SNiPAcard

Block annotations

Block info

genomic range	chr22:33,160,397-33,160,397
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-0.753	**gene(s) hit or close-by**	SYN3
phastCons	0	**eQTL gene(s)**	–
GERP++	-2.08	**potentially regulated gene(s)**	–
CADD score	0.809	**disease gene(s)**	–

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000293419 (promoter flanking region)	1	NHLF	DNase1
		HSMMtube	DNase1
		blood (K562)	H3K27me3
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1
		lung (IMR90)	DNase1, H3K18ac
		nervous (NH-A)	DNase1
		skin (NHEK)	H3K27me3

Putative effect on transcript

Intron variant

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