SNiPAcard

Block annotations

Block info

genomic range	chr4:74,701,512-74,703,999
block size	2,488 bp
variant count	2 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = 0.118 [0.075 – 0.161]	**gene(s) hit or close-by**	CXCL6
phastCons	μ = 0.519 [0.04 – 0.999]	**eQTL gene(s)**	CXCL6, PF4V1
GERP++	μ = 1.190 [0 – 2.38]	**potentially regulated gene(s)**	–
CADD score	μ = 7.585 [1.391 – 13.78]	**disease gene(s)**	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
CXCL6	?	ENSG00000124875	tibial nerve	2.03×10^{-7} (p-value)	GTEx Portal V6	2
CXCL6	?	ENSG00000124875	pancreas	5.79×10^{-7} (p-value)	GTEx Portal V6	1
PF4V1	ENST00000226524	ILMN_1745522	monocyte	1.91×10^{-17} (p-value)	Zeller et al.	1

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
CXCL6	upstream gene variant	1392	ENST00000503446	?	?	1
CXCL6	upstream gene variant, downstream gene variant	845	ENST00000515050	?	ENSP00000424819	2
CXCL6	upstream gene variant	702	ENST00000226317	NM_002993.3	ENSP00000226317	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
CXCL6	ENST00000503446	?	?	1

3'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
CXCL6	ENST00000226317	NM_002993.3	ENSP00000226317	1