SNiPAcard

Block annotations

Block info

genomic range	chr5:40,496,930-40,570,075
block size	73,146 bp
variant count	29 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.853 [-4.636 – 1.79]	**gene(s) hit or close-by**	–
phastCons	μ = 0.047 [0 – 0.998]	**eQTL gene(s)**	PTGER4
GERP++	μ = 0.045 [-4.53 – 4.26]	**potentially regulated gene(s)**	–
CADD score	μ = 4.166 [0.028 – 19.99]	**disease gene(s)**	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
PTGER4	?	ENSG00000171522	transformed fibroblasts	1.57×10^{-6} (p-value)	GTEx Portal V6	23

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001408868 (enhancer)	1	muscle (HSMM)	DNase1
ENSR00001278871 (promoter flanking region)	1	NHLF	DNase1
		embryonic stem cell (H1ESC)	DNase1
		HSMMtube	DNase1
		Osteobl	H3K4me2, H3K27ac
		skin (NHDF-AD)	DNase1
		breast (HMEC)	H3K4me2, H3K27ac
		muscle (HSMM)	H3K27ac, H3K4me2, DNase1
		cervix (HeLa-S3)	Cjun, Jund, Max, Cfos, DNase1
		endothelium (HUVEC)	DNase1, Cjun, H3K4me2, H3K4me1, H3K27ac
		lung (IMR90)	DNase1, H4K8ac, H3K27ac, H3K4ac, H2BK120ac, H2BK20ac
		A549	H3K4me2, H3K9ac, DNase1, H3K27ac, H3K36me3, H3K4me3
		nervous (NH-A)	H3K9ac, H3K27ac, DNase1
		skin (NHEK)	DNase1, H3K4me1, H3K27ac
ENSR00001278876 (promoter flanking region)	1	embryonic stem cell (H1ESC)	DNase1
		skin (NHDF-AD)	H3K4me1, DNase1
		muscle (HSMM)	H3K4me1, DNase1
		cervix (HeLa-S3)	DNase1
		monocytes (Monocytes-CD14+)	DNase1
		endothelium (HUVEC)	Cjun, DNase1, H3K4me1
		liver (HepG2)	DNase1
		lung (IMR90)	DNase1
		blood (GM12878)	BATF, Pax5