Locus 394 (rs1846899)

SNiPAcard

Block annotations

Block info

genomic range	chr3:186,472,816-186,475,666
block size	2,851 bp
variant count	2 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.641 [-1.457 – 0.176]	**gene(s) hit or close-by**	PSMD10P2, RP11-573D15.8
phastCons	μ = 0.250 [0 – 0.5]	**eQTL gene(s)**	–
GERP++	μ = -1.788 [-3.68 – 0.104]	**potentially regulated gene(s)**	–
CADD score	μ = 6.903 [2.027 – 11.78]	**disease gene(s)**	–

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001381876 (promoter flanking region)	1	endothelium (HUVEC)	H3K27me3
		HSMMtube	H3K27me3
		Osteobl	H3K27me3
		blood (K562)	H3K27me3
		nervous (NH-A)	H3K27me3
		skin (NHEK)	H3K4me2, H3K9ac, H3K27ac, H3K4me1, DNase1

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
PSMD10P2	upstream gene variant	3227	ENST00000432890	?	?	1
PSMD10P2	upstream gene variant	2816	ENST00000626135	?	?	1
PSMD10P2	upstream gene variant	3137	ENST00000627340	?	?	1
RP11-573D15.8	upstream gene variant	1272	ENST00000596632	?	?	2
RP11-573D15.8	upstream gene variant	150	ENST00000626586	?	?	1
RP11-573D15.8	downstream gene variant	1998	ENST00000608173	?	?	1
RP11-573D15.8	upstream gene variant	358	ENST00000625690	?	?	1
RP11-573D15.8	upstream gene variant	1563	ENST00000609652	?	?	2
RP11-573D15.8	upstream gene variant	659	ENST00000629201	?	?	1
RP11-573D15.8	upstream gene variant	209	ENST00000599314	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
RP11-573D15.8	ENST00000625869	?	?	2
RP11-573D15.8	ENST00000596329	?	?	2
RP11-573D15.8	ENST00000625690	?	?	1
RP11-573D15.8	ENST00000626520	?	?	2
RP11-573D15.8	ENST00000629954	?	?	2

RP11-573D15.8	ENST00000599314	?	?	1
RP11-573D15.8	ENST00000626586	?	?	1
RP11-573D15.8	ENST00000626978	?	?	2
RP11-573D15.8	ENST00000629201	?	?	1
RP11-573D15.8	ENST00000628291	?	?	2
RP11-573D15.8	ENST00000608173	?	?	1