

Block annotations

Block info

genomic range	chr9:136,195,607-136,201,191 <i>e!</i>
block size	5,585 bp
variant count	2 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.777$ [-0.783 – -0.771]	gene(s) hit or close-by	MED22 <i>e!</i> , RP11-244N20.7 <i>e!</i> , SURF6 <i>e!</i> , Y_RNA <i>e!</i>
phastCons	$\mu = 0.005$ [0 – 0.011]	eQTL gene(s)	–
GERP++	$\mu = -0.451$ [-0.451 – -0.451]	potentially regulated gene(s)	–
CADD score	$\mu = 2.429$ [0.053 – 4.804]	disease gene(s)	–

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
MED22 <i>e!</i>	downstream gene variant	3968	ENST00000610672 <i>e!</i> ?		ENSP00000482438 <i>e!</i>	1
RP11-244N20.7 <i>e!</i>	upstream gene variant	4635	ENST00000439130 <i>e!</i> ?		?	1
SURF6 <i>e!</i>	downstream gene variant	3	ENST00000372022 <i>e!</i> NM_006753.5		ENSP00000361092 <i>e!</i>	1
SURF6 <i>e!</i>	downstream gene variant, upstream gene variant	1416	ENST00000468290 <i>e!</i> ?		?	2
Y_RNA <i>e!</i>	downstream gene variant	3373	ENST00000364581 <i>e!</i> ?		?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
SURF6 <i>e!</i>	ENST00000372022 <i>e!</i>	NM_006753.5	ENSP00000361092 <i>e!</i>	1

