# Locus 439 (rs9811674)

SNiPAcard

## Block annotations

### Block info

| | |
|---|---|
| genomic range | chr3:190,287,162-190,290,917 |
| block size | 3,756 bp |
| variant count | 2 variants |

### Basic features

| Conservation/deleteriousness | | Linked genes | |
|---|---|---|---|
| phyloP | μ = -0.081 [-0.149 – -0.013] | gene(s) hit or close-by | IL1RAP |
| phastCons | μ = 0.000 [0 – 0] | eQTL gene(s) | – |
| GERP++ | μ = 1.190 [0 – 2.38] | potentially regulated gene(s) | – |
| CADD score | μ = 6.082 [3.796 – 8.369] | disease gene(s) | – |

## Putative effect on regulation

### Variation proximal to gene

| gene | variant type | min(distance) | transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|---|---|
| IL1RAP | downstream gene variant | 4856 | ENST00000461629 | ? | ? | 1 |
| IL1RAP | downstream gene variant | 4955 | ENST00000482913 | ? | ? | 1 |
| IL1RAP | downstream gene variant | 4705 | ENST00000473566 | ? | ? | 1 |

## Putative effect on transcript

### Intron variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| IL1RAP | ENST00000317757 | NM_001167931.1 | ENSP00000314807 | 2 |
| IL1RAP | ENST00000439062 | NM_001167928.1 | ENSP00000401132 | 2 |
| IL1RAP | ENST00000342550 | ? | ENSP00000345829 | 2 |
| IL1RAP | ENST00000453359 | ? | ENSP00000412008 | 2 |
| IL1RAP | ENST00000072516 | NM_001167929.1 | ENSP00000072516 | 2 |
| IL1RAP | ENST00000422940 | NM_001167930.1 | ENSP00000387371 | 2 |
| IL1RAP | ENST00000434491 | ? | ENSP00000391899 | 2 |
| IL1RAP | ENST00000422485 | NM_134470.3 | ENSP00000409352 | 2 |
| IL1RAP | ENST00000447382 | NM_002182.3 | ENSP00000390541 | 2 |
| IL1RAP | ENST00000422625 | ? | ENSP00000389149 | 2 |
| IL1RAP | ENST00000413869 | ? | ENSP00000416296 | 2 |
| IL1RAP | ENST00000412504 | ? | ENSP00000412053 | 2 |
| IL1RAP | ENST00000443369 | ? | ENSP00000408893 | 2 |