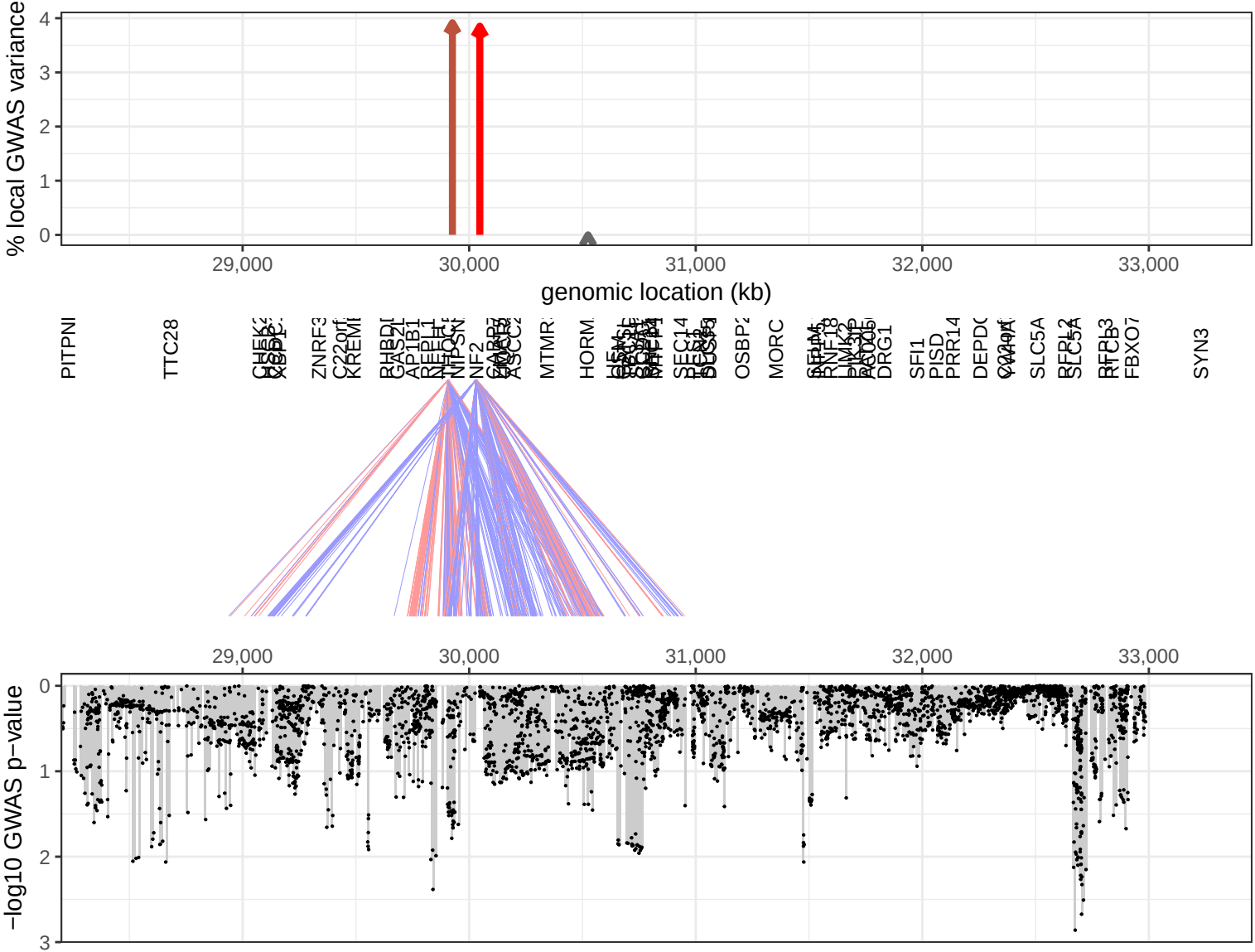
% local GWAS variance
0
1
2
3
4
29,000
30,000
31,000
32,000
33,000
genomic location (kb)
PITPNI
TTC28
ZNRF3
C22orf
KREMI
RHBDI
GAS2L
AP1B1
REEH
NF2
MTMR
HORM
SEC14
OSBP2
MORC
DRG1
SFI1
PISD
PRR14
DEPDC
SLC5A
RFFL2
RFFL3
FBXO7
SYN3
29,000
30,000
31,000
32,000
33,000
−log10 GWAS p−value
0
1
2
3