SUPPLEMENTARY FIGURES FOR:

Soil microbial community composition and tolerance to contaminants in an urban brownfield site

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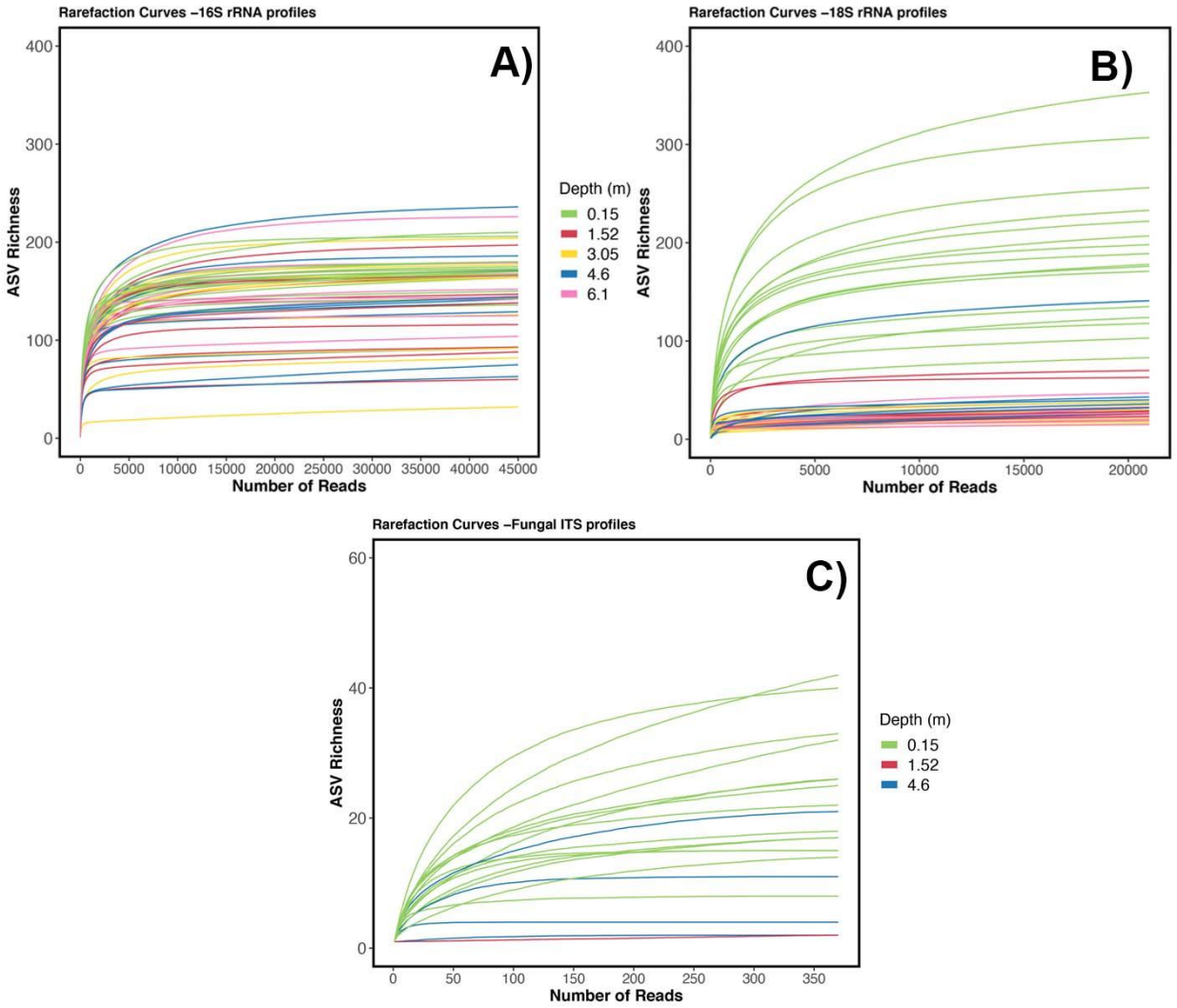


Figure S1. Rarefaction curves of soil microbiome ASV richness for the three gene markers studied. Plotted are the number of ASVs (ASV Richness) recovered with an increasing number of sequences, after subsampling to 45,000 sequences/sample for 16S rRNA profiles, 20,000 sequences/sample for 18S rRNA profiles, and 370 sequences/sample for FITS profiles. Samples with fewer sequences than the cutoff were excluded. Each curve represents a unique sample and is color-coded by sample depth. All curves plateau indicating that the sequencing cutoff was appropriate and accurately captured community diversity.

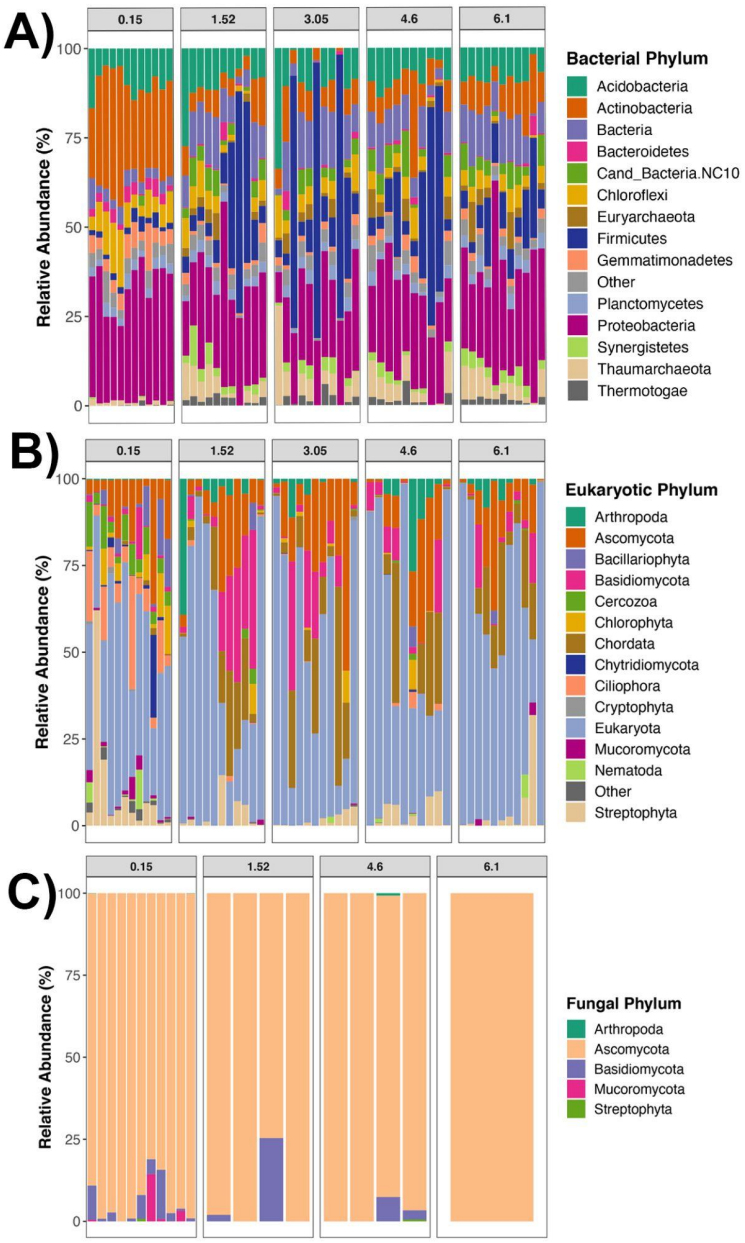


Figure S2. Predominant phyla of the soil microbiome in a contaminated brownfield site. Stacked bar plots showing the relative frequency of sequences assigned to each microbial phylum across samples for **A)**16S rRNA, **B)** 18S rRNA, and **C)** fungal ITS gene profiles. Samples are grouped by depth, and each color represents a microbial phylum. Microbial abundance data was not rarefied for these plots, but identical plots using rarefied data are found at the end of the supplemental section.

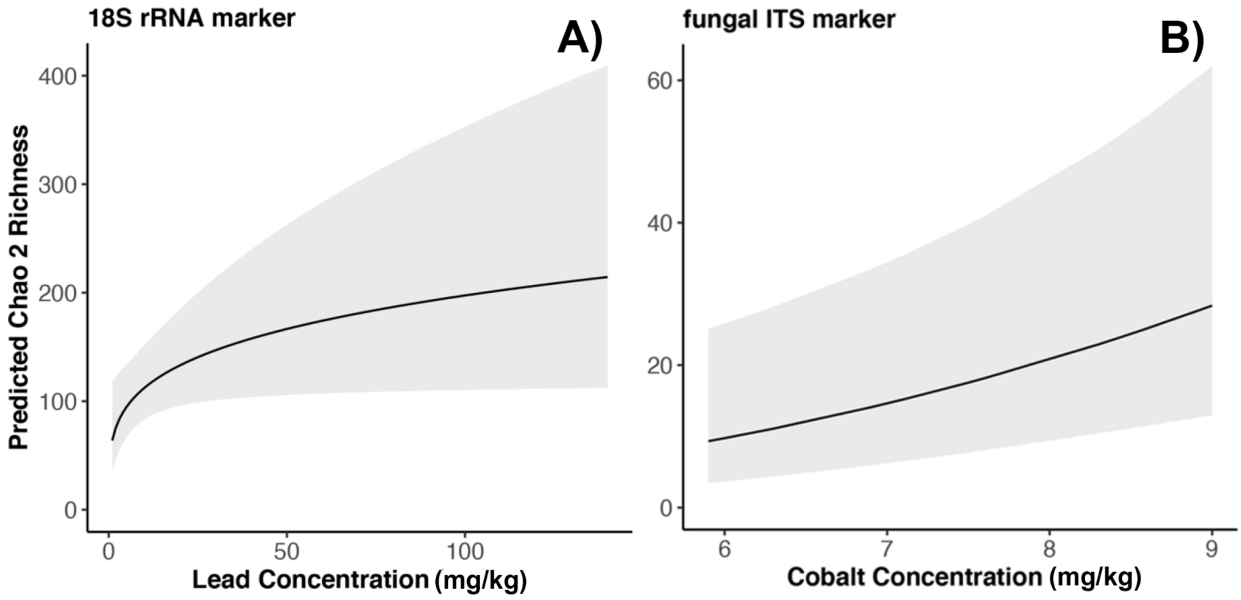


Figure S3. Soil microbiome richness is correlated with concentrations of heavy metals. Plots showing Chao 2 richness predicted from a linear model relating the concentrations of Lead (*μ*g/kg) and Cobalt (*μ*g/kg) to soil microbiome alpha diversity for A) 18S rRNA profiles and B) fungal ITS profiles. Only samples from depths with known concentrations of heavy metals were included. The shaded areas represent 95% CI. Model statistical output is in Table S5.

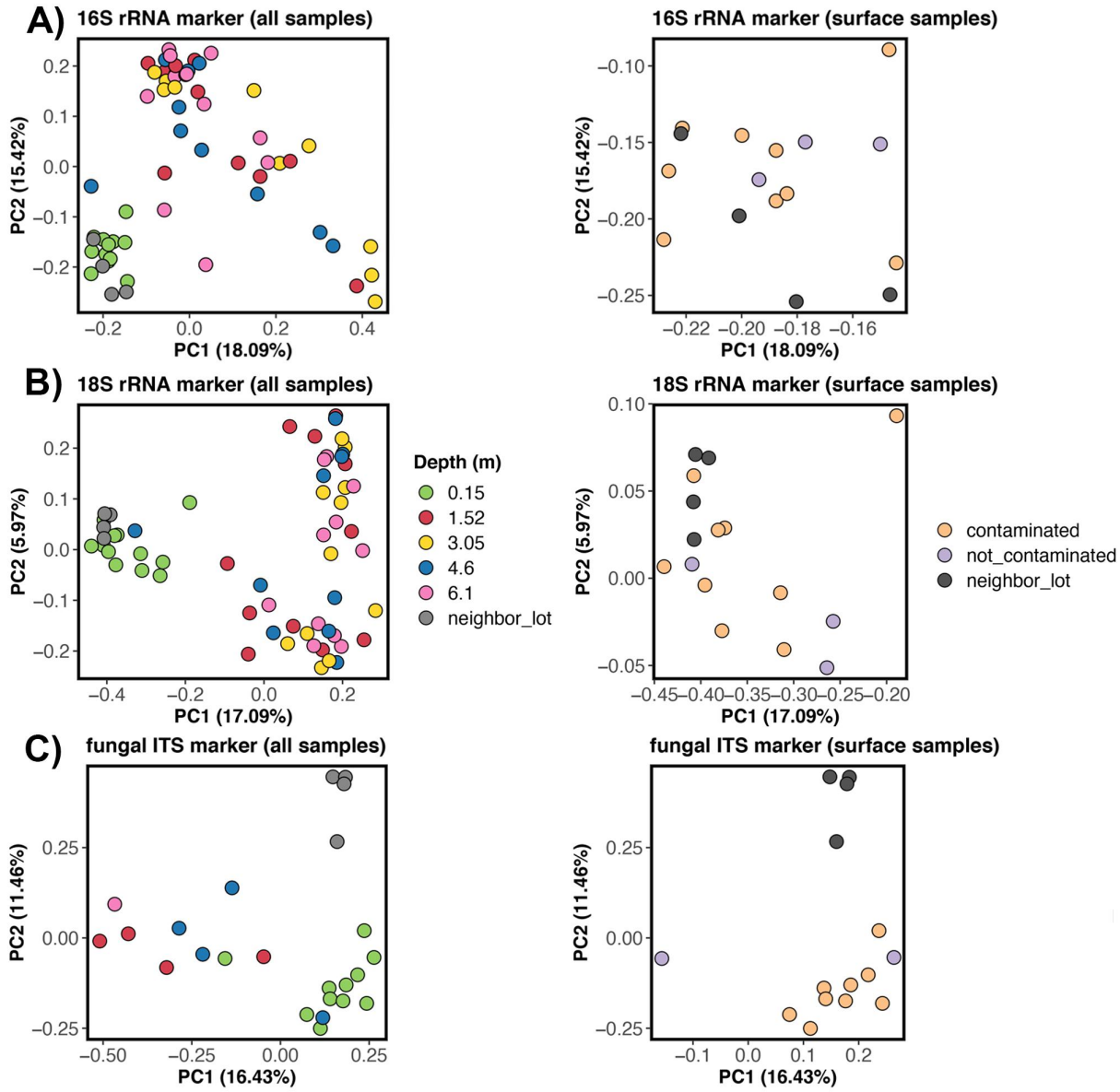
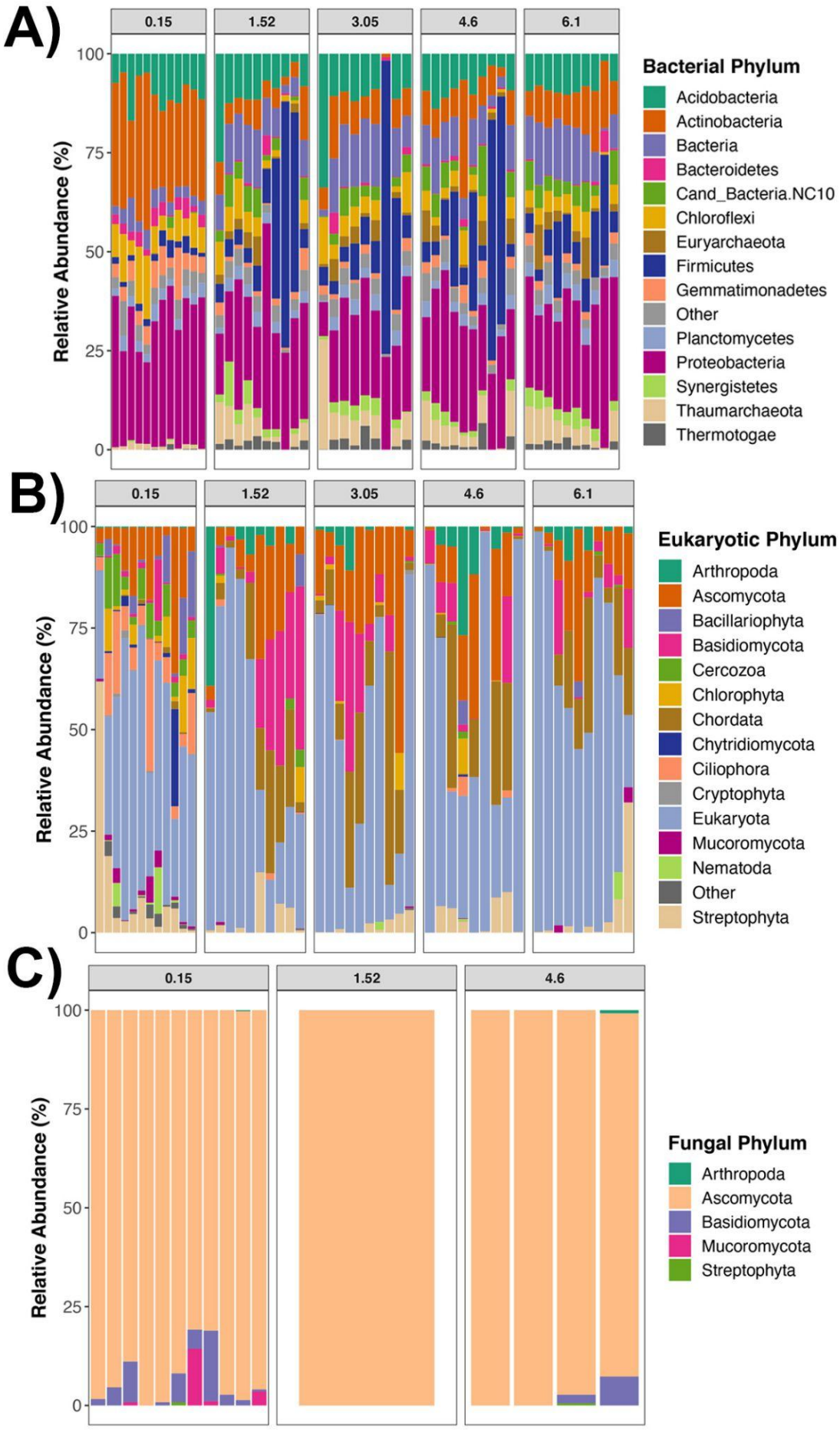


Figure S4. Stratification of soil microbiome by sampling depth. Shown here are PCoA plots constructed from Jaccard dissimilarity matrices for A) 16S rRNA, B) 18S rRNA, and C) fungal ITS data. Each point represents a sample and is color-coded by depth (left) or a binary category for pollutant contamination (surface samples only; right). Closeness of points indicates high community similarity. The percentage of variance accounted for by each principal-coordinate axis is shown in the axis labels.


A)
0.15
1.52
3.05
4.6
6.1
Relative Abundance (%)
100
75
50
25
0
Bacterial Phylum
Acidobacteria
Actinobacteria
Bacteria
Bacteroidetes
Cand_Bacteria.NC10
Chloroflexi
Euryarchaeota
Firmicutes
Gemmatimonadetes
Other
Planctomycetes
Proteobacteria
Synergistetes
Thaumarchaeota
Thermotogae
B)
0.15
1.52
3.05
4.6
6.1
Relative Abundance (%)
100
75
50
25
0
Eukaryotic Phylum
Arthropoda
Ascomycota
Bacillariophyta
Basidiomycota
Cercozoa
Chlorophyta
Chordata
Chytridiomycota
Ciliophora
Cryptophyta
Eukaryota
Mucoromycota
Nematoda
Other
Streptophyta
C)
0.15
1.52
4.6
Relative Abundance (%)
100
75
50
25
0
Fungal Phylum
Arthropoda
Ascomycota
Basidiomycota
Mucoromycota
Streptophyta

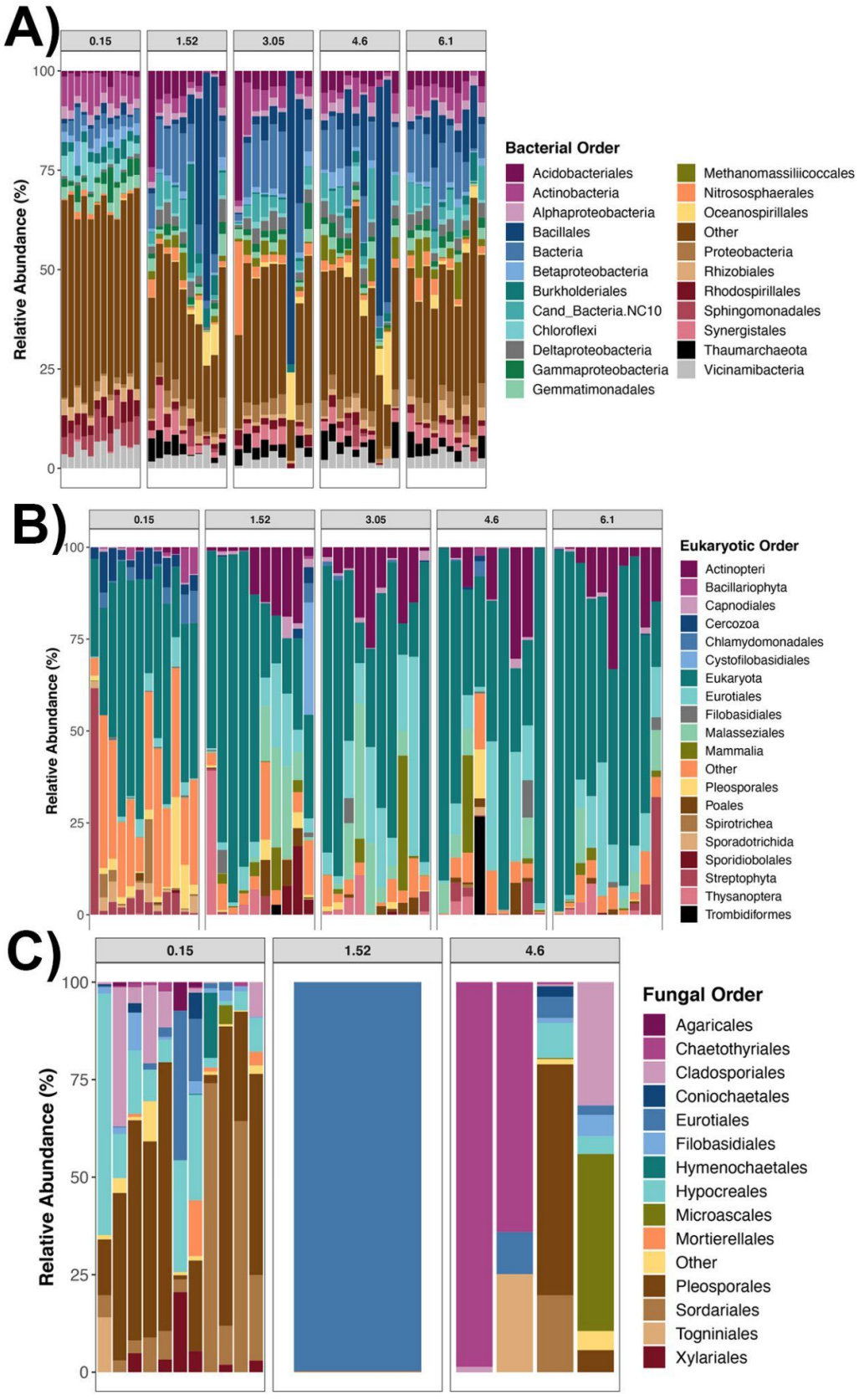


Figure S5. Microbial community composition plots using rarefied data. Stacked bar plots showing the relative frequency of sequences assigned to each microbial phylum (top) and order (bottom) across samples for **A)**16S rRNA, **B)** 18S rRNA, and **C)** fungal ITS gene profiles that have been subsampled to 42,000 reads (16S rRNA data), 21,000 reads (18S rRNA data), and 370 reads per sample (FITS data). Samples are grouped by depth, and each color represents a microbial group.