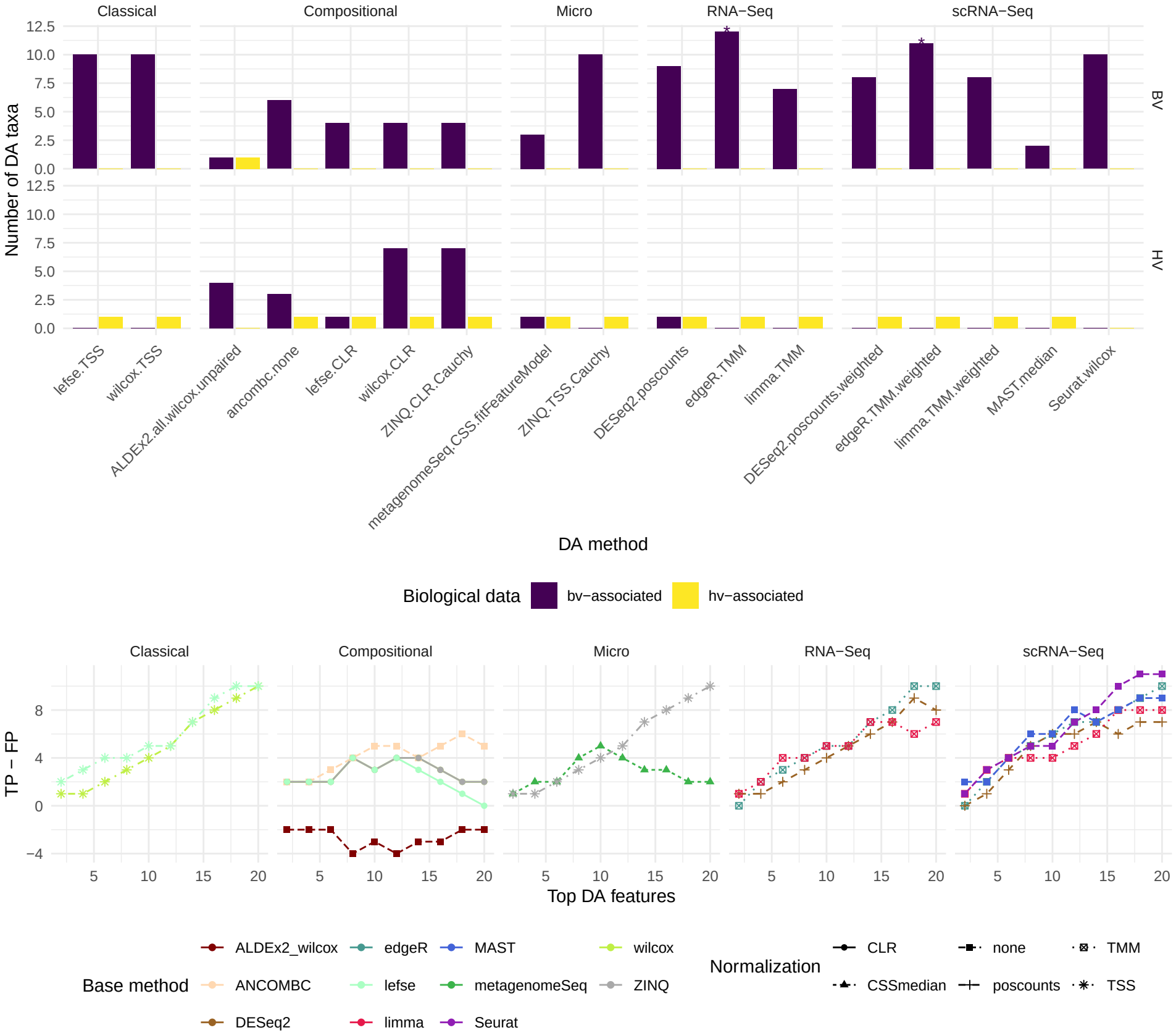
Classical
Compositional
Micro
RNA−Seq
scRNA−Seq
Number of DA taxa
BV
HV
lefse.TSS
wilcox.TSS
ALDEx2.all.wilcox.unpaired
ancombc.none
lefse.CLR
wilcox.CLR
ZINQ.CLR.Cauchy
metagenomeSeq.CSS.fitFeatureModel
ZINQ.TSS.Cauchy
DESeq2.poscounts
edgeR.TMM
limma.TMM
DESeq2.poscounts.weighted
edgeR.TMM.weighted
limma.TMM.weighted
MAST.median
Seurat.wilcox
DA method
Biological data
bv−associated
hv−associated
TP − FP
Top DA features
Base method
ALDEx2_wilcox
ANCOMBC
DESeq2
edgeR
lefse
limma
MAST
metagenomeSeq
Seurat
wilcox
ZINQ
Normalization
CLR
CSSmedian
none
poscounts
TMM
TSS