





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	TBFS for En-1
<i>MBL2</i>	T	A	0.119	0.016	6.25	ENSECAE000000138507	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



no predicted effect



missense mutation



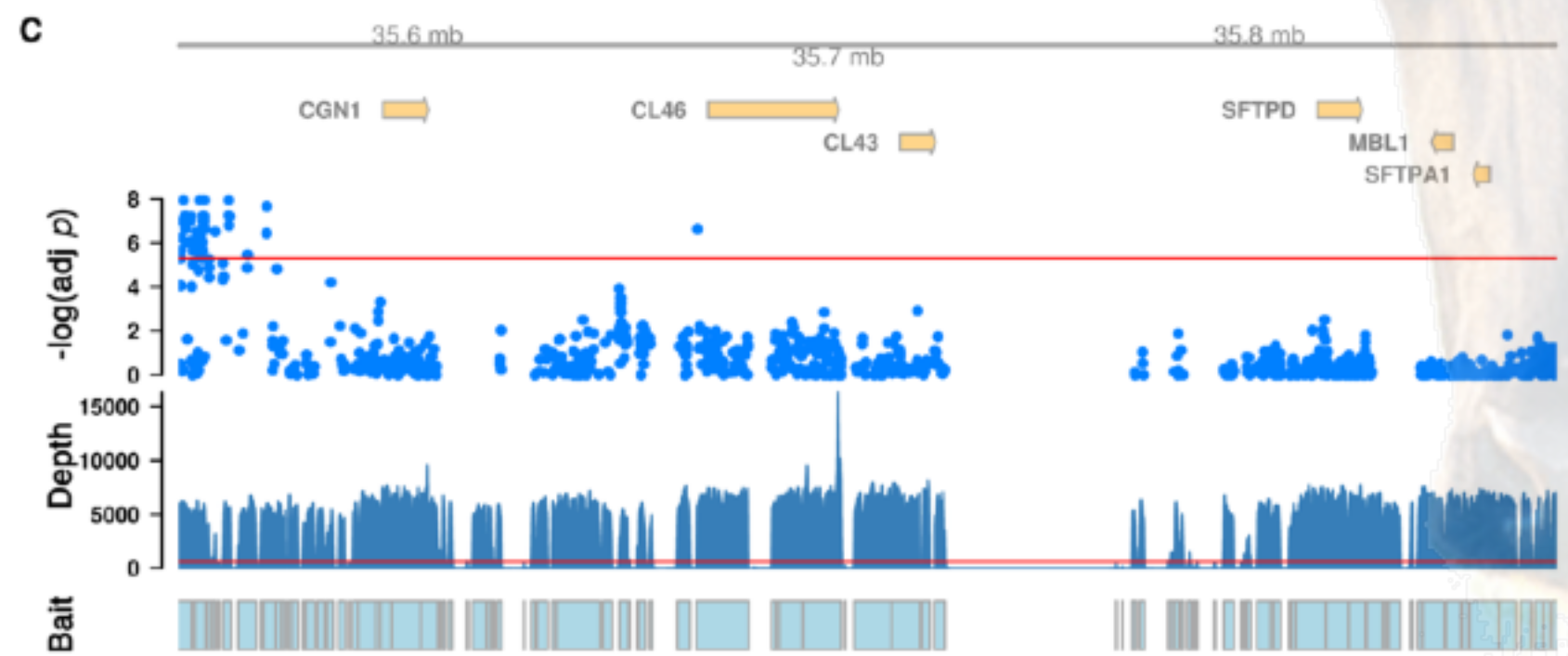
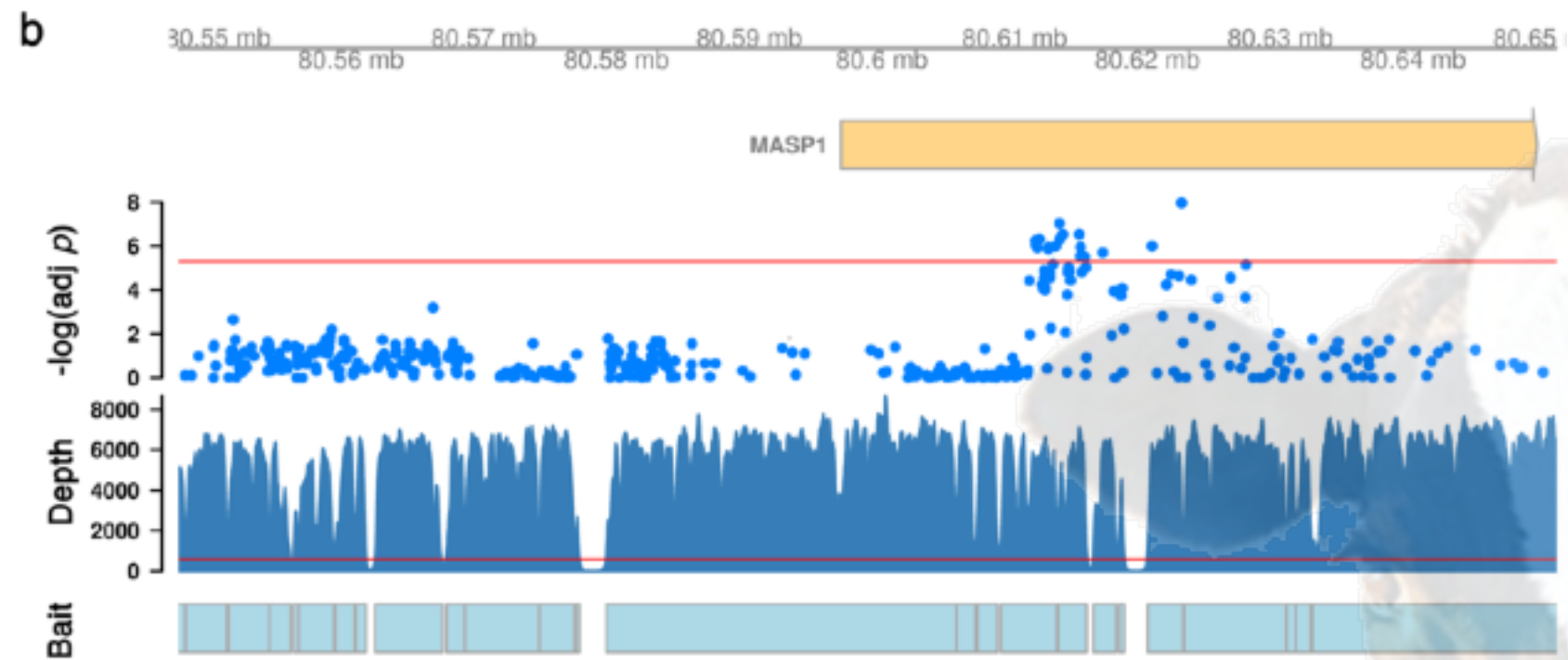
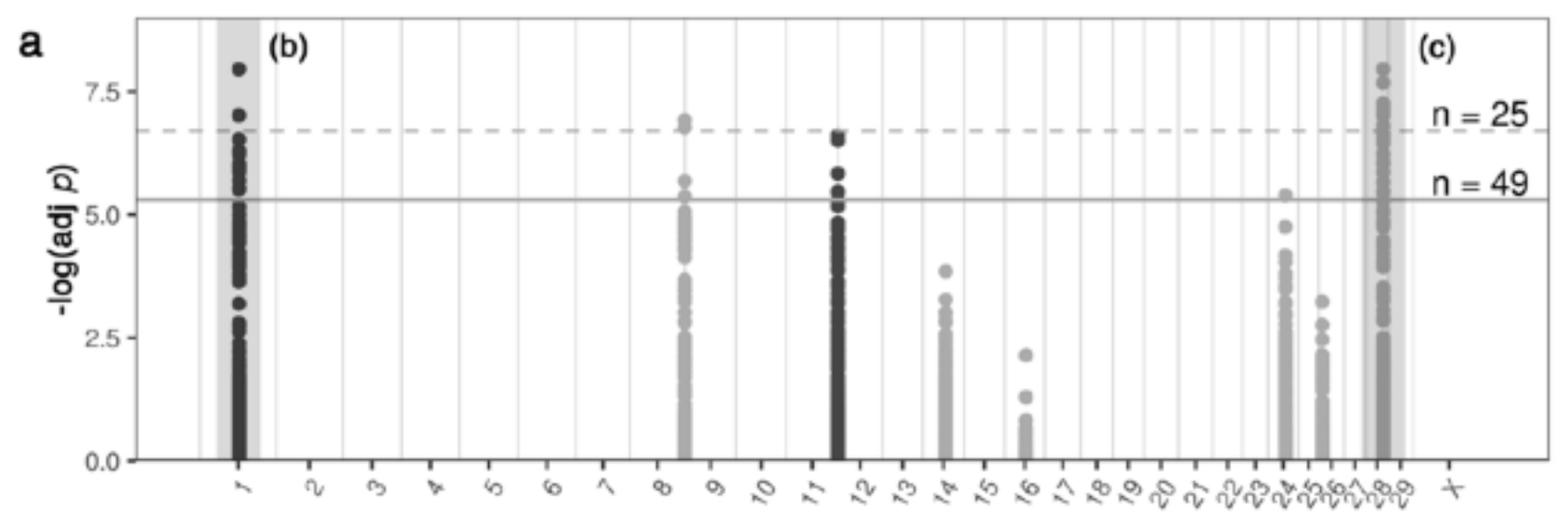
transcription factor binding site



miRNA binding site







# 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