SNiPAcard

Block annotations

Block info

genomic range	chr2:103,105,611-103,166,325
block size	60,715 bp
variant count	5 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.928 [-2.359 – 0.089]	**gene(s) hit or close-by**	SLC9A4
phastCons	μ = 0.001 [0 – 0.002]	**eQTL gene(s)**	AC007278.3, IL18RAP
GERP++	μ = -2.044 [-6.09 – 0.158]	**potentially regulated gene(s)**	–
CADD score	μ = 0.546 [0.126 – 1.397]	**disease gene(s)**	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
AC007278.3	?	ENSG00000234389	atrial appendage	1.67×10^{-7} (p-value)	GTEx Portal V6	5
IL18RAP	?	ENSG00000115607	blood	1.37×10^{-7} (p-value)	GTEx Portal V6	5
AC007278.3	?	ENSG00000234389	blood	3.34×10^{-10} (p-value)	GTEx Portal V6	5

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
SLC9A4	ENST00000295269	NM_001011552.3	ENSP00000295269	3