



Figure S1. A geographical map of the area where the fields under study are located. The green color represents the area used for growing crops in the organic farming system. The red color indicates the location of a field where growing crops are produced using conventional farming methods. The crosses indicate approximate soil sampling locations. The map was provided by the Yandex service (accesses on 17 November 2024, <https://yandex.ru/maps/>)

Table S1. Metabarcoding sequencing statistics

Sample ID	Raw reads	Filtered reads	Number of merged reads	Reads after removal of chimeric sequences
O_1_0-5	122412	106564	70463	58215
O_2_0-5	122309	105919	69196	57381
O_3_0-5	123220	106092	73106	61886
O_4_0-5	123779	106666	73224	60678

O_1_5-15	121837	103858	73507	62235
O_2_5-15	122643	107735	70783	59961
O_3_5-15	120060	106413	67954	56776
O_4_5-15	122332	105486	75910	65288
C_1_0-5	120549	104282	68911	56848
C_2_0-5	124294	108195	75157	62098
C_3_0-5	123855	108591	77682	64909
C_4_0-5	122696	105881	74694	62807
C_1_5-15	124106	108062	74299	63671
C_2_5-15	122371	107882	71579	60769
C_3_5-15	123540	107156	72390	60622
C_4_5-15	120879	101889	67938	56981

Table S2. Relative abundance of most abundant (> 0.5%) bacterial phyla in the two farming systems.

Taxonomy	Farming systems	
	Conventional	Organic
Actinobacteriota	45.11%	51.06%
Proteobacteria	19.49%	16.14%
Chloroflexota	11.69%	10.89%
Acidobacteriota	9.11%	10.37%
Firmicutes	4.63%	2.91%
Gemmatimonadota	2.25%	2.06%
Not_Assigned	1.28%	1.48%
Myxococcota	1.35%	1.12%
Bacteroidota	2.26%	0.94%
Desulfobacterota_B	0.85%	0.87%
Methylomirabilota	0.26%	0.55%
Planctomycetota	0.53%	0.51%

Table S3. The most abundant genera (>0.5%) of bacteria from the conventional and organic soils.

Genera	Farming systems	
	Conventional	Organic
<i>Unclassified</i> bacteria	13.22%	17.16%
AC_32 (<i>Gaiellaceae</i>)	4.68%	4.97%
<i>Blastococcus</i>	3.43%	4.24%
CADCWL01 (<i>Thermomicrobiales</i>)	3.55%	3.14%
SCSIO_52909 (<i>Rubrobacteraceae</i>)	2.93%	2.96%
<i>Luteitalea</i>	2.19%	2.69%
<i>Microvirga</i>	2.64%	2.54%
AC_64 (<i>Solirubrobacteraceae</i>)	1.91%	1.86%
<i>Skermanella</i>	2.50%	1.59%
<i>Microtholunatus</i>	1.64%	1.58%
JACDCA01 (<i>Vicinamibacterales</i>)	1.34%	1.50%
<i>Pseudonocardia</i>	1.36%	1.48%
<i>Arthrobacter_H</i>	1.80%	1.45%
GMQP_bins7 (<i>Gaiellaceae</i>)	1.18%	1.29%
<i>Solirubrobacter</i>	1.25%	1.22%
CF_46 (<i>Limnocyndrales</i>)	1.06%	1.16%
<i>Arboricoccus</i>	1.10%	1.12%
<i>Sphingomicrobium</i>	1.43%	0.95%
<i>Bacillus_BD</i>	1.40%	0.91%
<i>Micromonospora_E</i>	1.04%	0.90%
C_114 (<i>Limnocyndrales</i>)	0.70%	0.89%
CF_154 (<i>Ktedonobacteraceae</i>)	0.96%	0.88%
JACDDX01 (<i>Gemmatimonadales</i>)	0.89%	0.85%

<i>Jiangella</i>	0.38%	0.85%
SIRX01 (<i>Rubrobacteraceae</i>)	0.89%	0.82%
AC_51 (<i>Actinobacteriota</i>)	0.50%	0.76%
QHWT01 (<i>Vicinamibacterales</i>)	0.84%	0.75%
CF_167 (<i>Limnocyndria</i>)	0.61%	0.73%
Z2_YC6860 (<i>Xanthobacteraceae</i>)	0.63%	0.72%
AC_69 (<i>Actinobacteriota</i>)	0.38%	0.72%
VGBV01 (<i>Solirubrobacterales</i>)	0.75%	0.71%
VFZN01 (<i>Vicinamibacterales</i>)	0.44%	0.63%
CADCWI01(<i>Thermomicrobiales</i>)	0.97%	0.62%
<i>Nocardioides_B</i>	0.67%	0.60%
Gp6_AA45 (<i>Vicinamibacterales</i>)	0.45%	0.58%
WHTF01 (<i>Binatia</i>)	0.52%	0.55%
<i>Bradyrhizobium</i>	0.67%	0.54%
<i>Mycobacterium</i>	0.43%	0.52%
<i>Geodermatophilus</i>	0.45%	0.52%
<i>Ilumatobacter</i>	0.53%	0.49%
QHXM01 (<i>Pyrinomonadaceae</i>)	0.30%	0.48%
<i>Nocardioides</i>	0.63%	0.47%
VAZQ01 (<i>Xanthobacteraceae</i>)	0.42%	0.47%
<i>Asanoa</i>	0.31%	0.46%
<i>Streptomyces</i>	0.54%	0.44%

Table S4. Diversity indices (Chao1 and Shannon) for the bacterial community in the two studied farming systems (mean \pm SD).

Index	Conventional system	Organic system	<i>p</i>-value
Chao1	2440.93 \pm 73.19	2434.36 \pm 111.75	0.96
Shannon	6.89 \pm 0.06	6.90 \pm 0.07	0.88

Table S5. Reliable differentiation of soil bacterial genera in the two studied farming systems.

Phylum	Class	Order	Family	Genus	Organic	Conventional
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Jiangellales</i>	<i>Jiangellaceae</i>	<i>Jiangella</i>	0.85%	0.38%
<i>Actinobacteriota</i>	<i>Acidimicrobiia</i>	IMCC26256	JACPCJ01	JACPCJ01	0.19%	0.07%
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Streptomycetales</i>	<i>Streptomycetaceae</i>	<i>Streptacidiphilus_A</i>	0.06%	0.02%
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Mycobacteriales</i>	<i>Geodermatophilaceae</i>	<i>Modestobacter</i>	0.05%	0.01%
<i>Methyloirabilota</i>	<i>Methyloirabilia</i>	<i>Rokubacteriales</i>	CSP1_6	AR19	0.21%	0.08%
<i>Methyloirabilota</i>	<i>Methyloirabilia</i>	<i>Rokubacteriales</i>	CSP1_6	DSHD01	0.03%	0.01%
<i>Verrucomicrobiota</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacterales</i>	UBA10450	AV80	0.03%	0.00%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderiales</i>	SG8_39	RBG_16_66_20	0.04%	0.00%
<i>Acidobacteriota</i>	<i>Blastocatellia</i>	<i>Pyrinomonadales</i>	<i>Pyrinomonadaceae</i>	UBA11740	0.08%	0.03%
<i>Gemmatimonadota</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonadales</i>	<i>Gemmatimonadaceae</i>	UBA4720	0.06%	0.01%
<i>Eisenbacteria</i>	RBG_16_71_46	RBG_16_71_46	RBG_16_71_46	JACRPT01	0.02%	0.00%
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>Saccharimonadales</i>	AMD01	GCA_2861585	0.01%	0.00%
<i>Desulfobacterota_B</i>	<i>Binatia</i>	UBA9968	UBA9968	DP_1	0.06%	0.01%
<i>Nitrospirota</i>	<i>Nitrospira</i>	<i>Nitrospirales</i>	NS_4	SCTG01	0.07%	0.03%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderiales</i>	<i>Nitrosomonadaceae</i>	<i>Nitrosospira</i>	0.03%	0.10%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Janthinobacterium</i>	0.11%	0.65%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Lysobacter</i>	0.02%	0.08%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Pseudoduganella</i>	0.01%	0.10%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonadales</i>	<i>Pseudomonadaceae</i>	<i>Pseudomonas_E</i>	0.01%	0.12%

<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Rhodoferax_B</i>	0.00%	0.05%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Aquabacterium</i>	0.00%	0.01%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Rhodanobacteraceae</i>	<i>Dokdonella_A</i>	0.00%	0.01%
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Luteimonas_C</i>	0.00%	0.01%
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Xanthobacteraceae</i>	<i>Nitrobacter</i>	0.00%	0.04%
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Actinomycetales</i>	<i>Dermatophilaceae</i>	<i>Humibacillus</i>	0.11%	0.33%
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Actinomycetales</i>	<i>Micrococcaceae</i>	<i>Arthrobacter_F</i>	0.04%	0.09%
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Mycobacteriales</i>	<i>Micromonosporaceae</i>	<i>Catenuloplanes</i>	0.02%	0.05%
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Mycobacteriales</i>	<i>Pseudonocardiaceae</i>	<i>Saccharopolyspora_C</i>	0.00%	0.02%
<i>Actinobacteriota</i>	<i>Actinomycetia</i>	<i>Streptosporangiales</i>	<i>Streptosporangiaceae</i>	<i>Sphaerisporangium</i>	0.00%	0.02%
<i>Actinobacteriota</i>	<i>Acidimicrobiia</i>	<i>Acidimicrobiales</i>	<i>SZUA_35</i>	<i>CADEDH01</i>	0.00%	0.01%
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales_B</i>	<i>Domibacillaceae</i>	<i>Domibacillus</i>	0.04%	0.10%
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Bacillaceae_H</i>	<i>Priestia</i>	0.05%	0.14%
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales_D</i>	<i>Amphibacillaceae</i>	<i>Terribacillus</i>	0.01%	0.04%
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales_B</i>	<i>DSM_18226</i>	<i>Robertmurraya</i>	0.01%	0.03%
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Lactobacillales</i>	<i>Lactobacillaceae</i>	<i>Limosilactobacillus</i>	0.00%	0.12%
<i>Firmicutes_A</i>	<i>Clostridia</i>	<i>Peptostreptococcales</i>	<i>Peptostreptococcaceae</i>	<i>Tepidibacter</i>	0.01%	0.10%
<i>Firmicutes_A</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>Clostridiaceae</i>	<i>Clostridium_J</i>	0.00%	0.02%
<i>Acidobacteriota</i>	<i>Acidobacteriae</i>	<i>Acidobacteriales</i>	<i>Gp1_AA117</i>	<i>Gp1_AA17</i>	0.01%	0.06%
<i>Bacteroidota</i>	<i>Bacteroidia</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>	0.03%	0.91%
<i>Myxococcota</i>	<i>Myxococcia</i>	<i>Myxococcales</i>	<i>Anaeromyxobacteraceae</i>	<i>Anaeromyxobacter</i>	0.01%	0.03%

<i>Myxococcota</i>	<i>Myxococcia</i>	<i>Myxococcales</i>	<i>Anaeromyxobacteraceae</i>	<i>R267</i>	0.00%	0.02%
<i>Chloroflexota</i>	<i>Anaerolineae</i>	<i>Aggregatilineales</i>	<i>A4b</i>	<i>OLB13</i>	0.02%	0.10%