

SNiPACard

Block annotations

Block info

genomic range	chr17:34,318,565-34,352,415 <i>e!</i>
block size	33,851 bp
variant count	10 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = 0.150$ [-0.96 – 1.902]	gene(s) hit or close-by	CCL14 <i>e!</i> , CCL15 <i>e!</i> , CCL15-CCL14 <i>e!</i> , CCL23 <i>e!</i> , CTB-186H2.3 <i>e!</i> , RP11-104J23.1 <i>e!</i> , RP11-104J23.2 <i>e!</i>
phastCons	$\mu = 0.144$ [0.001 – 0.834]	eQTL gene(s)	-
GERP++	$\mu = 0.306$ [-0.237 – 2.23]	potentially regulated gene(s)	-
CADD score	$\mu = 4.766$ [0.246 – 14.22]	disease gene(s)	-

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
CCL14 <i>e!</i>	upstream gene variant	4771	ENST00000618404 <i>e!</i>	NM_032963.3	ENSP00000481023 <i>e!</i>	1
CCL14 <i>e!</i>	upstream gene variant	4525	ENST00000614009 <i>e!</i>	?	ENSP00000483186 <i>e!</i>	1
CCL14 <i>e!</i>	upstream gene variant	4880	ENST00000622526 <i>e!</i>	NM_032962.4	ENSP00000479097 <i>e!</i>	1
CCL14 <i>e!</i>	upstream gene variant	4854	ENST00000620991 <i>e!</i>	?	ENSP00000484818 <i>e!</i>	1
CCL15 <i>e!</i>	downstream gene variant, upstream gene variant	1297	ENST00000617897 <i>e!</i>	NM_032965.4	ENSP00000484078 <i>e!</i>	3
CCL15 <i>e!</i>	downstream gene variant	155	ENST00000614368 <i>e!</i>	?	ENSP00000484262 <i>e!</i>	3
CCL15-CCL14 <i>e!</i>	upstream gene variant	2301	ENST00000616694 <i>e!</i>	?	ENSP00000481402 <i>e!</i>	1
CCL15-CCL14 <i>e!</i>	upstream gene variant	2371	ENST00000610751 <i>e!</i>	?	ENSP00000481940 <i>e!</i>	1
CCL23 <i>e!</i>	downstream gene variant	592	ENST00000613876 <i>e!</i>	?	ENSP00000479076 <i>e!</i>	3
CCL23 <i>e!</i>	downstream gene variant	593	ENST00000615050 <i>e!</i>	NM_005064.4	ENSP00000481357 <i>e!</i>	3
CCL23 <i>e!</i>	downstream gene variant	591	ENST00000612516 <i>e!</i>	NM_145898.2	ENSP00000484748 <i>e!</i>	3
CTB-186H2.3 <i>e!</i>	downstream gene variant	4819	ENST00000617687 <i>e!</i>	?	?	1
CTB-186H2.3 <i>e!</i>	downstream gene variant	1259	ENST00000612584 <i>e!</i>	?	?	2
RP11-104J23.1 <i>e!</i>	upstream gene variant, downstream gene variant	580	ENST00000617328 <i>e!</i>	?	?	3
RP11-104J23.1 <i>e!</i>	downstream gene variant	2053	ENST00000619334 <i>e!</i>	?	?	1
RP11-104J23.2 <i>e!</i>	upstream gene variant	39	ENST00000617747 <i>e!</i>	?	?	3

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
CCL15-CCL14 <i>e!</i>	ENST00000616694 <i>e!</i>	?	ENSP00000481402 <i>e!</i>	3
CCL15-CCL14 <i>e!</i>	ENST00000610751 <i>e!</i>	?	ENSP00000481940 <i>e!</i>	3
RP11-104J23.1 <i>e!</i>	ENST00000619334 <i>e!</i>	?	?	3



