

Supplementary Material

Table S1. Total precipitation and mean temperatures in the study site.

	Total precipitation (mm)	Mean temperature (°C)
Winter	121	2.2
Spring	91	12.7
Summer	165	22.5
Autumn	165	12.3

Table S2. Soil characteristics at the three study plots over one year.

Plot	Vegetation ¹	Season	pH	P	K	TOC	N _{tot}	Labile C	Pot.	min-	Sand	Silt	Clay
										(%)	(%)	(%)	(%)
Fluvisol	CC	Winter	7.17 ^{a2}	155 ^a	474 ^a	1.92 ^a	0.2 ^a	650 ^a	54.21 ^a	NA	NA	NA	NA
Fluvisol	CC	Spring	7.22	141	578	2.34	0.23	744	126.02	NA	NA	NA	NA
Fluvisol	CC	Summer	7.15	145	570.33	2.56	0.24	745.67	86.26	34.47	38.87	27.53	
Fluvisol	CC	Autumn	7.37	155.67	518.33	2.24	0.21	774.67	58.92	NA	NA	NA	
Cambisol	G	Winter	7.07 ^{ab}	203 ^a	696 ^b	2.67 ^b	0.24 ^b	776 ^b	164.95 ^a	NA	NA	NA	
Cambisol	G	Spring	7.17	191	624	2.52	0.25	774	185.23	NA	NA	NA	
Cambisol	G	Summer	7.14	195	619	2.43	0.23	715	118.04	46.53	33.13	20.2	
Cambisol	G	Autumn	7.24	188.33	561.33	2.19	0.21	706	78.71	NA	NA	NA	
Luvisol	CC	Winter	7.27 ^b	143 ^b	323 ^c	1.71 ^b	0.17 ^b	582 ^b	104.08 ^a	NA	NA	NA	
Luvisol	CC	Spring	7.39	108	282	1.65	0.16	550	107.36	NA	NA	NA	
Luvisol	CC	Summer	7.33	137	279.67	1.58	0.15	536.33	78.75	21.17	59.83	19.7	
Luvisol	CC	Autumn	7.44	136.33	329.33	1.81	0.17	613.33	92.94	NA	NA	NA	

¹ CC indicate cover crop in between the wine rows, G indicates grassland in between vineyards.

² Lowercase letters indicate significant differences in the measured chemical parameter between the plots, using all the samples (pairwise comparisons; adjusted $p \leq 0.05$),

Table S3. 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 S4. Variance partitioning (PERMANOVA) of the effects of sample types, season and soil type on the prokaryote and fungal communities.

Attached file

Table_ADONIS.xlsx

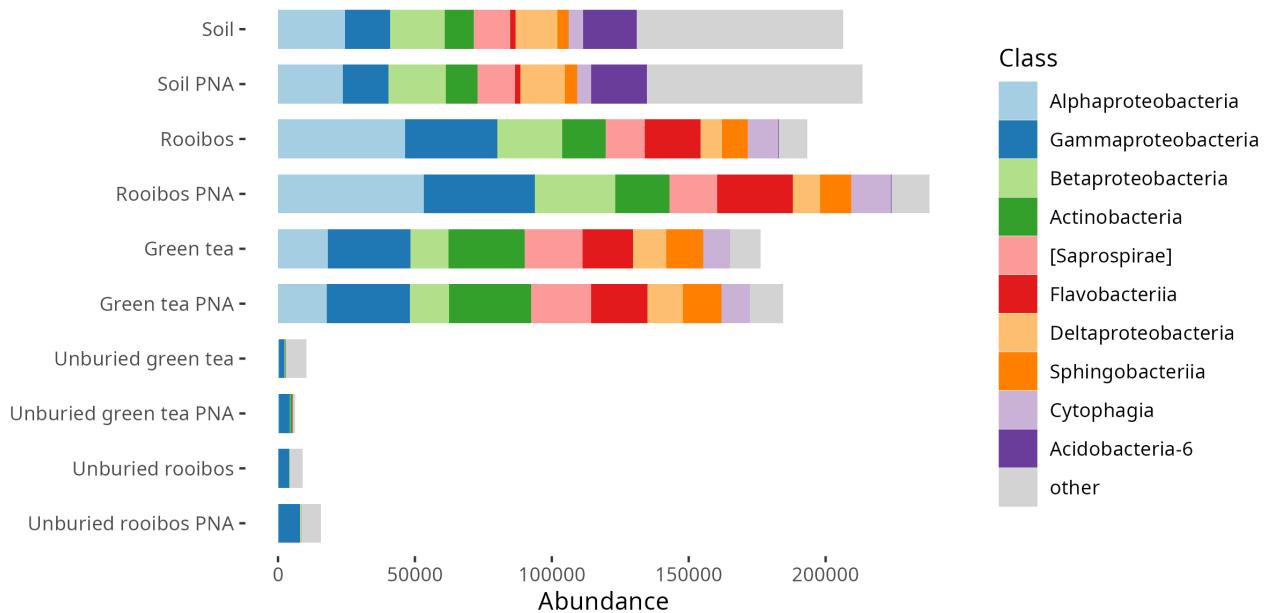


Figure S1. The bacterial community composition (after removal of chloroplast sequences) on the unburied vs buried tea material and the effect of using a chloroplast blocker (pPNA).

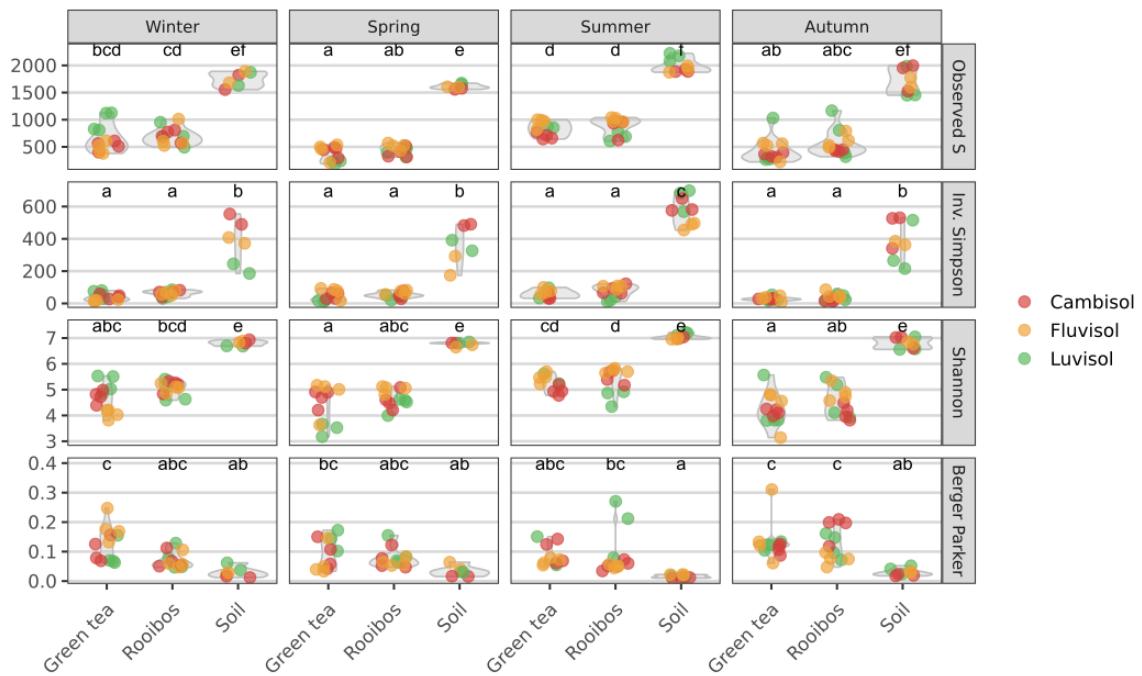
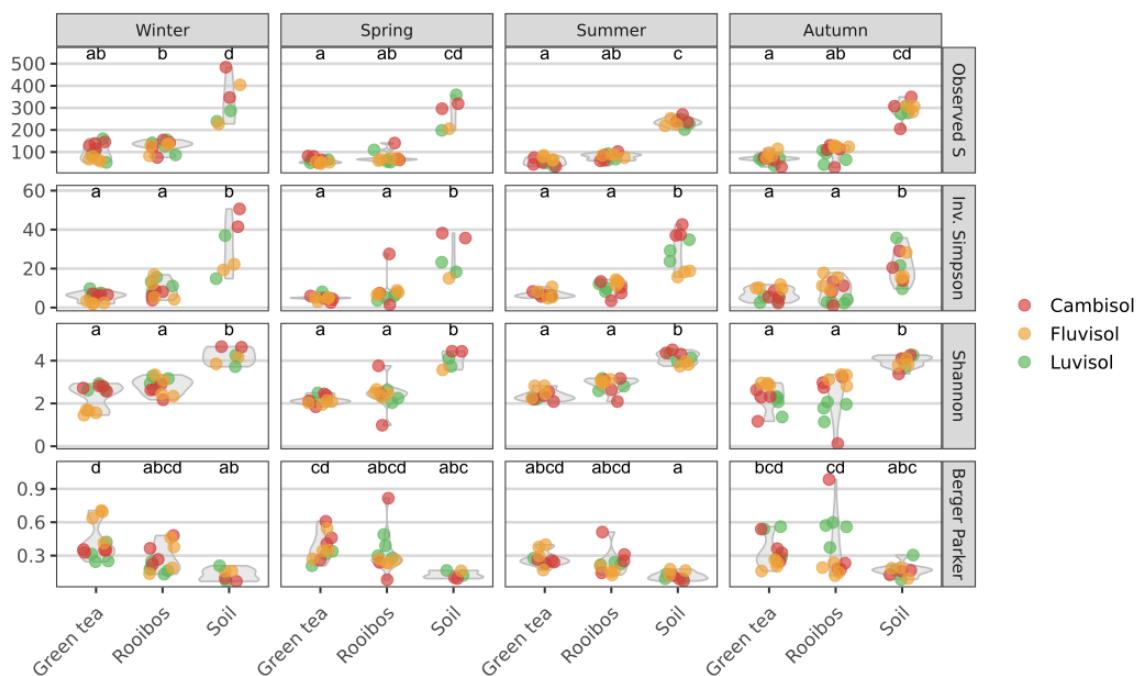
A**B**

Figure S2. Observed richness and diversity based on partial prokaryotic ribosomal SSU genes (A) and on partial fungal intergenic 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 ($p_{adj} \leq 0.01$).

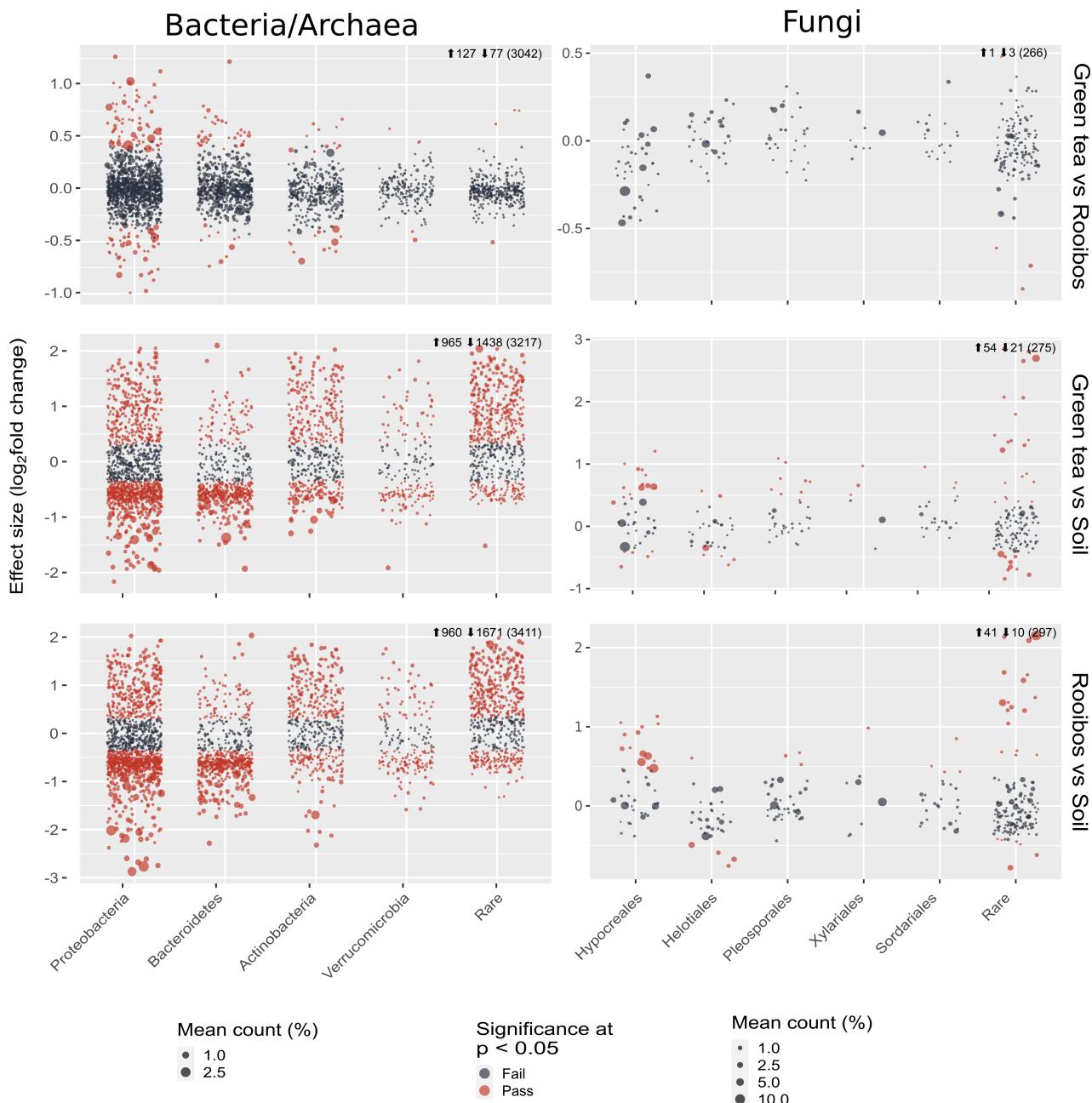


Figure S3. Differentially abundant ASVs between each sample-type pair using ALDEx2 for 16S rRNA gene (bacteria and archaea) and ITS (fungi). Each circle denotes a single ASV, and its size is its mean relative abundance across all samples in the comparison. The x-axis shows the phylum of each ASV, whereas 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.

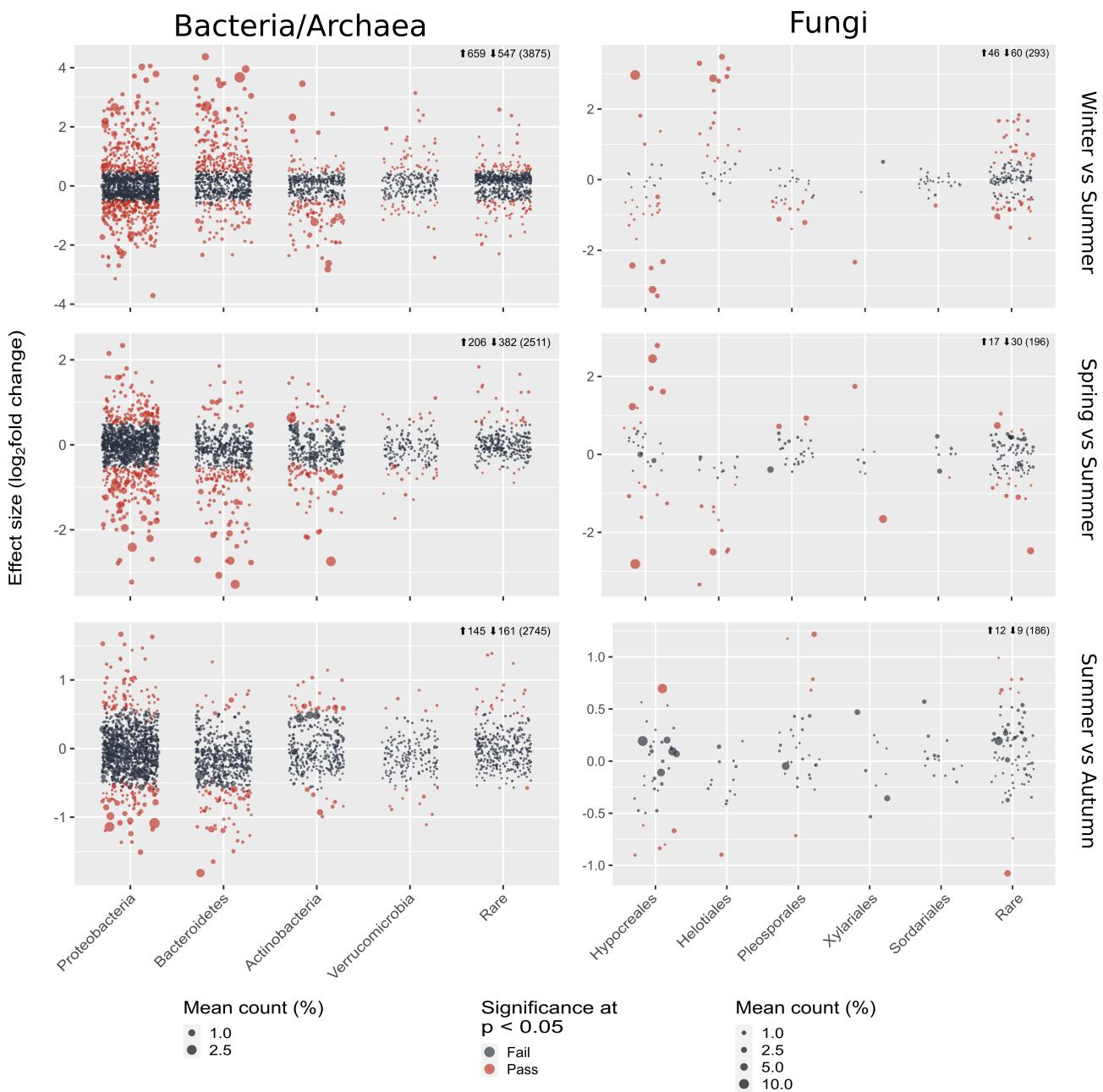


Figure S4. Differentially abundant ASVs between representative season pairs using ALDEEx2 for 16S rRNA gene (bacteria and archaea) and ITS (fungi). Only comparisons between the summer and other seasons are shown. Each circle denotes a single ASV, and its size is its mean relative abundance across all 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 log₂ 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.