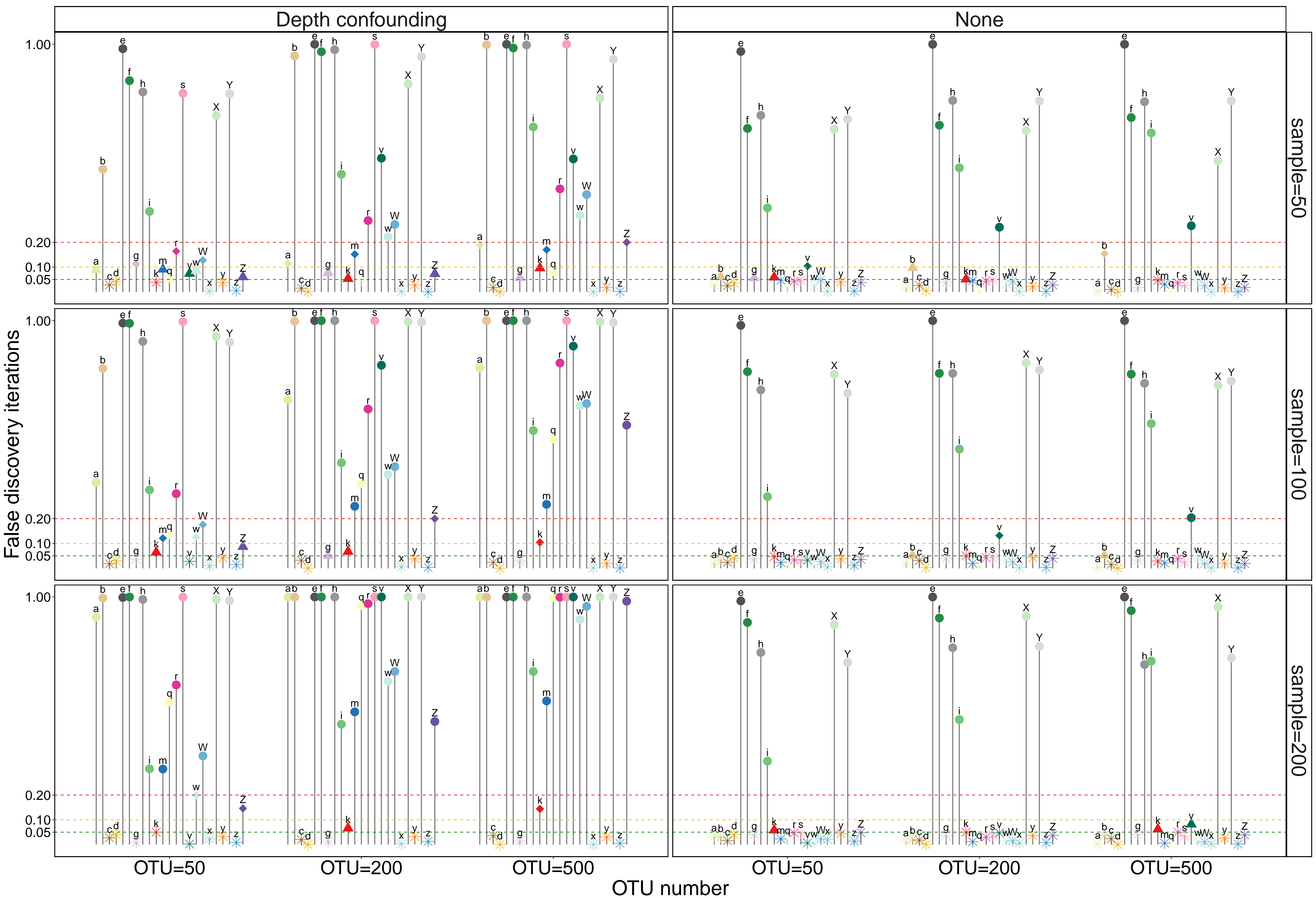


# Default: no differential taxa (binary–Stool)

- a:Aldex2(Wilcoxon)
- b:ANCOM-BC
- c:Beta-binomial
- d:DACOMP
- e:DESeq2
- f:edgeR
- g:GLM(quasipoisson)
- h:GMPR+DESeq2
- i:GMPR+edgeR
- k:LDM
- m:metagenomeSeq
- q:Aldex2(t-test)
- r:eBay(t-test)
- s:eBay(Wilcoxon)
- v:mbzinb
- w:RAIDA
- W:Wrench+metagenomeSeq
- x:Rarefy+t-test
- X:Wrench+edgeR
- y:Rarefy+Wilcoxon
- Y:Wrench+DESeq2
- z:TSS+t-test
- Z:TSS+Wilcoxon



False discovery iterations = iterations identify false positive / 1000 iterations