

## Supplementary Material

Table S1: Proportion of reads identified as chloroplast in each of the samples used for testing, without and with the application of the pPNA blocker.

	Without PNA					With PNA				
	Green tea unburied	Rooibos unburied	Green tea buried	Rooibos buried	Soil	Green tea unburied	Rooibos unburied	Green tea buried	Rooibos buried	Soil
c_Chloroplast;Other;Other;Other;Other	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d
c_Chloroplast;o_Chlorophyta;Other;Other;Other	n.d	n.d	n.d	n.d	n.d	0.1%	n.d	n.d	n.d	n.d
c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae;Other;Other	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d
c_Chloroplast;o_Chlorophyta;sf_Chlamydomonadaceae;g_Chlamydomonas;Other	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d
c_Chloroplast;o_Chlorophyta;f_Chlamydomonadaceae;g_Chlamydomonas;s_reinhardtii	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d
c_Chloroplast;o_Chlorophyta;f_Trebouxiophyceae;Other;Other	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d
c_Chloroplast;o_Chlorophyta;f_Trebouxiophyceae;g_Coccomyxa;Other	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d	n.d
c_Chloroplast;o_Stramenopiles;Other;Other;Other	n.d	n.d	n.d	n.d	2.4%	n.d	n.d	n.d	n.d	2.3%
c_Chloroplast;o_Streptophyta;Other;Other;Other	64.5%	15.4%	n.d	n.d	0.1%	2.2%	0.1%	n.d	n.d	0.1%

Table S2 Variance partitioning (PERMANOVA) of the effects of sample types, season and soil type on the prokaryote and fungal communities.

Attached file

Table\_ADONIS.xlsx

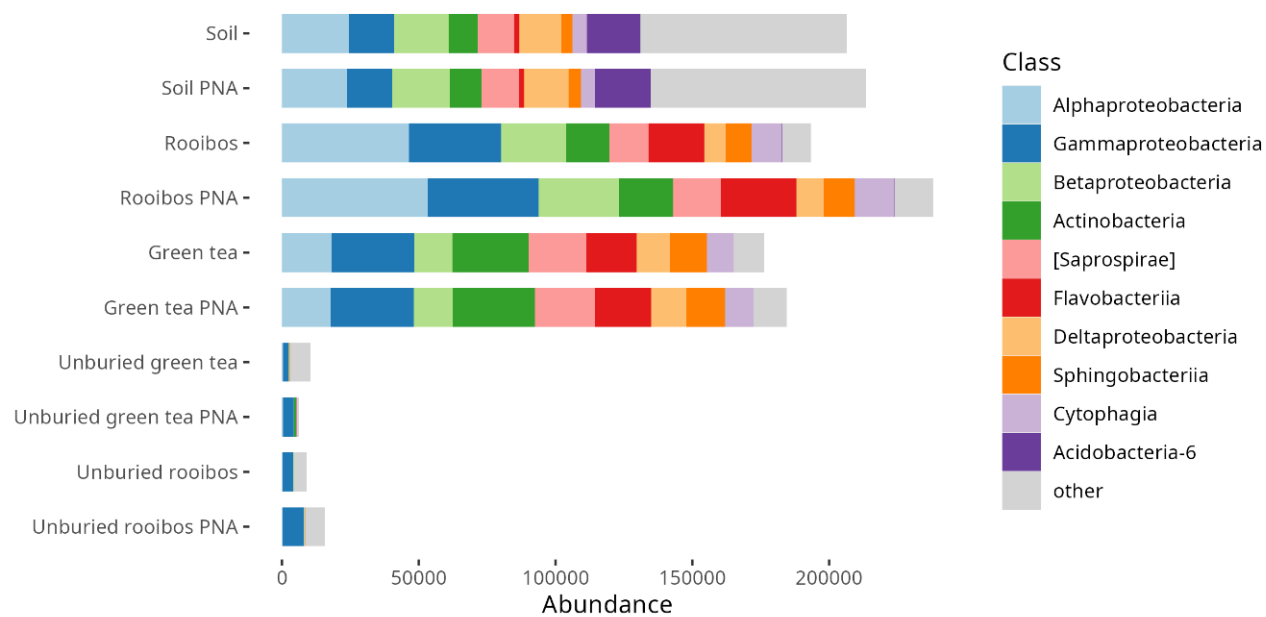


Figure S1: The bacterial community composition (after removal of chloroplast sequences) on the unburied vs buried tea material and the effect of using a chloroplast blocker (pPNA).

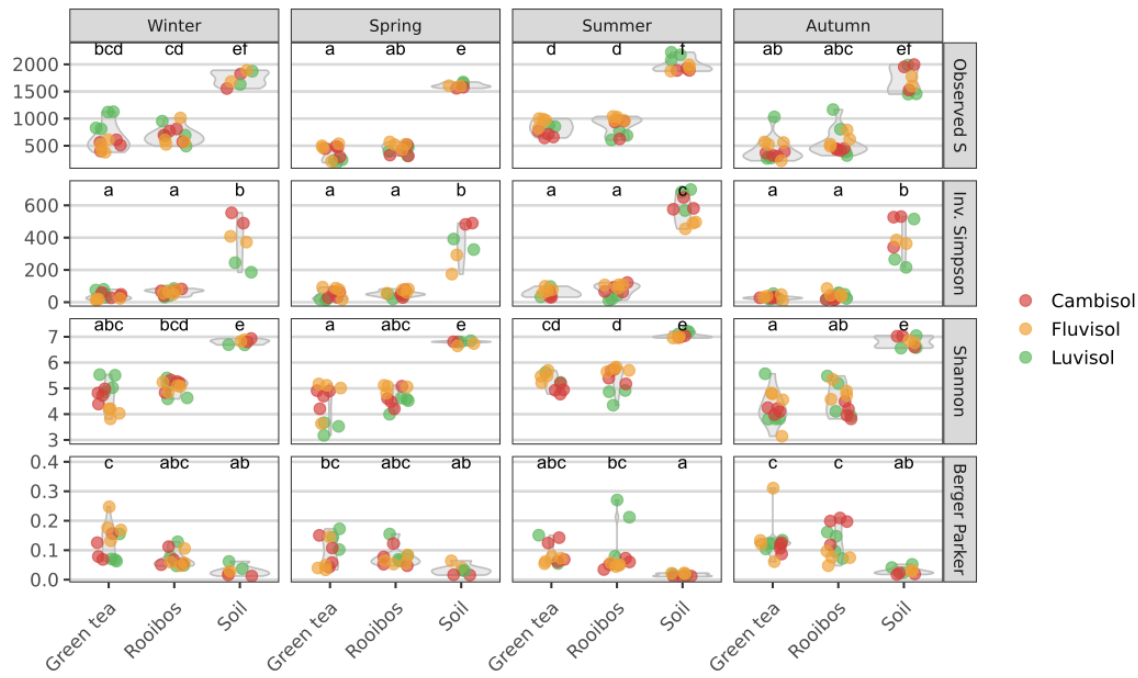
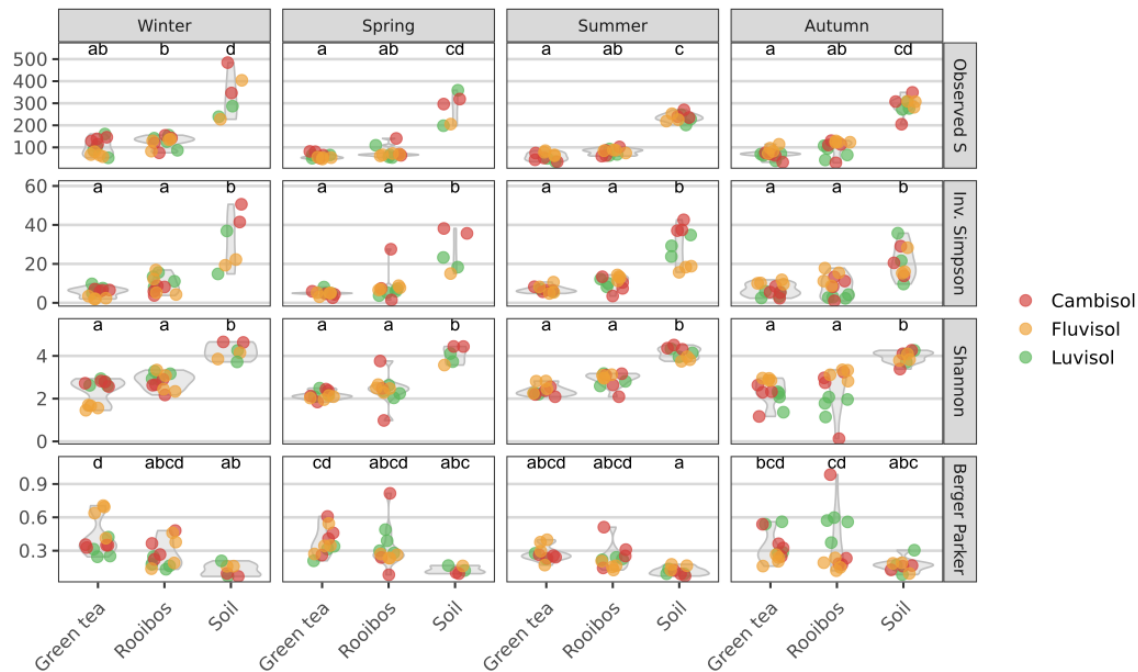
**A****B**

Figure S2: Observed richness and diversity based on partial prokaryotic ribosomal SSU genes (A) and on partial fungal inter-genic spacer region sequences (B) derived from green tea and rooibos teabags and soil. Observed S – number of observed ASVs; Inv. Simpson – estimated inverse Simpson index; Shannon – estimated Shannon index; Berger Parker – estimated Berger Parker index. Horizontal lines with asterisks denote significant differences between sample types for each site ( $p_{adj.} \leq 0.01$ ).

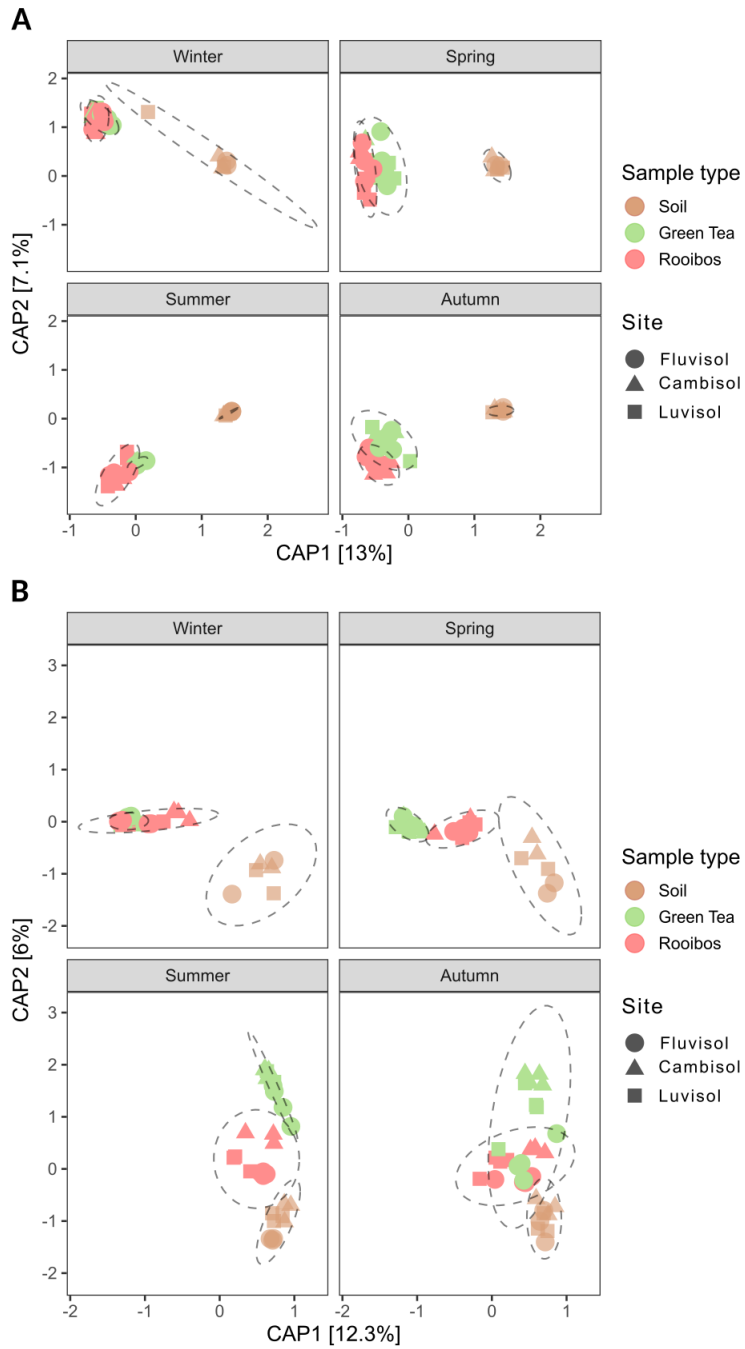


Figure S3: Principal coordinate analyses plots of prokaryotic (A) and fungal (B) community compositions based on Morisita-Horn distances of 16S rRNA gene and ITS region ASVs derived from soil, green tea and rooibos teabags. The models were contained using the formula: Distance matrix  $\sim$  Field + Sample type  $\times$  Season.

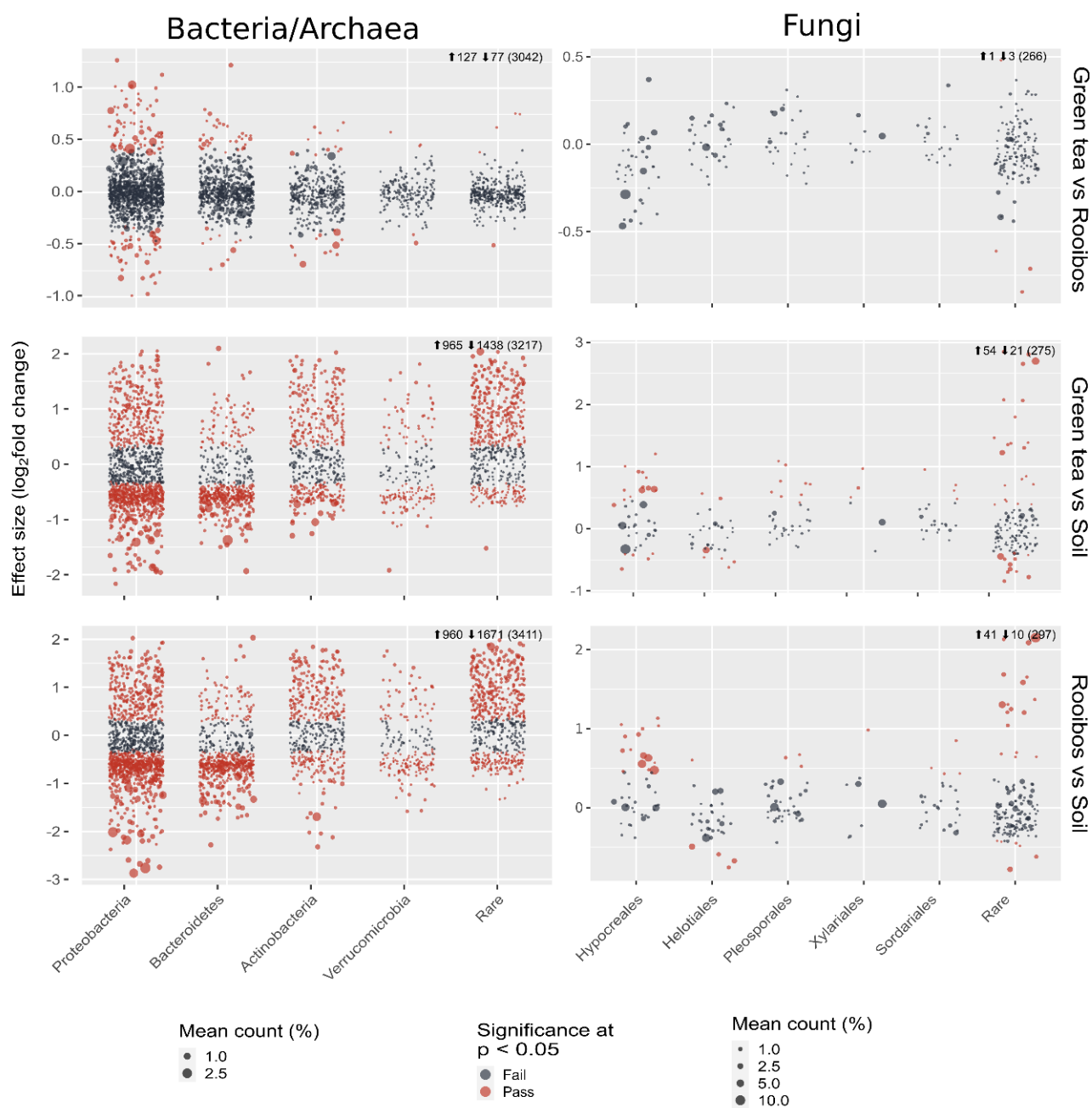


Figure S4: Differentially abundant ASVs between each sample-type pair using ALDEx2 for 16S rRNA gene (bacteria and archaea) and ITS (fungi). Each circle denotes a single ASV, and its size is its mean relative abundance across all samples in the comparison. The x-axis shows the phylum of each ASV, whereas the y axis shows the effect size in terms of the  $\log_2$  fold difference in relative abundance between each sample-type pair. Red circles are ASVs that show significant differential abundance at the  $P < 0.05$  level. Numbers next to the arrows indicate the number of significant differentially abundant ASVs that are either more abundant (up arrow) or less abundant (down arrow) in the first vs the second sample type. Numbers in brackets indicate the total number of ASVs in each pair-wise comparison.

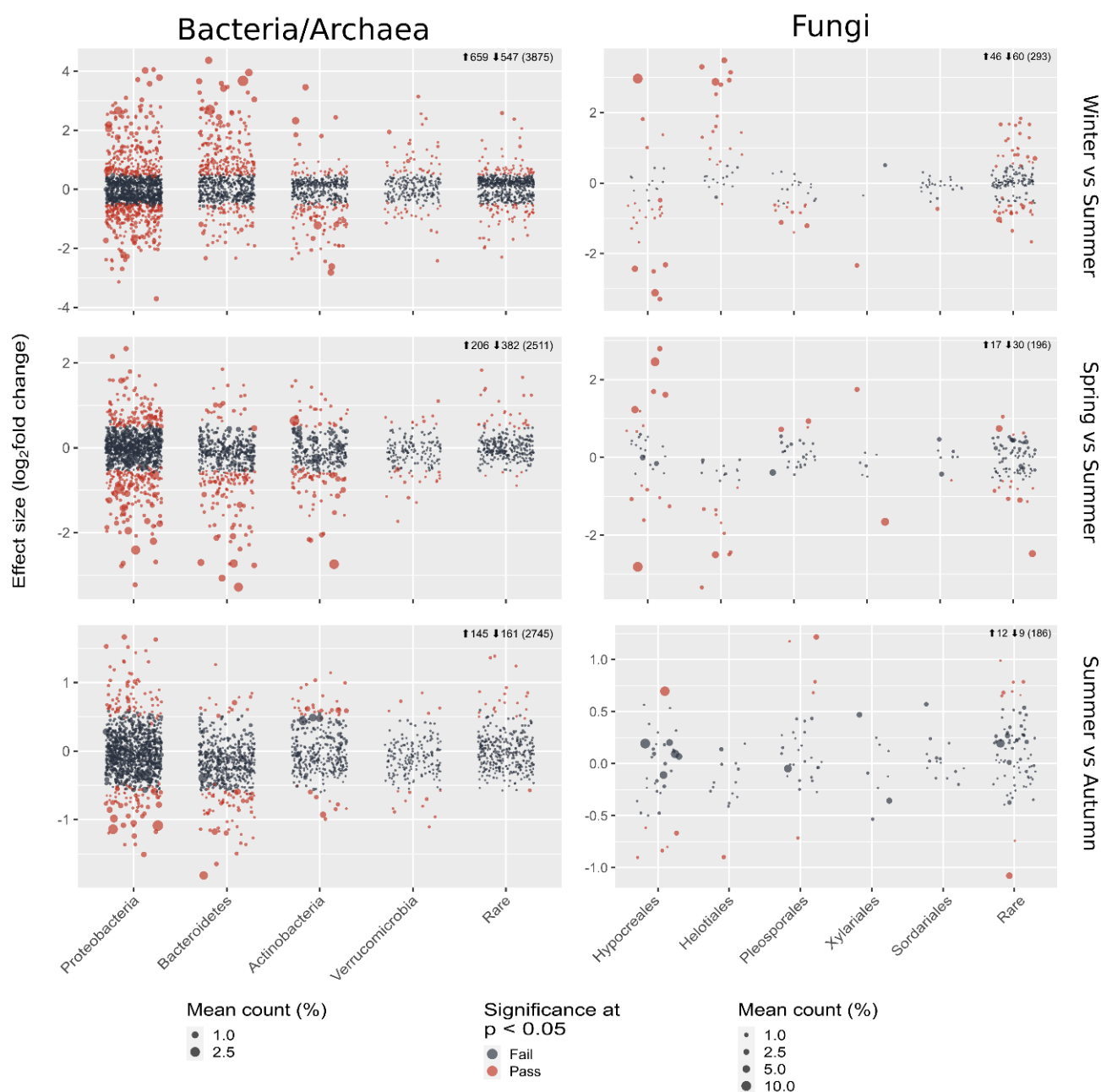


Figure S5: Differentially abundant ASVs between representative season pairs using ALDEx2 for 16S rRNA gene (bacteria and archaea) and ITS (fungi). Only comparisons between the summer and other seasons are shown. Each circle denotes a single ASV, and its size is its mean relative abundance across all samples in the comparison. The x-axis shows the phylum of each ASV, whereas the y axis shows the effect size in terms of the  $\log_2$  fold difference in relative abundance between each sample-type pair. Red circles are ASVs that show significant differential abundance at the  $P < 0.05$  level. Numbers next to the arrows indicate the number of significant differentially abundant ASVs that are either more abundant (up arrow) or less abundant (down arrow) in the first vs the second sample type. Numbers in brackets indicate the total number of ASVs in each pair-wise comparison.