max_aaf_all	chrom	start	ref	alt	impact	gene	clinvar_sig	clinvar_disease_name
0.6831	chr8	2048830	A	G	missense_variant	MYOM2	None	None
0.6716	chr8	6479041	C	T	missense_variant	MCPH1	benign	Primary_autosomal_recessive_microcephaly_1|not_specified|Primary_Microcephaly,_Recessive
0.935555555556	chr8	6681255	A	C	splice_region_variant	XKR5	None	None
-1.0	chr8	11666217	GTCCCAC	G	conservative_inframe_deletion	FDFT1	None	None
0.671189839572	chr8	12042879	T	C	splice_region_variant	FAM86B1	None	None
0.6916	chr8	12044200	A	G	splice_region_variant	FAM86B1	None	None
0.7798	chr8	12878806	T	G	missense_variant	KIAA1456	None	None
0.8221	chr8	12879098	G	A	missense_variant	KIAA1456	None	None
0.8221	chr8	12879538	A	G	missense_variant	KIAA1456	None	None
0.8313	chr8	17434640	G	C	splice_region_variant	PDGFRL	None	None
0.847026781661	chr8	17743019	G	A	missense_variant	FGL1	None	None
-1.0	chr8	17796381	AC	GT	missense_variant	PCM1	None	None
0.842472840145	chr8	17814914	A	G	missense_variant	PCM1	None	None
0.872843628269	chr8	17827259	A	AC	splice_region_variant	PCM1	None	None
0.1302	chr8	19819723	C	G	stop_gained	LPL	likely-benign,benign	LIPOPROTEIN_LIPASE_POLYMORPHISM|Hyperlipoproteinemia,_type_I
0.4582	chr8	22570906	GT	G	frameshift_variant	PEBP4	None	None
0.4582	chr8	22570934	T	C	missense_variant	PEBP4	None	None
0.8298	chr8	27324821	T	C	missense_variant	CHRNA2	benign,other	not_specified|Nocturnal_Frontal_Lobe_Epilepsy
0.0532413434002	chr8	48586505	G	C	splice_region_variant	SPIDR	None	None
0.32633279483	chr8	52321685	C	T	missense_variant	PXDNL	None	None
0.471153846154	chr8	52321842	G	C	missense_variant	PXDNL	None	None
0.301014458955	chr8	52325766	T	G	missense_variant	PXDNL	None	None
0.814837257618	chr8	72942209	G	T	splice_region_variant	TRPA1	None	None
0.7398	chr8	73982160	A	G	missense_variant	SBSPON	None	None
0.649	chr8	74005130	A	G	missense_variant	SBSPON	None	None
0.0170295742606	chr8	82370675	C	T	splice_region_variant	FABP9	None	None
3.24886289799e-05	chr8	86385979	G	A	stop_gained	CA2	None	None
0.470533642691	chr8	87076519	C	A	missense_variant	PSKH2	None	None
0.332	chr8	87567192	C	T	missense_variant	CPNE3	None	None

#family_id	name	paternal_id	maternal_id	sex	phenotype
#family_id	name	paternal_id	maternal_id	sex	phenotype
FAM	father	0	0	1	1
FAM	mother	0	0	2	1
FAM	proband	father	mother	1	2