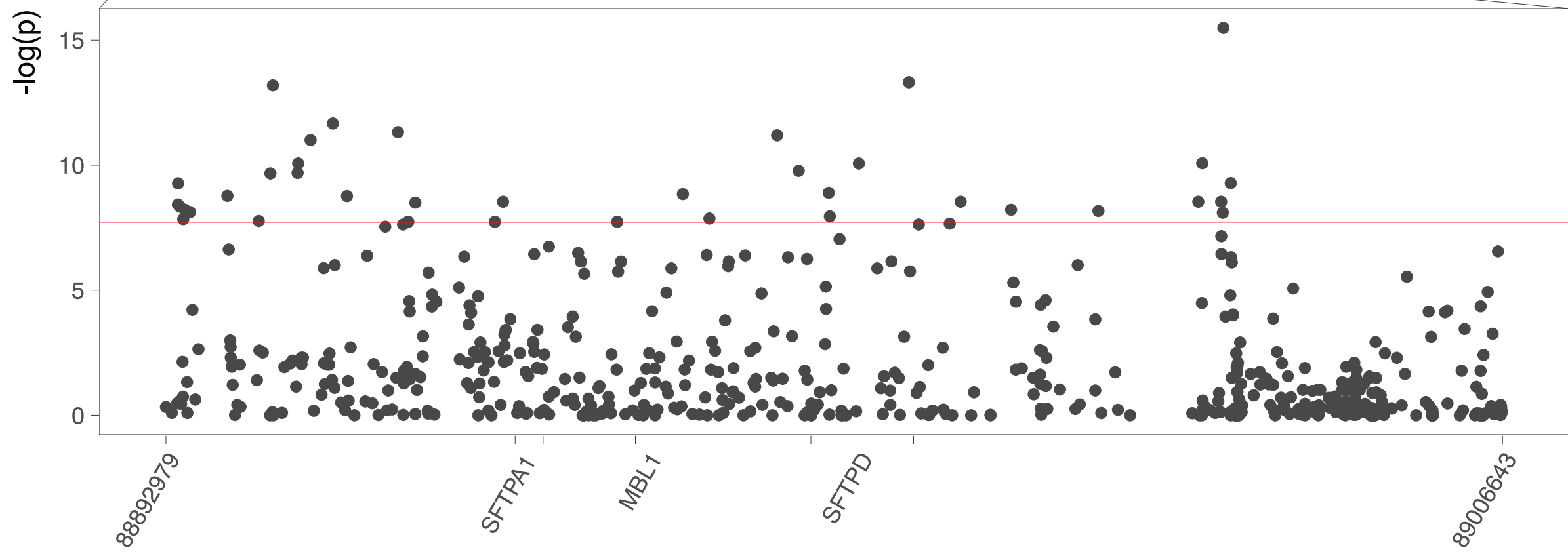
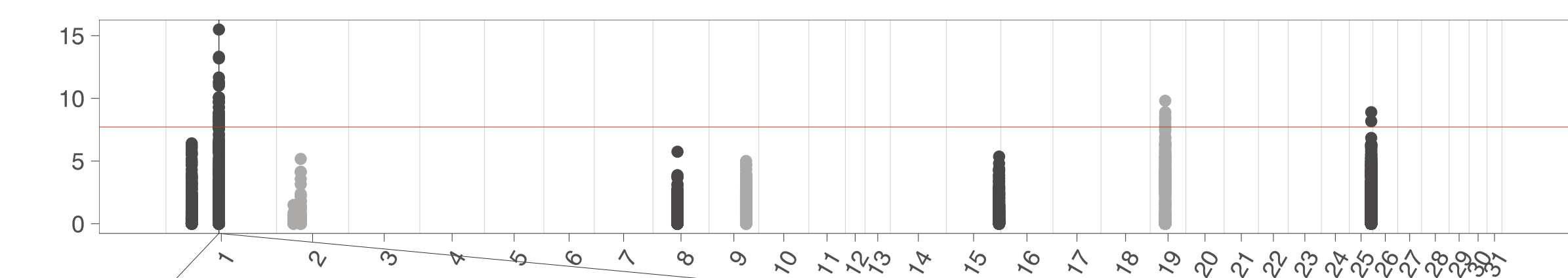




Aleluciatior





Functional effects

| Gene | Ref | Alt | Freq in Non-Infectious | Freq in Infectious | -log(p)* | Gene region | Predicted impact (<i>in silico</i>) |
|------------------|-----|-----|------------------------|--------------------|----------|--------------------|---|
| <i>SFTPD</i> | T | G | 0.338 | 0.673 | 15.49 | Upstream 5 - 50 kb | - |
| <i>SFTPD</i> | G | C | 0.192 | 0.014 | 13.32 | Intron 2-3 | - |
| <i>SFTPA1</i> | G | A | 0.208 | 0.022 | 13.19 | Upstream 5 - 50 kb | - |
| <i>SFTPD</i> | C | T | 0.151 | 0.008 | 11.19 | Downstream 3 kb | MRE for eca-miR-221 |
| <i>MBL1</i> | C | T | 0.157 | 0.019 | 8.84 | Downstream 3 kb | MRE for eca-miR-8954 |
| <i>SFTPA1</i> | G | A | 0.157 | 0.022 | 8.54 | Upstream 5 kb | TFBS for Msx-1 |
| <i>MBL1</i> | G | A | 0.149 | 0.022 | 7.74 | Upstream 5 kb | TFBS for ZF5 |
| <i>SFTPD</i> | A | G | 0.459 | 0.689 | 7.66 | Upstream 5 kb | TFBS for Msx-1, Zic1, Zic2, Zic3, and VDR |
| <i>FCN1-like</i> | T | C | 0.205 | 0.062 | 6.31 | Upstream 5 kb | TFBS for En-1 |
| <i>MBL2</i> | T | A | 0.119 | 0.016 | 6.25 | ENSECAE00000138507 | Gln174Leu |
| <i>FCN1-like</i> | G | A | 0.176 | 0.046 | 6.15 | Upstream 5 kb | TFBS for Zic1, Zic2, Zic3, and VDR |
| <i>FCN1-like</i> | G | A | 0.176 | 0.046 | 6.15 | Upstream 5 kb | TFBS for ZF5 |
| <i>MBL2</i> | T | C | 0.081 | 0.003 | 6.15 | Upstream 5 kb | TFBS for Zic2 |

miRNA binding site
 transcription factor binding site
 missense mutation
 no predicted effect

Allelic association

