SNiPAcard

Block annotations

Block info

genomic range	chr1:248,038,212-248,040,104
block size	1,893 bp
variant count	4 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.718 [-1.477 – 0.039]	**gene(s) hit or close-by**	TRIM58
phastCons	μ = 0.071 [0 – 0.28]	**eQTL gene(s)**	–
GERP++	μ = -2.271 [-6.98 – 1.88]	**potentially regulated gene(s)**	–
CADD score	μ = 4.373 [0.202 – 13.74]	**disease gene(s)**	–

Trait annotations

Variant association

trait	min(p-value)	source DB	source entry/link	variant(s)
Hypertension	5.36×10^{-5}	dbGaP	pha003041 dbGaP	1

Direct effect on transcript

Amino acid sequence alteration

gene	effect type	affected transcript	RefSeq id	protein	exchanged AA's	exchanged codons	SIFT prediction	PolyPhen prediction	variant(s)
TRIM58	missense variant	ENST00000366481	NM_015431.3	ENSP00000355437	I/V	Atc/Gtc	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
TRIM58	ENST00000366481	NM_015431.3	ENSP00000355437	2

3'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
TRIM58	ENST00000366481	NM_015431.3	ENSP00000355437	1