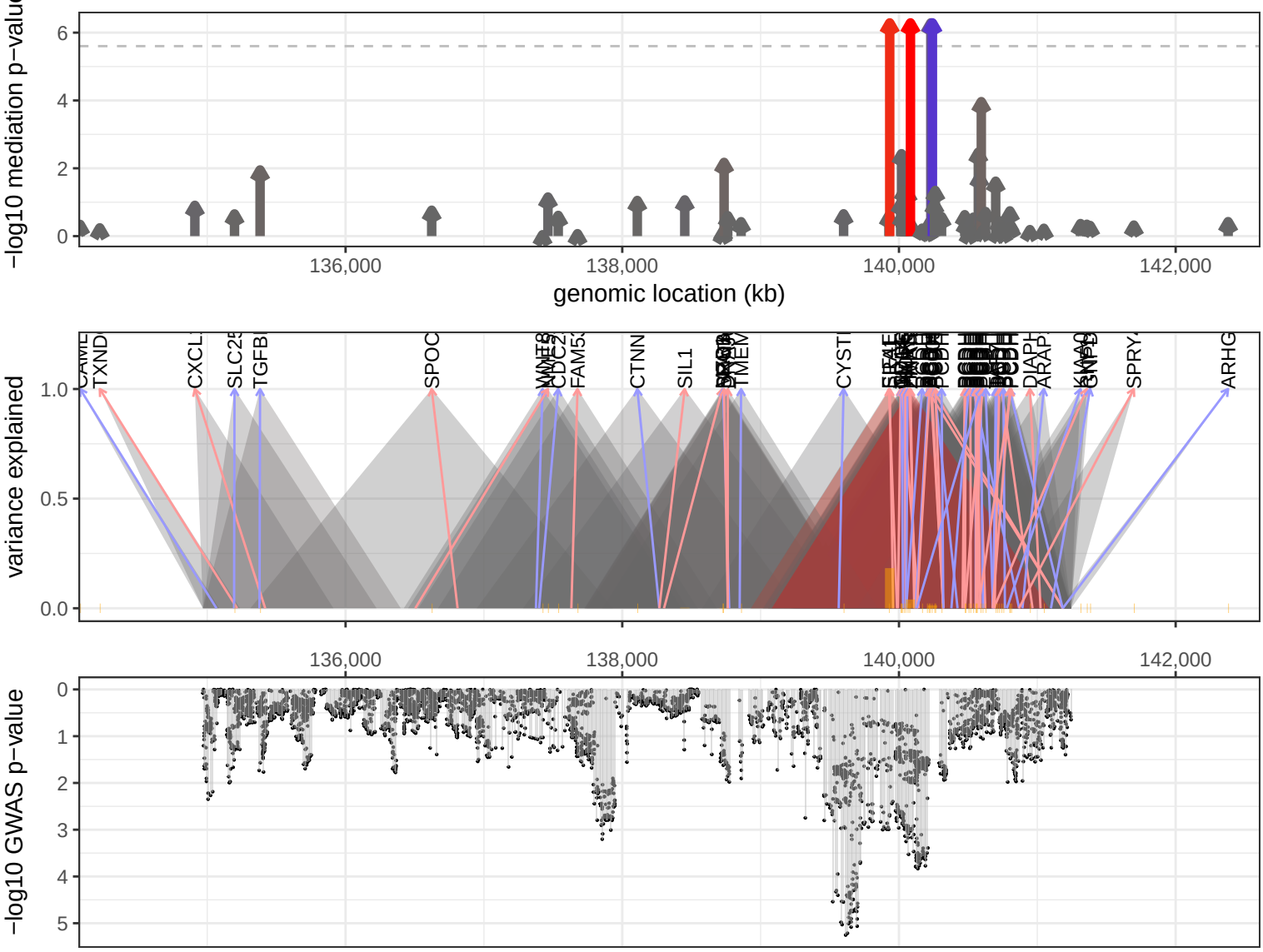
−log10 mediation p−value
6
4
2
0
136,000
138,000
140,000
142,000
genomic location (kb)
variance explained
1.0
0.5
0.0
TXND
CXCL
SLC25
TGFB
SPOC
CDC2
FAM5
CTNN
SIL1
TMEM
CYST
DIAPH
ARAP
SPRY
ARHG
136,000
138,000
140,000
142,000
−log10 GWAS p−value
0
1
2
3
4
5