

Default: no differential taxa (continuous–Stool)

- b:ANCOM-BC

c:Beta-binomial

d:DACOMP
- e:DESeq2

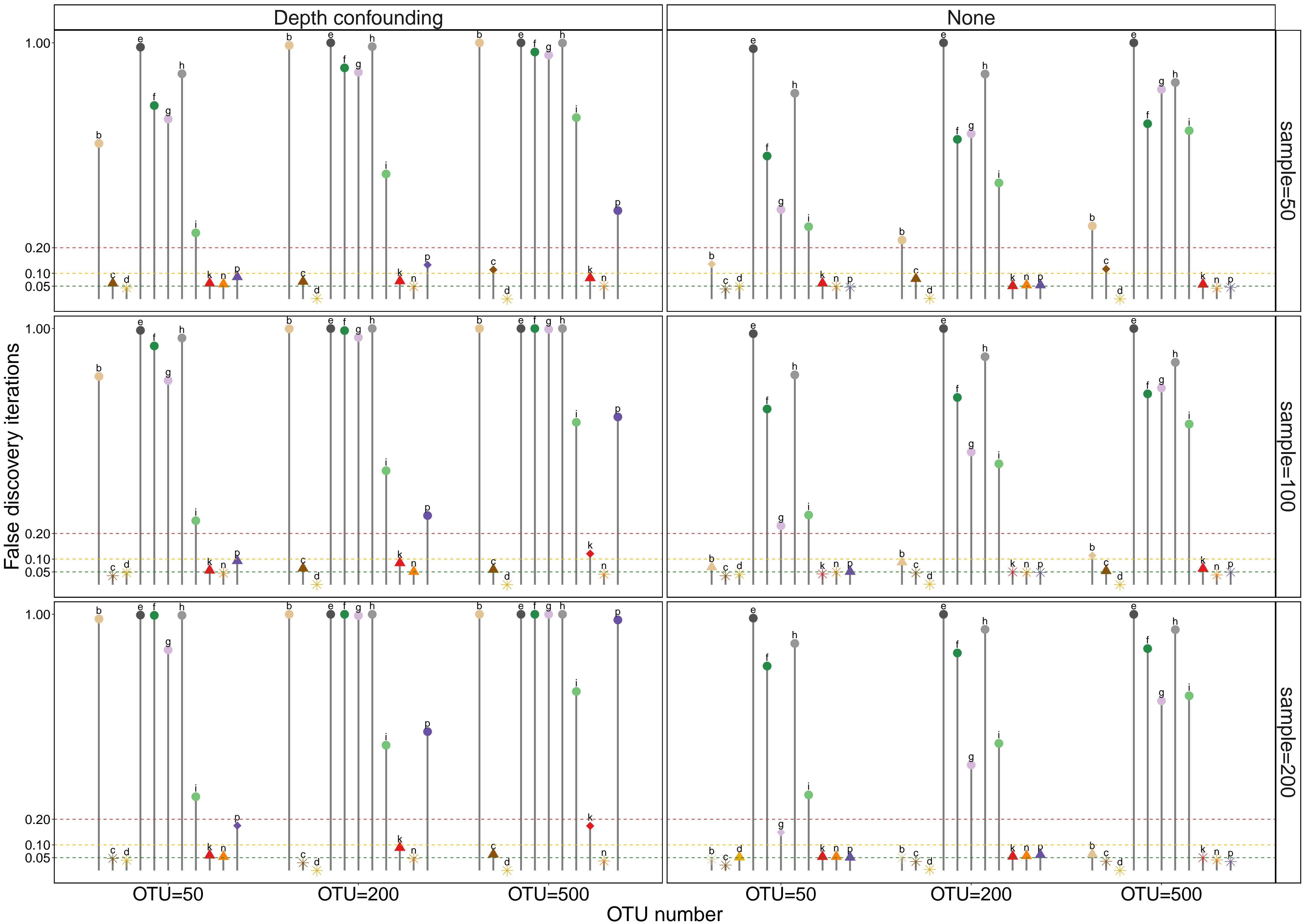
f:edgeR

g:GLM(quasipoisson)
- h:GMPR+DESeq2

i:GMPR+edgeR

k:LDM
- n:Rarefy+Spearman

p:TSS+Spearman



False discovery iterations = iterations identify false positive / 1000 iterations