

SNiPACard

Block annotations

Block info

genomic range	chr6:160,964,135-160,964,135 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	1.009	gene(s) hit or close-by	LPA <i>e!</i>
phastCons	0.012	eQTL gene(s)	-
GERP++	0.476	potentially regulated gene(s)	-
CADD score	2.631	disease gene(s)	-

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
LPA <i>e!</i>	ENST00000316300 <i>e!</i>	NM_005577.2	ENSP00000321334 <i>e!</i>	1

