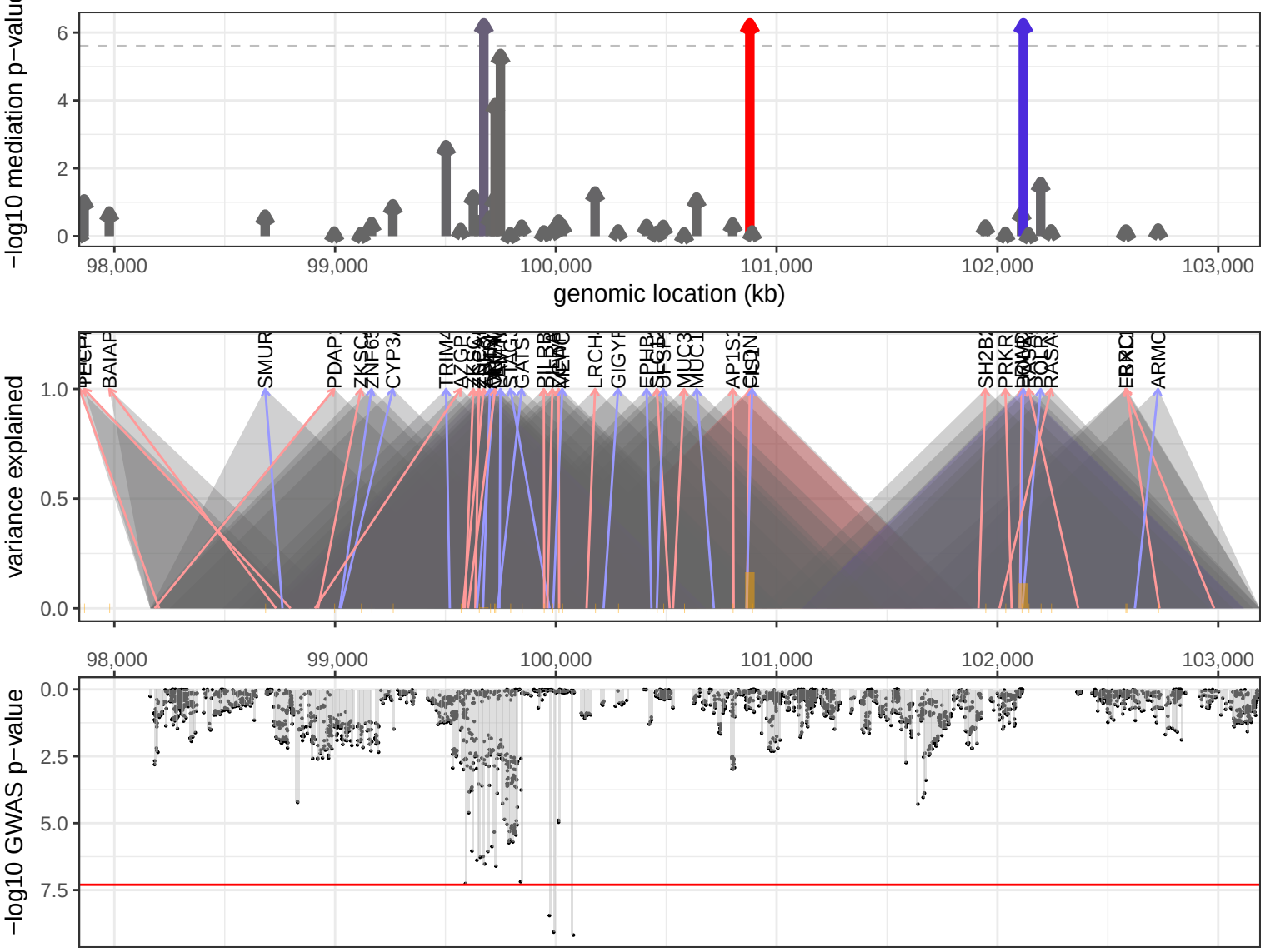
−log10 mediation p−value
6
4
2
0
98,000
99,000
100,000
101,000
102,000
103,000
genomic location (kb)
variance explained
1.0
0.5
0.0
BAIAF
SMUR
PDAP
CYP3
TRIM4
GATS
LRCH
GIGYF
MUC1
AP1S
SH2B
PRKR
RASA
ARMC
98,000
99,000
100,000
101,000
102,000
103,000
−log10 GWAS p−value
0.0
2.5
5.0
7.5