CHROM	POS	REF	ALT	TYPE	AF_primary	AF_meta	VariantCategory
chr1	109745855	T	G	SNV	0.118	0.219	downstream_gene_variant
chr1	114224782	AT	A	INDEL	0.256	0.169	intron_variant
chr1	119962130	G	A	SNV	0.165	0.219	missense_variant
chr1	148344615	G	GC	INDEL	0.132	0.101	upstream_gene_variant
chr1	154461505	G	A	SNV	0.128	0.331	upstream_gene_variant
chr1	155005648	C	T	SNV	0.116	0.167	missense_variant
chr1	155280104	C	CT	INDEL	0.133	0.184	splice_region_variant&intron_variant
chr1	157660172	C	T	SNV	0.087	0.305	synonymous_variant
chr1	158582497	GA	G	INDEL	0.217	0.196	upstream_gene_variant
chr1	158670040	T	A	SNV	0.054	0.319	missense_variant
chr1	159684121	CT	C	INDEL	0.326	0.274	upstream_gene_variant
chr1	16388875	GCC	G	INDEL	1.000	0.667	intron_variant
chr1	169101273	T	TG	INDEL	0.710	0.716	3_prime_UTR_variant
chr1	170633186	AT	A	INDEL	1.000	0.688	5_prime_UTR_variant
chr1	171558447	GT	G	INDEL	0.400	0.301	intron_variant
chr1	196397312	C	T	SNV	0.040	0.155	missense_variant
chr1	200558286	GA	G	INDEL	0.467	1.000	intron_variant
chr1	201981116	G	GT	INDEL	0.507	0.456	frameshift_variant
chr1	207091138	AT	A	INDEL	0.245	0.227	intron_variant
chr1	210001471	G	T	SNV	0.075	0.181	missense_variant
chr1	212526422	G	A	SNV	0.128	0.372	upstream_gene_variant
chr1	216246651	T	C	SNV	0.219	0.429	intron_variant
chr1	242122274	C	T	SNV	0.041	0.187	non_coding_transcript_exon_variant
chr1	247091604	CA	C	INDEL	0.214	0.250	intron_variant
chr1	43805083	A	T	SNV	0.109	0.187	missense_variant
chr1	93691855	GT	G	INDEL	0.300	0.256	intron_variant
chr1	94312544	G	GGC	INDEL	0.085	0.067	upstream_gene_variant
chr2	10188712	C	G	SNV	0.054	0.138	synonymous_variant
chr2	10188713	A	G	SNV	0.055	0.127	missense_variant
chr2	10269043	AAG	A	INDEL	0.078	0.184	frameshift_variant
chr2	11273407	GTC	G	INDEL	0.254	0.234	5_prime_UTR_variant

chr2	120714401	CT	C	INDEL	0.229	0.290	splice_region_variant&intron_variant
chr2	121746076	G	A	SNV	0.125	0.240	synonymous_variant
chr2	166810161	G	GCCCGCCC	INDEL	0.208	0.320	upstream_gene_variant
chr2	179415787	G	A	SNV	0.047	0.191	missense_variant
chr2	185800489	T	C	SNV	0.160	0.231	intron_variant
chr2	187529823	ATT	A	INDEL	0.246	0.293	upstream_gene_variant
chr2	217142458	G	A	SNV	0.071	0.197	missense_variant
chr2	219920551	G	A	SNV	0.164	0.198	missense_variant
chr2	29445163	T	C	SNV	0.094	0.204	intron_variant
chr2	32842836	C	T	SNV	0.104	0.229	synonymous_variant
chr2	55186296	A	G	SNV	0.156	0.232	missense_variant
chr2	96517957	ATT	A	INDEL	0.094	0.071	downstream_gene_variant
chr2	96605652	CAA	C	INDEL	1.000	0.500	intron_variant
chr3	124774779	A	AGGGCAG	INDEL	1.000	0.217	5_prime_UTR_variant
chr3	126268280	T	C	SNV	0.211	0.417	downstream_gene_variant
chr3	160955882	CTT	C	INDEL	0.571	0.500	splice_region_variant&intron_variant
chr3	183884669	G	A	SNV	0.081	0.159	missense_variant
chr3	32568145	C	CCA	INDEL	0.092	0.158	3_prime_UTR_variant
chr3	38639339	T	G	SNV	0.053	0.199	missense_variant
chr3	47018447	CA	C	INDEL	0.286	0.444	5_prime_UTR_variant
chr3	47449947	G	A	SNV	0.070	0.177	missense_variant
chr3	48697209	G	A	SNV	0.085	0.250	synonymous_variant
chr3	51422741	CGGA	C	INDEL	0.091	0.061	start_lost&conservative_inframe_deletion
chr3	58817341	G	T	SNV	0.048	0.210	intron_variant
chr3	75718167	GC	G	INDEL	0.118	0.078	upstream_gene_variant
chr4	169086540	CA	C	INDEL	0.333	0.364	intron_variant
chr5	10263451	TGGAG	T	INDEL	0.794	0.745	downstream_gene_variant
chr5	140503037	C	T	SNV	0.066	0.313	missense_variant
chr5	140764320	G	A	SNV	0.099	0.273	synonymous_variant
chr5	140768679	C	T	SNV	0.051	0.271	missense_variant
chr5	140810918	C	T	SNV	0.134	0.325	missense_variant
chr5	151169791	CA	C	INDEL	0.250	0.333	downstream_gene_variant

chr5	179233663	A	AGGC	INDEL	0.250	0.125	5_prime_UTR_variant
chr5	38427422	C	A	SNV	0.093	0.262	downstream_gene_variant
chr5	68862363	TGG	T	INDEL	0.545	0.385	downstream_gene_variant
chr5	74930800	G	T	SNV	0.111	0.263	synonymous_variant
chr6	109659589	TCA	T	INDEL	0.833	0.625	upstream_gene_variant
chr6	121433737	C	A	SNV	0.101	0.156	missense_variant
chr6	131211616	GA	G	INDEL	0.500	0.221	upstream_gene_variant
chr6	142409507	C	T	SNV	0.085	0.235	missense_variant
chr6	143792157	G	A	SNV	0.044	0.202	missense_variant
chr6	158294104	CT	C	INDEL	0.207	0.300	downstream_gene_variant
chr6	22146818	AT	A	INDEL	0.933	0.615	upstream_gene_variant
chr6	29694336	A	ATG	INDEL	1.000	1.000	upstream_gene_variant
chr6	31976139	GG	G	INDEL	0.297	0.492	upstream_gene_variant
chr6	32147291	CT	C	INDEL	0.203	0.145	upstream_gene_variant
chr6	32551947	CG	C	INDEL	0.111	0.091	frameshift_variant
chr6	32551954	CG	C	INDEL	0.122	0.105	frameshift_variant
chr6	32557375	T	TA	INDEL	0.123	0.147	intron_variant
chr6	32610140	T	TTTCTTTC	INDEL	0.135	0.064	downstream_gene_variant
chr6	33101200	T	TA	INDEL	0.317	0.381	downstream_gene_variant
chr6	401586	A	C	SNV	0.035	0.268	missense_variant
chr6	41712723	GTCTGTC	G	INDEL	0.205	0.224	intron_variant
chr7	105278904	G	A	SNV	0.039	0.145	synonymous_variant
chr7	128298973	G	GT	INDEL	0.233	0.292	upstream_gene_variant
chr7	129846823	TA	T	INDEL	0.375	0.278	splice_region_variant&intron_variant
chr7	138356734	G	GTTGGCT	INDEL	0.088	0.082	intron_variant
chr7	139746599	AGT	A	INDEL	0.229	0.213	intron_variant
chr7	141536351	CAG	C	INDEL	0.089	0.088	intron_variant
chr7	150754000	G	A	SNV	0.071	0.150	synonymous_variant
chr7	151814026	C	T	SNV	0.061	0.159	missense_variant
chr7	151882622	TAG	T	INDEL	0.061	0.143	upstream_gene_variant
chr7	154002658	CGT	C	INDEL	0.074	0.061	intron_variant
chr7	155465438	CAAAA	C	INDEL	0.250	0.438	sequence_feature

chr7	35851738	CA	C	INDEL	0.625	0.667	intron_variant
chr7	38543104	G	GC	INDEL	0.588	0.430	intron_variant
chr7	50450230	C	T	SNV	0.037	0.166	splice_region_variant&intron_variant
chr7	73929947	A	G	SNV	0.161	0.134	intron_variant
chr7	933611	AAGCCGG	A	INDEL	0.181	0.168	splice_region_variant&intron_variant
chr7	99711096	G	A	SNV	0.148	0.376	upstream_gene_variant
chr8	105509428	C	CA	INDEL	0.131	0.439	frameshift_variant
chr8	132051740	GGCGAAG	G	INDEL	0.078	0.206	frameshift_variant
chr8	144240312	G	A	SNV	0.137	0.345	missense_variant
chr8	22009453	C	G	SNV	0.077	0.205	synonymous_variant
chr8	25268493	GCGCGCG	G	INDEL	0.222	0.222	intron_variant
chr8	52321783	G	A	SNV	0.080	0.115	missense_variant
chr9	117129727	T	C	SNV	0.040	0.163	intron_variant
chr9	123762336	C	CA	INDEL	0.200	0.267	splice_region_variant&intron_variant
chr9	134379628	C	T	SNV	0.059	0.198	missense_variant
chr9	135204150	G	T	SNV	0.058	0.188	missense_variant
chr9	84267021	TAC	T	INDEL	0.167	0.189	intron_variant
chr10	112697017	CT	C	INDEL	0.160	0.119	upstream_gene_variant
chr10	134016407	C	T	SNV	0.055	0.168	upstream_gene_variant
chr10	14569998	C	CTT	INDEL	0.667	0.583	3_prime_UTR_variant
chr10	17898179	CA	C	INDEL	0.400	0.327	downstream_gene_variant
chr10	19678455	C	T	SNV	0.150	0.254	stop_gained
chr10	24498289	G	GA	INDEL	0.345	0.337	intron_variant
chr10	28274145	C	CAA	INDEL	0.400	0.462	splice_region_variant&intron_variant
chr10	38260558	AACACAC	A	INDEL	0.500	0.625	intron_variant
chr10	42941685	T	TA	INDEL	0.500	0.667	intron_variant
chr10	52502792	G	GTGCA	INDEL	0.092	0.076	intron_variant
chr10	54011325	T	A	SNV	0.047	0.239	splice_region_variant&intron_variant
chr10	61574357	AAC	A	INDEL	0.076	0.122	upstream_gene_variant
chr10	74098315	C	CAA	INDEL	0.286	0.344	upstream_gene_variant
chr10	89720633	C	CT	INDEL	0.800	0.286	splice_acceptor_variant&intron_variant
chr10	97725542	TTG	T	INDEL	0.182	0.500	intron_variant

chr11	104872624	TAC	T	INDEL	0.060	0.078	upstream_gene_variant
chr11	10711918	TA	T	INDEL	0.171	0.115	splice_region_variant&intron_variant
chr11	120292373	T	C	SNV	0.112	0.045	intron_variant
chr11	1213573	T	TCCACAC	INDEL	0.181	0.129	non_coding_transcript_exon_variant
chr11	33770312	G	A	SNV	0.103	0.235	intron_variant
chr11	43413157	TTTGCG	T	INDEL	0.125	0.179	upstream_gene_variant
chr11	45924491	G	T	SNV	0.100	0.205	synonymous_variant
chr11	47755552	CA	C	INDEL	0.235	0.286	upstream_gene_variant
chr11	58379663	CGT	C	INDEL	0.062	0.068	upstream_gene_variant
chr11	62751721	C	CT	INDEL	0.563	0.301	upstream_gene_variant
chr11	65636047	C	T	SNV	0.042	0.222	missense_variant
chr11	67795291	C	T	SNV	0.105	0.163	missense_variant
chr11	73675860	G	GCGCGCG(	INDEL	0.087	0.228	upstream_gene_variant
chr12	103352681	ACCCGCTC	A	INDEL	0.063	0.279	frameshift_variant
chr12	10586978	A	AT	INDEL	0.300	0.296	upstream_gene_variant
chr12	12630578	A	G	SNV	0.064	0.220	missense_variant
chr12	132313098	G	GGCTGCC(	INDEL	0.714	0.813	disruptive_inframe_insertion
chr12	132398254	AAC	A	INDEL	0.277	0.263	upstream_gene_variant
chr12	14946973	C	CA	INDEL	1.000	0.286	intron_variant
chr12	29596260	TCAGTAG(	T	INDEL	0.083	0.087	splice_region_variant&intron_variant
chr12	306372	C	CATCATCC	INDEL	0.316	0.382	downstream_gene_variant
chr12	51857449	C	G	SNV	0.154	0.192	missense_variant
chr12	56502908	CA	C	INDEL	0.286	0.467	upstream_gene_variant
chr12	80889165	T	TTTG	INDEL	0.250	0.389	intron_variant
chr12	9583167	AG	A	INDEL	0.163	0.137	intron_variant
chr13	114312605	G	GA	INDEL	0.852	0.844	upstream_gene_variant
chr13	25671272	AG	A	INDEL	0.070	0.080	frameshift_variant
chr13	25671310	TTATGA	T	INDEL	0.150	0.129	frameshift_variant
chr13	42042873	ACT	A	INDEL	0.063	0.131	intron_variant
chr14	100742719	G	T	SNV	0.057	0.162	downstream_gene_variant
chr14	106067207	C	G	SNV	0.067	0.159	upstream_gene_variant
chr14	50649285	C	A	SNV	0.099	0.256	stop_gained

chr14	57942425	TA	T	INDEL	0.357	0.421	splice_region_variant&intron_variant
chr14	65392929	CT	C	INDEL	0.500	0.667	downstream_gene_variant
chr14	68008899	T	TA	INDEL	0.471	0.463	intron_variant
chr14	73959703	C	CTT	INDEL	0.188	0.242	upstream_gene_variant
chr14	76446873	A	G	SNV	0.062	0.171	downstream_gene_variant
chr14	91710562	GACAC	G	INDEL	0.156	0.400	intron_variant
chr14	93107606	G	A	SNV	0.044	0.139	missense_variant
chr14	94008977	G	A	SNV	0.064	0.202	missense_variant
chr15	28326952	G	A	SNV	0.133	0.244	synonymous_variant
chr15	28518114	TC	T	INDEL	0.095	0.069	frameshift_variant
chr15	30437549	A	AG	INDEL	0.333	0.199	downstream_gene_variant
chr15	38641776	A	AAATTAG	INDEL	0.833	1.000	intron_variant
chr15	40235552	CT	C	INDEL	0.500	0.385	intron_variant
chr15	40583923	G	A	SNV	0.046	0.232	3_prime_UTR_variant
chr15	40862191	G	GGTTTTGT	INDEL	0.163	0.213	upstream_gene_variant
chr15	48826427	GA	G	INDEL	0.500	0.379	sequence_feature
chr15	68500317	G	GAC	INDEL	0.682	0.727	3_prime_UTR_variant
chr15	90328748	AAGATT	A	INDEL	0.129	0.099	intron_variant
chr15	90328754	C	G	SNV	0.135	0.111	intron_variant
chr15	93007468	C	G	SNV	0.107	0.146	synonymous_variant
chr15	93410345	A	ATC	INDEL	0.171	0.203	intergenic_region
chr15	99514423	TGGGGGG	T	INDEL	0.463	0.387	intron_variant
chr16	1493826	GGT	G	INDEL	0.071	0.207	frameshift_variant
chr16	15457634	A	T	SNV	0.356	0.052	missense_variant
chr16	15457638	A	G	SNV	0.324	0.037	missense_variant
chr16	15609245	C	T	SNV	0.033	0.235	missense_variant
chr16	15865292	CT	C	INDEL	0.250	0.255	downstream_gene_variant
chr16	16381738	T	TA	INDEL	0.255	0.157	downstream_gene_variant
chr16	19278429	T	TAA	INDEL	0.400	0.302	3_prime_UTR_variant
chr16	21412275	T	TA	INDEL	1.000	0.800	downstream_gene_variant
chr16	4546127	CTT	C	INDEL	0.769	0.500	splice_region_variant&intron_variant
chr16	50186988	G	A	SNV	0.152	0.235	upstream_gene_variant

chr16	57059758	A	T	SNV	0.071	0.219	missense_variant
chr16	89346098	G	A	SNV	0.095	0.283	synonymous_variant
chr16	89784471	CT	C	INDEL	0.062	0.076	upstream_gene_variant
chr16	89981345	T	TTG	INDEL	0.379	0.357	5_prime_UTR_variant
chr17	11659920	G	A	SNV	0.113	0.255	synonymous_variant
chr17	17931884	C	CA	INDEL	0.200	0.267	upstream_gene_variant
chr17	29647361	TA	T	INDEL	0.204	0.269	upstream_gene_variant
chr17	40837178	A	G	SNV	0.110	0.335	upstream_gene_variant
chr17	7578550	G	A	SNV	0.116	0.294	structural_interaction_variant
chr17	7700419	CAA	C	INDEL	0.143	0.173	intron_variant
chr17	80915236	T	C	SNV	0.096	0.295	missense_variant&splice_region_variant
chr18	10718236	C	T	SNV	0.083	0.165	missense_variant
chr18	13746320	G	A	SNV	0.079	0.169	missense_variant
chr18	29672592	AG	A	INDEL	0.400	0.333	5_prime_UTR_variant
chr18	29693953	C	G	SNV	0.094	0.226	downstream_gene_variant
chr18	3188664	TAC	T	INDEL	0.067	0.081	upstream_gene_variant
chr18	40503735	GA	G	INDEL	0.324	0.244	splice_region_variant&intron_variant
chr18	43487885	TA	T	INDEL	0.389	0.318	intron_variant
chr19	1005265	G	A	SNV	0.113	0.273	missense_variant
chr19	10229240	CA	C	INDEL	0.324	0.314	splice_region_variant&intron_variant
chr19	13318300	G	A	SNV	0.073	0.303	missense_variant
chr19	15932574	CCACACAC	C	INDEL	0.500	0.439	downstream_gene_variant
chr19	1827020	T	TGGA	INDEL	0.231	0.149	conservative_inframe_insertion
chr19	2979962	CA	C	INDEL	0.192	0.168	upstream_gene_variant
chr19	36003877	TCAA	T	INDEL	0.171	0.105	upstream_gene_variant
chr19	39071143	C	T	SNV	0.067	0.178	missense_variant&splice_region_variant
chr19	39226648	AGGTCTCC	A	INDEL	0.800	0.826	upstream_gene_variant
chr19	4885688	T	TG	INDEL	0.444	0.800	downstream_gene_variant
chr19	50302897	C	T	SNV	0.083	0.225	synonymous_variant
chr19	51331204	T	TTG	INDEL	0.800	0.811	upstream_gene_variant
chr19	53875365	G	A	SNV	0.060	0.200	intron_variant
chr19	55488178	C	CTCTT	INDEL	0.097	0.068	downstream_gene_variant

chr19	55598003	G	GC	INDEL	0.259	0.286	upstream_gene_variant
chr19	5667204	AC	A	INDEL	0.250	0.157	sequence_feature
chr19	7529500	G	T	SNV	0.055	0.184	missense_variant
chr19	8601051	G	GTC	INDEL	0.227	0.478	downstream_gene_variant
chr20	17462058	A	AGAG	INDEL	0.667	0.304	upstream_gene_variant
chr20	18414185	CA	C	INDEL	0.313	0.259	upstream_gene_variant
chr20	25756020	CA	C	INDEL	0.238	0.143	upstream_gene_variant
chr20	26061746	CT	C	INDEL	0.394	0.324	downstream_gene_variant
chr20	2673644	GGGCGCT	G	INDEL	1.000	0.800	5_prime_UTR_variant
chr20	29623257	TTG	T	INDEL	0.070	0.065	splice_region_variant&intron_variant
chr20	29624020	G	GT	INDEL	0.326	0.230	splice_region_variant&intron_variant
chr20	33500343	T	C	SNV	0.070	0.046	upstream_gene_variant
chr20	36628853	A	ACGGCCA(	INDEL	0.188	0.173	intron_variant
chr21	10969894	A	G	SNV	0.186	0.102	intron_variant
chr21	15746137	C	T	SNV	0.084	0.154	missense_variant
chr21	19628809	CT	C	INDEL	0.304	0.139	splice_region_variant&intron_variant
chr21	30438952	AT	A	INDEL	0.429	0.333	upstream_gene_variant
chr21	40636354	TAAA	T	INDEL	0.375	0.250	intron_variant
chr21	48064255	G	A	SNV	0.101	0.207	missense_variant
chr22	17600985	C	T	SNV	0.087	0.234	missense_variant
chr22	20656732	AG	A	INDEL	0.083	0.172	intron_variant
chr22	24141236	CA	C	INDEL	0.222	0.214	intron_variant
chr22	30051705	CT	C	INDEL	0.439	0.311	sequence_feature
chr22	39882149	AT	A	INDEL	0.368	0.519	splice_region_variant&intron_variant
chr22	40364462	AAC	A	INDEL	0.833	0.526	upstream_gene_variant
chr22	42951978	GC	G	INDEL	0.700	0.667	upstream_gene_variant
chr22	47882347	C	T	SNV	0.109	0.218	intron_variant
chr22	50547296	A	T	SNV	0.088	0.222	downstream_gene_variant
chr22	51043245	C	T	SNV	0.192	0.244	synonymous_variant
chr22	51135989	GTT	G	INDEL	1.000	1.000	frameshift_variant
chrX	114141233	A	C	SNV	0.182	0.416	missense_variant
chrX	123184949	CT	C	INDEL	0.333	0.333	splice_region_variant&intron_variant

chrX	135961586	TG	T	INDEL	0.207	0.270	frameshift_variant
chrX	148851540	TG	T	INDEL	0.698	0.656	upstream_gene_variant
chrX	15262814	T	TA	INDEL	0.737	0.765	intron_variant
chrX	153151280	G	GCC	INDEL	1.000	1.000	frameshift_variant
chrX	153151284	GT	G	INDEL	1.000	1.000	frameshift_variant
chrX	19380975	TA	T	INDEL	0.375	0.308	splice_region_variant&intron_variant
chrX	44758425	T	G	SNV	0.185	0.467	intron_variant
chrX	44772989	GTA	G	INDEL	0.316	0.132	intron_variant
chrX	52654061	A	G	SNV	0.228	0.461	non_coding_transcript_exon_variant
chrX	71933512	TCA	T	INDEL	0.143	0.306	downstream_gene_variant
chrX	76965132	TA	T	INDEL	0.500	0.500	intron_variant
chrY	13310690	TTC	T	INDEL	0.159	0.128	intergenic_region
chrY	24052494	AG	A	INDEL	0.375	1.000	intron_variant

CHROM	POS	PutativeImpact	GeneSymbol	EnsemblID	NucleotideChange	AAChange
chr1	109745855	MODIFIER	KIAA1324	ENSG00000116299	c.*221T>G	
chr1	114224782	MODIFIER	MAGI3	ENSG00000081026	c.3329-721delT	
chr1	119962130	MODERATE	HSD3B2	ENSG00000203859	c.232G>A	p.Val78Ile
chr1	148344615	MODIFIER	PFN1P3	ENSG00000234367	n.-4641_-4640insC	
chr1	154461505	MODIFIER	SHE	ENSG00000169291	c.-2986C>T	
chr1	155005648	MODERATE	DCST2	ENSG00000163354	c.361G>A	p.Glu121Lys
chr1	155280104	LOW	FDPS	ENSG00000160752	n.255-8dupT	
chr1	157660172	LOW	FCRL3	ENSG00000160856	c.1563G>A	p.Ser521Ser
chr1	158582497	MODIFIER	SPTA1	ENSG00000163554	n.-683delT	
chr1	158670040	MODERATE	OR6K2	ENSG00000196171	c.403A>T	p.Met135Leu
chr1	159684121	MODIFIER	CRP	ENSG00000132693	n.-565delA	
chr1	16388875	MODIFIER	FAM131C	ENSG00000185519	c.174+117_174+118delGG	
chr1	169101273	MODIFIER	ATP1B1	ENSG00000143153	c.*480_*481insG	
chr1	170633186	MODIFIER	PRRX1	ENSG00000116132	c.-162delT	
chr1	171558447	MODIFIER	PRRC2C	ENSG00000117523	c.8200-39delT	
chr1	196397312	MODERATE	KCNT2	ENSG00000162687	c.907G>A	p.Val303Ile
chr1	200558286	MODIFIER	KIF14	ENSG00000118193	c.3114+58delT	
chr1	201981116	HIGH	ELF3	ENSG00000163435	c.197dupT	p.Trp67fs
chr1	207091138	MODIFIER	FAIM3	ENSG00000162894	c.38-3700delA	
chr1	210001471	MODERATE	DIEXF	ENSG00000117597	c.63G>T	p.Lys21Asn
chr1	212526422	MODIFIER	RP11-384C4.2	ENSG00000229832	n.-4338G>A	
chr1	216246651	MODIFIER	USH2A	ENSG00000042781	c.5573-9A>G	
chr1	242122274	MODIFIER	BECN1P1	ENSG00000196289	n.1233C>T	
chr1	247091604	MODIFIER	AHCTF1	ENSG00000153207	c.98+2826delT	
chr1	43805083	MODERATE	MPL	ENSG00000117400	c.533A>T	p.Asn178Ile
chr1	93691855	MODIFIER	CCDC18	ENSG00000122483	c.2332-19delT	
chr1	94312544	MODIFIER	RP4-561L24.3	ENSG00000260464	n.-186_-185insGC	
chr2	10188712	LOW	KLF11	ENSG00000172059	c.1248C>G	p.Arg416Arg
chr2	10188713	MODERATE	KLF11	ENSG00000172059	c.1249A>G	p.Thr417Ala
chr2	10269043	HIGH	RRM2	ENSG00000171848	c.1051_1052delGA	p.Glu351fs
chr2	11273407	MODIFIER	C2orf50	ENSG00000150873	c.-36_-35delCT	

chr2	120714401	LOW	PTPN4	ENSG00000088179	c.1981-3delT	
chr2	121746076	LOW	GLI2	ENSG00000074047	c.2586G>A	p.Ala862Ala
chr2	166810161	MODIFIER	AC010127.3	ENSG00000236107	n.-3748_-3747insCCCGCCCGCTCA	
chr2	179415787	MODERATE	TTN	ENSG00000155657	c.91471C>T	p.Arg30491Cys
chr2	185800489	MODIFIER	ZNF804A	ENSG00000170396	c.387-21T>C	
chr2	187529823	MODIFIER	ITGAV	ENSG00000138448	n.-29_-28delTT	
chr2	217142458	MODERATE	MARCH4	ENSG00000144583	c.802C>T	p.Arg268Cys
chr2	219920551	MODERATE	IHH	ENSG00000163501	c.614C>T	p.Pro205Leu
chr2	29445163	MODIFIER	ALK	ENSG00000171094	c.3515+47A>G	
chr2	32842836	LOW	BIRC6	ENSG00000115760	c.14439C>T	p.Cys4813Cys
chr2	55186296	MODERATE	EML6	ENSG00000214595	c.4751A>G	p.His1584Arg
chr2	96517957	MODIFIER	ANKRD36C	ENSG00000174501	n.*79_*80delAA	
chr2	96605652	MODIFIER	ANKRD36C	ENSG00000174501	c.1532-891_1532-890delTT	
chr3	124774779	MODIFIER	HEG1	ENSG00000173706	c.-52_-46dupGCTGCCC	
chr3	126268280	MODIFIER	C3orf22	ENSG00000180697	c.*431A>G	
chr3	160955882	LOW	NMD3	ENSG00000169251	c.578-5_578-4delTT	
chr3	183884669	MODERATE	DVL3	ENSG00000161202	c.1104G>A	p.Met368Ile
chr3	32568145	MODIFIER	DYNC1LI1	ENSG00000144635	c.*144_*145dupTG	
chr3	38639339	MODERATE	SCN5A	ENSG00000183873	c.2143A>C	p.Met715Leu
chr3	47018447	MODIFIER	CCDC12	ENSG00000160799	c.-93delT	
chr3	47449947	MODERATE	PTPN23	ENSG00000076201	c.1297G>A	p.Asp433Asn
chr3	48697209	LOW	CELSR3	ENSG00000008300	c.2859C>T	p.Asp953Asp
chr3	51422741	HIGH	MANF	ENSG00000145050	c.-2_1delGGA	p.Met1del
chr3	58817341	MODIFIER	C3orf67	ENSG00000163689	c.1800+71C>A	
chr3	75718167	MODIFIER	LINC00960	ENSG00000242516	n.-3374delC	
chr4	169086540	MODIFIER	ANXA10	ENSG00000109511	c.480+80delA	
chr5	10263451	MODIFIER	CTD-2256P15	ENSG00000271980	n.*1254_*1257delCTCC	
chr5	140503037	MODERATE	PCDHB4	ENSG00000081818	c.1457C>T	p.Thr486Ile
chr5	140764320	LOW	PCDHGA7	ENSG00000253537	c.1854G>A	p.Ala618Ala
chr5	140768679	MODERATE	PCDHGB4	ENSG00000253953	c.1228C>T	p.Arg410Cys
chr5	140810918	MODERATE	PCDHGA12	ENSG00000253159	c.592C>T	p.Arg198Cys
chr5	151169791	MODIFIER	G3BP1	ENSG00000145907	n.*2845delA	

chr5	179233663	MODIFIER	MGAT4B	ENSG00000161013	c.-83_-81dupGCC	
chr5	38427422	MODIFIER	CTD-2108O9.4	ENSG00000248234	n.*2572G>T	
chr5	68862363	MODIFIER	GTF2H2C	ENSG00000183474	n.*1404_*1405delGG	
chr5	74930800	LOW	ANKDD1B	ENSG00000189045	c.678G>T	p.Leu226Leu
chr6	109659589	MODIFIER	CCDC162P	ENSG00000203799	n.-88_-87delCA	
chr6	121433737	MODERATE	TBC1D32	ENSG00000146350	c.3361G>T	p.Asp1121Tyr
chr6	131211616	MODIFIER	EPB41L2	ENSG00000079819	c.-54delT	
chr6	142409507	MODERATE	NMBR	ENSG00000135577	c.289G>A	p.Val97Ile
chr6	143792157	MODERATE	PEX3	ENSG00000034693	c.391G>A	p.Val131Ile
chr6	158294104	MODIFIER	RP11-52J3.2	ENSG00000229502	n.*1037delA	
chr6	22146818	MODIFIER	CASC15	ENSG00000272168	n.-618delT	
chr6	29694336	MODIFIER	HCG4P11	ENSG00000225864	n.-2590_-2589dupCA	
chr6	31976139	MODIFIER	C4A-AS1	ENSG00000233627	n.-4842delC	
chr6	32147291	MODIFIER	AGPAT1	ENSG00000204310	c.-8019delA	
chr6	32551947	HIGH	HLA-DRB1	ENSG00000196126	c.308delC	p.Ala103fs
chr6	32551954	HIGH	HLA-DRB1	ENSG00000196126	c.301delC	p.Arg101fs
chr6	32557375	MODIFIER	HLA-DRB1	ENSG00000196126	c.100+44_100+45insT	
chr6	32610140	MODIFIER	HLA-DQA1	ENSG00000196735	c.*4832_*4833insTTCTTTC	
chr6	33101200	MODIFIER	HLA-DPB2	ENSG00000224557	n.*4339_*4340insA	
chr6	401586	MODERATE	IRF4	ENSG00000137265	c.908A>C	p.Asn303Thr
chr6	41712723	MODIFIER	PGC	ENSG00000096088	c.60-183_60-178delGACAGA	
chr7	105278904	LOW	ATXN7L1	ENSG00000146776	c.1098C>T	p.Ser366Ser
chr7	128298973	MODIFIER	AC018638.1	ENSG00000229413	n.-4985_-4984insA	
chr7	129846823	LOW	TMEM209	ENSG00000146842	c.31-6delT	
chr7	138356734	MODIFIER	SVOPL	ENSG00000157703	c.273+29_273+30insAGCCAA	
chr7	139746599	MODIFIER	PARP12	ENSG00000059378	c.986+83_986+84delAC	
chr7	141536351	MODIFIER	PRSS37	ENSG00000165076	c.568-18_568-17delCT	
chr7	150754000	LOW	CDK5	ENSG00000164885	c.189C>T	p.Ile63Ile
chr7	151814026	MODERATE	GALNT11	ENSG00000178234	c.191C>T	p.Pro64Leu
chr7	151882622	MODIFIER	KMT2C	ENSG00000055609	c.-3320_-3319delCT	
chr7	154002658	MODIFIER	DPP6	ENSG00000130226	c.244-140627_244-140626delTG	
chr7	155465438	MODERATE	RBM33	ENSG00000184863	c.123-122_123-119delAAAA	

chr7	35851738	MODIFIER	SEPT7	ENSG00000122545	c.69+74delA	
chr7	38543104	MODIFIER	AMPH	ENSG00000078053	c.205+145_205+146insG	
chr7	50450230	LOW	IKZF1	ENSG00000185811	c.422-8C>T	
chr7	73929947	MODIFIER	GTF2IRD1	ENSG00000006704	c.517+21A>G	
chr7	933611	LOW	GET4	ENSG00000239857	c.895+8_895+36delGGGGCGCCCTT GTCACACCCACTCCAGCC	
chr7	99711096	MODIFIER	TAF6	ENSG00000106290	n.-2149C>T	
chr8	105509428	HIGH	LRP12	ENSG00000147650	c.1351dupT	p.Cys451fs
chr8	132051740	HIGH	ADCY8	ENSG00000155897	c.824_839delTCTTCACGCTCTTCGC	p.Leu275fs
chr8	144240312	MODERATE	LY6H	ENSG00000176956	c.158C>T	p.Thr53Ile
chr8	22009453	LOW	LGI3	ENSG00000168481	c.555G>C	p.Leu185Leu
chr8	25268493	MODIFIER	DOCK5	ENSG00000147459	c.5509-213_5509-206delGCGCACGC	
chr8	52321783	MODERATE	PXDNL	ENSG00000147485	c.2401C>T	p.Arg801Cys
chr9	117129727	MODIFIER	AKNA	ENSG00000106948	c.1728+96A>G	
chr9	123762336	LOW	C5	ENSG00000106804	n.166-8dupT	
chr9	134379628	MODERATE	POMT1	ENSG00000130714	c.23C>T	p.Pro8Leu
chr9	135204150	MODERATE	SETX	ENSG00000107290	c.2835C>A	p.Asp945Glu
chr9	84267021	MODIFIER	TLE1	ENSG00000196781	c.372+106_372+107delGT	
chr10	112697017	MODIFIER	RPL13AP6	ENSG00000234118	n.-27delA	
chr10	134016407	MODIFIER	DPYSL4	ENSG00000151640	n.-650C>T	
chr10	14569998	MODIFIER	FAM107B	ENSG00000065809	c.*11_*12dupAA	
chr10	17898179	MODIFIER	MRC1L1	ENSG00000183748	c.*1348delA	
chr10	19678455	HIGH	MALRD1	ENSG00000204740	c.2869C>T	p.Arg957*
chr10	24498289	MODIFIER	KIAA1217	ENSG00000120549	c.70+111dupA	
chr10	28274145	LOW	ARMC4	ENSG00000169126	c.383-7_383-6dupTT	
chr10	38260558	MODIFIER	ZNF25	ENSG00000175395	c.15+70_15+77delGTGTGTGT	
chr10	42941685	MODIFIER	CCNYL2	ENSG00000182632	n.698+5371dupT	
chr10	52502792	MODIFIER	ASAH2B	ENSG00000204147	c.86+25_86+26insATGC	
chr10	54011325	LOW	PRKG1	ENSG00000185532	c.1077-5T>A	
chr10	61574357	MODIFIER	CCDC6	ENSG00000108091	n.-1873_-1872delGT	
chr10	74098315	MODIFIER	DNAJB12	ENSG00000148719	n.-1694_-1693dupTT	
chr10	89720633	HIGH	PTEN	ENSG00000171862	c.802-3dupT	

chr10	97725542	MODIFIER	ENTPD1-AS1	ENSG00000226688	n.276-89127_276-89126delCA	
chr11	104872624	MODIFIER	CASP5	ENSG00000137757	c.-2873_-2872delGT	
chr11	10711918	LOW	MRVI1	ENSG00000072952	c.-882-3delT	
chr11	120292373	MODIFIER	ARHGEF12	ENSG00000196914	c.299-139T>C	
chr11	1213573	MODIFIER	MUC5AC	ENSG00000215182	n.815_816insCACACC	
chr11	33770312	MODIFIER	FBXO3	ENSG00000110429	c.1048+11C>T	
chr11	43413157	MODIFIER	TTC17	ENSG00000052841	n.-4528_-4524delTTGCG	
chr11	45924491	LOW	MAPK8IP1	ENSG00000121653	c.1173G>T	p.Leu391Leu
chr11	47755552	MODIFIER	FNBP4	ENSG00000109920	n.-1743delT	
chr11	58379663	MODIFIER	AP001350.1	ENSG00000269570	c.-906_-905delAC	
chr11	62751721	MODIFIER	SLC22A6	ENSG00000197901	n.-358dupA	
chr11	65636047	MODERATE	EFEMP2	ENSG00000172638	c.781G>A	p.Glu261Lys
chr11	67795291	MODERATE	ALDH3B1	ENSG00000006534	c.1285C>T	p.Arg429Cys
chr11	73675860	MODIFIER	DNAJB13	ENSG00000187726	c.-3449_-3448insCGCGCGCGCGCGCC	
chr12	103352681	HIGH	ASCL1	ENSG00000139352	c.664_673delCTCAGCCCCG	p.Leu222fs
chr12	10586978	MODIFIER	KLRC2	ENSG00000205809	c.-476dupA	
chr12	12630578	MODERATE	DUSP16	ENSG00000111266	c.1187T>C	p.Leu396Pro
chr12	132313098	MODERATE	MMP17	ENSG00000198598	c.62_70dupTGCCGCTGC	p.Leu21_Leu23dup
chr12	132398254	MODIFIER	ULK1	ENSG00000177169	c.-2766_-2765delAC	
chr12	14946973	MODIFIER	WBP11	ENSG00000084463	c.722-118dupT	
chr12	29596260	LOW	OVCH1	ENSG00000187950	c.3157+6_3157+33delTGATTTCCCATGAATCTCTATGCTACTG	
chr12	306372	MODIFIER	RP11-283I3.1	ENSG00000255671	n.*3076_*3077insATCATCCTCCCCCTCCTCTTTCTCATGGTA	
chr12	51857449	MODERATE	SLC4A8	ENSG00000050438	c.1300C>G	p.Gln434Glu
chr12	56502908	MODIFIER	PA2G4	ENSG00000170515	n.-744delA	
chr12	80889165	MODIFIER	PTPRQ	ENSG00000139304	c.1870+33_1870+35dupGTT	
chr12	9583167	MODIFIER	DDX12P	ENSG00000214826	n.1493+16delC	
chr13	114312605	MODIFIER	ATP4B	ENSG00000186009	c.-147_-146insT	
chr13	25671272	HIGH	PABPC3	ENSG00000151846	c.937delG	p.Ala313fs
chr13	25671310	HIGH	PABPC3	ENSG00000151846	c.976_980delATGAT	p.Met326fs
chr13	42042873	MODIFIER	RGCC	ENSG00000102760	c.344-19_344-18delTC	

chr14	100742719	MODIFIER	AL157871.2	ENSG00000259052	n.*3577C>A	
chr14	106067207	MODIFIER	AL928742.12	ENSG00000227468	n.-831G>C	
chr14	50649285	HIGH	SOS2	ENSG00000100485	c.754G>T	p.Glu252*
chr14	57942425	LOW	C14orf105	ENSG00000100557	c.653-4delT	
chr14	65392929	MODIFIER	CHURC1	ENSG00000258289	n.*1728delT	
chr14	68008899	MODIFIER	PLEKHH1	ENSG00000054690	c.126+189_126+190insA	
chr14	73959703	MODIFIER	HEATR4	ENSG00000187105	n.-1221_-1220dupAA	
chr14	76446873	MODIFIER	TGFB3	ENSG00000119699	n.*46T>C	
chr14	91710562	MODIFIER	GPR68	ENSG00000119714	c.-99-9043_-99-9040delGTGT	
chr14	93107606	MODERATE	RIN3	ENSG00000100599	c.464G>A	p.Arg155Gln
chr14	94008977	MODERATE	UNC79	ENSG00000133958	c.1690G>A	p.Val564Ile
chr15	28326952	LOW	OCA2	ENSG00000104044	c.69C>T	p.Ser23Ser
chr15	28518114	HIGH	HERC2	ENSG00000128731	c.836delG	p.Gly279fs
chr15	30437549	MODIFIER	RN7SL469P	ENSG00000241167	n.*1346_*1347insG	
chr15	38641776	MODIFIER	SPRED1	ENSG00000166068	c.684+52_684+53insAATTAGT	
chr15	40235552	MODIFIER	EIF2AK4	ENSG00000128829	c.258-12delT	
chr15	40583923	MODIFIER	PLCB2	ENSG00000137841	c.*44C>T	
chr15	40862191	MODIFIER	C15orf57	ENSG00000128891	c.-6997_-6978dupAAAACAAAACAAAACAAAAC	
chr15	48826427	LOW	FBN1	ENSG00000166147	c.737-26delT	
chr15	68500317	MODIFIER	CLN6	ENSG00000128973	c.*159_*160dupGT	
chr15	90328748	MODIFIER	ANPEP	ENSG00000166825	c.2752-21_2752-17delAATCT	
chr15	90328754	MODIFIER	ANPEP	ENSG00000166825	c.2752-22G>C	
chr15	93007468	LOW	ST8SIA2	ENSG00000140557	c.981C>G	p.Val327Val
chr15	93410345	MODIFIER	RN7SL599P-A	ENSG00000264123-ENSG00000272888	n.93410345_93410346insTC	
chr15	99514423	MODIFIER	RP11-654A16.	ENSG00000259475	n.267-5131_267-5125delCCCCCCC	
chr16	1493826	HIGH	CCDC154	ENSG00000197599	c.193_194delAC	p.Thr65fs
chr16	15457634	MODERATE	NPIPA5	ENSG00000183793	c.935T>A	p.Leu312Gln
chr16	15457638	MODERATE	NPIPA5	ENSG00000183793	c.931T>C	p.Cys311Arg
chr16	15609245	MODERATE	C16orf45	ENSG00000166780	c.190C>T	p.Arg64Trp

chr16	15865292	MODIFIER	MYH11	ENSG00000133392	n.*4406delA	
chr16	16381738	MODIFIER	RP11-517A5.5	ENSG00000262848	n.*2253dupT	
chr16	19278429	MODIFIER	SYT17	ENSG00000103528	c.*46_*47dupAA	
chr16	21412275	MODIFIER	NPIPB3	ENSG00000169246	c.*1329_*1330insT	
chr16	4546127	LOW	HMOX2	ENSG00000103415	n.293-4_293-3delTT	
chr16	50186988	MODIFIER	RPL10P14	ENSG00000260031	n.-1500C>T	
chr16	57059758	MODERATE	NLRC5	ENSG00000140853	c.903A>T	p.Gln301His
chr16	89346098	LOW	ANKRD11	ENSG00000167522	c.6852C>T	p.Ala2284Ala
chr16	89784471	MODIFIER	ZNF276	ENSG00000158805	c.-3577delT	
chr16	89981345	MODIFIER	MC1R	ENSG00000258839	c.-771_-770dupTG	
chr17	11659920	LOW	DNAH9	ENSG00000007174	c.6774G>A	p.Leu2258Leu
chr17	17931884	MODIFIER	ATPAF2	ENSG00000171953	n.-2940dupT	
chr17	29647361	MODIFIER	CTD-2370N5..	ENSG00000265118	c.-1514delT	
chr17	40837178	MODIFIER	CCR10	ENSG00000184451	c.-3337T>C	
chr17	7578550	HIGH	TP53	ENSG00000141510	c.380C>T	
chr17	7700419	MODIFIER	DNAH2	ENSG00000183914	c.7864-56_7864-55delAA	
chr17	80915236	MODERATE	B3GNTL1	ENSG00000175711	c.860A>G	p.Lys287Arg
chr18	10718236	MODERATE	PIEZO2	ENSG00000154864	c.4952G>A	p.Arg1651Gln
chr18	13746320	MODERATE	RNMT	ENSG00000101654	c.1241G>A	p.Arg414Gln
chr18	29672592	MODIFIER	RNF138	ENSG00000134758	c.-145delG	
chr18	29693953	MODIFIER	RP11-53I6.2	ENSG00000263917	n.*2211C>G	
chr18	3188664	MODIFIER	RP13-270P17.	ENSG00000265399	n.-1730_-1729delAC	
chr18	40503735	LOW	RIT2	ENSG00000152214	c.235-8delT	
chr18	43487885	MODIFIER	EPG5	ENSG00000152223	c.4329+37delT	
chr19	1005265	MODERATE	GRIN3B	ENSG00000116032	c.1765G>A	p.Ala589Thr
chr19	10229240	LOW	EIF3G	ENSG00000130811	c.301-8delT	
chr19	13318300	MODERATE	CACNA1A	ENSG00000141837	c.7348C>T	p.Arg2450Cys
chr19	15932574	MODIFIER	ZNF861P	ENSG00000267235	n.*24_*31delTGTGTGTG	
chr19	1827020	MODERATE	REXO1	ENSG00000079313	c.1765_1767dupTCC	p.Ser589dup
chr19	2979962	MODIFIER	TLE6	ENSG00000104953	n.-3941delA	
chr19	36003877	MODIFIER	DMKN	ENSG00000161249	c.-2768_-2766delTTG	
chr19	39071143	MODERATE	RYR1	ENSG00000196218	c.14645C>T	p.Thr4882Met

chr19	39226648	MODIFIER	CTD-2540F13	ENSG00000267892	n.-2275_-2258delGGTCTCGGGGGTCTCGGG	
chr19	4885688	MODIFIER	AC027319.1	ENSG00000221535	n.*3526_*3527insC	
chr19	50302897	LOW	AP2A1	ENSG00000196961	c.1146C>T	p.Asp382Asp
chr19	51331204	MODIFIER	KLK1	ENSG00000167748	c.-4201_-4200insCA	
chr19	53875365	MODIFIER	ZNF525	ENSG00000203326	c.-67-103G>A	
chr19	55488178	MODIFIER	CTC-550B14.1	ENSG00000243494	n.*2393_*2394insTCTT	
chr19	55598003	MODIFIER	EPS8L1	ENSG00000131037	n.-142_-141insC	
chr19	5667204	MODERATE	SAFB	ENSG00000160633	c.2453+30delC	
chr19	7529500	MODERATE	CTD-2207O23	ENSG00000268861	c.2135G>T	p.Arg712Leu
chr19	8601051	MODIFIER	MYO1F	ENSG00000142347	c.*5733_*5734dupGA	
chr20	17462058	MODIFIER	DYNLT3P1	ENSG00000232241	n.-1983_-1982insCTC	
chr20	18414185	MODIFIER	RNA5SP476	ENSG00000252422	n.-300delA	
chr20	25756020	MODIFIER	FAM182B	ENSG00000175170	n.-113delT	
chr20	26061746	MODIFIER	FAM182A	ENSG00000125804	n.*4671delT	
chr20	2673644	MODIFIER	EBF4	ENSG00000088881	c.-137_-132delCTGGCG	
chr20	29623257	LOW	FRG1B	ENSG00000149531	c.66+7_66+8delGT	
chr20	29624020	LOW	FRG1B	ENSG00000149531	c.71-6dupT	
chr20	33500343	MODIFIER	ACSS2	ENSG00000131069	n.-553T>C	
chr20	36628853	MODIFIER	TTI1	ENSG00000101407	c.2653-1153_2653-1124dupCCCACGCGGGAGGGAAGCCTGCGCTGGCCG	
chr21	10969894	MODIFIER	TPTE	ENSG00000166157	c.119+115T>C	
chr21	15746137	MODERATE	HSPA13	ENSG00000155304	c.1217G>A	p.Gly406Glu
chr21	19628809	LOW	CHODL	ENSG00000154645	c.80-4delT	
chr21	30438952	MODIFIER	CCT8	ENSG00000156261	n.-3765delA	
chr21	40636354	MODIFIER	BRWD1	ENSG00000185658	c.1885+29_1885+31delTTT	
chr21	48064255	MODERATE	PRMT2	ENSG00000160310	c.182G>A	p.Arg61Lys
chr22	17600985	MODERATE	CECR6	ENSG00000183307	c.1033G>A	p.Ala345Thr
chr22	20656732	MODIFIER	AC011718.2	ENSG00000223579	n.347-2393delC	
chr22	24141236	MODIFIER	SMARCB1	ENSG00000099956	c.336-1876delA	

chr22	30051705	LOW	NF2	ENSG00000186575	c.599+41delT	
chr22	39882149	LOW	MGAT3	ENSG00000128268	c.1-3delT	
chr22	40364462	MODIFIER	GRAP2	ENSG00000100351	n.-916_-915delAC	
chr22	42951978	MODIFIER	Z93241.1	ENSG00000265106	n.-3700delG	
chr22	47882347	MODIFIER	LL22NC03-75	ENSG00000218357	c.50+132G>A	
chr22	50547296	MODIFIER	MOV10L1	ENSG00000073146	c.*18608A>T	
chr22	51043245	LOW	MAPK8IP2	ENSG00000008735	c.1515C>T	p.Tyr505Tyr
chr22	51135989	HIGH	SHANK3	ENSG00000251322	c.1393_1394delTT	p.Phe465fs
chrX	114141233	MODERATE	HTR2C	ENSG00000147246	c.632A>C	p.Asp211Ala
chrX	123184949	LOW	STAG2	ENSG00000101972	c.1018-3delT	
chrX	135961586	HIGH	RBMX	ENSG00000147274	c.3delC	p.Asn1fs
chrX	148851540	MODIFIER	HSFX1	ENSG00000171116	c.-4799delG	
chrX	15262814	MODIFIER	ASB9	ENSG00000102048	c.761-63dupT	
chrX	153151280	HIGH	LCA10	ENSG00000196987	c.650_651insCC	p.Gly218fs
chrX	153151284	HIGH	LCA10	ENSG00000196987	c.655delT	p.Tyr219fs
chrX	19380975	LOW	MAP3K15	ENSG00000180815	c.3567-8delT	
chrX	44758425	MODIFIER	KDM6A	ENSG00000147050	c.225+25192T>G	
chrX	44772989	MODIFIER	KDM6A	ENSG00000147050	c.225+39770_225+39771delAT	
chrX	52654061	MODIFIER	SSX8	ENSG00000157965	n.297A>G	
chrX	71933512	MODIFIER	PHKA1-AS1	ENSG00000231944	n.*1323_*1324delCA	
chrX	76965132	MODIFIER	ATRX	ENSG00000085224	c.133+7475delT	
chrY	13310690	MODIFIER	RP1-85D24.1-	ENSG00000270570-ENSG00000263502	n.13310691_13310692delTC	
chrY	24052494	MODIFIER	RBMY1E	ENSG00000242389	c.881+10delC	