Locus 437 (rs7260110)

SNiPAcard

Block annotations

Block info

genomic range	chr19:14,500,714-14,504,025
block size	3,312 bp
variant count	3 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = 0.292 [0.197 – 0.445]	gene(s) hit or close-by	ADGRE5
phastCons	μ = 0.166 [0.06 – 0.337]	eQTL gene(s)	–
GERP++	μ = 0.982 [0.113 – 2.33]	potentially regulated gene(s)	–
CADD score	μ = 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)
ADGRE5	downstream gene variant	2016	ENST00000587606	?	ENSP00000465800	1
ADGRE5	upstream gene variant	4267	ENST00000586849	?	?	1
ADGRE5	upstream gene variant	3037	ENST00000591737	?	?	1
ADGRE5	upstream gene variant	4201	ENST00000593028	?	?	1
ADGRE5	upstream gene variant	4520	ENST00000587319	?	?	1
ADGRE5	upstream gene variant	4520	ENST00000590567	?	?	1
ADGRE5	downstream gene variant	1721	ENST00000591080	?	?	1
ADGRE5	upstream gene variant	4520	ENST00000592341	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
ADGRE5	ENST00000358600	NM_001784.4	ENSP00000351413	3
ADGRE5	ENST00000586517	?	ENSP00000467351	3
ADGRE5	ENST00000587728	?	?	3
ADGRE5	ENST00000242786	NM_078481.3	ENSP00000242786	3
ADGRE5	ENST00000591080	?	?	2
ADGRE5	ENST00000357355	NM_001025160.2	ENSP00000349918	3
ADGRE5	ENST00000592261	?	ENSP00000467478	3
ADGRE5	ENST00000587606	?	ENSP00000465800	2
ADGRE5	ENST00000587535	?	?	3