# SNiPAcard

## Block annotations

### Block info

| | |
|---|---|
| **genomic range** | chr22:33,159,092-33,167,869 |
| **block size** | 8,778 bp |
| **variant count** | 19 variants |

### Basic features

| Conservation/deleteriousness | | Linked genes | |
|---|---|---|---|
| **phyloP** | μ = -0.235 [-3.023 – 2.015] | **gene(s) hit or close-by** | SYN3 |
| **phastCons** | μ = 0.069 [0 – 0.983] | **eQTL gene(s)** | – |
| **GERP++** | μ = 0.074 [-6.84 – 2.32] | **potentially regulated gene(s)** | – |
| **CADD score** | μ = 4.567 [0.694 – 16.06] | **disease gene(s)** | – |

## Putative effect on regulation

### Regulatory feature cluster

| element id | variant(s) | tissue/cell | factors |
|---|---|---|---|
| ENSR00000293419 (promoter flanking region) | 3 | NHLF | DNase1 |
| | | HSMMtube | DNase1 |
| | | blood (K562) | H3K27me3 |
| | | skin (NHDF-AD) | DNase1 |
| | | muscle (HSMM) | DNase1 |
| | | lung (IMR90) | DNase1, H3K18ac |
| | | nervous (NH-A) | DNase1 |
| | | skin (NHEK) | H3K27me3 |

## Putative effect on transcript

### Intron variant

| gene | affected transcript | RefSeq id | protein | variant(s) |
|---|---|---|---|---|
| SYN3 | ENST00000462268 | ? | ? | 19 |
| SYN3 | ENST00000358763 | NM_003490.3, NM_001135774.1, NM_133633.2 | ENSP00000351614 | 19 |