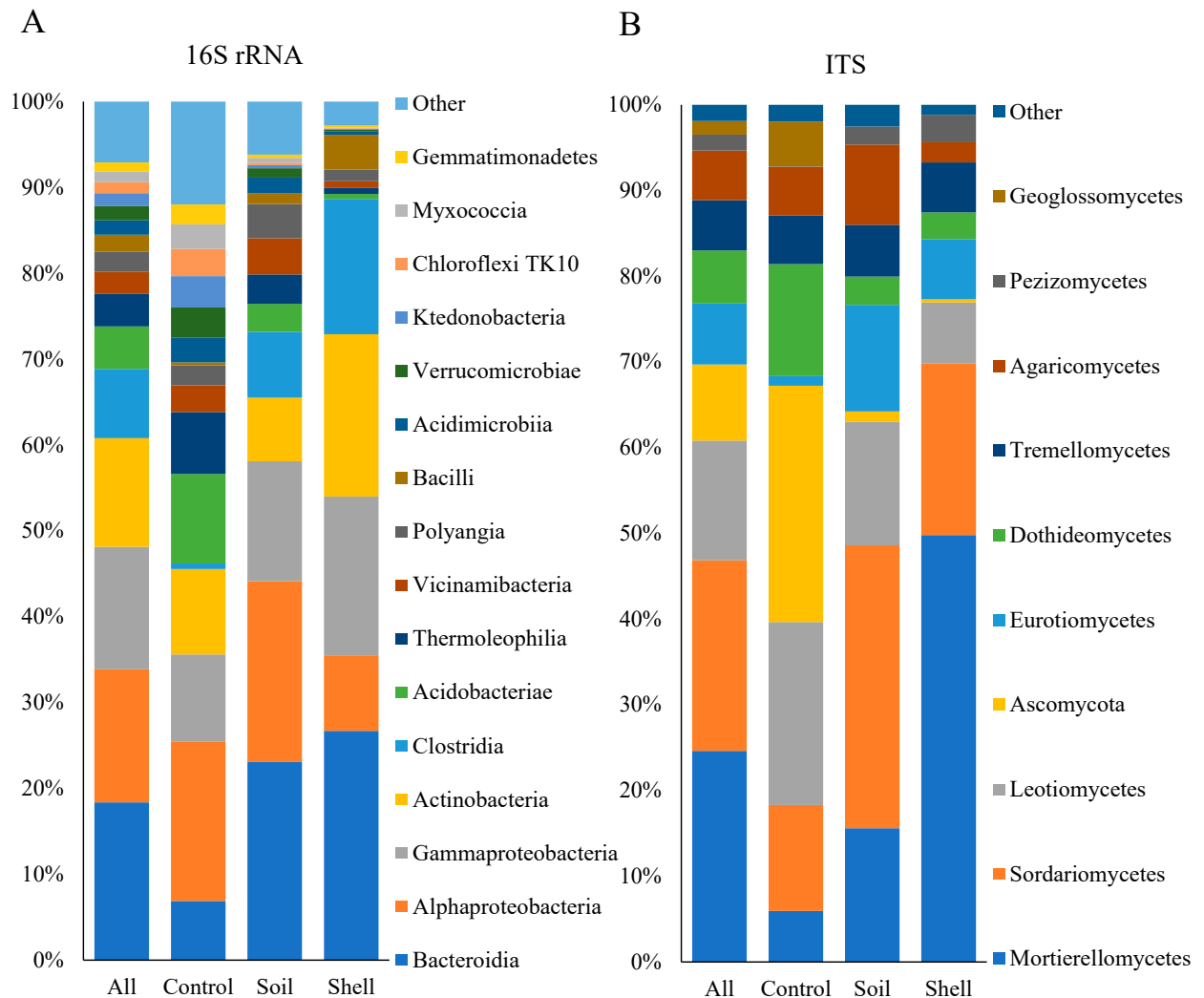
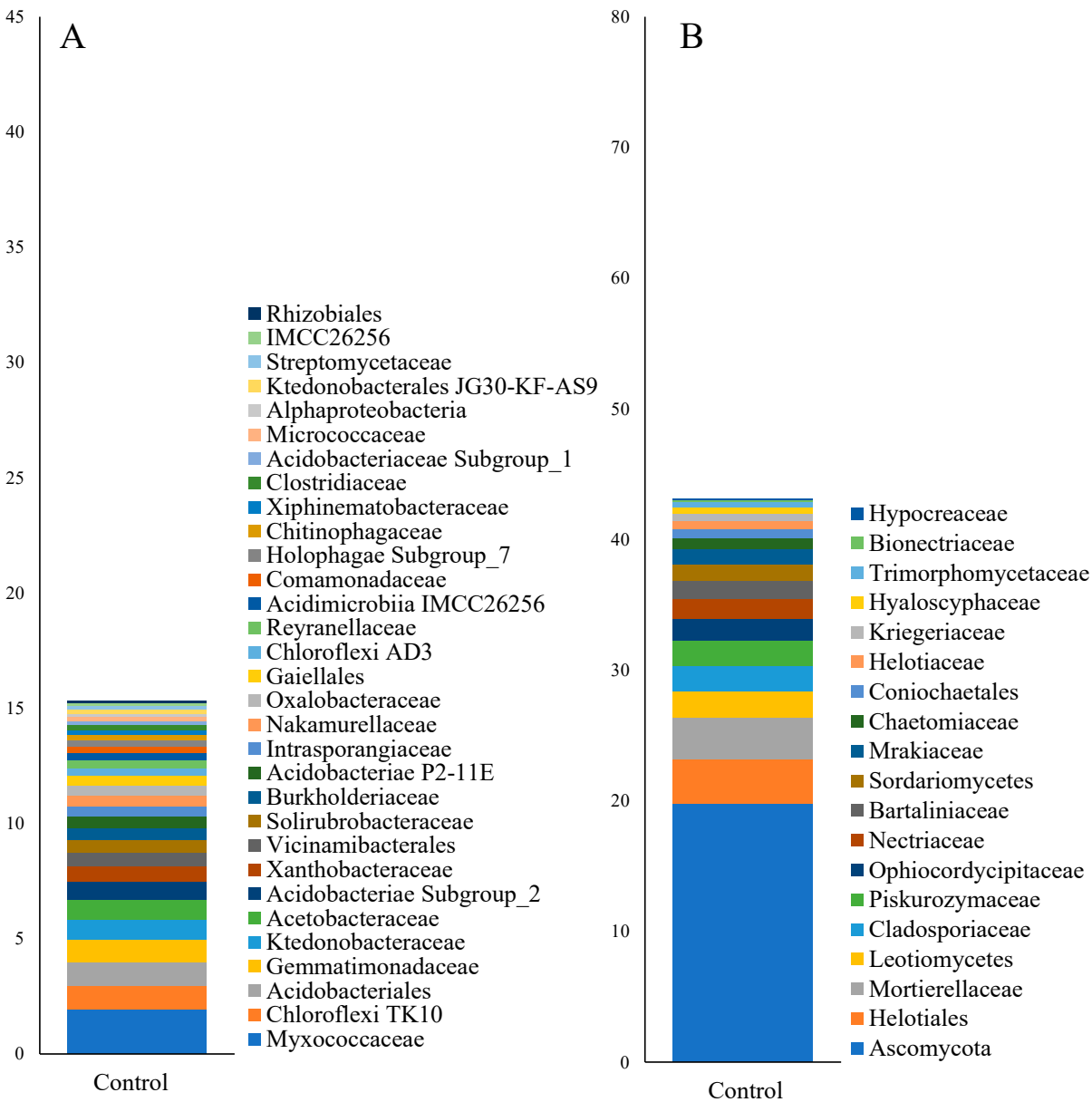


## Supplementary Figures

**Figure S1:** Microbial classes identified in the study. A, bacterial 16S rRNA; B, fungal ITS.



**Figure S2:** Microbial families identified in the core microbiomes. A, bacterial 16S rRNA; B, fungal ITS.



## Supplementary Tables

**Table S1:** Variation in sample groupings as explained by weighted UniFrac dissimilarity distances.

	16S rRNA	ITS2
<b>Control x Soil x Shell</b>	0.699***	0.663***
<b>Control x Soil</b>	0.737***	0.583***
<b>Control x Shell</b>	0.681***	0.690***
<b>Soil x Shell</b>	0.417***	0.492***

*Adonis tests were used to assess whether beta-diversity is related to sample groupings, 999 permutations, R<sup>2</sup>, \*\*\*P < 0.001.*