Mineral Fertilizers Determine Differences in Soils Microbial Composition and Resistome: Exploration of Conventional versus Organic Cropping Systems

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TableS1. Whole-metagenome sequencing statistics

Sample ID	Raw reads	Filtered reads	GC (%)	Contigs	Largest contig	Total length
O_1_0-5	47849547	29057102	63,91	259615	71145	2,02E+08
O_2_0-5	42717295	25680006	63,57	195358	52235	1,5E+08
O_3_0-5	39942046	23281866	63,85	185045	31411	1,45E+08
O_4_0-5	43597757	25736542	63,27	214213	73025	1,69E+08
O_1_5-15	45840812	25899721	64,4	218092	54462	1,73E+08
O_2_5-15	44359583	26256170	65,04	214343	21573	1,71E+08
O_3_5-15	41569400	23444351	63,68	196708	47560	1,55E+08
O_4_5-15	42185183	24310725	62,86	211813	69326	1,69E+08
C_1_0-5	43043801	26385577	63,44	252421	51184	1,98E+08
C_2_0-5	43592684	25810201	63,38	254839	46321	2,01E+08
C_3_0-5	42594049	25397003	63,26	234682	52097	1,84E+08
C_4_0-5	42525450	23577565	62,9	205787	63031	1,58E+08
C_1_5-15	42367252	25136117	64,4	218092	54462	1,73E+08
C_2_5-15	42314322	24020133	62,96	206686	40780	1,56E+08

O-Organic cropping system; C- Conventional cropping system.

Table S2. The differences between conventional soil comparing to organic soil microbiomes of the studied cropping systems expressed as log2fold value

No	Genera	Log2fold values	Standard deviation	*p*-value
1	*Paracoccus*	4.44	2.72	0.007
2	*Corynebacterium*	4.37	2.82	0.008
3	*Halomonas*	3.13	3.18	0.006
4	*Hymenobacter*	2.09	2.50	0.004
5	*Cryobacterium*	2.09	2.59	0.002
6	*Nostoc*	2.08	2.50	6.47E-08
7	*Tetrasphaera*	2.05	2.46	0.008
8	*Pseudorhodoplanes*	1.99	2.56	0.017
9	*Baekduia*	1.99	2.84	0.033
10	*Labilithrix*	1.95	2.97	0.020
11	*Myxococcus*	1.87	2.60	3.41E-04
12	*Rhizobium*	1.26	0.41	5.33E-04
13	*Lysobacter*	1.22	0.39	5.48E-04
14	*Marmoricola*	1.14	0.38	0.030
15	*Nitrosospira*	1.12	0.52	0.004
16	*Desertimonas*	1.12	0.22	6.24E-04
17	*Micromonospora*	1.10	0.24	0.002
18	*Gemmatimonas*	1.10	0.35	0.008
19	*Actinoplanes*	1.08	0.58	0.018
20	*Paludisphaera*	1.08	0.12	8.19E-06
21	*Reyranella*	1.07	0.53	0.018
22	*Nakamurella*	1.06	0.15	0.004
23	*Ramlibacter*	1.05	0.28	2.98E-05
24	*Chitinophaga*	1.05	0.41	0.004
25	*Azospirillum*	1.04	0.38	0.006

26	*Microlunatus*	1.03	0.11	0.006
27	*Patulibacter*	1.03	0.37	0.036
28	*Cupriavidus*	1.01	0.12	6.79E-05
29	*Pedosphaera*	1.01	0.44	0.037
30	*Bradyrhizobium*	1.00	0.31	5.23E-04
31	*Novosphingobium*	1.00	0.40	0.006
32	*Caulobacter*	1.00	0.19	9.82E-06
33	*Aquisphaera*	1.00	0.40	0.005
34	*Bosea*	0.99	0.55	0.021
35	*Devosia*	0.98	0.81	0.037
36	*Phenylobacterium*	0.98	0.23	0.002
37	*Massilia*	0.97	0.52	0.008
38	*Altererythrobacter*	0.97	0.39	0.016
39	*Gemmata*	0.96	0.54	0.025
40	*Afipia*	0.94	0.46	0.012
41	*Pedobacter*	0.94	0.58	0.024
42	*Opitutus*	0.93	0.43	0.004
43	*Aeromicrobium*	0.92	0.17	6.05E-04
44	*Belnapia*	0.92	0.35	0.020
45	*Anaeromyxobacter*	0.88	1.14	0.038
46	*Luteitalea*	0.86	0.51	0.021
47	*Pseudoxanthomonas*	0.84	0.84	0.014
48	*Frankia*	0.79	0.17	0.012
49	*Bacillus*	0.79	0.49	0.044
50	*Methylobacterium*	0.77	0.69	0.042
51	*Pseudomonas*	0.67	0.49	0.028
52	*Skermanella*	0.51	0.48	0.027
53	*Acrocarpospora*	0.02	0.04	0.014

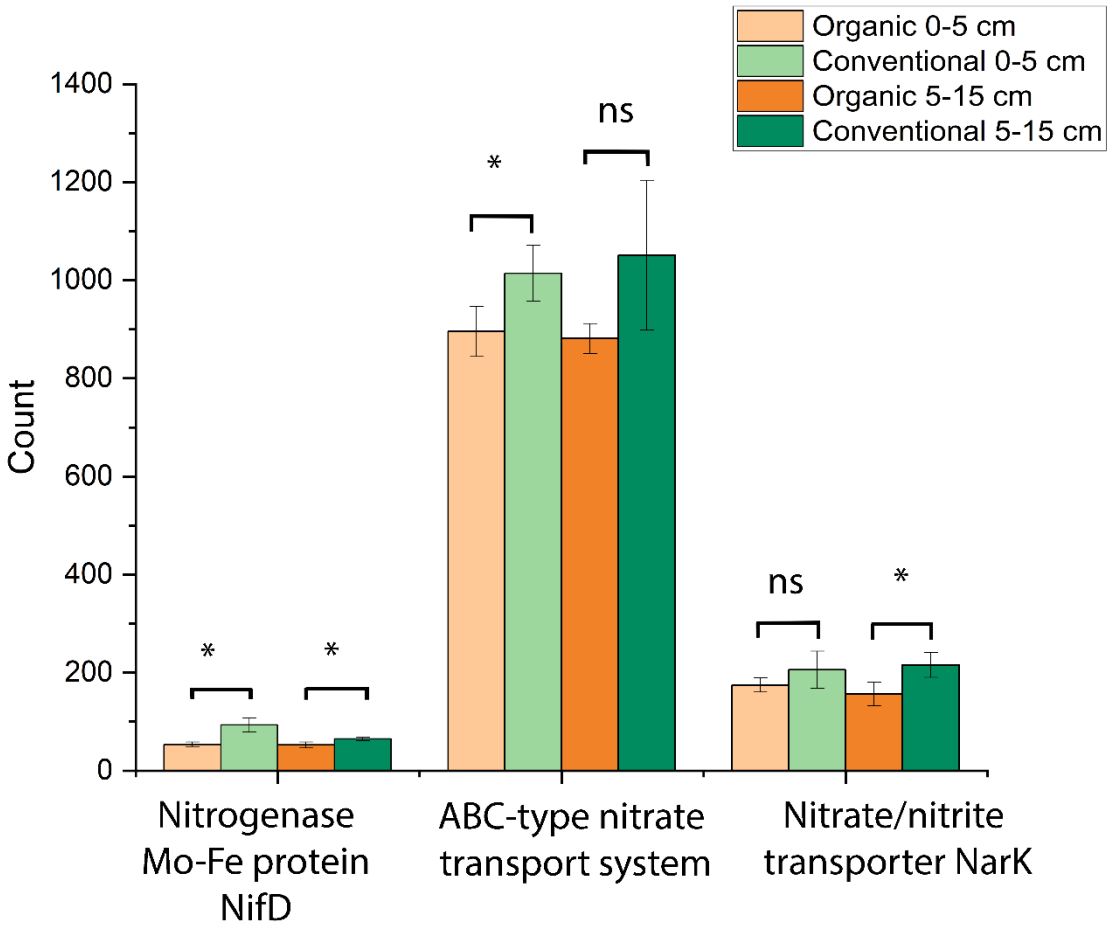

Figure S1. The distribution of functional genes depending of cropping systems and sampling depth. As a result of metagenomic analysis, 23 genes were found whose products are involved in the nitrogen cycle. Only gene products that are significantly different (* $p < 0.05$) between the study groups are presented.

Table S3. Statistics on the reconstructed genomes (MAGs)

MAG ID	Total length	GC (%)	Compl	Contam	Coverage, x	Domain	Phylum	Class	Order	Family	Genus
Binatia_bacterium_cn-1-5-15_WHTF01	3238136	54.1	68.28	1.29	7.5	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_cn-3-0-5_WHTF01	3098994	54.0	67.43	2.12	8.0	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_cn-3-5-15_WHTF01	3637332	53.9	70.15	1.77	8.4	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_cn-4-0-5_WHTF01	3590980	54.0	77.25	3.25	8.5	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_cn-4-5-15_WHTF01	4281509	54.0	84.14	2.58	9.8	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_on-1-5-15_WHTF01	3245865	53.9	65.28	4.77	7.4	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_on-2-0-5_WHTF01	2998526	53.8	67.99	2.58	7.5	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_on-3-5-15_WHTF01	4178679	53.9	75.99	7.46	9.2	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Binatia_bacterium_on-4-5-15_WHTF01	5150289	53.9	81.79	5.56	8.8	Bacteria	Binatota	Binatia	UBA9968	UBA9968	WHTF01
Entotheonellia_bacterium_on-4-5-15_J063	3016061	60.0	59.46	6.46	7.4	Bacteria	Tectomicrobia	Entotheonellia	J063	-	-
Gaiellaceae_bacterium_cn-3-5-15_JACDAN01	2073141	68.8	56.39	3.76	12.0	Bacteria	Actinobacteriota	Thermoleophilia	Gaiellales	Gaiellaceae	JACDAN01
Gaiellaceae_bacterium_cn-4-0-5_JACDAN01	1722759	68.8	55.34	0.43	15.4	Bacteria	Actinobacteriota	Thermoleophilia	Gaiellales	Gaiellaceae	JACDAN01

MAG ID	Total length	GC (%)	Compl	Contam	Coverage, x	Domain	Phylum	Class	Order	Family	Genus
Gaiellaceae_bacterium_on-3-0-5_JACDAN01	2142866	68.8	68.4	7.88	18.7	Bacteria	Actinobacteriota	Thermoleophilia	Gaiellales	Gaiellaceae	JACDAN01
Nitrososphaera_sp._cn-1-0-5	2231118	43.1	94.66	3.88	30.1	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._cn-1-5-15	1968333	43.2	91.42	1.94	13.1	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._cn-2-0-5	1877413	43.5	88.83	1.94	23.7	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._cn-2-5-15	1844670	43.3	83.66	2.02	12.7	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._cn-3-0-5	1965454	43.1	87.86	4.85	13.3	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._cn-3-5-15	2017109	43.2	92.64	2.91	21.0	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._cn-4-0-5	2284611	43.1	94.17	3.88	30.2	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._cn-4-5-15	2391571	42.9	93.2	2.91	25.1	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._on-1-0-5	1943870	43.5	94.17	2.91	34.6	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera

MAG ID	Total length	GC (%)	Compl	Contam	Coverage, x	Domain	Phylum	Class	Order	Family	Genus
Nitrososphaera_sp._on-1-5-15	2038668	43.2	93.85	2.91	16.6	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._on-2-0-5	1910831	43.2	93.2	1.94	36.8	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._on-2-5-15	1737819	43.6	89.48	2.91	13.6	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._on-3-0-5	1838331	43.5	91.75	3.24	33.0	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._on-3-5-15	2306422	43.6	93.2	2.91	34.3	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._on-4-0-5	1773233	43.6	90.29	1.94	35.1	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaera_sp._on-4-5-15	2071797	43.1	87.95	3.4	21.1	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	Nitrososphaera
Nitrososphaeraceae_archaeon_cn-1-0-5_JACDAN01	1354225	35.5	73.95	7.62	10.2	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	JAFAQB01
Nitrososphaeraceae_archaeon_cn-4-0-5_JACDAN01	1527027	36.0	70.15	6.45	9.1	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	JAFAQB01
Nitrososphaeraceae_archaeon_cn-4-5-15_TH5893	1254743	36.4	63.59	4.82	9.0	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	TH5893

MAG ID	Total length	GC (%)	Compl	Contam	Coverage, x	Domain	Phylum	Class	Order	Family	Genus
Nitrososphaeraceae_archaeon_on-2-0-5_JACDAN01	2015688	35.6	82.52	6.31	14.3	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	JAFAQB01
Nitrososphaeraceae_archaeon_on-3-0-5_JACDAN01	2105715	35.9	79.29	3.51	11.0	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	JAFAQB01
Nitrososphaeraceae_archaeon_on-3-0-5_TH5893	808252	41.2	56.98	1.12	7.5	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	TH5893
Nitrososphaeraceae_archaeon_on-4-0-5_JACDAN01	1584090	35.5	85.11	7.83	13.1	Archaea	Thermoproteota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	JAFAQB01
Nitrospiraceae_bacterium_on-3-5-15	1625429	57.8	60.03	0.96	6.7	Bacteria	Nitrospirota	Nitrospiria	Nitrospirales	Nitrospiraceae	Nitrospira_C
Propionibacteriaceae_bacterium_cn-1-0-5	2701653	65.6	76.91	1.99	16.0	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-
Propionibacteriaceae_bacterium_cn-4-0-5	2617094	65.4	76.26	3.2	12.6	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-
Propionibacteriaceae_bacterium_on-1-0-5	3098211	65.5	89.09	2.5	18.0	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-
Propionibacteriaceae_bacterium_on-1-5-15	2182504	65.0	75.04	0.25	9.7	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-
Propionibacteriaceae_bacterium_on-2-0-5	2881091	65.4	74.22	3.1	12.7	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-

MAG ID	Total length	GC (%)	Compl	Contam	Coverage, x	Domain	Phylum	Class	Order	Family	Genus
Propionibacteriaceae_bacterium_on-3-0-5	2975218	65.4	87.12	1.11	12.6	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-
Propionibacteriaceae_bacterium_on-3-5-15	2171394	65.3	57.06	6.68	7.2	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-
Propionibacteriaceae_bacterium_on-4-0-5	3135040	65.6	75.01	3.28	11.1	Bacteria	Actinobacteriota	Actinomycetia	Propionibacteriales	Propionibacteriaceae	-
Solirubrobacterales_bacterium_on-2-0-5_70-9	1350622	68.2	53.93	2.59	12.9	Bacteria	Actinobacteriota	Thermoleophilia	Solirubrobacterales	70-9	-

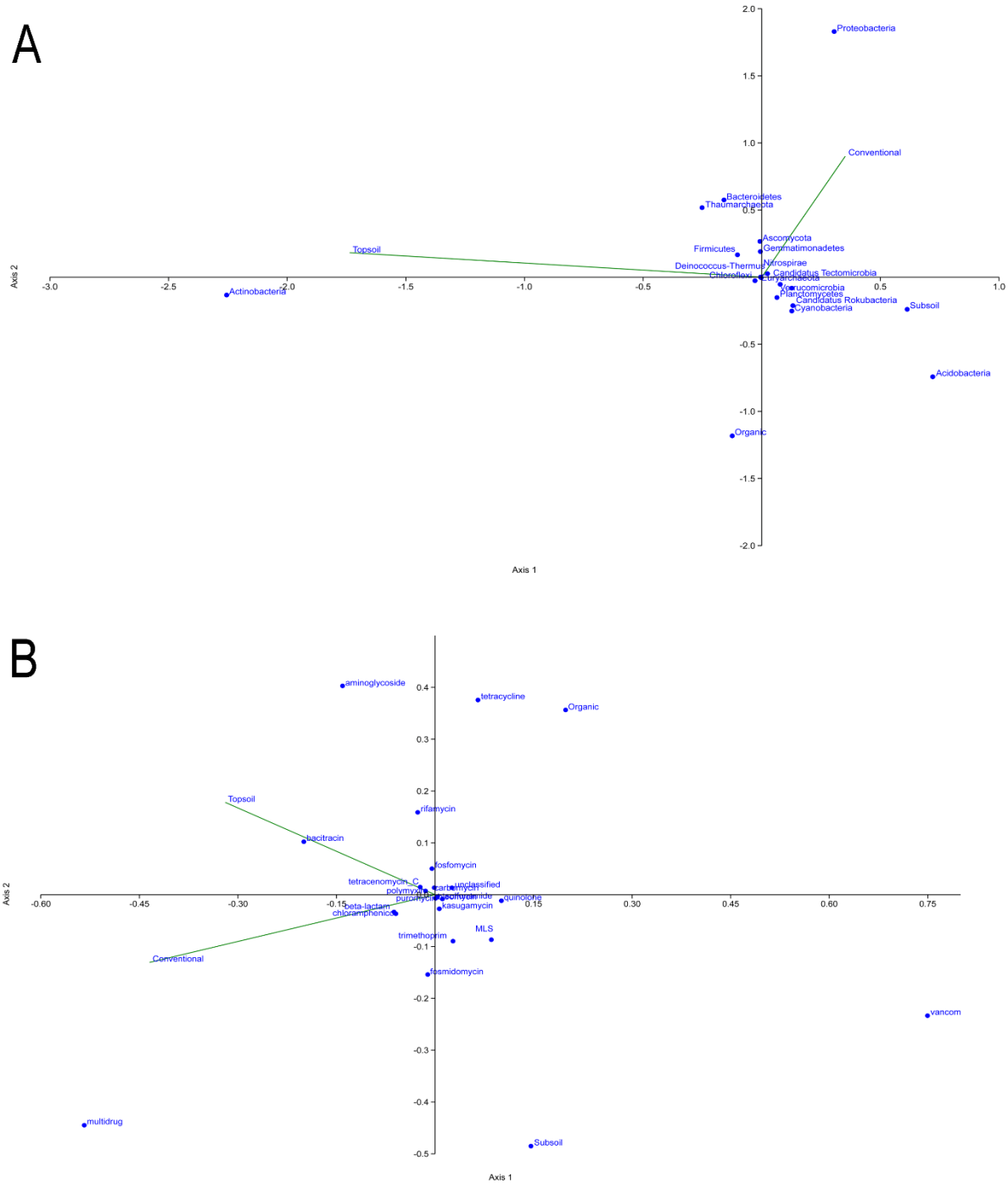

Figure S2. The redundancy analysis of the dependence of the microbiome at phylum level (A) and ARGs profile (B) on land use and soil sampling depths.

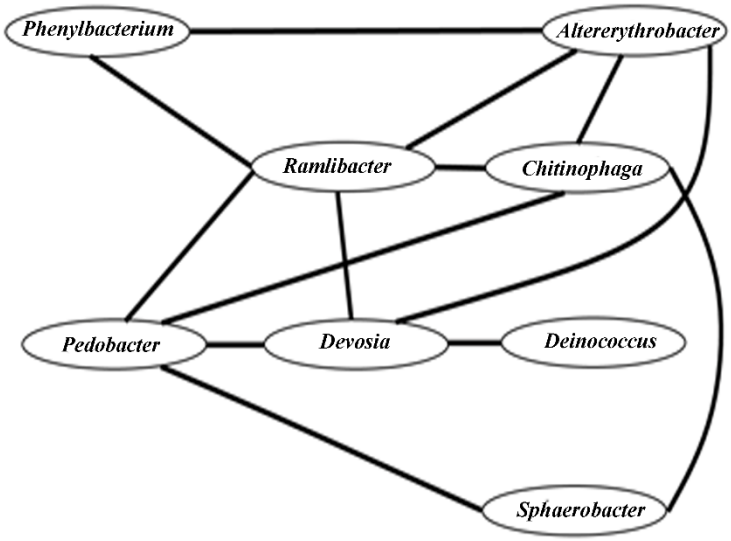

Figure S3. The structure of high correlations inside the group of bacteria significantly correlated with beta-lactam. Solid lines connect taxa correlated to each other with the correlation coefficient greater than 0.8.