

SNiPAcad

Block annotations

Block info

genomic range	chr19:52,115,833-52,128,795 <i>e!</i>
block size	12,963 bp
variant count	4 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.206$ [-0.505 – 0.179]	gene(s) hit or close-by	RPL9P33 <i>e!</i> , SIGLEC5 <i>e!</i> , SIGLEC5 <i>e!</i>
phastCons	$\mu = 0.013$ [0 – 0.032]	eQTL gene(s)	SIGLEC14 <i>e!</i>
GERP++	$\mu = -0.546$ [-2.66 – 1.26]	potentially regulated gene(s)	-
CADD score	$\mu = 2.647$ [1.725 – 4.652]	disease gene(s)	-

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
SIGLEC14 <i>e!</i>	?	ENSG00000254415 <i>e!</i>	subcutaneous adipocytes	8.46×10 ⁻⁷ (p-value)	GTEx Portal V6 <i>mq</i>	2

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
RPL9P33 <i>e!</i>	downstream gene variant	2995	ENST00000484311 <i>e!</i>	?	?	2

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
SIGLEC5 <i>e!</i>	ENST00000599649 <i>e!</i>	?	ENSP00000470259 <i>e!</i>	4
SIGLEC5 <i>e!</i>	ENST00000534261 <i>e!</i>	?	ENSP00000473238 <i>e!</i>	4
SIGLEC5 <i>e!</i>	ENST00000570106 <i>e!</i>	NM_003830.3	ENSP00000455510 <i>e!</i>	4
SIGLEC5 <i>e!</i>	ENST00000429354 <i>e!</i>	?	ENSP00000415200 <i>e!</i>	4

