Additional file 1: Supplementary Figures

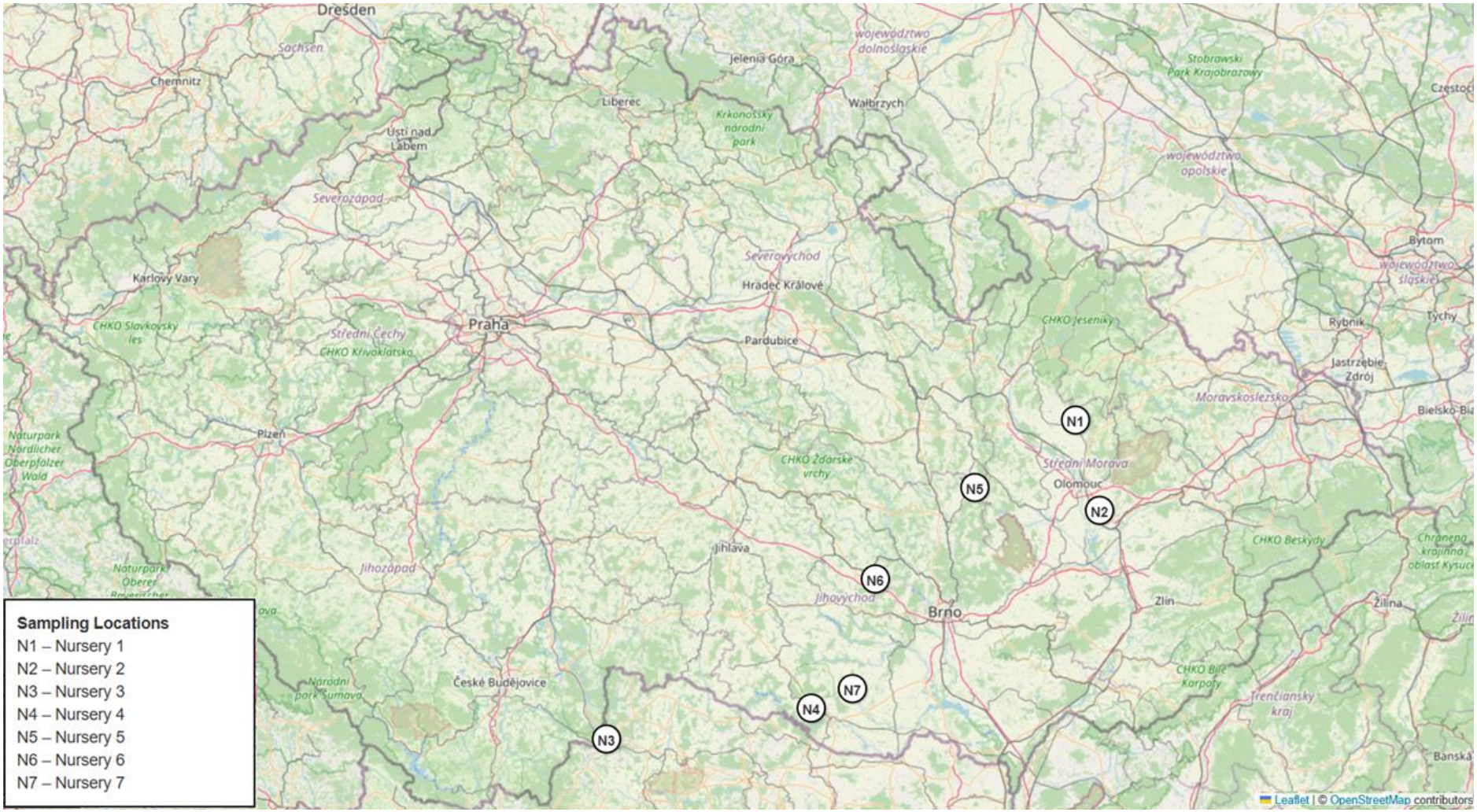
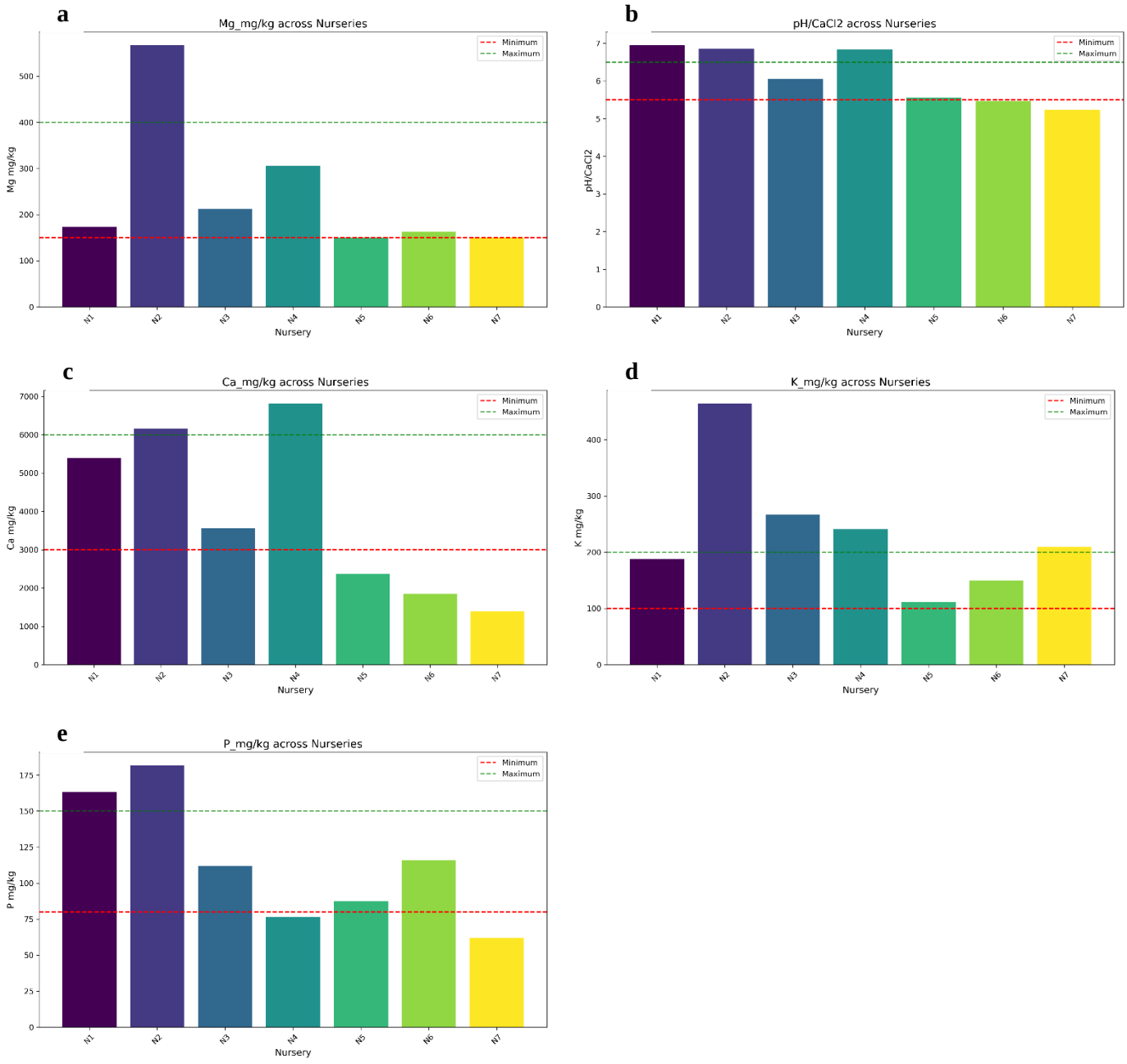
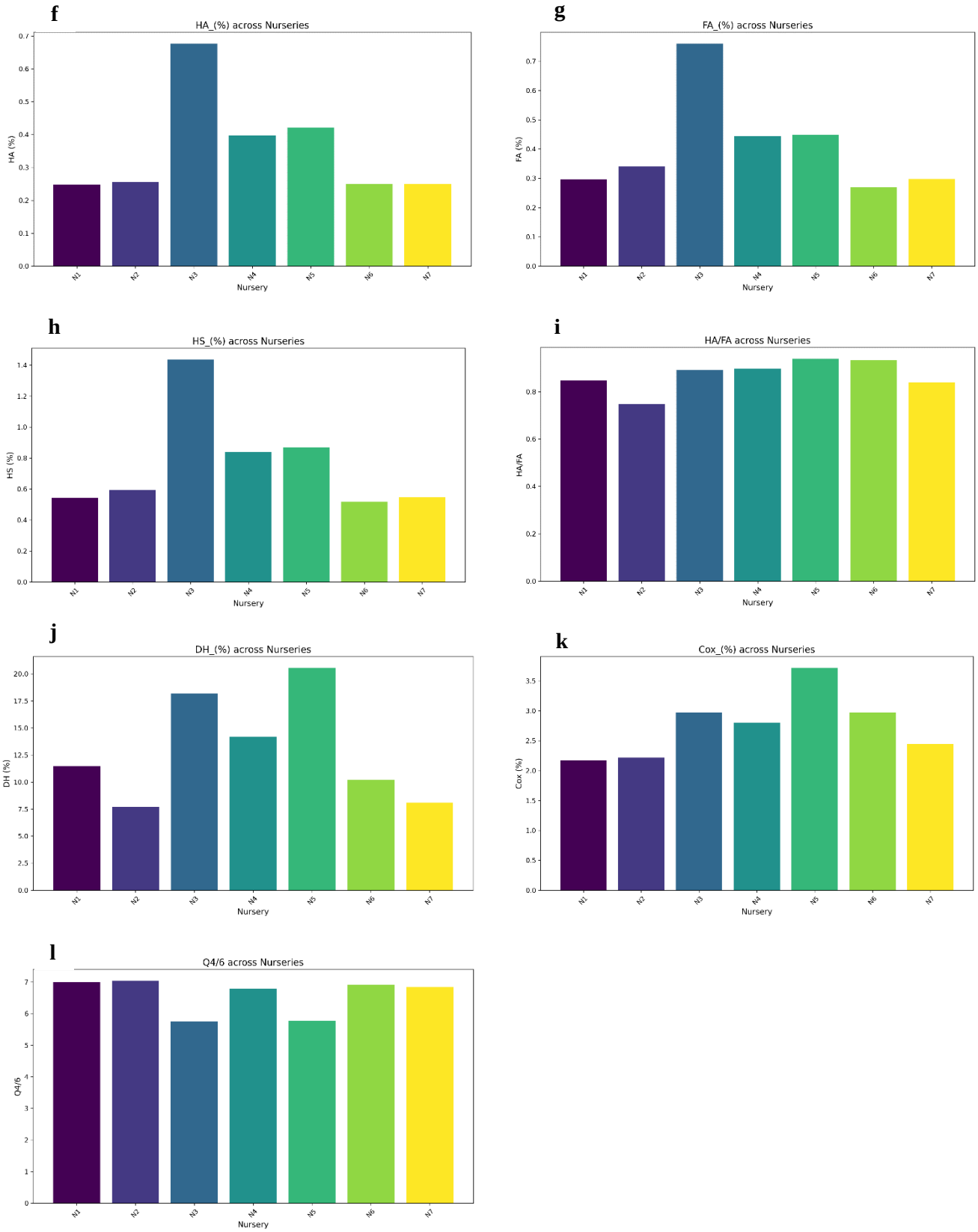


Figure S0 *Map of the sampled forest nurseries (N1-N7), generated using Folium (Python library).*

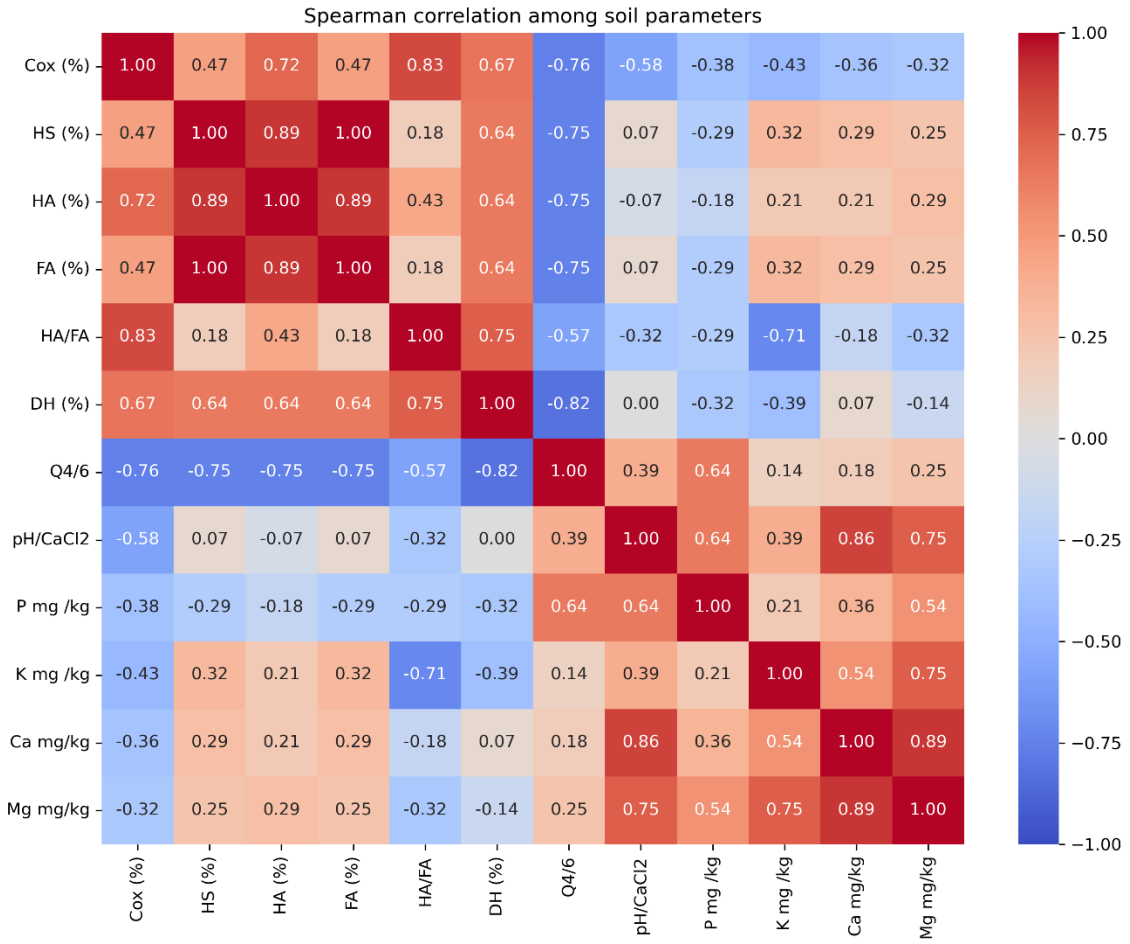
Figure S2 Sampling design - *(a - b) Forest nursery N5, (c) Forest nursery N7, (d) sampled soil, (e) washed seedlings, (f) sterile cuts, (g) morphotyping, (h-k) symptomatic seedlings, (l-m) necrotic tissue, (n) fragments cultivation on PDA with streptomycine*



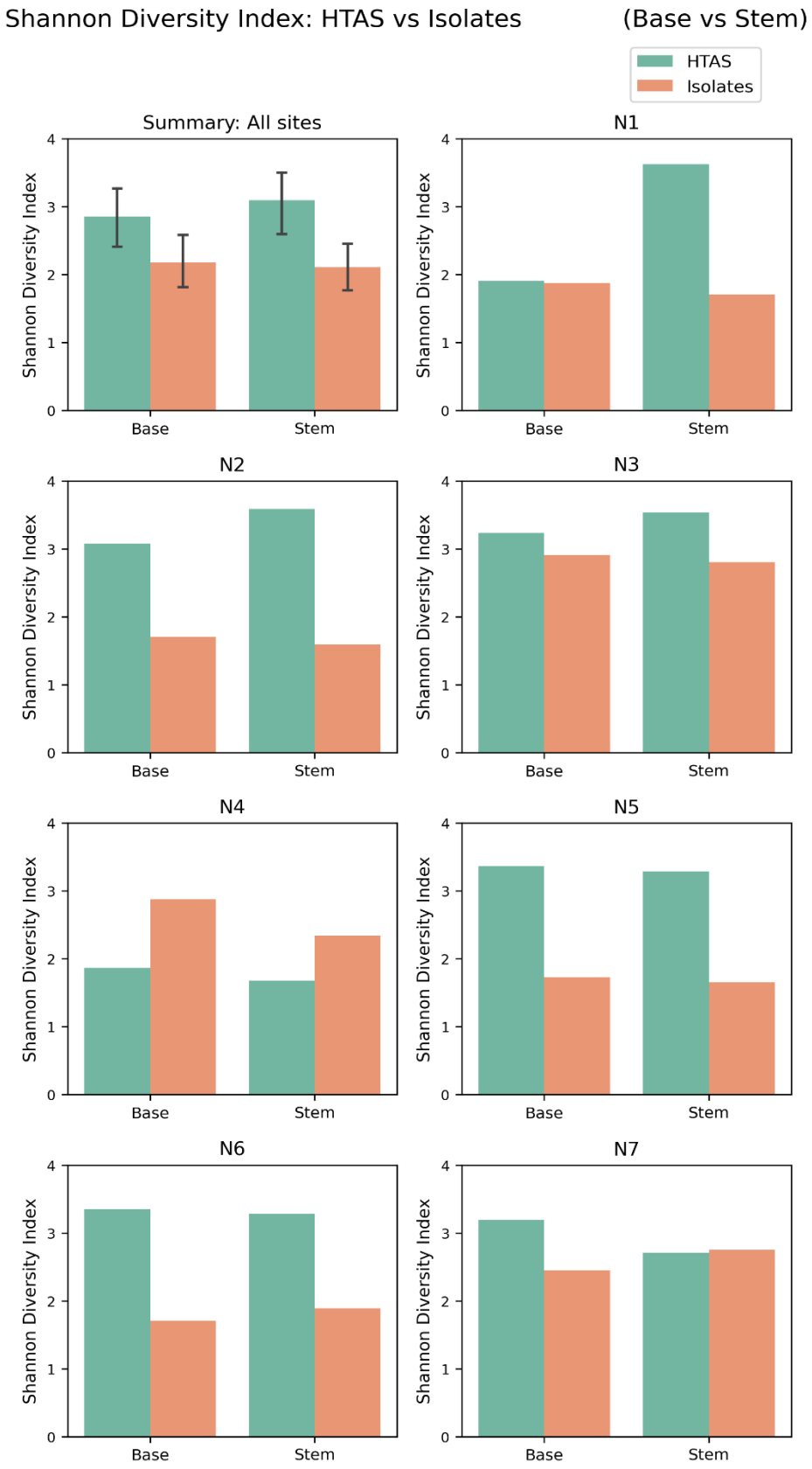
Supplementary Figure S3 *Inorganic soil parameters across the seven forest nurseries. The horizontal red and green dashed lines the thresholds for deficiency and sufficiency, respectively, according to forest soil nutrient recommendations* [98]. *Each subplot (a–e) corresponds to one measured parameter.*



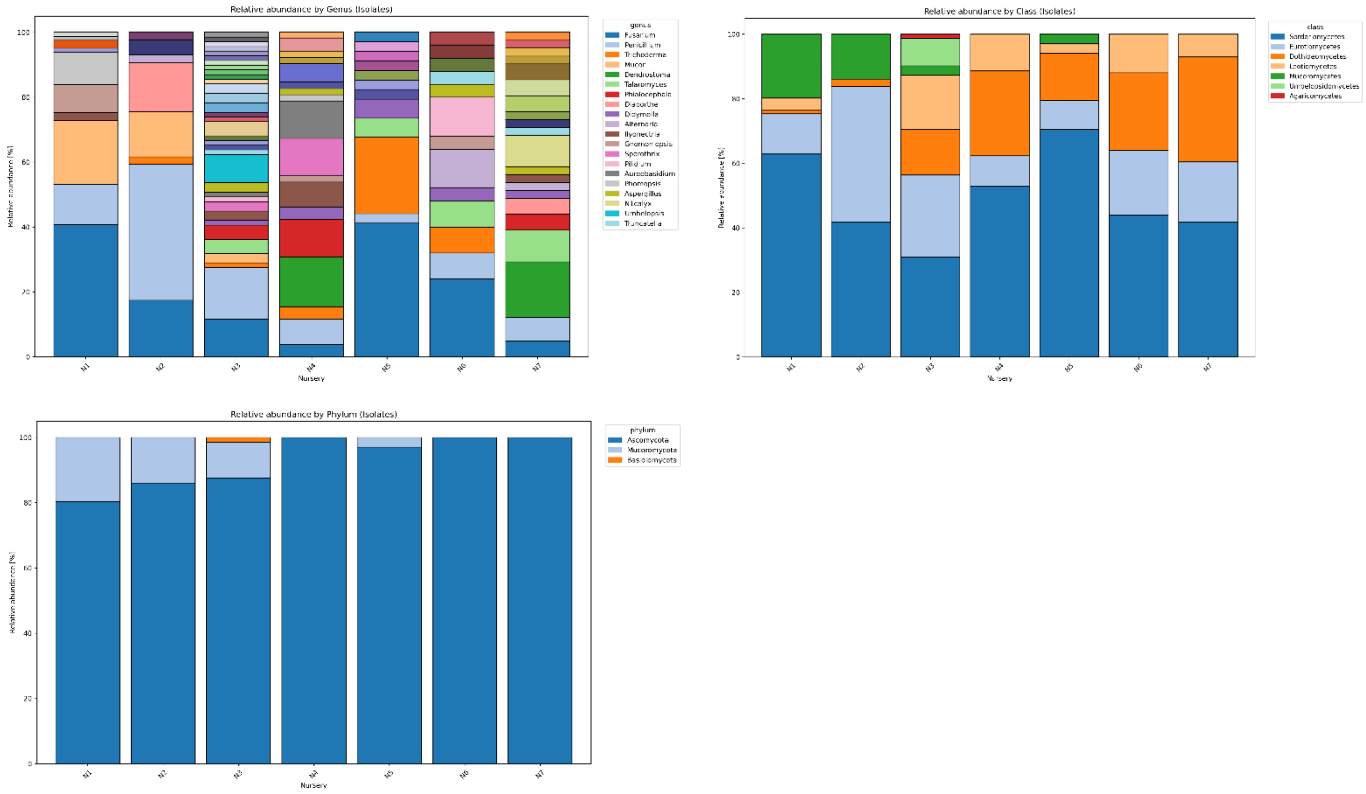
Supplementary Figure S4 *Organic soil parameters across the seven forest nurseries.Each subplot (f–l) corresponds to one measured parameter.*



Supplementary Figure S5 *Spearman correlation matrix among soil parameters aggregated by nursery. Matrix visualizes pairwise Spearman's rank correlations between all measured soil chemical parameters, including organic fractions (Cox, HS, HA, FA), humus ratios (HA/FA, $Q_{4/6}$), soil Ph/$CaCl_2$, and inorganic nutrients (P, K, Ca, Mg). Strong positive associations are marked in dark red, strong negative in dark blue. Notable correlations include strong co-variation among carbon fractions and between pH and cation availability (Ca, Mg).*

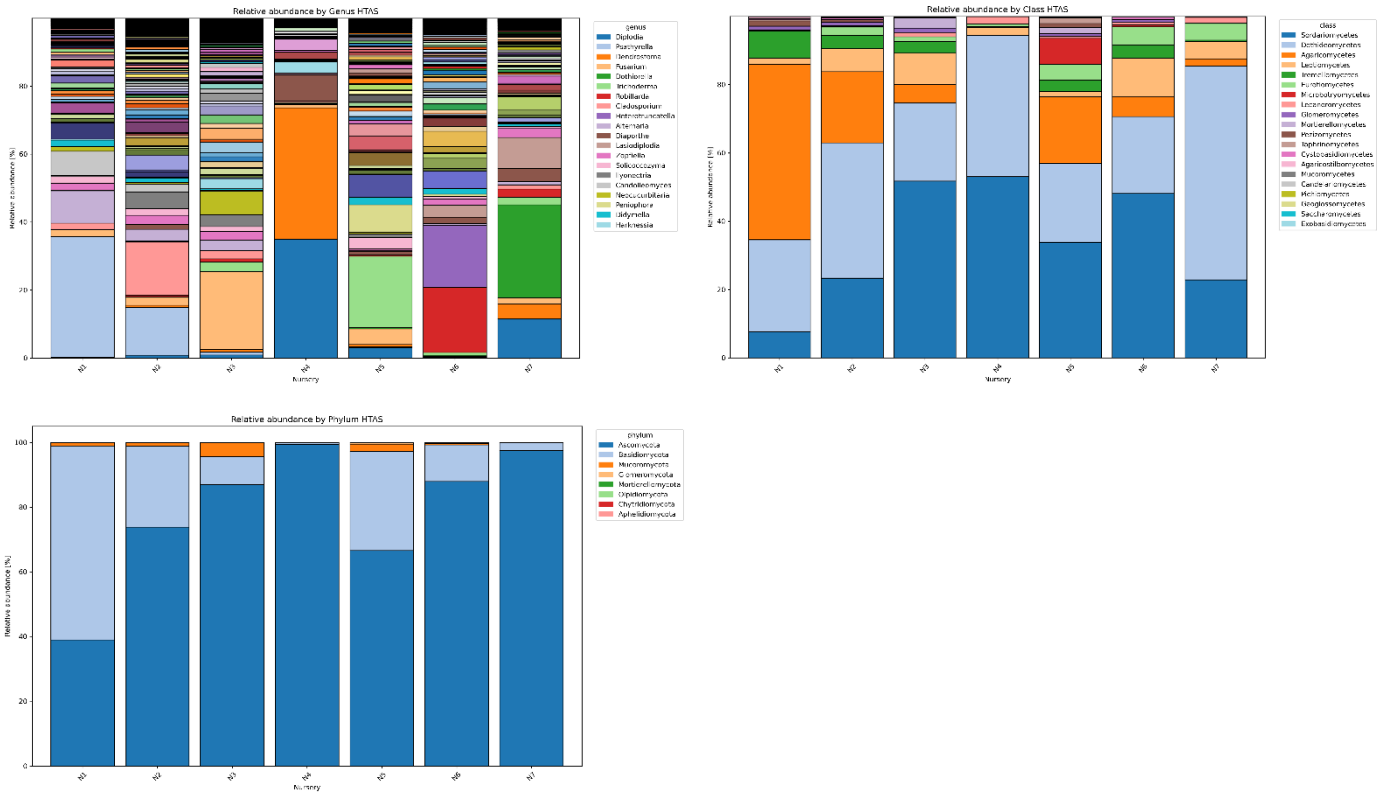


Supplementary Figure S6 *Comparison of fungal Shannon diversity index between HTAS and isolate-based datasets across sites and plant organ. Bar plots show Shannon diversity for fungal communities detected by HTAS (green) and Isolate (orange) in the base and stems of the seedlings. The top-left is the summary of the overall trend across all sites, while remaining graphs display results for each individual forest nursery. HTAS consistently captured higher fungal diversity compared to the Isolation, with some nursery and organ specific variation.*

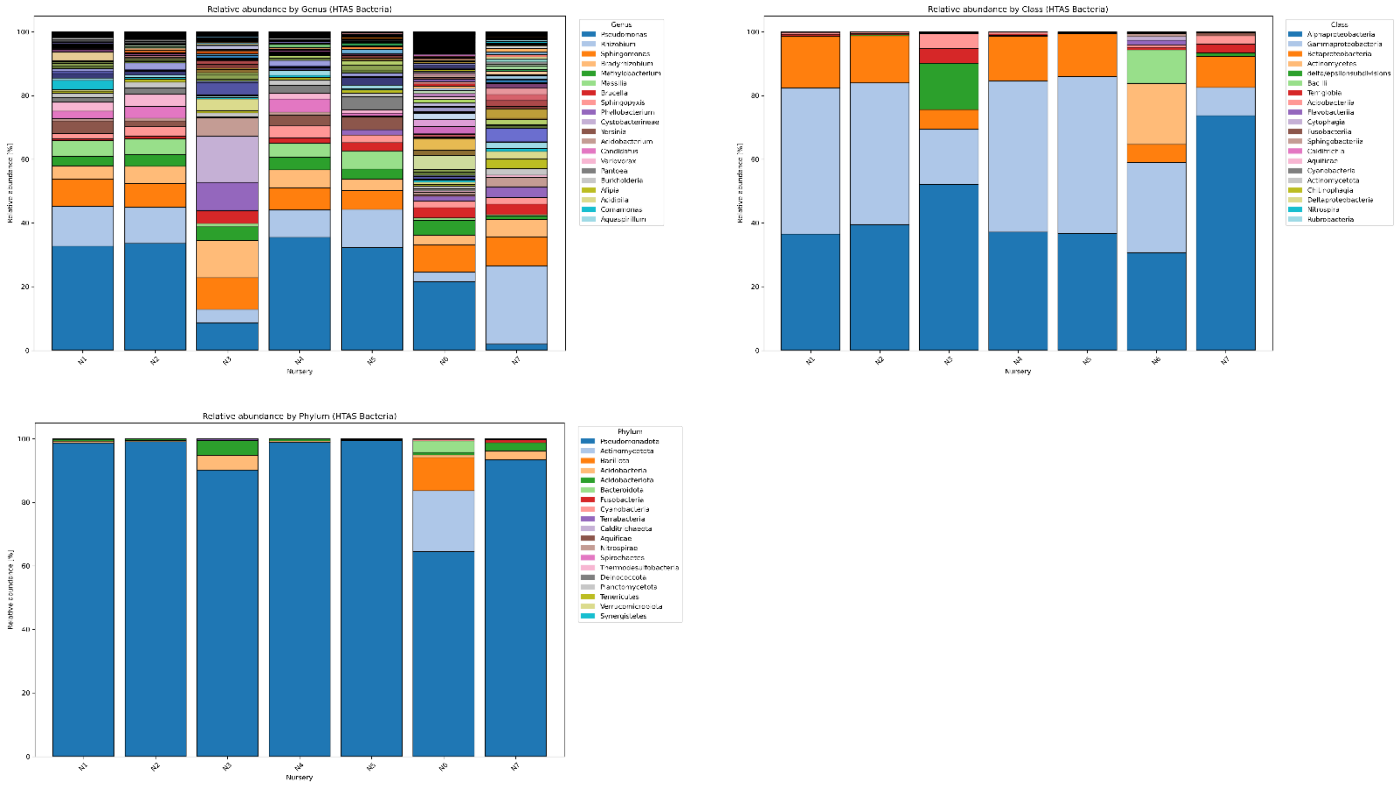


Supplementary Figure S8 *Relative abundance of fungal isolates across nurseries. Stacked barplots show the normalized relative abundance of fungal isolates assigned at the genus, class, and phylum level across nurseries. In Genus plot only top 20 taxa are included in legend.*

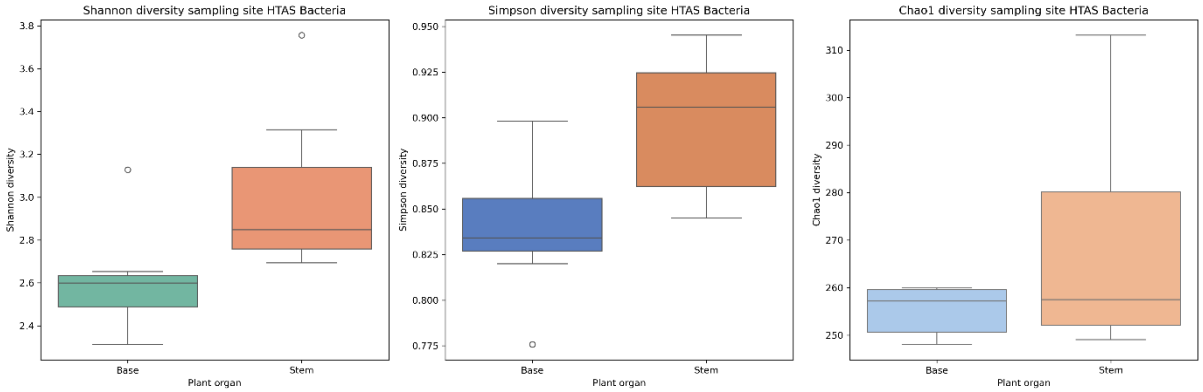
Supplementary Figure S9 *Normalized relative abundance of fungal trophic modes across sampling sites based on HTAS. Stacked barplot shows the relative proportions of trophic assignments (FUNGuild) across all nurseries and plant organ (B-base; S-stem).*



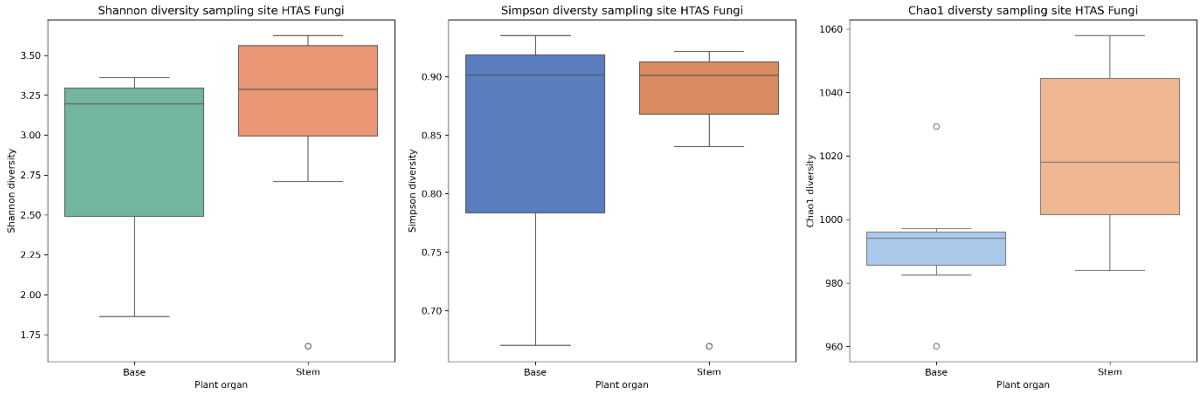
Supplementary Figure S10 *Relative abundance of fungal HTAS across location. Stacked barplots show the normalized relative abundance of fungi assigned at the genus, class, and phylum level across nurseries. In Genus plot only top 20 taxa are included in legend.*



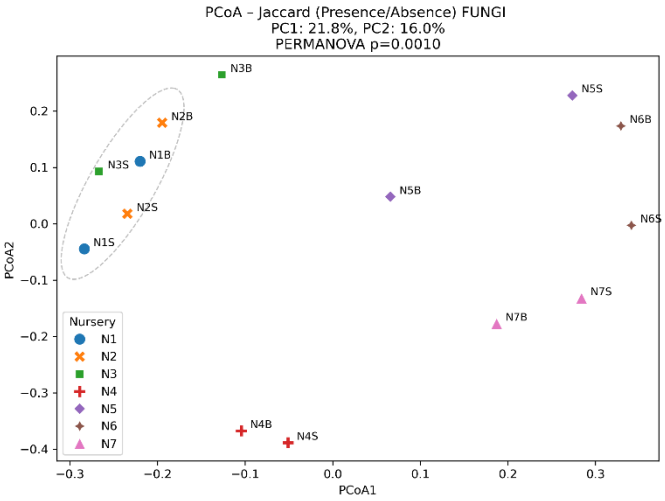
Supplementary Figure S12 *Relative abundance of bacterial HTAS across location. Stacked barplots show the normalized relative abundance of bacterias assigned at the genus, class, and phylum across nurseries. In Genus plot only top 20 taxa are included in legend.*

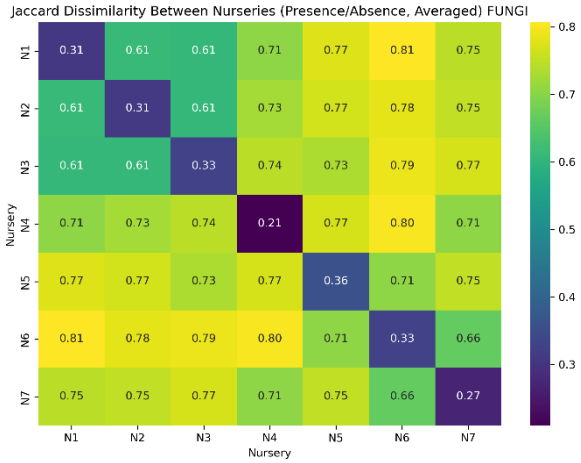


Supplementary Figure S13 *Alpha diversity of bacterial communities across sampling site (base, stem) based on HTAS data. Diversity metrics include Shannon index (left), Simpson index (center), and Chao1 richness estimator (right).*

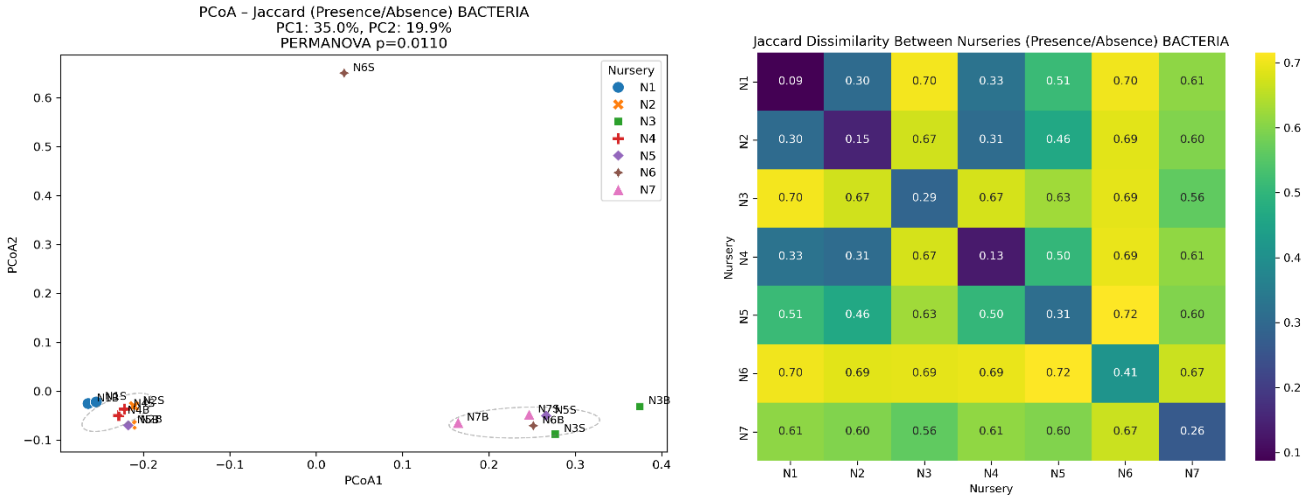


Supplementary Figure S14 *Alpha diversity of fungal communities across sampling site (base, stem) based on HTAS data. Diversity metrics include Shannon index (left), Simpson index (center), and Chao1 richness estimator (right).*

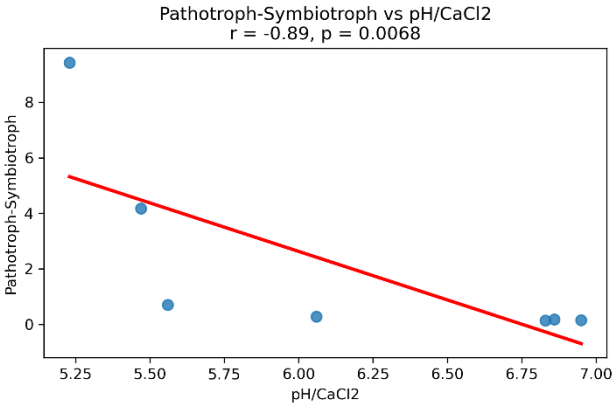




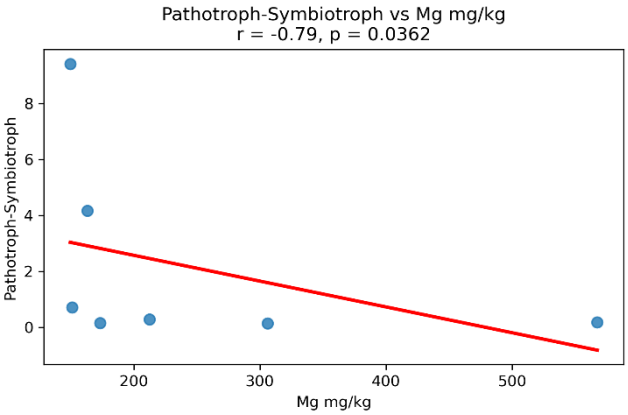
Supplementary Figure S17 *Jaccard-based community dissimilarity among fungal sequences across sites. PCoA based on presence/absence data shows clear separation of localities (PC1 = 21.8%, PC2 = 16.0%). Clustered Jaccard distance matrix reveals grouping of locations with higher overlap in fungal OTU occurrence. Notably, N7 and N5 form one cluster, while N1 and N2 exhibit more distinct profiles from the rest.*



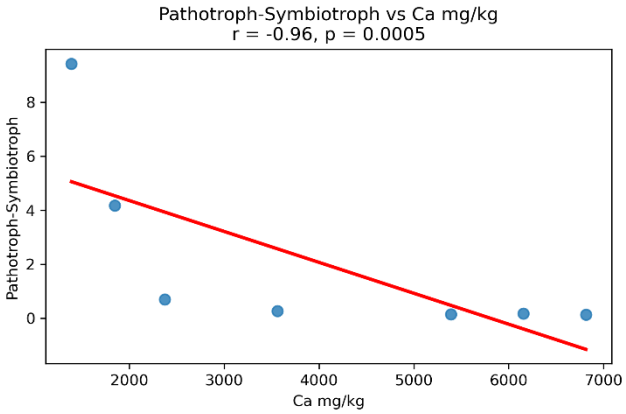
Supplementary Figure S18 *Jaccard-based community dissimilarity among bacterial sequences across sites. PCoA based on presence/absence data shows clear separation of localities (PC1 = 35.0%, PC2 = 19.9%). Notably partial separation of N7 and N3 from other sites. Jaccard dissimilarity heatmap with hierarchical clustering further highlights compositional differences between sites, particularly between N7 and the rest.*



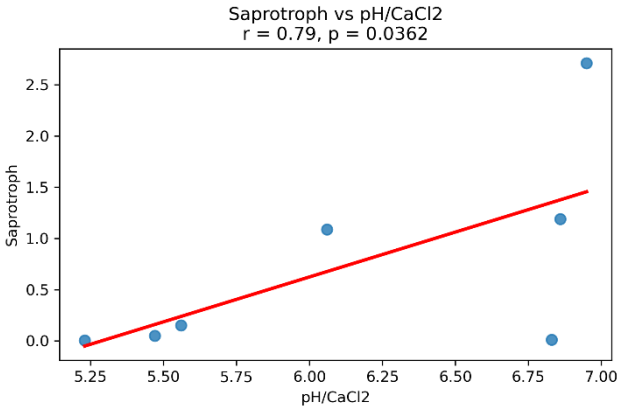
Supplementary Figure S20 *Negative correlation between the relative abundance of the Pathotroph–Symbiotroph fungal group and soil pH/CaCl₂. Spearman's correlation revealed a strong and statistically significant relationship (ρ = –0.89, p = 0.0068), suggesting that this functional group is more prevalent in more acidic soils.*



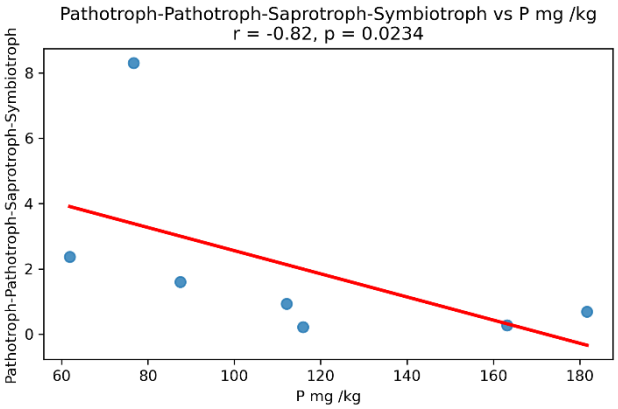
Supplementary Figure S21 *Negative correlation between the relative abundance of the Pathotroph–Symbiotroph group and soil Mg (mg/kg). Spearman's correlation revealed a statistically significant relationship ($\rho = -0.79$, $p = 0.0362$), suggesting that this functional group is more prevalent in soil with less amount of Mg.*



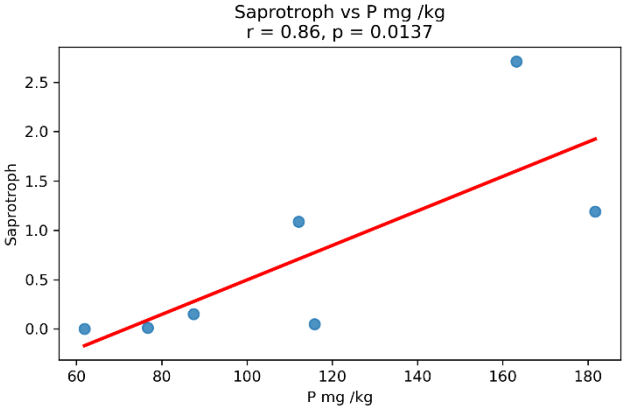
Supplementary Figure S22 *Negative correlation between the relative abundance of the Pathotroph-Symbiotroph group and soil Ca (mg/kg). Spearman's correlation revealed a strong statistically significant relationship ($\rho = -0.96$, $p = 0.0005$), suggesting that this functional group is more prevalent in soil with less amount of Ca.*



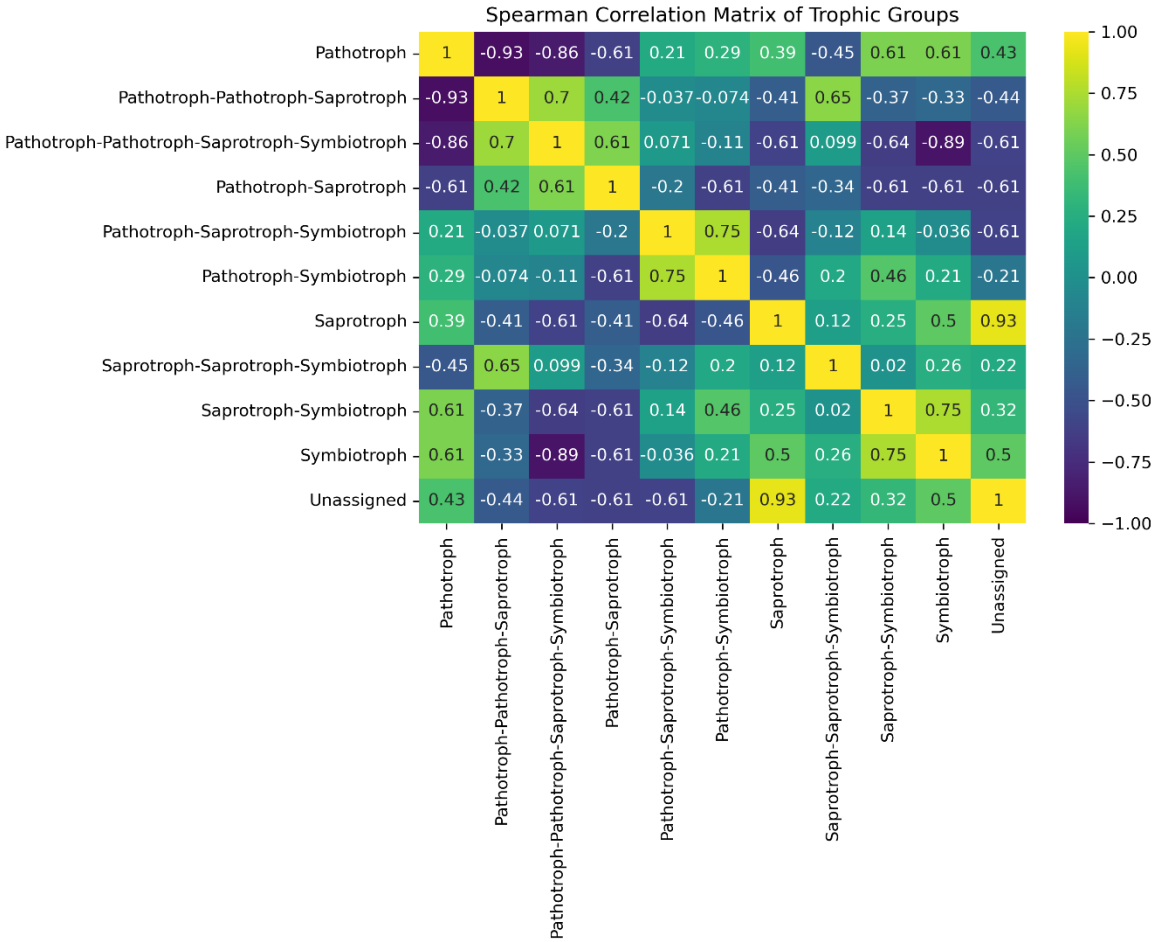
Supplementary Figure S23 *Positive correlation between the relative abundance of the Saprotroph group and soil pH/$CaCl_2$. Spearman's correlation revealed a statistically significant relationship (ρ = 0.79, p = 0.0362), suggesting that this functional group is more prevalent in soil with higher pH/$CaCl_2$.*



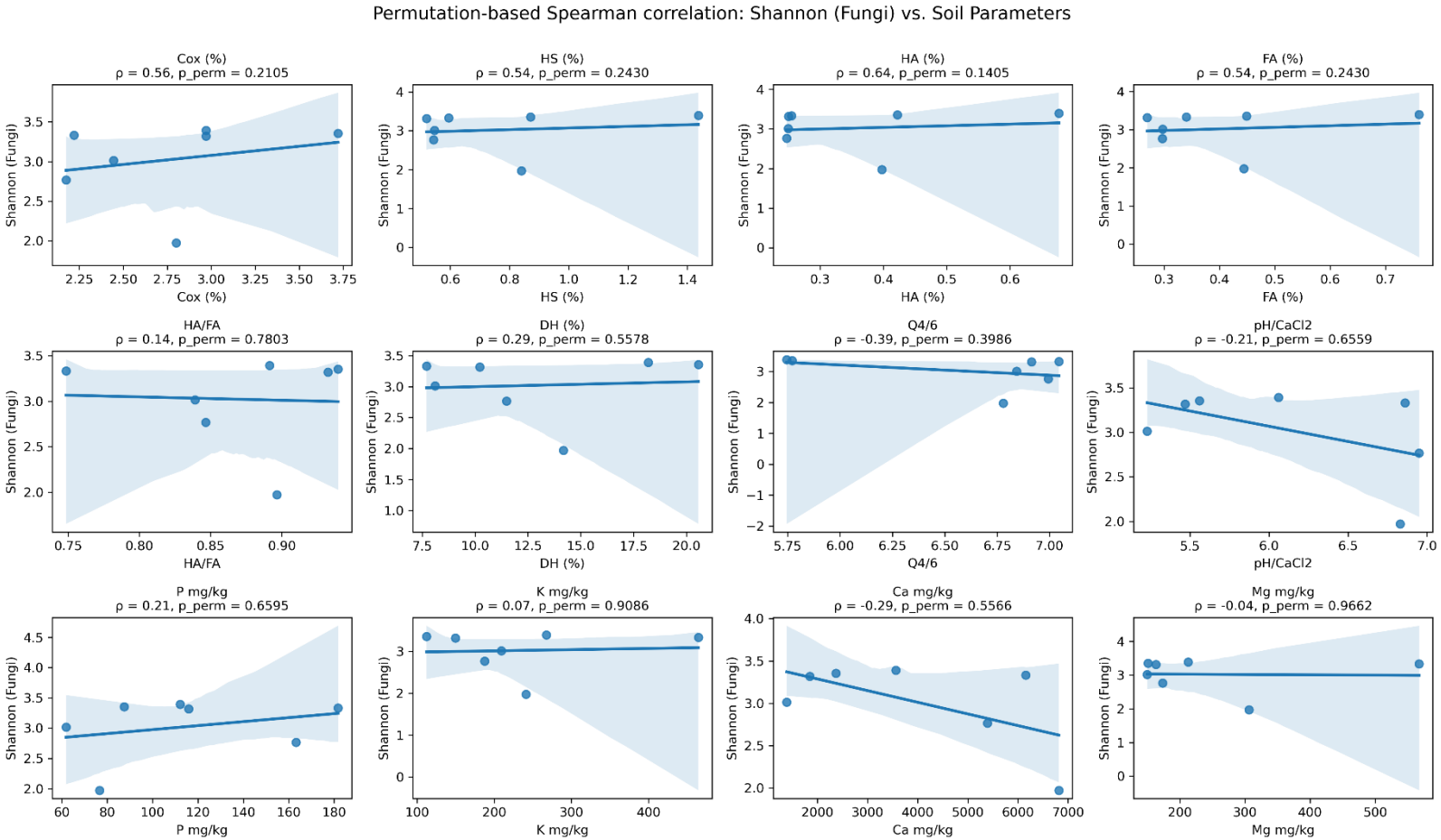
Supplementary Figure S24 *Negative correlation between the relative abundance of the Pathotroph-Pathotroph-Saproroph-Symbiotroph group and soil P (mg/kg). Spearman's correlation revealed a statistically significant relationship (ρ = –0.82, p = 0.0234), suggesting that this functional group is more prevalent in soil with less amount of P.*



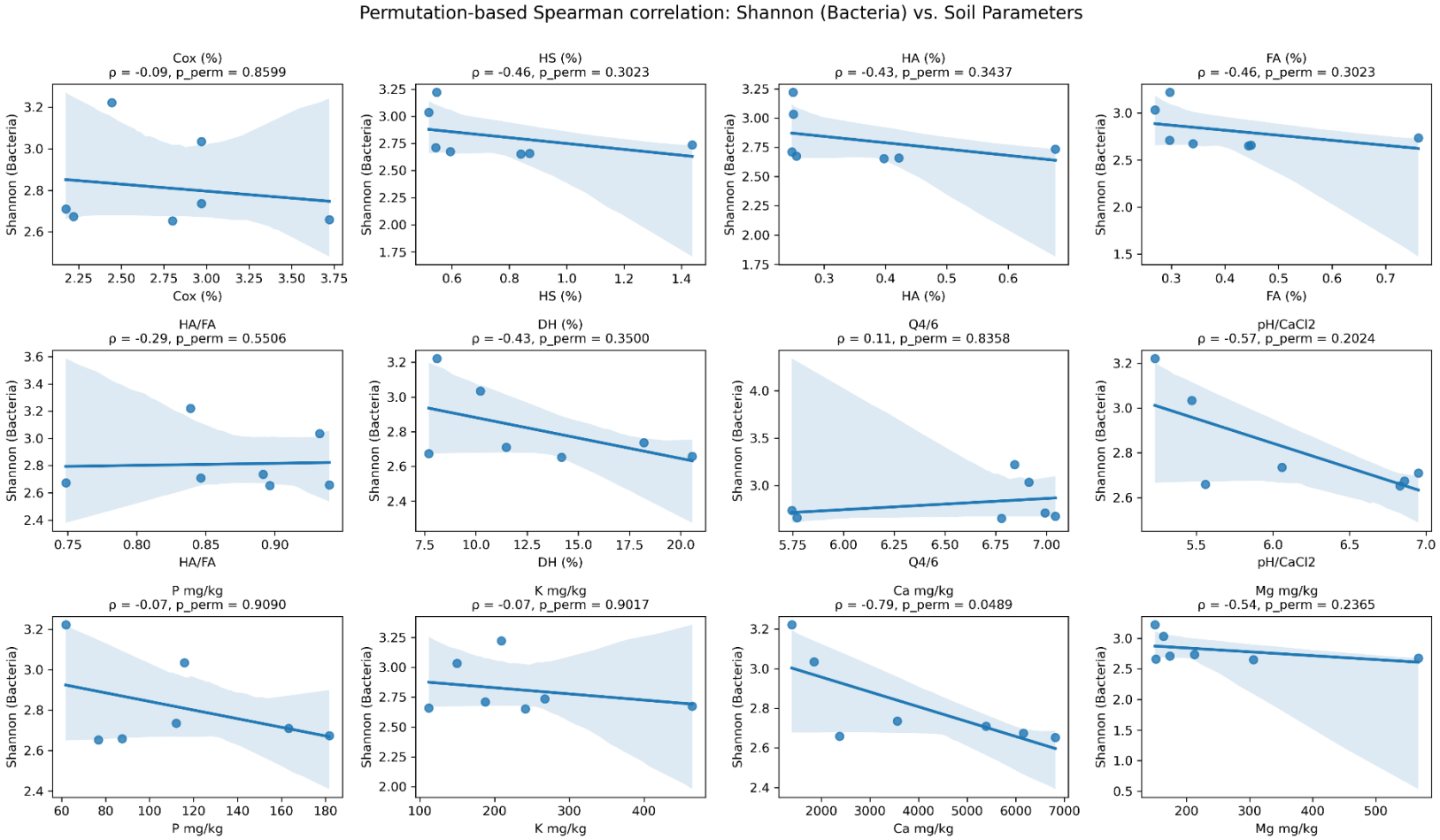
Supplementary Figure S25 *Positive correlation between the relative abundance of the Saprotroph group and soil P (mg/kg). Spearman's correlation revealed a statistically significant relationship ($\rho = 0.86$, $p = 0.0137$), suggesting that this functional group is more prevalent in soil with higher P.*



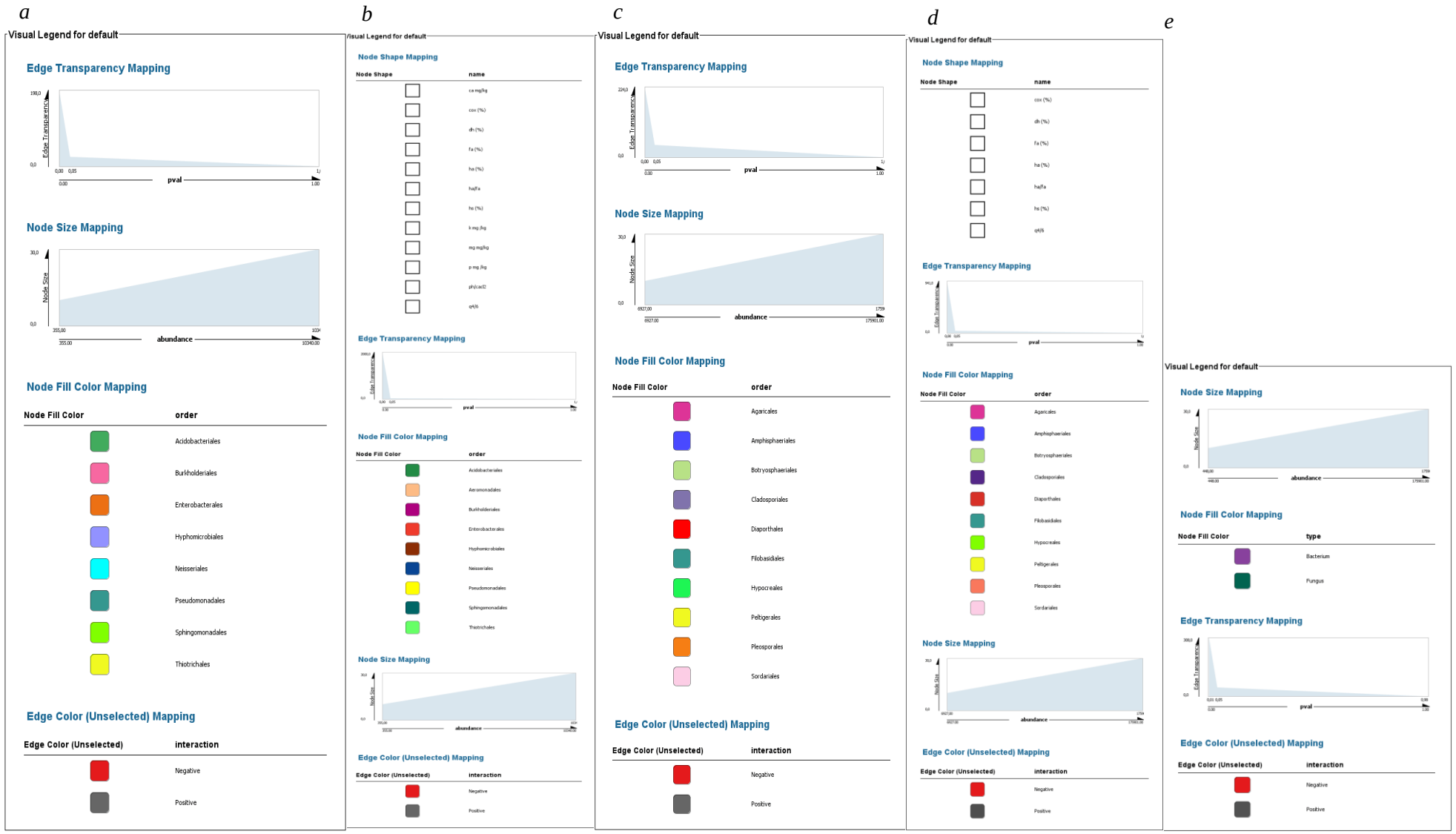
Supplementary Figure S26 *Spearman correlation matrix among fungal trophic modes based on raw relative abundance data across all samples. Positive and negative correlations indicate potential co-occurrence or exclusion patterns between functional groups. Notably, strong negative correlations were observed between Pathotroph–Symbiotroph and both Saprotroph (ρ = –0.70) and Symbiotroph (ρ = –0.71), while Pathotroph and Pathotroph–Symbiotroph showed a strong positive association (ρ = 0.53).*



Supplementary Figure S28 *Permutation-based Spearman correlation between fungal Shannon diversity and soil parameters. Each panel shows the correlation between Shannon diversity (fungi) and one soil parameter, based on average values per location. Correlation coefficients (ρ) and permutation-based p-values (p_{perm}, 10,000 permutations) are indicated in the title of each plot. None of the tested parameters reached statistical significance. While some humus fractions (e.g., C_{ox}, HA, HS) showed moderate positive trends, inorganic parameters such as pH/$CaCl_2$, Ca, Mg, and P displayed weak or inconsistent associations with fungal diversity.*



Supplementary Figure S29 *Permutation-based Spearman correlation between bacterial Shannon diversity and soil parameters. Each panel shows the correlation between Shannon diversity and one soil parameter, based on average values per location. Correlation coefficients (ρ) and permutation-based p-values (p_{perm}, 10,000 permutations) are indicated in the title of each plot. None of the tested parameters reached statistical significance. While some humus fractions (e.g., Cox, HA, HS) showed moderate positive trends, inorganic parameters such as pH, Ca, Mg, and P displayed weak or inconsistent associations with bacterial diversity.*



Supplementary Figure S30 *Visual legend showing node and edge mappings: color by order, type, or soil factor, top 20 taxa, and transparency by p-value statistically significant. (a-b) bacterial hubs, (c-d) fungal hubs, (f) crosskingdom.*