

Supplementary Information

Supplementary Table S1 | Numbers of 16S rRNA gene and ITS amplicon sequencing samples that passed sequencing QC steps.

Phyllosphere	AP13		WBC		VS16		DAC	
	Bacteria/ Archaea	Fungi	Bacteria/A rchaea	Fungi	Bacteria/ Archaea	Fungi	Bacteria/ Archae a	Fungi
Harvested + Fertilized	5	5	6	6	5	5	6	6
Harvested + Unfertilized	6	6	5	5	6	6	6	6
Unharvested + Fertilized	6	5	6	5	6	5	6	6
Unharvested + Unfertilized	5	5	6	5	6	6	5	6
Leaf endosphere	AP13		WBC		VS16		DAC	
	Bacteria/ Archaea	Fungi	Bacteria/ Archaea	Fungi	Bacteri a/Archae ea	Fungi	Bacteria/ Archaea	Fungi
Harvested + Fertilized	6	1	6	1	6	2	6	4
Harvested + Unfertilized	6	2	5	1	6	2	6	3
Unharvested + Fertilized	1	4	0	0	1	4	0	6
Unharvested + Unfertilized	1	3	1	1	0	4	0	5

Supplementary Table S2 | Permuted multivariate analysis of variance (PERMANOVA) tables for all hypothesis tests for difference in community beta diversity. Only significant results are shown. “Genotype (Ecotype)” denotes that the analysis was performed as Genotype nested within Ecotype.

Bacteria	Factor	R2	p-value
All	Compartment	27.3	0.001
	Genotype	1.63	0.007
Leaf surface	Harvest	7.4	0.001
	Genotype (Ecotype)	10.0	0.001
	Ecotype	5.3	0.001
Leaf endosphere	Ecotype	19.8	0.001
Fungi	Factor	R2	p-value
Leaf surface	Harvest	4.5	0.001
	Genotype	2.1	0.001
	Ecotype	1.8	0.007
Leaf endosphere	Ecotype	4.7	0.002
	Genotype	7.2	0.002

Supplementary Table S3 | Number of significantly enriched ASVs in the phyllosphere compared to leaf endosphere grouped by genus (A) and average frequency of significantly different abundant ASVs per genotype across phyllosphere samples (B). Taxa were classified at the highest level possible.

A)

# of ASVs	Taxonomy	Phylum/Class
2	<i>Acidobacteriia</i> Subgroup 2	<i>Acidobacteria</i>
2	<i>Bifidobacterium</i>	<i>Actinobacteria</i>
1	<i>Corynebacteriaceae</i>	<i>Actinobacteria</i>
2	<i>Kineococcus</i>	<i>Actinobacteria</i>
2	<i>Microbacteriaceae</i>	<i>Actinobacteria</i>
4	<i>Curtobacterium</i>	<i>Actinobacteria</i>
2	<i>Streptomyces</i>	<i>Actinobacteria</i>
2	<i>Chitinophagaceae</i>	<i>Bacteroidetes</i>

2	<i>Obscuribacterales</i>	<i>Cyanobacteria</i>
4	<i>Bacilli</i>	<i>Firmicutes</i>
2	<i>Thermobacillus xylanilyticus</i>	<i>Firmicutes</i>
5	<i>Lactobacillus</i>	<i>Firmicutes</i>
2	<i>Desulfosporosinus</i>	<i>Firmicutes</i>
2	<i>Turcibacter</i>	<i>Firmicutes</i>
5	<i>Methylobacterium</i>	<i>Alphaproteobacteria</i>
6	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium</i>	<i>Alphaproteobacteria</i>
2	<i>Mesorhizobium</i>	<i>Alphaproteobacteria</i>
2	<i>Ochrobactrum</i>	<i>Alphaproteobacteria</i>
4	<i>Xanthobacteraceae</i>	<i>Alphaproteobacteria</i>
2	<i>Bradyrhizobium</i>	<i>Alphaproteobacteria</i>
5	<i>Sphingomonas</i>	<i>Alphaproteobacteria</i>
2	Uncultured <i>Alkalilimnicola</i> sp.	<i>Gammaproteobacteria</i>
6	<i>Massilia</i>	<i>Gammaproteobacteria</i>
4	<i>Ralstonia</i>	<i>Gammaproteobacteria</i>
2	<i>Enterobacteriaceae</i>	<i>Gammaproteobacteria</i>
4	<i>Pseudomonas</i>	<i>Gammaproteobacteria</i>
1	<i>Rhodanobacteraceae</i>	<i>Gammaproteobacteria</i>
6	<i>Xanthomonadaceae</i>	<i>Gammaproteobacteria</i>

B)

Test-Statistic	P_{FDR}	AP1 3	WB C	VS16	DAC	Taxonomy	Phylum/Class
25.4	0.01	984	752	721	5151	<i>Enterobacteriaceae</i>	<i>Gammaproteobacteria</i>
25.2	0.01	964	754	792	5890	<i>Enterobacteriaceae</i>	<i>Gammaproteobacteria</i>
23.7	0.02	134	40	11	27	<i>Methylophilaceae</i>	<i>Alphaproteobacteria</i>
23.5	0.02	262	308	47	36	<i>Xanthomonadaceae</i>	<i>Gammaproteobacteria</i>
22.8	0.02	302	330	62	39	<i>Xanthomonadaceae</i>	<i>Gammaproteobacteria</i>

22.2	0.02	145	43	292	895	<i>Allorhizobium- Neorhizobium- Pararhizobium- Rhizobium</i>	<i>Alphaproteobacteria</i>
22.1	0.02	0	0	0	24	<i>Acetobacteraceae</i>	<i>Alphaproteobacteria</i>
20.1	0.04	108	51	8	22	<i>Methylophilaceae</i>	<i>Alphaproteobacteria</i>

Supplementary Table S4 | Core bacteria across a range of sample fractions. Computation was conducted across all samples (A), phyllosphere (B) and leaf endosphere (C). Core community composition is depicted in Figure 5.

A)

Fraction of samples [%]	ASV count	Fraction of community [%]
50	44	2.1
55	20	1.0
60	13	0.6
70	1	0.05
75	1	0.05

80	0	0.0
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B)

Fraction of samples [%]	ASV count	Fraction of community [%]
50	143	7.1
55	112	5.5
60	93	4.6
65	70	3.5
75	41	2.0
80	24	1.2
85	10	0.5
90	10	0.5
95	4	0.2
100	0	0.0

C)

Fraction of samples [%]	ASV count	Fraction of community [%]
50	2	21.1
55	2	21.1
60	1	13.5
65	1	13.5
70	0	0.0

Supplementary Table S5 | Core bacterial ASVs in 65% of upland or lowland leaf endosphere samples. No ASVs were shared in >65% of lowland samples and no ASVs were shared in >75% of upland samples.

Core ASV in 65% of samples and associated ASV ID	# of ASVs in upland plants	# of ASVs in lowland plants
<i>Pseudomonas</i> spp. (e9fd312214016f62f5e539b1291863a5)	1	0
<i>Pseudomonas</i> spp. (affa8b9097e979324b1a9dd9694e42cb)	0	1

Supplementary Table S6 | Core bacterial (A) and fungal (B) ASVs in 90% of samples by harvest level.
A

Core bacterial genera/families in 90% of samples	# of ASVs in harvested plants	# of ASVs in unharvested plants
<i>Methylobacterium</i>	4	5
<i>Enterobacteriaceae</i>	2	0
<i>Curtobacterium</i>	2	4
<i>Sphingomonas</i>	2	1
<i>Pseudomonas</i>	1	0
<i>Mesorhizobium</i>	1	0
<i>Chitinophagaceae</i>	1	0
<i>Bradyrhizobium</i>	0	2
<i>Obscuribacterales</i>	0	2
<i>Acidobacteriia</i>	0	2
Total	13	16

B

Core fungal genera/families in 90% of samples	# of ASVs in harvested plants	# of ASVs in unharvested plants
<i>Cladosporium</i>	8	8
<i>Nigrospora</i>	6	6
<i>Aureobasidium</i>	6	4
<i>Ustilaginaceae</i>	3	3
<i>Pleosporales</i>	5	5
<i>Curvularia</i>	2	2
<i>Periconia</i>	2	3
<i>Meira</i>	1	1
<i>Filobasidium</i>	1	1
<i>Nectriaceae</i>	1	0

<i>Alternaria</i>	1	1
<i>Keissleriella</i>	1	0
<i>Epicoccum</i>	1	0
<i>Exophiala</i>	0	1
Total	38	37

Supplementary Table S7 | Core fungal ASVs across a range of sample fractions. Computation is conducted across all samples (A) and the leaf surface (B). The leaf endosphere was omitted from this analysis since many LE samples failed. Core community composition is depicted in Figure 5.

A)

Fraction of samples [%]	ASV count	Fraction of community [%]
50	30	77.1
55	7	56.9
60	4	52.7

65	2	40.8
75	2	40.8
80	2	40.8
85	1	15.2

B)

Fraction of samples [%]	ASV count	Fraction of community [%]
50	128	92.1
55	112	90.6
60	102	87.3
65	88	86.7
70	80	86.1
80	59	82.5
85	45	80.8
90	38	79.0

95	29	76.9
100	2	3.5

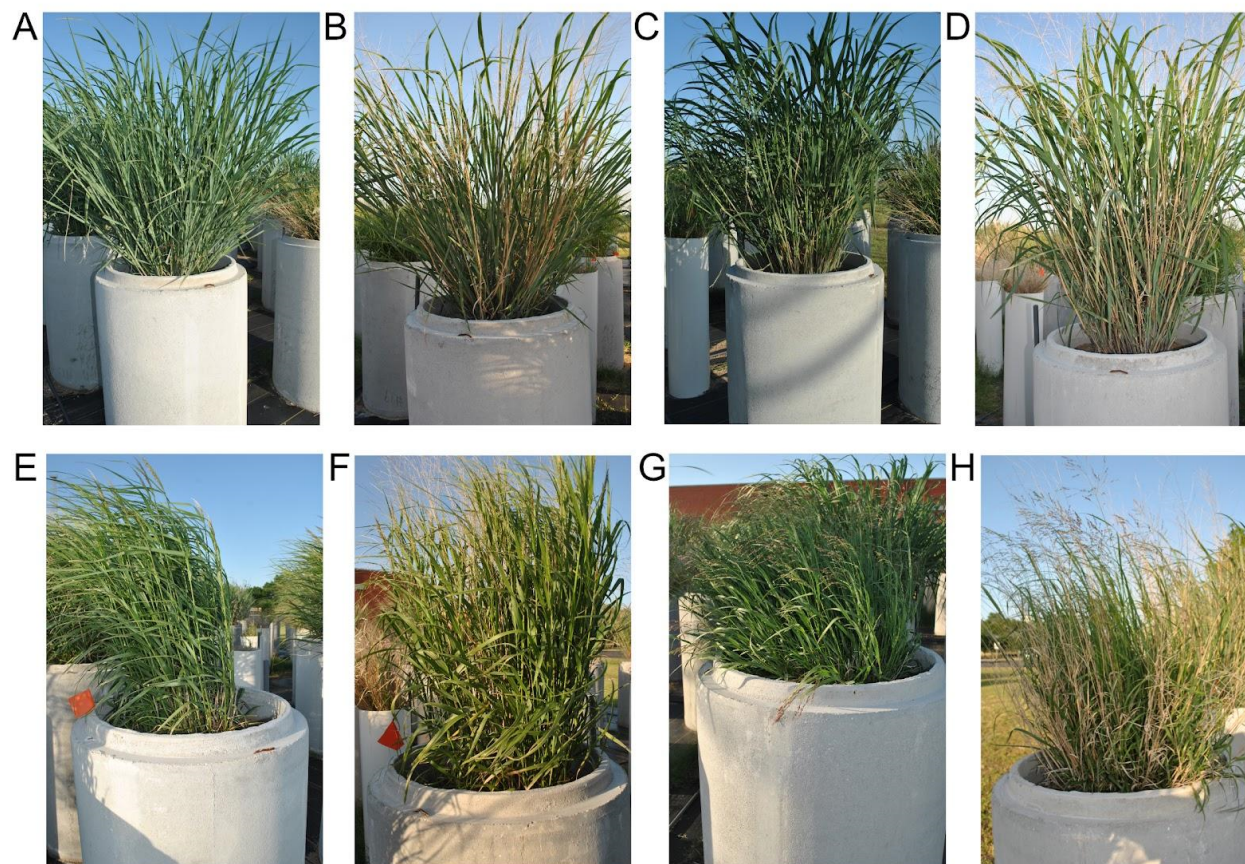


Figure S1 | Aboveground phenotypic differences between switchgrass plants from harvested and unharvested lowland (AP13, WBC) and upland (VS16, DAC) plants. (A) Harvested AP13, (B) unharvested AP13, (C) harvested WBC, (D) unharvested WBC, (E) harvested VS16, (F) unharvested VS16, (G) harvested DAC, (H) unharvested DAC.



Figure S2 | Experimental setup. 96 plants were individually placed in concrete cylinders preventing exchange between plants.

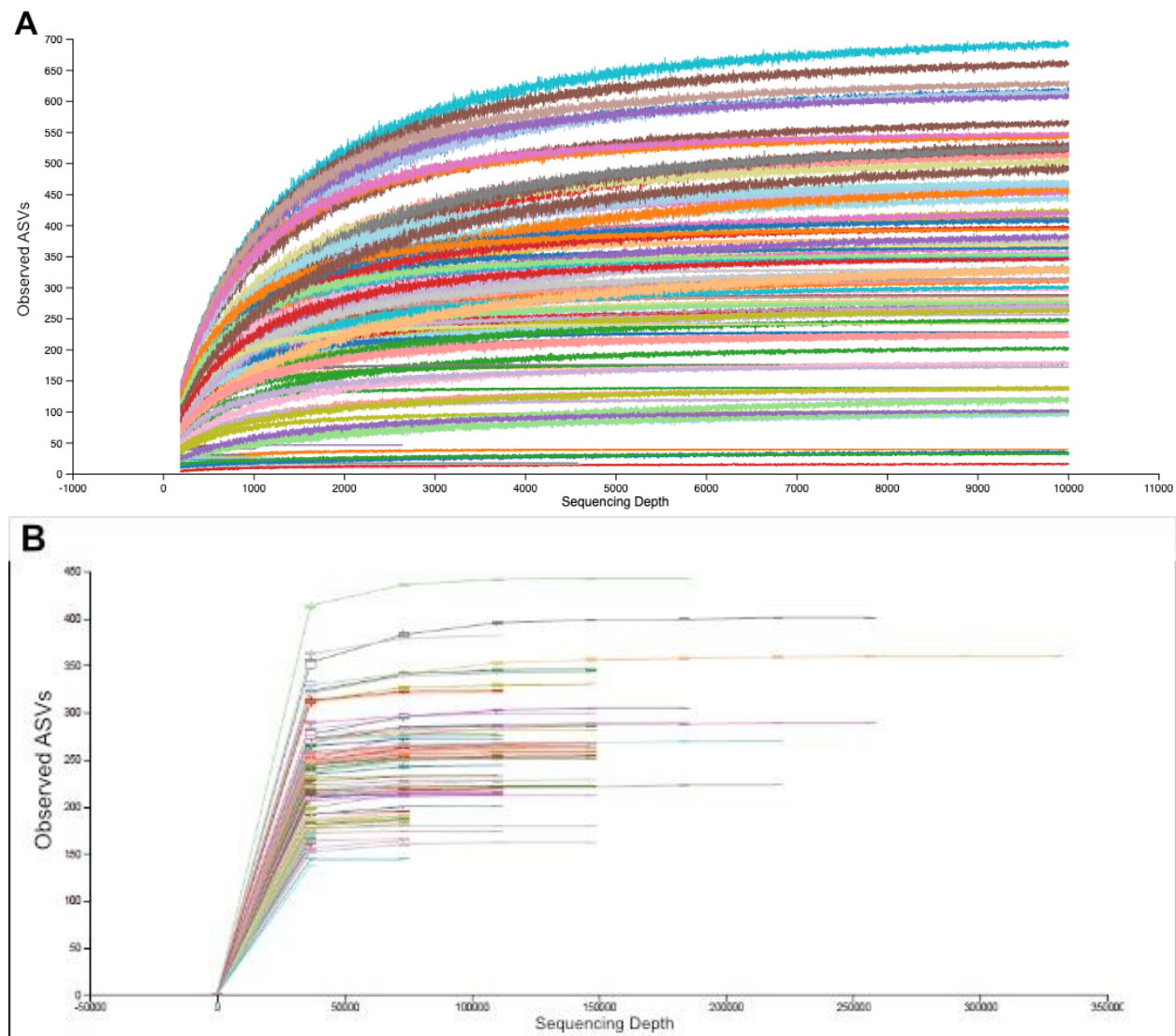


Figure S3 | Rarefaction curves based on A) 16S rRNA gene sequencing and on B) ITS sequencing.

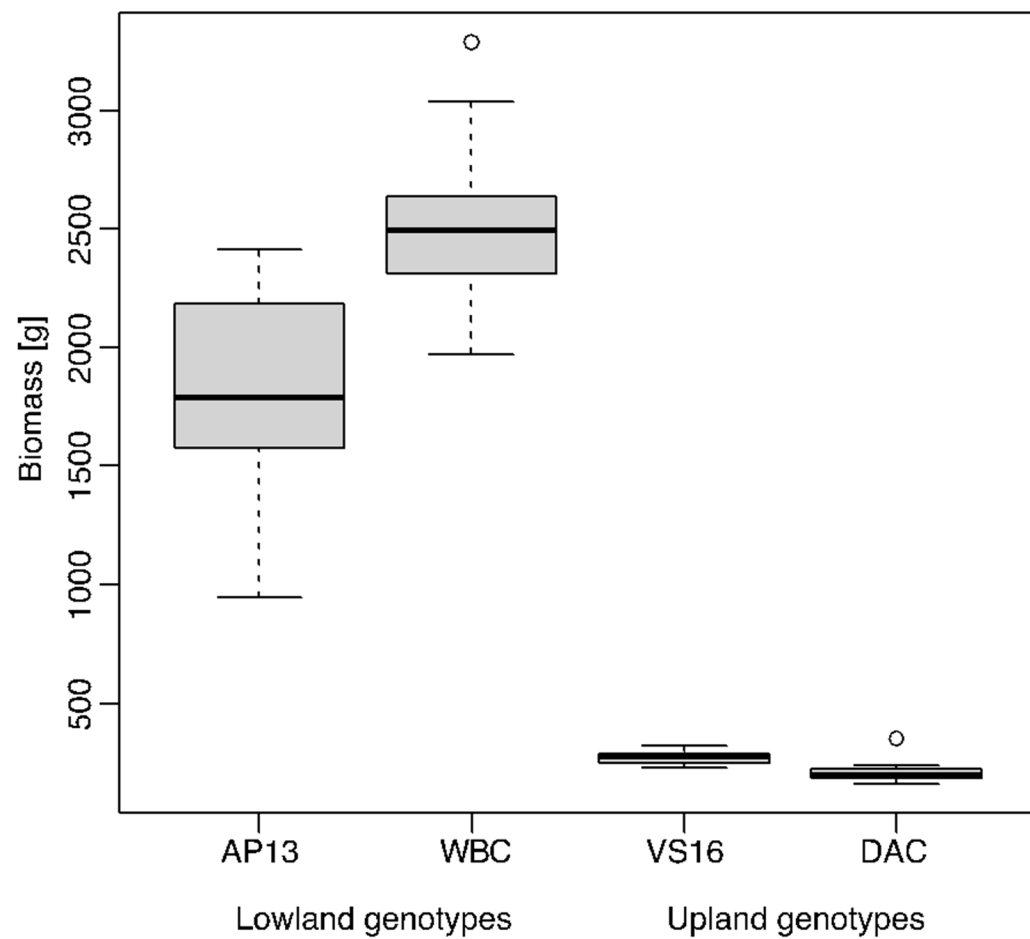


Figure S4 | Biomass differences between switchgrass genotypes/ecotypes.

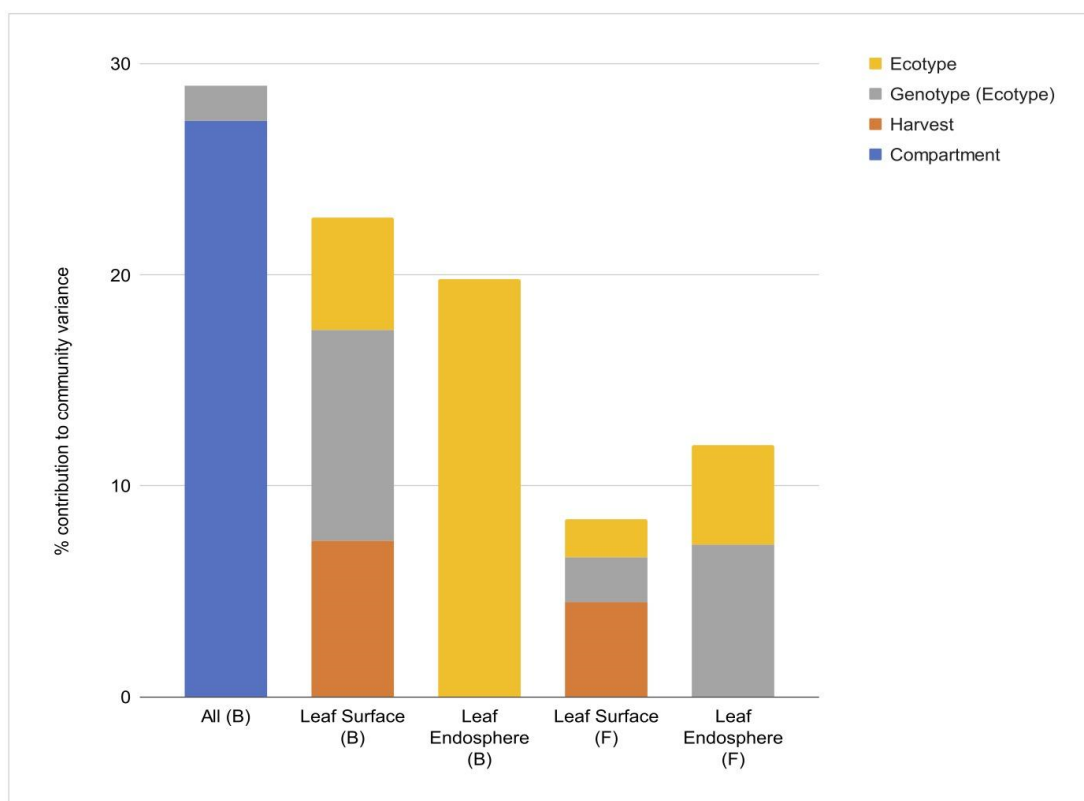


Figure S5 | Relative contribution of experimental factors to microbial community variance. (B) = Bacteria; (F) = Fungi.

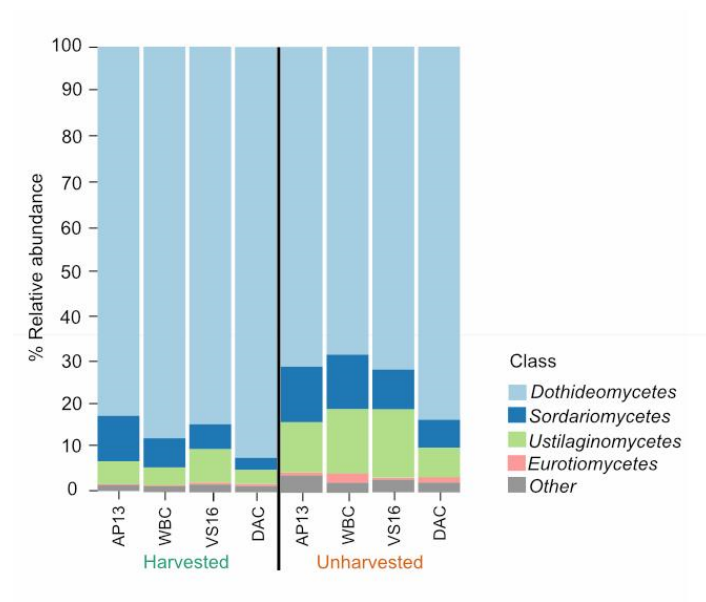
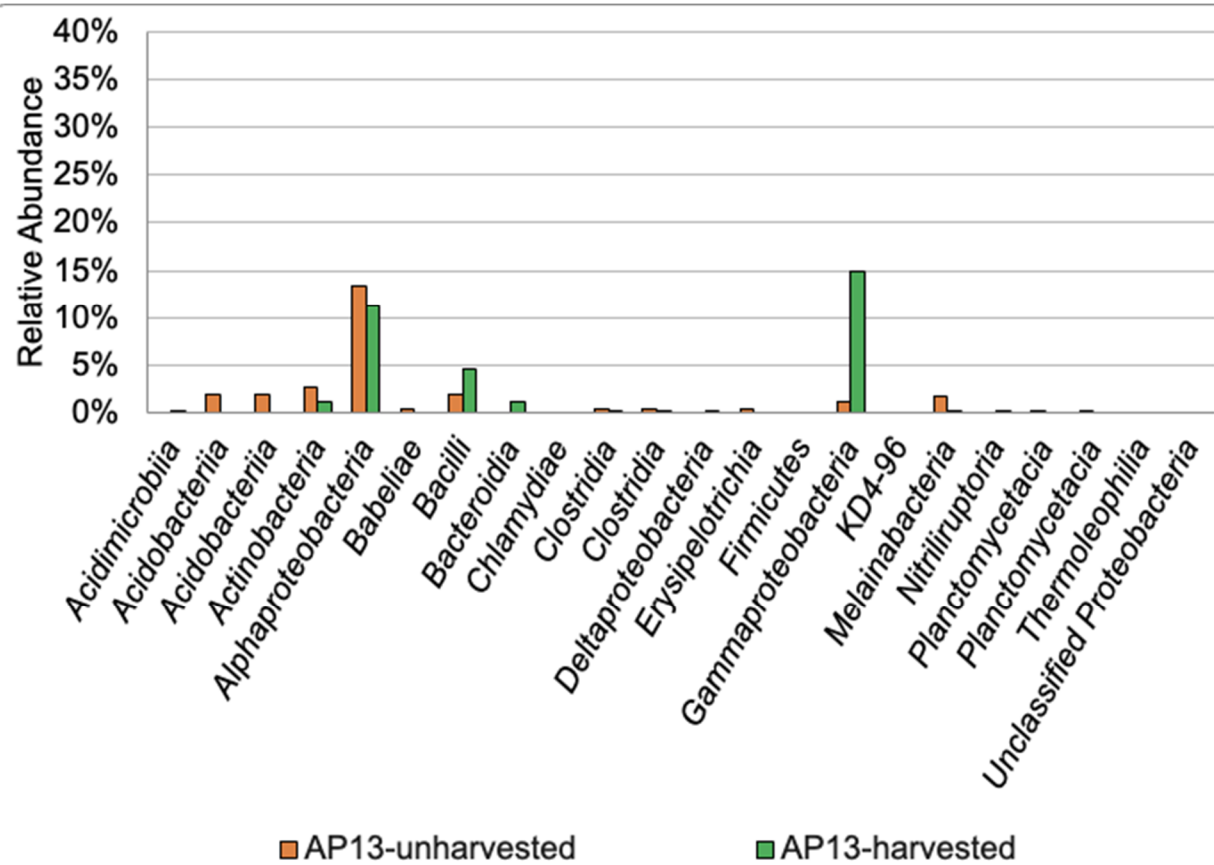
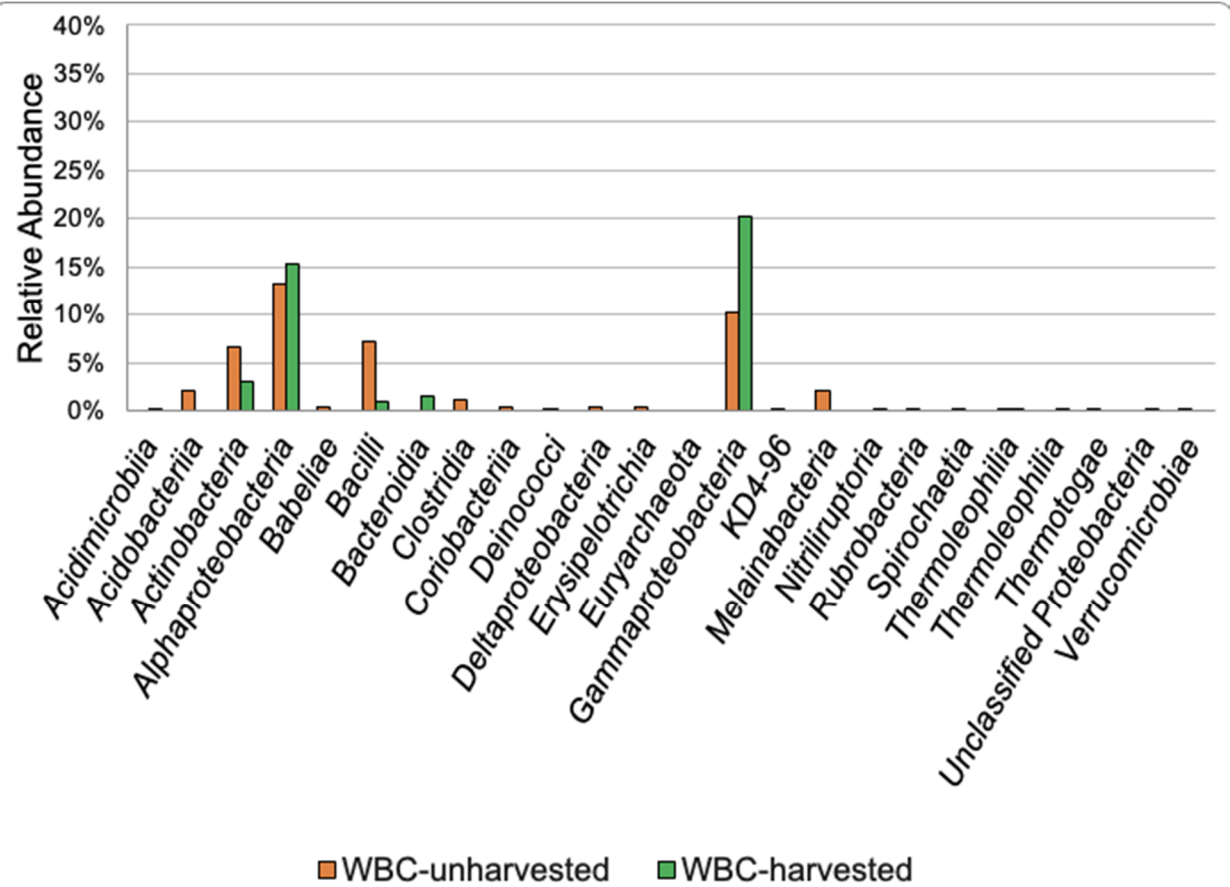
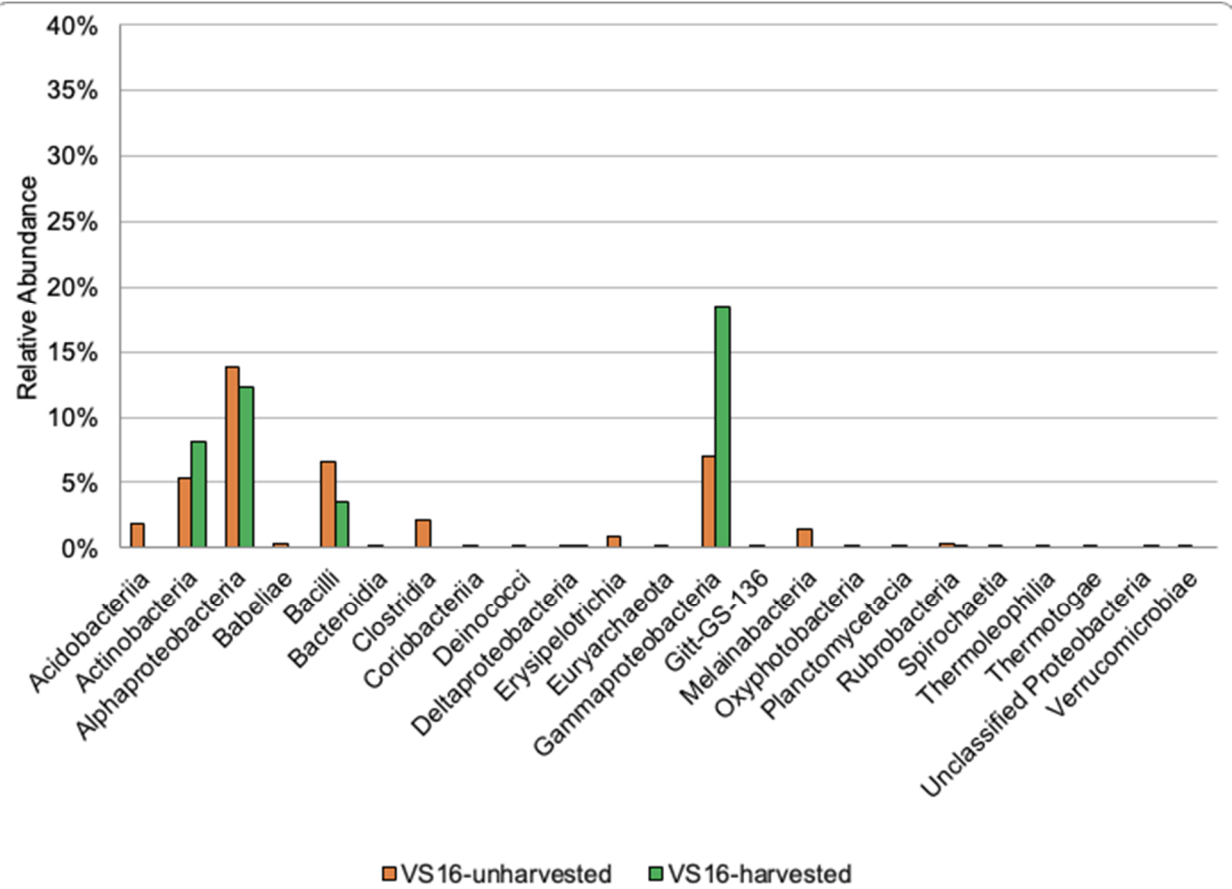


Figure S6 | Community composition of fungi in phyllosphere samples at the class level grouped by harvest level and genotype.







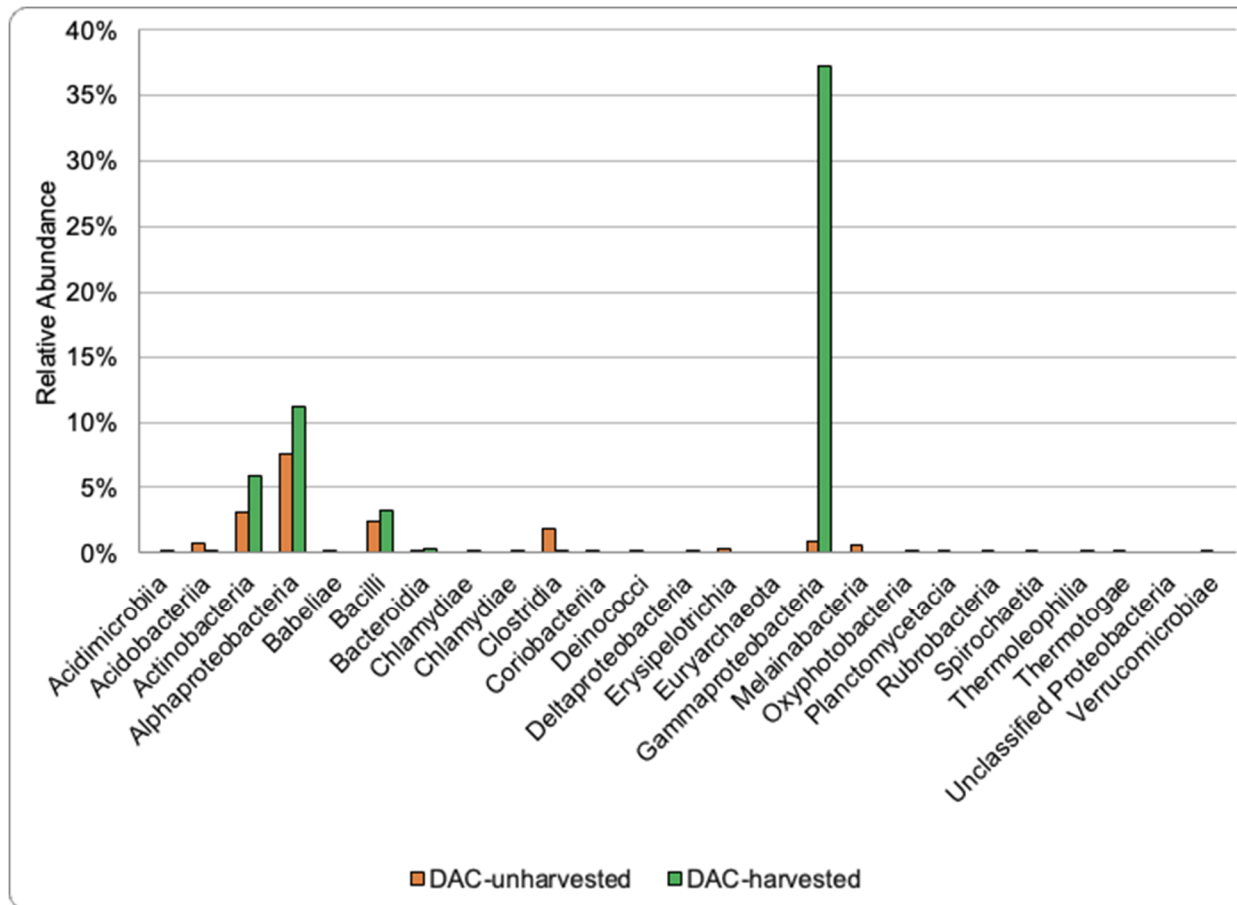


Figure S7 | Taxa enriched in harvested vs. unharvested switchgrass phyllosphere samples by genotype. A) AP13 genotype, lowland ecotype; B) WBC genotype, lowland ecotype; C) VS16 genotype, upland ecotype; D) DAC genotype, upland ecotype.

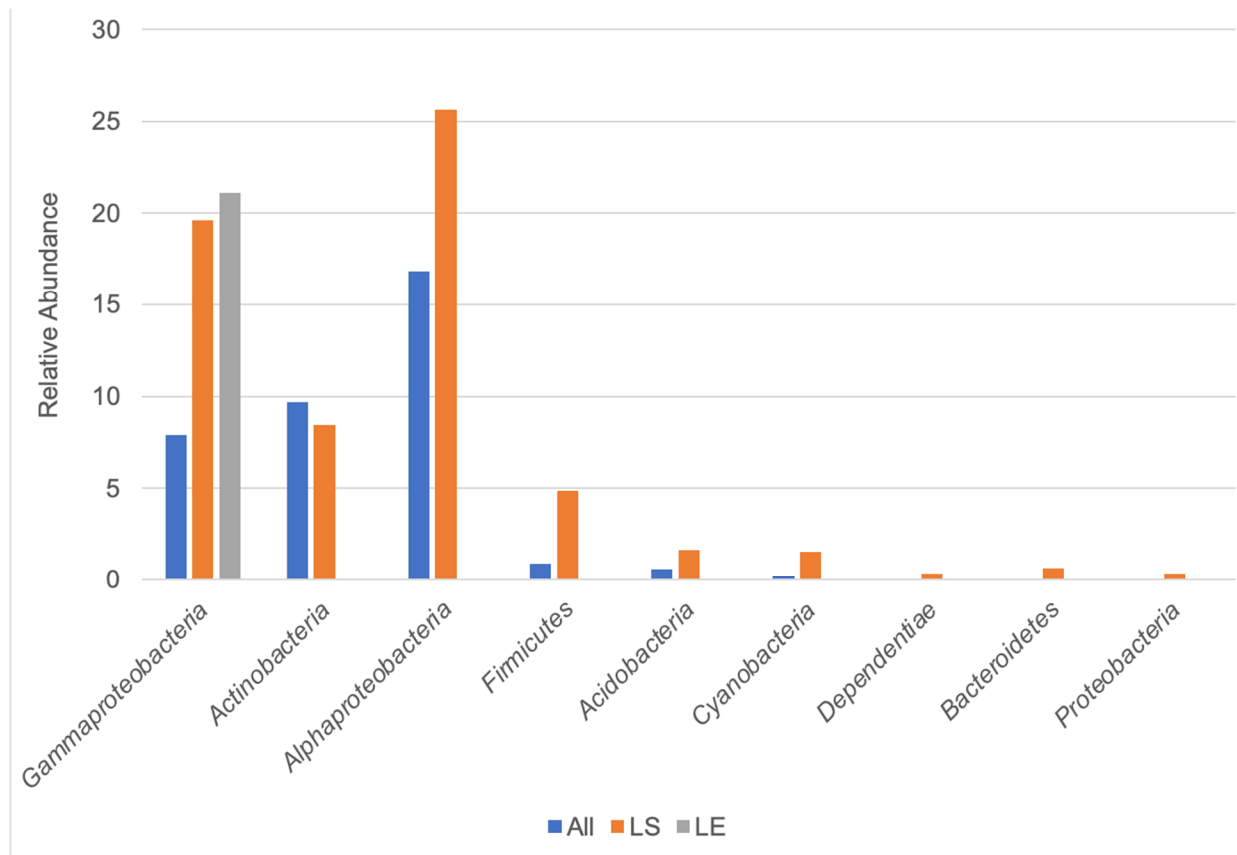


Figure S9 | Bacterial core microbiome composition shared among 50% of all, leaf surface (LS), and leaf endosphere (LE) samples.

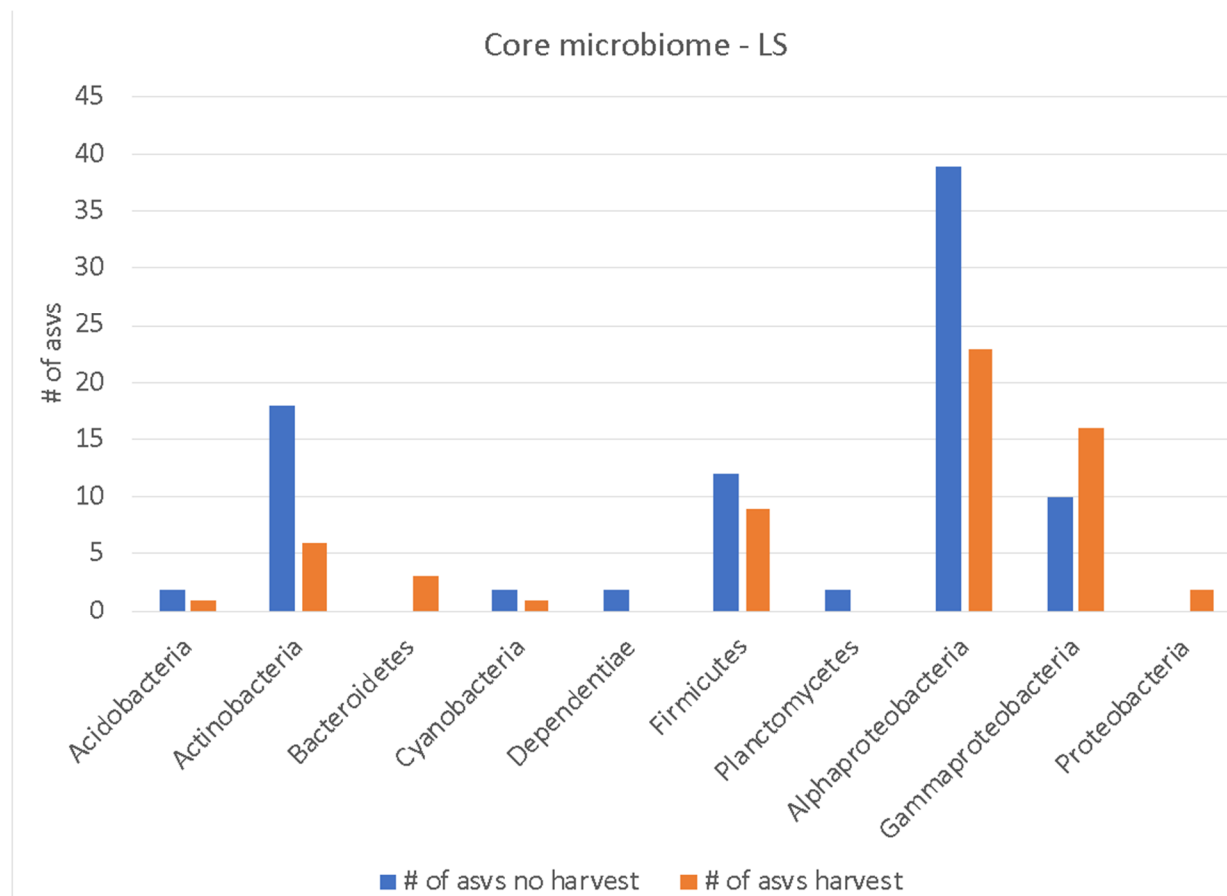


Figure S10 | Core microbiome in the phyllosphere by harvest level.

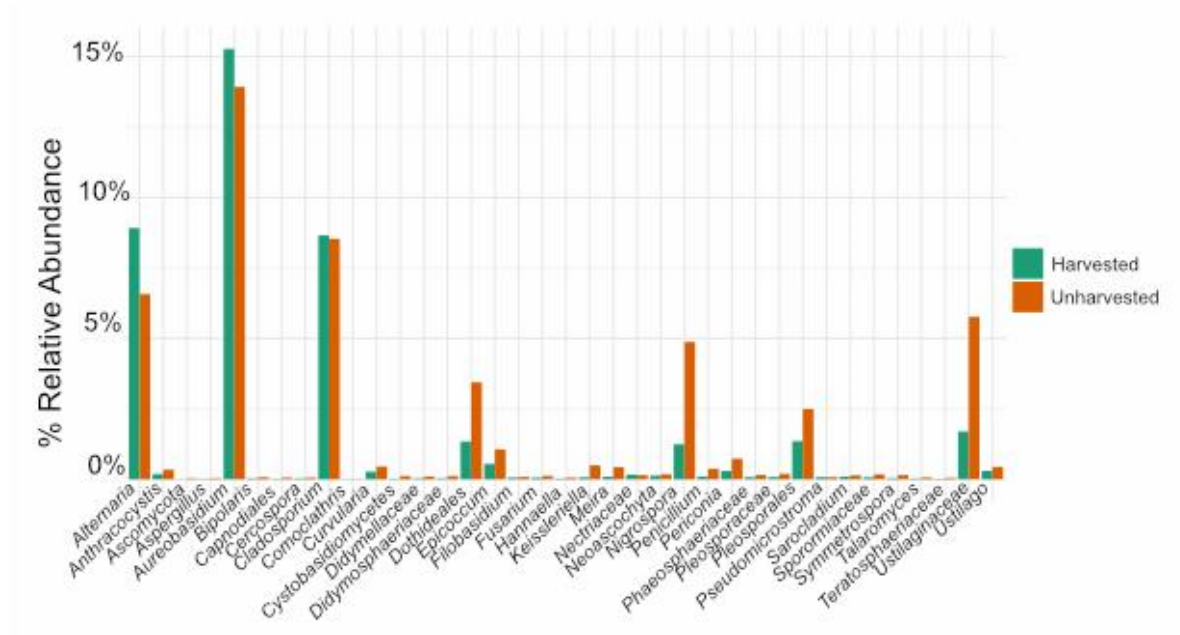


Figure S11 | Relative abundance of fungal taxa in harvested vs. unharvested phyllosphere samples.