# SNiPAcard

## Block annotations

### Block info

| | |
|---|---|
| **genomic range** | chr1:109,817,192-109,822,166 |
| **block size** | 4,975 bp |
| **variant count** | 10 variants |

### Basic features

| Conservation/deleteriousness | | Linked genes | |
|---|---|---|---|
| **phyloP** | μ = -0.610 [-1.832 – 0.394] | **gene(s) hit or close-by** | CELSR2, PSRC1 |
| **phastCons** | μ = 0.102 [0 – 0.992] | **eQTL gene(s)** | CELSR2, PSRC1, SORT1 |
| **GERP++** | μ = -1.693 [-9 – 3.35] | **potentially regulated gene(s)** | AMPD2 |
| **CADD score** | μ = 4.646 [0.153 – 13.51] | **disease gene(s)** | SORT1, AMPD2 |

## Trait annotations

### Variant association

| trait | min(p-value) | source DB | source entry/link | variant(s) |
|---|---|---|---|---|
| Coronary Artery Disease | $<1.00\times10^{-8}$ | GWAS Catalog | 24262325 | 1 |
| Coronary artery disease or large artery stroke | $<8.00\times10^{-17}$ | GWAS Catalog | 24262325 | 1 |
| Coronary artery disease or ischemic stroke | $<1.00\times10^{-8}$ | GWAS Catalog | 24262325 | 1 |
| Cholesterol, total | $<2.00\times10^{-170}$ | GWAS Catalog | 24097068 | 1 |
| LDL cholesterol | $<5.00\times10^{-241}$ | GWAS Catalog | 24097068 | 1 |
| Lipoprotein-associated phospholipase A2 activity and mass | $<2.00\times10^{-22}$ | GWAS Catalog | 23118302 | 1 |
| Lipoprotein-associated phospholipase A2 activity and mass | $<1.00\times10^{-17}$ | GWAS Catalog | 22003152 | 1 |
| Cardiovascular disease risk factors | $<2.00\times10^{-22}$ | GWAS Catalog | 21943158 | 1 |
| Metabolite levels | $<2.00\times10^{-19}$ | GWAS Catalog | 21909109 | 1 |
| Coronary heart disease | $<3.00\times10^{-10}$ | GWAS Catalog | 21378990 | 1 |
| Coronary heart disease | $<6.00\times10^{-10}$ | GWAS Catalog | 21378988 | 1 |
| LDL cholesterol | $<9.00\times10^{-29}$ | GWAS Catalog | 21347282 | 1 |
| Coronary Artery Disease | $<8.00\times10^{-11}$ | GWAS Catalog | 21239051 | 1 |
| Progranulin levels | $<2.00\times10^{-30}$ | GWAS Catalog | 21087763 | 1 |
| LDL cholesterol | $<1.00\times10^{-26}$ | GWAS Catalog | 20864672 | 1 |
| Cholesterol, total | $<6.00\times10^{-131}$ | GWAS Catalog | 20686565 | 1 |
| LDL cholesterol | $<1.00\times10^{-170}$ | GWAS Catalog | 20686565 | 1 |
| Lipoprotein-associated phospholipase A2 activity and mass | $<3.00\times10^{-15}$ | GWAS Catalog | 20442857 | 1 |
| Response to statin therapy | $<4.00\times10^{-6}$ | GWAS Catalog | 20339536 | 1 |
| Lipid metabolism phenotypes | $<2.00\times10^{-53}$ | GWAS Catalog | 19936222 | 1 |
| Myocardial infarction (early onset) | $<8.00\times10^{-12}$ | GWAS Catalog | 19198609 | 1 |
| Cholesterol, total | $<9.00\times10^{-22}$ | GWAS Catalog | 19060911 | 1 |
| LDL cholesterol | $<8.00\times10^{-23}$ | GWAS Catalog | 19060911 | 1 |
| LDL cholesterol | $<2.00\times10^{-12}$ | GWAS Catalog | 19060910 | 1 |
| LDL cholesterol | $<2.00\times10^{-42}$ | GWAS Catalog | 19060906 | 1 |
| LDL cholesterol | $<1.00\times10^{-33}$ | GWAS Catalog | 18262040 | 1 |

| | | | | |
|---|---|---|---|---|
| LDL cholesterol | $<3.00\times10^{-29}$ | GWAS Catalog | 18193044 | 1 |
| LDL cholesterol | $<6.00\times10^{-33}$ | GWAS Catalog | 18193043 | 1 |
| LDL cholesterol | $<1.00\times10^{-7}$ | GWAS Catalog | 18179892 | 1 |
| Coronary heart disease | $<4.00\times10^{-9}$ | GWAS Catalog | 17634449 | 1 |
| cholesterol | $5.02\times10^{-9}$ | Metabolomics GWAS Server | 24816252 | 7 |
| Cholesterol | $2.68\times10^{-5}$ | dbGaP | pha003078 | 1 |
| Cholesterol | $7.39\times10^{-5}$ | dbGaP | pha003073 | 1 |
| Lipoproteins, ldl | $2.19\times10^{-12}$ | dbGaP | pha002902 | 1 |

## Variant annotation

| trait | type | source DB | source entry/link | Variant(s) |
|---|---|---|---|---|
| Low density lipoprotein cholesterol level quantitative trait locus 6 | association | ClinVar | RCV000007497.1 | 1 |
| ? | HGMD curated | HGMD | CR114612 | 1 |
| ? | HGMD curated | HGMD | CR105220 | 1 |
| LOW DENSITY LIPOPROTEIN CHOLESTEROL LEVEL QUANTITATIVE TRAIT LOCUS 6 | OMIM curated | OMIM | MIM:602458 | 1 |

## Disease gene annotation

| gene | trait | source DB | source entry/link |
|---|---|---|---|
| SORT1 | LOW DENSITY LIPOPROTEIN CHOLESTEROL LEVEL QUANTITATIVE TRAIT [...] | OMIM | MIM:613589 |
| AMPD2 | PONTOCEREBELLAR HYPOPLASIA, TYPE 9 | OMIM | MIM:615809 |
| AMPD2 | SPASTIC PARAPLEGIA 63, AUTOSOMAL RECESSIVE | OMIM | MIM:615686 |
| AMPD2 | Autosomal recessive spastic paraplegia type 63 | OrphaNet | OrphaNet:401805 |
| AMPD2 | Pontocerebellar hypoplasia, type 9 | OrphaNet | OrphaNet:369920 |

# Direct effect on regulation

## *cis*-eQTL

| gene | transcript | probe | tissue | min(statistic) (type) | source | variant(s) |
|---|---|---|---|---|---|---|
| PSRC1 | ? | ENSG00000134222 | pancreas | $2.83\times10^{-7}$ (p-value) | GTEx Portal V6 | 10 |
| SORT1 | ? | ENSG00000134243 | pancreas | $2.33\times10^{-6}$ (p-value) | GTEx Portal V6 | 5 |
| PSRC1 | ? | ENSG00000134222 | blood | $1.98\times10^{-7}$ (p-value) | GTEx Portal V6 | 5 |
| PSRC1 | ? | ENSG00000134222 | esophagus mucosa | $5.45\times10^{-12}$ (p-value) | GTEx Portal V6 | 10 |
| CELSR2 | ? | ENSG00000143126 | esophagus mucosa | $4.25\times10^{-7}$ (p-value) | GTEx Portal V6 | 7 |
| PSRC1 | ENST00000369907 | ILMN_1671843 | monocyte | $6.65\times10^{-18}$ (p-value) | Fairfax et al. | 4 |
| PSRC1 | ENST00000369909 | | | | | |
| PSRC1 | ENST00000369904 | | | | | |
| PSRC1 | ENST00000409138 | | | | | |
| PSRC1 | ENST00000409267 | | | | | |
| PSRC1 | ENST00000492431 | | | | | |
| PSRC1 | ENST00000369903 | | | | | |
| CELSR2 | ? | ENSG00000143126 | skeletal muscle | $7.42\times10^{-36}$ (p-value) | GTEx Portal V6 | 10 |
| PSRC1 | ? | ENSG00000134222 | testis | $3.79\times10^{-8}$ (p-value) | GTEx Portal V6 | 10 |
| SORT1 | ? | ENSG00000134243 | liver | $3.42\times10^{-27}$ (p-value) | GTEx Portal V6 | 10 |
| PSRC1 | ? | ENSG00000134222 | liver | $4.39\times10^{-19}$ (p-value) | GTEx Portal V6 | 10 |

| | | | | | | |
|---|---|---|---|---|---|---|
| CELSR2 | ? | ENSG00000143126 | liver | 3.42×10-19 (p-value) | GTEx Portal V6 | 10 |
| CELSR2 | ? | ENSG00000143126 | sun exposed skin | 7.33×10-6 (p-value) | GTEx Portal V6 | 2 |
| CELSR2 | ENST00000498157 | ILMN_1711208 | liver | <2.2×10-16 (p-value) | Innocenti et al. | 1 |
| CELSR2 | ENST00000271332 | | | | | |
| SORT1 | ENST00000538502 | ILMN_1707077 | liver | <2.2×10-16 (p-value) | Innocenti et al. | 1 |
| SORT1 | ENST00000256637 | | | | | |
| PSRC1 | ? | ENSG00000134222 | cortex | 8.68×10-7 (p-value) | GTEx Portal V6 | 6 |
| PSRC1 | ? | ENSG00000134222 | unexposed skin | 2.73×10-6 (p-value) | GTEx Portal V6 | 3 |
| PSRC1 | ENST00000369907 | ILMN_1671843 | monocyte | 7.21×10-61 (p-value) | Zeller et al. | 2 |
| PSRC1 | ENST00000369909 | | | | | |
| PSRC1 | ENST00000369904 | | | | | |
| PSRC1 | ENST00000409138 | | | | | |
| PSRC1 | ENST00000409267 | | | | | |
| PSRC1 | ENST00000369903 | | | | | |
| PSRC1 | ENST00000492431 | | | | | |
| PSRC1 | ENST00000369909 | ILMN_2315964 | monocyte | 3.05×10-13 (p-value) | Zeller et al. | 2 |
| PSRC1 | ENST00000369904 | | | | | |
| PSRC1 | ENST00000409267 | | | | | |
| PSRC1 | ENST00000369907 | | | | | |
| PSRC1 | ENST00000409138 | | | | | |
| PSRC1 | ENST00000474126 | | | | | |
| PSRC1 | ENST00000492431 | | | | | |
| PSRC1 | ENST00000369903 | | | | | |
| PSRC1 | ? | ENSG00000134222 | thyroid | 1.44×10-5 (p-value) | GTEx Portal V6 | 1 |

## Putative effect on regulation

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

| SNiPA enhancer id | variant(s) | associated SNiPA promoter id | associated gene(s) |
|---|---|---|---|
| ENCE00000031690 | 1 | ENCP00000003684 | AMPD2 |

### Regulatory feature cluster

| element id | variant(s) | tissue/cell | factors |
|---|---|---|---|
| ENSR00001523273 (promoter flanking region) | 5 | embryonic stem cell (H1ESC) | H3K36me3, H3K27me3, Rad21, CTCF, DNase1 |
| | | HSMMtube | CTCF |
| | | blood (K562) | Rad21, CTCF, H3K36me3, DNase1, H3K4me1, MEF2A, Max, PU1, H3K9ac |
| | | skin (NHDF-AD) | CTCF |
| | | muscle (HSMM) | CTCF, H3K36me3, DNase1 |
| | | liver (HepG2) | PolII, Rad21, H3K4me1, H3K4me2, FOXA1, H3K27ac, CTCF, Cmyc, DNase1 |
| | | lung (IMR90) | H3K36me3, CTCF |
| | | blood (GM12878) | DNase1, H2AZ, Rad21, CTCF |
| | | nervous (NH-A) | CTCF, H3K4me1, H3K4me2, DNase1 |
| | | skin (NHEK) | DNase1, H3K36me3, CTCF |
| | | NHLF | DNase1, CTCF |
| | | Osteobl | H3K4me2, CTCF, H3K36me3 |
| | | blood (DND-41) | CTCF, H3K36me3 |
| | | breast (HMEC) | H3K27ac, H3K4me3, H3K9ac, H3K4me2, CTCF |
| | | cervix (HeLa-S3) | H3K9ac, H3K4me2, H3K27ac, H3K4me3, H3K4me1, Max, PolII, CTCF, DNase1 |
| | | monocytes (Monocytes-CD14+) | CTCF, H3K36me3 |
| | | endothelium (HUVEC) | H3K36me3, DNase1, CTCF, Max |
| | | A549 | DNase1, H3K27ac, H3K36me3, CTCF, H3K4me2, H3K4me3 |

## Variation in RISC binding site

| gene | variant(s) | affected transcript(s) | targeting miRNA(s) |
|---|---|---|---|
| CELSR2 | 1 | ENST00000271332<br>ENST00000498157 | hsa-miR-4319 |

## Variation proximal to gene

| gene | variant type | min(distance) | transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|---|---|
| CELSR2 | downstream gene variant | 158 | ENST00000271332 | NM_001408.2 | ENSP00000271332 | 6 |
| CELSR2 | downstream gene variant | 261 | ENST00000489018 | ? | ? | 8 |
| CELSR2 | downstream gene variant | 77 | ENST00000498157 | ? | ? | 7 |
| PSRC1 | downstream gene variant | 1611 | ENST00000418914 | ? | ENSP00000413186 | 5 |
| PSRC1 | downstream gene variant | 13 | ENST00000369909 | NM_001032291.2, NM_032636.7 | ENSP00000358925 | 10 |
| PSRC1 | downstream gene variant | 1442 | ENST00000429031 | ? | ENSP00000387791 | 5 |
| PSRC1 | downstream gene variant | 12 | ENST00000369904 | NM_001005290.3 | ENSP00000358920 | 10 |
| PSRC1 | downstream gene variant | 12 | ENST00000369907 | ? | ENSP00000358923 | 10 |
| PSRC1 | downstream gene variant | 21 | ENST00000409138 | ? | ENSP00000474667 | 10 |
| PSRC1 | downstream gene variant | 12 | ENST00000409267 | ? | ENSP00000386323 | 10 |
| PSRC1 | downstream gene variant | 1265 | ENST00000474126 | ? | ENSP00000474682 | 6 |
| PSRC1 | downstream gene variant | 23 | ENST00000492431 | ? | ? | 10 |
| PSRC1 | downstream gene variant | 2075 | ENST00000471740 | ? | ? | 5 |
| PSRC1 | downstream gene variant | 41 | ENST00000369903 | ? | ENSP00000358919 | 9 |
| PSRC1 | downstream gene variant | 1860 | ENST00000459765 | ? | ? | 5 |

# Putative effect on transcript

## 3'-UTR variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| CELSR2 | ENST00000271332 | NM_001408.2 | ENSP00000271332 | 4 |

## Non-coding exon variant

| gene | affected transcript | RefSeq id | variant(s) |
|---|---|---|---|
| CELSR2 | ENST00000498157 | ? | 3 |