Supplementary information for

Microbial Electrochemical Systems outperform fixed-bed biofilters for cleaning-up urban wastewater

AUTHORS:

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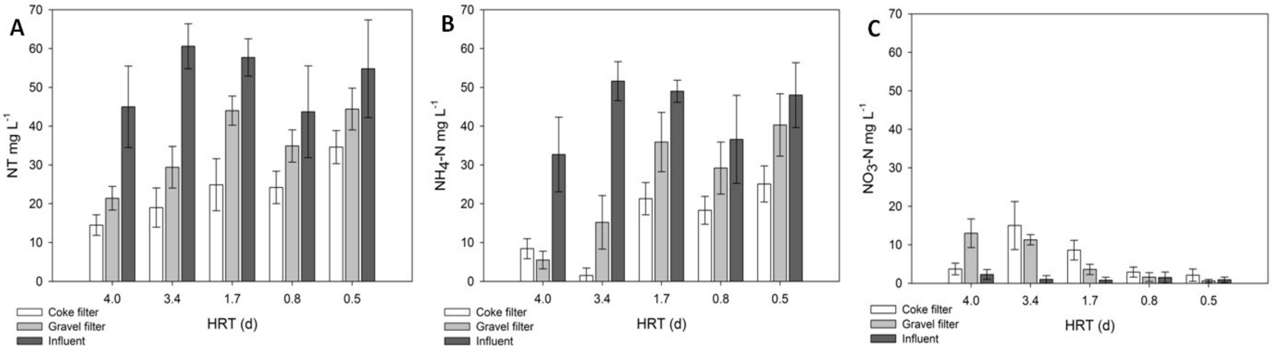


Fig.1S Total nitrogen (A), ammonia (B) and nitrate (C) influent and effluent average values of the coke and the gravel biofilters. Error bars represent 95% confidence interval.

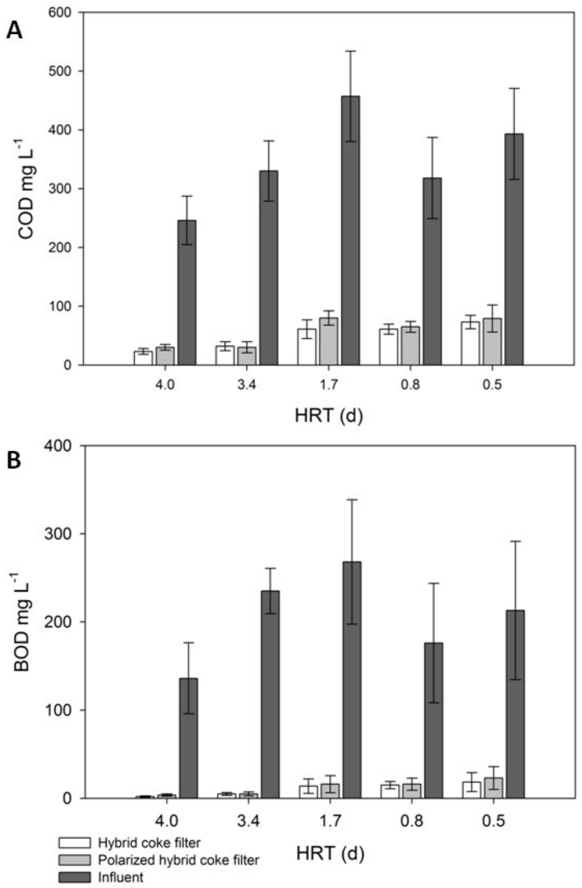
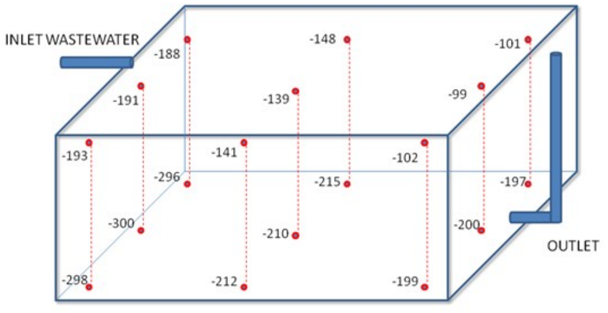
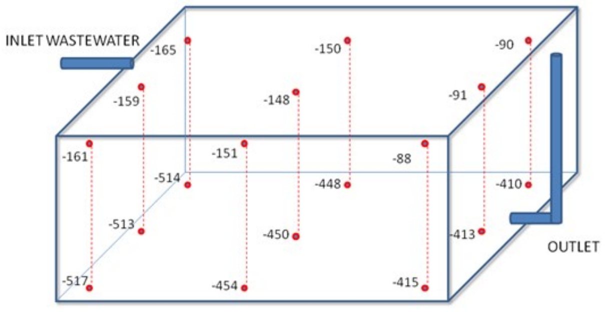


Fig. 2S Influent and effluent COD (A) and BOD5 (B) average values of the hybrid biofilter and the hybrid polarized biofilter. Error bars represent 95% confidence interval.



GRAVEL BIOFILTER



COKE BIOFILTER

Fig. 3S Redox potential measured in the coke and the gravel biofilters

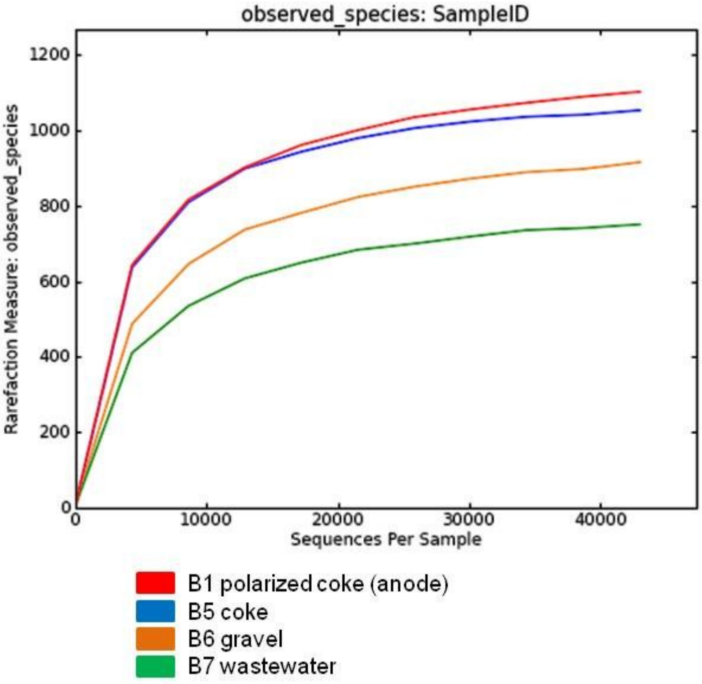


Fig. 4S Rarefaction curves calculated for each sample based on the OTU computations.

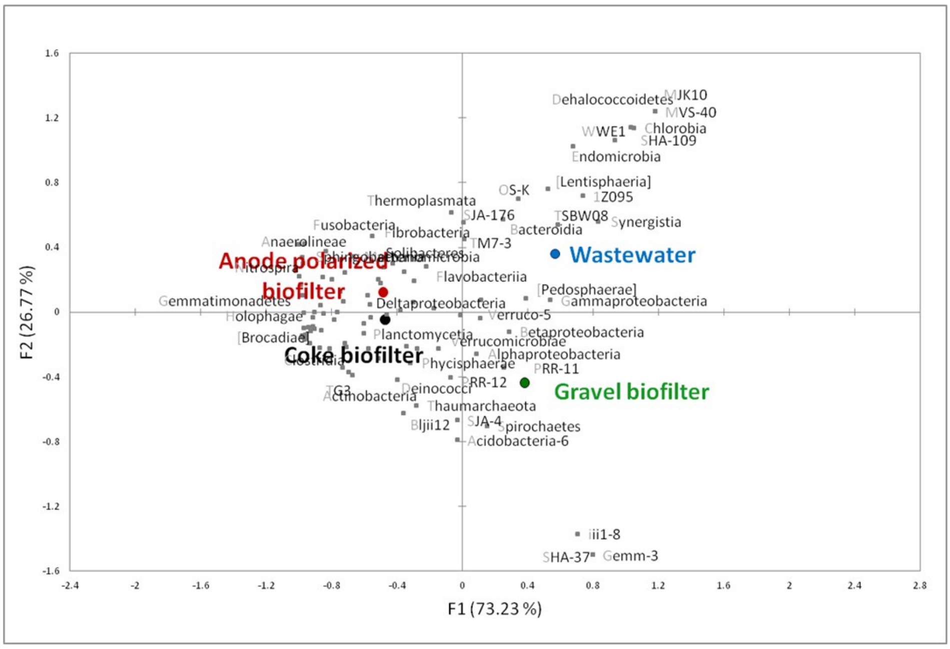


Fig. 5S Correspondence analysis biplot of classes' distribution from pyrosequencing analysis.

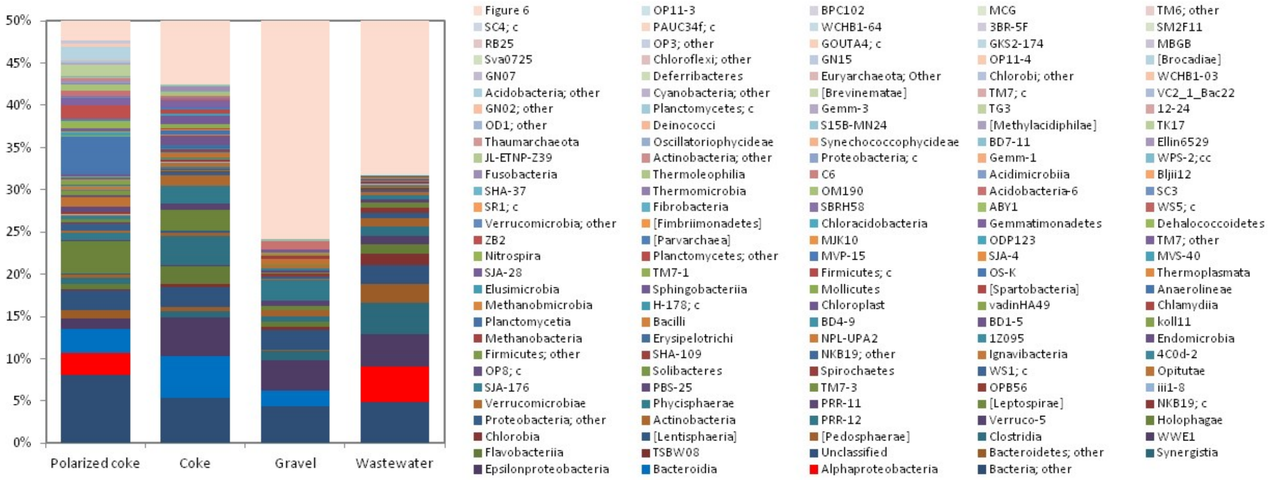


Fig. 6S. Relative abundance of classes of the category 'other' at class level.

Table 1S Influent pre-treated wastewater and effluents characteristics. Averages ± SD

HRT (d)		4.0	3.4	1.7	0.8	0.5
Influent	COD (mg L^{-1})	246 ± 114	330 ± 107	457 ± 92	318 ± 143	393 ± 101
	BOD$_5$ (mg L^{-1})	136 ± 86	235 ± 36	268 ± 81	176 ± 127	213 ± 112
	TN (mg L^{-1})	45.0 ± 17.4	60.6 ± 7.5	57.7 ± 3.9	43.7 ± 16.5	54.8 ± 10.1
	NH_4-N (mg L^{-1})	32.7 ± 18.7	51.6 ± 6.5	49.0 ± 2.3	36.6 ± 15.9	47.0 ± 8.8
	NO_3-N (mg L^{-1})	2.3 ± 3.6	1.0 ± 1.6	0.8 ± 0.6	1.5 ± 2.0	0.9 ± 0.6
	TP (mg L^{-1})	6.1 ± 2.3	7.5 ± 1.1	7.3 ± 0.8	7.0 ± 1.3	8.6 ± 2.2
	TSS (mg L^{-1})	62 ± 36	102 ± 29	141 ± 32	207 ± 156	239 ± 168
	EC (µS cm^{-1})	1519 ± 209	1133 ± 66	1177 ± 31	1312 ± 93	1207 ± 130
	ORP (mV)	-220 ± 19	-180 ± 17	-178 ± 17	-78 ± 190	-101 ± 98
	pH	7.7 ± 0.2	7.5 ± 0.3	7.3 ± 0.3	7.5 ± 0.4	7.2 ± 0.2
	T (ºC)	19.5 ± 5.0	23.3 ± 2.8	20.1 ± 4.0	19.9 ± 2.3	21.8 ± 1.1
	DO (mg L-1)	0.6 ± 0.4	0.7 ± 0.3	0.6 ± 0.1	1.3 ± 0.6	1.3 ± 0.4
Coke Biofilter	TSS (mg L-1)	41 ± 21	2 ± 3	2 ± 2	15 ± 5	14 ± 9
	EC (µS cm-1)	1641 ± 283	1026 ± 56	1011 ± 64	1226 ± 107	1120 ± 69
	ORP (mV)	-44 ± 13	-72 ± 18	-111 ± 19	-98 ± 26	-61 ± 19
	pH	7.5 ± 0.3	7.7 ± 0.2	7.3 ± 0.1	7.5 ± 0.3	7.5 ± 0.1
	T (ºC)	18.5 ± 4.9	22.3 ± 2.8	19.8 ± 4.0	18.5 ± 2.2	20.9 ± 0.9
Gravel biofilter	TSS (mg L-1)	4 ± 3	2 ± 1	11 ± 7	13 ± 5	16 ± 6
	EC (µS cm-1)	1448 ± 235	971 ± 49	1102 ± 75	1288 ± 103	1179 ± 95
	ORP (mV)	-31 ± 11	-65 ± 15	-88 ± 13	-80 ± 20	-54 ± 18
	pH	8.0 ±0.2	7.7 ± 0.1	7.6 ± 0.1	7.7 ± 0.3	7.6 ± 0.2
	T (ºC)	18.5 ± 4.9	22.4 ±2.8	19.8 ± 4.0	18.5 ± 2.2	20.8 ± 0.8

Table 2S. Organic matter removal rates (COD and BOD) and percentage removal efficiencies (in brackets). Averages ± SD (COD: n=30; BOD_5: n=15)

HRT (days)		4.0	3.4	1.7	0.8	0.5
Surface Inlet load	COD	3.6 ± 1.7	6.0 ± 1.9	15.8 ± 3.2	25.1 ± 11.3	44.4 ± 11.4
	BOD_5	2.0 ± 1.0	4.2 ± 0.7	9.2 ± 2.8	13.8 ± 9.5	24.0 ± 12.7
Volume Inlet load	COD	19.0 ± 9.1	31.0 ± 10.1	82.0 ± 16.5	130.9 ± 59.0	231.2 ± 59.2
	BOD_5	10.4 ± 6.6	22.1 ± 3.4	48.1 ± 14.5	71.9 ± 49.4	125.0 ± 65.9
Coke biofilter	COD	17.6 ± 8.7 (91±8)	28.7 ± 10.1 (93±5)	76.6 ± 17.9 (93±6)	117.2 ± 58.8 (90±8)	213.5 ± 71.2 (90±8)
	BOD_5	10.1 ± 6.5 (97±3)	21.9 ± 3.4 (99±1)	47.0 ± 14.5 (98±2)	69.8 ± 52.6 (96±3)	119.4 ± 65.0 (95±2)
Gravel biofilter	COD	15.4 ± 8.7 (80±9)	25.8 ± 9.6 (83±7)	64.9 ± 19.3 (78±8)	95.6 ± 59.4 (73±10)	168.9 ± 67.5 (73±9)
	BOD_5	10.0 ± 6.6 (92±5)	21.0 ± 3.2 (95±2)	43.2 ± 14.4 (90±6)	62.0 ± 54.4 (78±10)	107.8 ± 65.0 (82±4)
Hybrid biofilter	COD	16.4 ± 8.7 (88±8)	27.9 ± 10.2 (89±8)	71.0 ± 18.5 (87±6)	107.6 ± 58.0 (80±8)	186.5 ± 57.4 (81±6)
	BOD_5	10.2 ± 6.1 (98±2)	21.7 ± 3.3 (98±1)	45.6 ± 14.9 (94±4)	66.5 ± 51.5 (88±7)	114.3 ± 66.1 (90±9)
Hybrid polarized biofilter	COD	16.7 ± 8.6 (86±8)	27.8 ± 10.5 (89±8)	67.7 ± 15.7 (83±4)	108.2 ± 55.8 (80±8)	182.8 ± 69.3 (79±9)
	BOD_5	10.1 ± 6.5 (97±3)	21.6 ± 3.2 (98±2)	45.2 ± 14.5 (94±4)	66.0 ± 51.2 (88±7)	111.5 ± 68.0 (88±8)

Surface Inlet loads are given in g $m^{-2}d^{-1}$. Rest of the values are given in g $m^{-3}d^{-1}$.

Table 3S Statistical test and p-values of the coke and gravel biofilters effluents comparison (*significant differences). W = Wilcoxon test; t = T-test

HRT		4.0	3.4	1.7	0.8	0.5
COD	Test	W=115.0	t=4.7358	t=4.97003	t=5.9989	t=6.07078
	P-value	3.39014E-7*	0.0000335879*	0.000205645*	5.71257E-7*	0.0000214144*
BOD_5	Test	t=3.35102	W=14.0	W=0.0	W=3.5	t=6.15014
	P-value	0.00183017*	0.00668291*	0.0121858*	0.00118219*	0.000846891*
NT	Test	t=3.7542	t=2.27672	t=3.28567	t=2.78791	t=3.54823
	P-value	0.000978189*	0.0390336*	0.0110934*	0.0121472*	0.00752885*
NH_4-N	Test	t=-1.81134	W=1.0	t=3.36448	t=2.90737	W=0
	P-value	0.0794836	0.00133738*	0.0120106*	0.00939458*	0.0121858*
NO_3	Test	W=20.0	W=40.0	t=-2.7704	T=-1.64259	W=20.0
	P-value	0.143672	0.430216	0.0242818*	0.117822	0.143672

Table 4S Overall averages ± SD (n=15) of total nitrogen and ammonia removal rates and average removal efficiencies (in brackets)

HRT (days)		4.0	3.4	1.7	0.8	0.5
Surface inlet load	TN	0.7 ± 0.3	1.1 ± 0.1	2.0 ± 0.1	3.5 ± 1.3	6.2 ± 1.1
	NH4-N	0.5 ± 0.3	0.9 ± 0.1	1.7 ± 0.1	2.9 ± 1.3	5.4 ± 0.8
Volume inlet load	TN	3.4 ± 1.3	5.7 ± 0.7	10.4 ± 0.7	18.0 ± 6.8	32.2 ± 6.0
	NH_4-N	2.5 ± 1.4	4.8 ± 0.6	8.8 ± 0.4	15.1 ± 6.5	28.2 ± 4.0
Coke biofilter	TN	2.3 ± 1.4 (68 ± 12)	4.0 ± 0.9 (69 ± 12)	4.1 ± 1.4 (40 ± 11)	8.0 ± 4.7 (45 ± 10)	11.9 ± 8.6 (37 ±12)
	NH_4-N	1.9 ± 1.5 (74 ± 21)	4.8 ± 0.7 (97 ± 5)	6.6 ± 1.4 (57 ±10)	7.6 ± 4.6 (49 ±10)	11.2 ± 6.8 (39 ±11)
Gravel biofilter	TN	1.8 ± 1.3 (52 ± 14)	3.0 ± 0.8 (51 ± 13)	2.5 ± 0.7 (24 ± 6)	3.7 ± 3.4 (20 ± 9)	6.6 ± 6.0 (19 ± 9)
	NH_4-N	2.1 ± 1.5 (83 ± 22)	3.5 ± 0.7 (71 ± 15)	2.3 ± 0.9 (27 ± 11)	3.0 ± 3.1 (20 ± 12)	4.6 ± 3.9 (16 ± 13)
Hybrid biofilter	TN	1.8 ± 1.3 (59 ± 14)	3.4 ± 0.9 (56 ± 13)	2.2 ± 0.8 (24 ± 14)	7.7 ± 5.6 (24 ±14)	8.4 ± 5.6 (23 ±12)
	NH_4-N	2.0 ± 1.5 (78 ± 25)	4.2 ± 0.8 (87 ± 14)	2.6 ± 0.6 (30 ± 8)	5.3 ± 4.4 (28 ± 13)	7.0 ± 4.1 (24 ± 12)
Hybrid polarized biofilter	TN	2.0 ± 1.4 (59 ± 14)	3.2 ± 0.7 (56 ± 13)	2.5 ± 1.6 (24 ± 14)	5.6 ± 5.6 (23 ± 13)	6.9 ± 5.3 (22 ±12)
	NH_4-N	2.2 ± 1.5 (81 ± 21)	4.2 ± 0.9 (87 ± 14)	2.3 ± 1.1 (27 ± 13)	4.9 ± 4.4 (25 ± 12)	5.7 ± 3.1 (20 ± 9)

Surface inlet loads are given in g m^{-2} d^{-1}. Rest of the values are given in g m^{-3} d^{-1}.

Table 5S Alpha diversity metrics of the bacterial populations

Sample ID	Description	Total reads	Observed OTUs	Chao 1	Shannon	Good's Coverage
B1	Coke granules anode	167,678	1,219	1,263	7.13	0.99
B5	Coke granules single electrode	178,772	1,121	1,151	7.38	0.99
B6	Gravel	173,665	1,006	1,042	6.89	0.99
B7	Inlet wastewater	169,876	832	914	6.27	0.99

Table 6S. Main taxa of bacteria identified in the analysed communities (over 0.1), in percentage.

Taxon	Coke polarized	Coke	Gravel	Waste water
Bacteria;Other;Other;Other;Other;Other	8.04	5.35	4.35	4.91
Acidobacteria;Acidobacteria-6;iii1-15;;	0.43	0.21	0.94	0.00
Acidobacteria;Holophagae;Holophagales;Holophagaceae;	0.09	0.12	0.17	0.49
Acidobacteria;Holophagae;Holophagales;Holophagaceae;Geothrix	3.21	2.24	0.19	0.00
Acidobacteria;Holophagae;Holophagales;Other;Other	0.54	0.16	0.06	0.04
Acidobacteria;iii1-8;DS-18	0.02	0.00	0.35	0.00
Acidobacteria;iii1-8;SJA-36	0.10	0.17	5.67	0.09
Acidobacteria;iii1-8;Other;Other;Other	0.04	0.02	0.13	0.01
Acidobacteria;Solibacteres;Solibacterales;Solibacteraceae;CandidatusSolibacter	0.50	0.10	0.13	0.04
Actinobacteria;Acidimicrobiia;Acidimicrobiales;C111	0.10	0.02	0.01	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Dietziaceae;Dietzia	0.00	0.23	0.00	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Geodermatophilaceae	0.00	0.12	0.04	0.00
Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Other	0.00	0.22	0.02	0.06
Actinobacteria;Actinobacteria;Actinomycetales;Other;Other	0.03	0.46	0.01	0.20
Actinobacteria;Actinobacteria;Bifidobacteriales;Bifidobacteriaceae;Bifidobacterium	0.01	0.11	0.05	0.01
Bacteroidetes;Bacteroidia;Bacteroidales	2.47	3.33	1.20	6.73
Bacteroidetes;Bacteroidia;Bacteroidales;BA008	0.22	0.61	0.11	0.21
Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0.02	0.11	0.04	0.55
Bacteroidetes;Bacteroidia;Bacteroidales;GZB119	0.07	0.61	0.37	0.01
Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Parabacteroides	0.01	0.20	0.06	1.30
Bacteroidetes;Flavobacteriia;Flavobacteriales;Cryomorphaceae	0.15	0.34	0.01	0.00
Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Flavobacterium	0.16	1.33	0.38	0.97
Bacteroidetes;Flavobacteriia;Flavobacteriales;Flavobacteriaceae;Other	0.02	0.31	0.21	0.13
Bacteroidetes;Flavobacteriia;Flavobacteriales;Other;Other	0.25	0.08	0.01	0.00
Bacteroidetes;Sphingobacteriia;Sphingobacteriales;;	4.79	0.24	0.01	0.00
Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Chitinophagaceae;	0.15	0.15	0.01	0.00
Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Cyclobacteriaceae;	0.02	0.42	0.00	0.00
Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Flammeovirgaceae;A4	0.13	0.01	0.00	0.00
Bacteroidetes;Sphingobacteriia;Sphingobacteriales;Other;Other	0.23	0.09	0.12	0.00
Bacteroidetes;Other;Other;Other;Other	0.96	0.56	0.07	2.30
BRC1;PRR-11	0.03	0.18	0.28	0.11
Chlorobi;Chlorobia;Chlorobiales;Chlorobiaceae;	0.02	0.02	0.01	0.58
Chlorobi;Ignavibacteria;Ignavibacteriales;Ignavibacteriaceae	0.41	0.06	0.02	0.03
Chlorobi;OPB56	0.20	0.27	0.06	0.09
Chlorobi;SJA-28	0.34	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolinaceae;	0.18	0.01	0.00	0.00
Chloroflexi;Anaerolineae;Anaerolineales;Anaerolinaceae;WCHB1-05	0.17	0.03	0.00	0.00
Chloroflexi;Anaerolineae;Caldilineales;Caldilineaceae	0.15	0.02	0.00	0.00
Chloroflexi;Anaerolineae;envOPS12	2.85	0.00	0.00	0.00
Chloroflexi;Anaerolineae;Other;Other;Other	0.78	0.00	0.00	0.00
Chloroflexi;TK17;mle1-48	1.26	0.00	0.00	0.00
Cyanobacteria;4C0d-2;MLE1-12	0.11	0.01	0.01	0.01
Cyanobacteria;4C0d-2;YS2	0.03	0.17	0.00	0.03
Cyanobacteria;Chloroplast;Stramenopiles	0.12	0.01	0.00	0.00
Cyanobacteria;Chloroplast;Streptophyta	0.12	0.00	0.00	0.01
Elusimicrobia;Elusimicrobia;Elusimicrobiales;Elusimicrobiaceae;Elusimicrobium	0.36	0.15	0.02	0.00
Firmicutes	0.02	0.59	0.01	0.03
Firmicutes;Clostridia;Clostridiales;Catabacteriaceae	0.07	0.61	0.01	0.15
Firmicutes;Clostridia;Clostridiales;Christensenellaceae	0.04	0.23	0.00	0.01
Firmicutes;Clostridia;Clostridiales;Clostridiaceae	0.05	0.29	0.04	0.09
Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Clostridium	0.04	0.18	0.00	0.01
Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Fusibacter	0.00	0.38	0.02	0.01
Firmicutes;Clostridia;Clostridiales;Peptococcaceae;	0.22	0.37	0.00	0.00
Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae;	0.02	0.14	0.10	0.08
Firmicutes;Clostridia;Clostridiales;Veillonellaceae;	0.00	0.31	0.26	0.36
Firmicutes;Clostridia;Clostridiales;Other;Other	0.05	0.15	0.01	0.11
Firmicutes;Clostridia;Coriobacteriales;Coriobacteriaceae;	0.10	0.12	0.01	0.00
Firmicutes;Clostridia;Other;Other;Other	0.03	0.11	0.02	0.02
Firmicutes;Erysipelotrichi;Erysipelotrichales;Erysipelotrichaceae;PSB-M-3	0.02	0.23	0.00	0.01
Fusobacteria;Fusobacteria	0.06	0.49	0.00	0.00
Gemmatimonadetes;Gemmatimonadetes	0.38	0.16	0.01	0.00
Gemmatimonadetes;Gemmatimonadetes;Gemmatimonadales;Gemmatimonadaceae;Gemmatimonas	0.00	0.51	0.00	0.00

Taxon	**Coke polarized**	**Coke**	**Gravel**	**Waste water**
Gemmatimonadetes;Gemmatimonadetes;KD8-87	0.45	0.04	0.00	0.00
GN02;BD1-5	0.02	1.02	0.00	0.02
Lentisphaerae;[Lentisphaeria];Victivallales;Victivallaceae;	0.01	0.08	0.03	0.62
Nitrospirae;Nitrospira;Nitrospirales;Thermodesulfovibrionaceae;GOUTA19	0.80	0.00	0.00	0.00
NKB19	0.10	0.08	0.30	0.18
NKB19;TSBW08	0.19	0.38	0.38	1.38
OD1;ZB2	1.68	0.01	0.00	0.00
OP11;OP11-4	0.36	0.00	0.00	0.00
OP3;koll11	0.44	0.00	0.00	0.00
OP3;PBS-25	0.56	0.03	0.00	0.06
Planctomycetes;[Brocadiae];Brocadiales;Brocadiaceae	1.71	0.00	0.00	0.00
Planctomycetes;C6;MVS-107	0.40	0.00	0.01	0.00
Planctomycetes;OM190;agg27	0.12	0.01	0.02	0.00
Planctomycetes;OM190;CL500-15	0.69	0.54	0.05	0.00
Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Phycisphaera	0.38	0.24	0.27	0.11
Planctomycetes;Planctomycetia;Pirellulales;Pirellulaceae	0.25	0.46	0.16	0.00
Proteobacteria;Alphaproteobacteria;BD7-3	0.50	0.87	0.52	0.02
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0.05	0.48	0.18	0.03
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Phenylobacterium	0.04	0.20	0.45	0.00
Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Other	0.10	0.38	0.27	0.06
Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Other	0.00	0.01	0.00	0.17
Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae;Other	0.05	0.03	0.46	0.01
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Devosia	0.02	0.19	0.03	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Rhodoplanes	0.23	0.15	0.27	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales;Phyllobacteriaceae;Other	0.01	0.12	0.01	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;	0.00	0.10	0.07	0.00
Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Other	0.06	0.46	1.10	0.05
Proteobacteria;Alphaproteobacteria;Rhizobiales;Other;Other	0.16	0.96	0.72	0.03
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Hyphomonadaceae;Hyphomonas	0.01	0.15	0.01	0.00
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacter	0.02	1.11	1.06	0.03
Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Other	0.13	0.90	2.16	0.03
Proteobacteria;Alphaproteobacteria;Rhodospirillales	0.17	0.03	0.79	0.00
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Acetobacteraceae;Roseomonas	0.01	0.11	0.18	0.25
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;	0.27	0.07	0.25	0.01
Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Oleomonas	0.04	0.00	0.00	2.91
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	0.03	0.18	0.14	0.04
Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingopyxis	0.02	0.22	0.09	0.00
Proteobacteria;Alphaproteobacteria;Other;Other;Other	0.22	0.17	0.14	0.18
Proteobacteria;Betaproteobacteria	0.17	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae;Other	0.00	0.09	0.02	0.82
Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;	0.31	0.31	0.77	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Aquabacterium	0.02	0.13	0.21	0.02
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Hydrogenophaga	0.43	0.65	0.35	5.47
Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Other	1.82	2.37	2.05	11.20
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Janthinobacterium	5.58	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Burkholderiales;Oxalobacteraceae;Other	0.20	0.02	0.01	0.00
Proteobacteria;Betaproteobacteria;Ellin6067	0.48	0.01	0.16	0.00
Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;	0.01	0.02	0.45	0.00
Proteobacteria;Betaproteobacteria;Hydrogenophilales;Hydrogenophilaceae;Thiobacillus	0.72	1.28	12.98	0.01
Proteobacteria;Betaproteobacteria;Methylophilales;Methylophilaceae;Methylotenera	0.02	0.10	0.01	0.56
Proteobacteria;Betaproteobacteria;Methylophilales;Other;Other	0.01	1.03	0.01	0.00
Proteobacteria;Betaproteobacteria;Nitrosomonadales;Nitrosomonadaceae;	0.17	0.17	0.01	0.00
Proteobacteria;Betaproteobacteria;Procabacteriales;Procabacteriaceae;	0.00	0.02	0.00	0.19
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dechloromonas	0.02	0.27	0.33	0.65
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Denitratisoma	0.22	0.23	0.01	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Dok59	1.63	0.94	2.05	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Methyloversatilis	0.11	0.24	0.51	0.07
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Propionivibrio	0.01	0.10	0.14	0.24
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Sterolibacterium	0.39	0.00	0.00	0.00
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Thauera	0.01	1.41	1.20	0.19
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Zoogloea	0.00	0.02	0.10	0.17
Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Other	1.94	1.29	1.69	0.07
Proteobacteria;Betaproteobacteria;SC-I-84	0.12	0.01	0.04	0.00
Proteobacteria;Betaproteobacteria;Thiobacterales;;	0.42	0.22	2.58	0.00
Proteobacteria;Betaproteobacteria;Thiobacterales;Other;Other	0.03	0.43	1.02	0.03
Proteobacteria;Betaproteobacteria;Other;Other;Other	2.25	2.20	4.55	6.91

Taxon	**Coke polarized**	**Coke**	**Gravel**	**Waste water**
Proteobacteria;Deltaproteobacteria	0.05	0.18	0.00	0.06
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoracaceae;	0.07	0.20	0.02	0.00
Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrio	0.20	0.04	0.02	0.00
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;	20.72	17.83	2.23	0.01
Proteobacteria;Deltaproteobacteria;Desulfobacterales;Desulfobulbaceae;Desulfobulbus	0.01	0.09	0.24	0.12
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfomicrobiaceae;Desulfomicrobium	0.03	0.40	0.75	0.41
Proteobacteria;Deltaproteobacteria;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio	0.01	0.16	0.11	0.51
Proteobacteria;Deltaproteobacteria;Desulfurellales	0.02	0.06	0.02	0.24
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Geobacter	0.25	2.88	0.28	0.45
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Geobacteraceae;Other	0.14	2.72	1.36	3.39
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Pelobacteraceae;	0.06	0.96	1.30	0.00
Proteobacteria;Deltaproteobacteria;Desulfuromonadales;Other;Other	0.25	0.18	1.10	0.02
Proteobacteria;Deltaproteobacteria;Myxococcales	0.09	0.27	0.02	0.00
Proteobacteria;Deltaproteobacteria;Myxococcales;0319-6G20;	0.11	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Myxococcales;Myxococcaceae;Anaeromyxobacter	0.12	0.00	0.01	0.00
Proteobacteria;Deltaproteobacteria;Myxococcales;Other;Other	0.36	0.00	0.00	0.00
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Desulfobacteraceae;	0.01	0.45	0.20	0.08
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Desulfobacteraceae;Desulfobacter	0.01	0.19	0.23	0.37
Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Desulfobacteraceae;Other	0.09	0.16	0.05	0.05
Proteobacteria;Deltaproteobacteria;Other;Other;Other	0.36	0.13	0.02	0.03
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	0.05	2.90	2.21	3.70
Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas	1.00	1.64	1.38	0.00
Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;	0.01	0.03	0.05	0.11
Proteobacteria;Gammaproteobacteria;Alteromonadales;[Chromatiaceae];Rheinheimera	0.57	0.01	0.00	0.21
Proteobacteria;Gammaproteobacteria;Alteromonadales;125ds10;	0.16	0.38	1.63	0.00
Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Other	0.01	0.17	0.11	0.00
Proteobacteria;Gammaproteobacteria;Chromatiales;;	0.03	1.24	0.01	0.00
Proteobacteria;Gammaproteobacteria;Chromatiales;Halothiobacillaceae;Thiovirga	0.01	0.01	0.02	0.49
Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Other	0.00	0.01	2.64	0.00
Proteobacteria;Gammaproteobacteria;FCPT525;FCPT525;	0.09	0.01	0.30	0.02
Proteobacteria;Gammaproteobacteria;HTCC2188;;	0.08	0.00	0.15	0.00
Proteobacteria;Gammaproteobacteria;HTCC2188;HTCC2188;HTCC	0.47	0.20	0.00	0.00
Proteobacteria;Gammaproteobacteria;Legionellales;Francisellaceae;Francisella	0.00	0.00	0.00	5.02
Proteobacteria;Gammaproteobacteria;Methylococcales;Methylococcaceae;Methylomonas	0.21	0.01	0.10	0.01
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	0.00	0.05	0.06	0.20
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	0.04	0.25	0.67	1.39
Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Other	0.06	0.45	0.59	15.18
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Sinobacteraceae;	0.29	0.04	0.04	0.27
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Sinobacteraceae;Other	0.66	0.00	1.36	0.00
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;	0.15	0.83	0.13	0.01
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Aquimonas	0.01	0.36	0.01	0.19
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Arenimonas	0.11	1.36	4.90	0.00
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Pseudoxanthomonas	0.05	0.04	0.11	0.01
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0.00	0.01	0.02	0.72
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Thermomonas	0.48	1.63	5.74	0.05
Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Other	0.11	0.39	0.55	0.16
Proteobacteria;Gammaproteobacteria;Other;Other;Other	2.09	0.64	0.98	2.11
Proteobacteria;Other;Other;Other;Other	0.90	0.34	0.26	0.29
Spirochaetes;[Leptospirae];[Leptospirales];Leptospiraceae;Leptospira	0.15	0.00	0.00	0.00
Spirochaetes;[Leptospirae];[Leptospirales];Sediment-4;	0.13	0.01	0.01	0.02
Spirochaetes;MVP-15;PL-11B10;;	0.04	0.24	0.02	0.00
Spirochaetes;Spirochaetes;Spirochaetales;Spirochaetaceae;Treponema	0.06	0.09	0.41	0.02
Spirochaetes;WWE1;[Cloacamonales];[Cloacamonaceae];W22	0.04	0.05	0.02	0.97
Synergistetes;Synergistia;Synergistales;Dethiosulfovibrionaceae;HA73	0.01	0.25	0.51	0.35
Synergistetes;Synergistia;Synergistales;Dethiosulfovibrionaceae;PD-UASB-13	0.00	0.06	0.09	0.16
Synergistetes;Synergistia;Synergistales;Synergistaceae;	0.00	0.02	0.01	0.67
Synergistetes;Synergistia;Synergistales;Synergistaceae;vadinCA02	0.03	0.25	0.45	2.20
Tenericutes;Mollicutes	0.11	0.04	0.00	0.00
Tenericutes;Mollicutes;Acholeplasmatales;Acholeplasmataceae;	0.01	0.37	0.00	0.00
Verrucomicrobia;[Methylacidiphilae]	0.11	0.00	0.00	0.00
Verrucomicrobia;[Pedosphaerae];[Pedosphaerales]	0.17	0.01	0.02	0.02
Verrucomicrobia;[Pedosphaerae];[Pedosphaerales];Ellin515;	0.05	0.15	0.43	0.04
Verrucomicrobia;[Pedosphaerae];[Pedosphaerales];R4-41B;	0.01	0.12	0.07	0.90
Verrucomicrobia;[Pedosphaerae];[Pedosphaerales];Other;Other	0.16	0.09	0.16	0.02
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;	0.44	0.43	0.44	0.01
Verrucomicrobia;Opitutae;Opitutales;Opitutaceae;Opitutus	0.68	0.23	0.16	0.01

Taxon	**Coke polarized**	**Coke**	**Gravel**	**Waste water**
Verrucomicrobia;Verruco-5;WCHB1-41;RFP12;	0.05	0.66	0.53	0.41
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Luteolibacter	0.00	0.05	0.13	0.09
Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;Prosthecobacter	0.08	0.35	0.18	0.01
WS3;PRR-12;GN03;;	0.19	1.98	2.11	0.47
WS3;PRR-12;GN03;KSB4;	0.56	0.01	0.31	0.00
WS3;PRR-12;GN03;Other;Other	0.14	0.00	0.00	0.00
WS5	0.04	0.11	0.00	0.00
Unclassified;Other;Other;Other;Other;Other	2.29	2.33	2.35	2.20

Table 7S Main genera of bacteria identified in the analyzed communities (over 0.1), in percentage.

Genus	Coke polarized biofilter	Coke biofilter	Gravel biofilter	Waste water
A4	0.13	0.01	0.01	0.01
Acinetobacter	0.00	0.05	0.06	0.20
Anaeromyxobacter	0.12	0.00	0.01	0.00
Aquabacterium	0.02	0.13	0.21	0.02
Aquimonas	0.01	0.36	0.01	0.19
Arcobacter	0.05	2.90	2.21	3.70
Arenimonas	0.11	1.36	4.90	0.00
Bacteroides	0,02	0,11	0,04	0,55
Bdellovibrio	0.20	0.04	0.02	0.00
Bifidobacterium	0.03	0.46	0.01	0.20
Brevundimonas	0.05	0.48	0.18	0.03
Candidatus solibacter	0.50	0.10	0.13	0.04
Clostridium	0.04	0.18	0.00	0.01
Dechloromonas	0.02	0.27	0.33	0.65
Denitratisoma	0.22	0.23	0.01	0.00
Desulfobacter	0.01	0.19	0.23	0.37
Desulfobulbus	0.01	0.09	0.24	0.12
Desulfobulbaceae	20,72	17,83	2,23	0,01
Desulfomicrobium	0.03	0.40	0.75	0.41
Desulfovibrio	0,01	0,16	0,11	0,51
Devosia	0,02	0,19	0,03	0,00
Dietzia	0.00	0.23	0.00	0.00
Dok59	1,63	0,94	2,05	0,00
Flavobacterium	0,16	1,33	0,38	0,97
Francisella	0.00	0.00	0.00	5.02
Fusibacter	0.00	0.38	0.02	0.01
Gemmatimonas	0.01	0.51	0.01	0.01
Geobacter	0,25	2,88	0,28	0,45
Geobacteraceae (family)	0,14	2,72	1,36	3,39
Geothrix	3,21	2,24	0,19	0,00
GOUTA19	0.80	0.00	0.00	0.00
HA73	0,01	0,25	0,51	0,35
HTCC	0.47	0.20	0.00	0.00
Hydrogenophaga	0,43	0,65	0,35	5,47
Hyphomonas	0.01	0.15	0.01	0.00
Janthinobacterium	5.58	0.00	0.00	0.00
Leptospira	0.15	0.00	0.00	0.00
Luteolibacter	0.00	0.05	0.13	0.09
Methylomonas	0.21	0.01	0.10	0.01
Methylotenera	0.02	0.10	0.01	0.56
Methyloversatilis	0.11	0.24	0.51	0.07
Nitrosomonadaceae (family)	0.17	0.17	0.01	0.00
Novosphingobium	0.03	0.18	0.14	0.04
Oleomonas	0.04	0.0	0.0	2.91
Opitutus	0.68	0.23	0.16	0.01
Parabacteroides	0.01	0.20	0.06	1.30
PD-UASB-13	0.00	0.06	0.09	0.16
Phenylobacterium	0.04	0.20	0.45	0.00
Phycisphaera	0.38	0.24	0.27	0.11
Propionivibrio	0.01	0.10	0.14	0.24
Prosthecobacter	0.08	0.35	0.18	0.01
PSB-M-3	0.02	0.23	0.00	0.01
Pseudomonas	0.04	0.25	0.67	1.35
Pseudonomadaceae (family)	0.06	0.45	0.59	15.18
Pseudoxanthomonas	0.05	0.04	0.11	0.01
Rheinheimera	0.57	0.01	0.00	0.21
Rhodobacter	0.02	1.11	1.06	0.03
Rhodoplanes	0.23	0.15	0.27	0.00
Roseomonas	0.01	0.11	0.18	0.25
Sphingopyxis	0.02	0.22	0.09	0.00
Stenotrophomonas	0.00	0.01	0.02	0.72
Sterolibacterium	0.39	0.00	0.00	0.00
Sulfurimonas	1.00	1.64	1.38	0.00
Thauera	0.01	1.41	1.20	0.19
Thermomonas	0.48	1.63	5.74	0.05
Thiobacillus	0.72	1.28	12.98	0.01
Thiovirga	0.01	0.01	0.02	0.49
Treponema	0.06	0.09	0.41	0.02
vadinCA02	0.03	0.25	0.45	2.20
W22	0.04	0.05	0.02	0.97
WCHB1-05	0.17	0.03	0.00	0.00
Zoogloea	0.00	0.02	0.10	0.17