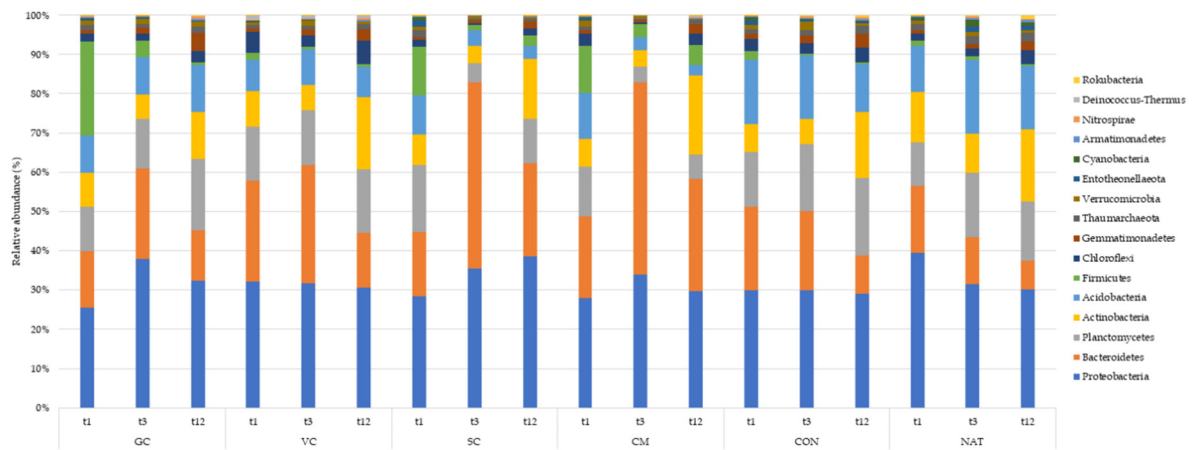


Figure S1. Bacterial community at phylum level with a relative abundance $\geq 0.1\%$.



Footnotes: GC: greenhouse crop residues compost; VC: vermicompost; SC: organic compost derived from the mixture of chicken and sheep manure; CM: manure from chickens raised on the soil of organic farms; CON: unamended control soils; NAT: natural reference soil. t1: initial soil sampling; t3: soil sampling at 3 months; t12: soil sampling at 12 months.

Table S1. Results of different multivariate PERMANOVA analysis ($p < 0.05$; 999 perm) by the factors treatment (GC, VC, SC, CM CON and NAT soils) and time (t1, t3 and t12) for the data of soil physico-chemical properties and bacterial composition (phylum level and genus or the next upper taxonomic level identified).

a) Physico-chemical soil properties:

Factor	DF	SS	MS	F-Value	P-Value
Treatment	5	4.63E+05	9,26E+05	43,882	0,001
Time	2	5.91E+05	2,95E+05	13,996	0,001
Treatment x Time	10	3,02E+0	30257	1,433	0,194
Residual	36	7,60E+05	21112		
Total	53	6,29E+06			

b) Soil bacterial community at phylum level:

Factor	DF	SS	MS	F-Value	P-Value
Treatment	5	3758,1	751,62	10,432	0,001
Time	2	2030,5	1015,2	14,091	0,001
Treatment x Time	10	2309,6	230,96	3,2055	0,001
Residual	36	2593,8	72,051		
Total	53	10692			

c) Soil bacterial community at genus or the next upper taxonomic level identified:

Factor	DF	SS	MS	F-Value	P-Value
Treatment	5	9452,4	1890,5	6,1747	0,001
Time	2	5395,8	2697,9	8,8118	0,001
Treatment x Time	10	6318,4	631,84	2,0637	0,001
Residual	36	11022	306,17		
Total	53	32189			

Table S2. Component loadings on all principal-component-analysis (PCA) solution for physico-chemical soil properties and nutrient stoichiometry ratios in restored, natural and control soils.

Variable	PC1	PC2	PC3	PC4	PC5
EC	0.373	-0.154	-0.389	0.081	-0.393
pH	-0.211	0.19	0.677	0.12	-0.048
TOC	-0.082	-0.629	0.144	0.118	-0.164
TN	0.15	-0.596	-0.024	-0.005	0.101
AP	0.371	-0.185	0.252	0.389	0.653
C:N	-0.369	-0.282	0.272	0.206	-0.43
C:P	-0.459	-0.049	-0.326	0.324	0.2
N:P	-0.447	0.02	-0.354	0.341	0.212
AW	-0.322	-0.27	-0.007	-0.742	0.33

EC: electrical conductivity; TOC: total organic carbon; TN: total nitrogen; AP: assimilable phosphorus; C:N: carbon to nitrogen ratio; C:P: carbon to phosphorus ratio; N:P: nitrogen to phosphorus ratio; AW: available plant water. CG: greenhouse crop residues compost; VC: vermicompost; CS: organic compost derived from the mixture of chicken and sheep manure; CM: manure from chickens raised on the soil of organic farms; CON: unamended control soils; NAT: natural reference soil.

Table S3. Distance-based redundancy analysis results, explanatory variance and contribution of relative abundance of bacterial taxa and abiotic properties (physico-chemical properties and nutrient stoichiometry) of the soil.

AICc	345.14	R ²	0.37
Percentage of variation explained by individual axes (% explained variation out of total variation)			
Axis	Individual	Cumulative	
1	21.87	21.87	
2	5.16	27.03	
<u>Weights</u>			
(Coefficients for linear combinations of X's in the formation of dbRDA coordinates)			
Variable	dbRDA1	dbRDA2	
EC	-0,64	4,06	
pH	-1,40	0,59	
TOC	-1,33	36,82	
TN	1,07	-32,13	
AP	-16,90	-3,70	
C:N	22,32	-19,30	
C:P	-220,04	-6,19	
N:P	183,50	5,25	
AW	2,49	1,59	

EC: electrical conductivity; TOC: total organic carbon; TN: total nitrogen; AP: assimilable phosphorus; C:N: carbon to nitrogen ratio; C:P: carbon to phosphorus ratio; N:P: nitrogen to phosphorus ratio; AW: available plant water.

Table S4. Results of the analysis of indicator species at the phylum and genus or the next upper taxonomic level identified for each type of restored, control and natural reference soil.

Treatment	Phylum	Soil Bacterial taxa	Indicator value	p-value	Sig.
GC	Firmicutes	g_Staphylococcus	0.674	0.0001	***
GC	Firmicutes	f_Bacillaceae	0.506	0.0046	**
GC	Proteobacteria	f_Blrii41_g_uncultured	0.414	0.0410	*
GC	Proteobacteria	g_Halomonas	0.455	0.0185	*
GC	Proteobacteria	g_Arenimonas	0.454	0.0187	*
VC	Bacteroidetes	g_Chryseolinea	0.663	0.0001	***
VC	Bacteroidetes	g_Alistipes	0.509	0.0034	**
VC	Bacteroidetes	f_Flavobacteriaceae	0.410	0.0056	**
VC	Deinococcus-Thermus	g_Truepera	0.776	0.0001	***
VC	Chloroflexi	o_SBR1031_g_anaerobic bacterium MO-CFX2	0.834	0.0001	***
VC	Chloroflexi	o_Ardenticatenales_g_bacterium YC-LK-LKJ3	0.895	0.0001	***
VC	Proteobacteria	f_Xanthomonadaceae	0.810	0.0001	***
CM	Actinobacteria	g_Arthrobacter	0.526	0.0008	***
CM	Actinobacteria	g_Leifsonia	0.524	0.0011	**
CM	Bacteroidetes	g_Sphingobacterium	0.495	0.0050	**
CM	Bacteroidetes	g_Pontibacter	0.623	0.0003	***
CM	Bacteroidetes	g_Myroides	0.430	0.0419	*
CM	Firmicutes	g_Atopostipes	0.550	0.0010	***
CM	Firmicutes	o_Bacillales	0.627	0.0001	***
CM	Proteobacteria	g_Alcaligenes	0.579	0.0008	***
CM	Proteobacteria	g_Stenotrophomonas	0.477	0.0148	*
CM	Proteobacteria	g_Nitrosospira	0.618	0.0004	***
SC	Bacteroidetes	g_Flavobacterium	0.507	0.0054	**
SC	Proteobacteria	g_Cellvibrio	0.503	0.0054	**
SC	Proteobacteria	g_Phenylobacterium	0.401	0.0089	**
CON	Acidobacteria	c_Subgroup 6_o_unknown_f_unknown	0.500	0.0008	***
CON	Actinobacteria	p_Actinobacteria_g_uncultured	0.446	0.0164	*
CON	Bacteroidetes	f_Microscillaceae	0.491	0.0013	**
CON	Bacteroidetes	g_Parasegetibacter	0.541	0.0009	***
CON	Chloroflexi	f_Anaerolineaceae_g_UTCFX1	0.584	0.0003	***
NAT	Acidobacteria	f_Pyrinomonadaceae_g_RB41	0.890	0.0001	***
NAT	Acidobacteria	f_Blastocatellaceae	0.617	0.0001	***
NAT	Acidobacteria	o_Subgroup 7_g_uncultured	0.667	0.0001	***
NAT	Actinobacteria	o_Gaiellales_f_uncultured_g_uncultured	0.449	0.0156	*
NAT	Actinobacteria	g_Blastococcus	0.602	0.0001	***
NAT	Actinobacteria	o_Gaiellales_f_uncultured	0.841	0.0001	***
NAT	Actinobacteria	g_Solirubrobacter	0.793	0.0001	***
NAT	Actinobacteria	g_Parviterribacter	0.516	0.0020	**
NAT	Actinobacteria	g_Rubrobacteria	0.650	0.0001	***
NAT	Bacteroidetes	g_Segetibacter	0.417	0.0378	*
NAT	Chloroflexi	f_JG30-KF-CM45_g_uncultured	0.579	0.0004	***
NAT	Cyanobacteria	g_Tychonema CCAP 1459-11B	0.535	0.0020	**
NAT	Planctomycetes	g_Zavarzinella	0.672	0.0001	***
NAT	Proteobacteria	f_Beijerinckiaceae	0.922	0.0001	***
NAT	Proteobacteria	f_Archangiaceae	0.443	0.0168	*
NAT	Proteobacteria	g_Psychroglaciecola	0.811	0.0001	***
NAT	Proteobacteria	g_PMMR1	0.861	0.0001	***

NAT	Proteobacteria	g_Reyranella	0.631	0.0002	***
NAT	Proteobacteria	o_Elsterales_f_uncultured_g_uncultured	0.768	0.0001	***
NAT	Proteobacteria	g_Rhodoplanes	0.694	0.0001	***
NAT	Proteobacteria	o_Rhizobiales_f_uncultured_g_uncultured	0.813	0.0001	***
NAT	Proteobacteria	o_Betaproteobacteriales_f_TRA3-20	0.883	0.0001	***
NAT	Proteobacteria	g_Ellin6067	0.706	0.0001	***

GC: greenhouse crop residues compost; VC: vermicompost; SC: organic compost derived from the mixture of chicken and sheep manure; CM: manure from chickens raised on the soil of organic farms; CON: unamended control soils; NAT: natural reference soil. Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1