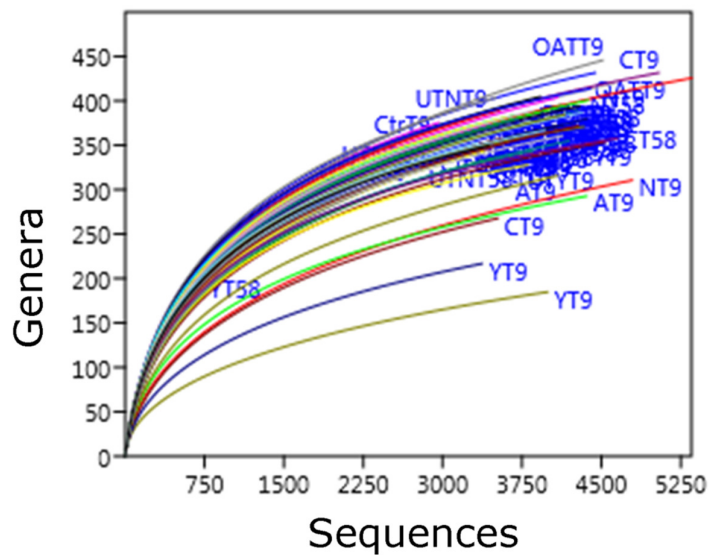


## Supplementary material

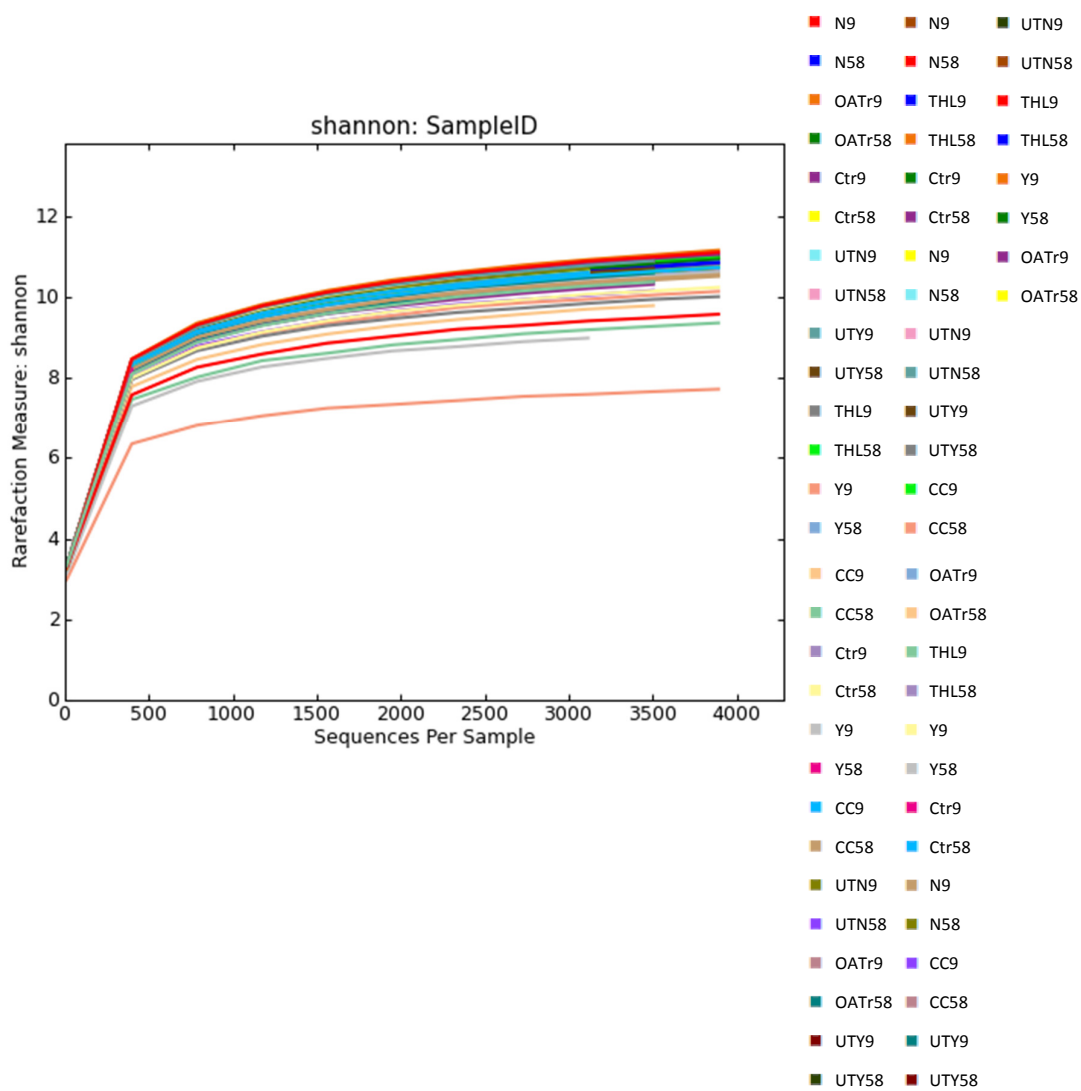
### Response of bacterial communities upon application of different innovative organic fertilizers in a greenhouse experiment using low-nutrient soil cultivated with *Cynodon dactylon*

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**Fig. S1A. Rarefaction analysis at genus level**

Diversity of bacterial communities derived from agricultural soil subject to the different fertilization conditions and sampled at the two time points T9 and T58.



**Fig. S1B. Rarefaction analysis of the Shannon index**

Saturation of the community diversity (Shannon diversity index  $H$ ) stemming from the analysis of the sequences.

			Sum of Squares	df	Mean Square	F	Sig.
Cumulative average height * Treatment	Between Groups	(Combined)	278.0	13	21.4	14.127	.000
	Within Groups		63.6	42	1.5		
	Total		341.5	55			
Cumulative average fresh weight * Treatment	Between Groups	(Combined)	27981.0	13	2152.4	44.915	.000
	Within Groups		2012.7	42	47.9		
	Total		29993.7	55			
Cumulative average dry weight * Treatment	Between Groups	(Combined)	1773.0	13	136.4	45.916	.000
	Within Groups		124.8	42	3.0		
	Total		1897.7	55			

**Table S1. Plant growth differences significance**

In the table, the results obtained from the ANOVA test done considering the three plant growth parameters in respect to the different treatments are reported.

Phylum	N. of genera
Proteobacteria	296
Actinobacteria	123
Firmicutes	110
Chloroflexi	66
Bacteroidetes	52
Acidobacteria	34
Verucomicrobia	34
Planctomycetes	33
Cyanobacteria	29
Gemmatimonadetes	16
Armatimonadetes	13
Chlorobi	11
TM7	9
WS3	8
Nitrospirae	7
Elusimicrobia	6
OD1	6
Spirochaetes	6
GN02	5
GN04	3
NKB19	3
OP3	3
TM6	3
Fibrobacteres	2
OP11	2
Tenericutes	2
Thermi	2
BRC1	1
Caldithrix	1
FCPU426	1
Fusobacteria	1
GAL15	1
Lentisphaerae	1
MVP21	1
Other	1
SR1	1
Synergistetes	1
Unclassified	1
Unclassified; Other	1
WPS2	1
WS2	1
WS4	1
WYO	1

**Table S2.** Number of genera detected across all samples within each phylum.

Taxon	THL D58/D9	CC D58/D9	N D58/D9	OATr D58/D9	UTY D58/D9	UTN D58/D9	Y D58/D9	Ctrl D58/D9
Acidobacteria_c_Acidobacteria-6_o_iii1-15_f_g	1.82	1.43	2.19	1.07	1.31	1.42	3.00	1.17
Acidobacteria_c_Acidobacteria-6_o_iii1-15_fm2424_g	2.23	2.11	3.24	1.09	1.70	1.76	2.80	1.28
Acidobacteria_c_Chloracidobacteria_o_f_g	2.62	1.66	2.30	1.11	1.51	1.56	3.33	1.41
Acidobacteria_c_iii1-8_o_DS-18_f_g	2.77	3.64	1.89	0.93	1.52	1.19	5.29	1.67
Acidobacteria_c_o_f_g	4.86	1.89	3.43	1.26	1.59	1.90	2.66	3.58
Acidobacteria_c_S035_o_f_g	2.42	1.14	2.25	0.91	1.24	0.89	1.47	0.77
Actinobacteria_c_Actinimicrobia_o_Actinimicrobiales_f_EB1017_g	2.59	3.47	1.72	1.41	1.24	0.86	6.35	1.16
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Geodermatophilaceae_g_Geodermatophilus	4.08	0.0003	0.0001	3.06	2.55	0.0005	0.0001	0.0003
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Intrasporangiaceae_g_Phycococcus	1.00	1.43	1.01	0.26	0.48	0.86	1.75	2.58
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Intrasporangiaceae_Other	1.12	1.14	1.30	0.36	1.30	0.91	3.23	1.34
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Micromonosporaceae_g	0.00	2.74	12.27	0.43	2.13	0.00	4.86	0.19
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Micromonosporaceae_Other	1.48	4.01	2.23	0.86	3.51	0.78	8.12	0.79
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Mycobacteriaceae_g_Mycobacterium	1.10	1.68	1.48	0.65	0.82	0.95	7.73	1.01
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Mycobacteriaceae_Other	0.46	0.60	0.68	0.16	0.69	0.46	1.47	0.52
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Pseudonocardiaceae_g_Pseudonocardia	2.41	1.49	0.0003	3.69	1.20	1.77	14.02	1.39
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Sporichthyaceae_g_Sporichthya	0.00	0.0002	3.98	0.00	0.0001	1.99	0.0000	0.00
Actinobacteria_c_Actinobacteria_o_Actinomycetales_f_Thermomonosporaceae_g	0.0000	0.0000	0.0000	0.0001	0.0000	0.0000	0.0000	0.0000
Actinobacteria_c_Actinobacteria_o_Actinomycetales_Other_Other	1.41	1.30	1.18	0.60	1.04	1.08	2.08	0.90
Actinobacteria_c_MB-A2-108_o_0319-7L14_f_g	3.34	4.97	6.65	2.19	2.65	2.09	11.09	1.28
Actinobacteria_c_Rubrobacteria_o_Rubrobacterales_f_Rubrobacteraceae_g_Rubrobacter	1.87	0.94	1.30	0.37	0.83	0.78	2.31	0.83
Actinobacteria_c_Thermoleptophila_o_Gaiallales_f_Gaiallaceae_g	2.24	2.49	4.14	1.12	1.38	1.36	4.64	1.09
Actinobacteria_c_Thermoleptophila_o_Solirubrobacterales_f_g	2.60	2.63	2.88	0.90	1.64	1.59	4.29	0.99
Actinobacteria_c_Thermoleptophila_o_Solirubrobacterales_Other_Other	1.98	1.34	1.94	1.54	1.55	1.51	2.37	1.22
Actinobacteria_Other_Other_Other	1.77	1.46	1.76	1.06	1.78	1.32	1.41	0.76
Armatimonadetes_c_[Fimbrimonadetes]_o_[Fimbrimonadales]_f_[Fimbrimonadaceae]_Other	7.78	0.36	2.67	0.38	0.52	0.22	0.00	1.81
Armatimonadetes_Other_Other_Other	2.64	0.79	2.37	1.25	1.36	1.90	7.84	1.13
Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_g	0.05	0.01	0.02	0.93	0.02	0.00	0.01	0.02
Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Porphyrimonadaceae_g_Dysgonomonas	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.00	0.0000
Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Porphyrimonadaceae_g_Parabacteroides	0.00	0.00	0.00	0.0000	0.0000	0.0000	0.00	0.0000
Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Porphyrimonadaceae_Other	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.00	0.0000
Bacteroidetes_c_Bacteroidia_o_Bacteroidales_Other_Other	0.00	0.00	0.00	0.0000	0.0000	0.98	0.00	0.00
Bacteroidetes_c_Flavobacteria_o_Flavobacteriales_f_Flavobacteriaceae_g_Riemerella	0.00	0.00	0.00	0.0000	0.00	0.0000	0.00	0.0000
Bacteroidetes_c_Flavobacteria_o_Flavobacteriales_f_Flavobacteriaceae_Other	0.00	0.00	0.00	0.67	0.00	0.00	0.00	0.00
Bacteroidetes_c_Sphingobacteria_o_Sphingobacteriales_f_Chitinophagaceae_g_Flavisolibacter	0.74	0.61	0.38	0.47	0.52	0.55	0.63	0.35
Bacteroidetes_Other_Other_Other	1.51	1.53	0.65	2.40	0.93	1.66	4.42	0.71
Chloroflexi_c_Anaerolineae_o_Caldilineales_f_Caldilineaceae_g	1.85	1.27	1.94	0.86	1.05	1.19	3.07	1.14
Chloroflexi_c_Bjiii12_o_f_g	1.63	0.0005	3.07	1.29	3.30	1.67	2.15	0.94
Chloroflexi_c_Chloroflexi_o_Roseiflexales_f_g	0.0000	0.0000	0.0001	0.00	0.0001	0.0000	0.0000	0.0000
Chloroflexi_c_Thermomicrobia_o_f_g	0.0000	0.0002	0.0002	0.0001	0.0002	0.0000	0.0003	0.00
Cyanobacteria_c_4C0d-2_o_SM1D11_f_g	24.26	10.49	16.81	0.63	16.39	0.0007	12.95	6.51
Cyanobacteria_c_Nostocophycidae_o_Nostocales_f_Nostocaceae_g_Nostoc	0.00	2.35	0.76	0.11	6.98	0.00	0.0005	0.24
Cyanobacteria_c_Synechococophycidae_o_Pseudanabaenales_f_Pseudanabaenaceae_g_Leptolyngbya	0.00	0.00	0.29	0.00	3.30	0.0000	0.0001	0.37
Firmicutes_c_Bacilli_o_Bacillales_f_Bacillaceae_Other	0.59	0.18	0.29	0.71	0.98	0.33	0.41	1.07
Firmicutes_c_Bacilli_o_Bacillales_f_Planococcaceae_g_Sporosarcina	0.0002	1.13	0.32	1.02	1.51	0.0001	0.00	2.25
Firmicutes_c_Bacilli_o_Bacillales_f_Thermoactinomyetaceae_g_Planifilum	0.00	0.0000	3.69	4.13	0.0001	0.60	0.0001	0.00
Firmicutes_c_Bacilli_Other_Other	0.91	0.32	0.91	0.49	1.21	0.43	0.00	0.60
Firmicutes_c_Clostridia_o_Clostridiales_f_Catabacteriaceae_g	0.0000	0.00	0.00	0.0000	0.00	0.0000	0.00	0.00
Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g	0.08	0.00	0.21	0.00	0.00	0.15	0.03	0.10
Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_Caloramator	0.07	0.13	0.27	0.00	0.00	0.00	0.08	0.38
Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_g_Clostridium	0.25	0.84	0.63	0.48	0.35	0.17	0.67	0.46
Firmicutes_c_Clostridia_o_Clostridiales_f_Clostridiaceae_Other	0.06	0.18	0.22	0.19	0.13	0.09	0.09	0.16
Firmicutes_c_Clostridia_o_Clostridiales_f_Dehalobacteriaceae_g	0.40	0.87	0.49	0.00	0.09	0.00	1.07	0.40
Firmicutes_c_Clostridia_o_Clostridiales_f_Dehalobacteriaceae_g_Dehaloacterium	0.00	0.0000	0.00	0.0001	0.0001	0.00	0.0000	0.00
Firmicutes_c_Clostridia_o_Clostridiales_f_Peptococcaceae_g_Desulfibacterium	2.01	0.22	0.33	0.0000	0.00	0.00	0.47	0.0000
Firmicutes_c_Clostridia_o_Clostridiales_f_Peptococcaceae_g_WCHB1-84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes_c_Clostridia_o_Clostridiales_f_Peptococcaceae_Other	0.29	0.31	0.33	0.07	0.00	0.04	0.26	0.20
Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_g_Oscillospira	0.25	0.00	0.69	0.0000	0.00	0.00	2.06	0.0000
Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae_Other	0.00	0.00	0.00	0.00	0.00	0.81	0.00	0.00
Firmicutes_c_Clostridia_o_Clostridiales_f_Symbiobacteriaceae_g_Symbiobacterium	0.01	0.11	0.03	0.00	0.03	0.00	0.12	0.03
Firmicutes_c_Clostridia_o_Clostridiales_f_Symbiobacteriaceae_Other	0.08	0.11	0.10	0.00	0.10	1.16	0.00	0.00
Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Desulfosporomusa	0.05	0.69	0.25	0.00	0.07	0.03	0.17	0.07
Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_G07	0.60	0.20	0.11	0.00	0.27	0.00	0.15	0.33
Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Propionispora	0.0000	0.0000	0.00	0.0000	0.0000	0.0000	0.0000	0.0000
Firmicutes_c_Clostridia_o_Clostridiales_f_Veillonellaceae_g_Thermosinus	0.04	0.00	0.00	0.33	0.12	0.18	0.00	0.21
Firmicutes_c_Clostridia_o_Clostridiales_Other_Other	0.16	0.20	0.18	0.11	0.16	0.12	0.15	0.22
Firmicutes_c_Clostridia_Other_Other	0.24	0.19	0.10	0.23	0.23	0.23	0.05	0.29
Firmicutes_c_Erysipelotrichi_o_Erysipelotrichales_f_Erysipelotrichaceae_Other	0.0000	0.00	0.00	0.0000	0.0000	0.00	0.00	0.00
Firmicutes_c_o_f_g	0.11	0.00	0.00	0.0000	0.00	0.00	0.20	0.00
Firmicutes_Other_Other_Other	0.11	0.07	0.09	0.39	0.05	0.06	0.05	0.16
Gemmatimonadetes_c_Gemm-1_o_f_g	3.68	2.65	2.60	1.27	1.32	1.41	8.94	1.21
Gemmatimonadetes_c_Gemm-5_o_f_g	4.79	2.64	3.45	1.51	1.61	2.05	6.50	1.64
Gemmatimonadetes_c_Gemmatimonadetes_o_C114_f_g	0.0000	0.0000	0.69	0.00	4.34	0.00	0.0000	0.50
Gemmatimonadetes_c_Gemmatimonadetes_o_N1423WL_f_g	2.09	0.56	1.86	0.84	1.05	1.12	3.26	1.24
MVP-21_c_o_f_g	0.0000	0.0000	0.0000	0.0000	0.0002	0.0002	0.0000	0.0000
Nitrospirae_c_Nitrospira_o_Nitrospirales_f_g	1.83	1.38	2.15	1.78	1.02	1.84	3.08	1.63
OP11_c_OP11-4_o_f_g	0.0010	3.19	0.0003	18.88	0.0001	0.0004	0.0001	0.0005
Planctomycetes_c_C6_o_d113_f_g	0.0000	0.0000	0.0000	0.0001	0.0000	0.0000	0.0000	0.0000
Planctomycetes_c_Planctomycetia_o_Gemmatales_f_Gemmataceae_g	2.22	1.54	4.08	1.64	1.44	1.99	5.37	1.37
Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_Hyphomicrobiaceae_g	2.95	1.68	1.73	1.55	0.98	0.95	2.08	1.56
Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_Hyphomicrobiaceae_g_Rhodoplates	2.39	2.00	1.98	1.49	1.57	1.42	4.43	1.10
Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_Hyphomicrobiaceae_Other	2.02	2.04	1.77	1.24	1.22	1.18	2.95	0.99
Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_f_Rhodobiaceae_g	4.83	2.20	6.51	0.88	0.84	0.97	3.82	1.32
Proteobacteria_c_Alphaproteobacteria_o_Rhizobiales_Other_Other	1.34	1.54	1.46	0.92	1.34	1.21	1.69	1.13
Proteobacteria_c_Alphaproteobacteria_o_Rhodobacteriales_f_Rhodobacteraceae_Other	0.87	8.68	1.04	3.17	2.24	1.57	0.0008	0.94
Proteobacteria_c_Alphaproteobacteria_o_Rhodospirillales_f_Rhodospirillaceae_g_Azospirillum	0.10	1.67	0.60	0.0001	0.12	0.03	2.08	0.63
Proteobacteria_c_Alphaproteobacteria_o_Rhodospirillales_f_Rhodospirillaceae_g_Skermanella	1.82	1.37	1.30	0.89	1.28	1.39	5.05	1.24
Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales_f_mitochondria_g	3.06	2.72	1.56	2.19	1.01	1.62	3.61	1.91
Proteobacteria_c_Alphaproteobacteria_o_Sphingomonadales_f_Erythrobacteraceae_g	1.54	1.15	0.92	0.46	0.54	0.74	3.21	2.12
Proteobacteria_c_Alphaproteobacteria_Other_Other	2.53	2.91	2.53	1.85	2.04	1.23	3.77	1.67
Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Comamonadaceae_g_Pelomonas	0.00	0.04	0.00	0.18	0.00	0.34	0.00	0.22
Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Comamonadaceae_g_Polaromonas	0.77	0.00	0.00	0.32	0.00	0.00	0.00	0.65
Proteobacteria_c_Betaproteobacteria_o_Burkholderiales_f_Oxalobacteraceae_Other	0.25	0.31	0.35	0.32	0.24	0.29	0.40	0.37
Proteobacteria_c_Betaproteobacteria_o_MND1_f_g	4.26	2.42	4.13	2.81	2.83	3.03	6.69	2.32
Proteobacteria_c_Betaproteobacteria_o_Rhodocyclales_f_Rhodocyclaceae_g_Zoogloea	0.00	0.00	0.00	0.0000	0.00	0.00	0.00	0.51
Proteobacteria_c_Deltaproteobacteria_o_[Entothoonellales]_f_[Entothoonellaceae]_g	2.20	1.36	1.85	1.05	0.99	1.13	2.05	1.39
Proteobacteria_c_Deltaproteobacteria_o_Myxococcales_f_g	2.02	1.56	2.26	1.38	1.24	1.49	2.21	1.29
Proteobacteria_c_Deltaproteobacteria_o_Myxococcales_f_Haliangiaceae_g_Haliangium	4.51	7.66	4.74	21.74	3.34	0.0036	0.0032	0.0039

Proteobacteria_c_Deltaproteobacteria_o_Syntrophobacterales_f_Syntrophaceae_g_Smithella	0.0002	0.0000	2.90	4.12	0.0004	0.0002	0.0004	0.0001
Proteobacteria_c_Deltaproteobacteria_o_Syntrophobacterales_f_Syntrophobacteraceae_g_	2.41	1.35	2.35	0.96	1.22	1.06	3.57	1.09
Proteobacteria_c_Deltaproteobacteria_Other_Other_Other	1.65	1.55	1.50	0.89	1.30	1.09	2.42	1.22
Proteobacteria_c_Epsilonproteobacteria_o_Campylobacterales_f_Campylobacteraceae_g_Sulfurospirillum	0.00	0.00	0.00	0.0000	0.0000	0.0000	0.00	0.00
Proteobacteria_c_Gammaproteobacteria_o_Enterobacterales_f_Enterobacteriaceae_g_Enterobacter	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria_c_Gammaproteobacteria_o_Legionellales_f_Legionellaceae_g_Legionella	0.0006	11.35	0.0006	3.23	9.78	0.0001	2.15	5.13
Proteobacteria_c_Gammaproteobacteria_o_Xanthomonadales_f_Sinobacteraceae_g_Hydrocarboniphaga	0.0005	5.78	0.0003	0.0004	0.0003	0.0002	0.0008	0.0002
Proteobacteria_c_Gammaproteobacteria_o_Xanthomonadales_f_Sinobacteraceae_g_Steroidobacter	2.21	2.15	2.13	1.26	1.42	1.29	3.20	1.24
Proteobacteria_Other_Other_Other_Other	1.41	1.41	1.37	1.59	1.37	1.64	2.23	1.43
TM7_c_TM7-3_o_1025_f_g_	1.46	0.00	0.0002	0.00	0.0000	0.30	0.0000	0.00
Verrucomicrobia_c_[Spartobacteria]_o_[Chthoniobacterales]_f_[Chthoniobacteraceae]_g_DA101	2.30	1.95	0.73	0.63	0.20	0.00	0.0006	1.80
Verrucomicrobia_c_Verrucomicrobiae_o_Verrucomicrobiales_f_Verrucomicrobiaceae_g_Prostheobacter	1.27	4.23	3.36	0.00	7.88	2.17	0.0000	0.0006

35	34	36	36	31	36	36	36
4	6	8	7	7	6	2	10
5	5	4	18	9	13	1	13
17	25	19	16	28	29	5	26
31	24	29	11	15	4	44	7
1	0	0	1	0	0	0	0

Legend	$x < 0.5$	$0.5 \leq x < 0.85$	$0.85 \leq x < 1.15$	$1.15 \leq x < 2$	$2 \leq x < 20$	$x > 0.20$
	White cells: Taxon absent at day9. In these boxes, the % of the taxon in the sample at day58 is shown, not the ratio.					

**Table S3. Genus level variation of taxa over time.** The ratios between the presence percentage of each genus at day 58 and at day 9 are reported, and each box is coloured depending on the resulting value (from green, when the presence percentage of the genus is higher at day 58 than at day 9, to red, when the percentage of the genus is lower at day 58). Below the data a six-line summary table reports the number of genera which changed with each of the six ratio classes, using the corresponding background colour described in the legend.