

Supplementary Table Guide

Supplementary Table 1.xlsx: Samples used in this study.

Supplementary Table 2.xlsx: Soil gene catalogue statistics.

Supplementary Table 3.xlsx: GLS models of diversity and biomass.

Supplementary Table 4.xlsx: Correlation of fungal OG categories to C/N ratio.

Supplementary Table 5.xlsx: Structural equation model parameters.

Supplementary Table 6.xlsx: Average number of ARGs found in bacterial phyla.

Supplementary Table 7.xlsx: ARG classes correlating to fungi.

Supplementary Table 8.xlsx: Correlations of bacterial/fungal Taxa to ARG.

Supplementary Table 9.xlsx: Abundance of taxa in soil and oceans.

Supplementary Table 10.xlsx: Genomes used in metagenomic simulations.

Supplementary Table 11.xlsx: Antibiotic producing fungal gene clusters.

Supplementary Table 12.xlsx: Biosynthetic clusters in public fungal genomes.

Supplementary Table 13.xlsx: Environmental variables used in model selection.

Supplementary Table 14.xlsx: Cross biome differences in microbial structure and function.

Supplementary Table 15.xlsx: Antibiotics and ARGs as defined in ARDB.

Supplementary Table 16.xlsx: Pathway correlations of bacterial KEGG to environment.

Supplementary Table 17.xlsx: Taxonomic and functional abundances across biomes.

Supplementary Table 18.xlsx: Taxa correlating to CARD ARGs.

Supplementary Table 19.xlsx: Antibiotic production prediction in Oomycetes.