Supplementary information:

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

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Table S1 The locations and basic properties of the five soils used in our pot experiment.

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
Clasification	Brown Dermosol	Orthic Tenosol	Red Ferrosol	Red Ferrosol	Brown Dermosol
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

Table S2 Genotypes included in our survey of the Australian Banana Germplasm Collection.

Cultivar	Subgroup/Species & Subspecies	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	Not available	--
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	Not available	AABB
FHIA-17	Highgate hybrid	AAAA
FHIA-18	Pome hybrid	AAAB
FHIA-23	Highgate hybrid	AAAA
FHIA-25	Not available	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
Santa Catarina Prata	Pome	AAB
SH-3142	Not available	AA
SH-3362	Not available	AA
Sugar	Silk	AAB
Yangambi Km5	Ibota	AAA
Zebrina	*Musa acuminata* ssp. *zebrina*	AA

Table S3 Studies included in our meta-analysis of banana-associated bacterial taxa.

Study	Method	Plant compartments	Cultivar	Taxonomic focus	Country	Study description	Title	Accession
De la Torre-González et al. (2021) [1]	Culture independent (Illumina MiSeq)	Ectorhizosphere, bulk soil	*Musa acuminata* (cultivar not given)	Bacteria	Mexico	Examine how different climate, soils, and crop management practices influence bacterial diversity in the banana plant microbiome	Response to edaphoclimatic conditions and crop management of the bacterial microbiome of *Musa acuminata* rhizosphere profiled by 16S rRNA gene amplicon sequencing	PRJNA673638
Du et al. (2018) [2]	Culture independent (Illumina MiSeq)	Pseudostem	Giant Cavendish Baxi	Actinobacteriota	China	The use of Actinobateria specific primers to examine the endophytic communities from Giant Cavendish (AAA) shoot tips.	Illumina-based sequencing analysis directed selection for actinobacterial probiotic candidates for banana plants	SRP062458
Fu et al. (2017) [3]	Culture independent (454)	Ectorhizosphere	Brazil	Bacteria	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

Gómez-Lama Cabanás et al. (2021) [4]	Culture independent (Illumina MiSeq)	Endorhizosphere	Pequeña Enana (synonymous with Dwarf Cavendish)	Bacteria/fungi	Spain (Canary Islands)	Examine microbial community diversity in mother and sucker plants across various farm in the Canary Islands.	The banana root endophytome: differences between mother plants and suckers and evaluation of selected bacteria to control *Fusarium oxysporum* f. sp. *cubense*	MT445188-MT445196
Karthik et al. (2017) [5]	Culture dependent (Platform unknown)	Leaf	Rasthali, Hill banana, Co1, Nattu Poovan and Red banana	Bacteria	India	Leaf endophytes of field grown Rasthali, Hill banana, Co1, Nattu Poovan and Red banana plants.	Endophytic bacteria associated with banana cultivars and their inoculation effect on plant growth	KF036177 - KF036193
Kaushal et al. (2020) [6]	Culture independent (Illumina, specific platform unknown)	Ectorhizosphere, endorhizosphere, rhizome (corm)	Sukari Ndizi (*Musa* subgroup AAB)	Bacteria	Tanzania	Assess the diversity of bacterial microbiome of banana plants with and without Fusarium Wilt symptoms	Unlocking the microbiome communities of banana (*Musa* spp.) under disease stressed (fusarium wilt) and non-stressed conditions	PRJNA493905 and PRJNA494050
Köberl et al. (2015) [7]	Culture independent (Illumina MiSeq)	Ectorhizosphere, endorhizosphere, pseudostem, leaves	Gros Michel	Gammaproteobacteria	Costa Rica and Nicaragua	Gammaproteobacterial communities found in the roots, pseudostem and leaves of field-grown plants.	Agroforestry leads to shifts within the gammaproteobacterial microbiome of banana plants cultivated in Central America	PRJEB8107

Köberl et al. (2017) [8]	Culture independent (Illumina MiSeq)	Ectorhizosphere, endorhizosphere, pseudostem, leaves	Gros Michel	Gammaproteobacteria	Costa Rica and Nicaragua	Gammaproteobacterial communities found in the roots, pseudostem and leaves of field-grown Fusarium wilt affected plants.	Members of Gammaproteobacteria as indicator species of healthy banana plants on Fusarium wilt-infested fields in Central America	PRJEB12550
Pereira et al. (2018) [9]	Culture dependent (Sanger)	Endorhizosphere	Prata Anã (AAB)	Bacteria	Brazil	Root communities from field grown Prata Anã (AAB) banana.	Characterization and activity of endophytic bacteria from 'Prata Anã' banana crop (*Musa* sp., AAB)	KX189587 - KX189625
Rossman et al. (2012) [10]	Culture dependent and indepedent (Culture based 16S sequences, DGGE, 454 Pyrosequencing, FISH, qPCR)	Bulk soil ectorhizosphere, pseudostem exterior	Unknown	Bacteria/Fungi Enteric sequences	Uganda	Examination of soil and pseudostem of field-grown banana.	Banana-associated microbial communities in Uganda are highly diverse but dominated by *Enterobacteriaceae*	HE588041 - HE588079
Shen et al. (2014) [11]	Culture independent (454)	Bulk soil	Brazil	Bacteria	China	The effect of a biocontrol on the bulk soil bacterial community of field grown banana plants.	Deep 16S rRNA pyrosequencing reveals a bacterial community associated with banana fusarium wilt disease suppression induced by bio-organic fertilizer application	DRA001282

Shen et al. (2015) [12]	Culture independent (454)	Bulk soil	Brazil	Bacteria	China	Comparing wilt suppressive/susceptible	Soils naturally suppressive to banana Fusarium wilt disease harbor unique bacterial communities	DRA002235
Souza, S. A. et al. (2013) [13]	Culture dependent (ABI-PRISM 3100 GA)	Endorhizosphere	Prata Anã (AAB)	Bacteria	Brazil	Root communities from field grown Prata Anã (AAB) banana.	Endophytic bacterial diversity in banana 'Prata Anã' (*Musa* spp.) roots	JQ979307 - JQ979408
Suhaimi et al. (2017) [14]	Culture independent (Illumina MiSeq)	Pseudostem	Nipah	Bacteria	Malaysia	Pseudostem from healthy and bacterial wilt effected field grown Nipah banana plants.	Diversity of microbiota associated with symptomatic and non-symptomatic bacterial wilt-diseased banana plants determined using 16S rRNA metagenome sequencing	SRP056352
Thomas et al. (2008) [15]	Culture dependent (Platform unknown)	Pseudostem	Grand Naine	Bacteria	India	Examination of field grown Grand Naine (AAA) shoot tips.	Identification of culturable and originally non-culturable endophytic bacteria isolated from shoot tip cultures of banana cv. Grand Naine	Various (see article)
Thomas & Soly, (2009) [16]	Culture dependent (Platform unknown)	Pseudostem	Grand Naine	Bacteria	India	Examination of field grown Grand Naine (AAA) shoot tips.	Endophytic bacteria associated with growing shoot tips of banana (*Musa* sp.) cv. Grand Naine and the affinity of endophytes to the host	EU518689-EU518713 & FJ447493-FJ447497

Thomas & Sekhar (2017) [17]	Culture independent and dependent (Illumina MiSeq)	Pseudostem	Grand Naine	Bacteria	India	Examination of field grown Grand Naine (AAA) shoot tips.	Cultivation versus molecular analysis of banana (*Musa* sp.) shoot-tip tissue reveals enormous diversity of normally uncultivable endophytic bacteria	KT944215 - KT944251, KT946872 - KT946901, SRR2664411, SRR2664412, SRR3646184, SRR3646239
Sekhar & Thomas (2015) [18]	Culture dependent (Platform unknown)	Pseudostem	Grand Naine	Bacteria	India	Examining bacteria present in banana plant shoot tips	Isolation and identification of shoot - tip associated endophytic bacteria from banana cv. Grand Naine and testing for antagonistic activity against *Fusarium oxysporum* f. sp. *cubense*	KP798811 - KP798857
Wang et al. (2013) [19]	Culture dependent (Platform unknown)	Bulk soil	Unknown	Bacteria	China	Isolation of suppressive strains from the rhizosphere of banana plants grown in a Fusarium Wilt suppressive field	Effects of novel bioorganic fertilizer produced by *Bacillus amyloliquefaciens* W19 on antagonism of Fusarium wilt of banana	JQ740889
Wang et al. (2015) [20]	Culture independent (454)	Bulk soil	Unknown	Bacteria/Fungi	China	Field soil from a field in which banana was grown after rotation with pineapple.	Pineapple-banana rotation reduced the amount of *Fusarium oxysporum* more than maize-banana rotation mainly through modulating fungal communities	DRA002471

Xue et al. (2015) [21]	Culture independent and dependent (454)	Ectorhizosphere	Brazil	Bacteria	China	Roots from field grown Brazil (AAA) banana affected by Fusarium wilt and then either treated with a biocontrol or not.	Manipulating the banana rhizosphere microbiome for biological control of Panama disease.	KJ600797 - KJ600996 & SRR1185515-SRR1185517
Zhai et al. (2016) [22]	Culture independent (Illumina MiSeq)	Pseudostem	Giant Cavendish Baxi	Actinobacteriota	China	The use of Actinobacteria specific primers to examine the root endophytes of field grown plants	A new approach to analyzing endophytic actinobacterial population in the roots of banana plants (*Musa* sp., AAA)	SRP061867

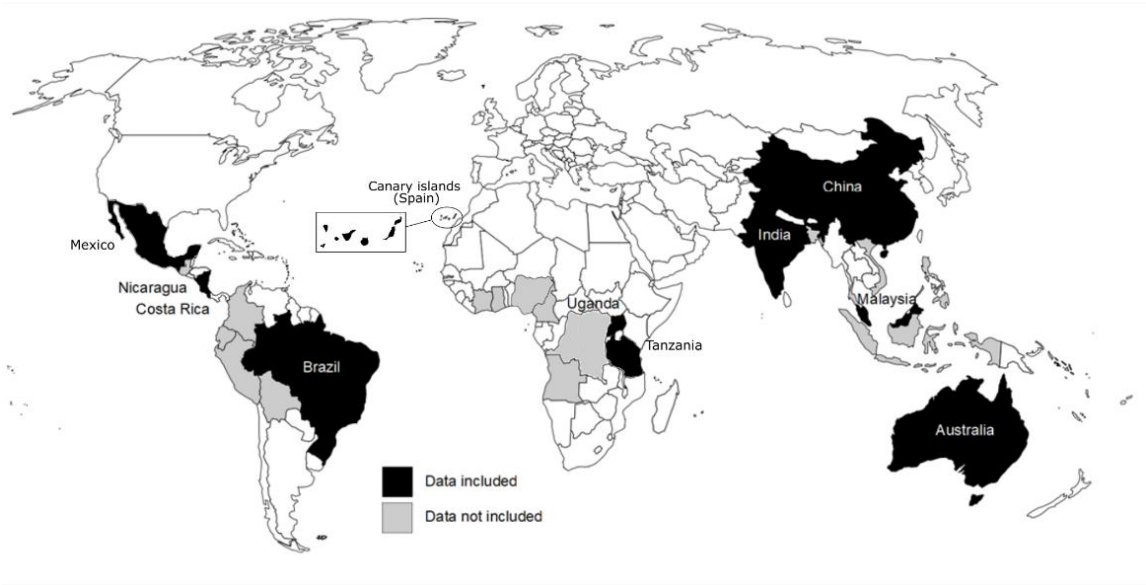

Fig. S1 A map showing, in black, countries included in the meta-analysis of the bacterial microbiome of *Musa* spp. Countries in grey are major producers (FAOSTAT, 2017) for which data were not available and were not included in meta-analysis.

Table S4 The impact of soil, genotype and plant compartment on alpha diversity metrics assessed by ANOVA from the bacterial microbiome of *Musa* spp.

Response variable	Predictor variable	*F* value	*P* value
Predicted OTUs (Chao 1)	Compartment	272.0	<0.001 ***
	Soil	1.7	0.151
	Compartment: Soil	3.4	<0.001 ***
Shannon's Diversity Index	Compartment	154.0	<0.001 ***
	Soil	1.2	0.290
	Compartment: Soil	2.9	<0.001 ***
Phylogenetic Diversity (Faith's)	Compartment	242.8	<0.001 ***
	Soil	1.5	0.193
	Compartment: Soil	4.3	<0.001 ***
Predicted OTUs (Chao 1)	Compartment	118.1	<0.001 ***
	Genotype	0.4	0.695
	Compartment: Genotype	0.7	0.728
Shannon's Diversity Index	Compartment	74.3	<0.001 ***
	Genotype	0.3	0.747
	Compartment: Genotype	0.9	0.593
Phylogenetic Diversity (Faith's)	Compartment	109.9	<0.001 ***
	Genotype	0.6	0.562
	Compartment: Genotype	0.6	0.850

Table S5 The impact of soil, genotype and plant compartment on beta diversity assessed by PERMANOVA from Weighted UniFrac relative abundance data from the bacterial microbiome of banana.

Response variable	Predictor variable	*F* value	R^2 (%)	*P* value
Community composition (Weighted unifrac)	Compartment	82.9	56.8	<0.001 ***
	Soil	5.5	2.2	<0.001 ***
	Compartment: Soil	2.4	6.4	<0.001 ***
Community composition (Weighted unifrac)	Compartment	35.8	51.9	<0.001 ***
	Genotype	0.3	0.1	0.799
	Compartment: Genotype	1.6	4.3	0.064

Table S6 Average percentage similarity plus/minus the standard deviation of 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	-	84.6 ± 5	67.3 ± 11	87.9 ± 3	77.1 ± 6	38.6 ± 11	25.6 ± 17	0.9 ± 2
AER	81.4 ± 10	-	76.4 ± 10	90.7 ± 4	82.1 ± 7	59.5 ± 12	37.7 ± 20	21.2 ± 15
AEnR	47.6 ± 34	78.1 ± 25	-	73.0 ± 26	87.4 ± 14	81.2 ± 16	66.2 ± 28	40.3 ± 30
BER	89.5 ± 3	90.4 ± 4	69.4 ± 12	-	81.7 ± 7	46.1 ± 12	27.7 ± 20	10.6 ± 12
BEnR	54.0 ± 31	81.8 ± 19	85.2 ± 13	80.9 ± 19	-	76.7 ± 19	60.7 ± 33	37.0 ± 35
R	36.0 ± 30	81.9 ± 17	84.8 ± 16	75.7 ± 22	82.8 ± 18	-	79.0 ± 19	62.9 ± 22
PS	54.9 ± 38	70.7 ± 31	77.1 ± 29	67.5 ± 33	75.0 ± 30	82.3 ± 28	-	63.2 ± 33
L	6.5 ± 20	74.2 ± 23	75.5 ± 30	60.3 ± 27	70.5 ± 28	95.9 ± 5	95.8 ± 4	-

Table S7 ANOVA test results of soils on a per compartment basis on alpha diversity of the *Musa* spp. bacterial microbiome.

Response variable	Compartment	*F* value	*P* value	
Chao1	Bulk soil	2.4	0.062	
	Apical ectorhizosphere	3.1	0.024	*
	Apical endorhizosphere	5.5	0.001	**
	Basal ectorhizosphere	5.3	0.001	**
	Basal endorhizosphere	1.6	0.200	
	Rhizome	0.8	0.519	
	Pseudostem	3.1	0.026	*
	Leaf	1.5	0.210	
Shannon	Bulk soil	6.1	<0.001	***
	Apical ectorhizosphere	2.4	0.060	
	Apical endorhizosphere	5.1	0.002	**
	Basal ectorhizosphere	10.4	<0.001	***
	Basal endorhizosphere	2.9	0.013	*
	Rhizome	1.2	0.308	
	Pseudostem	1.4	0.237	
	Leaf	0.4	0.829	
Phylogenetic diversity (Faith's)	Bulk soil	4.1	0.007	**
	Apical ectorhizosphere	3.7	0.011	*
	Apical endorhizosphere	7.7	<0.001	***
	Basal ectorhizosphere	3.9	0.009	**
	Basal endorhizosphere	3.6	0.012	*
	Rhizome	0.5	0.714	
	Pseudostem	3.0	0.027	*
	Leaf	1.3	0.283	

Table S8 PERMANOVA results to assess the impact of soils on community composition assessed from Weighted UniFrac distance on a per compartment basis.

Compartment	*F* value	R^2 (%)	*P* value
Bulk soil	5.2	31.4	<0.001 ***
Apical ectorhizosphere	1.5	11.7	0.193
Apical endorhizosphere	4.2	28.5	0.005 **
Basal ectorhizosphere	7.6	40.3	<0.001 ***
Basal endorhizosphere	4.0	26.3	0.004 **
Rhizome	3.7	24.5	0.012 *
Pseudostem	1.2	9.9	0.318
Leaf	0.6	5.0	0.679

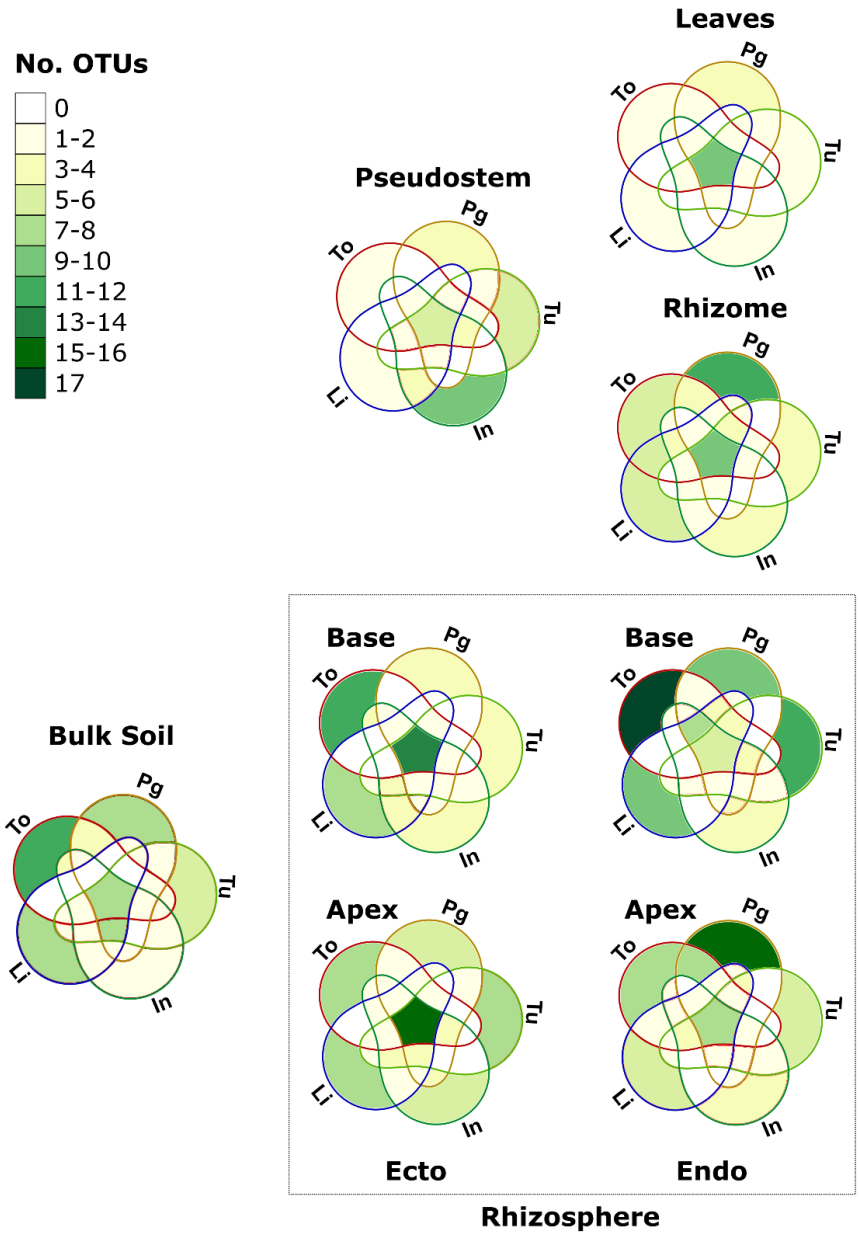

Fig. S2 Venn diagrams to show the numbers of shared candidate-core OTUs between soils (Pg, Tu, In, Li, and To) within compartments. Candidate-core OTUs are those that were present in ≥50% of the ten replicates within each treatment combination at a mean relative abundance of ≥0.5%. Core OTUs are those that were shared between all soils within each compartment.

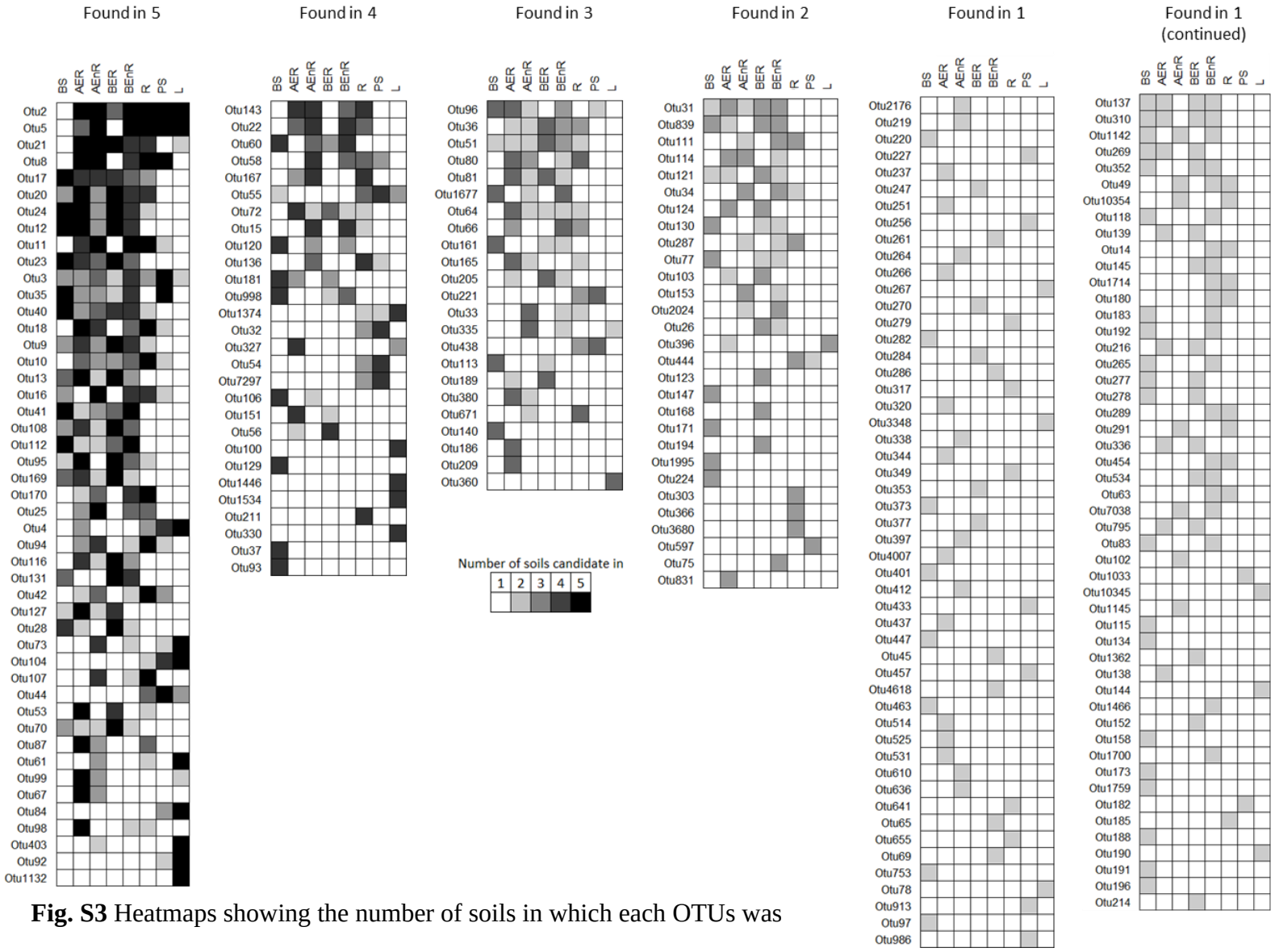

Fig. S3 Heatmaps showing the number of soils in which each OTUs was considered a ‘candidate-core’ population on a per compartment basis

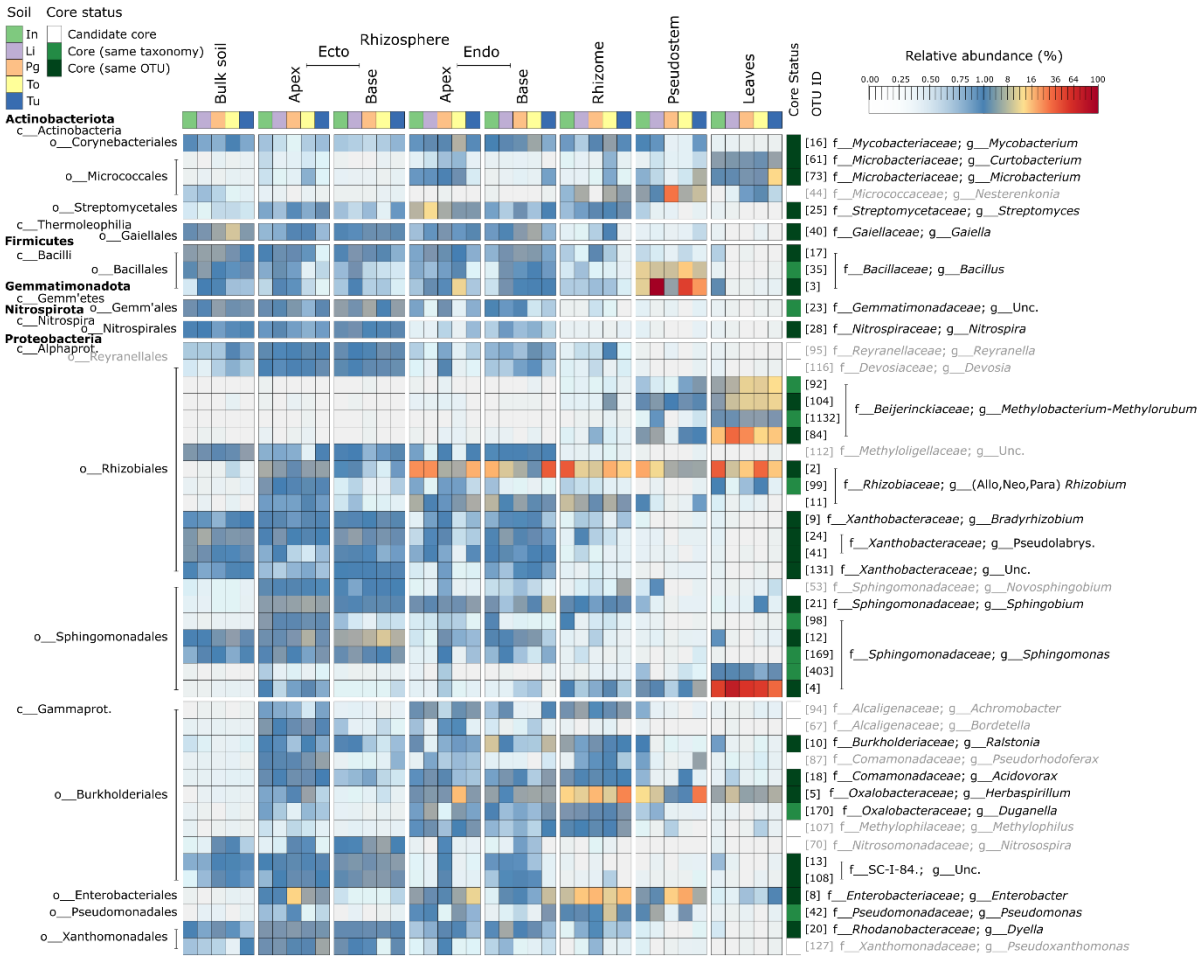

Fig. S4 The 'candidate' core bacterial microbiome of *Musa* spp. The heatmap highlights the relative abundances of core OTUs in each compartment and soil. Each cell represents the mean of the replicates for that treatment. OTUs in grey indicate 'candidates' that were not found in field-grown plants and were subsequently dropped. Those with black text were found in field plants and were elevated to full core status.

Table S9 OTUs found as candidate-core in one to five soils or as key constituents in the field.

	Total	OTUs
Considered as candidate core in 5 soils	47	Otu2, Otu5, Otu21, Otu8, Otu17, Otu20, Otu24, Otu12, Otu11, Otu23, Otu3, Otu35, Otu40, Otu18, Otu9, Otu10, Otu13, Otu16, Otu41, Otu108, Otu112, Otu95, Otu169, Otu170, Otu25, Otu4, Otu94, Otu116, Otu131, Otu42, Otu127, Otu28, Otu73, Otu104, Otu107, Otu44, Otu53, Otu70, Otu87, Otu61, Otu99, Otu67, Otu84, Otu98, Otu403, Otu92, Otu1132
Considered as candidate core in 4 soils	28	Otu143, Otu22, Otu60, Otu58, Otu167, Otu55 Otu72, Otu15, Otu120, Otu136, Otu181, Otu998, Otu1374, Otu32, Otu327, Otu54, Otu7297, Otu106, Otu151, Otu56, Otu100, Otu129, Otu1446, Otu1534, Otu211, Otu330, Otu37, Otu93
Considered as candidate core in 3 soils	23	Otu96, Otu36, Otu51, Otu80, Otu81, Otu1677, Otu64, Otu66, Otu161, Otu165, Otu205, Otu221, Otu33, Otu335, Otu438, Otu113, Otu189, Otu380, Otu671, Otu140, Otu186, Otu209, Otu360
Considered as candidate core in 2 soils	29	Otu31, Otu839, Otu111, Otu114, Otu121, Otu34, Otu124, Otu130, Otu287, Otu77, Otu103, Otu153, Otu2024, Otu26, Otu396, Otu444, Otu123, Otu147, Otu168, Otu171, Otu194, Otu1995, Otu224, Otu303, Otu366, Otu3680, Otu597, Otu75, Otu831
Considered as candidate core in 1 soil	101	Otu137, Otu310, Otu1142, Otu269, Otu352, Otu49, Otu10354, Otu118, Otu139, Otu14, Otu145, Otu1714, Otu180, Otu183, Otu192, Otu216, Otu265, Otu277, Otu278, Otu289, Otu291, Otu336, Otu454, Otu534, Otu63, Otu7038, Otu795, Otu83, Otu102, Otu1033, Otu10345, Otu1145, Otu115, Otu134, Otu1362, Otu138, Otu144, Otu1466, Otu152, Otu158, Otu1700, Otu173, Otu1759, Otu182, Otu185, Otu188, Otu190, Otu191, Otu196, Otu214, Otu2176, Otu219, Otu220, Otu227, Otu237, Otu247, Otu251, Otu256, Otu261, Otu264, Otu266, Otu267, Otu270, Otu279, Otu282, Otu284, Otu286, Otu317, Otu320, Otu3348, Otu338, Otu344, Otu349, Otu353, Otu373, Otu377, Otu397, Otu4007, Otu401, Otu412, Otu433, Otu437, Otu447, Otu45, Otu457, Otu4618, Otu463, Otu514, Otu525, Otu531, Otu610, Otu636, Otu641, Otu65, Otu655, Otu69, Otu753, Otu78, Otu913, Otu97, Otu986
Key field constituents	90	Otu129, Otu101, Otu9, Otu40, Otu195, Otu68, Otu146, Otu56, Otu77, Otu130, Otu37, Otu38, Otu27, Otu24, Otu191, Otu118, Otu23, Otu13, Otu26, Otu57, Otu82, Otu62, Otu1677, Otu93, Otu86, Otu41, Otu131, Otu134, Otu47, Otu17, Otu75, Otu60, Otu29, Otu12, Otu83, Otu43, Otu88, Otu839, Otu108, Otu10, Otu46, Otu36, Otu30, Otu76, Otu72, Otu50, Otu28, Otu128, Otu3, Otu21, Otu133, Otu103, Otu20, Otu65, Otu164, Otu48, Otu2, Otu25, Otu18, Otu8, Otu34, Otu14, Otu5, Otu11, Otu1194, Otu16, Otu203, Otu135, Otu3680, Otu59, Otu73, Otu4, Otu6, Otu156, Otu218, Otu100, Otu335, Otu63, Otu52, Otu104, Otu229, Otu1333, Otu61, Otu1614, Otu239, Otu84, Otu446, Otu78, Otu436, Otu324

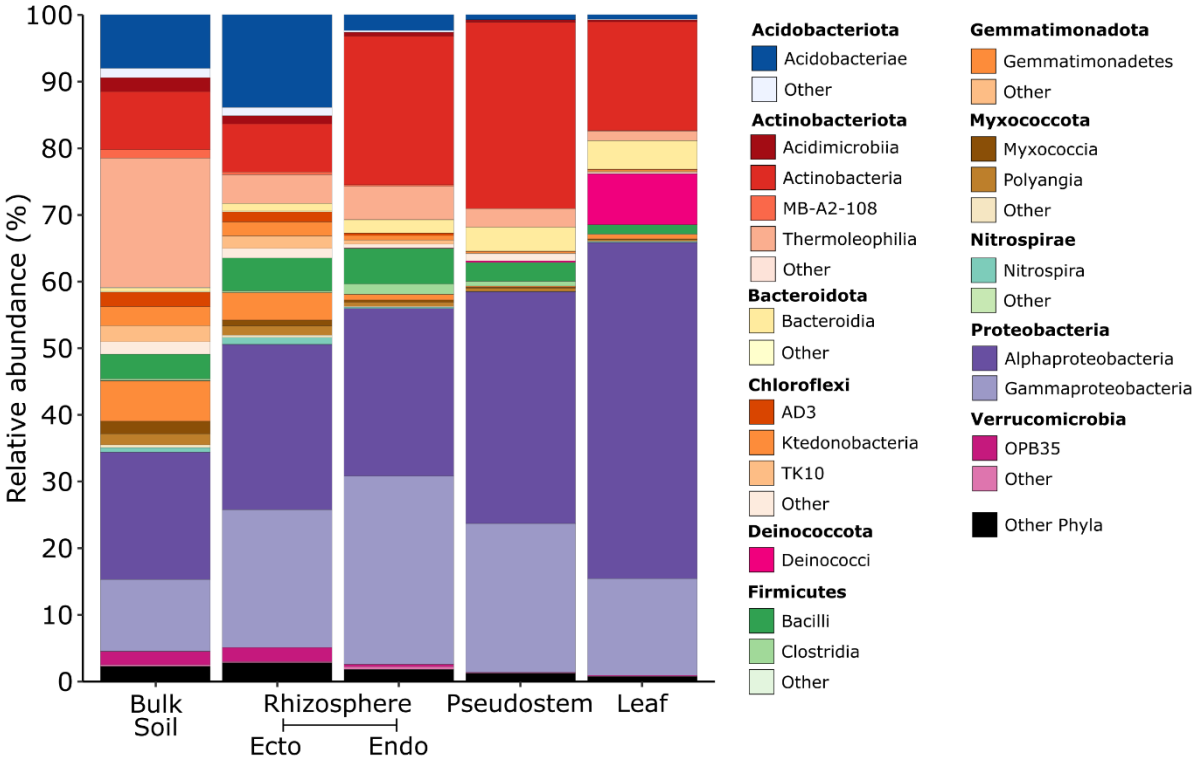

Fig. S5 The mean relative frequencies of bacterial classes associated with each compartment in field-grown *Musa* spp. Within each phylum, classes represented at <1% mean relative abundance are grouped as other.

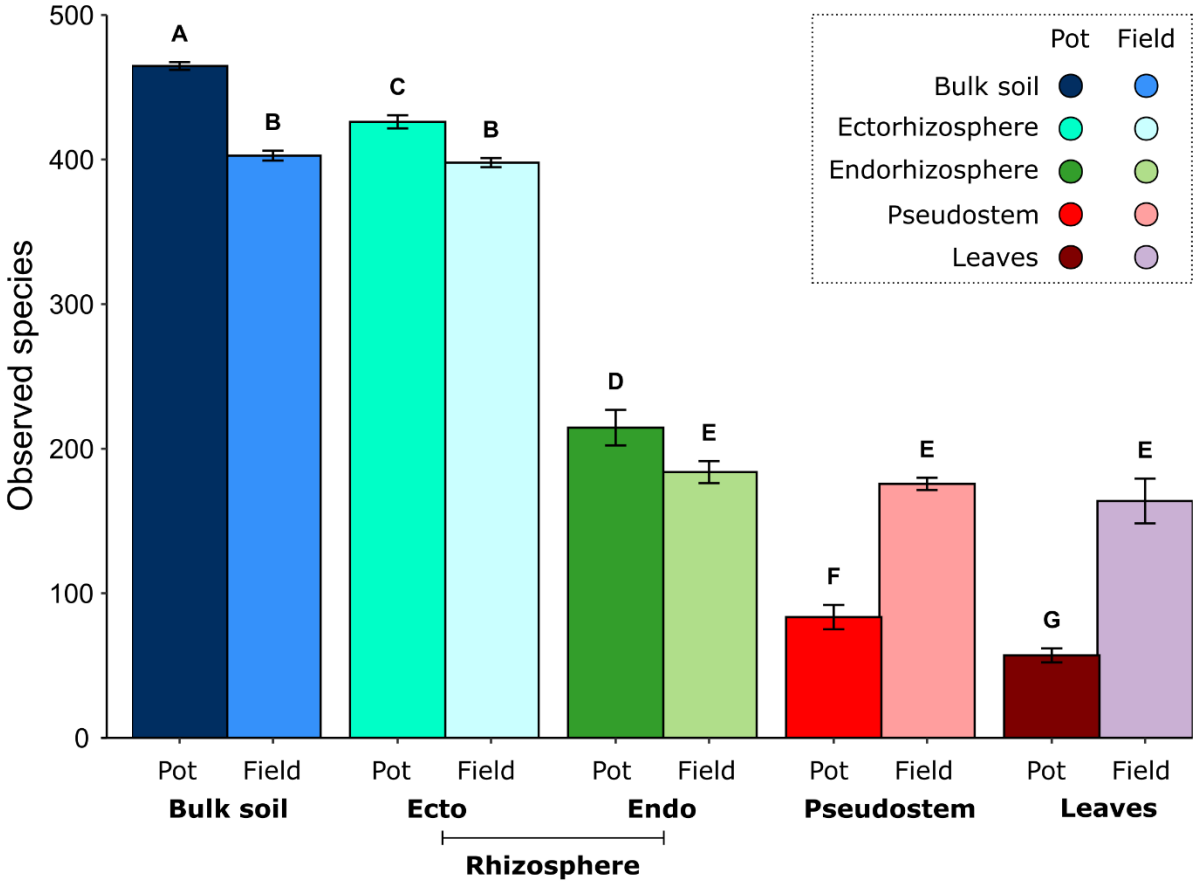

Fig. S6 Numbers of observed bacterial OTUs associated with different compartments and settings (pot vs. field). Error bars represent standard errors of the means. The letters indicate treatments that differ across soils according to estimated marginal means *post hoc* tests with Bejamini-Hochberg corrections. Members of the same groupings share the same letter.

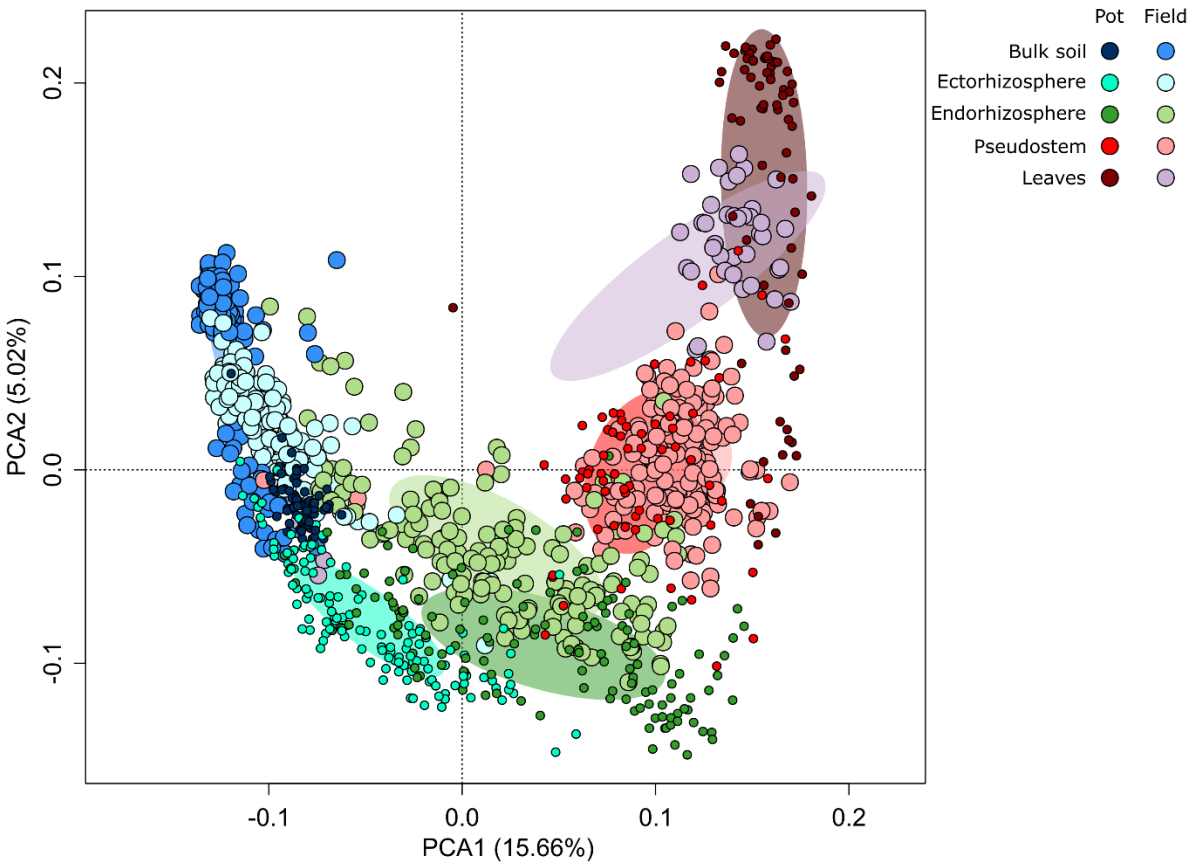

Fig. S7 A Principal Coordinate Analysis (DCA) ordination highlighting differences in the composition of bacterial communities (Hellinger transformed OTUs) associated with pot and field-grown plants in different plant compartments. Points representing field samples are larger than those representing pot samples. The ellipses represent standard deviations of the group centroids.

Table S10 SPIEC-EASI network centrality metrics for core OTUs.

OTU	Status	Taxonomy	Degree	Weighted degree	Betweenness	Closeness	Markov	PageRank
Otu12	Core	g__Sphingomonas	77	6.765	23148	4.36E-05	6.15E-04	1.58E-02
Otu13	Core	o__SC-I-84; f__; g__	43	3.347	10863	4.35E-05	6.02E-04	1.05E-02
Otu17	Core	g__Bacillus	39	2.714	5218	4.33E-05	5.98E-04	9.42E-03
Otu73	Core	g__Microbacterium	33	2.613	5390	4.32E-05	5.93E-04	8.35E-03
Otu41	Core	g__Pseudolabrys	27	2.380	4489	4.32E-05	5.81E-04	1.03E-02
Otu108	Core	o__SC-I-84;f__;g__	23	2.316	4777	4.33E-05	5.81E-04	8.39E-03
Otu28	Core	g__Nitrospira	22	1.360	1903	4.33E-05	5.80E-04	5.16E-03
Otu2	Core	g__(Allo,Neo,Para) Rhizobium	21	1.323	1869	4.32E-05	5.73E-04	6.39E-03
Otu24	Core	g__Pseudolabrys	21	1.315	1159	4.33E-05	5.77E-04	5.28E-03
Otu23	Core	f__Gemmatimonadaceae; g__	19	0.896	2440	4.32E-05	5.69E-04	4.45E-03
Otu40	Core	g__Gaiella	18	1.448	1571	4.32E-05	5.62E-04	6.82E-03
Otu61	Core	g__Curtobacterium	17	1.602	470	4.28E-05	5.56E-04	5.46E-03
Otu131	Core	f__Xanthobacteraceae; g__	15	1.167	1233	4.32E-05	5.55E-04	4.79E-03
Otu104	Core	g__Methylobacterium-Methylorubum	11	0.720	210	4.28E-05	5.27E-04	2.55E-03
Otu25	Core	g__Streptomyces	10	1.250	1648	4.27E-05	4.93E-04	6.33E-03
Otu4	Core	g__Sphingomonas	9	0.911	193	4.28E-05	5.08E-04	3.42E-03
Otu5	Core	g__Acidovorax	9	0.327	1572	4.32E-05	5.15E-04	1.15E-03
Otu9	Core	g__Bradyrhizobium	9	0.676	2153	4.30E-05	5.08E-04	2.76E-03
Otu11	Core	g__ (Allo,Neo,Para) Rhizobium	9	0.470	1338	4.28E-05	4.83E-04	3.34E-03
Otu21	Core	g__Sphingobium	8	0.380	144	4.30E-05	5.13E-04	1.83E-03
Otu84	Core	g__Methylobacterium-Methylorubum	8	1.279	129	4.26E-05	4.92E-04	4.46E-03
Otu403	Core	g__Sphingomonas	8	0.742	411	4.28E-05	5.04E-04	3.04E-03
Otu18	Core	g__Herbaspirillum	7	0.328	767	4.31E-05	4.93E-04	1.36E-03
Otu20	Core	g__Dyella	7	0.488	451	4.25E-05	4.51E-04	3.39E-03
Otu98	Core	g__Sphingomonas	6	0.569	9	4.27E-05	4.64E-04	2.73E-03
Otu99	Core	g__(Allo,Neo,Para) Rhizobium	6	0.234	110	4.28E-05	4.73E-04	1.38E-03
Otu170	Core	g__Duganella	6	0.255	937	4.29E-05	4.56E-04	2.95E-03
Otu8	Core	g__Enterobacter	5	0.590	200	4.27E-05	4.40E-04	4.03E-03
Otu10	Core	g__Ralstonia	5	0.409	296	4.30E-05	4.56E-04	1.90E-03
Otu42	Core	g__Pseudomonas	5	0.196	49	4.30E-05	4.59E-04	8.33E-04
Otu92	Core	g__Methylobacterium-Methylorubum	5	0.424	202	4.27E-05	4.52E-04	1.78E-03
Otu169	Core	g__Sphingomonas	5	0.564	310	4.32E-05	4.64E-04	2.37E-03
Otu16	Core	g__Mycobacterium	4	0.609	969	4.26E-05	4.18E-04	3.11E-03
Otu3	Core	g__Bacillus	3	0.573	0	4.28E-05	3.33E-04	2.78E-03
Otu35	Core	g__Bacillus	2	0.213	0	4.26E-05	3.00E-04	1.25E-03
Otu1132	Core	g__Methylobacterium-Methylorubum	0	-	-	-	-	-
Otu87	Non-core	g__Pseudorhodoferax	12	0.445	307	4.29E-05	5.37E-04	2.25E-03
Otu70	Non-core	g__Nitrosospira	9	0.688	778	4.28E-05	4.99E-04	3.51E-03
Otu127	Non-core	g__Pseudoxanthomonas	7	0.322	48	4.29E-05	4.95E-04	1.56E-03
Otu95	Non-core	g__Reyranella	6	0.501	116	4.31E-05	4.78E-04	2.23E-03
Otu112	Non-core	f__Methyloligellaceae; g__	5	0.113	111	4.25E-05	4.33E-04	1.34E-03
Otu116	Non-core	g__Devosia	4	0.314	312	4.30E-05	4.33E-04	1.36E-03
Otu94	Non-core	g__Achromobacter	3	0.255	86	4.26E-05	3.68E-04	1.94E-03
Otu107	Non-core	g__Methylophilus	3	0.143	24	4.25E-05	3.76E-04	1.07E-03
Otu44	Non-core	g__Nesterenkonia	1	0.006	0	5.31E-06	7.43E-05	2.53E-03
Otu53	Non-core	g__Novosphingobium	0	0.000	0	5.30E-06	7.41E-05	3.80E-04
Otu67	Non-core	g__Bordetella	0	-	-	-	-	-
Core median			8	0.57	411	4.29E-05	4.93E-04	2.95E-03
Non-core median			5	0.29	49	4.27E-05	4.37E-04	2.71E-03

*Otu67 & Otu1132 were not included in the field network as they did not meet the abundance / prevalence threshold

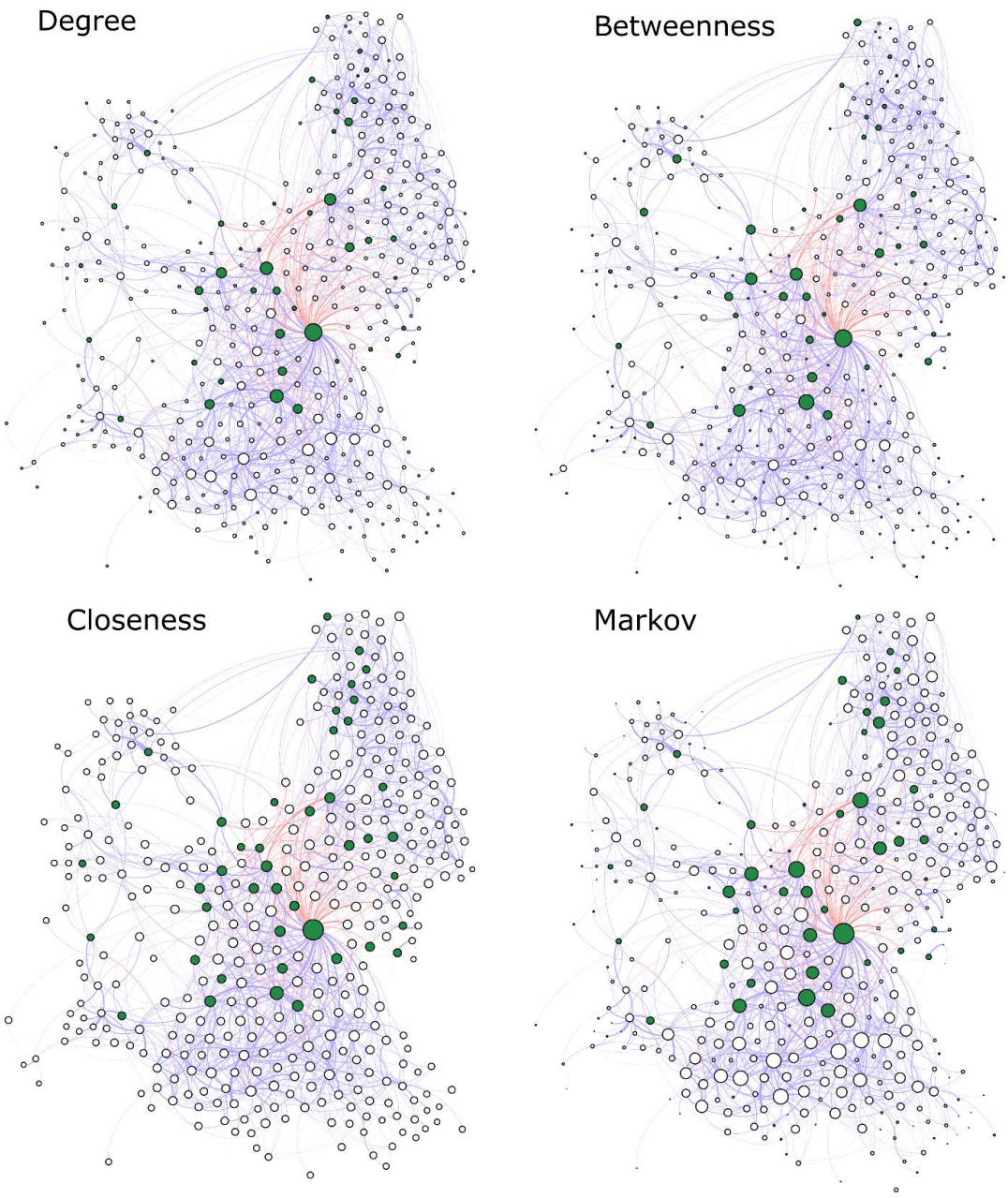

Fig. S8 SPIEC-EASI network graphs showing the co-occurrences of core and non-core bacteria in field-grown *Musa* spp. Nodes are coloured by core status and size is positively associated with a range of centrality metrics. Edge colours represent positive (blue) and negative (red) associations between taxa. Edge width is positively associated with the coefficient for the co-occurrence between the taxa. The node layout in each graph is the same as in Figure 4, which shows the OTU IDs.

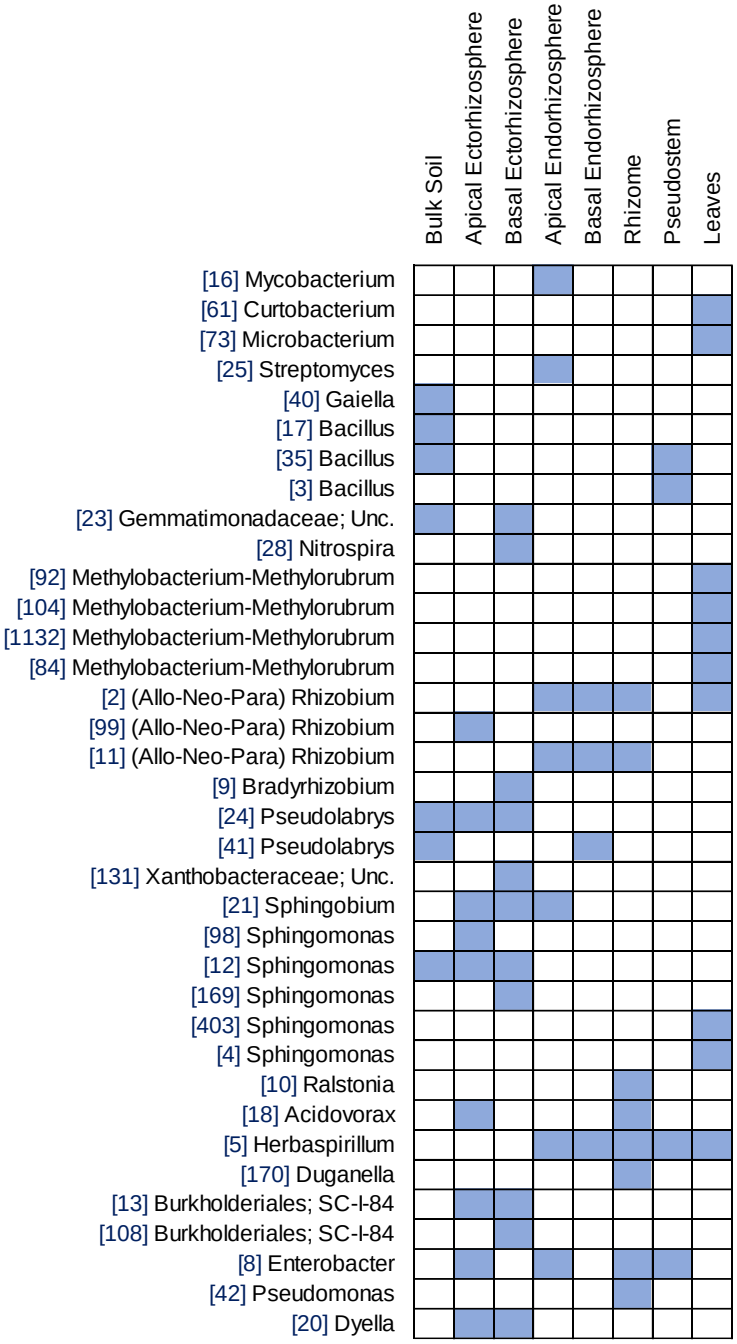

Fig. S9 The common core bacterial microbiome of *Musa* spp. Blue tiles highlight which OTUs are core within each plant compartment.

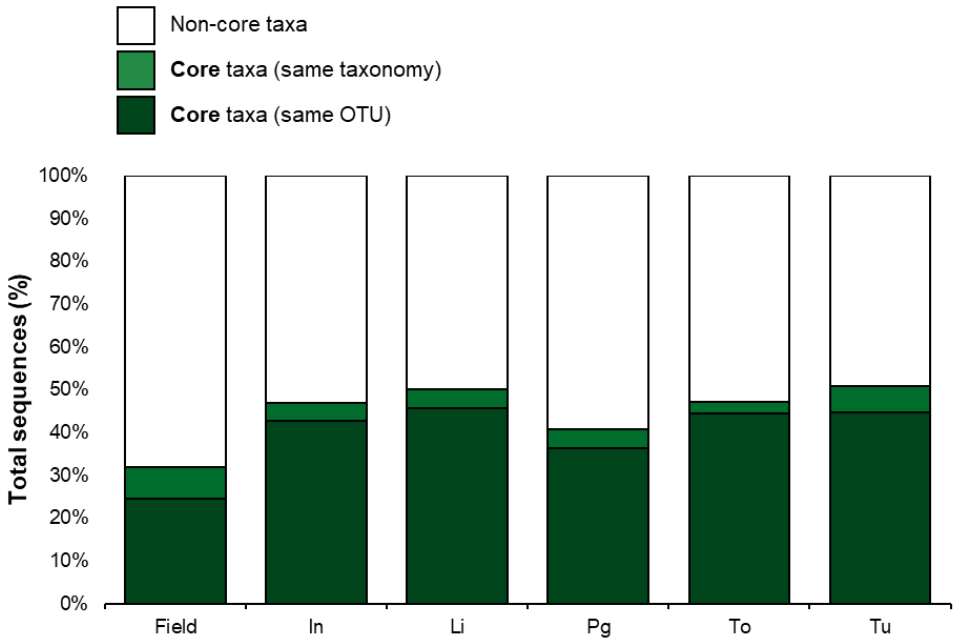

Fig. S10 Percentage of total bacterial sequences attributable to core OTUs and non-core OTUs within *Musa* spp. grown in the field or in pots containing different soils.

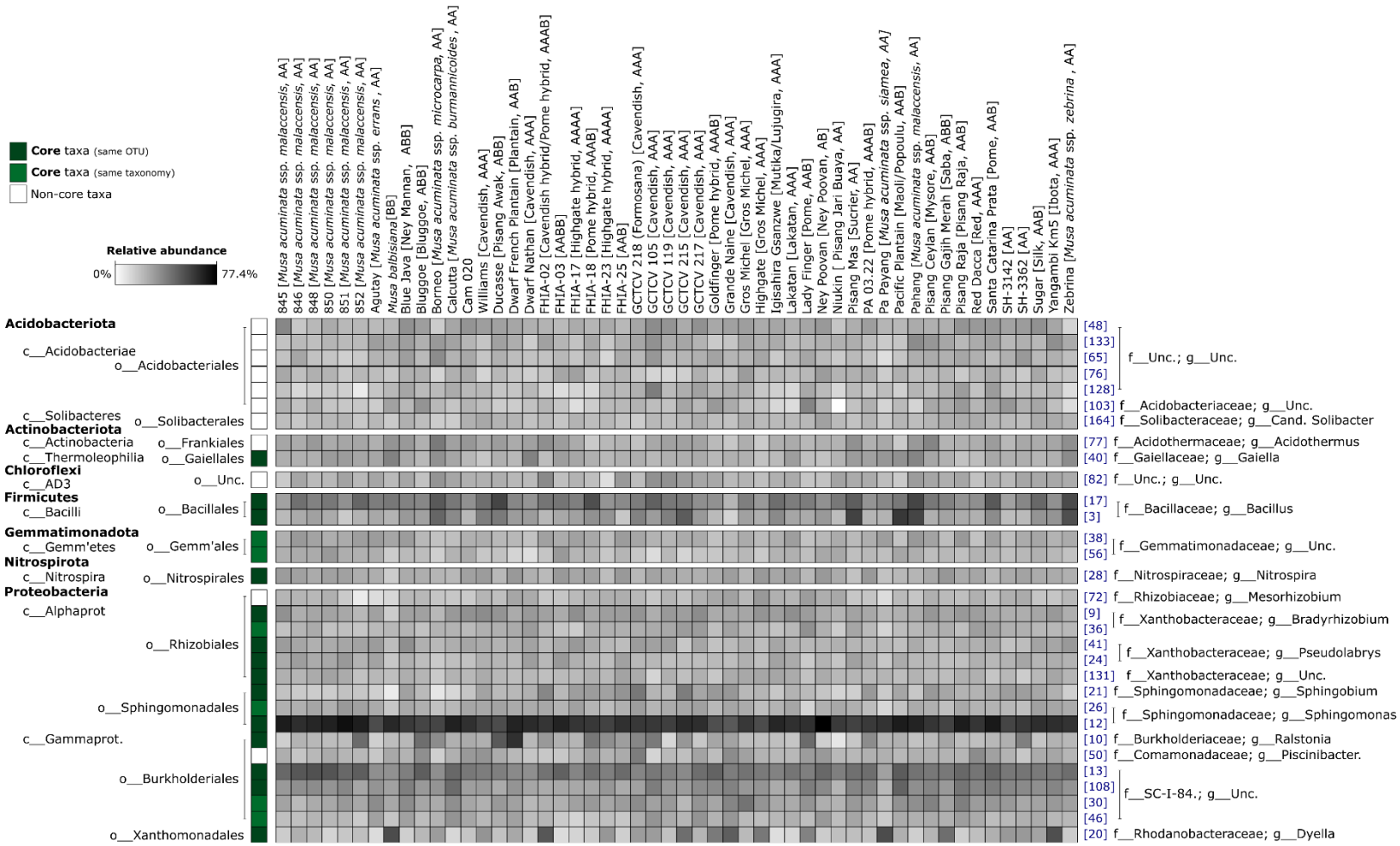

Fig. S11 A heatmap representing the mean relative abundances of key constituent OTUs in the ectorhizosphere of field-grown banana plants (i.e. present at ≥0.5% relative abundance in ≥50% of samples). The green squares indicate taxa that are members of the core microbiome.

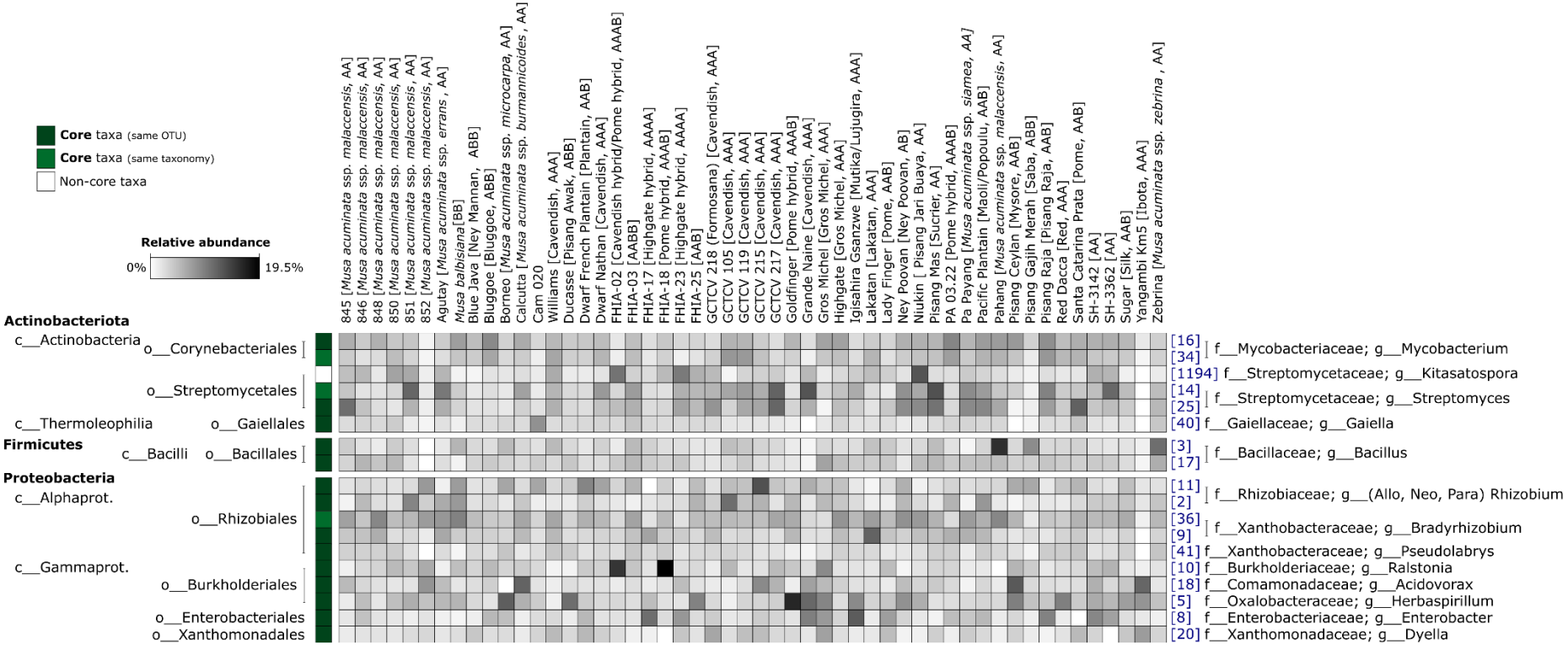

Fig. S12 A heatmap representing the mean relative abundances of key constituent OTUs in the endorhizosphere of field-grown banana plants (i.e. present at ≥0.5% relative abundance in ≥50% of samples). The green squares indicate taxa that are members of the core microbiome.

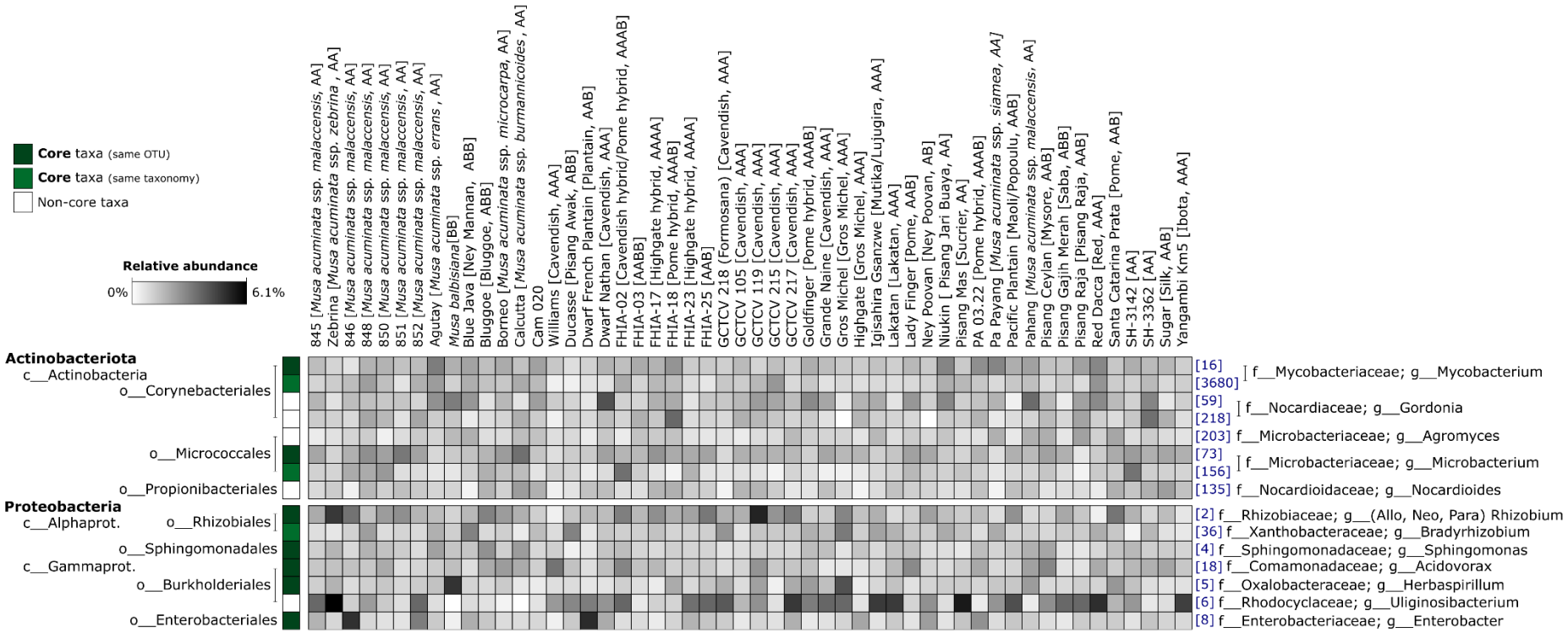

Fig. S13 A heatmap representing the mean relative abundances of key constituent OTUs in the pseudostem of field-grown banana plants (i.e. present at ≥0.5% relative abundance in ≥50% of samples). The green squares indicate taxa that are members of the core microbiome.

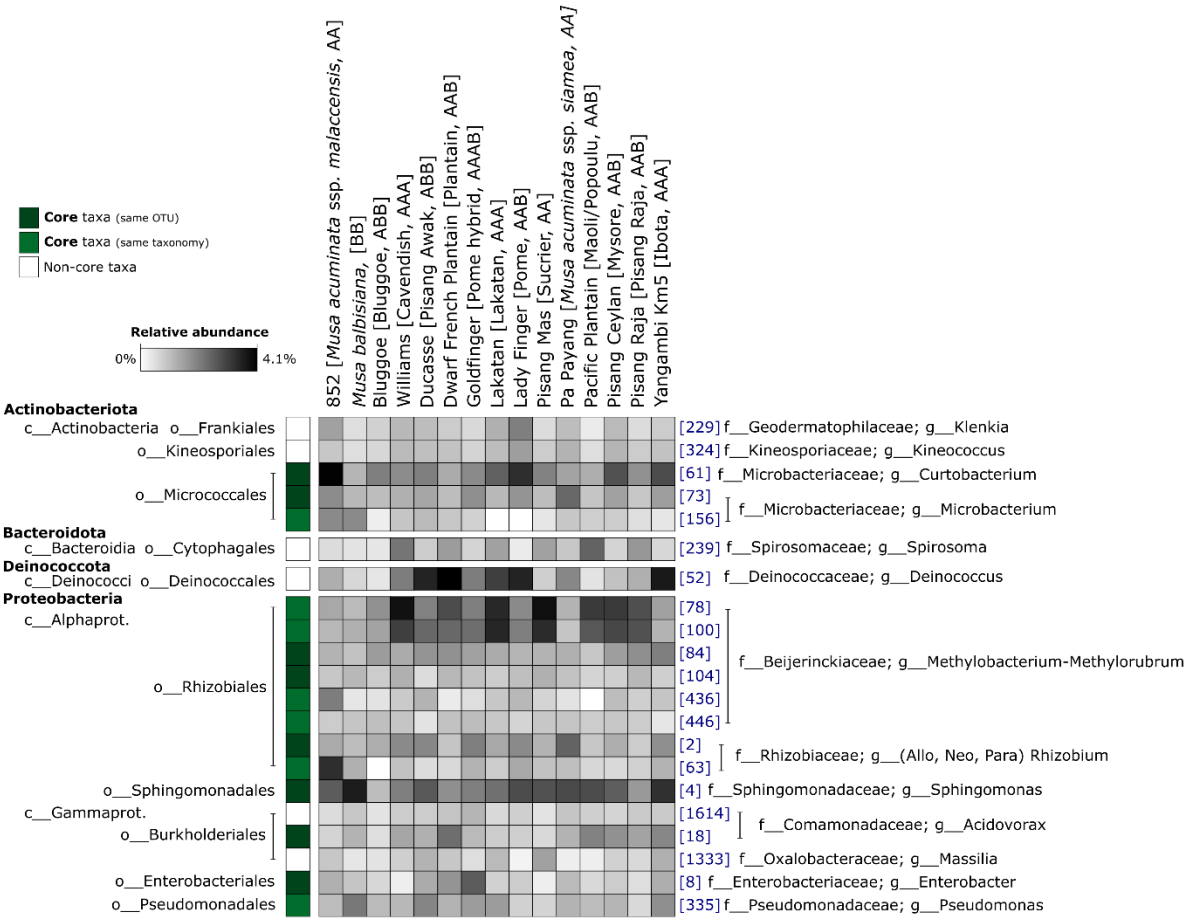

Fig. S14 A heatmap representing the mean relative abundances of key constituent OTUs in the leaves of field-grown banana plants (i.e. present at ≥0.5% relative abundance in ≥50% of samples). The green squares indicate taxa that are members of the core microbiome.

Table S11 Representative sequences the 47 candidate-core OTUs found in all soils. OTUs that were elevated to full core-status are marked as core in bold text.

OTU	Sequence (5'-3')
Otu2 Core	GTAGTCCACGCCGTAAACGATGAATGTTAGCCGTCGGGCAGTATACTGTTCGGTGGCGCAGCTAACGCATTAAACATTCCGCCTGGGGAGTACGGTCGCAAGA TTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAGCTCTTGACATTCGGGGTAT GGGCATTGGAGACGATGTCCTTCAGTTAGGCTGGCCCCAGAACA
Otu3 Core	GTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAA GACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTCTGA CAACTCTAGAGATAGAGCGTTCCCCTTCGGGGGACAGAGTGACA
Otu4 Core	GTAGTCCACGCCGTAAACGATGATAACTAGCTGTCCGGGCACTTGGTGCTTGGGTGGCGCAGCTAACGCATTAAGTTATCCGCCTGGGGAGTACGGCCGCAAG GTTAAAACTCAAAGGAATTGACGGGGGCCTGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAGCGTTTGACATGTCCGGAC GACTTCCAGAGATGGATTTCTTCCCTTCGGGGACTGGAACACAG
Otu5 Core	GTAGTCCACGCCCTAAACGATGTCTACTAGTTGTCGGGTCTTAATTGACTTGGTAACGCAGCTAACGCGTGAAGTAGACCGCCTGGGGAGTACGGTCGCAAGA TTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGGATGGAAT CCTGAAGAGATTTGGGAGTGCTCGAAAGAGAACCATCACACAGG
Otu8 Core	GTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCAAG GTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAA CTTAGCAGAGATGCTTTGGTGCCTTCGGGAACTCTGAGACAGGT
Otu9 Core	GTAGTCCACGCCGTAAACGATGAATGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAACGCTTTAAGCATTCCGCCTGGGGAGTACGGTCGCAAGA TTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGACGCAACGCGCAGAACCTTACCAGCCCTTGACATCCCGGTCGC GGACTCCAGAGACGGAGTTCTTCAGTTCGGCTGGACCGGAGACA
Otu10 Core	GTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGGATTCATTTCCTTAGTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCAAGA TTAAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGCCACTAAC GAAGCAGAGATGCATTAGGTGCTCGAAAGAGAAAGTGGACACAG

Otu11 Core

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CCTCTAGAGATAGGGGGTCCACTTCGGTGGCGCAGAGACAGGTG

Otu12 Core

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Otu13 Core

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Otu16 Core

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Otu17 Core

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Otu18 Core

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Otu20 Core

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Otu21 Core

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Otu23 Core

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Otu24 Core

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Otu25 Core

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Otu28 Core

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Otu35 Core

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Otu87

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Otu92 Core

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Otu98 Core

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Otu99 Core

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Otu104 Core

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Otu107

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Otu108 Core

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Otu112

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Otu116

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Otu127

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Otu131 Core

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Otu169 Core

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Otu403 Core

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Otu1132 Core

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CATGGAGAGATCCATGGTCCTCTTCGGAGGCGTGCACACAGGTG

Table S12 Examples from the literature where core and candidate-core taxa identified in this study have been reported to be important to *Musa* spp. plant fitness or associated with the plant.

OTUs	Taxonomy	Culture independent Study?	Comparison/ management intervention	Outcome	Link to plant fitness	References
17, 35, 3	*Bacillus*	Both	Inoculation of *Bacillus*	Increase in relative abundance	Negatively associated with Fusarium Wilt and Banana Bunchy Top Virus symptoms	[3, 11, 12, 19, 21, 23-28]
		Yes	Fusarium Wilt affected plants vs. healthy	Increases in abundance or shifts between different *Bacillus* species	Negatively associated with Fusarium Wilt symptoms	[21,29,30]
		No	Co-culture with *Fusarium oxysporum* f. sp. *cubense*	-	Suppression of plant pathogen on plates	[18]
			None applied – reported to be associated with *Musa* spp.	No change		[9, 13, 16, 17]
9	*Bradyrhizobium*	Yes	Pineapple plant rotation with *Musa* spp.	Increased relative abundance	Negatively associated with Fusarium Wilt symptoms	[20]
			Fusarium Wilt affected plants vs. healthy	Increased relative abundance	Highest in Fusarium Wilt effected plants or near to effected plants but not showing symptoms	[29]
			Fusarium Wilt affected plants vs. healthy	Increased relative abundance	Positively associated with Fusarium Wilt symptoms	[31]
			Fusarium Wilt affected plants vs. healthy	No change		[30]

61	*Curtobacterium*	No	None applied – reported to be associated with *Musa* spp.	No change	-	[18]
116	*Devosia*	Yes	Lime applied to soil	Increased relative abundance	Lower plant biomass in first 65 days of growth	[32]
			Fusarium Wilt affected plants vs. healthy and examination of tissue culture plantlets	No change	Present in all adult plants regardless of Wilt but not found in tissue culture plants	[29]
			Addition of organic matter to soil in which plant is grown	Increased relative abundance	Negatively associated with Fusarium Wilt symptoms	[31]
			Bacterial Wilt affected plants vs. healthy	Not present during wilting	-	[10]
20	*Dyella*	Yes	Bacterial Wilt affected plants vs. healthy	Not present during wilting	-	[14]
8	*Enterobacteria*	Yes	Location, agroforestry co-production, herbicide use, Fusarium Wilt affected plants vs. healthy, and Bacterial Wilt affected plants vs. healthy	No change	-	[7,8,14,30]
		No	None applied – reported to be associated with *Musa* spp.	No change	-	[9,13,15,18,33]
40	*Gaiella*	Yes	Fusarium Wilt affected plants vs. healthy or Bacterial Wilt affected plants vs. healthy	Decrease in relative abundance	Negatively associated with Fusarium Wilt symptoms	[26]
			Soil fumigation before growing plants affected by Fusarium Wilt	Fumigation increased abundance	Negatively associated with Fusarium Wilt symptoms	[28]

23	*Gemmatimonadaceae*	Yes	Fusarium Wilt affected plants vs. healthy, *Bacillus* inoculated compost, or chili rotation	Increase when treatment results in Fusarium Wilt decrease	Positively associated with an increase in plant biomass	[11,27,31,34]
			Addition of *Bacillus* inoculated sterile compost to control Fusarium Wilt	Decreased relative abundance	Positively associated with Fusarium Wilt symptoms	[21]
			Plants grown in fields with a different history of monoculture. Plants are either affected by Fusarium Wilt or healthy	Dominant regardless of treatment	-	[26]
			Bacterial Wilt affected plants vs. healthy	Not present during wilting	-	[14]
92, 104, 1132, 84	*Methylobacterium-Methylorubum*	Yes	Fusarium Wilt affected plants vs. healthy or Bacterial Wilt affected plants vs. healthy	Present regardless	-	[29,14]
		No	None applied – reported to be associated with *Musa* spp.	No change	-	[35]
73	*Microbacterium*	Yes	Fusarium Wilt affected plants vs. healthy	Present in healthy plants near to those wilting and wilting plants	-	[29]
			Bacterial Wilt affected plants vs. healthy	No change	-	[14]
		Both	None applied – reported to be associated with *Musa* spp.	No change	-	[22,36]
16	*Mycobacterium*	Yes	Fusarium Wilt affected plants vs. healthy	Present in wilting plants only	Positively associated with Fusarium Wilt symptoms	[29]

			Fumigation and addition of *Bacillus* inoculated sterile compost or conventional compost	No change	-	[14]
			None applied – reported to be associated with *Musa* spp.	No change	-	[2,22]
28	*Nitrospira*	Yes	Addition of *Bacillus* inoculated compost to control Fusarium Wilt	No change	-	[11]
			Comparison of wilt suppressive and conducive fields	No change	-	[24]
			Bacterial Wilt affected plants vs. healthy	Not present under wilting conditions	-	[14]
			Soil fumigation to control Fusarium Wilt	Reduced	Negatively associated with Fusarium Wilt symptoms	[28]
			Plants grown in fields with a different history of monoculture. Plants are either affected by Fusarium Wilt or healthy	No change	-	[19]
42	*Pseudomonas*	No	Inoculation of *Pseudomonas* strains	Increase in relative abundance	Negatively associated with Banana Bunchy Top Virus symptoms	[23]
			None applied – reported to be associated with *Musa* spp.	No change	-	[15,5]
			Co-culture with *Fusarium oxysporum* f. sp. *cubense*	No change	Suppression of plant pathogen on plates	[18]
		Yes	Agroforestry co-production with *Musa* spp.	Increased relative abundance	-	[7]

Plants grown in different locations	Increased relative abundance	-	[8]
Fusarium Wilt affected plants vs. healthy	Changes in the composition of *Pseudomonas* spp.	-	[30]
Fusarium Wilt affected plants vs. healthy	Present regardless	-	[29]
Comparison of Fusarium Wilt suppressive and conducive fields	Increased relative abundance in suppressive field	Negatively associated with Fusarium Wilt symptoms	[24]
Bacterial Wilt affected plants vs. healthy	No change	-	[14]
Addition of *Bacillus* inoculated compost to control Fusarium Wilt	Increased relative abundance	Negatively associated with Fusarium Wilt symptoms	[21]
	No change	-	[25]
Addition of *Bacillus* inoculated compost after soil fumigation to control Fusarium Wilt	Decrease in relative abundance	Positively associated with Fusarium Wilt symptoms	[23]
Addition of *Bacillus* inoculated compost after soil fumigation to control Fusarium Wilt	Increase in relative abundance	Negatively associated with Fusarium Wilt symptoms	[27]
Addition of pig manure	Increase in relative abundance		[28]
Compared with a chili plant rotation over time	Found in only one of two years recorded but negatively associated with *Fusarium oxysporum* f. sp. *cubense*	Negatively associated with Fusarium Wilt symptoms	[34]

			Agroforestry co-production with banana or herbicide used	Clustering of *Pseudomonas* communities depending on treatment	-	[10]
10	*Ralstonia*	Yes	Fusarium Wilt affected plants vs. healthy	Decrease in relative abundance	Negatively associated with Fusarium Wilt symptoms	[30]
			Fusarium Wilt affected plants vs. healthy	Present in wilting plants and those not showing symptoms next to wilting	-	[29]
			Addition of *Bacillus* inoculated compost to control Fusarium Wilt	Decrease in relative abundance	Positively associated with Fusarium Wilt symptoms	[36]
			Bacterial Wilt affected plants vs. healthy	No change	-	[14]
2, 99, 11	*(Allo,Neo,Para) Rhizobium*	No	None applied – reported to be associated with *Musa* spp.	No change	-	[13,9,5]
			Inoculation	Increased abundance	Increased plant biomass	[33]
		Yes	Bacterial Wilt affected plants vs. healthy	No change	-	[14]
			Fusarium Wilt affected plants vs. healthy	Found in wilting plants and those that were healthy next to wilting plants	-	[29]
			Addition of *Bacillus* inoculated compost to control Fusarium Wilt	Highest under conventional fertiliser (most abundant genus)	Positively associated with Fusarium Wilt symptoms	[31]
			Addition of *Bacillus* inoculated compost and fumigation to control Fusarium Wilt	No change	-	[36]

			Addition of *Bacillus* inoculated compost and fumigation to control Fusarium Wilt	No change	-	[28]
21	*Sphingobium*	Yes	Agroforestry co-production with banana or herbicide used	No change	-	[10]
			Compared with a chili plant rotation over time	Found in only one of two years recorded but negatively associated with *Fusarium oxysporum* f. sp. *cubense*	Negatively associated with Fusarium Wilt symptoms	[34]
			Addition of *Bacillus* inoculated compost to control Fusarium Wilt vs. healthy	Increased abundance	Negatively associated with Fusarium Wilt symptoms	[21,36]
				No change	-	[31]
			Fusarium Wilt affected plants vs. healthy	Found in wilting plants and those that were healthy next to wilting plants	-	[29]
			Bacterial Wilt affected plants vs. healthy	No change	-	[14]
98, 12, 169, 403, 4	*Sphingomonas*	No	None applied – reported to be associated with *Musa* spp.	No change	-	[18]
		Yes	Addition of *Bacillus* inoculated compost to control Fusarium Wilt	Increased abundance	Negatively associated with Fusarium Wilt symptoms	[11,21]
			Addition of *Bacillus* inoculated compost to control Fusarium Wilt	Increased under low addition, high addition no different from control	Negatively associated with Fusarium Wilt symptoms	[25]

			Changes in fertiliser management	Highest under conventional fertiliser	Positively associated with Fusarium Wilt symptoms	[31]
			Plants grown in fields with a different history of monoculture. Plants are either affected by Fusarium Wilt or healthy	Lower abundance	Negatively associated with Fusarium Wilt symptoms and length of time in monoculture	[26]
			Addition of *Bacillus* inoculated compost and fumigation to control Fusarium Wilt	Increased abundance	Negatively associated with Fusarium Wilt symptoms	[28]
			Lime applied to soil	Increased abundance	Lower plant biomass in first 65 days of growth	[32]
			Compared with a chili plant rotation over time	Found in only one of two years recorded but negatively associated with *Fusarium oxysporum* f. sp. *cubense*	Negatively associated with Fusarium Wilt symptoms	[34]
			Fusarium Wilt affected plants vs. healthy	Found in tissue culture plants, wilting plants and those that were healthy next to wilting plants	-	[29]
25	*Streptomyces*	Both	None applied – reported to be associated with *Musa* spp.	No change	-	[17]
		Yes	Addition of organic matter to soil	Increased abundance	-	[32]
			Fusarium Wilt affected plants vs. healthy	Found in wilting plants and those that were healthy next to wilting plants	-	[29]

		Addition of *Bacillus* inoculated compost to control Fusarium Wilt	Increased abundance	Negatively associated with Fusarium Wilt symptoms	[21]
		Addition of *Bacillus* inoculated compost and fumigation to control Fusarium Wilt	No change	-	[28]
	Both	Inoculation of *Streptomyces*	Increase in relative abundance	Negatively associated with Fusarium Wilt symptoms	[2]

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