Supplementary materials

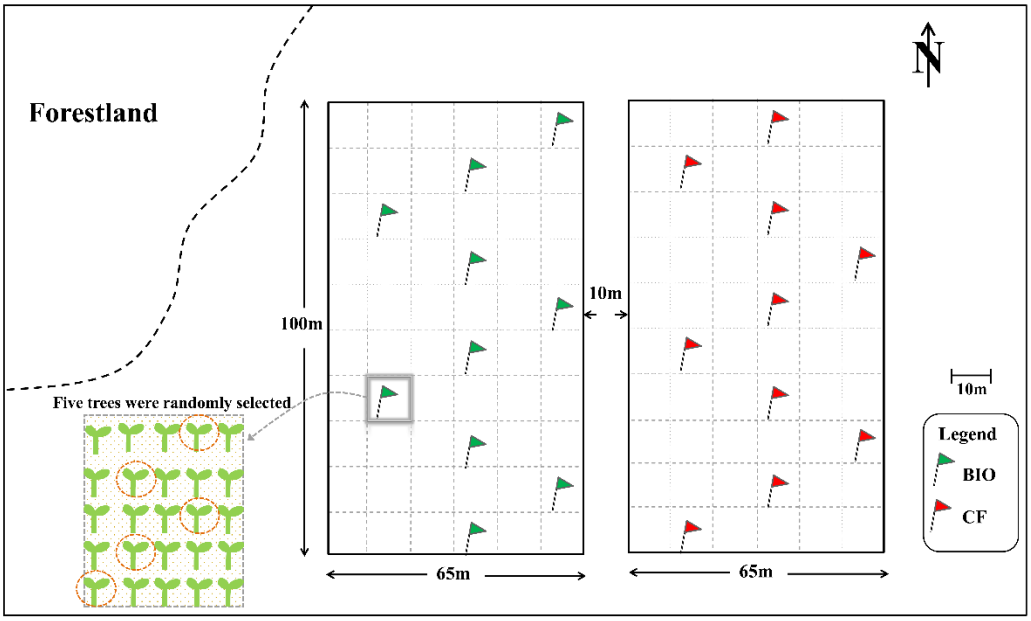

Fig. S1 Schematic of the sampling sites in the field experiment (Hainan, China). Flags represent the different sampling locations. In each of the replicated locations per treatment, five banana plants were selected randomly at least 4 m apart and soils were sampled and pooled into one composite replicate, giving ten replicates per treatment. The management regimes applied to the soil are indicated in the colored right panel. Colored flags indicate the approximate sampling location of soil and root samples within each plot.

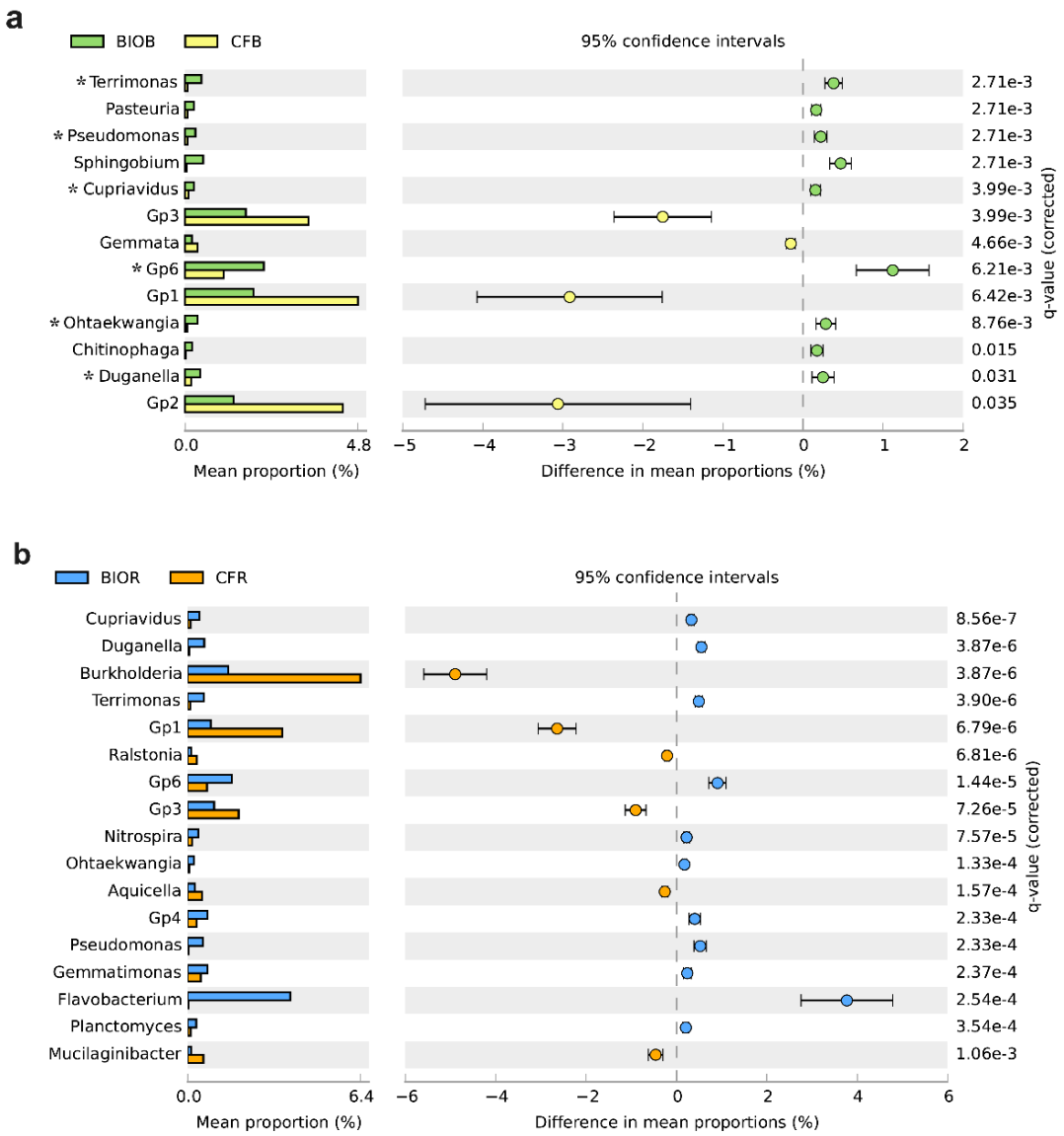

Fig. S2 STAMP analysis of bacterial community composition in genus level among all (a) bulk and (b) rhizosphere soil samples. BIOB, bulk soil from bio-organic system; CFB, bulk soil from organic system; BIOR, rhizosphere soil from bio-organic system; CFR, rhizosphere soil from organic system. The error bars show calculated standard variation of decuplicate samples, and asterisks indicate more abundant phyla in BIO group regardless of bulk soil and rhizosphere ($q < 0.05$). Corrected *P*-values (q) were calculated using the Benjamini-Hochberg false discovery rate approach ($P < 0.05$).

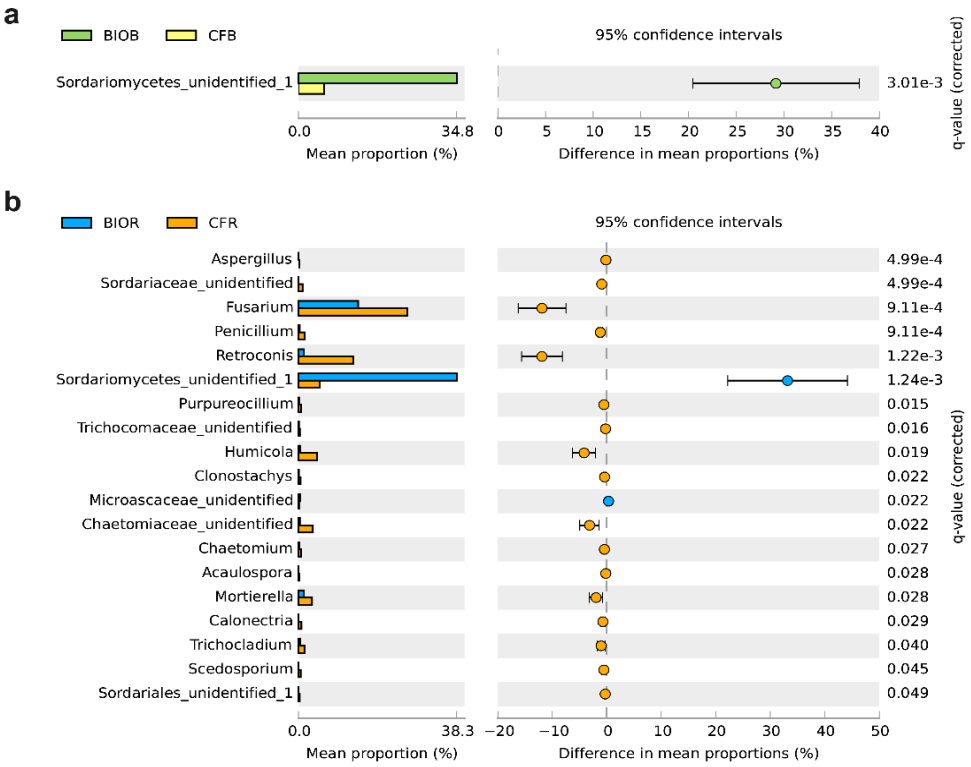

Fig. S3 STAMP analysis of fungal community composition in genus level among all (a) bulk and (b) rhizosphere soil samples. BIOB, bulk soil from bio-organic system; CFB, bulk soil from organic system; BIOR, rhizosphere soil from bio-organic system; CFR, rhizosphere soil from organic system. Corrected *P*-values (*q*) were calculated using the Benjamini-Hochberg false discovery rate approach ($P < 0.05$).

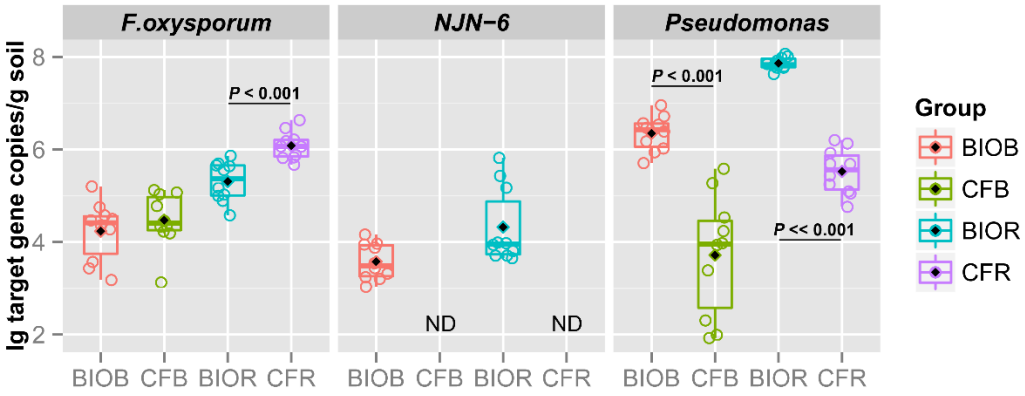

Fig. S4 Abundance of *Fusarium oxysporum*, strain NJN-6, and *Pseudomonas* among all rhizosphere and bulk soil samples. Box plots show the median (thick colored line), mean (blacked diamond), the first quartile (lower box bound), the third quartile (upper box bound), the range of data values that deviate from the box no more than 1.5 times the height of the box (vertical lines). BIOB, bulk soil from bio-organic system; CFB, bulk soil from organic system; BIOR, rhizosphere soil from bio-organic system; CFR, rhizosphere soil from organic system. *P*-values over paired columns indicate that the means are significantly different according to the two-tailed Student's or Welch's *t*-test ($P < 0.05$). ND, not determined.

Table S1 Sequences of oligonucleotide primers and probes required for real-time quantitative PCR

Target group	Primer/probe name and sequence (5′–3′)	Annealing temp/°C	Amplicon size/bp	Reference
Bacteria	Eub338F, ACTCCTACGGGAGGCAGCAG	53	200	[15]
	Eub518R, ATTACCGCGGCTGCTGG	53		
Fungi	ITS1f, TCC GTA GGT GAA CCT GCG G	53	300	[15]
	5.8s, CGC TGC GTT CTT CAT CG	53		
F. oxysporum	FOF1, ACATACCACTTGTTGCCTCG	58	340	[16]
	FOR1, CGCCAATCAATTTGAGGAACG	58		
NJN-6	Ba425F, GCTGCGTTCACTATTTCC	55	217	[4]
	Ba641R, TGTCTTTATCCGTCTCCC	55		
Pseudomonas	Pse435F, ACTTTAAGTTGGGAGGAAGGG	60	251	[17]
	Pse686R, ACACAGGAAATTCCACCACCC	60		
	Pse449 (Probe), Fam-ACAGAATAAGCACCGGCTAACBHQ	60		

Table S2 Primer sequences used for bacterial 16S rRNA and fungal ITS MiSeq sequencing

Target group	Primer name	Sequence (5′–3′)
Bacteria	515F	GTGCCAGCMGCCGCGGTAA
	806R	GGACTACHVGGGTWTCTAAT
Fungi	ITS1F	TCCGTAGGTGAACCTGCGG
	ITS2	GCTGCGTTCTTCATCGATGC

Table S3 Treatment and soil compartment effects on bacterial and fungal β-diversity

Main test[a]	*Bacteria*			*Fungi*		
	PERMANOVA		ANOSIM	PERMANOVA		ANOSIM
	F (*P*)	R^2	*R*	F (*P*)	R^2	*R*
Treatment	20.09^{***}	0.28	0.603^{***}	15.76^{***}	0.14	0.625^{***}
Soil compartment	10.44^{***}	0.14	0.510^{***}	10.63^{***}	0.16	0.255^{***}
Treatment×Soil compartment	5.90^{***}	0.08	-	3.77^{***}	0.05	-

Note: PERMANOVA, permutational multivariate analysis of variance; ANOSIM, analysis of similarities.[a] Main factors represent treatments (BIO, CF), soil compartment (rhizosphere, bulk soil). Values in table represent the *pseudo*-F ratio (F), the level of significance (***$P < 0.001$) and the estimation of the variance component (R^2) for PERMANOVA as well as the global *R* and the level of significance for ANOSIM.