Unlocking the bacterial and fungal communities assemblages of sugarcane microbiome

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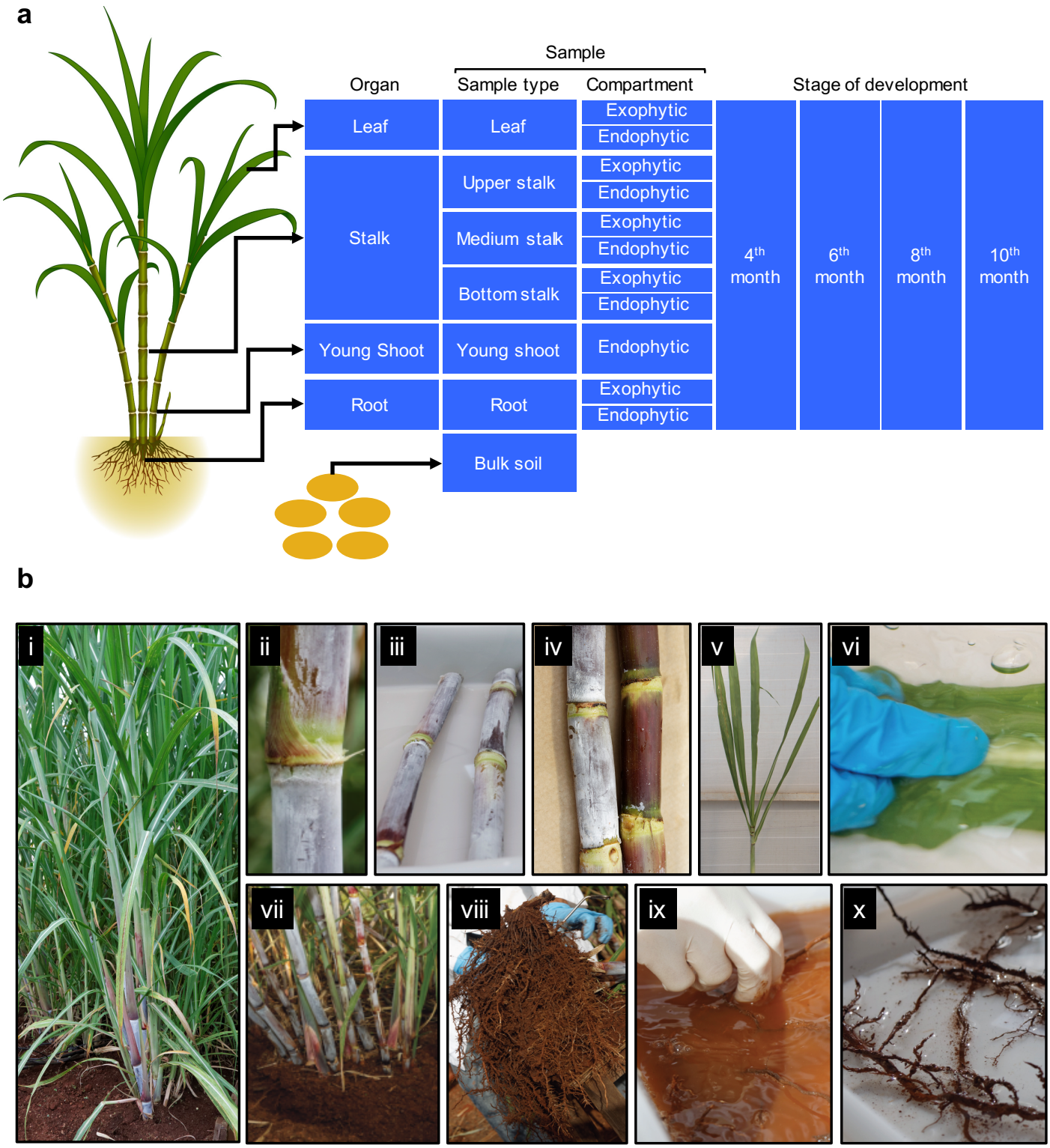
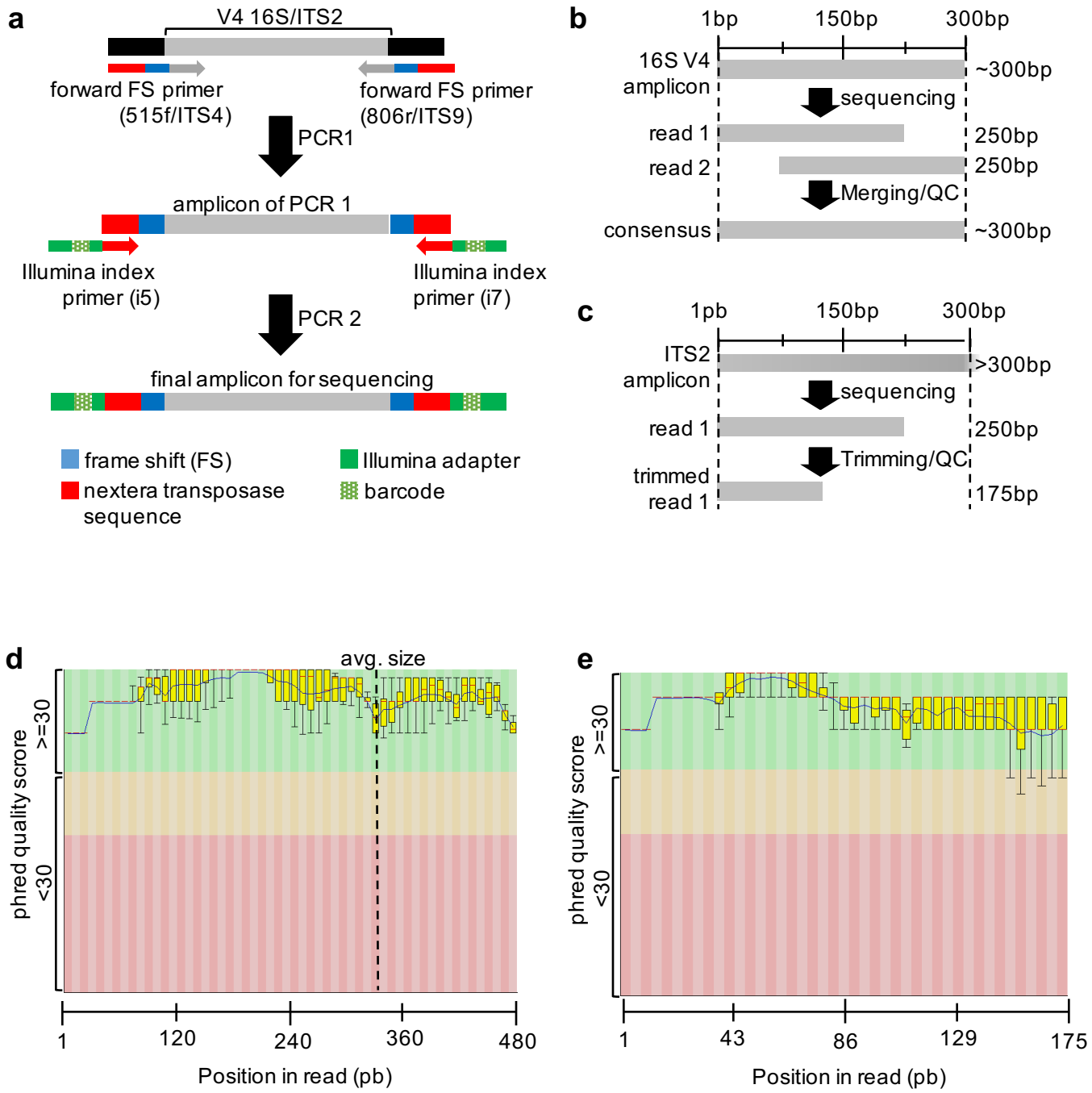
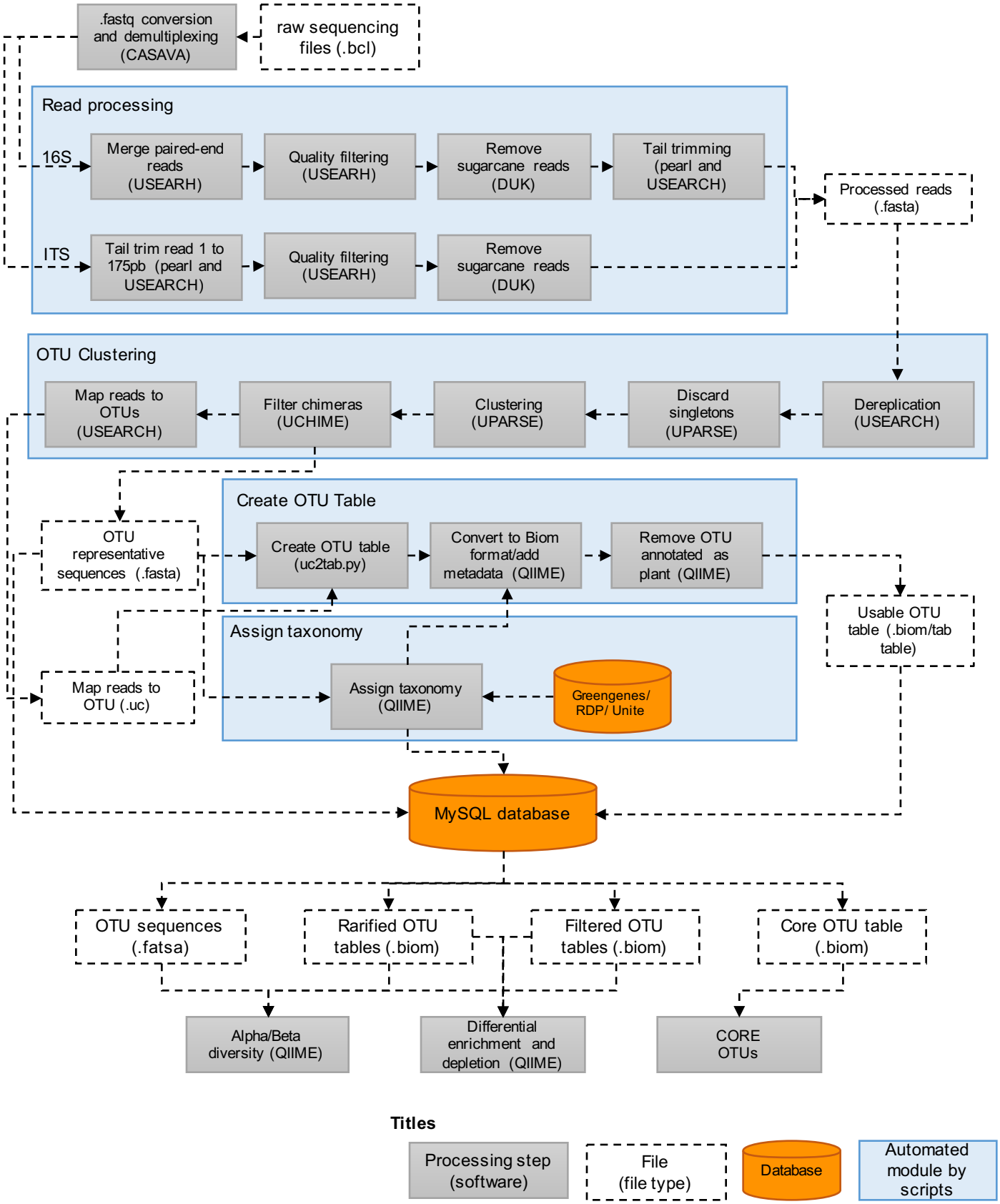
Supplementary Figures



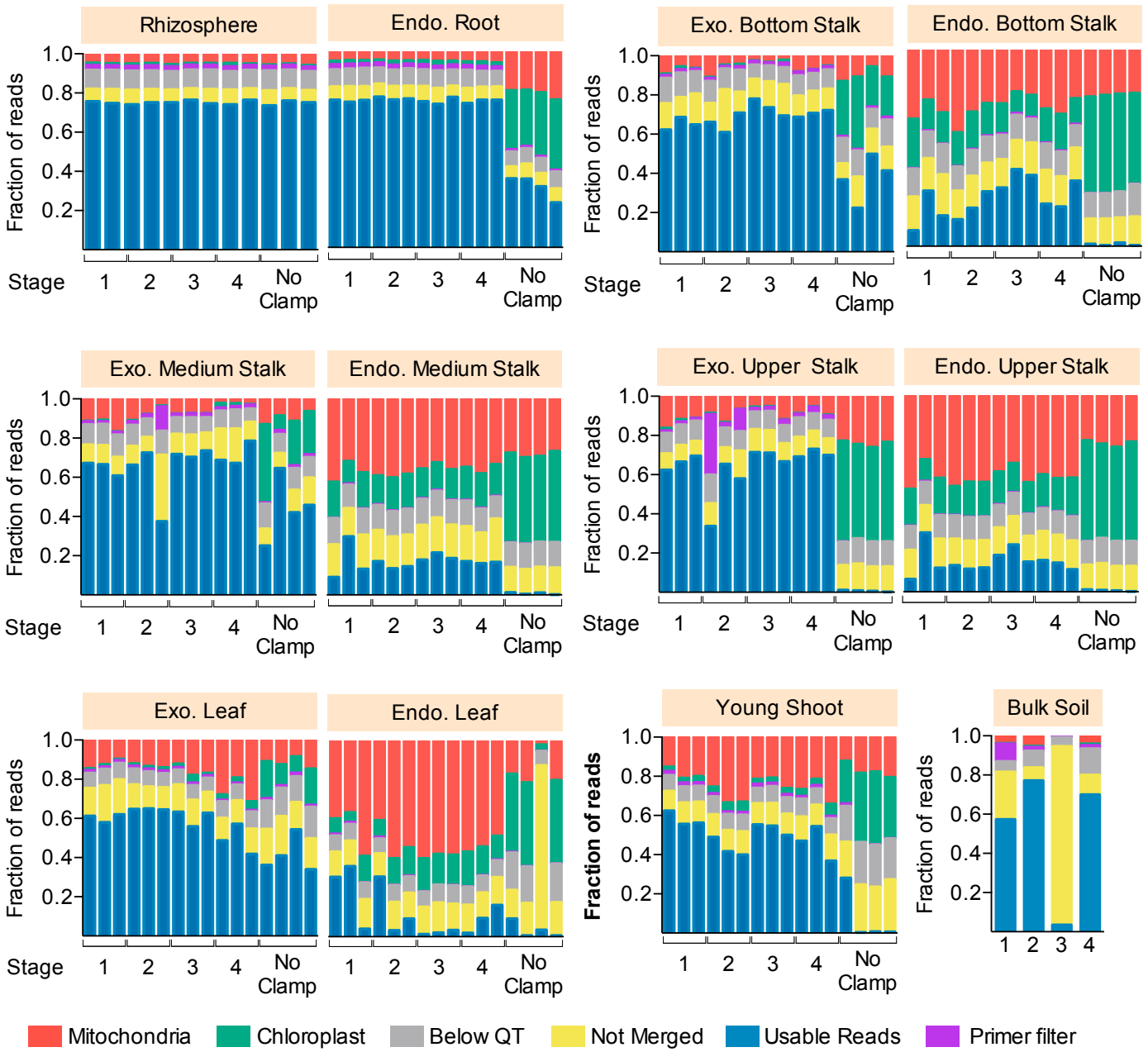
Supplementary Figure 1 - Experimental design and sampling plan overview. (a) Roots, young shoot, stalks and leaf of commercial sugarcane variety SP80-3280 had their microbial community sampled. Stalk has been portioned in bottom, medium and upper stalk. Bulk soil has also been collected from a area where no sugarcane plant has been planted summarizing 7 different sample types. Sugarcane tissues were accessed in two different compartments, endophytic and exophytic, with the except of young shoot from which only endophytic sample was collected. Each combination of sample-type and compartment, here defined as sample, where collected from sugarcane plants in its third annual cycle after 4, 6, 8 and 10 month of shoot germination. **(b)** Harvesting photos. (i) Sugarcane ratoon at 4th month after budding; (ii and iii) Stalks detail; (iv) Stalk pieces before (left) and after (right) microbiome sampling procedure; (v) Sampled leafs. (vi) Detail of leaf during sampling procedure. (vii) Sugarcane ratoon being excavated. (viii) Detachment of root from soil. (ix and x) Roots during sampling procedure.



Supplementary Figure 2 - Sequencing library preparation schema, amplicon processing and read quality. **(a)** The V4 region of 16S and ITS2 were amplified and tagged with barcodes and Illumina adapters through a two-step PCR. The first step of PCR (PCR 1) amplifies target gene regions and adds frame shift sequence (FS) amended with the Nextera transposase sequence. The second step of PCR (PCR 2) uses the Illumina index primer to amplify the PCR 1 product and to add Illumina adapters with a dual index barcode system. **(b)** Amplicon sequencing and read processing for V4 16S amplicons. Amplicons were sequenced with HiSeq 2500 with paired-end reads of 250 bp. The reads were merged to a consensus. The paired-end reads of 16S libraries were merged to consensus. **(c)** Amplicon sequencing and read processing for ITS 2 amplicons. Read 1 was trimmed to a fixed length of 175bp. **(d)** The quality score per base along the 16S consensus after reads merging to a consensus and quality filtering. **(e)** Quality score per base along trimmed read of ITS amplicons and quality filtering. pb.: base pair; avg.: average.



Supplemental Figure 3 - Schematic representation of the bioinformatic pipeline for data processing and analysis of 16S and ITS amplicons. Raw data from the HiSeq equipment was demultiplexed and inputted into an automated pipeline for read processing, OTU clustering, OTU table creation and taxonomy assignment. Information was stored in a MySQL database and retrieved for downstream analysis, such as alpha and beta diversity, community enrichment evaluation and core OTUs discovery.



Supplementary Figure 4 - Sequence statistics of 16S libraries after read processing. Each sample was quality filtered, paired-end merged, filtered by chloroplast and mitochondrial sequences, and tail trimmed by the start of the primer sequences. For each sample type, we included 4 control libraries in which no clamp for mitochondria and chloroplast sequences were used to evaluate its efficiency.

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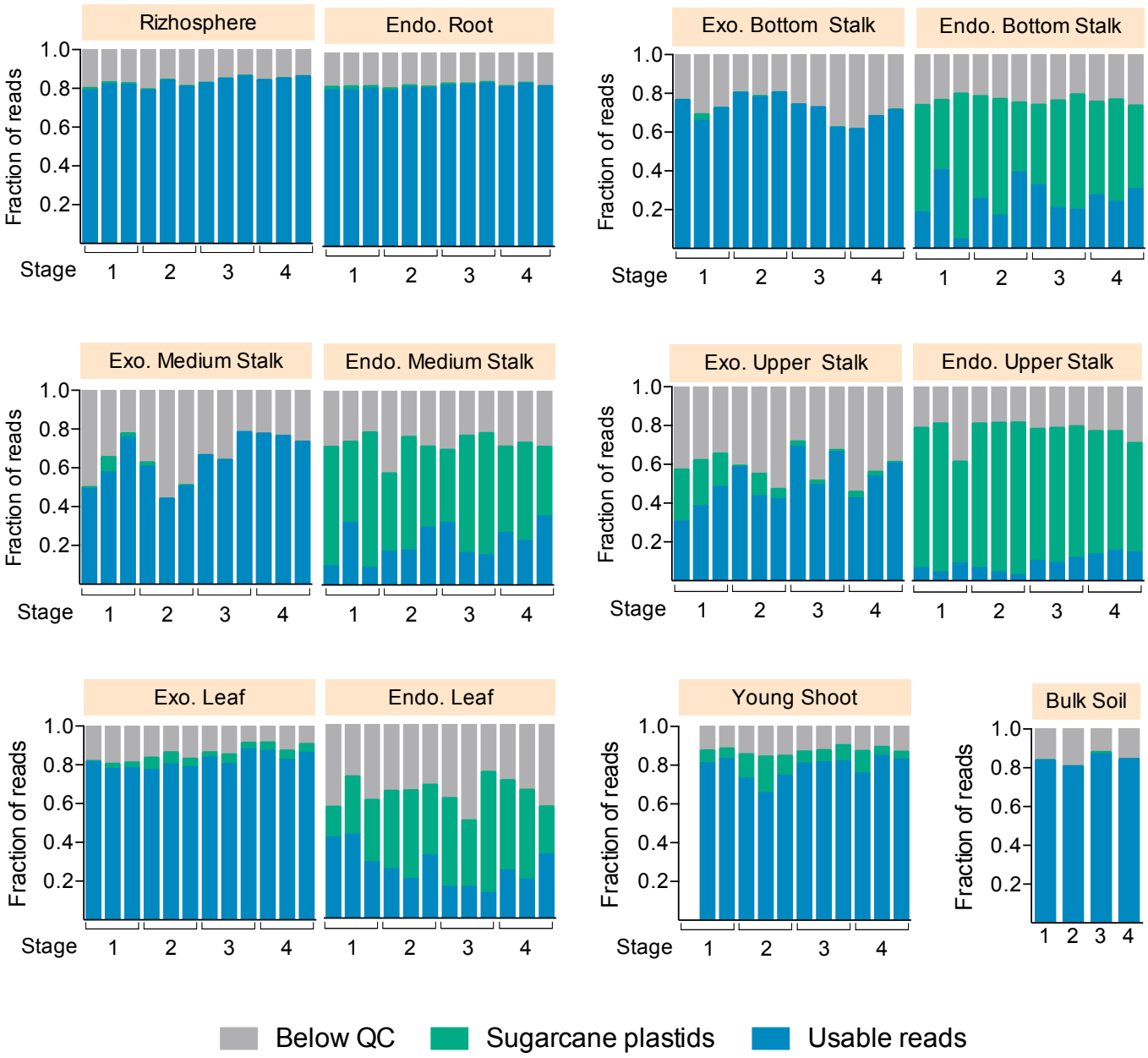
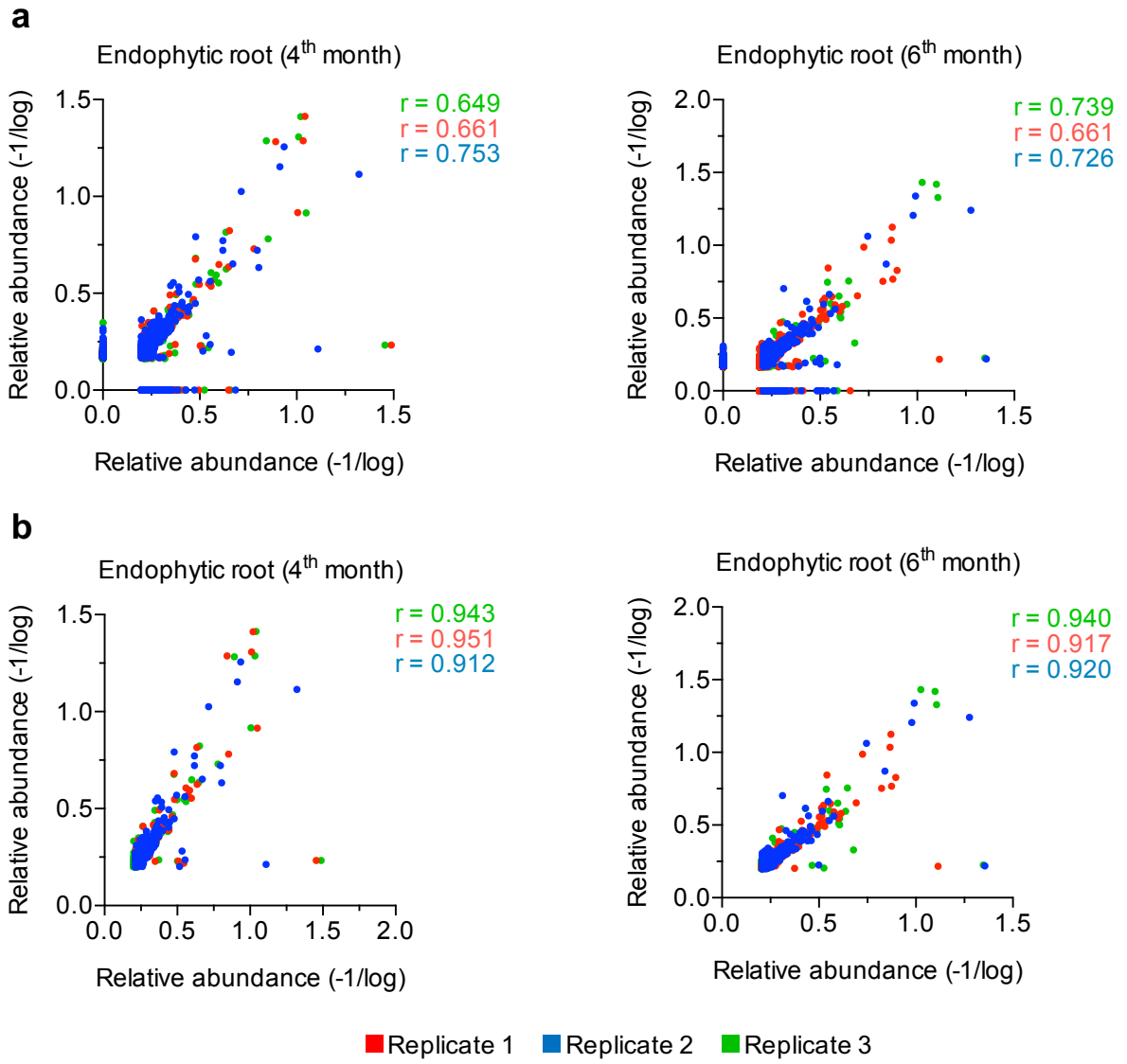
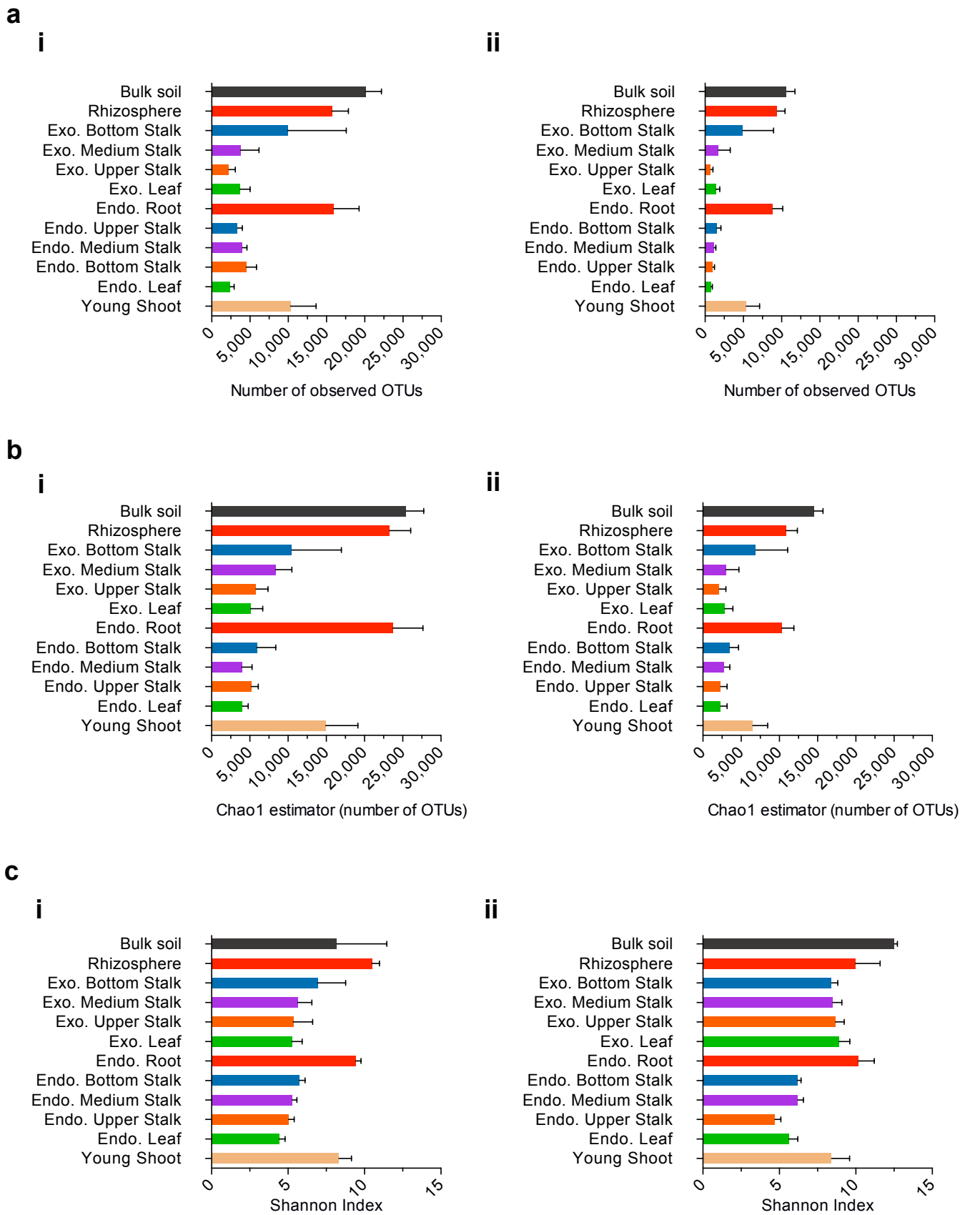


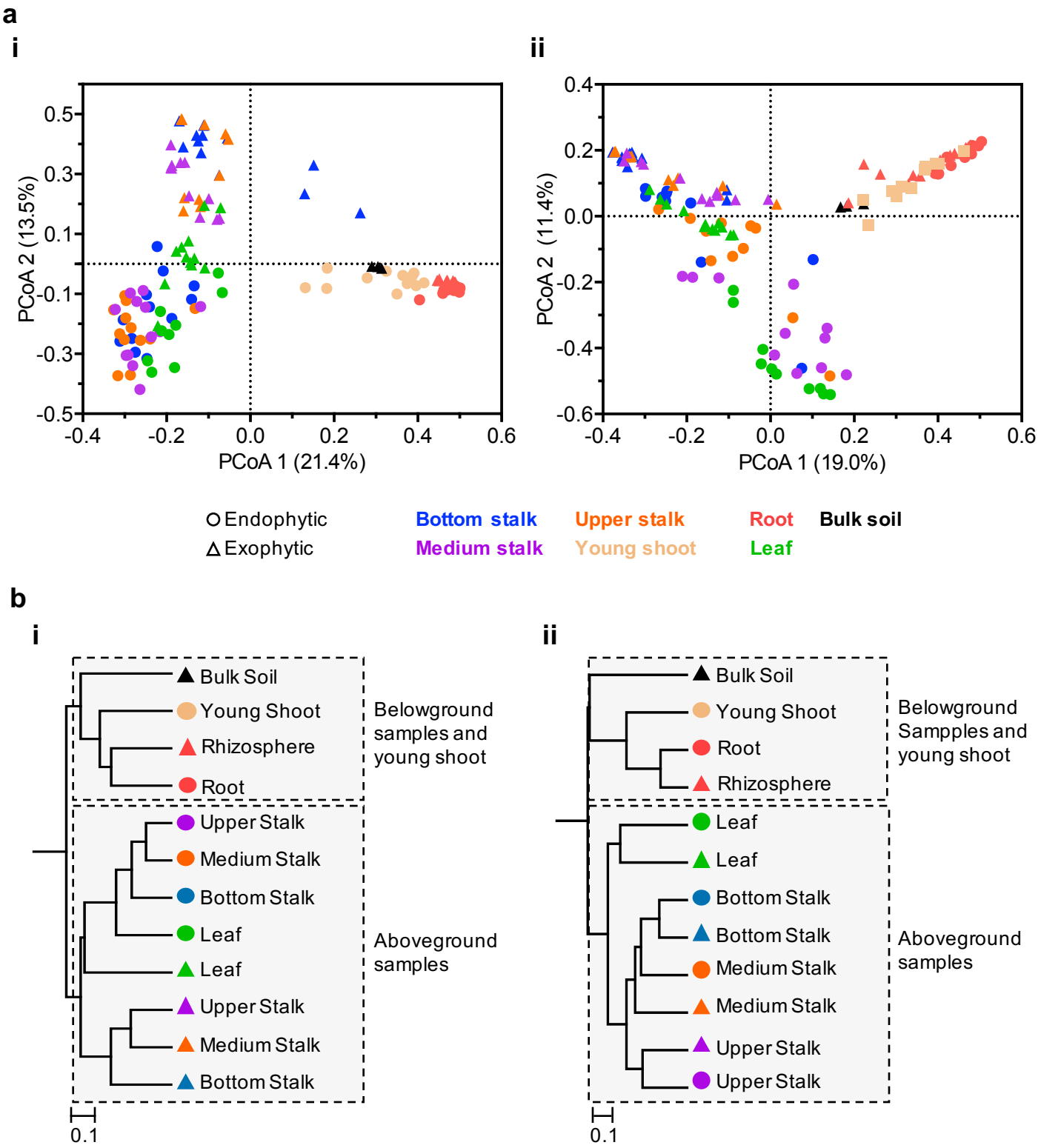
Supplementary Figure 5 - Sequencing statistics of ITS libraries after read processing. The reads of each sample were quality filtered and tail trimmed to a fixed position of 175 pb. Sugarcane ITS sequences were removed, resulting in usable reads that were inputted into a clustering pipeline.



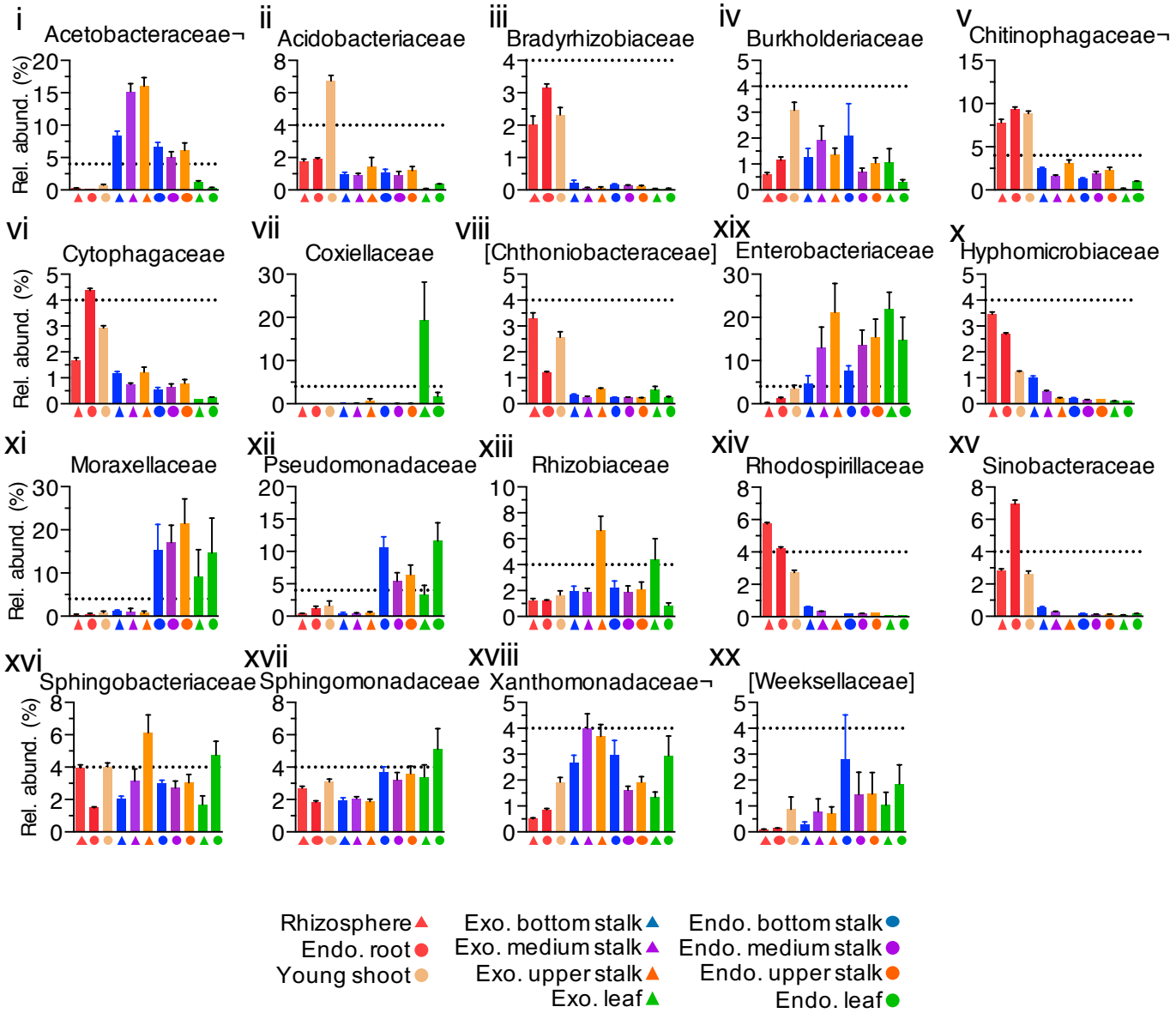
Supplementary Figure 6 - Technical reproducibility of library preparation and sequencing. Reproducibility was assessed using 6 different samples of endophytic root microbiota: 3 samples from the 4th month after shoot germination (replicates 1, 2 and 3) and 3 from the 6th month after shoot germination. The same DNA samples were used for library preparation and sequencing twice independently (technical replicates). Each OTU's relative abundance was -1/log transformed and plotted against its technical replicate (x-axis *VS.* y-axis). The Pearson correlation (r) was calculated for each pair of technical replicates. **(a)** No abundance filter was applied. **(b)** An abundance filter was applied (only an OTU with a relative abundance of >0.0005).



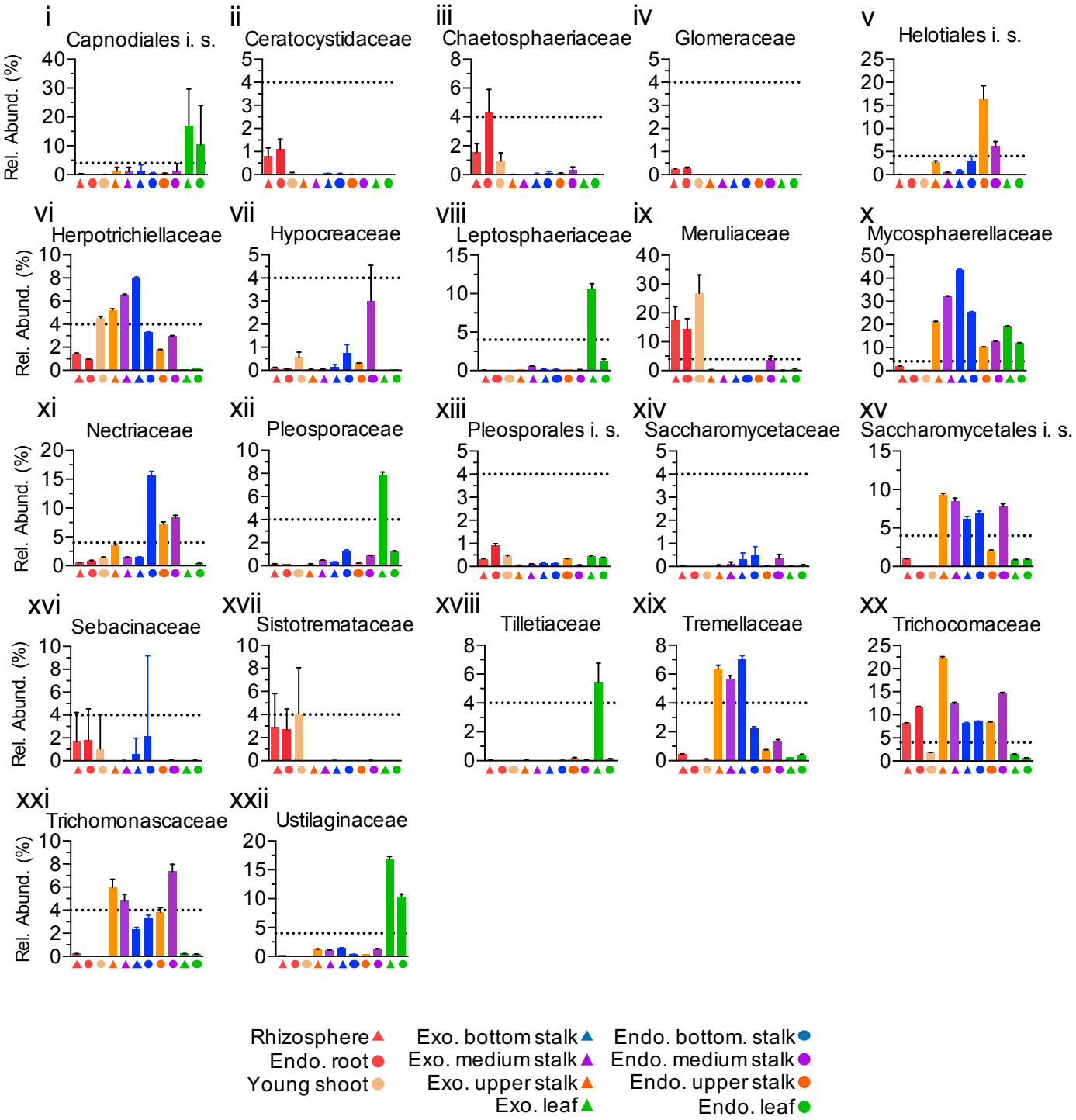
Supplementary Figure 7 - Diversity metrics. **(a)** Number of observed OTUs for (i) bacterial and (ii) fungal communities. OTUs were counted on a usable OTU table using MySQL query. **(b)** Chaos1 estimator for (i) bacterial and (ii) fungal communities. **(c)** Shannon index diversity for (i) bacterial and (ii) fungal communities. Samples were rarefied to 2 MM reads. (Samples with reads less than 2 MM rarefied to the maximum number of reads.) Exo.: Exophytic; Endo.: Endophytic.



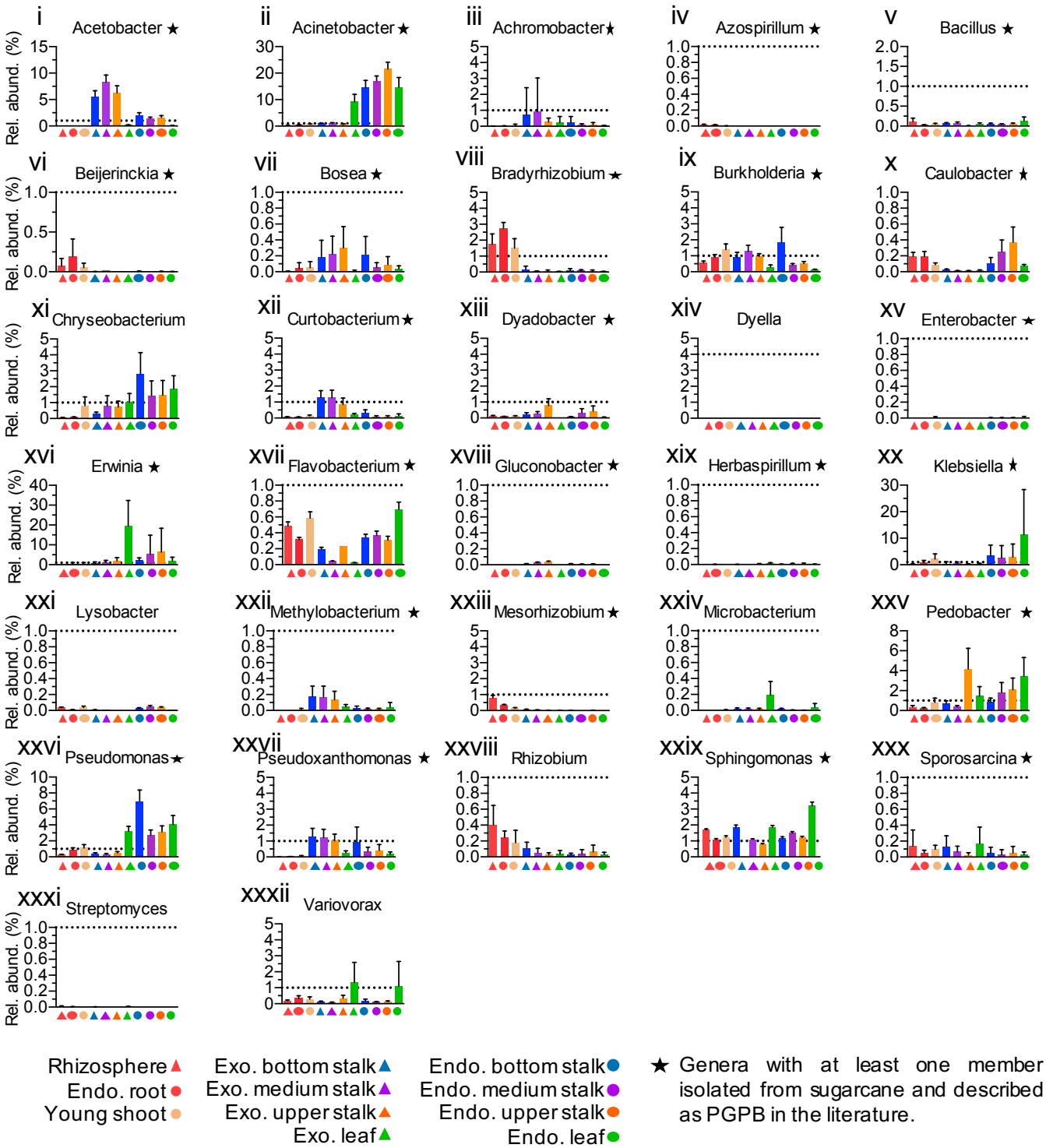
Supplementary Figure 8 - Aboveground and belowground samples showed differences in their compositions and structure in bacterial and fungal communities. (a) Principal coordinate analysis (PCoA) of pairwise, usable, Bray-Curtis distance matrix of the usable rarified OTU table for the **(i)** bacterial and **(ii)** fungal datasets. **(b)** Bray-Curtis dissimilarity of sample types for **(i)** prokaryotic and **(ii)** fungal datasets. The filtered OTU table was rarefied to 18,000 counts per sample and grouped hierarchically by sample type (UPGMA method) to highlight the relationships among sample types.



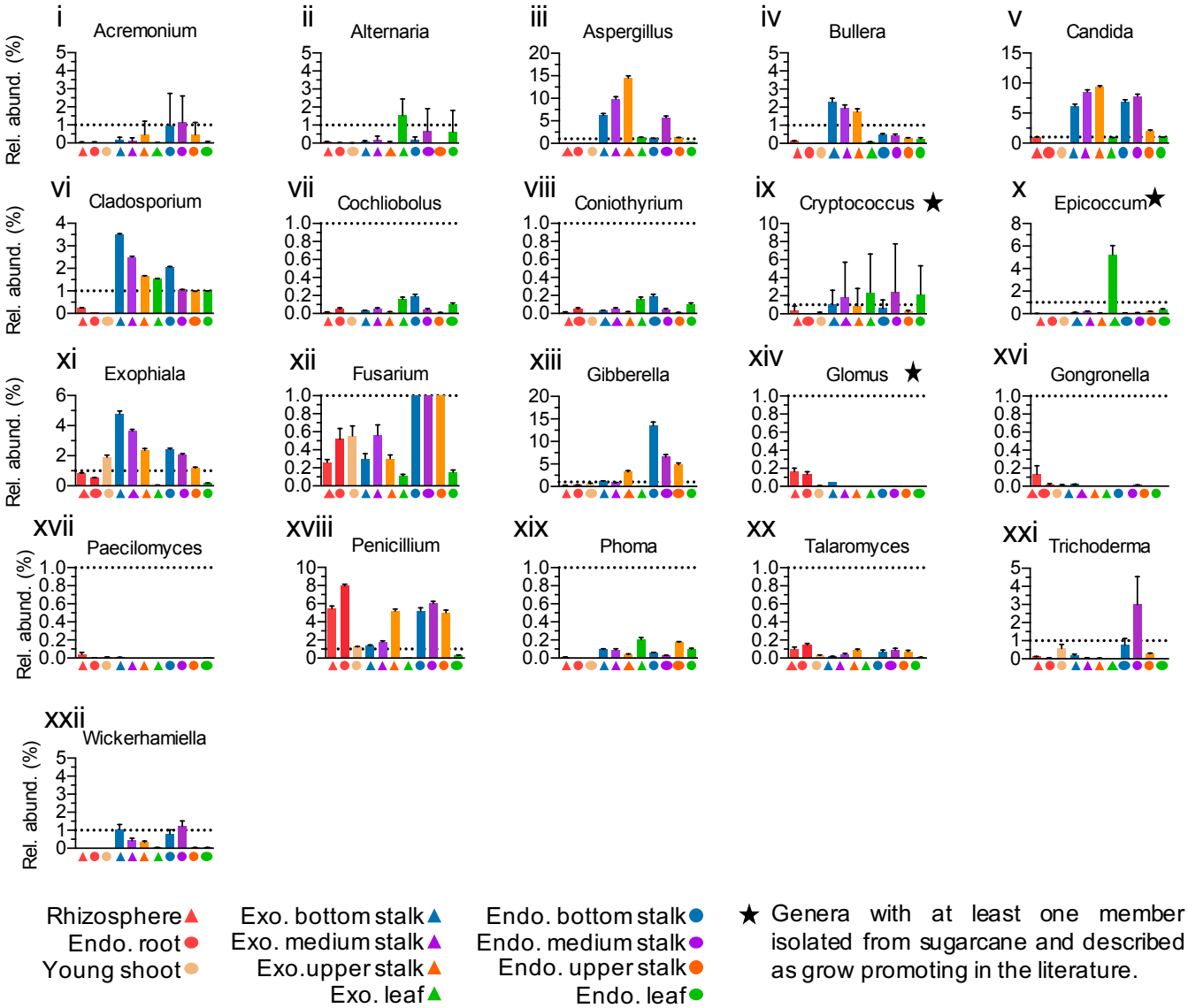
Supplementary Figure 9 - Relative abundance of relevant bacterial families in the core microbiome. Relative abundance was calculated as the sum of the relative abundance of core OTUs assigned to a given bacterial family. The horizontal line highlights the same relative abundance value in all graphs for comparative purposes. Exo.: Exophytic; Endo.: Endophytic.



Supplementary Figure 10 - Relative abundance of relevant fungal families in the core microbiome. Relative abundance was calculated as the sum of the relative abundance of the core OTU assigned to a given fungal group. The horizontal line highlights the same relative abundance value in all graphs for comparative purposes. Exo.: Exophytic; Endo.: Endophytic.



Supplementary Figure 11 - Relative abundance of bacteria genera for which at least one member is isolated and described as plant growth-promoting bacteria (PGPB) in the literature. Literature mining was performed for each bacterial genus looking for representatives with described plant growth-promoting traits. Genera with at least one member isolated from sugarcane and described as growth promoting in the literature are highlighted. The horizontal line highlights the equivalent value for relative abundance in all graphs for comparative purposes. Exo.: Exophytic; Endo.: Endophytic.



Supplementary Figure 12 - Relative abundance of fungi genera for which at least one member is isolated and described as plant growth promoting (PGP) in the literature. Literature mining was performed for each fungal genus looking for representatives with the described plant growth-promoting traits. Genera for which at least one member is isolated from sugarcane and described as growth promoting in the literature are highlighted. The horizontal line highlights the equivalent value for relative abundance in all graphs for comparative purposes. Exo.: Exophytic; Endo.: Endophytic.

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Supplementary Tables

Supplementary Table 1 - Number of raw, unmerged, below QC, chloroplasts, mitochondria and primer-filtered reads per sample for 16S dataset. Demultiplexed raw reads were inputted into the read-processing module of the automated pipeline (Supplementary Fig. 3). Unmerged, low-quality (QC) sequences and sequences of sugarcane plastids were discarded. Sequences without recognizable primer ends were also discarded. The resulting reads (usable) were used for OTU clustering.

	Sample	Number of reads						
		Raw paired-end	Unmerged paired-ends	Below QC	Chloroplast	Mitochondria	Primer filter	Usable
Exophytic	Rhizosphere	6,406,547	438,092	616,886	64,294	320,954	158,429	4,807,892
	Bottom stalk	18,766,849	2,479,006	1,973,686	113,347	1,044,556	316,817	12,839,437
	Medium stalk	14,983,374	1,568,492	1,374,686	60,136	1,202,838	271,937	10,505,285
	Upper stalk	11,555,639	1,110,733	1,199,925	63,565	1,134,329	670,190	7,376,897
	Leaf	7,955,303	1,137,091	652,253	173,139	1,499,041	90,782	4,402,997
	Bulk soil	39,461,273	5,922,837	3,265,103	202,897	1,724,984	1,918,605	26,426,847
Endophytic	Root	12,911,028	916,606	1,125,265	260,227	621,590	315,679	9,671,661
	Bottom stalk	12,851,231	2,075,040	1,650,326	2,082,440	3,680,107	76,834	3,286,484
	Medium stalk	12,251,593	2,110,722	1,553,816	1,968,319	4,475,064	43,202	2,100,470
	Upper stalk	16,092,080	2,274,553	1,893,750	2,676,662	6,629,517	51,457	2,566,141
	Leaf	8,564,385	1,193,540	731,012	1,145,570	4,535,408	28,518	930,337
	Young shoot	11,707,552	1,312,132	975,475	396,275	2,881,375	195,031	5,947,264
Total		**173,506,854**	**22,538,844**	**17,012,183**	**9,206,871**	**29,749,763**	**4,137,481**	**90,861,712**

Supplementary Table 2 - Number of raw R1 reads, below QC, and representing sugarcane sequences on the ITS dataset. Demultiplexed raw reads were imputed in the read-processing module of the automated pipeline (Supplementary Fig. 3). Only the first read (R1) was used for read processing. Low-quality (QC) sequences and sequences of sugarcane genomes were discarded. The resulting reads (usable) were used for OTU clustering.

	Sample	Number of reads			
		Raw R1 reads	**Below QC**	**Sugarcane**	**Usable**
Exophytic	Rhizosphere	1,537,301	252,069	7,990	1,277,242
	Bottom stalk	17,334,599	5,031,008	111,968	12,191,623
	Medium stalk	35,838,785	9,143,680	188,113	26,506,992
	Upper stalk	18,364,987	7,807,749	1,354,075	9,203,163
	Leaf	6,259,061	898,039	248,609	5,112,413
	Bulk soil	10,396,898	1,654,617	45,617	8,696,664
Endophytic	Root	3,382,608	567,808	30,886	2,783,914
	Bottom stalk	20,653,943	4,999,983	10,367,463	5,286,497
	Medium stalk	25,375,979	6,618,640	13,245,076	5,512,263
	Upper stalk	15,564,397	3,354,085	10,710,630	1,499,682
	Leaf	2,876,956	1,025,934	1,046,744	804,278
	Young shoot	9,807,600	1,225,097	696,722	7,885,781
Total		**167,393,114**	**42,578,709**	**38,053,893**	**86,760,512**

Supplementary Table 3 - Prokaryotic orders with significant differences in relative abundance in at least two sample types. The average relative abundance of sample types was used in Kruskal-Wallis tests on the order level to identify taxa whose average abundance differed significantly between sample types. A threshold of P<0,001 (FDR corrected) was used.
Un.:Unknown; Exo.: Exophytic; Endo.: Endophytic

Order	P value	P value (FDR corrected)	Relative abundance											
			Bulk Soil	Rhizo.	Endo. Root	Young Shoot	Exo. Bottom Stalk	Endo. Bottom Stalk	Exo. Medium Stalk	Endo. Medium Stalk	Exo. Upper Stalk	Endo. Upper Stalk	Exo. Leaf	Endo. Leaf
Pseudomonadales	0.000	0.000	0.0778%	0.7833%	1.7778%	2.3778%	1.4417%	26.5255%	1.1970%	22.9028%	0.9455%	28.1505%	12.7375%	32.1735%
Enterobacteriales	0.000	0.000	0.0796%	0.2523%	1.1912%	3.5292%	4.8245%	7.5352%	13.6333%	13.7389%	22.7136%	15.6236%	23.7954%	18.7660%
Rhodospirillales	0.000	0.000	10.2296%	8.4796%	5.2593%	6.7319%	9.6792%	7.1569%	16.3722%	5.3977%	16.1722%	6.4472%	1.1699%	0.2253%
Rhizobiales	0.000	0.000	4.3019%	10.4931%	9.3856%	8.2269%	4.8042%	3.3944%	3.6288%	2.6412%	9.2843%	2.8718%	5.2620%	1.0105%
[Saprospirales]	0.000	0.000	4.4852%	9.7074%	11.3870%	11.5505%	4.0819%	1.6778%	4.8323%	3.4917%	5.2773%	3.8866%	0.4102%	0.3710%
Un.	0.000	0.000	0.1204%	0.1671%	12.2056%	2.4162%	19.2282%	0.9051%	13.5359%	0.7653%	8.0480%	0.3560%	1.7653%	1.2994%
Xanthomonadales	0.000	0.000	5.5444%	4.0014%	8.7676%	5.2019%	3.2625%	2.9667%	4.0975%	1.4477%	3.4601%	1.6708%	1.3394%	3.4685%
Sphingobacteriales	0.000	0.000	1.9556%	5.2778%	2.4023%	5.7389%	2.5843%	2.1278%	2.9187%	2.6685%	6.2778%	2.8819%	0.9245%	3.0204%
Legionellales	0.000	0.000	0.7796%	2.6921%	0.7241%	0.8977%	0.2838%	0.0449%	0.4520%	0.0477%	0.7146%	0.0384%	19.6139%	1.6642%
Acidobacteriales	0.000	0.000	4.4556%	2.5319%	2.6931%	10.2208%	1.4278%	0.7375%	0.8823%	0.6880%	1.3571%	0.8713%	0.0514%	0.0753%
Cytophagales	0.000	0.000	1.4037%	2.4639%	5.5977%	3.4639%	1.4384%	0.7426%	0.8187%	0.6477%	1.1076%	0.7079%	0.8477%	0.1043%
Un.	0.000	0.000	0.0185%	0.0111%	0.1792%	0.5569%	0.9630%	2.3130%	0.7480%	4.0574%	1.3066%	2.7588%	0.8144%	5.9142%
Un. Alphaproteobacteria	0.000	0.000	0.5630%	0.4880%	0.5097%	1.2208%	2.8227%	5.3148%	1.7293%	1.3514%	1.3919%	1.6190%	0.6120%	0.1716%
[Chthoniobacterales]	0.000	0.000	0.2370%	4.5185%	1.7264%	3.1231%	0.2620%	0.1593%	0.0212%	0.1301%	0.1783%	0.1394%	0.0074%	0.0049%
Tremblayales	0.000	0.000	0.0000%	0.0014%	0.0000%	0.1120%	0.9583%	0.2199%	3.8162%	1.0347%	6.4444%	1.1898%	0.8093%	0.0932%
Ellin329	0.000	0.000	5.0426%	1.7648%	1.5444%	2.0449%	0.3361%	0.0370%	0.0364%	0.0231%	0.0035%	0.0190%	0.0079%	0.0074%
Solibacterales	0.000	0.000	5.5722%	1.4593%	0.7037%	1.6694%	0.5296%	0.0472%	0.0359%	0.0162%	0.0000%	0.0060%	0.0491%	0.0056%
iii1-15	0.000	0.000	3.9981%	2.9847%	0.7181%	0.3032%	0.4588%	0.0176%	0.0313%	0.0069%	0.0000%	0.0065%	0.0162%	0.0031%
Un. Betaproteobacteria	0.000	0.000	8.1148%	1.3069%	0.1093%	0.1801%	0.1755%	0.0042%	0.0192%	0.0028%	0.0000%	0.0028%	0.0023%	0.0012%
MND1	0.000	0.000	7.1611%	1.7593%	0.1241%	0.0824%	0.2176%	0.0037%	0.0283%	0.0028%	0.0000%	0.0032%	0.0116%	0.0019%
Myxococcales	0.000	0.000	0.7315%	1.2426%	4.4176%	1.8431%	0.5144%	0.0588%	0.0813%	0.0532%	0.0207%	0.0875%	0.2972%	0.0123%
[Pedosphaerales]	0.000	0.000	2.9833%	1.4935%	1.0444%	2.4500%	0.5495%	0.0384%	0.0389%	0.0171%	0.0000%	0.0148%	0.0213%	0.0080%
Actinomycetales	0.000	0.000	1.2111%	0.7380%	1.1255%	0.5060%	1.8005%	0.4995%	1.2586%	0.2690%	0.6419%	0.1620%	0.4574%	0.1315%
Caulobacterales	0.000	0.000	0.1296%	1.2153%	1.1722%	0.7704%	0.4769%	0.2477%	0.4217%	0.4602%	0.5854%	0.3597%	0.1028%	0.3086%
Chlamydiales	0.000	0.000	1.4519%	2.1806%	0.4051%	0.4282%	0.0829%	0.0681%	0.1232%	0.0236%	0.1045%	0.0333%	0.0042%	0.0056%
Bacillales	0.000	0.000	0.5222%	0.4069%	0.1176%	0.3241%	0.6278%	0.6565%	0.3611%	0.3199%	0.0904%	0.3551%	1.4273%	0.3142%
Rubrobacterales	0.000	0.000	0.0000%	0.0005%	0.0148%	0.0042%	0.7199%	1.1222%	0.3773%	1.1528%	0.2460%	0.5060%	0.8593%	0.2593%
Rickettsiales	0.000	0.000	0.1389%	0.2153%	0.0653%	0.1310%	0.1588%	0.2347%	0.1030%	0.0333%	0.2848%	0.0231%	1.5421%	2.0704%
Opitutales	0.000	0.000	0.6796%	1.3806%	0.6403%	0.6028%	0.1560%	0.0088%	0.0101%	0.0079%	0.0020%	0.0060%	0.0005%	0.0025%
Lactobacillales	0.000	0.000	0.0000%	0.0000%	0.0023%	0.0926%	0.8769%	0.5741%	0.4722%	0.3162%	0.0884%	0.1843%	0.3519%	1.0235%
Gemmatales	0.000	0.000	0.1444%	1.4736%	0.1639%	0.4056%	0.0792%	0.0106%	0.0081%	0.0074%	0.0303%	0.0125%	0.0000%	0.0019%
Syntrophobacterales	0.000	0.000	1.1778%	0.8264%	0.3338%	0.2157%	0.2824%	0.0153%	0.0187%	0.0065%	0.0010%	0.0069%	0.0037%	0.0043%
Un. Acidobacteria-5	0.000	0.000	2.6741%	0.2940%	0.1051%	0.1069%	0.1921%	0.0069%	0.0106%	0.0005%	0.0000%	0.0005%	0.0028%	0.0012%
Un. SJA-4	0.000	0.000	0.1463%	1.1458%	0.2454%	0.1551%	0.0370%	0.0037%	0.0040%	0.0120%	0.0000%	0.0106%	0.0005%	0.0031%
Rhodobacterales	0.000	0.000	0.4093%	0.3528%	0.8162%	0.3991%	0.0648%	0.0144%	0.0056%	0.0218%	0.0000%	0.0231%	0.0306%	0.0105%
[Fimbriimonadales]	0.000	0.000	0.0241%	0.7356%	0.4190%	0.3213%	0.0815%	0.0125%	0.0177%	0.0056%	0.0197%	0.0106%	0.0028%	0.0049%
Pirellulales	0.000	0.000	0.2500%	0.6495%	0.2412%	0.3639%	0.1037%	0.0093%	0.0030%	0.0005%	0.0000%	0.0032%	0.0009%	0.0000%
Ellin5290	0.000	0.000	1.7574%	0.1181%	0.0245%	0.0162%	0.0690%	0.0032%	0.0030%	0.0042%	0.0000%	0.0028%	0.0000%	0.0000%
Spirochaetales	0.000	0.000	0.0241%	0.3995%	0.9130%	0.1912%	0.0333%	0.0111%	0.0025%	0.0056%	0.0000%	0.0000%	0.0005%	0.0025%
Methylacidiphilales	0.000	0.000	0.0000%	0.3120%	0.2356%	1.0986%	0.0079%	0.0037%	0.0000%	0.0023%	0.0000%	0.0032%	0.0000%	0.0000%
RB41	0.000	0.000	0.3296%	0.3074%	0.3977%	0.4042%	0.1907%	0.0046%	0.0035%	0.0028%	0.0000%	0.0046%	0.0111%	0.0031%
Un. Gemm-1	0.000	0.000	1.1500%	0.3046%	0.0546%	0.0255%	0.0671%	0.0005%	0.0045%	0.0005%	0.0000%	0.0032%	0.0000%	0.0000%
SBR1031	0.000	0.000	0.1056%	0.5653%	0.3981%	0.1921%	0.0444%	0.0005%	0.0010%	0.0009%	0.0000%	0.0014%	0.0000%	0.0006%
DH61	0.000	0.000	0.0093%	0.8250%	0.1032%	0.0435%	0.0463%	0.0009%	0.0015%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%
Ellin6067	0.000	0.000	0.7907%	0.3782%	0.0310%	0.0620%	0.0741%	0.0014%	0.0111%	0.0000%	0.0000%	0.0000%	0.0144%	0.0006%
Planctomycetales	0.000	0.000	0.0722%	0.5389%	0.1106%	0.2444%	0.1102%	0.0111%	0.0101%	0.0111%	0.0596%	0.0125%	0.0000%	0.0012%
Pasteurellales	0.000	0.000	0.0000%	0.0000%	0.0005%	0.0255%	0.1269%	0.0690%	0.1965%	0.2903%	0.4848%	0.3454%	0.1046%	0.0364%
Gaiellales	0.000	0.000	0.6648%	0.3005%	0.0477%	0.0477%	0.2241%	0.0037%	0.0242%	0.0032%	0.0000%	0.0009%	0.0218%	0.0006%
Thiotrichales	0.000	0.000	0.9111%	0.2148%	0.0801%	0.0894%	0.0537%	0.0097%	0.0076%	0.0000%	0.0000%	0.0000%	0.0042%	0.0006%
Clostridiales	0.000	0.000	0.0000%	0.0162%	0.0000%	0.7023%	0.0296%	0.0759%	0.0298%	0.2958%	0.0773%	0.2509%	0.0833%	0.0043%
Verrucomicrobiales	0.000	0.000	0.0056%	0.2634%	0.1014%	0.1190%	0.2338%	0.0495%	0.0601%	0.0440%	0.2662%	0.0491%	0.0000%	0.0000%
Un. Gemm-1	0.000	0.000	0.7722%	0.1759%	0.0884%	0.0324%	0.0269%	0.0000%	0.0000%	0.0019%	0.0000%	0.0000%	0.0000%	0.0012%
Ellin6513	0.000	0.000	0.6722%	0.1523%	0.1292%	0.0856%	0.0500%	0.0005%	0.0035%	0.0023%	0.0000%	0.0000%	0.0019%	0.0000%
Neisseriales	0.000	0.000	0.0000%	0.2931%	0.2759%	0.0792%	0.0125%	0.0375%	0.0025%	0.0481%	0.0025%	0.0750%	0.0204%	0.0290%
FAC88	0.000	0.000	0.5481%	0.1602%	0.1139%	0.1356%	0.0352%	0.0014%	0.0020%	0.0014%	0.0000%	0.0056%	0.0023%	0.0006%
Acidimicrobiales	0.000	0.000	0.2833%	0.2949%	0.0606%	0.0444%	0.1185%	0.0102%	0.0040%	0.0032%	0.0000%	0.0060%	0.0083%	0.0006%
Un. Alphaproteobacteria	0.000	0.000	0.0889%	0.2162%	0.3477%	0.1736%	0.0208%	0.0014%	0.0010%	0.0014%	0.0015%	0.0074%	0.0019%	0.0025%
Solirubrobacterales	0.000	0.000	0.3130%	0.1458%	0.0366%	0.1375%	0.2056%	0.0222%	0.0207%	0.0028%	0.0010%	0.0190%	0.0148%	0.0025%
Un. Gammaproteobacteri	0.000	0.000	0.2778%	0.2583%	0.0819%	0.1009%	0.0389%	0.0009%	0.0030%	0.0046%	0.0000%	0.0005%	0.0028%	0.0302%
Un. Betaproteobacteria	0.000	0.000	0.1000%	0.2491%	0.1468%	0.1630%	0.0338%	0.0125%	0.0030%	0.0273%	0.0005%	0.0338%	0.0019%	0.0056%
Anaeroplasmatales	0.000	0.000	0.0000%	0.0074%	0.9648%	0.0194%	0.0023%	0.0042%	0.0000%	0.0023%	0.0000%	0.0000%	0.0009%	0.0037%
BD7-3	0.000	0.000	0.3185%	0.1907%	0.1875%	0.0750%	0.0241%	0.0005%	0.0015%	0.0042%	0.0025%	0.0097%	0.0014%	0.0043%
Sediment-1	0.000	0.000	0.2204%	0.2856%	0.0926%	0.0273%	0.0801%	0.0019%	0.0045%	0.0009%	0.0000%	0.0000%	0.0009%	0.0000%
Nitrososphaerales	0.000	0.000	0.2019%	0.2801%	0.0741%	0.0296%	0.0806%	0.0051%	0.0051%	0.0037%	0.0000%	0.0023%	0.0009%	0.0000%
MLE1-12	0.000	0.000	0.1407%	0.2685%	0.0787%	0.1597%	0.0060%	0.0051%	0.0000%	0.0046%	0.0020%	0.0116%	0.0000%	0.0000%
Un.	0.000	0.000	0.0037%	0.2699%	0.0477%	0.0523%	0.0403%	0.2102%	0.0025%	0.0028%	0.0086%	0.0014%	0.0005%	0.0000%
Rhodocyclales	0.000	0.000	0.0056%	0.2176%	0.0977%	0.1880%	0.0380%	0.0125%	0.0227%	0.0241%	0.0136%	0.0231%	0.0069%	0.0006%
[Cerasicoccales]	0.000	0.000	0.5611%	0.1343%	0.0032%	0.0079%	0.0069%	0.0019%	0.0000%	0.0069%	0.0025%	0.0028%	0.0000%	0.0000%
Alteromonadales	0.000	0.000	0.0167%	0.2718%	0.1148%	0.0995%	0.0454%	0.0005%	0.0015%	0.0000%	0.0000%	0.0028%	0.0028%	0.0012%
Un. Gammaproteobacteri	0.000	0.000	0.2500%	0.1060%	0.2898%	0.0356%	0.0204%	0.0042%	0.0020%	0.0000%	0.0000%	0.0005%	0.0000%	0.0043%
Phycisphaerales	0.000	0.000	0.2741%	0.1046%	0.1097%	0.1903%	0.0213%	0.0023%	0.0000%	0.0028%	0.0000%	0.0060%	0.0005%	0.0000%
258ds10	0.000	0.000	0.0130%	0.2741%	0.1630%	0.0440%	0.0356%	0.0014%	0.0020%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Sva0725	0.000	0.000	0.0463%	0.2532%	0.0986%	0.0227%	0.1139%	0.0000%	0.0131%	0.0005%	0.0000%	0.0000%	0.0014%	0.0000%
Un. Chlamydiia	0.000	0.000	0.0000%	0.3241%	0.0287%	0.0759%	0.0176%	0.0000%	0.0000%	0.0005%	0.0000%	0.0005%	0.0000%	0.0006%
Nitrospirales	0.000	0.000	0.2333%	0.1681%	0.0560%	0.0241%	0.0949%	0.0014%	0.0106%	0.0000%	0.0000%	0.0023%	0.0005%	0.0012%
Cenarchaeales	0.000	0.000	0.7148%	0.0130%	0.0009%	0.0000%	0.0060%	0.0005%	0.0000%	0.0009%	0.0000%	0.0042%	0.0000%	0.0000%
Bdellovibrionales	0.000	0.000	0.1815%	0.0667%	0.0889%	0.0958%	0.0370%	0.0009%	0.0045%	0.0718%	0.0596%	0.0699%	0.0056%	0.0006%
Un.	0.000	0.000	0.1796%	0.1949%	0.0546%	0.0903%	0.0093%	0.0005%	0.0005%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%
Un. S085	0.000	0.000	0.3444%	0.1662%	0.0088%	0.0120%	0.0231%	0.0000%	0.0005%	0.0005%	0.0000%	0.0005%	0.0014%	0.0000%
Un.	0.000	0.000	0.2074%	0.0000%	0.0000%	0.0000%	0.0069%	0.1366%	0.0126%	0.1301%	0.0035%	0.0958%	0.0019%	0.1235%
[Entotheonellales]	0.000	0.000	0.3648%	0.1319%	0.0157%	0.0037%	0.0157%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Nov-24	0.000	0.000	0.0648%	0.1329%	0.1157%	0.2079%	0.0051%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%
B07_WMSP1	0.000	0.000	0.2167%	0.1694%	0.0019%	0.0046%	0.0222%	0.0014%	0.0000%	0.0009%	0.0000%	0.0000%	0.0005%	0.0000%
Un. SBRH58	0.000	0.000	0.0407%	0.2181%	0.0208%	0.0528%	0.0194%	0.0037%	0.0015%	0.0046%	0.0000%	0.0000%	0.0000%	0.0000%
Un. Mb-NB09	0.000	0.000	0.1019%	0.1755%	0.1144%	0.0000%	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%	0.0019%	0.0000%	0.0000%
Un. TM7-1	0.000	0.000	0.3296%	0.0898%	0.0241%	0.0056%	0.0023%	0.0000%	0.0000%	0.0042%	0.0126%	0.0028%	0.0037%	0.0000%
IS-44	0.000	0.000	0.1185%	0.1106%	0.0398%	0.1208%	0.0542%	0.0000%	0.0061%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
AKYG885	0.000	0.000	0.0574%	0.2171%	0.0213%	0.0088%	0.0329%	0.0000%	0.0010%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%
KD8-87	0.000	0.000	0.3722%	0.0755%	0.0167%	0.0051%	0.0093%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
SC-I-84	0.000	0.000	0.0648%	0.1009%	0.0324%	0.1491%	0.0495%	0.0046%	0.0030%	0.0023%	0.0000%	0.0000%	0.0014%	0.0000%
SM1D11	0.000	0.000	0.0407%	0.1046%	0.0384%	0.0718%	0.0718%	0.0009%	0.0000%	0.0032%	0.0631%	0.0042%	0.0009%	0.0000%
CCU21	0.000	0.000	0.0093%	0.1375%	0.1662%	0.0213%	0.0106%	0.0023%	0.0000%	0.0000%	0.0000%	0.0000%	0.0009%	0.0000%
Un.	0.000	0.000	0.3704%	0.0361%	0.0157%	0.0083%	0.0148%	0.0000%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. Chlamydiia	0.000	0.000	0.0037%	0.2046%	0.0375%	0.0185%	0.0028%	0.0000%	0.0010%	0.0019%	0.0000%	0.0051%	0.0000%	0.0000%

MIZ46	0.000	0.000	0.2093%	0.0440%	0.0755%	0.0736%	0.0208%	0.0005%	0.0015%	0.0037%	0.0000%	0.0009%	0.0000%	0.0012%
Un. Gemmatimonadetes	0.000	0.000	0.2500%	0.0500%	0.0162%	0.0218%	0.0676%	0.0028%	0.0030%	0.0028%	0.0000%	0.0000%	0.0079%	0.0000%
Un. Deltaproteobacteria	0.000	0.000	0.1185%	0.0963%	0.0602%	0.0537%	0.0060%	0.0000%	0.0000%	0.0019%	0.0000%	0.0009%	0.0000%	0.0000%
PK29	0.000	0.000	0.0963%	0.0537%	0.1583%	0.0181%	0.0236%	0.0028%	0.0005%	0.0009%	0.0000%	0.0019%	0.0009%	0.0000%
Un.	0.000	0.000	0.3315%	0.0222%	0.0014%	0.0019%	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
WD2101	0.000	0.000	0.1296%	0.0282%	0.0338%	0.1000%	0.0343%	0.0074%	0.0015%	0.0019%	0.0071%	0.0019%	0.0056%	0.0000%
FW68	0.000	0.000	0.0019%	0.1287%	0.0431%	0.0472%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. Ellin6529	0.000	0.000	0.0741%	0.0884%	0.0269%	0.0111%	0.0486%	0.0000%	0.0025%	0.0037%	0.0000%	0.0019%	0.0000%	0.0000%
Procabacteriales	0.000	0.000	0.0093%	0.0875%	0.0060%	0.0477%	0.0042%	0.0338%	0.0010%	0.0185%	0.0000%	0.0264%	0.0042%	0.0068%
Armatimonadales	0.000	0.000	0.0000%	0.0926%	0.0310%	0.0440%	0.0278%	0.0069%	0.0242%	0.0005%	0.0066%	0.0000%	0.0005%	0.0000%
Aeromonadales	0.000	0.000	0.0000%	0.0000%	0.0005%	0.0000%	0.0000%	0.1185%	0.0000%	0.0815%	0.0000%	0.1176%	0.0000%	0.0056%
Un.	0.000	0.000	0.0148%	0.1051%	0.0352%	0.0514%	0.0042%	0.0000%	0.0000%	0.0000%	0.0000%	0.0009%	0.0000%	0.0019%
Un.	0.000	0.000	0.1278%	0.0861%	0.0111%	0.0014%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
CL500-15	0.000	0.000	0.1204%	0.0667%	0.0269%	0.0139%	0.0139%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%	0.0000%
Un.	0.000	0.000	0.1259%	0.0278%	0.0454%	0.0264%	0.0431%	0.0000%	0.0051%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0241%	0.0167%	0.0444%	0.0505%	0.1259%	0.0111%	0.0005%	0.0000%	0.0000%	0.0000%	0.0079%	0.0000%
IIb	0.000	0.000	0.2056%	0.0366%	0.0046%	0.0060%	0.0056%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0019%	0.0000%
Un. SJA-28	0.000	0.000	0.0333%	0.1111%	0.0264%	0.0023%	0.0079%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
GIF10	0.000	0.000	0.1111%	0.0444%	0.0597%	0.0083%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Kiloniellales	0.000	0.000	0.0000%	0.0565%	0.0671%	0.0731%	0.0009%	0.0000%	0.0000%	0.0019%	0.0000%	0.0120%	0.0000%	0.0000%
Un. 0319-6E2	0.000	0.000	0.0167%	0.1181%	0.0069%	0.0037%	0.0009%	0.0000%	0.0005%	0.0000%	0.0000%	0.0014%	0.0005%	0.0000%
Un. ABY1	0.000	0.000	0.1426%	0.0454%	0.0042%	0.0046%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
PHOS-HD29	0.000	0.000	0.0037%	0.0866%	0.0241%	0.0292%	0.0037%	0.0000%	0.0000%	0.0032%	0.0000%	0.0009%	0.0000%	0.0006%
DS-18	0.000	0.000	0.0259%	0.0847%	0.0167%	0.0019%	0.0139%	0.0000%	0.0035%	0.0000%	0.0000%	0.0000%	0.0009%	0.0006%
Desulfuromonadales	0.000	0.000	0.0000%	0.0880%	0.0023%	0.0458%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0051%	0.0000%
WCHD3-30	0.000	0.000	0.1944%	0.0106%	0.0000%	0.0000%	0.0042%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. EC1113	0.000	0.000	0.0907%	0.0542%	0.0009%	0.0046%	0.0116%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. TM1	0.000	0.000	0.1333%	0.0301%	0.0120%	0.0069%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0014%	0.0000%
[Roseiflexales]	0.000	0.000	0.0074%	0.0569%	0.0644%	0.0139%	0.0074%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
CFB-26	0.000	0.000	0.0426%	0.0588%	0.0403%	0.0009%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0296%	0.0352%	0.0028%	0.0889%	0.0069%	0.0005%	0.0005%	0.0009%	0.0000%	0.0005%	0.0000%	0.0006%
p04_C01	0.000	0.000	0.0148%	0.0667%	0.0171%	0.0139%	0.0093%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0963%	0.0306%	0.0111%	0.0014%	0.0037%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
PK329	0.000	0.000	0.1130%	0.0204%	0.0139%	0.0000%	0.0042%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%
NB1-j	0.000	0.000	0.0278%	0.0250%	0.0787%	0.0019%	0.0083%	0.0009%	0.0000%	0.0009%	0.0000%	0.0000%	0.0023%	0.0000%
Un.	0.000	0.000	0.0259%	0.0417%	0.0384%	0.0111%	0.0106%	0.0000%	0.0010%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. VHS-B5-50	0.000	0.000	0.0444%	0.0583%	0.0060%	0.0005%	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Holophagales	0.000	0.000	0.0037%	0.0648%	0.0102%	0.0093%	0.0060%	0.0009%	0.0020%	0.0069%	0.0000%	0.0009%	0.0000%	0.0000%
HTCC2188	0.000	0.000	0.0204%	0.0352%	0.0231%	0.0389%	0.0130%	0.0000%	0.0015%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Spirobacillales	0.000	0.000	0.0037%	0.0162%	0.0722%	0.0181%	0.0269%	0.0014%	0.0000%	0.0000%	0.0005%	0.0000%	0.0023%	0.0093%
Un. OPB56	0.000	0.000	0.0056%	0.0495%	0.0130%	0.0278%	0.0167%	0.0000%	0.0015%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%
Un. 3BR-5F	0.000	0.000	0.0037%	0.0713%	0.0120%	0.0023%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
agg27	0.000	0.000	0.0296%	0.0324%	0.0310%	0.0194%	0.0093%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
[Leptospirales]	0.000	0.000	0.0000%	0.0236%	0.0815%	0.0130%	0.0023%	0.0000%	0.0000%	0.0014%	0.0000%	0.0009%	0.0000%	0.0006%
Un. SM2F11	0.000	0.000	0.1185%	0.0097%	0.0019%	0.0060%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. SC3	0.000	0.000	0.0667%	0.0343%	0.0069%	0.0005%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. VC2_1_Bac22	0.000	0.000	0.0000%	0.0120%	0.0403%	0.0681%	0.0065%	0.0014%	0.0000%	0.0005%	0.0000%	0.0009%	0.0005%	0.0000%
Un.	0.000	0.000	0.0593%	0.0301%	0.0185%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. ML635J-21	0.000	0.000	0.0148%	0.0491%	0.0005%	0.0125%	0.0065%	0.0000%	0.0020%	0.0000%	0.0000%	0.0000%	0.0014%	0.0012%
MVS-107	0.000	0.000	0.0426%	0.0370%	0.0079%	0.0023%	0.0060%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Elusimicrobiales	0.000	0.000	0.0944%	0.0162%	0.0009%	0.0023%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
CV90	0.000	0.000	0.0000%	0.0481%	0.0139%	0.0162%	0.0023%	0.0000%	0.0000%	0.0000%	0.0000%	0.0019%	0.0000%	0.0000%
Un. Gemm-2	0.000	0.000	0.0630%	0.0264%	0.0000%	0.0005%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Chromatiales	0.000	0.000	0.0093%	0.0227%	0.0532%	0.0032%	0.0032%	0.0000%	0.0000%	0.0019%	0.0000%	0.0000%	0.0000%	0.0000%
Un. Deltaproteobacteria	0.000	0.000	0.0333%	0.0343%	0.0069%	0.0037%	0.0028%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. PAUC37f	0.000	0.000	0.0241%	0.0269%	0.0134%	0.0097%	0.0125%	0.0000%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0574%	0.0259%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0333%	0.0282%	0.0088%	0.0014%	0.0065%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0006%
TK10	0.000	0.000	0.0481%	0.0255%	0.0000%	0.0032%	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
ArcA07	0.000	0.000	0.1019%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
B97	0.000	0.000	0.0000%	0.0356%	0.0255%	0.0042%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Gemellales	0.000	0.000	0.0000%	0.0000%	0.0000%	0.0000%	0.0074%	0.0250%	0.0000%	0.0370%	0.0005%	0.0083%	0.0218%	0.0000%
YLA114	0.000	0.000	0.0778%	0.0074%	0.0014%	0.0009%	0.0023%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0389%	0.0250%	0.0019%	0.0009%	0.0014%	0.0000%	0.0000%	0.0009%	0.0000%	0.0000%	0.0005%	0.0000%
Un.	0.000	0.000	0.0222%	0.0190%	0.0111%	0.0069%	0.0065%	0.0019%	0.0010%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
N1423WL	0.000	0.000	0.0352%	0.0120%	0.0051%	0.0139%	0.0079%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%	0.0006%
Un. Gemm-3	0.000	0.000	0.0389%	0.0088%	0.0005%	0.0032%	0.0176%	0.0000%	0.0010%	0.0000%	0.0000%	0.0000%	0.0060%	0.0000%
Un.	0.000	0.000	0.0796%	0.0000%	0.0000%	0.0014%	0.0009%	0.0000%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%
d113	0.000	0.000	0.0241%	0.0255%	0.0019%	0.0000%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0009%	0.0000%	0.0000%
Fusobacteriales	0.000	0.000	0.0000%	0.0000%	0.0000%	0.0000%	0.0032%	0.0125%	0.0000%	0.0176%	0.0000%	0.0167%	0.0278%	0.0000%
Un. C0119	0.000	0.000	0.0000%	0.0171%	0.0032%	0.0347%	0.0042%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%
LD1-PA13	0.000	0.000	0.0500%	0.0093%	0.0023%	0.0042%	0.0009%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. [Chloracidobacteria]	0.000	0.000	0.0148%	0.0194%	0.0065%	0.0051%	0.0065%	0.0000%	0.0005%	0.0019%	0.0000%	0.0000%	0.0000%	0.0000%
Mariprofundales	0.000	0.000	0.0259%	0.0106%	0.0130%	0.0028%	0.0083%	0.0000%	0.0010%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
H39	0.000	0.000	0.0093%	0.0213%	0.0102%	0.0042%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%	0.0000%
Un. P2-11E	0.000	0.000	0.0537%	0.0074%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%
Un. BME43	0.000	0.000	0.0000%	0.0139%	0.0259%	0.0106%	0.0042%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%
Un. koll11	0.000	0.000	0.0426%	0.0079%	0.0074%	0.0019%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
envOPS12	0.000	0.000	0.0204%	0.0185%	0.0042%	0.0019%	0.0037%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. MSB-5A5	0.000	0.000	0.0111%	0.0273%	0.0005%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Ktedonobacterales	0.000	0.000	0.0019%	0.0042%	0.0306%	0.0153%	0.0056%	0.0009%	0.0005%	0.0019%	0.0000%	0.0000%	0.0005%	0.0000%
0319-7L14	0.000	0.000	0.0185%	0.0167%	0.0005%	0.0005%	0.0102%	0.0005%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0019%	0.0019%	0.0000%	0.0014%	0.0019%	0.0083%	0.0030%	0.0088%	0.0000%	0.0065%	0.0000%	0.0222%
A89	0.000	0.000	0.0056%	0.0222%	0.0051%	0.0005%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. OP11-4	0.000	0.000	0.0463%	0.0046%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
d153	0.000	0.000	0.0037%	0.0236%	0.0005%	0.0005%	0.0023%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
DS-100	0.000	0.000	0.0000%	0.0069%	0.0273%	0.0074%	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. Opitutae	0.000	0.000	0.0130%	0.0069%	0.0213%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0000%	0.0213%	0.0000%	0.0046%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0037%	0.0190%	0.0000%	0.0009%	0.0056%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
I025	0.000	0.000	0.0111%	0.0153%	0.0046%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
JH-WHS99	0.000	0.000	0.0093%	0.0181%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
HOC36	0.001	0.001	0.0000%	0.0125%	0.0019%	0.0102%	0.0079%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
mle1-48	0.000	0.000	0.0093%	0.0144%	0.0000%	0.0014%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%
Un.	0.000	0.000	0.0000%	0.0134%	0.0042%	0.0065%	0.0023%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
C114	0.000	0.000	0.0000%	0.0176%	0.0000%	0.0000%	0.0056%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. TK10	0.000	0.000	0.0130%	0.0116%	0.0000%	0.0000%	0.0037%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. SHA-109	0.000	0.000	0.0000%	0.0167%	0.0000%	0.0000%	0.0060%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
32-20	0.000	0.000	0.0111%	0.0056%	0.0088%	0.0037%	0.0046%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. Ktedonobacteria	0.000	0.000	0.0204%	0.0069%	0.0000%	0.0014%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
JG30-KF-AS9	0.000	0.000	0.0204%	0.0009%	0.0000%	0.0088%	0.0065%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Ellin7246	0.000	0.000	0.0074%	0.0139%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0009%	0.0000%
SJA-22	0.000	0.000	0.0000%	0.0005%	0.0120%	0.0245%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
A31	0.000	0.000	0.0037%	0.0130%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%
CPla-3	0.000	0.000	0.0037%	0.0032%	0.0046%	0.0194%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. TK17	0.000	0.000	0.0241%	0.0056%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%

Un. Endomicrobia	0.000	0.000	0.0093%	0.0097%	0.0060%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Micrococcales	0.000	0.000	0.0093%	0.0093%	0.0000%	0.0000%	0.0056%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
MVP-88	0.000	0.000	0.0259%	0.0023%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
GCA004	0.000	0.000	0.0000%	0.0153%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. GN07	0.000	0.000	0.0000%	0.0148%	0.0009%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
FAC87	0.000	0.000	0.0093%	0.0014%	0.0005%	0.0134%	0.0037%	0.0000%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%
Pla1	0.000	0.000	0.0148%	0.0056%	0.0000%	0.0005%	0.0019%	0.0000%	0.0000%	0.0019%	0.0000%	0.0000%	0.0000%	0.0000%
S1198	0.000	0.000	0.0000%	0.0134%	0.0000%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0006%
Un. Gemmatimonadetes	0.001	0.001	0.0167%	0.0023%	0.0000%	0.0000%	0.0014%	0.0000%	0.0015%	0.0000%	0.0000%	0.0000%	0.0014%	0.0000%
Un.	0.000	0.000	0.0093%	0.0074%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. S035	0.000	0.000	0.0111%	0.0042%	0.0000%	0.0000%	0.0046%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0000%	0.0116%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Chthonomonadales	0.000	0.000	0.0019%	0.0009%	0.0000%	0.0153%	0.0028%	0.0005%	0.0000%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0222%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. IIB17	0.000	0.000	0.0000%	0.0069%	0.0074%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. Thermomicrobia	0.000	0.000	0.0167%	0.0000%	0.0000%	0.0000%	0.0019%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. PBS-25	0.000	0.000	0.0000%	0.0069%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%	0.0000%
Mycoplasmatales	0.000	0.000	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0009%	0.0000%	0.0074%	0.0000%	0.0037%	0.0000%	0.0025%
Un.	0.000	0.000	0.0148%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un.	0.000	0.000	0.0093%	0.0019%	0.0000%	0.0000%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Caldilineales	0.000	0.000	0.0000%	0.0046%	0.0000%	0.0000%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. BD7-11	0.000	0.000	0.0000%	0.0051%	0.0000%	0.0019%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Nitrosomonadales	0.000	0.000	0.0074%	0.0000%	0.0000%	0.0014%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0019%	0.0000%
SJA-36	0.001	0.001	0.0000%	0.0037%	0.0032%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Un. SAR202	0.000	0.000	0.0037%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
CCM11a	0.000	0.000	0.0037%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
E2	0.000	0.000	0.0019%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%

Supplementary Table 4 - Fungal orders with significant differences in relative abundance in at least two sample types. The average relative abundance of sample types was used in Kruskal-Wallis tests on the order level to identify taxa whose average abundance differed significantly between sample types. A threshold of P<0,001 (FDR corrected) was used. Un.:Unknown; Exo.: Exophytic; Endo.: Endophytic

Order	P value	P value (FDR corrected)	Sample Type											
			Bulk Soil	Rhizosphere	Endophytic Root	Young Shoot	Exophytic Bottom Stalk	Endophytic Bottom Stalk	Exophytic Medium Stalk	Endophytic Medium Stalk	Exophytic Upper Stalk	Endophytic Upper Stalk	Exophytic Leaf	Endophytic Leaf
Capnodiales	0.000	0.000	7.1139%	2.4167%	0.1232%	0.2813%	48.6898%	36.2167%	20.9146%	23.1620%	28.5866%	12.8742%	9.8318%	13.1617%
Unkown	0.000	0.000	36.9236%	12.8045%	8.3030%	11.1187%	1.0380%	4.3801%	2.6136%	4.9051%	7.9134%	12.7091%	33.8894%	47.3222%
Eurotiales	0.000	0.000	7.0000%	8.1828%	11.7480%	1.9460%	8.2625%	12.5750%	23.1045%	1.4231%	8.4403%	14.7758%	8.0783%	0.4389%
Saccharomycetales	0.000	0.000	0.2708%	0.9712%	0.0040%	0.2500%	10.6287%	16.8102%	19.5939%	1.2435%	14.2269%	17.8914%	6.6323%	1.1011%
Polyporales	0.000	0.000	0.0778%	23.1490%	16.4939%	32.8298%	0.0148%	0.0005%	0.0101%	0.1222%	0.0259%	2.5813%	0.2288%	0.4011%
Unkown	0.000	0.000	4.4681%	4.0970%	3.3899%	2.0818%	5.0870%	7.8824%	9.8914%	1.0028%	3.5995%	4.8081%	9.2005%	10.5078%
Hypocreales	0.000	0.000	3.0917%	1.4934%	2.0672%	2.4742%	1.8634%	1.7074%	4.5545%	0.2583%	18.4843%	14.2419%	7.7136%	0.2783%
Unkown Agaricomycetes	0.000	0.000	3.1625%	19.0298%	17.8818%	14.4419%	0.2208%	0.0519%	0.0222%	0.1407%	0.4602%	0.2005%	0.3025%	1.1233%
Pleosporales	0.000	0.000	1.0083%	0.7328%	1.4172%	0.4116%	0.7167%	1.3750%	0.4465%	24.9972%	0.9319%	0.6298%	0.1899%	4.3078%
Unkown	0.000	0.000	4.1819%	4.8389%	11.6202%	3.5439%	0.1620%	0.0690%	0.0303%	0.1287%	1.3602%	1.2859%	3.5470%	4.8883%
Chaetothyriales	0.000	0.000	0.4306%	1.4914%	1.0530%	5.3414%	7.9773%	6.5528%	5.1126%	0.1870%	3.2065%	2.7187%	1.3646%	0.0861%
Ustilaginales	0.000	0.000	0.0111%	0.1172%	0.0000%	0.0121%	1.3824%	0.9838%	1.1854%	17.7958%	0.2662%	0.9409%	0.0414%	12.1111%
Helotiales	0.000	0.000	0.0569%	0.0106%	0.0010%	0.0237%	0.8329%	0.4495%	2.7187%	0.0806%	2.4236%	6.7429%	17.2399%	0.0600%
Tremellales	0.000	0.000	0.3528%	0.4480%	0.1985%	0.4414%	7.2662%	5.8171%	6.6530%	0.7236%	2.3338%	1.4157%	0.5096%	0.3561%
Unkown Sordariomycetes	0.000	0.000	0.7611%	3.8707%	4.1808%	7.2030%	0.1898%	0.0764%	0.0889%	0.0296%	0.3856%	0.4783%	0.1136%	0.0178%
Agaricales	0.000	0.000	6.3333%	3.8949%	4.3611%	1.7995%	0.0269%	0.0014%	0.0126%	0.2856%	0.0000%	0.0091%	0.0904%	0.0461%
Filobasidiales	0.000	0.000	0.2444%	0.3965%	0.0045%	0.0697%	1.0634%	1.9912%	0.8293%	2.6074%	0.6537%	2.4126%	0.0939%	1.8344%
Trichosphaeriales	0.000	0.000	0.1028%	0.0247%	0.0035%	0.0061%	0.1593%	0.1528%	0.1242%	9.5176%	0.6403%	0.1520%	0.0924%	0.8056%
Sebacinales	0.000	0.000	0.0167%	2.2737%	3.3157%	1.9333%	0.5856%	0.0023%	0.0051%	0.0005%	3.3782%	0.0934%	0.0187%	0.0200%
Spizellomycetales	0.000	0.000	7.9722%	0.0030%	0.0061%	0.0010%	0.0023%	0.0000%	0.0000%	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%
Incertae_sedis	0.000	0.000	0.0736%	0.3646%	0.2394%	5.9717%	0.1065%	0.0111%	0.0051%	0.0324%	0.0542%	0.8354%	0.0010%	0.0167%
Chaetosphaeriales	0.000	0.000	0.0681%	1.4904%	4.2222%	1.1889%	0.0074%	0.0000%	0.0045%	0.0000%	0.0653%	0.0803%	0.1854%	0.0039%
Sordariales	0.000	0.000	5.5028%	0.4859%	0.6273%	0.2283%	0.0130%	0.0000%	0.0000%	0.0356%	0.0144%	0.0066%	0.0091%	0.0050%
unidentified	0.000	0.000	0.6139%	1.0692%	2.2843%	1.2763%	0.3375%	0.3954%	0.4076%	0.2227%	0.1838%	0.0510%	0.0354%	0.0472%
unidentified	0.000	0.000	0.4264%	1.2258%	2.3692%	0.9500%	0.0162%	0.0282%	0.0247%	0.6787%	0.0435%	0.0253%	0.2237%	0.0361%
Tilletiales	0.000	0.000	0.0000%	0.0172%	0.0000%	0.0035%	0.0292%	0.0171%	0.0187%	5.7926%	0.0088%	0.0136%	0.0247%	0.0778%
Incertae_sedis	0.000	0.000	0.0000%	0.0919%	0.0000%	0.0303%	1.4255%	1.0509%	0.8848%	1.4403%	0.1889%	0.1015%	0.0399%	0.0978%
Microascales	0.000	0.000	1.6153%	1.0520%	1.6000%	0.1020%	0.0065%	0.0000%	0.0000%	0.0051%	0.0042%	0.0040%	0.0000%	0.0011%
Dothideales	0.000	0.000	0.0111%	0.1323%	0.0000%	0.0000%	1.1153%	0.3750%	0.0545%	0.8699%	0.6019%	0.0187%	0.0308%	0.2861%
Cantharellales	0.000	0.000	0.0000%	0.3944%	0.4343%	1.5258%	0.0019%	0.0366%	0.0076%	0.0190%	0.0102%	0.9172%	0.0111%	0.0028%
Unkown Dothideomycetes	0.000	0.000	0.1903%	0.1020%	0.1823%	0.4455%	0.0829%	0.1324%	0.3384%	0.5792%	0.0241%	0.0081%	0.0328%	0.1311%
Glomerales	0.000	0.000	0.0931%	0.5823%	0.9975%	0.0485%	0.0083%	0.0000%	0.0005%	0.0005%	0.0005%	0.0005%	0.0076%	0.0028%
Unkown Eurotiomycetes	0.000	0.000	1.2236%	0.0949%	0.0495%	0.0005%	0.0134%	0.0181%	0.0227%	0.0014%	0.0000%	0.0000%	0.0152%	0.0022%
Onygenales	0.000	0.000	1.2486%	0.0374%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Unkown Leotiomycetes	0.000	0.000	1.2208%	0.0071%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0102%	0.0000%	0.0000%	0.0000%	0.0000%
unidentified	0.000	0.000	0.3819%	0.0338%	0.0717%	0.4561%	0.0023%	0.0023%	0.0005%	0.0435%	0.0000%	0.0015%	0.0025%	0.0061%
Microstromatales	0.000	0.000	0.0000%	0.0030%	0.0000%	0.0005%	0.1954%	0.3944%	0.0439%	0.2681%	0.0324%	0.0000%	0.0000%	0.0283%
Rhizophlyctidales	0.000	0.000	0.8597%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%
unidentified	0.000	0.000	0.0083%	0.7798%	0.0197%	0.0247%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Mucorales	0.000	0.000	0.2431%	0.4025%	0.0652%	0.0121%	0.0046%	0.0000%	0.0000%	0.0384%	0.0000%	0.0030%	0.0000%	0.0000%
Xylariales	0.000	0.000	0.0000%	0.0035%	0.0000%	0.0308%	0.0083%	0.0120%	0.0040%	0.1981%	0.3806%	0.0045%	0.0000%	0.0494%
unidentified	0.000	0.000	0.1861%	0.1641%	0.2697%	0.0636%	0.0005%	0.0000%	0.0000%	0.0000%	0.0000%	0.0061%	0.0000%	0.0000%
Unkown	0.000	0.000	0.0569%	0.3788%	0.0444%	0.0131%	0.0028%	0.0005%	0.0318%	0.0315%	0.0032%	0.0025%	0.0136%	0.0017%
Corticiales	0.000	0.000	0.5542%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0014%	0.0005%	0.0000%	0.0000%	0.0011%
unidentified	0.000	0.000	0.0861%	0.0364%	0.0015%	0.0470%	0.0005%	0.0102%	0.0000%	0.1051%	0.0333%	0.2273%	0.0000%	0.0044%
Orbiliales	0.000	0.000	0.0167%	0.1005%	0.0495%	0.2581%	0.0231%	0.0000%	0.0000%	0.0000%	0.0954%	0.0020%	0.0000%	0.0000%
Russulales	0.000	0.000	0.0000%	0.0000%	0.0000%	0.0000%	0.0009%	0.0009%	0.0020%	0.2912%	0.0005%	0.0702%	0.0000%	0.0600%
unidentified	0.000	0.000	0.0000%	0.0167%	0.0000%	0.0005%	0.1116%	0.0907%	0.1025%	0.0481%	0.0199%	0.0222%	0.0000%	0.0061%
Botryosphaeriales	0.000	0.000	0.3264%	0.0000%	0.0000%	0.0000%	0.0000%	0.0037%	0.0005%	0.0468%	0.0199%	0.0000%	0.0000%	0.0000%
Phyllachorales	0.000	0.000	0.0000%	0.0000%	0.0025%	0.0010%	0.0000%	0.0745%	0.0000%	0.0366%	0.2454%	0.0000%	0.0000%	0.0056%
Auriculariales	0.000	0.000	0.0167%	0.0975%	0.1212%	0.1071%	0.0000%	0.0000%	0.0040%	0.0060%	0.0000%	0.0000%	0.0096%	0.0000%
unidentified	0.000	0.000	0.0000%	0.1141%	0.0753%	0.1424%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
unidentified	0.000	0.000	0.0278%	0.0005%	0.0000%	0.0000%	0.0056%	0.0398%	0.0000%	0.1491%	0.0296%	0.0025%	0.0025%	0.0183%
unidentified	0.000	0.000	0.0000%	0.0086%	0.0000%	0.0000%	0.1324%	0.0426%	0.0121%	0.0000%	0.0264%	0.0288%	0.0000%	0.0000%
Mortierellales	0.000	0.000	0.0875%	0.0515%	0.0025%	0.0278%	0.0125%	0.0074%	0.0000%	0.0000%	0.0167%	0.0000%	0.0000%	0.0000%
Incertae_sedis	0.000	0.000	0.1625%	0.0162%	0.0253%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%	0.0000%
Malasseziales	0.000	0.000	0.0347%	0.0071%	0.0000%	0.0000%	0.0000%	0.0000%	0.0015%	0.0301%	0.0042%	0.0157%	0.0157%	0.0894%
Unkown Tremellomycetes	0.000	0.000	0.1361%	0.0146%	0.0025%	0.0071%	0.0023%	0.0000%	0.0000%	0.0046%	0.0000%	0.0000%	0.0000%	0.0000%
Rhizophydiales	0.000	0.000	0.1181%	0.0419%	0.0005%	0.0025%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Cystobasidiales	0.000	0.000	0.0069%	0.0015%	0.0000%	0.0000%	0.0528%	0.0458%	0.0146%	0.0069%	0.0051%	0.0197%	0.0000%	0.0000%
Ophiostomatales	0.000	0.000	0.0583%	0.0197%	0.0025%	0.0348%	0.0023%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Unkown	0.000	0.000	0.0917%	0.0091%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
unidentified	0.000	0.000	0.0000%	0.0828%	0.0000%	0.0086%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Incertae_sedis	0.000	0.000	0.0417%	0.0202%	0.0061%	0.0015%	0.0005%	0.0000%	0.0000%	0.0088%	0.0000%	0.0010%	0.0000%	0.0100%
Unkown Chytridiomycetes	0.000	0.000	0.0375%	0.0283%	0.0000%	0.0086%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Erythrobasidiales	0.000	0.000	0.0000%	0.0025%	0.0010%	0.0000%	0.0005%	0.0042%	0.0025%	0.0421%	0.0000%	0.0000%	0.0000%	0.0083%
Diversisporales	0.000	0.000	0.0000%	0.0237%	0.0273%	0.0025%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Blastocladiales	0.000	0.000	0.0028%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0025%	0.0481%	0.0000%	0.0000%	0.0000%	0.0000%
Unkown	0.000	0.000	0.0000%	0.0146%	0.0111%	0.0263%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Hymenochaetales	0.000	0.000	0.0000%	0.0202%	0.0000%	0.0000%	0.0000%	0.0000%	0.0015%	0.0222%	0.0032%	0.0010%	0.0000%	0.0000%
Kickxellales	0.000	0.000	0.0222%	0.0237%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0009%	0.0000%	0.0000%	0.0000%
Incertae_sedis	0.000	0.000	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0005%	0.0000%	0.0282%	0.0000%	0.0000%	0.0000%	0.0028%
Archaeorhizomycetales	0.000	0.000	0.0278%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%	0.0000%
Wallemiales	0.000	0.001	0.0028%	0.0025%	0.0000%	0.0000%	0.0000%	0.0000%	0.0020%	0.0102%	0.0019%	0.0000%	0.0000%	0.0000%

Supplementary Table 5 - Identified bacterial genera and its growth-promoting traits. Bacterial genera with representatives described as plant-growth promoters were searched in the online tool Web of Science (http://www.webofknowledge.com) using a query comprised of the genus name amended by “AND ((PGPR) OR (PGPB) OR ("plant growth-promoting") OR ("plant growth-promotion") OR (plant*growth*) OR (plant*associat*))”. A query with the genus name amended by “AND ((sugar*cane) OR (Saccharum))” was used to verify if a genus representative was isolated from sugarcane. The source tissue of isolation in sugarcane was informed in cases where a member was isolated from sugarcane and described as beneficial to plant growth. Only publications describing growth-promotion traits through *in vivo* or *in vitro* assays were considered. During the survey, publications were sorted by number of citation and chosen based on their relevance to this work. Whenever possible, at least three publications per genus were cited. Additionally, the authors included publications they considered relevant to the discussion. rz: root zone; st: stalk. lf: leaf; ACC: ACC deaminase; AM: ammonia production; ANT: anti-microbial activity; CK: cytokinin production; EPS: exopolysaccharide production; GA: gibberellin production; HCN: HCN production; HMS: heavy metal solubilization; SID: siderophore production; IAA: indoleacetic acid production; N2: nitrogen fixation; PS: phosphate solubilization. Ref.: reference.

Genus	Growth-promoting trait	Isolated from sugarcane? (organ)	Ref.
Acetobacter	IAA, N2	rt, st, lf	[1–4]
Achromobacter	ACC, AM, EPS, HCN, N2, SID	rt, st	[5–10]
Acidisoma	-	-	-
Acidocella	-	-	-
Acidovorax	AM, IAA,HCN, PS, SID	-	[11,12]
Acinetobacter	ACC, ANT, IAA, N2, PS, SID	st	[13–16]
Actinoallomurus	-	-	-
Actinomadura	IAA	-	[17]
Actinomyces	-	-	-
Actinoplanes	-	-	-
Actinopolymorpha	-	-	-
Afifella	-	-	-
Agrobacterium	ACC, IAA, N2	st	[18–20]
Alicyclobacillus	-	-	-
Ammoniphilus	-	-	-
Amycolatopsis	-	-	-
Aquicella	-	-	-
Arthrospira	-	-	-
Asteroleplasma	-	-	-
Asticcacaulis	-	-	-
Azospirillum	N2	rt	[21,22]

Azovibrio	-	-	-
Bacillus	ACC, AM, ANT, GA, HCN, IAA, PS, SID	rt,st	[16,23–41]
Balneimonas	-	-	-
Bdellovibrio	-	-	-
Beijerinckia	GA, IAA, N2	rt	[42–44]
Blastochloris	-	-	-
Blastomonas	-	-	-
Bosea	IAA, N2	-	[45,46]
Bradyrhizobium	AM, EPS, HMS, HCN, IAA, PS, SID	rz	[47–55]
Burkholderia	ACC, HMS, IAA, N2, PS, SID	rz,st,lf	[38,39,43,56–60]
Catellatospora	-	-	-
Caulobacter	N2	rz	[61,62]
Cellvibrio	-	-	-
Chitinophaga	-	-	-
Chondromyces	-	-	-
Chromobacterium	ANT	-	[63]
Chryseobacterium	PS	-	[64,65]
Chthoniobacter	-	-	-
Cloacibacterium	-	-	-
Cohnella	-	-	-
Collimonas	-	-	-
Corynebacterium	-	-	-
Crocinitomix	-	-	-
Cryocola	-	-	-
Cupriavidus	-	-	-
Curtobacterium	IAA	st	[45,66]
Curvibacter	-	-	-
Cytophaga	-	-	-
DA101	-	-	-
Dactylosporangium	-	-	-
Dechloromonas	-	-	-
Devosia	-	-	-
Dokdonella	-	-	-
Dyadobacter	-	-	-
Dyella	ACC, IAA, PS	-	[67,68]
Edaphobacter	-	-	-
Emticicia	-	-	-
Enhydrobacter	-	-	-
Enterobacter	ACC, AM, EPS, HCN, IAA, N2, PS, SID	rz,st,lf	[38,43,45,61,69–72]
Erwinia	IAA, ACC, PS	-	[16]
Fimbriimonas	-	-	-

Flavisolibacter	-	-	-
Flavobacterium	IAA, N2, SID	lf	[73–75]
Fluviicola	-	-	-
Gemmata	-	-	-
Geobacter	-	-	-
Geodermatophilus	-	-	-
Geothrix	-	-	-
Gluconobacter	N2, IAA	rt, st, lf	[1–3,76–80]
Glycomyces	-	-	-
Gordonia	-	-	-
Haemophilus	-	-	-
Herbaspirillum	N2	st, lf	[81–84]
heteroC45_4W	-	-	-
Hylemonella	-	-	-
Hyphomicrobium	-	-	-
Iamia	-	-	-
Inquilinus	-	-	-
Janthinobacterium	IAA	-	[85]
Kaistia	-	-	-
Kaistobacter	-	-	-
Kibdelosporangium	SID	-	[86]
Klebsiella	IAA, N2, PS	rt, st	[61,70,87,88]
Kribbella	-	-	-
Labrys	-	-	-
Legionella	-	-	-
Leptothrix	-	-	-
Leuconostoc	-	-	-
Luteibacter	-	-	-
Luteimonas	-	-	-
Luteolibacter	-	-	-
Lysobacter	ANT, PS	-	[89,90]
Mesorhizobium	IAA, PS , N2	rt	[23,63,91–93]
Methylibium	-	-	-
Methylobacterium	N2, PS	-	[94,95]
Microbacterium	ACC, AM, EPS, HCN, PS, SID	st	[38]
Mycobacterium	IAA, SID	-	[34,96,97]
Mycoplana	-	-	-
Mycoplasma	-	-	-
Neisseria	-	-	-
Nevskia	-	-	-
Niastella	-	-	-
Nitrospira	-	-	-
Nocardia	-	-	-

Nocardioides	-	-	-
Novosphingobium	-	-	-
Ochrobactrum	-	-	-
Opitutus	-	-	-
OR-59	-	-	-
Paenibacillus	ACC, CK, IAA, SID	rt, st, lf	[24,25,70,81,98–100]
Pandoraea	-	-	-
Paracoccus	-	-	-
Parvibaculum	-	-	-
Pedobacter	IAA		[73]
Pedomicrobium	-	-	-
Pedosphaera	-	-	-
Phaeospirillum	-	-	-
Phenylobacterium	-	-	-
Pigmentiphaga	-	-	-
Pilimelia	-	-	-
Pimelobacter	-	-	-
Pirellula	-	-	-
Planctomyces	-	-	-
Plesiocystis	-	-	-
Polaromonas	-	-	-
Pontibacter	-	-	-
Propionibacterium	-	-	-
Prosthecobacter	-	-	-
Pseudomonas	ACC, AM, ANT, CK, EPS, HCN, HMS, IAA, N2, PS, SID	rt, st, lf	[24,25,29,30,32,34,38,39,81,92,97,101–106]
Pseudonocardia	-	-	-
Pseudoxanthomonas	AM, EPS, HCN, SID	-	[9]
Ralstonia	-	-	-
Rathayibacter	-	-	-
Rhizobium	AM, CK, EPS, HCN, IAA, PS, SID	rz,st,	[25,34,50,53,61,85,92,97,107–112]
Rhodoferax	-	-	-
Rhodoplanes	-	-	-
Rickettsia	-	-	-
Rickettsiella	-	-	-
Rubrivivax	-	-	-
Rubrobacter	-	-	-
Saccharopolyspora	-	-	-
Salinibacterium	-	-	-
Salinispora	-	-	-
Sediminibacterium	-	-	-

Serratia	IAA, ANT, GA, HCN, PS	-	[113,114]
Shinella	-	-	-
Solirubrobacter	-	-	-
Sphingobacterium	IAA, HCN	-	[115]
Sphingobium	-	-	-
Sphingomonas	IAA, N2	rt, st, lf	[8,34,38]
Sphingopyxis	-	-	-
Spirochaeta	-	-	-
Spirosoma	-	-	-
Sporocytophaga	-	-	-
Sporosarcina	PS, SID	-	[116]
Staphylococcus	-	-	-
Stenotrophomonas	-	-	-
Steroidobacter	-	-	-
Streptococcus	-	-	-
Streptomyces	ACC, SID, IAA	rz	[38,117]
Swaminathania	-	-	-
Telmatospirillum	-	-	-
Terriglobus	-	-	-
Thermomonas	-	-	-
Turneriella	-	-	-
Uliginosibacterium	-	-	-
Variovorax	IAA, SID	-	[74]
Wolbachia	-	-	-
Yonghaparkia	-	-	-

Reference for Supplementary Table 5

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Supplementary Table 6 - Identified fungal genera and its growth-promoting traits. Fungal genera with representatives described as plant growth promoters were searched in the online tool Web of Science (http://www.webofknowledge.com) using a query comprised of the genus name amended by “AND ((PGPR) OR (PGPB) OR ("plant growth-promoting") OR ("plant growth-promotion") OR (plant*growth*) OR (plant*associat*))”. A query with the genus name amended by “AND ((sugar*cane) OR (Saccharum))” was used to search whether a genus representative was isolated from sugarcane. The source tissue of isolation in sugarcane was informed in cases where a member was isolated from sugarcane and described as beneficial to plant growth. Only publications describing growth-promoting traits through *in vivo* or *in vitro* assays were considered. During the survey, publications were sorted by number of citation and chosen based on their relevance to this work. Whenever possible, at least three publications per genus were cited. Additionally, the authors included publications they considered relevant to the discussion. rz: root zone; st: stalk; lf: leaf; ANT: anti-microbial activity; AST: abiotic/biotic stress tolerance; EDP: enhanced defense against pathogens; GA: gibberellin production; IAA: indoleacetic acid production; N2: nitrogen fixation; PG: plant growth (publications that evaluated growth-promoting effects but did not describe the responsible trait); SID: siderophore production. PS: phosphate solubilization. Ref.: reference.

Genus	Growth promoting trait	Isolated from sugarcane? (organ)	Ref.
Acremonium	ANT, PG	-	[1,2]
Alternaria	EDP	-	[3]
Aporospora	-	-	-
Aspergillus	IAA, GA, PG, PS	-	[4–7]
Aureobasidium	-	-	-
Bipolaris	-	-	-
Bullera	-	-	-
Candida	IAA, ACC, PS	-	[8,9]
Capnobotryella	-	-	-
Capnodium	-	-	-
Cladophialophora	-	-	-
Cladosporium+AD90:AD117	-	-	-
Cladosporium	GA	-	[10]
Clitopilus	-	-	-
Cochliobolus	PG	-	[11]
Codinaeopsis	-	-	-

Colletotrichum	AST	-	[12]
Coniothyrium	-	-	-
Cryptococcus	PG, IAA, N2	lf	[9,13,14]
Curvularia	-	-	-
Cytospora	-	-	-
Dactylella	-	-	-
Debaryomyces	-	-	-
Devriesia	-	-	-
Dictyosporium	-	-	-
Didymella	-	-	-
Dissoconium	-	-	-
Epicoccum	ANT, PG	lf	[15,16]
Erythrobasidium	-	-	-
Exophiala	AST	-	[17]
Fusarium	PG, GA	-	[18,19]
Gibberella	GA	-	[19,20]
Glomus	PG, PS	rt	[21,22]
Gongronella	-	-	-
Hanseniaspora	-	-	-
Jaminaea	-	-	-
Khuskia	-	-	-
Lasiodiplodia	-	-	-
Leptosphaeria	-	-	-
Leptoxyphium	-	-	-
Magnaporthe	-	-	-
Malassezia	-	-	-
Mariannaea	-	-	-
Meira	-	-	-
Meyerozyma	-	-	-
Microdiplodia	-	-	-
Mycenella	-	-	-
Mycosphaerella	-	-	-
Myrmecridium	-	-	-
Neurospora	-	-	-
Nigrospora	-	-	-
Occultifur	-	-	-
Paecilomyces	PG, AST	-	[23]
Paraconiothyrium	-	-	-

Paraphaeosphaeria	-	-	-
Passalora	-	-	-
Penicillium	AST, PS, GA, PG	-	[19,24–27]
Penidiella	-	-	-
Periconia	-	-	-
Pestalotiopsis	-	-	-
Phaeosphaeria	-	-	-
Phaeosphaeriopsis	-	-	-
Phialophora	-	-	-
Phoma	ANT,GA, PG		[28–31]
Piriformospora	-	-	-
Pseudocercospora	-	-	-
Ramichloridium	-	-	-
Resinicium	-	-	-
Rhinocladiella	-	-	-
Rhizophagus	AST,PG, PS		[32–34]
Scytalidium	-	-	-
Serendipita	-	-	-
Sporisorium	-	-	-
Strelitziana	-	-	-
Talaromyces	PG	-	[35]
Teratosphaeria	-	-	-
Thielaviopsis	-	-	-
Tilletia	-	-	-
Toxicocladosporium	-	-	-
Trechispora	-	-	-
Tremella	-	-	-
Trichoderma	ANT, PG, PS,	-	[36–40]
Ustilago	-	-	-
Wickerhamiella	-	-	-
Xylaria	-	-	-
Zygoascus	-	-	-
Zygosaccharomyces	-	-	-

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Unlocking the bacterial and fungal communities assemblages of sugarcane microbiome

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Supplementary Data

Supplementary Data

PCR 1 - PRIMERS FOR V4 REGION OF 16S GENE

Oligo	Orientation	Appends			Complete Sequence (5'->3')
		Append to 5' (Nextera transposase sequence)	rame Shift	primer (rRNA)	
515f_FS1	Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	NNNNNN	GTGCCAGCMGCCGCGGTAA	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNNNNNGTGCCAGCMGCCGCGGTAA
515f_FS2	Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	NNNNN	GTGCCAGCMGCCGCGGTAA	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNNNNGTGCCAGCMGCCGCGGTAA
515f_FS3	Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	NNNN	GTGCCAGCMGCCGCGGTAA	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNNNGTGCCAGCMGCCGCGGTAA
806r_FS	Reverse	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG	NNNNNN	GGACTACHVGGGTWTCTAAT	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGNNNNNNGGACTACHVGGGTWTCTAAT

PCR 1 - PRIMERS FOR ITS GENE

Oligo	Orientation	Appends			Complete Sequence (5'->3')
		Append to 5' (Nextera transposase sequence)	rame Shift	primer (rRNA)	
ITS9f_FS1	Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	NNNNNN	GAACGCAGCRAAIIGYGA	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNNNNNGAACGCAGCRAAIIGYGA
ITS9f_FS2	Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	NNNNN	GAACGCAGCRAAIIGYGA	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNNNNGAACGCAGCRAAIIGYGA
ITS9f_FS3	Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	NNNN	GAACGCAGCRAAIIGYGA	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGNNNNGAACGCAGCRAAIIGYGA
ITS4r_FS	Reverse	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG	NNNNNN	TCCTCCGCTTATTGATATGC	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGNNNNNNTCCTCCGCTTATTGATATGC

i5 PRIMERS

Oligo	Sequence (5'->3')
S501	AATGATACGGCGACCACCGAGATCTACACTAGATCGCTCGTCGGCAGCGTC
S502	AATGATACGGCGACCACCGAGATCTACACCTCTCTATTCGTCGGCAGCGTC
S503	AATGATACGGCGACCACCGAGATCTACACTATCCTCTTCGTCGGCAGCGTC
S504	AATGATACGGCGACCACCGAGATCTACACAGAGTAGATCGTCGGCAGCGTC
S505	AATGATACGGCGACCACCGAGATCTACACGTAAGGAGTCGTCGGCAGCGTC
S506	AATGATACGGCGACCACCGAGATCTACACACTGCATATCGTCGGCAGCGTC
S507	AATGATACGGCGACCACCGAGATCTACACAAGGAGTATCGTCGGCAGCGTC
S508	AATGATACGGCGACCACCGAGATCTACACCTAAGCCTTCGTCGGCAGCGTC

i7 PRIMERS

Oligo	Sequence (5'->3')
N701	CAAGCAGAAGACGGCATACGAGATTCGCCTTAGTCTCGTGGGCTCGG
N702	CAAGCAGAAGACGGCATACGAGATCTAGTACGGTCTCGTGGGCTCGG
N703	CAAGCAGAAGACGGCATACGAGATTTCTGCCTGTCTCGTGGGCTCGG
N704	CAAGCAGAAGACGGCATACGAGATGCTCAGGAGTCTCGTGGGCTCGG
N705	CAAGCAGAAGACGGCATACGAGATAGGAGTCCGTCTCGTGGGCTCGG
N706	CAAGCAGAAGACGGCATACGAGATCATGCCTAGTCTCGTGGGCTCGG
N707	CAAGCAGAAGACGGCATACGAGATGTAGAGAGGTCTCGTGGGCTCGG
N708	CAAGCAGAAGACGGCATACGAGATCCTCTCTGGTCTCGTGGGCTCGG
N709	CAAGCAGAAGACGGCATACGAGATAGCGTAGCGTCTCGTGGGCTCGG
N710	CAAGCAGAAGACGGCATACGAGATCAGCCTCGGTCTCGTGGGCTCGG
N711	CAAGCAGAAGACGGCATACGAGATTGCCTCTTGTCTCGTGGGCTCGG
N712	CAAGCAGAAGACGGCATACGAGATTCCTCTACGTCTCGTGGGCTCGG