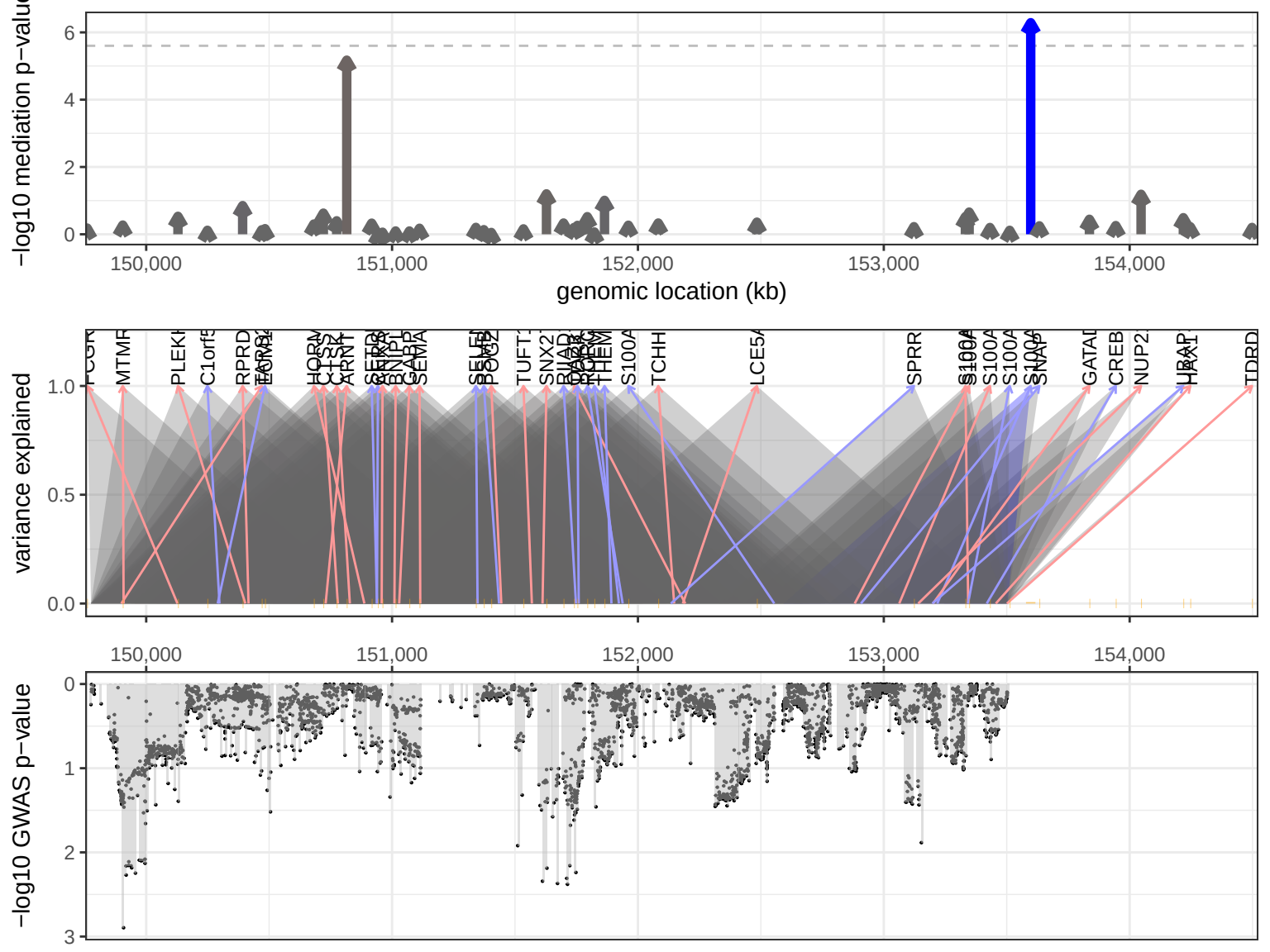
−log10 mediation p−value
6
4
2
0
150,000
151,000
152,000
153,000
154,000
genomic location (kb)
variance explained
1.0
0.5
0.0
MTMR
PLEKH
C1orf5
RPRD
HORM
ARNT
SEMA
TUFT
SNX2
S100A
TCHH
LCE5A
SPRR
S100A
S100A
S100A
SNAP
GATAD
CREB
NUP2
TDRD
150,000
151,000
152,000
153,000
154,000
−log10 GWAS p−value
0
1
2
3