SNiPAcard

Block annotations

Block info

genomic range	chr6:161,410,911-161,466,180
block size	55,270 bp
variant count	7 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = 0.059 [-0.379 – 0.364]	**gene(s) hit or close-by**	MAP3K4, RP3-428L16.2
phastCons	μ = 0.099 [0 – 0.351]	**eQTL gene(s)**	MAP3K4
GERP++	μ = 0.739 [-0.629 – 2.91]	**potentially regulated gene(s)**	–
CADD score	μ = 5.009 [1.938 – 8.622]	**disease gene(s)**	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
MAP3K4	ENST00000366919	ILMN_1678087	blood	2.80×10-5 (p-value)	Westra et al.	4
MAP3K4	ENST00000348824					
MAP3K4	ENST00000544041					
MAP3K4	ENST00000490904					
MAP3K4	ENST00000392142					
MAP3K4	ENST00000366920					
MAP3K4	ENST00000536852					

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
MAP3K4	upstream gene variant	903	ENST00000544041	?	ENSP00000445018	2
MAP3K4	upstream gene variant	903	ENST00000490904	NM_001291958.1	ENSP00000446303	2
MAP3K4	upstream gene variant	828	ENST00000542952	?	ENSP00000439377	2
MAP3K4	upstream gene variant	873	ENST00000366920	NM_001301072.1	ENSP00000355887	2
MAP3K4	upstream gene variant	786	ENST00000366919	NM_006724.2	ENSP00000355886	2
MAP3K4	upstream gene variant	873	ENST00000348824	?	ENSP00000297332	2
MAP3K4	upstream gene variant	843	ENST00000392142	NM_005922.2	ENSP00000375986	2
RP3-428L16.2	downstream gene variant, upstream gene variant	439	ENST00000608721	?	?	2

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
MAP3K4	ENST00000348824	?	ENSP00000297332	5
MAP3K4	ENST00000366919	NM_006724.2	ENSP00000355886	5
MAP3K4	ENST00000542952	?	ENSP00000439377	5

MAP3K4	ENST00000544041	?	ENSP00000445018	5
MAP3K4	ENST00000490904	NM_001291958.1	ENSP00000446303	5
MAP3K4	ENST00000392142	NM_005922.2	ENSP00000375986	5
MAP3K4	ENST00000366920	NM_001301072.1	ENSP00000355887	5
MAP3K4	ENST00000446500	?	?	3

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
RP3-428L16.2	ENST00000608721	?	1