

Block annotations

Block info

genomic range	chr22:33,168,562-33,175,471 <i>e!</i>
block size	6,910 bp
variant count	5 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.974$ [-1.494 – -0.145]	gene(s) hit or close-by	LL22NC01-116C6.1 <i>e!</i> , SYN3 <i>e!</i>
phastCons	$\mu = 0.000$ [0 – 0.001]	eQTL gene(s)	-
GERP++	$\mu = -1.872$ [-5.06 – 0.149]	potentially regulated gene(s)	-
CADD score	$\mu = 0.806$ [0.213 – 1.804]	disease gene(s)	-

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
LL22NC01-116C6.1 <i>e!</i>	upstream gene variant	3692	ENST00000444982 <i>e!</i>	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
SYN3 <i>e!</i>	ENST00000462268 <i>e!</i>	?	?	5
SYN3 <i>e!</i>	ENST00000358763 <i>e!</i>	NM_003490.3, NM_001135774.1, NM_133633.2	ENSP00000351614 <i>e!</i>	5

