

Block annotations

Block info





genomic range	chr17:34,352,666-34,352,666 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-0.07	gene(s) hit or close-by	-
phastCons	0.16	eQTL gene(s)	CCL14 <i>e!</i> , CCL15-CCL14 <i>e!</i> , CCL23 <i>e!</i>
GERP++	-2	potentially regulated gene(s)	-
CADD score	1.631	disease gene(s)	-

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
CCL23 <i>e!</i>	ENST00000613876 <i>e!</i>	ILMN_1764030 <i>e!</i>	skin	3.00×10 ⁻⁵ (p-value)	MuTHER consortium 	1
CCL23 <i>e!</i>	ENST00000615050 <i>e!</i>					
CCL23 <i>e!</i>	ENST00000613876 <i>e!</i>	ILMN_1686109 <i>e!</i>	skin	2.01×10 ⁻⁵ (p-value)	MuTHER consortium 	1
CCL23 <i>e!</i>	ENST00000615050 <i>e!</i>		adipocyte	2.10×10 ⁻⁵ (p-value)	MuTHER consortium 	1
CCL23 <i>e!</i>	ENST00000612516 <i>e!</i>					
CCL14 <i>e!</i>	ENST00000622526 <i>e!</i>	ILMN_1740609 <i>e!</i>	adipocyte	6.68×10 ⁻⁸ (p-value)	MuTHER consortium 	1
CCL15-CCL14 <i>e!</i>	ENST00000616694 <i>e!</i>					
CCL15-CCL14 <i>e!</i>	ENST00000610751 <i>e!</i>					
CCL14 <i>e!</i>	ENST00000618404 <i>e!</i>					
CCL14 <i>e!</i>	ENST00000614009 <i>e!</i>					
CCL14 <i>e!</i>	ENST00000620991 <i>e!</i>					

