SNiPAcard

Block annotations

Block info

genomic range	chr13:46,536,291-46,536,291
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	0.774	**gene(s) hit or close-by**	ZC3H13
phastCons	0.001	**eQTL gene(s)**	–
GERP++	2.91	**potentially regulated gene(s)**	–
CADD score	4.899	**disease gene(s)**	–

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
ZC3H13	downstream gene variant	20	ENST00000282007	NM_015070.4	ENSP00000282007	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
ZC3H13	ENST00000242848	?	ENSP00000242848	1