# Locus 88 (rs41341749)

SNiPAcard

## Block annotations

### Block info

| | |
|---|---|
| genomic range | chr17:34,310,702-34,322,110 |
| block size | 11,409 bp |
| variant count | 5 variants |

### Basic features

| Conservation/deleteriousness | | Linked genes | |
|---|---|---|---|
| phyloP | μ = 0.125 [-0.459 – 0.909] | gene(s) hit or close-by | CCL14, CCL15, CCL15-CCL14, CCL16, CTB-186H2.3 |
| phastCons | μ = 0.055 [0 – 0.268] | eQTL gene(s) | – |
| GERP++ | μ = -1.285 [-5.68 – 2.44] | potentially regulated gene(s) | CCL14, CCL14 |
| CADD score | μ = 5.865 [3.257 – 9.467] | disease gene(s) | – |

## Putative effect on regulation

### ENCODE promoter-associated DHS

| SNiPA promoter id | variant(s) | associated gene(s) |
|---|---|---|
| ENCP00000022624 | | CCL14 |

### Variation proximal to gene

| gene | variant type | min(distance) | transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|---|---|
| CCL14 | upstream gene variant | 230 | ENST00000622526 | NM_032962.4 | ENSP00000479097 | 1 |
| CCL14 | downstream gene variant, upstream gene variant | 21 | ENST00000620991 | ? | ENSP00000484818 | 2 |
| CCL14 | upstream gene variant | 121 | ENST00000618404 | NM_032963.3 | ENSP00000481023 | 1 |
| CCL15 | downstream gene variant | 1366 | ENST00000614368 | ? | ENSP00000484262 | 1 |
| CCL15 | downstream gene variant | 2508 | ENST00000617897 | NM_032965.4 | ENSP00000484078 | 1 |
| CCL16 | upstream gene variant | 2205 | ENST00000610493 | ? | ENSP00000478934 | 3 |
| CCL16 | upstream gene variant | 2170 | ENST00000611905 | NM_004590.2 | ENSP00000478024 | 3 |
| CTB-186H2.3 | downstream gene variant | 169 | ENST00000617687 | ? | ? | 1 |
| CTB-186H2.3 | upstream gene variant, downstream gene variant | 40 | ENST00000612584 | ? | ? | 4 |

## Putative effect on transcript

### Intron variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| CCL14 | ENST00000622526 | NM_032962.4 | ENSP00000479097 | 2 |
| CCL14 | ENST00000620991 | ? | ENSP00000484818 | 2 |
| CCL14 | ENST00000618404 | NM_032963.3 | ENSP00000481023 | 2 |
| CCL15-CCL14 | ENST00000616694 | ? | ENSP00000481402 | 4 |
| CCL15-CCL14 | ENST00000610751 | ? | ENSP00000481940 | 4 |
| CTB-186H2.3 | ENST00000617687 | ? | ? | 2 |

### 3'-UTR variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| CCL14 | ENST00000614009 | ? | ENSP00000483186 | 1 |

| | | | | |
|---|---|---|---|---|
| CCL14 | ENST00000622526 | NM_032962.4 | ENSP00000479097 | 1 |
| CCL14 | ENST00000618404 | NM_032963.3 | ENSP00000481023 | 1 |
| CCL15-CCL14 | ENST00000616694 | ? | ENSP00000481402 | 1 |
| CCL15-CCL14 | ENST00000610751 | ? | ENSP00000481940 | 1 |

## 5'-UTR variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| CCL14 | ENST00000614009 | ? | ENSP00000483186 | 3 |

## Non-coding exon variant

| gene | affected transcript | RefSeq id | variant(s) |
|---|---|---|---|
| CTB-186H2.3 | ENST00000617687 | ? | 1 |
| CTB-186H2.3 | ENST00000612584 | ? | 1 |