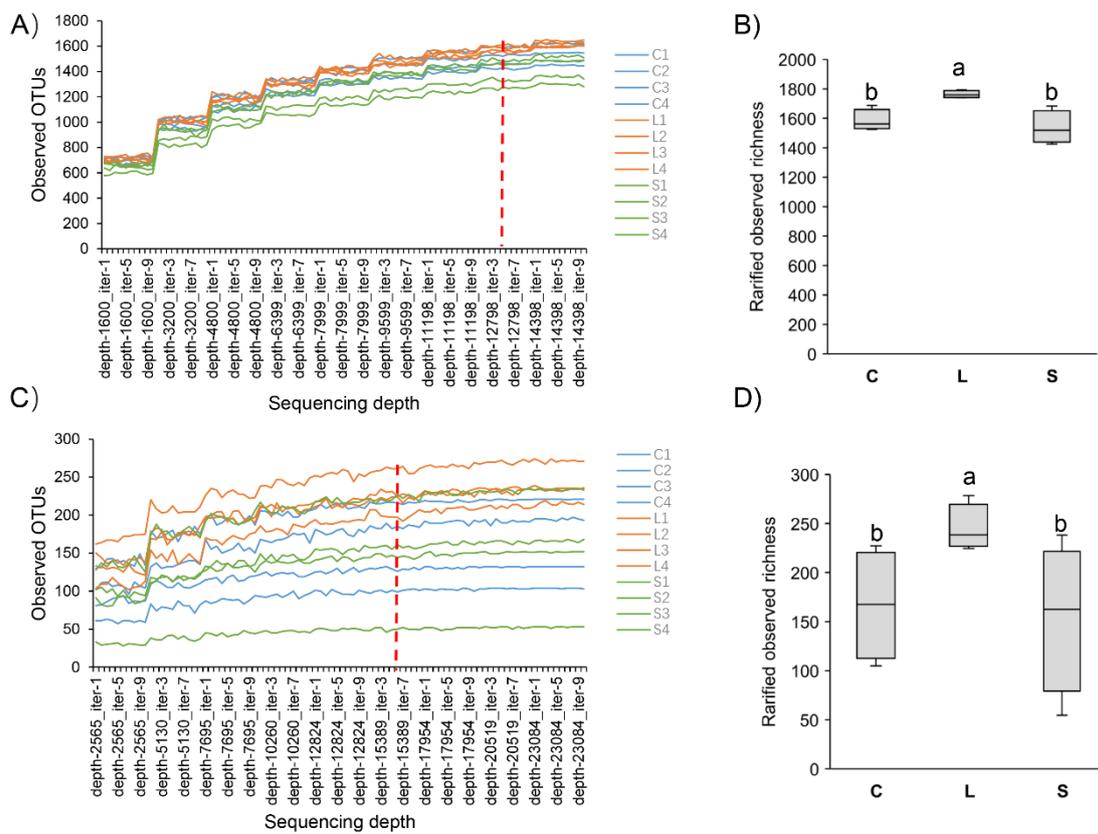


Supplementary Material



**Figure S1.** Rarefaction curves for bacteria (A, B) and fungi (C, D) observed OTUs richness. The dashed red line indicates the selected rarefaction sequencing depth used to generate the box plots of rarified observed richness: 12,798 and 15,389 sequences per sample for bacterial and fungal communities, respectively. C = Control forest soil with no influence from mushroom cultivation; L = Soil forest from furrows with low influence by mushroom cultivation; S = Forest soil below fungal beds strongly influenced by mushroom cultivation. Different letters indicate significant differences at  $p = 0.05$  (ANOVA) between means (Tukey's HSD pairwise comparisons,  $n = 4$ ).