Supplemental tables

Table S1*:* Primers used qPCR and amplicons sequencing. Specific overhang Illumina adapters are in italics and underlined.

Primer	Primer sequence (5'- to -3')	Target and size of the amplicon	Reference
qPCR			
515R	CCTACGGGAGGCAGCAG	Bacterial 16S rRNA gene (174 bp)	(López-Gutiérrez et al., 2004)
341F	ATTACCGCGGCTGCTGGCA		
Arch1060R	GGCCATGCACCWCCTCTC	Archaeal 16S rRNA gene (140 bp)	(Cadillo-Quiroz et al., 2006)
Arch967F	ATTGGCGGGGGAGCAC		
FR1	AICCATTCAATCGGTAIT	Fungal 18S rRNA gene (340 bp)	(Vainio and Hantula, 2000)
FF390	CGATAACGAACGAGACCT		
Amplicons sequencing			
341F	*TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG*CCTACGGGNGGCWGCAG	Bacterial 16SrRNA gene V3-V4 regions (464 bp)	(Klindworth et al., 2013)
785R	*GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG*GACTACHVGGGTATCTAATCC		
ITS1F	*TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG*CTTGGTCATTTAGAGGAAGTAA	Fungal ITS1 region (highly variable)	(Gardes and Bruns, 1993)
ITS2	*GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG*GCTGCGTTCTTCATCGATGC		(White et al., 1990)
AMV4.5Nf	*TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG*AAGCTCGTAGTTGAATTTCG	Fungal SSU 18SrRNA gene (350 bp)	(Suzuki et al., 2020)
AMDGr	*GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG*CCCAACTATCCCTATTAATCAT		

Cadillo-Quiroz, H., Bräuer, S., Yashiro, E., Sun, C., Yavitt, J., and Zinder, S. (2006). Vertical profiles of methanogenesis and methanogens in two contrasting acidic peatlands in central New York State, USA. *Environ. Microbiol.* 8, 1428–1440. doi: 10.1111/j.1462-2920.2006.01036.x.

Gardes, M., and Bruns, T. D. (1993). ITS primers with enhanced specificity for basidiomycetes - application to the identification of mycorrhizae and rusts. *Mol. Ecol.* 2, 113–118.

Klindworth, A., Pruesse, E., Schweer, T., Peplies, J., Quast, C., Horn, M., et al. (2013). Evaluation of

general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. *Nucleic Acids Res.* 41, 1–11. doi: 10.1093/nar/gks808.

López-Gutiérrez, J. C., Henry, S., Hallet, S., Martin-Laurent, F., Catroux, G., and Philippot, L. (2004). Quantification of a novel group of nitrate-reducing bacteria in the environment by real-time PCR. *J. Microbiol. Methods* 57, 399–407. doi: 10.1016/j.mimet.2004.02.009.

Suzuki, K., Takahashi, K., and Harada, N. (2020). Evaluation of primer pairs for studying arbuscular mycorrhizal fungal community compositions using a MiSeq platform. Biol. Fertil. Soils 56, 853–858.

Vainio, E. J., and Hantula, J. (2000). Direct analysis of wood-inhabiting fungi using denaturing gradient gel electrophoresis of amplified ribosomal DNA. *Mycol. Res.* 104, 927–936. doi: 10.1017/S0953756200002471.

White, T. J., Bruns, T. D., Lee, S. B., and Taylor, J. W. (1990). "Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics," in *PCR protocols: a guide to methods and applications*, eds. M. A. Innis, D. H. Gelfand, J. J. Sninsky, and T. J. White (United States: Academic Press, Inc.), 315–322.

Table S2: Percentage of growth promotion or inhibition in *Lepidium sativum* stem and root parameters compared to water-treated control. Results of one-way ANOVA using inoculum combination as factor are presented (n=15).

Combination	Stem mass $F(95,192) = 1.81$ $P < 0.001$	Root mass $F(95,192) = 3.29$ $P < 0.001$	Stem length $F(95,1324) = 3.79$ $P < 0.001$	Root length $F(95,192) = 4.15$ $P < 0.001$
A	37	31	7	22
B	28	30	-14	28
C	47	76	2	40
D	31	51	0	18
E	9	11	6	21
F	49	32	11	29
G	33	4	11	18
H	5	-16	-10	3
A×B	34	33	-11	24
A×C	77	124	39	47
A×D	30	29	18	27
A×E	37	36	4	-3
A×F	32	58	16	28
A×G	34	39	6	25
A×H	38	58	21	45
B×C	10	20	-12	9
B×D	70	69	7	42
B×E	40	19	9	27
B×F	44	44	41	30
B×G	15	10	-13	16
B×H	31	21	-17	13
C×D	30	31	-14	23
C×E	26	21	1	30
C×F	28	15	11	35
C×G	44	52	28	9
C×H	46	52	26	22
D×E	24	31	7	26
D×F	42	15	-12	0
D×G	26	45	-8	16
D×H	36	16	20	27
E×F	17	13	14	23
E×G	24	15	8	38
E×H	31	47	15	19
F×G	14	24	4	18
F×H	-14	-21	-18	16
G×H	35	38	-3	34
A×B×C	65	31	28	52
A×B×D	40	23	15	53
A×B×E	62	20	15	68
A×B×F	63	23	6	43
A×B×G	43	15	15	42

A×B×H	72	55	40	77
B×C×D	38	34	0	38
B×C×E	33	2	8	46
B×C×F	69	45	24	60
B×C×G	50	27	17	58
B×C×H	39	25	13	39
B×D×E	71	63	60	66
C×D×E	74	75	63	72
C×D×F	78	31	30	59
C×D×G	54	39	25	42
C×D×H	37	2	19	50
C×E×F	8	-8	-20	18
C×E×G	57	35	37	62
D×E×F	43	14	-3	47
D×E×G	51	15	34	77
D×E×H	98	64	25	71
D×F×G	32	24	0	38
D×F×H	42	23	10	37
D×G×H	31	-14	5	58
E×F×G	60	29	35	67
E×F×H	-3	-35	-28	19
E×G×H	42	5	-1	49
F×G×H	24	-2	21	21
A×C×D	17	-12	-4	20
A×C×E	21	-3	-3	17
A×C×F	28	6	-12	21
A×C×G	16	-8	13	17
A×C×H	15	-25	-12	23
A×D×E	1	-25	-21	0
A×D×F	13	-24	-37	12
A×D×G	24	1	-11	25
A×D×H	26	6	25	31
A×E×F	7	-1	-4	20
A×E×G	6	-19	-6	-6
A×E×H	11	-8	1	22
A×F×G	8	-9	3	27
A×F×H	14	-26	-7	34
A×G×H	32	23	7	31
B×D×F	10	2	-23	9
B×D×G	-10	-38	-38	-2
B×D×H	0	18	6	31
B×E×F	15	4	-19	10
B×E×G	2	-22	-39	0
B×E×H	25	14	-12	35
B×F×G	25	-13	-17	13
B×F×H	21	-19	-20	42

B×G×H	16	-9	12	27
C×E×H	28	-2	-5	18
C×F×G	32	3	1	29
C×F×H	21	8	-33	-1
C×G×H	8	17	-25	40
Mix	37	31	7	22

Table S3: Percentage of growth promotion or inhibition in 1103P plantlets shoot and root parameters compared to water-treated control. Results of one-way ANOVA or Kruskal-Wallis using inoculum combination as factor are presented (n=15).

	Leaves and stem mass $\chi^2(37) = 106$, $P < 0.001$	Root mass $\chi^2(37) = 62$, $P = 0.006$	Stem length $\chi^2(37) = 45$, $P = 0.160$	Total petiole length $\chi^2(37) = 53$, $P = 0.040$	Secondary root length $\chi^2(37) = 67$, $P = 0.002$	Number of secondary roots $\chi^2(37) = 41$, $P = 0.299$	Primary root length $\chi^2(37) = 168$, $P < 0.001$
A	-22	-2	-9	6	46	188	-27
B	-3	7	4	9	-5	94	5
C	-26	22	-15	-18	69	150	13
D	-33	49	-27	-14	12	88	26
E	-20	36	-17	6	59	212	-10
F	-24	31	-13	0	63	97	33
G	-4	26	-12	-9	63	153	-7
H	-19	51	-4	-6	-18	6	25
A×B	0	54	8	23	228	365	20
B×C	-14	18	-2	0	75	106	6
C×D	-17	44	0	-9	28	141	26
D×E	-7	29	3	3	117	124	8
E×F	-10	11	-7	-5	-31	24	4
F×G	-24	-7	-16	-19	-52	29	-13
G×H	-35	29	-23	-15	-30	128	2
A×C	24	41	19	20	135	171	75
B×D	18	-24	0	-21	-55	-29	-48
C×E	20	-6	3	-12	-37	-17	-44
D×F	52	43	10	1	82	83	6
E×G	13	2	-4	-27	-26	26	-38
F×H	41	36	8	-20	68	51	-34
A×D	44	10	1	3	102	93	-12
B×E	51	41	8	-5	45	47	-28
D×G	17	-3	-5	-22	24	61	-37
E×H	16	24	-3	-25	33	83	-39
A×E	37	-4	8	-10	-12	-51	-36
C×F	22	-3	6	-16	23	-18	-22
B×F	17	16	0	-18	-21	11	-24
C×G	40	66	5	-8	31	226	-9
D×H	27	19	-1	-1	16	-19	-4
A×F	38	16	8	2	29	-2	-32
B×G	33	5	1	-12	3	22	-41
C×H	3	36	-9	-23	30	19	22
A×G	19	61	-6	-17	41	40	-38
B×H	15	-6	2	-16	-8	-42	-53
A×H	23	24	-5	-11	60	11	-18

Table S4: Phenotypic measurements of the aerial and root systems of grapevines grown in the greenhouse experiment (n = 10). Different letters indicate statistically significant differences between groups ($P < 0.05$).

		Leaves number	Foliar surface (cm^2)	Aerial biomass (g)	Branch diameter (cm)	Dry root biomass (g)	Dry trunk biomass (g)
After 2 months	Untreated	22.7 ± 4 a	623 ± 137 a	6.1 ± 2 a	1.1 ± 0.2 a	5.1 ± 1.8 a	27.6 ± 6.9 a
	Myc+Bac	24.8 ± 4.3 a	699 ± 114 a	6.6 ± 1.4 a	1.1 ± 0.2 a	4 ± 0.8 a	25.6 ± 6.3 a
	Myc	22.9 ± 5.9 a	743 ± 198 a	6.8 ± 1.8 a	1.2 ± 0.2 a	4.8 ± 1.1 a	30.3 ± 6.5 a
	Bac	25.1 ± 5.3 a	747 ± 132 a	6.4 ± 1.4 a	1.1 ± 0.2 a	3.9 ± 1.1 a	23.3 ± 6.3 a
After 5 months	Untreated	27.3 ± 3.9 a	434 ± 80 a	12.2 ± 4 a	3.2 ± 0.2 **a**	11.3 ± 2.5 **ab**	32 ± 8 a
	Myc+Bac	28 ± 4.7 a	444 ± 159 a	11.9 ± 3.5 a	1.3 ± 0.3 **b**	14.2 ± 5.1 **b**	35.5 ± 12.3 a
	Myc	29.1 ± 4.4 a	441 ± 79 a	12.3 ± 2.4 a	1.5 ± 0.4 **b**	10.9 ± 2.5 **a**	36.4 ± 9.4 a
	Bac	27.4 ± 5.9 a	585 ± 554 a	10.8 ± 2.2 a	3.6 ± 0.5 **a**	11.2 ± 1.9 **a**	31.1 ± 9.3 a

Supplemental figures

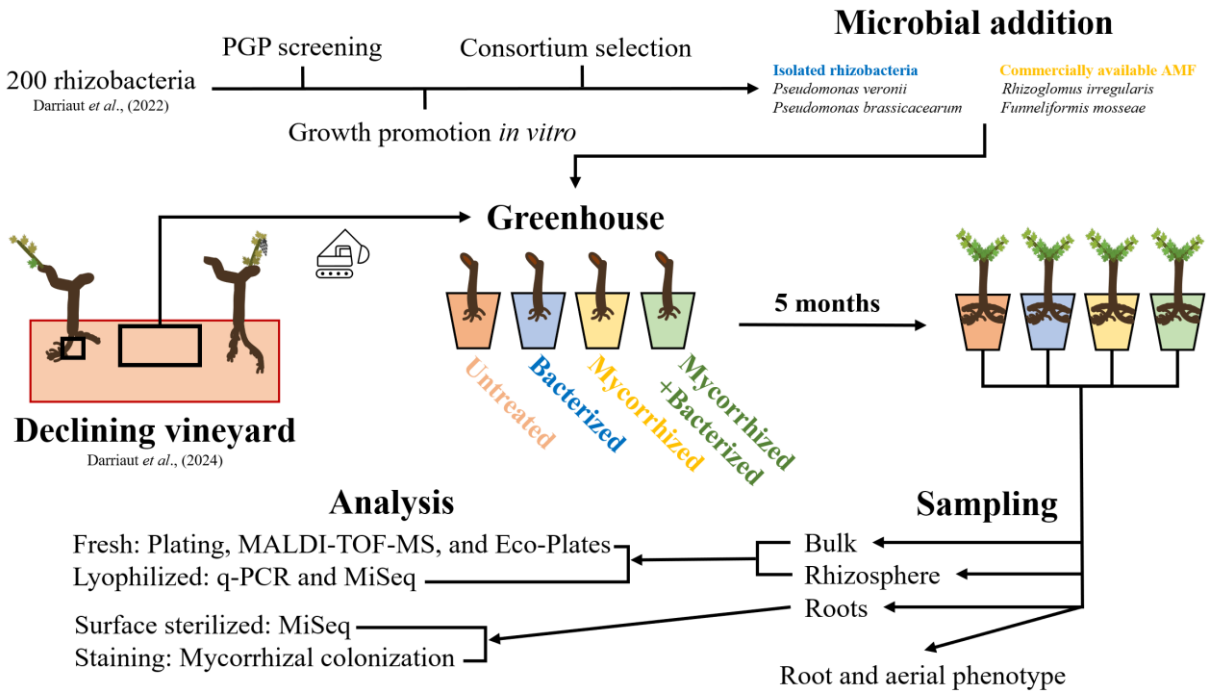

Figure S1: Schematic overview of the experimental design carried out, from the vineyard soil excavation and selection of the bacterial treatment used to the greenhouse setup. Soil from declining vineyard studied in Darriaut *et al.* (2024) was transplanted in April 2021 to start the greenhouse experiment. Grafted vines were planted in the pots with the soil under different microbial treatment: bacterized (i.e., root inoculated with rhizobacteria isolates *P. veronii* and *P. brassicacearum*, mycorrhized (*i.e.*, root inoculated with commercially available arbuscular mycorrhizal fungi), and both mycorrhized and bacterized treatments. After 5 months of growth, grapevines were phenotyped (n = 10), and samples of roots, rhizosphere and bulk soils were harvested as described in the methods (n = 3 pools of 3 random subsamples × 4 treatments).

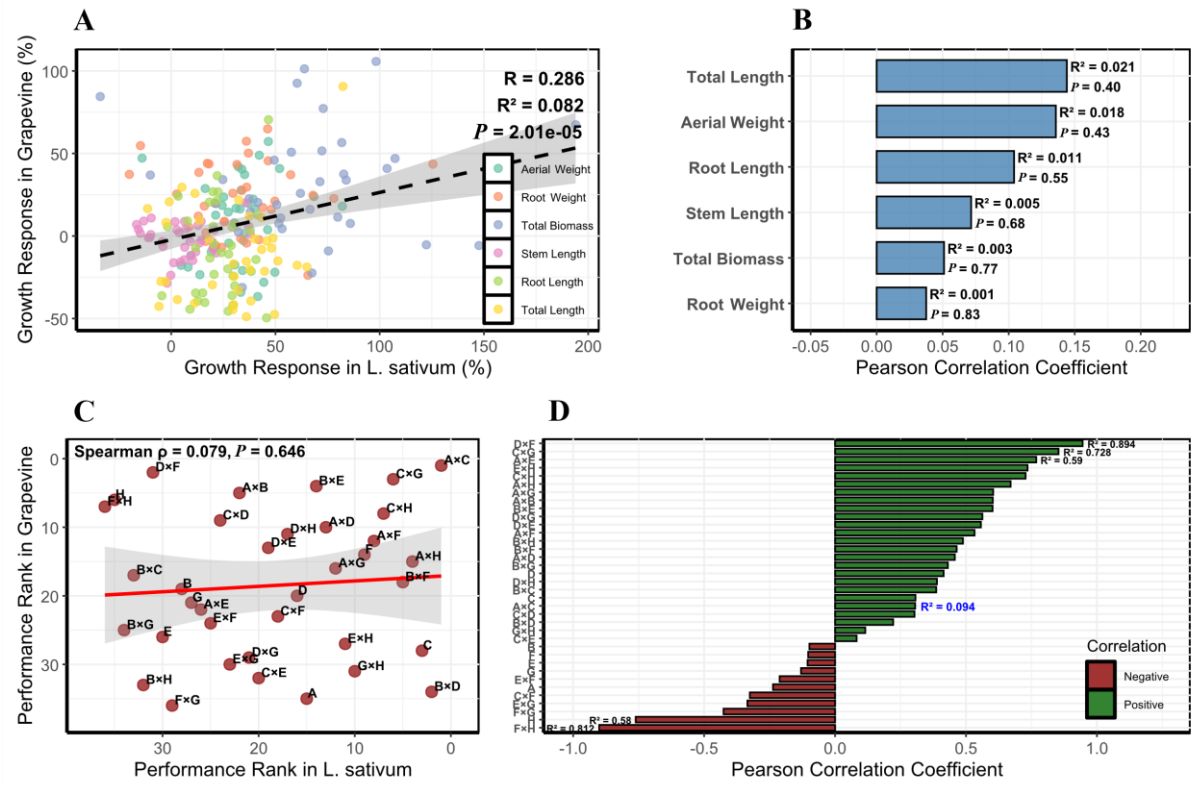

Figure S2: Cross-species correlation analysis between L. sativum and grapevine growth responses to microbial combinations. **(A)** Overall correlation across all variables showing individual data points colored by measured variable (aerial fresh weight, root fresh weight, root length, stem length, total biomass, total length) with linear regression line and 95% confidence interval. Statistical parameters: Pearson correlation coefficient (R), coefficient of determination (R^2), and p-value are displayed. **(B)** Variable-specific correlation coefficients for each growth parameter between the two plant species, with R^2 values and p-values shown for each variable. **(C)** Performance ranking correlation between species, where each point represents a microbial combination labeled with treatment codes (A×B, A×C, etc.). Lower ranks indicate better performance. Spearman rank correlation (ρ) and significance are reported. **(D)** Individual combination correlation analysis showing Pearson correlation coefficients for each microbial treatment when comparing all six growth variables between species. Positive correlations (green) indicate consistent effects across species, while negative correlations (red) suggest species-specific responses. Top combinations are labeled with R^2 values. Data represent means from biological replicates (n=5 per treatment) with treatments including single inoculations (A, B, C, etc.) and dual combinations (A×B, A×C, etc.) compared to uninoculated controls.

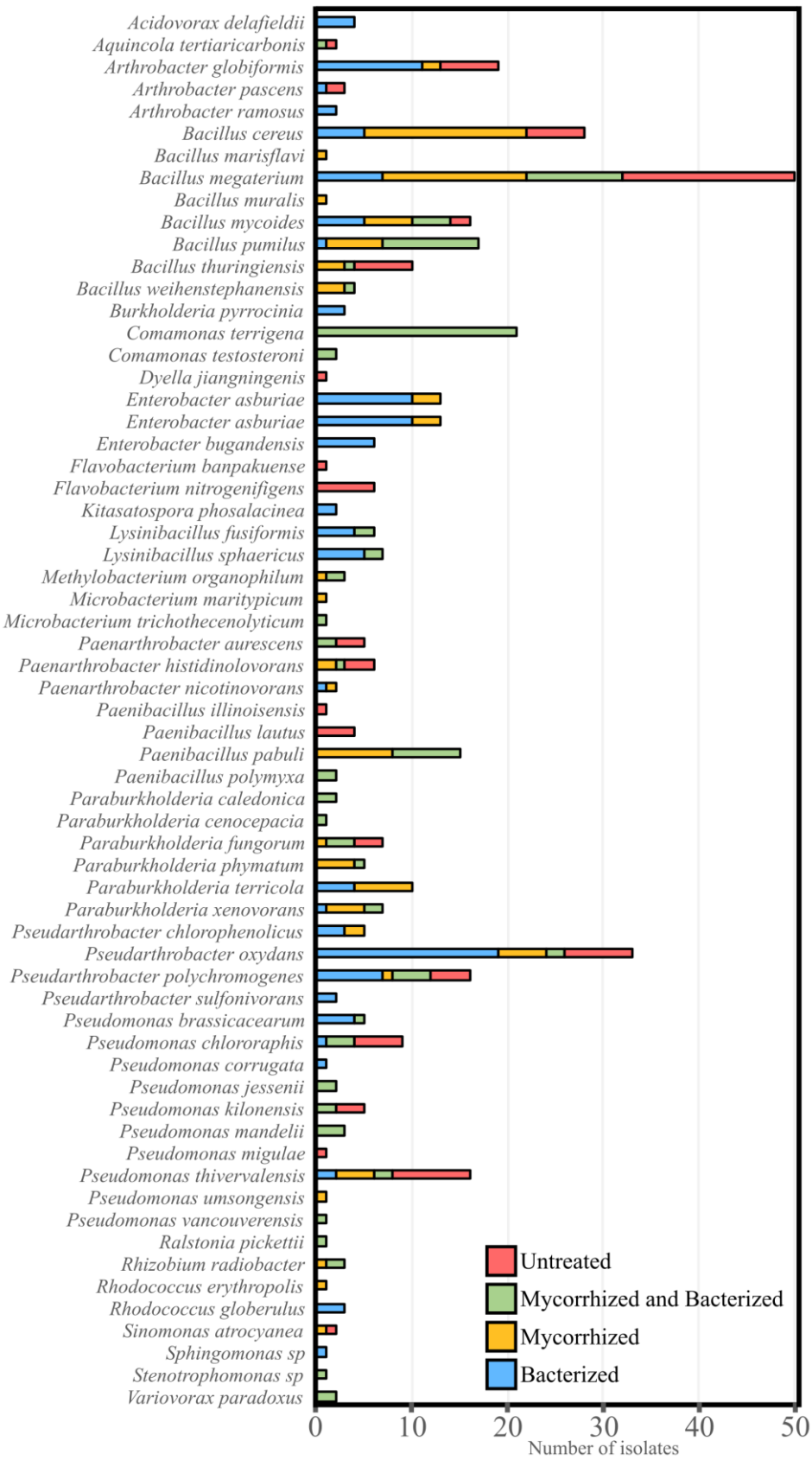

Figure S3: Rhizobacterial isolates identified at the species level using MALDI-TOF MS technology amongst the four conditions: untreated, mycorrhized, bacterized, both mycorrhized and bacterized (n = 50).

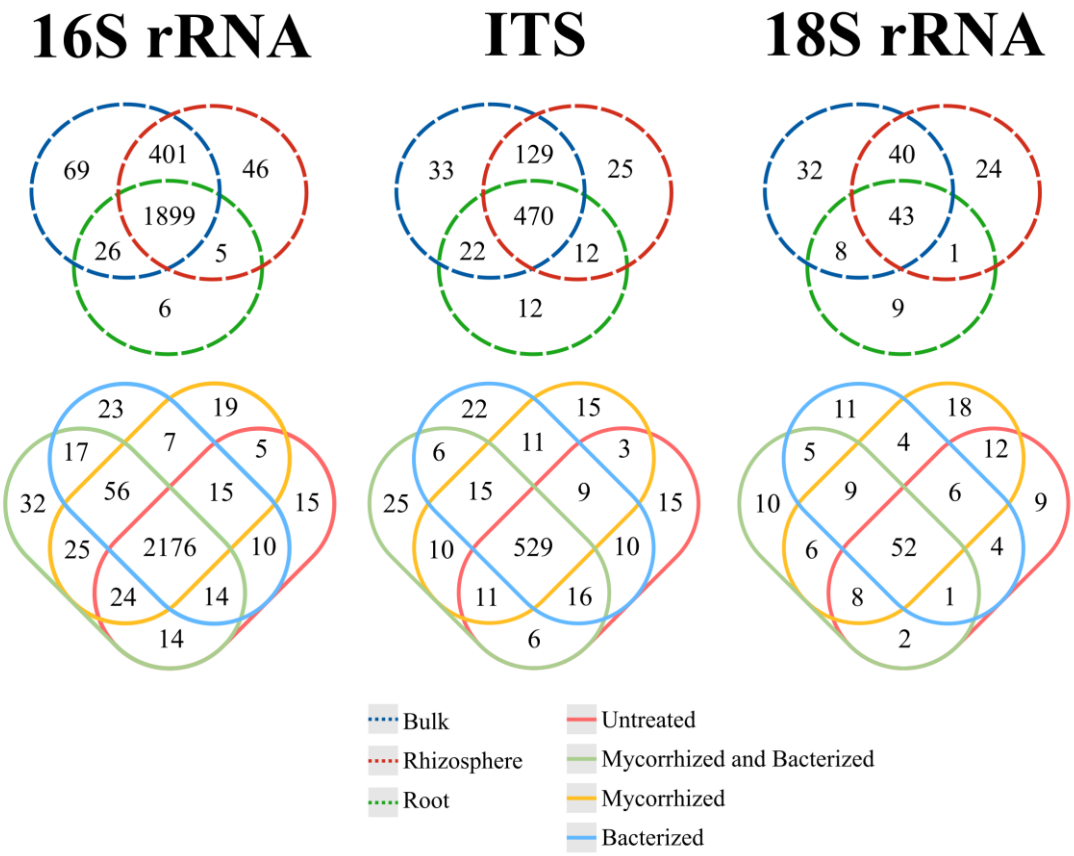

Figure S4: Venn diagrams presenting the shared OTUs between the compartments represented with dashed line: root, rhizosphere and bulk soil, and the treatment represented with solid line: untreated, mycorrhized, bacterized, and both mycorrhized and bacterized (n = 3 pools of 3 subsamples × 4 treatments).

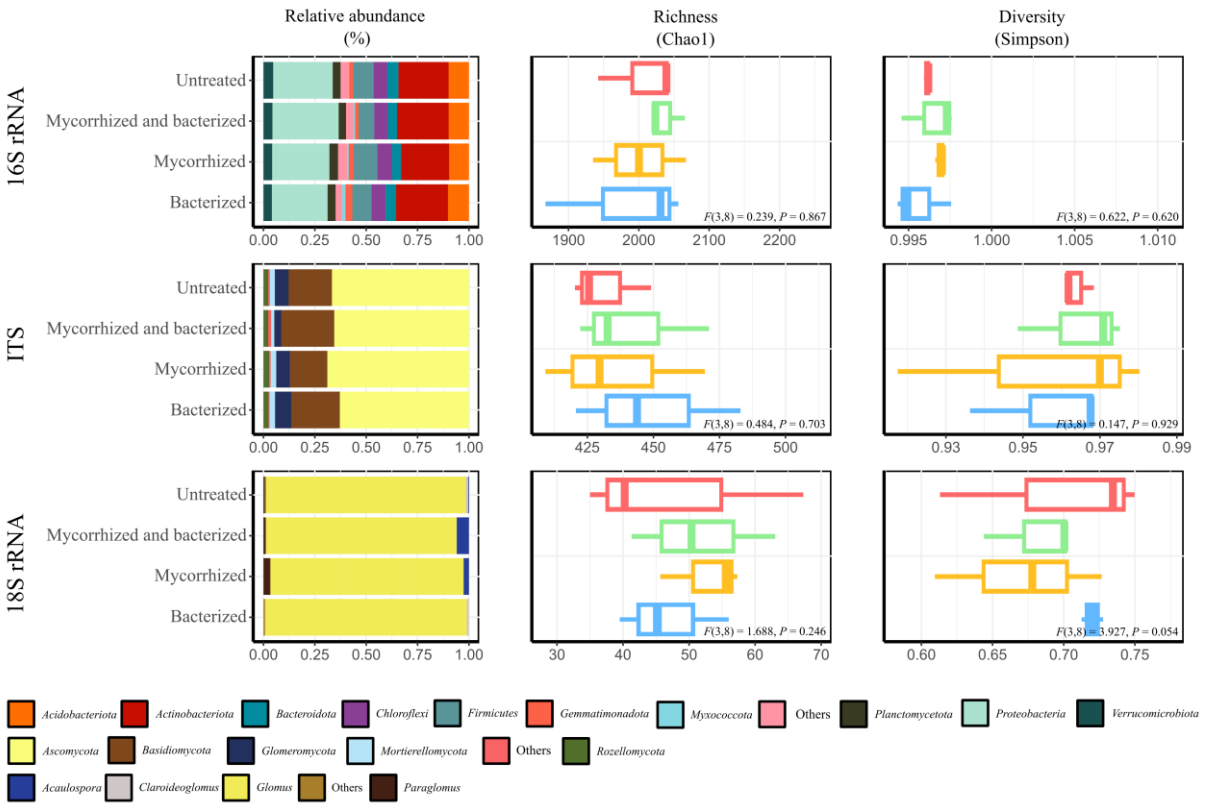

Figure S5: Microbial composition metrics of bacterial (16S rRNA gene), fungal (ITS), and Glomeromycota (18S rRNA gene) communities within bulk soil in untreated, both mycorrhized and bacterized, mycorrhized, and bacterized samples. Relative abundances, Chao1 richness, and Simpson's diversity are represented with the associated ANOVA. No letters indicate no significant differences using pairwise comparisons ($\alpha = 0.05$).

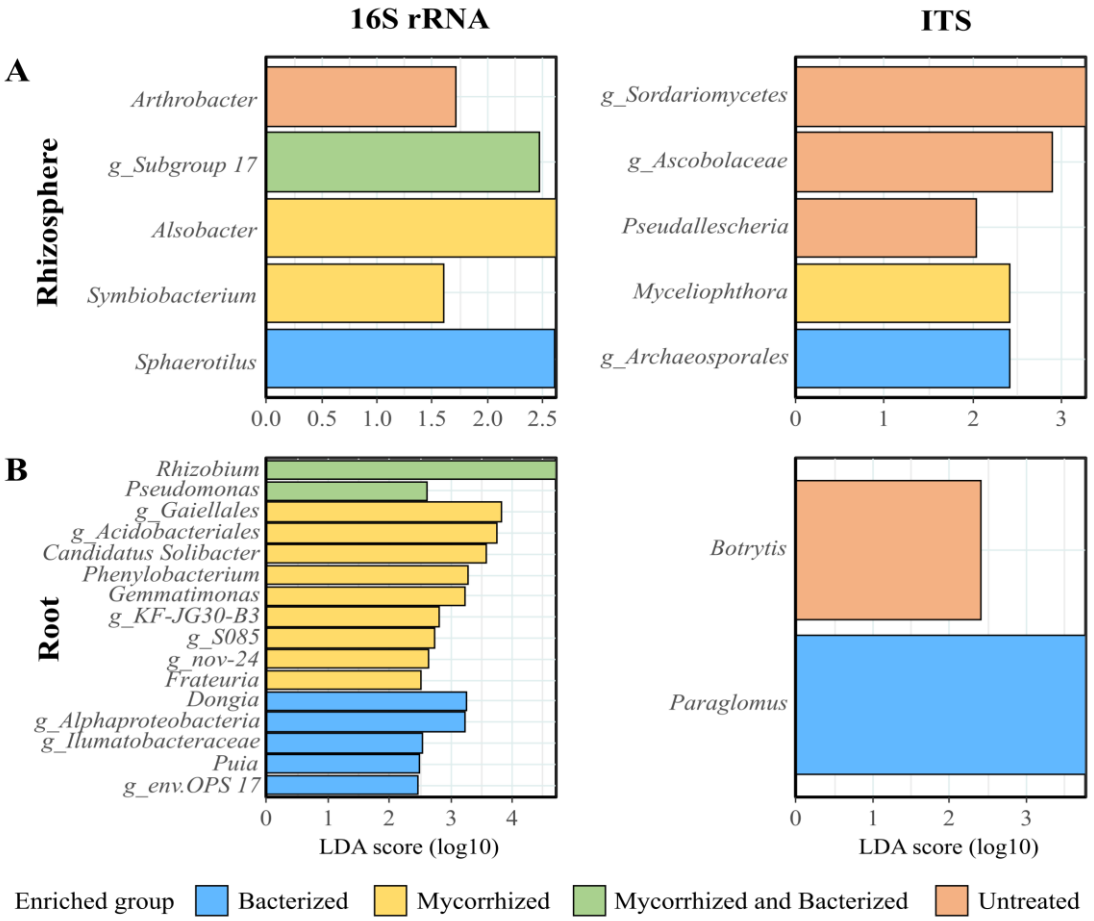

Figure S6: Enriched (16S rRNA) bacterial and (ITS) fungal genera among the treated and untreated conditions in (**A**) rhizosphere, and (**B**) root compartments, detected using LEfSe (FDR-adjusted, $P < 0.05$).

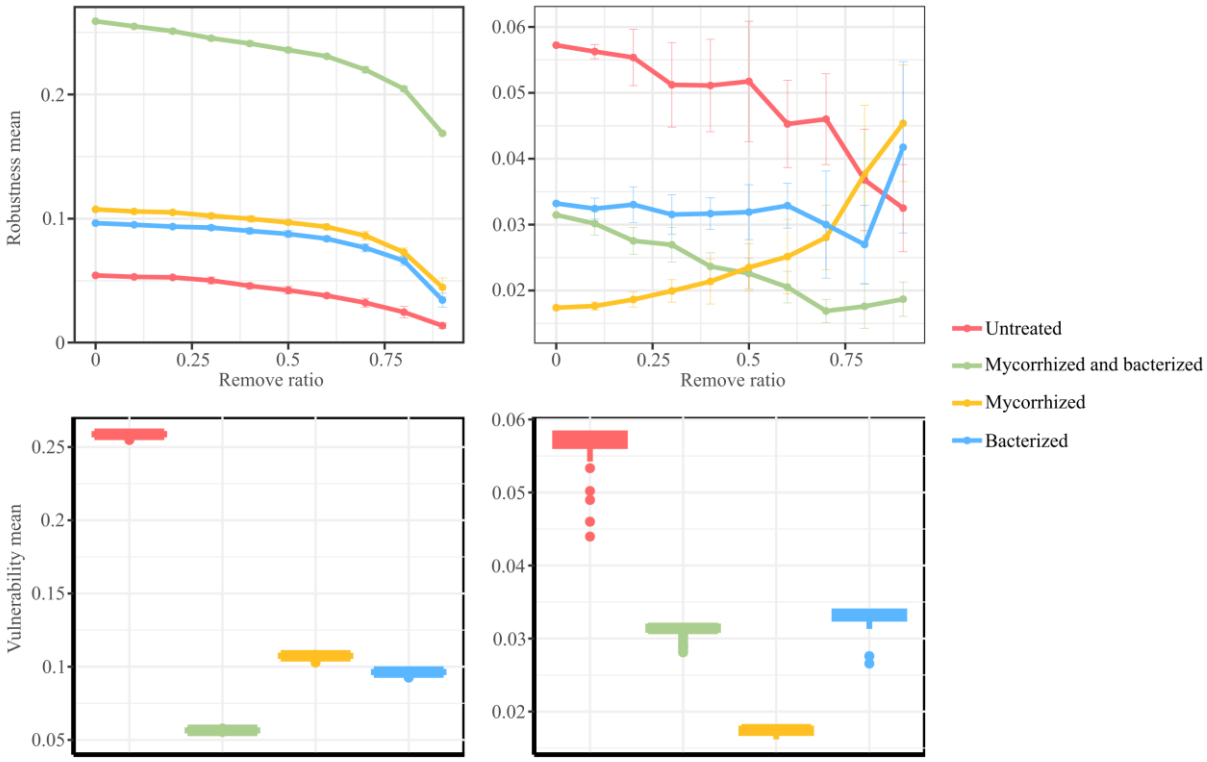

Figure S7: Network stability indexes including robustness mean in relation to removed ratio, and vulnerability mean.