

Appendix. Detailed description of the different taxonomic families and genera of the prokaryotic and fungal dataset

We calculated a linear discriminant analysis (LDA) effect size (LEfSe) algorithm to determine features (taxa and ASVs) significantly associated with a particular SOM management. In the prokaryotic dataset, LEfSe identified nine families and 25 genera (LDA score >2 and $p < 0.05$; Figs. S2-S3). Some of these microbial taxa included abundant lineages clearly associated to different SOM managements (LDA >3, $p < 0.05$), like the families *Rhodocyclaceae* (associated to ORG) and *Pedospaeraceae* (CM), and the genera *Thauera* (ORG), *Actinomadura* (CMOM), *Pirellula* (CM) and candidate MM2 (CM). In a closer look at ASV level, LEfSe identified 52 significant ASVs (LDA >2, $p < 0.05$; Fig. S4A), covering a broad phylogenetic spectrum (10 phyla). Overall, three of the five phyla with higher effect size ASVs (LDA >3, $p < 0.05$), were Bacteroidetes, Proteobacteria and Acidobacteria, which were associated to ORG soils, and one (Gemmatimonadetes) to CM (Fig. S4B). The predicted functional enzymatic gene profiles of prokaryotic communities identified eight enzymatic types significantly associated to particular SOM managements (Fig. S5). The LDA-LEfSe algorithm analysis on soil fungal communities identified did not identify families or genera associated to any management. In a closer look, four ASVs associated to ORG management (LDA >3, $p < 0.05$) belonging to the Ascomycota and Basidiomycota phyla (Fig. S6).

Table S1. Microbial abundance and prokaryote:fungi ratio determined by qPCR. Values are mean $\pm$ 1 SE. Different letters in a column show significant differences ($p < 0.05$) between treatments (Fischer LSD post-hoc comparison).

Management ^[1]	Prokaryote Log₁₀(16S copies g⁻¹)	Fungi Log₁₀(ITS copies g⁻¹)	Prokaryote:Fungi
CM	8.39 $\pm$ 0.29 A	5.26 $\pm$ 1.19 A	7062.47 $\pm$ 3502.75 A
CMOM	8.91 $\pm$ 0.43 A	5.69 $\pm$ 0.60 A	3632.35 $\pm$ 1906.68 A
ORG	8.77 $\pm$ 0.61 A	5.69 $\pm$ 1.12 A	4103.12 $\pm$ 2352.98 A

^[1] CM: conventional soil management with no OM application; CMOM: conventional management with OM application, and ORG: fully organic management with yearly OM application and no chemicals added.

Table S2. Results of Kruskal-Wallis analysis of total ASV richness and Shannon index comparing the different SOM managements. Legend of greenhouse managements as in table S1.

	Prokaryota (16S)				Fungi (ITS)			
	Shannon		Observed ASVs		Shannon		Observed ASVs	
	H	p-value	H	p-value	H	p-value	H	p-value
Factor ^[1]								
Management	0.14	0.93	0.42	0.81	0.50	0.78	0.02	0.99
Managements ^[2]								
CM-CMOM	0.10	0.75	0.10	0.75	0.88	0.35	0.04	0.83
CM-ORG	0.10	0.75	0.27	0.60	0.01	0.92	0.10	0.75
CMOM-ORG	0.01	0.92	0.27	0.60	0.01	0.92	0.01	0.92

^[1] Effects of factor “Management” were assessed by Kruskal-Wallis analysis taking into account all groups. Values represent the univariate H statistic and the p-value at 95% confidence level. ^[2] Pairwise comparisons between management systems. Values represent the univariate H statistic and the p-value at 95% confidence level assessed by Kruskal-Wallis analysis.

Table S3. PERMANOVA analysis of β -diversity based on Bray-Curtis and Jaccard distances comparing the three SOM management practices. Legend of greenhouse managements as in table S1.

	Prokaryota (16S)				Fungi (ITS)			
	Bray-Curtis		Jaccard		Bray-Curtis		Jaccard	
	Pseudo-F	p-value	Pseudo-F	p-value	Pseudo-F	p-value	Pseudo-F	p-value
Factor ^[1]								
Management	0.97	0.57	1.00	0.47	1.00	0.46	1.00	0.50
Managements ^[2]								
CM-CMOM	1.07	0.24	1.06	0.18	1.00	0.51	1.03	0.40
CM-ORG	1.01	0.36	1.00	0.40	0.85	0.67	0.94	0.74
CMOM-ORG	0.85	0.91	0.94	0.80	1.15	0.13	1.02	0.34

^[1] Effects of factor “Management” were assessed by PERMANOVA analysis taking into account all groups. Values represent the univariate Pseudo-F and the p-value at 95% confidence level. ^[2] Pairwise comparisons between management systems. Values represent the univariate Pseudo-F and the p-value at 95% confidence level assessed by PERMANOVA analysis.

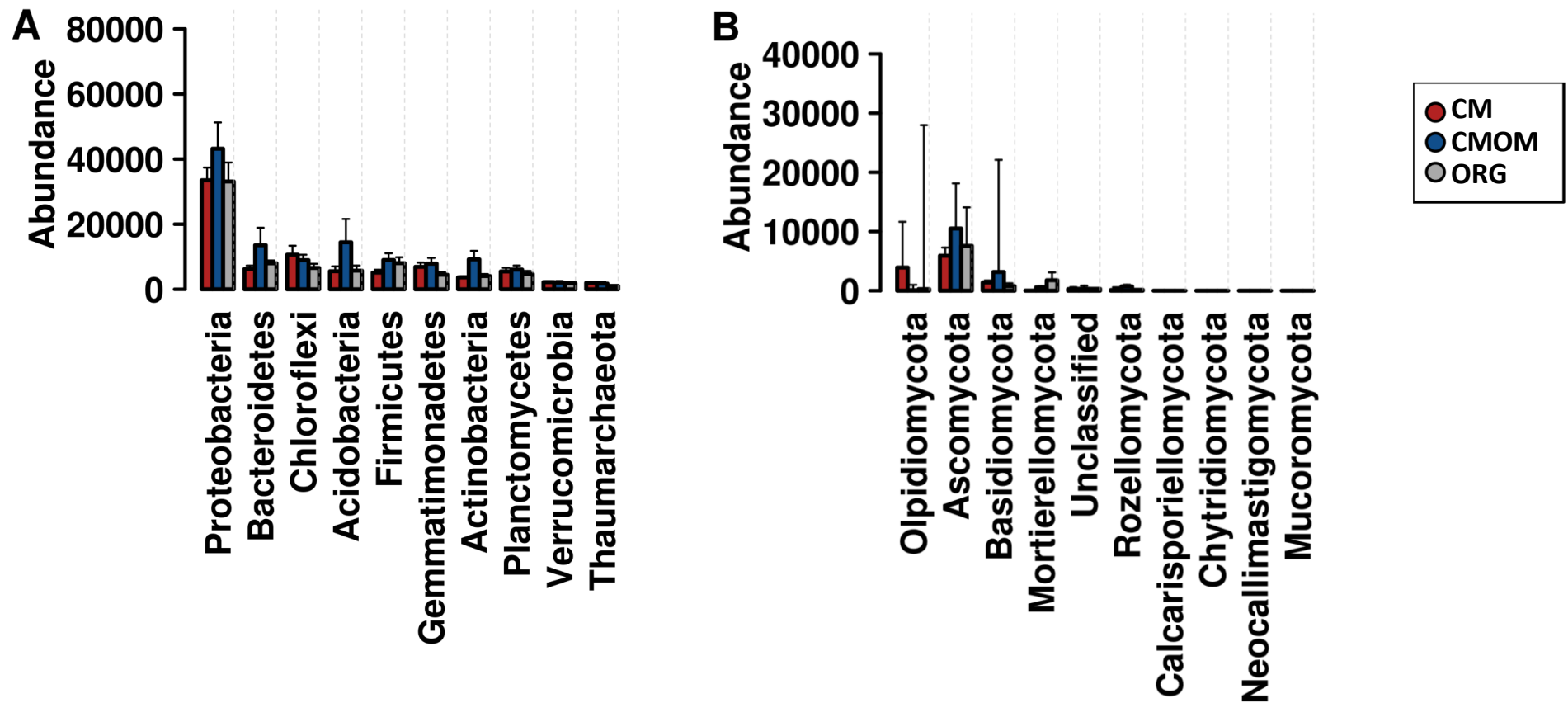


Figure S1. Relative abundance of the ten more frequent prokaryotic (A) and fungal (B) phyla. Bars represent mean ± 1 SE. CM: conventional soil management with no OM application; CMOM: conventional management with OM application, and ORG: fully organic management with yearly OM application and no chemicals added.

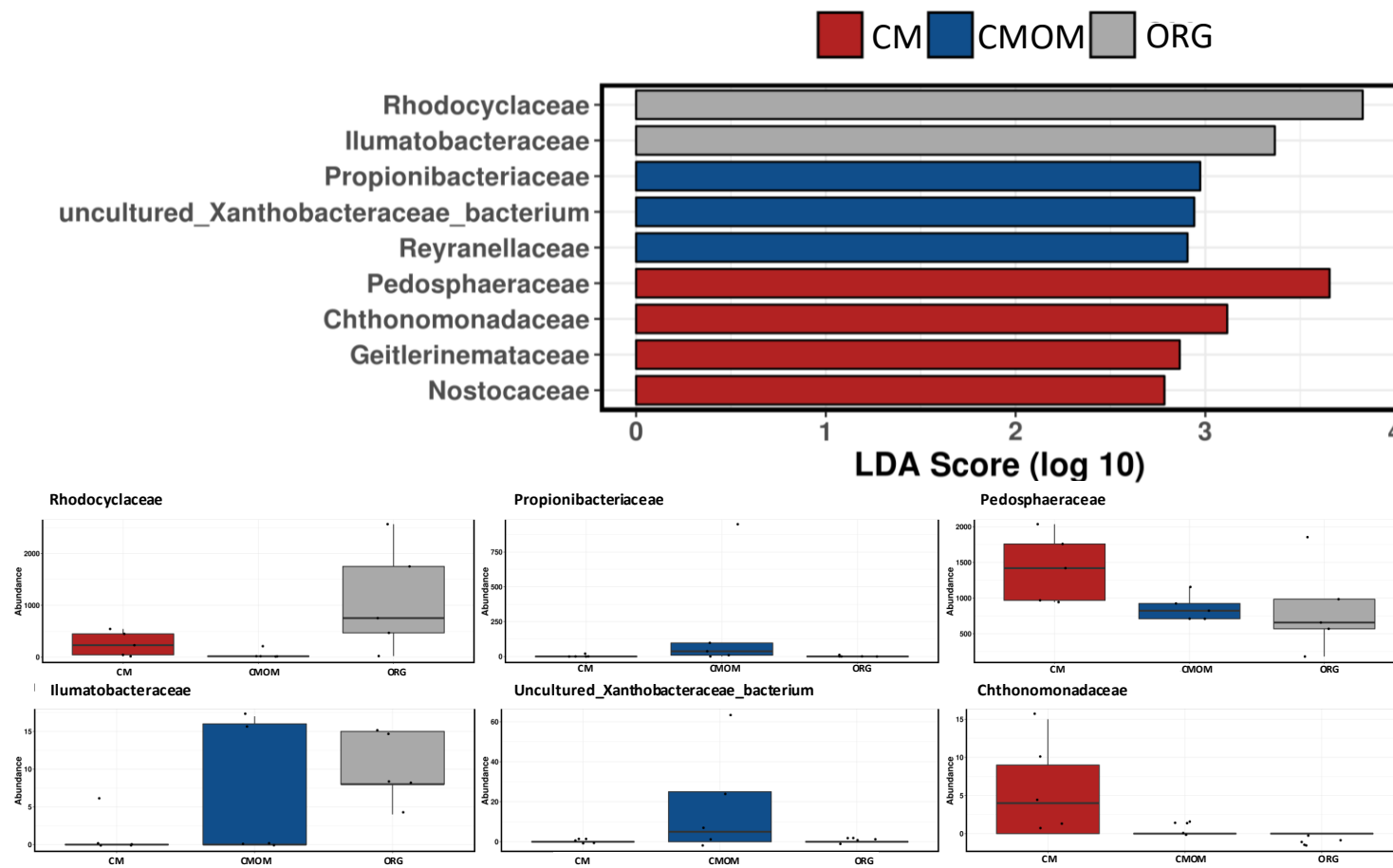


Figure S2. Prokaryotic families associated to particular OM management practices, $LDA > 2$, $p < 0.05$ (above). Boxplots represent relative abundance of the highly significant features, $LDA > 3$, $p < 0.05$ (below). Legend of greenhouse managements as in Fig. S1.

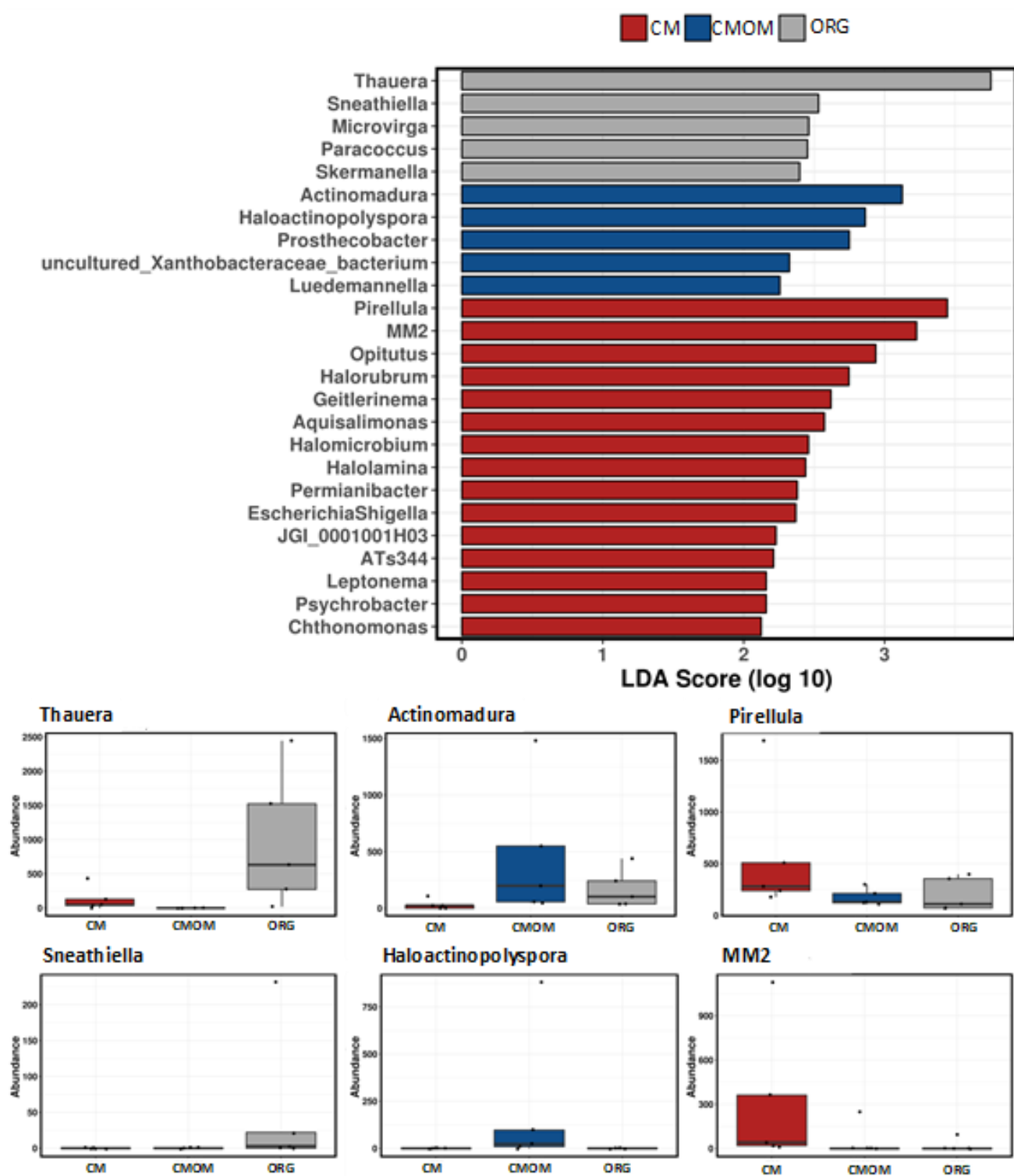


Figure S3. Prokaryotic genera associated to organic matter management practices, LDA>2, $p<0.05$ (above). Boxplots representing relative abundances of the highly significant features, LDA>3, $p<0.05$ (below). Legend of greenhouse managements as in Fig. S1.

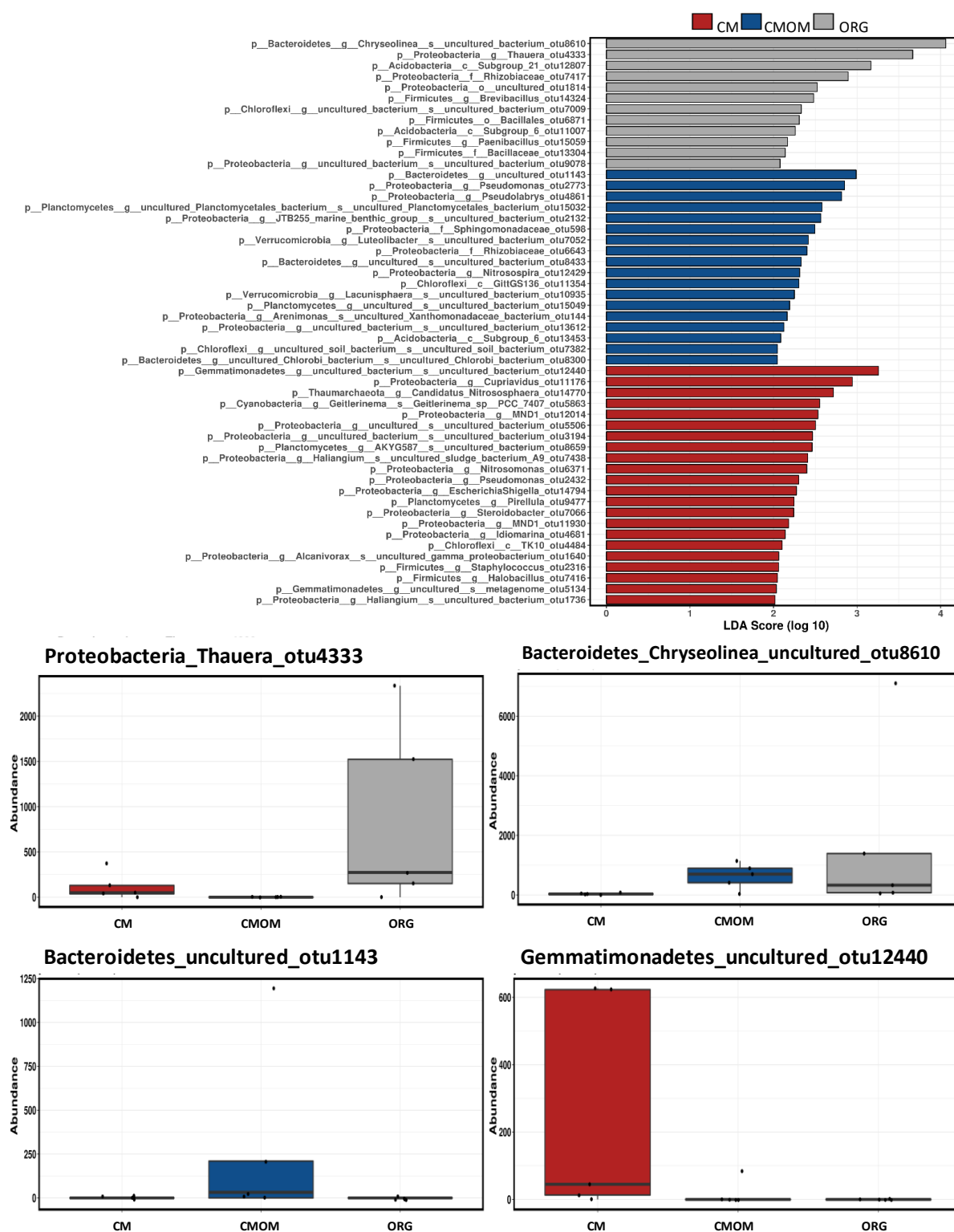
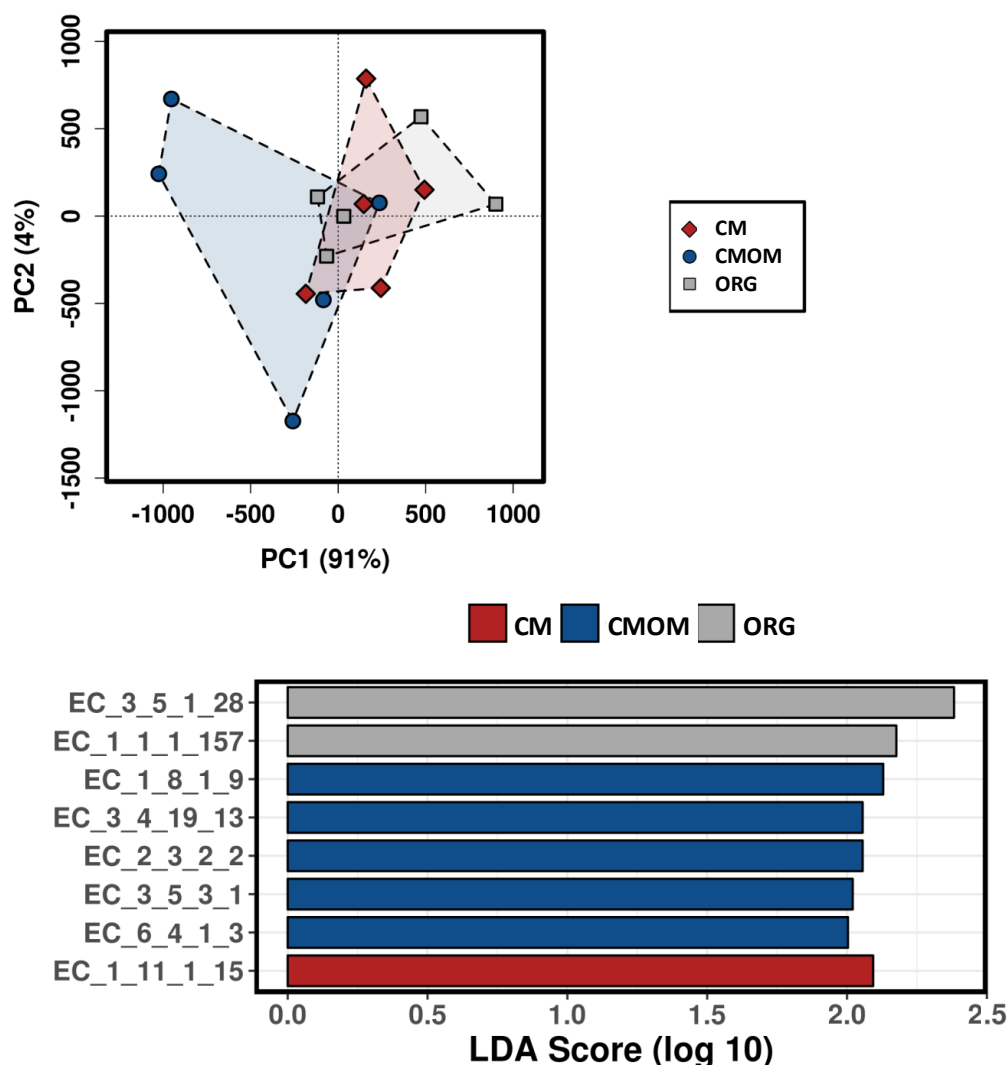


Figure S4. Prokaryotic ASVs associated to OM management practices (LDA>2, $p<0.05$) (above). Boxplots represent relative abundances of the highly significant features, LDA>3, $p<0.05$ (below). Legend of greenhouse managements as in Fig. S1.



Selected feature	Predicted functional pathway	LDA Score	Associated Group
EC_3_5_1_28	N-acetylmuramoyl-L-alanine amidase	2.3825781	ORG
EC_1_1_1_157	3-hydroxybutyryl-CoA dehydrogenase	2.1763900	ORG
EC_1_8_1_9	Thioredoxin-disulfide reductase	2.1294294	CMOM
EC_2_3_2_2	Gamma-glutamyltransferase	2.0557693	CMOM
EC_3_4_19_13	Pyroglutamyl-peptidase I	2.0557693	CMOM
EC_3_5_3_1	Arginase	2.0203345	CMOM
EC_6_4_1_3	Propionyl-CoA carboxylase	2.0033495	CMOM
EC_1_11_1_15	Peroxioredoxin	2.0934232	CM

Figure S5. Principal coordinates analysis (PCoA) based on the Bray-Curtis distance of Enzymes Classification (EC) data inferred by Picrust2 (above). Results of linear discriminant analysis effect size (LDA-LEfSe) showing the EC numbers significantly associated to particular OM managements (LDA>2, $p<0.05$) (below). Description of EC numbers identified by LEfSe (C). Legend of greenhouse managements as in Fig. S1.

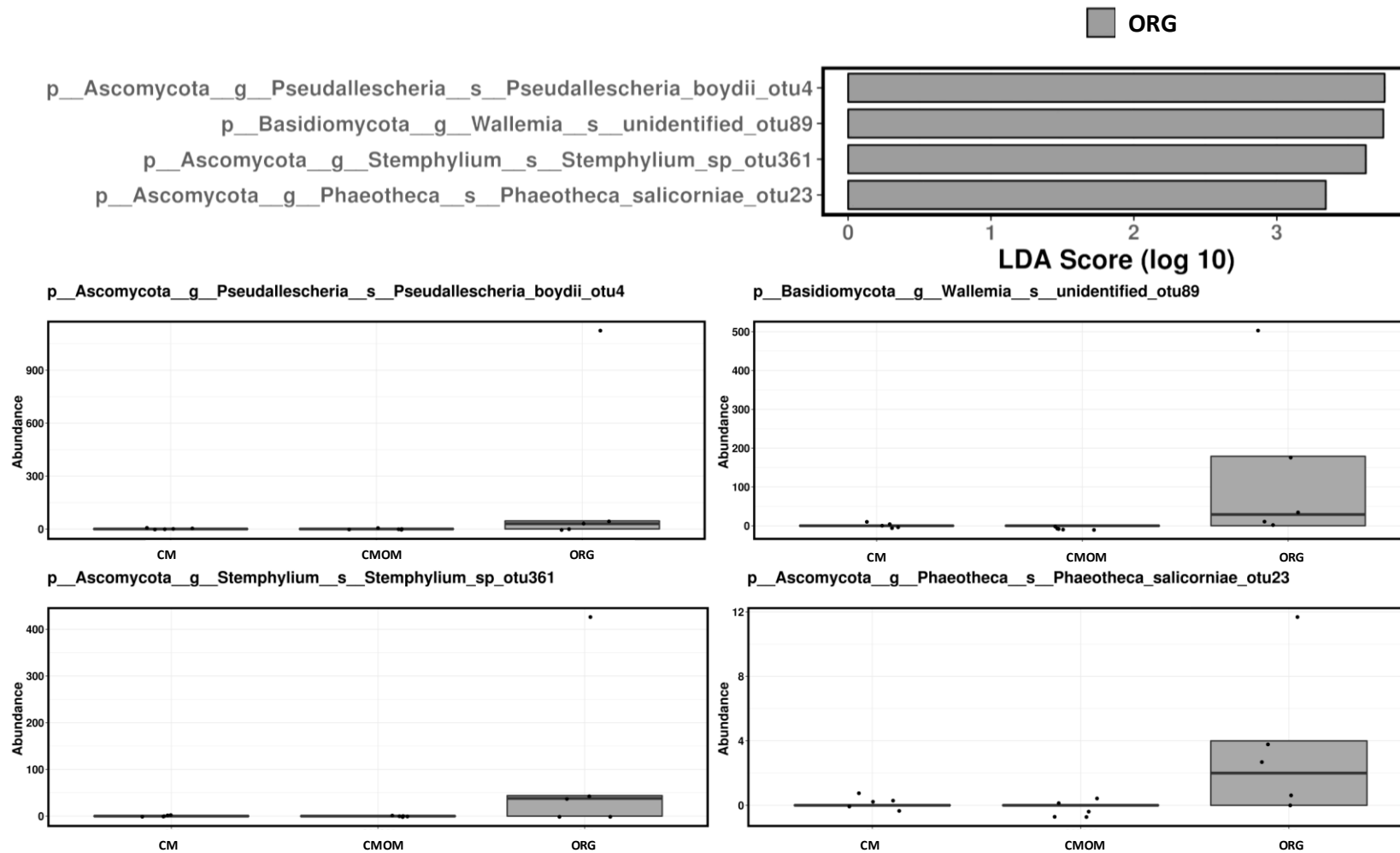


Figure S6. Fungal amplicon sequence variants (ASVs) associated to particular organic matter management practices, $LDA > 2$, $p < 0.05$ (above). Boxplots represent relative abundances of the highly significant features, $LDA > 3$, $p < 0.05$ (below). Legend of greenhouse managements as in Fig S1.