

SNiPACard

Block annotations

Block info

genomic range	chr17:34,383,107-34,391,237 <i>e!</i>
block size	8,131 bp
variant count	5 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.784$ [-2.213 – 0.281]	gene(s) hit or close-by	CCL18 <i>e!</i>
phastCons	$\mu = 0.008$ [0 – 0.027]	eQTL gene(s)	-
GERP++	$\mu = -2.376$ [-4.62 – 0.235]	potentially regulated gene(s)	-
CADD score	$\mu = 1.184$ [0.023 – 3.986]	disease gene(s)	-

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
CCL18 <i>e!</i>	upstream gene variant	403	ENST00000616054 <i>e!</i>	NM_002988.2	ENSP00000479955 <i>e!</i>	3

