SNiPAcard

Block annotations

Block info

genomic range	chr14:95,007,744-95,007,744
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-1.604	**gene(s) hit or close-by**	–
phastCons	0	**eQTL gene(s)**	–
GERP++	0.617	**potentially regulated gene(s)**	–
CADD score	3.096	**disease gene(s)**	–

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000423034 (promoter flanking region)	1	embryonic stem cell (H1ESC)	CTCF, Rad21
		HSMMtube	CTCF, DNase1
		Osteobl	CTCF
		blood (DND-41)	H3K27me3
		blood (K562)	H3K27me3
		muscle (HSMM)	CTCF, DNase1
		endothelium (HUVEC)	H3K36me3, CTCF
		liver (HepG2)	CTCF, H3K4me2, H3K4me1, Rad21, H3K4me3
		A549	H3K27me3