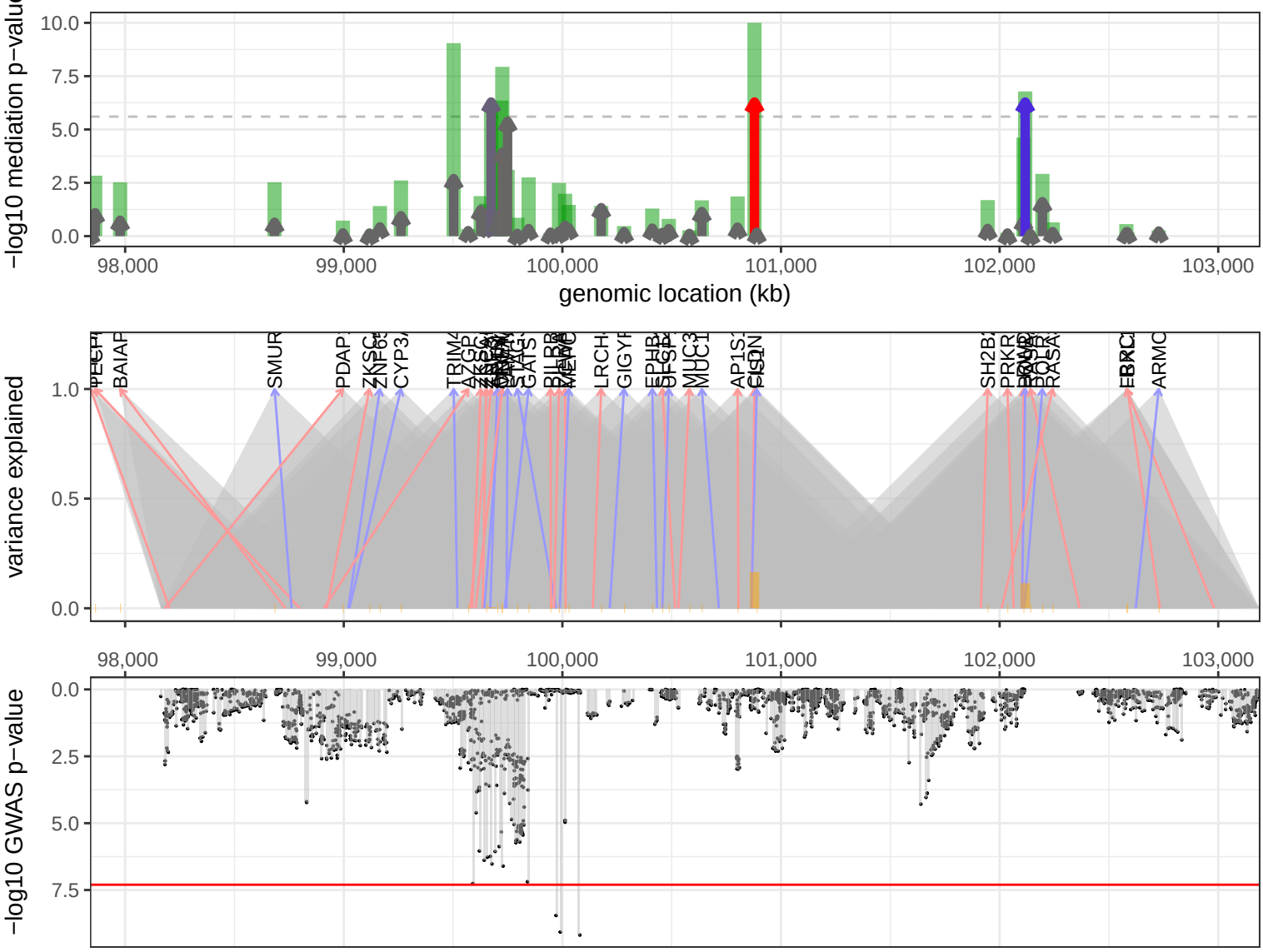
−log10 mediation p−value
10.0
7.5
5.0
2.5
0.0
98,000
99,000
100,000
101,000
102,000
103,000
genomic location (kb)
variance explained
1.0
0.5
0.0
BAIAP
SMUR
PDAP
CYP3
LRCH
GIGYF
MUC3
AP1S
SH2B
PRKR
RASA
ARMC
−log10 GWAS p−value
0.0
2.5
5.0
7.5