

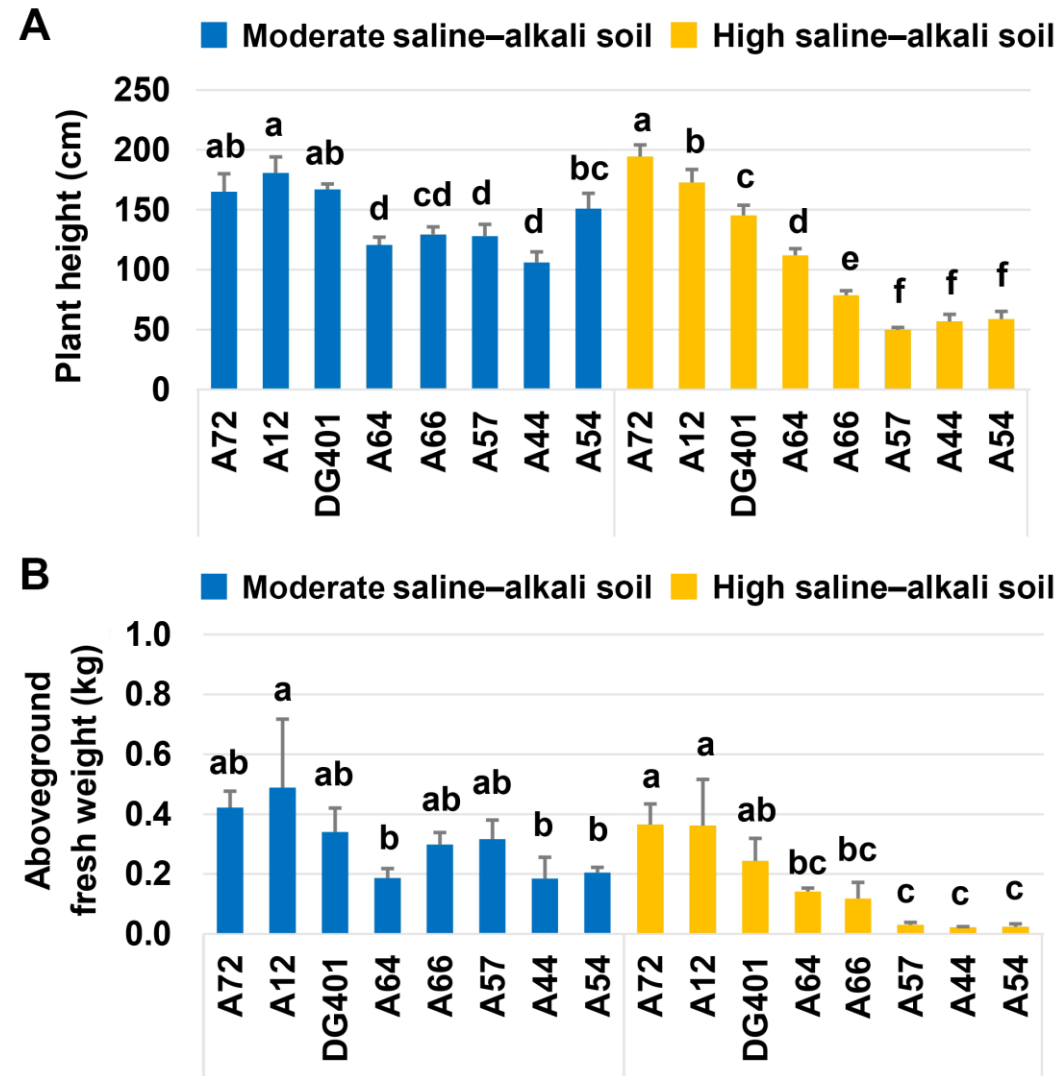


Fig. S1 Plant height (A) and aboveground fresh weight (B) of maize inbred lines under moderate and high saline-alkali conditions at harvest.

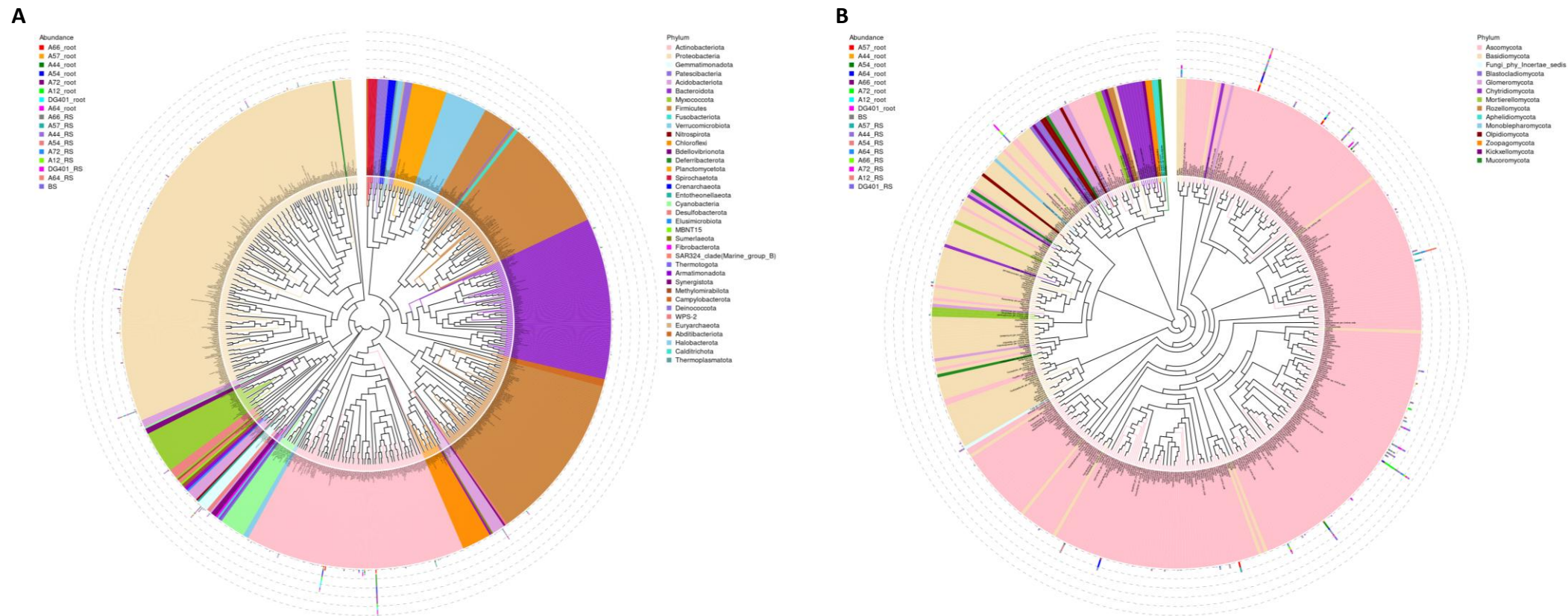


Fig. S2 Phylogenetic trees of representative bacterial (A) and fungal (B) genera from root-associated communities.

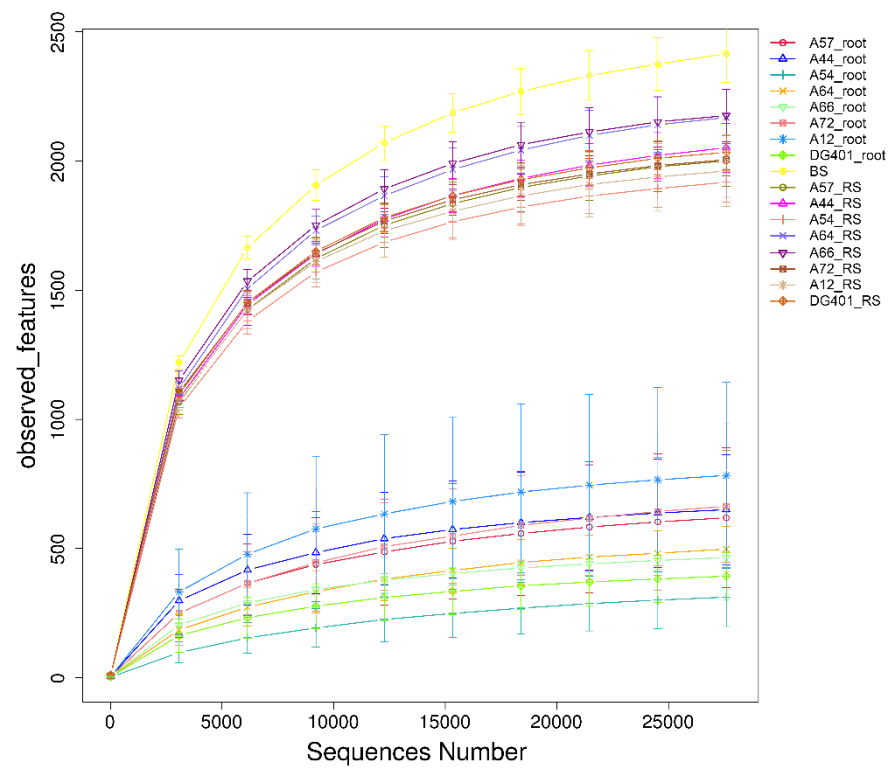
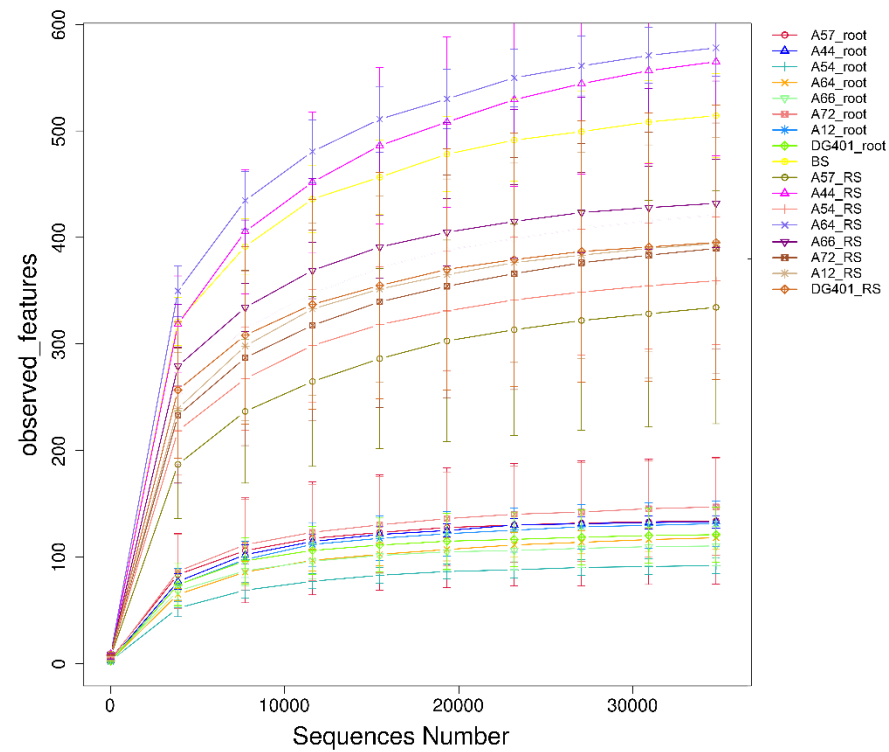
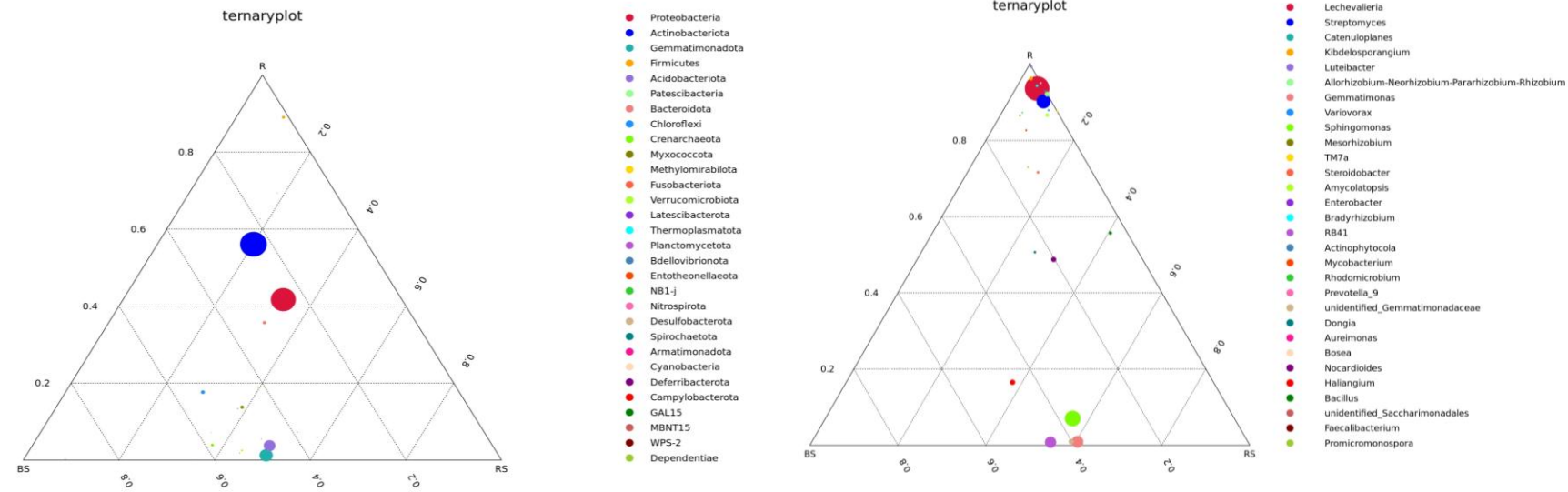
A**B**

Fig. S3 ASV-based rarefaction curves of 16S rRNA (A) and ITS (B) sequencing data.

A



B

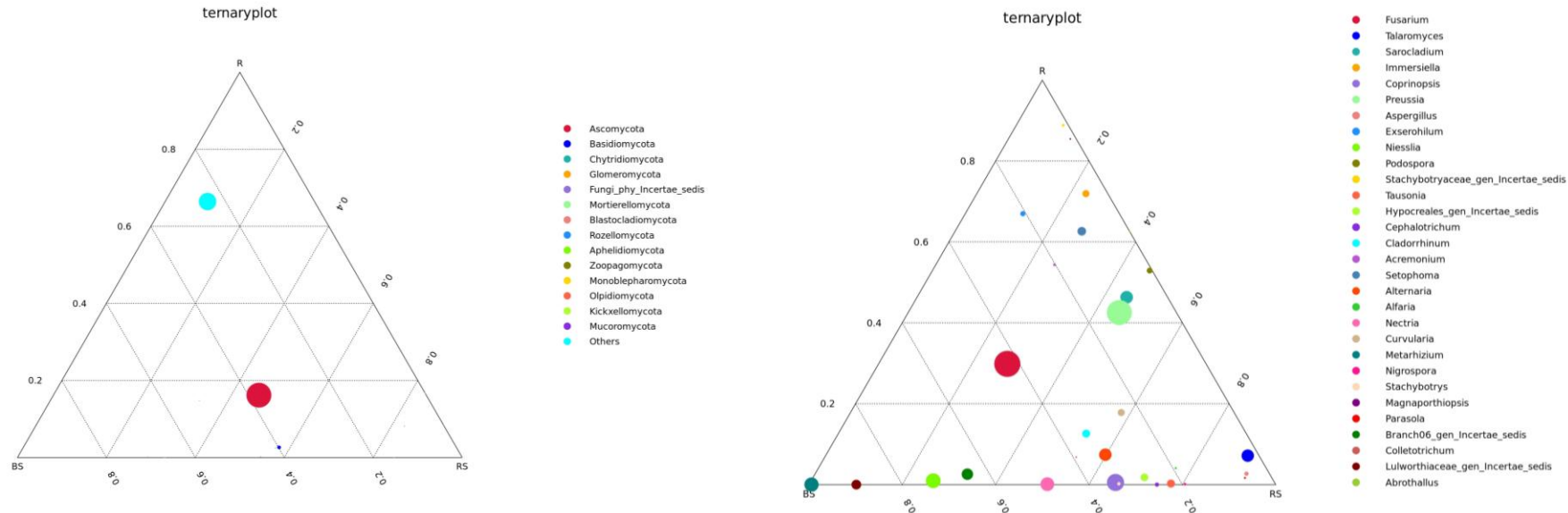


Fig. S4 Ternary diagrams showing the distribution of bacterial (A) and fungal (B) taxa across compartments at the phylum (left) and genus (right) levels.

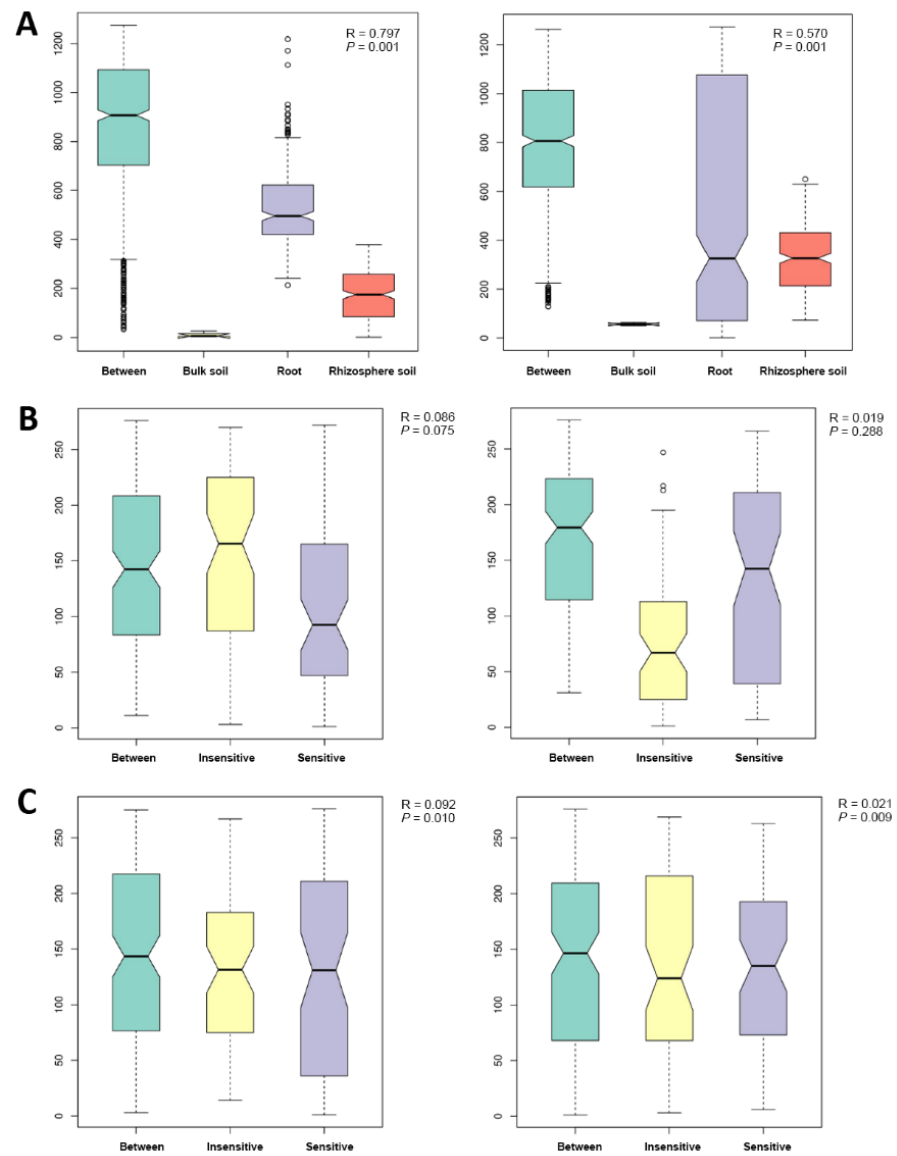


Fig. S5 Similarity analysis of bacterial (left) and fungal (right) community structures across compartments (A) and within the rhizosphere (B) and root (C) compartments between tolerant and sensitive groups.

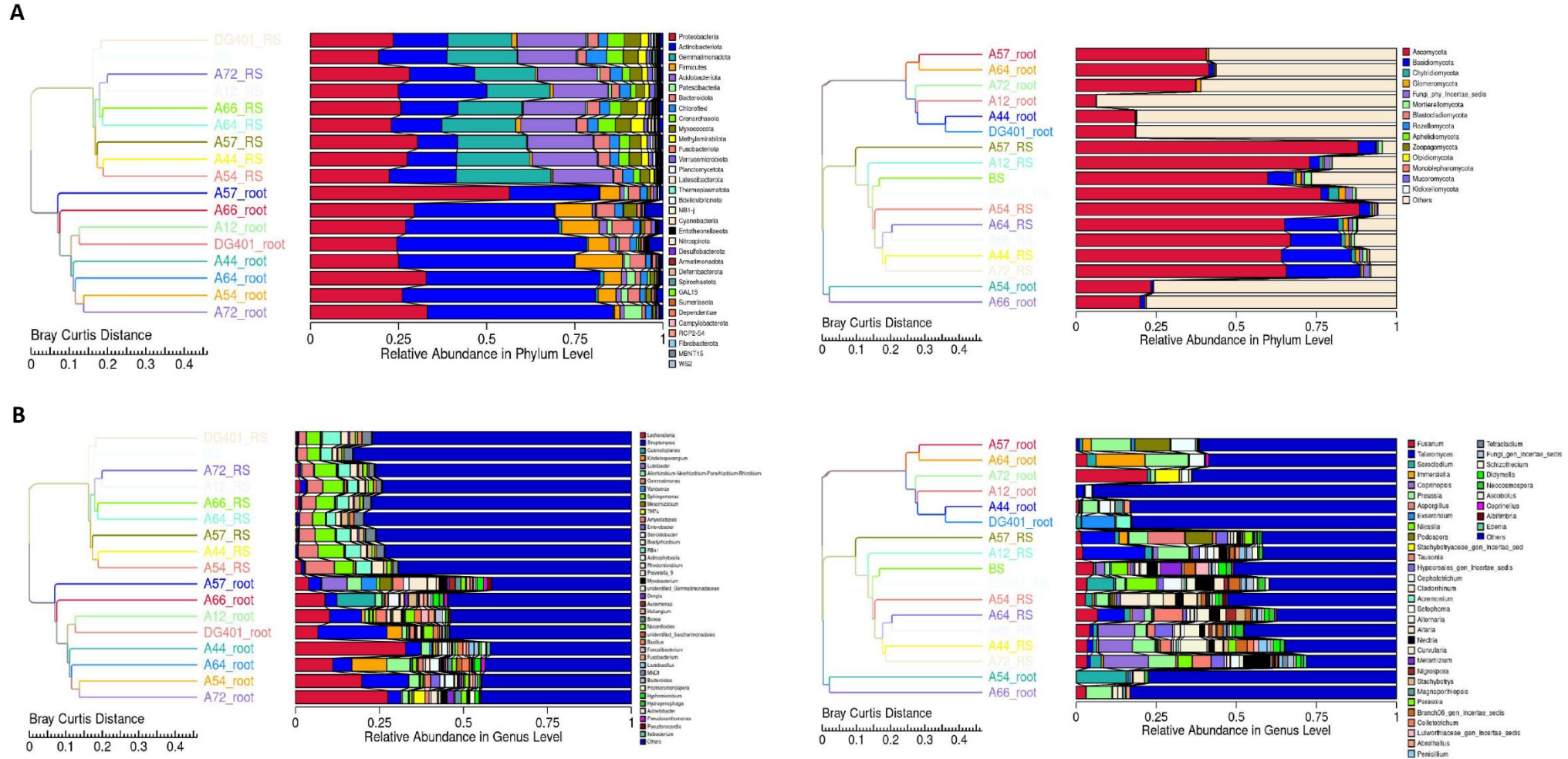


Fig. S6 UPGMA clustering of bacterial (left) and fungal (right) communities at the phylum (A) and genus (B) levels.

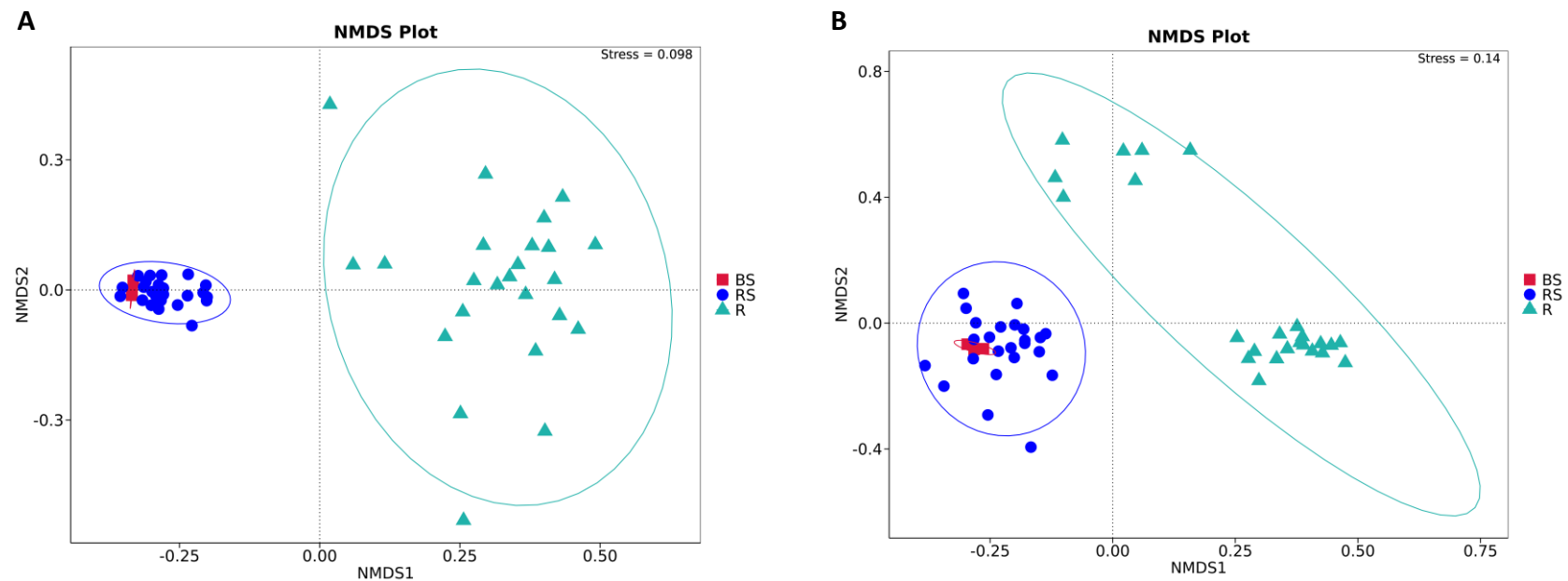


Fig. S7 NMDS analysis of bacterial (A) and fungal (B) communities across compartments using Bray-Curtis distances.

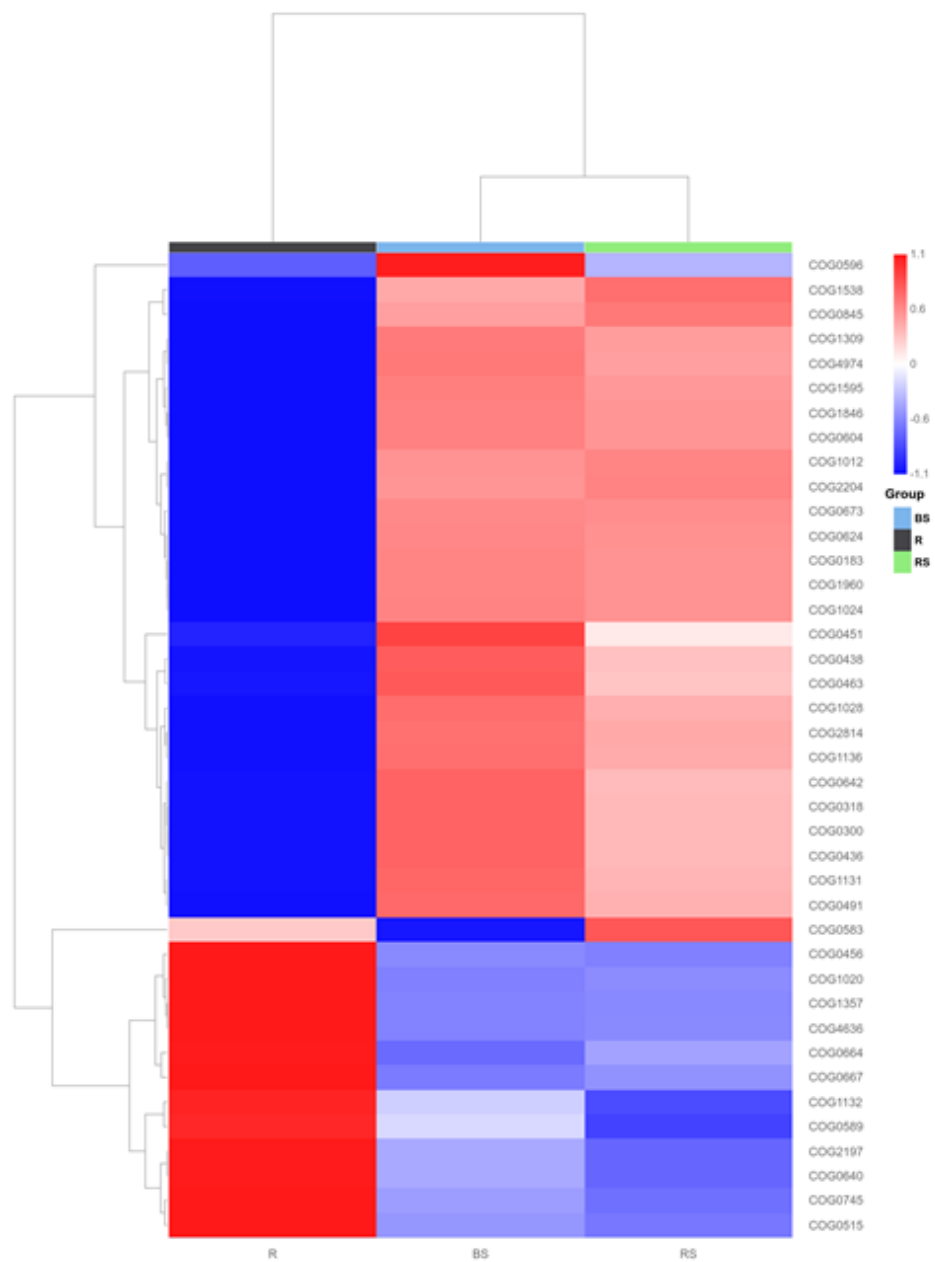


Fig. S8 Hierarchical clustering of predicted protein functional profiles in bacterial communities across compartments.

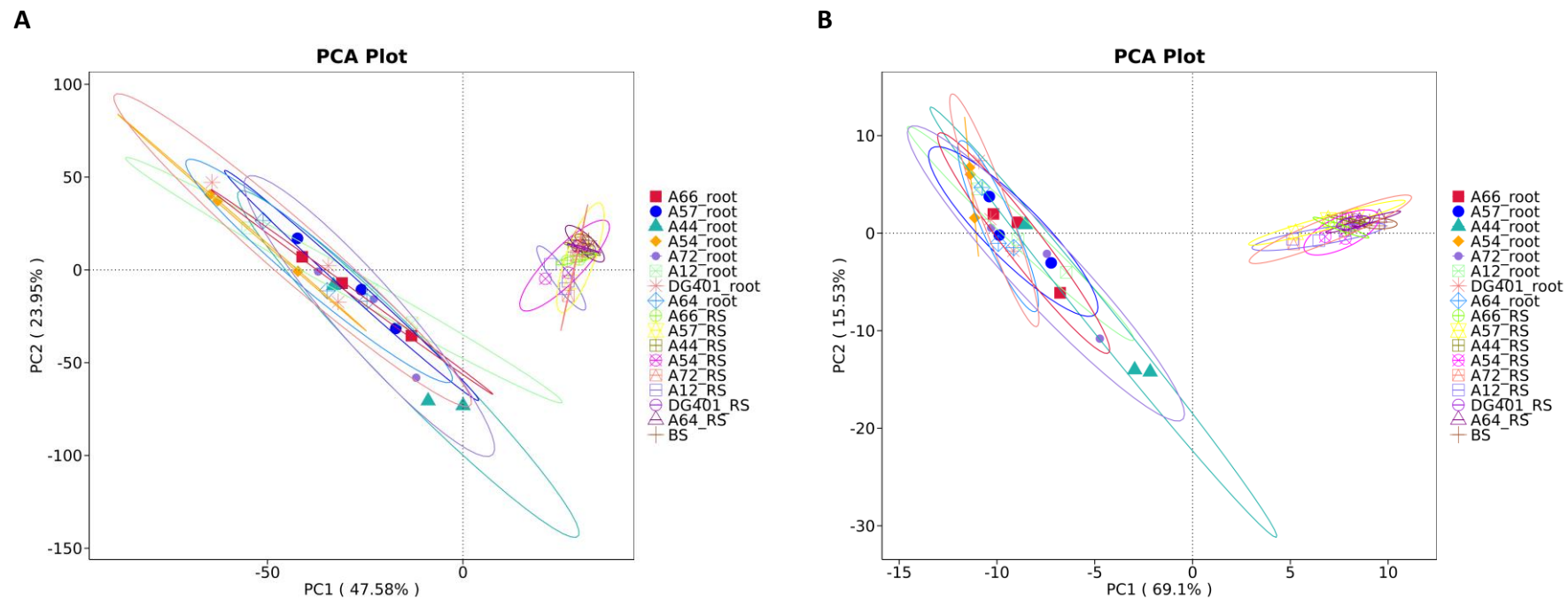


Fig. S9 PCA of bacterial communities based on predicted protein functional profiles (A) and biological pathways (B) across compartments.

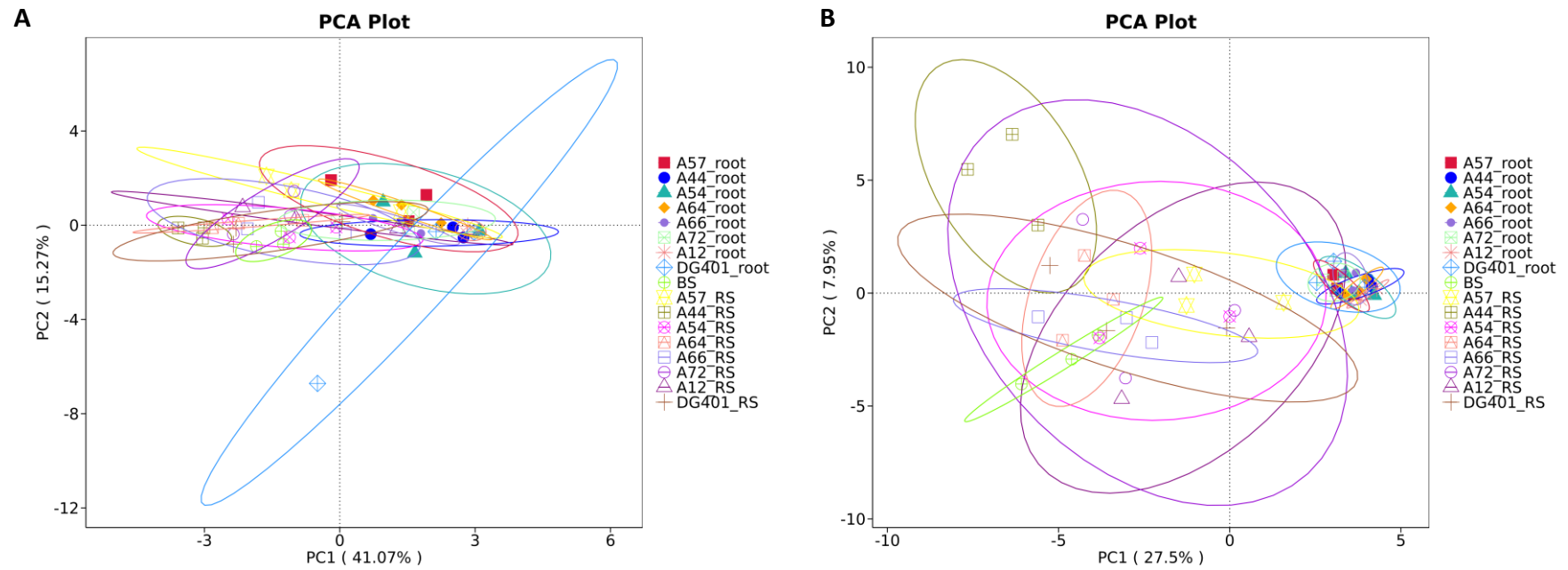


Fig. S10 PCA of fungal communities based on their trophic modes (A) and functional guilds (B) across compartments.

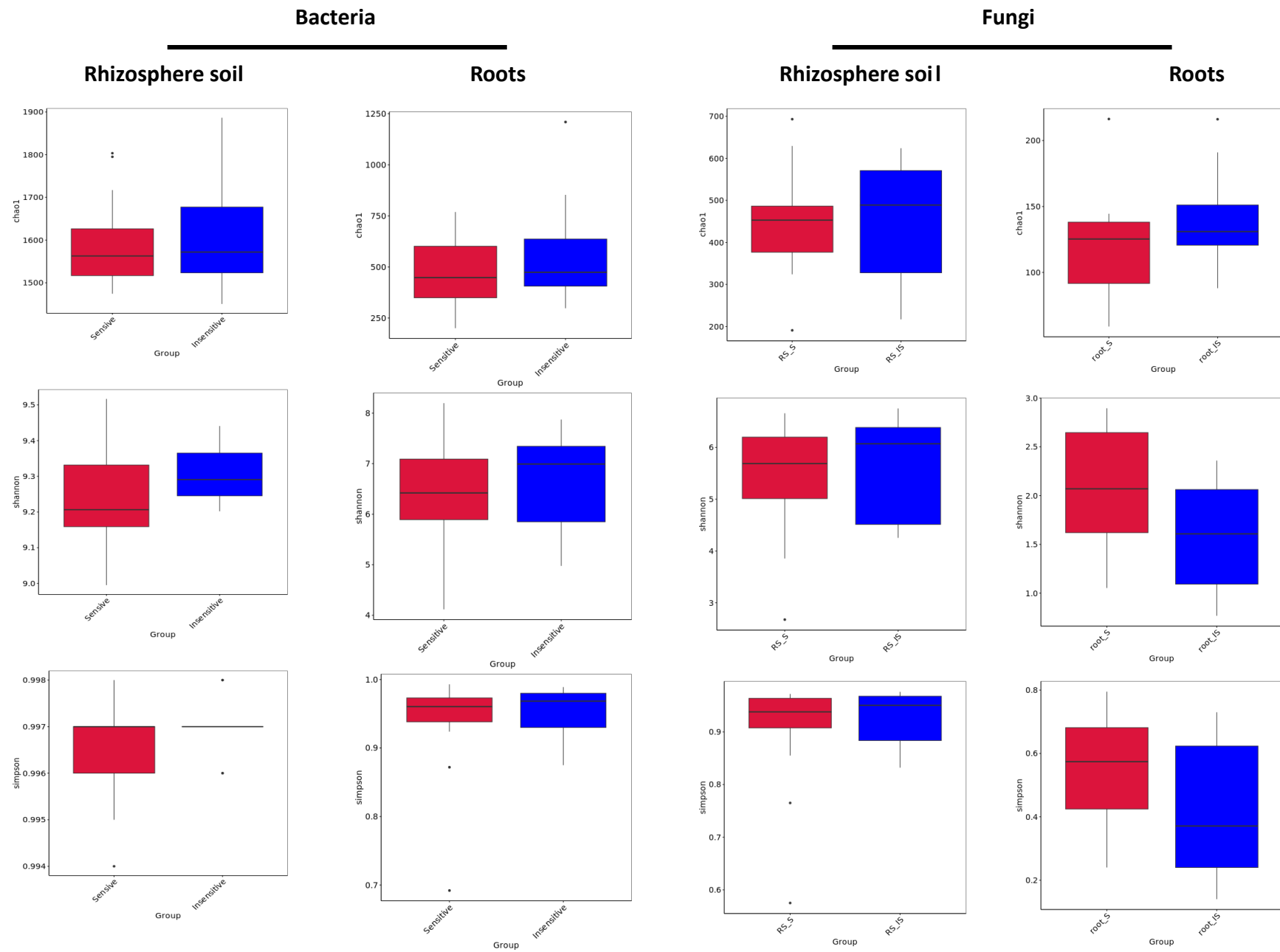


Fig. S11 Alpha diversity comparison of microbial communities in rhizosphere and root endosphere between tolerant and sensitive groups.

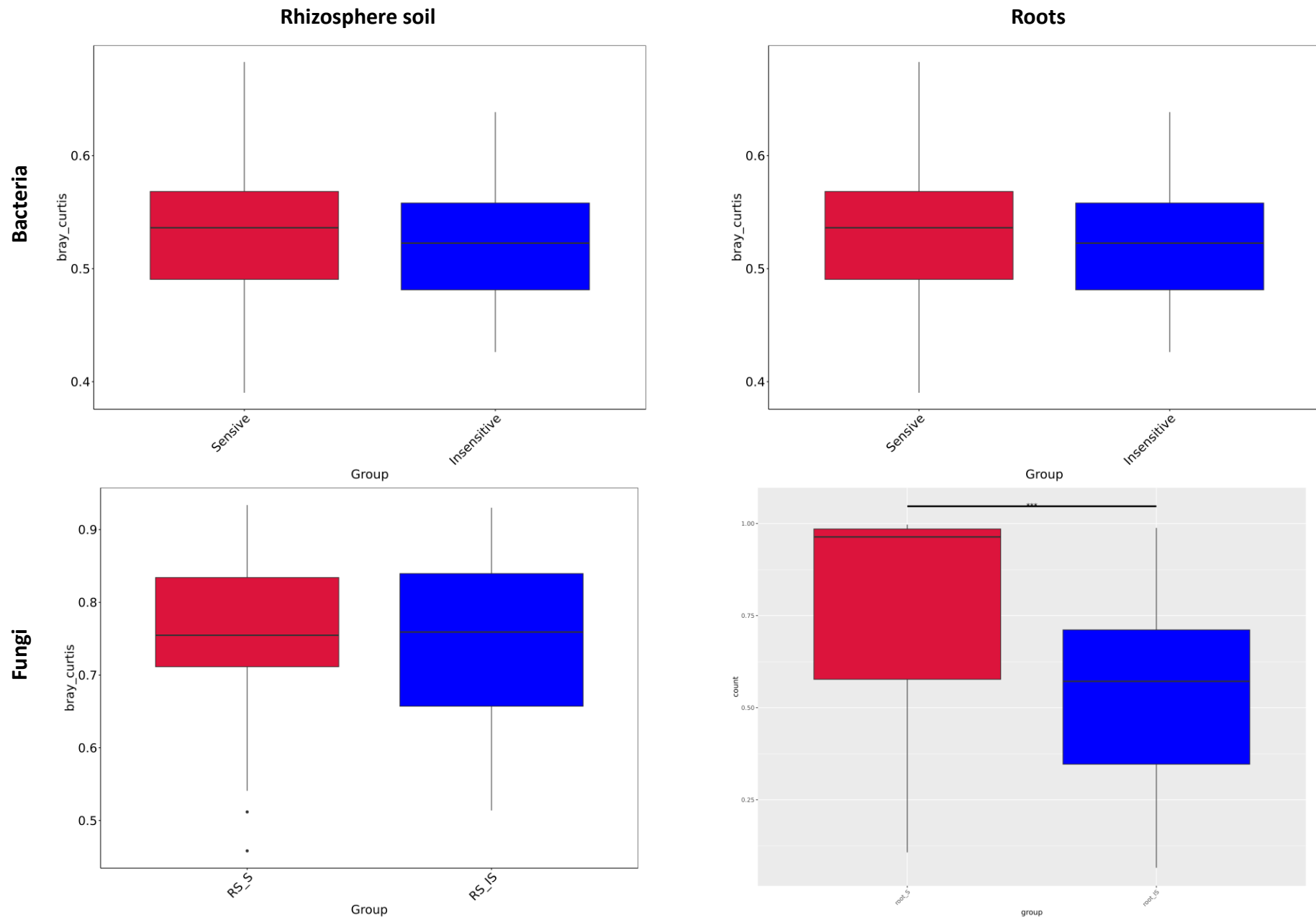


Fig. S12 Differences in beta diversity of microbial communities in rhizosphere and root endosphere between tolerant and sensitive groups.

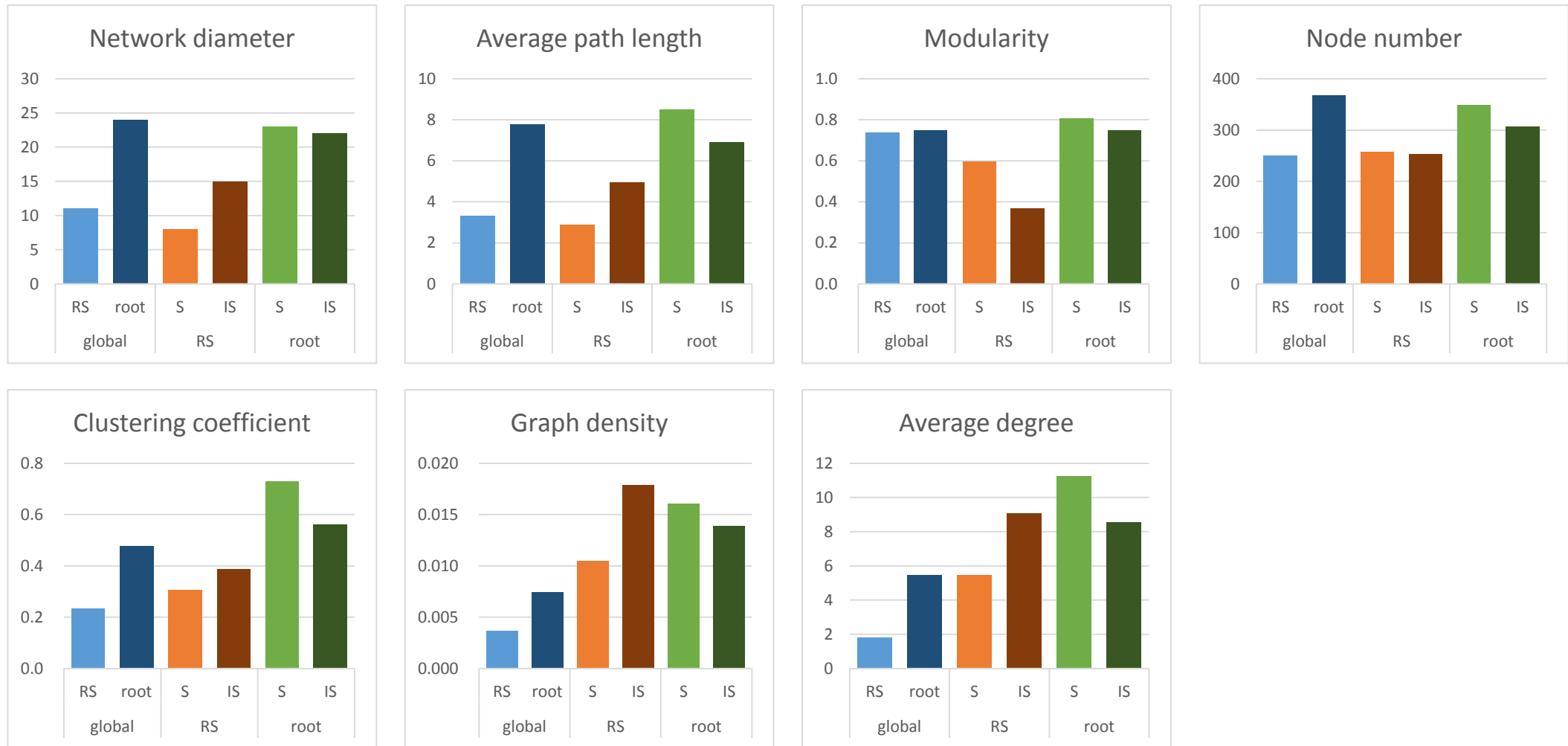


Fig. S13 Topology properties of bacterial co-occurrence networks in different soil–plant compartments.

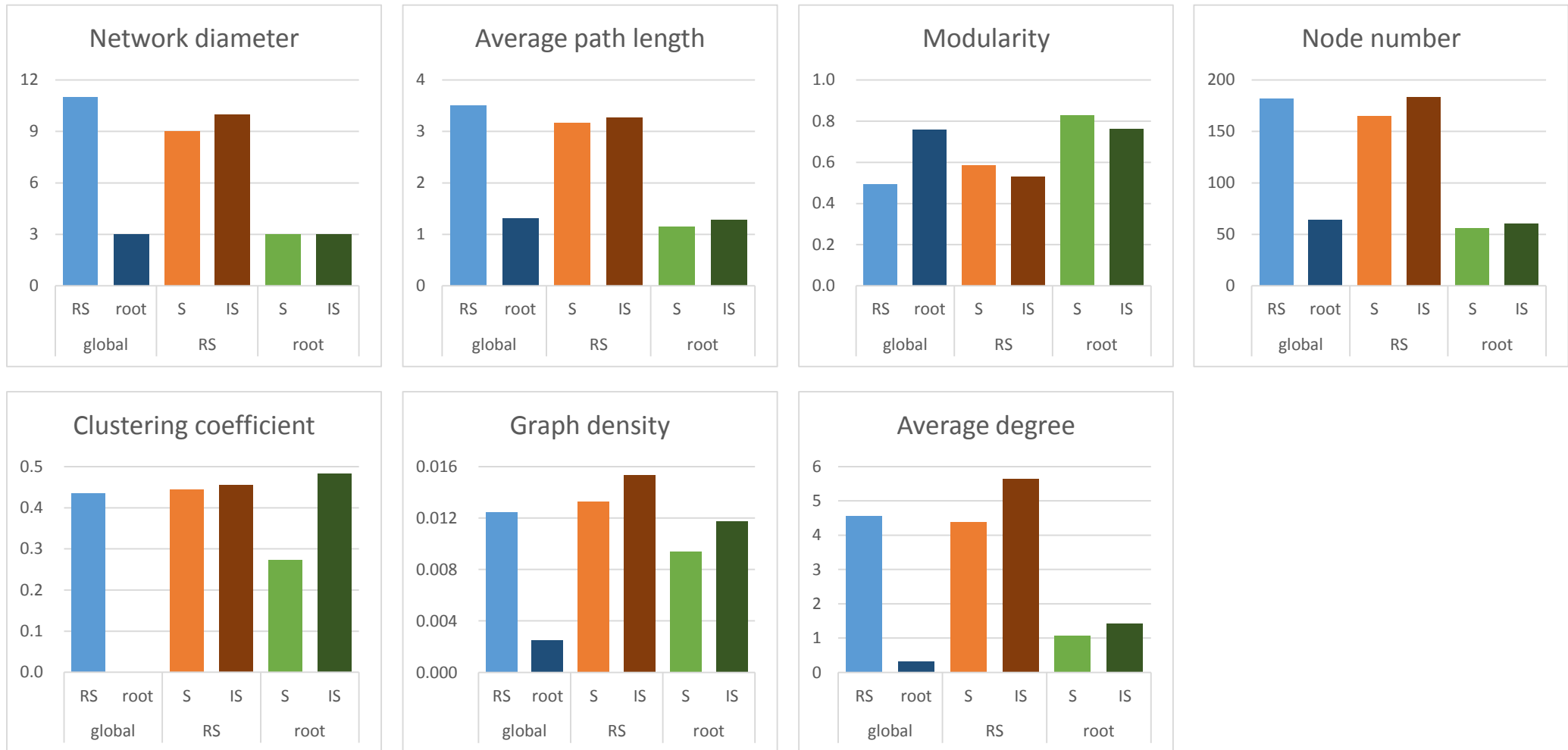


Fig. S14 Topology properties of fungal co-occurrence networks in different soil–plant compartments.