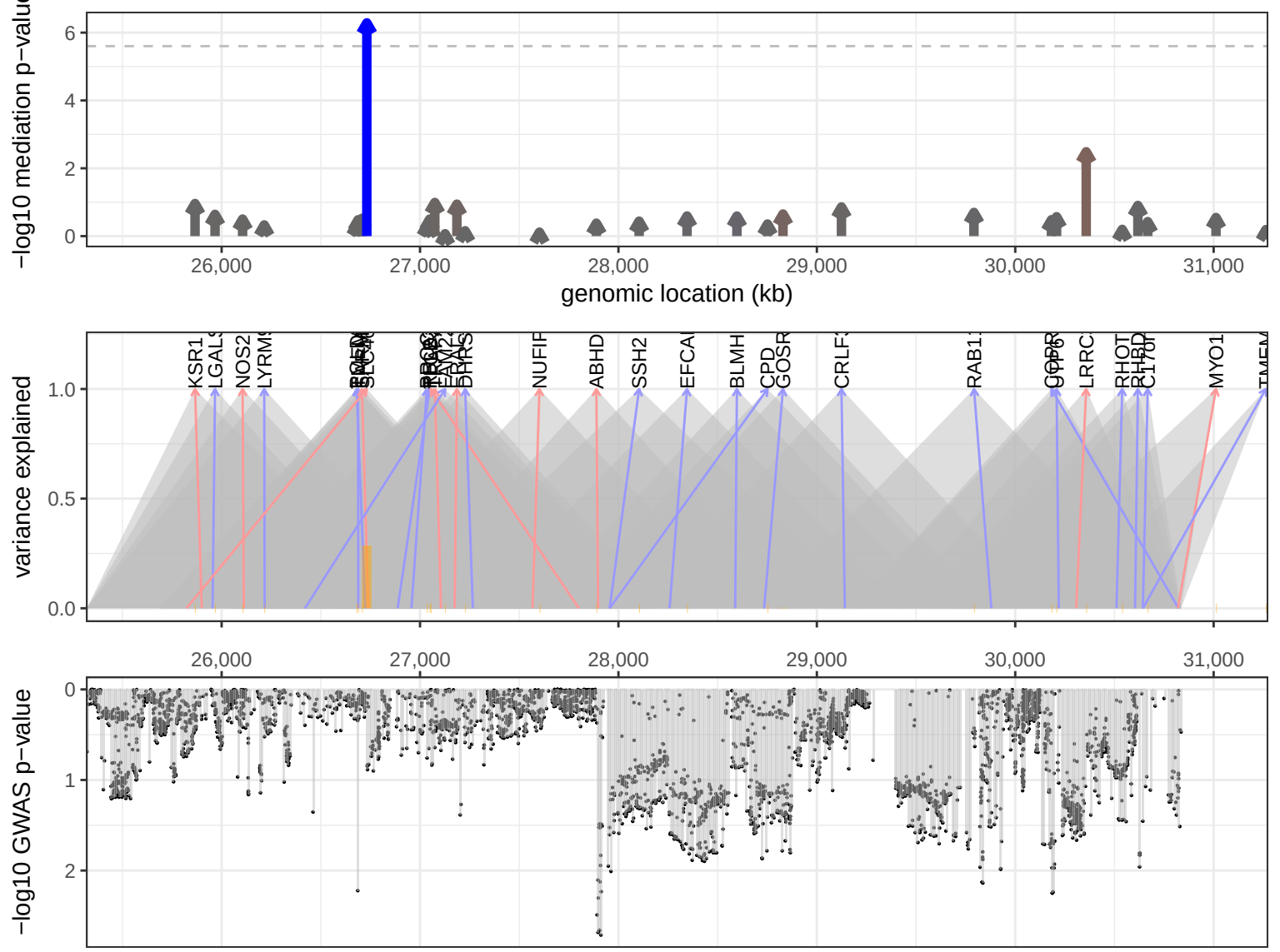
−log10 mediation p−value
6
4
2
0
26,000
27,000
28,000
29,000
30,000
31,000
genomic location (kb)
variance explained
1.0
0.5
0.0
KSR1
LGALS
NOS2
LYRM
NUFIP
ABHD
SSH2
EFCA
BLMH
CPD
GOSR
CRLF
RAB1
LRRC
RHOT
MYO1
−log10 GWAS p−value
0
1
2