

Block annotations

Block info

genomic range	chr10:52,032,893-52,043,336 <i>e!</i>
block size	10,444 bp
variant count	19 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.432$ [-3.86 – 0.643]	gene(s) hit or close-by	-
phastCons	$\mu = 0.010$ [0 – 0.177]	eQTL gene(s)	-
GERP++	$\mu = -0.877$ [-5.99 – 3.01]	potentially regulated gene(s)	-
CADD score	$\mu = 2.725$ [0.089 – 7.564]	disease gene(s)	-

