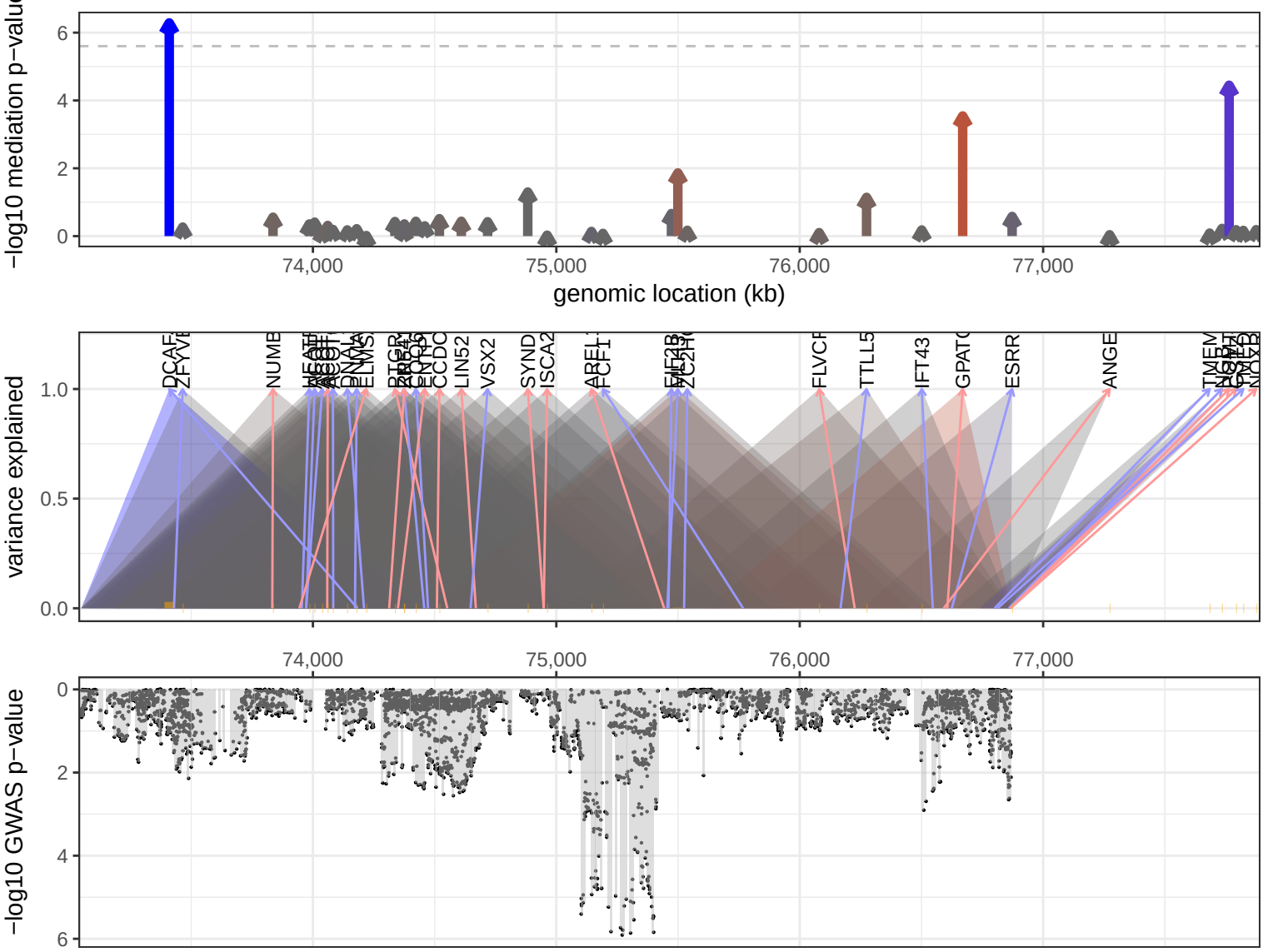
−log10 mediation p−value
6
4
2
0
74,000
75,000
76,000
77,000
genomic location (kb)
variance explained
1.0
0.5
0.0
NUMB
LIN52
VSX2
SYND
ISCA2
FLVCR
TTLL5
IFT43
GPAT
ESRR
ANGE
74,000
75,000
76,000
77,000
−log10 GWAS p−value
0
2
4
6