

SNiPACard

Block annotations

Block info



genomic range	chr19:7,779,733-7,789,796 <i>e!</i>
block size	10,064 bp
variant count	11 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.795$ [-1.99 – 0.075]	gene(s) hit or close-by	CLEC4G <i>e!</i>
phastCons	$\mu = 0.023$ [0 – 0.077]	eQTL gene(s)	CD209 <i>e!</i> , CLEC4G <i>e!</i> , FCER2 <i>e!</i> , MCEMP1 <i>e!</i> , TGFBR3L <i>e!</i> , XAB2 <i>e!</i>
GERP++	$\mu = -0.107$ [-0.858 – 0.13]	potentially regulated gene(s)	C19orf45 <i>e!</i> , CCL25 <i>e!</i>
CADD score	$\mu = 2.398$ [0.127 – 5.545]	disease gene(s)	CD209 <i>e!</i>










Trait annotations

Disease gene annotation

gene	trait	source DB	source entry/link
CD209 <i>e!</i>	DENGUE VIRUS, SUSCEPTIBILITY TODENGUE FEVER, SUSCEPTIBILITY TO, [...]	OMIM	MIM:614371 
CD209 <i>e!</i>	MYCOBACTERIUM TUBERCULOSIS, SUSCEPTIBILITY TOMYCOBACTERIUM TUBERCULOSIS, [...]	OMIM	MIM:607948 

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
TGFBR3L <i>e!</i>	?	ENSG00000260001 <i>e!</i>	prostate	3.22×10 ⁻⁷ (p-value)	GTEEx Portal V6 	3
XAB2 <i>e!</i>	?	ENSG00000076924 <i>e!</i>	left ventricle	3.84×10 ⁻⁶ (p-value)	GTEEx Portal V6 	1
FCER2 <i>e!</i>	?	ENSG00000104921 <i>e!</i>	tibial nerve	3.82×10 ⁻⁶ (p-value)	GTEEx Portal V6 	1
FCER2 <i>e!</i>	?	ENSG00000104921 <i>e!</i>	subcutaneous adipocytes	9.02×10 ⁻⁷ (p-value)	GTEEx Portal V6 	2
FCER2 <i>e!</i>	?	ENSG00000104921 <i>e!</i>	visceral adipocytes	3.72×10 ⁻⁶ (p-value)	GTEEx Portal V6 	1
CLEC4G <i>e!</i>	ENST00000620128 <i>e!</i>	ILMN_2193817 <i>e!</i>	monocyte	4.97×10 ⁻⁷ (p-value)	Fairfax et al. 	1
CLEC4G <i>e!</i>	ENST00000328853 <i>e!</i>					
MCEMP1 <i>e!</i>	ENST00000333598 <i>e!</i>	ILMN_1762713 <i>e!</i>	monocyte	7.18×10 ⁻⁵ (p-value)	Fairfax et al. 	1
MCEMP1 <i>e!</i>	ENST00000597445 <i>e!</i>					
MCEMP1 <i>e!</i>	ENST00000598851 <i>e!</i>					
CLEC4G <i>e!</i>	ENST00000620128 <i>e!</i>	ILMN_2193817 <i>e!</i>	monocyte	7.61×10 ⁻⁴⁵ (p-value)	Zeller et al. 	1
CLEC4G <i>e!</i>	ENST00000328853 <i>e!</i>					
CD209 <i>e!</i>	ENST00000315599 <i>e!</i>	ILMN_1676372 <i>e!</i>	monocyte	1.36×10 ⁻¹⁷ (p-value)	Zeller et al. 	1

Putative effect on regulation

ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000222798 <i>e!</i>	1	ENCP00000024006	C19orf45 <i>e!</i>
ENCE00000223049 <i>e!</i>	1	ENCP00000024014	CCL25 <i>e!</i>

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
CLEC4G <i>e!</i>	downstream gene variant	4048	ENST00000620128 <i>e!</i>	?	ENSP00000483109 <i>e!</i>	1
CLEC4G <i>e!</i>	downstream gene variant	4047	ENST00000328853 <i>e!</i>	NM_198492.3, NM_001244856.1	ENSP00000327599 <i>e!</i>	1

