# SNiPAcard

## Block annotations

### Block info

| | |
|---|---|
| **genomic range** | chr3:46,275,570-46,482,980 |
| **block size** | 207,411 bp |
| **variant count** | 90 variants |

### Basic features

| Conservation/deleteriousness | | Linked genes | |
|---|---|---|---|
| **phyloP** | μ = -0.456 [-4.588 – 1.248] | **gene(s) hit or close-by** | CCR2, CCR3, CCR5, CCRL2, LTF, RP11-24F11.2, UQCRC2P1 |
| **phastCons** | μ = 0.052 [0 – 0.59] | **eQTL gene(s)** | CCR3, LIMD1, LIMD1-AS1, LRRC2 |
| **GERP++** | μ = -0.526 [-10.7 – 3.83] | **potentially regulated gene(s)** | AC104304.1, ALS2CL, CCR1, CCR2, CCR3, CCR5, CCR9, CCRL2, CXCR6, LRRC2, LTF, LZTFL1, PRSS44, PRSS50, RP11-24F11.2, XCR1 |
| **CADD score** | μ = 3.969 [0.056 – 10.62] | **disease gene(s)** | LZTFL1, CCR5, LTF, CCR2 |

## Trait annotations

### Variant association

| trait | min(p-value) | source DB | source entry/link | variant(s) |
|---|---|---|---|---|
| Cerebrospinal fluid levels of Alzheimer's disease-related proteins | $<2.00\times10^{-13}$ | GWAS Catalog | 25340798 | 1 |

### Disease gene annotation

| gene | trait | source DB | source entry/link |
|---|---|---|---|
| LZTFL1 | BARDET-BIEDL SYNDROME 17 | OMIM | MIM:615994 |
| CCR5 | WEST NILE VIRUS, SUSCEPTIBILITY TO | OMIM | MIM:610379 |
| CCR5 | DIABETES MELLITUS, INSULIN-DEPENDENT, 22 | OMIM | MIM:612522 |
| CCR5 | HUMAN IMMUNODEFICIENCY VIRUS TYPE 1, SUSCEPTIBILITY TO | OMIM | MIM:609423 |
| LTF | SPECIFIC GRANULE DEFICIENCY | OMIM | MIM:245480 |
| CCR2 | HUMAN IMMUNODEFICIENCY VIRUS TYPE 1, SUSCEPTIBILITY TO | OMIM | MIM:609423 |
| LZTFL1 | BARDET-BIEDL SYNDROME | OrphaNet | OrphaNet:110 |

## Direct effect on transcript

### Amino acid sequence alteration

| gene | effect type | affected transcript | RefSeq id | protein | exchanged AA's | exchanged codons | SIFT prediction | PolyPhen prediction | variant(s) |
|---|---|---|---|---|---|---|---|---|---|
| CCRL2 | missense variant | ENST00000399036 | NM_003965.4 | ENSP00000381994 | M/V | Atg/Gtg | ? | ? | 1 |
| CCRL2 | missense variant | ENST00000357392 | NM_001130910.1 | ENSP00000349967 | M/V | Atg/Gtg | ? | ? | 1 |
| CCRL2 | missense variant | ENST00000400880 | ? | ENSP00000383677 | M/V | Atg/Gtg | ? | ? | 1 |
| CCRL2 | missense variant | ENST00000400882 | ? | ENSP00000383678 | M/V | Atg/Gtg | ? | ? | 1 |
| CCRL2 | missense variant | ENST00000433848 | ? | ENSP00000414957 | M/V | Atg/Gtg | ? | ? | 1 |

## Direct effect on regulation

### *cis*-eQTL

| gene | transcript | probe | tissue | min(statistic) (type) | source | variant(s) |
|---|---|---|---|---|---|---|
| LIMD1-AS1 | ? | ENSG00000230530 | tibial nerve | 5.71×10-6 (p-value) | GTEx Portal V6 | 23 |
| LIMD1 | ? | ENSG00000144791 | tibial nerve | 9.94×10-7 (p-value) | GTEx Portal V6 | 48 |
| LRRC2 | ? | ENSG00000163827 | transformed fibroblasts | 4.59×10-8 (p-value) | GTEx Portal V6 | 84 |
| LIMD1-AS1 | ? | ENSG00000230530 | tibial artery | 9.71×10-6 (p-value) | GTEx Portal V6 | 8 |
| LIMD1 | ? | ENSG00000144791 | tibial artery | 2.16×10-6 (p-value) | GTEx Portal V6 | 31 |
| CCR3 | ? | ENSG00000183625 | blood | 6.66×10-6 (p-value) | GTEx Portal V6 | 8 |

## Putative effect on regulation

### FANTOM5 expressed promoter

| SNiPA promoter id | variant(s) | associated transcript(s) | gene |
|---|---|---|---|
| FFCP00000607398 | 1 | ENST00000443496, ENST00000417439, ENST00000493056, ENST00000426532, ENST00000478874, ENST00000231751 | LTF |

### ENCODE promoter-associated DHS

| SNiPA promoter id | variant(s) | associated gene(s) |
|---|---|---|
| ENCP00000036249 | | |

### ENCODE promoter-associated distal DHS (Enhancer)

| SNiPA enhancer id | variant(s) | associated SNiPA promoter id | associated gene(s) |
|---|---|---|---|
| ENCE00000337650 | 1 | ENCP00000036251 | RP11-24F11.2<br>CCRL2 |
| | | ENCP00000036271 | ALS2CL |
| | | ENCP00000036243 | CCR3 |
| | | ENCP00000036252 | CCRL2 |
| | | ENCP00000036239 | XCR1 |
| | | ENCP00000036242 | CCR1 |
| ENCE00000337509 | 1 | ENCP00000036231 | LZTFL1 |
| | | ENCP00000036227 | LZTFL1 |
| | | ENCP00000036250 | CCR5 |
| | | ENCP00000036230 | CCR9 |
| | | ENCP00000036232 | LZTFL1 |
| | | ENCP00000036234 | CXCR6 |
| ENCE00000337805 | 1 | ENCP00000036249 | CCR5 |
| ENCE00000337856 | 1 | ENCP00000036254 | LTF |
| ENCE00000337664 | 1 | ENCP00000036251 | RP11-24F11.2<br>CCRL2 |
| | | ENCP00000036243 | CCR3 |
| | | ENCP00000036271 | ALS2CL |
| | | ENCP00000036252 | CCRL2 |
| | | ENCP00000036239 | XCR1 |
| | | ENCP00000036242 | CCR1 |
| ENCE00000337563 | 3 | ENCP00000036231 | LZTFL1 |
| | | ENCP00000036250 | CCR5 |
| | | ENCP00000036230 | CCR9 |
| | | ENCP00000036232 | LZTFL1 |
| | | ENCP00000036234 | CXCR6 |
| ENCE00000337711 | 1 | ENCP00000036261 | LRRC2 |

| | | | |
|---|---|---|---|
| | | ENCP00000036273 | PRSS50 |
| | | ENCP00000036248 | CCR2 |
| | | ENCP00000036263 | AC104304.1 |
| | | ENCP00000036277 | PRSS44 |
| | | ENCP00000036262 | AC104304.1 |
| | | ENCP00000036244 | CCR3 |
| ENCE00000337859 | 1 | ENCP00000036254 | LTF |
| ENCE00000337713 | 1 | ENCP00000036261 | LRRC2 |
| | | ENCP00000036273 | PRSS50 |
| | | ENCP00000036248 | CCR2 |
| | | ENCP00000036263 | AC104304.1 |
| | | ENCP00000036277 | PRSS44 |
| | | ENCP00000036262 | AC104304.1 |
| | | ENCP00000036244 | CCR3 |
| ENCE00000337671 | 1 | ENCP00000036243 | CCR3 |
| | | ENCP00000036271 | ALS2CL |
| | | ENCP00000036239 | XCR1 |
| | | ENCP00000036242 | CCR1 |
| ENCE00000337715 | 2 | ENCP00000036261 | LRRC2 |
| | | ENCP00000036248 | CCR2 |
| | | ENCP00000036263 | AC104304.1 |
| | | ENCP00000036262 | AC104304.1 |
| | | ENCP00000036277 | PRSS44 |
| | | ENCP00000036244 | CCR3 |
| | | ENCP00000036258 | LTF |
| | | ENCP00000036273 | PRSS50 |

## Regulatory feature cluster

| element id | variant(s) | tissue/cell | factors |
|---|---|---|---|
| ENSR00001478830 (CTCF binding site) | 1 | cervix (HeLa-S3) | H3K27me3 |
| | | embryonic stem cell (H1ESC) | CTCF, Rad21 |
| | | endothelium (HUVEC) | H3K36me3 |
| | | HSMMtube | H3K27me3 |
| | | Osteobl | H3K27me3 |
| | | blood (K562) | H3K27me3 |
| ENSR00001362902 (open chromatin region) | 1 | embryonic stem cell (H1ESC) | DNase1 |
| | | blood (K562) | H3K27me3 |
| ENSR00001362911 (promoter flanking region) | 1 | monocytes (Monocytes-CD14+) | H3K27ac, H3K4me1 |
| | | lung (IMR90) | H3K27me3 |
| | | blood (GM12878) | H3K4me1 |
| | | blood (DND-41) | H3K4me1, H3K27ac |
| | | blood (K562) | H3K27me3 |
| | | skin (NHEK) | DNase1 |
| ENSR00001674590 (enhancer) | 1 | NHLF | H3K27me3 |
| | | HSMMtube | H3K27me3 |
| | | Osteobl | H3K27me3 |
| | | blood (K562) | H3K27me3 |
| | | blood (DND-41) | H3K4me1, H3K27ac |
| | | muscle (HSMM) | H3K27me3 |
| | | monocytes (Monocytes-CD14+) | H3K27ac, H3K4me1 |
| | | blood (GM12878) | PU1, H3K4me1, H3K27ac |
| | | lung (IMR90) | H3K27me3 |
| | | A549 | H3K27me3 |
| ENSR00001362921 (promoter flanking region) | 1 | HSMMtube | H3K27me3, DNase1 |
| | | Osteobl | H3K27me3 |
| | | blood (K562) | H3K27me3 |
| | | skin (NHDF-AD) | DNase1, H3K27me3 |

| | | | |
|---|---|---|---|
| | | muscle (HSMM) | DNase1 |
| | | cervix (HeLa-S3) | DNase1, H3K27me3 |
| | | monocytes (Monocytes-CD14+) | DNase1, H3K4me1, H3K4me2, H3K27ac, H3K4me3, H3K36me3 |
| | | endothelium (HUVEC) | H3K27me3 |
| | | blood (GM12878) | BATF, H3K4me1 |
| | | lung (IMR90) | H3K27me3 |
| | | A549 | H3K27me3 |
| | | nervous (NH-A) | H3K27me3 |
| ENSR00001478841 (CTCF binding site) | 1 | embryonic stem cell (H1ESC) | Rad21, CTCF, DNase1 |
| | | HSMMtube | CTCF, H3K27me3 |
| | | blood (K562) | H3K27me3, CTCF |
| | | skin (NHDF-AD) | H3K27me3 |
| | | muscle (HSMM) | CTCF |
| | | liver (HepG2) | CTCF |
| | | blood (GM12878) | Rad21, CTCF |
| | | lung (IMR90) | H3K27me3 |
| | | nervous (NH-A) | H3K27me3 |
| | | skin (NHEK) | CTCF |
| | | Osteobl | H3K27me3 |
| | | blood (DND-41) | H3K4me1, CTCF |
| | | cervix (HeLa-S3) | CTCF |
| | | monocytes (Monocytes-CD14+) | DNase1, CTCF |
| | | endothelium (HUVEC) | H3K36me3, H3K27me3 |
| | | A549 | H3K27me3 |
| ENSR00001478842 (promoter flanking region) | 1 | endothelium (HUVEC) | H3K27me3 |
| | | HSMMtube | H3K27me3 |
| | | Osteobl | H3K27me3 |
| | | lung (IMR90) | H3K27me3 |
| | | nervous (NH-A) | H3K27me3 |
| | | blood (DND-41) | H3K4me1, H3K27ac |
| | | blood (K562) | H3K27me3 |
| ENSR00001674606 (enhancer) | 3 | HSMMtube | H3K27me3 |
| | | Osteobl | H3K27me3 |
| | | blood (DND-41) | H3K4me1, H3K27ac |
| | | blood (K562) | H3K27me3 |
| | | endothelium (HUVEC) | H3K27me3 |
| | | lung (IMR90) | H3K27me3 |
| | | A549 | H3K27me3 |
| | | nervous (NH-A) | H3K27me3 |
| ENSR00001478843 (promoter flanking region) | 3 | embryonic stem cell (H1ESC) | DNase1, H3K27me3 |
| | | blood (K562) | H3K27me3, DNase1 |
| | | blood (DND-41) | H3K4me1, H3K27ac |
| | | skin (NHDF-AD) | H3K27me3 |
| | | breast (HMEC) | DNase1, H3K27ac |
| | | cervix (HeLa-S3) | PolII, DNase1 |
| | | monocytes (Monocytes-CD14+) | DNase1 |
| | | endothelium (HUVEC) | Cjun, DNase1 |
| | | nervous (NH-A) | DNase1 |
| | | skin (NHEK) | DNase1 |
| ENSR00001674607 (CTCF binding site) | 1 | cervix (HeLa-S3) | H3K27ac, DNase1 |
| | | embryonic stem cell (H1ESC) | DNase1 |
| | | HSMMtube | H3K27me3 |
| | | lung (IMR90) | H3K27me3 |
| | | blood (K562) | Max, DNase1, H3K27me3 |
| | | blood (DND-41) | H3K27ac, H3K4me1 |
| | | nervous (NH-A) | H3K27me3 |
| ENSR00001362934 (promoter flanking region) | 1 | cervix (HeLa-S3) | PolII, H3K27ac, DNase1 |
| | | embryonic stem cell (H1ESC) | DNase1 |
| | | HSMMtube | H3K27me3 |
| | | lung (IMR90) | H3K27me3 |
| | | nervous (NH-A) | H3K27me3 |
| | | blood (K562) | H3K27me3, DNase1, Max |
| | | blood (DND-41) | H3K4me1, H3K27ac |
| ENSR00001362946 | 1 | HSMMtube | H3K27me3 |

| | | | |
|---|---|---|---|
| (enhancer) | | liver (HepG2) | H3K27me3 |
| | | Osteobl | H3K27me3 |
| | | blood (K562) | DNase1, H2AZ |
| | | blood (DND-41) | H3K4me1 |
| ENSR00001362947 (open chromatin region) | 3 | embryonic stem cell (H1ESC) | DNase1 |
| | | blood (K562) | H3K27me3 |
| ENSR00001362952 (open chromatin region) | 2 | A549 | H3K27me3 |
| | | blood (K562) | H3K27me3 |
| | | skin (NHEK) | DNase1, H3K4me1, H3K4me2, H3K27ac |
| ENSR00001674619 (enhancer) | 1 | lung (IMR90) | H3K27me3 |
| | | blood (DND-41) | H3K4me1, H3K27ac |
| | | blood (K562) | H3K27me3 |
| | | skin (NHDF-AD) | H3K27me3 |

## Variation proximal to gene

| gene | variant type | min(distance) | transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|---|---|
| CCR2 | downstream gene variant | 1779 | ENST00000445132 | NM_001123396.1 | ENSP00000399285 | 1 |
| CCR2 | downstream gene variant | 276 | ENST00000292301 | NM_001123041.2 | ENSP00000292301 | 1 |
| CCR2 | downstream gene variant | 269 | ENST00000400888 | ? | ENSP00000383681 | 1 |
| CCR2 | downstream gene variant | 2509 | ENST00000465202 | ? | ? | 1 |
| CCR2 | downstream gene variant | 679 | ENST00000421659 | ? | ENSP00000396736 | 2 |
| CCR3 | upstream gene variant | 2491 | ENST00000457243 | ? | ENSP00000401822 | 2 |
| CCR3 | upstream gene variant | 2461 | ENST00000395940 | NM_178329.2, NM_001837.3 | ENSP00000379271 | 2 |
| CCR3 | upstream gene variant | 2411 | ENST00000545097 | NM_178328.1, NM_001164680.1 | ENSP00000441600 | 2 |
| CCR3 | upstream gene variant | 2491 | ENST00000484025 | ? | ? | 2 |
| CCR3 | upstream gene variant | 2490 | ENST00000452454 | ? | ENSP00000389336 | 2 |
| CCR3 | upstream gene variant | 3681 | ENST00000395942 | ? | ENSP00000379273 | 1 |
| CCR3 | upstream gene variant | 1943 | ENST00000475150 | ? | ? | 2 |
| CCR5 | upstream gene variant, downstream gene variant | 684 | ENST00000292303 | NM_001100168.1, NM_000579.3 | ENSP00000292303 | 4 |
| CCR5 | upstream gene variant | 2500 | ENST00000445772 | ? | ENSP00000404881 | 2 |
| CCRL2 | upstream gene variant, downstream gene variant | 489 | ENST00000400882 | ? | ENSP00000383678 | 15 |
| CCRL2 | upstream gene variant, downstream gene variant | 411 | ENST00000495870 | ? | ? | 16 |
| CCRL2 | upstream gene variant, downstream gene variant | 488 | ENST00000357392 | NM_001130910.1 | ENSP00000349967 | 15 |
| CCRL2 | upstream gene variant, downstream gene variant | 488 | ENST00000399036 | NM_003965.4 | ENSP00000381994 | 16 |
| CCRL2 | upstream gene variant, downstream gene variant | 279 | ENST00000400880 | ? | ENSP00000383677 | 15 |
| CCRL2 | upstream gene variant, downstream gene variant | 662 | ENST00000433848 | ? | ENSP00000414957 | 15 |
| CCRL2 | upstream gene variant, downstream gene variant | 121 | ENST00000441909 | ? | ? | 19 |
| LTF | downstream gene variant | 2014 | ENST00000231751 | NM_002343.4 | ENSP00000231751 | 4 |
| LTF | downstream gene variant | 2388 | ENST00000426532 | NM_001199149.1 | ENSP00000405719 | 4 |
| LTF | downstream gene variant | 2570 | ENST00000443496 | ? | ENSP00000397427 | 3 |
| LTF | downstream gene variant | 2562 | ENST00000417439 | ? | ENSP00000405546 | 3 |
| LTF | downstream gene variant | 1695 | ENST00000493056 | ? | ? | 5 |
| LTF | downstream gene variant | 1756 | ENST00000478874 | ? | ? | 5 |

| | | | | | | |
|---|---|---|---|---|---|---|
| RP11-24F11.2 | downstream gene variant, upstream gene variant | 1314 | ENST00000451485 | ? | ? | 9 |
| UQCRC2P1 | downstream gene variant, upstream gene variant | 1366 | ENST00000417777 | ? | ? | 2 |

## Putative effect on transcript

### Synonymous coding variant

| gene | affected transcript | RefSeq id | protein | AA's | exchanged codons | variant(s) |
|---|---|---|---|---|---|---|
| CCR2 | ENST00000445132 | NM_001123396.1 | ENSP00000399285 | T | acA/acG | 1 |
| CCRL2 | ENST00000357392 | NM_001130910.1 | ENSP00000349967 | G | ggT/ggG | 1 |
| CCRL2 | ENST00000400882 | ? | ENSP00000383678 | G | ggT/ggG | 1 |
| CCRL2 | ENST00000433848 | ? | ENSP00000414957 | G | ggT/ggG | 1 |
| CCRL2 | ENST00000400880 | ? | ENSP00000383677 | G | ggT/ggG | 1 |
| CCRL2 | ENST00000399036 | NM_003965.4 | ENSP00000381994 | G | ggT/ggG | 1 |

### Intron variant (splice region)

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| LTF | ENST00000417439 | ? | ENSP00000405546 | 1 |
| LTF | ENST00000443496 | ? | ENSP00000397427 | 1 |
| LTF | ENST00000426532 | NM_001199149.1 | ENSP00000405719 | 1 |
| LTF | ENST00000231751 | NM_002343.4 | ENSP00000231751 | 1 |
| LTF | ENST00000493056 | ? | ? | 1 |
| LTF | ENST00000478874 | ? | ? | 1 |

### Intron variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| CCR2 | ENST00000292301 | NM_001123041.2 | ENSP00000292301 | 1 |
| CCR2 | ENST00000400888 | ? | ENSP00000383681 | 1 |
| CCR3 | ENST00000452454 | ? | ENSP00000389336 | 6 |
| CCR3 | ENST00000457243 | ? | ENSP00000401822 | 6 |
| CCR3 | ENST00000484025 | ? | ? | 6 |
| CCR3 | ENST00000545097 | NM_178328.1, NM_001164680.1 | ENSP00000441600 | 6 |
| CCR3 | ENST00000357422 | ? | ENSP00000350003 | 11 |
| CCR3 | ENST00000395940 | NM_178329.2, NM_001837.3 | ENSP00000379271 | 6 |
| CCRL2 | ENST00000441909 | ? | ? | 5 |
| LTF | ENST00000417439 | ? | ENSP00000405546 | 3 |
| LTF | ENST00000443496 | ? | ENSP00000397427 | 3 |
| LTF | ENST00000426532 | NM_001199149.1 | ENSP00000405719 | 3 |
| LTF | ENST00000231751 | NM_002343.4 | ENSP00000231751 | 3 |
| LTF | ENST00000493056 | ? | ? | 1 |
| LTF | ENST00000478874 | ? | ? | 1 |
| RP11-24F11.2 | ENST00000451485 | ? | ? | 30 |

### 3'-UTR variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| CCRL2 | ENST00000357392 | NM_001130910.1 | ENSP00000349967 | 1 |
| CCRL2 | ENST00000400882 | ? | ENSP00000383678 | 1 |
| CCRL2 | ENST00000399036 | NM_003965.4 | ENSP00000381994 | 1 |

## Non-coding exon variant

| gene | affected transcript | RefSeq id | variant(s) |
|---|---|---|---|
| CCR2 | ENST00000465202 | ? | 1 |