

Block annotations

Block info

genomic range	chr19:8,105,520-8,107,703 <i>e!</i>
block size	2,184 bp
variant count	4 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -1.185$ [-2.036 – 0.169]	gene(s) hit or close-by	ELAVL1 <i>e!</i>
phastCons	$\mu = 0.012$ [0.002 – 0.024]	eQTL gene(s)	-
GERP++	$\mu = -0.042$ [-0.167 – 0]	potentially regulated gene(s)	-
CADD score	$\mu = 1.701$ [0.781 – 3.285]	disease gene(s)	-

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
ELAVL1 <i>e!</i>	ENST00000351593 <i>e!</i>	?	ENSP00000264073 <i>e!</i>	4

