SNiPAcard

Block annotations

Block info

genomic range	chr4:88,478,750-88,481,387
block size	2,638 bp
variant count	3 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = 0.475 [-0.199 – 0.83]	**gene(s) hit or close-by**	–
phastCons	μ = 0.018 [0 – 0.051]	**eQTL gene(s)**	HSD17B13, SPARCL1
GERP++	μ = 0.249 [-1.55 – 1.44]	**potentially regulated gene(s)**	–
CADD score	μ = 2.523 [1 – 3.358]	**disease gene(s)**	–

Trait annotations

Variant association

trait	min(p-value)	source DB	source entry/link	variant(s)
stearidonate (18:4n3)	1.92×10^{-5}	Metabolomics GWAS Server	24816252	1

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
SPARCL1	?	ENSG00000152583	tibial nerve	8.50×10^{-6} (p-value)	GTEx Portal V6	3
SPARCL1	?	ENSG00000152583	subcutaneous adipocytes	6.18×10^{-6} (p-value)	GTEx Portal V6	2
HSD17B13	?	ENSG00000170509	thyroid	4.47×10^{-6} (p-value)	GTEx Portal V6	3

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001686562 (enhancer)	1	blood (DND-41)	H3K27me3