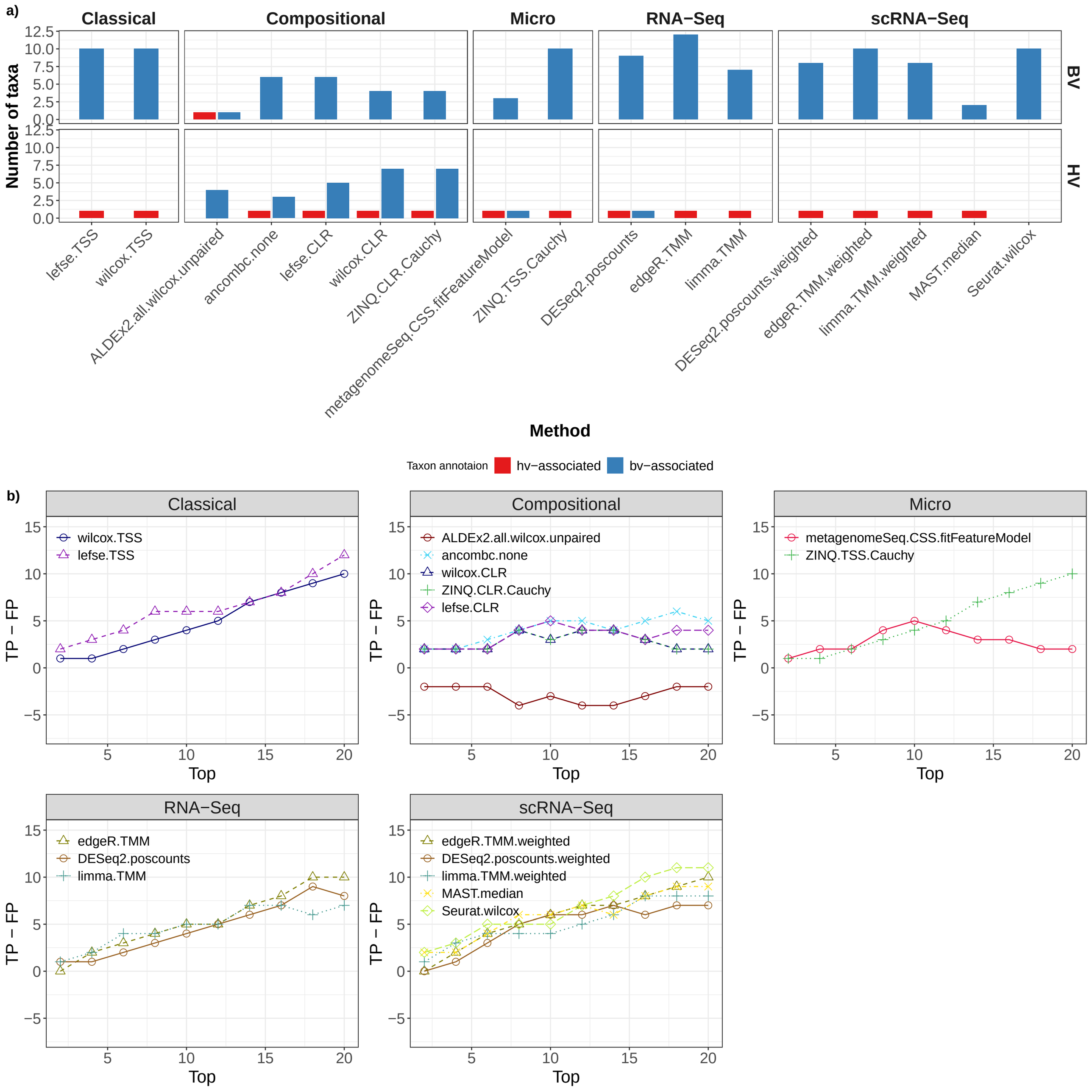
a)
Classical
Compositional
Micro
RNA−Seq
scRNA−Seq
Number of taxa
BV
HV
lefse.TSS
wilcox.TSS
ALDEx2.all.wilcox.unpaired
ancombc.none
lefse.CLR
wilcox.CLR
ZINQ.CLR.Cauchy
metagenomeSeq.CSS.fitFeatureModel
ZINQ.TSS.Cauchy
DESeq2.poscounts
edgeR.TMM
limma.TMM
DESeq2.poscounts.weighted
edgeR.TMM.weighted
limma.TMM.weighted
MAST.median
Seurat.wilcox
Method
Taxon annotaion
hv−associated
bv−associated
b)
Classical
wilcox.TSS
lefse.TSS
Compositional
ALDEx2.all.wilcox.unpaired
ancombc.none
wilcox.CLR
ZINQ.CLR.Cauchy
lefse.CLR
Micro
metagenomeSeq.CSS.fitFeatureModel
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RNA−Seq
edgeR.TMM
DESeq2.poscounts
limma.TMM
scRNA−Seq
edgeR.TMM.weighted
DESeq2.poscounts.weighted
limma.TMM.weighted
MAST.median
Seurat.wilcox
TP − FP
Top