

SNiPacard

Block annotations

Block info


genomic range	chr18:72,209,543-72,209,543 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	0.179	gene(s) hit or close-by	CNDP1 <i>e!</i>
phastCons	0	eQTL gene(s)	CNDP1 <i>e!</i>
GERP++	1.25	potentially regulated gene(s)	-
CADD score	5.184	disease gene(s)	-

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
CNDP1 <i>e!</i>	?	ENSG00000150656 <i>e!</i>	testis	1.15×10 ⁻⁵ (p-value)	GTEx Portal V6 	1

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001645555 <i>e!</i> (promoter flanking region)	1	cervix (HeLa-S3)	DNase1
		HSMMtube	H3K27me3
		liver (HepG2)	DNase1, HNF4G, Polr1, H3K27ac, H3K9ac, HNF4A, H3K4me2, H3K4me1
		Osteobl	H3K27me3
		lung (IMR90)	H3K27me3
		blood (K562)	H3K27me3
		blood (DND-41)	H3K27me3

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
CNDP1 <i>e!</i>	ENST00000358821 <i>e!</i>	NM_032649.5	ENSP00000351682 <i>e!</i>	1
CNDP1 <i>e!</i>	ENST00000582365 <i>e!</i>	?	ENSP00000462096 <i>e!</i>	1
CNDP1 <i>e!</i>	ENST00000585136 <i>e!</i>	?	?	1

