

Block annotations

Block info

genomic range	chr12:94,621,186-94,630,029 <i>e!</i>
block size	8,844 bp
variant count	11 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.564$ [-1.928 – 1.142]	gene(s) hit or close-by	PLXNC1 <i>e!</i>
phastCons	$\mu = 0.166$ [0 – 0.99]	eQTL gene(s)	-
GERP++	$\mu = -0.797$ [-3.36 – 3.49]	potentially regulated gene(s)	-
CADD score	$\mu = 4.859$ [0.817 – 16.82]	disease gene(s)	-

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
PLXNC1 <i>e!</i>	downstream gene variant	386	ENST00000546659 <i>e!</i>	?	?	7

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
PLXNC1 <i>e!</i>	ENST00000258526 <i>e!</i>	NM_005761.2	ENSP00000258526 <i>e!</i>	11

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
PLXNC1 <i>e!</i>	ENST00000546659 <i>e!</i>	?	1

