

SNiPAcad

Block annotations

Block info


genomic range	chr10:101,329,158-101,329,158 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-2.395	gene(s) hit or close-by	-
phastCons	0	eQTL gene(s)	DNMBP-AS1 <i>e!</i>
GERP++	-2.75	potentially regulated gene(s)	-
CADD score	1.456	disease gene(s)	-

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
DNMBP-AS1 <i>e!</i>	?	ENSG00000227695 <i>e!</i>	cerebellum	1.44×10 ⁻⁵ (p-value)	GTEEx Portal V6 	1

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000360276 <i>e!</i> (open chromatin region)	1	endothelium (HUVEC)	H3K27me3
		embryonic stem cell (H1ESC)	DNase1
		lung (IMR90)	H3K27me3
		blood (K562)	H3K27me3

