

Gene	Variant	Alleles	MAF (%)	GERP	SIFT (cutoff=0.05)	Polyphen2(Class:Score)	Condel	Mutpred	SNPs&GO	GeneAccession	HGVIS Protein Variant	HGVIS CDNA Variant	FunctionGVIS
TRPC3	Chr4:122824185 G>A	C>T	0.0077	5.9	Damaging	probably-damaging:0.989	Deleterious	0.775	Disease-Associated	NM_001130698.1	p.R762H	c.2285G>A	missense
TRPC3	Chr4:122853695 G>T	C>A	0.0077	5.66	Damaging	probably-damaging:1.0	Deleterious	0.929	Disease-Associated	NM_001130698.1	p.A240S	c.718G>T	missense
TRPC3	Chr4:122839575 C>T	G>A	0.0077	5.5	Damaging	probably-damaging:0.994	Deleterious	0.777	Disease-Associated	NM_001130698.1	p.P434L	c.1301C>T	missense
TRPC3	Chr4:122846208 C>T	G>A	0.0077	5.92	Damaging	probably-damaging:1.0	Deleterious	0.744	Disease-Associated	NM_001130698.1	p.R381C	c.1141C>T	missense
TRPC3	Chr4:122853824 C>T	G>A	0.0077	5.81	Damaging	probably-damaging:1.0	Deleterious	0.467	Disease-Associated	NM_001130698.1	p.H197Y	c.589C>G	missense
TRPC3	Chr4:122803932 C>G	G>C	0.0077	6.18	Damaging	possibly-damaging:0.956	Deleterious	0.357	Neutral	NM_001130698.1	p.L909V	c.2725C>G	missense
TRPC3	Chr4:122820775 C>T	G>A	0.0077	5.62	Damaging	probably-damaging:0.997	Deleterious	0.506	Neutral	NM_001130698.1	p.R847C	c.2539C>T	missense
TRPC3	Chr4:122836062 C>T	G>A	0.0154	5.5	Damaging	probably-damaging:0.999	Deleterious	0.723	Neutral	NM_001130698.1	p.T405M	c.1214C>T	missense
TRPC3	Chr4:122853484 C>T	G>A	0.0077	5.34	Damaging	probably-damaging:0.999	Deleterious	0.615	Neutral	NM_001130698.1	p.T310M	c.929C>T	missense
TRPC3	Chr4:122835948 C>T	G>A	0.0077	5.5	Damaging	possibly-damaging:0.85	Neutral	0.564	Disease-Associated	NM_001130698.1	p.A443V	c.1328C>T	missense
TRPC3	Chr4:122853923 G>A	C>T	0.0077	5.95	Damaging	probably-damaging:0.974	Neutral	0.665	Neutral	NM_001130698.1	p.E164K	c.490G>A	missense
TRPC3	Chr4:122800922 A>C	T>G	0.0077	4.92	Damaging	possibly-damaging:0.57	Neutral	0.223	Neutral	NM_001130698.1	p.K912T	c.2735A>G	missense
TRPC3	Chr4:122800971 A>G	T>C	0.0461	4.94	Damaging	benign:0.417	Deleterious	0.286	Neutral	NM_001130698.1	p.R896G	c.2686A>G	missense
TRPC3	Chr4:122825542 A>G	T>C	0.0077	5.52	Tolerated	possibly-damaging:0.949	Neutral	0.534	Disease-Associated	NM_001130698.1	p.R105H	c.2188A>G	missense
TRPC3	Chr4:122846297 G>A	C>T	0.0077	5.92	Tolerated	probably-damaging:0.977	Neutral	0.678	Disease-Associated	NM_001130698.1	p.R351Q	c.1052G>A	missense
TRPC3	Chr4:122824086 G>C	C>G	0.0077	5.77	Tolerated	possibly-damaging:0.776	Neutral	0.557	Disease-Associated	NM_001130698.1	p.R795P	c.2384G>C	missense
TRPC3	Chr4:122854150 A>G	T>C	0.0077	5.8	Damaging	benign:0.034	Neutral	0.237	Neutral	NM_001130698.1	p.E88G	c.263A>G	missense
TRPC3	Chr4:122846193 A>G	T>C	0.0308	5.92	Tolerated	possibly-damaging:0.947	Neutral	0.614	Neutral	NM_001130698.1	p.I360V	c.1156A>G	missense
TRPC3	Chr4:122829809 T>C	A>G	0.0077	5.5	Tolerated	probably-damaging:0.989	Neutral	0.67	Neutral	NM_001130698.1	p.F636L	c.1906T>C	missense
TRPC3	Chr4:122835991 G>A	C>T	0.0308	5.5	Tolerated	possibly-damaging:0.93	Neutral	0.502	Neutral	NM_001130698.1	p.V429M	c.1285G>A	missense
TRPC3	Chr4:122835999 T>C	A>G	0.0231	5.5	Tolerated	possibly-damaging:0.621	Neutral	0.533	Neutral	NM_001130698.1	p.V426A	c.1277T>C	missense
TRPC3	Chr4:122800957 G>C	C>G	0.0077	4.44	Tolerated	possibly-damaging:0.588	Neutral	0.199	Neutral	NM_001130698.1	p.E900D	c.2700C>G	missense
TRPC3	Chr4:122853895 C>A	G>T	0.0077	5.07	Tolerated	probably-damaging:0.969	Neutral	0.601	Neutral	NM_001130698.1	p.A172E	c.518C>A	missense
TRPC3	Chr4:122825566 G>A	C>T	0.0077	4.67	Tolerated	possibly-damaging:0.469	Neutral	0.372	Neutral	NM_001130698.1	p.V713C	c.2164G>A	missense
TRPC3	Chr4:122824032 T>C	A>G	0.0154	5.9	Tolerated	benign:0.03	Neutral	0.3	Neutral	NM_001130698.1	p.M813T	c.2438T>C	missense
TRPC3	Chr4:122833191 A>G	T>C	0.0231	5.21	Tolerated	benign:0.006	Neutral	0.512	Neutral	NM_001130698.1	p.I467V	c.1399A>G	missense
TRPC3	Chr4:122854099 G>A	C>T	0.0077	5.94	Tolerated	benign:0.011	Neutral	0.458	Neutral	NM_001130698.1	p.R105H	c.314G>A	missense
TRPC3	Chr4:122828630 A>G	T>C	0.0154	5.5	Tolerated	benign:0.303	Neutral	0.453	Neutral	NM_001130698.1	p.I629V	c.1885A>G	missense
TRPC3	Chr4:122824103 T>A	A>T	0.0077	4.59	Tolerated	benign:0.0	Neutral	0.413	Neutral	NM_001130698.1	p.F789L	c.2367T>A	missense
TRPC3	Chr4:122835964 A>T	T>A	0.1153	5.5	Tolerated	benign:0.002	Neutral	0.531	Neutral	NM_001130698.1	p.I438F	c.1312A>T	missense
TRPC3	Chr4:122836015 A>G	T>C	0.0077	3.04	Tolerated	benign:0.001	Neutral	0.315	Neutral	NM_001130698.1	p.I421V	c.1261A>G	missense
TRPC3	Chr4:122824011 C>T	G>A	0.0077	5.9	Tolerated	benign:0.001	Neutral	0.369	Neutral	NM_001130698.1	p.S80F	c.2459C>T	missense
TRPC3	Chr4:122836023 C>A	G>T	0.0077	5.5	Tolerated	benign:0.005	Neutral	0.448	Neutral	NM_001130698.1	p.T418N	c.1253C>A	missense
TRPC3	Chr4:122800929 A>G	T>C	0.0077	6.16	Tolerated	benign:0.0	Neutral	0.224	Neutral	NM_001130698.1	p.S910G	c.2728A>G	missense
TRPC3	Chr4:122824093 A>T	T>A	0.0077	0.21	Tolerated	benign:0.0	Neutral	0.449	Neutral	NM_001130698.1	p.I793F	c.2377A>T	missense
TRPC3	Chr4:122831390 C>T	G>A	0.0077	5.56	-	-	-	-	-	NM_001130698.1	p.Q571*	c.1711C>T	stop-gained
TRPC3	Chr4:122833074 C>T	G>A	0.0077	5.47	-	-	-	-	-	NM_001130698.1	p.Q506*	c.1516C>T	stop-gained
TRPC3	Chr4:122831423 A>T	T>A	0.0077	2.9	-	-	-	-	-	NM_001130698.1	p.R660*	c.1678A>T	stop-gained
TRPC3	Chr4:122854029 G>A	C>A	0.0154	5.95	Tolerated	-	-	-	-	NM_001130698.1	p.V128*	c.384G>T	coding-synonymous
TRPC3	Chr4:122820845 C>T	G>A	0.0154	4.86	Tolerated	-	-	-	-	NM_001130698.1	p.N823*	c.2469C>T	coding-synonymous
TRPC3	Chr4:122833090 C>T	G>A	0.0077	5.47	Tolerated	-	-	-	-	NM_001130698.1	p.F500*	c.1500C>T	coding-synonymous
TRPC3	Chr4:122836058 C>T	G>A	0.0308	4.66	Tolerated	-	-	-	-	NM_001130698.1	p.I406*	c.1218C>T	coding-synonymous
TRPC3	Chr4:122853501 C>T	G>A	0.0384	5.34	Tolerated	-	-	-	-	NM_001130698.1	p.S304*	c.912C>T	coding-synonymous
TRPC3	Chr4:122803944 C>T	G>A	0.0077	5.31	Tolerated	-	-	-	-	NM_001130698.1	p.I411V	c.2713C>T	coding-synonymous
TRPC3	Chr4:122835983 G>A	C>T	0.0077	5.5	Tolerated	-	-	-	-	NM_001130698.1	p.L431*	c.1293G>A	coding-synonymous
TRPC3	Chr4:122853939 G>A	C>T	0.0231	9.5	Tolerated	-	-	-	-	NM_001130698.1	p.E158*	c.474G>A	coding-synonymous
TRPC3	Chr4:122828484 G>A	C>T	0.0077	4.65	Tolerated	-	-	-	-	NM_001130698.1	p.G677*	c.2031G>A	coding-synonymous
TRPC3	Chr4:122853900 C>T	G>A	0.0077	5.95	Tolerated	-	-	-	-	NM_001130698.1	p.N171*	c.513C>T	coding-synonymous
TRPC3	Chr4:122800987 A>G	T>C	2.1913	3.76	Tolerated	-	-	-	-	NM_001130698.1	p.E890*	c.2670A>G	coding-synonymous
TRPC3	Chr4:122853882 C>T	G>A	0.0077	3.28	Tolerated	-	-	-	-	NM_001130698.1	p.D177*	c.531C>T	coding-synonymous
TRPC3	Chr4:122825603 C>A	G>T	0.0077	2.99	Tolerated	-	-	-	-	NM_001130698.1	p.L709*	c.2127C>A	coding-synonymous
TRPC3	Chr4:122853609 G>A	C>T	0.6382	2.95	Tolerated	-	-	-	-	NM_001130698.1	p.K268*	c.804G>A	coding-synonymous
TRPC3	Chr4:122824052 G>A	C>T	26.4263	2.65	Tolerated	-	-	-	-	NM_001130698.1	p.R806*	c.2418G>A	coding-synonymous
TRPC3	Chr4:122828667 C>T	G>A	0.0154	2.14	Tolerated	-	-	-	-	NM_001130698.1	p.A616*	c.1848C>T	coding-synonymous
TRPC3	Chr4:122833102 C>G	G>C	0.0154	1.57	Tolerated	-	-	-	-	NM_001130698.1	p.P496*	c.1488C>G	coding-synonymous
TRPC3	Chr4:122835980 C>T	G>A	1.7992	1.47	Tolerated	-	-	-	-	NM_001130698.1	p.G432*	c.2163C>T	coding-synonymous
TRPC3	Chr4:122853501 A>G	C>T	0.0946	1.31	Tolerated	-	-	-	-	NM_001130698.1	p.D118*	c.2454G>C	coding-synonymous
TRPC3	Chr4:122853750 C>T	G>A	0.0692	0.95	Tolerated	-	-	-	-	NM_001130698.1	p.I905*	c.663C>T	coding-synonymous
TRPC3	Chr4:122853690 G>A	C>T	0.0154	0.47	Tolerated	-	-	-	-	NM_001130698.1	p.A241*	c.723G>A	coding-synonymous
TRPC3	Chr4:122853879 C>T	G>A	0.0077	-0.97	Tolerated	-	-	-	-	NM_001130698.1	p.A178*	c.534C>T	coding-synonymous
TRPC3	Chr4:122854116 C>G	G>C	7.2362	-0.99	Tolerated	-	-	-	-	NM_001130698.1	p.A99*	c.297C>G	coding-synonymous
TRPC3	Chr4:122824040 T>C	A>G	0.0077	-1.37	Tolerated	-	-	-	-	NM_001130698.1	p.D810*	c.2430T>C	coding-synonymous
TRPC3	Chr4:122833132 G>A	C>T	0.0077	-2.1	Tolerated	-	-	-	-	NM_001130698.1	p.T486*	c.1458G>A	coding-synonymous
TRPC3	Chr4:122854095 C>T	G>A	0.0077	-2.32	Tolerated	-	-	-	-	NM_001130698.1	p.G106*	c.318C>T	coding-synonymous
TRPC3	Chr4:122831394 G>A	C>T	0.223	-2.89	Tolerated	-	-	-	-	NM_001130698.1	p.K569*	c.1707G>A	coding-synonymous
TRPC3	Chr4:122833201 A>G	T>C	0.0077	-5.32	Tolerated	-	-	-	-	NM_001130698.1	p.A463*	c.1389A>G	coding-synonymous
TRPC3	Chr4:122831472 T>C	A>G	0.0154	-5.41	Tolerated	-	-	-	-	NM_001130698.1	p.N543*	c.1629T>C	coding-synonymous
TRPC3	Chr4:122854098 C>T	G>A	0.0077	-7.02	Tolerated	-	-	-	-	NM_001130698.1	p.R105*	c.315C>T	coding-synonymous
TRPC3	Chr4:122825567 C>T	G>A	0.0308	-9.01	Tolerated	-	-	-	-	NM_001130698.1	p.Y721*	c.2163C>T	coding-synonymous
TRPC3	Chr4:122824016 A>G	T>C	0.0077	-9.88	Tolerated	-	-	-	-	NM_001130698.1	p.S818*	c.2454G>C	coding-synonymous
TRPC3	Chr4:122853717 G>A	C>T	0.0077	-10	Tolerated	-	-	-	-	NM_001130698.1	p.P232*	c.698G>A	coding-synonymous
TRPC3	Chr4:122828634 G>A	C>T	0.0077	-11	Tolerated	-	-	-	-	NM_001130698.1	p.A627*	c.1881G>A	coding-synonymous
TRPC3	Chr4:122836061 G>T	C>A	0.0077	-11	Tolerated	-	-	-	-	NM_001130698.1	p.T405*	c.1215G>A	coding-synonymous
TRPC3	Chr4:122824106 A>G	T>C	0.0231	-11.4	Tolerated	-	-	-	-	NM_001130698.1	p.S788*	c.2364A>G	coding-synonymous
TRPC3	Chr4:122825612 C>A	G>T	0.0308	-11.5	Tolerated	-	-	-	-	NM_001130698.1	p.S706*	c.2118C>A	coding-synonymous
TRPC3	Chr4:122824233 insT	GAAAA>GAAAAA;GAAAA>G	0.4574	1.35	-								