Supplementary information:

The Core Fungal Microbiome of Banana (*Musa* spp.)

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Table S1 The abiotic characteristics of five soils used to determine the candidate core fungal microbiome of *Musa* spp. as published previously in Birt et al. (2022).

Parameter	**Innisfail**	**Liverpool**	**Pin Gin**	**Tolga**	**Tully**
Latitude (°S)	17.485122	17.454604	17.592257	17.010557	17.481890
Longitude (°E)	145.859047	145.864289	145.833088	145.527065	145.858678
Texture	Clay Loam	Clay Loam	Clay	Clay	Clay loam
Clay (%)	27	26	39	56	28
pH	6.7	7.1	7.1	5.6	6.6
Total C (%)	2.067	1.558	2.417	2.843	2.837
Total N (%)	0.180	0.143	0.212	0.190	0.210
C:N	11.2	10.8	11.5	14.9	13.5

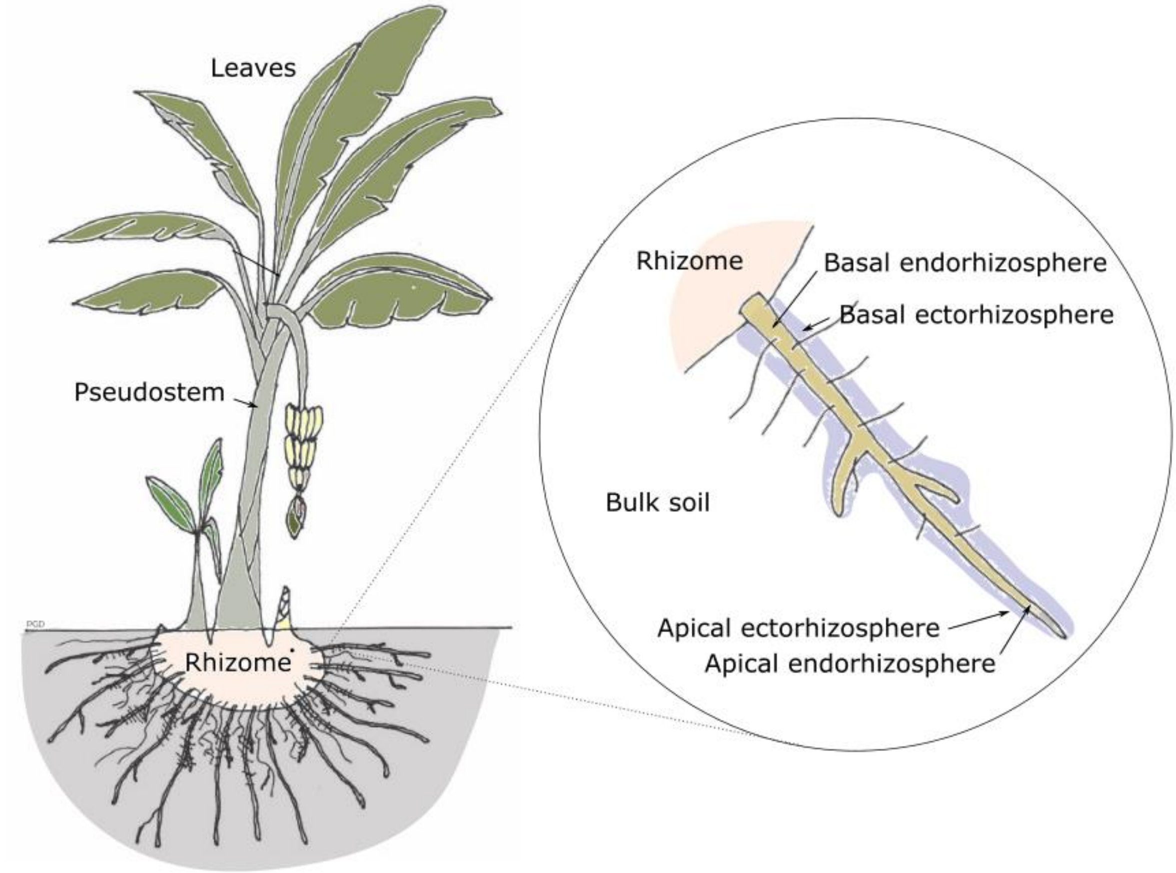


Fig. S1 A diagram showing the various plant compartments sampled in this study.

Table S2 Varieties of *Musa* spp. investigated in the field survey in this study as published in Birt et al. (2022).

Variety	**Classification**	**Genome**
845	*Musa acuminata* ssp. *Malaccensis*	AA
846	*Musa acuminata* ssp. *Malaccensis*	AA
848	*Musa acuminata* ssp. *Malaccensis*	AA
850	*Musa acuminata* ssp. *Malaccensis*	AA
851	*Musa acuminata* ssp. *Malaccensis*	AA
852	*Musa acuminata* ssp. *Malaccensis*	AA
Agutay	*Musa acuminata* ssp. *Errans*	AA
Musa balbisiana	*Musa balbisiana*	BB
Blue Java	Ney Mannan	ABB
Bluggoe	Bluggoe	ABB
Borneo	*Musa acuminata* ssp. *Microcarpa*	AA
Calcutta	*Musa acuminata* ssp. *Burmannicoides*	AA
Cam 020	Musa acuminata	AA
Williams	Cavendish	AAA
Ducasse	Pisang Awak	ABB
Dwarf French Plantain	Plantain	AAB
Dwarf Nathan	Cavendish	AAA
FHIA-02	Cavendish hybrid/Pome hybrid	AAAB
FHIA-03	Cooking hybrid	AABB
FHIA-17	Highgate hybrid	AAAA
FHIA-18	Pome hybrid	AAAB
FHIA-23	Highgate hybrid	AAAA
FHIA-25	Cooking hybrid	AAB
GCTCV 218 (Formosana)	Cavendish	AAA
GCTCV 105	Cavendish	AAA
GCTCV 119	Cavendish	AAA
GCTCV 215	Cavendish	AAA
GCTCV 217	Cavendish	AAA
Goldfinger	Pome hybrid	AAAB
Grande Naine	Cavendish	AAA
Gros Michel	Gros Michel	AAA
Highgate	Gros Michel	AAA
Igisahira Gsanzwe	Mutika/Lujugira	AAA
Lakatan	Lakatan	AAA
Lady Finger	Pome	AAB
Ney Poovan	Ney Poovan	AB
Niukin	Pisang Jari Buaya	AA
Pisang Mas	Sucrier	AA
PA 03.22	Pome hybrid	AAAB
Pa Payang	*Musa acuminata* ssp. *Siamea*	AA
Pacific Plantain	Maoli/Popoulu	AAB
Pahang	*Musa acuminata* ssp. *Malaccensis*	AA
Pisang Ceylan	Mysore	AAB
Pisang Gajih Merah	Saba	ABB
Pisang Raja	Pisang Raja	AAB
Red Dacca	Red	AAA
Red Dacca	Red	AAA
Santa Catarina Prata	Pome	AAB
SH-3142	*Musa acuminata*	AA
SH-3142	*Musa acuminata*	AA
SH-3142	*Musa acuminata*	AA
SH-3362	*Musa acuminata*	AA
Sugar	Silk	AAB
Yangambi Km5	Ibota	AAA
Zebrina	*Musa acuminata ssp. Zebrina*	AA

Table S3 The number of replicates in the treatment combinations of soil and plant compartment in plants grown under controlled conditions in this study.

Compartment	Innisfail	Liverpool	Pin Gin	Tolga	Tully
Bulk soil	10	10	10	8	10
Basal ectorhizosphere	10	10	9	10	10
Basal endorhizosphere	10	9	10	9	10
Apical ectorhizosphere	10	10	10	10	10
Apical endorhizosphere	10	9	10	10	9
Rhizome	8	9	4	7	7
Pseudostem	7	10	7	9	7
Leaf	8	6	6	6	5

Table S4 The number of replicates in the treatment combinations of genotype and plant compartment in plants grown under controlled conditions in this study.

Compartment	**Cavendish**	**Gold finger**	**Lady finger**
Bulk soil	10	8	7
Basal ectorhizosphere	10	9	10
Basal endorhizosphere	10	10	10
Apical ectorhizosphere	10	9	10
Apical endorhizosphere	10	10	10
Rhizome	8	6	8
Pseudostem	8	10	5
Leaf	7	8	7

Table S5 The number of replicates for each plant compartment and the total number of genotypes examined in the field survey in this study.

	Bulk soil	**Ectorhizosphere**	**Endorhizosphere**	**Pseudostem**	**Leaf**
Total number of replicates	164	165	27	26	21
Number of genotypes examined	52	52	18	22	11

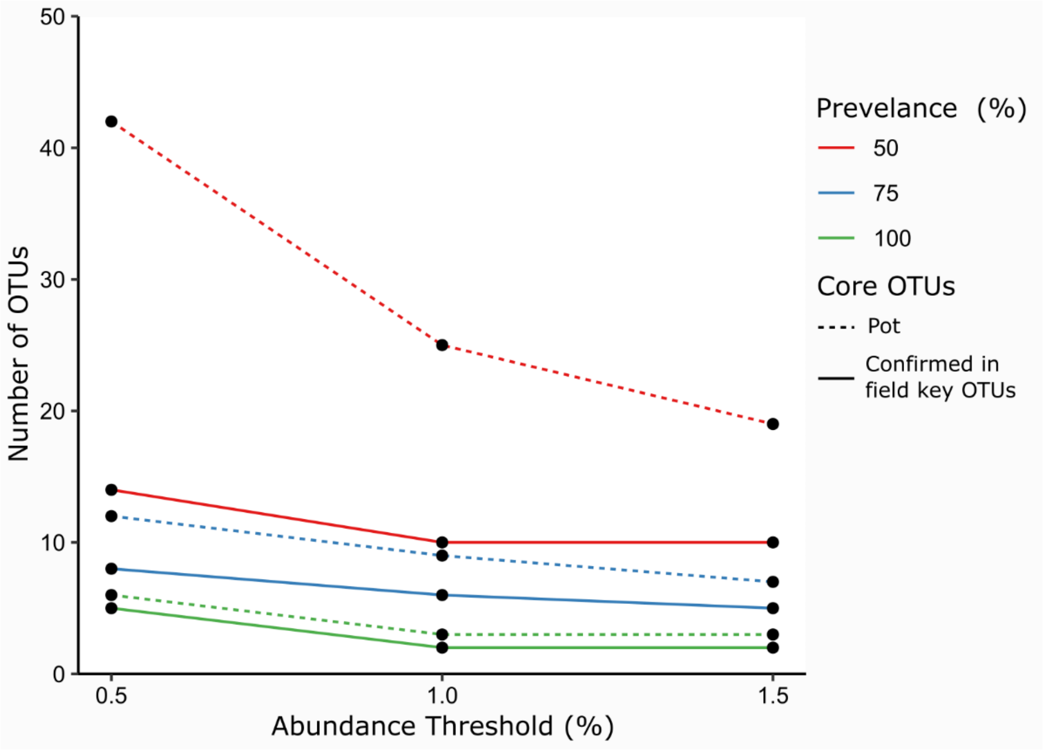


Fig. S2 The impact of different abundance and prevalence thresholds on the number of candidate-core OTUs defined in the pot dataset (dotted line) and confirmed in the key OTUs from the field survey (solid line).

Table S6 Studies included in the meta-analysis in this study.

Study	Method	Plant compartment	Cultivar	Country	Study description	Title	Accession
Fu et al. 2017	Culture independent (454 sequencing of ITS2 region)	Ectorhizosphere	Information not given	China	The effect of a biocontrol on the rhizosphere community of field grown banana plants.	*Inducing the rhizosphere microbiome by biofertilizer application to suppress banana Fusarium wilt disease*	SRP070868
Liu et al. 2019	Culture independent (Illumina MiSeq sequencing of ITS2 region)	Roots and ‘shoots’	*Musa* (AAA Group, Cavendish Subgroup) ‘Baxi’	China	Examining key microbes present in a plant experiencing Fusarium wilt	*Engineering banana endosphere microbiome to improve Fusarium wilt resistance in banana*	SRP061527
Rames et al. 2018	Culture independent (Illumina MiSeq sequencing of ITS2 region)	Bulk soil	*Musa* (ABB Group, Pisang Awak Subgroup) ‘Ducasse’	Australia	Examining the effect of ground cover on the microbiome of banana	*Soil microbial community changes associated with ground cover management in cultivation of Ducasse banana (Musa sp. ABB,*	PRJNA397084

						Pisang Awak subgroup) and suppression of Fusarium oxysporum	
Rossman et al 2012	Culture dependent	Bulk soil, ectorhizosphere, pseudostem exterior	Information not given	Uganda	Examination of the soil and pseudostem of field-grown bananas.	*Banana-associated microbial communities in Uganda are highly diverse but dominated by Enterobacteriaceae*	HE586686 to HE586734
Shen et al. 2015a	Culture independent (454 sequencing of ITS2 region)	Bulk soil	*Musa* (AAA Group, Cavendish Subgroup) ‘Brazil’	China	Comparing fields of where a biocontrol has been applied with one where it has not	*Rhizosphere microbial community manipulated by 2 years of consecutive biofertilizer application associated with banana Fusarium wilt disease suppression*	DRA002434

Shen et al. 2015b	Culture independent (Illumina MiSeq sequencing of ITS2 region)	Bulk soil	*Musa* (AAA Group, Cavendish Subgroup) 'Brazil'	China	Introduction of biofertiliser to control Fusarium wilt in pots.	*Effect of biofertilizer for suppressing Fusarium wilt disease of banana as well as enhancing microbial and chemical properties of soil under greenhouse trial*	DRA002820
Shen et al. 2018a	Culture independent (Illumina MiSeq sequencing of ITS2 region)	Bulk Soil	*Musa* (AAA Group, Cavendish Subgroup) 'Brazil'	China	The effect of soil fumigation on the soil microbiome	*Soil pre-fumigation could effectively improve the disease suppressiveness of biofertilizer to banana Fusarium wilt disease by reshaping the soil microbiome*	SRP112719
Shen et al. 2018b	Culture independent (Illumina MiSeq sequencing of ITS2 region)	Bulk soil	*Musa* (AAA Group, Cavendish	China	Effect of monoculture span on the soil microbiome	*Banana fusarium wilt disease incidence is influenced by shifts of soil microbial*	DRA004913

			Subgroup) ‘Brazil’			*communities under different monoculture spans*	
Shen et al. 2019	Culture independent (Illumina HiSeq sequencing of ITS1 region)	Bulk soil	*Musa* (AAA Group, Cavendish Subgroup) ‘Brazil’	China	Soil samples from pot experiment after fumigation and the addition of a biocontrol to control Fusarium wilt.	*Suppression of banana Panama disease induced by soil microbiome reconstruction through an integrated agricultural strategy*	SRP111447
Wang et al. 2015	Culture independent (454 sequencing of ITS2 region)	Bulk soil	Information not given	China	The effect of crop rotation on the soil microbiome	*Pineapple-banana rotation reduced the amount of Fusarium oxysporum more than maize-banana rotation mainly through modulating fungal communities*	DRA002472

Zhang et al. 2019	Culture independent (Illumina HiSeq sequencing of 18S region)	Bulk soil	*Musa* (AAA Group, Cavendish Subgroup) 'Williams'	China	The effect of liming and organic fertiliser on the soil microbiome	*Organic fertilizer, but not heavy liming, enhances banana biomass, increases soil organic carbon and modifies soil microbiota*	SRP139145

Table S7 The impact of soil, genotype and plant compartment on alpha diversity metrics assessed by ANOVA from the fungal microbiome of *Musa* spp. These results derive from our pot experiment which included five distinct soils, three *Musa* spp. genotypes, and eight compartments.

Response variable	**Predictor variable**	***F* value**	***P* value**
Observed OTUs	Compartment	23.4	<0.001 ***
	Soil	1.1	0.347
	Compartment: Soil	1.0	0.503
Predicted OTUs (Chao 1)	Compartment	16.3	<0.001 ***
	Soil	1.6	0.162
	Compartment: Soil	0.9	0.622
Observed OTUs	Compartment	16.2	<0.001 ***
	Genotype	1.1	0.320
	Compartment: Genotype	1.1	0.389
Predicted OTUs (Chao 1)	Compartment	12.5	<0.001 ***
	Genotype	1.9	0.159
	Compartment: Genotype	1.2	0.277

Table S8 Average percentage similarity plus/minus the standard deviation of fungal community composition in various *Musa* spp. plant compartments. Percentages were produced using a Bayesian approach implemented through SourceTracker.

	Source							
Sink	**BS**	**AER**	**AEnR**	**BER**	**BEnR**	**R**	**PS**	**L**
BS	-	94.3 ± 1	75.6 ± 13	95.9 ± 1	77.3 ± 9	67.1 ± 11	63.4 ± 11	61.1 ± 11
AER	94.6 ± 1	-	81.0 ± 8	96.1 ± 1	80.1 ± 6	71.1 ± 5	63.2 ± 10	59.7 ± 12
AEnR	93.8 ± 6	95.1 ± 6	-	94.9 ± 6	92.9 ± 4	89.8 ± 5	83.7 ± 8	83.2 ± 8
BER	94.5 ± 2	94.9 ± 1	76.3 ± 11	-	78.3 ± 10	65.1 ± 13	57.6 ± 9	68.1 ± 9
BEnR	78.8 ± 6	80.0 ± 5	79.4 ± 9	79.8 ± 5	-	80.2 ± 9	67.9 ± 12	55.8 ± 11
R	74.1 ± 2	71.9 ± 9	75.0 ± 13	75.6 ± 4	83.5 ± 10	-	79.6 ± 13	76.7 ± 13
PS	61.9 ± 6	62.3 ± 8	62.3 ± 18	63.4 ± 10	87.6 ± 7	91.0 ± 3	-	91.3 ± 2
L	40.1 ± 11	53.5 ± 8	44.1 ± 18	43.7 ± 14	55.5 ± 12	66.7 ± 9	63.3 ± 15	-

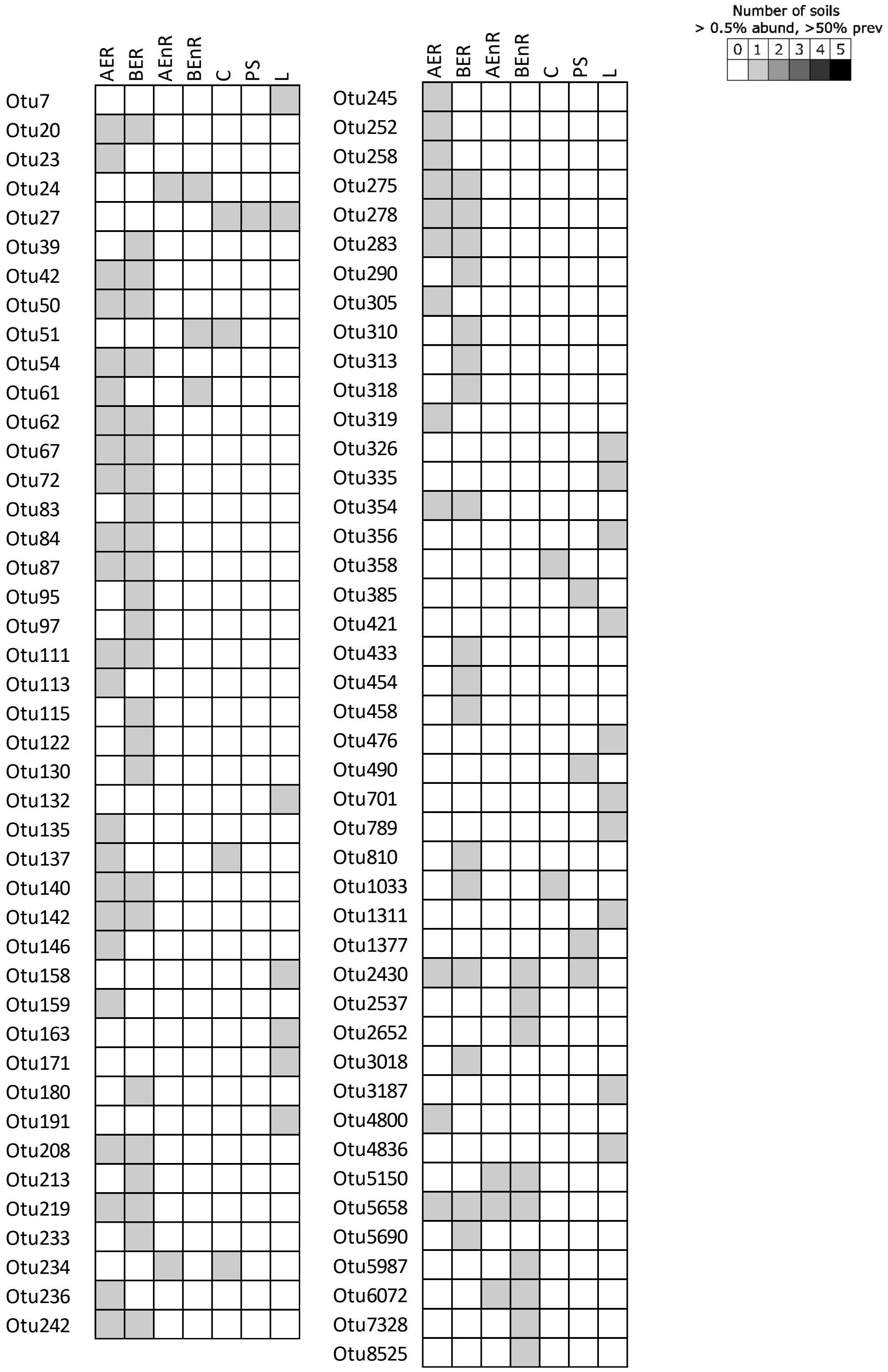


Fig. S3 Heatmaps to show the number of OTUs identified as abundant and prevelant in plant compartments of *Musa* (AAA Group, Cavendish Subgroup) ‘Williams’ grown in a single soil

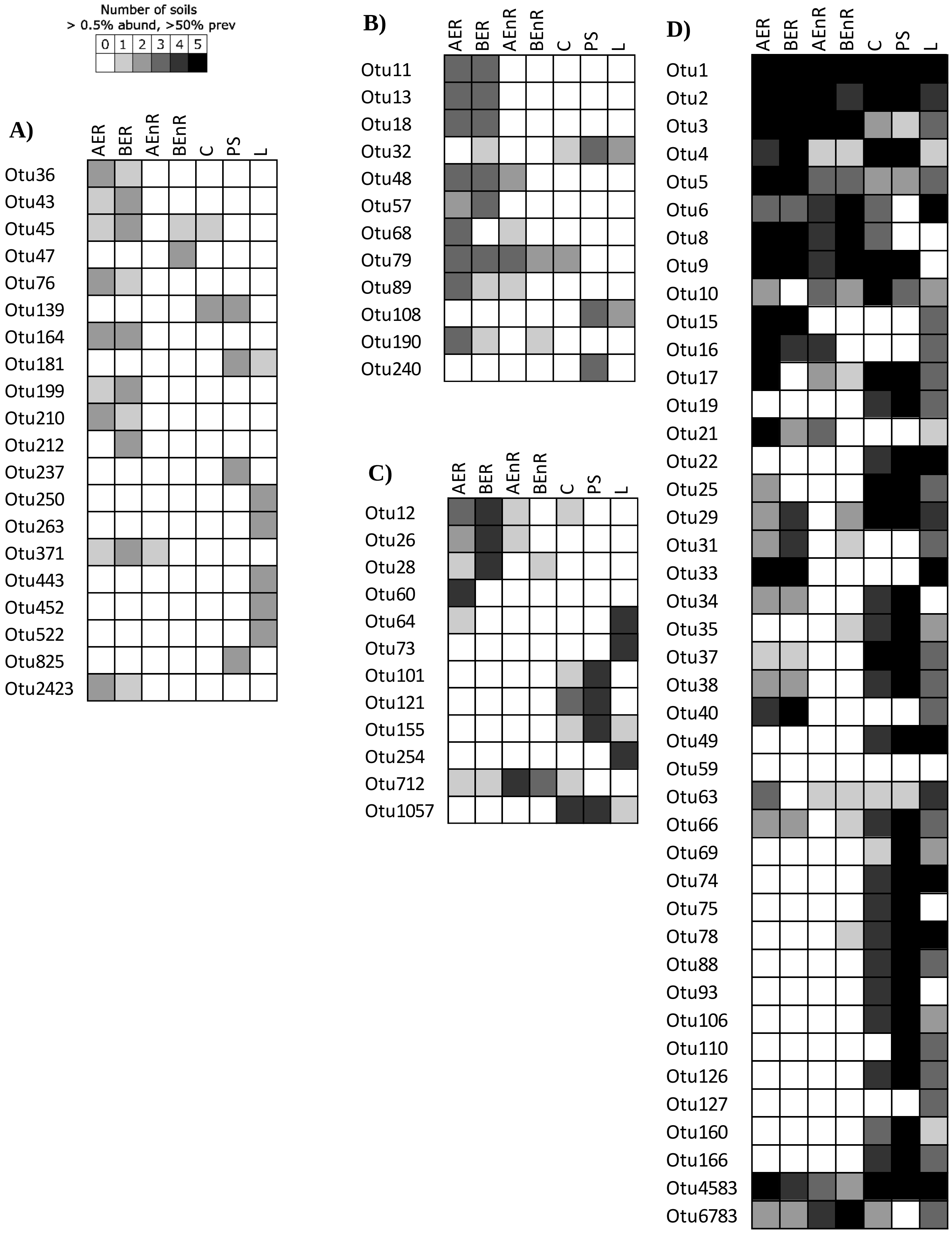


Fig. S4 The OTUs identified as abundant and prevalent in plant compartments of *Musa* (AAA Group, Cavendish Subgroup) ‘Williams’ grown in two (A), three (B), four (C), and five (D) soils

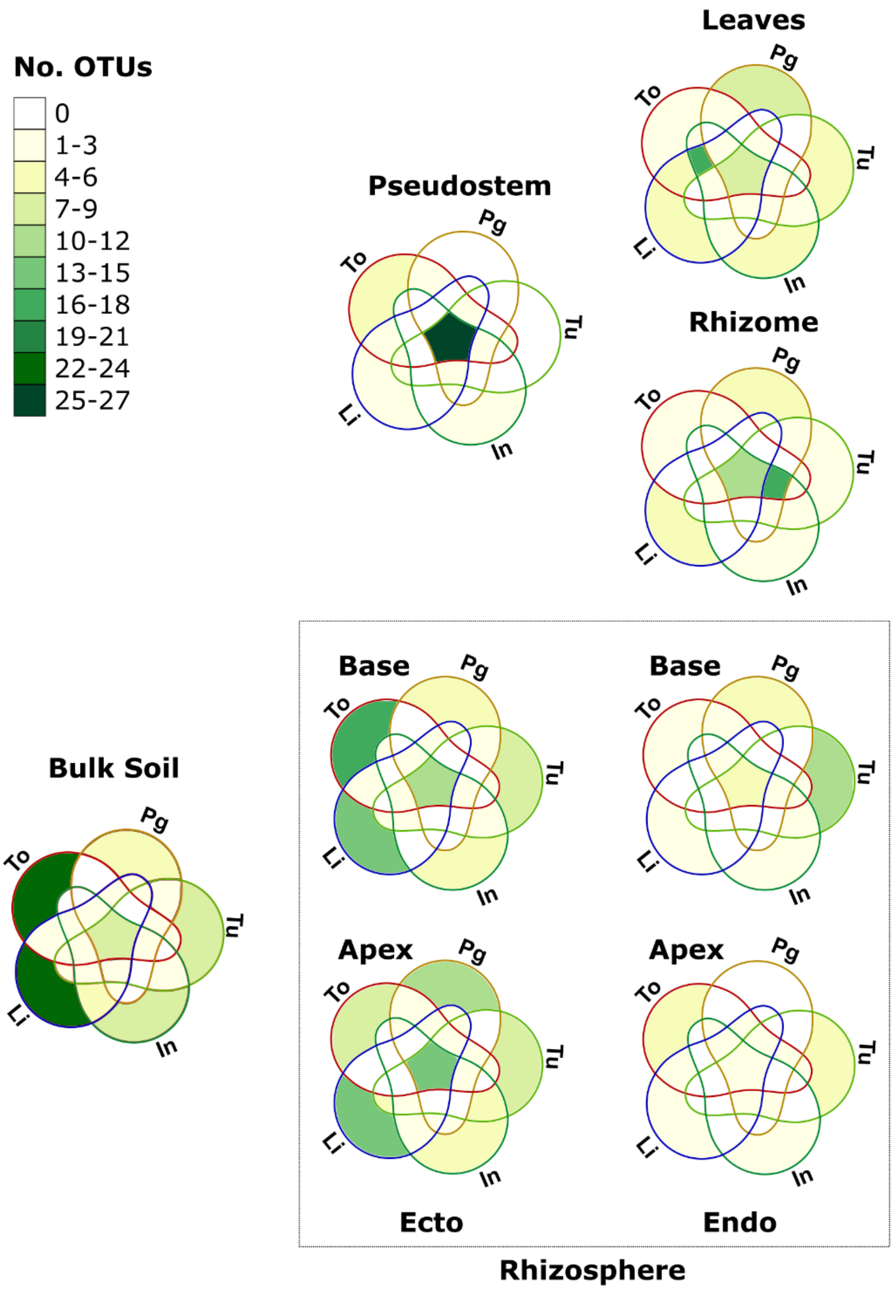


Fig. S5 Venn diagrams showing the number of OTUs found at an average abundance > 0.5% and prevelance > 50% in *Musa* (AAA Group, Cavendish Subgroup) 'Williams' plants grown in five distinct soils.

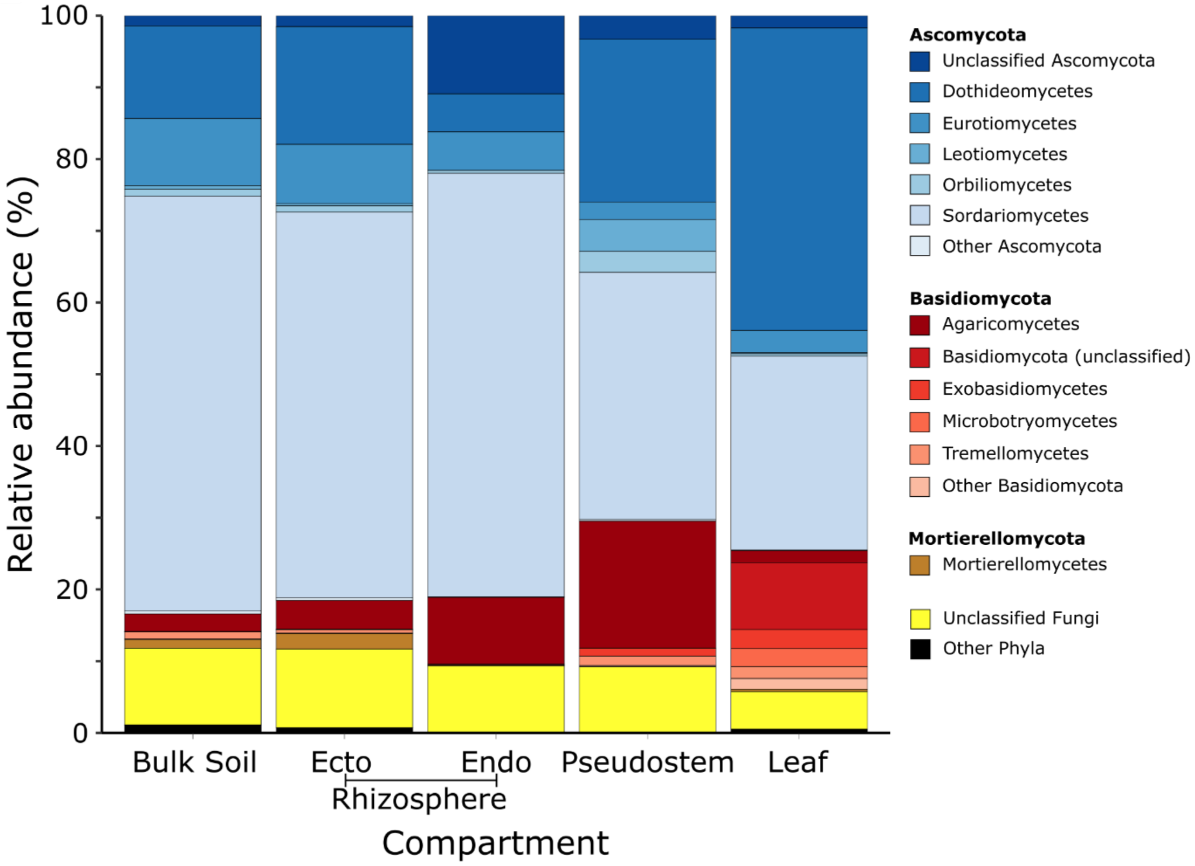


Fig. S6 The mean relative frequencies of fungal classes in different plant compartments associated with various field grown *Musa* genotypes. Within each phylum, classes represented at <1% mean relative abundance are grouped as other. Abbreviations are as follows: endo – endorhizosphere, ecto – ectorhizosphere.

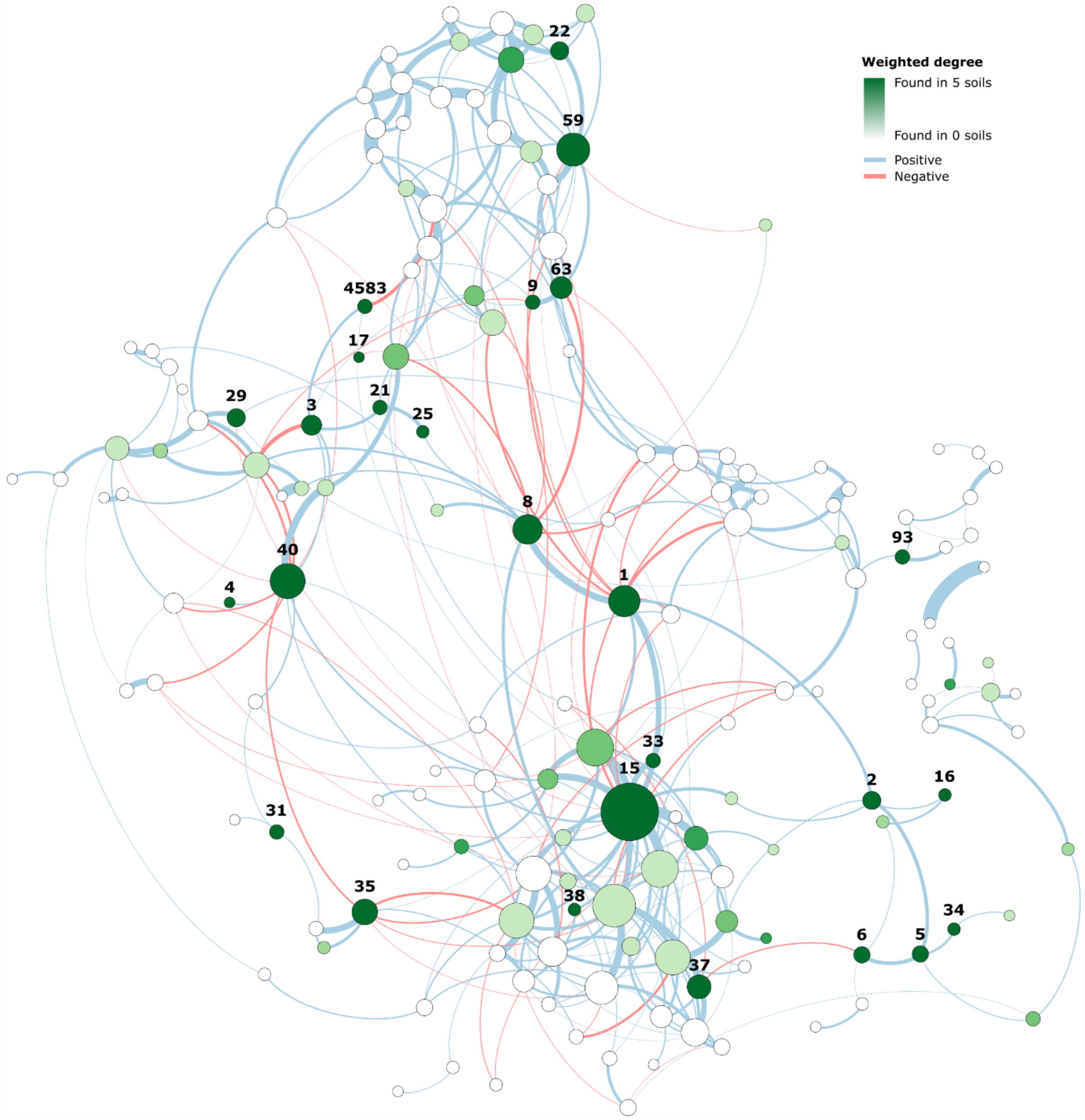


Fig. S7 A network showing co-occurrence between fungal OTUs associated with adult *Musa* spp. in a field setting. Node size is proportional to node degree. Nodes are coloured by the number of soils each OTU was present in according to a previous pot experiment.

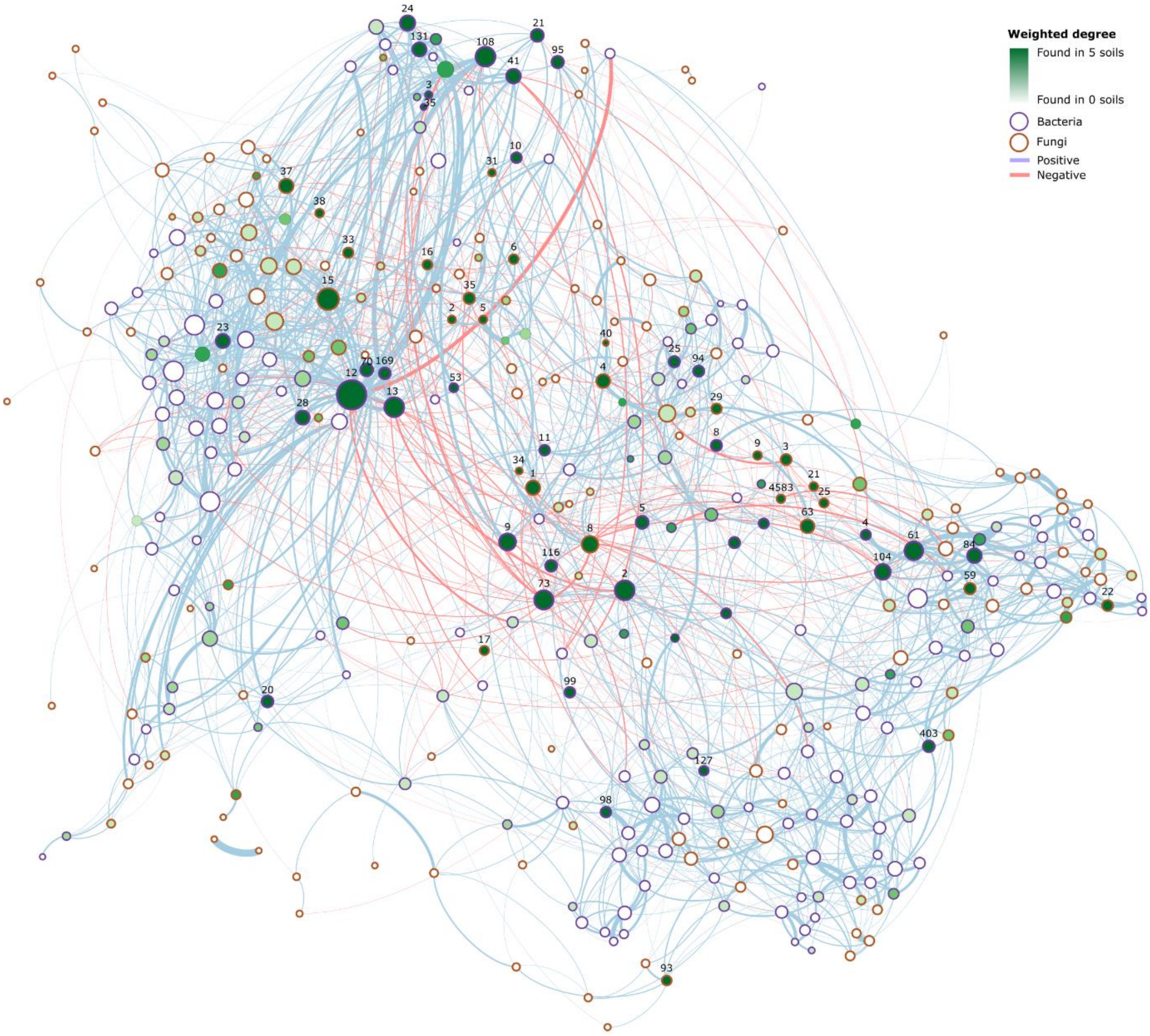
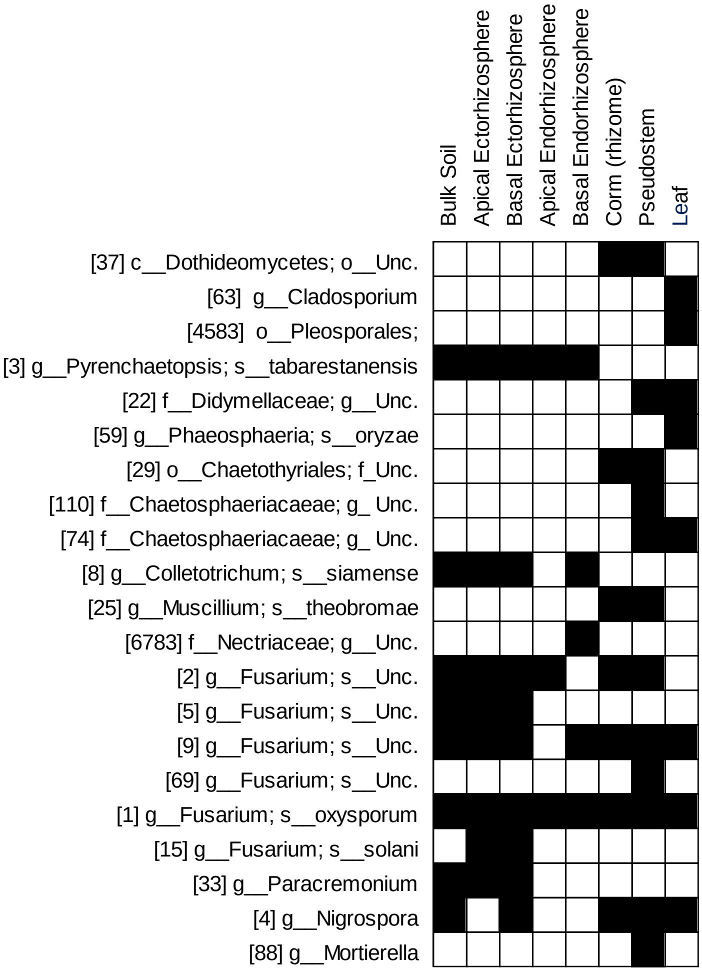


Fig. S8 A dual amplicon (16S and ITS2) network showing co-occurrence between fungal and bacterial OTUs associated with 52 adult *Musa* spp. in a field setting. Node size is proportional to node degree.



	Bulk Soil	Apical Ectorhizosphere	Basal Ectorhizosphere	Apical Endorhizosphere	Basal Endorhizosphere	Corm (rhizome)	Pseudostem	Leaf
[37] c__Dothideomycetes; o__Unc.	□	□	□	□	□	■	■	□
[63] g__Cladosporium	□	□	□	□	□	□	□	■
[4583] o__Pleosporales;	□	□	□	□	□	□	□	■
[3] g__Pyrenchaetopsis; s__tabarestanensis	■	■	■	■	■	□	□	□
[22] f__Didymellaceae; g__Unc.	□	□	□	□	□	□	■	■
[59] g__Phaeosphaeria; s__oryzae	□	□	□	□	□	□	□	■
[29] o__Chaetothyriales; f_Unc.	□	□	□	□	□	■	■	□
[110] f__Chaetosphaeriacaeae; g_ Unc.	□	□	□	□	□	□	■	□
[74] f__Chaetosphaeriacaeae; g_ Unc.	□	□	□	□	□	□	■	■
[8] g__Colletotrichum; s__siamense	■	■	■	□	■	□	□	□
[25] g__Muscillium; s__theobromae	□	□	□	□	□	■	■	□
[6783] f__Nectriaceae; g__Unc.	□	□	□	□	■	□	□	□
[2] g__Fusarium; s__Unc.	■	■	■	■	□	■	■	□
[5] g__Fusarium; s__Unc.	■	■	■	□	□	□	□	□
[9] g__Fusarium; s__Unc.	■	■	■	□	■	■	■	■
[69] g__Fusarium; s__Unc.	□	□	□	□	□	□	■	□
[1] g__Fusarium; s__oxysporum	■	■	■	■	■	■	■	■
[15] g__Fusarium; s__solani	□	■	■	□	□	□	□	□
[33] g__Paracremonium	■	■	■	□	□	□	□	□
[4] g__Nigrospora	■	□	■	□	□	■	■	■
[88] g__Mortierella	□	□	□	□	□	□	■	□

Fig. S9 The final core *Musa* spp. fungal microbiome. Black tiles indicate which plant compartments each OTU was identified as core.

Table S9 Representative sequences the 42 candidate-core OTUs found in all soils from *Musa* spp. grown under controlled conditions. OTUs that were elevated to full core-status are marked as core in bold text.

OTU	Sequence (5'-3')
Otu1 **Core**	CAACCCTCAAGCACAGCTTGGTGTTGGGACTCGCGTTAATTCGCGTTCCTCAAATTGATTGGCGGTCACGTCGAGCTTCCATAGCGTAGTAGTAAAACCCTCGTTACTGGTAATCGTCGCGGCCACGCCGTTAAACCCCAACTTCTGAA
Otu2 **Core**	CAACCCTCAGGCCCCCGGGCCTGGCGTTGGGGATCGGCGGAAAGCCCCCTGTGGGCATACGCCGTCCCCTAAATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAACTGGAGAGCGGCGCGGCCAAGCCGTAAAACCCCCAACTTCTGAA
Otu3 **Core**	TGTACCCTCAAGCACTGCTTGGTGTTGGGCGTTTGTCCTGCAAAGGACTCGCCTGAAAGCGATTGGCGGCCAACGTACTGGTGGTAGAGCGCAGCACAATTTGCGTCTCTCCCTTCTACGTCGGCGTCCATGAAGCCTTTTTTCAAC
Otu4 **Core**	CAACCCCTAAGCACAGCTTATTGTTGGGAATCTACGCCCTAGTAGTTCCTCAAAGACATTGGCGGAGTGGCAGTAGTCCTCTGAGCGTAGTAATTCTTTATCTCGCTTTTGTTAGGTGCTGCCTCCCCGGCCGTAAAACCCCCAATTTTTTCT
Otu5 **Core**	CATCCCTCAAGCCCCAGCGGCTTGGTGTTGGGCTTCGGCCGTCCTCAGCGGCGGCCGTGCCCCAAATACAGTGGCGGTCTCGCCCCCGGCTCCTCTGCGTAGTAGTAACATCTCGCACTGGGACGGAGCGAAGGCCACGCCGTAAAACAACCCAACTTTCTGAA
Otu6	CAACCCTCAAGCCCCCGGGCTTGGTGTTGGGGATCGGCGAGCCTCTGCGCCCGCCGTCCCCTAAATTGAGTGGCGGTCACGTTGTAACTTCCTCTGCGTAGTAGCACACTTAGCACTGGGAAACAGCGCGGCCACGCCGTAAAACCCCCAACTTTTGAAC
Otu8 **Core**	CAACCCTCAAGCTCTGCTTGGTGTTGGGGTACTACAGCCTCCTGTAGACCCTGTAACGTAGTGGCGGATCCTCTGTAAACCTGAGCGTAGTAGTTACTTCTCGCTTCTGGCAAGCAGCGGTTTCCACGCCGTGAAACCCATACTTTTAT
Otu9 **Core**	CAACCCTCAAGCTCAGCTTGGTGTTGGGACTCGCGGTAACCCGCGTTCCCCAAATCGATTGGCGGTCACGTCGAGCTTCCATAGCGTAGTAATCATACACCTCGTTACTGGTAATCGTCGCGGCCACGCCGTAAAACCCCAACTTCTGAA
Otu10	CAACCCTCAAGCCTAGCTTGGTGTTGGGCGTTTGTCCCGCCTCCGCGCGCCTGGACTCGCCTCAAAAACATTGGCGGCCGGTTCCCAGCAGGCCACGAGCGCAGCACAGCGAGCGCTGAAGTGGCTGCGGGTCGGCGCACCAGAAGCCCCCCCACACCAGAA

Otu15	CAACCCTCAGGCCCCCGGGCCTGGCGTTGGGGATCGGCGGAAGCCCCCTGCGGGCACAACGC
Core	CGTCCCCCAAATACAGTGGCGGTCCCGCCGCAGCTTCCATTGCGTAGTAGCTAACACCTCGCAA
	CTGGAGAGCGGCGCGGCCACGCCGTAAAACACCCAACTTCTGAA
Otu16	CAACCCTCGAGCCCTCGTGGCCCGGCGTTGGGGATCTGCCACGGCAGGCCCCGAAATACAGTG
	GCGGACCCGTTAGGCCCTTCCTTTGCGTAGTAGCATTAGCCTCGCATCGGGAGCCGGCGGGCT
	CTCCTGCCTCTAAACCCCCCAACAAGCCCGCTCCGGCGGCACCAA
Otu17	CAACCCTCGAGCCCCCGTGGCCCGGCGTTGGGGATCTGCCCAGGCAGGCCCCTAAAACCAGT
	GGCGGACCCGTTACAGGCCCTTCCTTTGCGTAGTAGCATCAGCCTCGCATCGGGAGCCAGCGG
	GCTTCTGGCCTCTAAACCCCCATCAAGTCCGCCCCGGCGGCACCAA
Otu19	ACACCCTCAAGCTCTGCTTGGTGTTGGGCGTCTGTCCCGCCTCCGTGCGCGGACTCGCCTCAA
	AGTCATTGGCAGCGGTCTCGTCGGCTTCTCGCGCAGCACATTTGCGCTTCTCGGAGCCCCGGC
	GGATCAGCGTCCAGCAAGCAATTTCATG
Otu21	CAACCCTCGAGCCCTCGTGGCCCGGCGTTGGGGATCTGCCCAGGCAGGCCCCGAAAACCAGT
	GGCGGACCCGTCCGGGACCTCTCCTTGCGTAGTAGCATCAGCCTCGCATCGGGAGCCGGCGG
	GCCTTCCGGCCTCTAAACCCCCCACAAGTCCGCTCCGGCGGCATCAA
Otu22	GTACCTTCAAGCTTTGCTTGGTGTTGGGTGTTTGTCTCGCCTCTGCGTGTAGACTCGCCTTAAAA
Core	CAATTGGCAGCCGGCGTATTGATTTCGGAGCGCAGTACATCTCGCGCTTTGCACTCATAACGAC
	GACGTCCAAAAGTACATTTTTACAC
Otu25	CAACCCTCGAGCCCCCGTGGCCCGGCGTTGGGGCCCTACGCGCCTTCTGGCAGTAGGCCCCG
Core	AAAAGCAGTGGCGGTCCCGTGTGGTCCTCTCCTTTGCGTAGTAGCATTAGCCTCGCTTTGGGAG
	CCCGCGGCGTGCCGGCCTCGAAACCATCAAGTCCGCTCCGGCGGCACCCA
Otu29	TCACCCCTCAAGCCCGGCTTGTTGTTGGACGCCGGCGGTGGCCTCTTTTGGCCCCGCCCGTCT
Core	CAAAGATAATGACGGCGTCTGTGAGGACTCCTGTACACTGAGCTTTCGGGCACGTACTAGGCAG
	CACTTCAGGCCCGGTCTTCGTCGAATCCCATCTCGGGTGCCGACAAACTTTTACCAA
Otu31	GTACCCTCAAGCTTTGCTTGGTGTTGGGCGTTTTTTGTCTTTGGTTTTGTCCAAAGACTCGCCTTA
	AAACGATTGGCAGCCGGCCTACTGGTTTCGCAGCGCAGCACATTTTTGCGCTTGCAATCAGCAA
	AAGAGGACGGCACTCCATCAAGACTCTATATCAC
Otu33	CAACCCTCAAGCCCCCTCGGGGGATTGGTGCTGGGGATCGGCCGTCATGGGCCGGCCCCGAA
Core	ATCGAGTGGCGGTCTCGCCGTCGCCTCCTCTGCGTAGTAGAAACACCTCGCACTGGGACGCGG
	CGCGGCCATGCCGTTAAACCCCCGACTTCTGAAA
Otu34	CAACCCTCAAGCCCCCCGGGCTTGGTGTTGGGGATCGGCACAAGGCCCCTCGCGGCCCGCCG
	TCCCCCAAATGCAGTGGCGGTCACGTCGCAGCCTTCTATGCGTAGTAGCAACACCTCGCACTGG
	AGCGCGACGCGGCCACGCCGTAAAACCCCCGACTTTTTTCT

Otu35	AGACTCAATCCCTCGGGTTTCCGAGGAGATTGGACTTGGGTGTTGCCGCTCTGCCGGCTCGCCTTAAAAGACTTAGCGGGATAGCACCGTAGTCGGCGTAATAAGTTTCGTCGGTGAAGGTTGTGATGACTGCTTACAATCGCCCTCGGGCAATTTTTGA
Otu37 **Core**	ACACCCCTCAAGCTCTGCTTGGTGTTGGGCGTCTGTCCGCCGCCGCGAGGCGGGGGACTCGCCCCAAAGGCATTGGCAGCGGCGTCCGCCGGGCTTTTCCCCATCAGCGCAGCACTGTTCGCGCACCTCGGGGACCCGCGCGGAGGCAGCGTCCACGAAGCGCCCACGTTTTTG
Otu38	CGACCCTCGCGCCCGGCTTCTGTCGGGGGCGGTGTTGGGGATCGGCCACACCCTTCAGTGGGAGGCCGGCCCCTAAATTCAGTGGCGACCACGCTGTAGCCTCCCCTGCGTAGTACTAAAACCACCTCGCAGGCGGAGAGCGGTGCGGCCCGCCGTAAAACCCCCCAACTTTTACAA
Otu40	CAACCCCTAAGCACAGCTTATTGTTGGGCGTCTACGTCTGTAGTGCCTCAAAGACATTGGCGGAGCGGCAGCAGTCCTCTGAGCGTAGTAATTCTTTATCTCGCTTCTGTTAGGCGCTGCCCCCCCGGCCGTAAAACCCCCAATTTTTTCT
Otu49	GAACCCTCAAGCTCTGCTTGGTGTTGGGTGTTTGTCCCGCCATTGCGCGTGGACTCGCCTTAAAGTAATTGGCAGCCATGTAATTCGGCTTTGAGCGCAGCACATTGCGTACTCTATGCTGGTACATTGGCATCCAGAAGCCCTTTTTTAC
Otu59 **Core**	GTACCTTCAAGCTTTGCTTGGTGTTGGGTGCTTGTCTTTTTGTTAAGACTCACCTCAAAGTCATTGGCAGCCAGTGTTTTGGTAGTAAGCGCAGCACATTTTGCGTCTTGGTCCCTTAACAGCAGCATCCATCAAGCCATTTTCTCAC
Otu63 **Core**	CACCACTCAAGCCTCGCTTGGTATTGGGCAACGCGGTCCGCCGCGTGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGGAAACTATTCGCTAAAGGGTGTTCGGGAGGCTACGCCGTAAAACAACCCCATTTCTAA
Otu66	CATCCCTCAAGCCCCTTCGGGCTTGGTGTTGGGCATCGGCCGTCCCTCCAGCGGCGGCCGTGCCCCAAATACAGTGGCGGTCTCGCCCCCGGCTCCTCTGCGTAGTAGTAACATCTCGCACTGGGACGGAGCGTAGGCCACGCCGTAAAACAACCCAACTTTCTGAA
Otu69 **Core**	CAACCCTCAGGCCCTGCCTGGTGTTGGAGGACTGCGCACCGCAGCCTCCCAAAGCAAGCGGCGGCGGCGCCCCATAACCGAACGCAGTAGTTACATCTCGTTCTGGGTCTGGGTCGTTGTCCTGCCGGAAAACCCCCATCTTTTTAAT
Otu74 **Core**	ACACCCCTCAAGCTCTGCTTGGTGTTGGGCGTCTGTCCGCCGCCGCGAGGCGGGAGGACTCGCCCCAAAGGCATTGGCAGCGGCGTCCGCCGGGCTTTCCCCATCAGCGCAGCACTGTTCGCGCACCAACGGGGACCCGCGCGGAGGCAGCGTCCAGGAAGCGCCCACTTTTTTG
Otu75	CAACCCTCAAGCTCTGCTTGGTATTGGGCCCTGCCGCTGGGCAGGCCTTAAAATCAGTGGCGGTGCCGTCGCGGCTCCAAGCGTAGTACATCTCTCGCTCCGGAGGCCCGGTGGTGTCTCGCCAGACAACCCCCAAATTGTCTTCTAT

Otu78	CATCATCATCTCCTCCCCGGTTTTGCCGGGTTCGGAAGGTGGACTTGGAGGACTTTTGCTGCTGCACAAGCGGCTCCTCTTGAATGCATCGGCTGTGCTCGAAAGGGCGCTCCTTGACGTTGTAATCTTCCTCGTCTCGGGCTTCTTTCTGACCGGCCTTGGCCTTTGCCTCTGGAGTGGCGGCCAACTTTTTACTTTGACATCTGACCTCGAATCGGG
Otu88 **Core**	AACACCTCAAAGCTTTTGATCTTTTTCAAAAGTTTTGGACTTGAGCAATCCCAACACCAGTCTTTTTGGATCGGTGGCGGGTTGCTTGAAATGCAGGTGCAGCTGGACATTCTCCTGAGCTAAAAGCATATTTATTTAGTCCCGTCAAACGGATTATTACTTTTGCTGCAGCTAATATAAAGGGAGTTTGACCGTTTTGGCTGACTGATGCAGGATTT
Otu93	CAACCCCTCGGACCCCCCGCGGCCCGGCGTTGGGGACCTGCCACGGCAGGCCCCGAAAACCAGCGGCGGACCCTCCGGGCCCTCTCCTTGCGCAGTAGCATCAGCCTCGCATCGGGAGCCCGGGCGGCGTCCGGCCCCTAAACACCCCCAAAGCCCGCCCCCGCGCGGCACCAA
Otu106	AAACCCTCAAGCCCCATGGGTGTTGTCCCGCCTCGTGCGCGGCCTTCGCCTGGCTTGGTGTTGGGTGCCTGTCCCTGCTCCCCGCGGGACTCACCCCAAATGCATTGGCAGCAGCCCCTCGGCTTCCCGCGCAGCACATTGCGCAGCGGAGCGTAGAGAGGCGTGCGTCCAGCAAGCAAACCCCAA
Otu110 **Core**	CAACCCTCAGGCCCTGCCTGGCGTTGGAGGACTGCGCACGCAGCCTCCCAAAGCGAGCGGCGGCGGCGCCCCGAAACCGAACGCAGTAGTTACTTCTCGTTCTGGGTCCGGGTCGTTGTCCTGCCGGAAAACCCCCTTCTAATCAAT
Otu126	CAACCCTCGAACCCCGGTTTTCTTTATGGATCCCGGGGATCGGTGTTGGGGCACTACGGAGGTCTTCTGACCGCCGTAGGCTTCGAAATACAGTGGCGGTCCCGCCGCGGCGCCCTCTGCGTAGTAATTTTCACCTCGCATTGGGTCCCGGCGAAGGCCAGCCGTCAAACCCTCTATTTTCTATG
Otu127	TGTACCCTCAAGCACTGCTTGGTGTTGGGCGTTTGTCCTGCAGAGGACTCGCCTGAAAGCGATTGGCGGCCAACGTAGTCGTGGCAGAGCGCAGCACAATCTCGCGTCTCTCCCCTCTGCGTCGGCGTCCATAAGCCTACAATCTCAAC
Otu160	ACACGATCAACTCTAGTTAGAGTTGGGATTGGCCTCATGCACTGTTATAGTGTATCTGGCTCGAATGGATCAAGTTGATGGGCTCCCCAGCGATGCTCGATGTGTGCTAGCGAGACAGTCGTCCCGATCTCACATTAGTGGTTTTGTTGCAGAGCTCTAATCACAGCTTGTTAACACATATACAAATCTA
Otu166	AACAAACCCATCGGGTGCTGGGATCCACGGATCCCTCACCCGGTTCTGAAGGTGGGATGCACGCAATCCCTCTTTGAAAGGAATCGGCGATGCTTGCTTGTCCATTTGGTTGCGTAGTAAAATTACCTTTACCTGTCGCAGTTGGACAAGCAATGATCTGCCATAAAACCGTAGAGCCTGCATGGCTTCAGT
Otu4583 **Core**	TGTACCCTTAAGCACTGCTTGGTGTTGGGCGTTTGCCCTGCAAAGGACTCGCCTGAAAGCGATTGGCGGCCAACGTACTGGTGGTAGAGTGCAGCACAATTTGCGTCTCTCCCCTCTGCGTCGGCGTCCATGAAGCCTTTTTTCAAC

Otu6783	CAACCCTCAAGCCCCTGGGCTTGGTGTTGGGGATCGGCGAGCCTCTGCGCCCGCCGTCCCCTA
Core	AATTTAGTGGCGGTCACGTTGTAACTTCCTCTGCGTAGTAGCACACTTCGCACTGGGAAACAGCGCGGCCACGCCGTAAACACCCCAACTTTTAAAC

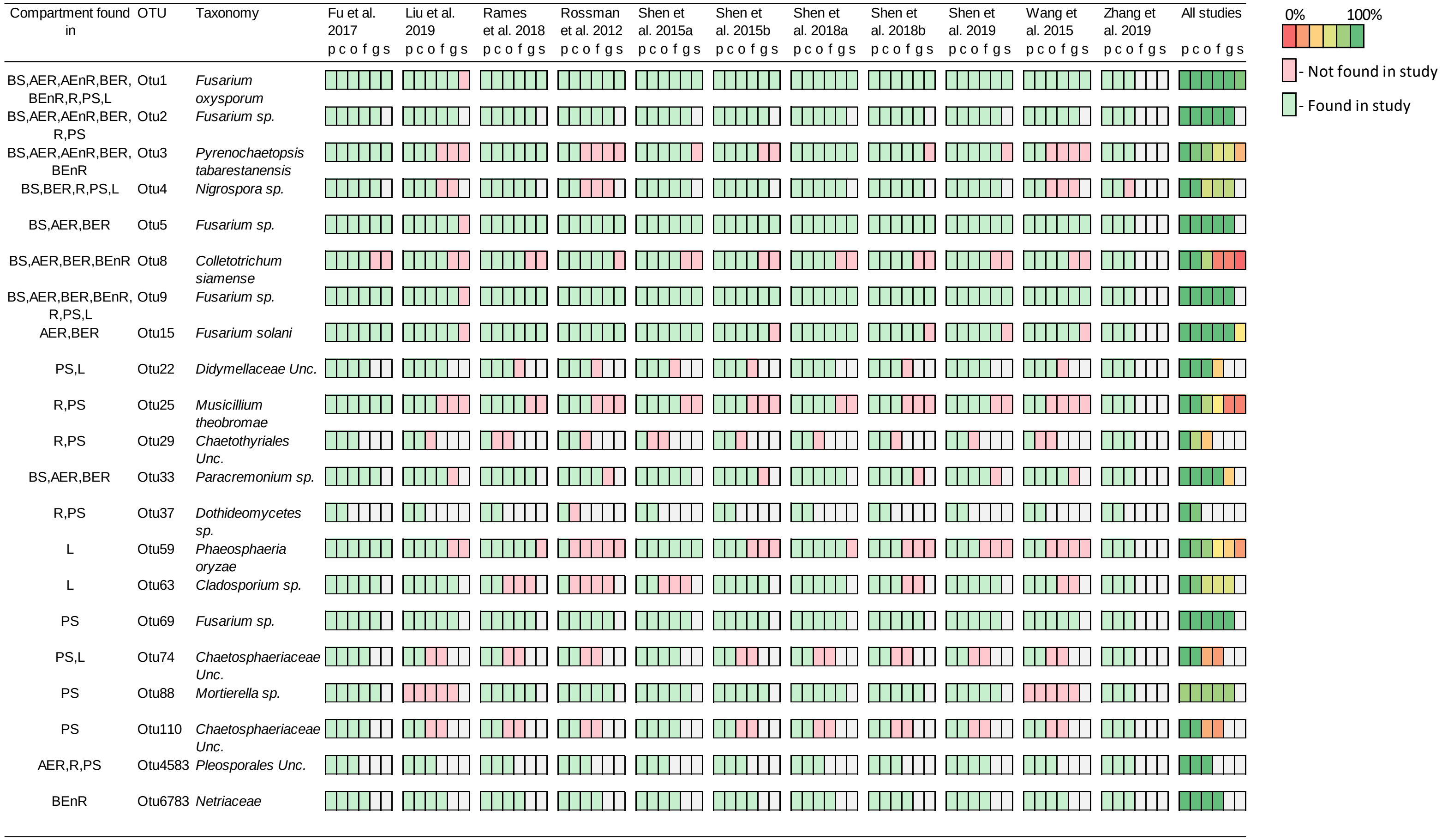


Fig S10 The presence of core OTUs in the taxonomy assigned to the top 10% of OTUs by maximum abundance in publicly available datasets that examine fungi associated with *Musa* spp. Green tiles represent presence of an OTU in a study with the same taxonomy as a core OTU, red indicates they were not present, white indicates they core OTU was not identified to that taxonomic rank. The final column represents a mean of all studies.

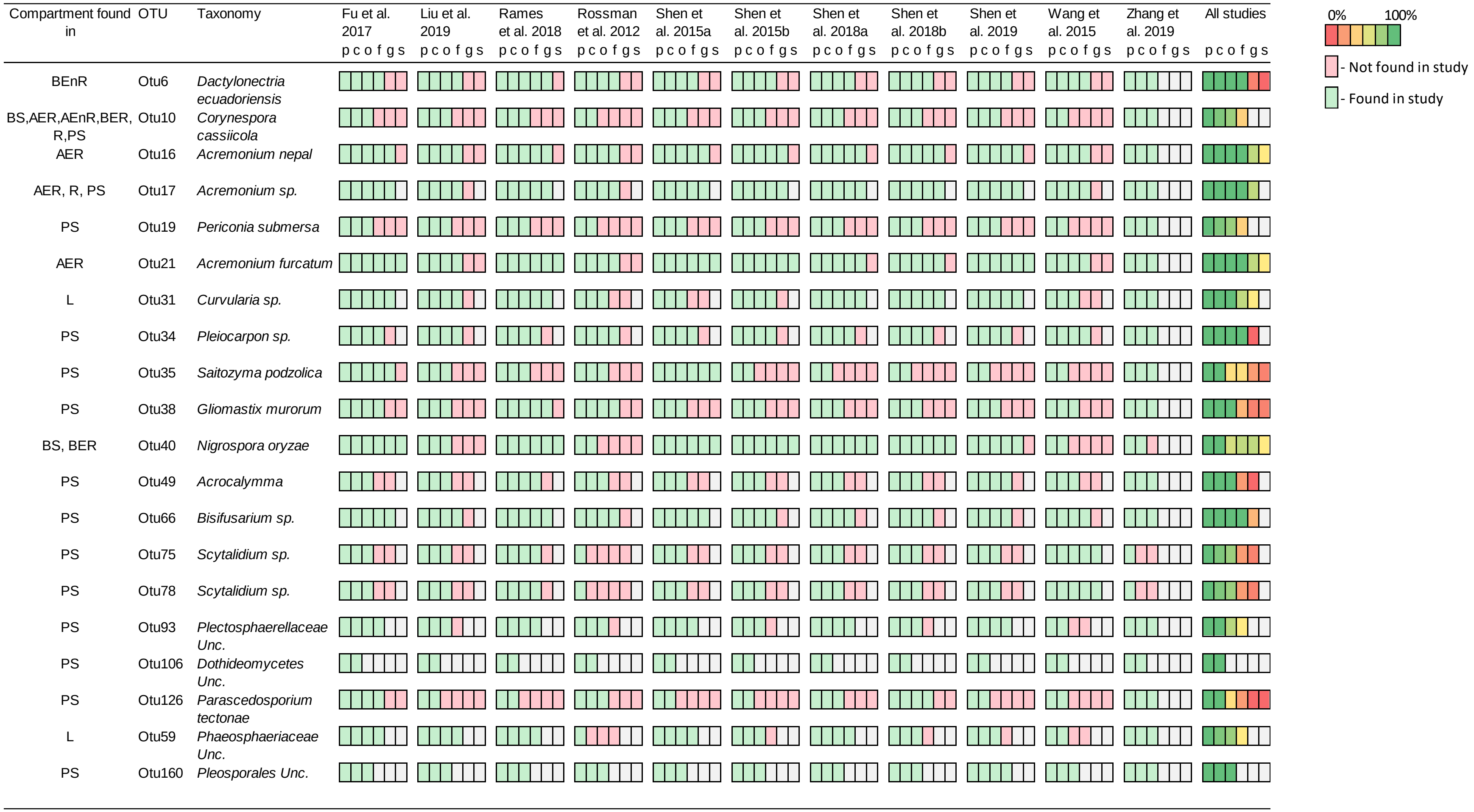


Fig S11 The presence of candidate-core OTUs in the taxonomy assigned to the top 10% of OTUs by maximum abundance in publicly available datasets that examine fungi associated with Musa spp. Green tiles represent presence of an OTU in a study with the same taxonomy as a core OTU, red indicates they were not present, white indicates they core OTU was not identified to that taxonomic rank. The final column represents a mean of all studies.