

Block annotations

Block info

genomic range	chr13:46,706,598-46,723,294 <i>e!</i>
block size	16,697 bp
variant count	3 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.108$ [-0.764 – 0.273]	gene(s) hit or close-by	LCP1 <i>e!</i>
phastCons	$\mu = 0.001$ [0 – 0.002]	eQTL gene(s)	–
GERP++	$\mu = 0.349$ [-1.92 – 3.66]	potentially regulated gene(s)	–
CADD score	$\mu = 5.530$ [3.363 – 9.165]	disease gene(s)	–

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
LCP1 <i>e!</i>	downstream gene variant	3622	ENST00000416500 <i>e!</i>	?	ENSP00000408052 <i>e!</i>	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
LCP1 <i>e!</i>	ENST00000494531 <i>e!</i>	?	?	1
LCP1 <i>e!</i>	ENST00000323076 <i>e!</i>	NM_002298.4	ENSP00000315757 <i>e!</i>	3
LCP1 <i>e!</i>	ENST00000398576 <i>e!</i>	?	ENSP00000381581 <i>e!</i>	3
LCP1 <i>e!</i>	ENST00000469227 <i>e!</i>	?	?	1

