803979	C/G	LILRA3	splice-3	0.009569	1463	dbSNP	9		NA	0.999	2.61	No alignment	NA	1.67904	0	0	2	2	
20	20270952	C/A	C20orf26	missense	0.008143	1535	1000Genomes	4	possibly-damaging	5	1	5.15	No alignment	NA	2.38391	0	0	1	2	<85% MIP data
20	31383232	C/T	DNMT3B	missense	0.000326	1535	dbSNP	10	probably-damaging	180	1	3.9	Damaging	-3	2.18819	0	0	1	2	
20	39832371	C/T	ZHX3	missense	0.003583	1535		9	possibly-damaging	29	1	5.53	Damaging	3	4.50361	0	0	1	2	<85% MIP data
20	57598607	C/T	TUBB1	nonsense	0	1535		16		NA	0.998	3.88	No alignment	NA	2.01896	0	0	1	2	
21	48063552	G/T	PRMT2	splice-5	0	1535		8		NA	1	3.4	No alignment	NA	1.63441	0	0	2	2	<85% MIP data
22	26839083	C/T	ASPHD2	missense	0.000326	1535		13		101	0.643	2.05	Damaging	-3	0.294961	1	0	1	1	
22	30776106	G/C	RNF215	missense	0.017613	1533		7	probably-damaging	103	0.009	1.45	Damaging	-2	0.703598	0	0	2	1	
22	32109640	C/G	C22orf30	missense	0	663	dbSNP	7	probably-damaging	22	0	1.31	Not damaging	0	0.244173	0	0	1	1	<85% MIP data
22	32134789	C/A	C22orf30	missense	0	663		3		32	0.996	4.51	Damaging	1	2.91209	1	0	1	1	
22	41522003	A/G	EP300	missense	0.003585	1534		1		21	1	4.23	Damaging	1	1.51706	0	0	1	2	
22	43933357	C/A	EFCAB6	missense	0.005537	1535		9, 10		110	0.356	4.36	Damaging	-1	1.91097	0	0	2	2	
22	45608215	G/A	C22orf9	nonsense	0.003257	1535		10		NA	0	-3.44	No alignment	4	0.027449	0	0	1	2	
22	50845251	G/A	SAPS2	missense	0	1535		4		58	0.994	4.35	Damaging	0	4.13111	0	0	1	2	