

Block annotations

Block info

genomic range	chr4:3,406,952-3,406,952 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-0.17	gene(s) hit or close-by	RGS12 <i>e!</i>
phastCons	0	eQTL gene(s)	-
GERP++	-1.39	potentially regulated gene(s)	-
CADD score	1.776	disease gene(s)	-

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001428857 <i>e!</i> (open chromatin region)	1	endothelium (HUVEC) blood (K562) skin (NHEK) muscle (HSMM)	H3K36me3 H3K27me3 H3K36me3 DNase1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
RGS12 <i>e!</i>	ENST00000514268 <i>e!</i>	?	ENSP00000424251 <i>e!</i>	1
RGS12 <i>e!</i>	ENST00000504194 <i>e!</i>	?	?	1
RGS12 <i>e!</i>	ENST00000506631 <i>e!</i>	?	?	1
RGS12 <i>e!</i>	ENST00000508158 <i>e!</i>	?	?	1
RGS12 <i>e!</i>	ENST00000344733 <i>e!</i>	NM_198229.2	ENSP00000339381 <i>e!</i>	1
RGS12 <i>e!</i>	ENST00000336727 <i>e!</i>	?	ENSP00000338509 <i>e!</i>	1
RGS12 <i>e!</i>	ENST00000513784 <i>e!</i>	?	?	1
RGS12 <i>e!</i>	ENST00000505570 <i>e!</i>	?	?	1
RGS12 <i>e!</i>	ENST00000506998 <i>e!</i>	?	?	1
RGS12 <i>e!</i>	ENST00000382788 <i>e!</i>	NM_002926.3	ENSP00000372238 <i>e!</i>	1
RGS12 <i>e!</i>	ENST00000338806 <i>e!</i>	NM_198227.1	ENSP00000342133 <i>e!</i>	1
RGS12 <i>e!</i>	ENST00000512990 <i>e!</i>	?	?	1
RGS12 <i>e!</i>	ENST00000503041 <i>e!</i>	?	?	1

