

Block annotations

Block info

genomic range	chr19:14,500,714-14,504,025 <i>e!</i>
block size	3,312 bp
variant count	3 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = 0.292$ [0.197 – 0.445]	gene(s) hit or close-by	ADGRES <i>e!</i>
phastCons	$\mu = 0.166$ [0.06 – 0.337]	eQTL gene(s)	–
GERP++	$\mu = 0.982$ [0.113 – 2.33]	potentially regulated gene(s)	–
CADD score	$\mu = 7.166$ [1.559 – 16.86]	disease gene(s)	–

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
ADGRES <i>e!</i>	downstream gene variant	2016	ENST00000587606 <i>e!</i>	?	ENSP00000465800 <i>e!</i>	1
ADGRES <i>e!</i>	upstream gene variant	4267	ENST00000586849 <i>e!</i>	?	?	1
ADGRES <i>e!</i>	upstream gene variant	3037	ENST00000591737 <i>e!</i>	?	?	1
ADGRES <i>e!</i>	upstream gene variant	4201	ENST00000593028 <i>e!</i>	?	?	1
ADGRES <i>e!</i>	upstream gene variant	4520	ENST00000587319 <i>e!</i>	?	?	1
ADGRES <i>e!</i>	upstream gene variant	4520	ENST00000590567 <i>e!</i>	?	?	1
ADGRES <i>e!</i>	downstream gene variant	1721	ENST00000591080 <i>e!</i>	?	?	1
ADGRES <i>e!</i>	upstream gene variant	4520	ENST00000592341 <i>e!</i>	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
ADGRES <i>e!</i>	ENST00000358600 <i>e!</i>	NM_001784.4	ENSP00000351413 <i>e!</i>	3
ADGRES <i>e!</i>	ENST00000586517 <i>e!</i>	?	ENSP00000467351 <i>e!</i>	3
ADGRES <i>e!</i>	ENST00000587728 <i>e!</i>	?	?	3
ADGRES <i>e!</i>	ENST00000242786 <i>e!</i>	NM_078481.3	ENSP00000242786 <i>e!</i>	3
ADGRES <i>e!</i>	ENST00000591080 <i>e!</i>	?	?	2
ADGRES <i>e!</i>	ENST00000357355 <i>e!</i>	NM_001025160.2	ENSP00000349918 <i>e!</i>	3
ADGRES <i>e!</i>	ENST00000592261 <i>e!</i>	?	ENSP00000467478 <i>e!</i>	3
ADGRES <i>e!</i>	ENST00000587606 <i>e!</i>	?	ENSP00000465800 <i>e!</i>	2
ADGRES <i>e!</i>	ENST00000587535 <i>e!</i>	?	?	3

