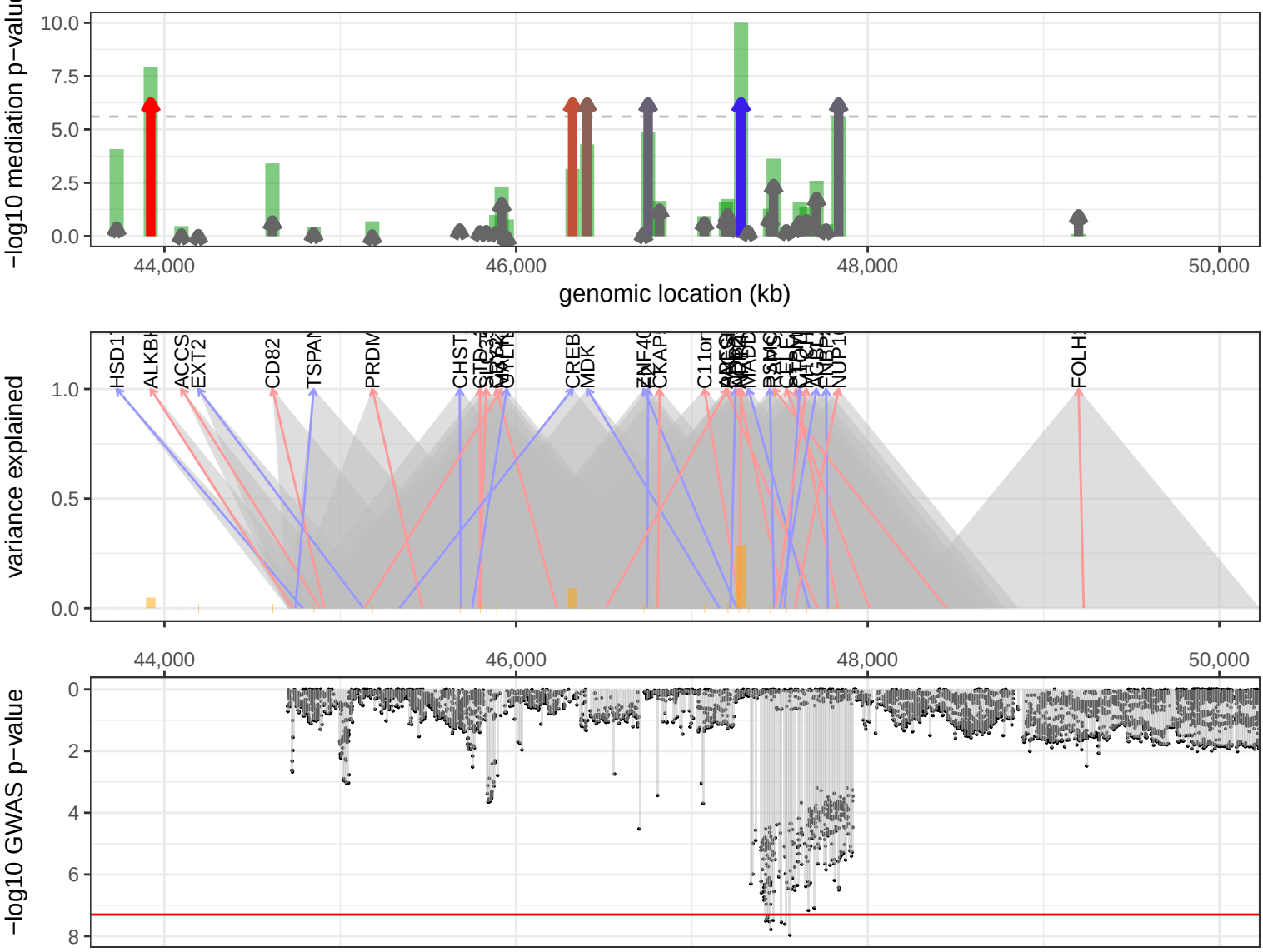
−log10 mediation p−value
10.0
7.5
5.0
2.5
0.0
44,000
46,000
48,000
50,000
genomic location (kb)
variance explained
1.0
0.5
0.0
HSD1
ALKBH
ACCS
EXT2
CD82
TSPAN
PRDM
CHST
CREB
MDK
ZNF40
CKAP
C11orf
NADB
NUP1
FOLH
44,000
46,000
48,000
50,000
−log10 GWAS p−value
0
2
4
6
8