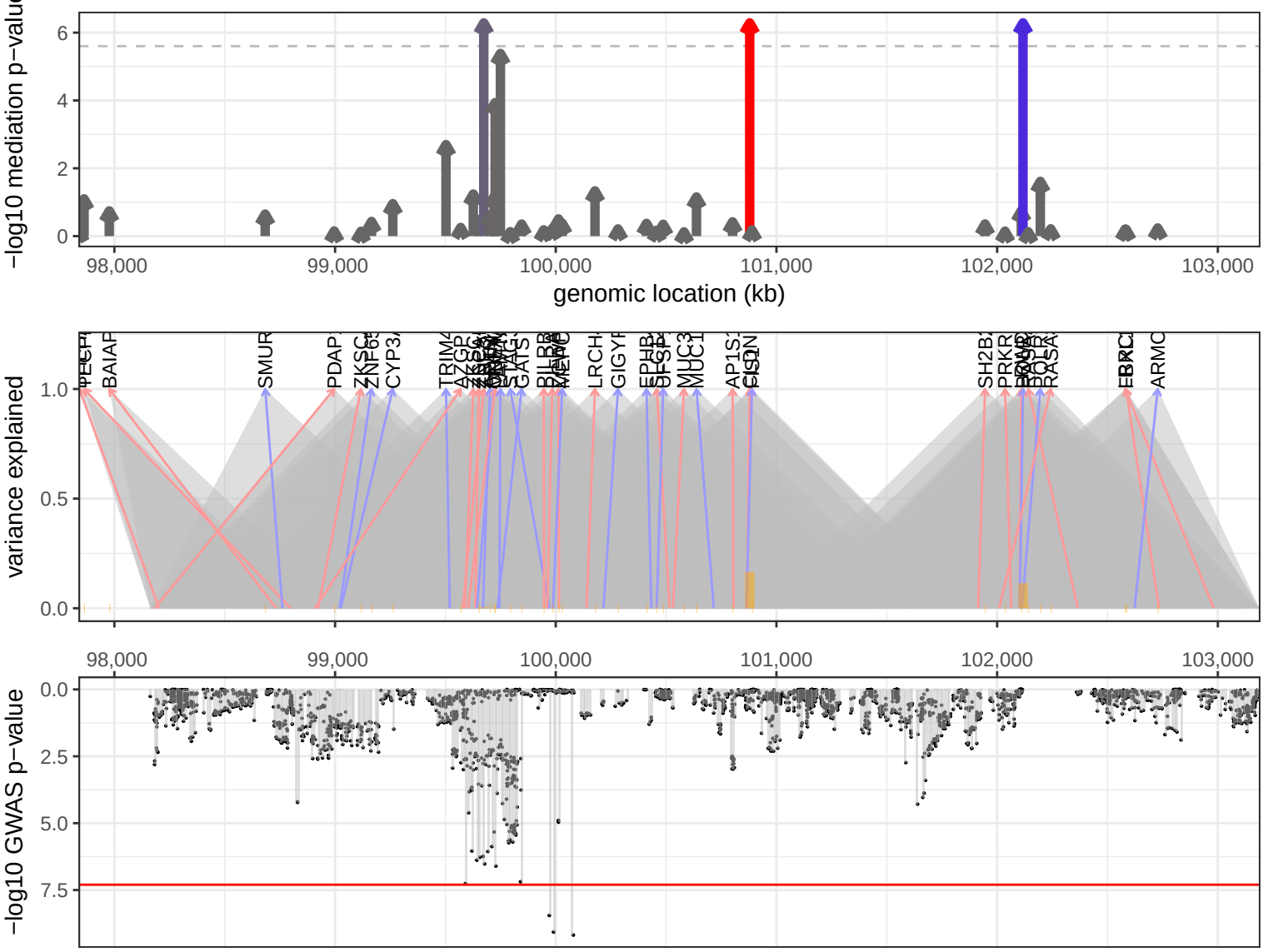
−log10 mediation p−value
6
4
2
0
98,000
99,000
100,000
101,000
102,000
103,000
genomic location (kb)
variance explained
1.0
0.5
0.0
BAIAF
SMUR
PDAP
CYP3
TRIM4
GATS
LRCH
GIGYF
MUC3
MUC1
AP1S
SH2B
PRKR
RASA
ARMC
−log10 GWAS p−value
0.0
2.5
5.0
7.5