Locus 27 (rs2097326)

SNiPAcard

Block annotations

Block info

genomic range	chr22:33,159,092-33,167,869
block size	8,778 bp
variant count	19 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.235 [-3.023 – 2.015]	gene(s) hit or close-by	SYN3
phastCons	μ = 0.069 [0 – 0.983]	eQTL gene(s)	–
GERP++	μ = 0.074 [-6.84 – 2.32]	potentially regulated gene(s)	–
CADD score	μ = 4.567 [0.694 – 16.06]	disease gene(s)	–

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000293419 (promoter flanking region)	3	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	?	?	19
SYN3	ENST00000358763	NM_003490.3, NM_001135774.1, NM_133633.2	ENSP00000351614	19