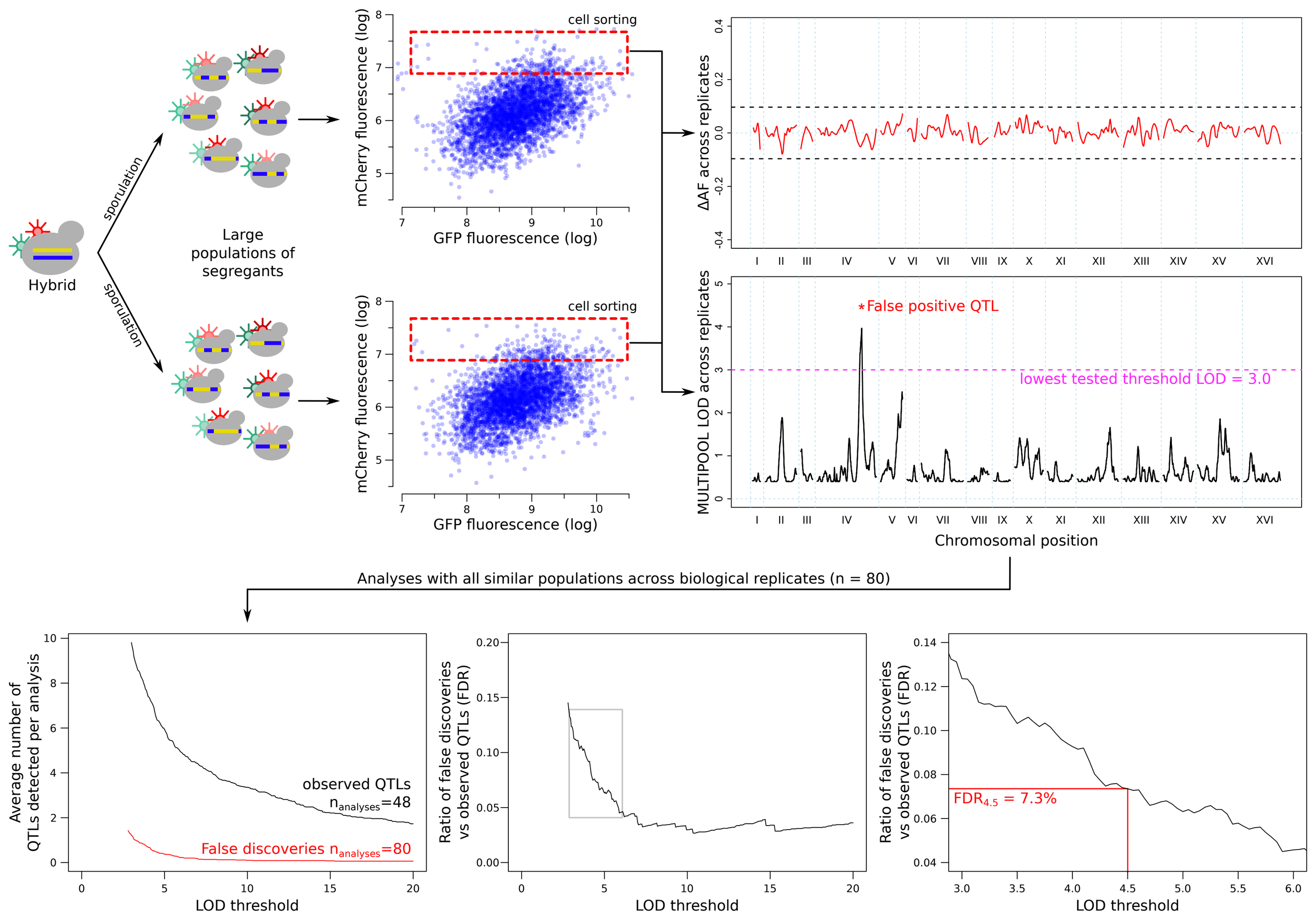
Hybrid
sporulation
sporulation
Large populations of segregants
cell sorting
mCherry fluorescence (log)
GFP fluorescence (log)
cell sorting
mCherry fluorescence (log)
GFP fluorescence (log)
ΔAF across replicates
MULTIPOOL LOD across replicates
*False positive QTL
lowest tested threshold LOD = 3.0
I II III IV V VI VII VIII IX X XI XII XIII XIV XV XVI
Chromosomal position
Analyses with all similar populations across biological replicates (n = 80)
Average number of QTLs detected per analysis
observed QTLs
n_analyses=48
False discoveries n_analyses=80
LOD threshold
Ratio of false discoveries vs observed QTLs (FDR)
LOD threshold
Ratio of false discoveries vs observed QTLs (FDR)
FDR4.5 = 7.3%
LOD threshold