Locus 366 (rs2056492)

SNiPAcard

Block annotations

Block info

genomic range	chr17:34,318,565-34,352,415
block size	33,851 bp
variant count	10 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = 0.150 [-0.96 – 1.902]	gene(s) hit or close-by	CCL14, CCL15, CCL15-CCL14, CCL23, CTB-186H2.3, RP11-104J23.1, RP11-104J23.2
phastCons	μ = 0.144 [0.001 – 0.834]	eQTL gene(s)	–
GERP++	μ = 0.306 [-0.237 – 2.23]	potentially regulated gene(s)	–
CADD score	μ = 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	upstream gene variant	4771	ENST00000618404	NM_032963.3	ENSP00000481023	1
CCL14	upstream gene variant	4525	ENST00000614009	?	ENSP00000483186	1
CCL14	upstream gene variant	4880	ENST00000622526	NM_032962.4	ENSP00000479097	1
CCL14	upstream gene variant	4854	ENST00000620991	?	ENSP00000484818	1
CCL15	downstream gene variant, upstream gene variant	1297	ENST00000617897	NM_032965.4	ENSP00000484078	3
CCL15	downstream gene variant	155	ENST00000614368	?	ENSP00000484262	3
CCL15-CCL14	upstream gene variant	2301	ENST00000616694	?	ENSP00000481402	1
CCL15-CCL14	upstream gene variant	2371	ENST00000610751	?	ENSP00000481940	1
CCL23	downstream gene variant	592	ENST00000613876	?	ENSP00000479076	3
CCL23	downstream gene variant	593	ENST00000615050	NM_005064.4	ENSP00000481357	3
CCL23	downstream gene variant	591	ENST00000612516	NM_145898.2	ENSP00000484748	3
CTB-186H2.3	downstream gene variant	4819	ENST00000617687	?	?	1
CTB-186H2.3	downstream gene variant	1259	ENST00000612584	?	?	2
RP11-104J23.1	upstream gene variant, downstream gene variant	580	ENST00000617328	?	?	3
RP11-104J23.1	downstream gene variant	2053	ENST00000619334	?	?	1
RP11-104J23.2	upstream gene variant	39	ENST00000617747	?	?	3

Putative effect on transcript

Intron variant

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

Locus 366 (sentinel SNP rs2056492 + proxy variants in LD r2 > 0.8). SNiPA block annotation (www.snipa.org) based on 1000 Genomes Project phase 3 v5 (European population) variant set and Ensembl 82 annotations.