

SNiPAcad

Block annotations

Block info

genomic range	chr9:137,840,809-137,857,978 <i>e!</i>
block size	17,170 bp
variant count	23 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.830$ [-4.588 – 0.787]	gene(s) hit or close-by	-
phastCons	$\mu = 0.003$ [0 – 0.046]	eQTL gene(s)	FCN1 <i>e!</i> , NELFB <i>e!</i> , OLFM1 <i>e!</i> , RP11-447M12.2 <i>e!</i>
GERP++	$\mu = -0.548$ [-4.14 – 1.89]	potentially regulated gene(s)	-
CADD score	$\mu = 2.698$ [0.166 – 6.591]	disease gene(s)	-

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
RP11-447M12.2 <i>e!</i>	?	ENSG00000236403 <i>e!</i>	blood	3.61×10^{-10} (p-value)	GTEx Portal V6 <i>!M</i>	23
FCN1 <i>e!</i>	?	ENSG00000085265 <i>e!</i>	blood	5.18×10^{-18} (p-value)	GTEx Portal V6 <i>!M</i>	23
OLFM1 <i>e!</i>	ENST00000371796 <i>e!</i>	ILMN_1742025 <i>e!</i>	monocyte	2.73×10^{-23} (p-value)	Fairfax et al. <i>!M</i>	4
OLFM1 <i>e!</i>	ENST00000371793 <i>e!</i>					
OLFM1 <i>e!</i>	ENST00000483042 <i>e!</i>					
OLFM1 <i>e!</i>	ENST00000252854 <i>e!</i>					
OLFM1 <i>e!</i>	ENST00000392991 <i>e!</i>	ILMN_1714709 <i>e!</i>	monocyte	1.15×10^{-19} (p-value)	Fairfax et al. <i>!M</i>	2
OLFM1 <i>e!</i>	ENST00000277415 <i>e!</i>					
NELFB <i>e!</i>	ENST00000343053 <i>e!</i>	ILMN_2290007 <i>e!</i>	monocyte	3.73×10^{-4} (p-value)	Fairfax et al. <i>!M</i>	2
OLFM1 <i>e!</i>	ENST00000392991 <i>e!</i>	ILMN_1714709 <i>e!</i>	monocyte	1.43×10^{-65} (p-value)	Zeller et al. <i>!M</i>	3
OLFM1 <i>e!</i>	ENST00000277415 <i>e!</i>					
OLFM1 <i>e!</i>	ENST00000371796 <i>e!</i>	ILMN_1742025 <i>e!</i>	monocyte	8.82×10^{-76} (p-value)	Zeller et al. <i>!M</i>	3
OLFM1 <i>e!</i>	ENST00000371793 <i>e!</i>					
OLFM1 <i>e!</i>	ENST00000252854 <i>e!</i>					
OLFM1 <i>e!</i>	ENST00000483042 <i>e!</i>					

