SNiPAcard

Block annotations

Block info

genomic range	chr2:102,776,518-102,776,518
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	0.364	gene(s) hit or close-by	IL1R1
phastCons	0.004	eQTL gene(s)	–
GERP++	0.235	potentially regulated gene(s)	–
CADD score	2.731	disease gene(s)	–

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
IL1R1	upstream gene variant	4716	ENST00000422532	?	ENSP00000390349	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
IL1R1	ENST00000409929	NM_001288706.1	ENSP00000386776	1
IL1R1	ENST00000452403	?	ENSP00000401646	1
IL1R1	ENST00000450319	?	ENSP00000411627	1
IL1R1	ENST00000442590	?	ENSP00000393296	1
IL1R1	ENST00000409288	?	ENSP00000386478	1
IL1R1	ENST00000430171	?	ENSP00000408101	1
IL1R1	ENST00000424272	?	ENSP00000415366	1
IL1R1	ENST00000410023	NM_000877.3	ENSP00000386380	1
IL1R1	ENST00000409589	?	ENSP00000386555	1
IL1R1	ENST00000428279	?	ENSP00000410461	1
IL1R1	ENST00000409329	?	ENSP00000387131	1
IL1R1	ENST00000413623	?	ENSP00000407017	1