

SNiPacard

Block annotations

Block info

genomic range	chr2:309,097-309,097 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-0.126	gene(s) hit or close-by	AC079779.5 <i>e!</i> , RP11-356M6.1 <i>e!</i>
phastCons	0.02	eQTL gene(s)	SH3YL1 <i>e!</i>
GERP++	-0.45	potentially regulated gene(s)	-
CADD score	1.239	disease gene(s)	-

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
SH3YL1 <i>e!</i>	?	ENSG00000035115 <i>e!</i>	muscularis mucosae	9.42×10 ⁻⁶ (p-value)	GTEx Portal V6 <i>!M</i>	1
SH3YL1 <i>e!</i>	?	ENSG00000035115 <i>e!</i>	tibial nerve	4.66×10 ⁻⁷ (p-value)	GTEx Portal V6 <i>!M</i>	1
SH3YL1 <i>e!</i>	?	ENSG00000035115 <i>e!</i>	esophagus mucosa	8.54×10 ⁻⁷ (p-value)	GTEx Portal V6 <i>!M</i>	1

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000584029 <i>e!</i> (open chromatin region)	1	embryonic stem cell (H1ESC) blood (K562) A549	DNase1 H3K27me3 H3K27me3

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
AC079779.5 <i>e!</i>	downstream gene variant	23	ENST00000591927 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	downstream gene variant	1199	ENST00000586715 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	2260	ENST00000591158 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	2501	ENST00000590255 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	830	ENST00000587073 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	1314	ENST00000588334 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	2575	ENST00000585703 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	1944	ENST00000591178 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	downstream gene variant	124	ENST00000589936 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	downstream gene variant	121	ENST00000591244 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	1940	ENST00000457938 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	1917	ENST00000588842 <i>e!</i>	?	?	1
AC079779.5 <i>e!</i>	upstream gene variant	2606	ENST00000592090 <i>e!</i>	?	?	1

Putative effect on transcript

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
AC079779.5 <i>e!</i>	ENST00000586772 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000589588 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000586311 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000586235 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000592366 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000585783 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000591122 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000592687 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000586673 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000590678 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000587796 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000416685 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000612487 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000592553 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000609984 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000591015 <i>e!</i>	?	1
AC079779.5 <i>e!</i>	ENST00000589124 <i>e!</i>	?	1
RP11-356M6.1 <i>e!</i>	ENST00000619113 <i>e!</i>	?	1

