

Block annotations

Block info

genomic range	chr3:186,359,810-186,360,409 <i>e!</i>
block size	600 bp
variant count	2 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -1.686$ [-2.582 -- -0.791]	gene(s) hit or close-by	FETUB <i>e!</i> , RP11-573D15.8 <i>e!</i>
phastCons	$\mu = 0.000$ [0 - 0]	eQTL gene(s)	-
GERP++	$\mu = -1.260$ [-1.57 -- -0.949]	potentially regulated gene(s)	-
CADD score	$\mu = 3.387$ [0.978 - 5.796]	disease gene(s)	-

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001681858 <i>e!</i> (enhancer)	1	monocytes (Monocytes-CD14+)	H3K27me3
		endothelium (HUVEC)	H3K27me3
		HSMMtube	H3K27me3
		Osteobl	H3K27me3
		lung (IMR90)	H3K27me3
		nervous (NH-A)	H3K27me3
		blood (DND-41)	H3K27me3

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
RP11-573D15.8 <i>e!</i>	downstream gene variant	4493	ENST00000630331 <i>e!</i>	?	?	1
RP11-573D15.8 <i>e!</i>	downstream gene variant	254	ENST00000629106 <i>e!</i>	?	?	1
RP11-573D15.8 <i>e!</i>	downstream gene variant	255	ENST00000626845 <i>e!</i>	?	?	1
RP11-573D15.8 <i>e!</i>	downstream gene variant	4499	ENST00000625741 <i>e!</i>	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
FETUB <i>e!</i>	ENST00000265029 <i>e!</i>	NM_014375.2	ENSP00000265029 <i>e!</i>	2
FETUB <i>e!</i>	ENST00000435961 <i>e!</i>	?	ENSP00000393851 <i>e!</i>	2
FETUB <i>e!</i>	ENST00000431018 <i>e!</i>	?	ENSP00000396581 <i>e!</i>	2
FETUB <i>e!</i>	ENST00000450521 <i>e!</i>	?	ENSP00000404288 <i>e!</i>	2
FETUB <i>e!</i>	ENST00000382134 <i>e!</i>	?	ENSP00000371569 <i>e!</i>	2
FETUB <i>e!</i>	ENST00000420570 <i>e!</i>	?	ENSP00000405438 <i>e!</i>	2
FETUB <i>e!</i>	ENST00000382136 <i>e!</i>	?	ENSP00000371571 <i>e!</i>	2
FETUB <i>e!</i>	ENST00000488561 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000625386 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000628505 <i>e!</i>	?	?	2

RP11-573D15.8 <i>e!</i>	ENST00000626649 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000428501 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000628190 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000630864 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000628253 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000625303 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000630315 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000629106 <i>e!</i>	?	?	1
RP11-573D15.8 <i>e!</i>	ENST00000455926 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000626633 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000630178 <i>e!</i>	?	?	2
RP11-573D15.8 <i>e!</i>	ENST00000626845 <i>e!</i>	?	?	1

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
RP11-573D15.8 <i>e!</i>	ENST00000625386 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000628505 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000626649 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000428501 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000628190 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000630864 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000628253 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000625303 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000630315 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000455926 <i>e!</i>	?	1
RP11-573D15.8 <i>e!</i>	ENST00000626633 <i>e!</i>	?	1

