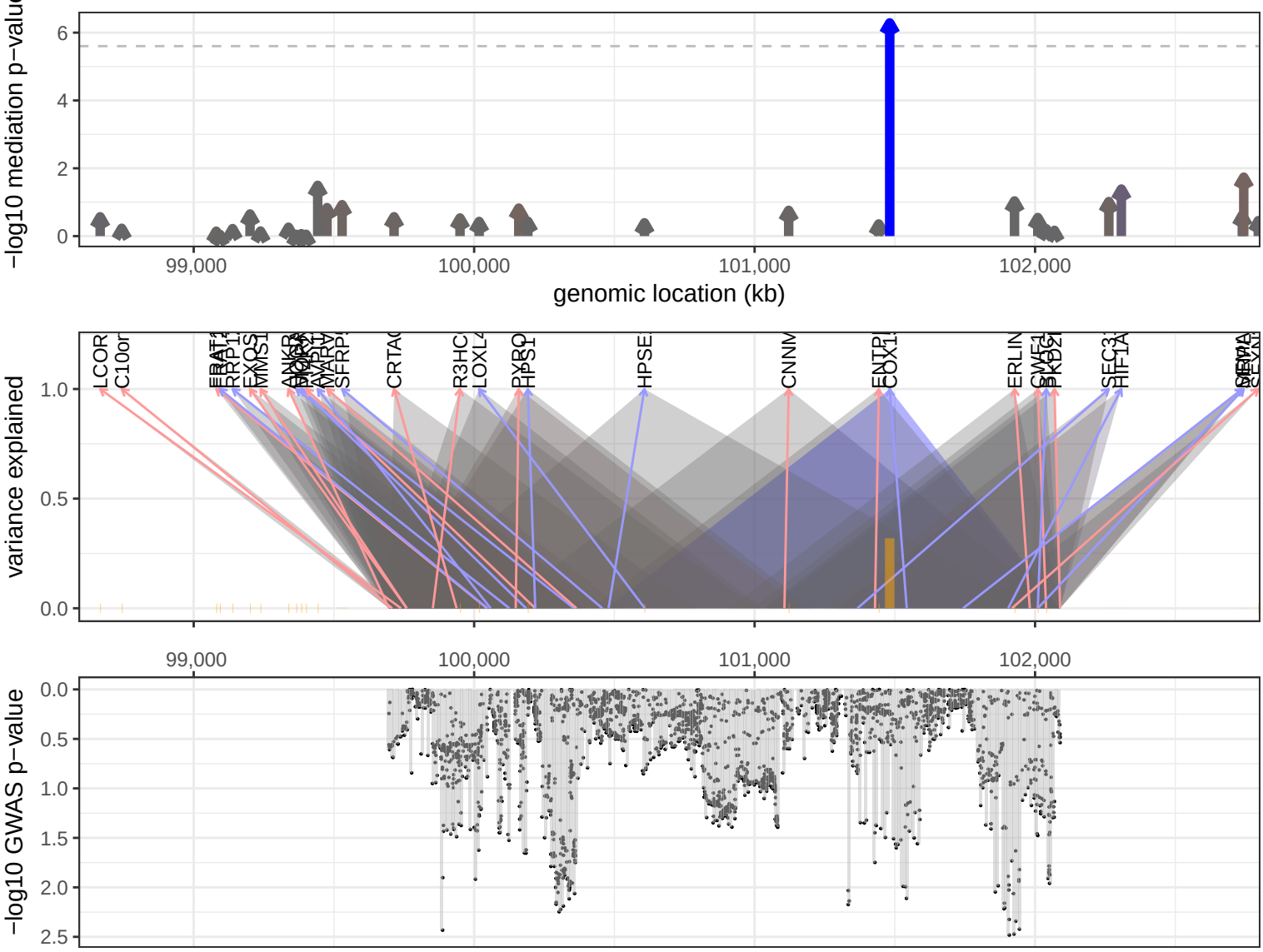
−log10 mediation p−value
6
4
2
0
99,000
100,000
101,000
102,000
genomic location (kb)
variance explained
1.0
0.5
0.0
LCOR
C10or
CRTAC
R3HC
LOXL4
HPSE
CNNM
ERLIN
SEC3
99,000
100,000
101,000
102,000
−log10 GWAS p−value
0.0
0.5
1.0
1.5
2.0
2.5