

Block annotations

Block info

genomic range	chr17:34,325,532-34,325,532 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-0.706	gene(s) hit or close-by	CCL15 <i>e!</i> , CCL15-CCL14 <i>e!</i> , RP11-104J23.1 <i>e!</i>
phastCons	0	eQTL gene(s)	-
GERP++	1.62	potentially regulated gene(s)	-
CADD score	5.599	disease gene(s)	-

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
CCL15 <i>e!</i>	upstream gene variant	126	ENST00000614368 <i>e!</i>	?	ENSP00000484262 <i>e!</i>	1
RP11-104J23.1 <i>e!</i>	upstream gene variant	2923	ENST00000619334 <i>e!</i>	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
CCL15 <i>e!</i>	ENST00000617897 <i>e!</i>	NM_032965.4	ENSP00000484078 <i>e!</i>	1
CCL15-CCL14 <i>e!</i>	ENST00000616694 <i>e!</i>	?	ENSP00000481402 <i>e!</i>	1
CCL15-CCL14 <i>e!</i>	ENST00000610751 <i>e!</i>	?	ENSP00000481940 <i>e!</i>	1

