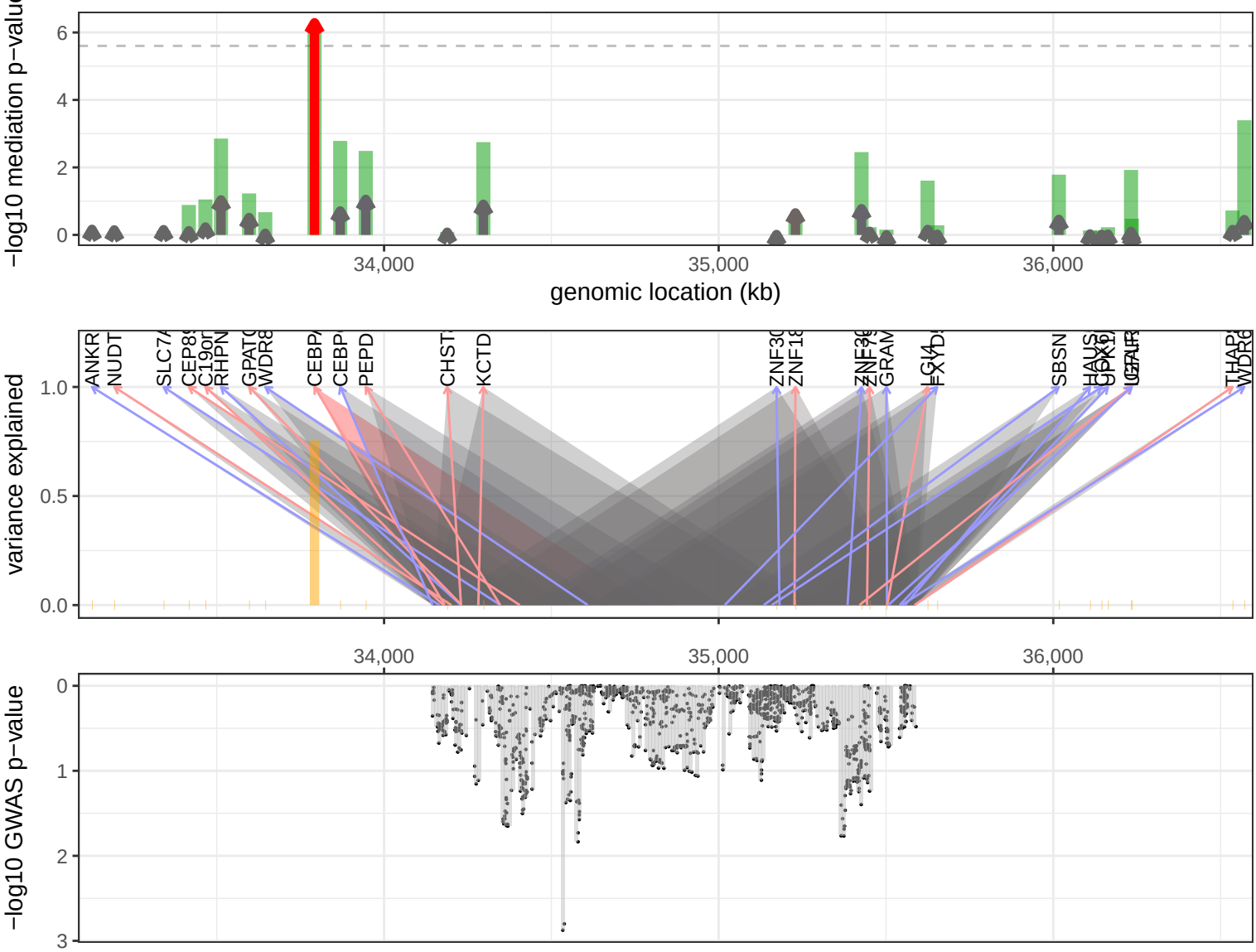
−log10 mediation p−value
6
4
2
0
34,000
35,000
36,000
genomic location (kb)
variance explained
1.0
0.5
0.0
ANKR
NUDT
SLC74
CEP89
C19orf
RHPN
GPATC
WDR8
CEBPA
CEBP
PEPD
CHST
KCTD
ZNF30
ZNF18
ZNF36
ZNF99
GRAM
FXYD
SBSN
HAUS
THAP
WDR6
34,000
35,000
36,000
−log10 GWAS p−value
0
1
2
3