

SNiPACard

Block annotations

Block info

genomic range	chr9:137,797,175-137,797,175 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-3.233	gene(s) hit or close-by	FCN1 <i>e!</i>
phastCons	0	eQTL gene(s)	-
GERP++	-1.67	potentially regulated gene(s)	-
CADD score	0.312	disease gene(s)	-

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
FCN1 <i>e!</i>	downstream gene variant	4256	ENST00000371806 <i>e!</i>	NM_002003.3	ENSP00000360871 <i>e!</i>	1
FCN1 <i>e!</i>	downstream gene variant	561	ENST00000616356 <i>e!</i>	?	ENSP00000479379 <i>e!</i>	1

