SNiPAcard

Block annotations

Block info

genomic range	chr22:33,147,483-33,147,526
block size	44 bp
variant count	2 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = 0.167 [-0.015 – 0.349]	**gene(s) hit or close-by**	SYN3
phastCons	μ = 0.003 [0.001 – 0.004]	**eQTL gene(s)**	–
GERP++	μ = 0.480 [-0.479 – 1.44]	**potentially regulated gene(s)**	–
CADD score	μ = 5.849 [4.562 – 7.137]	**disease gene(s)**	–

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
SYN3	ENST00000462268	?	?	2
SYN3	ENST00000358763	NM_003490.3, NM_001135774.1, NM_133633.2	ENSP00000351614	2