Water Research

Supplementary Material for:

Characterizing and Contrasting the Microbial Ecology of Laboratory and Full-scale EBPR Systems Cultured on Synthetic and Real Wastewaters

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This supplementary material contains four sections with additional data for the bulk solution performance of the lab-scale EBPR reactors (Section S1), qPCR (Section S2), genus-level Illuminia sequencing (Section S3), and BLASTN analyses (Section S4).

Section S1. EBPR performance

Table S1. EBPR bioreactor organic carbon utilization data.

Parameter	Units	Reactor	Average	SD	n
Anaerobic VFA uptake	$mg_{COD}\,L^{-1}$	S-EBPR	182.73	32.97	14
		V-EBPR	56.00	18.79	13
		G-EBPR	12.39	9.24	8
		R-EBPR	11.48	10.65	8
	$Cmmol\,L^{-1}$	S-EBPR	4.97	0.97	14
		V-EBPR	1.58	0.53	13
		G-EBPR	0.36	0.27	8
		R-EBPR	0.34	0.31	8
Anaerobic Glycogen Consumption	Cmmol	S-EBPR	3.60	1.25	4
		V-EBPR	2.55	1.24	5
		G-EBPR	2.62	0.94	4
		R-EBPR	0.00	0.12	4
Anaerobic PHA synthesis	Cmmol	S-EBPR	28.70	29.43	6
		V-EBPR	3.96	1.48	6
		G-EBPR	2.72	1.75	6
		R-EBPR	1.36	1.63	6

Table S2. Summary of anaerobic EBPR stoichiometric parameters.

Parameter	Units	Reactor	Average	SD	n
Anaerobic Phosphorus Release (P(rel))	$mg\,L^{-1}$	S-EBPR	65.31	22.42	38
		V-EBPR	10.03	5.59	38
		G-EBPR	0.87	1.16	17
		R-EBPR	2.66	1.91	17
Anaerobic P(rel):VFA(uptake) (P:C ratio)	$Pmol\,Cmol^{-1}$	S-EBPR	0.46	0.14	11
		V-EBPR	0.19	0.13	11
		G-EBPR	0.04	0.06	7
		R-EBPR	0.06	0.09	8
Anaerobic PHA:(Glycogen+VFAs+Glycerol)	$Cmmol\,Cmmol^{-1}$	S-EBPR	1.37	0.46	
		V-EBPR	0.71	0.30	
		G-EBPR	0.66	0.48	
		R-EBPR	0.52	0.51	
Anaerobic PHA:MLSS	$Cmmol\,g_{TSS}^{-1}$	S-EBPR	3.57	4.44	7
		V-EBPR	0.84	0.32	7
		G-EBPR	0.62	0.43	7
		R-EBPR	0.49	0.59	7

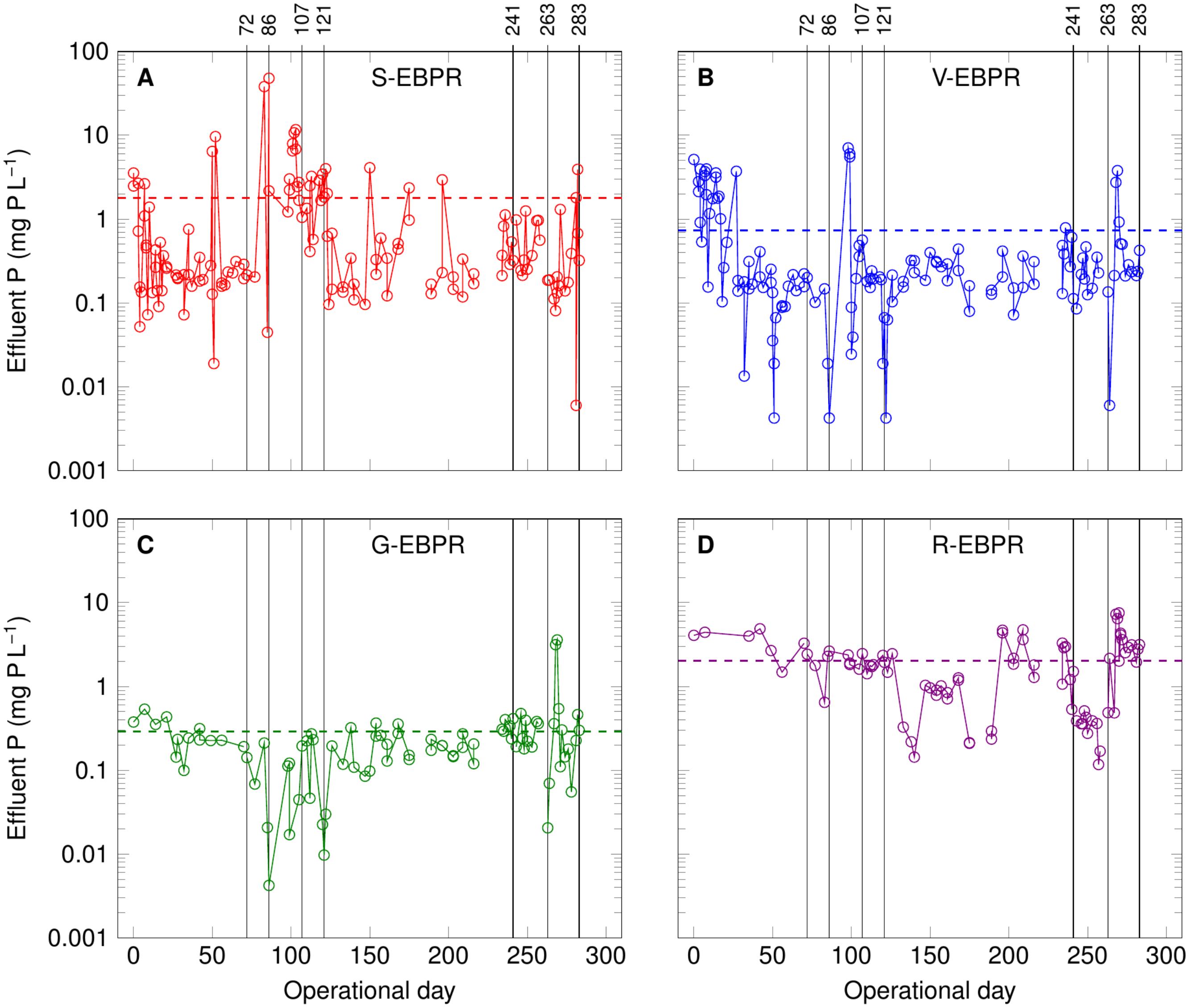

Figure S1. Effluent phosphorus for the four laboratory SBRs (**A**: S-EBPR, **B**: V-EBPR, **C**: G-EBPR, and **D**: R-EBPR) over the operational period. The thick dashed line in each denotes the average effluent phosphorus over the entire operational period. Solid vertical lines indicate the operational days on which system assessments occured.

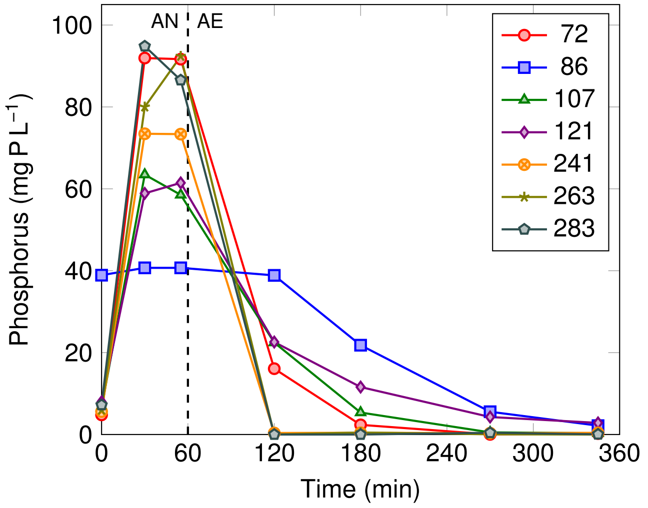

Figure S2. Intra-cycle bulk solution P for S-EBPR over a full SBR operational cycle on days 72, 86, 107, 121, 241, 263, and 283.

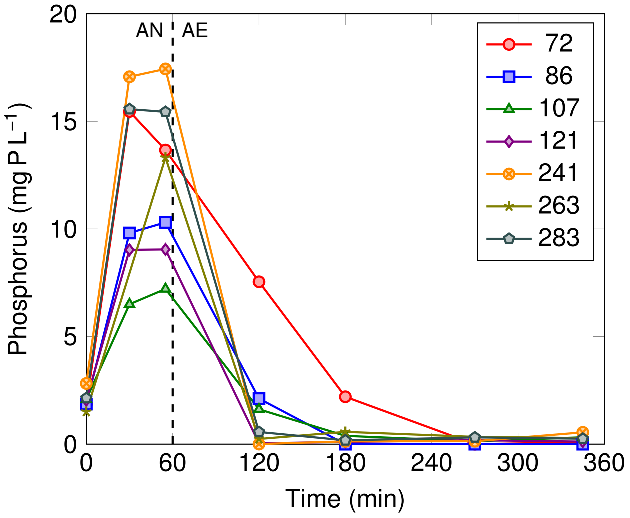

Figure S3. Intra-cycle bulk solution P for V-EBPR over a full SBR operational cycle on days 72, 86, 107, 121, 241, 263, and 283.

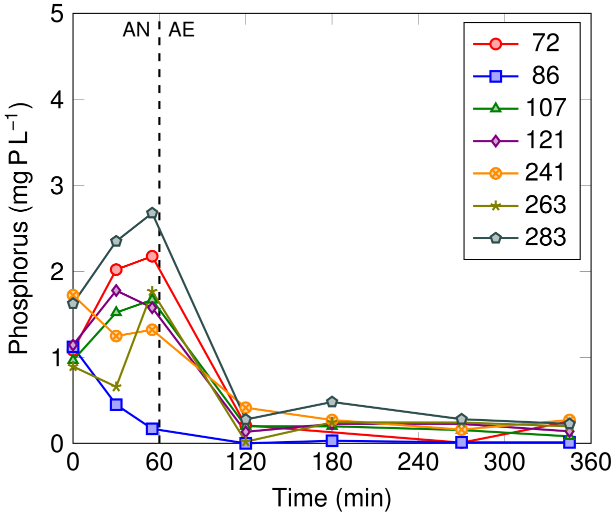

Figure S4. Intra-cycle bulk solution P for G-EBPR over a full SBR operational cycle on days 72, 86, 107, 121, 241, 263, and 283.

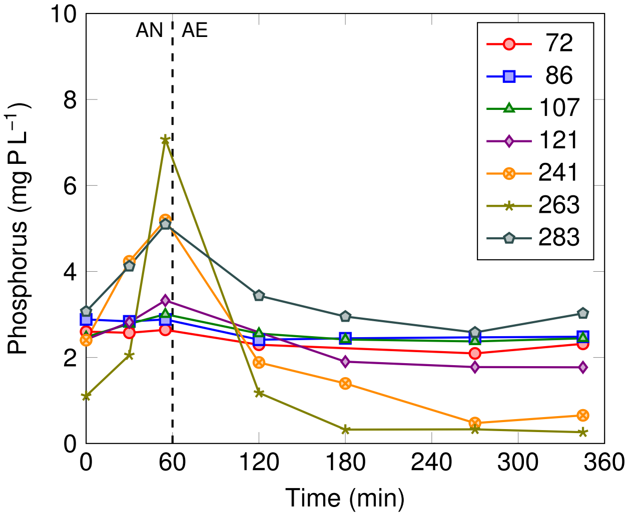

Figure S5. Intra-cycle bulk solution P for R-EBPR over a full SBR operational cycle on days 72, 86, 107, 121, 241, 263, and 283.

Section S2. qPCR results

Table S3. Results from quantitative PCR applied to DNA extracted from MLSS obtained from each reactor. Data shown for each operational day include average and standard deviation for triplicate analysis on each 96-well plate (P1, P2, P3) and a composite average.

qPCR Plate	S-EBPR		V-EBPR		G-EBPR		R-EBPR	
	PAOs Avg ± SD[a]	GAOs Avg ± SD[a]	PAOs Avg ± SD[a]	GAOs Avg ± SD[a]	PAOs Avg ± SD[a]	GAOs Avg ± SD[a]	PAOs Avg ± SD[a]	GAOs Avg ± SD[a]
Operational day 72								
P1	4.51 ± 0.27	0.32 ± 0.01	0.80 ± 0.14	0.68 ± 0.02	0.42 ± 0.05	0.08 ± 0.00	0.67 ± 0.08	0.07 ± 0.03
P2	3.62 ± 0.47	0.15 ± 0.02	0.57 ± 0.10	0.42 ± 0.04	0.54 ± 0.11	0.04 ± 0.00	0.42 ± 0.01	0.04 ± 0.00
P3	4.37 ± 0.41	0.15 ± 0.05	0.65 ± 0.03	0.25 ± 0.02	0.24 ± 0.03	0.02 ± 0.00	0.47 ± 0.05	0.02 ± 0.00
Composite	4.17 ± 0.53	0.21 ± 0.09	0.67 ± 0.13	0.45 ± 0.19	0.40 ± 0.14	0.05 ± 0.02	0.52 ± 0.12	0.04 ± 0.03
Operational day 86								
P1	5.07 ± 0.60	0.57 ± 0.03	0.40 ± 0.02	2.26 ± 0.67	0.28 ± 0.06	0.23 ± 0.01	1.44 ± 0.07	0.04 ± 0.00
P2	3.97 ± 0.49	0.28 ± 0.03	0.37 ± 0.04	1.96 ± 0.32	0.28 ± 0.02	0.13 ± 0.02	0.92 ± 0.04	0.02 ± 0.00
P3	4.39 ± 0.25	0.20 ± 0.02	0.43 ± 0.13	1.13 ± 0.12	0.27 ± 0.00	0.08 ± 0.00	1.06 ± 0.25	0.01 ± 0.00
Composite	4.48 ± 0.63	0.35 ± 0.17	0.40 ± 0.07	1.78 ± 0.63	0.27 ± 0.03	0.14 ± 0.07	1.14 ± 0.27	0.02 ± 0.01
Operational day 107								
P1	3.53 ± 0.05	0.24 ± 0.03	0.11 ± 0.02	0.01 ± 0.00	0.25 ± 0.04	0.10 ± 0.01	0.58 ± 0.09	0.00 ± 0.00
P2	5.49 ± 1.10	0.98 ± 0.10	0.15 ± 0.01	0.06 ± 0.01	0.32 ± 0.00	0.34 ± 0.02	0.79 ± 0.10	0.02 ± 0.00
P3	3.24 ± 0.15	0.39 ± 0.03	0.10 ± 0.02	0.04 ± 0.00	0.21 ± 0.05	0.24 ± 0.04	0.51 ± 0.05	0.01 ± 0.00
Composite	4.09 ± 1.19	0.54 ± 0.34	0.12 ± 0.03	0.04 ± 0.02	0.26 ± 0.06	0.23 ± 0.11	0.62 ± 0.14	0.01 ± 0.01
Operational day 121								
P1	4.63 ± 0.21	0.07 ± 0.00	0.39 ± 0.07	0.14 ± 0.03	0.29 ± 0.08	0.22 ± 0.03	0.14 ± 0.03	0.01 ± 0.00
P2	2.59 ± 0.13	0.08 ± 0.00	0.19 ± 0.02	0.16 ± 0.02	0.39 ± 0.00	0.75 ± 0.05	0.22 ± 0.04	0.07 ± 0.02
P3	1.54 ± 0.15	0.04 ± 0.01	0.15 ± 0.01	0.11 ± 0.01	0.27 ± 0.04	0.47 ± 0.03	0.15 ± 0.01	0.04 ± 0.00
Composite	2.92 ± 1.37	0.06 ± 0.02	0.24 ± 0.12	0.14 ± 0.03	0.32 ± 0.07	0.48 ± 0.23	0.17 ± 0.05	0.04 ± 0.03
Operational day 241								
P1	4.82 ± 1.21	0.11 ± 0.02	0.16 ± 0.04	1.95 ± 0.31	0.27 ± 0.06	0.65 ± 0.09	0.13 ± 0.05	0.01 ± 0.00
P2	8.10 ± 0.16	0.04 ± 0.00	0.30 ± 0.04	0.68 ± 0.04	0.63 ± 0.03	0.24 ± 0.01	0.19 ± 0.01	0.00 ± 0.00
P3	3.33 ± 0.43	0.06 ± 0.01	0.18 ± 0.06	0.92 ± 0.03	0.38 ± 0.10	0.32 ± 0.02	0.16 ± 0.02	0.00 ± 0.00
Composite	5.42 ± 2.21	0.07 ± 0.03	0.21 ± 0.08	1.18 ± 0.61	0.42 ± 0.17	0.40 ± 0.19	0.16 ± 0.04	0.00 ± 0.00
Operational day 263								
P1	0.55 ± 0.13	0.06 ± 0.02	0.28 ± 0.09	1.94 ± 0.17	0.46 ± 0.13	0.70 ± 0.02	0.06 ± 0.05	0.00 ± 0.00
P2	0.71 ± 0.05	0.02 ± 0.00	0.58 ± 0.03	0.66 ± 0.04	0.83 ± 0.02	0.19 ± 0.01	0.16 ± 0.00	0.00 ± 0.00
P3	0.58 ± 0.11	0.03 ± 0.00	0.41 ± 0.10	1.04 ± 0.07	1.08 ± 0.18	0.48 ± 0.04	0.13 ± 0.01	0.00 ± 0.00
Composite	0.61 ± 0.11	0.04 ± 0.02	0.42 ± 0.15	1.21 ± 0.58	0.79 ± 0.29	0.45 ± 1.32	0.11 ± 0.05	0.00 ± 0.00
Operational day 283								
P1	18.18 ± 1.01	0.12 ± 0.01	3.09 ± 0.53	3.24 ± 0.51	0.84 ± 0.28	2.56 ± 0.54	0.38 ± 0.01	0.03 ± 0.01
P2	10.49 ± 0.79	0.21 ± 0.02	2.03 ± 0.17	4.36 ± 0.59	0.70 ± 0.27	4.87 ± 1.55	0.21 ± 0.04	0.04 ± 0.01
P3	16.75 ± 1.70	0.16 ± 0.01	2.67 ± 0.15	3.58 ± 0.19	0.91 ± 0.16	3.55 ± 0.47	0.39 ± 0.03	0.04 ± 0.00
Composite	15.14 ± 3.70	0.16 ± 0.04	2.60 ± 0.54	3.73 ± 0.64	0.82 ± 0.23	3.66 ± 1.32	0.33 ± 0.09	0.03 ± 0.01

[a] Average and sample standard deviation with $n = 3$.

Table S4. qPCR primer sets for total eubacteria, PAOs, and GAOs.

Name	Sequence (5’–3’)	Specificity	Reference
EUB: Eubacterial 16S rRNA gene			
338f	`ACTCCTACGGGAGGCAGCAG`	Bacteria	(Huse et al., 2008)
533r	`TTACCGCGGCTGCTGGCAC`	Bacteria	(Huse et al., 2008)
PAO: Polyphosphate accumulating organisms 16S rRNA gene			
518f	`CCAGCAGCCGCGGTAAT`	Bacteria	(He et al., 2007)
846r	`GTTAGCTACGGCACTAAAAGG`	PAOs	(Crocetti et al., 2002)
GAO: Glycogen accumulating organisms 16S rRNA gene			
GAOQ431f	`AAGCCCTTTAGGCGGGGA`	*Candidatus* Competibacter phosphatis	(Crocetti et al., 2002)
GAOQ989r	`TTCCCCGGATGTCAAGGC`	*Candidatus* Competibacter phosphatis	(Crocetti et al., 2002)

Section S3. Genus-level Illumina sequencing results

Table S5. Tables summarizing the 16S rRNA gene sequencing results by primer set, system, and taxonomic level.

Reactor	domain	phylum	class	order	family	genus
EUB primer set						
S-EBPR	S14	S20	S26	S32	S38	S44
V-EBPR	S15	S21	S27	S33	S39	S45
G-EBPR	S16	S22	S28	S34	S40	S46
R-EBPR	S17	S23	S29	S35	S41	S47
Moscow WRRF	S18	S24	S30	S36	S42	S48
Summary	S19	S25	S31	S37	S43	S49
PAO primer set						
S-EBPR	S57	S63	S69	S75	S81	S87
V-EBPR	S58	S64	S70	S76	S82	S88
G-EBPR	S59	S65	S71	S77	S83	S89
R-EBPR	S60	S66	S72	S78	S84	S90
Moscow WRRF	S61	S67	S73	S79	S85	S91
Summary	S62	S68	S74	S80	S86	S92
GAO primer set						
S-EBPR	S100	S106	S112	S118	S124	S130
V-EBPR	S101	S107	S113	S119	S125	S131
G-EBPR	S102	S108	S114	S120	S126	S132
R-EBPR	S103	S109	S115	S121	S127	S133
Moscow WRRF	S104	S110	S116	S122	S128	S134
Summary	S105	S111	S117	S123	S129	S135

Table S6. PCR primers for DNA amplicon generation (first round[a]) for sequencing with Illumina MiSeq.

Name	Sequence (5'–3')[b,c,d]
EUB: Eubacterial 16S rRNA gene	
27F-1	ACACTGACGACATGGTTCTACA**GTAGAGTTTGATCCTGGCTCAG**
27F-2	ACACTGACGACATGGTTCTACAC**GTAGAGTTTGATCATGGCTCAG**
27F-3	ACACTGACGACATGGTTCTACAAC**GTAGAGTTTGATTCTGGCTCAG**
27F-4	ACACTGACGACATGGTTCTACATAC**GTAGAGTTTGATTATGGCTCAG**
533R-1	TACGGTAGCAGAGACTTGGTCT**TTACCGCGGCTGCTGGCAC**
533R-2	TACGGTAGCAGAGACTTGGTCTG**TTACCGCGGCTGCTGGCAC**
533R-3	TACGGTAGCAGAGACTTGGTCTTG**TTACCGCGGCTGCTGGCAC**
533R-4	TACGGTAGCAGAGACTTGGTCTATG**TTACCGCGGCTGCTGGCAC**
PAO: Polyphosphate accumulating organisms 16S rRNA gene	
518F-1	ACACTGACGACATGGTTCTACA**CCAGCAGCCGCGGTAAT**
518F-2	ACACTGACGACATGGTTCTACAC**CCAGCAGCCGCGGTAAT**
518F-3	ACACTGACGACATGGTTCTACAAC**CCAGCAGCCGCGGTAAT**
518F-4	ACACTGACGACATGGTTCTACATAC**CCAGCAGCCGCGGTAAT**
846R-PAO1	TACGGTAGCAGAGACTTGGTCT**GTTAGCTACGGCACTAAAAGG**
846R-PAO2	TACGGTAGCAGAGACTTGGTCTG**GTTAGCTACGGCACTAAAAGG**
846R-PAO3	TACGGTAGCAGAGACTTGGTCTTG**GTTAGCTACGGCACTAAAAGG**
846R-PAO4	TACGGTAGCAGAGACTTGGTCTATG**GTTAGCTACGGCACTAAAAGG**
GAO: Glycogen accumulating organisms 16S rRNA gene	
431F-GAO1	ACACTGACGACATGGTTCTACA**AAGCCCTTTAGGCGGGGA**
431F-GAO2	ACACTGACGACATGGTTCTACAC**AAGCCCTTTAGGCGGGGA**
431F-GAO3	ACACTGACGACATGGTTCTACAAC**AAGCCCTTTAGGCGGGGA**
431F-GAO4	ACACTGACGACATGGTTCTACATAC**AAGCCCTTTAGGCGGGGA**
989R-GAO1	TACGGTAGCAGAGACTTGGTCT**TTCCCCGGATGTCAAGGC**
989R-GAO1	TACGGTAGCAGAGACTTGGTCTG**TTCCCCGGATGTCAAGGC**
989R-GAO1	TACGGTAGCAGAGACTTGGTCTTG**TTCCCCGGATGTCAAGGC**
989R-GAO1	TACGGTAGCAGAGACTTGGTCTATG**TTCCCCGGATGTCAAGGC**

[a] Following the first round of PCR with the primers listed above, a second round of PCR was performed to attach the Illumina-specific adapter sequences and unique sequence barcodes with the adapter primers P7-CS2 and P5-CS1 given by `P7-NNNNNNNNTACGGTAGCAGAGACTTGGTCT` and `P5-NNNNNNNNACACTGACGACATGGTTCTACA`, respectively, where P7 and P5 are the Illumina-specific adapter sequences and `NNNNNNNN` denotes the eight bases constituting the unique sequence barcode. The underlined bases are the same as in the primers above[b].

[b] Underlined bases correspond to the universal tag sequences CS1 (`ACACTGACGACATGGTTCTACA`) and CS2 (`TACGGTAGCAGAGACTTGGTCT`) for forward and reverse primers, respectively.

[c] Highlighted bases were added to introduce base call variability during the Illumina sequencing.

[d] Bold bases denote the respective 16S rRNA primer sequences (e.g., the universal 27F for 27F-1 to 27F-4; the universal 533R for 533R-1 to 533R-4; the universal 518F for 518F-1 to 518F-4 (He et al., 2007); PAO846 for 846R-PAO1 to 846R-PAO4 (Crocetti et al., 2000); GAOQ431 for 431F-GAO1 to 431F-GAO4 (Crocetti et al., 2002); GAOQ989 for 989R-GAO1 to 989R-GAO4 (Crocetti et al., 2002).

EUB primer set

Diversity metrics

Table S7. Sample diversity and evenness indices and richness estimates using the EUB primer set.

Operational day	Total reads	Total phylotypes	Major[a] phylotypes	Minor[b] phylotypes	H'[c]	R[d]	D[e]	S_{Chao1}[f]
S-EBPR								
72	40 801	298	21	277	3.90	0.69	0.96	359.22
86	74 359	336	21	315	3.61	0.62	0.94	405.09
107	57 770	315	18	297	3.52	0.61	0.93	356.59
121	55 175	304	18	286	3.39	0.59	0.91	349.03
241	104 835	372	20	352	3.70	0.63	0.95	492.21
263	88 684	402	23	379	3.85	0.64	0.95	512.03
283	81 841	300	17	283	3.36	0.59	0.93	386.25
V-EBPR								
72	60 230	496	20	476	4.07	0.66	0.96	597.00
86	66 185	473	19	454	3.57	0.58	0.92	566.65
107	67 995	441	20	421	3.62	0.59	0.94	534.07
121	76 395	473	16	457	3.66	0.59	0.94	533.76
241	101 373	602	17	585	4.00	0.63	0.94	696.32
263	6 428	322	21	301	4.21	0.73	0.96	413.11
283	37 887	425	26	399	4.19	0.69	0.96	506.02
G-EBPR								
72	67 027	487	19	468	3.75	0.61	0.92	622.13
86	70 389	533	19	514	3.92	0.62	0.96	640.35
107	61 488	452	18	434	3.62	0.59	0.94	596.28
121	72 010	509	27	482	4.06	0.65	0.97	645.18
241	99 125	606	21	585	4.01	0.63	0.96	778.52
263	75 414	593	22	571	4.33	0.68	0.97	702.25
283	1 208	154	19	135	3.89	0.77	0.94	191.25
R-EBPR								
72	44 916	455	22	433	3.98	0.65	0.95	541.04
86	57 159	460	20	440	3.71	0.61	0.91	575.56
107	59 757	471	21	450	3.87	0.63	0.94	550.22
121	56 336	429	21	408	3.81	0.63	0.95	496.04
241	79 844	563	24	539	4.31	0.68	0.97	697.64
263	67 562	575	23	552	4.26	0.67	0.96	700.10
283	74 690	406	16	390	3.53	0.59	0.90	485.00
Moscow WRRF								
225	80 207	707	21	686	4.73	0.72	0.98	858.21
255	116 631	772	19	753	4.87	0.73	0.98	974.29
270	85 256	743	23	720	4.77	0.72	0.98	911.10
284	78 823	709	20	689	4.70	0.72	0.98	910.33
304	91 185	708	25	683	4.58	0.70	0.98	853.00
313	85 041	702	28	674	4.71	0.72	0.98	825.40

Table S7. Sample diversity and evenness indices and richness estimates using the EUB primer set continued.

Operational day	Total reads	Total phylotypes	Major[a] phylotypes	Minor[b] phylotypes	H'[c]	R[d]	D[e]	S_{Chao1}[f]
320	90 397	676	28	648	4.64	0.71	0.98	791.00

[a] Major phylotypes constitute at least 1% of the total relative abundance.

[b] Minor phylotypes constitute less than 1% of the total relative abundance.

[c] Shannon diversity index, given by $H' = -\sum_{i=1}^{S} \left(p_i \cdot \ln p_i\right)$ where S is the total number of phylotypes and p_i is the relative abundance of the i-th phylotype (Shannon, 1948).

[d] Pielou evenness index, given by $R = \frac{H'}{\ln S}$ where H' is the Shannon diversity index and S is the total number of phylotypes.

[e] Simpson's diversity index, given by $D = 1 - \sum_{i=1}^{S} p_i^2$ where S is the total number of phylotypes and p_i is the relative abundance of the i-th phylotype (Simpson, 1949).

[f] Bias-corrected Chao1 richness estimate, given by $S_{\text{Chao1}} = S + \frac{n+1}{n} \cdot \frac{F_1 \cdot (F_1 - 1)}{2 \cdot (F_2 + 1)}$ where S is the total number of phylotypes, n is the total number of sequences, F_1 is the total number of phylotypes to which only one sequence was assigned, and F_2 is the total number of phylotypes to which only two sequences were assigned.

Rarefaction analysis

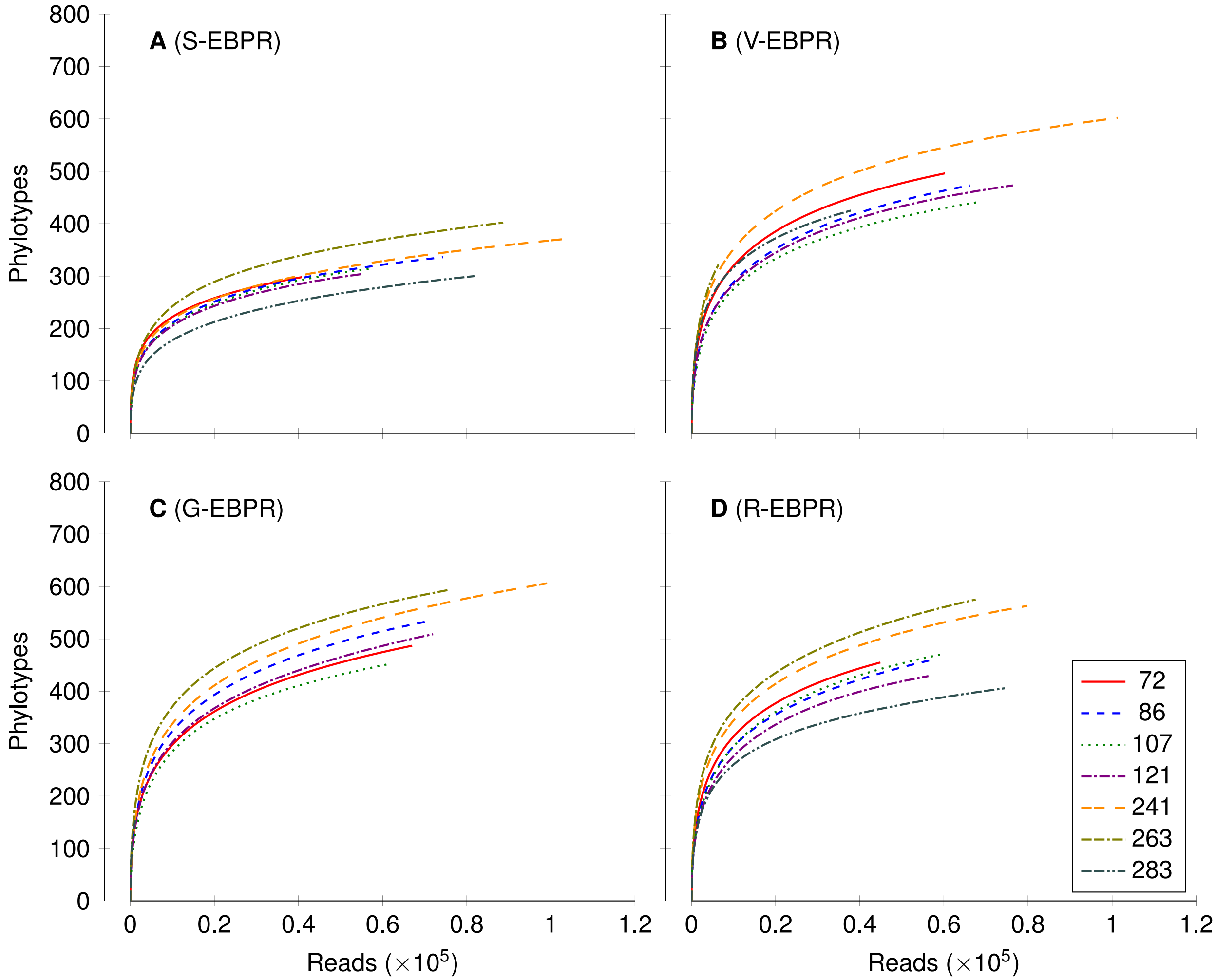

Figure S6. Rarefaction curves for the EUB primer set results for each lab-scale EBPR reactor.

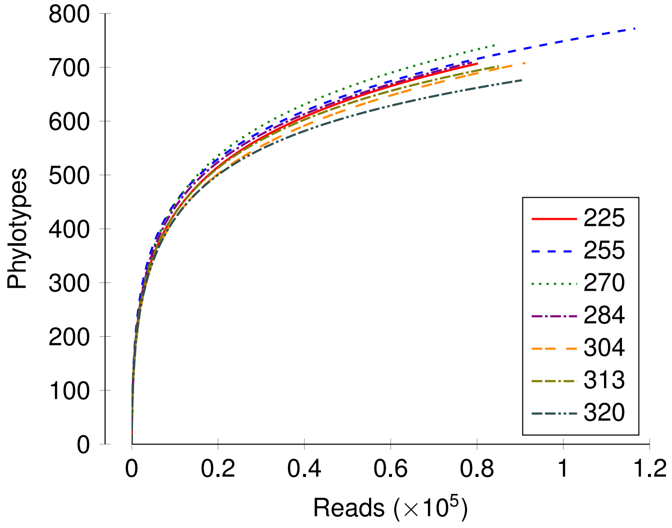

Figure S7. Rarefaction curves for the EUB primer set results for the Moscow WRRF.

Cluster analysis

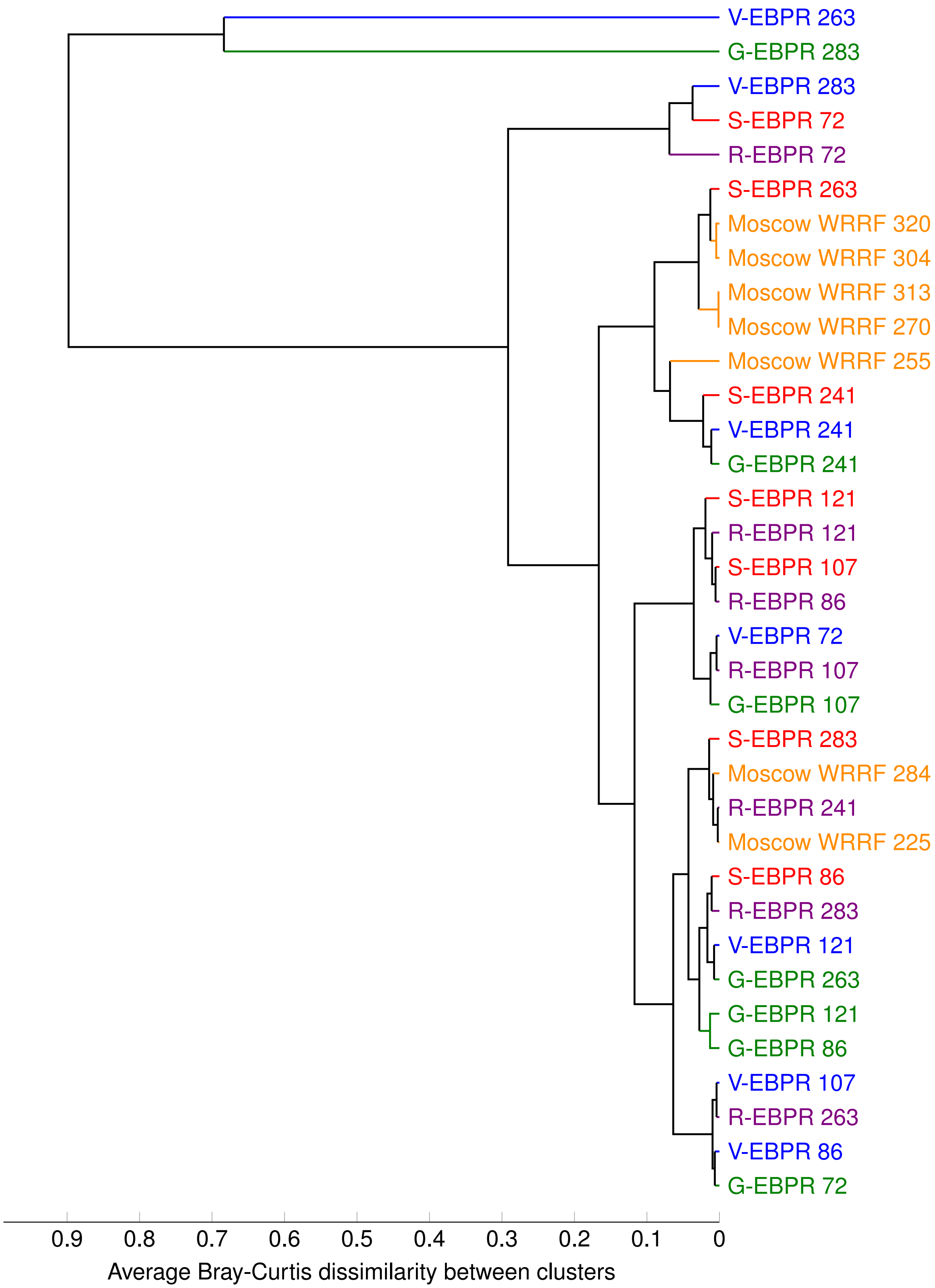

Figure S8. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the domain level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

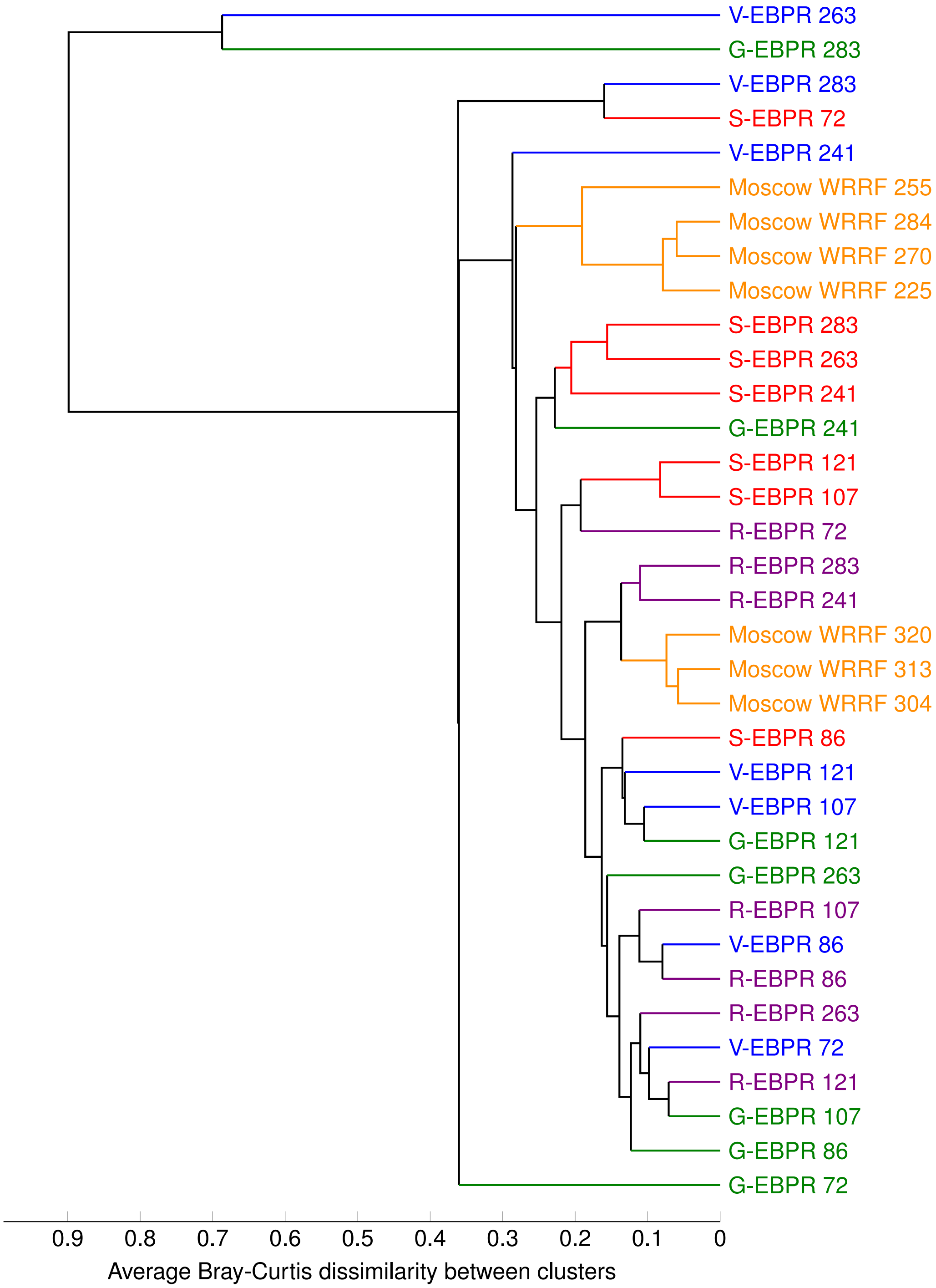

Figure S9. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the phylum level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

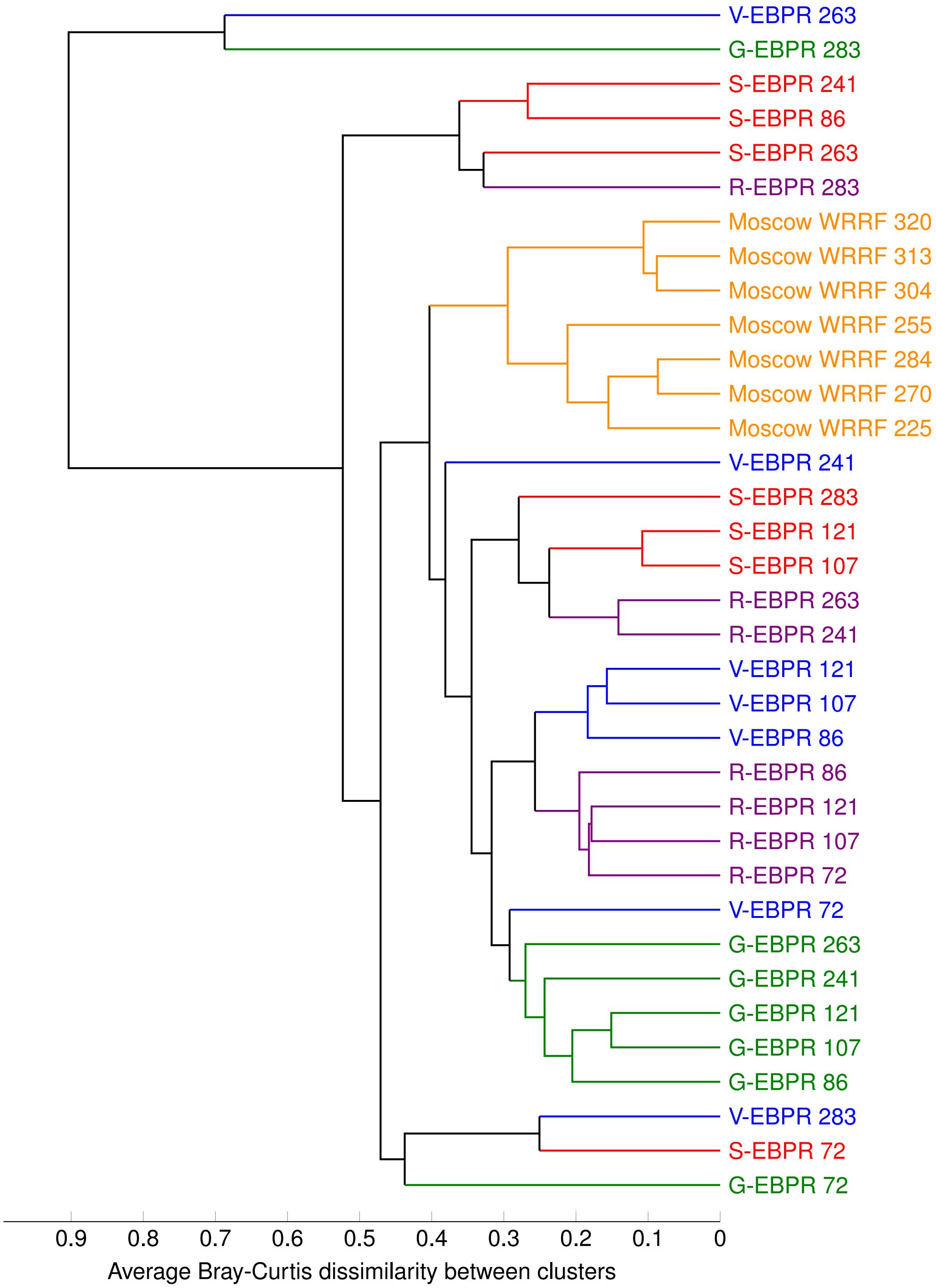

Figure S10. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the class level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

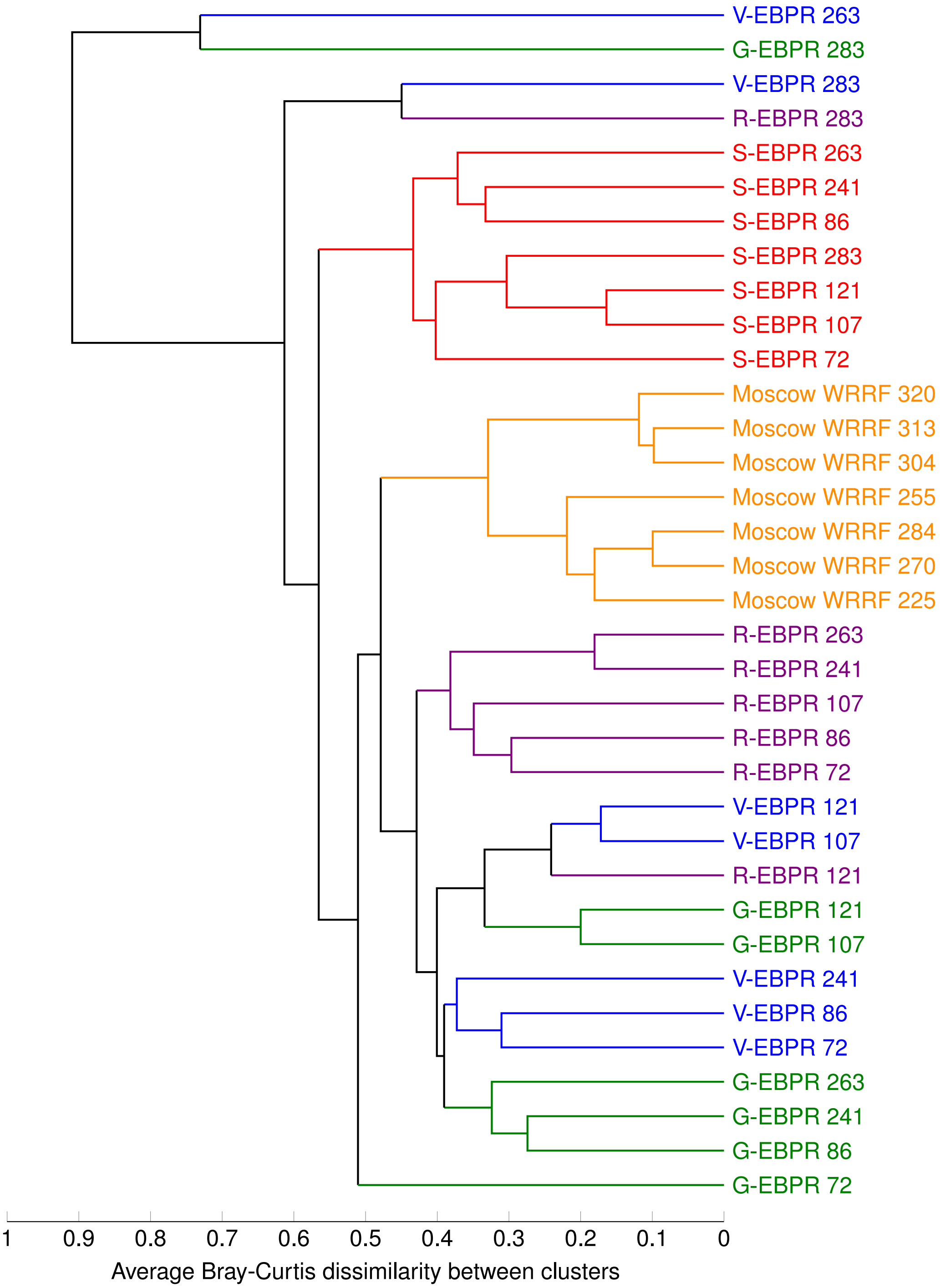

Figure S11. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the order level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

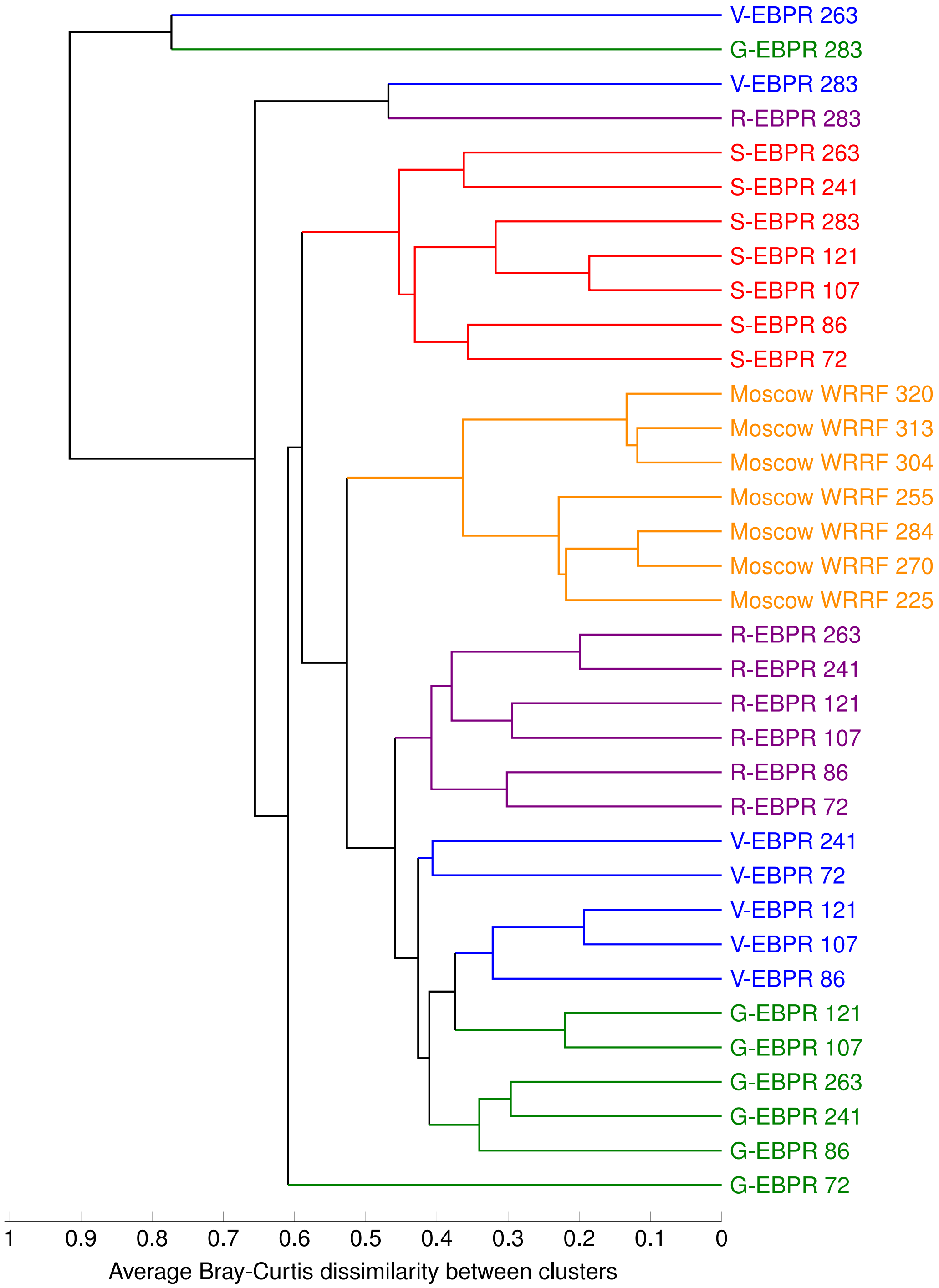

Figure S12. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the family level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

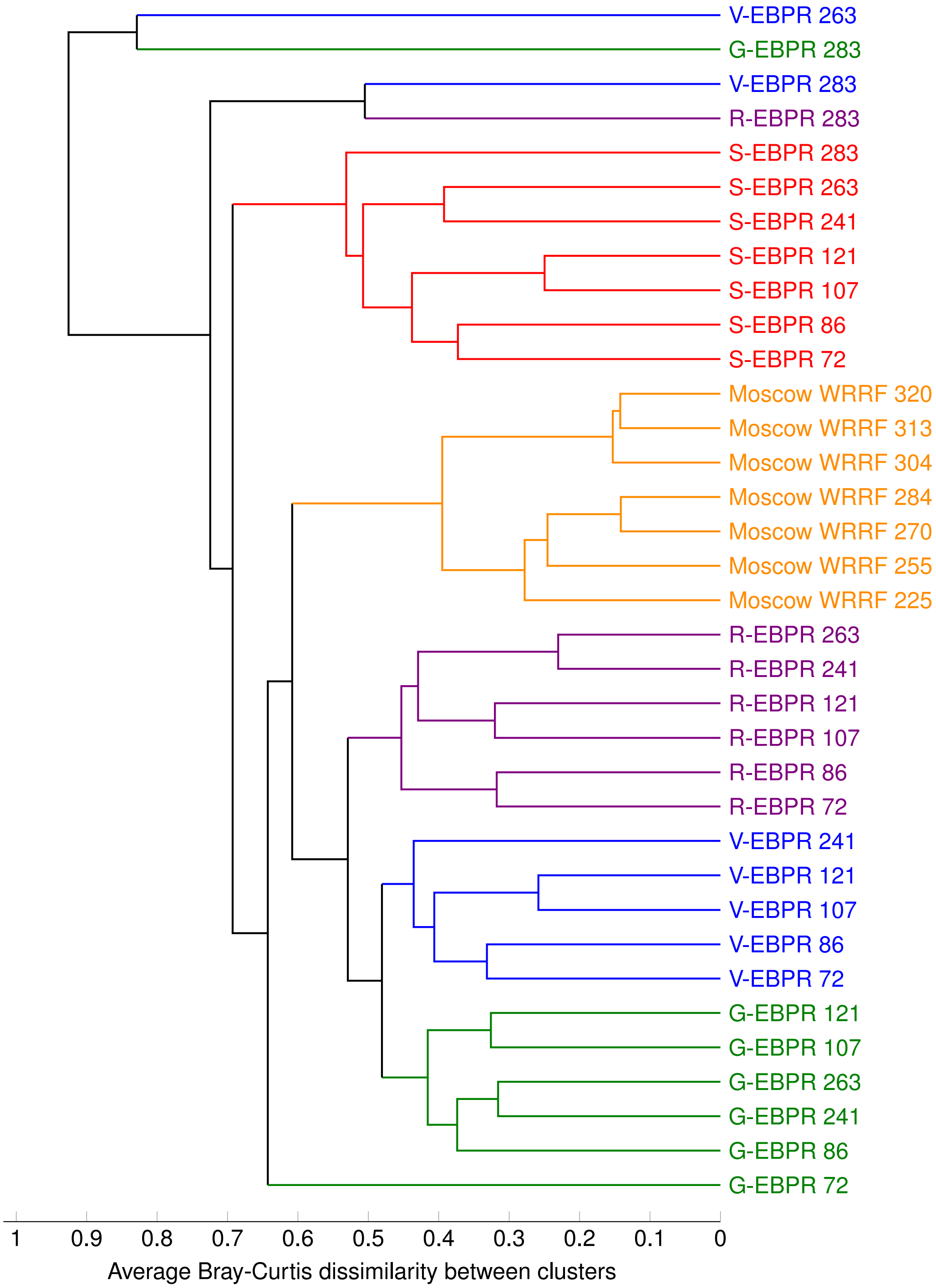

Figure S13. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the genus level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

Table S8. Dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the domain level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	37	0																																	
	107	45	46	0																																
	121	39	45	25	0																															
	241	53	40	47	48	0																														
	263	55	46	58	59	39	0																													
	283	56	55	45	57	50	55	0																												
V-EBPR	72	68	72	67	70	74	73	72	0																											
	86	74	76	69	75	78	78	76	33	0																										
	107	73	72	63	67	69	79	71	45	39	0																									
	121	73	71	57	62	70	77	74	43	36	26	0																								
	241	76	76	72	76	78	78	78	44	42	47	42	0																							
	263	88	92	90	90	94	93	93	83	83	85	85	88	0																						
	283	64	71	72	72	78	75	80	67	74	75	75	72	84	0																					
G-EBPR	72	70	71	74	74	74	75	81	64	69	71	68	71	86	73	0																				
	86	67	67	62	69	70	70	68	50	44	48	48	50	85	72	49	0																			
	107	72	71	59	71	74	75	56	55	53	54	55	53	84	73	63	38	0																		
	121	72	71	63	72	74	74	71	43	41	46	45	45	86	71	59	39	33	0																	
	241	74	73	68	75	75	75	74	46	44	50	48	44	89	72	53	33	45	36	0																
	263	67	71	69	71	75	73	76	45	44	53	51	46	86	67	57	42	47	44	32	0															
	283	97	98	98	98	99	98	98	97	98	98	98	98	83	94	98	98	97	98	98	98	0														
R-EBPR	72	75	79	76	76	80	79	78	53	55	55	57	60	80	68	67	57	64	60	62	59	96	0													
	86	75	77	76	77	78	78	80	60	42	51	51	58	84	73	69	54	66	63	60	59	97	32	0												
	107	66	69	62	67	72	76	69	56	41	46	47	57	85	70	67	48	59	56	55	54	97	45	38	0											
	121	64	66	57	58	64	74	71	55	48	36	35	57	84	74	61	46	57	54	55	54	97	48	43	32	0										
	241	63	64	59	63	65	72	67	51	53	47	48	53	87	66	60	48	57	52	50	51	98	47	49	44	41	0									
	263	64	66	61	63	69	74	72	55	51	48	47	50	85	64	64	49	56	52	49	48	97	46	46	43	44	23	0								
	283	65	63	72	71	71	72	78	75	82	83	81	77	92	50	76	73	77	76	75	73	97	80	83	77	78	70	69	0							
Moscow WRRF	225	64	65	64	65	67	71	69	60	65	68	68	59	89	67	65	61	63	55	60	59	98	67	68	63	65	54	53	65	0						
	255	67	64	67	68	66	68	70	61	68	67	69	57	92	72	68	64	63	55	59	62	98	72	72	67	70	56	56	70	28	0					
	270	61	61	63	64	64	67	69	58	65	65	65	55	90	68	64	56	57	50	55	58	98	68	69	66	65	53	49	66	26	20	0				
	284	62	62	62	64	65	68	69	58	64	64	65	56	89	68	64	56	58	52	57	58	98	67	68	65	64	54	50	68	29	29	14	0			
	304	65	63	60	64	63	68	65	58	58	63	65	60	90	73	68	55	58	50	57	60	98	69	68	60	65	60	58	72	39	42	39	37	0		
	313	64	61	59	63	61	66	63	58	59	64	65	61	90	71	68	55	56	49	57	59	98	68	68	59	64	58	57	71	38	39	36	36	14	0	
	320	66	66	61	64	64	70	66	59	59	63	65	61	90	73	70	57	59	52	59	61	98	69	69	58	66	60	59	74	42	44	42	41	16	14	0

Table S9. Dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the phylum level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	37	0																																	
	107	45	46	0																																
	121	39	45	25	0																															
	241	53	40	47	48	0																														
	263	55	46	58	59	39	0																													
	283	56	55	45	57	50	55	0																												
V-EBPR	72	68	72	67	70	74	73	72	0																											
	86	74	76	69	75	78	78	76	33	0																										
	107	73	72	63	67	69	79	71	45	39	0																									
	121	73	71	57	62	70	77	74	43	36	26	0																								
	241	76	76	72	76	78	78	78	44	42	47	42	0																							
	263	88	92	90	90	94	93	93	83	83	85	85	88	0																						
	283	64	71	72	72	78	75	80	67	74	75	75	72	84	0																					
G-EBPR	72	70	71	74	74	74	75	81	64	69	71	68	71	86	73	0																				
	86	67	67	62	69	70	70	68	50	44	48	48	50	85	72	49	0																			
	107	72	71	59	71	74	75	56	55	53	54	55	53	84	73	63	38	0																		
	121	72	71	63	72	74	74	71	43	41	46	45	45	86	71	59	39	33	0																	
	241	74	73	68	75	75	75	74	46	44	50	48	44	89	72	53	33	45	36	0																
	263	67	71	69	71	75	73	76	45	44	53	51	46	86	67	57	42	47	44	32	0															
	283	97	98	98	98	99	98	98	97	98	98	98	98	83	94	98	98	97	98	98	98	0														
R-EBPR	72	75	79	76	76	80	79	78	53	55	55	57	60	80	68	67	57	64	60	62	59	96	0													
	86	75	77	76	77	78	78	80	60	42	51	51	58	84	73	69	54	66	63	60	59	97	32	0												
	107	66	69	62	67	72	76	69	56	41	46	47	57	85	70	67	48	59	56	55	54	97	45	38	0											
	121	64	66	57	58	64	74	71	55	48	36	35	57	84	74	61	46	57	54	55	54	97	48	43	32	0										
	241	63	64	59	63	65	72	67	51	53	47	48	53	87	66	60	48	57	52	50	51	98	47	49	44	41	0									
	263	64	66	61	63	69	74	72	55	51	48	47	50	85	64	64	49	56	52	49	48	97	46	46	43	44	23	0								
	283	65	63	72	71	71	72	78	75	82	83	81	77	92	50	76	73	77	76	75	73	97	80	83	77	78	70	69	0							
Moscow WRRF	225	64	65	64	65	67	71	69	60	65	68	68	59	89	67	65	61	63	55	60	59	98	67	68	63	65	54	53	65	0						
	255	67	64	67	68	66	68	70	61	68	67	69	57	92	72	68	64	63	55	59	62	98	72	72	67	70	56	56	70	28	0					
	270	61	61	63	64	64	67	69	58	65	65	65	55	90	68	64	56	57	50	55	58	98	68	69	66	65	53	49	66	26	20	0				
	284	62	62	62	64	65	68	69	58	64	64	65	56	89	68	64	56	58	52	57	58	98	67	68	65	64	54	50	68	29	29	14	0			
	304	65	63	60	64	63	68	65	58	58	63	65	60	90	73	68	55	58	50	57	60	98	69	68	60	65	60	58	72	39	42	39	37	0		
	313	64	61	59	63	61	66	63	58	59	64	65	61	90	71	68	55	56	49	57	59	98	68	68	59	64	58	57	71	38	39	36	36	14	0	
	320	66	66	61	64	64	70	66	59	59	63	65	61	90	73	70	57	59	52	59	61	98	69	69	58	66	60	59	74	42	44	42	41	16	14	0

Table S10. Dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the class level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	37	0																																	
	107	45	46	0																																
	121	39	45	25	0																															
	241	53	40	47	48	0																														
	263	55	46	58	59	39	0																													
	283	56	55	45	57	50	55	0																												
V-EBPR	72	68	72	67	70	74	73	72	0																											
	86	74	76	69	75	78	78	76	33	0																										
	107	73	72	63	67	69	79	71	45	39	0																									
	121	73	71	57	62	70	77	74	43	36	26	0																								
	241	76	76	72	76	78	78	78	44	42	47	42	0																							
	263	88	92	90	90	94	93	93	83	83	85	85	88	0																						
	283	64	71	72	72	78	75	80	67	74	75	75	72	84	0																					
G-EBPR	72	70	71	74	74	74	75	81	64	69	71	68	71	86	73	0																				
	86	67	67	62	69	70	70	68	50	44	48	48	50	85	72	49	0																			
	107	72	71	59	71	74	75	56	55	53	54	55	53	84	73	63	38	0																		
	121	72	71	63	72	74	74	71	43	41	46	45	45	86	71	59	39	33	0																	
	241	74	73	68	75	75	75	74	46	44	50	48	44	89	72	53	33	45	36	0																
	263	67	71	69	71	75	73	76	45	44	53	51	46	86	67	57	42	47	44	32	0															
	283	97	98	98	98	99	98	98	97	98	98	98	98	83	94	98	98	97	98	98	98	0														
R-EBPR	72	75	79	76	76	80	79	78	53	55	55	57	60	80	68	67	57	64	60	62	59	96	0													
	86	75	77	76	77	78	78	80	60	42	51	51	58	84	73	69	54	66	63	60	59	97	32	0												
	107	66	69	62	67	72	76	69	56	41	46	47	57	85	70	67	48	59	56	55	54	97	45	38	0											
	121	64	66	57	58	64	74	71	55	48	36	35	57	84	74	61	46	57	54	55	54	97	48	43	32	0										
	241	63	64	59	63	65	72	67	51	53	47	48	53	87	66	60	48	57	52	50	51	98	47	49	44	41	0									
	263	64	66	61	63	69	74	72	55	51	48	47	50	85	64	64	49	56	52	49	48	97	46	46	43	44	23	0								
	283	65	63	72	71	71	72	78	75	82	83	81	77	92	50	76	73	77	76	75	73	97	80	83	77	78	70	69	0							
Moscow WRRF	225	64	65	64	65	67	71	69	60	65	68	68	59	89	67	65	61	63	55	60	59	98	67	68	63	65	54	53	65	0						
	255	67	64	67	68	66	68	70	61	68	67	69	57	92	72	68	64	63	55	59	62	98	72	72	67	70	56	56	70	28	0					
	270	61	61	63	64	64	67	69	58	65	65	65	55	90	68	64	56	57	50	55	58	98	68	69	66	65	53	49	66	26	20	0				
	284	62	62	62	64	65	68	69	58	64	64	65	56	89	68	64	56	58	52	57	58	98	67	68	65	64	54	50	68	29	29	14	0			
	304	65	63	60	64	63	68	65	58	58	63	65	60	90	73	68	55	58	50	57	60	98	69	68	60	65	60	58	72	39	42	39	37	0		
	313	64	61	59	63	61	66	63	58	59	64	65	61	90	71	68	55	56	49	57	59	98	68	68	59	64	58	57	71	38	39	36	36	14	0	
	320	66	66	61	64	64	70	66	59	59	63	65	61	90	73	70	57	59	52	59	61	98	69	69	58	66	60	59	74	42	44	42	41	16	14	0

Table S11. Dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the order level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	37	0																																	
	107	45	46	0																																
	121	39	45	25	0																															
	241	53	40	47	48	0																														
	263	55	46	58	59	39	0																													
	283	56	55	45	57	50	55	0																												
V-EBPR	72	68	72	67	70	74	73	72	0																											
	86	74	76	69	75	78	78	76	33	0																										
	107	73	72	63	67	69	79	71	45	39	0																									
	121	73	71	57	62	70	77	74	43	36	26	0																								
	241	76	76	72	76	78	78	78	44	42	47	42	0																							
	263	88	92	90	90	94	93	93	83	83	85	85	88	0																						
	283	64	71	72	72	78	75	80	67	74	75	75	72	84	0																					
G-EBPR	72	70	71	74	74	74	75	81	64	69	71	68	71	86	73	0																				
	86	67	67	62	69	70	70	68	50	44	48	48	50	85	72	49	0																			
	107	72	71	59	71	74	75	56	55	53	54	55	53	84	73	63	38	0																		
	121	72	71	63	72	74	74	71	43	41	46	45	45	86	71	59	39	33	0																	
	241	74	73	68	75	75	75	74	46	44	50	48	44	89	72	53	33	45	36	0																
	263	67	71	69	71	75	73	76	45	44	53	51	46	86	67	57	42	47	44	32	0															
	283	97	98	98	98	99	98	98	97	98	98	98	98	83	94	98	98	97	98	98	98	0														
R-EBPR	72	75	79	76	76	80	79	78	53	55	55	57	60	80	68	67	57	64	60	62	59	96	0													
	86	75	77	76	77	78	78	80	60	42	51	51	58	84	73	69	54	66	63	60	59	97	32	0												
	107	66	69	62	67	72	76	69	56	41	46	47	57	85	70	67	48	59	56	55	54	97	45	38	0											
	121	64	66	57	58	64	74	71	55	48	36	35	57	84	74	61	46	57	54	55	54	97	48	43	32	0										
	241	63	64	59	63	65	72	67	51	53	47	48	53	87	66	60	48	57	52	50	51	98	47	49	44	41	0									
	263	64	66	61	63	69	74	72	55	51	48	47	50	85	64	64	49	56	52	49	48	97	46	46	43	44	23	0								
	283	65	63	72	71	71	72	78	75	82	83	81	77	92	50	76	73	77	76	75	73	97	80	83	77	78	70	69	0							
Moscow WRRF	225	64	65	64	65	67	71	69	60	65	68	68	59	89	67	65	61	63	55	60	59	98	67	68	63	65	54	53	65	0						
	255	67	64	67	68	66	68	70	61	68	67	69	57	92	72	68	64	63	55	59	62	98	72	72	67	70	56	56	70	28	0					
	270	61	61	63	64	64	67	69	58	65	65	65	55	90	68	64	56	57	50	55	58	98	68	69	66	65	53	49	66	26	20	0				
	284	62	62	62	64	65	68	69	58	64	64	65	56	89	68	64	56	58	52	57	58	98	67	68	65	64	54	50	68	29	29	14	0			
	304	65	63	60	64	63	68	65	58	58	63	65	60	90	73	68	55	58	50	57	60	98	69	68	60	65	60	58	72	39	42	39	37	0		
	313	64	61	59	63	61	66	63	58	59	64	65	61	90	71	68	55	56	49	57	59	98	68	68	59	64	58	57	71	38	39	36	36	14	0	
	320	66	66	61	64	64	70	66	59	59	63	65	61	90	73	70	57	59	52	59	61	98	69	69	58	66	60	59	74	42	44	42	41	16	14	0

Table S12. Dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the family level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	37	0																																	
	107	45	46	0																																
	121	39	45	25	0																															
	241	53	40	47	48	0																														
	263	55	46	58	59	39	0																													
	283	56	55	45	57	50	55	0																												
V-EBPR	72	68	72	67	70	74	73	72	0																											
	86	74	76	69	75	78	78	76	33	0																										
	107	73	72	63	67	69	79	71	45	39	0																									
	121	73	71	57	62	70	77	74	43	36	26	0																								
	241	76	76	72	76	78	78	78	44	42	47	42	0																							
	263	88	92	90	90	94	93	93	83	83	85	85	88	0																						
	283	64	71	72	72	78	75	80	67	74	75	75	72	84	0																					
G-EBPR	72	70	71	74	74	74	75	81	64	69	71	68	71	86	73	0																				
	86	67	67	62	69	70	70	68	50	44	48	48	50	85	72	49	0																			
	107	72	71	59	71	74	75	56	55	53	54	55	53	84	73	63	38	0																		
	121	72	71	63	72	74	74	71	43	41	46	45	45	86	71	59	39	33	0																	
	241	74	73	68	75	75	75	74	46	44	50	48	44	89	72	53	33	45	36	0																
	263	67	71	69	71	75	73	76	45	44	53	51	46	86	67	57	42	47	44	32	0															
	283	97	98	98	98	99	98	98	97	98	98	98	98	83	94	98	98	97	98	98	98	0														
R-EBPR	72	75	79	76	76	80	79	78	53	55	55	57	60	80	68	67	57	64	60	62	59	96	0													
	86	75	77	76	77	78	78	80	60	42	51	51	58	84	73	69	54	66	63	60	59	97	32	0												
	107	66	69	62	67	72	76	69	56	41	46	47	57	85	70	67	48	59	56	55	54	97	45	38	0											
	121	64	66	57	58	64	74	71	55	48	36	35	57	84	74	61	46	57	54	55	54	97	48	43	32	0										
	241	63	64	59	63	65	72	67	51	53	47	48	53	87	66	60	48	57	52	50	51	98	47	49	44	41	0									
	263	64	66	61	63	69	74	72	55	51	48	47	50	85	64	64	49	56	52	49	48	97	46	46	43	44	23	0								
	283	65	63	72	71	71	72	78	75	82	83	81	77	92	50	76	73	77	76	75	73	97	80	83	77	78	70	69	0							
Moscow WRRF	225	64	65	64	65	67	71	69	60	65	68	68	59	89	67	65	61	63	55	60	59	98	67	68	63	65	54	53	65	0						
	255	67	64	67	68	66	68	70	61	68	67	69	57	92	72	68	64	63	55	59	62	98	72	72	67	70	56	56	70	28	0					
	270	61	61	63	64	64	67	69	58	65	65	65	55	90	68	64	56	57	50	55	58	98	68	69	66	65	53	49	66	26	20	0				
	284	62	62	62	64	65	68	69	58	64	64	65	56	89	68	64	56	58	52	57	58	98	67	68	65	64	54	50	68	29	29	14	0			
	304	65	63	60	64	63	68	65	58	58	63	65	60	90	73	68	55	58	50	57	60	98	69	68	60	65	60	58	72	39	42	39	37	0		
	313	64	61	59	63	61	66	63	58	59	64	65	61	90	71	68	55	56	49	57	59	98	68	68	59	64	58	57	71	38	39	36	36	14	0	
	320	66	66	61	64	64	70	66	59	59	63	65	61	90	73	70	57	59	52	59	61	98	69	69	58	66	60	59	74	42	44	42	41	16	14	0

Table S13. Dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the genus level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	37	0																																	
	107	45	46	0																																
	121	39	45	25	0																															
	241	53	40	47	48	0																														
	263	55	46	58	59	39	0																													
	283	56	55	45	57	50	55	0																												
V-EBPR	72	68	72	67	70	74	73	72	0																											
	86	74	76	69	75	78	78	76	33	0																										
	107	73	72	63	67	69	79	71	45	39	0																									
	121	73	71	57	62	70	77	74	43	36	26	0																								
	241	76	76	72	76	78	78	78	44	42	47	42	0																							
	263	88	92	90	90	94	93	93	83	83	85	85	88	0																						
	283	64	71	72	72	78	75	80	67	74	75	75	72	84	0																					
G-EBPR	72	70	71	74	74	74	75	81	64	69	71	68	71	86	73	0																				
	86	67	67	62	69	70	70	68	50	44	48	48	50	85	72	49	0																			
	107	72	71	59	71	74	75	56	55	53	54	55	53	84	73	63	38	0																		
	121	72	71	63	72	74	74	71	43	41	46	45	45	86	71	59	39	33	0																	
	241	74	73	68	75	75	75	74	46	44	50	48	44	89	72	53	33	45	36	0																
	263	67	71	69	71	75	73	76	45	44	53	51	46	86	67	57	42	47	44	32	0															
	283	97	98	98	98	99	98	98	97	98	98	98	98	83	94	98	98	97	98	98	98	0														
R-EBPR	72	75	79	76	76	80	79	78	53	55	55	57	60	80	68	67	57	64	60	62	59	96	0													
	86	75	77	76	77	78	78	80	60	42	51	51	58	84	73	69	54	66	63	60	59	97	32	0												
	107	66	69	62	67	72	76	69	56	41	46	47	57	85	70	67	48	59	56	55	54	97	45	38	0											
	121	64	66	57	58	64	74	71	55	48	36	35	57	84	74	61	46	57	54	55	54	97	48	43	32	0										
	241	63	64	59	63	65	72	67	51	53	47	48	53	87	66	60	48	57	52	50	51	98	47	49	44	41	0									
	263	64	66	61	63	69	74	72	55	51	48	47	50	85	64	64	49	56	52	49	48	97	46	46	43	44	23	0								
	283	65	63	72	71	71	72	78	75	82	83	81	77	92	50	76	73	77	76	75	73	97	80	83	77	78	70	69	0							
Moscow WRRF	225	64	65	64	65	67	71	69	60	65	68	68	59	89	67	65	61	63	55	60	59	98	67	68	63	65	54	53	65	0						
	255	67	64	67	68	66	68	70	61	68	67	69	57	92	72	68	64	63	55	59	62	98	72	72	67	70	56	56	70	28	0					
	270	61	61	63	64	64	67	69	58	65	65	65	55	90	68	64	56	57	50	55	58	98	68	69	66	65	53	49	66	26	20	0				
	284	62	62	62	64	65	68	69	58	64	64	65	56	89	68	64	56	58	52	57	58	98	67	68	65	64	54	50	68	29	29	14	0			
	304	65	63	60	64	63	68	65	58	58	63	65	60	90	73	68	55	58	50	57	60	98	69	68	60	65	60	58	72	39	42	39	37	0		
	313	64	61	59	63	61	66	63	58	59	64	65	61	90	71	68	55	56	49	57	59	98	68	68	59	64	58	57	71	38	39	36	36	14	0	
	320	66	66	61	64	64	70	66	59	59	63	65	61	90	73	70	57	59	52	59	61	98	69	69	58	66	60	59	74	42	44	42	41	16	14	0

Taxonomic hierarchy with relative abundance

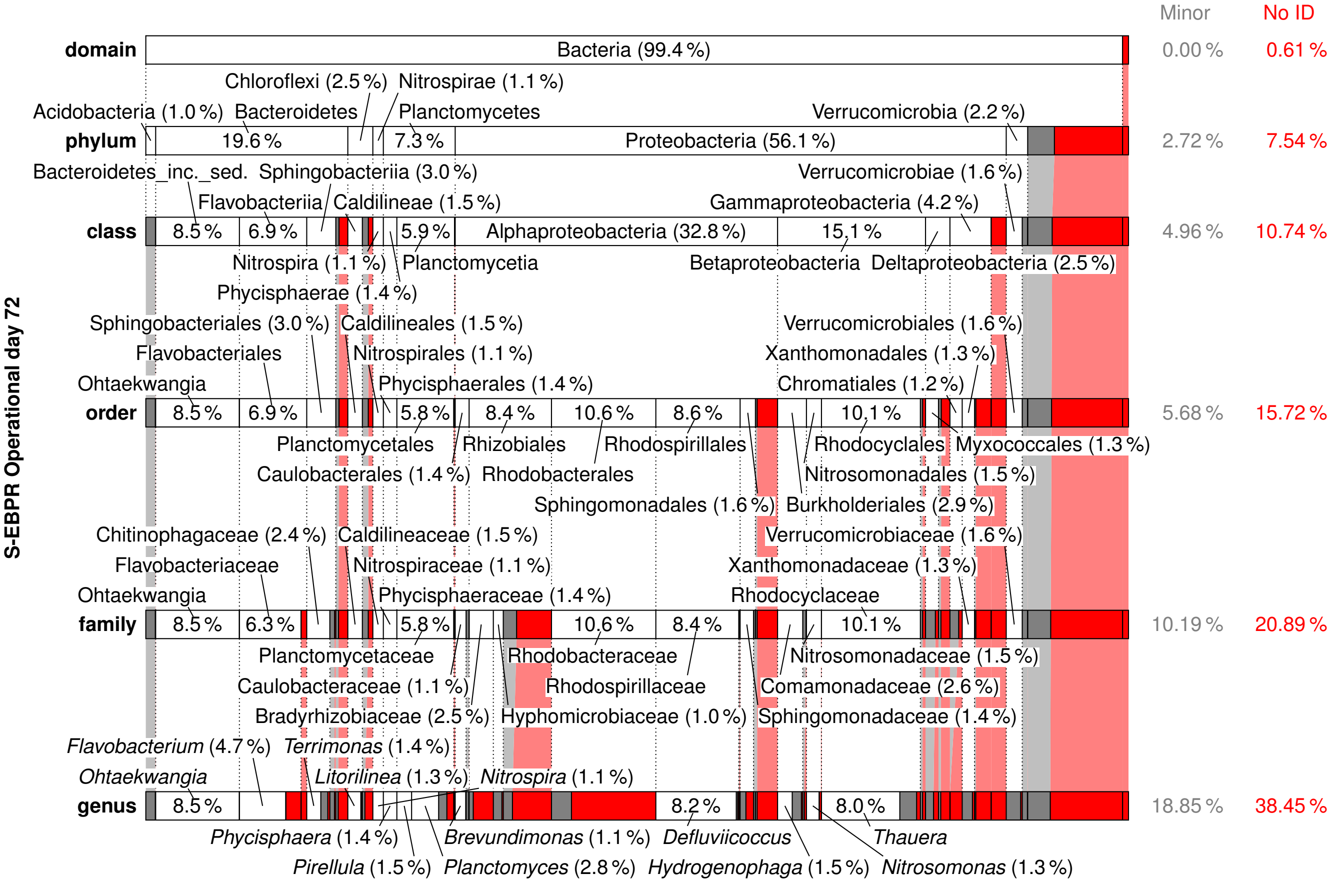

Figure S14. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

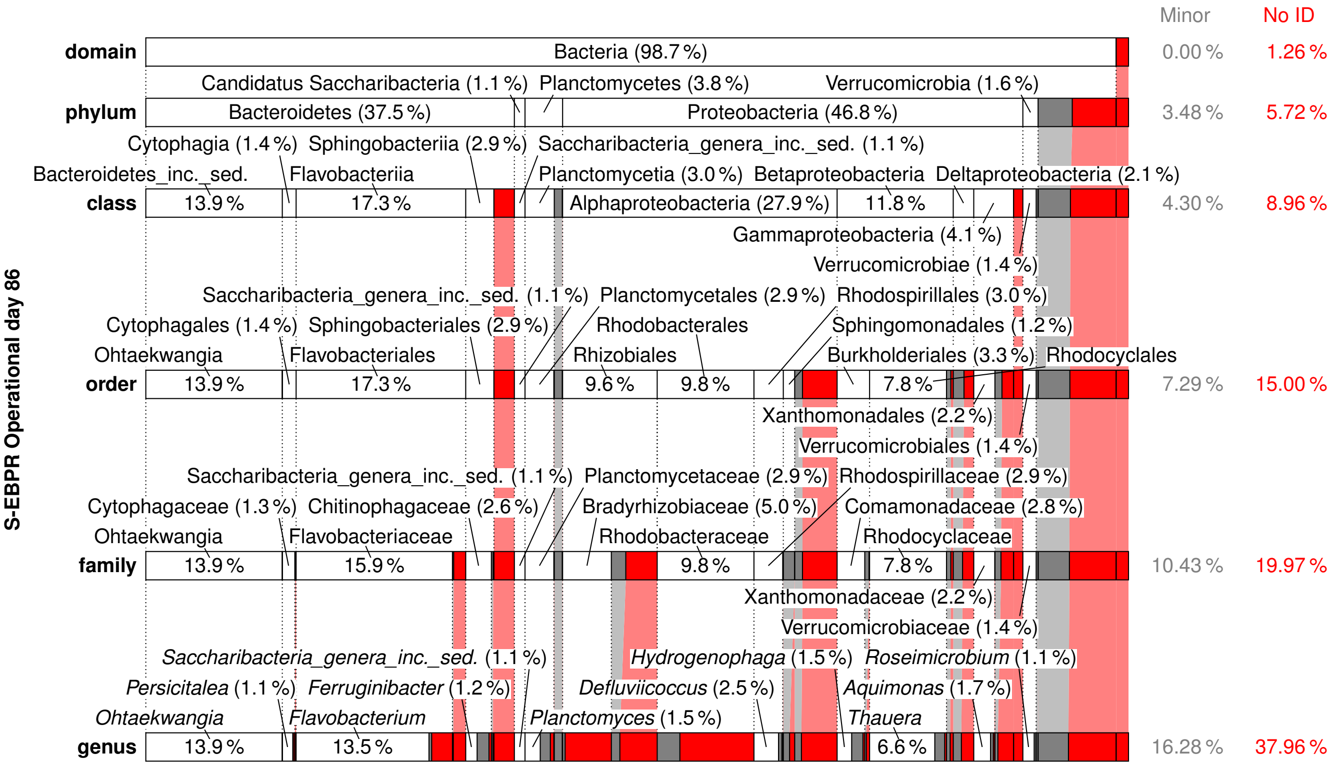

Figure S15. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

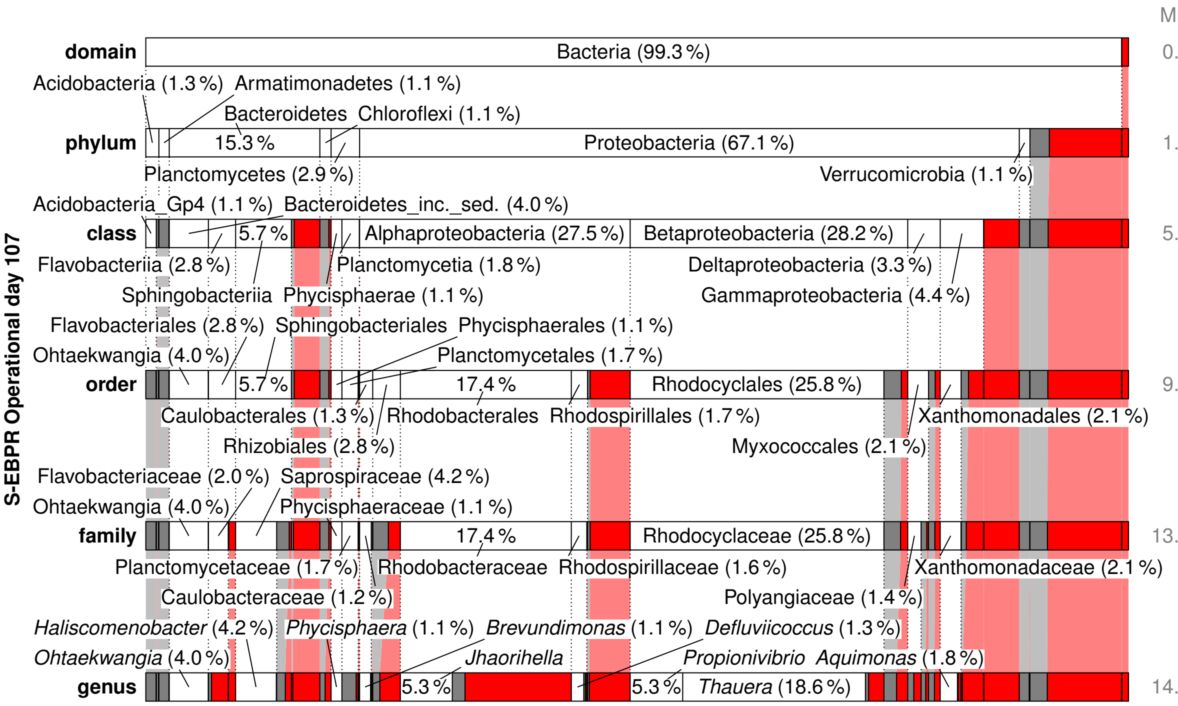

Figure S16. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

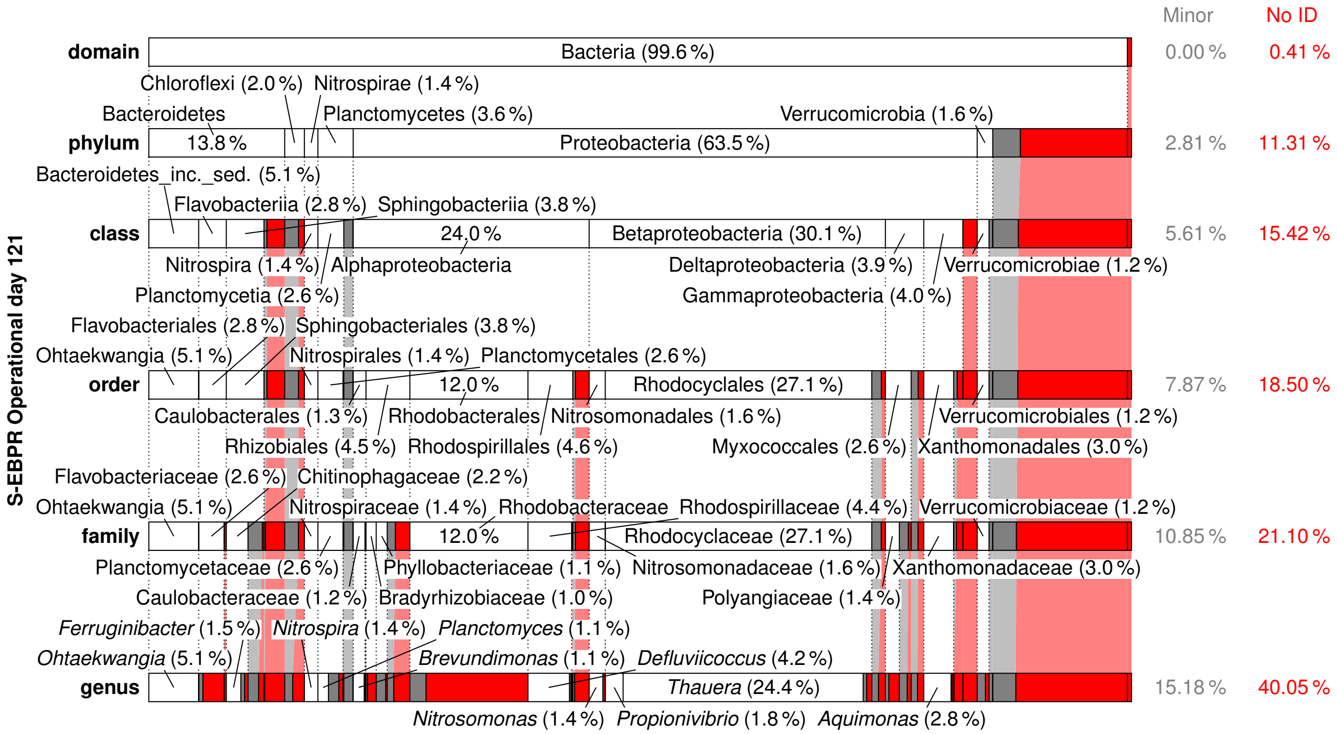

Figure S17. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

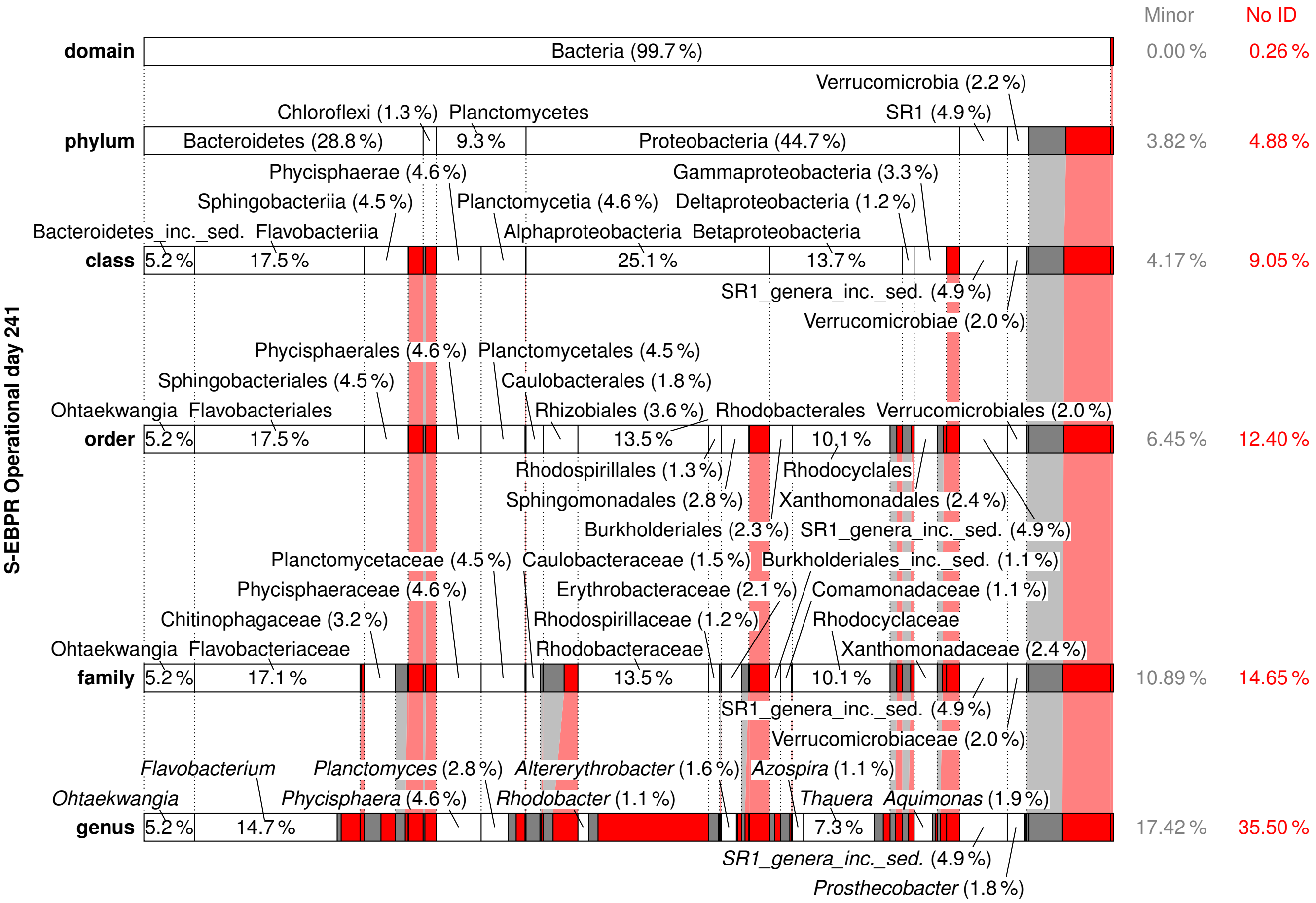

Figure S18. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

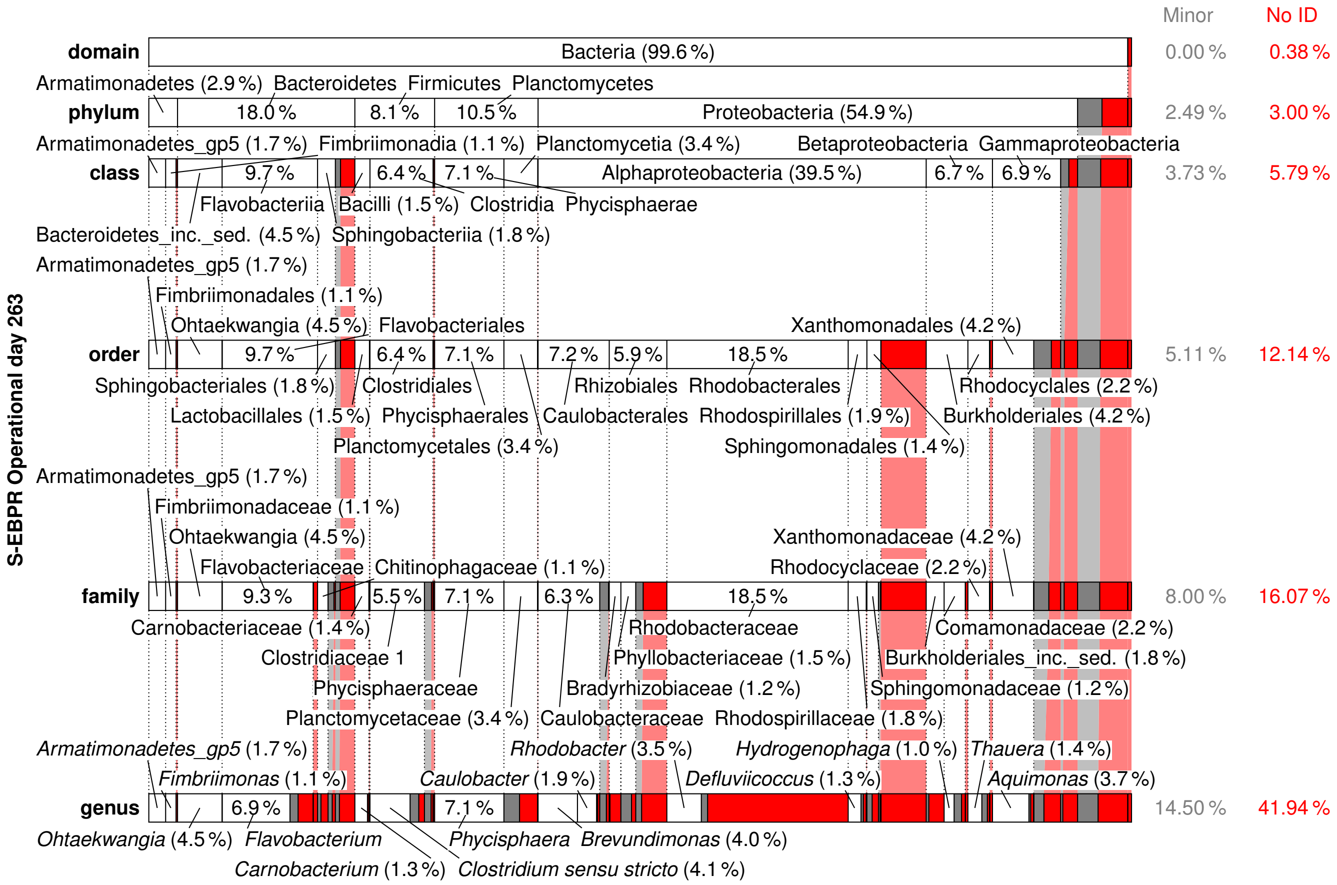

Figure S19. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

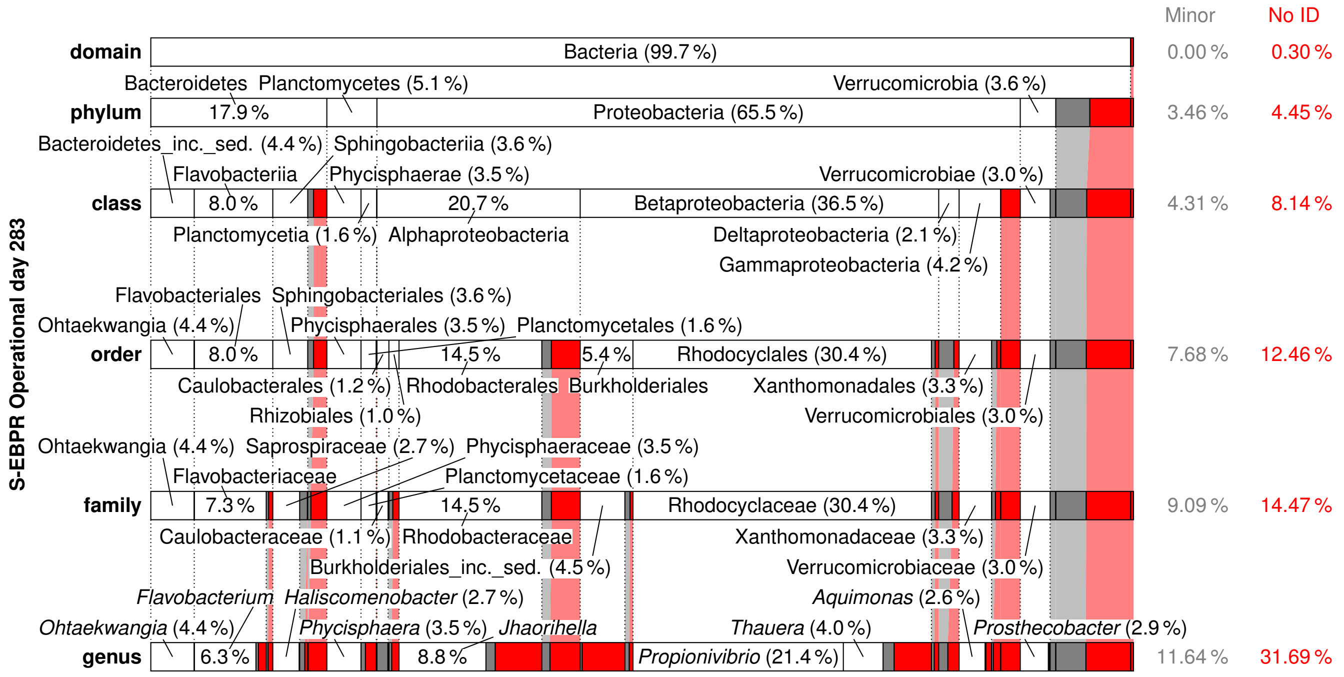

Figure S20. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

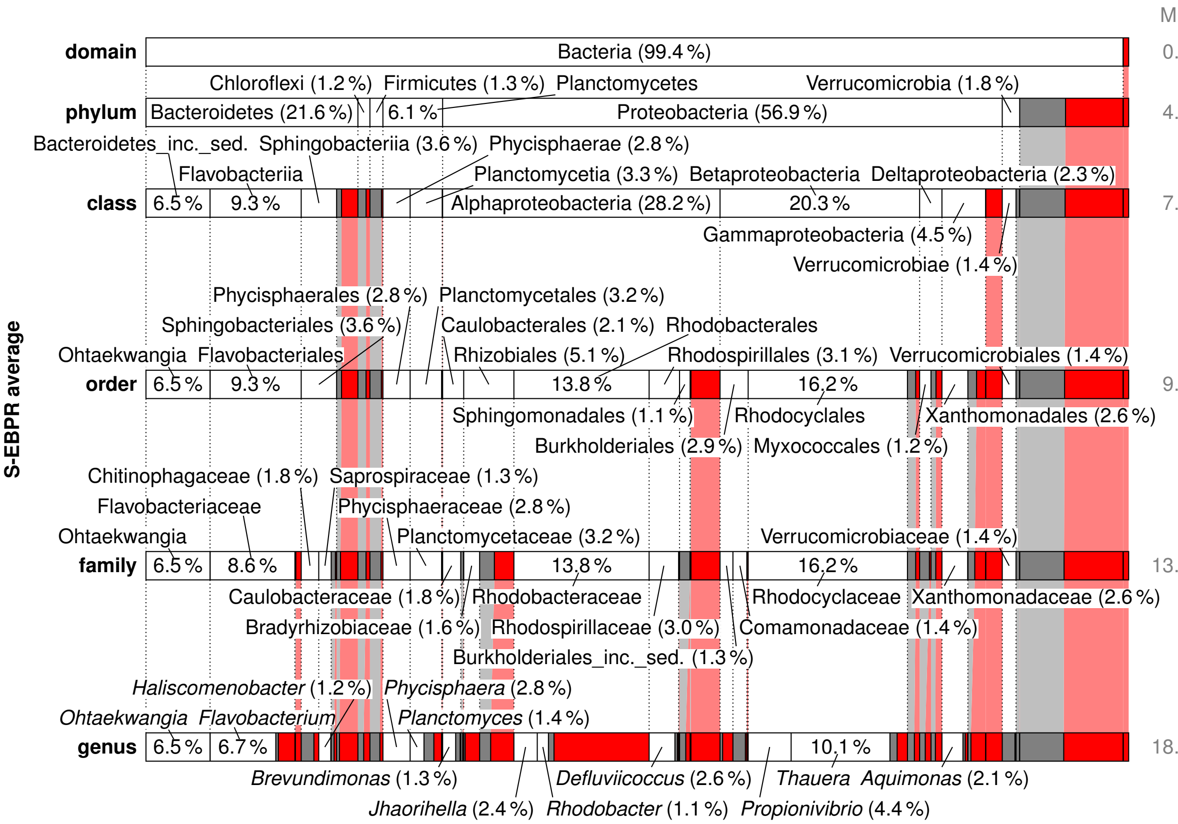

Figure S21. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for S-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

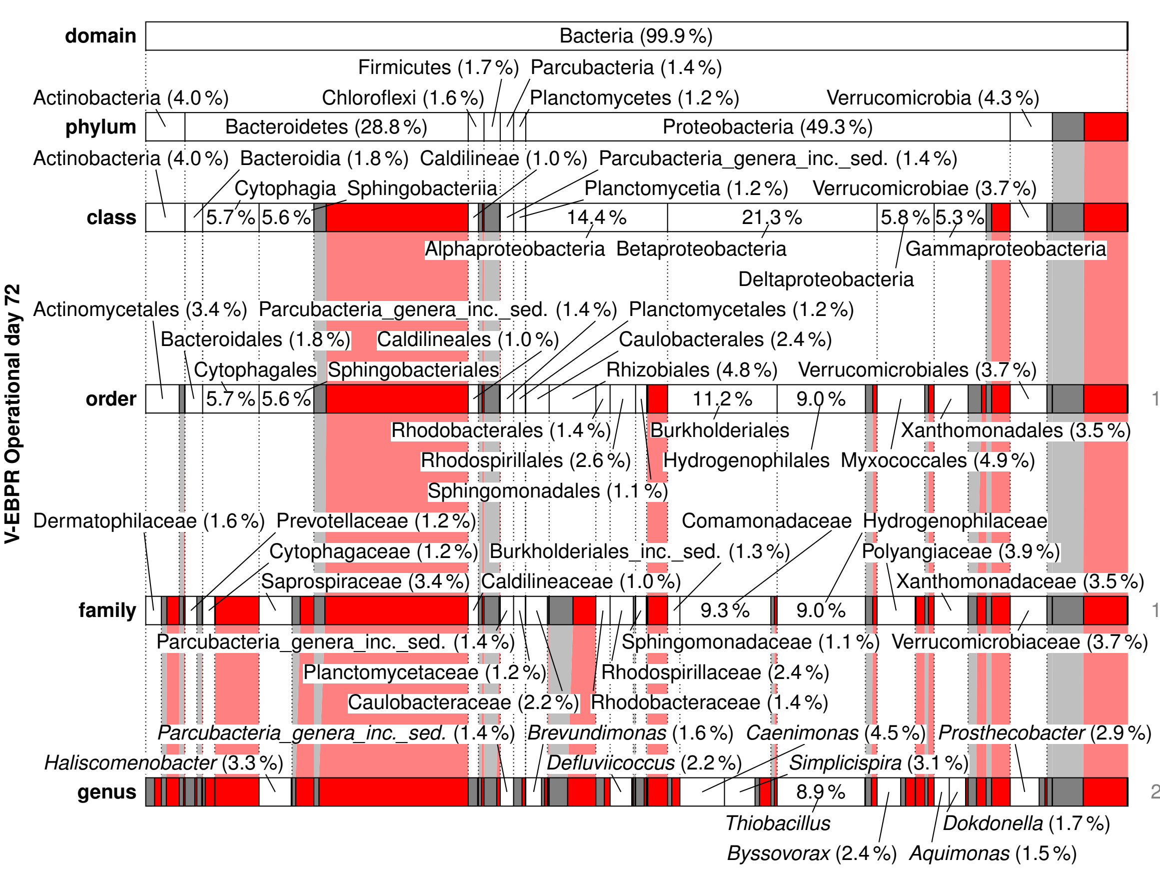

Figure S22. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

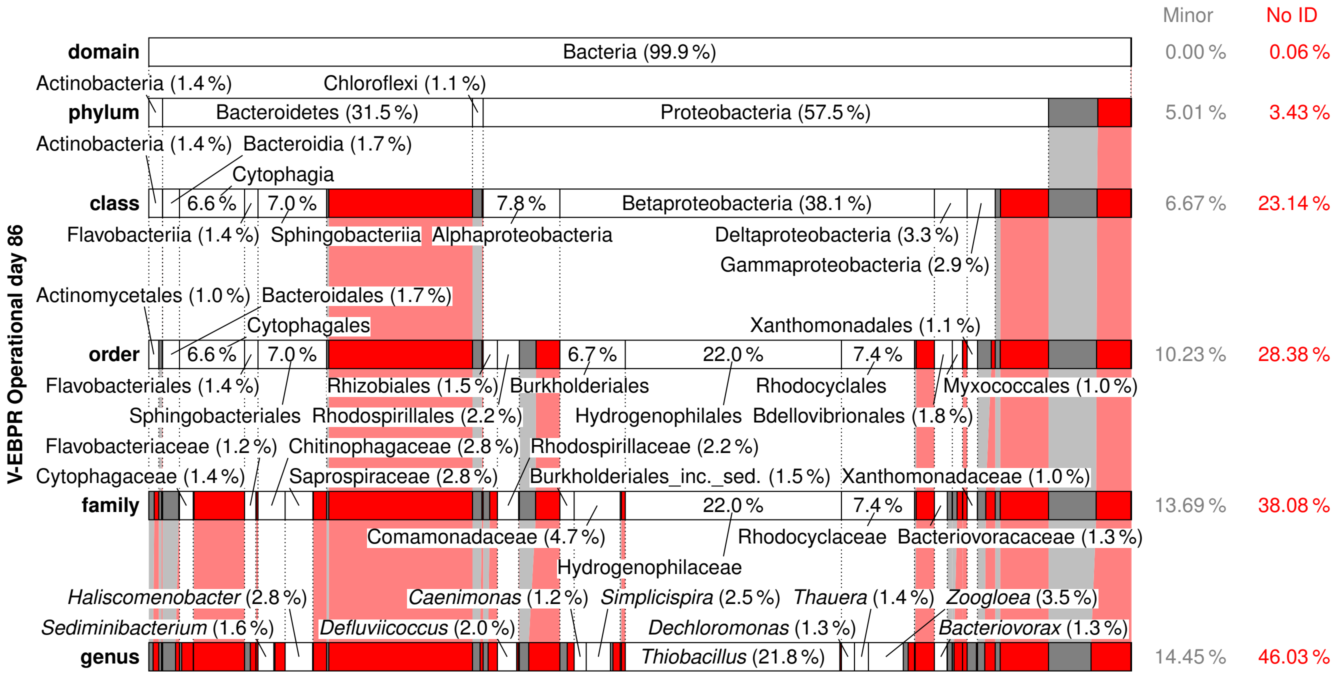

Figure S23. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

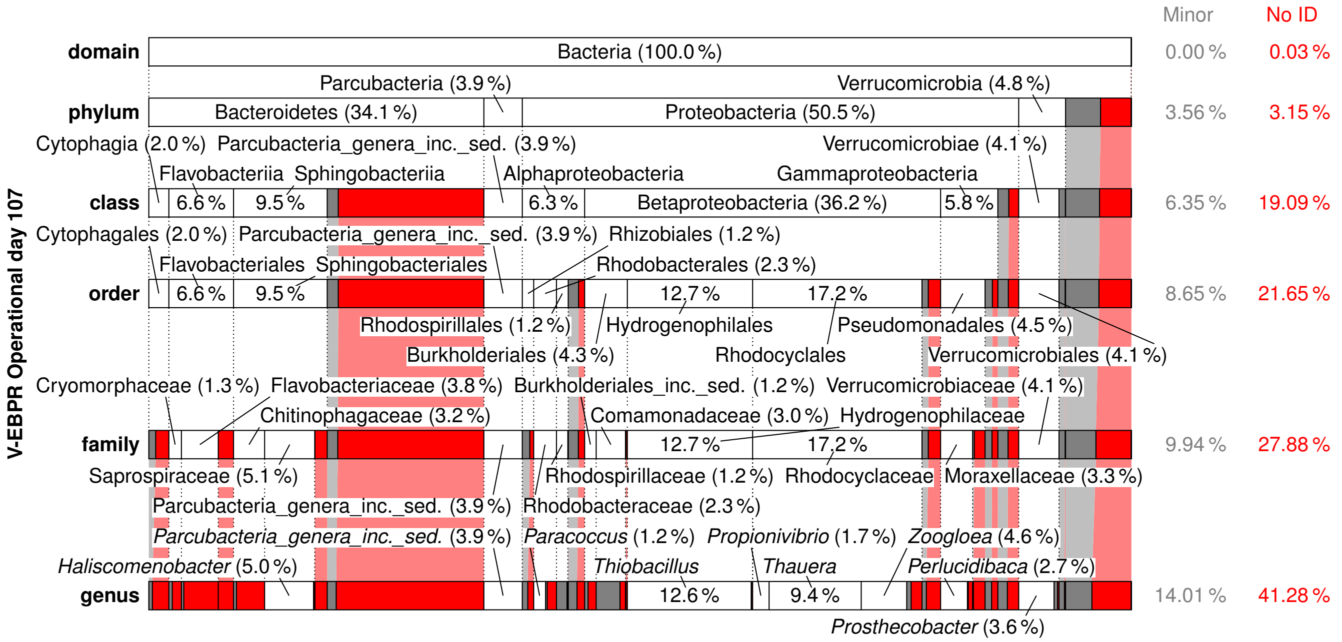

Figure S24. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

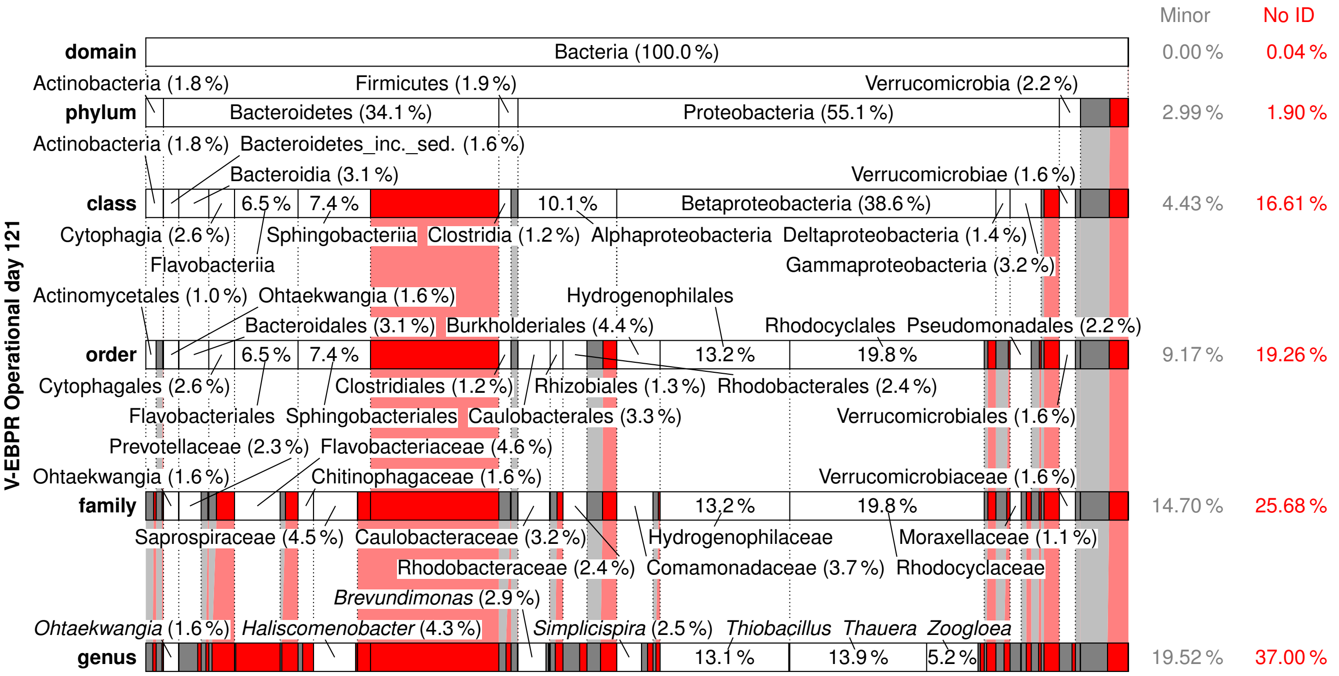

Figure S25. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

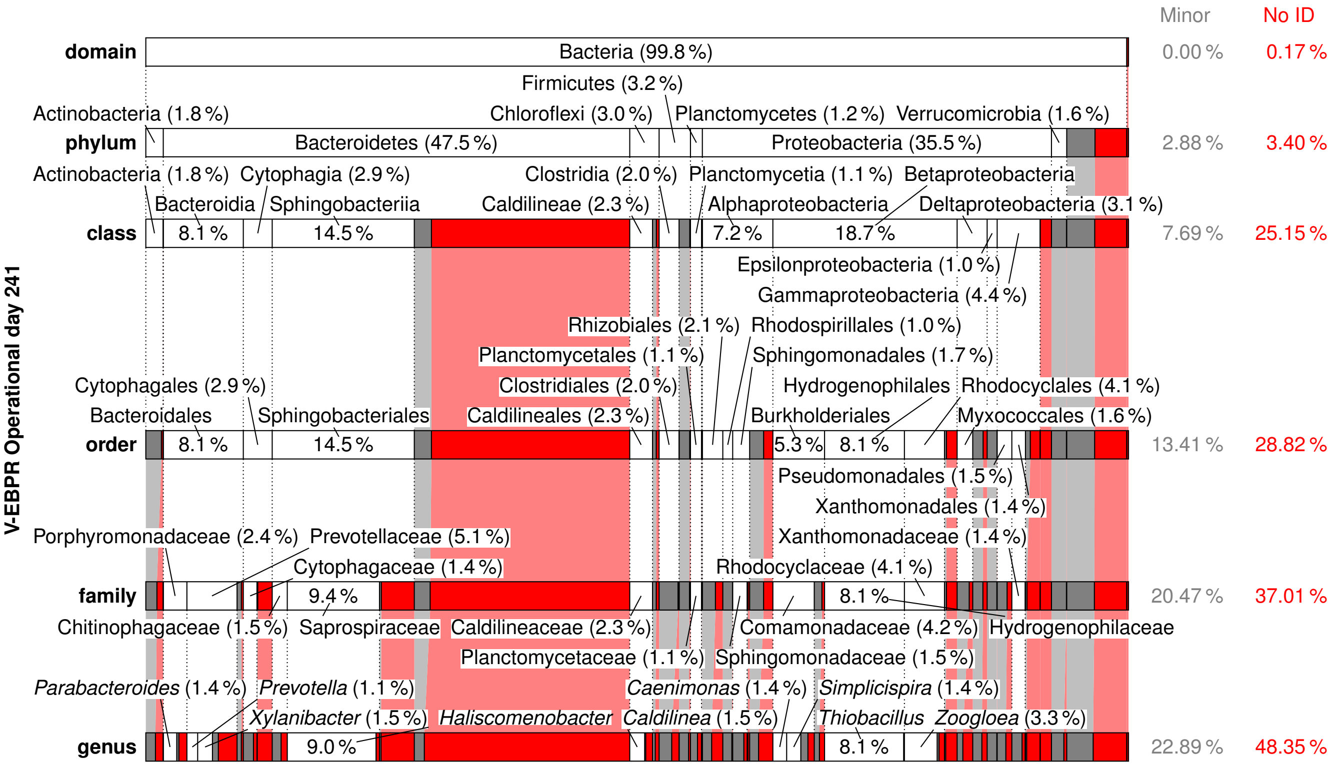

Figure S26. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

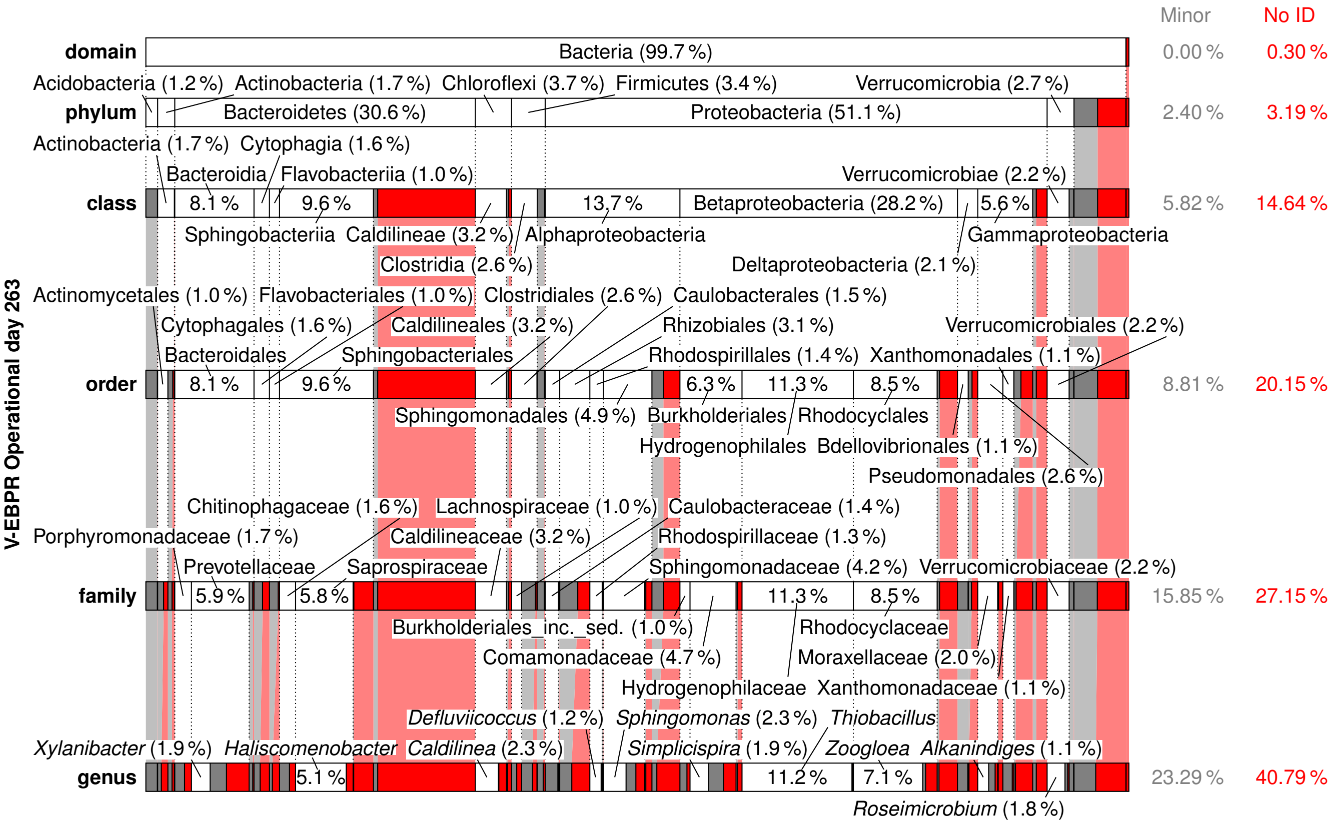

Figure S27. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

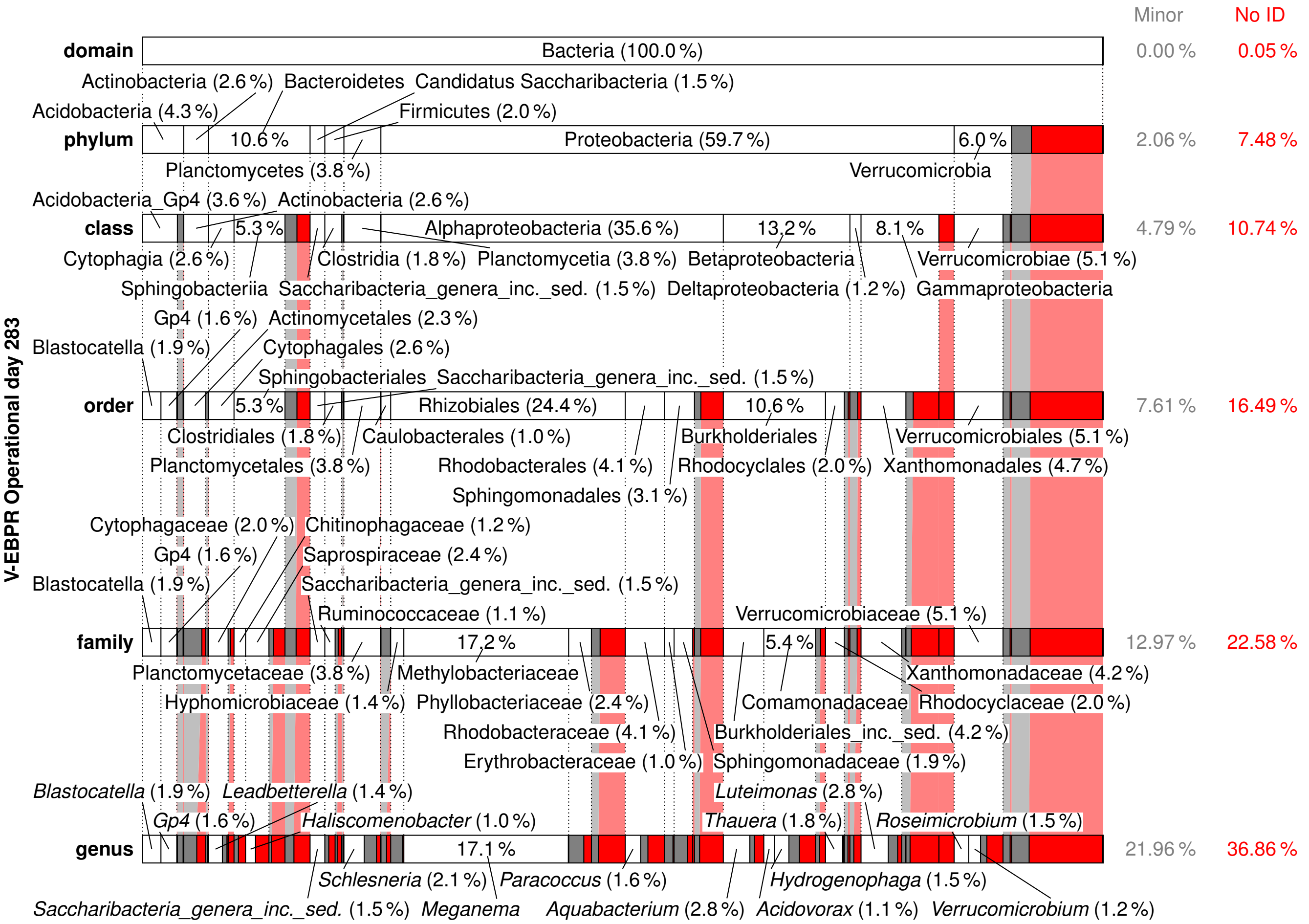

Figure S28. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

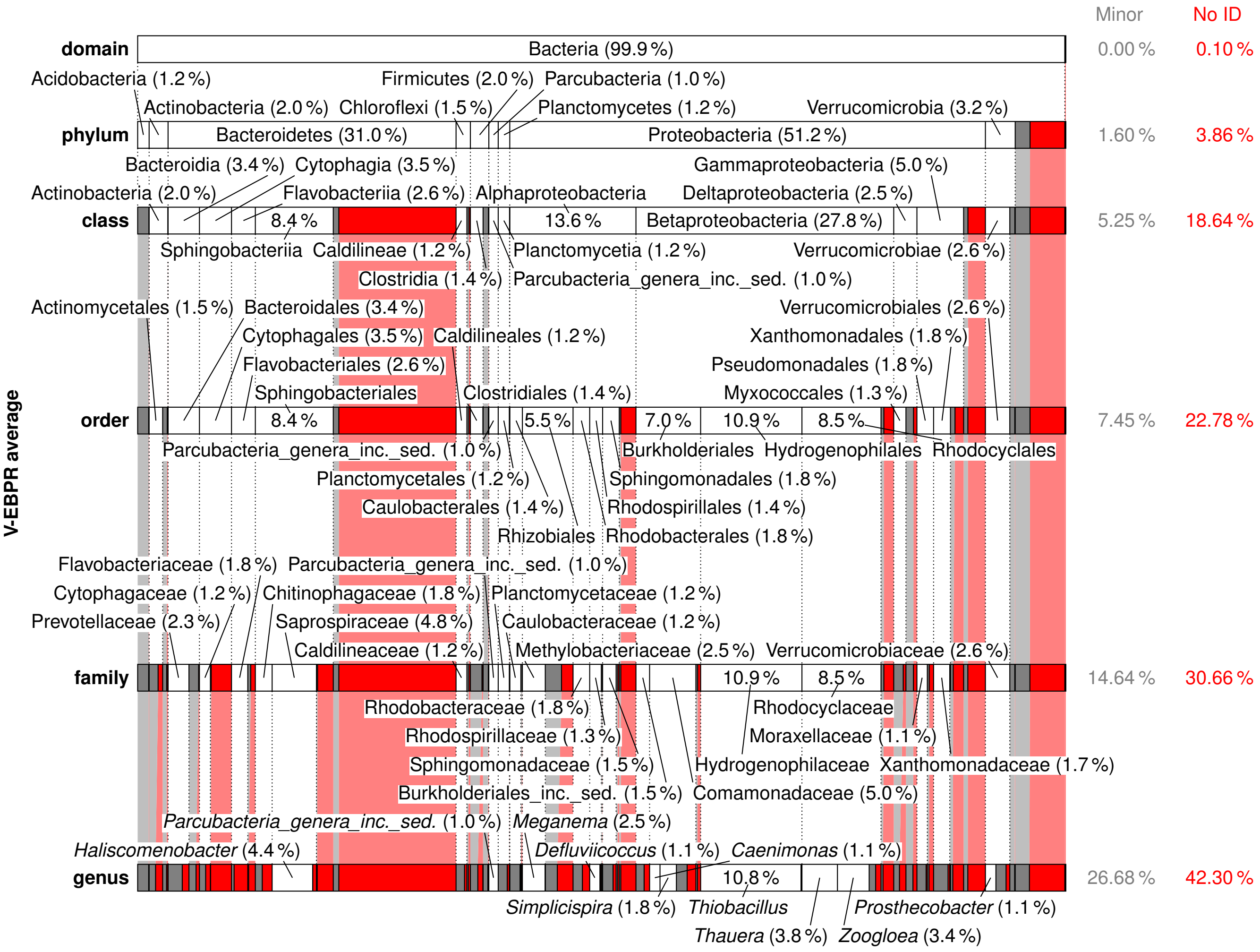

Figure S29. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for V-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

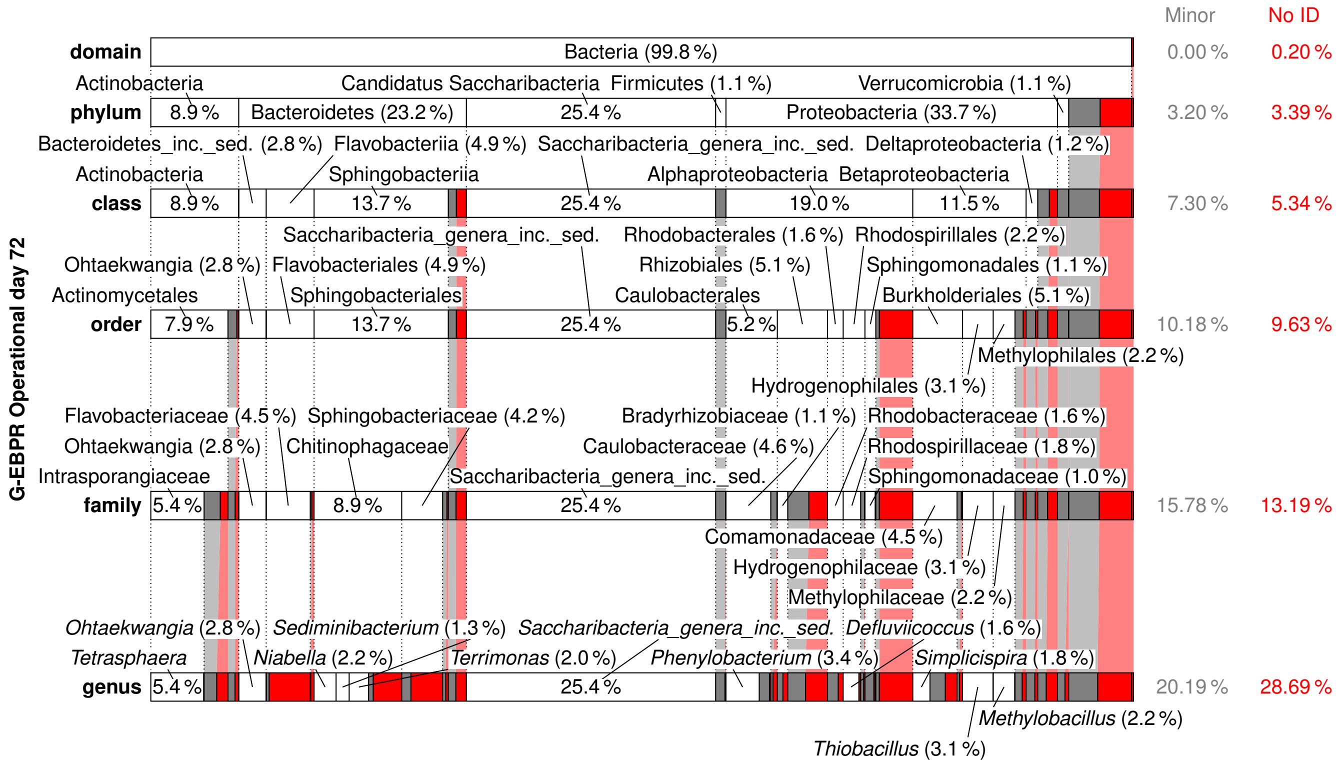

Figure S30. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

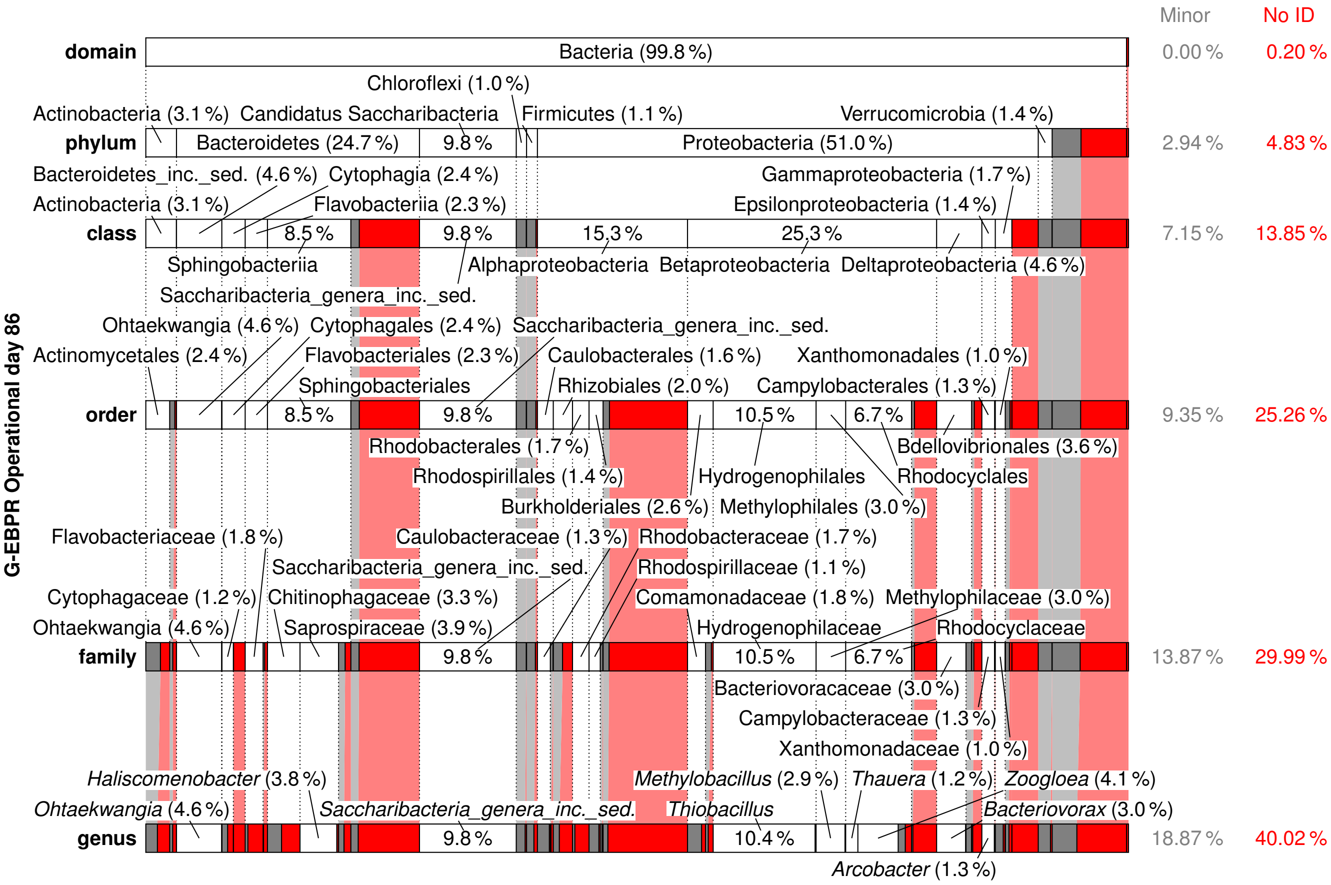

Figure S31. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

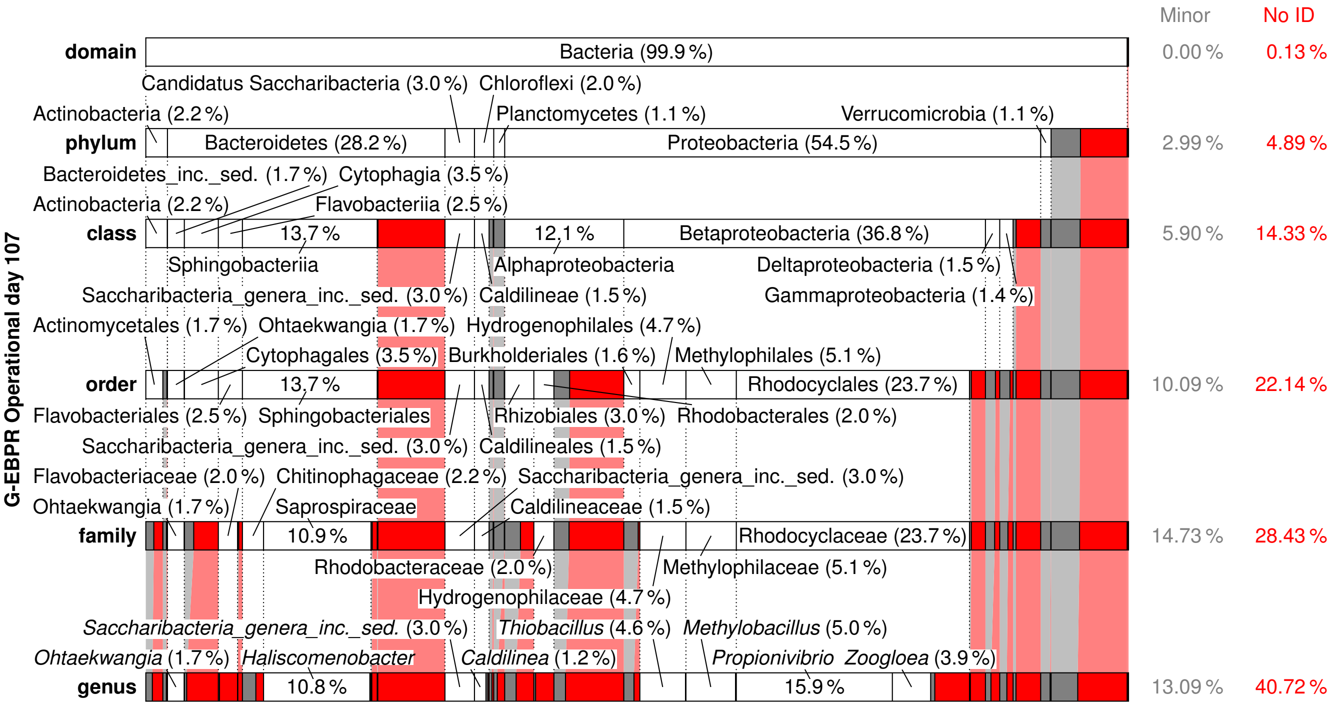

Figure S32. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

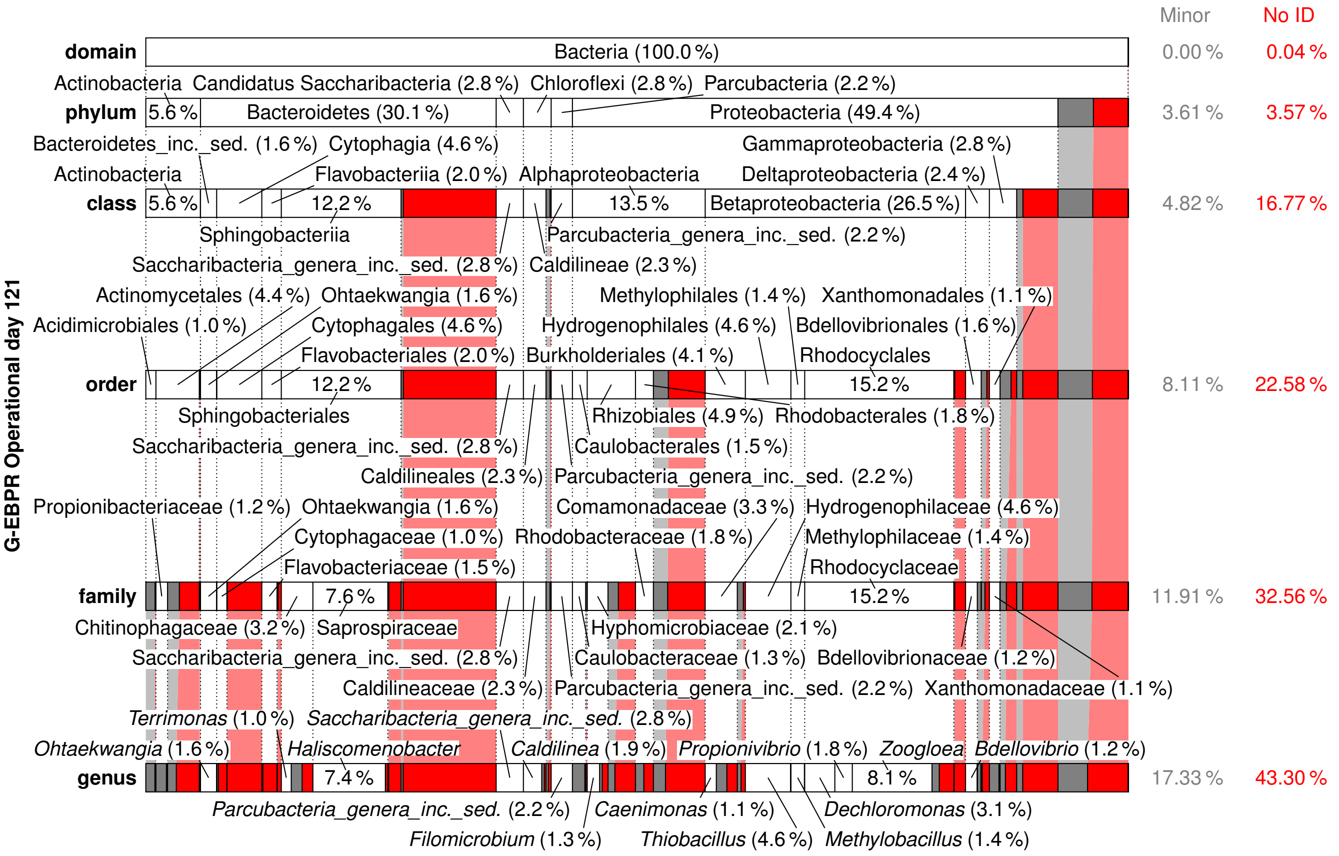

Figure S33. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

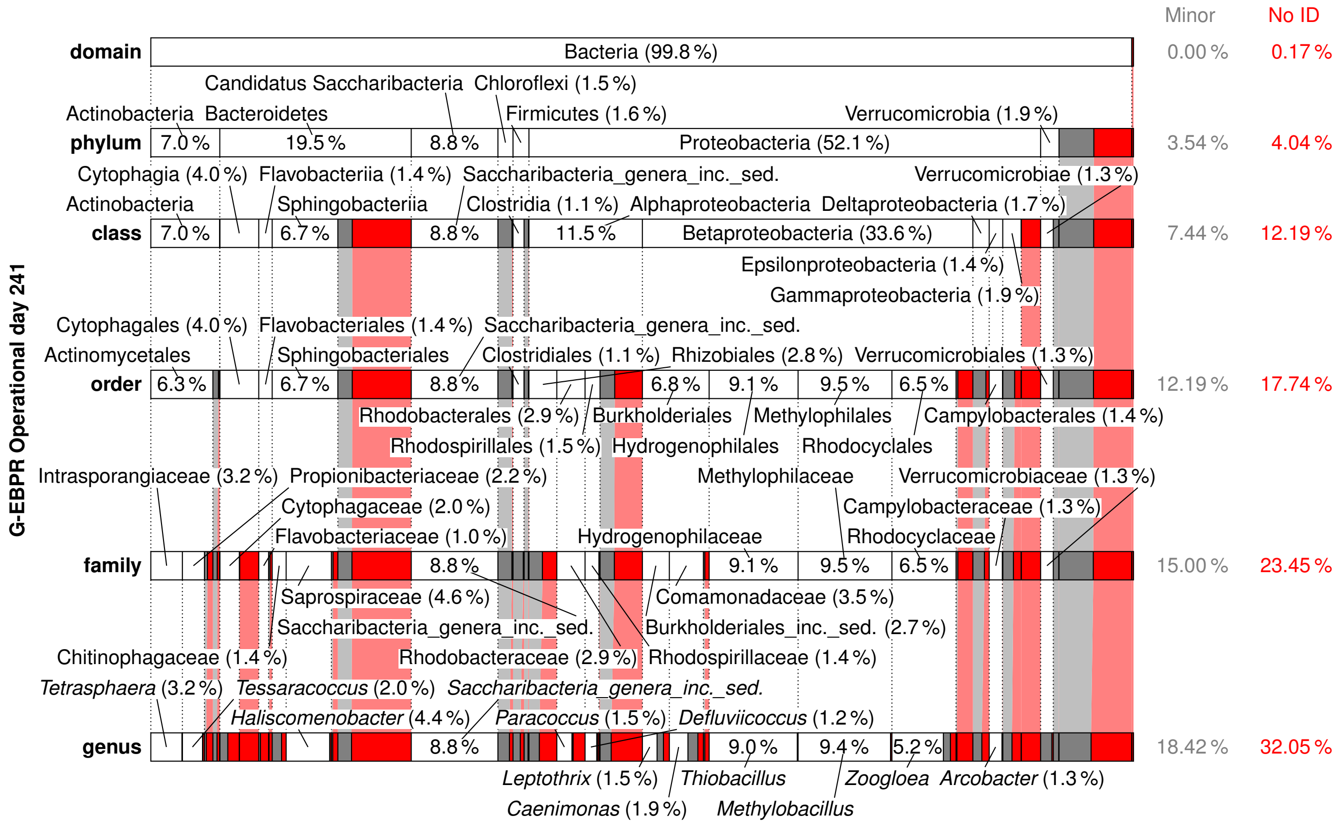

Figure S34. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

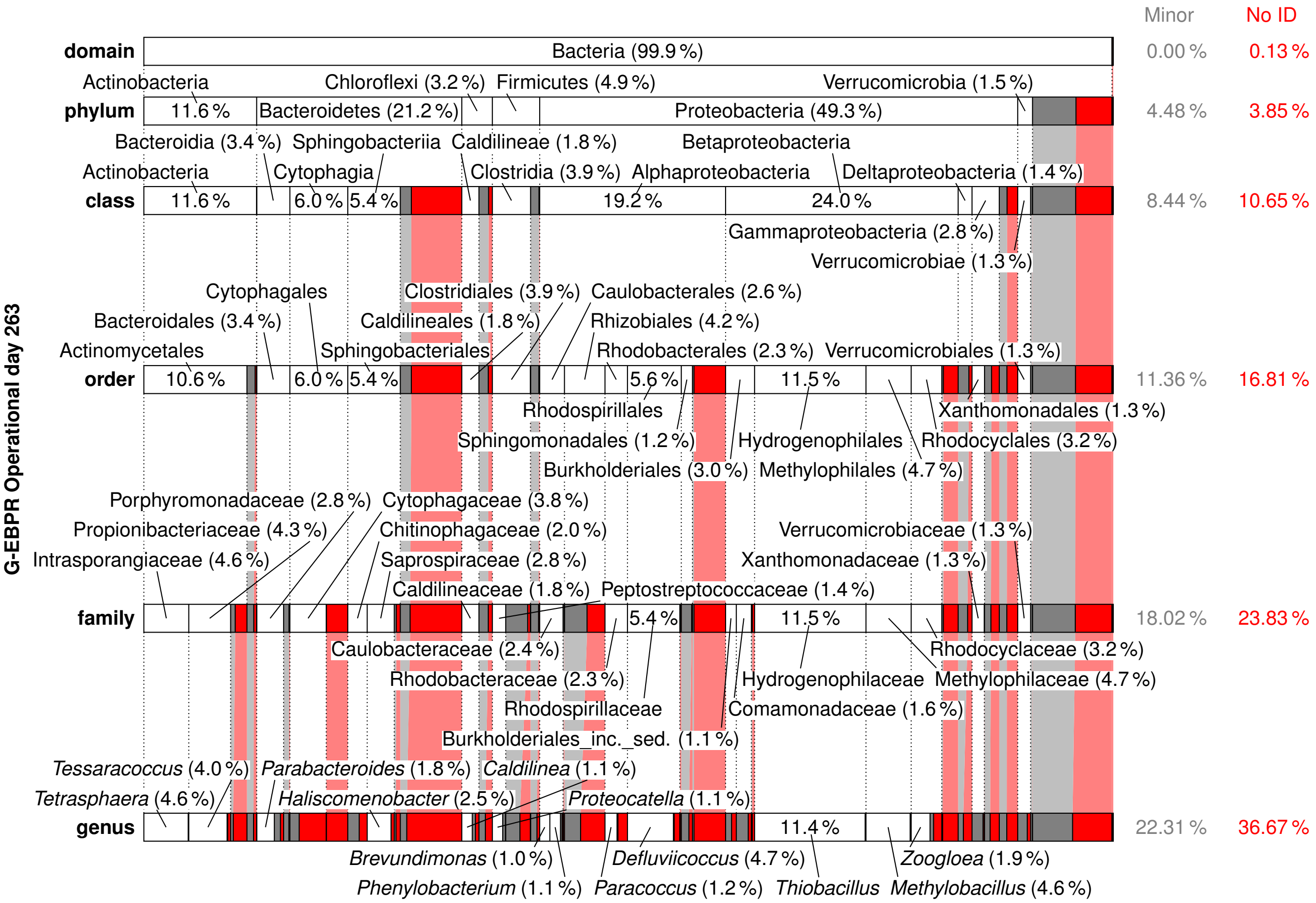

Figure S35. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

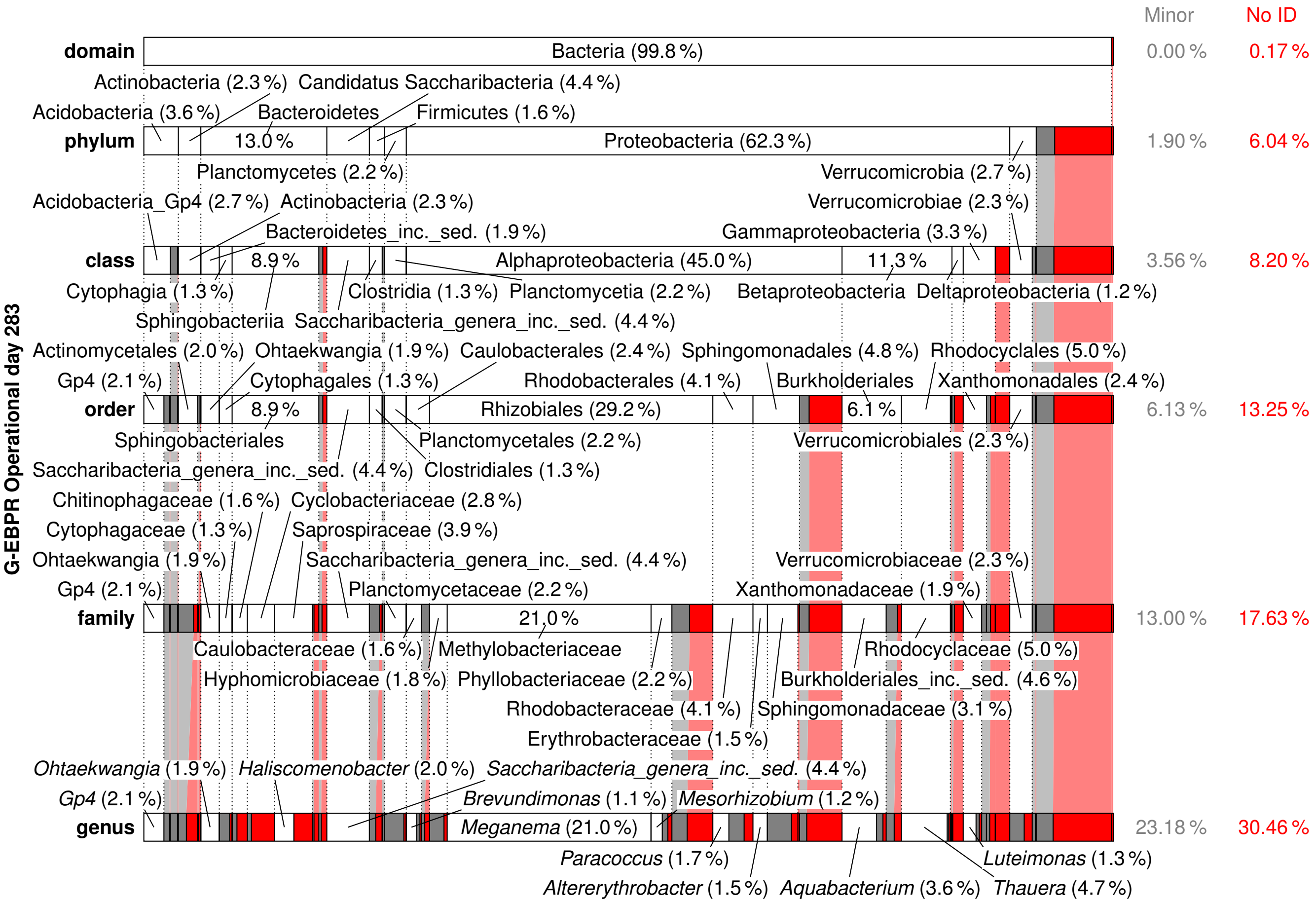

Figure S36. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

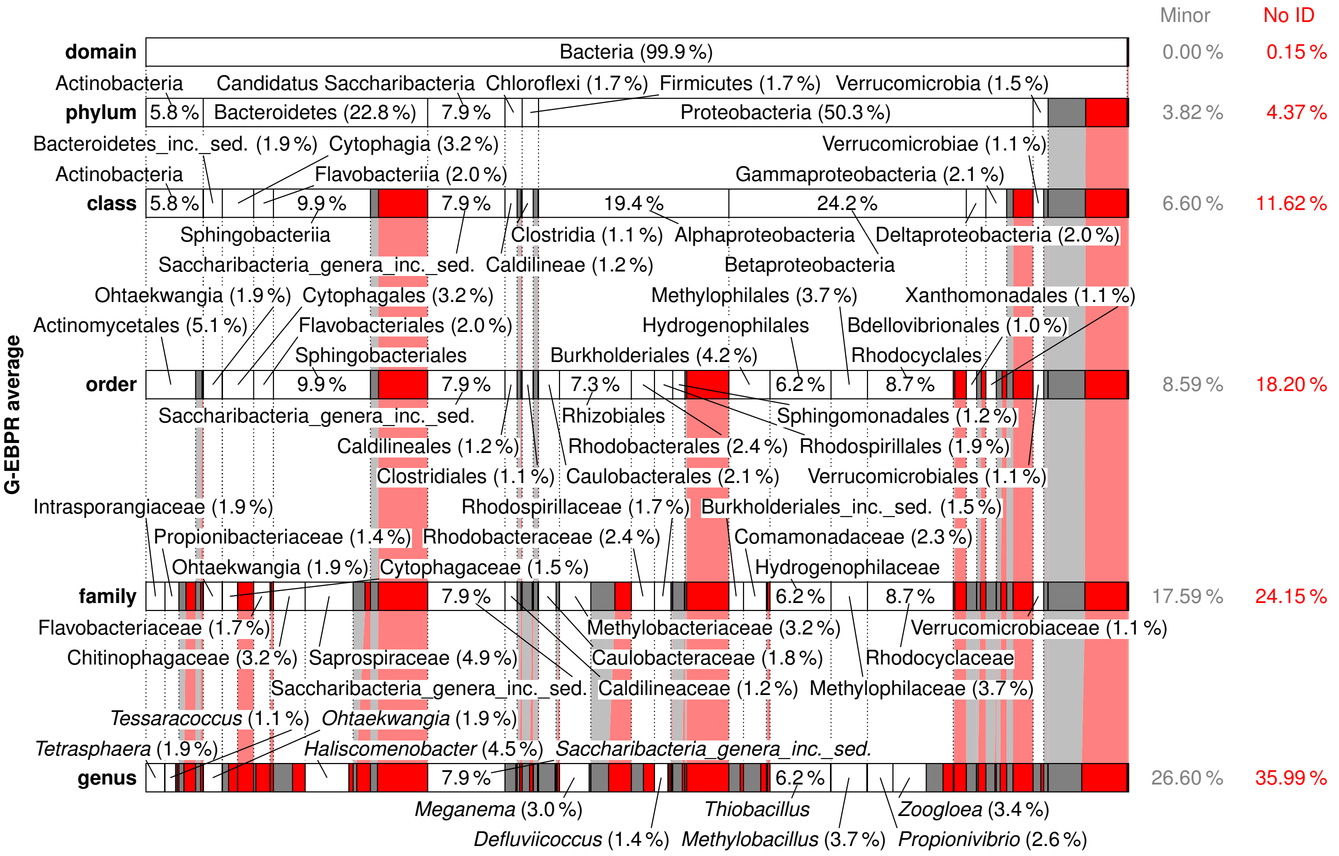

Figure S37. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for G-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

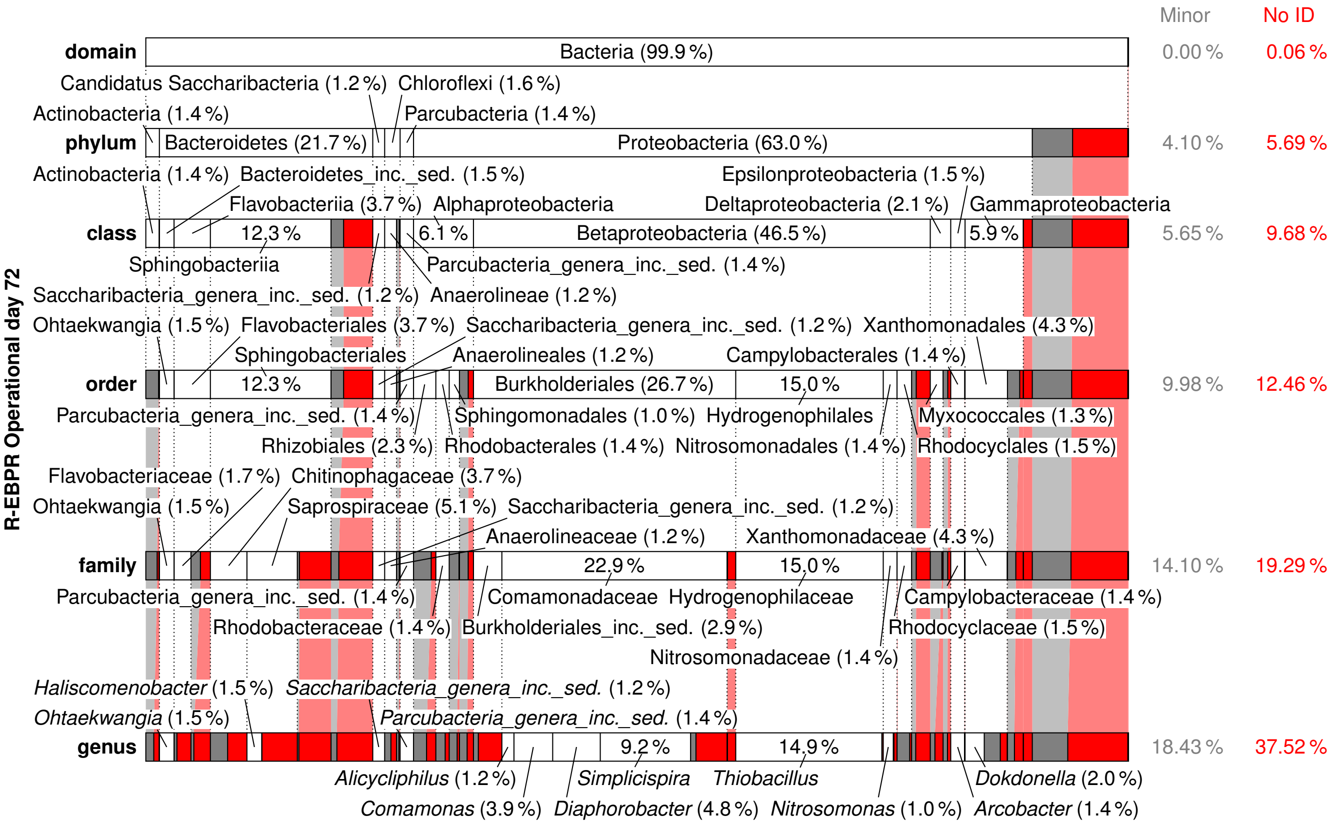

Figure S38. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

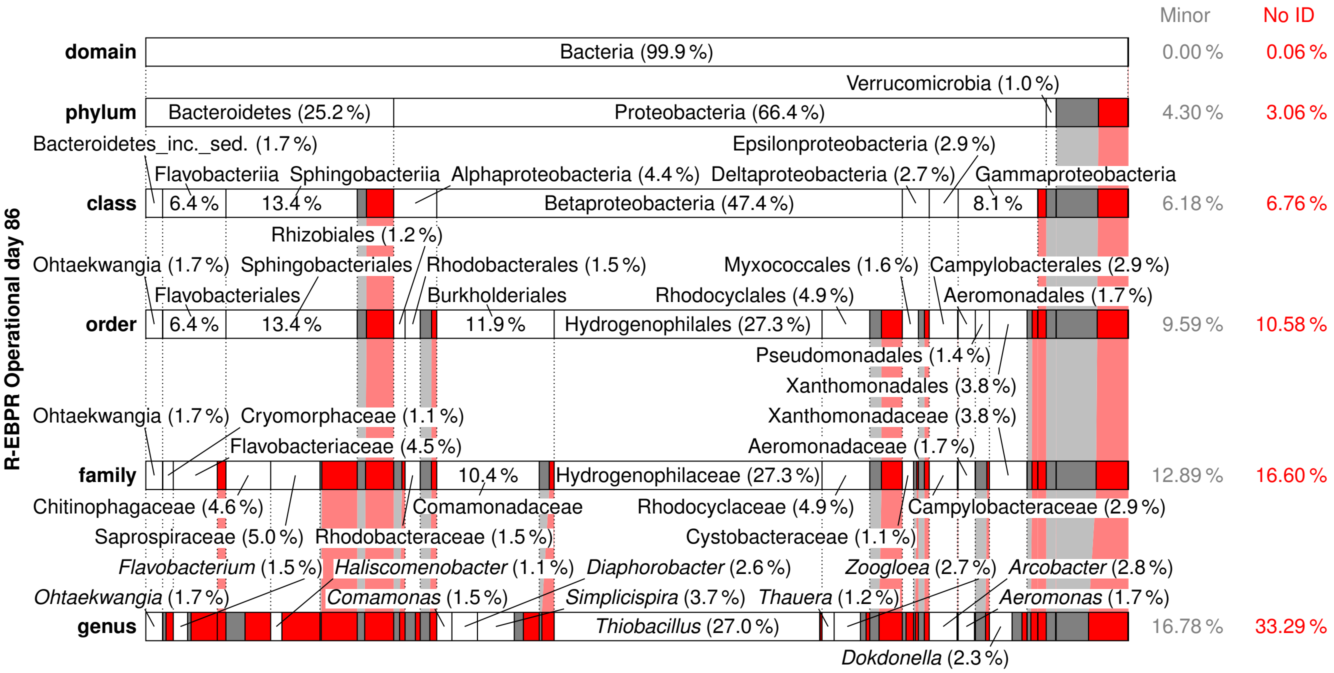

Figure S39. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

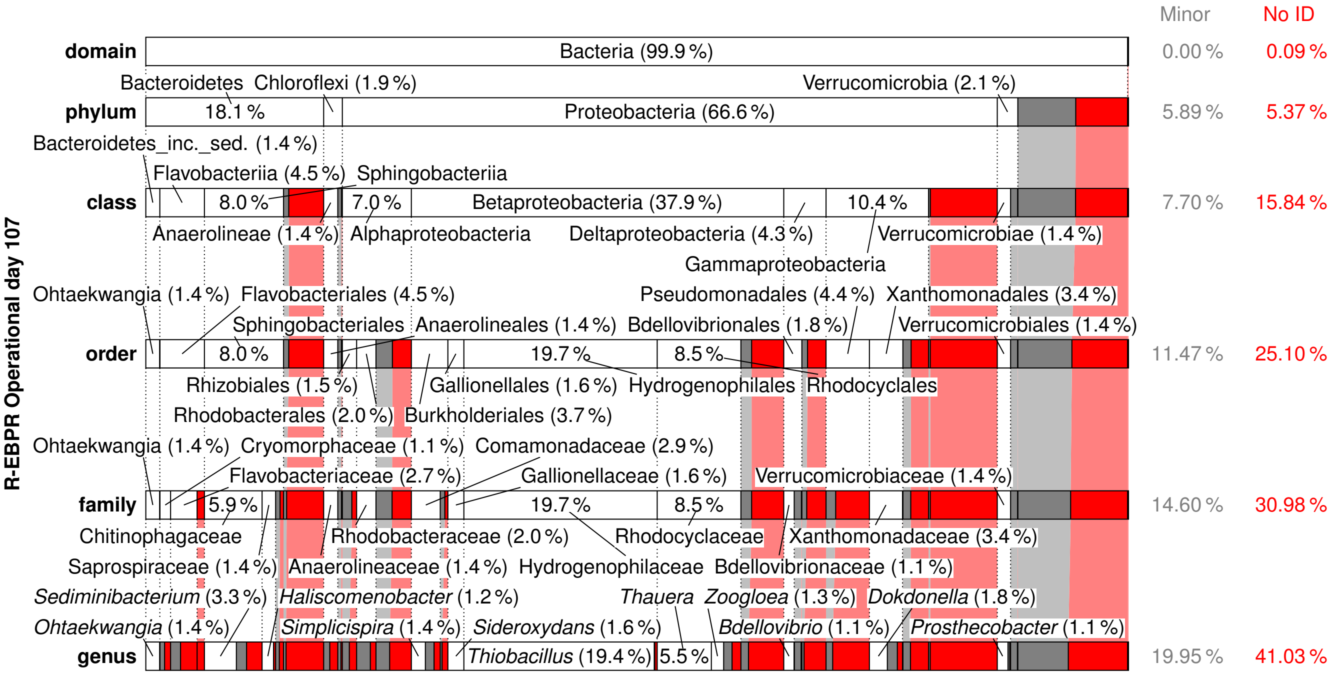

Figure S40. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

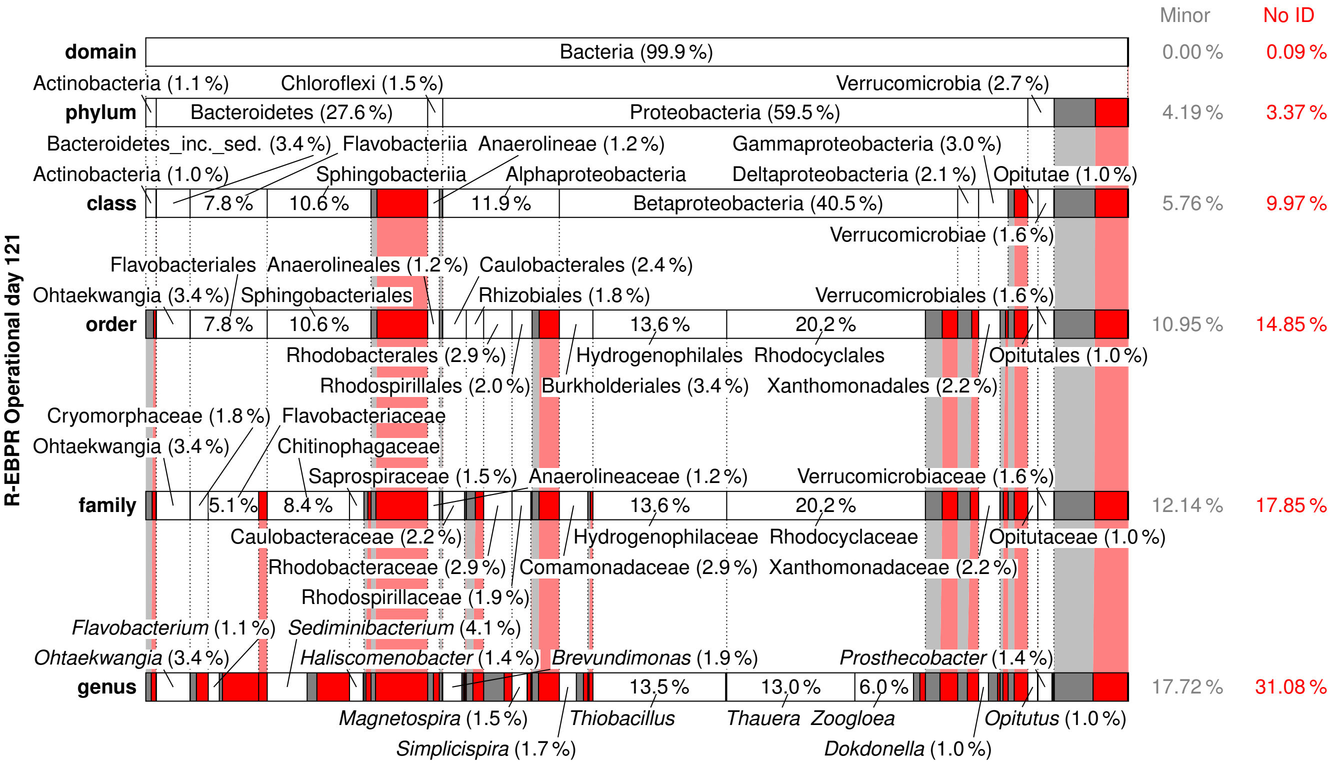

Figure S41. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

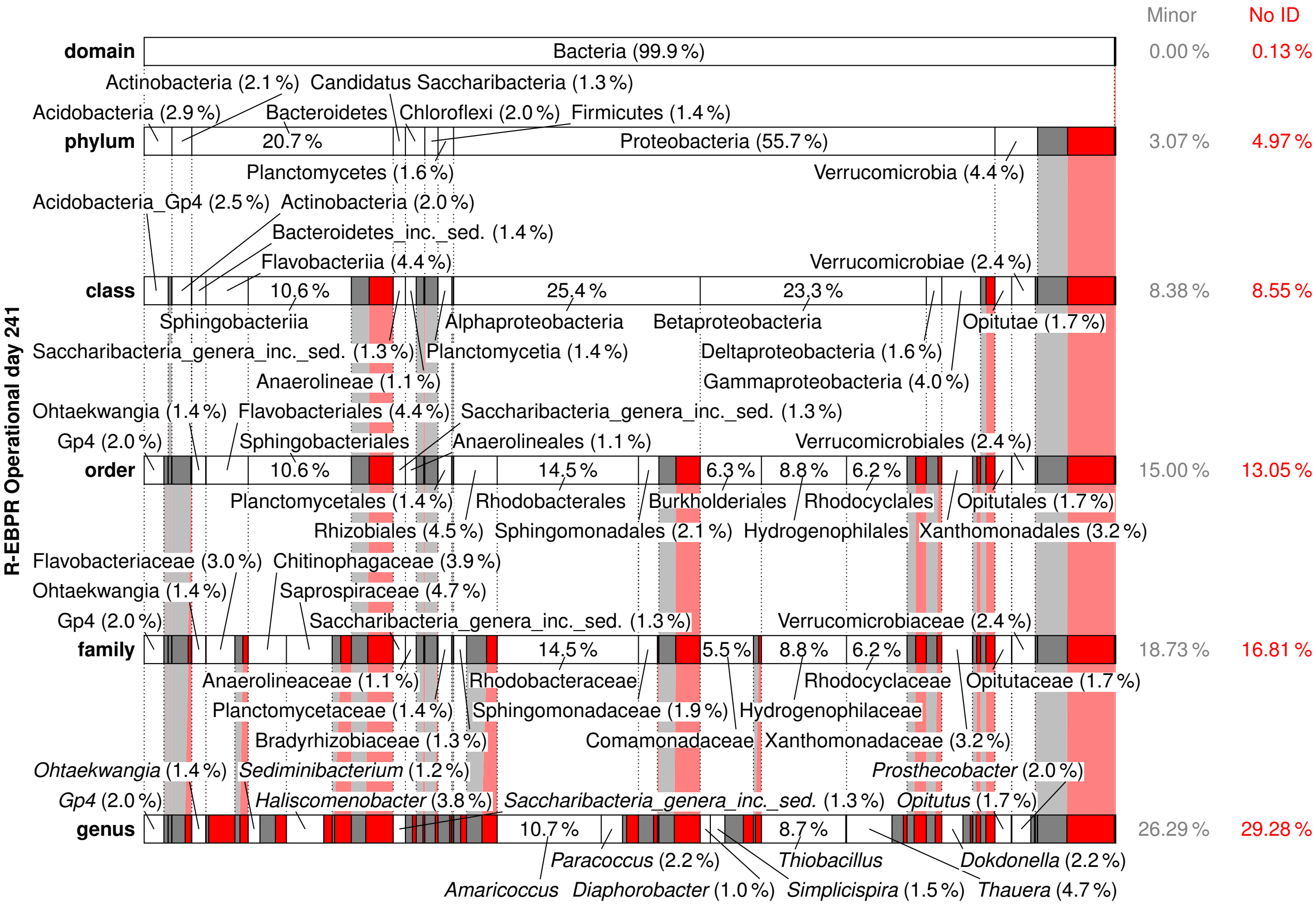

Figure S42. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

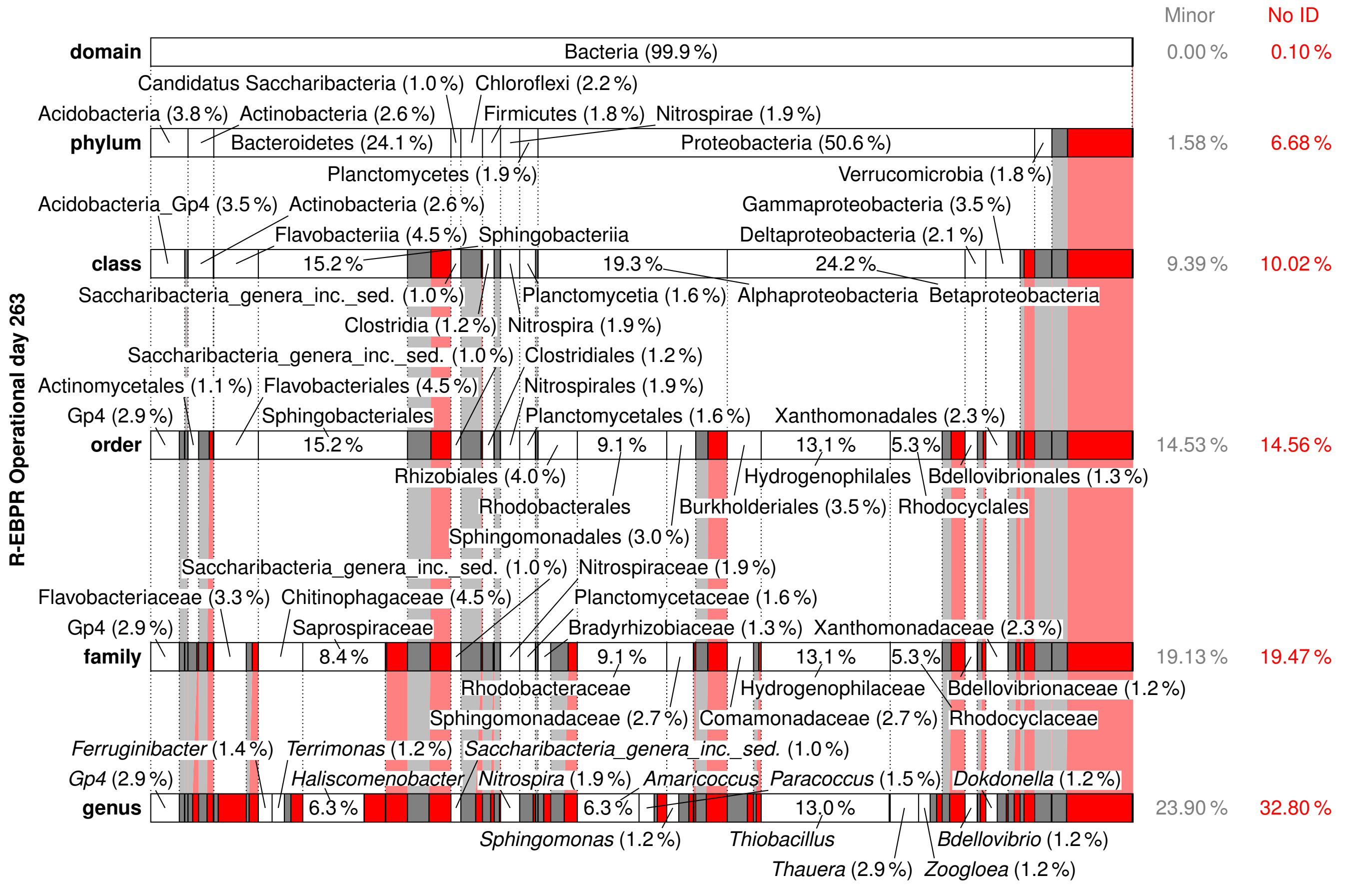

Figure S43. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

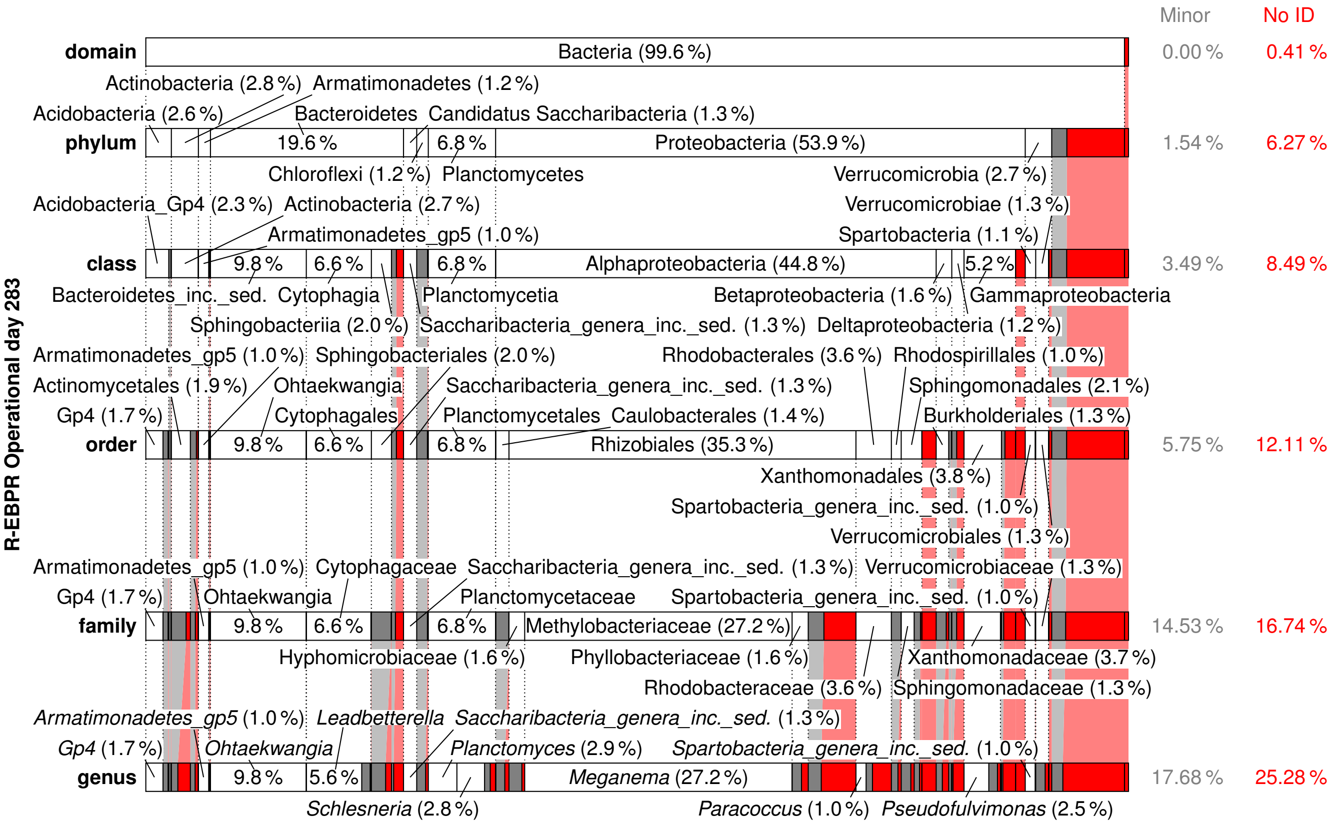

Figure S44. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

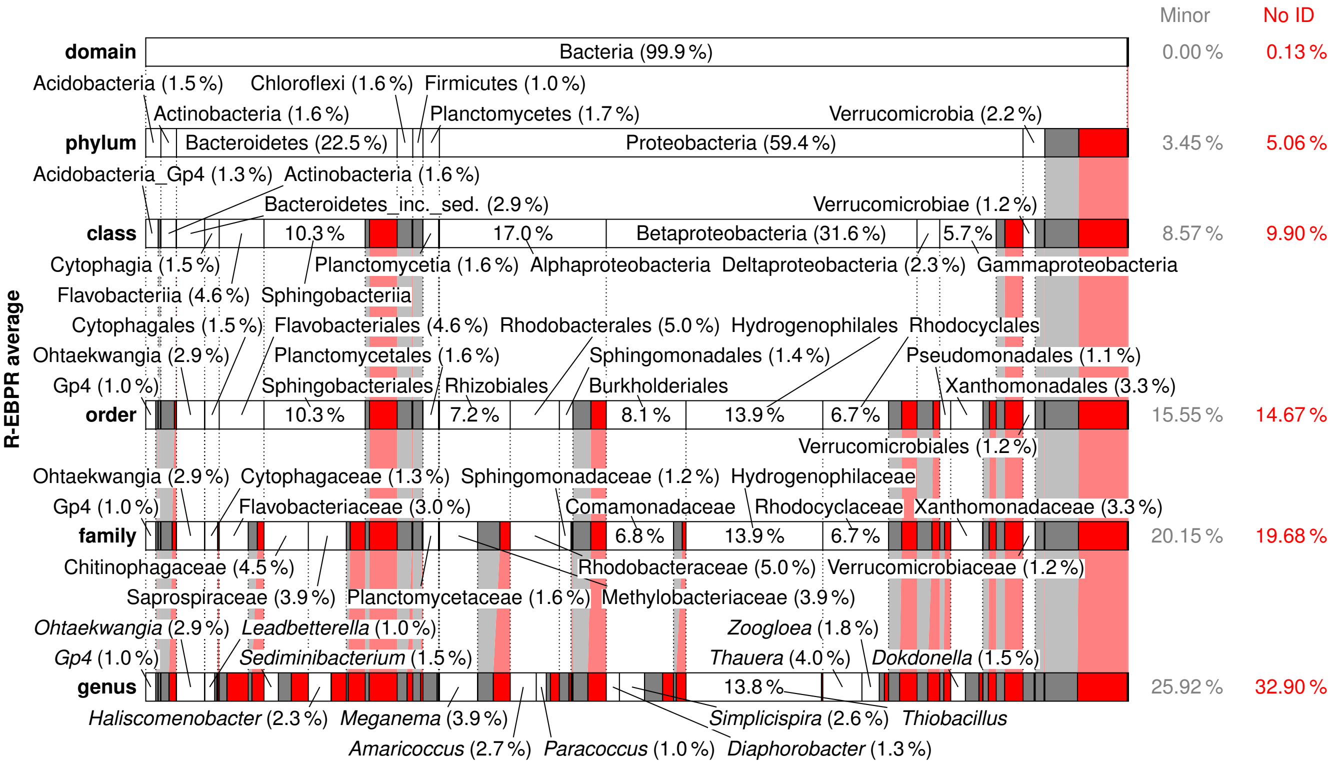

Figure S45. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for R-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

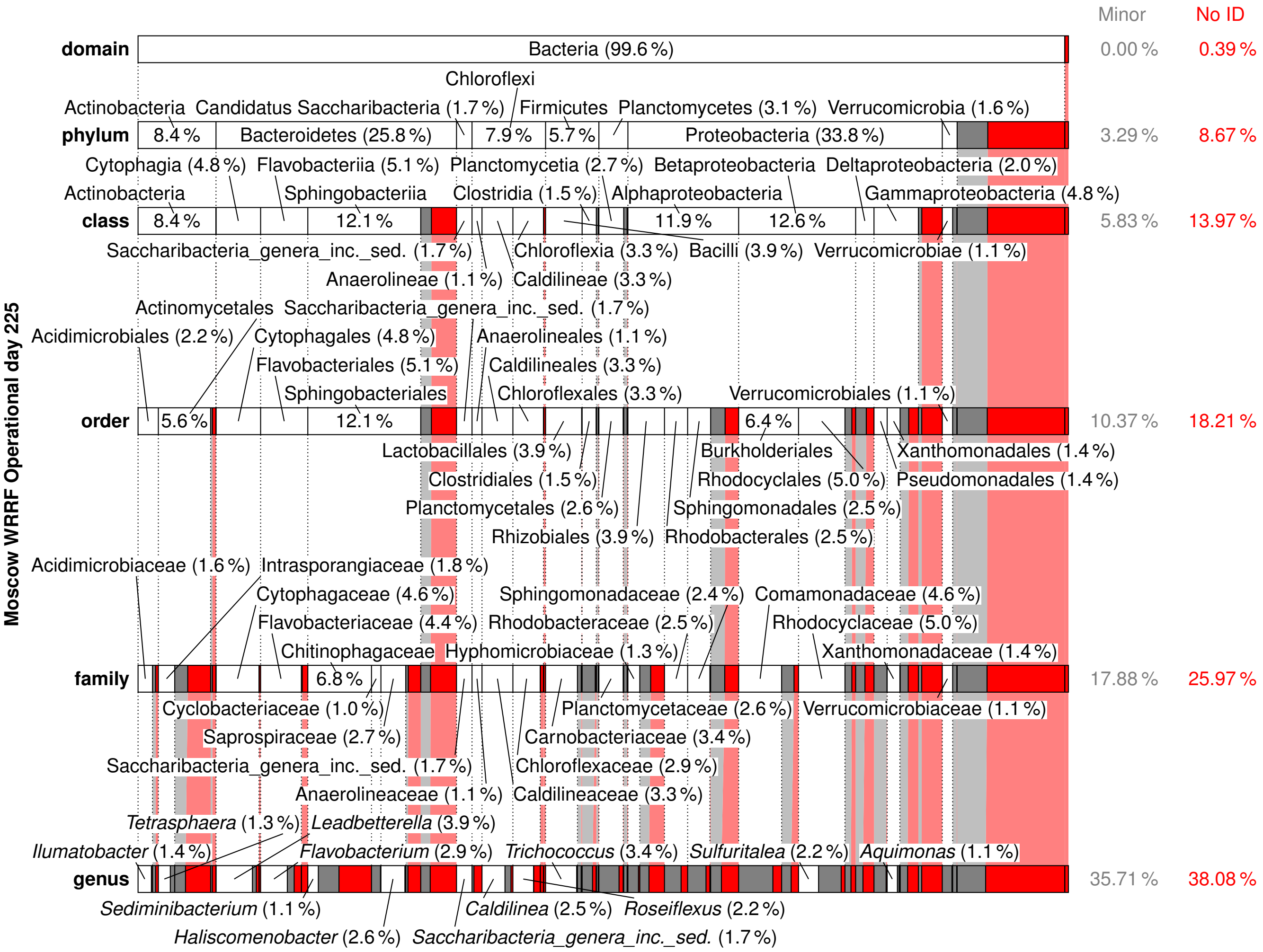

Figure S46. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF operational day 225. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

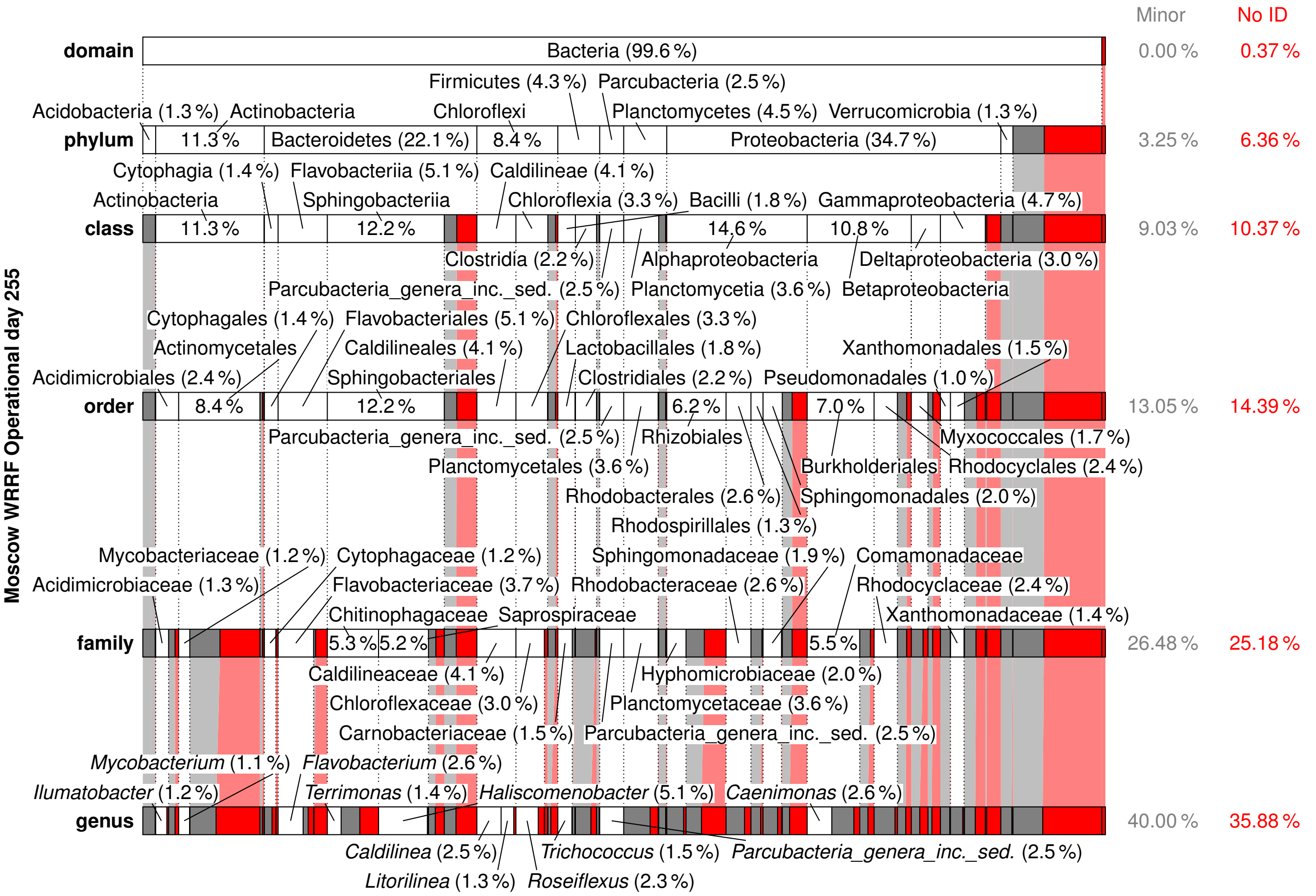

Figure S47. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF operational day 255. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

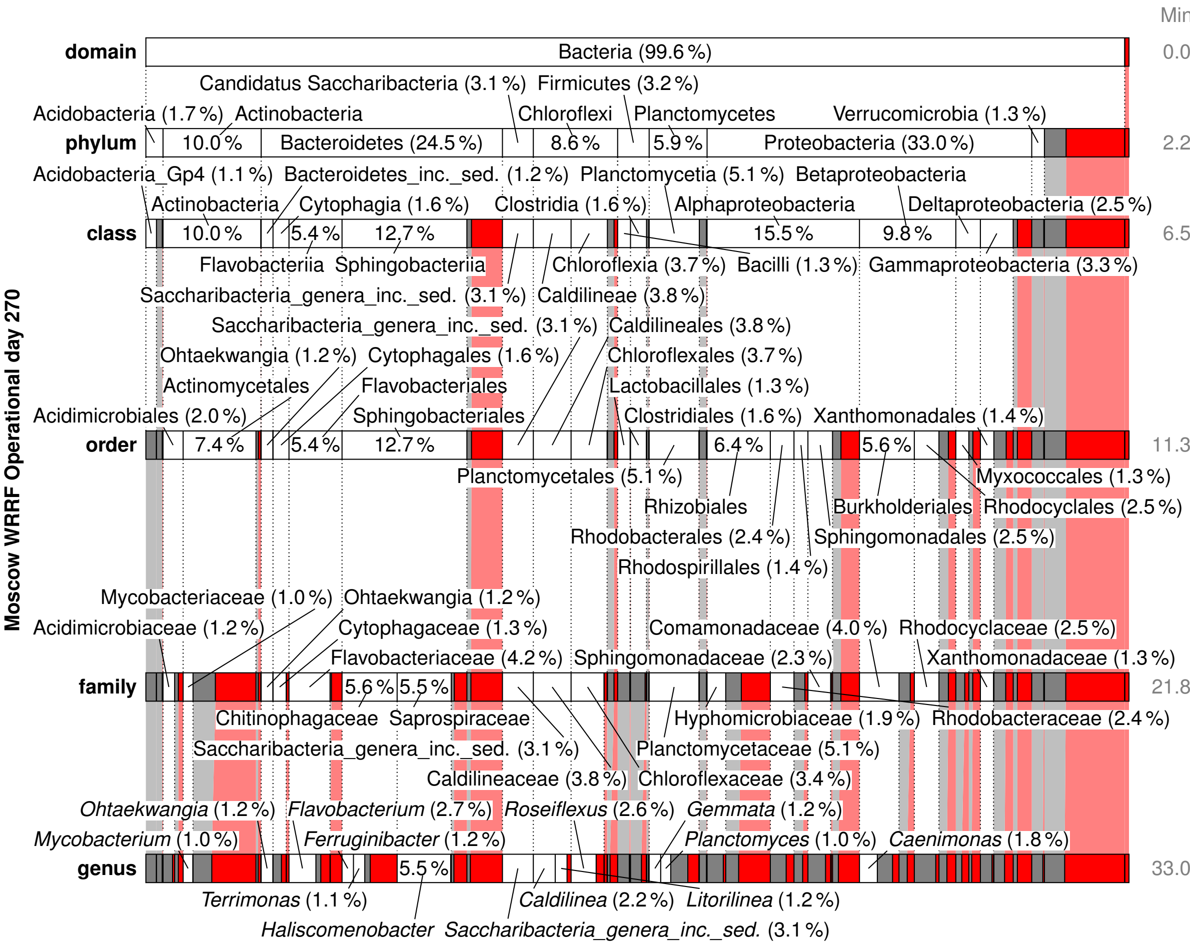

Figure S48. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF operational day 270. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

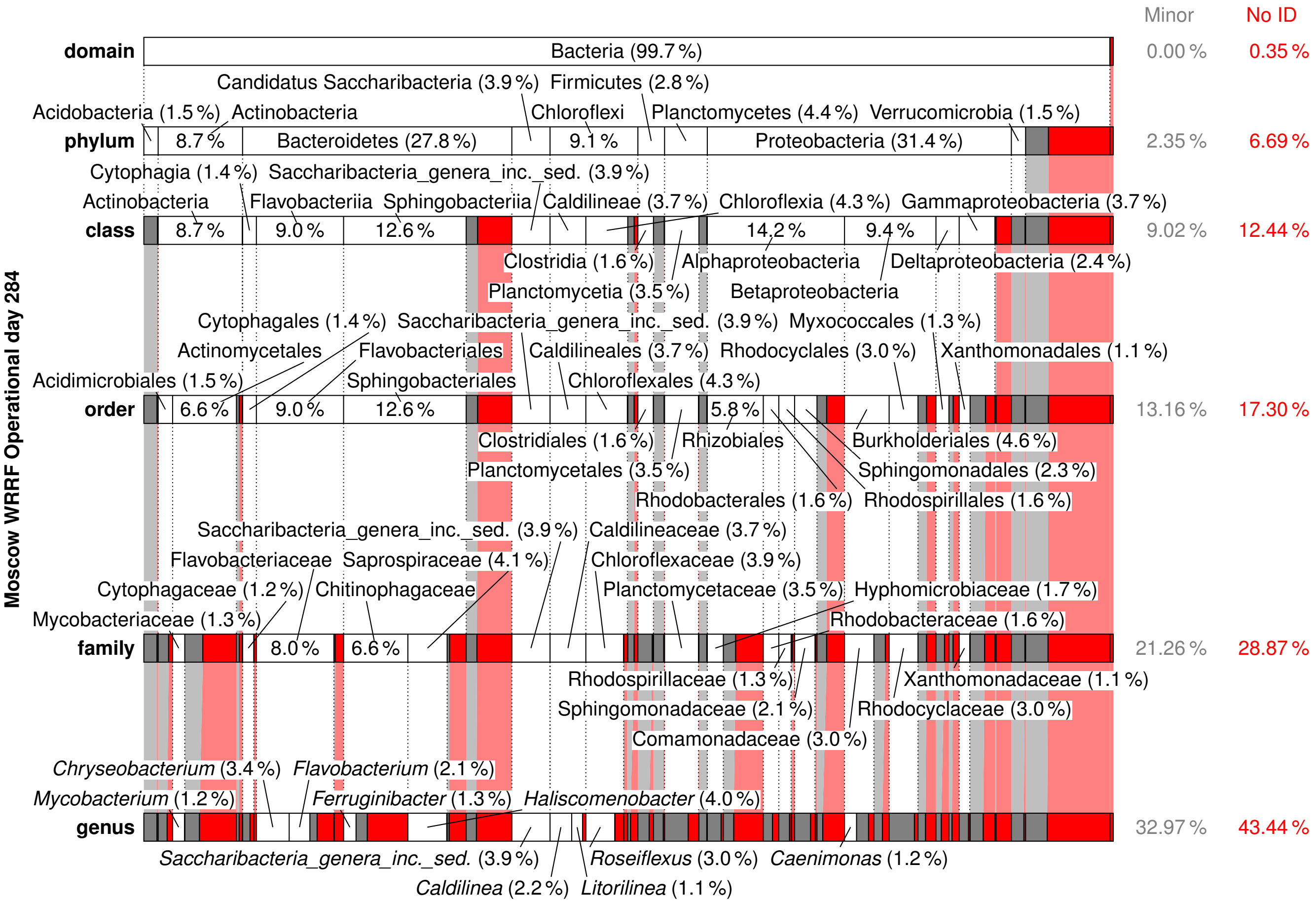

Figure S49. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF operational day 284. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

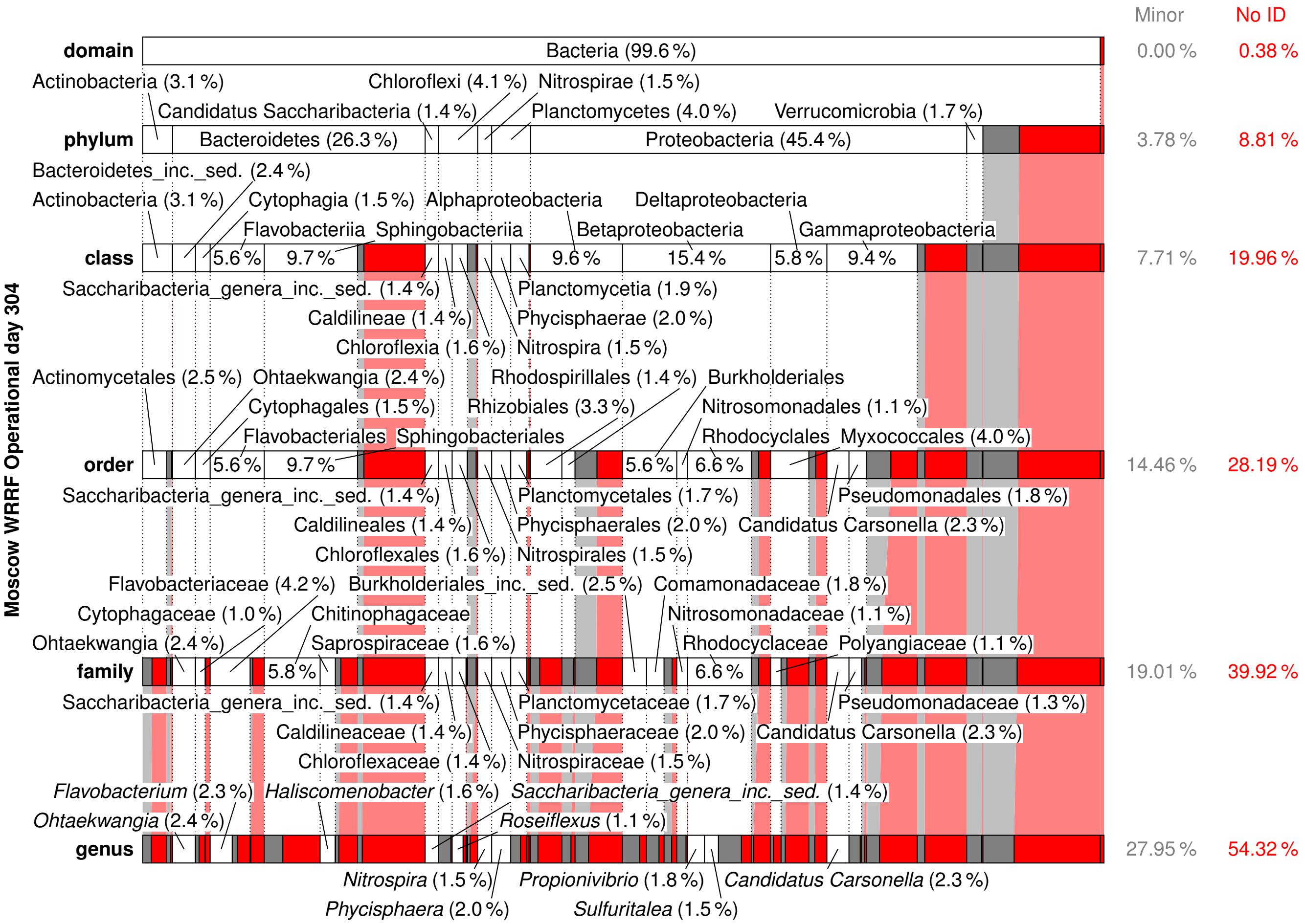

Figure S50. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF operational day 304. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

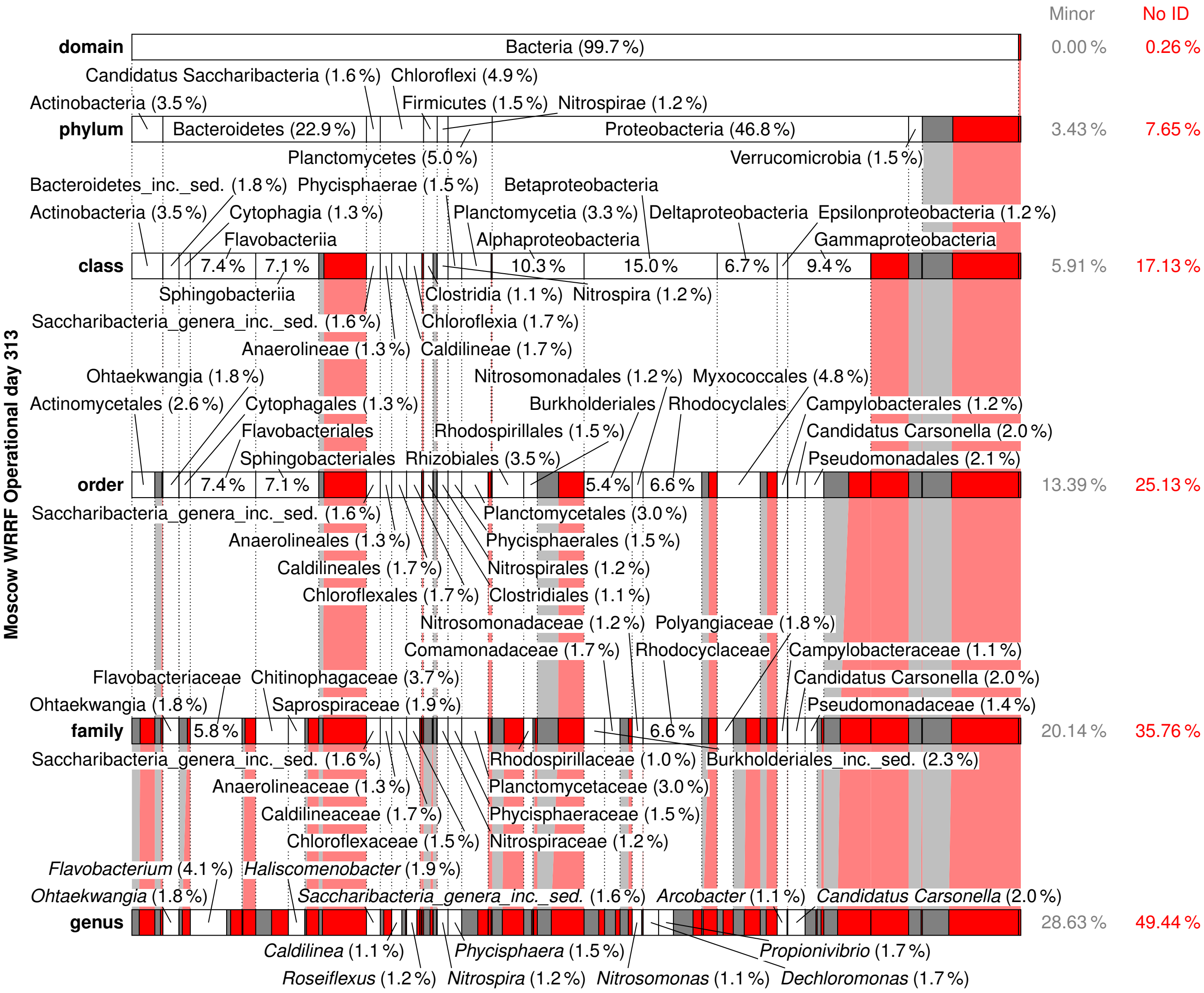

Figure S51. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF operational day 313. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

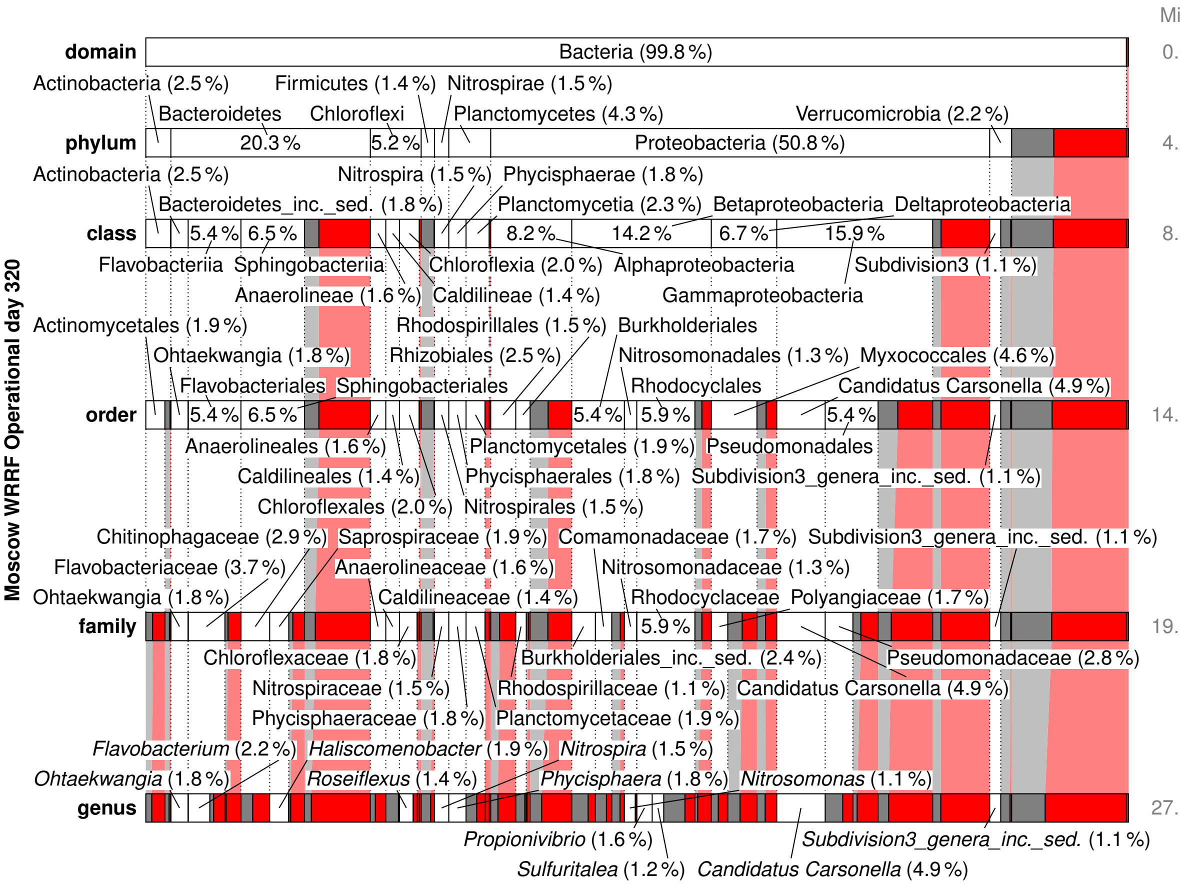

Figure S52. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF operational day 320. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

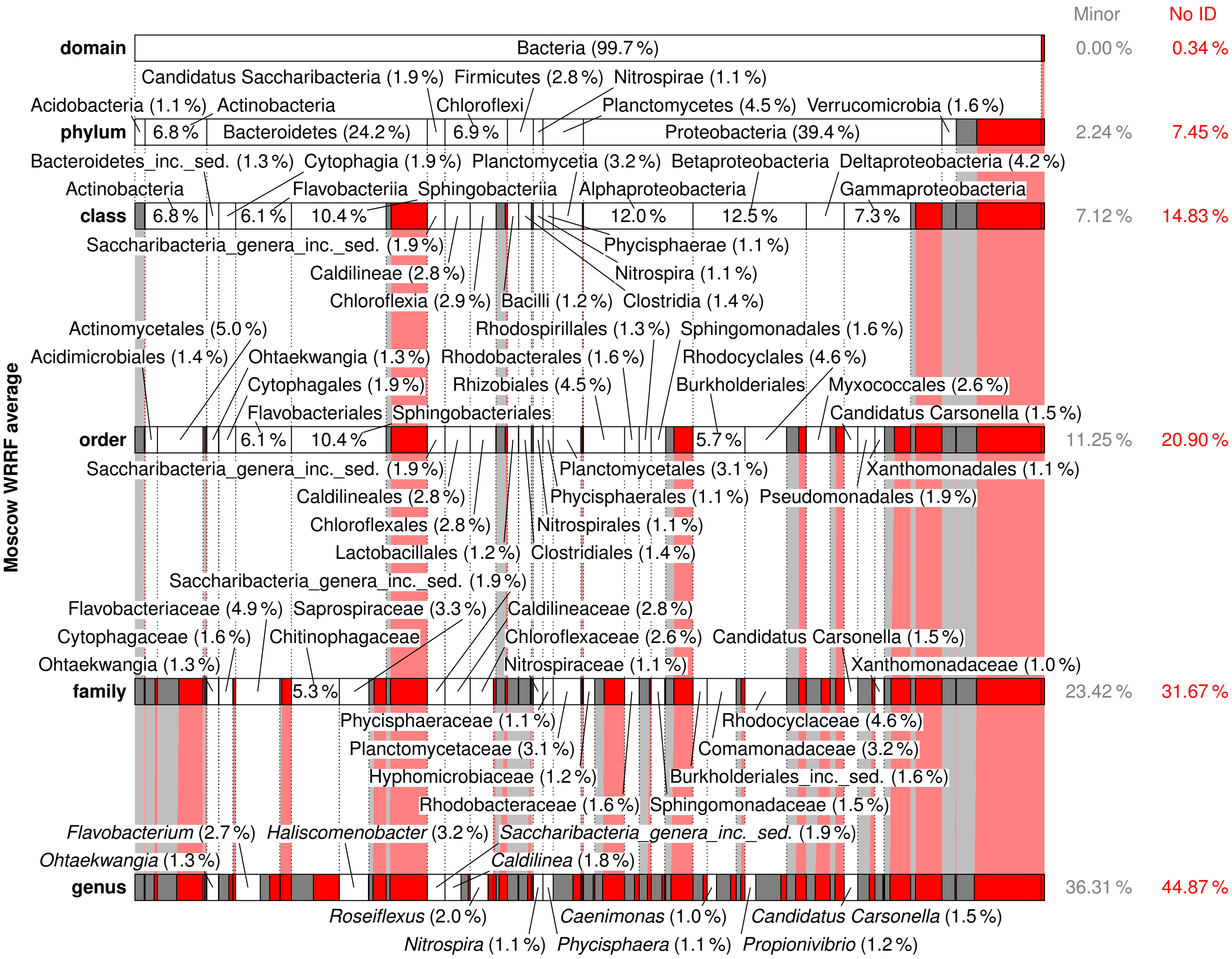

Figure S53. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for Moscow WRRF. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

Table S14. S-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.4	98.7	99.3	99.6	99.7	99.6	99.7	99.4	$\pm 3.46\cdot10^{-1}$
unknown	$6.08\cdot10^{-1}$	1.26	$6.91\cdot10^{-1}$	$4.13\cdot10^{-1}$	$2.62\cdot10^{-1}$	$3.78\cdot10^{-1}$	$2.99\cdot10^{-1}$	$5.59\cdot10^{-1}$	$\pm 3.46\cdot10^{-1}$
Minor phylotypes (1)[d]	N.D.[e]	$1.34\cdot10^{-3}$	N.D.[e]	$1.81\cdot10^{-3}$	$9.54\cdot10^{-4}$	N.D.[e]	N.D.[e]	$5.87\cdot10^{-4}$	$\pm 7.73\cdot10^{-4}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S15. V-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.9	99.9	100.0	100.0	99.8	99.7	100.0	99.9	$\pm 9.75\cdot10^{-2}$
Minor phylotypes (2)[d]	$8.63\cdot10^{-2}$	$5.74\cdot10^{-2}$	$3.09\cdot10^{-2}$	$3.80\cdot10^{-2}$	$1.75\cdot10^{-1}$	$2.96\cdot10^{-1}$	$4.75\cdot10^{-2}$	$1.04\cdot10^{-1}$	$\pm 9.75\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S16. G-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.8	99.8	99.9	100.0	99.8	99.9	99.8	99.9	$\pm 5.43\cdot10^{-2}$
Minor phylotypes (2)[d]	$1.98\cdot10^{-1}$	$2.00\cdot10^{-1}$	$1.25\cdot10^{-1}$	$4.44\cdot10^{-2}$	$1.70\cdot10^{-1}$	$1.29\cdot10^{-1}$	$1.66\cdot10^{-1}$	$1.48\cdot10^{-1}$	$\pm 5.43\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S17. R-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.9	99.9	99.9	99.9	99.9	99.9	99.6	99.9	$\pm 1.23\cdot10^{-1}$
Minor phylotypes (2)[d]	$6.23\cdot10^{-2}$	$5.77\cdot10^{-2}$	$8.53\cdot10^{-2}$	$8.52\cdot10^{-2}$	$1.34\cdot10^{-1}$	$1.01\cdot10^{-1}$	$4.07\cdot10^{-1}$	$1.33\cdot10^{-1}$	$\pm 1.23\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S18. Moscow WRRF domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	225	255	270	284	304	313	320	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.6	99.6	99.6	99.7	99.6	99.7	99.8	99.7	$\pm 7.92\cdot10^{-2}$
Minor phylotypes (2)[d]	$3.96\cdot10^{-1}$	$3.68\cdot10^{-1}$	$4.32\cdot10^{-1}$	$3.48\cdot10^{-1}$	$3.84\cdot10^{-1}$	$2.58\cdot10^{-1}$	$2.11\cdot10^{-1}$	$3.42\cdot10^{-1}$	$\pm 7.92\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S19. Summary of domain-level relative abundance by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	S-EBPR (S14)		V-EBPR (S15)		G-EBPR (S16)		R-EBPR (S17)		Moscow WRRF (S18)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
Bacteria	99.4	$\pm 3.46\cdot10^{-1}$	99.9	$\pm 9.75\cdot10^{-2}$	99.9	$\pm 5.43\cdot10^{-2}$	99.9	$\pm 1.23\cdot10^{-1}$	99.7	$\pm 7.92\cdot10^{-2}$
unknown	$5.59\cdot10^{-1}$	$\pm 3.46\cdot10^{-1}$	$1.03\cdot10^{-1}$	$\pm 9.74\cdot10^{-2}$	$1.47\cdot10^{-1}$	$\pm 5.49\cdot10^{-2}$	$1.33\cdot10^{-1}$	$\pm 1.23\cdot10^{-1}$	$3.40\cdot10^{-1}$	$\pm 7.88\cdot10^{-2}$
Minor phylotypes (1)[d]	$5.87\cdot10^{-4}$	$\pm 7.73\cdot10^{-4}$	$9.84\cdot10^{-4}$	$\pm 1.71\cdot10^{-3}$	$3.88\cdot10^{-4}$	$\pm 6.63\cdot10^{-4}$	$3.58\cdot10^{-4}$	$\pm 9.47\cdot10^{-4}$	$2.37\cdot10^{-3}$	$\pm 1.68\cdot10^{-3}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S20. S-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Proteobacteria	56.1	46.8	67.1	63.5	44.7	54.9	65.5	56.9	±8.90
Bacteroidetes	19.6	37.5	15.3	13.8	28.8	18.0	17.9	21.6	±8.52
Planctomycetes	7.31	3.83	2.90	3.59	9.27	10.5	5.10	6.07	±2.99
unknown d: *Bacteria*	6.93	4.46	7.37	10.9	4.62	2.63	4.15	5.86	±2.76
Verrucomicrobia	2.18	1.55	1.09	1.58	2.24	$1.60\cdot10^{-1}$	3.61	1.77	±1.07
Minor phylotypes (34)[d]	2.06	1.40	1.09	1.06	1.30	1.39	1.57	1.41	±$3.39\cdot10^{-1}$
Firmicutes	$2.43\cdot10^{-1}$	$1.18\cdot10^{-1}$	$1.40\cdot10^{-1}$	$2.23\cdot10^{-1}$	$2.90\cdot10^{-1}$	8.12	$1.34\cdot10^{-1}$	1.32	±3.00
Chloroflexi	2.55	$9.68\cdot10^{-1}$	1.14	2.00	1.35	$2.95\cdot10^{-1}$	$2.46\cdot10^{-1}$	1.22	±$8.43\cdot10^{-1}$
Armatimonadetes	$4.00\cdot10^{-1}$	$4.22\cdot10^{-1}$	1.05	$6.04\cdot10^{-1}$	$6.10\cdot10^{-1}$	2.92	$1.50\cdot10^{-1}$	$8.80\cdot10^{-1}$	±$9.42\cdot10^{-1}$
SR1	N.D.[e]	N.D.[e]	N.D.[e]	N.D.[e]	4.91	$7.10\cdot10^{-2}$	$2.68\cdot10^{-1}$	$7.50\cdot10^{-1}$	±1.84
Acidobacteria	1.00	$5.24\cdot10^{-1}$	1.33	$8.59\cdot10^{-1}$	$4.75\cdot10^{-1}$	$5.62\cdot10^{-1}$	$4.08\cdot10^{-1}$	$7.37\cdot10^{-1}$	±$3.39\cdot10^{-1}$
Nitrospirae	1.07	$4.03\cdot10^{-2}$	$7.22\cdot10^{-1}$	1.37	$9.96\cdot10^{-1}$	$1.13\cdot10^{-3}$	$6.88\cdot10^{-1}$	$6.98\cdot10^{-1}$	±$5.17\cdot10^{-1}$
unknown	$6.08\cdot10^{-1}$	1.26	$6.91\cdot10^{-1}$	$4.13\cdot10^{-1}$	$2.62\cdot10^{-1}$	$3.78\cdot10^{-1}$	$2.99\cdot10^{-1}$	$5.59\cdot10^{-1}$	±$3.46\cdot10^{-1}$
Candidatus Saccharibacteria	$1.47\cdot10^{-2}$	1.08	$1.90\cdot10^{-2}$	$7.07\cdot10^{-2}$	$1.41\cdot10^{-1}$	$2.26\cdot10^{-3}$	N.D.[e]	$1.90\cdot10^{-1}$	±$3.97\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S21. V-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Proteobacteria	49.3	57.5	50.5	55.1	35.5	51.1	59.7	51.2	± 7.92
Bacteroidetes	28.8	31.5	34.1	34.1	47.5	30.6	10.6	31.0	±10.9
unknown d: *Bacteria*	4.37	3.37	3.12	1.86	3.23	2.89	7.43	3.75	± 1.78
Verrucomicrobia	4.30	$9.91\cdot10^{-1}$	4.77	2.15	1.55	2.74	5.98	3.21	± 1.84
Actinobacteria	3.99	1.40	$9.88\cdot10^{-1}$	1.80	1.78	1.74	2.58	2.04	± $9.87\cdot10^{-1}$
Firmicutes	1.65	$8.04\cdot10^{-1}$	$9.16\cdot10^{-1}$	1.95	3.19	3.42	1.99	1.99	± 1.01
Chloroflexi	1.61	1.08	$3.25\cdot10^{-1}$	$4.88\cdot10^{-1}$	2.99	3.69	$6.26\cdot10^{-1}$	1.54	± 1.31
Planctomycetes	1.24	$9.46\cdot10^{-1}$	$5.50\cdot10^{-1}$	$4.08\cdot10^{-1}$	1.21	$5.13\cdot10^{-1}$	3.85	1.25	± 1.20
Acidobacteria	$7.74\cdot10^{-1}$	$9.96\cdot10^{-1}$	$2.40\cdot10^{-1}$	$2.51\cdot10^{-1}$	$8.89\cdot10^{-1}$	1.20	4.29	1.23	± 1.40
Minor phylotypes (36)[d]	2.23	$7.49\cdot10^{-1}$	$5.09\cdot10^{-1}$	$5.34\cdot10^{-1}$	1.39	1.38	1.33	1.16	± $6.13\cdot10^{-1}$
Parcubacteria	1.36	$1.98\cdot10^{-1}$	3.91	$9.15\cdot10^{-1}$	$3.86\cdot10^{-1}$	$1.40\cdot10^{-1}$	$1.53\cdot10^{-1}$	1.01	± 1.36

Table S21. V-EBPR phylum-level EUB results summary continued.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Candidatus Saccharibacteria	$3.29\cdot10^{-1}$	$3.85\cdot10^{-1}$	$6.32\cdot10^{-2}$	$4.28\cdot10^{-1}$	$3.86\cdot10^{-1}$	$6.53\cdot10^{-1}$	1.53	$5.40\cdot10^{-1}$	±	$4.71\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S22. G-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Proteobacteria	33.7	51.0	54.5	49.4	52.1	49.3	62.3	50.3	±	8.57
Bacteroidetes	23.2	24.7	28.2	30.1	19.5	21.2	13.0	22.8	±	5.72
Candidatus Saccharibacteria	25.4	9.85	3.00	2.77	8.82	$8.66\cdot10^{-1}$	4.39	7.87	±	8.38
Actinobacteria	8.95	3.12	2.20	5.56	7.02	11.6	2.32	5.83	±	3.60
unknown d: *Bacteria*	3.20	4.63	4.76	3.53	3.86	3.72	5.88	4.23	±	$9.24\cdot10^{-1}$
Chloroflexi	$9.86\cdot10^{-1}$	1.05	1.96	2.82	1.54	3.15	$7.45\cdot10^{-1}$	1.75	±	$9.40\cdot10^{-1}$
Firmicutes	1.05	1.11	$5.17\cdot10^{-1}$	$9.08\cdot10^{-1}$	1.62	4.88	1.57	1.67	±	1.47
Verrucomicrobia	1.14	1.41	1.06	$9.78\cdot10^{-1}$	1.87	1.53	2.73	1.53	±	$6.14\cdot10^{-1}$
Minor phylotypes (36)[d]	1.75	2.33	1.14	$7.22\cdot10^{-1}$	1.81	1.66	$9.11\cdot10^{-1}$	1.48	±	$5.71\cdot10^{-1}$
Acidobacteria	$2.22\cdot10^{-1}$	$4.19\cdot10^{-1}$	$6.86\cdot10^{-1}$	$5.78\cdot10^{-1}$	$5.45\cdot10^{-1}$	$9.57\cdot10^{-1}$	3.56	$9.95\cdot10^{-1}$	±	1.15
Planctomycetes	$4.33\cdot10^{-1}$	$3.18\cdot10^{-1}$	1.12	$4.65\cdot10^{-1}$	$5.59\cdot10^{-1}$	$8.43\cdot10^{-1}$	2.24	$8.53\cdot10^{-1}$	±	$6.68\cdot10^{-1}$
Parcubacteria	$5.97\cdot10^{-3}$	$6.82\cdot10^{-2}$	$7.76\cdot10^{-1}$	2.17	$7.97\cdot10^{-1}$	$2.86\cdot10^{-1}$	$4.14\cdot10^{-1}$	$6.45\cdot10^{-1}$	±	$7.39\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S23. R-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Proteobacteria	63.0	66.4	66.6	59.5	55.7	50.6	53.9	59.4	±	6.28
Bacteroidetes	21.7	25.2	18.1	27.6	20.7	24.1	19.6	22.5	±	3.36

Table S23. R-EBPR phylum-level EUB results summary continued.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
unknown d: *Bacteria*	5.63	3.00	5.28	3.29	4.84	6.58	5.87	4.93	± 1.33
Verrucomicrobia	$9.11\cdot10^{-1}$	1.01	2.09	2.68	4.39	1.76	2.70	2.22	± 1.19
Planctomycetes	$2.89\cdot10^{-1}$	$2.48\cdot10^{-1}$	$3.85\cdot10^{-1}$	$4.56\cdot10^{-1}$	1.60	1.87	6.85	1.67	± 2.38
Chloroflexi	1.57	$7.68\cdot10^{-1}$	1.90	1.53	2.00	2.20	1.18	1.59	± $4.97\cdot10^{-1}$
Actinobacteria	1.38	$4.01\cdot10^{-1}$	$8.55\cdot10^{-1}$	1.06	2.05	2.62	2.75	1.59	± $9.04\cdot10^{-1}$
Minor phylotypes (34)[d]	1.68	1.30	2.32	1.82	1.51	1.27	$8.68\cdot10^{-1}$	1.54	± $4.64\cdot10^{-1}$
Acidobacteria	$4.99\cdot10^{-1}$	$4.55\cdot10^{-1}$	$3.92\cdot10^{-1}$	$1.67\cdot10^{-1}$	2.85	3.80	2.60	1.54	± 1.49
Firmicutes	$7.90\cdot10^{-1}$	$8.96\cdot10^{-1}$	$7.13\cdot10^{-1}$	$9.25\cdot10^{-1}$	1.36	1.84	$7.43\cdot10^{-1}$	1.04	± $4.15\cdot10^{-1}$
Candidatus Saccharibacteria	1.21	$2.03\cdot10^{-1}$	$5.44\cdot10^{-1}$	$5.50\cdot10^{-1}$	1.25	1.01	1.34	$8.74\cdot10^{-1}$	± $4.40\cdot10^{-1}$
Parcubacteria	1.36	$8.22\cdot10^{-2}$	$7.40\cdot10^{-1}$	$3.11\cdot10^{-1}$	$7.78\cdot10^{-1}$	$1.82\cdot10^{-1}$	$3.37\cdot10^{-1}$	$5.42\cdot10^{-1}$	± $4.49\cdot10^{-1}$
Nitrospirae	N.D.[e]	$3.50\cdot10^{-3}$	$1.00\cdot10^{-2}$	$3.55\cdot10^{-3}$	$7.51\cdot10^{-1}$	1.95	N.D.[e]	$3.88\cdot10^{-1}$	± $7.42\cdot10^{-1}$
Armatimonadetes	N.D.[e]	$3.50\cdot10^{-3}$	$1.67\cdot10^{-2}$	$4.44\cdot10^{-2}$	$1.72\cdot10^{-1}$	$2.29\cdot10^{-1}$	1.23	$2.42\cdot10^{-1}$	± $4.43\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S24. Moscow WRRF phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c] %
Proteobacteria	33.8	34.7	33.0	31.4	45.4	46.8	50.8	39.4	± 7.95
Bacteroidetes	25.8	22.1	24.5	27.8	26.3	22.9	20.3	24.2	± 2.62
unknown d: *Bacteria*	8.27	5.99	5.96	6.34	8.43	7.39	7.39	7.11	± 1.03
Chloroflexi	7.91	8.41	8.58	9.06	4.07	4.87	5.17	6.87	± 2.08
Actinobacteria	8.38	11.3	9.98	8.71	3.12	3.49	2.55	6.79	± 3.63
Planctomycetes	3.12	4.47	5.89	4.41	4.04	4.97	4.27	4.45	± $8.49\cdot10^{-1}$
Firmicutes	5.73	4.35	3.21	2.75	$9.96\cdot10^{-1}$	1.54	1.36	2.85	± 1.74
Candidatus Saccharibacteria	1.67	$9.83\cdot10^{-1}$	3.14	3.94	1.40	1.56	$8.89\cdot10^{-1}$	1.94	± 1.15
Minor phylotypes (35)[d]	1.80	1.88	1.62	1.32	2.12	2.09	2.23	1.87	± $3.21\cdot10^{-1}$
Verrucomicrobia	1.60	1.26	1.29	1.47	1.69	1.55	2.23	1.58	± $3.24\cdot10^{-1}$
Acidobacteria	$5.98\cdot10^{-1}$	1.33	1.74	1.47	$7.59\cdot10^{-1}$	$9.64\cdot10^{-1}$	$9.48\cdot10^{-1}$	1.12	± $4.12\cdot10^{-1}$
Nitrospirae	$8.48\cdot10^{-1}$	$7.49\cdot10^{-1}$	$7.48\cdot10^{-1}$	$9.27\cdot10^{-1}$	1.46	1.21	1.45	1.06	± $3.14\cdot10^{-1}$

Table S24. Moscow WRRF phylum-level EUB results summary continued.

Phylum[a,b]	225	255	270	284	304	313	320	Average ±	SD[c]
	%	%	%	%	%	%	%	%	
Parcubacteria	$4.44\cdot10^{-1}$	2.50	$2.72\cdot10^{-1}$	$4.54\cdot10^{-1}$	$2.92\cdot10^{-1}$	$6.28\cdot10^{-1}$	$4.35\cdot10^{-1}$	$7.17\cdot10^{-1}$	$\pm 7.93\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S25. Summary of phylum-level relative abundance by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	S-EBPR (S20)		V-EBPR (S21)		G-EBPR (S22)		R-EBPR (S23)		Moscow WRRF (S24)	
	Average ±	SD[c]	Average ±	SD[c]	Average ±	SD[c]	Average ±	SD[c]	Average ±	SD[c]
	%		%		%		%		%	
Proteobacteria	56.9	± 8.90	51.2	± 7.92	50.3	± 8.57	59.4	± 6.28	39.4	± 7.95
Bacteroidetes	21.6	± 8.52	31.0	± 10.9	22.8	± 5.72	22.5	± 3.36	24.2	± 2.62
Candidatus Saccharibacteria	$1.90\cdot10^{-1}$	$\pm 3.97\cdot10^{-1}$	$5.40\cdot10^{-1}$	$\pm 4.71\cdot10^{-1}$	7.87	± 8.38	$8.74\cdot10^{-1}$	$\pm 4.40\cdot10^{-1}$	1.94	± 1.15
unknown d: *Bacteria*	5.86	± 2.76	3.75	± 1.78	4.23	$\pm 9.24\cdot10^{-1}$	4.93	± 1.33	7.11	± 1.03
Chloroflexi	1.22	$\pm 8.43\cdot10^{-1}$	1.54	± 1.31	1.75	$\pm 9.40\cdot10^{-1}$	1.59	$\pm 4.97\cdot10^{-1}$	6.87	± 2.08
Actinobacteria	$2.70\cdot10^{-1}$	$\pm 1.79\cdot10^{-1}$	2.04	$\pm 9.87\cdot10^{-1}$	5.83	± 3.60	1.59	$\pm 9.04\cdot10^{-1}$	6.79	± 3.63
Planctomycetes	6.07	± 2.99	1.25	± 1.20	$8.53\cdot10^{-1}$	$\pm 6.68\cdot10^{-1}$	1.67	± 2.38	4.45	$\pm 8.49\cdot10^{-1}$
Verrucomicrobia	1.77	± 1.07	3.21	± 1.84	1.53	$\pm 6.14\cdot10^{-1}$	2.22	± 1.19	1.58	$\pm 3.24\cdot10^{-1}$
Firmicutes	1.32	± 3.00	1.99	± 1.01	1.67	± 1.47	1.04	$\pm 4.15\cdot10^{-1}$	2.85	± 1.74
Acidobacteria	$7.37\cdot10^{-1}$	$\pm 3.39\cdot10^{-1}$	1.23	± 1.40	$9.95\cdot10^{-1}$	± 1.15	1.54	± 1.49	1.12	$\pm 4.12\cdot10^{-1}$
Minor phylotypes (32)[d]	$8.79\cdot10^{-1}$	$\pm 3.27\cdot10^{-1}$	$9.49\cdot10^{-1}$	$\pm 5.87\cdot10^{-1}$	1.23	$\pm 5.30\cdot10^{-1}$	1.26	$\pm 4.23\cdot10^{-1}$	1.36	$\pm 4.07\cdot10^{-1}$
Nitrospirae	$6.98\cdot10^{-1}$	$\pm 5.17\cdot10^{-1}$	$1.18\cdot10^{-3}$	$\pm 1.52\cdot10^{-3}$	$9.20\cdot10^{-4}$	$\pm 1.28\cdot10^{-3}$	$3.88\cdot10^{-1}$	$\pm 7.42\cdot10^{-1}$	1.06	$\pm 3.14\cdot10^{-1}$
Parcubacteria	$2.63\cdot10^{-1}$	$\pm 3.49\cdot10^{-1}$	1.01	± 1.36	$6.45\cdot10^{-1}$	$\pm 7.39\cdot10^{-1}$	$5.42\cdot10^{-1}$	$\pm 4.49\cdot10^{-1}$	$7.17\cdot10^{-1}$	$\pm 7.93\cdot10^{-1}$
Armatimonadetes	$8.80\cdot10^{-1}$	$\pm 9.42\cdot10^{-1}$	$7.80\cdot10^{-2}$	$\pm 8.72\cdot10^{-2}$	$8.83\cdot10^{-2}$	$\pm 8.71\cdot10^{-2}$	$2.42\cdot10^{-1}$	$\pm 4.43\cdot10^{-1}$	$1.30\cdot10^{-1}$	$\pm 7.27\cdot10^{-2}$
SR1	$7.50\cdot10^{-1}$	± 1.84	$2.96\cdot10^{-2}$	$\pm 4.39\cdot10^{-2}$	$4.33\cdot10^{-3}$	$\pm 6.34\cdot10^{-3}$	$1.44\cdot10^{-1}$	$\pm 1.78\cdot10^{-1}$	$3.85\cdot10^{-2}$	$\pm 3.03\cdot10^{-2}$
unknown	$5.59\cdot10^{-1}$	$\pm 3.46\cdot10^{-1}$	$1.03\cdot10^{-1}$	$\pm 9.74\cdot10^{-2}$	$1.47\cdot10^{-1}$	$\pm 5.49\cdot10^{-2}$	$1.33\cdot10^{-1}$	$\pm 1.23\cdot10^{-1}$	$3.40\cdot10^{-1}$	$\pm 7.88\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S26. S-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average	± %	SD[c]
Alphaproteobacteria	32.8	27.9	27.5	24.0	25.1	39.5	20.7	28.2	±	6.23
Betaproteobacteria	15.1	11.8	28.2	30.1	13.7	6.74	36.5	20.3	±	11.2
Flavobacteriia	6.85	17.3	2.77	2.81	17.5	9.71	7.99	9.28	±	6.11
Bacteroidetes_inc._sed.[d]	8.52	13.9	3.98	5.07	5.21	4.54	4.42	6.52	±	3.58
unknown d: *Bacteria*	6.93	4.46	7.37	10.9	4.62	2.63	4.15	5.86	±	2.76
Gammaproteobacteria	4.19	4.05	4.42	3.99	3.35	6.94	4.23	4.45	±	1.15
Sphingobacteriia	2.96	2.87	5.68	3.84	4.51	1.81	3.56	3.60	±	1.25
Planctomycetia	5.87	2.98	1.77	2.64	4.57	3.44	1.59	3.27	±	1.53
Minor phylotypes (79)[e]	3.91	1.97	2.79	3.10	2.33	2.64	2.67	2.77	±	$6.15\cdot10^{-1}$
Phycisphaerae	1.37	$8.11\cdot10^{-1}$	1.10	$9.30\cdot10^{-1}$	4.63	7.05	3.48	2.77	±	2.39
Deltaproteobacteria	2.49	2.09	3.31	3.90	1.22	$8.37\cdot10^{-1}$	2.07	2.27	±	1.08
unknown p: *Proteobacteria*	1.53	$9.47\cdot10^{-1}$	3.62	1.46	1.35	$8.87\cdot10^{-1}$	2.00	1.68	±	$9.32\cdot10^{-1}$
unknown p: *Bacteroidetes*	$8.97\cdot10^{-1}$	2.07	2.61	1.81	1.47	1.46	1.35	1.67	±	$5.54\cdot10^{-1}$
Verrucomicrobiae	1.63	1.35	$5.00\cdot10^{-1}$	1.20	2.01	$8.23\cdot10^{-2}$	3.04	1.40	±	$9.75\cdot10^{-1}$
Clostridia	$2.21\cdot10^{-2}$	$1.88\cdot10^{-2}$	$1.73\cdot10^{-2}$	$2.36\cdot10^{-2}$	$9.73\cdot10^{-2}$	6.43	$1.96\cdot10^{-2}$	$9.47\cdot10^{-1}$	±	2.42
SR1_genera_inc._sed.[d]	N.D.[f]	N.D.[f]	N.D.[f]	N.D.[f]	4.91	$7.10\cdot10^{-2}$	$2.68\cdot10^{-1}$	$7.50\cdot10^{-1}$	±	1.84
Nitrospira	1.07	$4.03\cdot10^{-2}$	$7.22\cdot10^{-1}$	1.37	$9.96\cdot10^{-1}$	$1.13\cdot10^{-3}$	$6.88\cdot10^{-1}$	$6.98\cdot10^{-1}$	±	$5.17\cdot10^{-1}$
unknown	$6.08\cdot10^{-1}$	1.26	$6.91\cdot10^{-1}$	$4.13\cdot10^{-1}$	$2.62\cdot10^{-1}$	$3.78\cdot10^{-1}$	$2.99\cdot10^{-1}$	$5.59\cdot10^{-1}$	±	$3.46\cdot10^{-1}$
Armatimonadetes_gp5	$3.53\cdot10^{-1}$	$3.63\cdot10^{-1}$	$4.55\cdot10^{-1}$	$5.47\cdot10^{-1}$	$3.41\cdot10^{-1}$	1.71	$1.17\cdot10^{-1}$	$5.55\cdot10^{-1}$	±	$5.26\cdot10^{-1}$
Cytophagia	$3.26\cdot10^{-1}$	1.41	$2.87\cdot10^{-1}$	$2.92\cdot10^{-1}$	$6.58\cdot10^{-2}$	$2.05\cdot10^{-1}$	$5.89\cdot10^{-1}$	$4.53\cdot10^{-1}$	±	$4.49\cdot10^{-1}$
Caldilineae	1.48	$8.65\cdot10^{-1}$	$2.39\cdot10^{-1}$	$3.62\cdot10^{-1}$	$4.96\cdot10^{-2}$	$2.48\cdot10^{-2}$	$1.10\cdot10^{-2}$	$4.33\cdot10^{-1}$	±	$5.50\cdot10^{-1}$
Acidobacteria_Gp4	$6.13\cdot10^{-1}$	$3.38\cdot10^{-1}$	1.07	$4.69\cdot10^{-1}$	$1.41\cdot10^{-1}$	$2.02\cdot10^{-1}$	$6.72\cdot10^{-2}$	$4.14\cdot10^{-1}$	±	$3.45\cdot10^{-1}$
unknown p: *Chloroflexi*	$4.56\cdot10^{-1}$	$6.99\cdot10^{-2}$	$2.28\cdot10^{-1}$	$6.00\cdot10^{-1}$	1.08	$1.09\cdot10^{-1}$	$1.92\cdot10^{-1}$	$3.91\cdot10^{-1}$	±	$3.58\cdot10^{-1}$
Fimbriimonadia	$3.43\cdot10^{-2}$	$4.71\cdot10^{-2}$	$5.66\cdot10^{-1}$	$5.26\cdot10^{-2}$	$2.54\cdot10^{-1}$	1.06	$3.30\cdot10^{-2}$	$2.93\cdot10^{-1}$	±	$3.92\cdot10^{-1}$
Bacilli	$4.90\cdot10^{-3}$	$4.03\cdot10^{-3}$	$6.92\cdot10^{-3}$	$3.62\cdot10^{-3}$	$1.81\cdot10^{-2}$	1.54	$1.22\cdot10^{-3}$	$2.25\cdot10^{-1}$	±	$5.79\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[d]	$1.47\cdot10^{-2}$	1.08	$1.90\cdot10^{-2}$	$7.07\cdot10^{-2}$	$1.41\cdot10^{-1}$	$2.26\cdot10^{-3}$	N.D.[f]	$1.90\cdot10^{-1}$	±	$3.97\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[f] N.D. = Not detected.

Table S27. V-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Betaproteobacteria	21.3	38.1	36.2	38.6	18.7	28.2	13.2	27.8	±	10.3
Alphaproteobacteria	14.4	7.81	6.34	10.1	7.18	13.7	35.6	13.6	±	10.2
unknown p: *Bacteroidetes*	14.5	14.6	14.8	13.1	20.2	9.93	1.37	12.6	±	5.82
Sphingobacteriia	5.58	6.98	9.53	7.37	14.5	9.55	5.31	8.40	±	3.16
Gammaproteobacteria	5.29	2.86	5.83	3.17	4.37	5.58	8.11	5.03	±	1.79
unknown d: *Bacteria*	4.37	3.37	3.12	1.86	3.23	2.89	7.43	3.75	±	1.78
Cytophagia	5.75	6.62	2.04	2.62	2.94	1.57	2.65	3.46	±	1.93
Bacteroidia	1.80	1.72	$8.04\cdot10^{-1}$	3.06	8.15	8.06	$7.65\cdot10^{-2}$	3.38	±	3.35
Minor phylotypes (83)[d]	4.62	2.41	2.04	2.05	4.30	3.87	3.33	3.23	±	1.08
Verrucomicrobiae	3.74	$6.12\cdot10^{-1}$	4.10	1.63	$9.79\cdot10^{-1}$	2.24	5.09	2.63	±	1.70
Flavobacteriia	$9.61\cdot10^{-1}$	1.37	6.58	6.47	$9.96\cdot10^{-1}$	1.03	$5.78\cdot10^{-1}$	2.57	±	2.71
Deltaproteobacteria	5.81	3.33	$6.25\cdot10^{-1}$	1.44	3.06	2.07	1.16	2.50	±	1.76
Actinobacteria	3.99	1.39	$9.81\cdot10^{-1}$	1.78	1.76	1.71	2.58	2.03	±	$9.90\cdot10^{-1}$
unknown p: *Proteobacteria*	1.90	4.89	1.01	1.56	1.15	1.10	1.58	1.88	±	1.36
Clostridia	1.00	$5.33\cdot10^{-1}$	$3.93\cdot10^{-1}$	1.24	2.03	2.61	1.77	1.37	±	$8.11\cdot10^{-1}$
Planctomycetia	1.22	$9.19\cdot10^{-1}$	$5.43\cdot10^{-1}$	$4.04\cdot10^{-1}$	1.13	$4.98\cdot10^{-1}$	3.84	1.22	±	1.20
Caldilineae	1.04	$6.74\cdot10^{-1}$	$1.65\cdot10^{-1}$	$3.70\cdot10^{-1}$	2.32	3.17	$4.25\cdot10^{-1}$	1.17	±	1.14
Parcubacteria_genera_inc._sed.[e]	1.36	$1.98\cdot10^{-1}$	3.91	$9.15\cdot10^{-1}$	$3.86\cdot10^{-1}$	$1.40\cdot10^{-1}$	$1.53\cdot10^{-1}$	1.01	±	1.36
Acidobacteria_Gp4	$1.83\cdot10^{-1}$	$4.26\cdot10^{-1}$	$7.35\cdot10^{-2}$	$9.82\cdot10^{-2}$	$4.76\cdot10^{-1}$	$5.76\cdot10^{-1}$	3.63	$7.80\cdot10^{-1}$	±	1.27
Bacteroidetes_inc._sed.[e]	$2.92\cdot10^{-1}$	$2.22\cdot10^{-1}$	$3.19\cdot10^{-1}$	1.56	$7.48\cdot10^{-1}$	$4.36\cdot10^{-1}$	$5.91\cdot10^{-1}$	$5.95\cdot10^{-1}$	±	$4.61\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	$3.29\cdot10^{-1}$	$3.85\cdot10^{-1}$	$6.32\cdot10^{-2}$	$4.28\cdot10^{-1}$	$3.86\cdot10^{-1}$	$6.53\cdot10^{-1}$	1.53	$5.40\cdot10^{-1}$	±	$4.71\cdot10^{-1}$
Epsilonproteobacteria	$5.58\cdot10^{-1}$	$5.35\cdot10^{-1}$	$4.87\cdot10^{-1}$	$2.96\cdot10^{-1}$	1.02	$3.58\cdot10^{-1}$	N.D.[f]	$4.65\cdot10^{-1}$	±	$3.10\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S28. G-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Betaproteobacteria	11.5	25.3	36.8	26.5	33.6	24.0	11.3	24.2	±	9.83
Alphaproteobacteria	19.0	15.3	12.1	13.5	11.5	19.2	45.0	19.4	±	11.7

Table S28. G-EBPR class-level EUB results summary continued.

Class[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Sphingobacteriia	13.7	8.49	13.7	12.2	6.68	5.42	8.94	9.87	±	3.35
Saccharibacteria_genera_inc._sed.[d]	25.4	9.85	3.00	2.77	8.82	$8.66\cdot10^{-1}$	4.39	7.87	±	8.38
Actinobacteria	8.94	3.12	2.20	5.56	7.02	11.6	2.32	5.83	±	3.60
unknown p: *Bacteroidetes*	1.02	6.13	6.82	9.45	6.00	5.20	$4.14\cdot10^{-1}$	5.00	±	3.22
unknown d: *Bacteria*	3.20	4.63	4.76	3.53	3.86	3.72	5.88	4.23	±	$9.24\cdot10^{-1}$
Minor phylotypes (83)[e]	3.02	3.85	3.22	2.78	3.90	4.54	2.57	3.41	±	$7.08\cdot10^{-1}$
Cytophagia	$6.40\cdot10^{-1}$	2.38	3.46	4.59	3.96	5.98	1.32	3.19	±	1.87
Gammaproteobacteria	$9.82\cdot10^{-1}$	1.69	1.36	2.78	1.88	2.81	3.31	2.12	±	$8.60\cdot10^{-1}$
unknown p: *Proteobacteria*	$8.35\cdot10^{-1}$	2.68	2.50	3.57	1.97	1.10	1.49	2.02	±	$9.66\cdot10^{-1}$
Flavobacteriia	4.87	2.27	2.45	1.98	1.37	$8.18\cdot10^{-1}$	$3.31\cdot10^{-1}$	2.01	±	1.48
Deltaproteobacteria	1.18	4.60	1.45	2.43	1.66	1.43	1.16	1.99	±	1.23
Bacteroidetes_inc._sed.[d]	2.79	4.61	1.72	1.65	$5.75\cdot10^{-1}$	$3.22\cdot10^{-1}$	1.90	1.94	±	1.44
Caldilineae	$7.82\cdot10^{-1}$	$8.78\cdot10^{-1}$	1.49	2.30	$8.49\cdot10^{-1}$	1.77	$5.79\cdot10^{-1}$	1.24	±	$6.32\cdot10^{-1}$
Clostridia	$3.86\cdot10^{-1}$	$5.68\cdot10^{-1}$	$1.79\cdot10^{-1}$	$3.56\cdot10^{-1}$	1.12	3.94	1.32	1.13	±	1.31
Verrucomicrobiae	$9.40\cdot10^{-1}$	$9.45\cdot10^{-1}$	$3.55\cdot10^{-1}$	$3.61\cdot10^{-1}$	1.29	1.33	2.32	1.08	±	$6.73\cdot10^{-1}$
Bacteroidia	$1.79\cdot10^{-1}$	$8.57\cdot10^{-1}$	$7.64\cdot10^{-2}$	$2.28\cdot10^{-1}$	$8.92\cdot10^{-1}$	3.43	$8.28\cdot10^{-2}$	$8.20\cdot10^{-1}$	±	1.20
Planctomycetia	$3.28\cdot10^{-1}$	$2.23\cdot10^{-1}$	$9.53\cdot10^{-1}$	$3.94\cdot10^{-1}$	$5.46\cdot10^{-1}$	$8.29\cdot10^{-1}$	2.24	$7.87\cdot10^{-1}$	±	$6.91\cdot10^{-1}$
Epsilonproteobacteria	$1.95\cdot10^{-1}$	1.37	$3.06\cdot10^{-1}$	$6.36\cdot10^{-1}$	1.38	$8.02\cdot10^{-1}$	N.D.[f]	$6.70\cdot10^{-1}$	±	$5.50\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[d]	$5.97\cdot10^{-3}$	$6.82\cdot10^{-2}$	$7.76\cdot10^{-1}$	2.17	$7.97\cdot10^{-1}$	$2.86\cdot10^{-1}$	$4.14\cdot10^{-1}$	$6.45\cdot10^{-1}$	±	$7.39\cdot10^{-1}$
Acidobacteria_Gp4	$1.33\cdot10^{-1}$	$1.79\cdot10^{-1}$	$2.86\cdot10^{-1}$	$2.82\cdot10^{-1}$	$2.37\cdot10^{-1}$	$6.10\cdot10^{-1}$	2.73	$6.37\cdot10^{-1}$	±	$9.36\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[f] N.D. = Not detected.

Table S29. R-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Betaproteobacteria	46.5	47.4	37.9	40.5	23.3	24.2	1.59	31.6	±	16.4
Alphaproteobacteria	6.10	4.38	7.02	11.9	25.4	19.3	44.8	17.0	±	14.5
Sphingobacteriia	12.3	13.4	8.05	10.6	10.6	15.2	2.05	10.3	±	4.29
Gammaproteobacteria	5.93	8.11	10.4	3.00	3.99	3.49	5.25	5.74	±	2.69

Table S29. R-EBPR class-level EUB results summary continued.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown d: *Bacteria*	5.63	3.00	5.28	3.29	4.84	6.58	5.87	4.93	±	1.33
Flavobacteriia	3.70	6.45	4.54	7.85	4.35	4.54	$4.69\cdot10^{-1}$	4.56	±	2.31
Minor phylotypes (80)[d]	3.19	2.59	3.71	3.33	4.54	4.67	3.04	3.58	±	$7.78\cdot10^{-1}$
Bacteroidetes_inc._sed.[e]	1.49	1.71	1.43	3.44	1.45	$7.90\cdot10^{-1}$	9.75	2.87	±	3.15
unknown p: *Bacteroidetes*	2.97	2.77	3.55	5.16	2.48	2.04	$7.23\cdot10^{-1}$	2.81	±	1.36
Deltaproteobacteria	2.08	2.74	4.30	2.13	1.59	2.12	1.25	2.32	±	$9.94\cdot10^{-1}$
unknown p: *Proteobacteria*	$9.11\cdot10^{-1}$	$8.57\cdot10^{-1}$	6.81	1.38	$9.16\cdot10^{-1}$	1.08	$9.83\cdot10^{-1}$	1.85	±	2.20
Planctomycetia	$2.87\cdot10^{-1}$	$2.38\cdot10^{-1}$	$3.41\cdot10^{-1}$	$4.21\cdot10^{-1}$	1.42	1.61	6.85	1.60	±	2.39
Actinobacteria	1.37	$3.90\cdot10^{-1}$	$8.42\cdot10^{-1}$	1.05	2.00	2.57	2.74	1.56	±	$8.93\cdot10^{-1}$
Cytophagia	$9.33\cdot10^{-1}$	$4.37\cdot10^{-1}$	$3.90\cdot10^{-1}$	$2.36\cdot10^{-1}$	$8.82\cdot10^{-1}$	$8.84\cdot10^{-1}$	6.62	1.48	±	2.28
Acidobacteria_Gp4	$1.54\cdot10^{-1}$	$1.94\cdot10^{-1}$	$1.42\cdot10^{-1}$	$7.81\cdot10^{-2}$	2.48	3.46	2.34	1.26	±	1.44
Verrucomicrobiae	$5.48\cdot10^{-1}$	$7.24\cdot10^{-1}$	1.35	1.62	2.42	$6.93\cdot10^{-1}$	1.31	1.24	±	$6.59\cdot10^{-1}$
Anaerolineae	1.21	$4.85\cdot10^{-1}$	1.44	1.18	1.11	$9.31\cdot10^{-1}$	N.D.[f]	$9.08\cdot10^{-1}$	±	$4.99\cdot10^{-1}$
Epsilonproteobacteria	1.46	2.94	$1.82\cdot10^{-1}$	$6.27\cdot10^{-1}$	$5.62\cdot10^{-1}$	$4.01\cdot10^{-1}$	N.D.[f]	$8.82\cdot10^{-1}$	±	1.02
Saccharibacteria_genera_inc._ sed.[e]	1.21	$2.03\cdot10^{-1}$	$5.44\cdot10^{-1}$	$5.50\cdot10^{-1}$	1.25	1.01	1.34	$8.74\cdot10^{-1}$	±	$4.40\cdot10^{-1}$
Opitutae	$2.94\cdot10^{-1}$	$2.73\cdot10^{-1}$	$6.89\cdot10^{-1}$	1.03	1.72	$9.04\cdot10^{-1}$	$4.15\cdot10^{-2}$	$7.08\cdot10^{-1}$	±	$5.74\cdot10^{-1}$
Clostridia	$3.78\cdot10^{-1}$	$6.81\cdot10^{-1}$	$2.90\cdot10^{-1}$	$3.09\cdot10^{-1}$	$9.51\cdot10^{-1}$	1.19	$5.22\cdot10^{-1}$	$6.17\cdot10^{-1}$	±	$3.43\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	1.36	$8.22\cdot10^{-2}$	$7.40\cdot10^{-1}$	$3.11\cdot10^{-1}$	$7.78\cdot10^{-1}$	$1.82\cdot10^{-1}$	$3.37\cdot10^{-1}$	$5.42\cdot10^{-1}$	±	$4.49\cdot10^{-1}$
Nitrospira	N.D.[f]	$3.50\cdot10^{-3}$	$1.00\cdot10^{-2}$	$3.55\cdot10^{-3}$	$7.51\cdot10^{-1}$	1.95	N.D.[f]	$3.88\cdot10^{-1}$	±	$7.42\cdot10^{-1}$
Armatimonadetes_gp5	N.D.[f]	$1.75\cdot10^{-3}$	$8.37\cdot10^{-3}$	$3.73\cdot10^{-2}$	$1.43\cdot10^{-1}$	$1.91\cdot10^{-1}$	1.05	$2.04\cdot10^{-1}$	±	$3.80\cdot10^{-1}$
Spartobacteria	$4.45\cdot10^{-2}$	$3.50\cdot10^{-3}$	$8.37\cdot10^{-3}$	$8.88\cdot10^{-3}$	$8.89\cdot10^{-2}$	$6.66\cdot10^{-2}$	1.06	$1.84\cdot10^{-1}$	±	$3.90\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S30. Moscow WRRF class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Betaproteobacteria	12.6	10.8	9.80	9.43	15.4	15.0	14.2	12.5	± 2.48
Alphaproteobacteria	11.9	14.6	15.5	14.2	9.58	10.3	8.25	12.0	± 2.78
Sphingobacteriia	12.1	12.2	12.7	12.6	9.71	7.09	6.47	10.4	± 2.69

Table S30. Moscow WRRF class-level EUB results summary continued.

Class[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Gammaproteobacteria	4.77	4.67	3.34	3.69	9.41	9.35	15.9	7.30	± 4.55
unknown d: *Bacteria*	8.27	5.99	5.96	6.34	8.43	7.39	7.39	7.11	± 1.03
Actinobacteria	8.37	11.3	9.95	8.69	3.10	3.47	2.54	6.77	± 3.62
Flavobacteriia	5.07	5.12	5.40	9.00	5.62	7.36	5.37	6.13	± 1.49
Deltaproteobacteria	1.97	3.02	2.50	2.40	5.85	6.75	6.66	4.16	± 2.15
unknown p: *Bacteroidetes*	2.70	2.09	3.15	3.53	6.37	4.78	5.24	3.98	± 1.53
Minor phylotypes (78)[d]	3.62	3.83	3.69	3.67	4.34	4.07	4.35	3.94	± $3.13\cdot10^{-1}$
Planctomycetia	2.67	3.64	5.10	3.55	1.90	3.30	2.35	3.22	± 1.05
unknown p: *Proteobacteria*	2.20	1.46	1.45	1.57	4.33	4.25	4.95	2.89	± 1.55
Chloroflexia	3.29	3.32	3.69	4.33	1.60	1.72	2.02	2.85	± 1.07
Caldilineae	3.32	4.06	3.84	3.69	1.41	1.67	1.39	2.77	± 1.22
Saccharibacteria_genera_inc._sed.[e]	1.67	$9.83\cdot10^{-1}$	3.14	3.94	1.40	1.56	$8.89\cdot10^{-1}$	1.94	± 1.15
Cytophagia	4.79	1.44	1.62	1.42	1.52	1.27	$9.44\cdot10^{-1}$	1.86	± 1.31
Clostridia	1.53	2.20	1.63	1.61	$7.49\cdot10^{-1}$	1.07	$9.65\cdot10^{-1}$	1.39	± $4.97\cdot10^{-1}$
Bacteroidetes_inc._sed.[e]	$4.58\cdot10^{-1}$	$7.94\cdot10^{-1}$	1.21	$7.71\cdot10^{-1}$	2.38	1.81	1.76	1.31	± $6.94\cdot10^{-1}$
Bacilli	3.93	1.83	1.31	$8.89\cdot10^{-1}$	$1.38\cdot10^{-1}$	$3.29\cdot10^{-1}$	$2.28\cdot10^{-1}$	1.24	± 1.34
Phycisphaerae	$3.68\cdot10^{-1}$	$7.22\cdot10^{-1}$	$7.24\cdot10^{-1}$	$8.07\cdot10^{-1}$	1.98	1.54	1.76	1.13	± $6.20\cdot10^{-1}$
Nitrospira	$8.48\cdot10^{-1}$	$7.49\cdot10^{-1}$	$7.48\cdot10^{-1}$	$9.27\cdot10^{-1}$	1.46	1.21	1.45	1.06	± $3.14\cdot10^{-1}$
Anaerolineae	1.07	$7.75\cdot10^{-1}$	$6.52\cdot10^{-1}$	$6.27\cdot10^{-1}$	$8.89\cdot10^{-1}$	1.28	1.57	$9.82\cdot10^{-1}$	± $3.50\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$4.44\cdot10^{-1}$	2.50	$2.72\cdot10^{-1}$	$4.54\cdot10^{-1}$	$2.92\cdot10^{-1}$	$6.28\cdot10^{-1}$	$4.35\cdot10^{-1}$	$7.17\cdot10^{-1}$	± $7.93\cdot10^{-1}$
Verrucomicrobiae	1.12	$7.87\cdot10^{-1}$	$5.58\cdot10^{-1}$	$5.33\cdot10^{-1}$	$3.90\cdot10^{-1}$	$6.03\cdot10^{-1}$	$5.66\cdot10^{-1}$	$6.51\cdot10^{-1}$	± $2.37\cdot10^{-1}$
Subdivision3	$2.97\cdot10^{-1}$	$2.92\cdot10^{-1}$	$5.36\cdot10^{-1}$	$4.88\cdot10^{-1}$	$6.88\cdot10^{-1}$	$5.93\cdot10^{-1}$	1.12	$5.74\cdot10^{-1}$	± $2.83\cdot10^{-1}$
Epsilonproteobacteria	$3.64\cdot10^{-1}$	$1.45\cdot10^{-1}$	$4.32\cdot10^{-1}$	$1.21\cdot10^{-1}$	$8.04\cdot10^{-1}$	1.18	$8.51\cdot10^{-1}$	$5.57\cdot10^{-1}$	± $3.98\cdot10^{-1}$
Acidobacteria_Gp4	$2.28\cdot10^{-1}$	$7.87\cdot10^{-1}$	1.08	$7.16\cdot10^{-1}$	$2.57\cdot10^{-1}$	$3.89\cdot10^{-1}$	$4.04\cdot10^{-1}$	$5.51\cdot10^{-1}$	± $3.16\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S31. Summary of class-level relative abundance by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	S-EBPR (S26)		V-EBPR (S27)		G-EBPR (S28)		R-EBPR (S29)		Moscow WRRF (S30)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
Betaproteobacteria	20.3	± 11.2	27.8	± 10.3	24.2	± 9.83	31.6	± 16.4	12.5	± 2.48
Alphaproteobacteria	28.2	± 6.23	13.6	± 10.2	19.4	± 11.7	17.0	± 14.5	12.0	± 2.78
unknown p: *Bacteroidetes*	1.67	± $5.54\cdot10^{-1}$	12.6	± 5.82	5.00	± 3.22	2.81	± 1.36	3.98	± 1.53
Sphingobacteriia	3.60	± 1.25	8.40	± 3.16	9.87	± 3.35	10.3	± 4.29	10.4	± 2.69
Flavobacteriia	9.28	± 6.11	2.57	± 2.71	2.01	± 1.48	4.56	± 2.31	6.13	± 1.49
Saccharibacteria_genera_inc._sed.[d]	$1.90\cdot10^{-1}$	± $3.97\cdot10^{-1}$	$5.40\cdot10^{-1}$	± $4.71\cdot10^{-1}$	7.87	± 8.38	$8.74\cdot10^{-1}$	± $4.40\cdot10^{-1}$	1.94	± 1.15
Gammaproteobacteria	4.45	± 1.15	5.03	± 1.79	2.12	± $8.60\cdot10^{-1}$	5.74	± 2.69	7.30	± 4.55
unknown d: *Bacteria*	5.86	± 2.76	3.75	± 1.78	4.23	± $9.24\cdot10^{-1}$	4.93	± 1.33	7.11	± 1.03
Actinobacteria	$2.69\cdot10^{-1}$	± $1.79\cdot10^{-1}$	2.03	± $9.90\cdot10^{-1}$	5.83	± 3.60	1.56	± $8.93\cdot10^{-1}$	6.77	± 3.62
Bacteroidetes_inc._sed.[d]	6.52	± 3.58	$5.95\cdot10^{-1}$	± $4.61\cdot10^{-1}$	1.94	± 1.44	2.87	± 3.15	1.31	± $6.94\cdot10^{-1}$
Deltaproteobacteria	2.27	± 1.08	2.50	± 1.76	1.99	± 1.23	2.32	± $9.94\cdot10^{-1}$	4.16	± 2.15
Cytophagia	$4.53\cdot10^{-1}$	± $4.49\cdot10^{-1}$	3.46	± 1.93	3.19	± 1.87	1.48	± 2.28	1.86	± 1.31
Bacteroidia	$4.82\cdot10^{-2}$	± $1.19\cdot10^{-1}$	3.38	± 3.35	$8.20\cdot10^{-1}$	± 1.20	$4.36\cdot10^{-1}$	± $3.18\cdot10^{-1}$	$5.45\cdot10^{-1}$	± $1.01\cdot10^{-1}$
Planctomycetia	3.27	± 1.53	1.22	± 1.20	$7.87\cdot10^{-1}$	± $6.91\cdot10^{-1}$	1.60	± 2.39	3.22	± 1.05
unknown p: *Proteobacteria*	1.68	± $9.32\cdot10^{-1}$	1.88	± 1.36	2.02	± $9.66\cdot10^{-1}$	1.85	± 2.20	2.89	± 1.55
Chloroflexia	$7.50\cdot10^{-3}$	± $6.73\cdot10^{-3}$	$5.72\cdot10^{-2}$	± $6.74\cdot10^{-2}$	$4.97\cdot10^{-2}$	± $3.18\cdot10^{-2}$	$5.91\cdot10^{-2}$	± $3.91\cdot10^{-2}$	2.85	± 1.07
Caldilineae	$4.33\cdot10^{-1}$	± $5.50\cdot10^{-1}$	1.17	± 1.14	1.24	± $6.32\cdot10^{-1}$	$4.79\cdot10^{-1}$	± $3.28\cdot10^{-1}$	2.77	± 1.22
Phycisphaerae	2.77	± 2.39	$1.99\cdot10^{-2}$	± $2.48\cdot10^{-2}$	$6.02\cdot10^{-2}$	± $5.35\cdot10^{-2}$	$7.24\cdot10^{-2}$	± $9.70\cdot10^{-2}$	1.13	± $6.20\cdot10^{-1}$
Verrucomicrobiae	1.40	± $9.75\cdot10^{-1}$	2.63	± 1.70	1.08	± $6.73\cdot10^{-1}$	1.24	± $6.59\cdot10^{-1}$	$6.51\cdot10^{-1}$	± $2.37\cdot10^{-1}$
Minor phylotypes (70)[e]	1.48	± $3.72\cdot10^{-1}$	1.83	± $8.08\cdot10^{-1}$	1.87	± $5.22\cdot10^{-1}$	1.79	± $2.45\cdot10^{-1}$	2.40	± $3.31\cdot10^{-1}$
Clostridia	$9.47\cdot10^{-1}$	± 2.42	1.37	± $8.11\cdot10^{-1}$	1.13	± 1.31	$6.17\cdot10^{-1}$	± $3.43\cdot10^{-1}$	1.39	± $4.97\cdot10^{-1}$
Acidobacteria_Gp4	$4.14\cdot10^{-1}$	± $3.45\cdot10^{-1}$	$7.80\cdot10^{-1}$	± 1.27	$6.37\cdot10^{-1}$	± $9.36\cdot10^{-1}$	1.26	± 1.44	$5.51\cdot10^{-1}$	± $3.16\cdot10^{-1}$
Bacilli	$2.25\cdot10^{-1}$	± $5.79\cdot10^{-1}$	$3.24\cdot10^{-1}$	± $1.50\cdot10^{-1}$	$3.74\cdot10^{-1}$	± $1.78\cdot10^{-1}$	$3.36\cdot10^{-1}$	± $1.61\cdot10^{-1}$	1.24	± 1.34
Nitrospira	$6.98\cdot10^{-1}$	± $5.17\cdot10^{-1}$	$1.18\cdot10^{-3}$	± $1.52\cdot10^{-3}$	$9.20\cdot10^{-4}$	± $1.28\cdot10^{-3}$	$3.88\cdot10^{-1}$	± $7.42\cdot10^{-1}$	1.06	± $3.14\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[d]	$2.63\cdot10^{-1}$	± $3.49\cdot10^{-1}$	1.01	± 1.36	$6.45\cdot10^{-1}$	± $7.39\cdot10^{-1}$	$5.42\cdot10^{-1}$	± $4.49\cdot10^{-1}$	$7.17\cdot10^{-1}$	± $7.93\cdot10^{-1}$
Anaerolineae	$3.43\cdot10^{-1}$	± $3.70\cdot10^{-1}$	$1.19\cdot10^{-1}$	± $1.03\cdot10^{-1}$	$2.81\cdot10^{-1}$	± $2.78\cdot10^{-1}$	$9.08\cdot10^{-1}$	± $4.99\cdot10^{-1}$	$9.82\cdot10^{-1}$	± $3.50\cdot10^{-1}$
Epsilonproteobacteria	N.D.[f]		$4.65\cdot10^{-1}$	± $3.10\cdot10^{-1}$	$6.70\cdot10^{-1}$	± $5.50\cdot10^{-1}$	$8.82\cdot10^{-1}$	± 1.02	$5.57\cdot10^{-1}$	± $3.98\cdot10^{-1}$
SR1_genera_inc._sed.[d]	$7.50\cdot10^{-1}$	± 1.84	$2.96\cdot10^{-2}$	± $4.39\cdot10^{-2}$	$4.33\cdot10^{-3}$	± $6.34\cdot10^{-3}$	$1.44\cdot10^{-1}$	± $1.78\cdot10^{-1}$	$3.85\cdot10^{-2}$	± $3.03\cdot10^{-2}$
Opitutae	$3.08\cdot10^{-1}$	± $1.84\cdot10^{-1}$	$3.97\cdot10^{-1}$	± $1.05\cdot10^{-1}$	$3.28\cdot10^{-1}$	± $2.31\cdot10^{-1}$	$7.08\cdot10^{-1}$	± $5.74\cdot10^{-1}$	$2.73\cdot10^{-1}$	± $1.77\cdot10^{-1}$
Subdivision3	$5.41\cdot10^{-2}$	± $2.87\cdot10^{-2}$	$4.49\cdot10^{-2}$	± $4.67\cdot10^{-2}$	$2.22\cdot10^{-2}$	± $2.19\cdot10^{-2}$	$3.71\cdot10^{-2}$	± $4.68\cdot10^{-2}$	$5.74\cdot10^{-1}$	± $2.83\cdot10^{-1}$
unknown	$5.59\cdot10^{-1}$	± $3.46\cdot10^{-1}$	$1.03\cdot10^{-1}$	± $9.74\cdot10^{-2}$	$1.47\cdot10^{-1}$	± $5.49\cdot10^{-2}$	$1.33\cdot10^{-1}$	± $1.23\cdot10^{-1}$	$3.40\cdot10^{-1}$	± $7.88\cdot10^{-2}$
Armatimonadetes_gp5	$5.55\cdot10^{-1}$	± $5.26\cdot10^{-1}$	$4.04\cdot10^{-2}$	± $4.68\cdot10^{-2}$	$5.86\cdot10^{-2}$	± $4.92\cdot10^{-2}$	$2.04\cdot10^{-1}$	± $3.80\cdot10^{-1}$	$5.37\cdot10^{-2}$	± $1.46\cdot10^{-2}$
unknown p: *Chloroflexi*	$3.91\cdot10^{-1}$	± $3.58\cdot10^{-1}$	$1.49\cdot10^{-1}$	± $9.47\cdot10^{-2}$	$1.15\cdot10^{-1}$	± $1.23\cdot10^{-1}$	$7.17\cdot10^{-2}$	± $3.52\cdot10^{-2}$	$2.44\cdot10^{-1}$	± $9.32\cdot10^{-2}$
Fimbriimonadia	$2.93\cdot10^{-1}$	± $3.92\cdot10^{-1}$	$1.36\cdot10^{-2}$	± $1.54\cdot10^{-2}$	$2.34\cdot10^{-2}$	± $3.84\cdot10^{-2}$	$2.13\cdot10^{-2}$	± $2.90\cdot10^{-2}$	$1.19\cdot10^{-2}$	± $7.92\cdot10^{-3}$

Table S31. Summary of class-level EUB results continued.

Class[a,b]	S-EBPR (S26) Average ± SD[c] %	V-EBPR (S27) Average ± SD[c] %	G-EBPR (S28) Average ± SD[c] %	R-EBPR (S29) Average ± SD[c] %	Moscow WRRF (S30) Average ± SD[c] %
Spartobacteria	$6.79\cdot10^{-4}$ ± $1.37\cdot10^{-3}$	$1.05\cdot10^{-1}$ ± $1.64\cdot10^{-1}$	$7.91\cdot10^{-2}$ ± $1.19\cdot10^{-1}$	$1.84\cdot10^{-1}$ ± $3.90\cdot10^{-1}$	$2.76\cdot10^{-2}$ ± $2.44\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[f] N.D. = Not detected.

Table S32. S-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Rhodocyclales	10.1	7.83	25.8	27.1	10.1	2.20	30.4	16.2 ± 11.2
Rhodobacterales	10.6	9.85	17.4	12.0	13.5	18.5	14.5	13.8 ± 3.27
Flavobacteriales	6.85	17.3	2.77	2.81	17.5	9.71	7.99	9.28 ± 6.11
Ohtaekwangia	8.52	13.9	3.98	5.07	5.21	4.54	4.42	6.52 ± 3.58
unknown d: *Bacteria*	6.93	4.46	7.37	10.9	4.62	2.63	4.15	5.86 ± 2.76
Minor phylotypes (173)[d]	6.60	4.40	6.12	5.55	4.48	5.01	4.70	5.27 ± $8.51\cdot10^{-1}$
Rhizobiales	8.38	9.62	2.81	4.46	3.59	5.86	1.03	5.11 ± 3.06
Sphingobacteriales	2.96	2.87	5.68	3.84	4.51	1.81	3.56	3.60 ± 1.25
Planctomycetales	5.80	2.94	1.66	2.56	4.54	3.43	1.55	3.21 ± 1.54
Rhodospirillales	8.58	2.99	1.65	4.56	1.33	1.90	$6.52\cdot10^{-1}$	3.09 ± 2.73
unknown c: *Alphaproteobacteria*	2.08	3.52	4.07	1.40	2.11	4.59	2.93	2.96 ± 1.17
Burkholderiales	2.94	3.30	$9.36\cdot10^{-1}$	$9.03\cdot10^{-1}$	2.34	4.24	5.37	2.86 ± 1.64
Phycisphaerales	1.37	$8.11\cdot10^{-1}$	1.10	$9.30\cdot10^{-1}$	4.63	7.05	3.48	2.77 ± 2.39
Xanthomonadales	1.26	2.15	2.13	3.04	2.38	4.20	3.31	2.64 ± $9.59\cdot10^{-1}$
Caulobacterales	1.42	$7.30\cdot10^{-1}$	1.34	1.30	1.77	7.24	1.22	2.15 ± 2.27
unknown p: *Proteobacteria*	1.53	$9.47\cdot10^{-1}$	3.62	1.46	1.35	$8.87\cdot10^{-1}$	2.00	1.68 ± $9.32\cdot10^{-1}$
unknown p: *Bacteroidetes*	$8.97\cdot10^{-1}$	2.07	2.61	1.81	1.47	1.46	1.35	1.67 ± $5.54\cdot10^{-1}$
Verrucomicrobiales	1.63	1.35	$5.00\cdot10^{-1}$	1.20	2.01	$8.23\cdot10^{-2}$	3.04	1.40 ± $9.75\cdot10^{-1}$
Myxococcales	1.32	$7.46\cdot10^{-1}$	2.12	2.62	$2.53\cdot10^{-1}$	$1.95\cdot10^{-1}$	$8.47\cdot10^{-1}$	1.16 ± $9.22\cdot10^{-1}$
Sphingomonadales	1.56	1.16	$1.58\cdot10^{-1}$	$1.79\cdot10^{-1}$	2.85	1.42	$2.20\cdot10^{-1}$	1.08 ± $9.90\cdot10^{-1}$
Clostridiales	$1.47\cdot10^{-2}$	$1.08\cdot10^{-2}$	$1.38\cdot10^{-2}$	$1.09\cdot10^{-2}$	$8.39\cdot10^{-2}$	6.42	$1.96\cdot10^{-2}$	$9.39\cdot10^{-1}$ ± 2.42

Table S32. S-EBPR order-level EUB results summary continued.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown c: *Gammaproteobacteria*	1.56	1.18	1.55	$5.84{\cdot}10^{-1}$	$3.09{\cdot}10^{-1}$	$9.46{\cdot}10^{-1}$	$3.95{\cdot}10^{-1}$	$9.31{\cdot}10^{-1}$	±	$5.21{\cdot}10^{-1}$
SR1_genera_inc._sed.[e]	N.D.[f]	N.D.[f]	N.D.[f]	N.D.[f]	4.91	$7.10{\cdot}10^{-2}$	$2.68{\cdot}10^{-1}$	$7.50{\cdot}10^{-1}$	±	1.84
Nitrosomonadales	1.53	$3.73{\cdot}10^{-1}$	$7.50{\cdot}10^{-1}$	1.64	$6.21{\cdot}10^{-1}$	$1.01{\cdot}10^{-2}$	$3.30{\cdot}10^{-1}$	$7.50{\cdot}10^{-1}$	±	$6.16{\cdot}10^{-1}$
Nitrospirales	1.07	$4.03{\cdot}10^{-2}$	$7.22{\cdot}10^{-1}$	1.37	$9.96{\cdot}10^{-1}$	$1.13{\cdot}10^{-3}$	$6.88{\cdot}10^{-1}$	$6.98{\cdot}10^{-1}$	±	$5.17{\cdot}10^{-1}$
Chromatiales	1.25	$3.90{\cdot}10^{-1}$	$6.42{\cdot}10^{-1}$	$3.26{\cdot}10^{-1}$	$3.55{\cdot}10^{-1}$	$6.45{\cdot}10^{-1}$	$3.41{\cdot}10^{-1}$	$5.64{\cdot}10^{-1}$	±	$3.32{\cdot}10^{-1}$
unknown	$6.08{\cdot}10^{-1}$	1.26	$6.91{\cdot}10^{-1}$	$4.13{\cdot}10^{-1}$	$2.62{\cdot}10^{-1}$	$3.78{\cdot}10^{-1}$	$2.99{\cdot}10^{-1}$	$5.59{\cdot}10^{-1}$	±	$3.46{\cdot}10^{-1}$
Armatimonadetes_gp5	$3.53{\cdot}10^{-1}$	$3.63{\cdot}10^{-1}$	$4.55{\cdot}10^{-1}$	$5.47{\cdot}10^{-1}$	$3.41{\cdot}10^{-1}$	1.71	$1.17{\cdot}10^{-1}$	$5.55{\cdot}10^{-1}$	±	$5.26{\cdot}10^{-1}$
Cytophagales	$3.26{\cdot}10^{-1}$	1.41	$2.87{\cdot}10^{-1}$	$2.92{\cdot}10^{-1}$	$6.58{\cdot}10^{-2}$	$2.05{\cdot}10^{-1}$	$5.89{\cdot}10^{-1}$	$4.53{\cdot}10^{-1}$	±	$4.49{\cdot}10^{-1}$
Caldilineales	1.48	$8.65{\cdot}10^{-1}$	$2.39{\cdot}10^{-1}$	$3.62{\cdot}10^{-1}$	$4.96{\cdot}10^{-2}$	$2.48{\cdot}10^{-2}$	$1.10{\cdot}10^{-2}$	$4.33{\cdot}10^{-1}$	±	$5.50{\cdot}10^{-1}$
unknown p: *Chloroflexi*	$4.56{\cdot}10^{-1}$	$6.99{\cdot}10^{-2}$	$2.28{\cdot}10^{-1}$	$6.00{\cdot}10^{-1}$	1.08	$1.09{\cdot}10^{-1}$	$1.92{\cdot}10^{-1}$	$3.91{\cdot}10^{-1}$	±	$3.58{\cdot}10^{-1}$
Fimbriimonadales	$3.43{\cdot}10^{-2}$	$4.71{\cdot}10^{-2}$	$5.66{\cdot}10^{-1}$	$5.26{\cdot}10^{-2}$	$2.54{\cdot}10^{-1}$	1.06	$3.30{\cdot}10^{-2}$	$2.93{\cdot}10^{-1}$	±	$3.92{\cdot}10^{-1}$
Lactobacillales	N.D.[f]	N.D.[f]	$1.73{\cdot}10^{-3}$	$1.81{\cdot}10^{-3}$	$1.62{\cdot}10^{-2}$	1.49	N.D.[f]	$2.15{\cdot}10^{-1}$	±	$5.61{\cdot}10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	$1.47{\cdot}10^{-2}$	1.08	$1.90{\cdot}10^{-2}$	$7.07{\cdot}10^{-2}$	$1.41{\cdot}10^{-1}$	$2.26{\cdot}10^{-3}$	N.D.[f]	$1.90{\cdot}10^{-1}$	±	$3.97{\cdot}10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S33. V-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown p: *Bacteroidetes*	14.5	14.6	14.8	13.1	20.2	9.93	1.37	12.6	± 5.82
Hydrogenophilales	8.99	22.0	12.7	13.2	8.13	11.3	$2.38{\cdot}10^{-2}$	10.9	± 6.60
Rhodocyclales	$6.11{\cdot}10^{-1}$	7.43	17.2	19.8	4.08	8.53	1.96	8.52	± 7.41
Sphingobacteriales	5.58	6.98	9.53	7.37	14.5	9.55	5.31	8.40	± 3.16
Burkholderiales	11.2	6.66	4.35	4.41	5.26	6.32	10.6	6.97	± 2.82
Minor phylotypes (174)[d]	7.50	4.57	4.26	3.99	7.79	6.69	5.03	5.69	± 1.59
Rhizobiales	4.75	1.45	1.16	1.30	2.08	3.06	24.4	5.46	± 8.45
unknown d: *Bacteria*	4.37	3.37	3.12	1.86	3.23	2.89	7.43	3.75	± 1.78
Cytophagales	5.75	6.62	2.04	2.62	2.94	1.57	2.65	3.46	± 1.93
Bacteroidales	1.80	1.72	$8.04{\cdot}10^{-1}$	3.06	8.15	8.06	$7.65{\cdot}10^{-2}$	3.38	± 3.35

Table S33. V-EBPR order-level EUB results summary continued.

Order[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Verrucomicrobiales	3.74	$6.12\cdot10^{-1}$	4.10	1.63	$9.79\cdot10^{-1}$	2.24	5.09	2.63	± 1.70
Flavobacteriales	$9.61\cdot10^{-1}$	1.37	6.58	6.47	$9.96\cdot10^{-1}$	1.03	$5.78\cdot10^{-1}$	2.57	± 2.71
unknown p: *Proteobacteria*	1.90	4.89	1.01	1.56	1.15	1.10	1.58	1.88	± 1.36
Xanthomonadales	3.47	1.06	$3.68\cdot10^{-1}$	$6.39\cdot10^{-1}$	1.39	1.12	4.67	1.82	± 1.61
Pseudomonadales	$5.31\cdot10^{-1}$	$9.58\cdot10^{-1}$	4.53	2.16	1.49	2.55	$3.67\cdot10^{-1}$	1.80	± 1.45
Rhodobacterales	1.45	$6.29\cdot10^{-1}$	2.32	2.44	$6.33\cdot10^{-1}$	$9.96\cdot10^{-1}$	4.08	1.79	± 1.25
Sphingomonadales	1.13	$4.58\cdot10^{-1}$	$4.18\cdot10^{-1}$	$7.49\cdot10^{-1}$	1.73	4.93	3.13	1.79	± 1.68
unknown c: *Alphaproteobacteria*	2.02	2.42	$6.16\cdot10^{-1}$	1.40	$9.40\cdot10^{-1}$	1.68	2.34	1.63	$\pm 6.88\cdot10^{-1}$
Actinomycetales	3.41	1.01	$5.94\cdot10^{-1}$	1.05	$8.17\cdot10^{-1}$	1.04	2.29	1.46	± 1.02
Rhodospirillales	2.60	2.23	1.19	$7.44\cdot10^{-1}$	1.01	1.38	$5.89\cdot10^{-1}$	1.39	$\pm 7.54\cdot10^{-1}$
Clostridiales	$9.91\cdot10^{-1}$	$5.21\cdot10^{-1}$	$3.93\cdot10^{-1}$	1.24	2.03	2.60	1.76	1.36	$\pm 8.09\cdot10^{-1}$
Caulobacterales	2.38	$4.74\cdot10^{-1}$	$3.63\cdot10^{-1}$	3.28	$5.12\cdot10^{-1}$	1.48	1.02	1.36	± 1.11
Myxococcales	4.86	1.03	$1.85\cdot10^{-1}$	$7.57\cdot10^{-1}$	1.59	$3.42\cdot10^{-1}$	$4.57\cdot10^{-1}$	1.32	± 1.63
Planctomycetales	1.20	$9.14\cdot10^{-1}$	$5.41\cdot10^{-1}$	$4.01\cdot10^{-1}$	1.12	$4.98\cdot10^{-1}$	3.80	1.21	± 1.18
Caldilineales	1.04	$6.74\cdot10^{-1}$	$1.65\cdot10^{-1}$	$3.70\cdot10^{-1}$	2.32	3.17	$4.25\cdot10^{-1}$	1.17	± 1.14
unknown c: *Betaproteobacteria*	$4.38\cdot10^{-1}$	1.86	1.25	$8.15\cdot10^{-1}$	1.09	1.82	$1.82\cdot10^{-1}$	1.06	$\pm 6.41\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	1.36	$1.98\cdot10^{-1}$	3.91	$9.15\cdot10^{-1}$	$3.86\cdot10^{-1}$	$1.40\cdot10^{-1}$	$1.53\cdot10^{-1}$	1.01	± 1.36
unknown c: *Gammaproteobacteria*	$4.67\cdot10^{-1}$	$4.03\cdot10^{-1}$	$5.54\cdot10^{-1}$	$1.86\cdot10^{-1}$	1.00	1.20	2.68	$9.27\cdot10^{-1}$	$\pm 8.50\cdot10^{-1}$
Bdellovibrionales	$3.07\cdot10^{-1}$	1.83	$3.84\cdot10^{-1}$	$4.71\cdot10^{-1}$	$9.27\cdot10^{-1}$	1.09	$2.35\cdot10^{-1}$	$7.49\cdot10^{-1}$	$\pm 5.74\cdot10^{-1}$
Ohtaekwangia	$2.92\cdot10^{-1}$	$2.22\cdot10^{-1}$	$3.19\cdot10^{-1}$	1.56	$7.48\cdot10^{-1}$	$4.36\cdot10^{-1}$	$5.91\cdot10^{-1}$	$5.95\cdot10^{-1}$	$\pm 4.61\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	$3.29\cdot10^{-1}$	$3.85\cdot10^{-1}$	$6.32\cdot10^{-2}$	$4.28\cdot10^{-1}$	$3.86\cdot10^{-1}$	$6.53\cdot10^{-1}$	1.53	$5.40\cdot10^{-1}$	$\pm 4.71\cdot10^{-1}$
Gp4	$1.43\cdot10^{-1}$	$2.13\cdot10^{-1}$	$2.06\cdot10^{-2}$	$6.94\cdot10^{-2}$	$3.29\cdot10^{-1}$	$4.36\cdot10^{-1}$	1.65	$4.09\cdot10^{-1}$	$\pm 5.66\cdot10^{-1}$
Blastocatella	$3.65\cdot10^{-2}$	$2.09\cdot10^{-1}$	$5.15\cdot10^{-2}$	$2.88\cdot10^{-2}$	$1.42\cdot10^{-1}$	$1.40\cdot10^{-1}$	1.91	$3.60\cdot10^{-1}$	$\pm 6.88\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S34. G-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Sphingobacteriales	13.7	8.49	13.7	12.2	6.68	5.42	8.94	9.87	± 3.35

Table S34. G-EBPR order-level EUB results summary continued.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Rhodocyclales	$7.76\cdot10^{-1}$	6.70	23.7	15.2	6.53	3.16	5.05	8.73	± 7.99
Saccharibacteria_genera_inc._sed.[d]	25.4	9.85	3.00	2.77	8.82	$8.66\cdot10^{-1}$	4.39	7.87	± 8.38
Rhizobiales	5.11	1.96	2.97	4.91	2.83	4.18	29.2	7.31	± 9.73
Hydrogenophilales	3.12	10.5	4.69	4.64	9.05	11.5	N.D.[e]	6.21	± 4.22
Minor phylotypes (175)[f]	4.66	6.35	5.55	5.81	7.00	8.29	5.63	6.19	± 1.18
Actinomycetales	7.85	2.43	1.74	4.41	6.32	10.6	1.99	5.05	± 3.37
unknown p: *Bacteroidetes*	1.02	6.13	6.82	9.45	6.00	5.20	$4.14\cdot10^{-1}$	5.00	± 3.22
unknown c: *Alphaproteobacteria*	3.40	7.94	5.51	3.75	2.81	3.26	3.39	4.30	± 1.82
unknown d: *Bacteria*	3.20	4.63	4.76	3.53	3.86	3.72	5.88	4.23	± $9.24\cdot10^{-1}$
Burkholderiales	5.06	2.61	1.63	4.09	6.79	2.99	6.13	4.19	± 1.90
Methylophilales	2.22	3.01	5.13	1.40	9.55	4.66	N.D.[e]	3.71	± 3.13
Cytophagales	$6.40\cdot10^{-1}$	2.38	3.46	4.59	3.96	5.98	1.32	3.19	± 1.87
Rhodobacterales	1.59	1.68	2.04	1.82	2.88	2.32	4.14	2.35	± $9.00\cdot10^{-1}$
Caulobacterales	5.23	1.61	$7.24\cdot10^{-1}$	1.50	$9.07\cdot10^{-1}$	2.56	2.40	2.13	± 1.53
unknown p: *Proteobacteria*	$8.35\cdot10^{-1}$	2.68	2.50	3.57	1.97	1.10	1.49	2.02	± $9.66\cdot10^{-1}$
Flavobacteriales	4.87	2.27	2.45	1.98	1.37	$8.18\cdot10^{-1}$	$3.31\cdot10^{-1}$	2.01	± 1.48
Ohtaekwangia	2.79	4.61	1.72	1.65	$5.75\cdot10^{-1}$	$3.22\cdot10^{-1}$	1.90	1.94	± 1.44
Rhodospirillales	2.21	1.43	$4.93\cdot10^{-1}$	$9.48\cdot10^{-1}$	1.53	5.55	$8.28\cdot10^{-1}$	1.86	± 1.72
Sphingomonadales	1.10	$5.44\cdot10^{-1}$	$2.98\cdot10^{-1}$	$3.85\cdot10^{-1}$	$4.25\cdot10^{-1}$	1.15	4.80	1.24	± 1.61
Caldilineales	$7.82\cdot10^{-1}$	$8.78\cdot10^{-1}$	1.49	2.30	$8.49\cdot10^{-1}$	1.77	$5.79\cdot10^{-1}$	1.24	± $6.32\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$2.98\cdot10^{-1}$	2.25	1.44	1.10	1.53	1.52	$8.28\cdot10^{-2}$	1.17	± $7.57\cdot10^{-1}$
Clostridiales	$3.86\cdot10^{-1}$	$5.67\cdot10^{-1}$	$1.77\cdot10^{-1}$	$3.56\cdot10^{-1}$	1.12	3.93	1.32	1.12	± 1.31
Verrucomicrobiales	$9.40\cdot10^{-1}$	$9.45\cdot10^{-1}$	$3.55\cdot10^{-1}$	$3.61\cdot10^{-1}$	1.29	1.33	2.32	1.08	± $6.73\cdot10^{-1}$
Xanthomonadales	$6.01\cdot10^{-1}$	1.01	$5.07\cdot10^{-1}$	1.09	$5.57\cdot10^{-1}$	1.29	2.40	1.07	± $6.61\cdot10^{-1}$
Bdellovibrionales	$6.59\cdot10^{-1}$	3.56	$4.93\cdot10^{-1}$	1.60	$6.75\cdot10^{-1}$	$2.60\cdot10^{-1}$	$8.28\cdot10^{-2}$	1.05	± 1.21
Bacteroidales	$1.79\cdot10^{-1}$	$8.57\cdot10^{-1}$	$7.64\cdot10^{-2}$	$2.28\cdot10^{-1}$	$8.92\cdot10^{-1}$	3.43	$8.28\cdot10^{-2}$	$8.20\cdot10^{-1}$	± 1.20
Planctomycetales	$3.28\cdot10^{-1}$	$2.22\cdot10^{-1}$	$9.32\cdot10^{-1}$	$3.79\cdot10^{-1}$	$5.39\cdot10^{-1}$	$8.18\cdot10^{-1}$	2.24	$7.79\cdot10^{-1}$	± $6.92\cdot10^{-1}$
Campylobacterales	$1.89\cdot10^{-1}$	1.31	$3.01\cdot10^{-1}$	$6.15\cdot10^{-1}$	1.35	$7.85\cdot10^{-1}$	N.D.[e]	$6.51\cdot10^{-1}$	± $5.33\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[d]	$5.97\cdot10^{-3}$	$6.82\cdot10^{-2}$	$7.76\cdot10^{-1}$	2.17	$7.97\cdot10^{-1}$	$2.86\cdot10^{-1}$	$4.14\cdot10^{-1}$	$6.45\cdot10^{-1}$	± $7.39\cdot10^{-1}$
Acidimicrobiales	$8.15\cdot10^{-1}$	$4.82\cdot10^{-1}$	$3.89\cdot10^{-1}$	1.03	$4.62\cdot10^{-1}$	$5.45\cdot10^{-1}$	$1.66\cdot10^{-1}$	$5.55\cdot10^{-1}$	± $2.84\cdot10^{-1}$

Table S34. G-EBPR order-level EUB results summary continued.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average	±	SD[c] %
Gp4	$9.25{\cdot}10^{-2}$	$6.68{\cdot}10^{-2}$	$1.37{\cdot}10^{-1}$	$2.10{\cdot}10^{-1}$	$6.66{\cdot}10^{-2}$	$3.67{\cdot}10^{-1}$	2.07	$4.30{\cdot}10^{-1}$	±	$7.31{\cdot}10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] N.D. = Not detected.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S35. R-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average	±	SD[c] %
Hydrogenophilales	15.0	27.3	19.7	13.6	8.76	13.1	$9.37{\cdot}10^{-3}$	13.9	±	8.50
Sphingobacteriales	12.3	13.4	8.05	10.6	10.6	15.2	2.05	10.3	±	4.29
Burkholderiales	26.7	11.9	3.72	3.42	6.30	3.45	1.28	8.11	±	8.88
Rhizobiales	2.27	1.16	1.45	1.77	4.49	4.00	35.3	7.21	±	12.5
Rhodocyclales	1.48	4.86	8.52	20.2	6.23	5.29	$2.68{\cdot}10^{-1}$	6.69	±	6.59
Minor phylotypes (167)[d]	4.32	3.57	5.57	4.41	6.63	7.39	5.20	5.30	±	1.35
Rhodobacterales	1.36	1.54	1.97	2.89	14.5	9.10	3.60	5.00	±	4.98
unknown d: *Bacteria*	5.63	3.00	5.28	3.29	4.84	6.58	5.87	4.93	±	1.33
Flavobacteriales	3.70	6.45	4.54	7.85	4.35	4.54	$4.69{\cdot}10^{-1}$	4.56	±	2.31
Xanthomonadales	4.32	3.84	3.41	2.19	3.17	2.27	3.81	3.29	±	$8.07{\cdot}10^{-1}$
Ohtaekwangia	1.49	1.71	1.43	3.44	1.45	$7.90{\cdot}10^{-1}$	9.75	2.87	±	3.15
unknown p: *Bacteroidetes*	2.97	2.77	3.55	5.16	2.48	2.04	$7.23{\cdot}10^{-1}$	2.81	±	1.36
unknown p: *Proteobacteria*	$9.11{\cdot}10^{-1}$	$8.57{\cdot}10^{-1}$	6.81	1.38	$9.16{\cdot}10^{-1}$	1.08	$9.83{\cdot}10^{-1}$	1.85	±	2.20
Planctomycetales	$2.87{\cdot}10^{-1}$	$2.38{\cdot}10^{-1}$	$3.30{\cdot}10^{-1}$	$4.12{\cdot}10^{-1}$	1.41	1.60	6.85	1.59	±	2.39
unknown c: *Alphaproteobacteria*	$5.34{\cdot}10^{-1}$	$5.27{\cdot}10^{-1}$	1.93	2.05	2.50	1.97	1.45	1.56	±	$7.70{\cdot}10^{-1}$
unknown c: *Betaproteobacteria*	1.43	2.13	3.27	1.58	1.09	1.42	$2.95{\cdot}10^{-2}$	1.56	±	$9.87{\cdot}10^{-1}$
Cytophagales	$9.33{\cdot}10^{-1}$	$4.37{\cdot}10^{-1}$	$3.90{\cdot}10^{-1}$	$2.36{\cdot}10^{-1}$	$8.82{\cdot}10^{-1}$	$8.84{\cdot}10^{-1}$	6.62	1.48	±	2.28
Sphingomonadales	1.04	$5.44{\cdot}10^{-1}$	$4.15{\cdot}10^{-1}$	$5.38{\cdot}10^{-1}$	2.10	2.95	2.10	1.39	±	$9.97{\cdot}10^{-1}$
Verrucomicrobiales	$5.48{\cdot}10^{-1}$	$7.24{\cdot}10^{-1}$	1.35	1.62	2.42	$6.93{\cdot}10^{-1}$	1.31	1.24	±	$6.59{\cdot}10^{-1}$
Pseudomonadales	$8.35{\cdot}10^{-1}$	1.43	4.41	$4.14{\cdot}10^{-1}$	$2.22{\cdot}10^{-1}$	$4.84{\cdot}10^{-1}$	$1.34{\cdot}10^{-2}$	1.12	±	1.53
Gp4	$1.22{\cdot}10^{-1}$	$1.47{\cdot}10^{-1}$	$1.07{\cdot}10^{-1}$	$6.75{\cdot}10^{-2}$	2.03	2.91	1.75	1.02	±	1.18

Table S35. R-EBPR order-level EUB results summary continued.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Caulobacterales	$6.48\cdot10^{-1}$	$4.29\cdot10^{-1}$	$8.90\cdot10^{-1}$	2.40	$7.13\cdot10^{-1}$	$5.40\cdot10^{-1}$	1.36	$9.97\cdot10^{-1}$	±	$6.87\cdot10^{-1}$
Anaerolineales	1.21	$4.85\cdot10^{-1}$	1.44	1.18	1.11	$9.31\cdot10^{-1}$	N.D.[e]	$9.08\cdot10^{-1}$	±	$4.99\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	1.21	$2.03\cdot10^{-1}$	$5.44\cdot10^{-1}$	$5.50\cdot10^{-1}$	1.25	1.01	1.34	$8.74\cdot10^{-1}$	±	$4.40\cdot10^{-1}$
Campylobacterales	1.43	2.90	$1.71\cdot10^{-1}$	$6.25\cdot10^{-1}$	$5.50\cdot10^{-1}$	$3.95\cdot10^{-1}$	N.D.[e]	$8.67\cdot10^{-1}$	±	1.00
Actinomycetales	$7.88\cdot10^{-1}$	$1.80\cdot10^{-1}$	$1.97\cdot10^{-1}$	$3.59\cdot10^{-1}$	$9.98\cdot10^{-1}$	1.08	1.93	$7.91\cdot10^{-1}$	±	$6.25\cdot10^{-1}$
Bdellovibrionales	$4.50\cdot10^{-1}$	$6.02\cdot10^{-1}$	1.84	$6.34\cdot10^{-1}$	$6.73\cdot10^{-1}$	1.26	$6.29\cdot10^{-2}$	$7.89\cdot10^{-1}$	±	$5.84\cdot10^{-1}$
Myxococcales	1.30	1.64	$5.24\cdot10^{-1}$	$7.86\cdot10^{-1}$	$4.48\cdot10^{-1}$	$5.37\cdot10^{-1}$	$5.36\cdot10^{-2}$	$7.56\cdot10^{-1}$	±	$5.43\cdot10^{-1}$
Nitrosomonadales	1.40	$7.30\cdot10^{-1}$	$9.44\cdot10^{-1}$	$9.14\cdot10^{-1}$	$5.71\cdot10^{-1}$	$6.59\cdot10^{-1}$	N.D.[e]	$7.45\cdot10^{-1}$	±	$4.26\cdot10^{-1}$
Opitutales	$2.89\cdot10^{-1}$	$2.69\cdot10^{-1}$	$6.71\cdot10^{-1}$	1.01	1.72	$9.00\cdot10^{-1}$	$4.15\cdot10^{-2}$	$6.99\cdot10^{-1}$	±	$5.71\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$3.67\cdot10^{-1}$	$5.76\cdot10^{-1}$	1.78	$2.61\cdot10^{-1}$	$3.76\cdot10^{-1}$	$3.88\cdot10^{-1}$	1.08	$6.90\cdot10^{-1}$	±	$5.52\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$2.98\cdot10^{-1}$	$4.90\cdot10^{-1}$	1.88	$6.98\cdot10^{-1}$	$3.84\cdot10^{-1}$	$2.66\cdot10^{-1}$	$7.46\cdot10^{-1}$	$6.81\cdot10^{-1}$	±	$5.61\cdot10^{-1}$
Rhodospirillales	$1.49\cdot10^{-1}$	$1.17\cdot10^{-1}$	$1.79\cdot10^{-1}$	2.04	$7.64\cdot10^{-1}$	$4.78\cdot10^{-1}$	1.00	$6.76\cdot10^{-1}$	±	$6.90\cdot10^{-1}$
Clostridiales	$3.72\cdot10^{-1}$	$6.79\cdot10^{-1}$	$2.86\cdot10^{-1}$	$3.05\cdot10^{-1}$	$9.47\cdot10^{-1}$	1.18	$5.21\cdot10^{-1}$	$6.13\cdot10^{-1}$	±	$3.44\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[f]	1.36	$8.22\cdot10^{-2}$	$7.40\cdot10^{-1}$	$3.11\cdot10^{-1}$	$7.78\cdot10^{-1}$	$1.82\cdot10^{-1}$	$3.37\cdot10^{-1}$	$5.42\cdot10^{-1}$	±	$4.49\cdot10^{-1}$
Gallionellales	$3.65\cdot10^{-1}$	$3.80\cdot10^{-1}$	1.63	$6.89\cdot10^{-1}$	$2.76\cdot10^{-1}$	$1.64\cdot10^{-1}$	$5.36\cdot10^{-3}$	$5.01\cdot10^{-1}$	±	$5.40\cdot10^{-1}$
Nitrospirales	N.D.[e]	$3.50\cdot10^{-3}$	$1.00\cdot10^{-2}$	$3.55\cdot10^{-3}$	$7.51\cdot10^{-1}$	1.95	N.D.[e]	$3.88\cdot10^{-1}$	±	$7.42\cdot10^{-1}$
Aeromonadales	$1.80\cdot10^{-1}$	1.75	$7.70\cdot10^{-2}$	$9.05\cdot10^{-2}$	$3.38\cdot10^{-2}$	$7.10\cdot10^{-2}$	N.D.[e]	$3.14\cdot10^{-1}$	±	$6.35\cdot10^{-1}$
Armatimonadetes_gp5	N.D.[e]	$1.75\cdot10^{-3}$	$8.37\cdot10^{-3}$	$3.73\cdot10^{-2}$	$1.43\cdot10^{-1}$	$1.91\cdot10^{-1}$	1.05	$2.04\cdot10^{-1}$	±	$3.80\cdot10^{-1}$
Spartobacteria_genera_inc._sed.[f]	$2.67\cdot10^{-2}$	$3.50\cdot10^{-3}$	$8.37\cdot10^{-3}$	$7.10\cdot10^{-3}$	$8.77\cdot10^{-2}$	$6.36\cdot10^{-2}$	1.02	$1.74\cdot10^{-1}$	±	$3.76\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

[f] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S36. Moscow WRRF order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	±	SD[c]
Sphingobacteriales	12.1	12.2	12.7	12.6	9.71	7.09	6.47	10.4	±	2.69
Minor phylotypes (169)[d]	6.97	7.69	7.32	7.36	9.40	9.57	9.11	8.20	±	1.11
unknown d: *Bacteria*	8.27	5.99	5.96	6.34	8.43	7.39	7.39	7.11	±	1.03
Flavobacteriales	5.07	5.12	5.40	9.00	5.62	7.36	5.37	6.13	±	1.49

Table S36. Moscow WRRF order-level EUB results summary continued.

Order[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Burkholderiales	6.44	6.95	5.58	4.60	5.64	5.41	5.36	5.71	$\pm 7.68\cdot10^{-1}$
Actinomycetales	5.62	8.45	7.41	6.58	2.48	2.58	1.94	5.01	± 2.65
Rhodocyclales	4.99	2.43	2.51	2.98	6.64	6.60	5.92	4.58	± 1.90
Rhizobiales	3.93	6.16	6.43	5.77	3.27	3.55	2.55	4.52	± 1.56
unknown p: *Bacteroidetes*	2.70	2.09	3.15	3.53	6.37	4.78	5.24	3.98	± 1.53
Planctomycetales	2.62	3.58	5.07	3.51	1.67	2.98	1.93	3.05	± 1.15
unknown p: *Proteobacteria*	2.20	1.46	1.45	1.57	4.33	4.25	4.95	2.89	± 1.55
Chloroflexales	3.28	3.29	3.67	4.28	1.58	1.69	2.02	2.83	± 1.06
Caldilineales	3.32	4.06	3.84	3.69	1.41	1.67	1.39	2.77	± 1.22
Myxococcales	$4.66\cdot10^{-1}$	1.73	1.33	1.34	3.97	4.84	4.65	2.62	± 1.81
unknown c: *Alphaproteobacteria*	1.45	1.56	1.88	1.84	2.66	2.87	2.40	2.10	$\pm 5.50\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	1.67	$9.83\cdot10^{-1}$	3.14	3.94	1.40	1.56	$8.89\cdot10^{-1}$	1.94	± 1.15
Pseudomonadales	1.41	1.04	$6.40\cdot10^{-1}$	$7.80\cdot10^{-1}$	1.82	2.10	5.38	1.88	± 1.63
Cytophagales	4.79	1.44	1.62	1.42	1.52	1.27	$9.44\cdot10^{-1}$	1.86	± 1.31
unknown c: *Gammaproteobacteria*	1.04	$9.12\cdot10^{-1}$	$7.12\cdot10^{-1}$	$9.76\cdot10^{-1}$	2.76	2.49	3.55	1.78	± 1.13
Rhodobacterales	2.49	2.59	2.41	1.60	$5.56\cdot10^{-1}$	$8.90\cdot10^{-1}$	$6.96\cdot10^{-1}$	1.60	$\pm 8.97\cdot10^{-1}$
Sphingomonadales	2.47	2.00	2.50	2.31	$7.50\cdot10^{-1}$	$6.77\cdot10^{-1}$	$4.75\cdot10^{-1}$	1.60	$\pm 9.21\cdot10^{-1}$
Candidatus Carsonella	$4.34\cdot10^{-1}$	$5.19\cdot10^{-1}$	$1.44\cdot10^{-1}$	$1.66\cdot10^{-1}$	2.30	1.96	4.93	1.49	± 1.75
Clostridiales	1.52	2.20	1.63	1.61	$7.46\cdot10^{-1}$	1.07	$9.58\cdot10^{-1}$	1.39	$\pm 4.96\cdot10^{-1}$
Acidimicrobiales	2.18	2.39	2.04	1.49	$4.08\cdot10^{-1}$	$6.20\cdot10^{-1}$	$3.72\cdot10^{-1}$	1.36	$\pm 8.80\cdot10^{-1}$
Rhodospirillales	$5.62\cdot10^{-1}$	1.25	1.42	1.63	1.37	1.53	1.46	1.32	$\pm 3.53\cdot10^{-1}$
Ohtaekwangia	$4.58\cdot10^{-1}$	$7.94\cdot10^{-1}$	1.21	$7.71\cdot10^{-1}$	2.38	1.81	1.76	1.31	$\pm 6.93\cdot10^{-1}$
Lactobacillales	3.88	1.79	1.27	$8.70\cdot10^{-1}$	$1.32\cdot10^{-1}$	$3.20\cdot10^{-1}$	$2.26\cdot10^{-1}$	1.21	± 1.33
Phycisphaerales	$3.68\cdot10^{-1}$	$7.22\cdot10^{-1}$	$7.24\cdot10^{-1}$	$8.07\cdot10^{-1}$	1.98	1.54	1.76	1.13	$\pm 6.20\cdot10^{-1}$
Xanthomonadales	1.39	1.45	1.38	1.13	$6.87\cdot10^{-1}$	$7.44\cdot10^{-1}$	$6.17\cdot10^{-1}$	1.06	$\pm 3.66\cdot10^{-1}$
Nitrospirales	$8.48\cdot10^{-1}$	$7.49\cdot10^{-1}$	$7.48\cdot10^{-1}$	$9.27\cdot10^{-1}$	1.46	1.21	1.45	1.06	$\pm 3.14\cdot10^{-1}$
Anaerolineales	1.07	$7.75\cdot10^{-1}$	$6.52\cdot10^{-1}$	$6.27\cdot10^{-1}$	$8.89\cdot10^{-1}$	1.28	1.57	$9.82\cdot10^{-1}$	$\pm 3.50\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$8.28\cdot10^{-1}$	$7.85\cdot10^{-1}$	$7.61\cdot10^{-1}$	$6.22\cdot10^{-1}$	1.16	1.13	1.09	$9.10\cdot10^{-1}$	$\pm 2.11\cdot10^{-1}$
Nitrosomonadales	$4.70\cdot10^{-1}$	$7.23\cdot10^{-1}$	$7.53\cdot10^{-1}$	$6.91\cdot10^{-1}$	1.12	1.23	1.26	$8.92\cdot10^{-1}$	$\pm 3.07\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$4.10\cdot10^{-1}$	$4.78\cdot10^{-1}$	$7.57\cdot10^{-1}$	$9.74\cdot10^{-1}$	1.24	$9.56\cdot10^{-1}$	$9.64\cdot10^{-1}$	$8.26\cdot10^{-1}$	$\pm 2.97\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$4.44\cdot10^{-1}$	2.50	$2.72\cdot10^{-1}$	$4.54\cdot10^{-1}$	$2.92\cdot10^{-1}$	$6.28\cdot10^{-1}$	$4.35\cdot10^{-1}$	$7.17\cdot10^{-1}$	$\pm 7.93\cdot10^{-1}$
Verrucomicrobiales	1.12	$7.87\cdot10^{-1}$	$5.58\cdot10^{-1}$	$5.33\cdot10^{-1}$	$3.90\cdot10^{-1}$	$6.03\cdot10^{-1}$	$5.66\cdot10^{-1}$	$6.51\cdot10^{-1}$	$\pm 2.37\cdot10^{-1}$
Subdivision3_genera_inc._sed.[e]	$2.97\cdot10^{-1}$	$2.92\cdot10^{-1}$	$5.36\cdot10^{-1}$	$4.88\cdot10^{-1}$	$6.88\cdot10^{-1}$	$5.93\cdot10^{-1}$	1.12	$5.74\cdot10^{-1}$	$\pm 2.83\cdot10^{-1}$

Table S36. Moscow WRRF order-level EUB results summary continued.

Order[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Campylobacterales	$3.54\cdot10^{-1}$	$1.31\cdot10^{-1}$	$4.23\cdot10^{-1}$	$1.17\cdot10^{-1}$	$7.76\cdot10^{-1}$	1.16	$8.35\cdot10^{-1}$	$5.42\cdot10^{-1}$	$\pm 3.92\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S37. Summary of order-level relative abundance by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	S-EBPR (S32)		V-EBPR (S33)		G-EBPR (S34)		R-EBPR (S35)		Moscow WRRF (S36)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
Rhodocyclales	16.2	± 11.2	8.52	± 7.41	8.73	± 7.99	6.69	± 6.59	4.58	± 1.90
Hydrogenophilales	$6.08\cdot10^{-3}$	$\pm 5.56\cdot10^{-3}$	10.9	± 6.60	6.21	± 4.22	13.9	± 8.50	$3.11\cdot10^{-3}$	$\pm 1.35\cdot10^{-3}$
Rhodobacterales	13.8	± 3.27	1.79	± 1.25	2.35	$\pm 9.00\cdot10^{-1}$	5.00	± 4.98	1.60	$\pm 8.97\cdot10^{-1}$
unknown p: *Bacteroidetes*	1.67	$\pm 5.54\cdot10^{-1}$	12.6	± 5.82	5.00	± 3.22	2.81	± 1.36	3.98	± 1.53
Sphingobacteriales	3.60	± 1.25	8.40	± 3.16	9.87	± 3.35	10.3	± 4.29	10.4	± 2.69
Flavobacteriales	9.28	± 6.11	2.57	± 2.71	2.01	± 1.48	4.56	± 2.31	6.13	± 1.49
Burkholderiales	2.86	± 1.64	6.97	± 2.82	4.19	± 1.90	8.11	± 8.88	5.71	$\pm 7.68\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[d]	$1.90\cdot10^{-1}$	$\pm 3.97\cdot10^{-1}$	$5.40\cdot10^{-1}$	$\pm 4.71\cdot10^{-1}$	7.87	± 8.38	$8.74\cdot10^{-1}$	$\pm 4.40\cdot10^{-1}$	1.94	± 1.15
Rhizobiales	5.11	± 3.06	5.46	± 8.45	7.31	± 9.73	7.21	± 12.5	4.52	± 1.56
unknown d: *Bacteria*	5.86	± 2.76	3.75	± 1.78	4.23	$\pm 9.24\cdot10^{-1}$	4.93	± 1.33	7.11	± 1.03
Ohtaekwangia	6.52	± 3.58	$5.95\cdot10^{-1}$	$\pm 4.61\cdot10^{-1}$	1.94	± 1.44	2.87	± 3.15	1.31	$\pm 6.93\cdot10^{-1}$
Actinomycetales	$1.03\cdot10^{-1}$	$\pm 7.30\cdot10^{-2}$	1.46	± 1.02	5.05	± 3.37	$7.91\cdot10^{-1}$	$\pm 6.25\cdot10^{-1}$	5.01	± 2.65
Minor phylotypes (152)[e]	1.86	$\pm 4.33\cdot10^{-1}$	2.47	$\pm 8.46\cdot10^{-1}$	2.66	$\pm 7.06\cdot10^{-1}$	2.64	$\pm 3.55\cdot10^{-1}$	4.87	± 1.13
unknown c: *Alphaproteobacteria*	2.96	± 1.17	1.63	$\pm 6.88\cdot10^{-1}$	4.30	± 1.82	1.56	$\pm 7.70\cdot10^{-1}$	2.10	$\pm 5.50\cdot10^{-1}$
Methylophilales	$2.59\cdot10^{-4}$	$\pm 6.85\cdot10^{-4}$	$3.74\cdot10^{-4}$	$\pm 9.90\cdot10^{-4}$	3.71	± 3.13	$1.17\cdot10^{-3}$	$\pm 2.01\cdot10^{-3}$	$1.84\cdot10^{-3}$	$\pm 2.16\cdot10^{-3}$
Cytophagales	$4.53\cdot10^{-1}$	$\pm 4.49\cdot10^{-1}$	3.46	± 1.93	3.19	± 1.87	1.48	± 2.28	1.86	± 1.31
Bacteroidales	$4.82\cdot10^{-2}$	$\pm 1.19\cdot10^{-1}$	3.38	± 3.35	$8.20\cdot10^{-1}$	± 1.20	$4.36\cdot10^{-1}$	$\pm 3.18\cdot10^{-1}$	$5.45\cdot10^{-1}$	$\pm 1.01\cdot10^{-1}$
Xanthomonadales	2.64	$\pm 9.59\cdot10^{-1}$	1.82	± 1.61	1.07	$\pm 6.61\cdot10^{-1}$	3.29	$\pm 8.07\cdot10^{-1}$	1.06	$\pm 3.66\cdot10^{-1}$
Planctomycetales	3.21	± 1.54	1.21	± 1.18	$7.79\cdot10^{-1}$	$\pm 6.92\cdot10^{-1}$	1.59	± 2.39	3.05	± 1.15
Rhodospirillales	3.09	± 2.73	1.39	$\pm 7.54\cdot10^{-1}$	1.86	± 1.72	$6.76\cdot10^{-1}$	$\pm 6.90\cdot10^{-1}$	1.32	$\pm 3.53\cdot10^{-1}$
unknown p: *Proteobacteria*	1.68	$\pm 9.32\cdot10^{-1}$	1.88	± 1.36	2.02	$\pm 9.66\cdot10^{-1}$	1.85	± 2.20	2.89	± 1.55

Table S37. Summary of order-level EUB results continued.

Order[a,b]	S-EBPR (S32)			V-EBPR (S33)			G-EBPR (S34)			R-EBPR (S35)			Moscow WRRF (S36)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%			%			%			%			%	
Chloroflexales	$5.64\cdot10^{-3}$	±	$7.11\cdot10^{-3}$	$5.69\cdot10^{-2}$	±	$6.75\cdot10^{-2}$	$4.70\cdot10^{-2}$	±	$3.15\cdot10^{-2}$	$5.91\cdot10^{-2}$	±	$3.91\cdot10^{-2}$	2.83	±	1.06
Caldilineales	$4.33\cdot10^{-1}$	±	$5.50\cdot10^{-1}$	1.17	±	1.14	1.24	±	$6.32\cdot10^{-1}$	$4.79\cdot10^{-1}$	±	$3.28\cdot10^{-1}$	2.77	±	1.22
Phycisphaerales	2.77	±	2.39	$1.99\cdot10^{-2}$	±	$2.48\cdot10^{-2}$	$6.02\cdot10^{-2}$	±	$5.35\cdot10^{-2}$	$7.24\cdot10^{-2}$	±	$9.70\cdot10^{-2}$	1.13	±	$6.20\cdot10^{-1}$
Verrucomicrobiales	1.40	±	$9.75\cdot10^{-1}$	2.63	±	1.70	1.08	±	$6.73\cdot10^{-1}$	1.24	±	$6.59\cdot10^{-1}$	$6.51\cdot10^{-1}$	±	$2.37\cdot10^{-1}$
Myxococcales	1.16	±	$9.22\cdot10^{-1}$	1.32	±	1.63	$4.06\cdot10^{-1}$	±	$2.41\cdot10^{-1}$	$7.56\cdot10^{-1}$	±	$5.43\cdot10^{-1}$	2.62	±	1.81
Caulobacterales	2.15	±	2.27	1.36	±	1.11	2.13	±	1.53	$9.97\cdot10^{-1}$	±	$6.87\cdot10^{-1}$	$5.80\cdot10^{-1}$	±	$1.46\cdot10^{-1}$
Pseudomonadales	$1.56\cdot10^{-1}$	±	$1.75\cdot10^{-1}$	1.80	±	1.45	$3.34\cdot10^{-1}$	±	$2.68\cdot10^{-1}$	1.12	±	1.53	1.88	±	1.63
Sphingomonadales	1.08	±	$9.90\cdot10^{-1}$	1.79	±	1.68	1.24	±	1.61	1.39	±	$9.97\cdot10^{-1}$	1.60	±	$9.21\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$9.31\cdot10^{-1}$	±	$5.21\cdot10^{-1}$	$9.27\cdot10^{-1}$	±	$8.50\cdot10^{-1}$	$4.58\cdot10^{-1}$	±	$2.43\cdot10^{-1}$	$6.90\cdot10^{-1}$	±	$5.52\cdot10^{-1}$	1.78	±	1.13
unknown c: *Betaproteobacteria*	$4.00\cdot10^{-1}$	±	$1.59\cdot10^{-1}$	1.06	±	$6.41\cdot10^{-1}$	1.17	±	$7.57\cdot10^{-1}$	1.56	±	$9.87\cdot10^{-1}$	$8.26\cdot10^{-1}$	±	$2.97\cdot10^{-1}$
Candidatus Carsonella	$4.51\cdot10^{-2}$	±	$3.99\cdot10^{-2}$	$1.03\cdot10^{-1}$	±	$1.63\cdot10^{-1}$	$1.31\cdot10^{-2}$	±	$1.55\cdot10^{-2}$	$1.09\cdot10^{-1}$	±	$2.48\cdot10^{-1}$	1.49	±	1.75
Clostridiales	$9.39\cdot10^{-1}$	±	2.42	1.36	±	$8.09\cdot10^{-1}$	1.12	±	1.31	$6.13\cdot10^{-1}$	±	$3.44\cdot10^{-1}$	1.39	±	$4.96\cdot10^{-1}$
Acidimicrobiales	$1.60\cdot10^{-1}$	±	$1.24\cdot10^{-1}$	$4.47\cdot10^{-1}$	±	$1.70\cdot10^{-1}$	$5.55\cdot10^{-1}$	±	$2.84\cdot10^{-1}$	$5.18\cdot10^{-1}$	±	$2.66\cdot10^{-1}$	1.36	±	$8.80\cdot10^{-1}$
Lactobacillales	$2.15\cdot10^{-1}$	±	$5.61\cdot10^{-1}$	$3.06\cdot10^{-1}$	±	$1.61\cdot10^{-1}$	$3.56\cdot10^{-1}$	±	$1.99\cdot10^{-1}$	$2.99\cdot10^{-1}$	±	$1.84\cdot10^{-1}$	1.21	±	1.33
Nitrospirales	$6.98\cdot10^{-1}$	±	$5.17\cdot10^{-1}$	$1.18\cdot10^{-3}$	±	$1.52\cdot10^{-3}$	$9.20\cdot10^{-4}$	±	$1.28\cdot10^{-3}$	$3.88\cdot10^{-1}$	±	$7.42\cdot10^{-1}$	1.06	±	$3.14\cdot10^{-1}$
Bdellovibrionales	$4.52\cdot10^{-1}$	±	$2.14\cdot10^{-1}$	$7.49\cdot10^{-1}$	±	$5.74\cdot10^{-1}$	1.05	±	1.21	$7.89\cdot10^{-1}$	±	$5.84\cdot10^{-1}$	$4.82\cdot10^{-1}$	±	$1.73\cdot10^{-1}$
Gp4	$1.71\cdot10^{-1}$	±	$1.54\cdot10^{-1}$	$4.09\cdot10^{-1}$	±	$5.66\cdot10^{-1}$	$4.30\cdot10^{-1}$	±	$7.31\cdot10^{-1}$	1.02	±	1.18	$4.41\cdot10^{-1}$	±	$2.63\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[d]	$2.63\cdot10^{-1}$	±	$3.49\cdot10^{-1}$	1.01	±	1.36	$6.45\cdot10^{-1}$	±	$7.39\cdot10^{-1}$	$5.42\cdot10^{-1}$	±	$4.49\cdot10^{-1}$	$7.17\cdot10^{-1}$	±	$7.93\cdot10^{-1}$
Anaerolineales	$3.43\cdot10^{-1}$	±	$3.70\cdot10^{-1}$	$1.19\cdot10^{-1}$	±	$1.03\cdot10^{-1}$	$2.81\cdot10^{-1}$	±	$2.78\cdot10^{-1}$	$9.08\cdot10^{-1}$	±	$4.99\cdot10^{-1}$	$9.82\cdot10^{-1}$	±	$3.50\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$6.04\cdot10^{-1}$	±	$2.47\cdot10^{-1}$	$3.70\cdot10^{-1}$	±	$2.02\cdot10^{-1}$	$4.64\cdot10^{-1}$	±	$2.69\cdot10^{-1}$	$6.81\cdot10^{-1}$	±	$5.61\cdot10^{-1}$	$9.10\cdot10^{-1}$	±	$2.11\cdot10^{-1}$
Nitrosomonadales	$7.50\cdot10^{-1}$	±	$6.16\cdot10^{-1}$	$1.80\cdot10^{-1}$	±	$1.30\cdot10^{-1}$	$2.23\cdot10^{-2}$	±	$2.18\cdot10^{-2}$	$7.45\cdot10^{-1}$	±	$4.26\cdot10^{-1}$	$8.92\cdot10^{-1}$	±	$3.07\cdot10^{-1}$
Campylobacterales	N.D.[f]			$4.54\cdot10^{-1}$	±	$3.02\cdot10^{-1}$	$6.51\cdot10^{-1}$	±	$5.33\cdot10^{-1}$	$8.67\cdot10^{-1}$	±	1.00	$5.42\cdot10^{-1}$	±	$3.92\cdot10^{-1}$
SR1_genera_inc._sed.[d]	$7.50\cdot10^{-1}$	±	1.84	$2.96\cdot10^{-2}$	±	$4.39\cdot10^{-2}$	$4.33\cdot10^{-3}$	±	$6.34\cdot10^{-3}$	$1.44\cdot10^{-1}$	±	$1.78\cdot10^{-1}$	$3.85\cdot10^{-2}$	±	$3.03\cdot10^{-2}$
Opitutales	$2.67\cdot10^{-1}$	±	$1.68\cdot10^{-1}$	$3.82\cdot10^{-1}$	±	$9.04\cdot10^{-2}$	$3.27\cdot10^{-1}$	±	$2.31\cdot10^{-1}$	$6.99\cdot10^{-1}$	±	$5.71\cdot10^{-1}$	$2.28\cdot10^{-1}$	±	$1.58\cdot10^{-1}$
Subdivision3_genera_inc._sed.[d]	$5.41\cdot10^{-2}$	±	$2.87\cdot10^{-2}$	$4.49\cdot10^{-2}$	±	$4.67\cdot10^{-2}$	$2.22\cdot10^{-2}$	±	$2.19\cdot10^{-2}$	$3.71\cdot10^{-2}$	±	$4.68\cdot10^{-2}$	$5.74\cdot10^{-1}$	±	$2.83\cdot10^{-1}$
Chromatiales	$5.64\cdot10^{-1}$	±	$3.32\cdot10^{-1}$	$1.99\cdot10^{-1}$	±	$1.98\cdot10^{-1}$	$4.64\cdot10^{-2}$	±	$2.89\cdot10^{-2}$	$5.03\cdot10^{-2}$	±	$5.39\cdot10^{-2}$	$1.34\cdot10^{-1}$	±	$8.26\cdot10^{-2}$
unknown	$5.59\cdot10^{-1}$	±	$3.46\cdot10^{-1}$	$1.03\cdot10^{-1}$	±	$9.74\cdot10^{-2}$	$1.47\cdot10^{-1}$	±	$5.49\cdot10^{-2}$	$1.33\cdot10^{-1}$	±	$1.23\cdot10^{-1}$	$3.40\cdot10^{-1}$	±	$7.88\cdot10^{-2}$
Armatimonadetes_gp5	$5.55\cdot10^{-1}$	±	$5.26\cdot10^{-1}$	$4.04\cdot10^{-2}$	±	$4.68\cdot10^{-2}$	$5.86\cdot10^{-2}$	±	$4.92\cdot10^{-2}$	$2.04\cdot10^{-1}$	±	$3.80\cdot10^{-1}$	$5.37\cdot10^{-2}$	±	$1.46\cdot10^{-2}$
Gallionellales	$5.19\cdot10^{-2}$	±	$7.34\cdot10^{-2}$	$3.27\cdot10^{-2}$	±	$5.82\cdot10^{-2}$	$1.23\cdot10^{-2}$	±	$3.11\cdot10^{-2}$	$5.01\cdot10^{-1}$	±	$5.40\cdot10^{-1}$	$1.02\cdot10^{-3}$	±	$1.43\cdot10^{-3}$
unknown p: *Chloroflexi*	$3.91\cdot10^{-1}$	±	$3.58\cdot10^{-1}$	$1.49\cdot10^{-1}$	±	$9.47\cdot10^{-2}$	$1.15\cdot10^{-1}$	±	$1.23\cdot10^{-1}$	$7.17\cdot10^{-2}$	±	$3.52\cdot10^{-2}$	$2.44\cdot10^{-1}$	±	$9.32\cdot10^{-2}$
Blastocatella	$2.38\cdot10^{-1}$	±	$2.31\cdot10^{-1}$	$3.60\cdot10^{-1}$	±	$6.88\cdot10^{-1}$	$1.95\cdot10^{-1}$	±	$1.82\cdot10^{-1}$	$2.25\cdot10^{-1}$	±	$2.49\cdot10^{-1}$	$7.22\cdot10^{-2}$	±	$7.07\cdot10^{-2}$
Aeromonadales	$3.72\cdot10^{-2}$	±	$9.79\cdot10^{-2}$	$6.35\cdot10^{-2}$	±	$3.16\cdot10^{-2}$	$5.02\cdot10^{-2}$	±	$3.44\cdot10^{-2}$	$3.14\cdot10^{-1}$	±	$6.35\cdot10^{-1}$	$1.27\cdot10^{-1}$	±	$5.60\cdot10^{-2}$
Fimbriimonadales	$2.93\cdot10^{-1}$	±	$3.92\cdot10^{-1}$	$1.36\cdot10^{-2}$	±	$1.54\cdot10^{-2}$	$2.34\cdot10^{-2}$	±	$3.84\cdot10^{-2}$	$2.13\cdot10^{-2}$	±	$2.90\cdot10^{-2}$	$1.19\cdot10^{-2}$	±	$7.92\cdot10^{-3}$

Table S37. Summary of order-level EUB results continued.

Order[a,b]	S-EBPR (S32)			V-EBPR (S33)			G-EBPR (S34)			R-EBPR (S35)			Moscow WRRF (S36)		
	Average %	±	SD[c]	Average %	±	SD[c]	Average %	±	SD[c]	Average %	±	SD[c]	Average %	±	SD[c]
Spartobacteria_genera_inc._sed.[d]	$1.61\cdot10^{-4}$	±	$4.26\cdot10^{-4}$	$1.01\cdot10^{-1}$	±	$1.60\cdot10^{-1}$	$7.76\cdot10^{-2}$	±	$1.20\cdot10^{-1}$	$1.74\cdot10^{-1}$	±	$3.76\cdot10^{-1}$	$2.66\cdot10^{-2}$	±	$2.40\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[f] N.D. = Not detected.

Table S38. S-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Rhodocyclaceae	10.1	7.83	25.8	27.1	10.1	2.20	30.4	16.2	±	11.2
Rhodobacteraceae	10.6	9.85	17.4	12.0	13.5	18.5	14.5	13.8	±	3.27
Flavobacteriaceae	6.27	15.9	2.02	2.59	17.1	9.27	7.33	8.64	±	5.95
Minor phylotypes (372)[d]	10.1	6.86	8.85	8.45	6.93	9.08	7.69	8.28	±	1.19
Ohtaekwangia	8.52	13.9	3.98	5.07	5.21	4.54	4.42	6.52	±	3.58
unknown d: *Bacteria*	6.93	4.46	7.37	10.9	4.62	2.63	4.15	5.86	±	2.76
Planctomycetaceae	5.80	2.94	1.66	2.56	4.54	3.43	1.55	3.21	±	1.54
Rhodospirillaceae	8.44	2.93	1.58	4.45	1.16	1.84	$6.23\cdot10^{-1}$	3.00	±	2.71
unknown c: *Alphaproteobacteria*	2.08	3.52	4.07	1.40	2.11	4.59	2.93	2.96	±	1.17
Phycisphaeraceae	1.37	$8.11\cdot10^{-1}$	1.10	$9.30\cdot10^{-1}$	4.63	7.05	3.48	2.77	±	2.39
Xanthomonadaceae	1.26	2.15	2.12	3.04	2.38	4.20	3.30	2.64	±	$9.58\cdot10^{-1}$
unknown o: *Rhizobiales*	3.55	3.19	1.23	1.47	1.42	2.41	$6.33\cdot10^{-1}$	1.99	±	1.09
Caulobacteraceae	1.11	$5.02\cdot10^{-1}$	1.19	1.20	1.48	6.28	1.14	1.84	±	1.98
Chitinophagaceae	2.35	2.61	$8.78\cdot10^{-1}$	2.21	3.20	1.07	$1.75\cdot10^{-1}$	1.79	±	1.09
unknown p: *Proteobacteria*	1.53	$9.47\cdot10^{-1}$	3.62	1.46	1.35	$8.87\cdot10^{-1}$	2.00	1.68	±	$9.32\cdot10^{-1}$
unknown p: *Bacteroidetes*	$8.97\cdot10^{-1}$	2.07	2.61	1.81	1.47	1.46	1.35	1.67	±	$5.54\cdot10^{-1}$
Bradyrhizobiaceae	2.47	4.96	$6.80\cdot10^{-1}$	1.04	$9.61\cdot10^{-1}$	1.18	$5.25\cdot10^{-2}$	1.62	±	1.64
Comamonadaceae	2.56	2.81	$4.64\cdot10^{-1}$	$3.33\cdot10^{-1}$	1.11	2.16	$4.79\cdot10^{-1}$	1.42	±	1.07
Verrucomicrobiaceae	1.63	1.35	$5.00\cdot10^{-1}$	1.20	2.01	$8.23\cdot10^{-2}$	3.04	1.40	±	$9.75\cdot10^{-1}$
Burkholderiales_inc._sed.[e]	$3.31\cdot10^{-1}$	$4.21\cdot10^{-1}$	$3.95\cdot10^{-1}$	$5.49\cdot10^{-1}$	1.13	1.82	4.55	1.31	±	1.53
Saprospiraceae	$4.04\cdot10^{-1}$	$8.20\cdot10^{-2}$	4.18	$9.53\cdot10^{-1}$	$3.33\cdot10^{-1}$	$1.83\cdot10^{-1}$	2.74	1.27	±	1.58

Table S38. S-EBPR family-level EUB results summary continued.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown c: *Gammaproteobacteria*	1.56	1.18	1.55	$5.84\cdot10^{-1}$	$3.09\cdot10^{-1}$	$9.46\cdot10^{-1}$	$3.95\cdot10^{-1}$	$9.31\cdot10^{-1}$	±	$5.21\cdot10^{-1}$
Clostridiaceae 1	N.D.[f]	N.D.[f]	$1.73\cdot10^{-3}$	N.D.[f]	N.D.[f]	5.54	$1.22\cdot10^{-3}$	$7.92\cdot10^{-1}$	±	2.10
Phyllobacteriaceae	$9.44\cdot10^{-1}$	$3.85\cdot10^{-1}$	$3.69\cdot10^{-1}$	1.12	$8.05\cdot10^{-1}$	1.51	$1.98\cdot10^{-1}$	$7.62\cdot10^{-1}$	±	$4.73\cdot10^{-1}$
SR1_genera_inc._sed.[e]	N.D.[f]	N.D.[f]	N.D.[f]	N.D.[f]	4.91	$7.10\cdot10^{-2}$	$2.68\cdot10^{-1}$	$7.50\cdot10^{-1}$	±	1.84
Nitrosomonadaceae	1.53	$3.73\cdot10^{-1}$	$7.50\cdot10^{-1}$	1.64	$6.21\cdot10^{-1}$	$1.01\cdot10^{-2}$	$3.30\cdot10^{-1}$	$7.50\cdot10^{-1}$	±	$6.16\cdot10^{-1}$
Nitrospiraceae	1.07	$4.03\cdot10^{-2}$	$7.22\cdot10^{-1}$	1.37	$9.96\cdot10^{-1}$	$1.13\cdot10^{-3}$	$6.88\cdot10^{-1}$	$6.98\cdot10^{-1}$	±	$5.17\cdot10^{-1}$
Sphingomonadaceae	1.37	$9.09\cdot10^{-1}$	$1.49\cdot10^{-1}$	$1.70\cdot10^{-1}$	$7.22\cdot10^{-1}$	1.18	$2.05\cdot10^{-1}$	$6.71\cdot10^{-1}$	±	$5.06\cdot10^{-1}$
unknown	$6.08\cdot10^{-1}$	1.26	$6.91\cdot10^{-1}$	$4.13\cdot10^{-1}$	$2.62\cdot10^{-1}$	$3.78\cdot10^{-1}$	$2.99\cdot10^{-1}$	$5.59\cdot10^{-1}$	±	$3.46\cdot10^{-1}$
Armatimonadetes_gp5	$3.53\cdot10^{-1}$	$3.63\cdot10^{-1}$	$4.55\cdot10^{-1}$	$5.47\cdot10^{-1}$	$3.41\cdot10^{-1}$	1.71	$1.17\cdot10^{-1}$	$5.55\cdot10^{-1}$	±	$5.26\cdot10^{-1}$
unknown o: *Flavobacteriales*	$5.74\cdot10^{-1}$	1.23	$6.92\cdot10^{-1}$	$2.05\cdot10^{-1}$	$2.95\cdot10^{-1}$	$4.19\cdot10^{-1}$	$4.22\cdot10^{-1}$	$5.47\cdot10^{-1}$	±	$3.40\cdot10^{-1}$
Polyangiaceae	$2.45\cdot10^{-1}$	$1.61\cdot10^{-2}$	1.36	1.42	$1.80\cdot10^{-1}$	$2.14\cdot10^{-2}$	$1.27\cdot10^{-1}$	$4.81\cdot10^{-1}$	±	$6.26\cdot10^{-1}$
Hyphomicrobiaceae	1.01	$5.57\cdot10^{-1}$	$2.86\cdot10^{-1}$	$5.64\cdot10^{-1}$	$2.58\cdot10^{-1}$	$3.95\cdot10^{-1}$	$5.38\cdot10^{-2}$	$4.46\cdot10^{-1}$	±	$3.07\cdot10^{-1}$
Caldilineaceae	1.48	$8.65\cdot10^{-1}$	$2.39\cdot10^{-1}$	$3.62\cdot10^{-1}$	$4.96\cdot10^{-2}$	$2.48\cdot10^{-2}$	$1.10\cdot10^{-2}$	$4.33\cdot10^{-1}$	±	$5.50\cdot10^{-1}$
Erythrobacteraceae	$1.91\cdot10^{-1}$	$2.41\cdot10^{-1}$	$5.19\cdot10^{-3}$	$7.25\cdot10^{-3}$	2.08	$2.11\cdot10^{-1}$	$1.34\cdot10^{-2}$	$3.93\cdot10^{-1}$	±	$7.51\cdot10^{-1}$
unknown p: *Chloroflexi*	$4.56\cdot10^{-1}$	$6.99\cdot10^{-2}$	$2.28\cdot10^{-1}$	$6.00\cdot10^{-1}$	1.08	$1.09\cdot10^{-1}$	$1.92\cdot10^{-1}$	$3.91\cdot10^{-1}$	±	$3.58\cdot10^{-1}$
Cytophagaceae	$2.75\cdot10^{-1}$	1.28	$2.03\cdot10^{-1}$	$1.23\cdot10^{-1}$	$1.91\cdot10^{-2}$	$1.59\cdot10^{-1}$	$1.17\cdot10^{-1}$	$3.10\cdot10^{-1}$	±	$4.33\cdot10^{-1}$
Fimbriimonadaceae	$3.43\cdot10^{-2}$	$4.71\cdot10^{-2}$	$5.66\cdot10^{-1}$	$5.26\cdot10^{-2}$	$2.54\cdot10^{-1}$	1.06	$3.30\cdot10^{-2}$	$2.93\cdot10^{-1}$	±	$3.92\cdot10^{-1}$
Carnobacteriaceae	N.D.[f]	N.D.[f]	$1.73\cdot10^{-3}$	$1.81\cdot10^{-3}$	$1.53\cdot10^{-2}$	1.43	N.D.[f]	$2.07\cdot10^{-1}$	±	$5.38\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	$1.47\cdot10^{-2}$	1.08	$1.90\cdot10^{-2}$	$7.07\cdot10^{-2}$	$1.41\cdot10^{-1}$	$2.26\cdot10^{-3}$	N.D.[f]	$1.90\cdot10^{-1}$	±	$3.97\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S39. V-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown p: *Bacteroidetes*	14.5	14.6	14.8	13.1	20.2	9.93	1.37	12.6	± 5.82
Hydrogenophilaceae	8.99	22.0	12.7	13.2	8.13	11.3	$2.38\cdot10^{-2}$	10.9	± 6.60
Minor phylotypes (365)[d]	11.9	7.95	6.16	7.10	12.1	11.9	12.2	9.91	± 2.71
Rhodocyclaceae	$6.11\cdot10^{-1}$	7.43	17.2	19.8	4.08	8.53	1.96	8.52	± 7.41

Table S39. V-EBPR family-level EUB results summary continued.

Family[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Comamonadaceae	9.26	4.69	2.98	3.69	4.21	4.68	5.39	4.99	± 2.04
Saprospiraceae	3.36	2.83	5.10	4.47	9.39	5.85	2.43	4.77	± 2.38
unknown d: *Bacteria*	4.37	3.37	3.12	1.86	3.23	2.89	7.43	3.75	± 1.78
Verrucomicrobiaceae	3.74	$6.12\cdot10^{-1}$	4.10	1.63	$9.79\cdot10^{-1}$	2.24	5.09	2.63	± 1.70
Methylobacteriaceae	$6.64\cdot10^{-3}$	$3.02\cdot10^{-3}$	N.D.[e]	$5.24\cdot10^{-3}$	$4.14\cdot10^{-2}$	$6.22\cdot10^{-2}$	17.2	2.47	± 6.48
Prevotellaceae	1.21	$9.58\cdot10^{-1}$	$3.62\cdot10^{-1}$	2.28	5.10	5.86	N.D.[e]	2.25	± 2.33
unknown o: *Cytophagales*	4.46	5.14	1.34	1.84	1.47	$7.00\cdot10^{-1}$	$3.54\cdot10^{-1}$	2.19	± 1.86
unknown p: *Proteobacteria*	1.90	4.89	1.01	1.56	1.15	1.10	1.58	1.88	± 1.36
Chitinophagaceae	$7.92\cdot10^{-1}$	2.76	3.16	1.57	1.53	1.63	1.20	1.81	± $8.46\cdot10^{-1}$
Rhodobacteraceae	1.45	$6.29\cdot10^{-1}$	2.32	2.44	$6.33\cdot10^{-1}$	$9.96\cdot10^{-1}$	4.08	1.79	± 1.25
Flavobacteriaceae	$7.77\cdot10^{-1}$	1.15	3.75	4.64	$8.38\cdot10^{-1}$	$8.25\cdot10^{-1}$	$2.96\cdot10^{-1}$	1.75	± 1.71
Xanthomonadaceae	3.45	1.05	$3.49\cdot10^{-1}$	$6.35\cdot10^{-1}$	1.36	1.12	4.23	1.74	± 1.49
unknown o: *Sphingobacteriales*	1.39	1.35	1.25	1.30	3.36	1.99	1.22	1.69	± $7.80\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	2.02	2.42	$6.16\cdot10^{-1}$	1.40	$9.40\cdot10^{-1}$	1.68	2.34	1.63	± $6.88\cdot10^{-1}$
Burkholderiales_inc._sed.[f]	1.25	1.45	1.18	$5.07\cdot10^{-1}$	$6.62\cdot10^{-1}$	1.03	4.22	1.47	± 1.25
Sphingomonadaceae	1.09	$4.09\cdot10^{-1}$	$3.87\cdot10^{-1}$	$6.90\cdot10^{-1}$	1.47	4.20	1.94	1.45	± 1.34
Rhodospirillaceae	2.37	2.16	1.16	$6.79\cdot10^{-1}$	$9.29\cdot10^{-1}$	1.26	$2.01\cdot10^{-1}$	1.25	± $7.76\cdot10^{-1}$
unknown o: *Rhizobiales*	2.33	$7.84\cdot10^{-1}$	$3.99\cdot10^{-1}$	$6.01\cdot10^{-1}$	$7.51\cdot10^{-1}$	1.23	2.61	1.24	± $8.79\cdot10^{-1}$
Planctomycetaceae	1.20	$9.14\cdot10^{-1}$	$5.41\cdot10^{-1}$	$4.01\cdot10^{-1}$	1.12	$4.98\cdot10^{-1}$	3.80	1.21	± 1.18
Caulobacteraceae	2.20	$3.88\cdot10^{-1}$	$3.13\cdot10^{-1}$	3.21	$4.34\cdot10^{-1}$	1.35	$4.83\cdot10^{-1}$	1.20	± 1.13
Cytophagaceae	1.23	1.40	$6.35\cdot10^{-1}$	$7.33\cdot10^{-1}$	1.39	$8.56\cdot10^{-1}$	2.03	1.18	± $4.87\cdot10^{-1}$
Caldilineaceae	1.04	$6.74\cdot10^{-1}$	$1.65\cdot10^{-1}$	$3.70\cdot10^{-1}$	2.32	3.17	$4.25\cdot10^{-1}$	1.17	± 1.14
Moraxellaceae	$3.02\cdot10^{-1}$	$1.98\cdot10^{-1}$	3.26	1.14	$9.17\cdot10^{-1}$	2.02	$2.11\cdot10^{-2}$	1.12	± 1.17
unknown c: *Betaproteobacteria*	$4.38\cdot10^{-1}$	1.86	1.25	$8.15\cdot10^{-1}$	1.09	1.82	$1.82\cdot10^{-1}$	1.06	± $6.41\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[f]	1.36	$1.98\cdot10^{-1}$	3.91	$9.15\cdot10^{-1}$	$3.86\cdot10^{-1}$	$1.40\cdot10^{-1}$	$1.53\cdot10^{-1}$	1.01	± 1.36
unknown c: *Gammaproteobacteria*	$4.67\cdot10^{-1}$	$4.03\cdot10^{-1}$	$5.54\cdot10^{-1}$	$1.86\cdot10^{-1}$	1.00	1.20	2.68	$9.27\cdot10^{-1}$	± $8.50\cdot10^{-1}$
Polyangiaceae	3.88	$3.60\cdot10^{-1}$	$1.46\cdot10^{-1}$	$4.69\cdot10^{-1}$	$8.35\cdot10^{-1}$	$7.78\cdot10^{-2}$	$3.99\cdot10^{-1}$	$8.81\cdot10^{-1}$	± 1.35
Porphyromonadaceae	$3.70\cdot10^{-1}$	$5.68\cdot10^{-1}$	$3.21\cdot10^{-1}$	$5.01\cdot10^{-1}$	2.40	1.70	$5.54\cdot10^{-2}$	$8.45\cdot10^{-1}$	± $8.64\cdot10^{-1}$
Phyllobacteriaceae	$5.69\cdot10^{-1}$	$1.22\cdot10^{-1}$	$1.69\cdot10^{-1}$	$1.68\cdot10^{-1}$	$4.37\cdot10^{-1}$	$4.98\cdot10^{-1}$	2.37	$6.19\cdot10^{-1}$	± $7.94\cdot10^{-1}$
Ohtaekwangia	$2.92\cdot10^{-1}$	$2.22\cdot10^{-1}$	$3.19\cdot10^{-1}$	1.56	$7.48\cdot10^{-1}$	$4.36\cdot10^{-1}$	$5.91\cdot10^{-1}$	$5.95\cdot10^{-1}$	± $4.61\cdot10^{-1}$
Ruminococcaceae	$3.10\cdot10^{-1}$	$1.06\cdot10^{-1}$	$1.46\cdot10^{-1}$	$5.51\cdot10^{-1}$	$8.66\cdot10^{-1}$	$8.56\cdot10^{-1}$	1.07	$5.58\cdot10^{-1}$	± $3.84\cdot10^{-1}$
Hyphomicrobiaceae	$8.88\cdot10^{-1}$	$2.54\cdot10^{-1}$	$1.94\cdot10^{-1}$	$2.07\cdot10^{-1}$	$3.41\cdot10^{-1}$	$5.60\cdot10^{-1}$	1.37	$5.45\cdot10^{-1}$	± $4.39\cdot10^{-1}$

Table S39. V-EBPR family-level EUB results summary continued.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Saccharibacteria_genera_inc._ sed.[f]	$3.29\cdot10^{-1}$	$3.85\cdot10^{-1}$	$6.32\cdot10^{-2}$	$4.28\cdot10^{-1}$	$3.86\cdot10^{-1}$	$6.53\cdot10^{-1}$	1.53	$5.40\cdot10^{-1}$	$\pm 4.71\cdot10^{-1}$
unknown o: *Flavobacteriales*	$1.31\cdot10^{-1}$	$1.74\cdot10^{-1}$	1.55	1.28	$1.31\cdot10^{-1}$	$1.40\cdot10^{-1}$	$7.92\cdot10^{-2}$	$4.99\cdot10^{-1}$	$\pm 6.33\cdot10^{-1}$
unknown o: *Actinomycetales*	1.26	$4.61\cdot10^{-1}$	$2.49\cdot10^{-1}$	$2.51\cdot10^{-1}$	$3.83\cdot10^{-1}$	$4.36\cdot10^{-1}$	$4.06\cdot10^{-1}$	$4.93\cdot10^{-1}$	$\pm 3.50\cdot10^{-1}$
unknown o: *Pseudomonadales*	$1.94\cdot10^{-1}$	$3.91\cdot10^{-1}$	1.09	$4.95\cdot10^{-1}$	$4.82\cdot10^{-1}$	$4.51\cdot10^{-1}$	$1.69\cdot10^{-1}$	$4.68\cdot10^{-1}$	$\pm 3.06\cdot10^{-1}$
Gp4	$1.43\cdot10^{-1}$	$2.13\cdot10^{-1}$	$2.06\cdot10^{-2}$	$6.94\cdot10^{-2}$	$3.29\cdot10^{-1}$	$4.36\cdot10^{-1}$	1.65	$4.09\cdot10^{-1}$	$\pm 5.66\cdot10^{-1}$
Lachnospiraceae	$3.69\cdot10^{-1}$	$1.15\cdot10^{-1}$	$1.12\cdot10^{-1}$	$4.63\cdot10^{-1}$	$6.46\cdot10^{-1}$	1.03	$7.39\cdot10^{-2}$	$4.01\cdot10^{-1}$	$\pm 3.49\cdot10^{-1}$
Dermatophilaceae	1.59	$3.48\cdot10^{-1}$	$1.03\cdot10^{-1}$	$2.46\cdot10^{-1}$	$1.18\cdot10^{-1}$	$1.87\cdot10^{-1}$	$2.64\cdot10^{-3}$	$3.70\cdot10^{-1}$	$\pm 5.48\cdot10^{-1}$
Blastocatella	$3.65\cdot10^{-2}$	$2.09\cdot10^{-1}$	$5.15\cdot10^{-2}$	$2.88\cdot10^{-2}$	$1.42\cdot10^{-1}$	$1.40\cdot10^{-1}$	1.91	$3.60\cdot10^{-1}$	$\pm 6.88\cdot10^{-1}$
Cryomorphaceae	$5.31\cdot10^{-2}$	$4.38\cdot10^{-2}$	1.28	$5.41\cdot10^{-1}$	$2.76\cdot10^{-2}$	$6.22\cdot10^{-2}$	$2.03\cdot10^{-1}$	$3.16\cdot10^{-1}$	$\pm 4.62\cdot10^{-1}$
Bacteriovoracaceae	$9.96\cdot10^{-2}$	1.32	$1.47\cdot10^{-3}$	$1.31\cdot10^{-3}$	$4.33\cdot10^{-1}$	$1.24\cdot10^{-1}$	$7.92\cdot10^{-3}$	$2.83\cdot10^{-1}$	$\pm 4.80\cdot10^{-1}$
Erythrobacteraceae	$1.83\cdot10^{-2}$	$2.57\cdot10^{-2}$	$8.82\cdot10^{-3}$	$2.23\cdot10^{-2}$	$9.57\cdot10^{-2}$	$1.09\cdot10^{-1}$	1.00	$1.83\cdot10^{-1}$	$\pm 3.63\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

[f] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S40. G-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Minor phylotypes (367)[d]	9.63	10.2	7.61	9.56	10.8	13.8	11.8	10.5	± 1.94
Rhodocyclaceae	$7.76\cdot10^{-1}$	6.70	23.7	15.2	6.53	3.16	5.05	8.73	± 7.99
Saccharibacteria_genera_inc._ sed.[e]	25.4	9.85	3.00	2.77	8.82	$8.66\cdot10^{-1}$	4.39	7.87	± 8.38
Hydrogenophilaceae	3.12	10.5	4.69	4.64	9.05	11.5	N.D.[f]	6.21	± 4.22
unknown p: *Bacteroidetes*	1.02	6.13	6.82	9.45	6.00	5.20	$4.14\cdot10^{-1}$	5.00	± 3.22
Saprospiraceae	$4.21\cdot10^{-1}$	3.92	10.9	7.62	4.60	2.79	3.89	4.88	± 3.43
unknown c: *Alphaproteobacteria*	3.40	7.94	5.51	3.75	2.81	3.26	3.39	4.30	± 1.82
unknown d: *Bacteria*	3.20	4.63	4.76	3.53	3.86	3.72	5.88	4.23	$\pm 9.24\cdot10^{-1}$
Methylophilaceae	2.22	3.01	5.13	1.40	9.55	4.66	N.D.[f]	3.71	± 3.13

Table S40. G-EBPR family-level EUB results summary continued.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Chitinophagaceae	8.92	3.31	2.15	3.21	1.42	2.00	1.57	3.23	± 2.62
Methylobacteriaceae	$1.58\cdot10^{-1}$	$1.42\cdot10^{-1}$	$2.54\cdot10^{-1}$	$2.06\cdot10^{-1}$	$2.53\cdot10^{-1}$	$2.59\cdot10^{-1}$	21.0	3.19	± 7.87
Rhodobacteraceae	1.59	1.68	2.04	1.82	2.88	2.32	4.14	2.35	± $9.00\cdot10^{-1}$
Comamonadaceae	4.51	1.83	$8.64\cdot10^{-1}$	3.27	3.47	1.55	$8.28\cdot10^{-1}$	2.33	± 1.42
unknown p: *Proteobacteria*	$8.35\cdot10^{-1}$	2.68	2.50	3.57	1.97	1.10	1.49	2.02	± $9.66\cdot10^{-1}$
Ohtaekwangia	2.79	4.61	1.72	1.65	$5.75\cdot10^{-1}$	$3.22\cdot10^{-1}$	1.90	1.94	± 1.44
Intrasporangiaceae	5.42	$1.22\cdot10^{-1}$	$4.07\cdot10^{-2}$	$1.01\cdot10^{-1}$	3.21	4.63	N.D.[f]	1.93	± 2.42
Caulobacteraceae	4.56	1.32	$5.66\cdot10^{-1}$	1.34	$7.36\cdot10^{-1}$	2.41	1.57	1.79	± 1.36
unknown o: *Rhizobiales*	1.90	1.01	1.36	1.75	1.46	1.85	2.40	1.68	± $4.46\cdot10^{-1}$
Rhodospirillaceae	1.78	1.14	$4.00\cdot10^{-1}$	$8.14\cdot10^{-1}$	1.41	5.40	$7.45\cdot10^{-1}$	1.67	± 1.71
Flavobacteriaceae	4.49	1.82	1.96	1.55	1.00	$5.89\cdot10^{-1}$	$2.48\cdot10^{-1}$	1.66	± 1.40
unknown o: *Cytophagales*	$2.39\cdot10^{-2}$	1.18	2.50	3.52	1.94	2.20	N.D.[f]	1.62	± 1.30
Cytophagaceae	$6.13\cdot10^{-1}$	1.17	$9.30\cdot10^{-1}$	1.04	1.99	3.76	1.32	1.55	± 1.06
Burkholderiales_inc._sed.[e]	$3.42\cdot10^{-1}$	$5.50\cdot10^{-1}$	$5.66\cdot10^{-1}$	$5.65\cdot10^{-1}$	2.74	1.11	4.55	1.49	± 1.58
Propionibacteriaceae	$6.24\cdot10^{-1}$	$5.23\cdot10^{-1}$	$3.74\cdot10^{-1}$	1.18	2.25	4.32	$6.62\cdot10^{-1}$	1.42	± 1.43
Caldilineaceae	$7.82\cdot10^{-1}$	$8.78\cdot10^{-1}$	1.49	2.30	$8.49\cdot10^{-1}$	1.77	$5.79\cdot10^{-1}$	1.24	± $6.32\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$2.98\cdot10^{-1}$	2.25	1.44	1.10	1.53	1.52	$8.28\cdot10^{-2}$	1.17	± $7.57\cdot10^{-1}$
Verrucomicrobiaceae	$9.40\cdot10^{-1}$	$9.45\cdot10^{-1}$	$3.55\cdot10^{-1}$	$3.61\cdot10^{-1}$	1.29	1.33	2.32	1.08	± $6.73\cdot10^{-1}$
Xanthomonadaceae	$5.92\cdot10^{-1}$	1.00	$4.96\cdot10^{-1}$	1.07	$5.50\cdot10^{-1}$	1.27	1.90	$9.85\cdot10^{-1}$	± $5.03\cdot10^{-1}$
unknown o: *Actinomycetales*	$7.85\cdot10^{-1}$	$9.40\cdot10^{-1}$	$9.22\cdot10^{-1}$	2.03	$5.48\cdot10^{-1}$	1.21	$4.14\cdot10^{-1}$	$9.79\cdot10^{-1}$	± $5.33\cdot10^{-1}$
Sphingomonadaceae	1.04	$4.75\cdot10^{-1}$	$2.62\cdot10^{-1}$	$3.44\cdot10^{-1}$	$3.48\cdot10^{-1}$	$9.72\cdot10^{-1}$	3.15	$9.41\cdot10^{-1}$	± 1.02
Hyphomicrobiaceae	$4.22\cdot10^{-1}$	$1.26\cdot10^{-1}$	$8.20\cdot10^{-1}$	2.11	$3.18\cdot10^{-1}$	$5.20\cdot10^{-1}$	1.82	$8.77\cdot10^{-1}$	± $7.79\cdot10^{-1}$
Sphingobacteriaceae	4.16	$6.29\cdot10^{-1}$	$9.43\cdot10^{-2}$	$8.89\cdot10^{-2}$	$1.61\cdot10^{-1}$	$2.00\cdot10^{-1}$	$1.66\cdot10^{-1}$	$7.86\cdot10^{-1}$	± 1.50
Planctomycetaceae	$3.28\cdot10^{-1}$	$2.22\cdot10^{-1}$	$9.32\cdot10^{-1}$	$3.79\cdot10^{-1}$	$5.39\cdot10^{-1}$	$8.18\cdot10^{-1}$	2.24	$7.79\cdot10^{-1}$	± $6.92\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$5.97\cdot10^{-3}$	$6.82\cdot10^{-2}$	$7.76\cdot10^{-1}$	2.17	$7.97\cdot10^{-1}$	$2.86\cdot10^{-1}$	$4.14\cdot10^{-1}$	$6.45\cdot10^{-1}$	± $7.39\cdot10^{-1}$
Campylobacteraceae	$1.88\cdot10^{-1}$	1.29	$2.98\cdot10^{-1}$	$6.08\cdot10^{-1}$	1.34	$7.70\cdot10^{-1}$	N.D.[f]	$6.43\cdot10^{-1}$	± $5.28\cdot10^{-1}$
Bacteriovoracaceae	$2.46\cdot10^{-1}$	2.99	$1.02\cdot10^{-1}$	$3.90\cdot10^{-1}$	$1.92\cdot10^{-1}$	$8.75\cdot10^{-2}$	N.D.[f]	$5.73\cdot10^{-1}$	± 1.07
Phyllobacteriaceae	$5.56\cdot10^{-1}$	$1.02\cdot10^{-1}$	$1.09\cdot10^{-1}$	$2.46\cdot10^{-1}$	$2.33\cdot10^{-1}$	$5.09\cdot10^{-1}$	2.15	$5.58\cdot10^{-1}$	± $7.25\cdot10^{-1}$
unknown o: *Sphingobacteriales*	$1.40\cdot10^{-1}$	$5.82\cdot10^{-1}$	$5.06\cdot10^{-1}$	1.24	$4.86\cdot10^{-1}$	$4.12\cdot10^{-1}$	$4.97\cdot10^{-1}$	$5.53\cdot10^{-1}$	± $3.36\cdot10^{-1}$
Bradyrhizobiaceae	1.06	$3.20\cdot10^{-1}$	$3.11\cdot10^{-1}$	$4.33\cdot10^{-1}$	$4.05\cdot10^{-1}$	$7.52\cdot10^{-1}$	$4.97\cdot10^{-1}$	$5.40\cdot10^{-1}$	± $2.74\cdot10^{-1}$
Porphyromonadaceae	$2.69\cdot10^{-2}$	$4.38\cdot10^{-1}$	$4.39\cdot10^{-2}$	$8.61\cdot10^{-2}$	$2.68\cdot10^{-1}$	2.78	$8.28\cdot10^{-2}$	$5.32\cdot10^{-1}$	± 1.00
Bdellovibrionaceae	$4.04\cdot10^{-1}$	$5.60\cdot10^{-1}$	$3.89\cdot10^{-1}$	1.20	$4.78\cdot10^{-1}$	$1.70\cdot10^{-1}$	$8.28\cdot10^{-2}$	$4.69\cdot10^{-1}$	± $3.64\cdot10^{-1}$
Gp4	$9.25\cdot10^{-2}$	$6.68\cdot10^{-2}$	$1.37\cdot10^{-1}$	$2.10\cdot10^{-1}$	$6.66\cdot10^{-2}$	$3.67\cdot10^{-1}$	2.07	$4.30\cdot10^{-1}$	± $7.31\cdot10^{-1}$
Cyclobacteriaceae	$1.79\cdot10^{-2}$	$4.12\cdot10^{-2}$	$3.25\cdot10^{-2}$	$1.39\cdot10^{-2}$	$9.08\cdot10^{-3}$	$7.96\cdot10^{-3}$	2.81	$4.20\cdot10^{-1}$	± 1.06
Peptostreptococcaceae	$1.64\cdot10^{-1}$	$1.02\cdot10^{-1}$	$6.18\cdot10^{-2}$	$1.01\cdot10^{-1}$	$1.64\cdot10^{-1}$	1.38	N.D.[f]	$2.82\cdot10^{-1}$	± $4.87\cdot10^{-1}$

Table S40. G-EBPR family-level EUB results summary continued.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Erythrobacteraceae	$3.73\cdot10^{-2}$	$2.84\cdot10^{-2}$	$1.63\cdot10^{-2}$	$2.78\cdot10^{-2}$	$5.04\cdot10^{-2}$	$9.95\cdot10^{-2}$	1.49	$2.50\cdot10^{-1}$	±	$5.48\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S41. R-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Hydrogenophilaceae	15.0	27.3	19.7	13.6	8.76	13.1	$9.37\cdot10^{-3}$	13.9	±	8.50
Minor phylotypes (365)[d]	8.50	7.23	9.45	7.17	11.2	12.0	12.0	9.66	±	2.13
Comamonadaceae	22.9	10.4	2.94	2.90	5.48	2.67	$6.13\cdot10^{-1}$	6.85	±	7.75
Rhodocyclaceae	1.48	4.86	8.52	20.2	6.23	5.29	$2.68\cdot10^{-1}$	6.69	±	6.59
Rhodobacteraceae	1.36	1.54	1.97	2.89	14.5	9.10	3.60	5.00	±	4.98
unknown d: *Bacteria*	5.63	3.00	5.28	3.29	4.84	6.58	5.87	4.93	±	1.33
Chitinophagaceae	3.72	4.55	5.87	8.37	3.94	4.52	$6.19\cdot10^{-1}$	4.51	±	2.34
Methylobacteriaceae	$6.68\cdot10^{-3}$	$1.05\cdot10^{-2}$	$1.67\cdot10^{-3}$	N.D.[e]	$7.51\cdot10^{-3}$	$5.92\cdot10^{-3}$	27.2	3.89	±	10.3
Saprospiraceae	5.13	5.02	1.38	1.47	4.71	8.40	$9.60\cdot10^{-1}$	3.87	±	2.73
Xanthomonadaceae	4.29	3.82	3.37	2.17	3.15	2.26	3.71	3.25	±	$7.95\cdot10^{-1}$
Flavobacteriaceae	1.72	4.48	2.70	5.13	2.98	3.31	$3.41\cdot10^{-1}$	2.95	±	1.61
Ohtaekwangia	1.49	1.71	1.43	3.44	1.45	$7.90\cdot10^{-1}$	9.75	2.87	±	3.15
unknown p: *Bacteroidetes*	2.97	2.77	3.55	5.16	2.48	2.04	$7.23\cdot10^{-1}$	2.81	±	1.36
unknown p: *Proteobacteria*	$9.11\cdot10^{-1}$	$8.57\cdot10^{-1}$	6.81	1.38	$9.16\cdot10^{-1}$	1.08	$9.83\cdot10^{-1}$	1.85	±	2.20
Planctomycetaceae	$2.87\cdot10^{-1}$	$2.38\cdot10^{-1}$	$3.30\cdot10^{-1}$	$4.12\cdot10^{-1}$	1.41	1.60	6.85	1.59	±	2.39
unknown c: *Alphaproteobacteria*	$5.34\cdot10^{-1}$	$5.27\cdot10^{-1}$	1.93	2.05	2.50	1.97	1.45	1.56	±	$7.70\cdot10^{-1}$
unknown c: *Betaproteobacteria*	1.43	2.13	3.27	1.58	1.09	1.42	$2.95\cdot10^{-2}$	1.56	±	$9.87\cdot10^{-1}$
unknown o: *Sphingobacteriales*	3.21	3.61	$3.51\cdot10^{-1}$	$3.16\cdot10^{-1}$	1.09	2.13	$3.21\cdot10^{-2}$	1.53	±	1.46
Cytophagaceae	$4.70\cdot10^{-1}$	$3.45\cdot10^{-1}$	$1.77\cdot10^{-1}$	$1.38\cdot10^{-1}$	$7.54\cdot10^{-1}$	$8.30\cdot10^{-1}$	6.58	1.33	±	2.33
Verrucomicrobiaceae	$5.48\cdot10^{-1}$	$7.24\cdot10^{-1}$	1.35	1.62	2.42	$6.93\cdot10^{-1}$	1.31	1.24	±	$6.59\cdot10^{-1}$
Sphingomonadaceae	$9.57\cdot10^{-1}$	$5.07\cdot10^{-1}$	$3.60\cdot10^{-1}$	$5.09\cdot10^{-1}$	1.95	2.71	1.32	1.19	±	$8.73\cdot10^{-1}$

Table S41. R-EBPR family-level EUB results summary continued.

Family[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
unknown o: *Rhizobiales*	$4.74\cdot10^{-1}$	$3.25\cdot10^{-1}$	$4.87\cdot10^{-1}$	$8.47\cdot10^{-1}$	1.09	$9.38\cdot10^{-1}$	3.26	1.06	±	1.01
Gp4	$1.22\cdot10^{-1}$	$1.47\cdot10^{-1}$	$1.07\cdot10^{-1}$	$6.75\cdot10^{-2}$	2.03	2.91	1.75	1.02	±	1.18
Cryomorphaceae	$9.64\cdot10^{-1}$	1.09	1.09	1.85	$8.22\cdot10^{-1}$	$6.01\cdot10^{-1}$	$3.21\cdot10^{-2}$	$9.21\cdot10^{-1}$	±	$5.51\cdot10^{-1}$
Anaerolineaceae	1.21	$4.85\cdot10^{-1}$	1.44	1.18	1.11	$9.31\cdot10^{-1}$	N.D.[e]	$9.08\cdot10^{-1}$	±	$4.99\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	1.21	$2.03\cdot10^{-1}$	$5.44\cdot10^{-1}$	$5.50\cdot10^{-1}$	1.25	1.01	1.34	$8.74\cdot10^{-1}$	±	$4.40\cdot10^{-1}$
Caulobacteraceae	$5.79\cdot10^{-1}$	$3.85\cdot10^{-1}$	$8.12\cdot10^{-1}$	2.22	$6.53\cdot10^{-1}$	$4.13\cdot10^{-1}$	$9.48\cdot10^{-1}$	$8.58\cdot10^{-1}$	±	$6.34\cdot10^{-1}$
Campylobacteraceae	1.42	2.87	$1.71\cdot10^{-1}$	$6.19\cdot10^{-1}$	$5.44\cdot10^{-1}$	$3.85\cdot10^{-1}$	N.D.[e]	$8.57\cdot10^{-1}$	±	$9.94\cdot10^{-1}$
Burkholderiales_inc._sed.[f]	2.89	$9.81\cdot10^{-1}$	$4.47\cdot10^{-1}$	$2.33\cdot10^{-1}$	$4.67\cdot10^{-1}$	$3.97\cdot10^{-1}$	$1.41\cdot10^{-1}$	$7.94\cdot10^{-1}$	±	$9.62\cdot10^{-1}$
Nitrosomonadaceae	1.40	$7.30\cdot10^{-1}$	$9.44\cdot10^{-1}$	$9.14\cdot10^{-1}$	$5.71\cdot10^{-1}$	$6.59\cdot10^{-1}$	N.D.[e]	$7.45\cdot10^{-1}$	±	$4.26\cdot10^{-1}$
Opitutaceae	$2.89\cdot10^{-1}$	$2.69\cdot10^{-1}$	$6.71\cdot10^{-1}$	1.01	1.72	$9.00\cdot10^{-1}$	$4.15\cdot10^{-2}$	$6.99\cdot10^{-1}$	±	$5.71\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$3.67\cdot10^{-1}$	$5.76\cdot10^{-1}$	1.78	$2.61\cdot10^{-1}$	$3.76\cdot10^{-1}$	$3.88\cdot10^{-1}$	1.08	$6.90\cdot10^{-1}$	±	$5.52\cdot10^{-1}$
unknown o: *Flavobacteriales*	1.01	$8.80\cdot10^{-1}$	$7.45\cdot10^{-1}$	$8.68\cdot10^{-1}$	$5.45\cdot10^{-1}$	$6.25\cdot10^{-1}$	$9.51\cdot10^{-2}$	$6.81\cdot10^{-1}$	±	$3.04\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$2.98\cdot10^{-1}$	$4.90\cdot10^{-1}$	1.88	$6.98\cdot10^{-1}$	$3.84\cdot10^{-1}$	$2.66\cdot10^{-1}$	$7.46\cdot10^{-1}$	$6.81\cdot10^{-1}$	±	$5.61\cdot10^{-1}$
Bradyrhizobiaceae	$9.04\cdot10^{-1}$	$2.36\cdot10^{-1}$	$2.95\cdot10^{-1}$	$2.70\cdot10^{-1}$	1.33	1.29	$3.87\cdot10^{-1}$	$6.74\cdot10^{-1}$	±	$4.92\cdot10^{-1}$
Bdellovibrionaceae	$3.50\cdot10^{-1}$	$5.97\cdot10^{-1}$	1.06	$6.18\cdot10^{-1}$	$6.51\cdot10^{-1}$	1.24	$6.29\cdot10^{-2}$	$6.54\cdot10^{-1}$	±	$3.99\cdot10^{-1}$
Hyphomicrobiaceae	$4.03\cdot10^{-1}$	$2.27\cdot10^{-1}$	$3.26\cdot10^{-1}$	$2.70\cdot10^{-1}$	$9.29\cdot10^{-1}$	$7.52\cdot10^{-1}$	1.60	$6.44\cdot10^{-1}$	±	$4.96\cdot10^{-1}$
unknown o: *Pseudomonadales*	$3.90\cdot10^{-1}$	$2.57\cdot10^{-1}$	3.43	$2.13\cdot10^{-1}$	$2.13\cdot10^{-2}$	$4.14\cdot10^{-2}$	N.D.[e]	$6.22\cdot10^{-1}$	±	1.25
Parcubacteria_genera_inc._sed.[f]	1.36	$8.22\cdot10^{-2}$	$7.40\cdot10^{-1}$	$3.11\cdot10^{-1}$	$7.78\cdot10^{-1}$	$1.82\cdot10^{-1}$	$3.37\cdot10^{-1}$	$5.42\cdot10^{-1}$	±	$4.49\cdot10^{-1}$
Gallionellaceae	$3.65\cdot10^{-1}$	$3.80\cdot10^{-1}$	1.63	$6.89\cdot10^{-1}$	$2.76\cdot10^{-1}$	$1.64\cdot10^{-1}$	$5.36\cdot10^{-3}$	$5.01\cdot10^{-1}$	±	$5.40\cdot10^{-1}$
Phyllobacteriaceae	$3.03\cdot10^{-1}$	$2.26\cdot10^{-1}$	$1.54\cdot10^{-1}$	$1.49\cdot10^{-1}$	$5.36\cdot10^{-1}$	$4.72\cdot10^{-1}$	1.64	$4.98\cdot10^{-1}$	±	$5.27\cdot10^{-1}$
Rhodospirillaceae	$4.90\cdot10^{-2}$	$5.60\cdot10^{-2}$	$5.36\cdot10^{-2}$	1.91	$6.91\cdot10^{-1}$	$4.04\cdot10^{-1}$	$2.21\cdot10^{-1}$	$4.84\cdot10^{-1}$	±	$6.73\cdot10^{-1}$
Cystobacteraceae	$8.57\cdot10^{-1}$	1.14	$3.68\cdot10^{-1}$	$2.84\cdot10^{-1}$	$2.66\cdot10^{-1}$	$2.03\cdot10^{-1}$	N.D.[e]	$4.46\cdot10^{-1}$	±	$4.04\cdot10^{-1}$
Nitrospiraceae	N.D.[e]	$3.50\cdot10^{-3}$	$1.00\cdot10^{-2}$	$3.55\cdot10^{-3}$	$7.51\cdot10^{-1}$	1.95	N.D.[e]	$3.88\cdot10^{-1}$	±	$7.42\cdot10^{-1}$
Aeromonadaceae	$1.80\cdot10^{-1}$	1.75	$7.70\cdot10^{-2}$	$9.05\cdot10^{-2}$	$3.38\cdot10^{-2}$	$7.10\cdot10^{-2}$	N.D.[e]	$3.14\cdot10^{-1}$	±	$6.35\cdot10^{-1}$
Armatimonadetes_gp5	N.D.[e]	$1.75\cdot10^{-3}$	$8.37\cdot10^{-3}$	$3.73\cdot10^{-2}$	$1.43\cdot10^{-1}$	$1.91\cdot10^{-1}$	1.05	$2.04\cdot10^{-1}$	±	$3.80\cdot10^{-1}$
Spartobacteria_genera_inc._sed.[f]	$2.67\cdot10^{-2}$	$3.50\cdot10^{-3}$	$8.37\cdot10^{-3}$	$7.10\cdot10^{-3}$	$8.77\cdot10^{-2}$	$6.36\cdot10^{-2}$	1.02	$1.74\cdot10^{-1}$	±	$3.76\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

[f] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S42. Moscow WRRF family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Minor phylotypes (365)[d]	15.1	18.6	16.5	15.7	15.3	17.2	16.3	16.4	± 1.21
unknown d: *Bacteria*	8.27	5.99	5.96	6.34	8.43	7.39	7.39	7.11	± 1.03
Chitinophagaceae	6.85	5.32	5.60	6.63	5.82	3.67	2.93	5.26	± 1.46
Flavobacteriaceae	4.38	3.69	4.18	8.00	4.16	5.82	3.74	4.85	± 1.56
Rhodocyclaceae	4.99	2.43	2.51	2.98	6.64	6.60	5.92	4.58	± 1.90
unknown p: *Bacteroidetes*	2.70	2.09	3.15	3.53	6.37	4.78	5.24	3.98	± 1.53
Saprospiraceae	2.67	5.19	5.51	4.05	1.58	1.87	1.94	3.26	± 1.64
Comamonadaceae	4.62	5.46	4.02	3.03	1.82	1.74	1.66	3.19	± 1.54
Planctomycetaceae	2.62	3.58	5.07	3.51	1.67	2.98	1.93	3.05	± 1.15
unknown p: *Proteobacteria*	2.20	1.46	1.45	1.57	4.33	4.25	4.95	2.89	± 1.55
Caldilineaceae	3.32	4.06	3.84	3.69	1.41	1.67	1.39	2.77	± 1.22
unknown o: *Actinomycetales*	2.46	4.15	4.13	3.47	1.51	1.65	1.25	2.66	± 1.25
Chloroflexaceae	2.94	2.97	3.36	3.90	1.45	1.50	1.79	2.56	± $9.75\cdot10^{-1}$
unknown o: *Rhizobiales*	1.49	2.26	2.95	2.85	2.30	2.21	1.65	2.24	± $5.48\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	1.45	1.56	1.88	1.84	2.66	2.87	2.40	2.10	± $5.50\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	1.67	$9.83\cdot10^{-1}$	3.14	3.94	1.40	1.56	$8.89\cdot10^{-1}$	1.94	± 1.15
unknown c: *Gammaproteobacteria*	1.04	$9.12\cdot10^{-1}$	$7.12\cdot10^{-1}$	$9.76\cdot10^{-1}$	2.76	2.49	3.55	1.78	± 1.13
Rhodobacteraceae	2.49	2.59	2.41	1.60	$5.56\cdot10^{-1}$	$8.90\cdot10^{-1}$	$6.96\cdot10^{-1}$	1.60	± $8.97\cdot10^{-1}$
Burkholderiales_inc._sed.[e]	$9.61\cdot10^{-1}$	$9.05\cdot10^{-1}$	$9.40\cdot10^{-1}$	$8.83\cdot10^{-1}$	2.50	2.30	2.41	1.56	± $7.94\cdot10^{-1}$
Cytophagaceae	4.63	1.21	1.35	1.16	1.00	$9.14\cdot10^{-1}$	$6.17\cdot10^{-1}$	1.55	± 1.37
Sphingomonadaceae	2.39	1.92	2.31	2.11	$6.74\cdot10^{-1}$	$6.15\cdot10^{-1}$	$4.38\cdot10^{-1}$	1.49	± $8.75\cdot10^{-1}$
Candidatus Carsonella	$4.34\cdot10^{-1}$	$5.19\cdot10^{-1}$	$1.44\cdot10^{-1}$	$1.66\cdot10^{-1}$	2.30	1.96	4.93	1.49	± 1.75
unknown o: *Sphingobacteriales*	1.34	$8.75\cdot10^{-1}$	1.28	1.71	1.74	1.18	1.19	1.33	± $3.07\cdot10^{-1}$
Ohtaekwangia	$4.58\cdot10^{-1}$	$7.94\cdot10^{-1}$	1.21	$7.71\cdot10^{-1}$	2.38	1.81	1.76	1.31	± $6.93\cdot10^{-1}$
Hyphomicrobiaceae	1.28	2.00	1.90	1.65	$5.43\cdot10^{-1}$	$7.93\cdot10^{-1}$	$5.38\cdot10^{-1}$	1.24	± $6.29\cdot10^{-1}$
Phycisphaeraceae	$3.68\cdot10^{-1}$	$7.22\cdot10^{-1}$	$7.24\cdot10^{-1}$	$8.07\cdot10^{-1}$	1.98	1.54	1.76	1.13	± $6.20\cdot10^{-1}$
unknown o: *Flavobacteriales*	$5.98\cdot10^{-1}$	1.22	1.08	$8.68\cdot10^{-1}$	1.21	1.21	1.32	1.07	± $2.53\cdot10^{-1}$
Nitrospiraceae	$8.48\cdot10^{-1}$	$7.49\cdot10^{-1}$	$7.48\cdot10^{-1}$	$9.27\cdot10^{-1}$	1.46	1.21	1.45	1.06	± $3.14\cdot10^{-1}$
Xanthomonadaceae	1.37	1.42	1.34	1.09	$6.01\cdot10^{-1}$	$6.78\cdot10^{-1}$	$5.35\cdot10^{-1}$	1.00	± $3.90\cdot10^{-1}$
Pseudomonadaceae	$4.48\cdot10^{-1}$	$4.73\cdot10^{-1}$	$2.42\cdot10^{-1}$	$3.50\cdot10^{-1}$	1.31	1.35	2.82	$9.99\cdot10^{-1}$	± $9.23\cdot10^{-1}$

Table S42. Moscow WRRF family-level EUB results summary continued.

Family[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
unknown o: *Myxococcales*	$1.28\cdot10^{-1}$	$5.07\cdot10^{-1}$	$4.16\cdot10^{-1}$	$4.58\cdot10^{-1}$	2.28	1.60	1.50	$9.85\cdot10^{-1}$	$\pm 8.05\cdot10^{-1}$
Anaerolineaceae	1.07	$7.75\cdot10^{-1}$	$6.52\cdot10^{-1}$	$6.27\cdot10^{-1}$	$8.89\cdot10^{-1}$	1.28	1.57	$9.82\cdot10^{-1}$	$\pm 3.50\cdot10^{-1}$
Carnobacteriaceae	3.43	1.50	$9.84\cdot10^{-1}$	$6.17\cdot10^{-1}$	$6.91\cdot10^{-2}$	$1.26\cdot10^{-1}$	$9.73\cdot10^{-2}$	$9.75\cdot10^{-1}$	± 1.21
Rhodospirillaceae	$4.20\cdot10^{-1}$	$9.87\cdot10^{-1}$	$9.72\cdot10^{-1}$	1.27	$9.86\cdot10^{-1}$	1.04	1.07	$9.63\cdot10^{-1}$	$\pm 2.61\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$8.28\cdot10^{-1}$	$7.85\cdot10^{-1}$	$7.61\cdot10^{-1}$	$6.22\cdot10^{-1}$	1.16	1.13	1.09	$9.10\cdot10^{-1}$	$\pm 2.11\cdot10^{-1}$
Nitrosomonadaceae	$4.70\cdot10^{-1}$	$7.23\cdot10^{-1}$	$7.53\cdot10^{-1}$	$6.91\cdot10^{-1}$	1.12	1.23	1.26	$8.92\cdot10^{-1}$	$\pm 3.07\cdot10^{-1}$
Polyangiaceae	$1.67\cdot10^{-1}$	$4.21\cdot10^{-1}$	$3.69\cdot10^{-1}$	$3.46\cdot10^{-1}$	1.08	1.81	1.68	$8.39\cdot10^{-1}$	$\pm 6.82\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$4.10\cdot10^{-1}$	$4.78\cdot10^{-1}$	$7.57\cdot10^{-1}$	$9.74\cdot10^{-1}$	1.24	$9.56\cdot10^{-1}$	$9.64\cdot10^{-1}$	$8.26\cdot10^{-1}$	$\pm 2.97\cdot10^{-1}$
Acidimicrobiaceae	1.55	1.34	1.18	$8.64\cdot10^{-1}$	$2.57\cdot10^{-1}$	$3.82\cdot10^{-1}$	$1.98\cdot10^{-1}$	$8.25\cdot10^{-1}$	$\pm 5.53\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$4.44\cdot10^{-1}$	2.50	$2.72\cdot10^{-1}$	$4.54\cdot10^{-1}$	$2.92\cdot10^{-1}$	$6.28\cdot10^{-1}$	$4.35\cdot10^{-1}$	$7.17\cdot10^{-1}$	$\pm 7.93\cdot10^{-1}$
Mycobacteriaceae	$1.66\cdot10^{-1}$	1.16	1.01	1.25	$4.53\cdot10^{-1}$	$3.53\cdot10^{-1}$	$2.26\cdot10^{-1}$	$6.59\cdot10^{-1}$	$\pm 4.64\cdot10^{-1}$
Verrucomicrobiaceae	1.12	$7.87\cdot10^{-1}$	$5.58\cdot10^{-1}$	$5.33\cdot10^{-1}$	$3.90\cdot10^{-1}$	$6.03\cdot10^{-1}$	$5.66\cdot10^{-1}$	$6.51\cdot10^{-1}$	$\pm 2.37\cdot10^{-1}$
Subdivision3_genera_inc._sed.[e]	$2.97\cdot10^{-1}$	$2.92\cdot10^{-1}$	$5.36\cdot10^{-1}$	$4.88\cdot10^{-1}$	$6.88\cdot10^{-1}$	$5.93\cdot10^{-1}$	1.12	$5.74\cdot10^{-1}$	$\pm 2.83\cdot10^{-1}$
Campylobacteraceae	$3.48\cdot10^{-1}$	$1.25\cdot10^{-1}$	$4.22\cdot10^{-1}$	$1.17\cdot10^{-1}$	$7.70\cdot10^{-1}$	1.15	$8.24\cdot10^{-1}$	$5.36\cdot10^{-1}$	$\pm 3.88\cdot10^{-1}$
Intrasporangiaceae	1.76	$9.13\cdot10^{-1}$	$5.03\cdot10^{-1}$	$3.34\cdot10^{-1}$	$6.80\cdot10^{-2}$	$4.94\cdot10^{-2}$	$5.75\cdot10^{-2}$	$5.27\cdot10^{-1}$	$\pm 6.29\cdot10^{-1}$
Cyclobacteriaceae	1.01	$6.41\cdot10^{-1}$	$2.35\cdot10^{-1}$	$1.50\cdot10^{-1}$	$2.54\cdot10^{-1}$	$1.36\cdot10^{-1}$	$1.54\cdot10^{-1}$	$3.69\cdot10^{-1}$	$\pm 3.34\cdot10^{-1}$
unknown o: *Pseudomonadales*	$1.87\cdot10^{-2}$	$1.03\cdot10^{-2}$	$1.41\cdot10^{-2}$	$2.66\cdot10^{-2}$	$1.65\cdot10^{-1}$	$2.42\cdot10^{-1}$	1.76	$3.19\cdot10^{-1}$	$\pm 6.40\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S43. Summary of family-level relative abundance by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	S-EBPR (S38) Average %	± SD[c]	V-EBPR (S39) Average %	± SD[c]	G-EBPR (S40) Average %	± SD[c]	R-EBPR (S41) Average %	± SD[c]	Moscow WRRF (S42) Average %	± SD[c]
Rhodocyclaceae	16.2	± 11.2	8.52	± 7.41	8.73	± 7.99	6.69	± 6.59	4.58	± 1.90
Hydrogenophilaceae	$6.08\cdot10^{-3}$	$\pm 5.56\cdot10^{-3}$	10.9	± 6.60	6.21	± 4.22	13.9	± 8.50	$3.11\cdot10^{-3}$	$\pm 1.35\cdot10^{-3}$
Rhodobacteraceae	13.8	± 3.27	1.79	± 1.25	2.35	$\pm 9.00\cdot10^{-1}$	5.00	± 4.98	1.60	$\pm 8.97\cdot10^{-1}$
unknown p: *Bacteroidetes*	1.67	$\pm 5.54\cdot10^{-1}$	12.6	± 5.82	5.00	± 3.22	2.81	± 1.36	3.98	± 1.53
Minor phylotypes (332)[d]	3.68	$\pm 9.21\cdot10^{-1}$	5.19	± 2.27	5.64	± 1.77	5.22	± 1.37	10.1	± 1.11

Table S43. Summary of family-level EUB results continued.

Family[a,b]	S-EBPR (S38) Average ± SD[c] %	V-EBPR (S39) Average ± SD[c] %	G-EBPR (S40) Average ± SD[c] %	R-EBPR (S41) Average ± SD[c] %	Moscow WRRF (S42) Average ± SD[c] %
Flavobacteriaceae	8.64 ± 5.95	1.75 ± 1.71	1.66 ± 1.40	2.95 ± 1.61	4.85 ± 1.56
Saccharibacteria_genera_inc._sed.[e]	$1.90\cdot10^{-1}$ ± $3.97\cdot10^{-1}$	$5.40\cdot10^{-1}$ ± $4.71\cdot10^{-1}$	7.87 ± 8.38	$8.74\cdot10^{-1}$ ± $4.40\cdot10^{-1}$	1.94 ± 1.15
unknown d: *Bacteria*	5.86 ± 2.76	3.75 ± 1.78	4.23 ± $9.24\cdot10^{-1}$	4.93 ± 1.33	7.11 ± 1.03
Comamonadaceae	1.42 ± 1.07	4.99 ± 2.04	2.33 ± 1.42	6.85 ± 7.75	3.19 ± 1.54
Ohtaekwangia	6.52 ± 3.58	$5.95\cdot10^{-1}$ ± $4.61\cdot10^{-1}$	1.94 ± 1.44	2.87 ± 3.15	1.31 ± $6.93\cdot10^{-1}$
Chitinophagaceae	1.79 ± 1.09	1.81 ± $8.46\cdot10^{-1}$	3.23 ± 2.62	4.51 ± 2.34	5.26 ± 1.46
Saprospiraceae	1.27 ± 1.58	4.77 ± 2.38	4.88 ± 3.43	3.87 ± 2.73	3.26 ± 1.64
unknown c: *Alphaproteobacteria*	2.96 ± 1.17	1.63 ± $6.88\cdot10^{-1}$	4.30 ± 1.82	1.56 ± $7.70\cdot10^{-1}$	2.10 ± $5.50\cdot10^{-1}$
Methylobacteriaceae	$1.62\cdot10^{-2}$ ± $7.19\cdot10^{-3}$	2.47 ± 6.48	3.19 ± 7.87	3.89 ± 10.3	$1.13\cdot10^{-2}$ ± $3.95\cdot10^{-3}$
Methylophilaceae	$2.59\cdot10^{-4}$ ± $6.85\cdot10^{-4}$	$3.74\cdot10^{-4}$ ± $9.90\cdot10^{-4}$	3.71 ± 3.13	$1.17\cdot10^{-3}$ ± $2.01\cdot10^{-3}$	$1.84\cdot10^{-3}$ ± $2.16\cdot10^{-3}$
Xanthomonadaceae	2.64 ± $9.58\cdot10^{-1}$	1.74 ± 1.49	$9.85\cdot10^{-1}$ ± $5.03\cdot10^{-1}$	3.25 ± $7.95\cdot10^{-1}$	1.00 ± $3.90\cdot10^{-1}$
Planctomycetaceae	3.21 ± 1.54	1.21 ± 1.18	$7.79\cdot10^{-1}$ ± $6.92\cdot10^{-1}$	1.59 ± 2.39	3.05 ± 1.15
Rhodospirillaceae	3.00 ± 2.71	1.25 ± $7.76\cdot10^{-1}$	1.67 ± 1.71	$4.84\cdot10^{-1}$ ± $6.73\cdot10^{-1}$	$9.63\cdot10^{-1}$ ± $2.61\cdot10^{-1}$
unknown p: *Proteobacteria*	1.68 ± $9.32\cdot10^{-1}$	1.88 ± 1.36	2.02 ± $9.66\cdot10^{-1}$	1.85 ± 2.20	2.89 ± 1.55
Caldilineaceae	$4.33\cdot10^{-1}$ ± $5.50\cdot10^{-1}$	1.17 ± 1.14	1.24 ± $6.32\cdot10^{-1}$	$4.79\cdot10^{-1}$ ± $3.28\cdot10^{-1}$	2.77 ± 1.22
Phycisphaeraceae	2.77 ± 2.39	$1.99\cdot10^{-2}$ ± $2.48\cdot10^{-2}$	$6.02\cdot10^{-2}$ ± $5.35\cdot10^{-2}$	$7.24\cdot10^{-2}$ ± $9.70\cdot10^{-2}$	1.13 ± $6.20\cdot10^{-1}$
unknown o: *Actinomycetales*	$3.36\cdot10^{-2}$ ± $3.97\cdot10^{-2}$	$4.93\cdot10^{-1}$ ± $3.50\cdot10^{-1}$	$9.79\cdot10^{-1}$ ± $5.33\cdot10^{-1}$	$1.42\cdot10^{-1}$ ± $1.41\cdot10^{-1}$	2.66 ± 1.25
Verrucomicrobiaceae	1.40 ± $9.75\cdot10^{-1}$	2.63 ± 1.70	1.08 ± $6.73\cdot10^{-1}$	1.24 ± $6.59\cdot10^{-1}$	$6.51\cdot10^{-1}$ ± $2.37\cdot10^{-1}$
Chloroflexaceae	$1.57\cdot10^{-3}$ ± $1.97\cdot10^{-3}$	$5.65\cdot10^{-2}$ ± $6.75\cdot10^{-2}$	$4.66\cdot10^{-2}$ ± $3.17\cdot10^{-2}$	$5.86\cdot10^{-2}$ ± $3.86\cdot10^{-2}$	2.56 ± $9.75\cdot10^{-1}$
Prevotellaceae	$2.82\cdot10^{-2}$ ± $7.16\cdot10^{-2}$	2.25 ± 2.33	$4.06\cdot10^{-2}$ ± $4.79\cdot10^{-2}$	$2.57\cdot10^{-2}$ ± $2.73\cdot10^{-2}$	$2.56\cdot10^{-2}$ ± $1.60\cdot10^{-2}$
unknown o: *Rhizobiales*	1.99 ± 1.09	1.24 ± $8.79\cdot10^{-1}$	1.68 ± $4.46\cdot10^{-1}$	1.06 ± 1.01	2.24 ± $5.48\cdot10^{-1}$
unknown o: *Cytophagales*	$1.04\cdot10^{-1}$ ± $8.80\cdot10^{-2}$	2.19 ± 1.86	1.62 ± 1.30	$1.48\cdot10^{-1}$ ± $1.46\cdot10^{-1}$	$2.85\cdot10^{-1}$ ± $1.02\cdot10^{-1}$
Intrasporangiaceae	$3.20\cdot10^{-3}$ ± $3.75\cdot10^{-3}$	$7.07\cdot10^{-2}$ ± $5.15\cdot10^{-2}$	1.93 ± 2.42	$6.91\cdot10^{-2}$ ± $7.93\cdot10^{-2}$	$5.27\cdot10^{-1}$ ± $6.29\cdot10^{-1}$
Caulobacteraceae	1.84 ± 1.98	1.20 ± 1.13	1.79 ± 1.36	$8.58\cdot10^{-1}$ ± $6.34\cdot10^{-1}$	$2.21\cdot10^{-1}$ ± $1.82\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$9.31\cdot10^{-1}$ ± $5.21\cdot10^{-1}$	$9.27\cdot10^{-1}$ ± $8.50\cdot10^{-1}$	$4.58\cdot10^{-1}$ ± $2.43\cdot10^{-1}$	$6.90\cdot10^{-1}$ ± $5.52\cdot10^{-1}$	1.78 ± 1.13
unknown o: *Sphingobacteriales*	$1.22\cdot10^{-1}$ ± $6.36\cdot10^{-2}$	1.69 ± $7.80\cdot10^{-1}$	$5.53\cdot10^{-1}$ ± $3.36\cdot10^{-1}$	1.53 ± 1.46	1.33 ± $3.07\cdot10^{-1}$
Bradyrhizobiaceae	1.62 ± 1.64	$3.34\cdot10^{-1}$ ± $1.71\cdot10^{-1}$	$5.40\cdot10^{-1}$ ± $2.74\cdot10^{-1}$	$6.74\cdot10^{-1}$ ± $4.92\cdot10^{-1}$	$4.20\cdot10^{-1}$ ± $2.72\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$4.00\cdot10^{-1}$ ± $1.59\cdot10^{-1}$	1.06 ± $6.41\cdot10^{-1}$	1.17 ± $7.57\cdot10^{-1}$	1.56 ± $9.87\cdot10^{-1}$	$8.26\cdot10^{-1}$ ± $2.97\cdot10^{-1}$
Burkholderiales_inc._sed.[e]	1.31 ± 1.53	1.47 ± 1.25	1.49 ± 1.58	$7.94\cdot10^{-1}$ ± $9.62\cdot10^{-1}$	1.56 ± $7.94\cdot10^{-1}$
Cytophagaceae	$3.10\cdot10^{-1}$ ± $4.33\cdot10^{-1}$	1.18 ± $4.87\cdot10^{-1}$	1.55 ± 1.06	1.33 ± 2.33	1.55 ± 1.37

Table S43. Summary of family-level EUB results continued.

Family[a,b]	S-EBPR (S38)		V-EBPR (S39)		G-EBPR (S40)		R-EBPR (S41)		Moscow WRRF (S42)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
Sphingomonadaceae	$6.71\cdot10^{-1}$	± $5.06\cdot10^{-1}$	1.45	± 1.34	$9.41\cdot10^{-1}$	± 1.02	1.19	± $8.73\cdot10^{-1}$	1.49	± $8.75\cdot10^{-1}$
Candidatus Carsonella	$4.51\cdot10^{-2}$	± $3.99\cdot10^{-2}$	$1.03\cdot10^{-1}$	± $1.63\cdot10^{-1}$	$1.31\cdot10^{-2}$	± $1.55\cdot10^{-2}$	$1.09\cdot10^{-1}$	± $2.48\cdot10^{-1}$	1.49	± 1.75
Propionibacteriaceae	$1.61\cdot10^{-4}$	± $4.26\cdot10^{-4}$	$6.11\cdot10^{-2}$	± $8.58\cdot10^{-2}$	1.42	± 1.43	$1.01\cdot10^{-1}$	± $2.27\cdot10^{-1}$	$4.09\cdot10^{-1}$	± $2.77\cdot10^{-1}$
Hyphomicrobiaceae	$4.46\cdot10^{-1}$	± $3.07\cdot10^{-1}$	$5.45\cdot10^{-1}$	± $4.39\cdot10^{-1}$	$8.77\cdot10^{-1}$	± $7.79\cdot10^{-1}$	$6.44\cdot10^{-1}$	± $4.96\cdot10^{-1}$	1.24	± $6.29\cdot10^{-1}$
Moraxellaceae	$6.69\cdot10^{-4}$	± $1.31\cdot10^{-3}$	1.12	± 1.17	$1.58\cdot10^{-1}$	± $1.26\cdot10^{-1}$	$3.61\cdot10^{-1}$	± $3.31\cdot10^{-1}$	$5.65\cdot10^{-1}$	± $2.29\cdot10^{-1}$
unknown o: *Flavobacteriales*	$5.47\cdot10^{-1}$	± $3.40\cdot10^{-1}$	$4.99\cdot10^{-1}$	± $6.33\cdot10^{-1}$	$2.35\cdot10^{-1}$	± $1.05\cdot10^{-1}$	$6.81\cdot10^{-1}$	± $3.04\cdot10^{-1}$	1.07	± $2.53\cdot10^{-1}$
Nitrospiraceae	$6.98\cdot10^{-1}$	± $5.17\cdot10^{-1}$	$1.18\cdot10^{-3}$	± $1.52\cdot10^{-3}$	$9.20\cdot10^{-4}$	± $1.28\cdot10^{-3}$	$3.88\cdot10^{-1}$	± $7.42\cdot10^{-1}$	1.06	± $3.14\cdot10^{-1}$
Gp4	$1.71\cdot10^{-1}$	± $1.54\cdot10^{-1}$	$4.09\cdot10^{-1}$	± $5.66\cdot10^{-1}$	$4.30\cdot10^{-1}$	± $7.31\cdot10^{-1}$	1.02	± 1.18	$4.41\cdot10^{-1}$	± $2.63\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$2.63\cdot10^{-1}$	± $3.49\cdot10^{-1}$	1.01	± 1.36	$6.45\cdot10^{-1}$	± $7.39\cdot10^{-1}$	$5.42\cdot10^{-1}$	± $4.49\cdot10^{-1}$	$7.17\cdot10^{-1}$	± $7.93\cdot10^{-1}$
Pseudomonadaceae	$1.54\cdot10^{-1}$	± $1.76\cdot10^{-1}$	$2.07\cdot10^{-1}$	± $1.77\cdot10^{-1}$	$9.36\cdot10^{-2}$	± $1.06\cdot10^{-1}$	$1.33\cdot10^{-1}$	± $1.26\cdot10^{-1}$	$9.99\cdot10^{-1}$	± $9.23\cdot10^{-1}$
unknown o: *Myxococcales*	$1.61\cdot10^{-1}$	± $1.15\cdot10^{-1}$	$2.95\cdot10^{-1}$	± $3.25\cdot10^{-1}$	$8.45\cdot10^{-2}$	± $6.90\cdot10^{-2}$	$1.06\cdot10^{-1}$	± $5.55\cdot10^{-2}$	$9.85\cdot10^{-1}$	± $8.05\cdot10^{-1}$
Anaerolineaceae	$3.43\cdot10^{-1}$	± $3.70\cdot10^{-1}$	$1.19\cdot10^{-1}$	± $1.03\cdot10^{-1}$	$2.81\cdot10^{-1}$	± $2.78\cdot10^{-1}$	$9.08\cdot10^{-1}$	± $4.99\cdot10^{-1}$	$9.82\cdot10^{-1}$	± $3.50\cdot10^{-1}$
Carnobacteriaceae	$2.07\cdot10^{-1}$	± $5.38\cdot10^{-1}$	$2.65\cdot10^{-1}$	± $1.41\cdot10^{-1}$	$3.20\cdot10^{-1}$	± $1.80\cdot10^{-1}$	$2.59\cdot10^{-1}$	± $1.79\cdot10^{-1}$	$9.75\cdot10^{-1}$	± 1.21
Cryomorphaceae	$9.08\cdot10^{-2}$	± $8.91\cdot10^{-2}$	$3.16\cdot10^{-1}$	± $4.62\cdot10^{-1}$	$1.14\cdot10^{-1}$	± $5.53\cdot10^{-2}$	$9.21\cdot10^{-1}$	± $5.51\cdot10^{-1}$	$2.12\cdot10^{-1}$	± $9.32\cdot10^{-2}$
unknown c: *Deltaproteobacteria*	$6.04\cdot10^{-1}$	± $2.47\cdot10^{-1}$	$3.70\cdot10^{-1}$	± $2.02\cdot10^{-1}$	$4.64\cdot10^{-1}$	± $2.69\cdot10^{-1}$	$6.81\cdot10^{-1}$	± $5.61\cdot10^{-1}$	$9.10\cdot10^{-1}$	± $2.11\cdot10^{-1}$
Nitrosomonadaceae	$7.50\cdot10^{-1}$	± $6.16\cdot10^{-1}$	$1.80\cdot10^{-1}$	± $1.30\cdot10^{-1}$	$2.23\cdot10^{-2}$	± $2.18\cdot10^{-2}$	$7.45\cdot10^{-1}$	± $4.26\cdot10^{-1}$	$8.92\cdot10^{-1}$	± $3.07\cdot10^{-1}$
Polyangiaceae	$4.81\cdot10^{-1}$	± $6.26\cdot10^{-1}$	$8.81\cdot10^{-1}$	± 1.35	$1.36\cdot10^{-1}$	± $1.44\cdot10^{-1}$	$1.11\cdot10^{-1}$	± $1.11\cdot10^{-1}$	$8.39\cdot10^{-1}$	± $6.82\cdot10^{-1}$
Campylobacteraceae	N.D.[f]		$4.50\cdot10^{-1}$	± $2.98\cdot10^{-1}$	$6.43\cdot10^{-1}$	± $5.28\cdot10^{-1}$	$8.57\cdot10^{-1}$	± $9.94\cdot10^{-1}$	$5.36\cdot10^{-1}$	± $3.88\cdot10^{-1}$
Porphyromonadaceae	$1.67\cdot10^{-2}$	± $4.19\cdot10^{-2}$	$8.45\cdot10^{-1}$	± $8.64\cdot10^{-1}$	$5.32\cdot10^{-1}$	± 1.00	$1.56\cdot10^{-1}$	± $1.15\cdot10^{-1}$	$2.90\cdot10^{-1}$	± $7.64\cdot10^{-2}$
Acidimicrobiaceae	$1.30\cdot10^{-1}$	± $1.09\cdot10^{-1}$	$2.37\cdot10^{-1}$	± $1.40\cdot10^{-1}$	$2.97\cdot10^{-1}$	± $2.61\cdot10^{-1}$	$2.88\cdot10^{-1}$	± $1.23\cdot10^{-1}$	$8.25\cdot10^{-1}$	± $5.53\cdot10^{-1}$
Clostridiaceae 1	$7.92\cdot10^{-1}$	± 2.10	$7.48\cdot10^{-2}$	± $4.91\cdot10^{-2}$	$1.21\cdot10^{-1}$	± $2.46\cdot10^{-1}$	$6.50\cdot10^{-2}$	± $5.57\cdot10^{-2}$	$1.82\cdot10^{-1}$	± $9.17\cdot10^{-2}$
Sphingobacteriaceae	$4.04\cdot10^{-1}$	± $2.90\cdot10^{-1}$	$7.07\cdot10^{-2}$	± $6.73\cdot10^{-2}$	$7.86\cdot10^{-1}$	± 1.50	$3.00\cdot10^{-1}$	± $2.87\cdot10^{-1}$	$1.97\cdot10^{-1}$	± $9.56\cdot10^{-2}$
Phyllobacteriaceae	$7.62\cdot10^{-1}$	± $4.73\cdot10^{-1}$	$6.19\cdot10^{-1}$	± $7.94\cdot10^{-1}$	$5.58\cdot10^{-1}$	± $7.25\cdot10^{-1}$	$4.98\cdot10^{-1}$	± $5.27\cdot10^{-1}$	$1.98\cdot10^{-1}$	± $1.07\cdot10^{-1}$
SR1_genera_inc._sed.[e]	$7.50\cdot10^{-1}$	± 1.84	$2.96\cdot10^{-2}$	± $4.39\cdot10^{-2}$	$4.33\cdot10^{-3}$	± $6.34\cdot10^{-3}$	$1.44\cdot10^{-1}$	± $1.78\cdot10^{-1}$	$3.85\cdot10^{-2}$	± $3.03\cdot10^{-2}$
Opitutaceae	$2.67\cdot10^{-1}$	± $1.68\cdot10^{-1}$	$3.82\cdot10^{-1}$	± $9.04\cdot10^{-2}$	$3.27\cdot10^{-1}$	± $2.31\cdot10^{-1}$	$6.99\cdot10^{-1}$	± $5.71\cdot10^{-1}$	$2.28\cdot10^{-1}$	± $1.58\cdot10^{-1}$
Mycobacteriaceae	$2.20\cdot10^{-3}$	± $1.99\cdot10^{-3}$	$3.76\cdot10^{-2}$	± $3.39\cdot10^{-2}$	$3.92\cdot10^{-2}$	± $5.92\cdot10^{-2}$	$2.23\cdot10^{-2}$	± $2.53\cdot10^{-2}$	$6.59\cdot10^{-1}$	± $4.64\cdot10^{-1}$
Bdellovibrionaceae	$4.31\cdot10^{-1}$	± $2.13\cdot10^{-1}$	$4.63\cdot10^{-1}$	± $2.53\cdot10^{-1}$	$4.69\cdot10^{-1}$	± $3.64\cdot10^{-1}$	$6.54\cdot10^{-1}$	± $3.99\cdot10^{-1}$	$4.11\cdot10^{-1}$	± $1.49\cdot10^{-1}$
unknown o: *Pseudomonadales*	$8.28\cdot10^{-4}$	± $1.05\cdot10^{-3}$	$4.68\cdot10^{-1}$	± $3.06\cdot10^{-1}$	$8.31\cdot10^{-2}$	± $1.35\cdot10^{-1}$	$6.22\cdot10^{-1}$	± 1.25	$3.19\cdot10^{-1}$	± $6.40\cdot10^{-1}$
Subdivision3_genera_inc._sed.[e]	$5.41\cdot10^{-2}$	± $2.87\cdot10^{-2}$	$4.49\cdot10^{-2}$	± $4.67\cdot10^{-2}$	$2.22\cdot10^{-2}$	± $2.19\cdot10^{-2}$	$3.71\cdot10^{-2}$	± $4.68\cdot10^{-2}$	$5.74\cdot10^{-1}$	± $2.83\cdot10^{-1}$
Bacteriovoracaceae	$1.36\cdot10^{-2}$	± $1.18\cdot10^{-2}$	$2.83\cdot10^{-1}$	± $4.80\cdot10^{-1}$	$5.73\cdot10^{-1}$	± 1.07	$1.24\cdot10^{-1}$	± $2.71\cdot10^{-1}$	$6.15\cdot10^{-2}$	± $3.16\cdot10^{-2}$
unknown	$5.59\cdot10^{-1}$	± $3.46\cdot10^{-1}$	$1.03\cdot10^{-1}$	± $9.74\cdot10^{-2}$	$1.47\cdot10^{-1}$	± $5.49\cdot10^{-2}$	$1.33\cdot10^{-1}$	± $1.23\cdot10^{-1}$	$3.40\cdot10^{-1}$	± $7.88\cdot10^{-2}$
Ruminococcaceae	$1.18\cdot10^{-3}$	± $2.07\cdot10^{-3}$	$5.58\cdot10^{-1}$	± $3.84\cdot10^{-1}$	$2.43\cdot10^{-1}$	± $2.13\cdot10^{-1}$	$1.63\cdot10^{-1}$	± $1.18\cdot10^{-1}$	$2.40\cdot10^{-1}$	± $5.83\cdot10^{-2}$
Armatimonadetes_gp5	$5.55\cdot10^{-1}$	± $5.26\cdot10^{-1}$	$4.04\cdot10^{-2}$	± $4.68\cdot10^{-2}$	$5.86\cdot10^{-2}$	± $4.92\cdot10^{-2}$	$2.04\cdot10^{-1}$	± $3.80\cdot10^{-1}$	$5.37\cdot10^{-2}$	± $1.46\cdot10^{-2}$
Gallionellaceae	$5.19\cdot10^{-2}$	± $7.34\cdot10^{-2}$	$3.27\cdot10^{-2}$	± $5.82\cdot10^{-2}$	$1.23\cdot10^{-2}$	± $3.11\cdot10^{-2}$	$5.01\cdot10^{-1}$	± $5.40\cdot10^{-1}$	$1.02\cdot10^{-3}$	± $1.43\cdot10^{-3}$
Cystobacteraceae	$2.63\cdot10^{-1}$	± $1.50\cdot10^{-1}$	$1.37\cdot10^{-1}$	± $1.36\cdot10^{-1}$	$1.30\cdot10^{-1}$	± $1.24\cdot10^{-1}$	$4.46\cdot10^{-1}$	± $4.04\cdot10^{-1}$	$1.05\cdot10^{-1}$	± $1.05\cdot10^{-1}$
Peptostreptococcaceae	$9.87\cdot10^{-2}$	± $2.61\cdot10^{-1}$	$1.58\cdot10^{-1}$	± $8.17\cdot10^{-2}$	$2.82\cdot10^{-1}$	± $4.87\cdot10^{-1}$	$1.71\cdot10^{-1}$	± $9.80\cdot10^{-2}$	$4.39\cdot10^{-1}$	± $1.83\cdot10^{-1}$

Table S43. Summary of family-level EUB results continued.

Family[a,b]	S-EBPR (S38) Average %	± SD[c]	V-EBPR (S39) Average %	± SD[c]	G-EBPR (S40) Average %	± SD[c]	R-EBPR (S41) Average %	± SD[c]	Moscow WRRF (S42) Average %	± SD[c]
Cyclobacteriaceae	$2.59\cdot10^{-2}$	± $1.76\cdot10^{-2}$	$5.10\cdot10^{-2}$	± $1.09\cdot10^{-1}$	$4.20\cdot10^{-1}$	± 1.06	$8.55\cdot10^{-2}$	± $1.36\cdot10^{-1}$	$3.69\cdot10^{-1}$	± $3.34\cdot10^{-1}$
Lachnospiraceae	$3.58\cdot10^{-3}$	± $7.43\cdot10^{-3}$	$4.01\cdot10^{-1}$	± $3.49\cdot10^{-1}$	$2.35\cdot10^{-1}$	± $2.81\cdot10^{-1}$	$1.26\cdot10^{-1}$	± $1.33\cdot10^{-1}$	$3.54\cdot10^{-1}$	± $1.48\cdot10^{-1}$
Erythrobacteraceae	$3.93\cdot10^{-1}$	± $7.51\cdot10^{-1}$	$1.83\cdot10^{-1}$	± $3.63\cdot10^{-1}$	$2.50\cdot10^{-1}$	± $5.48\cdot10^{-1}$	$1.21\cdot10^{-1}$	± $2.32\cdot10^{-1}$	$3.06\cdot10^{-2}$	± $1.84\cdot10^{-2}$
unknown p: *Chloroflexi*	$3.91\cdot10^{-1}$	± $3.58\cdot10^{-1}$	$1.49\cdot10^{-1}$	± $9.47\cdot10^{-2}$	$1.15\cdot10^{-1}$	± $1.23\cdot10^{-1}$	$7.17\cdot10^{-2}$	± $3.52\cdot10^{-2}$	$2.44\cdot10^{-1}$	± $9.32\cdot10^{-2}$
Dermatophilaceae	$1.05\cdot10^{-2}$	± $1.50\cdot10^{-2}$	$3.70\cdot10^{-1}$	± $5.48\cdot10^{-1}$	$1.31\cdot10^{-1}$	± $9.70\cdot10^{-2}$	$1.37\cdot10^{-2}$	± $1.72\cdot10^{-2}$	$4.30\cdot10^{-2}$	± $2.83\cdot10^{-2}$
Blastocatella	$2.38\cdot10^{-1}$	± $2.31\cdot10^{-1}$	$3.60\cdot10^{-1}$	± $6.88\cdot10^{-1}$	$1.95\cdot10^{-1}$	± $1.82\cdot10^{-1}$	$2.25\cdot10^{-1}$	± $2.49\cdot10^{-1}$	$7.22\cdot10^{-2}$	± $7.07\cdot10^{-2}$
Aeromonadaceae	$3.72\cdot10^{-2}$	± $9.79\cdot10^{-2}$	$6.35\cdot10^{-2}$	± $3.16\cdot10^{-2}$	$4.99\cdot10^{-2}$	± $3.40\cdot10^{-2}$	$3.14\cdot10^{-1}$	± $6.35\cdot10^{-1}$	$1.27\cdot10^{-1}$	± $5.56\cdot10^{-2}$
Fimbriimonadaceae	$2.93\cdot10^{-1}$	± $3.92\cdot10^{-1}$	$1.36\cdot10^{-2}$	± $1.54\cdot10^{-2}$	$2.34\cdot10^{-2}$	± $3.84\cdot10^{-2}$	$2.13\cdot10^{-2}$	± $2.90\cdot10^{-2}$	$1.19\cdot10^{-2}$	± $7.92\cdot10^{-3}$
Spartobacteria_genera_inc._sed.[e]	$1.61\cdot10^{-4}$	± $4.26\cdot10^{-4}$	$1.01\cdot10^{-1}$	± $1.60\cdot10^{-1}$	$7.76\cdot10^{-2}$	± $1.20\cdot10^{-1}$	$1.74\cdot10^{-1}$	± $3.76\cdot10^{-1}$	$2.66\cdot10^{-2}$	± $2.40\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S44. S-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Minor phylotypes (1441)[d]	19.4	13.4	13.8	14.9	14.3	19.5	12.0	15.3	± 2.95
Thauera	7.97	6.64	18.6	24.4	7.29	1.42	4.04	10.1	± 8.31
unknown f: *Rhodobacteraceae*	8.59	7.54	10.8	10.4	11.4	14.3	4.75	9.68	± 3.06
Flavobacterium	4.71	13.5	$2.75\cdot10^{-1}$	$4.11\cdot10^{-1}$	14.7	6.91	6.28	6.69	± 5.71
Ohtaekwangia	8.52	13.9	3.98	5.07	5.21	4.54	4.42	6.52	± 3.58
unknown d: *Bacteria*	6.93	4.46	7.37	10.9	4.62	2.63	4.15	5.86	± 2.76
Propionivibrio	$6.08\cdot10^{-1}$	$3.25\cdot10^{-1}$	5.35	1.82	$8.79\cdot10^{-1}$	$2.29\cdot10^{-1}$	21.4	4.37	± 7.72
unknown c: *Alphaproteobacteria*	2.08	3.52	4.07	1.40	2.11	4.59	2.93	2.96	± 1.17
Phycisphaera	1.37	$8.11\cdot10^{-1}$	1.10	$9.30\cdot10^{-1}$	4.63	7.05	3.48	2.77	± 2.39
Defluviicoccus	8.19	2.50	1.27	4.22	$7.12\cdot10^{-1}$	1.30	$1.82\cdot10^{-1}$	2.63	± 2.79
Jhaorihella	$3.36\cdot10^{-1}$	$7.21\cdot10^{-1}$	5.29	$8.19\cdot10^{-1}$	$6.20\cdot10^{-1}$	$2.03\cdot10^{-2}$	8.85	2.38	± 3.37
Aquimonas	$4.98\cdot10^{-1}$	1.71	1.75	2.78	1.88	3.71	2.65	2.14	± 1.02
unknown o: *Rhizobiales*	3.55	3.19	1.23	1.47	1.42	2.41	$6.33\cdot10^{-1}$	1.99	± 1.09

Table S44. S-EBPR genus-level EUB results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown f: *Flavobacteriaceae*	1.54	2.12	1.71	2.16	1.95	1.53	$7.93\cdot10^{-1}$	1.69	±$4.70\cdot10^{-1}$
unknown p: *Proteobacteria*	1.53	$9.47\cdot10^{-1}$	3.62	1.46	1.35	$8.87\cdot10^{-1}$	2.00	1.68	±$9.32\cdot10^{-1}$
unknown p: *Bacteroidetes*	$8.97\cdot10^{-1}$	2.07	2.61	1.81	1.47	1.46	1.35	1.67	±$5.54\cdot10^{-1}$
unknown f: *Bradyrhizobiaceae*	2.04	4.71	$6.08\cdot10^{-1}$	$8.84\cdot10^{-1}$	$8.99\cdot10^{-1}$	1.11	$4.28\cdot10^{-2}$	1.47	±1.55
Planctomyces	2.75	1.55	$8.74\cdot10^{-1}$	1.07	2.81	$6.73\cdot10^{-1}$	$1.41\cdot10^{-1}$	1.41	±1.03
Brevundimonas	1.07	$4.75\cdot10^{-1}$	1.13	1.12	$9.77\cdot10^{-1}$	4.01	$5.10\cdot10^{-1}$	1.33	±1.22
Haliscomenobacter	$4.02\cdot10^{-1}$	$7.80\cdot10^{-2}$	4.15	$9.46\cdot10^{-1}$	$3.21\cdot10^{-1}$	$7.33\cdot10^{-2}$	2.70	1.24	±1.58
Rhodobacter	$7.62\cdot10^{-1}$	$9.09\cdot10^{-1}$	$5.76\cdot10^{-1}$	$3.86\cdot10^{-1}$	1.10	3.51	$7.22\cdot10^{-1}$	1.14	±1.07
unknown f: *Rhodocyclaceae*	$3.82\cdot10^{-1}$	$1.87\cdot10^{-1}$	1.56	$5.18\cdot10^{-1}$	$6.97\cdot10^{-1}$	$2.16\cdot10^{-1}$	3.80	1.05	±1.30
unknown f: *Burkholderiales_inc._sed.*[e]	$1.69\cdot10^{-1}$	$2.73\cdot10^{-1}$	$1.90\cdot10^{-1}$	$2.16\cdot10^{-1}$	$5.99\cdot10^{-1}$	1.56	4.35	1.05	±1.54
unknown c: *Gammaproteobacteria*	1.56	1.18	1.55	$5.84\cdot10^{-1}$	$3.09\cdot10^{-1}$	$9.46\cdot10^{-1}$	$3.95\cdot10^{-1}$	$9.31\cdot10^{-1}$	±$5.21\cdot10^{-1}$
Prosthecobacter	$8.33\cdot10^{-1}$	$1.47\cdot10^{-1}$	$1.38\cdot10^{-1}$	$1.83\cdot10^{-1}$	1.80	$2.93\cdot10^{-2}$	2.86	$8.56\cdot10^{-1}$	±1.08
unknown f: *Planctomycetaceae*	$7.06\cdot10^{-1}$	$3.63\cdot10^{-1}$	$2.11\cdot10^{-1}$	$4.35\cdot10^{-1}$	$9.30\cdot10^{-1}$	1.84	1.10	$7.99\cdot10^{-1}$	±$5.60\cdot10^{-1}$
SR1_genera_inc._sed.[e]	N.D.[f]	N.D.[f]	N.D.[f]	N.D.[f]	4.91	$7.10\cdot10^{-2}$	$2.68\cdot10^{-1}$	$7.50\cdot10^{-1}$	±1.84
Nitrospira	1.07	$4.03\cdot10^{-2}$	$7.22\cdot10^{-1}$	1.37	$9.96\cdot10^{-1}$	$1.13\cdot10^{-3}$	$6.88\cdot10^{-1}$	$6.98\cdot10^{-1}$	±$5.17\cdot10^{-1}$
Hydrogenophaga	1.49	1.48	$9.17\cdot10^{-2}$	$1.36\cdot10^{-1}$	$5.43\cdot10^{-1}$	1.02	$3.18\cdot10^{-2}$	$6.85\cdot10^{-1}$	±$6.46\cdot10^{-1}$
Nitrosomonas	1.30	$3.08\cdot10^{-1}$	$6.09\cdot10^{-1}$	1.40	$4.97\cdot10^{-1}$	$7.89\cdot10^{-3}$	$2.36\cdot10^{-1}$	$6.22\cdot10^{-1}$	±$5.32\cdot10^{-1}$
Clostridium sensu stricto	N.D.[f]	N.D.[f]	N.D.[f]	N.D.[f]	N.D.[f]	4.08	$1.22\cdot10^{-3}$	$5.83\cdot10^{-1}$	±1.54
unknown	$6.08\cdot10^{-1}$	1.26	$6.91\cdot10^{-1}$	$4.13\cdot10^{-1}$	$2.62\cdot10^{-1}$	$3.78\cdot10^{-1}$	$2.99\cdot10^{-1}$	$5.59\cdot10^{-1}$	±$3.46\cdot10^{-1}$
Armatimonadetes_gp5	$3.53\cdot10^{-1}$	$3.63\cdot10^{-1}$	$4.55\cdot10^{-1}$	$5.47\cdot10^{-1}$	$3.41\cdot10^{-1}$	1.71	$1.17\cdot10^{-1}$	$5.55\cdot10^{-1}$	±$5.26\cdot10^{-1}$
unknown o: *Flavobacteriales*	$5.74\cdot10^{-1}$	1.23	$6.92\cdot10^{-1}$	$2.05\cdot10^{-1}$	$2.95\cdot10^{-1}$	$4.19\cdot10^{-1}$	$4.22\cdot10^{-1}$	$5.47\cdot10^{-1}$	±$3.40\cdot10^{-1}$
Azospira	$9.14\cdot10^{-1}$	$6.29\cdot10^{-1}$	$6.58\cdot10^{-2}$	$1.29\cdot10^{-1}$	1.15	$2.91\cdot10^{-1}$	$2.83\cdot10^{-1}$	$4.95\cdot10^{-1}$	±$4.14\cdot10^{-1}$
unknown f: *Chitinophagaceae*	$2.11\cdot10^{-1}$	$2.42\cdot10^{-1}$	$2.87\cdot10^{-1}$	$3.48\cdot10^{-1}$	1.50	$7.21\cdot10^{-1}$	$1.28\cdot10^{-1}$	$4.91\cdot10^{-1}$	±$4.83\cdot10^{-1}$
Pirellula	1.50	$7.25\cdot10^{-1}$	$2.32\cdot10^{-1}$	$3.62\cdot10^{-1}$	$2.30\cdot10^{-1}$	$2.16\cdot10^{-1}$	$9.29\cdot10^{-2}$	$4.80\cdot10^{-1}$	±$4.93\cdot10^{-1}$
Ferruginibacter	$4.53\cdot10^{-1}$	1.16	$1.59\cdot10^{-1}$	1.48	$1.91\cdot10^{-2}$	$6.77\cdot10^{-3}$	$2.44\cdot10^{-3}$	$4.69\cdot10^{-1}$	±$6.10\cdot10^{-1}$
Caulobacter	N.D.[f]	$8.07\cdot10^{-3}$	$1.04\cdot10^{-2}$	$7.25\cdot10^{-3}$	$4.50\cdot10^{-1}$	1.95	$6.00\cdot10^{-1}$	$4.32\cdot10^{-1}$	±$7.13\cdot10^{-1}$
Terrimonas	1.43	$8.63\cdot10^{-1}$	$5.54\cdot10^{-2}$	$2.90\cdot10^{-2}$	$5.29\cdot10^{-1}$	$2.59\cdot10^{-2}$	$9.78\cdot10^{-3}$	$4.21\cdot10^{-1}$	±$5.55\cdot10^{-1}$
unknown p: *Chloroflexi*	$4.56\cdot10^{-1}$	$6.99\cdot10^{-2}$	$2.28\cdot10^{-1}$	$6.00\cdot10^{-1}$	1.08	$1.09\cdot10^{-1}$	$1.92\cdot10^{-1}$	$3.91\cdot10^{-1}$	±$3.58\cdot10^{-1}$
Litorilinea	1.32	$7.87\cdot10^{-1}$	$2.16\cdot10^{-1}$	$3.35\cdot10^{-1}$	$4.29\cdot10^{-2}$	$1.80\cdot10^{-2}$	$1.10\cdot10^{-2}$	$3.91\cdot10^{-1}$	±$4.94\cdot10^{-1}$
Altererythrobacter	$1.79\cdot10^{-1}$	$2.19\cdot10^{-1}$	$3.46\cdot10^{-3}$	$5.44\cdot10^{-3}$	1.56	$1.47\cdot10^{-1}$	$9.78\cdot10^{-3}$	$3.04\cdot10^{-1}$	±$5.62\cdot10^{-1}$

Table S44. S-EBPR genus-level EUB results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Fimbriimonas	$3.43\cdot10^{-2}$	$4.71\cdot10^{-2}$	$5.66\cdot10^{-1}$	$5.26\cdot10^{-2}$	$2.54\cdot10^{-1}$	1.06	$3.30\cdot10^{-2}$	$2.93\cdot10^{-1}$	$\pm3.92\cdot10^{-1}$
Roseimicrobium	$4.04\cdot10^{-1}$	1.15	$2.63\cdot10^{-1}$	$5.26\cdot10^{-2}$	$8.87\cdot10^{-2}$	$2.14\cdot10^{-2}$	$3.67\cdot10^{-2}$	$2.88\cdot10^{-1}$	$\pm4.05\cdot10^{-1}$
unknown f: *Polyangiaceae*	$7.11\cdot10^{-2}$	$1.21\cdot10^{-2}$	$7.43\cdot10^{-1}$	1.07	$6.49\cdot10^{-2}$	$2.26\cdot10^{-3}$	$4.52\cdot10^{-2}$	$2.87\cdot10^{-1}$	$\pm4.35\cdot10^{-1}$
Persicitalea	$2.16\cdot10^{-1}$	1.07	$1.07\cdot10^{-1}$	$5.80\cdot10^{-2}$	$1.91\cdot10^{-3}$	$2.26\cdot10^{-3}$	$8.55\cdot10^{-3}$	$2.09\cdot10^{-1}$	$\pm3.86\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	$1.47\cdot10^{-2}$	1.08	$1.90\cdot10^{-2}$	$7.07\cdot10^{-2}$	$1.41\cdot10^{-1}$	$2.26\cdot10^{-3}$	N.D.[f]	$1.90\cdot10^{-1}$	$\pm3.97\cdot10^{-1}$
Carnobacterium	N.D.[f]	N.D.[f]	N.D.[f]	N.D.[f]	$1.43\cdot10^{-2}$	1.29	N.D.[f]	$1.86\cdot10^{-1}$	$\pm4.85\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S45. V-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Minor phylotypes (1430)[d]	24.3	14.9	14.2	14.2	23.5	25.0	28.8	20.7	± 6.08
unknown p: *Bacteroidetes*	14.5	14.6	14.8	13.1	20.2	9.93	1.37	12.6	± 5.82
Thiobacillus	8.94	21.8	12.6	13.1	8.06	11.2	$2.38\cdot10^{-2}$	10.8	± 6.55
Haliscomenobacter	3.28	2.81	4.98	4.30	9.04	5.15	1.04	4.37	± 2.50
Thauera	$1.99\cdot10^{-1}$	1.42	9.38	13.9	$3.26\cdot10^{-2}$	$3.11\cdot10^{-2}$	1.79	3.82	± 5.55
unknown d: *Bacteria*	4.37	3.37	3.12	1.86	3.23	2.89	7.43	3.75	± 1.78
Zoogloea	$9.63\cdot10^{-2}$	3.55	4.63	5.23	3.33	7.06	$2.64\cdot10^{-2}$	3.42	± 2.60
Meganema	$4.98\cdot10^{-3}$	$1.51\cdot10^{-3}$	N.D.[e]	$3.93\cdot10^{-3}$	$1.18\cdot10^{-2}$	$4.67\cdot10^{-2}$	17.1	2.46	± 6.47
unknown o: *Cytophagales*	4.46	5.14	1.34	1.84	1.47	$7.00\cdot10^{-1}$	$3.54\cdot10^{-1}$	2.19	± 1.86
unknown p: *Proteobacteria*	1.90	4.89	1.01	1.56	1.15	1.10	1.58	1.88	± 1.36
Simplicispira	3.11	2.46	$7.93\cdot10^{-1}$	2.52	1.44	1.90	$1.24\cdot10^{-1}$	1.76	± 1.05
unknown o: *Sphingobacteriales*	1.39	1.35	1.25	1.30	3.36	1.99	1.22	1.69	$\pm7.80\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	2.02	2.42	$6.16\cdot10^{-1}$	1.40	$9.40\cdot10^{-1}$	1.68	2.34	1.63	$\pm6.88\cdot10^{-1}$

Table S45. V-EBPR genus-level EUB results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown f: *Flavobacteriaceae*	$5.71\cdot10^{-1}$	$5.64\cdot10^{-1}$	3.51	4.52	$5.73\cdot10^{-1}$	$5.44\cdot10^{-1}$	$5.28\cdot10^{-2}$	1.48	± 1.77
unknown o: *Rhizobiales*	2.33	$7.84\cdot10^{-1}$	$3.99\cdot10^{-1}$	$6.01\cdot10^{-1}$	$7.51\cdot10^{-1}$	1.23	2.61	1.24	± $8.79\cdot10^{-1}$
Prosthecobacter	2.95	$3.94\cdot10^{-1}$	3.60	$4.92\cdot10^{-1}$	$2.03\cdot10^{-1}$	$6.22\cdot10^{-2}$	$2.35\cdot10^{-1}$	1.13	± 1.48
Caenimonas	4.54	1.23	$4.27\cdot10^{-2}$	$1.24\cdot10^{-1}$	1.40	$4.67\cdot10^{-1}$	$4.75\cdot10^{-2}$	1.12	± 1.61
Defluviicoccus	2.21	1.97	$9.84\cdot10^{-1}$	$6.17\cdot10^{-1}$	$7.80\cdot10^{-1}$	1.15	N.D.[e]	1.10	± $7.69\cdot10^{-1}$
unknown f: *Chitinophagaceae*	$4.57\cdot10^{-1}$	1.03	2.86	1.11	$6.30\cdot10^{-1}$	$6.22\cdot10^{-1}$	$7.44\cdot10^{-1}$	1.07	± $8.26\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$4.38\cdot10^{-1}$	1.86	1.25	$8.15\cdot10^{-1}$	1.09	1.82	$1.82\cdot10^{-1}$	1.06	± $6.41\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[f]	1.36	$1.98\cdot10^{-1}$	3.91	$9.15\cdot10^{-1}$	$3.86\cdot10^{-1}$	$1.40\cdot10^{-1}$	$1.53\cdot10^{-1}$	1.01	± 1.36
unknown f: *Comamonadaceae*	1.16	$7.46\cdot10^{-1}$	$5.59\cdot10^{-1}$	$5.54\cdot10^{-1}$	$6.44\cdot10^{-1}$	1.26	1.68	$9.43\cdot10^{-1}$	± $4.32\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$4.67\cdot10^{-1}$	$4.03\cdot10^{-1}$	$5.54\cdot10^{-1}$	$1.86\cdot10^{-1}$	1.00	1.20	2.68	$9.27\cdot10^{-1}$	± $8.50\cdot10^{-1}$
Brevundimonas	1.60	$2.16\cdot10^{-1}$	$2.28\cdot10^{-1}$	2.85	$1.60\cdot10^{-1}$	$9.65\cdot10^{-1}$	$2.11\cdot10^{-1}$	$8.90\cdot10^{-1}$	± 1.02
unknown f: *Rhodobacteraceae*	$5.86\cdot10^{-1}$	$4.38\cdot10^{-1}$	$9.43\cdot10^{-1}$	$7.42\cdot10^{-1}$	$4.13\cdot10^{-1}$	$6.69\cdot10^{-1}$	1.72	$7.88\cdot10^{-1}$	± $4.51\cdot10^{-1}$
Roseimicrobium	$4.91\cdot10^{-1}$	$1.30\cdot10^{-1}$	$3.46\cdot10^{-1}$	$7.84\cdot10^{-1}$	$2.85\cdot10^{-1}$	1.82	1.52	$7.68\cdot10^{-1}$	± $6.55\cdot10^{-1}$
unknown f: *Prevotellaceae*	$2.04\cdot10^{-1}$	$2.33\cdot10^{-1}$	$6.62\cdot10^{-2}$	$3.46\cdot10^{-1}$	1.90	2.30	N.D.[e]	$7.22\cdot10^{-1}$	± $9.57\cdot10^{-1}$
Xylanibacter	$2.74\cdot10^{-1}$	$2.49\cdot10^{-1}$	$1.53\cdot10^{-1}$	$9.03\cdot10^{-1}$	1.51	1.90	N.D.[e]	$7.12\cdot10^{-1}$	± $7.42\cdot10^{-1}$
Caldilinea	$5.00\cdot10^{-1}$	$2.89\cdot10^{-1}$	$8.38\cdot10^{-2}$	$1.52\cdot10^{-1}$	1.52	2.35	$5.54\cdot10^{-2}$	$7.07\cdot10^{-1}$	± $8.84\cdot10^{-1}$
Ohtaekwangia	$2.92\cdot10^{-1}$	$2.22\cdot10^{-1}$	$3.19\cdot10^{-1}$	1.56	$7.48\cdot10^{-1}$	$4.36\cdot10^{-1}$	$5.91\cdot10^{-1}$	$5.95\cdot10^{-1}$	± $4.61\cdot10^{-1}$
unknown f: *Rhodocyclaceae*	$7.80\cdot10^{-2}$	$6.47\cdot10^{-1}$	1.11	$3.98\cdot10^{-1}$	$5.56\cdot10^{-1}$	1.17	$1.06\cdot10^{-1}$	$5.80\cdot10^{-1}$	± $4.35\cdot10^{-1}$
Aquimonas	1.54	$3.23\cdot10^{-1}$	$9.56\cdot10^{-2}$	$3.77\cdot10^{-1}$	$6.39\cdot10^{-1}$	$6.38\cdot10^{-1}$	$4.28\cdot10^{-1}$	$5.78\cdot10^{-1}$	± $4.65\cdot10^{-1}$
Paracoccus	$8.63\cdot10^{-2}$	$3.48\cdot10^{-2}$	1.21	$8.84\cdot10^{-1}$	$7.89\cdot10^{-2}$	$1.24\cdot10^{-1}$	1.61	$5.74\cdot10^{-1}$	± $6.51\cdot10^{-1}$
Prevotella	$5.61\cdot10^{-1}$	$3.43\cdot10^{-1}$	$9.27\cdot10^{-2}$	$8.43\cdot10^{-1}$	1.09	$9.33\cdot10^{-1}$	N.D.[e]	$5.53\cdot10^{-1}$	± $4.25\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	$3.29\cdot10^{-1}$	$3.85\cdot10^{-1}$	$6.32\cdot10^{-2}$	$4.28\cdot10^{-1}$	$3.86\cdot10^{-1}$	$6.53\cdot10^{-1}$	1.53	$5.40\cdot10^{-1}$	± $4.71\cdot10^{-1}$
unknown f: *Cytophagaceae*	$9.73\cdot10^{-1}$	1.18	$2.94\cdot10^{-1}$	$4.12\cdot10^{-1}$	$3.55\cdot10^{-1}$	$2.49\cdot10^{-1}$	$1.21\cdot10^{-1}$	$5.11\cdot10^{-1}$	± $3.99\cdot10^{-1}$
Byssovorax	2.41	$1.28\cdot10^{-1}$	$5.29\cdot10^{-2}$	$3.06\cdot10^{-1}$	$5.45\cdot10^{-1}$	$6.22\cdot10^{-2}$	$1.32\cdot10^{-2}$	$5.02\cdot10^{-1}$	± $8.61\cdot10^{-1}$
unknown o: *Flavobacteriales*	$1.31\cdot10^{-1}$	$1.74\cdot10^{-1}$	1.55	1.28	$1.31\cdot10^{-1}$	$1.40\cdot10^{-1}$	$7.92\cdot10^{-2}$	$4.99\cdot10^{-1}$	± $6.33\cdot10^{-1}$
Sphingomonas	$1.56\cdot10^{-1}$	$3.17\cdot10^{-2}$	$1.18\cdot10^{-2}$	$2.17\cdot10^{-1}$	$5.55\cdot10^{-1}$	2.30	$1.87\cdot10^{-1}$	$4.95\cdot10^{-1}$	± $8.17\cdot10^{-1}$
unknown o: *Actinomycetales*	1.26	$4.61\cdot10^{-1}$	$2.49\cdot10^{-1}$	$2.51\cdot10^{-1}$	$3.83\cdot10^{-1}$	$4.36\cdot10^{-1}$	$4.06\cdot10^{-1}$	$4.93\cdot10^{-1}$	± $3.50\cdot10^{-1}$

Table S45. V-EBPR genus-level EUB results summary continued.

Genus[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
unknown o: *Pseudomonadales*	$1.94\cdot10^{-1}$	$3.91\cdot10^{-1}$	1.09	$4.95\cdot10^{-1}$	$4.82\cdot10^{-1}$	$4.51\cdot10^{-1}$	$1.69\cdot10^{-1}$	$4.68\cdot10^{-1}$	$\pm3.06\cdot10^{-1}$
Dokdonella	1.67	$6.12\cdot10^{-1}$	$2.12\cdot10^{-1}$	$1.85\cdot10^{-1}$	$3.55\cdot10^{-1}$	$2.33\cdot10^{-1}$	N.D.[e]	$4.66\cdot10^{-1}$	$\pm5.62\cdot10^{-1}$
Parabacteroides	$2.77\cdot10^{-1}$	$3.49\cdot10^{-1}$	$1.84\cdot10^{-1}$	$2.53\cdot10^{-1}$	1.37	$8.09\cdot10^{-1}$	N.D.[e]	$4.63\cdot10^{-1}$	$\pm4.71\cdot10^{-1}$
Aquabacterium	$2.49\cdot10^{-2}$	$3.02\cdot10^{-3}$	$4.71\cdot10^{-2}$	$4.71\cdot10^{-2}$	$1.63\cdot10^{-1}$	$3.11\cdot10^{-2}$	2.76	$4.40\cdot10^{-1}$	± 1.03
Perlucidibaca	$8.30\cdot10^{-3}$	$6.04\cdot10^{-2}$	2.73	$9.69\cdot10^{-2}$	$8.68\cdot10^{-2}$	N.D.[e]	$2.64\cdot10^{-3}$	$4.27\cdot10^{-1}$	± 1.02
Schlesneria	$2.37\cdot10^{-1}$	$1.84\cdot10^{-1}$	$1.37\cdot10^{-1}$	$7.85\cdot10^{-2}$	$1.13\cdot10^{-1}$	$6.22\cdot10^{-2}$	2.11	$4.18\cdot10^{-1}$	$\pm7.49\cdot10^{-1}$
Gp4	$1.43\cdot10^{-1}$	$2.13\cdot10^{-1}$	$2.06\cdot10^{-2}$	$6.94\cdot10^{-2}$	$3.29\cdot10^{-1}$	$4.36\cdot10^{-1}$	1.65	$4.09\cdot10^{-1}$	$\pm5.66\cdot10^{-1}$
Luteimonas	$4.98\cdot10^{-3}$	$1.51\cdot10^{-3}$	$1.47\cdot10^{-3}$	$1.18\cdot10^{-2}$	$1.97\cdot10^{-3}$	N.D.[e]	2.83	$4.08\cdot10^{-1}$	± 1.07
unknown f: *Saprospiraceae*	$7.64\cdot10^{-2}$	$1.21\cdot10^{-2}$	$1.25\cdot10^{-1}$	$1.69\cdot10^{-1}$	$3.48\cdot10^{-1}$	$7.00\cdot10^{-1}$	1.39	$4.03\cdot10^{-1}$	$\pm4.93\cdot10^{-1}$
unknown f: *Verrucomicrobiaceae*	$2.03\cdot10^{-1}$	$4.99\cdot10^{-2}$	$1.49\cdot10^{-1}$	$3.39\cdot10^{-1}$	$2.59\cdot10^{-1}$	$1.40\cdot10^{-1}$	1.68	$4.03\cdot10^{-1}$	$\pm5.71\cdot10^{-1}$
Sediminibacterium	$1.81\cdot10^{-1}$	1.61	$4.12\cdot10^{-2}$	$6.94\cdot10^{-2}$	$5.08\cdot10^{-1}$	$3.73\cdot10^{-1}$	N.D.[e]	$3.97\cdot10^{-1}$	$\pm5.66\cdot10^{-1}$
Blastocatella	$3.65\cdot10^{-2}$	$2.09\cdot10^{-1}$	$5.15\cdot10^{-2}$	$2.88\cdot10^{-2}$	$1.42\cdot10^{-1}$	$1.40\cdot10^{-1}$	1.91	$3.60\cdot10^{-1}$	$\pm6.88\cdot10^{-1}$
Acidovorax	$1.59\cdot10^{-1}$	$4.83\cdot10^{-2}$	$3.97\cdot10^{-2}$	$3.40\cdot10^{-2}$	$3.29\cdot10^{-1}$	$5.29\cdot10^{-1}$	1.10	$3.20\cdot10^{-1}$	$\pm3.91\cdot10^{-1}$
Alkanindiges	$3.15\cdot10^{-2}$	$4.08\cdot10^{-2}$	$4.41\cdot10^{-3}$	$9.29\cdot10^{-1}$	$1.22\cdot10^{-1}$	1.10	N.D.[e]	$3.19\cdot10^{-1}$	$\pm4.81\cdot10^{-1}$
Leadbetterella	$4.98\cdot10^{-3}$	$1.51\cdot10^{-3}$	$1.32\cdot10^{-2}$	$3.93\cdot10^{-3}$	$3.27\cdot10^{-1}$	$2.96\cdot10^{-1}$	1.44	$2.98\cdot10^{-1}$	$\pm5.23\cdot10^{-1}$
Bacteriovorax	$9.30\cdot10^{-2}$	1.31	$1.47\cdot10^{-3}$	$1.31\cdot10^{-3}$	$3.91\cdot10^{-1}$	$1.09\cdot10^{-1}$	N.D.[e]	$2.72\cdot10^{-1}$	$\pm4.76\cdot10^{-1}$
Propionivibrio	$6.64\cdot10^{-2}$	$5.74\cdot10^{-2}$	1.68	$1.44\cdot10^{-2}$	$3.85\cdot10^{-2}$	$1.56\cdot10^{-2}$	N.D.[e]	$2.67\cdot10^{-1}$	$\pm6.22\cdot10^{-1}$
Dechloromonas	$3.15\cdot10^{-2}$	1.33	$2.00\cdot10^{-1}$	$1.40\cdot10^{-1}$	$6.91\cdot10^{-3}$	$7.78\cdot10^{-2}$	N.D.[e]	$2.54\cdot10^{-1}$	$\pm4.78\cdot10^{-1}$
Hydrogenophaga	$3.98\cdot10^{-2}$	$1.66\cdot10^{-2}$	$1.32\cdot10^{-2}$	$2.62\cdot10^{-2}$	$6.91\cdot10^{-2}$	$6.22\cdot10^{-2}$	1.51	$2.48\cdot10^{-1}$	$\pm5.57\cdot10^{-1}$
Verrucomicrobium	$6.81\cdot10^{-2}$	$3.32\cdot10^{-2}$	$1.18\cdot10^{-2}$	$7.85\cdot10^{-3}$	$7.40\cdot10^{-2}$	$1.56\cdot10^{-1}$	1.23	$2.26\cdot10^{-1}$	$\pm4.47\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

[f] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S46. G-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Minor phylotypes (1436)[d]	21.0	18.4	13.3	17.3	19.6	26.9	31.1	21.1	± 6.04
Saccharibacteria_genera_inc._sed.[e]	25.4	9.85	3.00	2.77	8.82	$8.66\cdot10^{-1}$	4.39	7.87	± 8.38
Thiobacillus	3.10	10.4	4.65	4.61	8.98	11.4	N.D.[f]	6.16	± 4.19

Table S46. G-EBPR genus-level EUB results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown p: *Bacteroidetes*	1.02	6.13	6.82	9.45	6.00	5.20	$4.14\cdot10^{-1}$	5.00	± 3.22
Haliscomenobacter	$3.16\cdot10^{-1}$	3.75	10.8	7.38	4.44	2.46	1.99	4.45	± 3.58
unknown c: *Alphaproteobacteria*	3.40	7.94	5.51	3.75	2.81	3.26	3.39	4.30	± 1.82
unknown d: *Bacteria*	3.20	4.63	4.76	3.53	3.86	3.72	5.88	4.23	± $9.24\cdot10^{-1}$
Methylobacillus	2.20	2.95	5.05	1.38	9.41	4.57	N.D.[f]	3.65	± 3.08
Zoogloea	$2.72\cdot10^{-1}$	4.10	3.90	8.11	5.24	1.95	$1.66\cdot10^{-1}$	3.39	± 2.85
Meganema	$7.46\cdot10^{-3}$	$1.56\cdot10^{-2}$	$3.42\cdot10^{-2}$	$9.72\cdot10^{-3}$	$6.05\cdot10^{-3}$	$1.86\cdot10^{-2}$	21.0	3.02	± 7.94
Propionivibrio	$1.19\cdot10^{-2}$	$3.44\cdot10^{-1}$	15.9	1.78	$9.18\cdot10^{-2}$	$2.39\cdot10^{-2}$	N.D.[f]	2.59	± 5.89
unknown p: *Proteobacteria*	$8.35\cdot10^{-1}$	2.68	2.50	3.57	1.97	1.10	1.49	2.02	± $9.66\cdot10^{-1}$
Ohtaekwangia	2.79	4.61	1.72	1.65	$5.75\cdot10^{-1}$	$3.22\cdot10^{-1}$	1.90	1.94	± 1.44
Tetrasphaera	5.38	$1.15\cdot10^{-1}$	$3.09\cdot10^{-2}$	$9.44\cdot10^{-2}$	3.17	4.58	N.D.[f]	1.91	± 2.40
unknown o: *Rhizobiales*	1.90	1.01	1.36	1.75	1.46	1.85	2.40	1.68	± $4.46\cdot10^{-1}$
unknown o: *Cytophagales*	$2.39\cdot10^{-2}$	1.18	2.50	3.52	1.94	2.20	N.D.[f]	1.62	± 1.30
unknown f: *Flavobacteriaceae*	4.19	1.55	1.84	1.45	$8.27\cdot10^{-1}$	$2.69\cdot10^{-1}$	N.D.[f]	1.44	± 1.39
Defluviicoccus	1.60	$9.60\cdot10^{-1}$	$3.16\cdot10^{-1}$	$7.03\cdot10^{-1}$	1.19	4.74	N.D.[f]	1.36	± 1.58
unknown f: *Chitinophagaceae*	2.90	1.88	$7.81\cdot10^{-1}$	1.10	$4.68\cdot10^{-1}$	$8.26\cdot10^{-1}$	1.08	1.29	± $8.34\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$2.98\cdot10^{-1}$	2.25	1.44	1.10	1.53	1.52	$8.28\cdot10^{-2}$	1.17	± $7.57\cdot10^{-1}$
unknown f: *Rhodobacteraceae*	$5.03\cdot10^{-1}$	1.44	1.87	$9.75\cdot10^{-1}$	1.21	$9.83\cdot10^{-1}$	$9.11\cdot10^{-1}$	1.13	± $4.34\cdot10^{-1}$
Tessaracoccus	$4.01\cdot10^{-1}$	$1.52\cdot10^{-1}$	$1.64\cdot10^{-1}$	$8.42\cdot10^{-1}$	2.05	3.95	N.D.[f]	1.08	± 1.45
unknown f: *Rhodocyclaceae*	$6.42\cdot10^{-2}$	$6.36\cdot10^{-1}$	3.53	1.48	$5.73\cdot10^{-1}$	$8.49\cdot10^{-1}$	$1.66\cdot10^{-1}$	1.04	± 1.19
Phenylobacterium	3.39	$9.28\cdot10^{-1}$	$2.57\cdot10^{-1}$	$6.54\cdot10^{-1}$	$5.37\cdot10^{-1}$	1.10	$8.28\cdot10^{-2}$	$9.92\cdot10^{-1}$	± 1.11
unknown o: *Actinomycetales*	$7.85\cdot10^{-1}$	$9.40\cdot10^{-1}$	$9.22\cdot10^{-1}$	2.03	$5.48\cdot10^{-1}$	1.21	$4.14\cdot10^{-1}$	$9.79\cdot10^{-1}$	± $5.33\cdot10^{-1}$
Thauera	$2.00\cdot10^{-1}$	1.24	$8.29\cdot10^{-2}$	$7.92\cdot10^{-2}$	$4.14\cdot10^{-1}$	$7.56\cdot10^{-2}$	4.72	$9.73\cdot10^{-1}$	± 1.70
unknown f: *Cytophagaceae*	$1.34\cdot10^{-2}$	$5.82\cdot10^{-1}$	$6.99\cdot10^{-1}$	$8.71\cdot10^{-1}$	1.18	2.80	$2.48\cdot10^{-1}$	$9.12\cdot10^{-1}$	± $9.15\cdot10^{-1}$
Caldilinea	$5.43\cdot10^{-1}$	$6.15\cdot10^{-1}$	1.17	1.87	$6.05\cdot10^{-1}$	1.08	N.D.[f]	$8.40\cdot10^{-1}$	± $5.94\cdot10^{-1}$
Paracoccus	$1.30\cdot10^{-1}$	$4.12\cdot10^{-2}$	$7.97\cdot10^{-2}$	$7.39\cdot10^{-1}$	1.54	1.24	1.66	$7.76\cdot10^{-1}$	± $7.10\cdot10^{-1}$
Terrimonas	1.98	$8.79\cdot10^{-1}$	$6.25\cdot10^{-1}$	1.01	$1.93\cdot10^{-1}$	$2.10\cdot10^{-1}$	$1.66\cdot10^{-1}$	$7.23\cdot10^{-1}$	± $6.51\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$5.97\cdot10^{-3}$	$6.82\cdot10^{-2}$	$7.76\cdot10^{-1}$	2.17	$7.97\cdot10^{-1}$	$2.86\cdot10^{-1}$	$4.14\cdot10^{-1}$	$6.45\cdot10^{-1}$	± $7.39\cdot10^{-1}$

Table S46. G-EBPR genus-level EUB results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
Arcobacter	$1.82\cdot10^{-1}$	1.27	$2.78\cdot10^{-1}$	$6.00\cdot10^{-1}$	1.30	$6.44\cdot10^{-1}$	N.D.[f]	$6.11\cdot10^{-1}$	$\pm5.14\cdot10^{-1}$
unknown f: *Comamonadaceae*	1.20	$3.99\cdot10^{-1}$	$2.26\cdot10^{-1}$	1.06	$5.62\cdot10^{-1}$	$3.26\cdot10^{-1}$	$2.48\cdot10^{-1}$	$5.75\cdot10^{-1}$	$\pm3.97\cdot10^{-1}$
Caenimonas	$1.03\cdot10^{-1}$	$2.12\cdot10^{-1}$	$1.19\cdot10^{-1}$	1.13	1.89	$5.49\cdot10^{-1}$	N.D.[f]	$5.73\cdot10^{-1}$	$\pm7.01\cdot10^{-1}$
Brevundimonas	$8.30\cdot10^{-1}$	$1.97\cdot10^{-1}$	$1.58\cdot10^{-1}$	$4.72\cdot10^{-1}$	$9.68\cdot10^{-2}$	1.05	1.08	$5.54\cdot10^{-1}$	$\pm4.26\cdot10^{-1}$
unknown o: *Sphingobacteriales*	$1.40\cdot10^{-1}$	$5.82\cdot10^{-1}$	$5.06\cdot10^{-1}$	1.24	$4.86\cdot10^{-1}$	$4.12\cdot10^{-1}$	$4.97\cdot10^{-1}$	$5.53\cdot10^{-1}$	$\pm3.36\cdot10^{-1}$
Bacteriovorax	$2.24\cdot10^{-1}$	2.96	$7.64\cdot10^{-2}$	$3.49\cdot10^{-1}$	$1.07\cdot10^{-1}$	$6.63\cdot10^{-2}$	N.D.[f]	$5.40\cdot10^{-1}$	±1.07
Simplicispira	1.75	$6.15\cdot10^{-1}$	$2.73\cdot10^{-1}$	$5.35\cdot10^{-1}$	$3.43\cdot10^{-1}$	$1.95\cdot10^{-1}$	N.D.[f]	$5.30\cdot10^{-1}$	$\pm5.76\cdot10^{-1}$
Sediminibacterium	1.33	$7.96\cdot10^{-2}$	$3.43\cdot10^{-1}$	$6.33\cdot10^{-1}$	$5.26\cdot10^{-1}$	$7.81\cdot10^{-1}$	N.D.[f]	$5.28\cdot10^{-1}$	$\pm4.54\cdot10^{-1}$
Aquabacterium	$2.98\cdot10^{-2}$	$2.98\cdot10^{-2}$	$9.76\cdot10^{-3}$	$1.67\cdot10^{-2}$	$1.21\cdot10^{-2}$	$5.30\cdot10^{-3}$	3.56	$5.23\cdot10^{-1}$	±1.34
unknown f: *Sphingobacteriaceae*	3.22	$8.67\cdot10^{-2}$	$1.30\cdot10^{-2}$	$8.33\cdot10^{-3}$	$2.93\cdot10^{-2}$	$2.39\cdot10^{-2}$	N.D.[f]	$4.83\cdot10^{-1}$	±1.21
Dechloromonas	$1.49\cdot10^{-2}$	$1.99\cdot10^{-2}$	$9.11\cdot10^{-2}$	3.07	$2.82\cdot10^{-2}$	$1.59\cdot10^{-2}$	N.D.[f]	$4.62\cdot10^{-1}$	±1.15
Bdellovibrio	$4.04\cdot10^{-1}$	$5.34\cdot10^{-1}$	$3.69\cdot10^{-1}$	1.19	$4.54\cdot10^{-1}$	$1.60\cdot10^{-1}$	$8.28\cdot10^{-2}$	$4.57\cdot10^{-1}$	$\pm3.62\cdot10^{-1}$
unknown f: *Saprospiraceae*	$1.04\cdot10^{-1}$	$1.68\cdot10^{-1}$	$1.09\cdot10^{-1}$	$2.40\cdot10^{-1}$	$1.61\cdot10^{-1}$	$3.28\cdot10^{-1}$	1.90	$4.31\cdot10^{-1}$	$\pm6.54\cdot10^{-1}$
Gp4	$9.25\cdot10^{-2}$	$6.68\cdot10^{-2}$	$1.37\cdot10^{-1}$	$2.10\cdot10^{-1}$	$6.66\cdot10^{-2}$	$3.67\cdot10^{-1}$	2.07	$4.30\cdot10^{-1}$	$\pm7.31\cdot10^{-1}$
Niabella	2.24	$2.07\cdot10^{-1}$	$1.04\cdot10^{-1}$	$9.44\cdot10^{-2}$	$2.72\cdot10^{-2}$	$1.59\cdot10^{-2}$	N.D.[f]	$3.84\cdot10^{-1}$	$\pm8.21\cdot10^{-1}$
unknown f: *Cyclobacteriaceae*	$1.49\cdot10^{-2}$	$2.84\cdot10^{-2}$	$3.25\cdot10^{-2}$	$1.11\cdot10^{-2}$	$6.05\cdot10^{-3}$	$6.63\cdot10^{-3}$	2.40	$3.57\cdot10^{-1}$	$\pm9.01\cdot10^{-1}$
Parabacteroides	$1.49\cdot10^{-2}$	$1.56\cdot10^{-1}$	$2.11\cdot10^{-2}$	$3.89\cdot10^{-2}$	$1.35\cdot10^{-1}$	1.82	N.D.[f]	$3.13\cdot10^{-1}$	$\pm6.69\cdot10^{-1}$
Leptothrix	N.D.[f]	$2.42\cdot10^{-2}$	$2.24\cdot10^{-1}$	$5.42\cdot10^{-2}$	1.50	$2.47\cdot10^{-1}$	N.D.[f]	$2.92\cdot10^{-1}$	$\pm5.41\cdot10^{-1}$
Filomicrobium	$2.98\cdot10^{-3}$	$5.68\cdot10^{-3}$	$4.57\cdot10^{-1}$	1.26	$3.63\cdot10^{-2}$	$5.44\cdot10^{-2}$	$8.28\cdot10^{-2}$	$2.71\cdot10^{-1}$	$\pm4.64\cdot10^{-1}$
Mesorhizobium	$2.49\cdot10^{-1}$	$2.56\cdot10^{-2}$	$3.42\cdot10^{-2}$	$8.05\cdot10^{-2}$	$8.27\cdot10^{-2}$	$1.79\cdot10^{-1}$	1.16	$2.59\cdot10^{-1}$	$\pm4.05\cdot10^{-1}$
Altererythrobacter	$7.46\cdot10^{-3}$	$1.42\cdot10^{-3}$	$3.25\cdot10^{-3}$	$5.55\cdot10^{-3}$	$3.43\cdot10^{-2}$	$5.44\cdot10^{-2}$	1.49	$2.28\cdot10^{-1}$	$\pm5.57\cdot10^{-1}$
Luteimonas	$1.94\cdot10^{-2}$	$9.94\cdot10^{-3}$	N.D.[f]	$1.39\cdot10^{-3}$	N.D.[f]	$5.30\cdot10^{-3}$	1.32	$1.94\cdot10^{-1}$	$\pm4.98\cdot10^{-1}$
Proteocatella	N.D.[f]	$5.54\cdot10^{-2}$	$1.63\cdot10^{-2}$	$8.33\cdot10^{-3}$	$4.34\cdot10^{-2}$	1.07	N.D.[f]	$1.70\cdot10^{-1}$	$\pm3.97\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

Table S47. R-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Minor phylotypes (1434)[d]	20.5	16.2	19.1	15.8	23.3	23.6	22.8	20.2	±	3.28
Thiobacillus	14.9	27.0	19.4	13.5	8.68	13.0	$9.37\cdot10^{-3}$	13.8	±	8.41
unknown d: *Bacteria*	5.63	3.00	5.28	3.29	4.84	6.58	5.87	4.93	±	1.33
Thauera	$2.69\cdot10^{-1}$	1.23	5.51	13.0	4.68	2.89	$2.49\cdot10^{-1}$	3.98	±	4.50
Meganema	$6.68\cdot10^{-3}$	$1.05\cdot10^{-2}$	$1.67\cdot10^{-3}$	N.D.[e]	$6.26\cdot10^{-3}$	$4.44\cdot10^{-3}$	27.2	3.89	±	10.3
Ohtaekwangia	1.49	1.71	1.43	3.44	1.45	$7.90\cdot10^{-1}$	9.75	2.87	±	3.15
unknown p: *Bacteroidetes*	2.97	2.77	3.55	5.16	2.48	2.04	$7.23\cdot10^{-1}$	2.81	±	1.36
Amaricoccus	$1.18\cdot10^{-1}$	$9.10\cdot10^{-2}$	$4.42\cdot10^{-1}$	$8.72\cdot10^{-1}$	10.7	6.28	$4.15\cdot10^{-2}$	2.65	±	4.20
Simplicispira	9.19	3.75	1.43	1.73	1.49	$3.03\cdot10^{-1}$	$2.68\cdot10^{-3}$	2.56	±	3.16
Haliscomenobacter	1.52	1.15	1.17	1.41	3.85	6.25	$9.52\cdot10^{-1}$	2.33	±	1.99
unknown f: *Flavobacteriaceae*	1.43	2.67	1.69	3.69	2.70	2.86	$1.54\cdot10^{-1}$	2.17	±	1.17
unknown p: *Proteobacteria*	$9.11\cdot10^{-1}$	$8.57\cdot10^{-1}$	6.81	1.38	$9.16\cdot10^{-1}$	1.08	$9.83\cdot10^{-1}$	1.85	±	2.20
Zoogloea	$7.04\cdot10^{-1}$	2.67	1.25	5.97	$5.85\cdot10^{-1}$	1.18	N.D.[e]	1.77	±	2.03
unknown f: *Chitinophagaceae*	1.97	2.61	1.58	3.32	1.13	1.21	$2.92\cdot10^{-1}$	1.73	±	1.01
unknown c: *Alphaproteobacteria*	$5.34\cdot10^{-1}$	$5.27\cdot10^{-1}$	1.93	2.05	2.50	1.97	1.45	1.56	±	$7.70\cdot10^{-1}$
unknown c: *Betaproteobacteria*	1.43	2.13	3.27	1.58	1.09	1.42	$2.95\cdot10^{-2}$	1.56	±	$9.87\cdot10^{-1}$
unknown f: *Saprospiraceae*	3.61	3.87	$2.09\cdot10^{-1}$	$6.57\cdot10^{-2}$	$8.64\cdot10^{-1}$	2.15	$8.03\cdot10^{-3}$	1.54	±	1.68
unknown o: *Sphingobacteriales*	3.21	3.61	$3.51\cdot10^{-1}$	$3.16\cdot10^{-1}$	1.09	2.13	$3.21\cdot10^{-2}$	1.53	±	1.46
Dokdonella	1.95	2.31	1.83	1.00	2.18	1.16	$3.61\cdot10^{-2}$	1.50	±	$8.09\cdot10^{-1}$
Sediminibacterium	$7.99\cdot10^{-1}$	$6.21\cdot10^{-1}$	3.25	4.06	1.21	$3.06\cdot10^{-1}$	N.D.[e]	1.47	±	1.56
Diaphorobacter	4.84	2.60	$3.68\cdot10^{-1}$	$1.72\cdot10^{-1}$	1.04	$3.58\cdot10^{-1}$	N.D.[e]	1.34	±	1.78
unknown f: *Comamonadaceae*	3.16	1.62	$6.31\cdot10^{-1}$	$4.44\cdot10^{-1}$	1.04	$6.29\cdot10^{-1}$	$2.83\cdot10^{-1}$	1.12	±	1.01
unknown o: *Rhizobiales*	$4.74\cdot10^{-1}$	$3.25\cdot10^{-1}$	$4.87\cdot10^{-1}$	$8.47\cdot10^{-1}$	1.09	$9.38\cdot10^{-1}$	3.26	1.06	±	1.01
Leadbetterella	$1.09\cdot10^{-1}$	$2.31\cdot10^{-1}$	$6.19\cdot10^{-2}$	$8.52\cdot10^{-2}$	$4.00\cdot10^{-1}$	$6.35\cdot10^{-1}$	5.64	1.02	±	2.05
Paracoccus	$3.83\cdot10^{-1}$	$5.28\cdot10^{-1}$	$7.06\cdot10^{-1}$	$7.74\cdot10^{-1}$	2.19	1.53	1.03	1.02	±	$6.39\cdot10^{-1}$
Gp4	$1.22\cdot10^{-1}$	$1.47\cdot10^{-1}$	$1.07\cdot10^{-1}$	$6.75\cdot10^{-2}$	2.03	2.91	1.75	1.02	±	1.18
unknown f: *Rhodobacteraceae*	$4.10\cdot10^{-1}$	$4.92\cdot10^{-1}$	$5.74\cdot10^{-1}$	$7.99\cdot10^{-1}$	1.22	$9.62\cdot10^{-1}$	1.92	$9.11\cdot10^{-1}$	±	$5.28\cdot10^{-1}$
Comamonas	3.94	1.54	$1.44\cdot10^{-1}$	$2.57\cdot10^{-1}$	$9.14\cdot10^{-2}$	$1.45\cdot10^{-1}$	N.D.[e]	$8.75\cdot10^{-1}$	±	1.45

Table S47. R-EBPR genus-level EUB results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Saccharibacteria_genera_inc._ sed.[f]	1.21	$2.03\cdot10^{-1}$	$5.44\cdot10^{-1}$	$5.50\cdot10^{-1}$	1.25	1.01	1.34	$8.74\cdot10^{-1}$	±	$4.40\cdot10^{-1}$
Prosthecobacter	$2.76\cdot10^{-1}$	$5.63\cdot10^{-1}$	1.09	1.43	1.97	$4.91\cdot10^{-1}$	$1.70\cdot10^{-1}$	$8.55\cdot10^{-1}$	±	$6.64\cdot10^{-1}$
Arcobacter	1.41	2.84	$1.67\cdot10^{-1}$	$6.04\cdot10^{-1}$	$5.35\cdot10^{-1}$	$3.76\cdot10^{-1}$	N.D.[e]	$8.47\cdot10^{-1}$	±	$9.87\cdot10^{-1}$
Planctomyces	$2.00\cdot10^{-2}$	$1.12\cdot10^{-1}$	$1.64\cdot10^{-1}$	$2.63\cdot10^{-1}$	$8.30\cdot10^{-1}$	$7.83\cdot10^{-1}$	2.91	$7.26\cdot10^{-1}$	±	1.02
Opitutus	$2.89\cdot10^{-1}$	$2.66\cdot10^{-1}$	$6.58\cdot10^{-1}$	1.00	1.69	$8.93\cdot10^{-1}$	$4.15\cdot10^{-2}$	$6.91\cdot10^{-1}$	±	$5.62\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$3.67\cdot10^{-1}$	$5.76\cdot10^{-1}$	1.78	$2.61\cdot10^{-1}$	$3.76\cdot10^{-1}$	$3.88\cdot10^{-1}$	1.08	$6.90\cdot10^{-1}$	±	$5.52\cdot10^{-1}$
unknown o: *Flavobacteriales*	1.01	$8.80\cdot10^{-1}$	$7.45\cdot10^{-1}$	$8.68\cdot10^{-1}$	$5.45\cdot10^{-1}$	$6.25\cdot10^{-1}$	$9.51\cdot10^{-2}$	$6.81\cdot10^{-1}$	±	$3.04\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$2.98\cdot10^{-1}$	$4.90\cdot10^{-1}$	1.88	$6.98\cdot10^{-1}$	$3.84\cdot10^{-1}$	$2.66\cdot10^{-1}$	$7.46\cdot10^{-1}$	$6.81\cdot10^{-1}$	±	$5.61\cdot10^{-1}$
Bdellovibrio	$3.50\cdot10^{-1}$	$5.97\cdot10^{-1}$	1.06	$6.18\cdot10^{-1}$	$6.49\cdot10^{-1}$	1.24	$6.29\cdot10^{-2}$	$6.54\cdot10^{-1}$	±	$3.99\cdot10^{-1}$
Brevundimonas	$1.96\cdot10^{-1}$	$2.40\cdot10^{-1}$	$6.64\cdot10^{-1}$	1.94	$3.64\cdot10^{-1}$	$2.03\cdot10^{-1}$	$7.83\cdot10^{-1}$	$6.28\cdot10^{-1}$	±	$6.25\cdot10^{-1}$
unknown o: *Pseudomonadales*	$3.90\cdot10^{-1}$	$2.57\cdot10^{-1}$	3.43	$2.13\cdot10^{-1}$	$2.13\cdot10^{-2}$	$4.14\cdot10^{-2}$	N.D.[e]	$6.22\cdot10^{-1}$	±	1.25
unknown f: *Burkholderiales_inc._sed.*[f]	2.39	$7.47\cdot10^{-1}$	$2.78\cdot10^{-1}$	$1.37\cdot10^{-1}$	$3.46\cdot10^{-1}$	$2.61\cdot10^{-1}$	$9.10\cdot10^{-2}$	$6.07\cdot10^{-1}$	±	$8.16\cdot10^{-1}$
Flavobacterium	$1.78\cdot10^{-1}$	1.45	$7.48\cdot10^{-1}$	1.13	$1.73\cdot10^{-1}$	$2.26\cdot10^{-1}$	$5.22\cdot10^{-2}$	$5.66\cdot10^{-1}$	±	$5.51\cdot10^{-1}$
unknown f: *Cryomorphaceae*	$6.70\cdot10^{-1}$	$7.42\cdot10^{-1}$	$6.09\cdot10^{-1}$	1.20	$3.02\cdot10^{-1}$	$3.18\cdot10^{-1}$	$1.87\cdot10^{-2}$	$5.51\cdot10^{-1}$	±	$3.82\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[f]	1.36	$8.22\cdot10^{-2}$	$7.40\cdot10^{-1}$	$3.11\cdot10^{-1}$	$7.78\cdot10^{-1}$	$1.82\cdot10^{-1}$	$3.37\cdot10^{-1}$	$5.42\cdot10^{-1}$	±	$4.49\cdot10^{-1}$
Nitrosomonas	1.02	$4.43\cdot10^{-1}$	$7.01\cdot10^{-1}$	$7.67\cdot10^{-1}$	$4.16\cdot10^{-1}$	$3.51\cdot10^{-1}$	N.D.[e]	$5.28\cdot10^{-1}$	±	$3.32\cdot10^{-1}$
Sideroxydans	$3.65\cdot10^{-1}$	$3.80\cdot10^{-1}$	1.63	$6.89\cdot10^{-1}$	$2.76\cdot10^{-1}$	$1.64\cdot10^{-1}$	$5.36\cdot10^{-3}$	$5.01\cdot10^{-1}$	±	$5.40\cdot10^{-1}$
Schlesneria	$8.91\cdot10^{-3}$	$1.05\cdot10^{-2}$	$8.87\cdot10^{-2}$	$8.17\cdot10^{-2}$	$1.92\cdot10^{-1}$	$2.43\cdot10^{-1}$	2.82	$4.91\cdot10^{-1}$	±	1.03
Terrimonas	$1.54\cdot10^{-1}$	$4.93\cdot10^{-1}$	$1.82\cdot10^{-1}$	$2.89\cdot10^{-1}$	$8.27\cdot10^{-1}$	1.25	$9.91\cdot10^{-2}$	$4.70\cdot10^{-1}$	±	$4.25\cdot10^{-1}$
Nitrospira	N.D.[e]	$3.50\cdot10^{-3}$	$1.00\cdot10^{-2}$	$3.55\cdot10^{-3}$	$7.51\cdot10^{-1}$	1.95	N.D.[e]	$3.88\cdot10^{-1}$	±	$7.42\cdot10^{-1}$
Alicycliphilus	1.23	$5.88\cdot10^{-1}$	$1.26\cdot10^{-1}$	$4.08\cdot10^{-2}$	$4.37\cdot10^{-1}$	$1.66\cdot10^{-1}$	$5.36\cdot10^{-3}$	$3.71\cdot10^{-1}$	±	$4.35\cdot10^{-1}$
Magnetospira	$8.91\cdot10^{-3}$	$1.57\cdot10^{-2}$	$1.84\cdot10^{-2}$	1.54	$6.02\cdot10^{-1}$	$3.20\cdot10^{-1}$	$7.10\cdot10^{-2}$	$3.68\cdot10^{-1}$	±	$5.61\cdot10^{-1}$
Pseudofulvimonas	N.D.[e]	N.D.[e]	N.D.[e]	N.D.[e]	N.D.[e]	N.D.[e]	2.52	$3.60\cdot10^{-1}$	±	$9.53\cdot10^{-1}$
Sphingomonas	$7.12\cdot10^{-2}$	$3.15\cdot10^{-2}$	$5.02\cdot10^{-3}$	$1.95\cdot10^{-2}$	$8.40\cdot10^{-1}$	1.23	$1.27\cdot10^{-1}$	$3.31\cdot10^{-1}$	±	$4.94\cdot10^{-1}$
Ferruginibacter	$2.00\cdot10^{-2}$	$8.05\cdot10^{-2}$	$2.84\cdot10^{-2}$	$8.34\cdot10^{-2}$	$3.74\cdot10^{-1}$	1.40	$4.82\cdot10^{-2}$	$2.91\cdot10^{-1}$	±	$5.05\cdot10^{-1}$
Aeromonas	$1.36\cdot10^{-1}$	1.66	$5.69\cdot10^{-2}$	$7.10\cdot10^{-2}$	$2.63\cdot10^{-2}$	$4.88\cdot10^{-2}$	N.D.[e]	$2.85\cdot10^{-1}$	±	$6.06\cdot10^{-1}$
Armatimonadetes_gp5	N.D.[e]	$1.75\cdot10^{-3}$	$8.37\cdot10^{-3}$	$3.73\cdot10^{-2}$	$1.43\cdot10^{-1}$	$1.91\cdot10^{-1}$	1.05	$2.04\cdot10^{-1}$	±	$3.80\cdot10^{-1}$

Table S47. R-EBPR genus-level EUB results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Spartobacteria_genera_inc._sed.[f]	$2.67\cdot10^{-2}$	$3.50\cdot10^{-3}$	$8.37\cdot10^{-3}$	$7.10\cdot10^{-3}$	$8.77\cdot10^{-2}$	$6.36\cdot10^{-2}$	1.02	$1.74\cdot10^{-1}$	±	$3.76\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

[f] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S48. Moscow WRRF genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Minor phylotypes (1439)[d]	35.6	38.5	35.4	32.8	29.2	32.0	30.6	33.5	± 3.23
unknown d: *Bacteria*	8.27	5.99	5.96	6.34	8.43	7.39	7.39	7.11	± 1.03
unknown p: *Bacteroidetes*	2.70	2.09	3.15	3.53	6.37	4.78	5.24	3.98	± 1.53
Haliscomenobacter	2.59	5.08	5.45	4.02	1.57	1.85	1.93	3.21	± 1.62
unknown p: *Proteobacteria*	2.20	1.46	1.45	1.57	4.33	4.25	4.95	2.89	± 1.55
unknown f: *Chitinophagaceae*	3.50	1.95	2.74	4.19	3.88	1.88	1.73	2.84	± 1.02
Flavobacterium	2.87	2.60	2.74	2.14	2.30	4.09	2.20	2.71	± $6.70\cdot10^{-1}$
unknown o: *Actinomycetales*	2.46	4.15	4.13	3.47	1.51	1.65	1.25	2.66	± 1.25
unknown o: *Rhizobiales*	1.49	2.26	2.95	2.85	2.30	2.21	1.65	2.24	± $5.48\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	1.45	1.56	1.88	1.84	2.66	2.87	2.40	2.10	± $5.50\cdot10^{-1}$
Roseiflexus	2.23	2.32	2.55	2.99	1.14	1.17	1.40	1.97	± $7.34\cdot10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	1.67	$9.83\cdot10^{-1}$	3.14	3.94	1.40	1.56	$8.89\cdot10^{-1}$	1.94	± 1.15
unknown c: *Gammaproteobacteria*	1.04	$9.12\cdot10^{-1}$	$7.12\cdot10^{-1}$	$9.76\cdot10^{-1}$	2.76	2.49	3.55	1.78	± 1.13
Caldilinea	2.47	2.52	2.23	2.23	$8.65\cdot10^{-1}$	1.14	$9.26\cdot10^{-1}$	1.77	± $7.53\cdot10^{-1}$
Candidatus Carsonella	$4.34\cdot10^{-1}$	$5.19\cdot10^{-1}$	$1.44\cdot10^{-1}$	$1.66\cdot10^{-1}$	2.30	1.96	4.93	1.49	± 1.75
unknown o: *Sphingobacteriales*	1.34	$8.75\cdot10^{-1}$	1.28	1.71	1.74	1.18	1.19	1.33	± $3.07\cdot10^{-1}$
Ohtaekwangia	$4.58\cdot10^{-1}$	$7.94\cdot10^{-1}$	1.21	$7.71\cdot10^{-1}$	2.38	1.81	1.76	1.31	± $6.93\cdot10^{-1}$

Table S48. Moscow WRRF genus-level EUB results summary continued.

Genus[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Propionivibrio	$8.89\cdot10^{-1}$	$7.25\cdot10^{-1}$	$8.30\cdot10^{-1}$	$9.22\cdot10^{-1}$	1.76	1.67	1.57	1.20	$\pm 4.49\cdot10^{-1}$
Phycisphaera	$3.68\cdot10^{-1}$	$7.22\cdot10^{-1}$	$7.24\cdot10^{-1}$	$8.07\cdot10^{-1}$	1.98	1.54	1.76	1.13	$\pm 6.20\cdot10^{-1}$
unknown f: *Flavobacteriaceae*	$7.73\cdot10^{-1}$	$5.62\cdot10^{-1}$	$9.43\cdot10^{-1}$	1.73	1.32	1.28	1.15	1.11	$\pm 3.87\cdot10^{-1}$
unknown o: *Flavobacteriales*	$5.98\cdot10^{-1}$	1.22	1.08	$8.68\cdot10^{-1}$	1.21	1.21	1.32	1.07	$\pm 2.53\cdot10^{-1}$
Nitrospira	$8.48\cdot10^{-1}$	$7.49\cdot10^{-1}$	$7.48\cdot10^{-1}$	$9.27\cdot10^{-1}$	1.46	1.21	1.45	1.06	$\pm 3.14\cdot10^{-1}$
Caenimonas	$6.61\cdot10^{-1}$	2.56	1.82	1.24	$2.76\cdot10^{-1}$	$3.15\cdot10^{-1}$	$3.19\cdot10^{-1}$	1.03	$\pm 8.88\cdot10^{-1}$
unknown o: *Myxococcales*	$1.28\cdot10^{-1}$	$5.07\cdot10^{-1}$	$4.16\cdot10^{-1}$	$4.58\cdot10^{-1}$	2.28	1.60	1.50	$9.85\cdot10^{-1}$	$\pm 8.05\cdot10^{-1}$
Terrimonas	$9.45\cdot10^{-1}$	1.44	1.15	$7.31\cdot10^{-1}$	$9.55\cdot10^{-1}$	$9.94\cdot10^{-1}$	$6.18\cdot10^{-1}$	$9.76\cdot10^{-1}$	$\pm 2.68\cdot10^{-1}$
Trichococcus	3.35	1.47	$9.42\cdot10^{-1}$	$5.96\cdot10^{-1}$	$6.80\cdot10^{-2}$	$1.22\cdot10^{-1}$	$9.51\cdot10^{-2}$	$9.49\cdot10^{-1}$	± 1.18
Sulfuritalea	2.15	$3.58\cdot10^{-1}$	$2.24\cdot10^{-1}$	$1.97\cdot10^{-1}$	1.45	$9.97\cdot10^{-1}$	1.17	$9.36\cdot10^{-1}$	$\pm 7.30\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$8.28\cdot10^{-1}$	$7.85\cdot10^{-1}$	$7.61\cdot10^{-1}$	$6.22\cdot10^{-1}$	1.16	1.13	1.09	$9.10\cdot10^{-1}$	$\pm 2.11\cdot10^{-1}$
unknown f: *Planctomycetaceae*	$4.56\cdot10^{-1}$	$8.35\cdot10^{-1}$	1.14	1.07	$6.53\cdot10^{-1}$	1.17	$8.43\cdot10^{-1}$	$8.81\cdot10^{-1}$	$\pm 2.65\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$4.10\cdot10^{-1}$	$4.78\cdot10^{-1}$	$7.57\cdot10^{-1}$	$9.74\cdot10^{-1}$	1.24	$9.56\cdot10^{-1}$	$9.64\cdot10^{-1}$	$8.26\cdot10^{-1}$	$\pm 2.97\cdot10^{-1}$
Litorilinea	$6.43\cdot10^{-1}$	1.31	1.20	1.12	$4.12\cdot10^{-1}$	$4.22\cdot10^{-1}$	$3.61\cdot10^{-1}$	$7.83\cdot10^{-1}$	$\pm 4.16\cdot10^{-1}$
Nitrosomonas	$3.91\cdot10^{-1}$	$6.26\cdot10^{-1}$	$6.56\cdot10^{-1}$	$5.85\cdot10^{-1}$	$9.35\cdot10^{-1}$	1.07	1.11	$7.68\cdot10^{-1}$	$\pm 2.73\cdot10^{-1}$
Ferruginibacter	$6.10\cdot10^{-1}$	$9.58\cdot10^{-1}$	1.16	1.29	$5.44\cdot10^{-1}$	$4.08\cdot10^{-1}$	$2.33\cdot10^{-1}$	$7.43\cdot10^{-1}$	$\pm 3.97\cdot10^{-1}$
Leadbetterella	3.91	$3.04\cdot10^{-1}$	$2.80\cdot10^{-1}$	$3.77\cdot10^{-1}$	$9.76\cdot10^{-2}$	$1.00\cdot10^{-1}$	$5.86\cdot10^{-2}$	$7.33\cdot10^{-1}$	± 1.41
Dechloromonas	$4.20\cdot10^{-1}$	$3.60\cdot10^{-1}$	$3.07\cdot10^{-1}$	$2.60\cdot10^{-1}$	$9.67\cdot10^{-1}$	1.75	$9.80\cdot10^{-1}$	$7.21\cdot10^{-1}$	$\pm 5.46\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$4.44\cdot10^{-1}$	2.50	$2.72\cdot10^{-1}$	$4.54\cdot10^{-1}$	$2.92\cdot10^{-1}$	$6.28\cdot10^{-1}$	$4.35\cdot10^{-1}$	$7.17\cdot10^{-1}$	$\pm 7.93\cdot10^{-1}$
Ilumatobacter	1.44	1.17	$9.65\cdot10^{-1}$	$7.13\cdot10^{-1}$	$2.19\cdot10^{-1}$	$3.41\cdot10^{-1}$	$1.68\cdot10^{-1}$	$7.16\cdot10^{-1}$	$\pm 4.96\cdot10^{-1}$
unknown f: *Anaerolineaceae*	$8.68\cdot10^{-1}$	$4.96\cdot10^{-1}$	$4.02\cdot10^{-1}$	$3.70\cdot10^{-1}$	$6.26\cdot10^{-1}$	$8.96\cdot10^{-1}$	1.06	$6.74\cdot10^{-1}$	$\pm 2.70\cdot10^{-1}$
Aquimonas	1.10	$8.97\cdot10^{-1}$	$8.77\cdot10^{-1}$	$7.40\cdot10^{-1}$	$3.56\cdot10^{-1}$	$3.96\cdot10^{-1}$	$2.93\cdot10^{-1}$	$6.66\cdot10^{-1}$	$\pm 3.17\cdot10^{-1}$
Mycobacterium	$1.66\cdot10^{-1}$	1.15	1.00	1.24	$4.51\cdot10^{-1}$	$3.48\cdot10^{-1}$	$2.25\cdot10^{-1}$	$6.54\cdot10^{-1}$	$\pm 4.59\cdot10^{-1}$
unknown f: *Rhodocyclaceae*	$4.09\cdot10^{-1}$	$2.50\cdot10^{-1}$	$3.23\cdot10^{-1}$	$3.72\cdot10^{-1}$	1.04	$9.76\cdot10^{-1}$	1.02	$6.26\cdot10^{-1}$	$\pm 3.63\cdot10^{-1}$
Planctomyces	$9.00\cdot10^{-1}$	$7.84\cdot10^{-1}$	1.02	$5.77\cdot10^{-1}$	$2.79\cdot10^{-1}$	$4.32\cdot10^{-1}$	$2.37\cdot10^{-1}$	$6.04\cdot10^{-1}$	$\pm 3.07\cdot10^{-1}$
Subdivision3_genera_inc._sed.[e]	$2.97\cdot10^{-1}$	$2.92\cdot10^{-1}$	$5.36\cdot10^{-1}$	$4.88\cdot10^{-1}$	$6.88\cdot10^{-1}$	$5.93\cdot10^{-1}$	1.12	$5.74\cdot10^{-1}$	$\pm 2.83\cdot10^{-1}$
unknown f: *Polyangiaceae*	$9.85\cdot10^{-2}$	$3.20\cdot10^{-1}$	$2.65\cdot10^{-1}$	$2.93\cdot10^{-1}$	$7.93\cdot10^{-1}$	1.14	$9.65\cdot10^{-1}$	$5.54\cdot10^{-1}$	$\pm 4.05\cdot10^{-1}$
Chryseobacterium	$1.20\cdot10^{-1}$	$8.83\cdot10^{-2}$	$8.45\cdot10^{-2}$	3.38	$1.75\cdot10^{-2}$	$3.06\cdot10^{-2}$	$4.54\cdot10^{-2}$	$5.38\cdot10^{-1}$	± 1.25
Arcobacter	$3.39\cdot10^{-1}$	$1.21\cdot10^{-1}$	$4.19\cdot10^{-1}$	$1.12\cdot10^{-1}$	$7.37\cdot10^{-1}$	1.11	$7.87\cdot10^{-1}$	$5.17\cdot10^{-1}$	$\pm 3.72\cdot10^{-1}$
Gemmata	$1.62\cdot10^{-1}$	$5.02\cdot10^{-1}$	1.17	$6.38\cdot10^{-1}$	$2.27\cdot10^{-1}$	$3.95\cdot10^{-1}$	$2.54\cdot10^{-1}$	$4.79\cdot10^{-1}$	$\pm 3.49\cdot10^{-1}$
unknown o: *Pseudomonadales*	$1.87\cdot10^{-2}$	$1.03\cdot10^{-2}$	$1.41\cdot10^{-2}$	$2.66\cdot10^{-2}$	$1.65\cdot10^{-1}$	$2.42\cdot10^{-1}$	1.76	$3.19\cdot10^{-1}$	$\pm 6.40\cdot10^{-1}$

Table S48. Moscow WRRF genus-level EUB results summary continued.

Genus[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average ± SD[c] %	
Tetrasphaera	1.29	$3.88\cdot10^{-1}$	$2.21\cdot10^{-1}$	$1.40\cdot10^{-1}$	$3.62\cdot10^{-2}$	$2.94\cdot10^{-2}$	$3.21\cdot10^{-2}$	$3.05\cdot10^{-1}$	$\pm4.53\cdot10^{-1}$
Sediminibacterium	1.13	$4.94\cdot10^{-1}$	$1.54\cdot10^{-1}$	$6.34\cdot10^{-2}$	$3.62\cdot10^{-2}$	$3.29\cdot10^{-2}$	$1.22\cdot10^{-2}$	$2.75\cdot10^{-1}$	$\pm4.13\cdot10^{-1}$
unknown f: *Pseudomonadaceae*	$2.37\cdot10^{-2}$	$1.89\cdot10^{-2}$	$2.35\cdot10^{-2}$	$2.92\cdot10^{-2}$	$1.36\cdot10^{-1}$	$1.36\cdot10^{-1}$	1.04	$2.00\cdot10^{-1}$	$\pm3.72\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S49. Summary of genus-level relative abundance by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	S-EBPR (S44)		V-EBPR (S45)		G-EBPR (S46)		R-EBPR (S47)		Moscow WRRF (S48)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
Minor phylotypes (1367)[d]	10.0	±2.63	13.2	±5.36	13.0	±4.70	13.4	± 2.30	23.2	±1.87
Thiobacillus	$4.11\cdot10^{-3}$	$\pm3.70\cdot10^{-3}$	10.8	±6.55	6.16	±4.19	13.8	± 8.41	$2.95\cdot10^{-3}$	$\pm1.23\cdot10^{-3}$
unknown p: *Bacteroidetes*	1.67	$\pm5.54\cdot10^{-1}$	12.6	±5.82	5.00	±3.22	2.81	± 1.36	3.98	±1.53
Thauera	10.1	±8.31	3.82	±5.55	$9.73\cdot10^{-1}$	±1.70	3.98	± 4.50	$1.17\cdot10^{-1}$	$\pm3.11\cdot10^{-2}$
unknown f: *Rhodobacteraceae*	9.68	±3.06	$7.88\cdot10^{-1}$	$\pm4.51\cdot10^{-1}$	1.13	$\pm4.34\cdot10^{-1}$	$9.11\cdot10^{-1}$	$\pm5.28\cdot10^{-1}$	$5.14\cdot10^{-1}$	$\pm2.45\cdot10^{-1}$
Saccharibacteria_genera_inc._ sed.[e]	$1.90\cdot10^{-1}$	$\pm3.97\cdot10^{-1}$	$5.40\cdot10^{-1}$	$\pm4.71\cdot10^{-1}$	7.87	±8.38	$8.74\cdot10^{-1}$	$\pm4.40\cdot10^{-1}$	1.94	±1.15
unknown d: *Bacteria*	5.86	±2.76	3.75	±1.78	4.23	$\pm9.24\cdot10^{-1}$	4.93	± 1.33	7.11	±1.03
Flavobacterium	6.69	±5.71	$1.53\cdot10^{-1}$	$\pm1.59\cdot10^{-1}$	$1.13\cdot10^{-1}$	$\pm8.00\cdot10^{-2}$	$5.66\cdot10^{-1}$	$\pm5.51\cdot10^{-1}$	2.71	$\pm6.70\cdot10^{-1}$
Ohtaekwangia	6.52	±3.58	$5.95\cdot10^{-1}$	$\pm4.61\cdot10^{-1}$	1.94	±1.44	2.87	± 3.15	1.31	$\pm6.93\cdot10^{-1}$
Haliscomenobacter	1.24	±1.58	4.37	±2.50	4.45	±3.58	2.33	± 1.99	3.21	±1.62
Propionivibrio	4.37	±7.72	$2.67\cdot10^{-1}$	$\pm6.22\cdot10^{-1}$	2.59	±5.89	$2.11\cdot10^{-2}$	$\pm1.19\cdot10^{-2}$	1.20	$\pm4.49\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	2.96	±1.17	1.63	$\pm6.88\cdot10^{-1}$	4.30	±1.82	1.56	$\pm7.70\cdot10^{-1}$	2.10	$\pm5.50\cdot10^{-1}$
Meganema	$1.62\cdot10^{-2}$	$\pm7.19\cdot10^{-3}$	2.46	±6.47	3.02	±7.94	3.89	±10.3	$1.01\cdot10^{-2}$	$\pm3.97\cdot10^{-3}$
Methylobacillus	$2.59\cdot10^{-4}$	$\pm6.85\cdot10^{-4}$	$3.74\cdot10^{-4}$	$\pm9.90\cdot10^{-4}$	3.65	±3.08	$1.17\cdot10^{-3}$	$\pm2.01\cdot10^{-3}$	$4.92\cdot10^{-4}$	$\pm6.14\cdot10^{-4}$
Zoogloea	$4.65\cdot10^{-3}$	$\pm3.43\cdot10^{-3}$	3.42	±2.60	3.39	±2.85	1.77	± 2.03	$1.79\cdot10^{-1}$	$\pm4.14\cdot10^{-2}$
unknown p: *Proteobacteria*	1.68	$\pm9.32\cdot10^{-1}$	1.88	±1.36	2.02	$\pm9.66\cdot10^{-1}$	1.85	± 2.20	2.89	±1.55
unknown f: *Chitinophagaceae*	$4.91\cdot10^{-1}$	$\pm4.83\cdot10^{-1}$	1.07	$\pm8.26\cdot10^{-1}$	1.29	$\pm8.34\cdot10^{-1}$	1.73	± 1.01	2.84	±1.02

Table S49. Summary of genus-level EUB results continued.

Genus[a,b]	S-EBPR (S44)		V-EBPR (S45)		G-EBPR (S46)		R-EBPR (S47)		Moscow WRRF (S48)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
Phycisphaera	2.77	± 2.39	$1.99\cdot10^{-2}$	± $2.48\cdot10^{-2}$	$6.02\cdot10^{-2}$	± $5.35\cdot10^{-2}$	$7.24\cdot10^{-2}$	± $9.70\cdot10^{-2}$	1.13	± $6.20\cdot10^{-1}$
unknown o: *Actinomycetales*	$3.36\cdot10^{-2}$	± $3.97\cdot10^{-2}$	$4.93\cdot10^{-1}$	± $3.50\cdot10^{-1}$	$9.79\cdot10^{-1}$	± $5.33\cdot10^{-1}$	$1.42\cdot10^{-1}$	± $1.41\cdot10^{-1}$	2.66	± 1.25
Amaricoccus	$5.20\cdot10^{-4}$	± $8.89\cdot10^{-4}$	$1.10\cdot10^{-1}$	± $2.25\cdot10^{-1}$	$9.74\cdot10^{-2}$	± $2.00\cdot10^{-1}$	2.65	± 4.20	$5.58\cdot10^{-2}$	± $3.74\cdot10^{-2}$
Defluviicoccus	2.63	± 2.79	1.10	± $7.69\cdot10^{-1}$	1.36	± 1.58	$1.56\cdot10^{-3}$	± $1.68\cdot10^{-3}$	$6.58\cdot10^{-1}$	± $2.24\cdot10^{-1}$
Simplicispira	$6.44\cdot10^{-3}$	± $5.93\cdot10^{-3}$	1.76	± 1.05	$5.30\cdot10^{-1}$	± $5.76\cdot10^{-1}$	2.56	± 3.16	$3.26\cdot10^{-1}$	± $2.07\cdot10^{-1}$
Jhaorihella	2.38	± 3.37	$1.58\cdot10^{-2}$	± $3.85\cdot10^{-2}$	$3.90\cdot10^{-2}$	± $9.25\cdot10^{-2}$	$3.83\cdot10^{-4}$	± $1.01\cdot10^{-3}$	N.D.[f]	
unknown o: *Rhizobiales*	1.99	± 1.09	1.24	± $8.79\cdot10^{-1}$	1.68	± $4.46\cdot10^{-1}$	1.06	± 1.01	2.24	± $5.48\cdot10^{-1}$
unknown o: *Cytophagales*	$1.04\cdot10^{-1}$	± $8.80\cdot10^{-2}$	2.19	± 1.86	1.62	± 1.30	$1.48\cdot10^{-1}$	± $1.46\cdot10^{-1}$	$2.85\cdot10^{-1}$	± $1.02\cdot10^{-1}$
unknown f: *Flavobacteriaceae*	1.69	± $4.70\cdot10^{-1}$	1.48	± 1.77	1.44	± 1.39	2.17	± 1.17	1.11	± $3.87\cdot10^{-1}$
Aquimonas	2.14	± 1.02	$5.78\cdot10^{-1}$	± $4.65\cdot10^{-1}$	$3.03\cdot10^{-1}$	± $2.56\cdot10^{-1}$	$2.85\cdot10^{-1}$	± $2.68\cdot10^{-1}$	$6.66\cdot10^{-1}$	± $3.17\cdot10^{-1}$
Roseiflexus	N.D.[f]		$4.37\cdot10^{-2}$	± $6.10\cdot10^{-2}$	$2.73\cdot10^{-2}$	± $1.77\cdot10^{-2}$	$3.70\cdot10^{-2}$	± $2.99\cdot10^{-2}$	1.97	± $7.34\cdot10^{-1}$
Tetrasphaera	$2.73\cdot10^{-4}$	± $7.21\cdot10^{-4}$	$6.52\cdot10^{-2}$	± $5.18\cdot10^{-2}$	1.91	± 2.40	$5.94\cdot10^{-2}$	± $7.54\cdot10^{-2}$	$3.05\cdot10^{-1}$	± $4.53\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$9.31\cdot10^{-1}$	± $5.21\cdot10^{-1}$	$9.27\cdot10^{-1}$	± $8.50\cdot10^{-1}$	$4.58\cdot10^{-1}$	± $2.43\cdot10^{-1}$	$6.90\cdot10^{-1}$	± $5.52\cdot10^{-1}$	1.78	± 1.13
Caldilinea	$1.71\cdot10^{-2}$	± $2.58\cdot10^{-2}$	$7.07\cdot10^{-1}$	± $8.84\cdot10^{-1}$	$8.40\cdot10^{-1}$	± $5.94\cdot10^{-1}$	$1.68\cdot10^{-1}$	± $1.67\cdot10^{-1}$	1.77	± $7.53\cdot10^{-1}$
unknown o: *Sphingobacteriales*	$1.22\cdot10^{-1}$	± $6.36\cdot10^{-2}$	1.69	± $7.80\cdot10^{-1}$	$5.53\cdot10^{-1}$	± $3.36\cdot10^{-1}$	1.53	± 1.46	1.33	± $3.07\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$4.00\cdot10^{-1}$	± $1.59\cdot10^{-1}$	1.06	± $6.41\cdot10^{-1}$	1.17	± $7.57\cdot10^{-1}$	1.56	± $9.87\cdot10^{-1}$	$8.26\cdot10^{-1}$	± $2.97\cdot10^{-1}$
unknown f: *Saprospiraceae*	$2.89\cdot10^{-2}$	± $3.81\cdot10^{-2}$	$4.03\cdot10^{-1}$	± $4.93\cdot10^{-1}$	$4.31\cdot10^{-1}$	± $6.54\cdot10^{-1}$	1.54	± 1.68	$4.27\cdot10^{-2}$	± $3.61\cdot10^{-2}$
Dokdonella	$1.75\cdot10^{-2}$	± $1.60\cdot10^{-2}$	$4.66\cdot10^{-1}$	± $5.62\cdot10^{-1}$	$2.21\cdot10^{-1}$	± $1.42\cdot10^{-1}$	1.50	± $8.09\cdot10^{-1}$	$3.91\cdot10^{-2}$	± $1.74\cdot10^{-2}$
Candidatus Carsonella	$4.51\cdot10^{-2}$	± $3.99\cdot10^{-2}$	$1.03\cdot10^{-1}$	± $1.63\cdot10^{-1}$	$1.31\cdot10^{-2}$	± $1.55\cdot10^{-2}$	$1.09\cdot10^{-1}$	± $2.48\cdot10^{-1}$	1.49	± 1.75
unknown f: *Bradyrhizobiaceae*	1.47	± 1.55	$1.17\cdot10^{-1}$	± $8.79\cdot10^{-2}$	$1.99\cdot10^{-1}$	± $1.56\cdot10^{-1}$	$2.63\cdot10^{-1}$	± $2.80\cdot10^{-1}$	$6.68\cdot10^{-2}$	± $4.65\cdot10^{-2}$
Sediminibacterium	$4.94\cdot10^{-2}$	± $6.91\cdot10^{-2}$	$3.97\cdot10^{-1}$	± $5.66\cdot10^{-1}$	$5.28\cdot10^{-1}$	± $4.54\cdot10^{-1}$	1.47	± 1.56	$2.75\cdot10^{-1}$	± $4.13\cdot10^{-1}$
Planctomyces	1.41	± 1.03	$3.59\cdot10^{-1}$	± $1.31\cdot10^{-1}$	$2.01\cdot10^{-1}$	± $1.58\cdot10^{-1}$	$7.26\cdot10^{-1}$	± 1.02	$6.04\cdot10^{-1}$	± $3.07\cdot10^{-1}$
Diaphorobacter	$1.07\cdot10^{-2}$	± $2.06\cdot10^{-2}$	$1.62\cdot10^{-1}$	± $3.17\cdot10^{-1}$	$2.42\cdot10^{-2}$	± $2.40\cdot10^{-2}$	1.34	± 1.78	$6.43\cdot10^{-2}$	± $3.52\cdot10^{-2}$
Brevundimonas	1.33	± 1.22	$8.90\cdot10^{-1}$	± 1.02	$5.54\cdot10^{-1}$	± $4.26\cdot10^{-1}$	$6.28\cdot10^{-1}$	± $6.25\cdot10^{-1}$	$4.58\cdot10^{-2}$	± $5.39\cdot10^{-2}$
Rhodobacter	1.14	± 1.07	$1.59\cdot10^{-1}$	± $1.65\cdot10^{-1}$	$1.23\cdot10^{-1}$	± $2.02\cdot10^{-1}$	$2.61\cdot10^{-1}$	± $7.84\cdot10^{-2}$	$2.19\cdot10^{-1}$	± $1.74\cdot10^{-1}$
Prosthecobacter	$8.56\cdot10^{-1}$	± 1.08	1.13	± 1.48	$3.29\cdot10^{-1}$	± $2.72\cdot10^{-1}$	$8.55\cdot10^{-1}$	± $6.64\cdot10^{-1}$	$3.22\cdot10^{-1}$	± $1.08\cdot10^{-1}$
Caenimonas	$1.42\cdot10^{-1}$	± $1.68\cdot10^{-1}$	1.12	± 1.61	$5.73\cdot10^{-1}$	± $7.01\cdot10^{-1}$	$1.79\cdot10^{-1}$	± $2.45\cdot10^{-1}$	1.03	± $8.88\cdot10^{-1}$
unknown f: *Comamonadaceae*	$1.50\cdot10^{-1}$	± $1.16\cdot10^{-1}$	$9.43\cdot10^{-1}$	± $4.32\cdot10^{-1}$	$5.75\cdot10^{-1}$	± $3.97\cdot10^{-1}$	1.12	± 1.01	$6.19\cdot10^{-1}$	± $1.51\cdot10^{-1}$
Tessaracoccus	N.D.[f]		$5.53\cdot10^{-3}$	± $5.42\cdot10^{-3}$	1.08	± 1.45	$6.26\cdot10^{-3}$	± $6.24\cdot10^{-3}$	$9.21\cdot10^{-2}$	± $7.01\cdot10^{-2}$

Table S49. Summary of genus-level EUB results continued.

Genus[a,b]	S-EBPR (S44)		V-EBPR (S45)		G-EBPR (S46)		R-EBPR (S47)		Moscow WRRF (S48)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
unknown o: *Flavobacteriales*	$5.47\cdot10^{-1}$	± $3.40\cdot10^{-1}$	$4.99\cdot10^{-1}$	± $6.33\cdot10^{-1}$	$2.35\cdot10^{-1}$	± $1.05\cdot10^{-1}$	$6.81\cdot10^{-1}$	± $3.04\cdot10^{-1}$	1.07	± $2.53\cdot10^{-1}$
Nitrospira	$6.98\cdot10^{-1}$	± $5.17\cdot10^{-1}$	$1.18\cdot10^{-3}$	± $1.52\cdot10^{-3}$	$9.20\cdot10^{-4}$	± $1.28\cdot10^{-3}$	$3.88\cdot10^{-1}$	± $7.42\cdot10^{-1}$	1.06	± $3.14\cdot10^{-1}$
unknown f: *Rhodocyclaceae*	1.05	± 1.30	$5.80\cdot10^{-1}$	± $4.35\cdot10^{-1}$	1.04	± 1.19	$4.26\cdot10^{-1}$	± $2.88\cdot10^{-1}$	$6.26\cdot10^{-1}$	± $3.63\cdot10^{-1}$
unknown f: *Burkholderiales_inc._sed.*[e]	1.05	± 1.54	$5.92\cdot10^{-1}$	± $3.15\cdot10^{-1}$	$3.36\cdot10^{-1}$	± $1.55\cdot10^{-1}$	$6.07\cdot10^{-1}$	± $8.16\cdot10^{-1}$	$4.54\cdot10^{-1}$	± $2.37\cdot10^{-1}$
Leadbetterella	$8.78\cdot10^{-4}$	± $9.30\cdot10^{-4}$	$2.98\cdot10^{-1}$	± $5.23\cdot10^{-1}$	$2.00\cdot10^{-1}$	± $1.25\cdot10^{-1}$	1.02	± 2.05	$7.33\cdot10^{-1}$	± 1.41
Paracoccus	$1.12\cdot10^{-2}$	± $7.06\cdot10^{-3}$	$5.74\cdot10^{-1}$	± $6.51\cdot10^{-1}$	$7.76\cdot10^{-1}$	± $7.10\cdot10^{-1}$	1.02	± $6.39\cdot10^{-1}$	$1.82\cdot10^{-1}$	± $1.19\cdot10^{-1}$
Gp4	$1.71\cdot10^{-1}$	± $1.54\cdot10^{-1}$	$4.09\cdot10^{-1}$	± $5.66\cdot10^{-1}$	$4.30\cdot10^{-1}$	± $7.31\cdot10^{-1}$	1.02	± 1.18	$4.41\cdot10^{-1}$	± $2.63\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$2.63\cdot10^{-1}$	± $3.49\cdot10^{-1}$	1.01	± 1.36	$6.45\cdot10^{-1}$	± $7.39\cdot10^{-1}$	$5.42\cdot10^{-1}$	± $4.49\cdot10^{-1}$	$7.17\cdot10^{-1}$	± $7.93\cdot10^{-1}$
Phenylobacterium	$2.00\cdot10^{-2}$	± $2.65\cdot10^{-2}$	$1.61\cdot10^{-1}$	± $1.04\cdot10^{-1}$	$9.92\cdot10^{-1}$	± 1.11	$1.53\cdot10^{-1}$	± $9.45\cdot10^{-2}$	$9.50\cdot10^{-2}$	± $6.23\cdot10^{-2}$
unknown o: *Myxococcales*	$1.61\cdot10^{-1}$	± $1.15\cdot10^{-1}$	$2.95\cdot10^{-1}$	± $3.25\cdot10^{-1}$	$8.45\cdot10^{-2}$	± $6.90\cdot10^{-2}$	$1.06\cdot10^{-1}$	± $5.55\cdot10^{-2}$	$9.85\cdot10^{-1}$	± $8.05\cdot10^{-1}$
Terrimonas	$4.21\cdot10^{-1}$	± $5.55\cdot10^{-1}$	$1.85\cdot10^{-1}$	± $1.39\cdot10^{-1}$	$7.23\cdot10^{-1}$	± $6.51\cdot10^{-1}$	$4.70\cdot10^{-1}$	± $4.25\cdot10^{-1}$	$9.76\cdot10^{-1}$	± $2.68\cdot10^{-1}$
Trichococcus	$6.67\cdot10^{-4}$	± $8.60\cdot10^{-4}$	$2.51\cdot10^{-1}$	± $1.45\cdot10^{-1}$	$2.95\cdot10^{-1}$	± $1.71\cdot10^{-1}$	$2.27\cdot10^{-1}$	± $1.79\cdot10^{-1}$	$9.49\cdot10^{-1}$	± 1.18
Sulfuritalea	$3.60\cdot10^{-3}$	± $4.49\cdot10^{-3}$	$1.38\cdot10^{-2}$	± $1.73\cdot10^{-2}$	$6.49\cdot10^{-3}$	± $1.01\cdot10^{-2}$	$2.21\cdot10^{-2}$	± $2.95\cdot10^{-2}$	$9.36\cdot10^{-1}$	± $7.30\cdot10^{-1}$
unknown f: *Cytophagaceae*	$6.28\cdot10^{-2}$	± $5.15\cdot10^{-2}$	$5.11\cdot10^{-1}$	± $3.99\cdot10^{-1}$	$9.12\cdot10^{-1}$	± $9.15\cdot10^{-1}$	$8.55\cdot10^{-2}$	± $6.13\cdot10^{-2}$	$4.43\cdot10^{-1}$	± $1.20\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$6.04\cdot10^{-1}$	± $2.47\cdot10^{-1}$	$3.70\cdot10^{-1}$	± $2.02\cdot10^{-1}$	$4.64\cdot10^{-1}$	± $2.69\cdot10^{-1}$	$6.81\cdot10^{-1}$	± $5.61\cdot10^{-1}$	$9.10\cdot10^{-1}$	± $2.11\cdot10^{-1}$
unknown f: *Planctomycetaceae*	$7.99\cdot10^{-1}$	± $5.60\cdot10^{-1}$	$2.40\cdot10^{-1}$	± $1.45\cdot10^{-1}$	$2.39\cdot10^{-1}$	± $2.18\cdot10^{-1}$	$1.62\cdot10^{-1}$	± $1.90\cdot10^{-1}$	$8.81\cdot10^{-1}$	± $2.65\cdot10^{-1}$
Comamonas	$3.61\cdot10^{-2}$	± $7.52\cdot10^{-2}$	$5.11\cdot10^{-2}$	± $3.48\cdot10^{-2}$	$3.63\cdot10^{-2}$	± $4.24\cdot10^{-2}$	$8.75\cdot10^{-1}$	± 1.45	$6.80\cdot10^{-2}$	± $2.89\cdot10^{-2}$
Arcobacter	N.D.[f]		$4.40\cdot10^{-1}$	± $2.89\cdot10^{-1}$	$6.11\cdot10^{-1}$	± $5.14\cdot10^{-1}$	$8.47\cdot10^{-1}$	± $9.87\cdot10^{-1}$	$5.17\cdot10^{-1}$	± $3.72\cdot10^{-1}$
Litorilinea	$3.91\cdot10^{-1}$	± $4.94\cdot10^{-1}$	$2.05\cdot10^{-1}$	± $1.49\cdot10^{-1}$	$2.62\cdot10^{-1}$	± $1.18\cdot10^{-1}$	$2.56\cdot10^{-1}$	± $1.97\cdot10^{-1}$	$7.83\cdot10^{-1}$	± $4.16\cdot10^{-1}$
Roseimicrobium	$2.88\cdot10^{-1}$	± $4.05\cdot10^{-1}$	$7.68\cdot10^{-1}$	± $6.55\cdot10^{-1}$	$2.53\cdot10^{-1}$	± $2.16\cdot10^{-1}$	$9.51\cdot10^{-2}$	± $8.06\cdot10^{-2}$	$3.94\cdot10^{-2}$	± $2.22\cdot10^{-2}$
Nitrosomonas	$6.22\cdot10^{-1}$	± $5.32\cdot10^{-1}$	$1.29\cdot10^{-1}$	± $1.03\cdot10^{-1}$	$1.41\cdot10^{-2}$	± $1.65\cdot10^{-2}$	$5.28\cdot10^{-1}$	± $3.32\cdot10^{-1}$	$7.68\cdot10^{-1}$	± $2.73\cdot10^{-1}$
SR1_genera_inc._sed.[e]	$7.50\cdot10^{-1}$	± 1.84	$2.96\cdot10^{-2}$	± $4.39\cdot10^{-2}$	$4.33\cdot10^{-3}$	± $6.34\cdot10^{-3}$	$1.44\cdot10^{-1}$	± $1.78\cdot10^{-1}$	$3.85\cdot10^{-2}$	± $3.03\cdot10^{-2}$
Ferruginibacter	$4.69\cdot10^{-1}$	± $6.10\cdot10^{-1}$	$3.19\cdot10^{-2}$	± $2.72\cdot10^{-2}$	$3.15\cdot10^{-2}$	± $2.98\cdot10^{-2}$	$2.91\cdot10^{-1}$	± $5.05\cdot10^{-1}$	$7.43\cdot10^{-1}$	± $3.97\cdot10^{-1}$
unknown f: *Prevotellaceae*	$4.83\cdot10^{-3}$	± $1.28\cdot10^{-2}$	$7.22\cdot10^{-1}$	± $9.57\cdot10^{-1}$	$6.78\cdot10^{-3}$	± $7.88\cdot10^{-3}$	$4.14\cdot10^{-3}$	± $5.30\cdot10^{-3}$	$4.87\cdot10^{-3}$	± $5.44\cdot10^{-3}$
Dechloromonas	$1.31\cdot10^{-2}$	± $1.68\cdot10^{-2}$	$2.54\cdot10^{-1}$	± $4.78\cdot10^{-1}$	$4.62\cdot10^{-1}$	± 1.15	$2.25\cdot10^{-1}$	± $1.32\cdot10^{-1}$	$7.21\cdot10^{-1}$	± $5.46\cdot10^{-1}$
Ilumatobacter	$1.22\cdot10^{-1}$	± $1.04\cdot10^{-1}$	$2.23\cdot10^{-1}$	± $1.40\cdot10^{-1}$	$2.86\cdot10^{-1}$	± $2.58\cdot10^{-1}$	$2.76\cdot10^{-1}$	± $1.14\cdot10^{-1}$	$7.16\cdot10^{-1}$	± $4.96\cdot10^{-1}$
Xylanibacter	$9.69\cdot10^{-4}$	± $2.03\cdot10^{-3}$	$7.12\cdot10^{-1}$	± $7.42\cdot10^{-1}$	$3.34\cdot10^{-4}$	± $5.77\cdot10^{-4}$	$1.79\cdot10^{-4}$	± $4.73\cdot10^{-4}$	$2.24\cdot10^{-3}$	± $3.79\cdot10^{-3}$
Opitutus	$2.65\cdot10^{-1}$	± $1.68\cdot10^{-1}$	$3.78\cdot10^{-1}$	± $8.97\cdot10^{-2}$	$3.24\cdot10^{-1}$	± $2.28\cdot10^{-1}$	$6.91\cdot10^{-1}$	± $5.62\cdot10^{-1}$	$2.23\cdot10^{-1}$	± $1.53\cdot10^{-1}$
Hydrogenophaga	$6.85\cdot10^{-1}$	± $6.46\cdot10^{-1}$	$2.48\cdot10^{-1}$	± $5.57\cdot10^{-1}$	$1.49\cdot10^{-1}$	± $1.02\cdot10^{-1}$	$5.30\cdot10^{-2}$	± $5.41\cdot10^{-2}$	$4.56\cdot10^{-2}$	± $3.72\cdot10^{-2}$
unknown f: *Anaerolineaceae*	$2.13\cdot10^{-1}$	± $2.13\cdot10^{-1}$	$4.50\cdot10^{-2}$	± $4.35\cdot10^{-2}$	$1.02\cdot10^{-1}$	± $9.67\cdot10^{-2}$	$4.26\cdot10^{-1}$	± $2.73\cdot10^{-1}$	$6.74\cdot10^{-1}$	± $2.70\cdot10^{-1}$
Mycobacterium	$2.20\cdot10^{-3}$	± $1.99\cdot10^{-3}$	$3.72\cdot10^{-2}$	± $3.38\cdot10^{-2}$	$3.90\cdot10^{-2}$	± $5.87\cdot10^{-2}$	$2.22\cdot10^{-2}$	± $2.48\cdot10^{-2}$	$6.54\cdot10^{-1}$	± $4.59\cdot10^{-1}$

Table S49. Summary of genus-level EUB results continued.

Genus[a,b]	S-EBPR (S44)		V-EBPR (S45)		G-EBPR (S46)		R-EBPR (S47)		Moscow WRRF (S48)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
Bdellovibrio	$3.57\cdot10^{-1}$	$\pm1.74\cdot10^{-1}$	$4.61\cdot10^{-1}$	$\pm2.47\cdot10^{-1}$	$4.57\cdot10^{-1}$	$\pm3.62\cdot10^{-1}$	$6.54\cdot10^{-1}$	$\pm3.99\cdot10^{-1}$	$4.10\cdot10^{-1}$	$\pm1.49\cdot10^{-1}$
unknown o: *Pseudomonadales*	$8.28\cdot10^{-4}$	$\pm1.05\cdot10^{-3}$	$4.68\cdot10^{-1}$	$\pm3.06\cdot10^{-1}$	$8.31\cdot10^{-2}$	$\pm1.35\cdot10^{-1}$	$6.22\cdot10^{-1}$	±1.25	$3.19\cdot10^{-1}$	$\pm6.40\cdot10^{-1}$
Clostridium sensu stricto	$5.83\cdot10^{-1}$	±1.54	$4.79\cdot10^{-2}$	$\pm3.30\cdot10^{-2}$	$6.26\cdot10^{-2}$	$\pm1.27\cdot10^{-1}$	$3.60\cdot10^{-2}$	$\pm3.38\cdot10^{-2}$	$1.06\cdot10^{-1}$	$\pm5.33\cdot10^{-2}$
Subdivision3_genera_inc._sed.[e]	$5.41\cdot10^{-2}$	$\pm2.87\cdot10^{-2}$	$4.49\cdot10^{-2}$	$\pm4.67\cdot10^{-2}$	$2.22\cdot10^{-2}$	$\pm2.19\cdot10^{-2}$	$3.71\cdot10^{-2}$	$\pm4.68\cdot10^{-2}$	$5.74\cdot10^{-1}$	$\pm2.83\cdot10^{-1}$
unknown	$5.59\cdot10^{-1}$	$\pm3.46\cdot10^{-1}$	$1.03\cdot10^{-1}$	$\pm9.74\cdot10^{-2}$	$1.47\cdot10^{-1}$	$\pm5.49\cdot10^{-2}$	$1.33\cdot10^{-1}$	$\pm1.23\cdot10^{-1}$	$3.40\cdot10^{-1}$	$\pm7.88\cdot10^{-2}$
Armatimonadetes_gp5	$5.55\cdot10^{-1}$	$\pm5.26\cdot10^{-1}$	$4.04\cdot10^{-2}$	$\pm4.68\cdot10^{-2}$	$5.86\cdot10^{-2}$	$\pm4.92\cdot10^{-2}$	$2.04\cdot10^{-1}$	$\pm3.80\cdot10^{-1}$	$5.37\cdot10^{-2}$	$\pm1.46\cdot10^{-2}$
unknown f: *Polyangiaceae*	$2.87\cdot10^{-1}$	$\pm4.35\cdot10^{-1}$	$2.78\cdot10^{-1}$	$\pm3.29\cdot10^{-1}$	$6.65\cdot10^{-2}$	$\pm6.16\cdot10^{-2}$	$7.32\cdot10^{-2}$	$\pm7.58\cdot10^{-2}$	$5.54\cdot10^{-1}$	$\pm4.05\cdot10^{-1}$
Prevotella	$2.06\cdot10^{-2}$	$\pm5.46\cdot10^{-2}$	$5.53\cdot10^{-1}$	$\pm4.25\cdot10^{-1}$	$2.69\cdot10^{-2}$	$\pm3.28\cdot10^{-2}$	$1.54\cdot10^{-2}$	$\pm1.46\cdot10^{-2}$	$1.59\cdot10^{-2}$	$\pm6.05\cdot10^{-3}$
unknown f: *Cryomorphaceae*	$4.52\cdot10^{-2}$	$\pm5.00\cdot10^{-2}$	$2.26\cdot10^{-1}$	$\pm3.35\cdot10^{-1}$	$8.15\cdot10^{-2}$	$\pm3.88\cdot10^{-2}$	$5.51\cdot10^{-1}$	$\pm3.82\cdot10^{-1}$	$1.52\cdot10^{-1}$	$\pm5.64\cdot10^{-2}$
Bacteriovorax	$2.04\cdot10^{-3}$	$\pm1.81\cdot10^{-3}$	$2.72\cdot10^{-1}$	$\pm4.76\cdot10^{-1}$	$5.40\cdot10^{-1}$	±1.07	$1.12\cdot10^{-1}$	$\pm2.57\cdot10^{-1}$	$4.77\cdot10^{-2}$	$\pm2.70\cdot10^{-2}$
Chryseobacterium	$1.84\cdot10^{-2}$	$\pm4.00\cdot10^{-2}$	$2.76\cdot10^{-2}$	$\pm3.34\cdot10^{-2}$	$2.94\cdot10^{-2}$	$\pm6.02\cdot10^{-2}$	$5.66\cdot10^{-2}$	$\pm5.39\cdot10^{-2}$	$5.38\cdot10^{-1}$	±1.25
Aquabacterium	$2.83\cdot10^{-3}$	$\pm4.44\cdot10^{-3}$	$4.40\cdot10^{-1}$	±1.03	$5.23\cdot10^{-1}$	±1.34	$7.68\cdot10^{-3}$	$\pm1.25\cdot10^{-2}$	$1.59\cdot10^{-1}$	$\pm1.11\cdot10^{-1}$
Byssovorax	$1.18\cdot10^{-1}$	$\pm1.16\cdot10^{-1}$	$5.02\cdot10^{-1}$	$\pm8.61\cdot10^{-1}$	$6.51\cdot10^{-2}$	$\pm8.26\cdot10^{-2}$	$1.30\cdot10^{-2}$	$\pm1.16\cdot10^{-2}$	$1.61\cdot10^{-1}$	$\pm2.03\cdot10^{-1}$
Sideroxydans	$5.19\cdot10^{-2}$	$\pm7.34\cdot10^{-2}$	$3.27\cdot10^{-2}$	$\pm5.82\cdot10^{-2}$	$1.23\cdot10^{-2}$	$\pm3.11\cdot10^{-2}$	$5.01\cdot10^{-1}$	$\pm5.40\cdot10^{-1}$	$1.02\cdot10^{-3}$	$\pm1.43\cdot10^{-3}$
Sphingomonas	$4.12\cdot10^{-2}$	$\pm3.64\cdot10^{-2}$	$4.95\cdot10^{-1}$	$\pm8.17\cdot10^{-1}$	$1.64\cdot10^{-1}$	$\pm1.99\cdot10^{-1}$	$3.31\cdot10^{-1}$	$\pm4.94\cdot10^{-1}$	$3.91\cdot10^{-1}$	$\pm2.17\cdot10^{-1}$
Azospira	$4.95\cdot10^{-1}$	$\pm4.14\cdot10^{-1}$	$6.10\cdot10^{-4}$	$\pm1.15\cdot10^{-3}$	$9.13\cdot10^{-3}$	$\pm1.25\cdot10^{-2}$	$6.68\cdot10^{-4}$	$\pm8.47\cdot10^{-4}$	$2.38\cdot10^{-1}$	$\pm1.01\cdot10^{-1}$
Schlesneria	$1.55\cdot10^{-1}$	$\pm1.39\cdot10^{-1}$	$4.18\cdot10^{-1}$	$\pm7.49\cdot10^{-1}$	$1.52\cdot10^{-1}$	$\pm1.95\cdot10^{-1}$	$4.91\cdot10^{-1}$	±1.03	$2.78\cdot10^{-1}$	$\pm1.32\cdot10^{-1}$
Pirellula	$4.80\cdot10^{-1}$	$\pm4.93\cdot10^{-1}$	$1.31\cdot10^{-1}$	$\pm2.02\cdot10^{-1}$	$1.42\cdot10^{-1}$	$\pm2.68\cdot10^{-1}$	$9.19\cdot10^{-2}$	$\pm1.59\cdot10^{-1}$	$4.86\cdot10^{-1}$	$\pm2.30\cdot10^{-1}$
unknown f: *Sphingobacteriaceae*	$1.18\cdot10^{-1}$	$\pm1.32\cdot10^{-1}$	$7.77\cdot10^{-3}$	$\pm9.44\cdot10^{-3}$	$4.83\cdot10^{-1}$	±1.21	$1.36\cdot10^{-1}$	$\pm2.27\cdot10^{-1}$	$8.81\cdot10^{-2}$	$\pm7.70\cdot10^{-2}$
Gemmata	$2.12\cdot10^{-2}$	$\pm3.41\cdot10^{-2}$	$2.12\cdot10^{-2}$	$\pm3.12\cdot10^{-2}$	$7.82\cdot10^{-3}$	$\pm1.15\cdot10^{-2}$	$2.30\cdot10^{-2}$	$\pm3.16\cdot10^{-2}$	$4.79\cdot10^{-1}$	$\pm3.49\cdot10^{-1}$
Acidovorax	$7.14\cdot10^{-2}$	$\pm7.61\cdot10^{-2}$	$3.20\cdot10^{-1}$	$\pm3.91\cdot10^{-1}$	$1.63\cdot10^{-1}$	$\pm7.90\cdot10^{-2}$	$9.34\cdot10^{-2}$	$\pm8.61\cdot10^{-2}$	$4.75\cdot10^{-1}$	$\pm3.00\cdot10^{-1}$
Parabacteroides	$9.05\cdot10^{-3}$	$\pm2.34\cdot10^{-2}$	$4.63\cdot10^{-1}$	$\pm4.71\cdot10^{-1}$	$3.13\cdot10^{-1}$	$\pm6.69\cdot10^{-1}$	$6.72\cdot10^{-2}$	$\pm5.55\cdot10^{-2}$	$1.12\cdot10^{-1}$	$\pm2.06\cdot10^{-2}$
Luteimonas	$1.63\cdot10^{-2}$	$\pm1.70\cdot10^{-2}$	$4.08\cdot10^{-1}$	±1.07	$1.94\cdot10^{-1}$	$\pm4.98\cdot10^{-1}$	$4.55\cdot10^{-1}$	$\pm3.37\cdot10^{-1}$	$1.48\cdot10^{-2}$	$\pm1.28\cdot10^{-2}$
Caulobacter	$4.32\cdot10^{-1}$	$\pm7.13\cdot10^{-1}$	$5.63\cdot10^{-2}$	$\pm5.92\cdot10^{-2}$	$1.29\cdot10^{-1}$	$\pm5.73\cdot10^{-2}$	$3.73\cdot10^{-2}$	$\pm3.04\cdot10^{-2}$	$7.69\cdot10^{-2}$	$\pm7.02\cdot10^{-2}$
Perlucidibaca	$1.75\cdot10^{-4}$	$\pm4.62\cdot10^{-4}$	$4.27\cdot10^{-1}$	±1.02	$2.60\cdot10^{-2}$	$\pm2.54\cdot10^{-2}$	$9.48\cdot10^{-2}$	$\pm2.06\cdot10^{-1}$	$9.28\cdot10^{-2}$	$\pm1.12\cdot10^{-1}$
unknown f: *Verrucomicrobiaceae*	$1.10\cdot10^{-1}$	$\pm1.25\cdot10^{-1}$	$4.03\cdot10^{-1}$	$\pm5.71\cdot10^{-1}$	$2.89\cdot10^{-1}$	$\pm2.63\cdot10^{-1}$	$1.05\cdot10^{-1}$	$\pm1.07\cdot10^{-1}$	$7.09\cdot10^{-2}$	$\pm1.75\cdot10^{-2}$
Mesorhizobium	$3.98\cdot10^{-1}$	$\pm3.06\cdot10^{-1}$	$2.21\cdot10^{-1}$	$\pm2.79\cdot10^{-1}$	$2.59\cdot10^{-1}$	$\pm4.05\cdot10^{-1}$	$1.66\cdot10^{-1}$	$\pm1.28\cdot10^{-1}$	$7.46\cdot10^{-2}$	$\pm4.31\cdot10^{-2}$
unknown p: *Chloroflexi*	$3.91\cdot10^{-1}$	$\pm3.58\cdot10^{-1}$	$1.49\cdot10^{-1}$	$\pm9.47\cdot10^{-2}$	$1.15\cdot10^{-1}$	$\pm1.23\cdot10^{-1}$	$7.17\cdot10^{-2}$	$\pm3.52\cdot10^{-2}$	$2.44\cdot10^{-1}$	$\pm9.32\cdot10^{-2}$
Niabella	$2.32\cdot10^{-1}$	$\pm2.21\cdot10^{-1}$	$1.42\cdot10^{-2}$	$\pm2.34\cdot10^{-2}$	$3.84\cdot10^{-1}$	$\pm8.21\cdot10^{-1}$	$4.37\cdot10^{-3}$	$\pm5.98\cdot10^{-3}$	$1.30\cdot10^{-2}$	$\pm1.03\cdot10^{-2}$
Alicycliphilus	$8.96\cdot10^{-3}$	$\pm1.21\cdot10^{-2}$	$1.31\cdot10^{-1}$	$\pm1.53\cdot10^{-1}$	$2.52\cdot10^{-2}$	$\pm2.01\cdot10^{-2}$	$3.71\cdot10^{-1}$	$\pm4.35\cdot10^{-1}$	$4.82\cdot10^{-2}$	$\pm1.69\cdot10^{-2}$
Magnetospira	$1.01\cdot10^{-2}$	$\pm9.37\cdot10^{-3}$	$2.32\cdot10^{-2}$	$\pm3.44\cdot10^{-2}$	$6.46\cdot10^{-2}$	$\pm1.54\cdot10^{-1}$	$3.68\cdot10^{-1}$	$\pm5.61\cdot10^{-1}$	$9.41\cdot10^{-4}$	$\pm7.71\cdot10^{-4}$
Pseudofulvimonas	$3.16\cdot10^{-2}$	$\pm3.57\cdot10^{-2}$	N.D.[f]		$4.89\cdot10^{-2}$	$\pm1.01\cdot10^{-1}$	$3.60\cdot10^{-1}$	$\pm9.53\cdot10^{-1}$	$1.37\cdot10^{-3}$	$\pm8.63\cdot10^{-4}$
Blastocatella	$2.38\cdot10^{-1}$	$\pm2.31\cdot10^{-1}$	$3.60\cdot10^{-1}$	$\pm6.88\cdot10^{-1}$	$1.95\cdot10^{-1}$	$\pm1.82\cdot10^{-1}$	$2.25\cdot10^{-1}$	$\pm2.49\cdot10^{-1}$	$7.22\cdot10^{-2}$	$\pm7.07\cdot10^{-2}$

Table S49. Summary of genus-level EUB results continued.

Genus[a,b]	S-EBPR (S44)		V-EBPR (S45)		G-EBPR (S46)		R-EBPR (S47)		Moscow WRRF (S48)	
	Average ±	SD[c]	Average ±	SD[c]	Average ±	SD[c]	Average ±	SD[c]	Average ±	SD[c]
	%		%		%		%		%	
unknown f: *Cyclobacteriaceae*	$1.53\cdot10^{-2}$	$\pm 1.02\cdot10^{-2}$	$2.73\cdot10^{-2}$	$\pm 5.24\cdot10^{-2}$	$3.57\cdot10^{-1}$	$\pm 9.01\cdot10^{-1}$	$6.37\cdot10^{-2}$	$\pm 8.59\cdot10^{-2}$	$3.54\cdot10^{-2}$	$\pm 1.29\cdot10^{-2}$
Alkanindiges	$2.47\cdot10^{-4}$	$\pm 6.54\cdot10^{-4}$	$3.19\cdot10^{-1}$	$\pm 4.81\cdot10^{-1}$	$5.54\cdot10^{-3}$	$\pm 6.01\cdot10^{-3}$	$7.75\cdot10^{-3}$	$\pm 4.90\cdot10^{-3}$	$1.26\cdot10^{-2}$	$\pm 6.73\cdot10^{-3}$
Altererythrobacter	$3.04\cdot10^{-1}$	$\pm 5.62\cdot10^{-1}$	$1.37\cdot10^{-1}$	$\pm 3.12\cdot10^{-1}$	$2.28\cdot10^{-1}$	$\pm 5.57\cdot10^{-1}$	$7.70\cdot10^{-2}$	$\pm 1.96\cdot10^{-1}$	$2.04\cdot10^{-3}$	$\pm 1.63\cdot10^{-3}$
Fimbriimonas	$2.93\cdot10^{-1}$	$\pm 3.92\cdot10^{-1}$	$1.36\cdot10^{-2}$	$\pm 1.54\cdot10^{-2}$	$2.34\cdot10^{-2}$	$\pm 3.84\cdot10^{-2}$	$2.13\cdot10^{-2}$	$\pm 2.90\cdot10^{-2}$	$1.19\cdot10^{-2}$	$\pm 7.92\cdot10^{-3}$
Leptothrix	$5.70\cdot10^{-4}$	$\pm 1.09\cdot10^{-3}$	$9.52\cdot10^{-3}$	$\pm 8.75\cdot10^{-3}$	$2.92\cdot10^{-1}$	$\pm 5.41\cdot10^{-1}$	$3.49\cdot10^{-3}$	$\pm 4.88\cdot10^{-3}$	$5.41\cdot10^{-2}$	$\pm 7.02\cdot10^{-2}$
Aeromonas	$3.55\cdot10^{-2}$	$\pm 9.33\cdot10^{-2}$	$5.32\cdot10^{-2}$	$\pm 3.01\cdot10^{-2}$	$3.68\cdot10^{-2}$	$\pm 2.71\cdot10^{-2}$	$2.85\cdot10^{-1}$	$\pm 6.06\cdot10^{-1}$	$8.11\cdot10^{-2}$	$\pm 2.42\cdot10^{-2}$
Filomicrobium	$3.58\cdot10^{-3}$	$\pm 3.15\cdot10^{-3}$	$1.52\cdot10^{-2}$	$\pm 1.54\cdot10^{-2}$	$2.71\cdot10^{-1}$	$\pm 4.64\cdot10^{-1}$	$1.12\cdot10^{-2}$	$\pm 5.48\cdot10^{-3}$	$6.90\cdot10^{-3}$	$\pm 3.83\cdot10^{-3}$
Verrucomicrobium	$3.70\cdot10^{-3}$	$\pm 3.21\cdot10^{-3}$	$2.26\cdot10^{-1}$	$\pm 4.47\cdot10^{-1}$	$2.85\cdot10^{-2}$	$\pm 2.66\cdot10^{-2}$	$4.16\cdot10^{-2}$	$\pm 2.11\cdot10^{-2}$	$8.69\cdot10^{-2}$	$\pm 6.57\cdot10^{-2}$
Persicitalea	$2.09\cdot10^{-1}$	$\pm 3.86\cdot10^{-1}$	$1.10\cdot10^{-1}$	$\pm 4.81\cdot10^{-2}$	$1.11\cdot10^{-1}$	$\pm 1.03\cdot10^{-1}$	$2.94\cdot10^{-2}$	$\pm 3.71\cdot10^{-2}$	$6.15\cdot10^{-4}$	$\pm 5.87\cdot10^{-4}$
unknown f: *Pseudomonadaceae*	$2.32\cdot10^{-2}$	$\pm 2.78\cdot10^{-2}$	$2.84\cdot10^{-2}$	$\pm 3.04\cdot10^{-2}$	$1.28\cdot10^{-2}$	$\pm 1.72\cdot10^{-2}$	$1.84\cdot10^{-2}$	$\pm 1.71\cdot10^{-2}$	$2.00\cdot10^{-1}$	$\pm 3.72\cdot10^{-1}$
Carnobacterium	$1.86\cdot10^{-1}$	$\pm 4.85\cdot10^{-1}$	N.D.[f]		$1.89\cdot10^{-4}$	$\pm 5.01\cdot10^{-4}$	N.D.[f]		$3.56\cdot10^{-4}$	$\pm 9.42\cdot10^{-4}$
Spartobacteria_genera_inc._sed.[e]	$1.61\cdot10^{-4}$	$\pm 4.26\cdot10^{-4}$	$1.01\cdot10^{-1}$	$\pm 1.60\cdot10^{-1}$	$7.76\cdot10^{-2}$	$\pm 1.20\cdot10^{-1}$	$1.74\cdot10^{-1}$	$\pm 3.76\cdot10^{-1}$	$2.66\cdot10^{-2}$	$\pm 2.40\cdot10^{-2}$
Proteocatella	$4.83\cdot10^{-4}$	$\pm 1.28\cdot10^{-3}$	$8.56\cdot10^{-3}$	$\pm 1.31\cdot10^{-2}$	$1.70\cdot10^{-1}$	$\pm 3.97\cdot10^{-1}$	$2.10\cdot10^{-2}$	$\pm 3.66\cdot10^{-2}$	$2.98\cdot10^{-3}$	$\pm 2.23\cdot10^{-3}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] N.D. = Not detected.

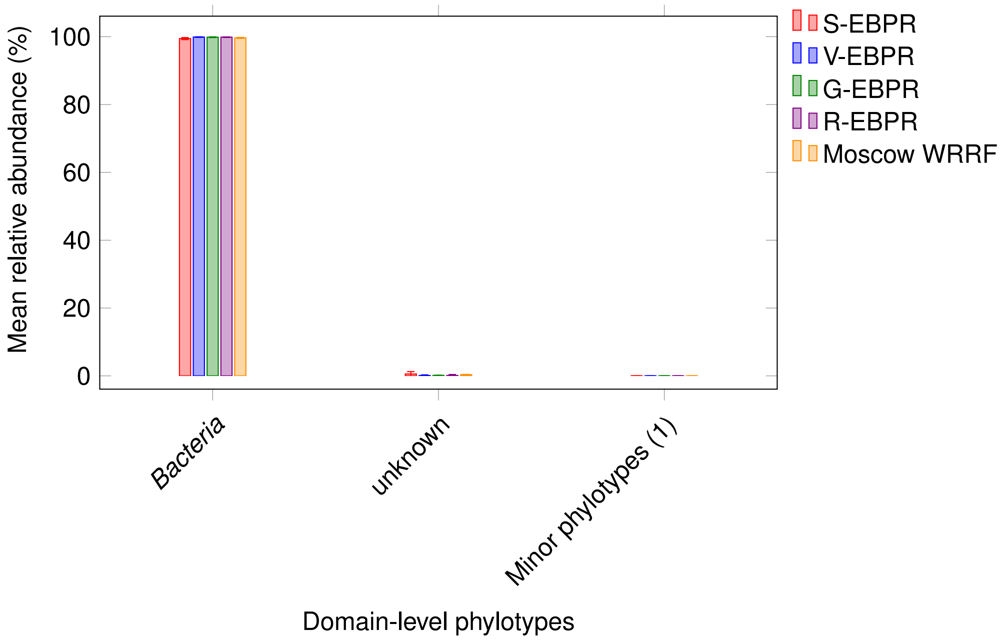

Figure S54. Mean relative abundance for phylotypes identified using the EUB primer set at the domain level (see Tables S14 to S18). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the domain level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

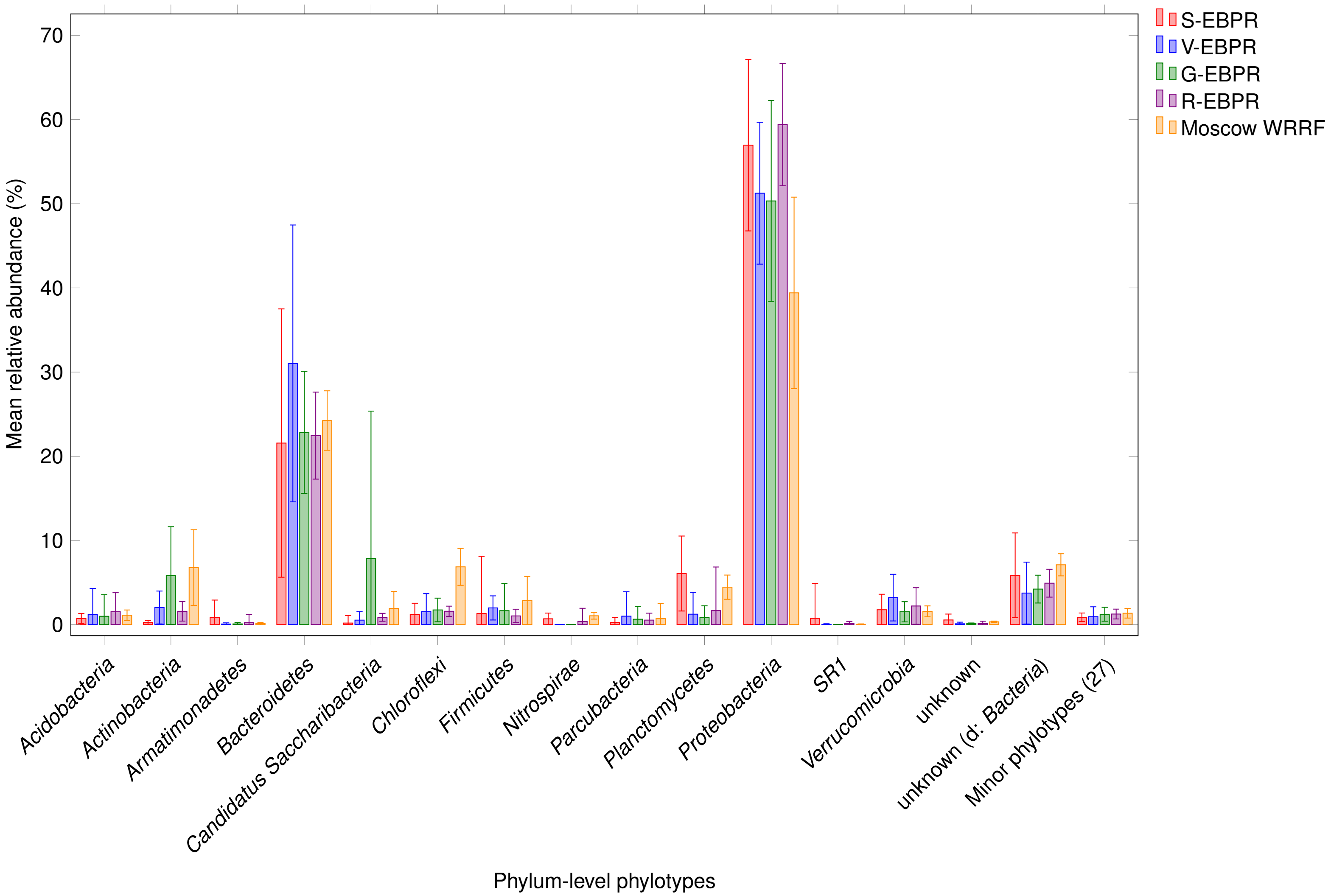

Figure S55. Mean relative abundance for phylotypes identified using the EUB primer set at the phylum level (see Tables S20 to S24). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the phylum level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

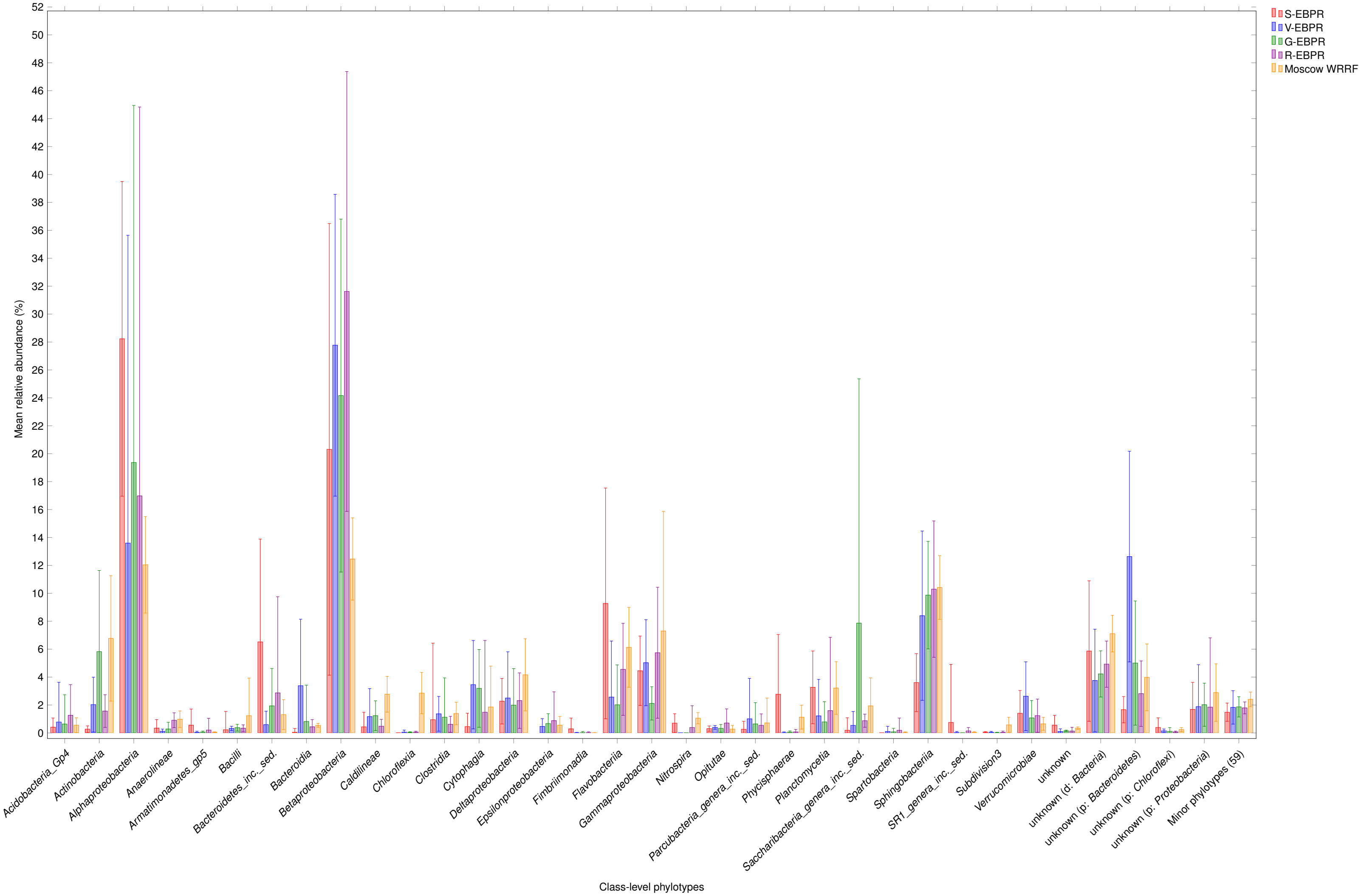

Figure S56. Mean relative abundance for phylotypes identified using the EUB primer set at the class level (see Tables S26 to S30). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the class level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

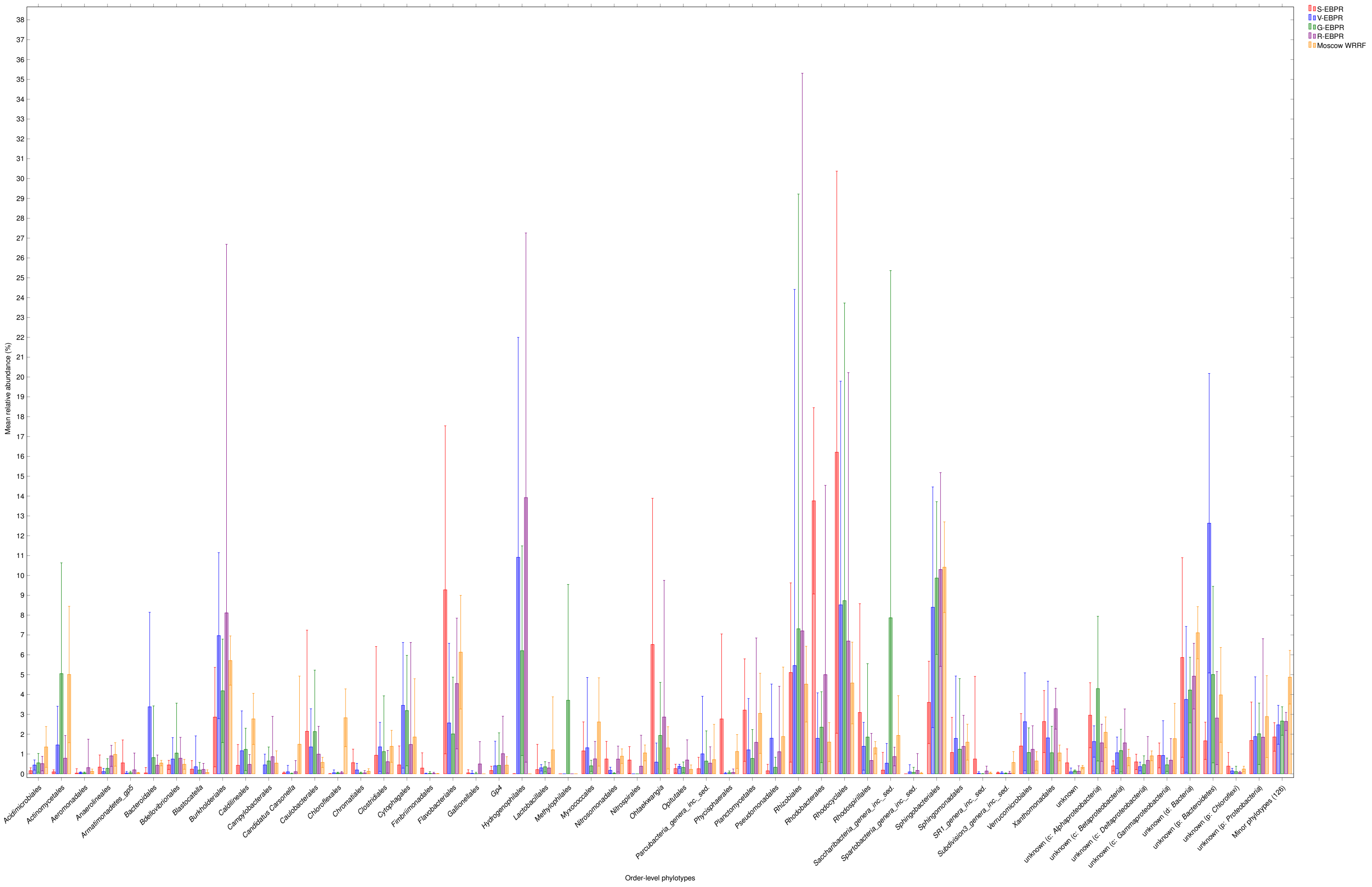

Figure S57. Mean relative abundance for phylotypes identified using the EUB primer set at the order level (see Tables S32 to S36). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the order level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

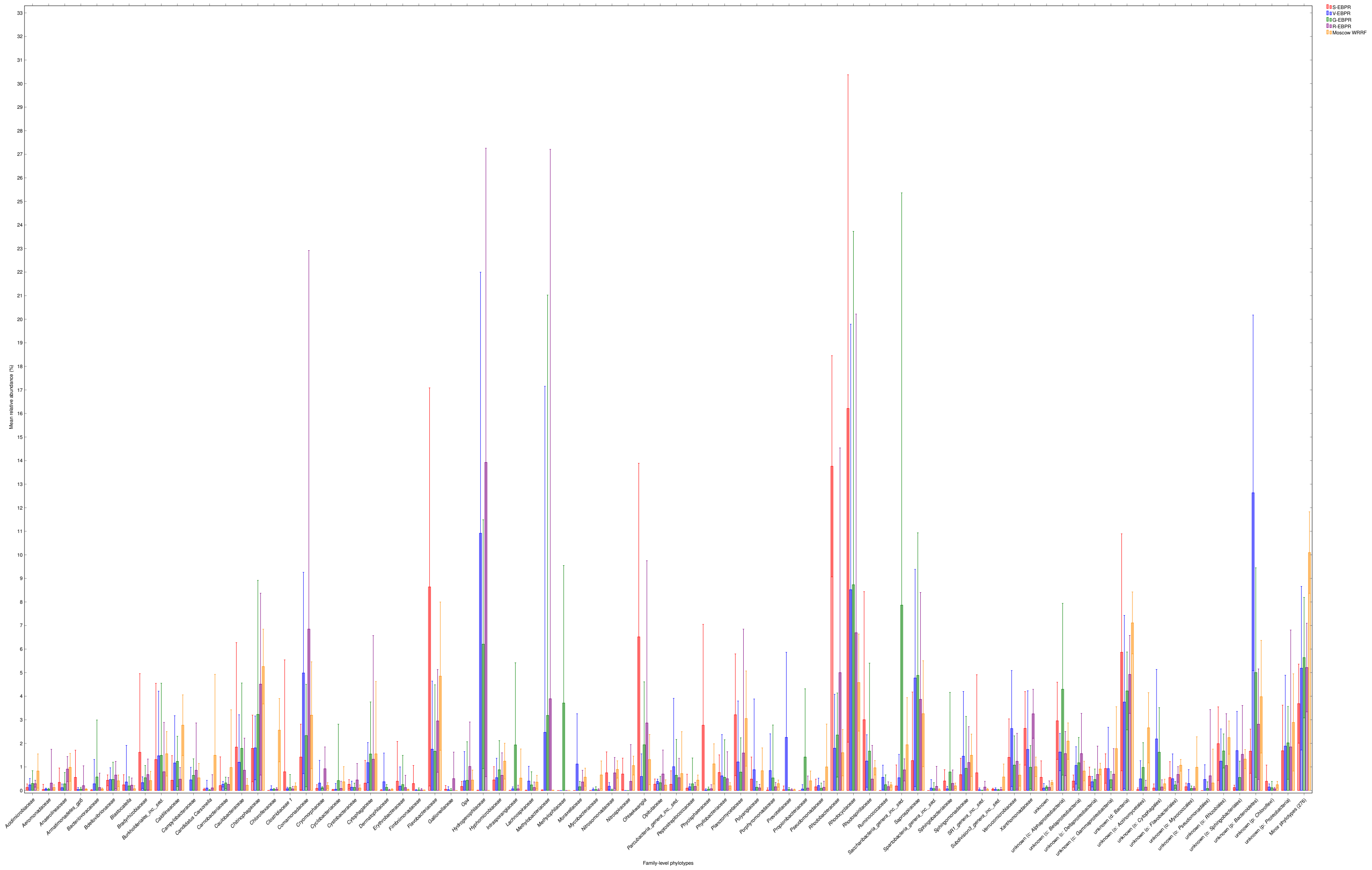

Figure S58. Mean relative abundance for phylotypes identified using the EUB primer set at the family level (see Tables S38 to S42). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the family level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

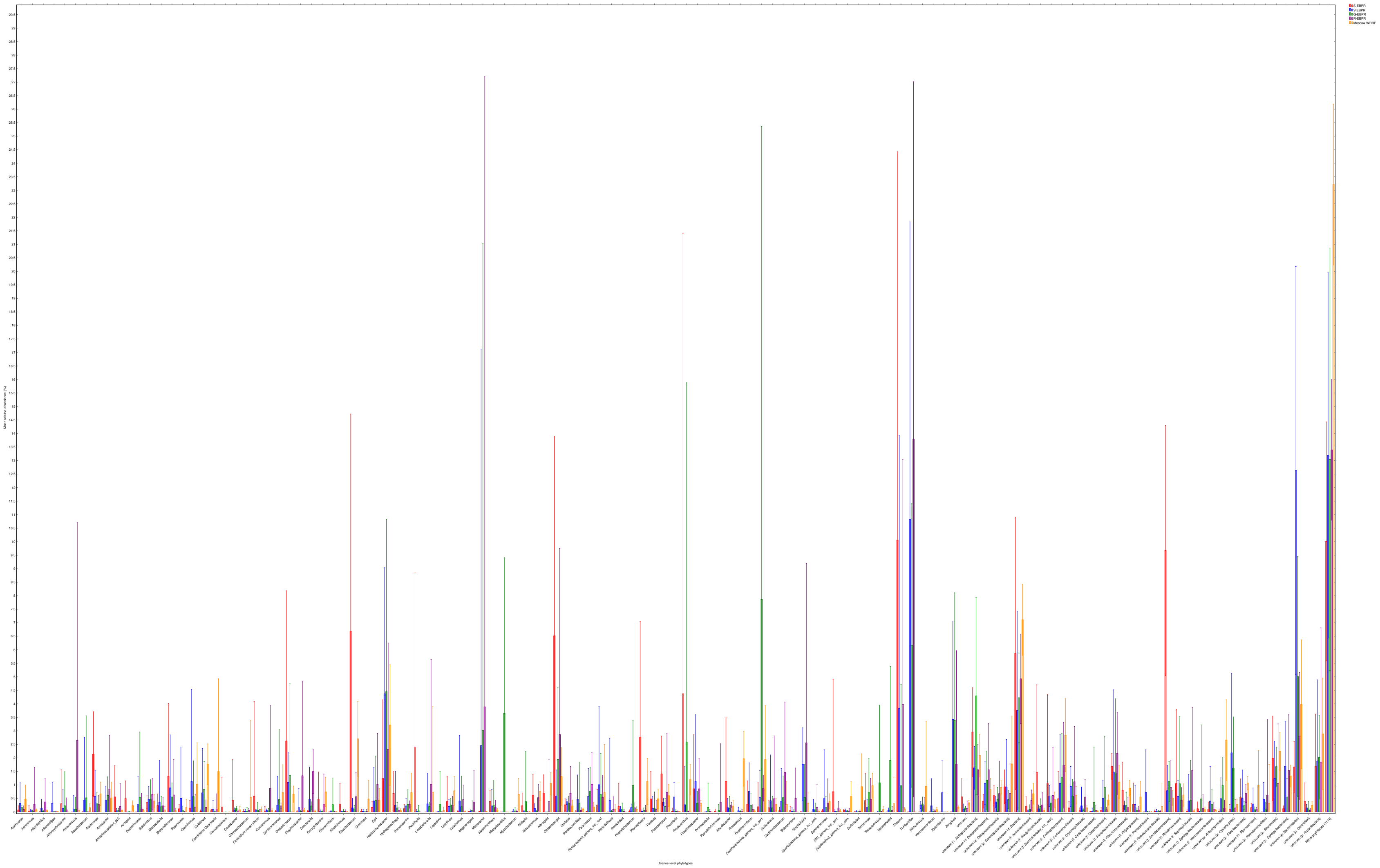

Figure S59. Mean relative abundance for phylotypes identified using the EUB primer set at the genus level (see Tables S44 to S48). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the genus level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

Heatmaps

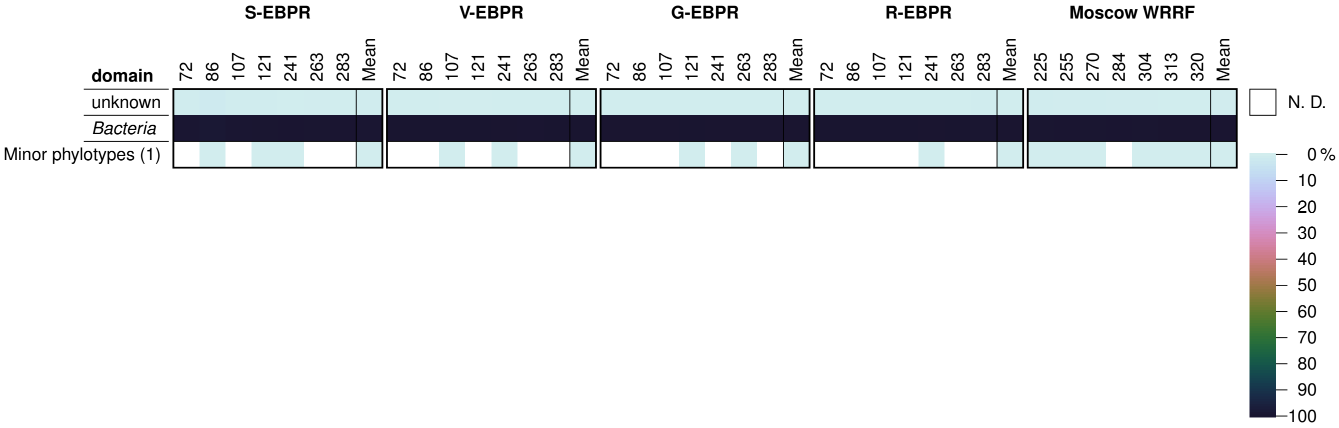

Figure S60. Heat map showing the relative abundance of phylotypes identified at the domain level using the EUB primer set (see Tables S14 to S18). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "∗" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

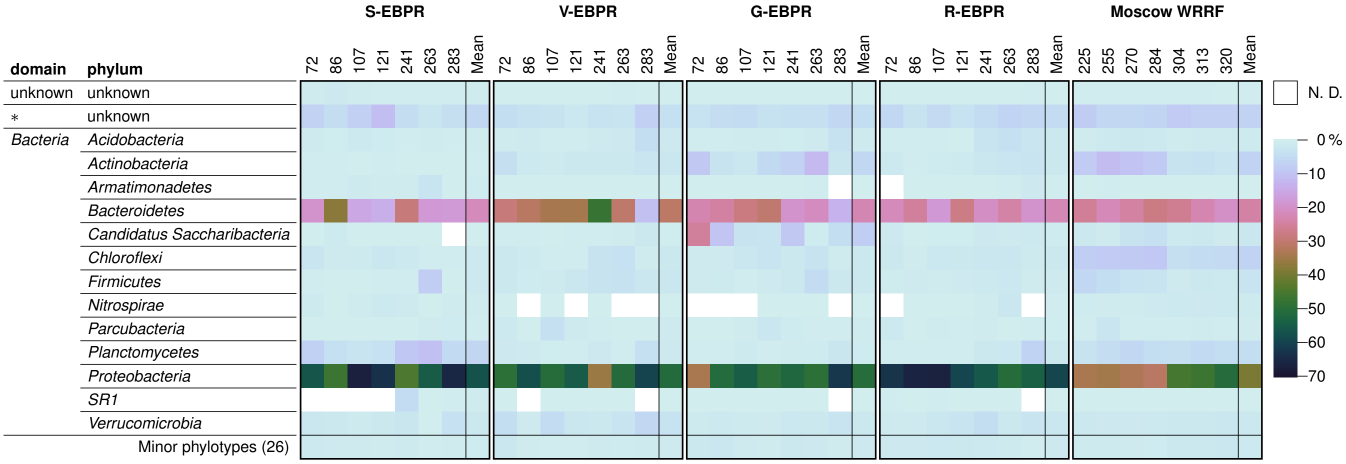

Figure S61. Heat map showing the relative abundance of phylotypes identified at the phylum level using the EUB primer set (see Tables S20 to S24). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "∗" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

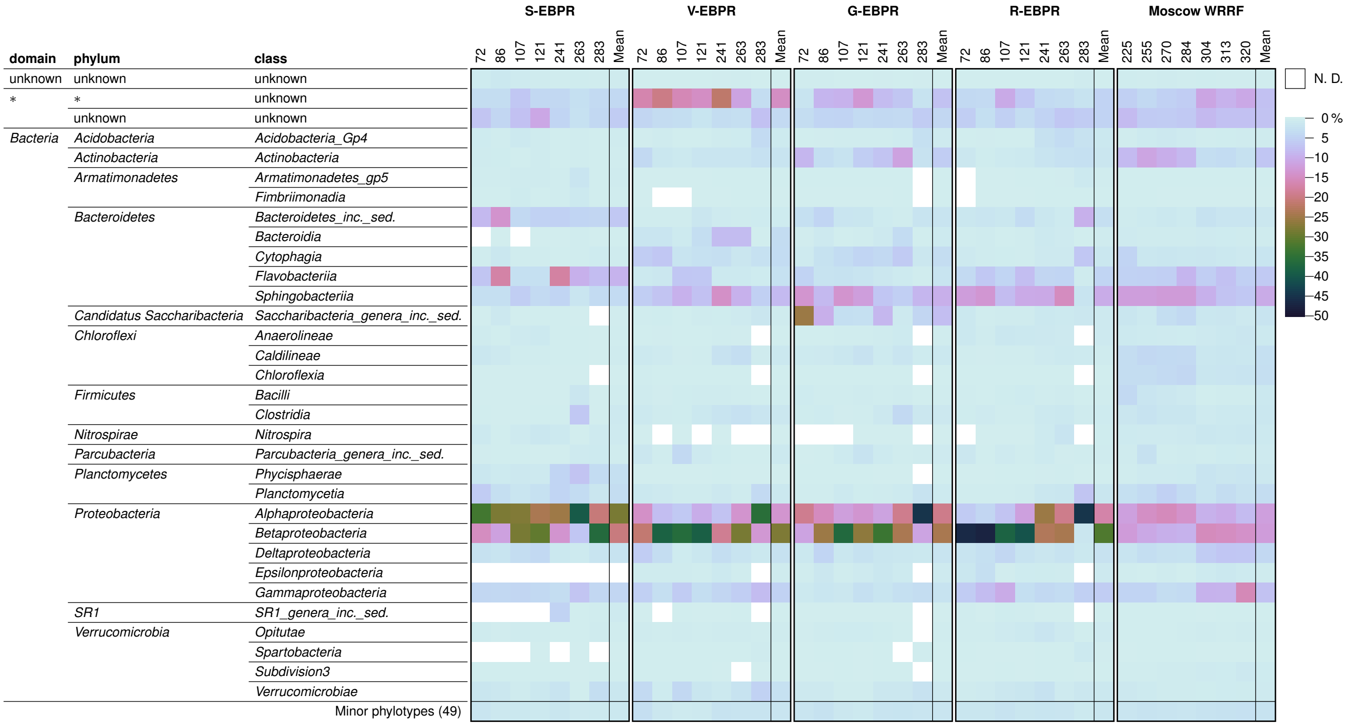

Figure S62. Heat map showing the relative abundance of phylotypes identified at the class level using the EUB primer set (see Tables S26 to S30). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

Figure S63. Heat map showing the relative abundance of phylotypes identified at the order level using the EUB primer set (see Tables S32 to S36). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as “unknown”) were aggregated by the most specific taxonomic level at which they were identified (the “*” is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted “Minor phylotypes” at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the line has been omitted.

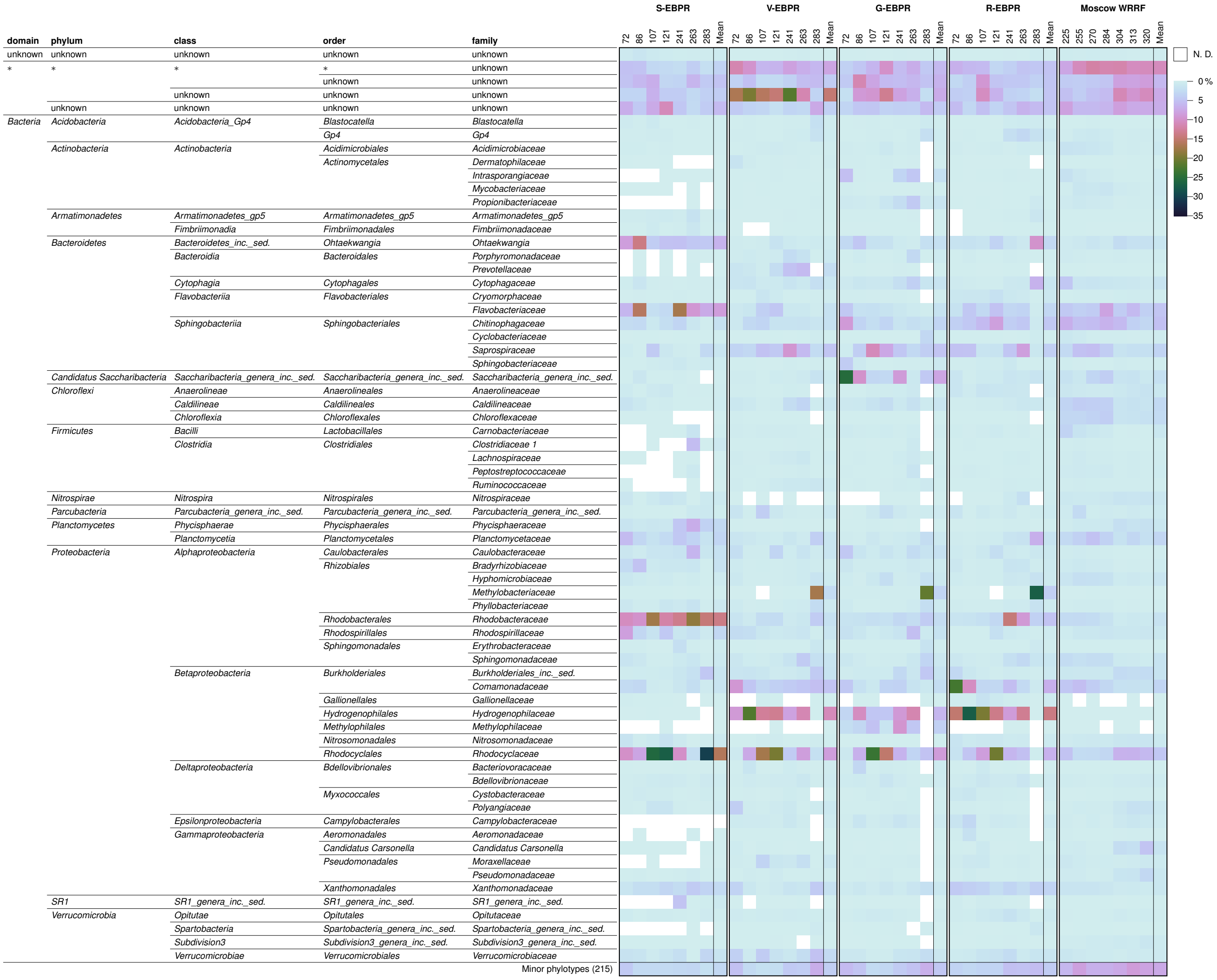

Figure S64. Heat map showing the relative abundance of phylotypes identified at the family level using the EUB primer set (see Tables S38 to S42). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

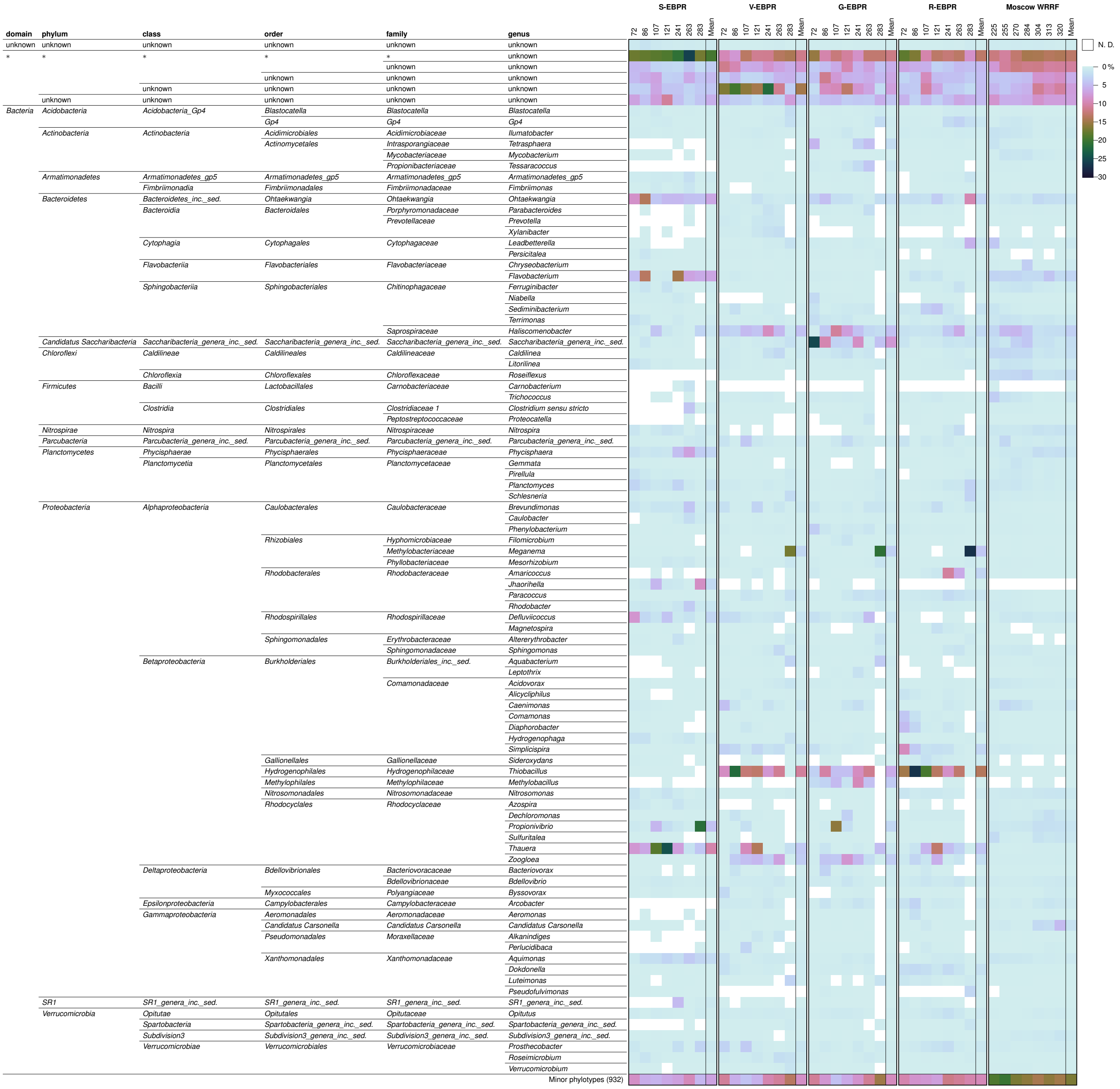

Figure S65. Heat map showing the relative abundance of phylotypes identified at the genus level using the EUB primer set (see Tables S44 to S48). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

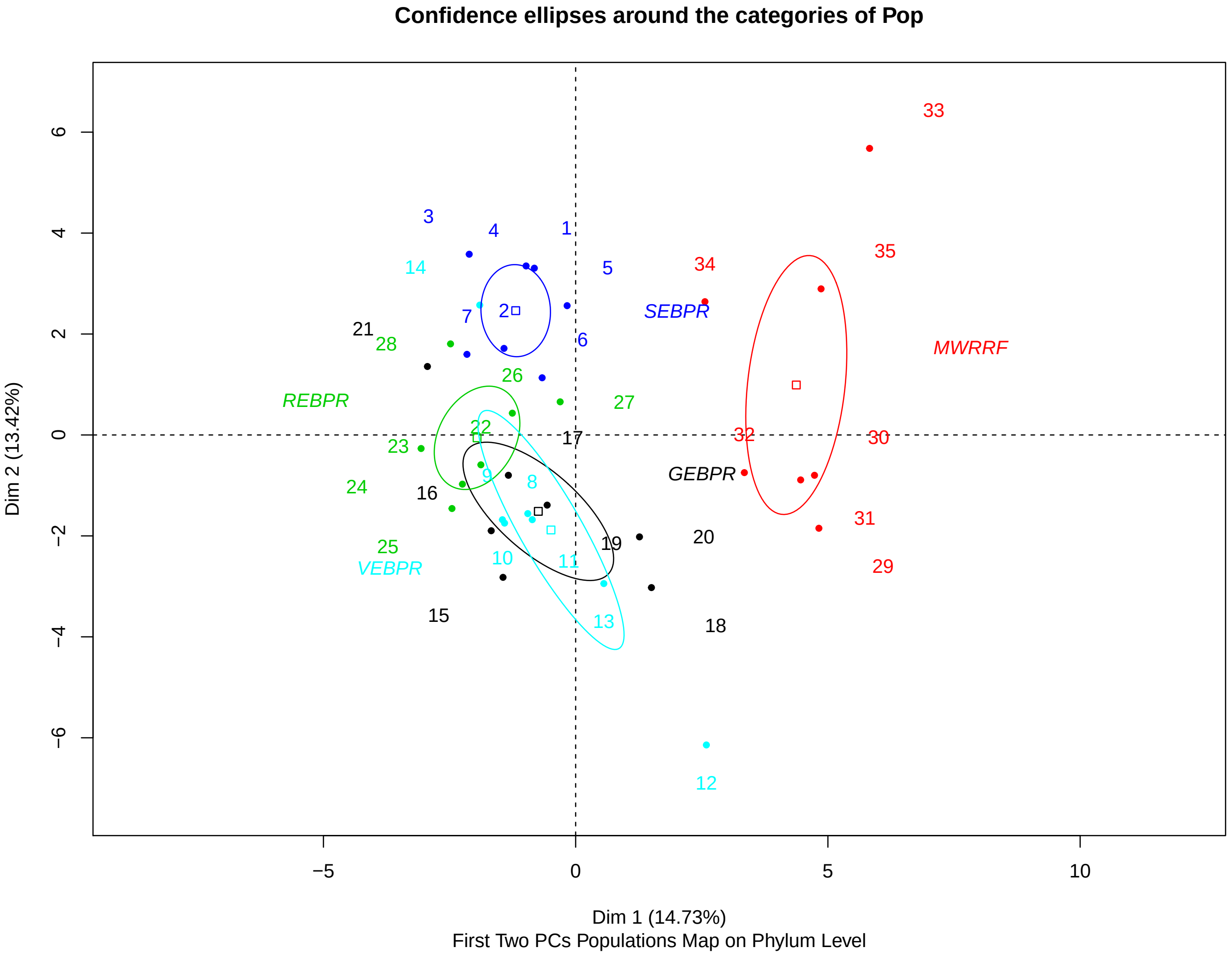

Figure S66. Bivariate plot of the first two principal component (Dim 1 and Dim 2) scores for the 16S rRNA gene sequencing results using the EUB primer set at the phylum level and the P removed. Samples have been grouped by system (distinguished by color) with the numbers corresponding to their index in an ordered list (i.e., sorted by operational day following an arbitrary system ordering: 1 to 7 are S-EBPR operational days 72 to 283; 8 to 14 are V-EBPR operational days 72 to 283; 15 to 21 are G-EBPR operational days 72 to 283; 22 to 28 are R-EBPR operational days 72 to 283; and 29 to 35 are Moscow WRRF operational days 225 to 320). The centroid for each group in the Dim 1-Dim 2 space is depicted as a square in the associated color and the ellipses denote the 95 % confidence regions for the associated centroids in the Dim 1-Dim 2 space.

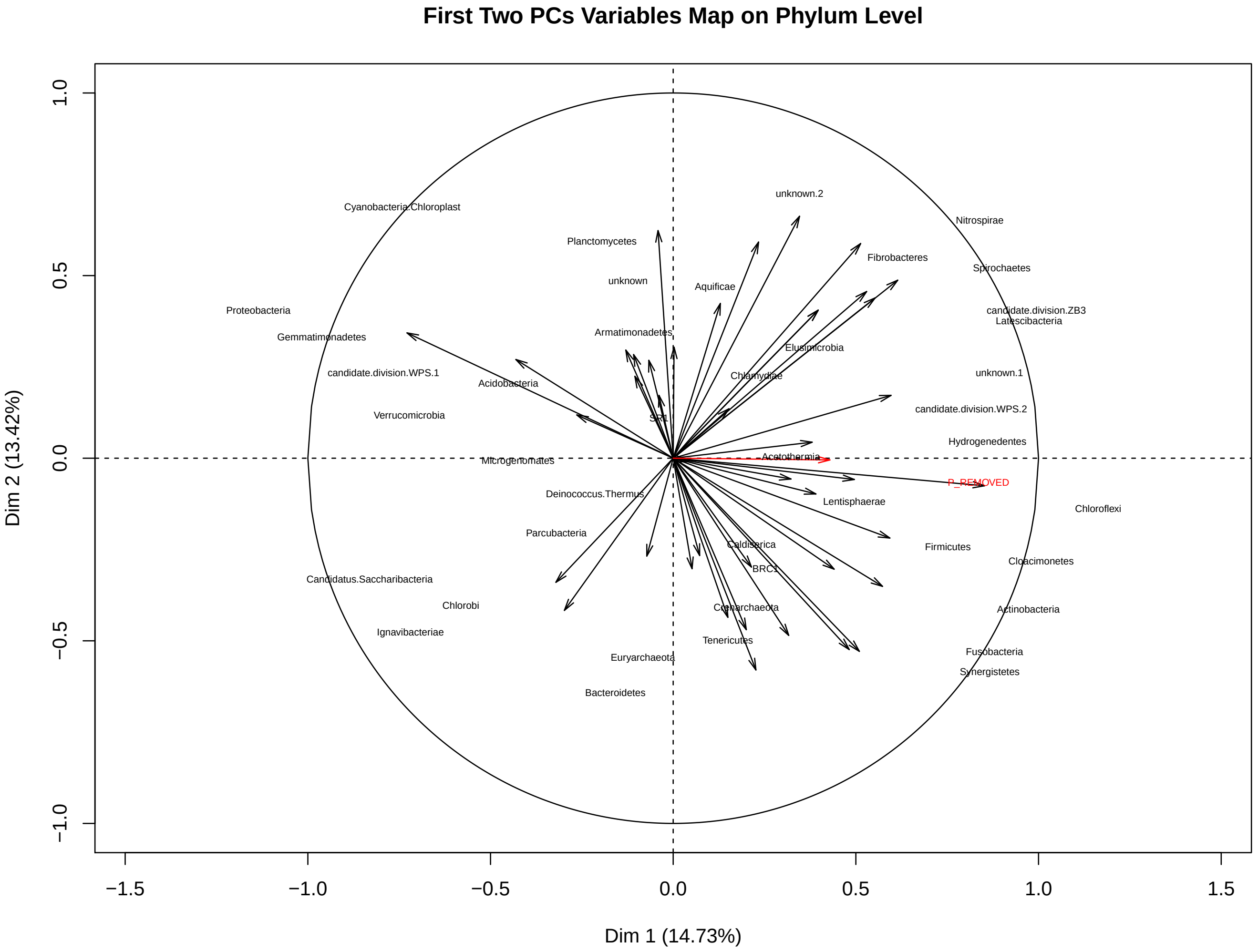

Figure S67. Bivariate plot depicting the correlation between each of the variables (the phylotypes identified by the 16S rRNA gene sequencing results using the EUB primer set at the phylum level and the P removed) and the first two principal components. Each variable is represented by a vector, the cosine of the angle between any two vectors represents the correlation between the two corresponding variables on the space defined by the first two principal components.

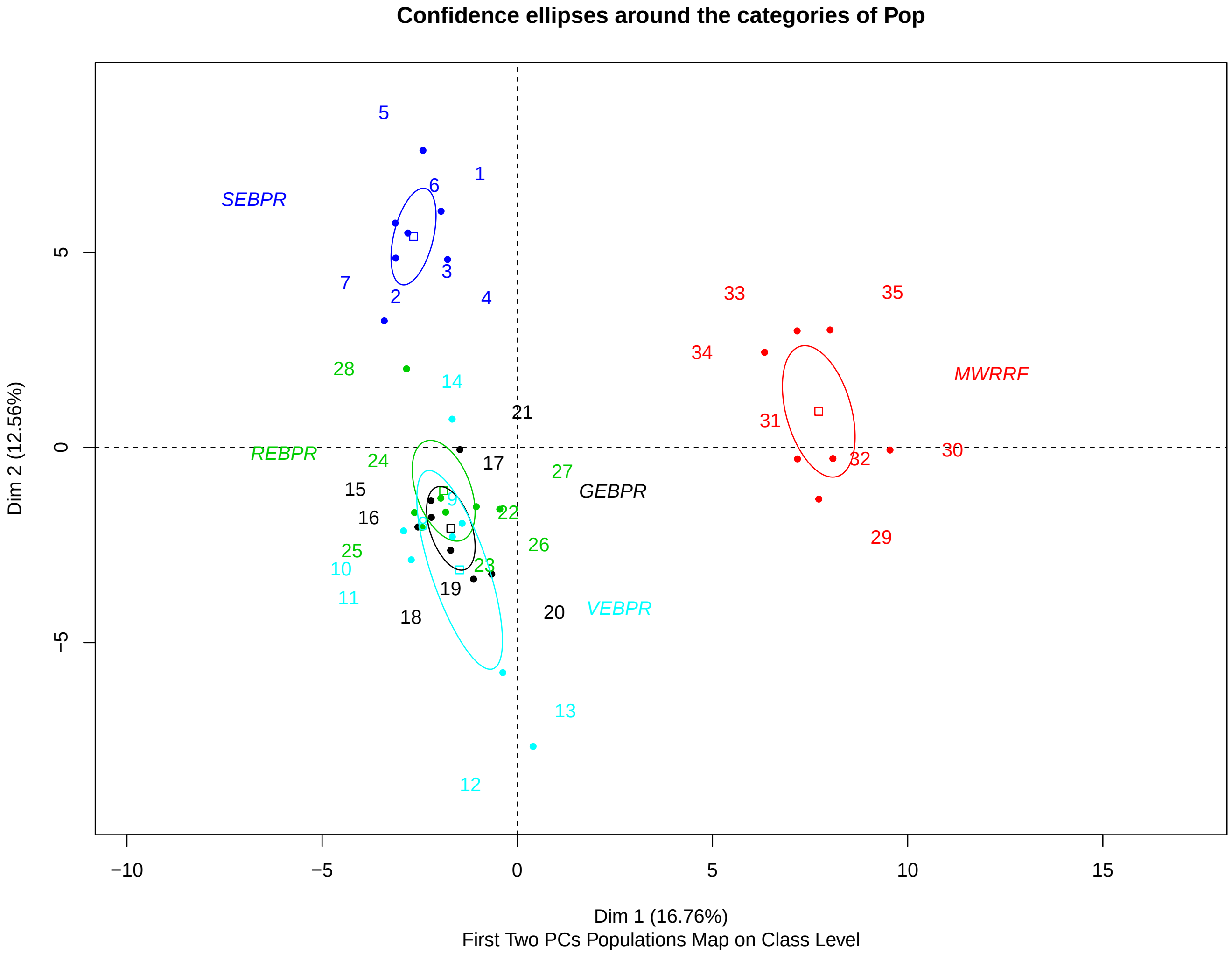

Figure S68. Bivariate plot of the first two principal component (Dim 1 and Dim 2) scores for the 16S rRNA gene sequencing results using the EUB primer set at the class level and the P removed. Samples have been grouped by system (distinguished by color) with the numbers corresponding to their index in an ordered list (i.e., sorted by operational day following an arbitrary system ordering: 1 to 7 are S-EBPR operational days 72 to 283; 8 to 14 are V-EBPR operational days 72 to 283; 15 to 21 are G-EBPR operational days 72 to 283; 22 to 28 are R-EBPR operational days 72 to 283; and 29 to 35 are Moscow WRRF operational days 225 to 320). The centroid for each group in the Dim 1-Dim 2 space is depicted as a square in the associated color and the ellipses denote the 95 % confidence regions for the associated centroids in the Dim 1-Dim 2 space.

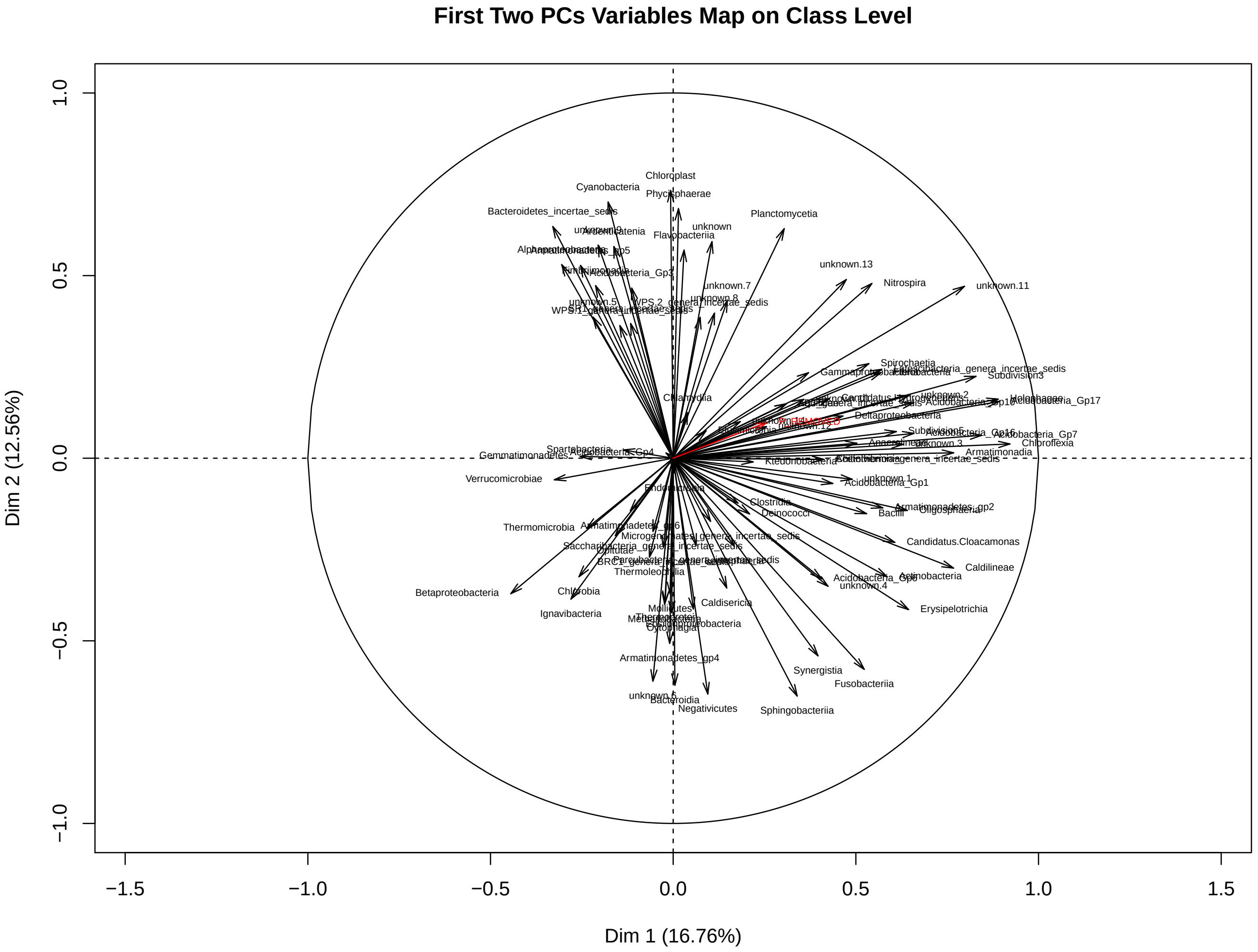

Figure S69. Bivariate plot depicting the correlation between each of the variables (the phylotypes identified by the 16S rRNA gene sequencing results using the EUB primer set at the class level and the P removed) and the first two principal components. Each variable is represented by a vector, the cosine of the angle between any two vectors represents the correlation between the two corresponding variables on the space defined by the first two principal components.

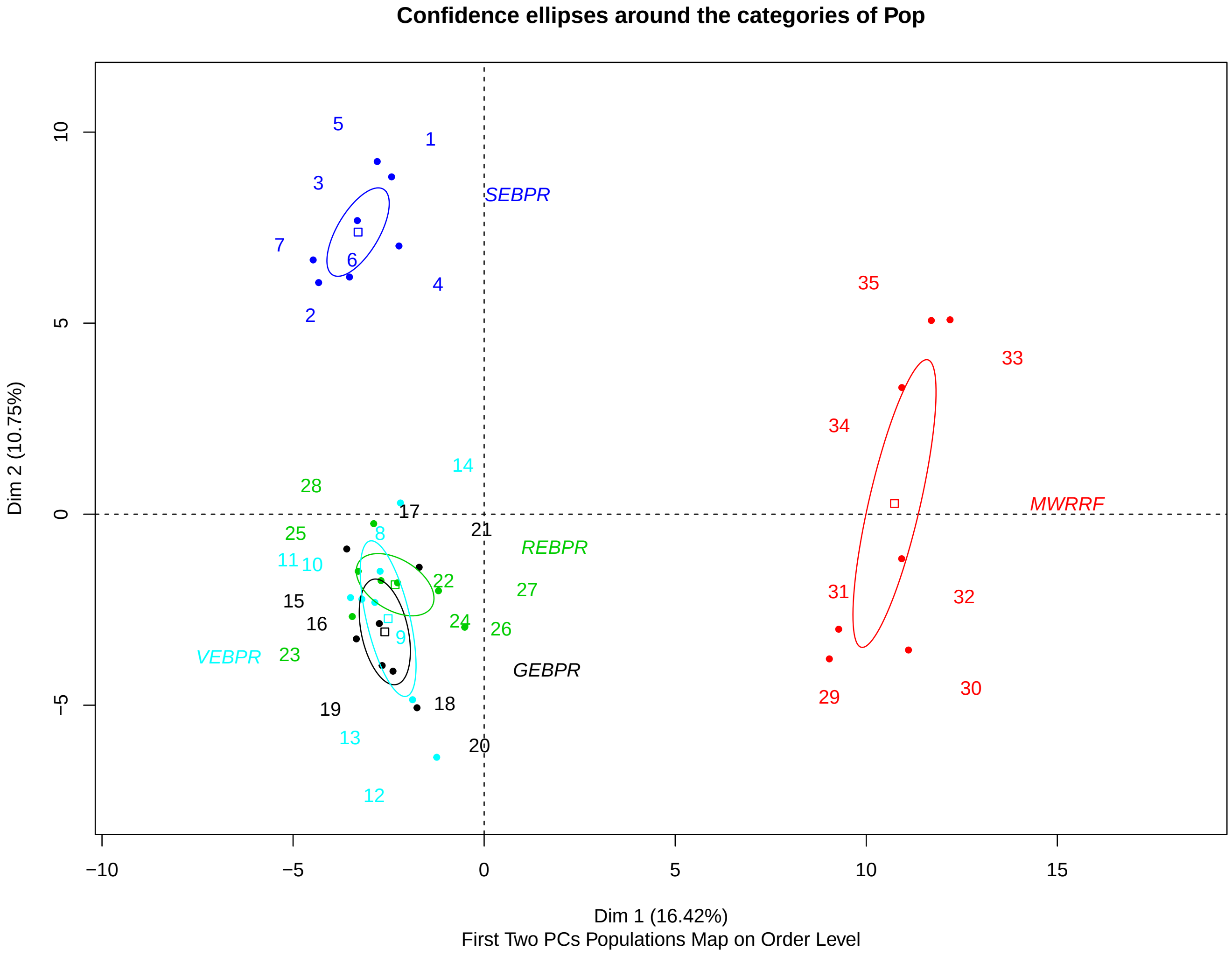

Figure S70. Bivariate plot of the first two principal component (Dim 1 and Dim 2) scores for the 16S rRNA gene sequencing results using the EUB primer set at the order level and the P removed. Samples have been grouped by system (distinguished by color) with the numbers corresponding to their index in an ordered list (i.e., sorted by operational day following an arbitrary system ordering: 1 to 7 are S-EBPR operational days 72 to 283; 8 to 14 are V-EBPR operational days 72 to 283; 15 to 21 are G-EBPR operational days 72 to 283; 22 to 28 are R-EBPR operational days 72 to 283; and 29 to 35 are Moscow WRRF operational days 225 to 320). The centroid for each group in the Dim 1-Dim 2 space is depicted as a square in the associated color and the ellipses denote the 95 % confidence regions for the associated centroids in the Dim 1-Dim 2 space.

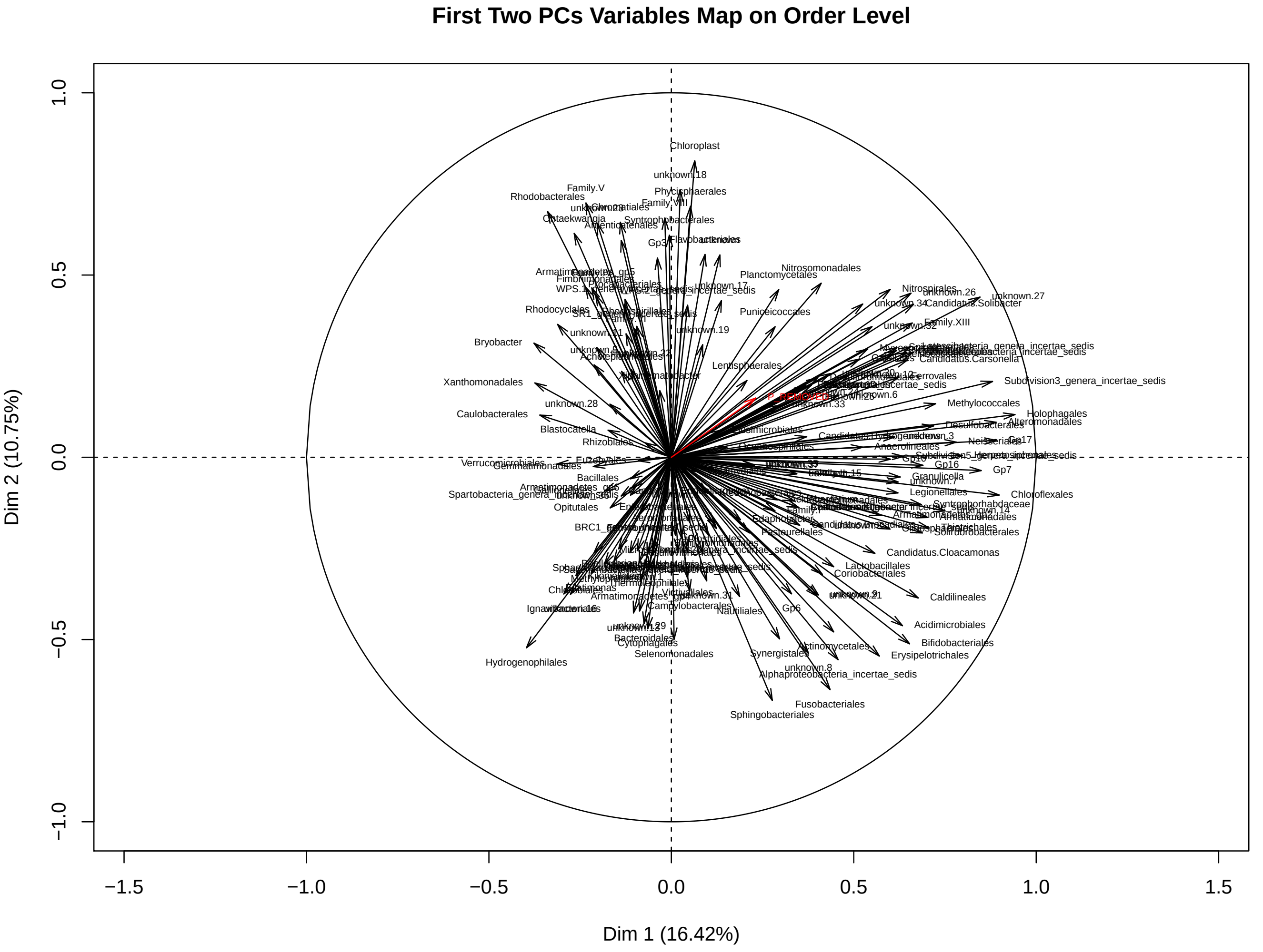

Figure S71. Bivariate plot depicting the correlation between each of the variables (the phylotypes identified by the 16S rRNA gene sequencing results using the EUB primer set at the order level and the P removed) and the first two principal components. Each variable is represented by a vector, the cosine of the angle between any two vectors represents the correlation between the two corresponding variables on the space defined by the first two principal components.

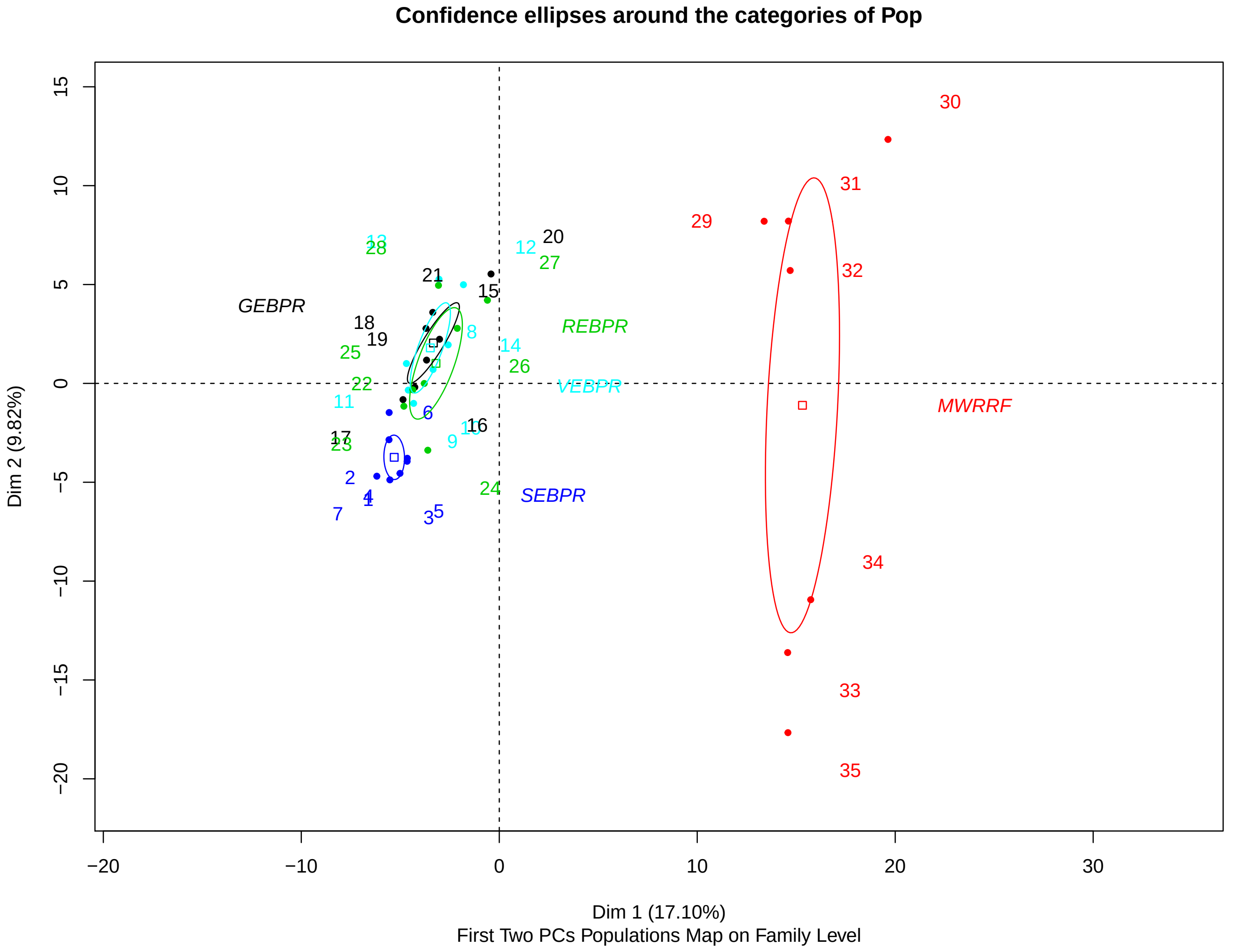

Figure S72. Bivariate plot of the first two principal component (Dim 1 and Dim 2) scores for the 16S rRNA gene sequencing results using the EUB primer set at the family level and the P removed. Samples have been grouped by system (distinguished by color) with the numbers corresponding to their index in an ordered list (i.e., sorted by operational day following an arbitrary system ordering: 1 to 7 are S-EBPR operational days 72 to 283; 8 to 14 are V-EBPR operational days 72 to 283; 15 to 21 are G-EBPR operational days 72 to 283; 22 to 28 are R-EBPR operational days 72 to 283; and 29 to 35 are Moscow WRRF operational days 225 to 320). The centroid for each group in the Dim 1-Dim 2 space is depicted as a square in the associated color and the ellipses denote the 95 % confidence regions for the associated centroids in the Dim 1-Dim 2 space.

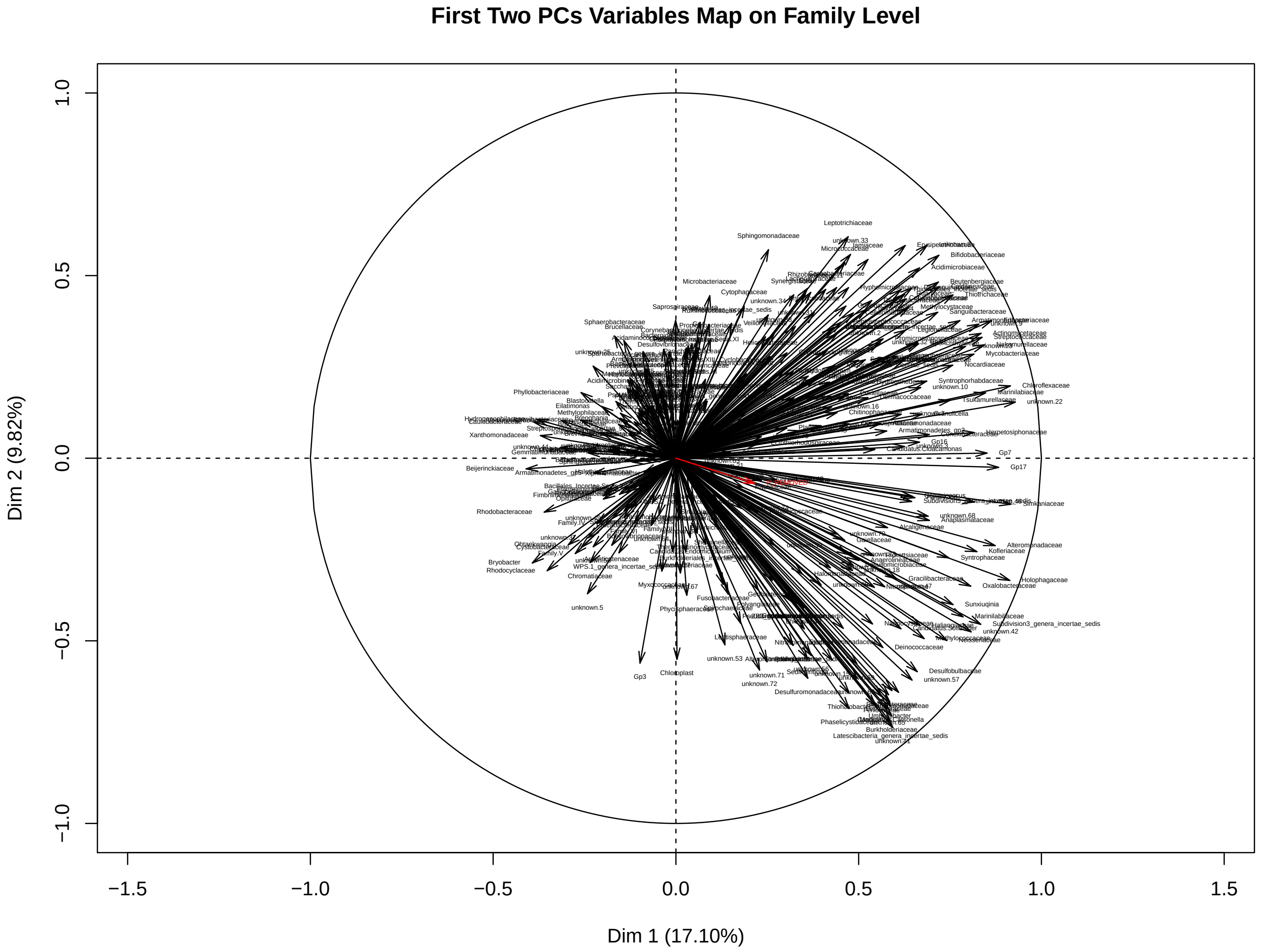

Figure S73. Bivariate plot depicting the correlation between each of the variables (the phylotypes identified by the 16S rRNA gene sequencing results using the EUB primer set at the family level and the P removed) and the first two principal components. Each variable is represented by a vector, the cosine of the angle between any two vectors represents the correlation between the two corresponding variables on the space defined by the first two principal components.

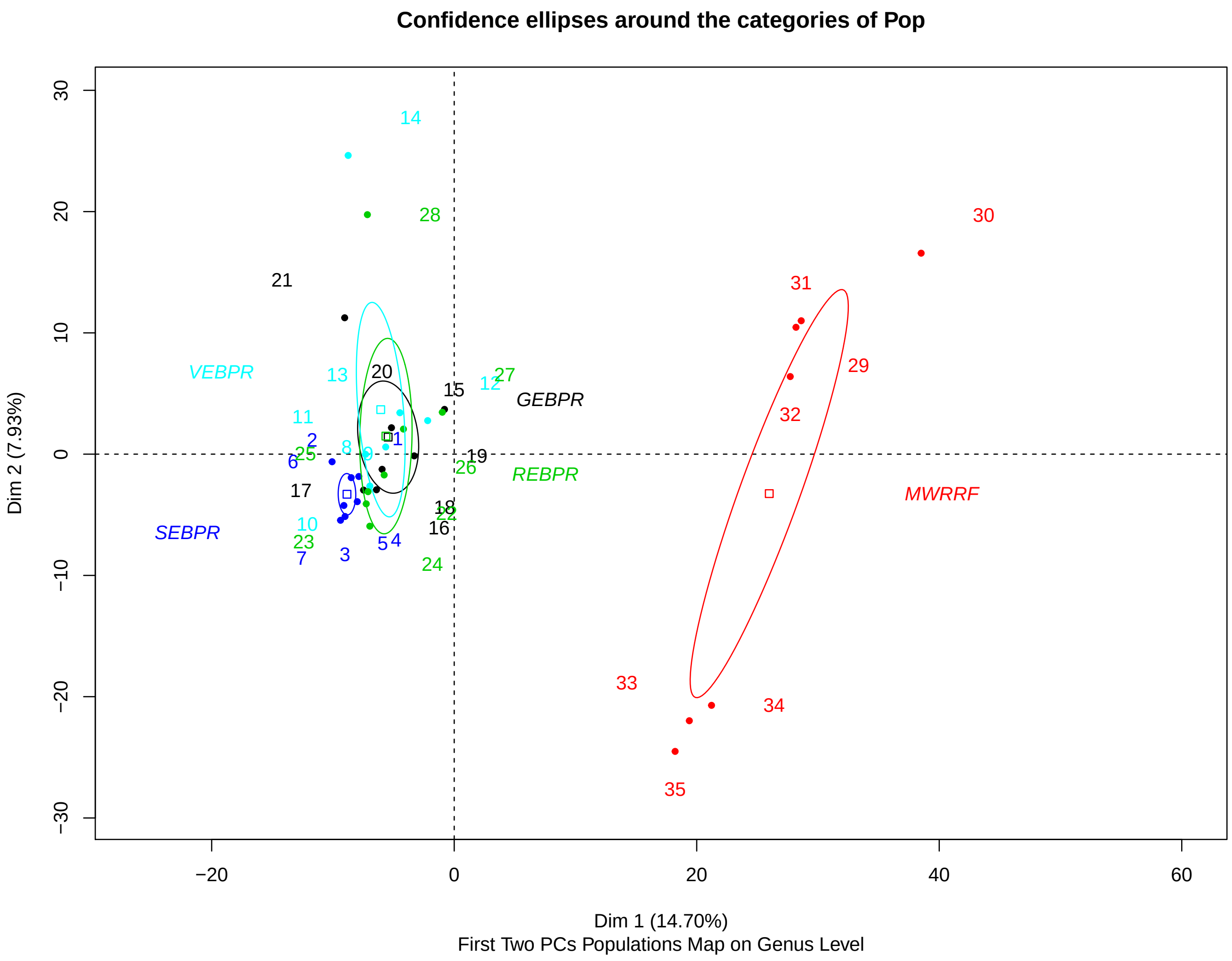

Figure S74. Bivariate plot of the first two principal component (Dim 1 and Dim 2) scores for the 16S rRNA gene sequencing results using the EUB primer set at the genus level and the P removed. Samples have been grouped by system (distinguished by color) with the numbers corresponding to their index in an ordered list (i.e., sorted by operational day following an arbitrary system ordering: 1 to 7 are S-EBPR operational days 72 to 283; 8 to 14 are V-EBPR operational days 72 to 283; 15 to 21 are G-EBPR operational days 72 to 283; 22 to 28 are R-EBPR operational days 72 to 283; and 29 to 35 are Moscow WRRF operational days 225 to 320). The centroid for each group in the Dim 1-Dim 2 space is depicted as a square in the associated color and the ellipses denote the 95 % confidence regions for the associated centroids in the Dim 1-Dim 2 space.

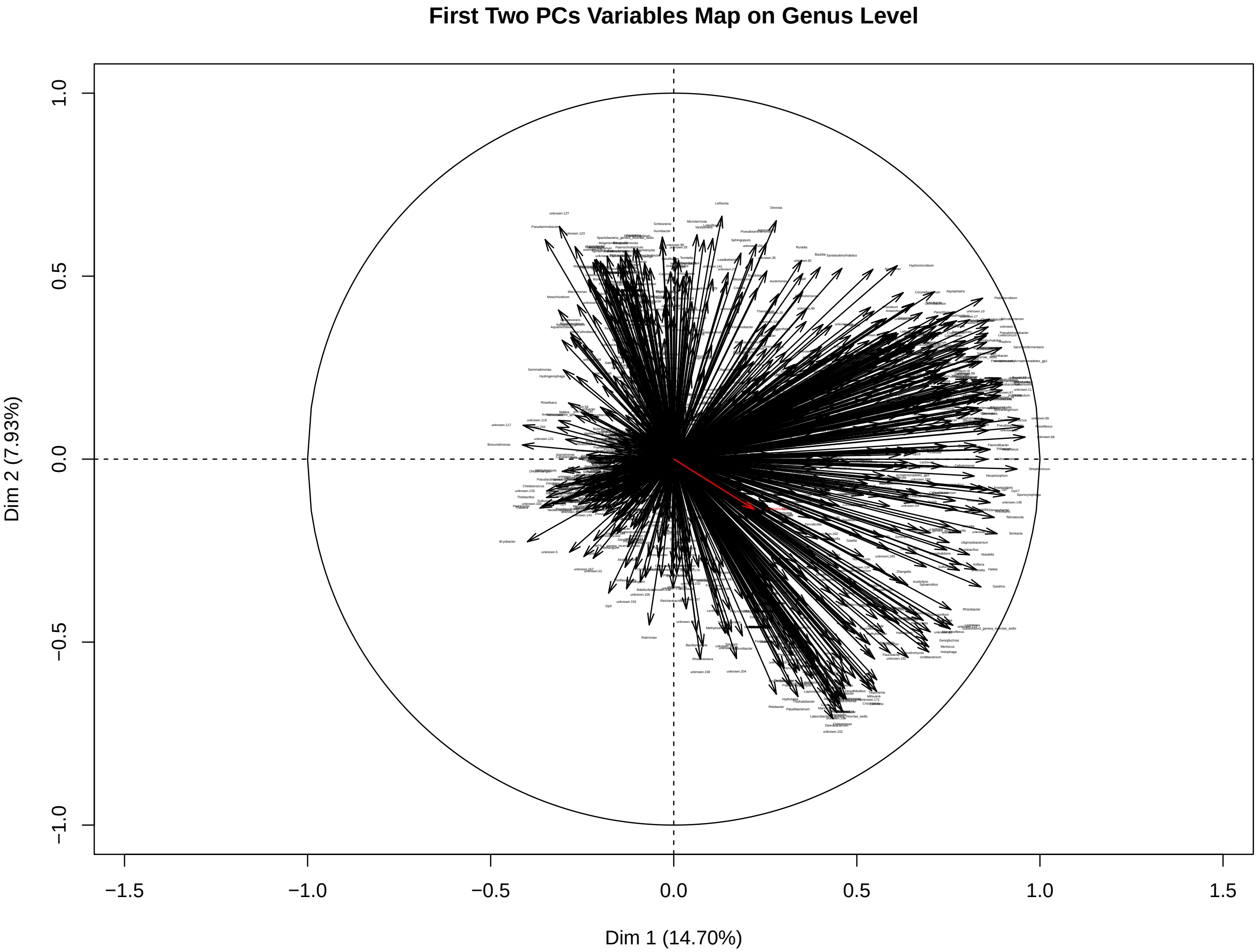

Figure S75. Bivariate plot depicting the correlation between each of the variables (the phylotypes identified by the 16S rRNA gene sequencing results using the EUB primer set at the genus level and the P removed) and the first two principal components. Each variable is represented by a vector, the cosine of the angle between any two vectors represents the correlation between the two corresponding variables on the space defined by the first two principal components.

PAO primer set

Diversity metrics

Table S50. Sample diversity and evenness indices and richness estimates using the PAO primer set.

Operational day	Total reads	Total phylotypes	Major[a] phylotypes	Minor[b] phylotypes	H'[c]	R[d]	D[e]	S_{Chao1}[f]
S-EBPR								
72	16 215	37	4	33	1.12	0.31	0.59	52.60
86	369	8	5	3	1.00	0.48	0.51	8.50
107	23 425	26	3	23	0.56	0.17	0.29	52.00
121	26 988	39	3	36	0.70	0.19	0.33	43.50
241	35 474	40	4	36	0.64	0.17	0.29	56.50
263	27 666	40	4	36	0.74	0.20	0.29	42.14
283	71 580	21	3	18	0.49	0.16	0.26	22.20
V-EBPR								
72	5 839	51	11	40	2.18	0.55	0.83	62.14
86	3 426	37	7	30	1.63	0.45	0.69	67.32
107	1 995	16	3	13	0.62	0.22	0.29	20.20
121	7 872	55	11	44	2.28	0.57	0.85	66.00
241	17 583	76	15	61	2.10	0.49	0.74	104.87
263	24 784	76	13	63	2.43	0.56	0.84	89.12
283	58 510	46	4	42	0.65	0.17	0.29	66.00
G-EBPR								
72	5 710	53	15	38	2.46	0.62	0.86	61.25
86	6 146	41	7	34	0.92	0.25	0.31	47.43
107	17 296	25	1	24	0.14	0.04	0.04	34.33
121	30 553	35	4	31	0.74	0.21	0.29	45.50
241	31 675	68	11	57	2.15	0.51	0.83	83.54
263	14 827	62	14	48	2.10	0.51	0.80	83.37
283	35 031	75	10	65	2.24	0.52	0.84	98.75
R-EBPR								
72	4 126	44	7	37	1.51	0.40	0.63	50.43
86	4 265	30	5	25	1.14	0.34	0.57	49.50
107	10 587	45	7	38	1.24	0.33	0.56	62.14
121	20 560	45	6	39	1.13	0.30	0.50	67.00
241	35 230	67	5	62	0.95	0.23	0.39	84.10
263	26 514	61	7	54	1.13	0.28	0.49	80.43
283	19 082	68	6	62	1.43	0.34	0.62	143.60
Moscow WRRF								
225	31 029	69	11	58	2.00	0.47	0.80	82.12
255	28 463	57	5	52	1.58	0.39	0.71	85.50
270	18 238	46	5	41	1.44	0.37	0.63	64.20
284	25 431	61	6	55	1.56	0.38	0.67	80.00
304	22 117	60	5	55	1.06	0.26	0.45	110.14
313	20 495	49	6	43	1.27	0.33	0.56	106.75

Table S50. Sample diversity and evenness indices and richness estimates using the PAO primer set continued.

Operational day	Total reads	Total phylotypes	Major[a] phylotypes	Minor[b] phylotypes	H'[c]	R[d]	D[e]	S_{Chao1}[f]
320	12	4	4	0	1.27	0.91	0.69	4.00

[a] Major phylotypes constitute at least 1% of the total relative abundance.

[b] Minor phylotypes constitute less than 1% of the total relative abundance.

[c] Shannon diversity index, given by $H' = -\sum_{i=1}^{S} \left(p_i \cdot \ln p_i\right)$ where S is the total number of phylotypes and p_i is the relative abundance of the i-th phylotype (Shannon, 1948).

[d] Pielou evenness index, given by $R = \frac{H'}{\ln S}$ where H' is the Shannon diversity index and S is the total number of phylotypes.

[e] Simpson's diversity index, given by $D = 1 - \sum_{i=1}^{S} p_i^2$ where S is the total number of phylotypes and p_i is the relative abundance of the i-th phylotype (Simpson, 1949).

[f] Bias-corrected Chao1 richness estimate, given by $S_{\text{Chao1}} = S + \frac{n+1}{n} \cdot \frac{F_1 \cdot (F_1 - 1)}{2 \cdot (F_2 + 1)}$ where S is the total number of phylotypes, n is the total number of sequences, F_1 is the total number of phylotypes to which only one sequence was assigned, and F_2 is the total number of phylotypes to which only two sequences were assigned.

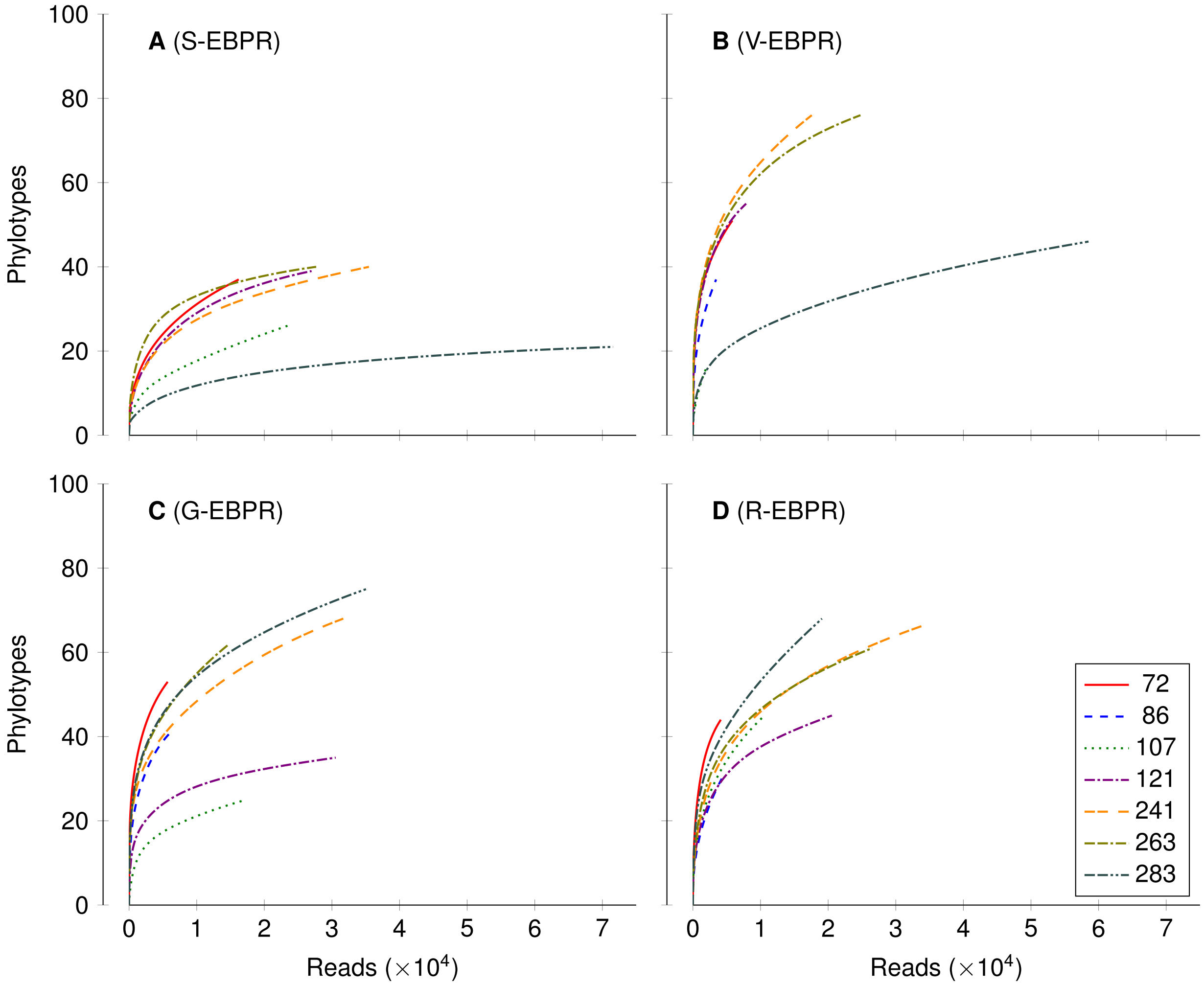

Figure S76. Rarefaction curves for the PAO primer set results for each lab-scale EBPR reactor.

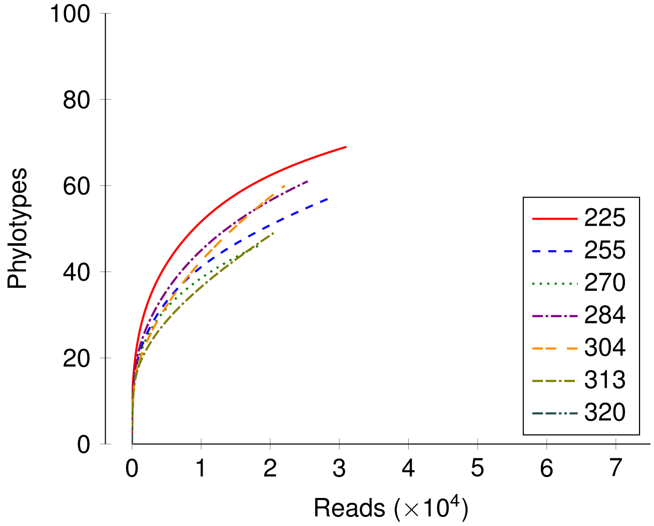

Figure S77. Rarefaction curves for the PAO primer set results for the Moscow WRRF.

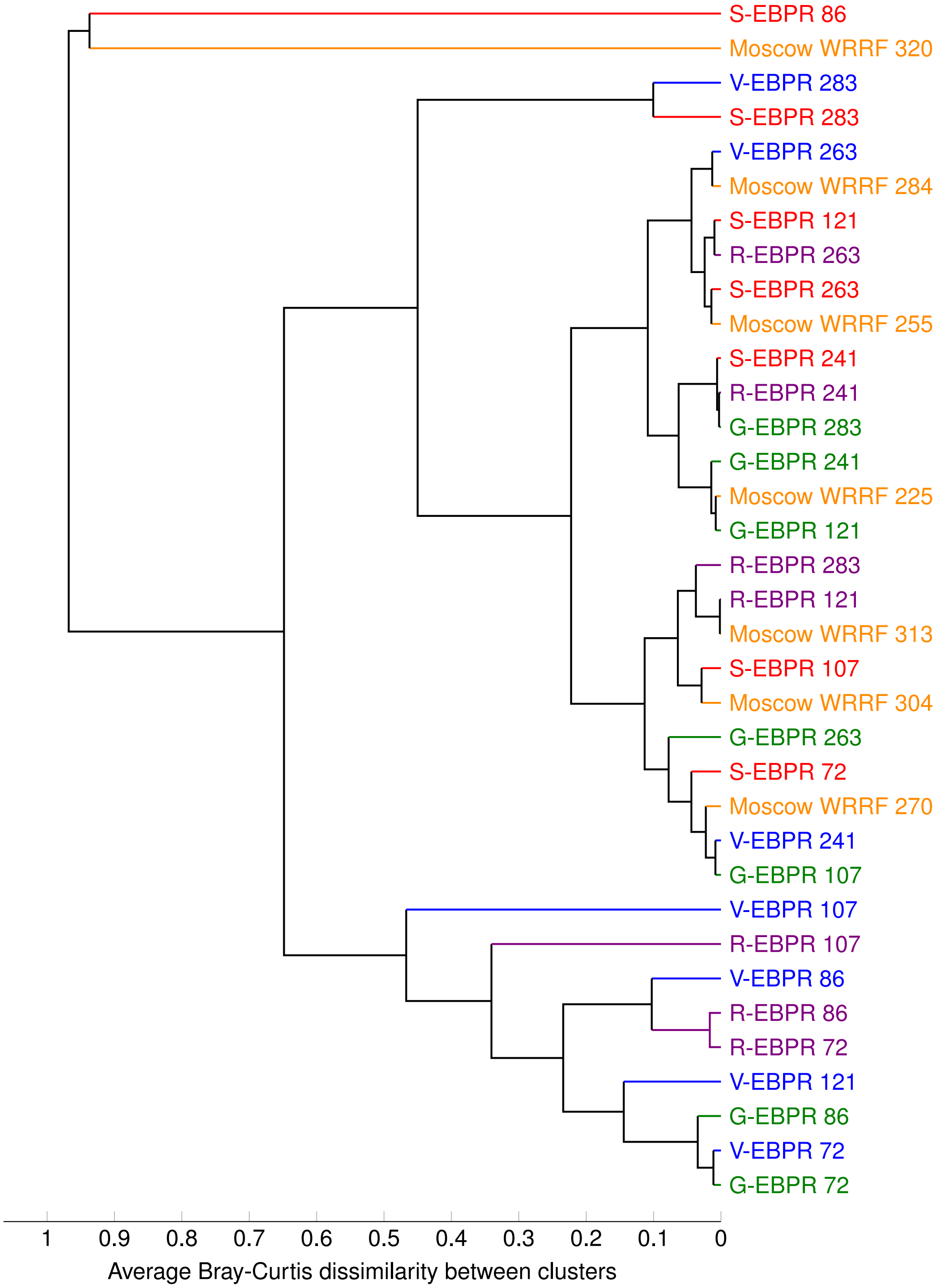

Figure S78. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the PAO primer set at the domain level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

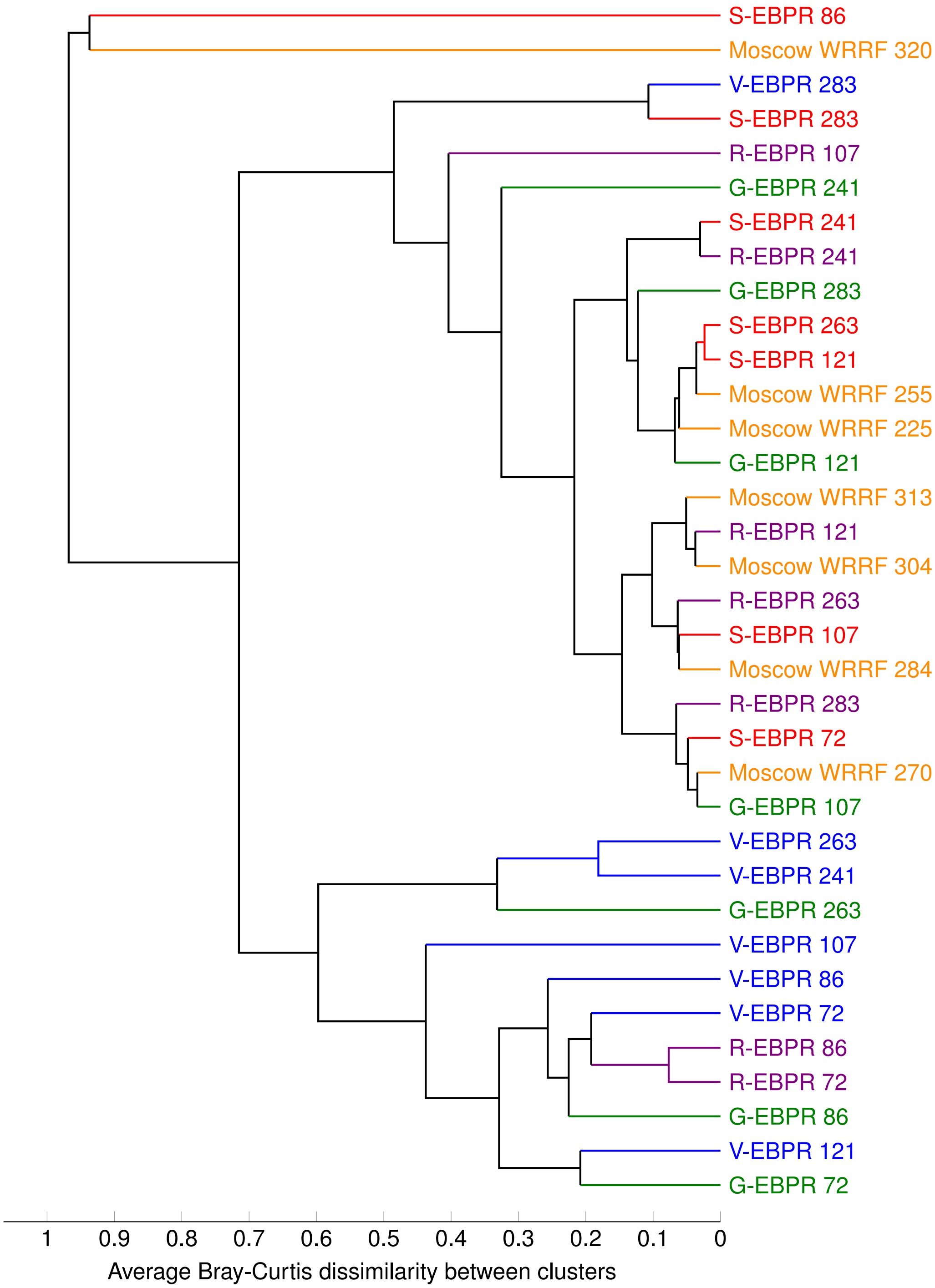

Figure S79. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the PAO primer set at the phylum level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

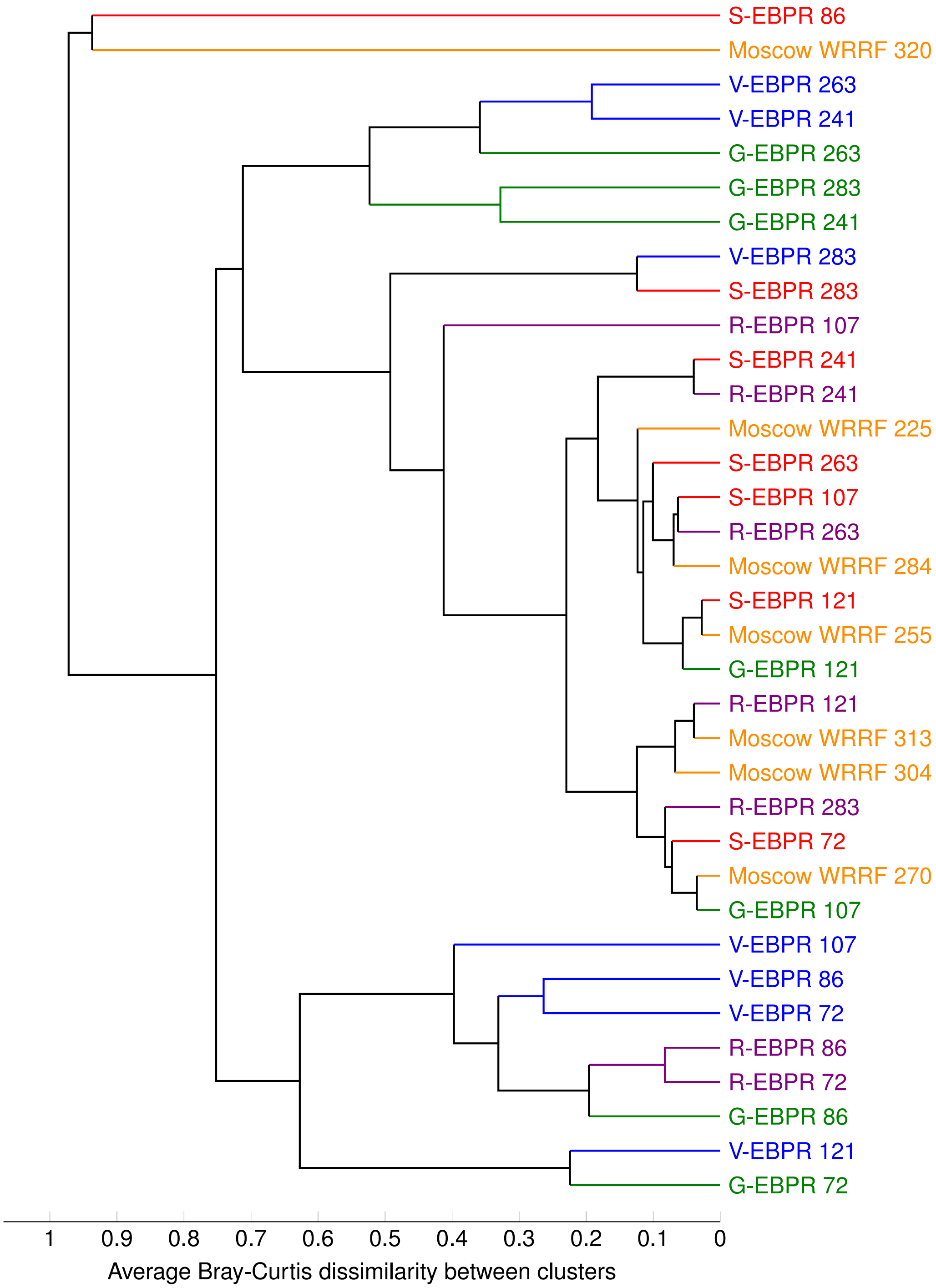

Figure S80. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the PAO primer set at the class level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

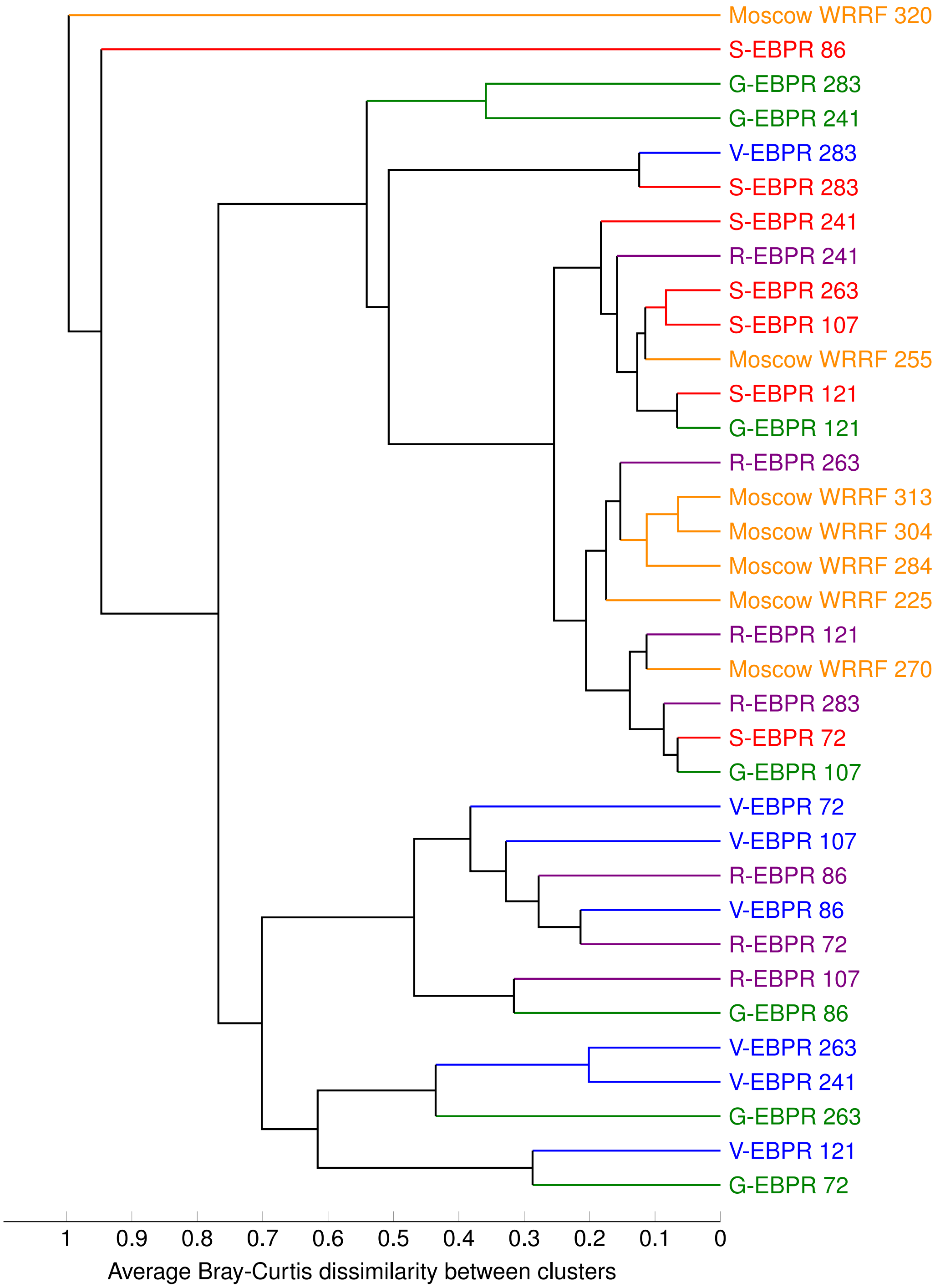

Figure S81. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the PAO primer set at the order level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

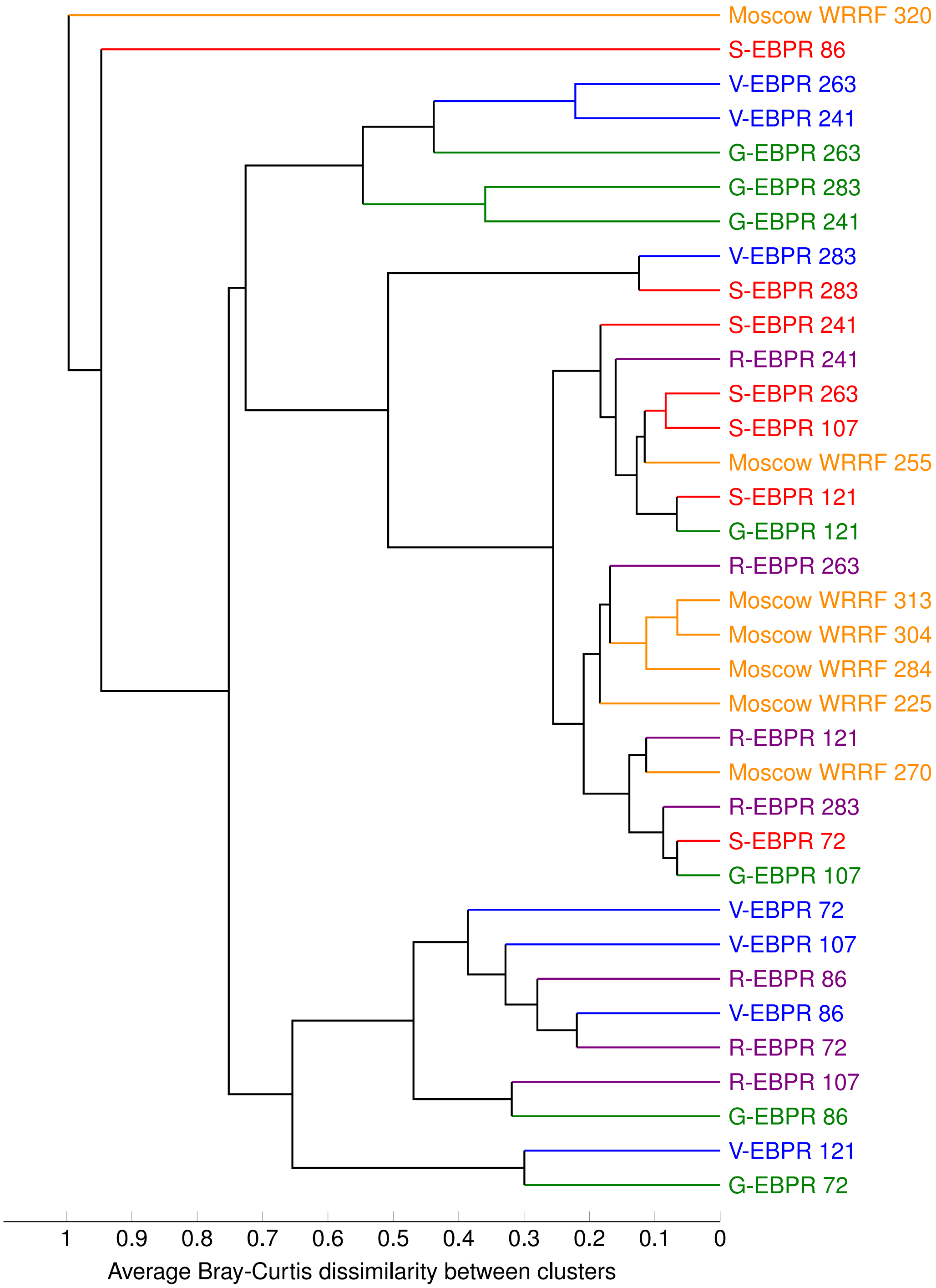

Figure S82. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the PAO primer set at the family level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

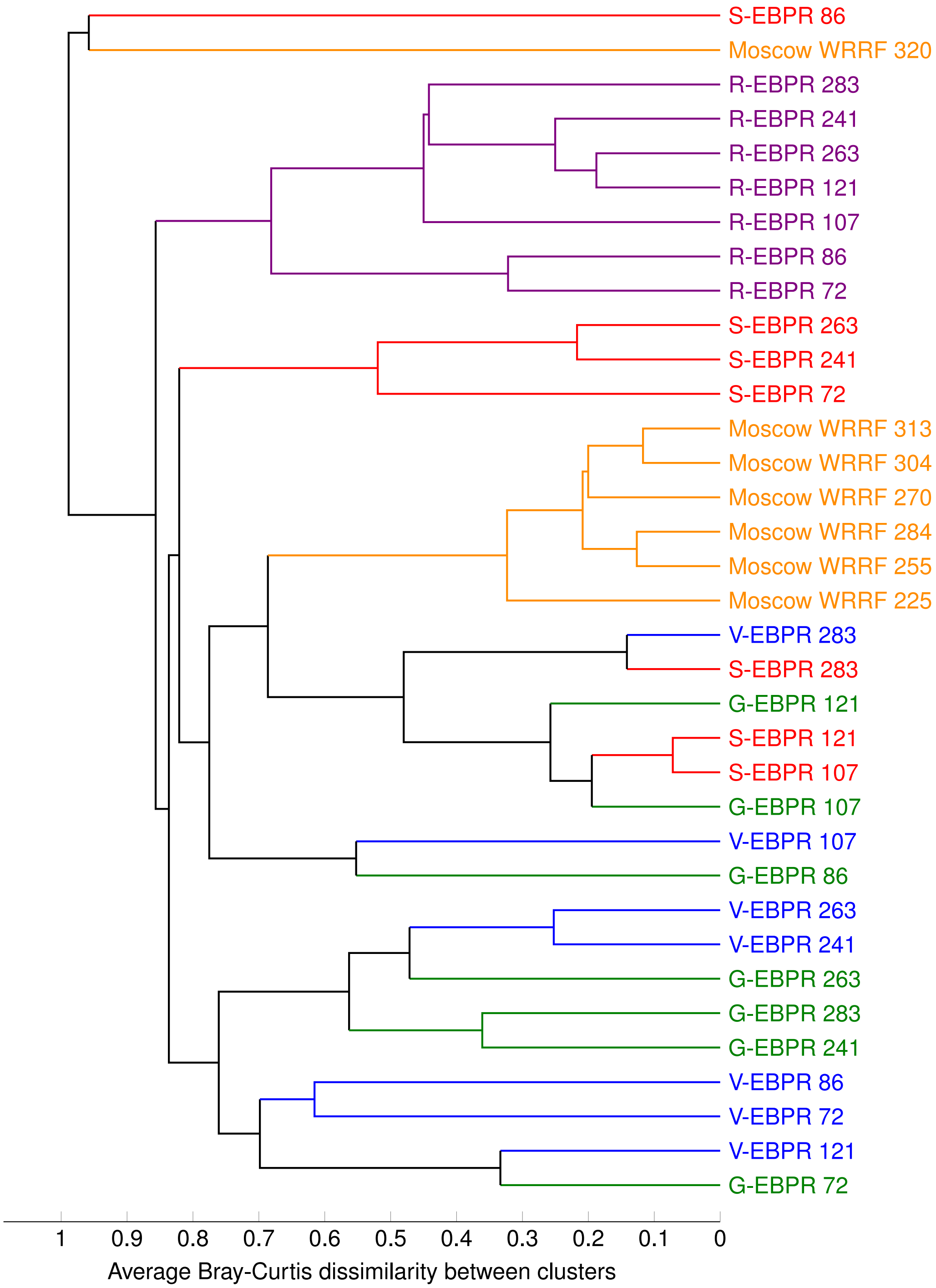

Figure S83. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the PAO primer set at the genus level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

Table S51. Dissimilarity matrix for samples with phylotypes identified using the PAO primer set at the domain level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	96	0																																	
	107	59	97	0																																
	121	58	98	7	0																															
	241	47	98	81	79	0																														
	263	56	97	94	91	22	0																													
	283	81	99	51	47	89	96	0																												
V-EBPR	72	75	96	80	82	88	85	93	0																											
	86	88	96	92	92	93	94	97	62	0																										
	107	79	96	85	87	90	94	95	65	83	0																									
	121	86	98	90	90	92	89	96	57	70	73	0																								
	241	80	96	86	86	87	86	94	64	88	80	71	0																							
	263	88	99	92	91	91	88	96	72	87	86	62	25	0																						
	283	79	100	44	40	89	97	14	89	92	93	89	90	89	0																					
G-EBPR	72	92	94	96	94	96	92	98	73	79	87	33	74	69	94	0																				
	86	52	98	64	68	78	94	86	72	87	55	74	73	82	82	79	0																			
	107	62	99	16	23	84	96	62	89	97	82	90	86	90	54	95	54	0																		
	121	71	100	27	23	86	95	49	88	85	88	82	82	82	37	87	67	28	0																	
	241	70	99	67	69	85	92	83	78	92	88	74	57	47	77	79	68	64	64	0																
	263	89	95	93	93	93	88	97	65	87	86	70	52	42	94	72	82	92	89	45	0															
	283	71	99	61	62	85	92	78	78	87	89	71	64	59	70	80	70	58	57	36	66	0														
R-EBPR	72	87	97	91	91	93	95	97	66	66	78	73	88	91	94	78	82	95	94	91	88	81	0													
	86	97	98	98	98	98	98	99	91	90	90	86	93	95	98	88	91	97	96	94	94	85	32	0												
	107	93	99	96	95	96	95	98	86	90	89	79	88	91	96	83	89	96	93	90	91	78	54	43	0											
	121	91	99	93	93	95	95	97	83	88	93	83	89	90	93	86	92	97	93	90	91	79	68	66	32	0										
	241	92	99	93	93	94	94	96	85	91	92	85	88	89	94	91	92	95	93	89	89	81	80	79	55	30	0									
	263	95	99	96	96	96	95	98	89	90	95	86	89	87	96	90	94	97	94	88	86	80	77	72	46	19	21	0								
	283	68	98	75	76	82	94	88	81	86	81	70	77	77	81	79	55	71	70	69	85	57	70	74	47	37	51	45	0							
Moscow WRRF	225	67	99	55	56	84	94	64	76	90	88	81	78	81	62	87	68	62	66	61	85	51	77	76	63	66	71	71	55	0						
	255	65	99	61	62	83	95	67	80	89	87	83	84	87	66	90	67	70	73	71	89	63	76	74	61	63	69	68	57	23	0					
	270	71	98	66	67	83	95	70	73	87	80	81	82	86	71	88	67	79	82	78	88	77	77	75	75	77	81	82	70	31	24	0				
	284	63	98	60	61	82	95	67	78	89	86	84	84	87	67	90	65	70	75	71	89	71	83	82	76	78	81	83	69	27	13	18	0			
	304	73	99	68	69	83	94	71	74	88	83	83	82	87	71	91	69	80	82	79	88	79	82	89	87	86	88	90	73	44	27	23	22	0		
	313	69	99	66	66	81	94	69	73	88	82	83	82	87	70	91	65	77	80	77	88	75	76	84	83	83	86	88	67	37	20	17	15	12	0	
	320	100	96	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	0

Table S52. Dissimilarity matrix for samples with phylotypes identified using the PAO primer set at the phylum level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	96	0																																	
	107	59	97	0																																
	121	58	98	7	0																															
	241	47	98	81	79	0																														
	263	56	97	94	91	22	0																													
	283	81	99	51	47	89	96	0																												
V-EBPR	72	75	96	80	82	88	85	93	0																											
	86	88	96	92	92	93	94	97	62	0																										
	107	79	96	85	87	90	94	95	65	83	0																									
	121	86	98	90	90	92	89	96	57	70	73	0																								
	241	80	96	86	86	87	86	94	64	88	80	71	0																							
	263	88	99	92	91	91	88	96	72	87	86	62	25	0																						
	283	79	100	44	40	89	97	14	89	92	93	89	90	89	0																					
G-EBPR	72	92	94	96	94	96	92	98	73	79	87	33	74	69	94	0																				
	86	52	98	64	68	78	94	86	72	87	55	74	73	82	82	79	0																			
	107	62	99	16	23	84	96	62	89	97	82	90	86	90	54	95	54	0																		
	121	71	100	27	23	86	95	49	88	85	88	82	82	82	37	87	67	28	0																	
	241	70	99	67	69	85	92	83	78	92	88	74	57	47	77	79	68	64	64	0																
	263	89	95	93	93	93	88	97	65	87	86	70	52	42	94	72	82	92	89	45	0															
	283	71	99	61	62	85	92	78	78	87	89	71	64	59	70	80	70	58	57	36	66	0														
R-EBPR	72	87	97	91	91	93	95	97	66	66	78	73	88	91	94	78	82	95	94	91	88	81	0													
	86	97	98	98	98	98	98	99	91	90	90	86	93	95	98	88	91	97	96	94	94	85	32	0												
	107	93	99	96	95	96	95	98	86	90	89	79	88	91	96	83	89	96	93	90	91	78	54	43	0											
	121	91	99	93	93	95	95	97	83	88	93	83	89	90	93	86	92	97	93	90	91	79	68	66	32	0										
	241	92	99	93	93	94	94	96	85	91	92	85	88	89	94	91	92	95	93	89	89	81	80	79	55	30	0									
	263	95	99	96	96	96	95	98	89	90	95	86	89	87	96	90	94	97	94	88	86	80	77	72	46	19	21	0								
	283	68	98	75	76	82	94	88	81	86	81	70	77	77	81	79	55	71	70	69	85	57	70	74	47	37	51	45	0							
Moscow WRRF	225	67	99	55	56	84	94	64	76	90	88	81	78	81	62	87	68	62	66	61	85	51	77	76	63	66	71	71	55	0						
	255	65	99	61	62	83	95	67	80	89	87	83	84	87	66	90	67	70	73	71	89	63	76	74	61	63	69	68	57	23	0					
	270	71	98	66	67	83	95	70	73	87	80	81	82	86	71	88	67	79	82	78	88	77	77	75	75	77	81	82	70	31	24	0				
	284	63	98	60	61	82	95	67	78	89	86	84	84	87	67	90	65	70	75	71	89	71	83	82	76	78	81	83	69	27	13	18	0			
	304	73	99	68	69	83	94	71	74	88	83	83	82	87	71	91	69	80	82	79	88	79	82	89	87	86	88	90	73	44	27	23	22	0		
	313	69	99	66	66	81	94	69	73	88	82	83	82	87	70	91	65	77	80	77	88	75	76	84	83	83	86	88	67	37	20	17	15	12	0	
	320	100	96	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	0

Table S53. Dissimilarity matrix for samples with phylotypes identified using the PAO primer set at the class level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	96	0																																	
	107	59	97	0																																
	121	58	98	7	0																															
	241	47	98	81	79	0																														
	263	56	97	94	91	22	0																													
	283	81	99	51	47	89	96	0																												
V-EBPR	72	75	96	80	82	88	85	93	0																											
	86	88	96	92	92	93	94	97	62	0																										
	107	79	96	85	87	90	94	95	65	83	0																									
	121	86	98	90	90	92	89	96	57	70	73	0																								
	241	80	96	86	86	87	86	94	64	88	80	71	0																							
	263	88	99	92	91	91	88	96	72	87	86	62	25	0																						
	283	79	100	44	40	89	97	14	89	92	93	89	90	89	0																					
G-EBPR	72	92	94	96	94	96	92	98	73	79	87	33	74	69	94	0																				
	86	52	98	64	68	78	94	86	72	87	55	74	73	82	82	79	0																			
	107	62	99	16	23	84	96	62	89	97	82	90	86	90	54	95	54	0																		
	121	71	100	27	23	86	95	49	88	85	88	82	82	82	37	87	67	28	0																	
	241	70	99	67	69	85	92	83	78	92	88	74	57	47	77	79	68	64	64	0																
	263	89	95	93	93	93	88	97	65	87	86	70	52	42	94	72	82	92	89	45	0															
	283	71	99	61	62	85	92	78	78	87	89	71	64	59	70	80	70	58	57	36	66	0														
R-EBPR	72	87	97	91	91	93	95	97	66	66	78	73	88	91	94	78	82	95	94	91	88	81	0													
	86	97	98	98	98	98	98	99	91	90	90	86	93	95	98	88	91	97	96	94	94	85	32	0												
	107	93	99	96	95	96	95	98	86	90	89	79	88	91	96	83	89	96	93	90	91	78	54	43	0											
	121	91	99	93	93	95	95	97	83	88	93	83	89	90	93	86	92	97	93	90	91	79	68	66	32	0										
	241	92	99	93	93	94	94	96	85	91	92	85	88	89	94	91	92	95	93	89	89	81	80	79	55	30	0									
	263	95	99	96	96	96	95	98	89	90	95	86	89	87	96	90	94	97	94	88	86	80	77	72	46	19	21	0								
	283	68	98	75	76	82	94	88	81	86	81	70	77	77	81	79	55	71	70	69	85	57	70	74	47	37	51	45	0							
Moscow WRRF	225	67	99	55	56	84	94	64	76	90	88	81	78	81	62	87	68	62	66	61	85	51	77	76	63	66	71	71	55	0						
	255	65	99	61	62	83	95	67	80	89	87	83	84	87	66	90	67	70	73	71	89	63	76	74	61	63	69	68	57	23	0					
	270	71	98	66	67	83	95	70	73	87	80	81	82	86	71	88	67	79	82	78	88	77	77	75	75	77	81	82	70	31	24	0				
	284	63	98	60	61	82	95	67	78	89	86	84	84	87	67	90	65	70	75	71	89	71	83	82	76	78	81	83	69	27	13	18	0			
	304	73	99	68	69	83	94	71	74	88	83	83	82	87	71	91	69	80	82	79	88	79	82	89	87	86	88	90	73	44	27	23	22	0		
	313	69	99	66	66	81	94	69	73	88	82	83	82	87	70	91	65	77	80	77	88	75	76	84	83	83	86	88	67	37	20	17	15	12	0	
	320	100	96	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	0

Table S54. Dissimilarity matrix for samples with phylotypes identified using the PAO primer set at the order level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	96	0																																	
	107	59	97	0																																
	121	58	98	7	0																															
	241	47	98	81	79	0																														
	263	56	97	94	91	22	0																													
	283	81	99	51	47	89	96	0																												
V-EBPR	72	75	96	80	82	88	85	93	0																											
	86	88	96	92	92	93	94	97	62	0																										
	107	79	96	85	87	90	94	95	65	83	0																									
	121	86	98	90	90	92	89	96	57	70	73	0																								
	241	80	96	86	86	87	86	94	64	88	80	71	0																							
	263	88	99	92	91	91	88	96	72	87	86	62	25	0																						
	283	79	100	44	40	89	97	14	89	92	93	89	90	89	0																					
G-EBPR	72	92	94	96	94	96	92	98	73	79	87	33	74	69	94	0																				
	86	52	98	64	68	78	94	86	72	87	55	74	73	82	82	79	0																			
	107	62	99	16	23	84	96	62	89	97	82	90	86	90	54	95	54	0																		
	121	71	100	27	23	86	95	49	88	85	88	82	82	82	37	87	67	28	0																	
	241	70	99	67	69	85	92	83	78	92	88	74	57	47	77	79	68	64	64	0																
	263	89	95	93	93	93	88	97	65	87	86	70	52	42	94	72	82	92	89	45	0															
	283	71	99	61	62	85	92	78	78	87	89	71	64	59	70	80	70	58	57	36	66	0														
R-EBPR	72	87	97	91	91	93	95	97	66	66	78	73	88	91	94	78	82	95	94	91	88	81	0													
	86	97	98	98	98	98	98	99	91	90	90	86	93	95	98	88	91	97	96	94	94	85	32	0												
	107	93	99	96	95	96	95	98	86	90	89	79	88	91	96	83	89	96	93	90	91	78	54	43	0											
	121	91	99	93	93	95	95	97	83	88	93	83	89	90	93	86	92	97	93	90	91	79	68	66	32	0										
	241	92	99	93	93	94	94	96	85	91	92	85	88	89	94	91	92	95	93	89	89	81	80	79	55	30	0									
	263	95	99	96	96	96	95	98	89	90	95	86	89	87	96	90	94	97	94	88	86	80	77	72	46	19	21	0								
	283	68	98	75	76	82	94	88	81	86	81	70	77	77	81	79	55	71	70	69	85	57	70	74	47	37	51	45	0							
Moscow WRRF	225	67	99	55	56	84	94	64	76	90	88	81	78	81	62	87	68	62	66	61	85	51	77	76	63	66	71	71	55	0						
	255	65	99	61	62	83	95	67	80	89	87	83	84	87	66	90	67	70	73	71	89	63	76	74	61	63	69	68	57	23	0					
	270	71	98	66	67	83	95	70	73	87	80	81	82	86	71	88	67	79	82	78	88	77	77	75	75	77	81	82	70	31	24	0				
	284	63	98	60	61	82	95	67	78	89	86	84	84	87	67	90	65	70	75	71	89	71	83	82	76	78	81	83	69	27	13	18	0			
	304	73	99	68	69	83	94	71	74	88	83	83	82	87	71	91	69	80	82	79	88	79	82	89	87	86	88	90	73	44	27	23	22	0		
	313	69	99	66	66	81	94	69	73	88	82	83	82	87	70	91	65	77	80	77	88	75	76	84	83	83	86	88	67	37	20	17	15	12	0	
	320	100	96	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	0

Table S55. Dissimilarity matrix for samples with phylotypes identified using the PAO primer set at the family level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	96	0																																	
	107	59	97	0																																
	121	58	98	7	0																															
	241	47	98	81	79	0																														
	263	56	97	94	91	22	0																													
	283	81	99	51	47	89	96	0																												
V-EBPR	72	75	96	80	82	88	85	93	0																											
	86	88	96	92	92	93	94	97	62	0																										
	107	79	96	85	87	90	94	95	65	83	0																									
	121	86	98	90	90	92	89	96	57	70	73	0																								
	241	80	96	86	86	87	86	94	64	88	80	71	0																							
	263	88	99	92	91	91	88	96	72	87	86	62	25	0																						
	283	79	100	44	40	89	97	14	89	92	93	89	90	89	0																					
G-EBPR	72	92	94	96	94	96	92	98	73	79	87	33	74	69	94	0																				
	86	52	98	64	68	78	94	86	72	87	55	74	73	82	82	79	0																			
	107	62	99	16	23	84	96	62	89	97	82	90	86	90	54	95	54	0																		
	121	71	100	27	23	86	95	49	88	85	88	82	82	82	37	87	67	28	0																	
	241	70	99	67	69	85	92	83	78	92	88	74	57	47	77	79	68	64	64	0																
	263	89	95	93	93	93	88	97	65	87	86	70	52	42	94	72	82	92	89	45	0															
	283	71	99	61	62	85	92	78	78	87	89	71	64	59	70	80	70	58	57	36	66	0														
R-EBPR	72	87	97	91	91	93	95	97	66	66	78	73	88	91	94	78	82	95	94	91	88	81	0													
	86	97	98	98	98	98	98	99	91	90	90	86	93	95	98	88	91	97	96	94	94	85	32	0												
	107	93	99	96	95	96	95	98	86	90	89	79	88	91	96	83	89	96	93	90	91	78	54	43	0											
	121	91	99	93	93	95	95	97	83	88	93	83	89	90	93	86	92	97	93	90	91	79	68	66	32	0										
	241	92	99	93	93	94	94	96	85	91	92	85	88	89	94	91	92	95	93	89	89	81	80	79	55	30	0									
	263	95	99	96	96	96	95	98	89	90	95	86	89	87	96	90	94	97	94	88	86	80	77	72	46	19	21	0								
	283	68	98	75	76	82	94	88	81	86	81	70	77	77	81	79	55	71	70	69	85	57	70	74	47	37	51	45	0							
Moscow WRRF	225	67	99	55	56	84	94	64	76	90	88	81	78	81	62	87	68	62	66	61	85	51	77	76	63	66	71	71	55	0						
	255	65	99	61	62	83	95	67	80	89	87	83	84	87	66	90	67	70	73	71	89	63	76	74	61	63	69	68	57	23	0					
	270	71	98	66	67	83	95	70	73	87	80	81	82	86	71	88	67	79	82	78	88	77	77	75	75	77	81	82	70	31	24	0				
	284	63	98	60	61	82	95	67	78	89	86	84	84	87	67	90	65	70	75	71	89	71	83	82	76	78	81	83	69	27	13	18	0			
	304	73	99	68	69	83	94	71	74	88	83	83	82	87	71	91	69	80	82	79	88	79	82	89	87	86	88	90	73	44	27	23	22	0		
	313	69	99	66	66	81	94	69	73	88	82	83	82	87	70	91	65	77	80	77	88	75	76	84	83	83	86	88	67	37	20	17	15	12	0	
	320	100	96	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	0

Table S56. Dissimilarity matrix for samples with phylotypes identified using the PAO primer set at the genus level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	96	0																																	
	107	59	97	0																																
	121	58	98	7	0																															
	241	47	98	81	79	0																														
	263	56	97	94	91	22	0																													
	283	81	99	51	47	89	96	0																												
V-EBPR	72	75	96	80	82	88	85	93	0																											
	86	88	96	92	92	93	94	97	62	0																										
	107	79	96	85	87	90	94	95	65	83	0																									
	121	86	98	90	90	92	89	96	57	70	73	0																								
	241	80	96	86	86	87	86	94	64	88	80	71	0																							
	263	88	99	92	91	91	88	96	72	87	86	62	25	0																						
	283	79	100	44	40	89	97	14	89	92	93	89	90	89	0																					
G-EBPR	72	92	94	96	94	96	92	98	73	79	87	33	74	69	94	0																				
	86	52	98	64	68	78	94	86	72	87	55	74	73	82	82	79	0																			
	107	62	99	16	23	84	96	62	89	97	82	90	86	90	54	95	54	0																		
	121	71	100	27	23	86	95	49	88	85	88	82	82	82	37	87	67	28	0																	
	241	70	99	67	69	85	92	83	78	92	88	74	57	47	77	79	68	64	64	0																
	263	89	95	93	93	93	88	97	65	87	86	70	52	42	94	72	82	92	89	45	0															
	283	71	99	61	62	85	92	78	78	87	89	71	64	59	70	80	70	58	57	36	66	0														
R-EBPR	72	87	97	91	91	93	95	97	66	66	78	73	88	91	94	78	82	95	94	91	88	81	0													
	86	97	98	98	98	98	98	99	91	90	90	86	93	95	98	88	91	97	96	94	94	85	32	0												
	107	93	99	96	95	96	95	98	86	90	89	79	88	91	96	83	89	96	93	90	91	78	54	43	0											
	121	91	99	93	93	95	95	97	83	88	93	83	89	90	93	86	92	97	93	90	91	79	68	66	32	0										
	241	92	99	93	93	94	94	96	85	91	92	85	88	89	94	91	92	95	93	89	89	81	80	79	55	30	0									
	263	95	99	96	96	96	95	98	89	90	95	86	89	87	96	90	94	97	94	88	86	80	77	72	46	19	21	0								
	283	68	98	75	76	82	94	88	81	86	81	70	77	77	81	79	55	71	70	69	85	57	70	74	47	37	51	45	0							
Moscow WRRF	225	67	99	55	56	84	94	64	76	90	88	81	78	81	62	87	68	62	66	61	85	51	77	76	63	66	71	71	55	0						
	255	65	99	61	62	83	95	67	80	89	87	83	84	87	66	90	67	70	73	71	89	63	76	74	61	63	69	68	57	23	0					
	270	71	98	66	67	83	95	70	73	87	80	81	82	86	71	88	67	79	82	78	88	77	77	75	75	77	81	82	70	31	24	0				
	284	63	98	60	61	82	95	67	78	89	86	84	84	87	67	90	65	70	75	71	89	71	83	82	76	78	81	83	69	27	13	18	0			
	304	73	99	68	69	83	94	71	74	88	83	83	82	87	71	91	69	80	82	79	88	79	82	89	87	86	88	90	73	44	27	23	22	0		
	313	69	99	66	66	81	94	69	73	88	82	83	82	87	70	91	65	77	80	77	88	75	76	84	83	83	86	88	67	37	20	17	15	12	0	
	320	100	96	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100	100	100	100	100	100	100	100	0

Taxonomic hierarchy with relative abundance

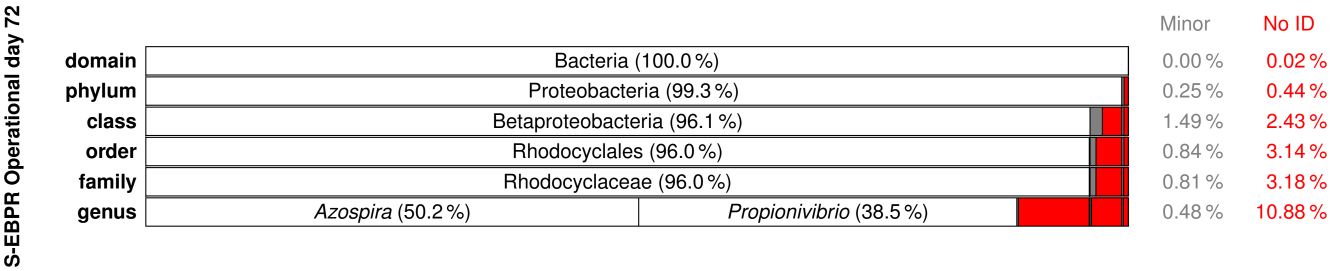

Figure S84. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

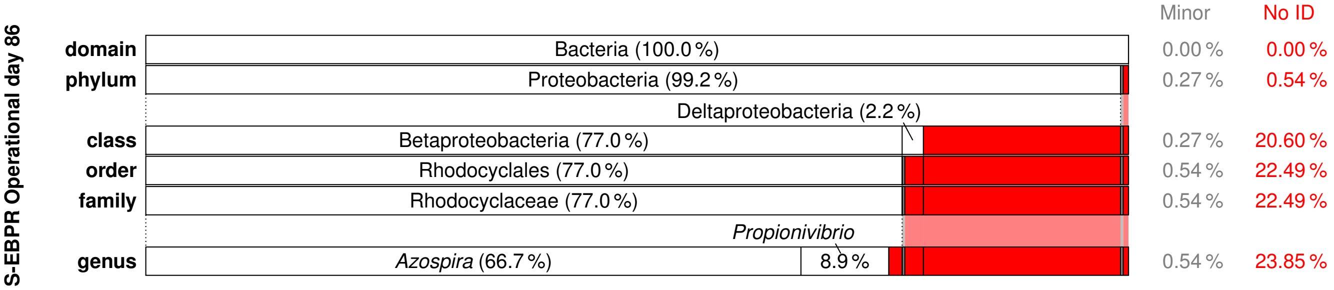

Figure S85. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

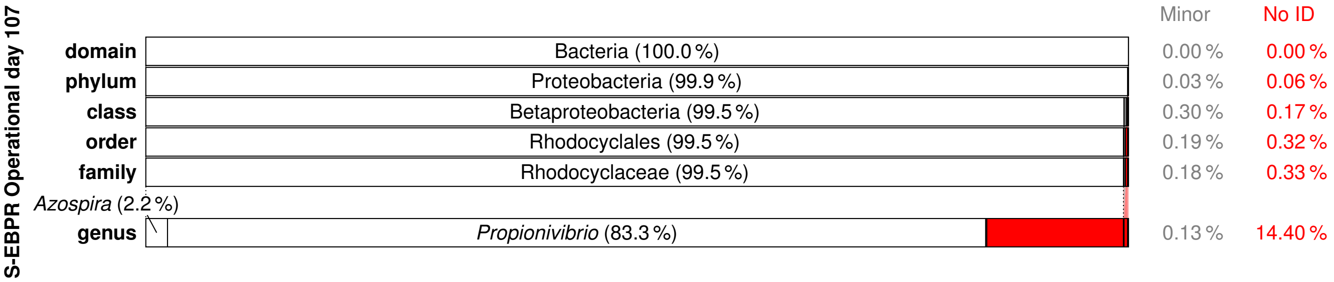

Figure S86. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

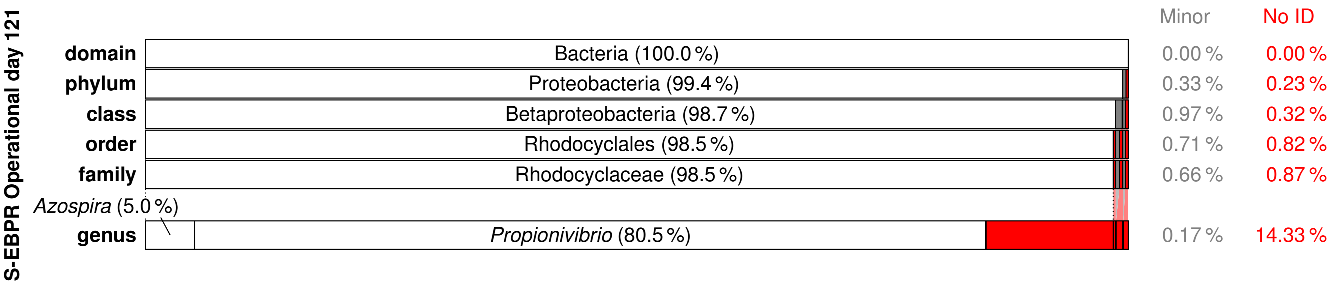

Figure S87. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

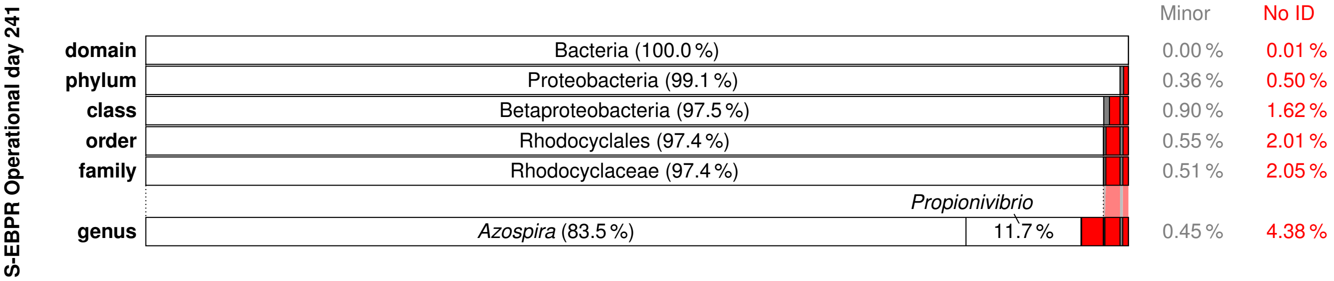

Figure S88. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

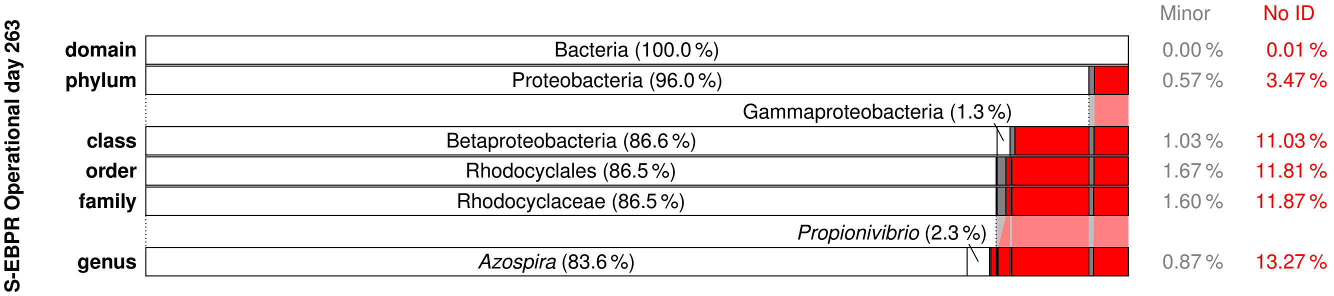

Figure S89. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

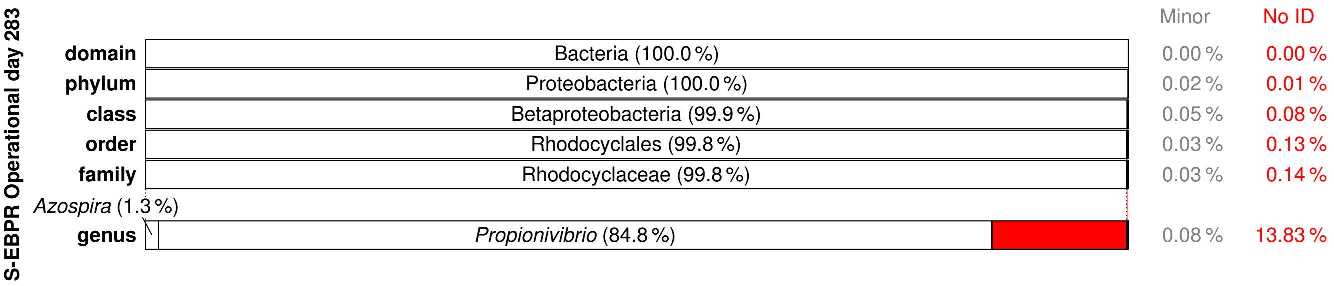

Figure S90. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

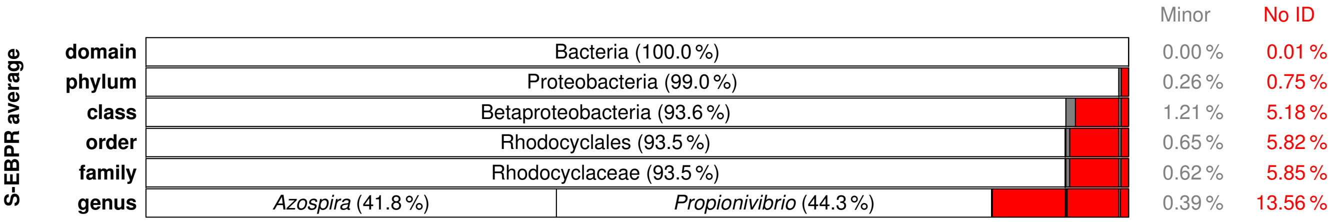

Figure S91. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for S-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

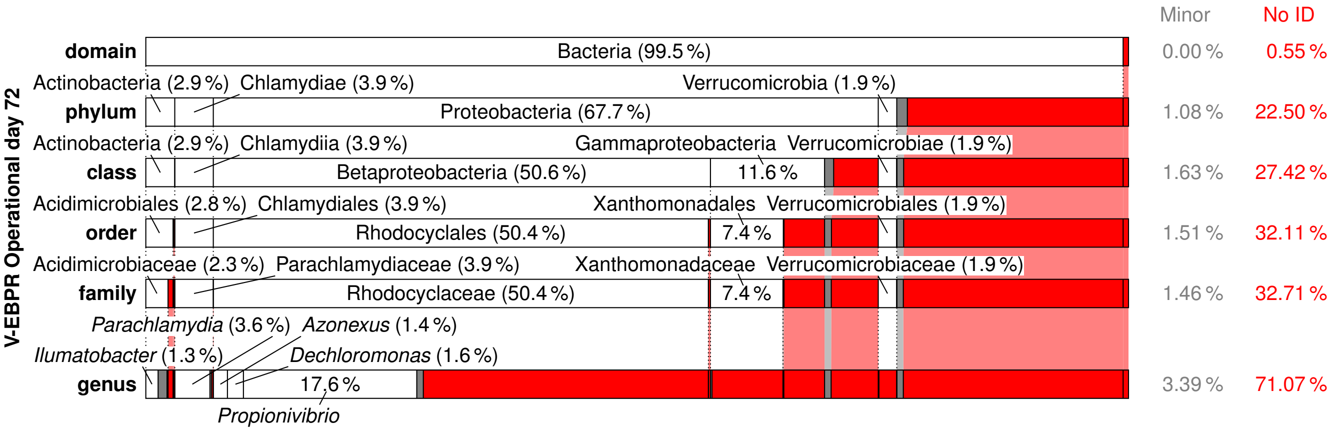

Figure S92. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

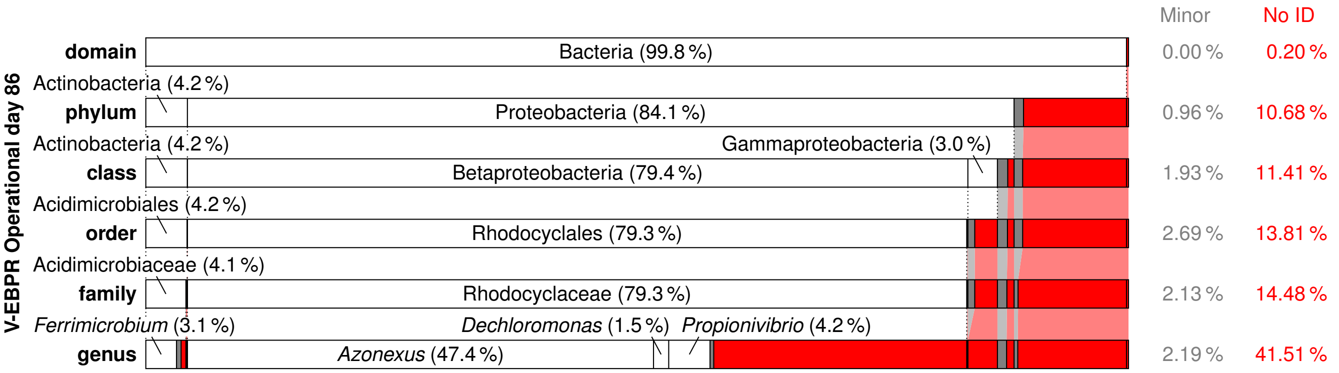

Figure S93. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

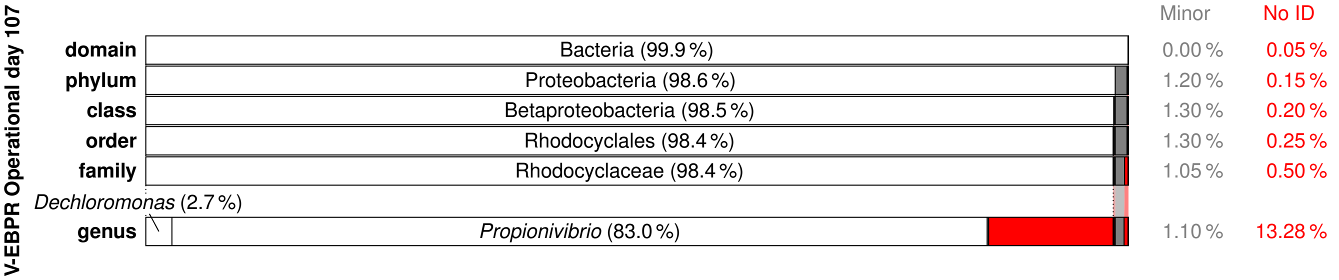

Figure S94. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

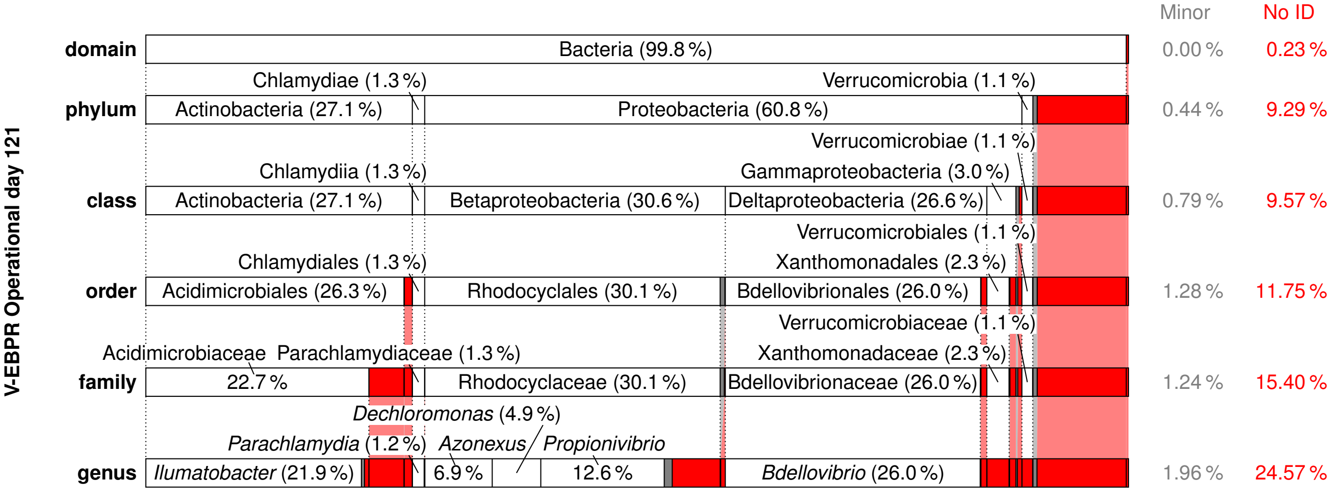

Figure S95. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

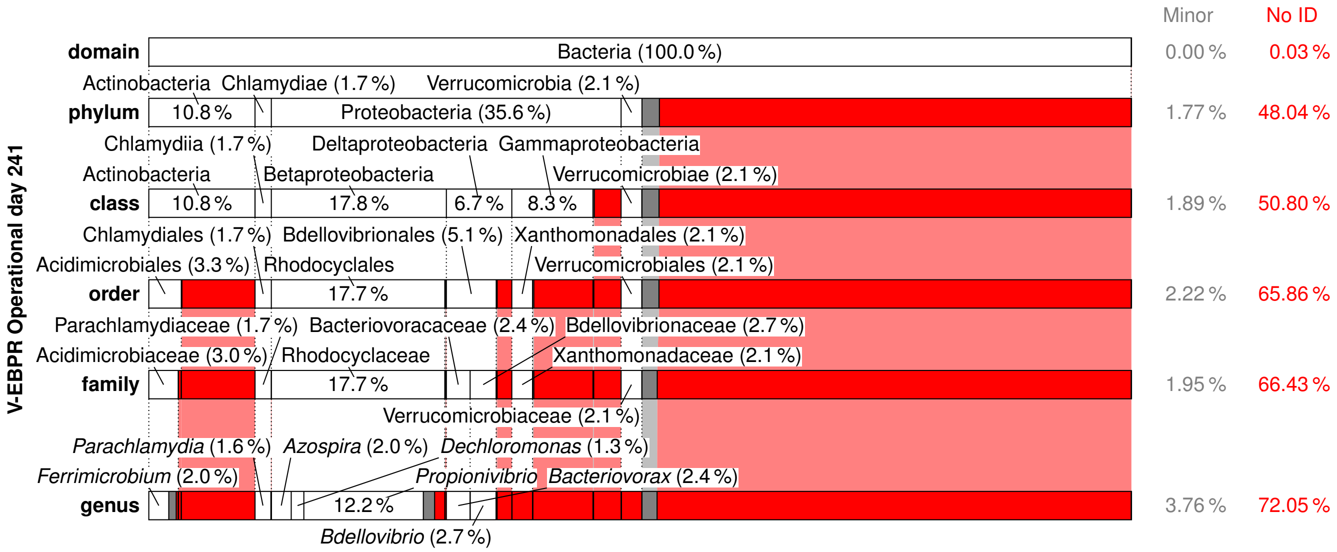

Figure S96. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

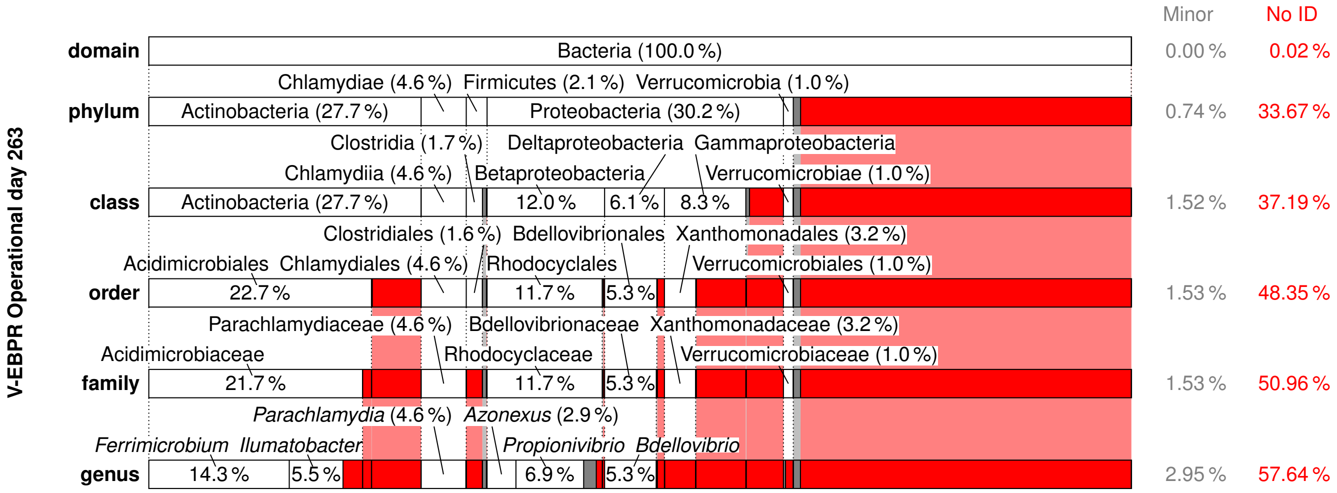

Figure S97. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

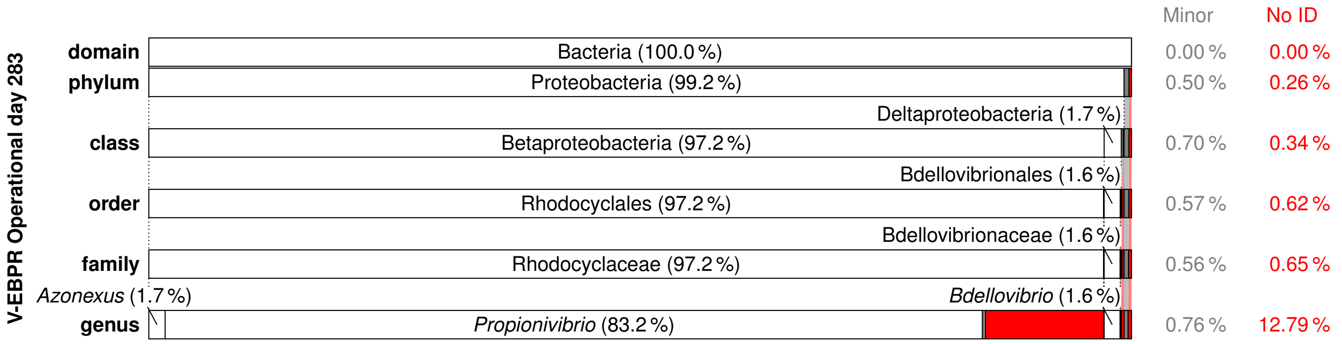

Figure S98. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

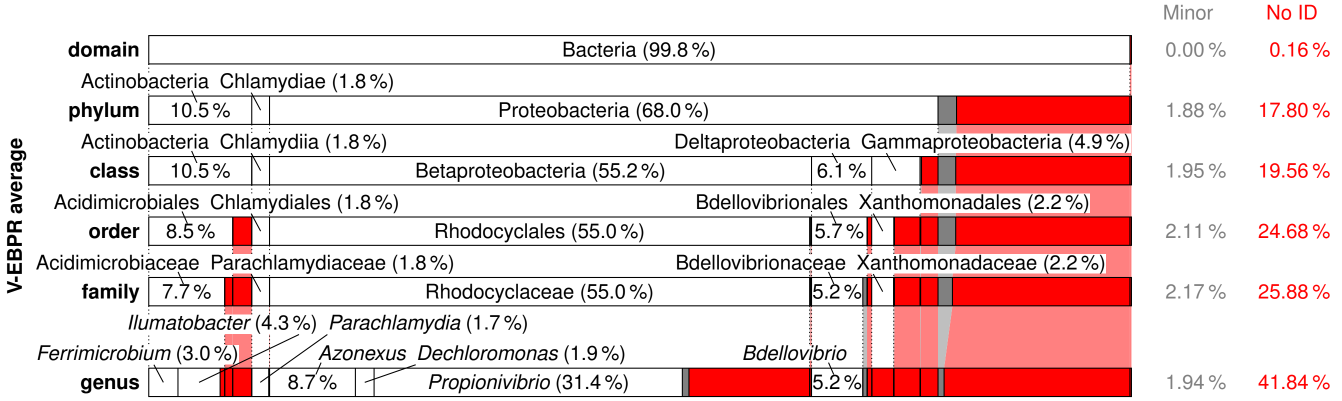

Figure S99. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for V-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

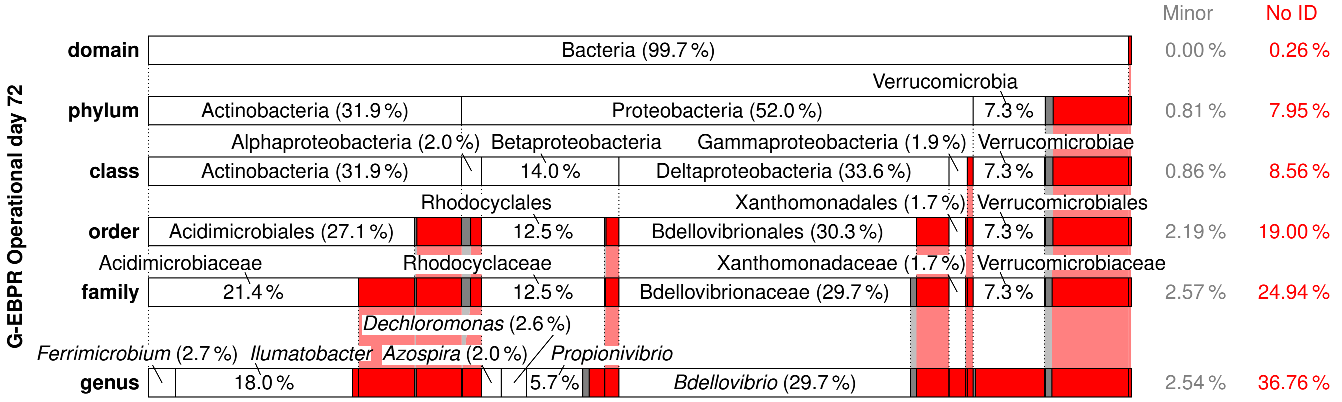

Figure S100. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

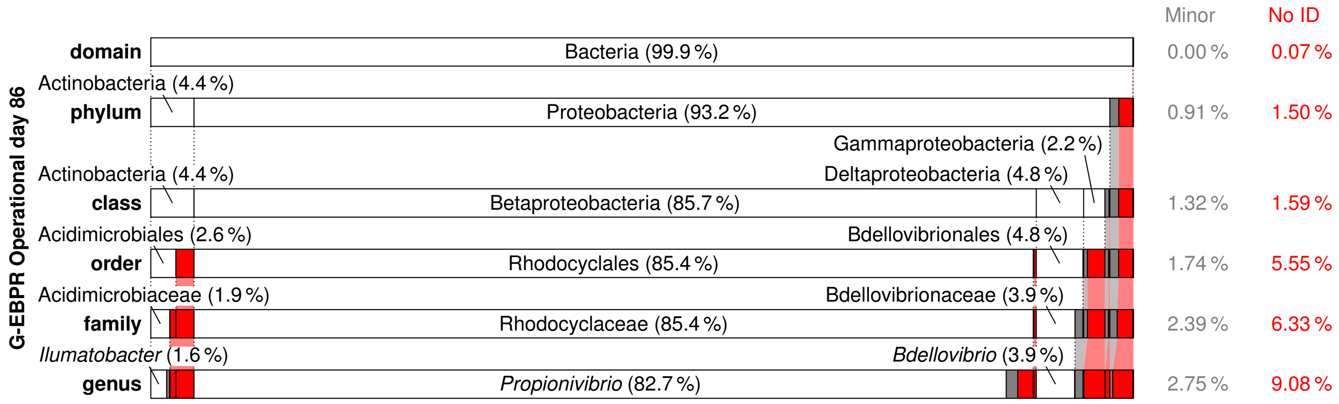

Figure S101. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

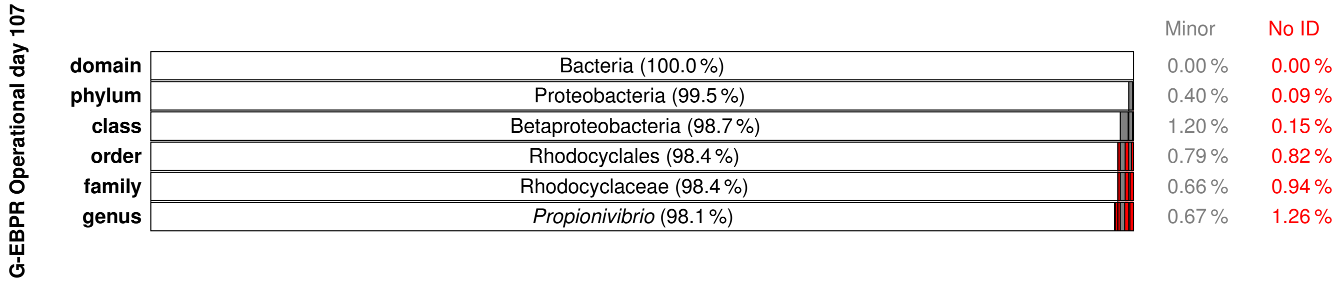

Figure S102. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

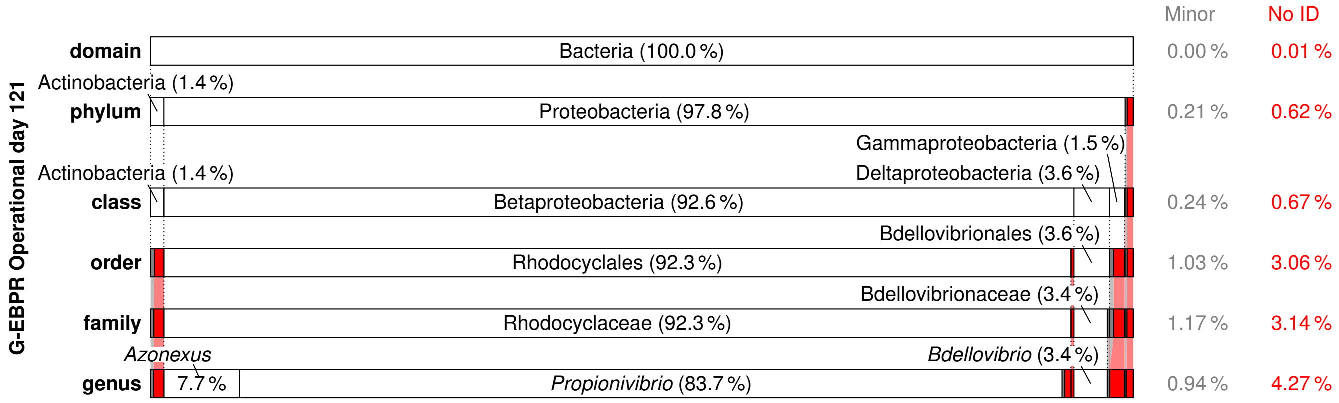

Figure S103. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

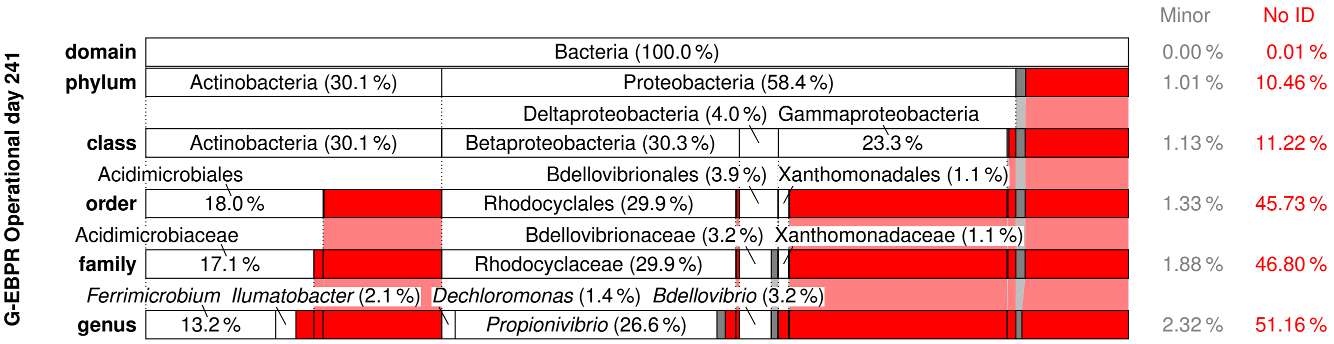

Figure S104. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

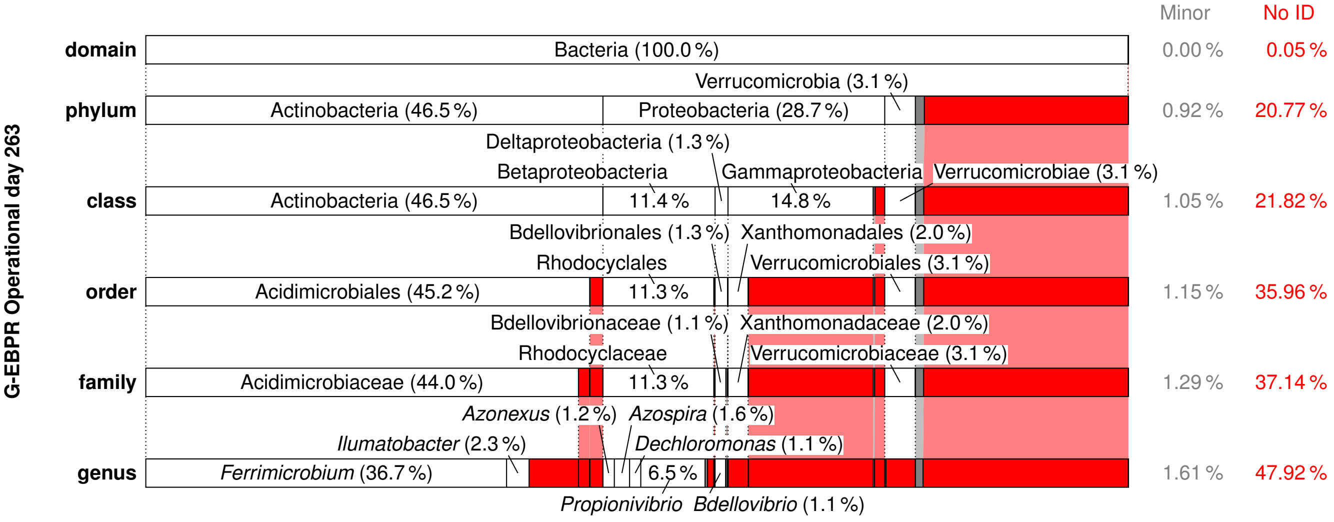

Figure S105. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

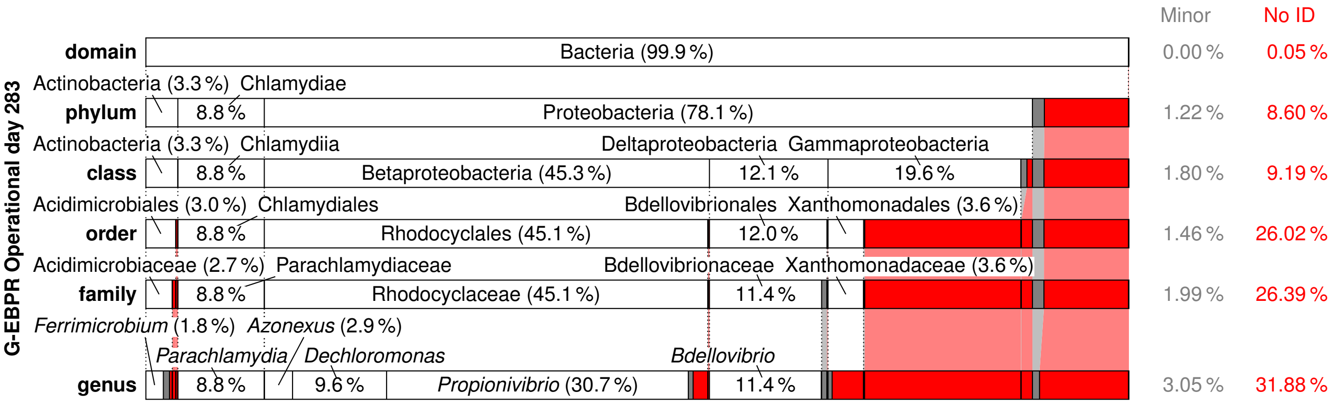

Figure S106. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

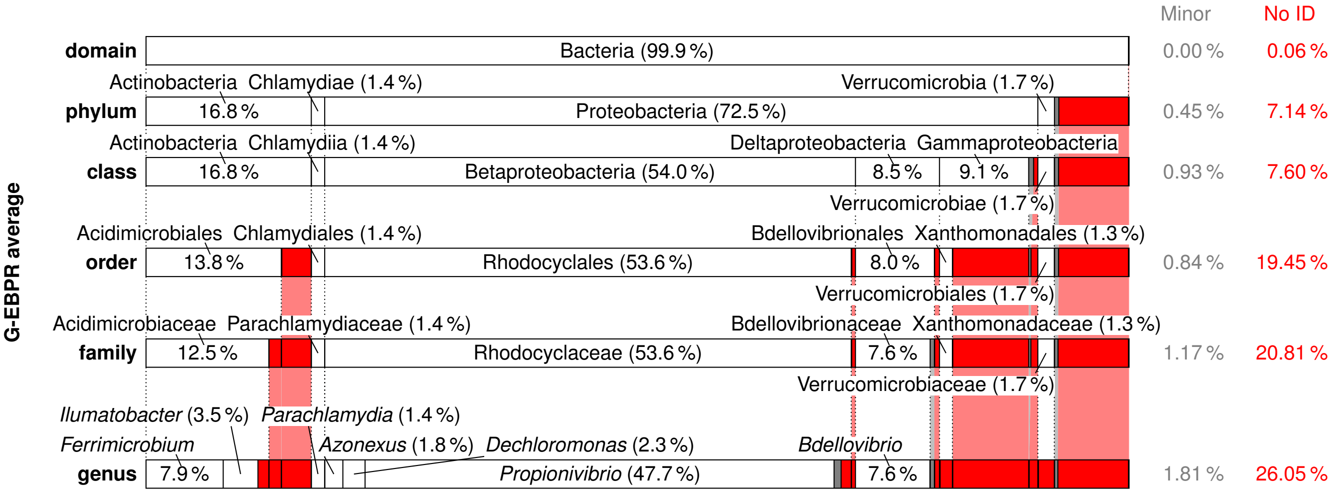

Figure S107. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for G-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

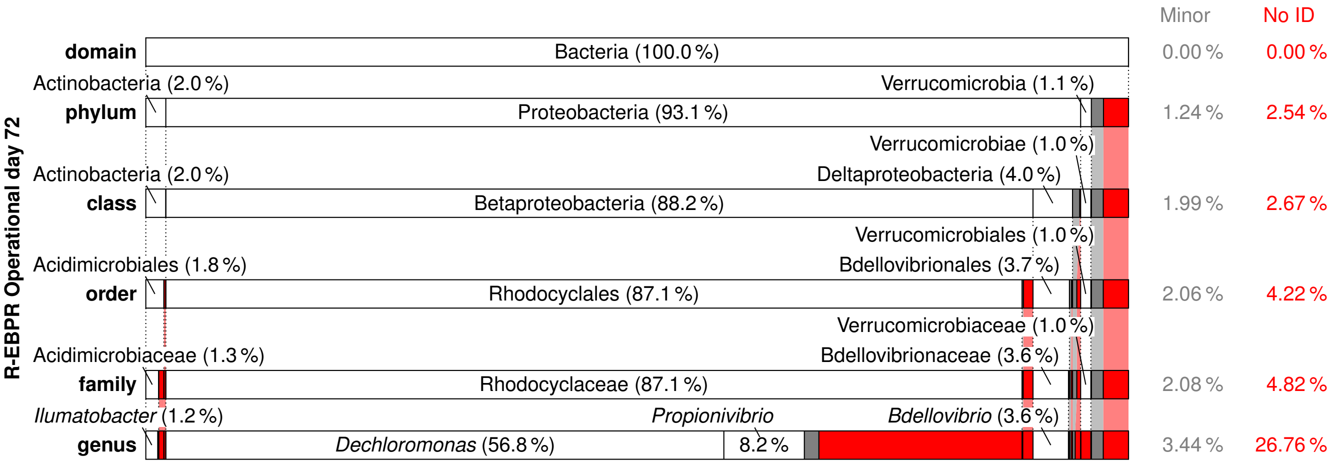

Figure S108. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

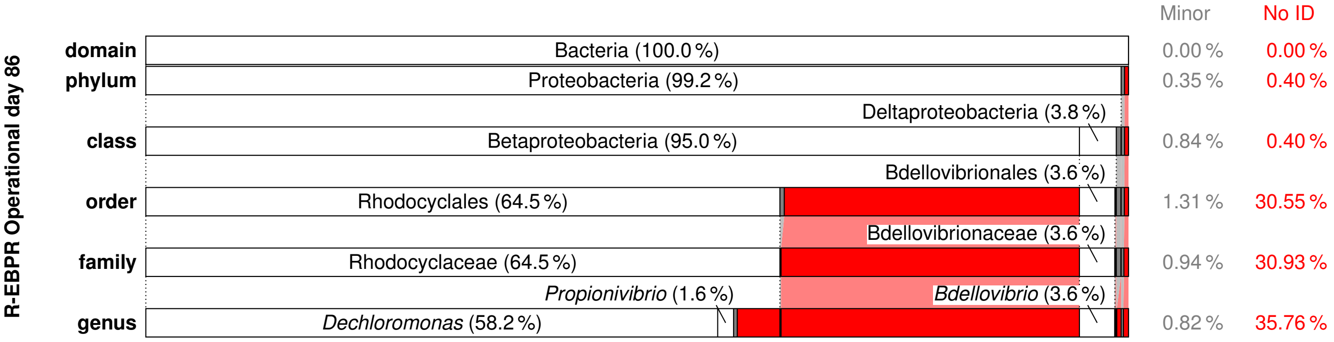

Figure S109. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

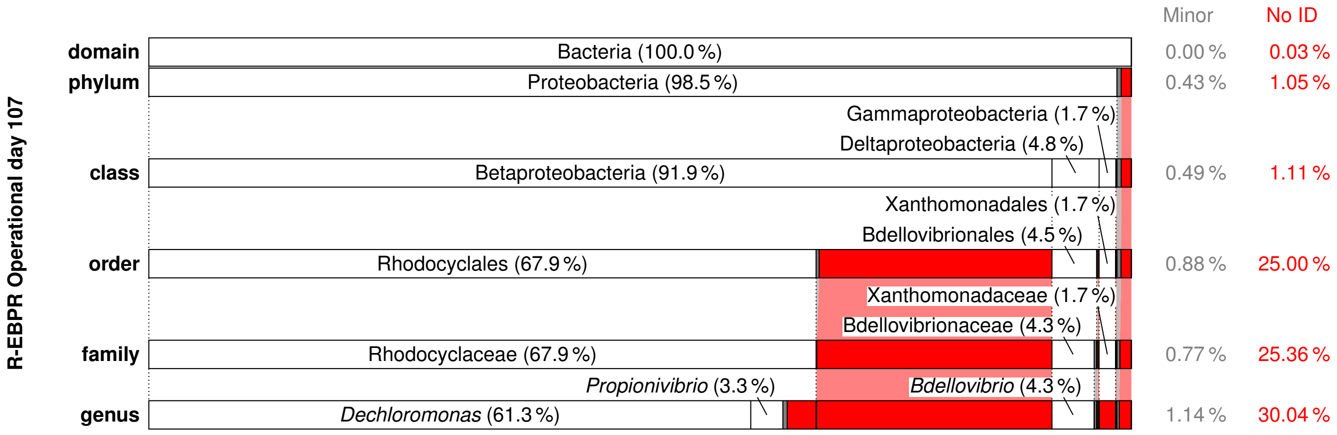

Figure S110. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

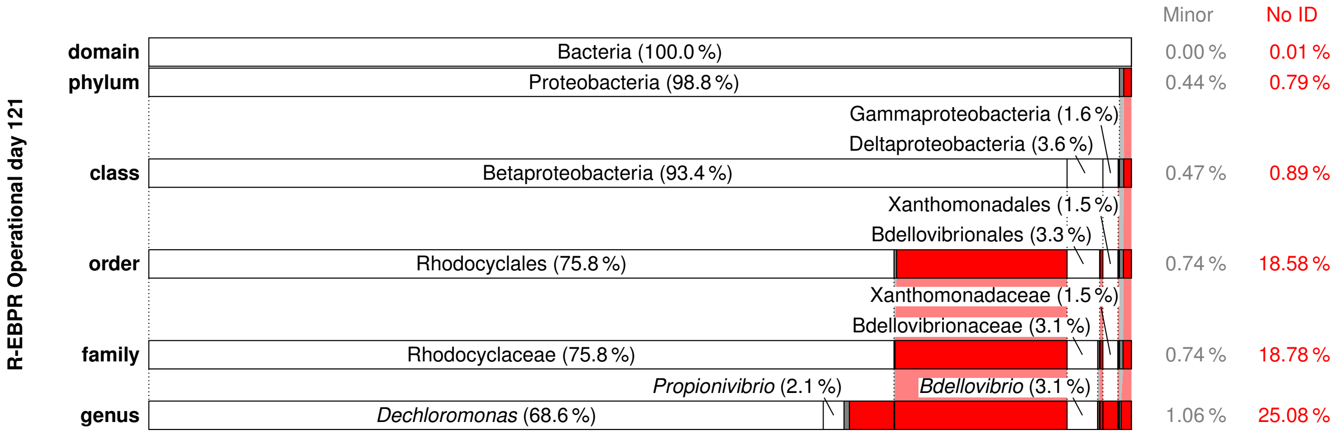

Figure S111. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

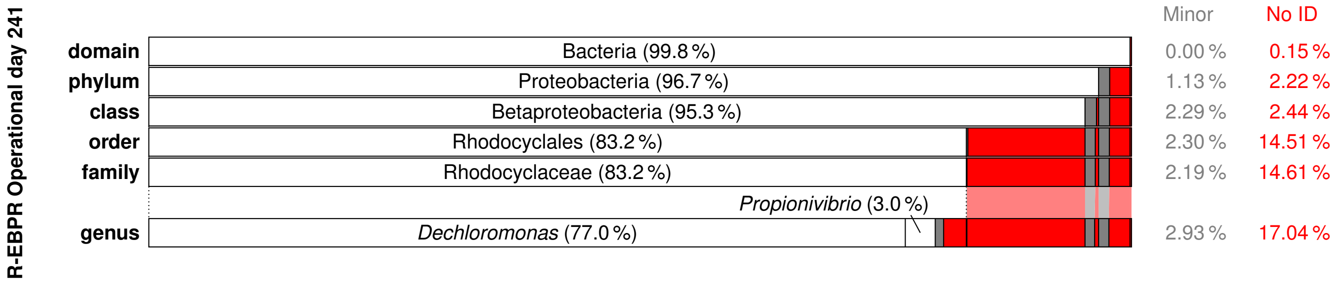

Figure S112. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

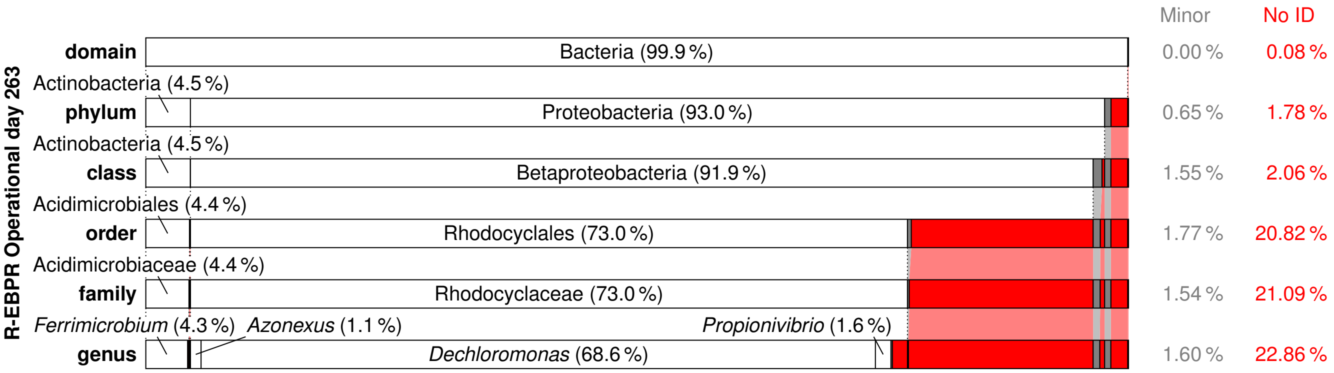

Figure S113. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

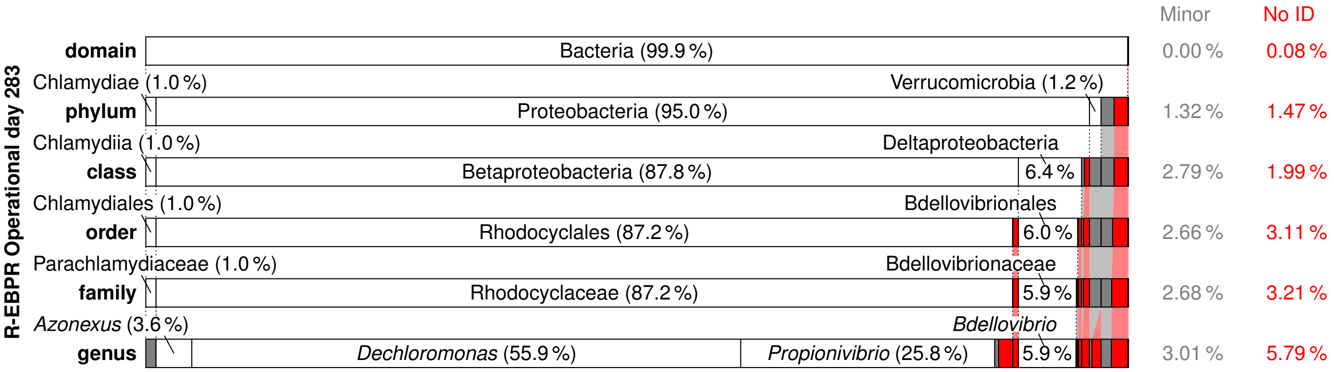

Figure S114. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

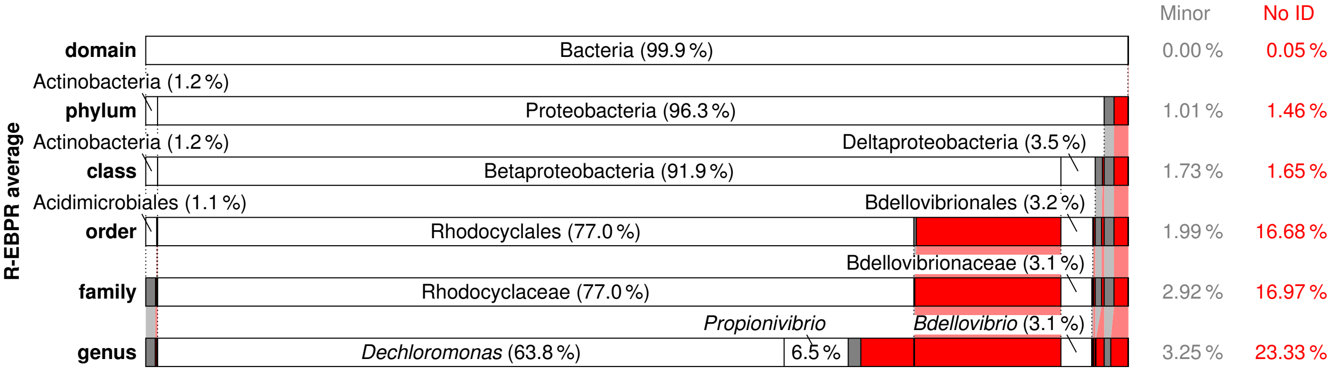

Figure S115. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for R-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

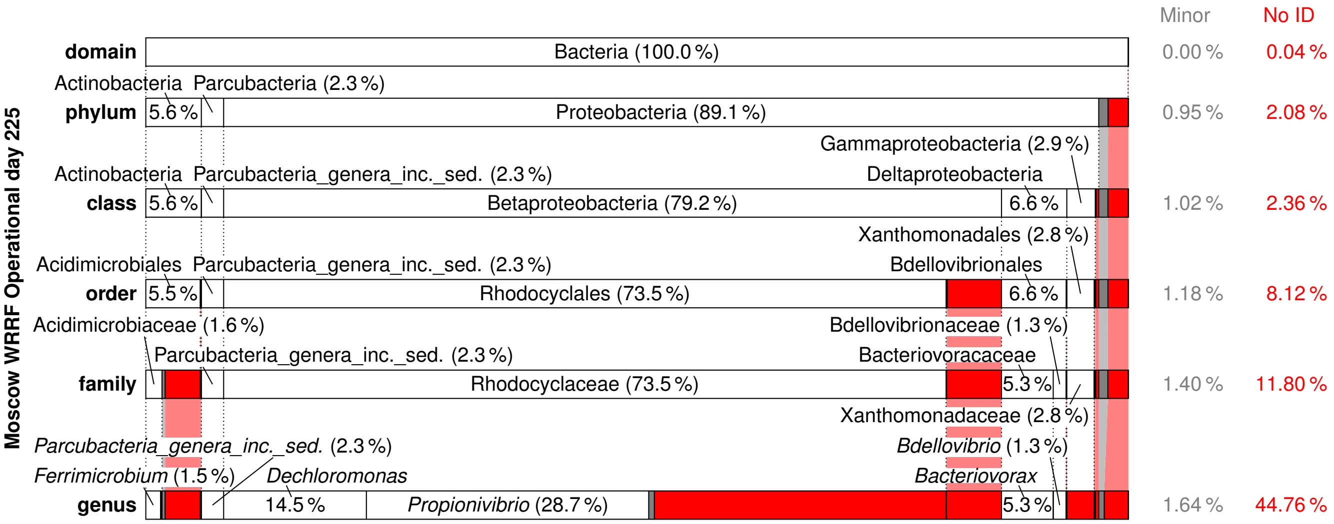

Figure S116. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF operational day 225. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

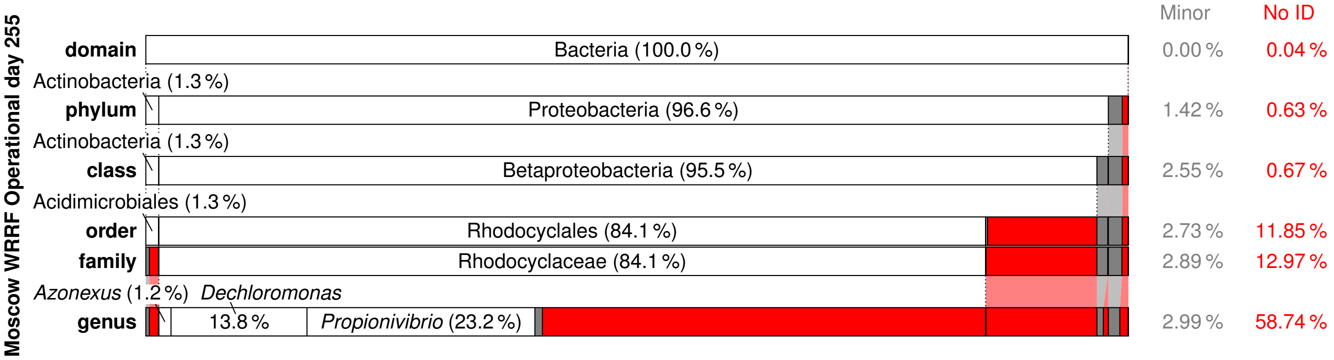

Figure S117. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF operational day 255. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

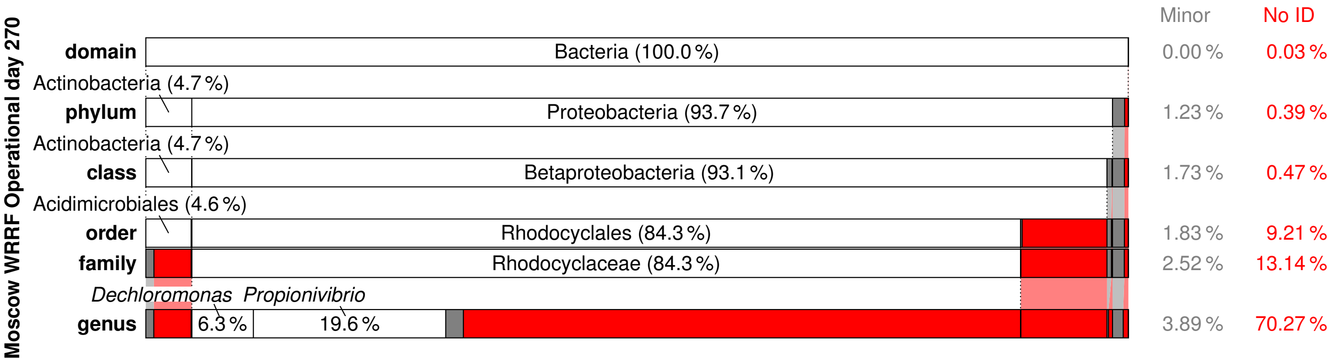

Figure S118. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF operational day 270. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

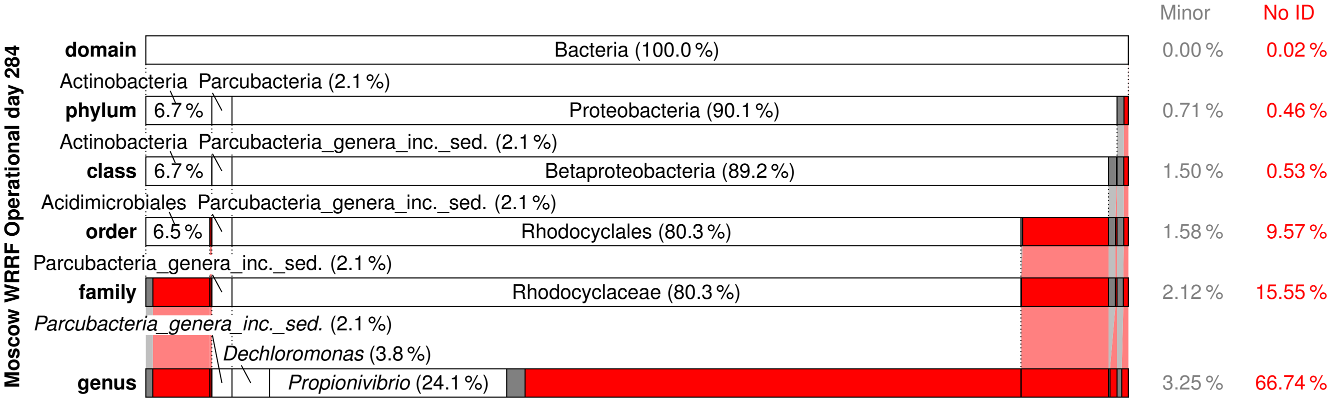

Figure S119. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF operational day 284. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

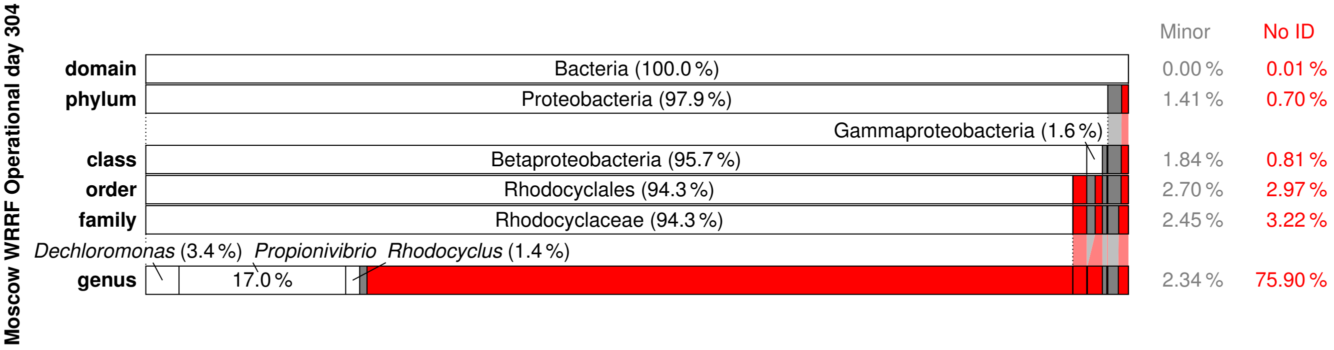

Figure S120. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF operational day 304. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

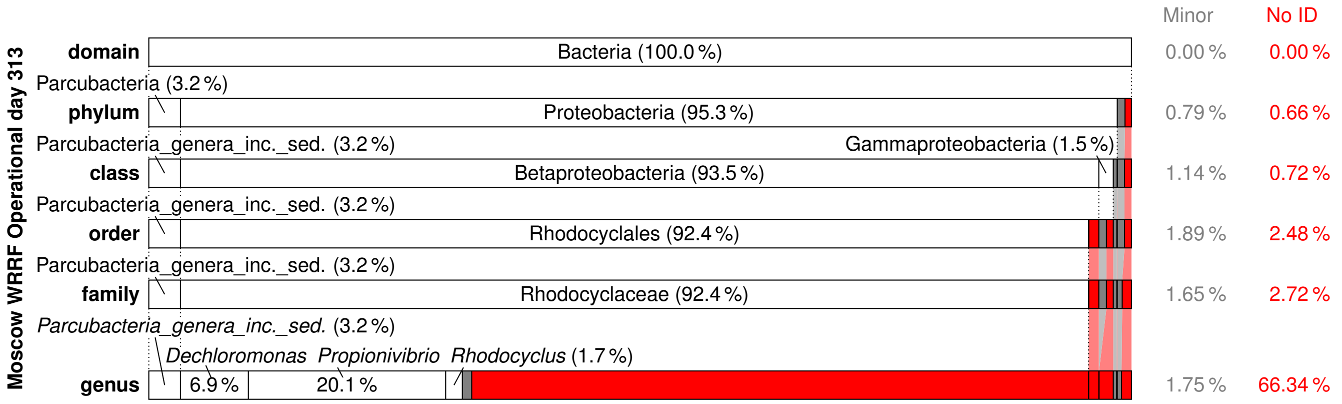

Figure S121. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF operational day 313. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

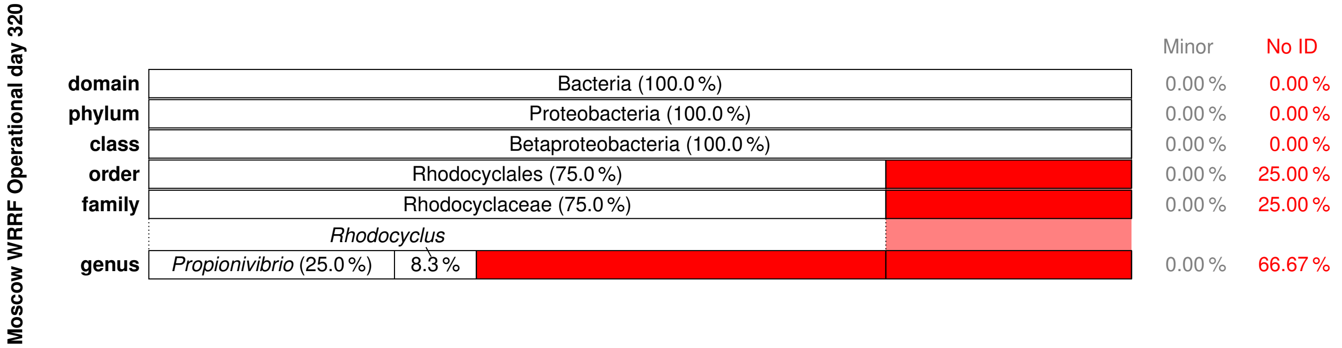

Figure S122. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF operational day 320. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

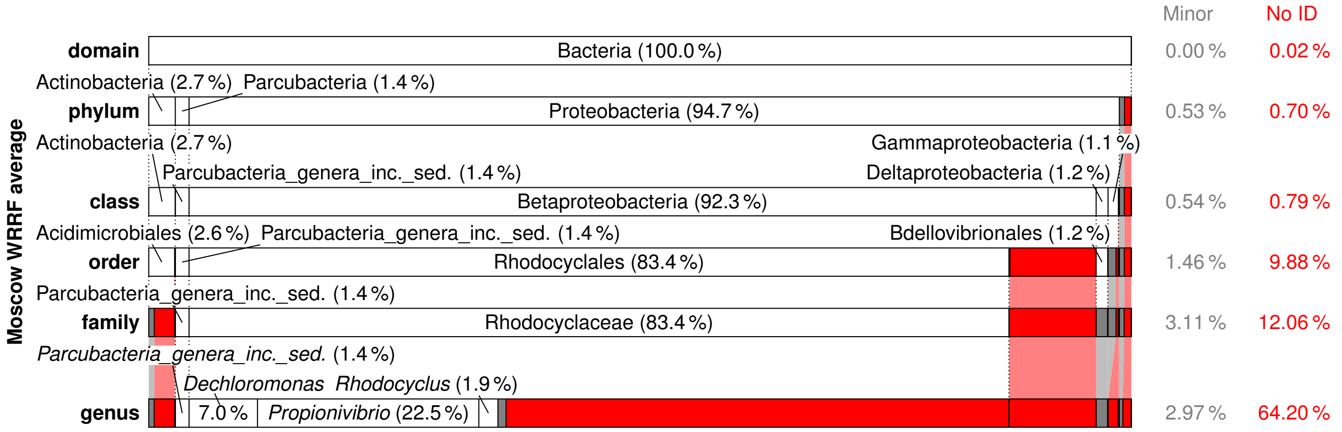

Figure S123. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing PAO primer set results for Moscow WRRF. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S57. S-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	$\pm 8.08{\cdot}10^{-3}$
Minor phylotypes (1)[d]	$1.85{\cdot}10^{-2}$	N.D.[e]	$4.27{\cdot}10^{-3}$	N.D.[e]	$1.41{\cdot}10^{-2}$	$1.45{\cdot}10^{-2}$	N.D.[e]	$7.33{\cdot}10^{-3}$	$\pm 8.08{\cdot}10^{-3}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S58. V-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.5	99.8	99.9	99.8	100.0	100.0	100.0	99.8	$\pm 1.95{\cdot}10^{-1}$
Minor phylotypes (1)[d]	$5.48{\cdot}10^{-1}$	$2.04{\cdot}10^{-1}$	$5.01{\cdot}10^{-2}$	$2.29{\cdot}10^{-1}$	$3.41{\cdot}10^{-2}$	$2.42{\cdot}10^{-2}$	$1.71{\cdot}10^{-3}$	$1.56{\cdot}10^{-1}$	$\pm 1.95{\cdot}10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S59. G-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.7	99.9	100.0	100.0	100.0	100.0	99.9	99.9	$\pm 9.15{\cdot}10^{-2}$
Minor phylotypes (1)[d]	$2.63{\cdot}10^{-1}$	$6.51{\cdot}10^{-2}$	N.D.[e]	$9.82{\cdot}10^{-3}$	$6.31{\cdot}10^{-3}$	$4.72{\cdot}10^{-2}$	$5.14{\cdot}10^{-2}$	$6.32{\cdot}10^{-2}$	$\pm 9.15{\cdot}10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S60. R-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Domain[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Bacteria	100.0	100.0	100.0	100.0	99.8	99.9	99.9	99.9	$\pm 5.63\cdot10^{-2}$
Minor phylotypes (1)[d]	N.D.[e]	N.D.[e]	$2.83\cdot10^{-2}$	$1.46\cdot10^{-2}$	$1.50\cdot10^{-1}$	$8.30\cdot10^{-2}$	$8.38\cdot10^{-2}$	$5.15\cdot10^{-2}$	$\pm 5.63\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S61. Moscow WRRF domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Domain[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Bacteria	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	$\pm 1.73\cdot10^{-2}$
Minor phylotypes (1)[d]	$4.19\cdot10^{-2}$	$4.22\cdot10^{-2}$	$2.74\cdot10^{-2}$	$1.57\cdot10^{-2}$	$9.04\cdot10^{-3}$	$4.88\cdot10^{-3}$	N.D.[e]	$2.02\cdot10^{-2}$	$\pm 1.73\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S62. Summary of domain-level relative abundance by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Domain[a,b]	S-EBPR (S57) Average %	 ± SD[c]	V-EBPR (S58) Average %	 ± SD[c]	G-EBPR (S59) Average %	 ± SD[c]	R-EBPR (S60) Average %	 ± SD[c]	Moscow WRRF (S61) Average %	 ± SD[c]
Bacteria	100.0	$\pm 8.08\cdot10^{-3}$	99.8	$\pm 1.95\cdot10^{-1}$	99.9	$\pm 9.15\cdot10^{-2}$	99.9	$\pm 5.63\cdot10^{-2}$	100.0	$\pm 1.73\cdot10^{-2}$
Minor phylotypes (1)[d]	$7.33\cdot10^{-3}$	$\pm 8.08\cdot10^{-3}$	$1.56\cdot10^{-1}$	$\pm 1.95\cdot10^{-1}$	$6.32\cdot10^{-2}$	$\pm 9.15\cdot10^{-2}$	$5.15\cdot10^{-2}$	$\pm 5.63\cdot10^{-2}$	$2.02\cdot10^{-2}$	$\pm 1.73\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S63. S-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
Proteobacteria	99.3	99.2	99.9	99.4	99.1	96.0	100.0	99.0	± 1.37
unknown d: *Bacteria*	$4.26\cdot10^{-1}$	$5.42\cdot10^{-1}$	$5.98\cdot10^{-2}$	$2.30\cdot10^{-1}$	$4.85\cdot10^{-1}$	3.45	$9.78\cdot10^{-3}$	$7.43\cdot10^{-1}$	± 1.21
Minor phylotypes (22)[d]	$2.65\cdot10^{-1}$	$2.71\cdot10^{-1}$	$2.99\cdot10^{-2}$	$3.26\cdot10^{-1}$	$3.78\cdot10^{-1}$	$5.82\cdot10^{-1}$	$1.82\cdot10^{-2}$	$2.67\cdot10^{-1}$	± $1.97\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S64. V-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
Proteobacteria	67.7	84.1	98.6	60.8	35.6	30.2	99.2	68.0	± 28.0
unknown d: *Bacteria*	22.0	10.5	$1.00\cdot10^{-1}$	9.06	48.0	33.7	$2.58\cdot10^{-1}$	17.6	± 17.9
Actinobacteria	2.95	4.23	$4.51\cdot10^{-1}$	27.1	10.8	27.7	$1.03\cdot10^{-1}$	10.5	± 12.1
Chlamydiae	3.92	$2.04\cdot10^{-1}$	$7.02\cdot10^{-1}$	1.26	1.66	4.60	$3.16\cdot10^{-1}$	1.81	± 1.76
Verrucomicrobia	1.88	$2.92\cdot10^{-2}$	$5.01\cdot10^{-2}$	1.12	2.13	1.00	$3.76\cdot10^{-2}$	$8.93\cdot10^{-1}$	± $8.90\cdot10^{-1}$
Firmicutes	$7.36\cdot10^{-1}$	$7.01\cdot10^{-1}$	N.D.[d]	$2.92\cdot10^{-1}$	$9.84\cdot10^{-1}$	2.12	$2.22\cdot10^{-2}$	$6.93\cdot10^{-1}$	± $7.31\cdot10^{-1}$
Minor phylotypes (18)[e]	$8.91\cdot10^{-1}$	$2.34\cdot10^{-1}$	$5.01\cdot10^{-2}$	$3.81\cdot10^{-1}$	$8.25\cdot10^{-1}$	$7.67\cdot10^{-1}$	$2.22\cdot10^{-2}$	$4.53\cdot10^{-1}$	± $3.72\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S65. G-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
Proteobacteria	52.0	93.2	99.5	97.8	58.4	28.7	78.1	72.5	± 27.0
Actinobacteria	31.9	4.39	$1.97\cdot10^{-1}$	1.36	30.1	46.5	3.25	16.8	± 18.9
unknown d: *Bacteria*	7.69	1.43	$8.67\cdot10^{-2}$	$6.12\cdot10^{-1}$	10.5	20.7	8.55	7.08	± 7.33

Table S65. G-EBPR phylum-level PAO results summary continued.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Verrucomicrobia	7.34	$4.88\cdot10^{-1}$	$1.73\cdot10^{-2}$	$5.56\cdot10^{-2}$	$3.35\cdot10^{-1}$	3.12	$4.88\cdot10^{-1}$	1.69	±	2.71
Chlamydiae	$3.15\cdot10^{-1}$	$3.25\cdot10^{-2}$	$5.20\cdot10^{-2}$	$1.15\cdot10^{-1}$	$9.47\cdot10^{-2}$	$1.42\cdot10^{-1}$	8.80	1.36	±	3.28
Minor phylotypes (19)[d]	$7.53\cdot10^{-1}$	$4.56\cdot10^{-1}$	$1.33\cdot10^{-1}$	$4.91\cdot10^{-2}$	$5.84\cdot10^{-1}$	$8.23\cdot10^{-1}$	$7.79\cdot10^{-1}$	$5.11\cdot10^{-1}$	±	$3.14\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S66. R-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Proteobacteria	93.1	99.2	98.5	98.8	96.7	93.0	95.0	96.3	±	2.66
unknown d: *Bacteria*	2.54	$3.99\cdot10^{-1}$	1.02	$7.73\cdot10^{-1}$	2.07	1.70	1.39	1.41	±	$7.51\cdot10^{-1}$
Actinobacteria	2.04	$2.11\cdot10^{-1}$	$1.98\cdot10^{-1}$	$1.07\cdot10^{-1}$	$5.65\cdot10^{-1}$	4.54	$7.49\cdot10^{-1}$	1.20	±	1.61
Verrucomicrobia	1.09	$4.69\cdot10^{-2}$	$1.13\cdot10^{-1}$	$2.29\cdot10^{-1}$	$7.10\cdot10^{-2}$	$4.90\cdot10^{-2}$	1.18	$3.97\cdot10^{-1}$	±	$5.09\cdot10^{-1}$
Minor phylotypes (19)[d]	$7.27\cdot10^{-1}$	$7.03\cdot10^{-2}$	$9.45\cdot10^{-2}$	$1.22\cdot10^{-1}$	$5.73\cdot10^{-1}$	$5.20\cdot10^{-1}$	$6.55\cdot10^{-1}$	$3.95\cdot10^{-1}$	±	$2.88\cdot10^{-1}$
Chlamydiae	$5.09\cdot10^{-1}$	$2.34\cdot10^{-2}$	$5.67\cdot10^{-2}$	N.D.[e]	$7.10\cdot10^{-2}$	$1.66\cdot10^{-1}$	1.04	$2.66\cdot10^{-1}$	±	$3.82\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S67. Moscow WRRF phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Phylum[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	±	SD[c]
Proteobacteria	89.1	96.6	93.7	90.1	97.9	95.3	100.0	94.7	±	4.02
Actinobacteria	5.65	1.32	4.68	6.72	$2.89\cdot10^{-1}$	$2.63\cdot10^{-1}$	N.D.[d]	2.70	±	2.88
Parcubacteria	2.27	$9.80\cdot10^{-1}$	$8.11\cdot10^{-1}$	2.05	$4.66\cdot10^{-1}$	3.22	N.D.[d]	1.40	±	1.14
unknown d: *Bacteria*	2.04	$5.90\cdot10^{-1}$	$3.67\cdot10^{-1}$	$4.44\cdot10^{-1}$	$6.92\cdot10^{-1}$	$6.59\cdot10^{-1}$	N.D.[d]	$6.84\cdot10^{-1}$	±	$6.41\cdot10^{-1}$

Table S67. Moscow WRRF phylum-level PAO results summary continued.

Phylum[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Minor phylotypes (20)[e]	$9.93 \cdot 10^{-1}$	$4.81 \cdot 10^{-1}$	$4.50 \cdot 10^{-1}$	$7.24 \cdot 10^{-1}$	$6.60 \cdot 10^{-1}$	$5.27 \cdot 10^{-1}$	N.D.[d]	$5.48 \cdot 10^{-1}$	$\pm 3.04 \cdot 10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S68. Summary of phylum-level relative abundance by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Phylum[a,b]	S-EBPR (S63)		V-EBPR (S64)		G-EBPR (S65)		R-EBPR (S66)		Moscow WRRF (S67)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
Proteobacteria	99.0	± 1.37	68.0	± 28.0	72.5	± 27.0	96.3	± 2.66	94.7	± 4.02
unknown d: *Bacteria*	$7.43 \cdot 10^{-1}$	± 1.21	17.6	± 17.9	7.08	± 7.33	1.41	$\pm 7.51 \cdot 10^{-1}$	$6.84 \cdot 10^{-1}$	$\pm 6.41 \cdot 10^{-1}$
Actinobacteria	$4.97 \cdot 10^{-2}$	$\pm 5.07 \cdot 10^{-2}$	10.5	± 12.1	16.8	± 18.9	1.20	± 1.61	2.70	± 2.88
Chlamydiae	$1.03 \cdot 10^{-2}$	$\pm 2.73 \cdot 10^{-2}$	1.81	± 1.76	1.36	± 3.28	$2.66 \cdot 10^{-1}$	$\pm 3.82 \cdot 10^{-1}$	$6.82 \cdot 10^{-2}$	$\pm 7.37 \cdot 10^{-2}$
Verrucomicrobia	$7.75 \cdot 10^{-2}$	$\pm 7.52 \cdot 10^{-2}$	$8.93 \cdot 10^{-1}$	$\pm 8.90 \cdot 10^{-1}$	1.69	± 2.71	$3.97 \cdot 10^{-1}$	$\pm 5.09 \cdot 10^{-1}$	$3.58 \cdot 10^{-1}$	$\pm 2.01 \cdot 10^{-1}$
Parcubacteria	N.D.[d]		$8.91 \cdot 10^{-2}$	$\pm 9.80 \cdot 10^{-2}$	$1.01 \cdot 10^{-1}$	$\pm 1.14 \cdot 10^{-1}$	$1.04 \cdot 10^{-1}$	$\pm 1.18 \cdot 10^{-1}$	1.40	± 1.14
Firmicutes	$1.47 \cdot 10^{-2}$	$\pm 3.06 \cdot 10^{-2}$	$6.93 \cdot 10^{-1}$	$\pm 7.31 \cdot 10^{-1}$	$2.65 \cdot 10^{-1}$	$\pm 1.41 \cdot 10^{-1}$	$1.80 \cdot 10^{-1}$	$\pm 1.77 \cdot 10^{-1}$	$6.33 \cdot 10^{-2}$	$\pm 3.28 \cdot 10^{-2}$
Minor phylotypes (17)[e]	$1.15 \cdot 10^{-1}$	$\pm 1.05 \cdot 10^{-1}$	$3.64 \cdot 10^{-1}$	$\pm 3.04 \cdot 10^{-1}$	$1.45 \cdot 10^{-1}$	$\pm 1.36 \cdot 10^{-1}$	$1.11 \cdot 10^{-1}$	$\pm 5.19 \cdot 10^{-2}$	$5.80 \cdot 10^{-2}$	$\pm 3.99 \cdot 10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S69. S-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Betaproteobacteria	96.1	77.0	99.5	98.7	97.5	86.6	99.9	93.6	± 8.63
unknown p: *Proteobacteria*	1.97	20.1	$1.02 \cdot 10^{-1}$	$6.30 \cdot 10^{-2}$	1.07	7.53	$7.12 \cdot 10^{-2}$	4.41	± 7.39

Table S69. S-EBPR class-level PAO results summary continued.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown d: *Bacteria*	$4.26\cdot10^{-1}$	$5.42\cdot10^{-1}$	$5.98\cdot10^{-2}$	$2.30\cdot10^{-1}$	$4.85\cdot10^{-1}$	3.45	$9.78\cdot10^{-3}$	$7.43\cdot10^{-1}$	±	1.21
Deltaproteobacteria	$7.15\cdot10^{-1}$	2.17	$9.82\cdot10^{-2}$	$3.08\cdot10^{-1}$	$2.00\cdot10^{-1}$	$3.94\cdot10^{-1}$	$1.26\cdot10^{-2}$	$5.57\cdot10^{-1}$	±	$7.46\cdot10^{-1}$
Gammaproteobacteria	$5.06\cdot10^{-1}$	N.D.[d]	$1.66\cdot10^{-1}$	$3.22\cdot10^{-1}$	$3.21\cdot10^{-1}$	1.31	$1.96\cdot10^{-2}$	$3.78\cdot10^{-1}$	±	$4.49\cdot10^{-1}$
Minor phylotypes (44)[e]	$3.02\cdot10^{-1}$	$2.71\cdot10^{-1}$	$3.84\cdot10^{-2}$	$3.63\cdot10^{-1}$	$4.40\cdot10^{-1}$	$6.87\cdot10^{-1}$	$1.82\cdot10^{-2}$	$3.03\cdot10^{-1}$	±	$2.32\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S70. V-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Betaproteobacteria	50.6	79.4	98.5	30.6	17.8	12.0	97.2	55.2	±	36.8
unknown d: *Bacteria*	22.0	10.5	$1.00\cdot10^{-1}$	9.06	48.0	33.7	$2.58\cdot10^{-1}$	17.6	±	17.9
Actinobacteria	2.95	4.23	$4.51\cdot10^{-1}$	27.1	10.8	27.7	$1.03\cdot10^{-1}$	10.5	±	12.1
Deltaproteobacteria	$7.88\cdot10^{-1}$	$9.63\cdot10^{-1}$	N.D.[d]	26.6	6.66	6.09	1.74	6.12	±	9.42
Gammaproteobacteria	11.6	3.01	$1.00\cdot10^{-1}$	2.96	8.26	8.28	$2.05\cdot10^{-1}$	4.92	±	4.48
Chlamydiia	3.92	$2.04\cdot10^{-1}$	$7.02\cdot10^{-1}$	1.26	1.66	4.60	$3.16\cdot10^{-1}$	1.81	±	1.76
unknown p: *Proteobacteria*	4.54	$6.42\cdot10^{-1}$	$5.01\cdot10^{-2}$	$2.79\cdot10^{-1}$	2.72	3.45	$7.86\cdot10^{-2}$	1.68	±	1.85
Minor phylotypes (40)[e]	1.73	$5.55\cdot10^{-1}$	$5.01\cdot10^{-2}$	1.02	1.77	1.61	$2.73\cdot10^{-2}$	$9.65\cdot10^{-1}$	±	$7.67\cdot10^{-1}$
Verrucomicrobiae	1.88	$2.92\cdot10^{-2}$	$5.01\cdot10^{-2}$	1.11	2.12	1.00	$3.76\cdot10^{-2}$	$8.89\cdot10^{-1}$	±	$8.87\cdot10^{-1}$
Clostridia	$3.43\cdot10^{-2}$	$4.67\cdot10^{-1}$	N.D.[d]	N.D.[d]	$1.93\cdot10^{-1}$	1.65	$1.71\cdot10^{-2}$	$3.37\cdot10^{-1}$	±	$6.03\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S71. G-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Class[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%	%		
Betaproteobacteria	14.0	85.7	98.7	92.6	30.3	11.4	45.3	54.0	±	37.7
Actinobacteria	31.9	4.39	$1.97\cdot10^{-1}$	1.36	30.1	46.5	3.25	16.8	±	18.9
Gammaproteobacteria	1.86	2.16	$3.41\cdot10^{-1}$	1.52	23.3	14.8	19.6	9.08	±	9.82
Deltaproteobacteria	33.6	4.82	$4.63\cdot10^{-1}$	3.62	3.97	1.32	12.1	8.55	±	11.7
unknown d: *Bacteria*	7.69	1.43	$8.67\cdot10^{-2}$	$6.12\cdot10^{-1}$	10.5	20.7	8.55	7.08	±	7.33
Verrucomicrobiae	7.27	$4.56\cdot10^{-1}$	$1.16\cdot10^{-2}$	$5.56\cdot10^{-2}$	$3.35\cdot10^{-1}$	3.12	$4.80\cdot10^{-1}$	1.67	±	2.69
Chlamydiia	$3.15\cdot10^{-1}$	$3.25\cdot10^{-2}$	$5.20\cdot10^{-2}$	$1.15\cdot10^{-1}$	$9.47\cdot10^{-2}$	$1.42\cdot10^{-1}$	8.80	1.36	±	3.28
Minor phylotypes (41)[d]	1.42	$5.69\cdot10^{-1}$	$1.97\cdot10^{-1}$	$9.16\cdot10^{-2}$	1.29	1.80	1.34	$9.59\cdot10^{-1}$	±	$6.66\cdot10^{-1}$
Alphaproteobacteria	2.03	$4.23\cdot10^{-1}$	N.D.[e]	$2.95\cdot10^{-2}$	$1.80\cdot10^{-1}$	$2.02\cdot10^{-1}$	$6.22\cdot10^{-1}$	$4.98\cdot10^{-1}$	±	$7.11\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S72. R-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Class[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%	%		
Betaproteobacteria	88.2	95.0	91.9	93.4	95.3	91.9	87.8	91.9	±	3.00
Deltaproteobacteria	4.02	3.75	4.80	3.64	$9.93\cdot10^{-1}$	$8.03\cdot10^{-1}$	6.43	3.49	±	2.01
unknown d: *Bacteria*	2.54	$3.99\cdot10^{-1}$	1.02	$7.73\cdot10^{-1}$	2.07	1.70	1.39	1.41	±	$7.51\cdot10^{-1}$
Actinobacteria	2.04	$2.11\cdot10^{-1}$	$1.98\cdot10^{-1}$	$1.07\cdot10^{-1}$	$5.65\cdot10^{-1}$	4.54	$7.49\cdot10^{-1}$	1.20	±	1.61
Minor phylotypes (42)[d]	1.24	$1.17\cdot10^{-1}$	$2.46\cdot10^{-1}$	$2.82\cdot10^{-1}$	$9.74\cdot10^{-1}$	$8.79\cdot10^{-1}$	1.47	$7.44\cdot10^{-1}$	±	$5.32\cdot10^{-1}$
Gammaproteobacteria	$3.64\cdot10^{-1}$	$4.69\cdot10^{-1}$	1.70	1.56	$5.11\cdot10^{-2}$	$5.28\cdot10^{-2}$	$1.89\cdot10^{-1}$	$6.26\cdot10^{-1}$	±	$7.03\cdot10^{-1}$
Verrucomicrobiae	1.04	$2.34\cdot10^{-2}$	$7.56\cdot10^{-2}$	$1.95\cdot10^{-1}$	$8.52\cdot10^{-3}$	$3.77\cdot10^{-3}$	$9.75\cdot10^{-1}$	$3.32\cdot10^{-1}$	±	$4.67\cdot10^{-1}$
Chlamydiia	$5.09\cdot10^{-1}$	$2.34\cdot10^{-2}$	$5.67\cdot10^{-2}$	N.D.[e]	$7.10\cdot10^{-2}$	$1.66\cdot10^{-1}$	1.04	$2.66\cdot10^{-1}$	±	$3.82\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S73. Moscow WRRF class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Class[a,b]	225	255	270	284	304	313	320	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Betaproteobacteria	79.2	95.5	93.1	89.2	95.7	93.5	100.0	92.3	± 6.65
Actinobacteria	5.65	1.32	4.68	6.72	$2.89\cdot10^{-1}$	$2.63\cdot10^{-1}$	N.D.[d]	2.70	± 2.88
Parcubacteria_genera_inc._sed.[e]	2.27	$9.80\cdot10^{-1}$	$8.11\cdot10^{-1}$	2.05	$4.66\cdot10^{-1}$	3.22	N.D.[d]	1.40	± 1.14
Deltaproteobacteria	6.65	$6.61\cdot10^{-1}$	$1.75\cdot10^{-1}$	$1.61\cdot10^{-1}$	$4.52\cdot10^{-1}$	$3.76\cdot10^{-1}$	N.D.[d]	1.21	± 2.41
Gammaproteobacteria	2.90	$4.43\cdot10^{-1}$	$3.24\cdot10^{-1}$	$6.25\cdot10^{-1}$	1.59	1.47	N.D.[d]	1.05	± 1.01
unknown d: *Bacteria*	2.04	$5.90\cdot10^{-1}$	$3.67\cdot10^{-1}$	$4.44\cdot10^{-1}$	$6.92\cdot10^{-1}$	$6.59\cdot10^{-1}$	N.D.[d]	$6.84\cdot10^{-1}$	$\pm 6.41\cdot10^{-1}$
Minor phylotypes (43)[f]	1.34	$5.41\cdot10^{-1}$	$5.15\cdot10^{-1}$	$8.02\cdot10^{-1}$	$7.60\cdot10^{-1}$	$5.56\cdot10^{-1}$	N.D.[d]	$6.45\cdot10^{-1}$	$\pm 4.04\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S74. Summary of class-level relative abundance by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Class[a,b]	S-EBPR (S69)		V-EBPR (S70)		G-EBPR (S71)		R-EBPR (S72)		Moscow WRRF (S73)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
Betaproteobacteria	93.6	± 8.63	55.2	± 36.8	54.0	± 37.7	91.9	± 3.00	92.3	± 6.65
unknown d: *Bacteria*	$7.43\cdot10^{-1}$	± 1.21	17.6	± 17.9	7.08	± 7.33	1.41	$\pm 7.51\cdot10^{-1}$	$6.84\cdot10^{-1}$	$\pm 6.41\cdot10^{-1}$
Actinobacteria	$4.97\cdot10^{-2}$	$\pm 5.07\cdot10^{-2}$	10.5	± 12.1	16.8	± 18.9	1.20	± 1.61	2.70	± 2.88
Gammaproteobacteria	$3.78\cdot10^{-1}$	$\pm 4.49\cdot10^{-1}$	4.92	± 4.48	9.08	± 9.82	$6.26\cdot10^{-1}$	$\pm 7.03\cdot10^{-1}$	1.05	± 1.01
Deltaproteobacteria	$5.57\cdot10^{-1}$	$\pm 7.46\cdot10^{-1}$	6.12	± 9.42	8.55	± 11.7	3.49	± 2.01	1.21	± 2.41
unknown p: *Proteobacteria*	4.41	± 7.39	1.68	± 1.85	$4.31\cdot10^{-1}$	$\pm 3.72\cdot10^{-1}$	$1.77\cdot10^{-1}$	$\pm 1.74\cdot10^{-1}$	$6.77\cdot10^{-2}$	$\pm 9.21\cdot10^{-2}$
Chlamydiia	$1.03\cdot10^{-2}$	$\pm 2.73\cdot10^{-2}$	1.81	± 1.76	1.36	± 3.28	$2.66\cdot10^{-1}$	$\pm 3.82\cdot10^{-1}$	$6.82\cdot10^{-2}$	$\pm 7.37\cdot10^{-2}$
Verrucomicrobiae	$7.66\cdot10^{-2}$	$\pm 7.52\cdot10^{-2}$	$8.89\cdot10^{-1}$	$\pm 8.87\cdot10^{-1}$	1.67	± 2.69	$3.32\cdot10^{-1}$	$\pm 4.67\cdot10^{-1}$	$1.30\cdot10^{-1}$	$\pm 1.25\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[d]	N.D.[e]		$8.91\cdot10^{-2}$	$\pm 9.80\cdot10^{-2}$	$1.01\cdot10^{-1}$	$\pm 1.14\cdot10^{-1}$	$1.04\cdot10^{-1}$	$\pm 1.18\cdot10^{-1}$	1.40	± 1.14
Minor phylotypes (38)[f]	$1.23\cdot10^{-1}$	$\pm 1.14\cdot10^{-1}$	$7.23\cdot10^{-1}$	$\pm 6.19\cdot10^{-1}$	$3.63\cdot10^{-1}$	$\pm 2.83\cdot10^{-1}$	$3.51\cdot10^{-1}$	$\pm 2.32\cdot10^{-1}$	$3.30\cdot10^{-1}$	$\pm 1.77\cdot10^{-1}$
Alphaproteobacteria	$3.56\cdot10^{-2}$	$\pm 3.82\cdot10^{-2}$	$1.53\cdot10^{-1}$	$\pm 1.48\cdot10^{-1}$	$4.98\cdot10^{-1}$	$\pm 7.11\cdot10^{-1}$	$1.07\cdot10^{-1}$	$\pm 1.19\cdot10^{-1}$	$3.00\cdot10^{-2}$	$\pm 2.60\cdot10^{-2}$

Table S74. Summary of class-level PAO results continued.

Class[a,b]	S-EBPR (S69)		V-EBPR (S70)		G-EBPR (S71)		R-EBPR (S72)		Moscow WRRF (S73)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
Clostridia	$7.46\cdot10^{-3}$	$\pm 1.34\cdot10^{-2}$	$3.37\cdot10^{-1}$	$\pm 6.03\cdot10^{-1}$	$6.36\cdot10^{-2}$	$\pm 6.71\cdot10^{-2}$	$5.09\cdot10^{-3}$	$\pm 9.59\cdot10^{-3}$	$1.97\cdot10^{-2}$	$\pm 1.47\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] N.D. = Not detected.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S75. S-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Rhodocyclales	96.0	77.0	99.5	98.5	97.4	86.5	99.8	93.5	± 8.61
unknown p: *Proteobacteria*	1.97	20.1	$1.02\cdot10^{-1}$	$6.30\cdot10^{-2}$	1.07	7.53	$7.12\cdot10^{-2}$	4.41	± 7.39
Minor phylotypes (80)[d]	1.01	$5.42\cdot10^{-1}$	$2.65\cdot10^{-1}$	1.00	$9.25\cdot10^{-1}$	2.18	$8.52\cdot10^{-2}$	$8.57\cdot10^{-1}$	$\pm 6.87\cdot10^{-1}$
unknown d: *Bacteria*	$4.26\cdot10^{-1}$	$5.42\cdot10^{-1}$	$5.98\cdot10^{-2}$	$2.30\cdot10^{-1}$	$4.85\cdot10^{-1}$	3.45	$9.78\cdot10^{-3}$	$7.43\cdot10^{-1}$	± 1.21
unknown c: *Deltaproteobacteria*	$5.86\cdot10^{-1}$	1.90	$8.54\cdot10^{-2}$	$2.37\cdot10^{-1}$	$7.33\cdot10^{-2}$	$3.18\cdot10^{-1}$	$2.79\cdot10^{-3}$	$4.57\cdot10^{-1}$	$\pm 6.65\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S76. V-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Rhodocyclales	50.4	79.3	98.4	30.1	17.7	11.7	97.2	55.0	± 36.9
unknown d: *Bacteria*	22.0	10.5	$1.00\cdot10^{-1}$	9.06	48.0	33.7	$2.58\cdot10^{-1}$	17.6	± 17.9
Acidimicrobiales	2.77	4.20	$4.51\cdot10^{-1}$	26.3	3.30	22.7	$9.06\cdot10^{-2}$	8.54	± 11.0
Bdellovibrionales	$5.99\cdot10^{-1}$	$9.34\cdot10^{-1}$	N.D.[d]	26.0	5.07	5.31	1.64	5.65	± 9.22

Table S76. V-EBPR order-level PAO results summary continued.

Order[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
unknown c: *Gammaproteobacteria*	4.13	2.31	N.D.[d]	$6.10 \cdot 10^{-1}$	6.02	5.03	$1.26 \cdot 10^{-1}$	2.60	±	2.48
Xanthomonadales	7.42	$6.71 \cdot 10^{-1}$	N.D.[d]	2.27	2.11	3.19	$7.52 \cdot 10^{-2}$	2.25	±	2.58
unknown c: *Actinobacteria*	$1.37 \cdot 10^{-1}$	$2.92 \cdot 10^{-2}$	N.D.[d]	$8.13 \cdot 10^{-1}$	7.43	4.97	$1.20 \cdot 10^{-2}$	1.91	±	3.03
Chlamydiales	3.92	$2.04 \cdot 10^{-1}$	$7.02 \cdot 10^{-1}$	1.26	1.66	4.60	$3.16 \cdot 10^{-1}$	1.81	±	1.76
unknown p: *Proteobacteria*	4.54	$6.42 \cdot 10^{-1}$	$5.01 \cdot 10^{-2}$	$2.79 \cdot 10^{-1}$	2.72	3.45	$7.86 \cdot 10^{-2}$	1.68	±	1.85
Minor phylotypes (72)[e]	2.04	$7.01 \cdot 10^{-1}$	$2.01 \cdot 10^{-1}$	1.69	2.23	2.07	$9.40 \cdot 10^{-2}$	1.29	±	$9.29 \cdot 10^{-1}$
Verrucomicrobiales	1.88	$2.92 \cdot 10^{-2}$	$5.01 \cdot 10^{-2}$	1.11	2.12	1.00	$3.76 \cdot 10^{-2}$	$8.89 \cdot 10^{-1}$	±	$8.87 \cdot 10^{-1}$
unknown c: *Deltaproteobacteria*	$1.88 \cdot 10^{-1}$	$2.92 \cdot 10^{-2}$	N.D.[d]	$5.84 \cdot 10^{-1}$	1.49	$7.18 \cdot 10^{-1}$	$8.89 \cdot 10^{-2}$	$4.43 \cdot 10^{-1}$	±	$5.40 \cdot 10^{-1}$
Clostridiales	$3.43 \cdot 10^{-2}$	$4.67 \cdot 10^{-1}$	N.D.[d]	N.D.[d]	$1.88 \cdot 10^{-1}$	1.64	$1.71 \cdot 10^{-2}$	$3.35 \cdot 10^{-1}$	±	$5.99 \cdot 10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S77. G-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Order[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Rhodocyclales	12.5	85.4	98.4	92.3	29.9	11.3	45.1	53.6	±	37.9
Acidimicrobiales	27.1	2.55	$7.52 \cdot 10^{-2}$	$3.60 \cdot 10^{-1}$	18.0	45.2	3.04	13.8	±	17.3
Bdellovibrionales	30.3	4.75	$4.45 \cdot 10^{-1}$	3.60	3.92	1.27	12.0	8.03	±	10.5
unknown c: *Gammaproteobacteria*	$1.58 \cdot 10^{-1}$	1.77	$2.89 \cdot 10^{-1}$	1.10	22.1	12.7	15.9	7.72	±	9.04
unknown d: *Bacteria*	7.69	1.43	$8.67 \cdot 10^{-2}$	$6.12 \cdot 10^{-1}$	10.5	20.7	8.55	7.08	±	7.33
unknown c: *Actinobacteria*	4.55	1.84	$1.21 \cdot 10^{-1}$	$9.72 \cdot 10^{-1}$	12.0	1.32	$2.08 \cdot 10^{-1}$	3.00	±	4.23
Verrucomicrobiales	7.27	$4.56 \cdot 10^{-1}$	$1.16 \cdot 10^{-2}$	$5.56 \cdot 10^{-2}$	$3.35 \cdot 10^{-1}$	3.12	$4.80 \cdot 10^{-1}$	1.67	±	2.69
Chlamydiales	$3.15 \cdot 10^{-1}$	$3.25 \cdot 10^{-2}$	$5.20 \cdot 10^{-2}$	$1.15 \cdot 10^{-1}$	$9.47 \cdot 10^{-2}$	$1.42 \cdot 10^{-1}$	8.80	1.36	±	3.28
Minor phylotypes (72)[d]	2.75	1.04	$2.20 \cdot 10^{-1}$	$1.41 \cdot 10^{-1}$	1.67	2.10	1.62	1.36	±	$9.60 \cdot 10^{-1}$
Xanthomonadales	1.68	$3.74 \cdot 10^{-1}$	$4.63 \cdot 10^{-2}$	$4.16 \cdot 10^{-1}$	1.06	2.04	3.62	1.32	±	1.25
unknown c: *Deltaproteobacteria*	3.31	$4.88 \cdot 10^{-2}$	$1.73 \cdot 10^{-2}$	$9.82 \cdot 10^{-3}$	$3.47 \cdot 10^{-2}$	$6.74 \cdot 10^{-3}$	$4.85 \cdot 10^{-2}$	$4.97 \cdot 10^{-1}$	±	1.24

Table S77. G-EBPR order-level PAO results summary continued.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown c: *Betaproteobacteria*	1.31	$2.44\cdot10^{-1}$	$2.37\cdot10^{-1}$	$2.98\cdot10^{-1}$	$2.78\cdot10^{-1}$	$9.44\cdot10^{-2}$	$1.20\cdot10^{-1}$	$3.69\cdot10^{-1}$	±	$4.23\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	1.10	$4.88\cdot10^{-2}$	N.D.[e]	$1.64\cdot10^{-2}$	$8.21\cdot10^{-2}$	$4.05\cdot10^{-2}$	$5.68\cdot10^{-1}$	$2.66\cdot10^{-1}$	±	$4.20\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S78. R-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
Rhodocyclales	87.1	64.5	67.9	75.8	83.2	73.0	87.2	77.0	±	9.13
unknown c: *Betaproteobacteria*	$9.69\cdot10^{-1}$	30.0	23.7	17.3	11.9	18.5	$5.55\cdot10^{-1}$	14.7	±	11.1
Bdellovibrionales	3.71	3.61	4.54	3.31	$8.83\cdot10^{-1}$	$6.19\cdot10^{-1}$	6.03	3.24	±	1.93
unknown d: *Bacteria*	2.54	$3.99\cdot10^{-1}$	1.02	$7.73\cdot10^{-1}$	2.07	1.70	1.39	1.41	±	$7.51\cdot10^{-1}$
Minor phylotypes (76)[d]	2.04	$7.50\cdot10^{-1}$	$8.60\cdot10^{-1}$	$9.34\cdot10^{-1}$	1.29	1.58	2.14	1.37	±	$5.65\cdot10^{-1}$
Acidimicrobiales	1.84	$1.88\cdot10^{-1}$	$1.79\cdot10^{-1}$	$7.30\cdot10^{-2}$	$5.36\cdot10^{-1}$	4.44	$6.03\cdot10^{-1}$	1.12	±	1.58
Xanthomonadales	$2.18\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.67	1.53	$2.27\cdot10^{-2}$	$1.89\cdot10^{-2}$	$1.05\cdot10^{-1}$	$5.73\cdot10^{-1}$	±	$7.19\cdot10^{-1}$
Verrucomicrobiales	1.04	$2.34\cdot10^{-2}$	$7.56\cdot10^{-2}$	$1.95\cdot10^{-1}$	$8.52\cdot10^{-3}$	$3.77\cdot10^{-3}$	$9.75\cdot10^{-1}$	$3.32\cdot10^{-1}$	±	$4.67\cdot10^{-1}$
Chlamydiales	$5.09\cdot10^{-1}$	$2.34\cdot10^{-2}$	$5.67\cdot10^{-2}$	N.D.[e]	$7.10\cdot10^{-2}$	$1.66\cdot10^{-1}$	1.04	$2.66\cdot10^{-1}$	±	$3.82\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S79. Moscow WRRF order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Order[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	±	SD[c]
Rhodocyclales	73.5	84.1	84.3	80.3	94.3	92.4	75.0	83.4	±	7.96

Table S79. Moscow WRRF order-level PAO results summary continued.

Order[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	±	SD[c]
unknown c: *Betaproteobacteria*	5.52	11.1	8.63	8.74	1.39	1.02	25.0	8.78	±	8.10
Acidimicrobiales	5.54	1.29	4.63	6.51	$2.76\cdot10^{-1}$	$2.63\cdot10^{-1}$	N.D.[d]	2.64	±	2.81
Parcubacteria_genera_inc._sed.[e]	2.27	$9.80\cdot10^{-1}$	$8.11\cdot10^{-1}$	2.05	$4.66\cdot10^{-1}$	3.22	N.D.[d]	1.40	±	1.14
Bdellovibrionales	6.58	$6.46\cdot10^{-1}$	$1.48\cdot10^{-1}$	$1.34\cdot10^{-1}$	$4.30\cdot10^{-1}$	$3.22\cdot10^{-1}$	N.D.[d]	1.18	±	2.39
Minor phylotypes (77)[f]	1.74	$8.12\cdot10^{-1}$	$7.90\cdot10^{-1}$	1.29	1.61	1.34	N.D.[d]	1.08	±	$5.99\cdot10^{-1}$
Xanthomonadales	2.79	$4.18\cdot10^{-1}$	$2.91\cdot10^{-1}$	$5.43\cdot10^{-1}$	$8.05\cdot10^{-1}$	$7.56\cdot10^{-1}$	N.D.[d]	$8.00\cdot10^{-1}$	±	$9.19\cdot10^{-1}$
unknown d: *Bacteria*	2.04	$5.90\cdot10^{-1}$	$3.67\cdot10^{-1}$	$4.44\cdot10^{-1}$	$6.92\cdot10^{-1}$	$6.59\cdot10^{-1}$	N.D.[d]	$6.84\cdot10^{-1}$	±	$6.41\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S80. Summary of order-level relative abundance by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Order[a,b]	S-EBPR (S75)			V-EBPR (S76)			G-EBPR (S77)			R-EBPR (S78)			Moscow WRRF (S79)		
	Average %	±	SD[c]	Average %	±	SD[c]	Average %	±	SD[c]	Average %	±	SD[c]	Average %	±	SD[c]
Rhodocyclales	93.5	±	8.61	55.0	±	36.9	53.6	±	37.9	77.0	±	9.13	83.4	±	7.96
unknown d: *Bacteria*	$7.43\cdot10^{-1}$	±	1.21	17.6	±	17.9	7.08	±	7.33	1.41	±	$7.51\cdot10^{-1}$	$6.84\cdot10^{-1}$	±	$6.41\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$5.96\cdot10^{-2}$	±	$7.58\cdot10^{-2}$	$8.13\cdot10^{-2}$	±	$6.31\cdot10^{-2}$	$3.69\cdot10^{-1}$	±	$4.23\cdot10^{-1}$	14.7	±	11.1	8.78	±	8.10
Acidimicrobiales	$4.69\cdot10^{-2}$	±	$4.78\cdot10^{-2}$	8.54	±	11.0	13.8	±	17.3	1.12	±	1.58	2.64	±	2.81
Bdellovibrionales	$8.78\cdot10^{-2}$	±	$9.38\cdot10^{-2}$	5.65	±	9.22	8.03	±	10.5	3.24	±	1.93	1.18	±	2.39
unknown c: *Gammaproteobacteria*	$1.19\cdot10^{-1}$	±	$1.63\cdot10^{-1}$	2.60	±	2.48	7.72	±	9.04	$2.30\cdot10^{-2}$	±	$1.22\cdot10^{-2}$	$2.36\cdot10^{-1}$	±	$3.29\cdot10^{-1}$
unknown p: *Proteobacteria*	4.41	±	7.39	1.68	±	1.85	$4.31\cdot10^{-1}$	±	$3.72\cdot10^{-1}$	$1.77\cdot10^{-1}$	±	$1.74\cdot10^{-1}$	$6.77\cdot10^{-2}$	±	$9.21\cdot10^{-2}$
unknown c: *Actinobacteria*	$2.77\cdot10^{-3}$	±	$3.74\cdot10^{-3}$	1.91	±	3.03	3.00	±	4.23	$7.56\cdot10^{-2}$	±	$6.99\cdot10^{-2}$	$5.39\cdot10^{-2}$	±	$7.10\cdot10^{-2}$
Xanthomonadales	$2.47\cdot10^{-1}$	±	$3.00\cdot10^{-1}$	2.25	±	2.58	1.32	±	1.25	$5.73\cdot10^{-1}$	±	$7.19\cdot10^{-1}$	$8.00\cdot10^{-1}$	±	$9.19\cdot10^{-1}$
Chlamydiales	$1.03\cdot10^{-2}$	±	$2.73\cdot10^{-2}$	1.81	±	1.76	1.36	±	3.28	$2.66\cdot10^{-1}$	±	$3.82\cdot10^{-1}$	$6.82\cdot10^{-2}$	±	$7.37\cdot10^{-2}$
Verrucomicrobiales	$7.66\cdot10^{-2}$	±	$7.52\cdot10^{-2}$	$8.89\cdot10^{-1}$	±	$8.87\cdot10^{-1}$	1.67	±	2.69	$3.32\cdot10^{-1}$	±	$4.67\cdot10^{-1}$	$1.30\cdot10^{-1}$	±	$1.25\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[d]	N.D.[e]			$8.91\cdot10^{-2}$	±	$9.80\cdot10^{-2}$	$1.01\cdot10^{-1}$	±	$1.14\cdot10^{-1}$	$1.04\cdot10^{-1}$	±	$1.18\cdot10^{-1}$	1.40	±	1.14

Table S80. Summary of order-level PAO results continued.

Order[a,b]	S-EBPR (S75) Average ± SD[c] %	V-EBPR (S76) Average ± SD[c] %	G-EBPR (S77) Average ± SD[c] %	R-EBPR (S78) Average ± SD[c] %	Moscow WRRF (S79) Average ± SD[c] %
Minor phylotypes (69)[f]	$1.99\cdot10^{-1} \pm 1.73\cdot10^{-1}$	$1.04 \pm 7.71\cdot10^{-1}$	$7.67\cdot10^{-1} \pm 6.71\cdot10^{-1}$	$7.66\cdot10^{-1} \pm 2.65\cdot10^{-1}$	$4.84\cdot10^{-1} \pm 2.35\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$4.57\cdot10^{-1} \pm 6.65\cdot10^{-1}$	$4.43\cdot10^{-1} \pm 5.40\cdot10^{-1}$	$4.97\cdot10^{-1} \pm 1.24$	$1.61\cdot10^{-1} \pm 1.02\cdot10^{-1}$	$1.45\cdot10^{-2} \pm 1.24\cdot10^{-2}$
Clostridiales	$6.93\cdot10^{-3} \pm 1.37\cdot10^{-2}$	$3.35\cdot10^{-1} \pm 5.99\cdot10^{-1}$	$6.36\cdot10^{-2} \pm 6.71\cdot10^{-2}$	$5.09\cdot10^{-3} \pm 9.59\cdot10^{-3}$	$1.97\cdot10^{-2} \pm 1.47\cdot10^{-2}$
unknown c: *Alphaproteobacteria*	$1.44\cdot10^{-3} \pm 2.76\cdot10^{-3}$	$7.66\cdot10^{-2} \pm 1.15\cdot10^{-1}$	$2.66\cdot10^{-1} \pm 4.20\cdot10^{-1}$	$5.94\cdot10^{-2} \pm 8.35\cdot10^{-2}$	$9.05\cdot10^{-3} \pm 1.36\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] N.D. = Not detected.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S81. S-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Rhodocyclaceae	96.0	77.0	99.5	98.5	97.4	86.5	99.8	93.5 ± 8.61
unknown p: *Proteobacteria*	1.97	20.1	$1.02\cdot10^{-1}$	$6.30\cdot10^{-2}$	1.07	7.53	$7.12\cdot10^{-2}$	4.41 ± 7.39
Minor phylotypes (138)[d]	1.01	$5.42\cdot10^{-1}$	$2.65\cdot10^{-1}$	1.00	$9.25\cdot10^{-1}$	2.18	$8.52\cdot10^{-2}$	$8.57\cdot10^{-1} \pm 6.87\cdot10^{-1}$
unknown d: *Bacteria*	$4.26\cdot10^{-1}$	$5.42\cdot10^{-1}$	$5.98\cdot10^{-2}$	$2.30\cdot10^{-1}$	$4.85\cdot10^{-1}$	3.45	$9.78\cdot10^{-3}$	$7.43\cdot10^{-1} \pm 1.21$
unknown c: *Deltaproteobacteria*	$5.86\cdot10^{-1}$	1.90	$8.54\cdot10^{-2}$	$2.37\cdot10^{-1}$	$7.33\cdot10^{-2}$	$3.18\cdot10^{-1}$	$2.79\cdot10^{-3}$	$4.57\cdot10^{-1} \pm 6.65\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S82. V-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Family[a,b]	72	86	107	121	241	263	283	Average ± SD[c]
	%	%	%	%	%	%	%	%
Rhodocyclaceae	50.4	79.3	98.4	30.1	17.7	11.7	97.2	55.0 ± 36.9
unknown d: *Bacteria*	22.0	10.5	$1.00\cdot10^{-1}$	9.06	48.0	33.7	$2.58\cdot10^{-1}$	17.6 ± 17.9
Acidimicrobiaceae	2.26	4.09	$2.01\cdot10^{-1}$	22.7	3.00	21.7	$8.55\cdot10^{-2}$	7.73 ± 10.0
Bdellovibrionaceae	$2.06\cdot10^{-1}$	$8.17\cdot10^{-1}$	N.D.[d]	26.0	2.66	5.26	1.63	5.22 ± 9.32
unknown c: *Gammaproteobacteria*	4.13	2.31	N.D.[d]	$6.10\cdot10^{-1}$	6.02	5.03	$1.26\cdot10^{-1}$	2.60 ± 2.48
Xanthomonadaceae	7.38	$6.71\cdot10^{-1}$	N.D.[d]	2.27	2.11	3.18	$7.52\cdot10^{-2}$	2.24 ± 2.57
unknown c: *Actinobacteria*	$1.37\cdot10^{-1}$	$2.92\cdot10^{-2}$	N.D.[d]	$8.13\cdot10^{-1}$	7.43	4.97	$1.20\cdot10^{-2}$	1.91 ± 3.03
Parachlamydiaceae	3.92	$2.04\cdot10^{-1}$	$7.02\cdot10^{-1}$	1.26	1.66	4.60	$3.16\cdot10^{-1}$	1.81 ± 1.76
unknown p: *Proteobacteria*	4.54	$6.42\cdot10^{-1}$	$5.01\cdot10^{-2}$	$2.79\cdot10^{-1}$	2.72	3.45	$7.86\cdot10^{-2}$	1.68 ± 1.85
Minor phylotypes (128)[e]	2.07	$7.01\cdot10^{-1}$	$2.01\cdot10^{-1}$	1.70	2.25	2.12	$9.57\cdot10^{-2}$	1.31 ± $9.44\cdot10^{-1}$
Verrucomicrobiaceae	1.88	$2.92\cdot10^{-2}$	$5.01\cdot10^{-2}$	1.11	2.12	1.00	$3.76\cdot10^{-2}$	$8.89\cdot10^{-1}$ ± $8.87\cdot10^{-1}$
unknown o: *Acidimicrobiales*	$5.14\cdot10^{-1}$	$1.17\cdot10^{-1}$	$2.51\cdot10^{-1}$	3.56	$3.01\cdot10^{-1}$	$8.96\cdot10^{-1}$	$5.13\cdot10^{-3}$	$8.06\cdot10^{-1}$ ± 1.25
unknown c: *Deltaproteobacteria*	$1.88\cdot10^{-1}$	$2.92\cdot10^{-2}$	N.D.[d]	$5.84\cdot10^{-1}$	1.49	$7.18\cdot10^{-1}$	$8.89\cdot10^{-2}$	$4.43\cdot10^{-1}$ ± $5.40\cdot10^{-1}$
Bacteriovoracaceae	$3.94\cdot10^{-1}$	$1.17\cdot10^{-1}$	N.D.[d]	$3.81\cdot10^{-2}$	2.42	$5.25\cdot10^{-2}$	$8.55\cdot10^{-3}$	$4.32\cdot10^{-1}$ ± $8.86\cdot10^{-1}$
unknown o: *Clostridiales*	$3.43\cdot10^{-2}$	$4.67\cdot10^{-1}$	N.D.[d]	N.D.[d]	$1.71\cdot10^{-1}$	1.61	$1.54\cdot10^{-2}$	$3.29\cdot10^{-1}$ ± $5.91\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S83. G-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Family[a,b]	72	86	107	121	241	263	283	Average ± SD[c]
	%	%	%	%	%	%	%	%
Rhodocyclaceae	12.5	85.4	98.4	92.3	29.9	11.3	45.1	53.6 ± 37.9
Acidimicrobiaceae	21.4	1.94	$6.94\cdot10^{-2}$	$3.31\cdot10^{-1}$	17.1	44.0	2.69	12.5 ± 16.4
unknown c: *Gammaproteobacteria*	$1.58\cdot10^{-1}$	1.77	$2.89\cdot10^{-1}$	1.10	22.1	12.7	15.9	7.72 ± 9.04
Bdellovibrionaceae	29.7	3.94	$4.39\cdot10^{-1}$	3.39	3.25	1.10	11.4	7.60 ± 10.4
unknown d: *Bacteria*	7.69	1.43	$8.67\cdot10^{-2}$	$6.12\cdot10^{-1}$	10.5	20.7	8.55	7.08 ± 7.33

Table S83. G-EBPR family-level PAO results summary continued.

Family[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
unknown c: *Actinobacteria*	4.55	1.84	$1.21\cdot10^{-1}$	$9.72\cdot10^{-1}$	12.0	1.32	$2.08\cdot10^{-1}$	3.00	±	4.23
Minor phylotypes (129)[d]	3.38	1.85	$2.25\cdot10^{-1}$	$3.53\cdot10^{-1}$	2.35	2.28	2.17	1.80	±	1.14
Verrucomicrobiaceae	7.27	$4.56\cdot10^{-1}$	$1.16\cdot10^{-2}$	$5.56\cdot10^{-2}$	$3.35\cdot10^{-1}$	3.12	$4.80\cdot10^{-1}$	1.67	±	2.69
Parachlamydiaceae	$3.15\cdot10^{-1}$	$3.25\cdot10^{-2}$	$5.20\cdot10^{-2}$	$1.15\cdot10^{-1}$	$9.47\cdot10^{-2}$	$1.42\cdot10^{-1}$	8.79	1.36	±	3.28
Xanthomonadaceae	1.68	$3.74\cdot10^{-1}$	$4.63\cdot10^{-2}$	$4.16\cdot10^{-1}$	1.06	2.04	3.62	1.32	±	1.25
unknown o: *Acidimicrobiales*	5.69	$6.18\cdot10^{-1}$	$5.78\cdot10^{-3}$	$2.95\cdot10^{-2}$	$9.38\cdot10^{-1}$	1.14	$3.54\cdot10^{-1}$	1.25	±	2.00
unknown c: *Deltaproteobacteria*	3.31	$4.88\cdot10^{-2}$	$1.73\cdot10^{-2}$	$9.82\cdot10^{-3}$	$3.47\cdot10^{-2}$	$6.74\cdot10^{-3}$	$4.85\cdot10^{-2}$	$4.97\cdot10^{-1}$	±	1.24
unknown c: *Betaproteobacteria*	1.31	$2.44\cdot10^{-1}$	$2.37\cdot10^{-1}$	$2.98\cdot10^{-1}$	$2.78\cdot10^{-1}$	$9.44\cdot10^{-2}$	$1.20\cdot10^{-1}$	$3.69\cdot10^{-1}$	±	$4.23\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	1.10	$4.88\cdot10^{-2}$	N.D.[e]	$1.64\cdot10^{-2}$	$8.21\cdot10^{-2}$	$4.05\cdot10^{-2}$	$5.68\cdot10^{-1}$	$2.66\cdot10^{-1}$	±	$4.20\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S84. R-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Family[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Rhodocyclaceae	87.1	64.5	67.9	75.8	83.2	73.0	87.2	77.0	±	9.13
unknown c: *Betaproteobacteria*	$9.69\cdot10^{-1}$	30.0	23.7	17.3	11.9	18.5	$5.55\cdot10^{-1}$	14.7	±	11.1
Bdellovibrionaceae	3.61	3.61	4.30	3.12	$8.71\cdot10^{-1}$	$6.11\cdot10^{-1}$	5.90	3.15	±	1.87
Minor phylotypes (134)[d]	2.67	$7.97\cdot10^{-1}$	1.22	1.16	1.31	1.64	2.36	1.59	±	$6.81\cdot10^{-1}$
unknown d: *Bacteria*	2.54	$3.99\cdot10^{-1}$	1.02	$7.73\cdot10^{-1}$	2.07	1.70	1.39	1.41	±	$7.51\cdot10^{-1}$
Acidimicrobiaceae	1.31	$1.41\cdot10^{-1}$	$6.61\cdot10^{-2}$	$3.89\cdot10^{-2}$	$5.25\cdot10^{-1}$	4.39	$5.08\cdot10^{-1}$	$9.97\cdot10^{-1}$	±	1.56
Xanthomonadaceae	$2.18\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.67	1.53	$2.27\cdot10^{-2}$	$1.89\cdot10^{-2}$	$1.05\cdot10^{-1}$	$5.73\cdot10^{-1}$	±	$7.19\cdot10^{-1}$
Verrucomicrobiaceae	1.04	$2.34\cdot10^{-2}$	$7.56\cdot10^{-2}$	$1.95\cdot10^{-1}$	$8.52\cdot10^{-3}$	$3.77\cdot10^{-3}$	$9.75\cdot10^{-1}$	$3.32\cdot10^{-1}$	±	$4.67\cdot10^{-1}$

Table S84. R-EBPR family-level PAO results summary continued.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Parachlamydiaceae	$5.09\cdot10^{-1}$	$2.34\cdot10^{-2}$	$5.67\cdot10^{-2}$	N.D.[e]	$7.10\cdot10^{-2}$	$1.66\cdot10^{-1}$	1.04	$2.66\cdot10^{-1}$ ± $3.82\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S85. Moscow WRRF family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Family[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average ± SD[c] %
Rhodocyclaceae	73.5	84.1	84.3	80.3	94.3	92.4	75.0	83.4 ± 7.96
unknown c: *Betaproteobacteria*	5.52	11.1	8.63	8.74	1.39	1.02	25.0	8.78 ± 8.10
unknown o: *Acidimicrobiales*	3.58	$9.28\cdot10^{-1}$	3.80	5.79	$2.35\cdot10^{-1}$	$2.15\cdot10^{-1}$	N.D.[d]	2.08 ± 2.29
Parcubacteria_genera_inc._sed.[e]	2.27	$9.80\cdot10^{-1}$	$8.11\cdot10^{-1}$	2.05	$4.66\cdot10^{-1}$	3.22	N.D.[d]	1.40 ± 1.14
Minor phylotypes (133)[f]	2.06	$8.96\cdot10^{-1}$	1.13	1.61	1.64	1.36	N.D.[d]	1.24 ± $6.64\cdot10^{-1}$
Bacteriovoracaceae	5.26	$2.14\cdot10^{-1}$	$6.03\cdot10^{-2}$	$1.97\cdot10^{-2}$	$4.07\cdot10^{-2}$	$6.34\cdot10^{-2}$	N.D.[d]	$8.09\cdot10^{-1}$ ± 1.97
Xanthomonadaceae	2.78	$4.18\cdot10^{-1}$	$2.91\cdot10^{-1}$	$5.43\cdot10^{-1}$	$8.05\cdot10^{-1}$	$7.56\cdot10^{-1}$	N.D.[d]	$8.00\cdot10^{-1}$ ± $9.18\cdot10^{-1}$
unknown d: *Bacteria*	2.04	$5.90\cdot10^{-1}$	$3.67\cdot10^{-1}$	$4.44\cdot10^{-1}$	$6.92\cdot10^{-1}$	$6.59\cdot10^{-1}$	N.D.[d]	$6.84\cdot10^{-1}$ ± $6.41\cdot10^{-1}$
Acidimicrobiaceae	1.65	$2.81\cdot10^{-1}$	$4.83\cdot10^{-1}$	$4.05\cdot10^{-1}$	$1.36\cdot10^{-2}$	$2.93\cdot10^{-2}$	N.D.[d]	$4.08\cdot10^{-1}$ ± $5.81\cdot10^{-1}$
Bdellovibrionaceae	1.32	$4.32\cdot10^{-1}$	$8.77\cdot10^{-2}$	$1.10\cdot10^{-1}$	$3.89\cdot10^{-1}$	$2.59\cdot10^{-1}$	N.D.[d]	$3.71\cdot10^{-1}$ ± $4.47\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S86. Summary of family-level relative abundance by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Family[a,b]	S-EBPR (S81) Average ± SD[c] %	V-EBPR (S82) Average ± SD[c] %	G-EBPR (S83) Average ± SD[c] %	R-EBPR (S84) Average ± SD[c] %	Moscow WRRF (S85) Average ± SD[c] %
Rhodocyclaceae	93.5 ± 8.61	55.0 ± 36.9	53.6 ± 37.9	77.0 ± 9.13	83.4 ± 7.96
unknown d: *Bacteria*	$7.43\cdot10^{-1} \pm 1.21$	17.6 ± 17.9	7.08 ± 7.33	$1.41 \pm 7.51\cdot10^{-1}$	$6.84\cdot10^{-1} \pm 6.41\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$5.96\cdot10^{-2} \pm 7.58\cdot10^{-2}$	$8.13\cdot10^{-2} \pm 6.31\cdot10^{-2}$	$3.69\cdot10^{-1} \pm 4.23\cdot10^{-1}$	14.7 ± 11.1	8.78 ± 8.10
Acidimicrobiaceae	$1.90\cdot10^{-2} \pm 2.85\cdot10^{-2}$	7.73 ± 10.0	12.5 ± 16.4	$9.97\cdot10^{-1} \pm 1.56$	$4.08\cdot10^{-1} \pm 5.81\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$1.19\cdot10^{-1} \pm 1.63\cdot10^{-1}$	2.60 ± 2.48	7.72 ± 9.04	$2.30\cdot10^{-2} \pm 1.22\cdot10^{-2}$	$2.36\cdot10^{-1} \pm 3.29\cdot10^{-1}$
Bdellovibrionaceae	$4.62\cdot10^{-2} \pm 4.80\cdot10^{-2}$	5.22 ± 9.32	7.60 ± 10.4	3.15 ± 1.87	$3.71\cdot10^{-1} \pm 4.47\cdot10^{-1}$
unknown p: *Proteobacteria*	4.41 ± 7.39	1.68 ± 1.85	$4.31\cdot10^{-1} \pm 3.72\cdot10^{-1}$	$1.77\cdot10^{-1} \pm 1.74\cdot10^{-1}$	$6.77\cdot10^{-2} \pm 9.21\cdot10^{-2}$
unknown c: *Actinobacteria*	$2.77\cdot10^{-3} \pm 3.74\cdot10^{-3}$	1.91 ± 3.03	3.00 ± 4.23	$7.56\cdot10^{-2} \pm 6.99\cdot10^{-2}$	$5.39\cdot10^{-2} \pm 7.10\cdot10^{-2}$
Xanthomonadaceae	$2.47\cdot10^{-1} \pm 3.00\cdot10^{-1}$	2.24 ± 2.57	1.32 ± 1.25	$5.73\cdot10^{-1} \pm 7.19\cdot10^{-1}$	$8.00\cdot10^{-1} \pm 9.18\cdot10^{-1}$
unknown o: *Acidimicrobiales*	$1.54\cdot10^{-2} \pm 1.58\cdot10^{-2}$	$8.06\cdot10^{-1} \pm 1.25$	1.25 ± 2.00	$1.26\cdot10^{-1} \pm 1.83\cdot10^{-1}$	2.08 ± 2.29
Parachlamydiaceae	$1.03\cdot10^{-2} \pm 2.73\cdot10^{-2}$	1.81 ± 1.76	1.36 ± 3.28	$2.66\cdot10^{-1} \pm 3.82\cdot10^{-1}$	$6.82\cdot10^{-2} \pm 7.37\cdot10^{-2}$
Verrucomicrobiaceae	$7.66\cdot10^{-2} \pm 7.52\cdot10^{-2}$	$8.89\cdot10^{-1} \pm 8.87\cdot10^{-1}$	1.67 ± 2.69	$3.32\cdot10^{-1} \pm 4.67\cdot10^{-1}$	$1.30\cdot10^{-1} \pm 1.25\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[d]	N.D.[e]	$8.91\cdot10^{-2} \pm 9.80\cdot10^{-2}$	$1.01\cdot10^{-1} \pm 1.14\cdot10^{-1}$	$1.04\cdot10^{-1} \pm 1.18\cdot10^{-1}$	1.40 ± 1.14
Minor phylotypes (125)[f]	$2.17\cdot10^{-1} \pm 2.02\cdot10^{-1}$	$1.06 \pm 7.83\cdot10^{-1}$	$7.80\cdot10^{-1} \pm 6.77\cdot10^{-1}$	$7.69\cdot10^{-1} \pm 2.65\cdot10^{-1}$	$6.46\cdot10^{-1} \pm 3.50\cdot10^{-1}$
Bacteriovoracaceae	$4.16\cdot10^{-2} \pm 1.01\cdot10^{-1}$	$4.32\cdot10^{-1} \pm 8.86\cdot10^{-1}$	$4.34\cdot10^{-1} \pm 3.01\cdot10^{-1}$	$9.81\cdot10^{-2} \pm 9.79\cdot10^{-2}$	$8.09\cdot10^{-1} \pm 1.97$
unknown c: *Deltaproteobacteria*	$4.57\cdot10^{-1} \pm 6.65\cdot10^{-1}$	$4.43\cdot10^{-1} \pm 5.40\cdot10^{-1}$	$4.97\cdot10^{-1} \pm 1.24$	$1.61\cdot10^{-1} \pm 1.02\cdot10^{-1}$	$1.45\cdot10^{-2} \pm 1.24\cdot10^{-2}$
unknown o: *Clostridiales*	$1.76\cdot10^{-3} \pm 4.66\cdot10^{-3}$	$3.29\cdot10^{-1} \pm 5.91\cdot10^{-1}$	$5.54\cdot10^{-2} \pm 6.17\cdot10^{-2}$	$1.15\cdot10^{-3} \pm 2.09\cdot10^{-3}$	$1.70\cdot10^{-2} \pm 1.50\cdot10^{-2}$
unknown c: *Alphaproteobacteria*	$1.44\cdot10^{-3} \pm 2.76\cdot10^{-3}$	$7.66\cdot10^{-2} \pm 1.15\cdot10^{-1}$	$2.66\cdot10^{-1} \pm 4.20\cdot10^{-1}$	$5.94\cdot10^{-2} \pm 8.35\cdot10^{-2}$	$9.05\cdot10^{-3} \pm 1.36\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] N.D. = Not detected.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S87. S-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Propionivibrio	38.5	8.94	83.3	80.5	11.7	2.28	84.8	44.3 ± 37.8
Azospira	50.2	66.7	2.21	5.00	83.5	83.6	1.30	41.8 ± 38.1
unknown f: *Rhodocyclaceae*	7.22	1.36	13.9	12.9	2.22	$5.31\cdot10^{-1}$	13.7	7.40 ± 6.10
unknown p: *Proteobacteria*	1.97	20.1	$1.02\cdot10^{-1}$	$6.30\cdot10^{-2}$	1.07	7.53	$7.12\cdot10^{-2}$	4.41 ± 7.39
Minor phylotypes (242)[d]	1.17	$5.42\cdot10^{-1}$	$3.76\cdot10^{-1}$	1.04	$9.87\cdot10^{-1}$	2.31	$1.49\cdot10^{-1}$	$9.39\cdot10^{-1}$ ± $7.13\cdot10^{-1}$
unknown d: *Bacteria*	$4.26\cdot10^{-1}$	$5.42\cdot10^{-1}$	$5.98\cdot10^{-2}$	$2.30\cdot10^{-1}$	$4.85\cdot10^{-1}$	3.45	$9.78\cdot10^{-3}$	$7.43\cdot10^{-1}$ ± 1.21
unknown c: *Deltaproteobacteria*	$5.86\cdot10^{-1}$	1.90	$8.54\cdot10^{-2}$	$2.37\cdot10^{-1}$	$7.33\cdot10^{-2}$	$3.18\cdot10^{-1}$	$2.79\cdot10^{-3}$	$4.57\cdot10^{-1}$ ± $6.65\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S88. V-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Propionivibrio	17.6	4.20	83.0	12.6	12.2	6.89	83.2	31.4 ± 35.6
unknown d: *Bacteria*	22.0	10.5	$1.00\cdot10^{-1}$	9.06	48.0	33.7	$2.58\cdot10^{-1}$	17.6 ± 17.9
unknown f: *Rhodocyclaceae*	29.0	25.7	12.7	4.88	1.04	$6.01\cdot10^{-1}$	12.0	12.3 ± 11.4
Azonexus	1.44	47.4	N.D.[d]	6.87	$8.30\cdot10^{-1}$	2.94	1.66	8.74 ± 17.2
Bdellovibrio	$2.06\cdot10^{-1}$	$8.17\cdot10^{-1}$	N.D.[d]	26.0	2.66	5.26	1.63	5.22 ± 9.32
Ilumatobacter	1.25	$4.67\cdot10^{-1}$	$1.00\cdot10^{-1}$	21.9	$7.56\cdot10^{-1}$	5.47	$3.93\cdot10^{-2}$	4.29 ± 8.01
Ferrimicrobium	$9.08\cdot10^{-1}$	3.12	$1.00\cdot10^{-1}$	$3.18\cdot10^{-1}$	2.03	14.3	$3.59\cdot10^{-2}$	2.97 ± 5.12
unknown c: *Gammaproteobacteria*	4.13	2.31	N.D.[d]	$6.10\cdot10^{-1}$	6.02	5.03	$1.26\cdot10^{-1}$	2.60 ± 2.48
unknown f: *Xanthomonadaceae*	7.23	$6.71\cdot10^{-1}$	N.D.[d]	2.26	2.09	3.15	$7.18\cdot10^{-2}$	2.21 ± 2.51
unknown c: *Actinobacteria*	$1.37\cdot10^{-1}$	$2.92\cdot10^{-2}$	N.D.[d]	$8.13\cdot10^{-1}$	7.43	4.97	$1.20\cdot10^{-2}$	1.91 ± 3.03
Dechloromonas	1.63	1.55	2.66	4.94	1.29	$9.97\cdot10^{-1}$	$2.63\cdot10^{-1}$	1.90 ± 1.52
Minor phylotypes (228)[e]	3.13	1.05	$3.01\cdot10^{-1}$	2.36	2.67	2.59	$1.64\cdot10^{-1}$	1.75 ± 1.22
Parachlamydia	3.58	$1.17\cdot10^{-1}$	$7.02\cdot10^{-1}$	1.21	1.62	4.56	$3.16\cdot10^{-1}$	1.73 ± 1.70

Table S88. V-EBPR genus-level PAO results summary continued.

Genus[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
unknown p: *Proteobacteria*	4.54	$6.42\cdot10^{-1}$	$5.01\cdot10^{-2}$	$2.79\cdot10^{-1}$	2.72	3.45	$7.86\cdot10^{-2}$	1.68	±	1.85
unknown f: *Verrucomicrobiaceae*	1.82	$2.92\cdot10^{-2}$	$5.01\cdot10^{-2}$	1.09	2.08	$7.91\cdot10^{-1}$	$3.42\cdot10^{-2}$	$8.41\cdot10^{-1}$	±	$8.64\cdot10^{-1}$
unknown o: *Acidimicrobiales*	$5.14\cdot10^{-1}$	$1.17\cdot10^{-1}$	$2.51\cdot10^{-1}$	3.56	$3.01\cdot10^{-1}$	$8.96\cdot10^{-1}$	$5.13\cdot10^{-3}$	$8.06\cdot10^{-1}$	±	1.25
unknown f: *Acidimicrobiaceae*	$1.03\cdot10^{-1}$	$4.96\cdot10^{-1}$	N.D.[d]	$4.45\cdot10^{-1}$	$2.16\cdot10^{-1}$	1.99	$1.03\cdot10^{-2}$	$4.65\cdot10^{-1}$	±	$6.99\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	$1.88\cdot10^{-1}$	$2.92\cdot10^{-2}$	N.D.[d]	$5.84\cdot10^{-1}$	1.49	$7.18\cdot10^{-1}$	$8.89\cdot10^{-2}$	$4.43\cdot10^{-1}$	±	$5.40\cdot10^{-1}$
Bacteriovorax	$3.94\cdot10^{-1}$	$1.17\cdot10^{-1}$	N.D.[d]	$3.81\cdot10^{-2}$	2.42	$5.25\cdot10^{-2}$	$8.55\cdot10^{-3}$	$4.32\cdot10^{-1}$	±	$8.86\cdot10^{-1}$
Azospira	$1.71\cdot10^{-1}$	$1.17\cdot10^{-1}$	$5.01\cdot10^{-2}$	$2.29\cdot10^{-1}$	2.02	$1.09\cdot10^{-1}$	$3.42\cdot10^{-3}$	$3.86\cdot10^{-1}$	±	$7.26\cdot10^{-1}$
unknown o: *Clostridiales*	$3.43\cdot10^{-2}$	$4.67\cdot10^{-1}$	N.D.[d]	N.D.[d]	$1.71\cdot10^{-1}$	1.61	$1.54\cdot10^{-2}$	$3.29\cdot10^{-1}$	±	$5.91\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S89. G-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Genus[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Propionivibrio	5.71	82.7	98.1	83.7	26.6	6.54	30.7	47.7	±	39.3
Ferrimicrobium	2.75	$3.09\cdot10^{-1}$	$5.78\cdot10^{-3}$	$1.90\cdot10^{-1}$	13.2	36.7	1.78	7.85	±	13.6
unknown c: *Gammaproteobacteria*	$1.58\cdot10^{-1}$	1.77	$2.89\cdot10^{-1}$	1.10	22.1	12.7	15.9	7.72	±	9.04
Bdellovibrio	29.7	3.90	$4.39\cdot10^{-1}$	3.39	3.24	1.08	11.4	7.58	±	10.4
unknown d: *Bacteria*	7.69	1.43	$8.67\cdot10^{-2}$	$6.12\cdot10^{-1}$	10.5	20.7	8.55	7.08	±	7.33
Ilumatobacter	18.0	1.61	$5.20\cdot10^{-2}$	$1.08\cdot10^{-1}$	2.06	2.29	$6.25\cdot10^{-1}$	3.53	±	6.44
unknown c: *Actinobacteria*	4.55	1.84	$1.21\cdot10^{-1}$	$9.72\cdot10^{-1}$	12.0	1.32	$2.08\cdot10^{-1}$	3.00	±	4.23
Dechloromonas	2.59	$8.14\cdot10^{-1}$	$8.09\cdot10^{-2}$	$2.29\cdot10^{-1}$	1.37	1.14	9.57	2.26	±	3.33
Minor phylotypes (229)[d]	3.71	1.95	$2.31\cdot10^{-1}$	$3.93\cdot10^{-1}$	2.65	2.69	2.80	2.06	±	1.30
Azonexus	$5.78\cdot10^{-1}$	$2.44\cdot10^{-1}$	N.D.[e]	7.71	$3.66\cdot10^{-1}$	1.16	2.87	1.85	±	2.76
unknown f: *Verrucomicrobiaceae*	7.04	$4.56\cdot10^{-1}$	$1.16\cdot10^{-2}$	$5.56\cdot10^{-2}$	$3.19\cdot10^{-1}$	2.99	$4.31\cdot10^{-1}$	1.62	±	2.61

Table S89. G-EBPR genus-level PAO results summary continued.

Genus[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Parachlamydia	$2.80\cdot10^{-1}$	$3.25\cdot10^{-2}$	$5.20\cdot10^{-2}$	$1.11\cdot10^{-1}$	$9.16\cdot10^{-2}$	$1.35\cdot10^{-1}$	8.78	1.36	±	3.28
unknown f: *Xanthomonadaceae*	1.68	$3.74\cdot10^{-1}$	$4.05\cdot10^{-2}$	$4.16\cdot10^{-1}$	1.04	2.04	3.20	1.26	±	1.12
unknown o: *Acidimicrobiales*	5.69	$6.18\cdot10^{-1}$	$5.78\cdot10^{-3}$	$2.95\cdot10^{-2}$	$9.38\cdot10^{-1}$	1.14	$3.54\cdot10^{-1}$	1.25	±	2.00
unknown f: *Acidimicrobiaceae*	$6.30\cdot10^{-1}$	$1.63\cdot10^{-2}$	$1.16\cdot10^{-2}$	$3.27\cdot10^{-2}$	1.82	5.02	$2.85\cdot10^{-1}$	1.12	±	1.84
unknown f: *Rhodocyclaceae*	1.56	1.58	$2.49\cdot10^{-1}$	$6.28\cdot10^{-1}$	1.06	$6.34\cdot10^{-1}$	1.49	1.03	±	$5.35\cdot10^{-1}$
Azospira	2.00	$4.88\cdot10^{-2}$	N.D.[e]	$1.31\cdot10^{-2}$	$2.24\cdot10^{-1}$	1.55	$3.68\cdot10^{-1}$	$6.00\cdot10^{-1}$	±	$8.22\cdot10^{-1}$
unknown c: *Deltaproteobacteria*	3.31	$4.88\cdot10^{-2}$	$1.73\cdot10^{-2}$	$9.82\cdot10^{-3}$	$3.47\cdot10^{-2}$	$6.74\cdot10^{-3}$	$4.85\cdot10^{-2}$	$4.97\cdot10^{-1}$	±	1.24
unknown c: *Betaproteobacteria*	1.31	$2.44\cdot10^{-1}$	$2.37\cdot10^{-1}$	$2.98\cdot10^{-1}$	$2.78\cdot10^{-1}$	$9.44\cdot10^{-2}$	$1.20\cdot10^{-1}$	$3.69\cdot10^{-1}$	±	$4.23\cdot10^{-1}$
unknown c: *Alphaproteobacteria*	1.10	$4.88\cdot10^{-2}$	N.D.[e]	$1.64\cdot10^{-2}$	$8.21\cdot10^{-2}$	$4.05\cdot10^{-2}$	$5.68\cdot10^{-1}$	$2.66\cdot10^{-1}$	±	$4.20\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S90. R-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Genus[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Dechloromonas	56.8	58.2	61.3	68.6	77.0	68.6	55.9	63.8	±	7.86
unknown c: *Betaproteobacteria*	$9.69\cdot10^{-1}$	30.0	23.7	17.3	11.9	18.5	$5.55\cdot10^{-1}$	14.7	±	11.1
Propionivibrio	8.19	1.62	3.27	2.11	3.05	1.58	25.8	6.52	±	8.82
unknown f: *Rhodocyclaceae*	20.7	4.34	2.94	4.54	2.31	1.53	1.43	5.39	±	6.85
Bdellovibrio	3.61	3.61	4.30	3.12	$8.69\cdot10^{-1}$	$6.11\cdot10^{-1}$	5.86	3.14	±	1.86
Minor phylotypes (237)[d]	4.02	1.13	1.61	1.37	1.81	2.07	3.90	2.27	±	1.19
unknown d: *Bacteria*	2.54	$3.99\cdot10^{-1}$	1.02	$7.73\cdot10^{-1}$	2.07	1.70	1.39	1.41	±	$7.51\cdot10^{-1}$
Azonexus	$7.27\cdot10^{-1}$	$1.17\cdot10^{-1}$	$1.42\cdot10^{-1}$	$3.50\cdot10^{-1}$	$4.80\cdot10^{-1}$	1.08	3.64	$9.34\cdot10^{-1}$	±	1.24
Ferrimicrobium	$7.27\cdot10^{-2}$	$4.69\cdot10^{-2}$	$4.72\cdot10^{-2}$	$3.89\cdot10^{-2}$	$4.94\cdot10^{-1}$	4.25	$2.93\cdot10^{-1}$	$7.50\cdot10^{-1}$	±	1.55

Table S90. R-EBPR genus-level PAO results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown f: *Xanthomonadaceae*	$1.70\cdot10^{-1}$	$4.22\cdot10^{-1}$	1.65	1.52	$2.84\cdot10^{-3}$	$1.13\cdot10^{-2}$	$9.96\cdot10^{-2}$	$5.54\cdot10^{-1}$	±	$7.21\cdot10^{-1}$
unknown f: *Verrucomicrobiaceae*	1.02	$2.34\cdot10^{-2}$	$6.61\cdot10^{-2}$	$1.95\cdot10^{-1}$	$5.68\cdot10^{-3}$	$3.77\cdot10^{-3}$	$9.38\cdot10^{-1}$	$3.21\cdot10^{-1}$	±	$4.54\cdot10^{-1}$
Ilumatobacter	1.21	$7.03\cdot10^{-2}$	$1.89\cdot10^{-2}$	N.D.[e]	$2.84\cdot10^{-3}$	$3.02\cdot10^{-2}$	$1.94\cdot10^{-1}$	$2.18\cdot10^{-1}$	±	$4.43\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S91. Moscow WRRF genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Genus[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	±	SD[c]
unknown f: *Rhodocyclaceae*	29.7	45.1	56.7	50.5	71.8	62.8	41.7	51.2	±	14.0
Propionivibrio	28.7	23.2	19.6	24.1	17.0	20.1	25.0	22.5	±	3.94
unknown c: *Betaproteobacteria*	5.52	11.1	8.63	8.74	1.39	1.02	25.0	8.78	±	8.10
Dechloromonas	14.5	13.8	6.27	3.82	3.38	6.91	N.D.[d]	6.96	±	5.42
unknown o: *Acidimicrobiales*	3.58	$9.28\cdot10^{-1}$	3.80	5.79	$2.35\cdot10^{-1}$	$2.15\cdot10^{-1}$	N.D.[d]	2.08	±	2.29
Rhodocyclus	$3.51\cdot10^{-1}$	$4.85\cdot10^{-1}$	$5.65\cdot10^{-1}$	$7.59\cdot10^{-1}$	1.42	1.70	8.33	1.95	±	2.86
Minor phylotypes (235)[e]	2.30	1.21	1.74	2.41	2.03	1.86	N.D.[d]	1.65	±	$8.29\cdot10^{-1}$
Parcubacteria_genera_inc._sed.[f]	2.27	$9.80\cdot10^{-1}$	$8.11\cdot10^{-1}$	2.05	$4.66\cdot10^{-1}$	3.22	N.D.[d]	1.40	±	1.14
Bacteriovorax	5.26	$2.14\cdot10^{-1}$	$5.48\cdot10^{-2}$	$1.97\cdot10^{-2}$	$4.07\cdot10^{-2}$	$6.34\cdot10^{-2}$	N.D.[d]	$8.08\cdot10^{-1}$	±	1.97
unknown f: *Xanthomonadaceae*	2.77	$4.15\cdot10^{-1}$	$2.85\cdot10^{-1}$	$5.39\cdot10^{-1}$	$7.78\cdot10^{-1}$	$7.47\cdot10^{-1}$	N.D.[d]	$7.90\cdot10^{-1}$	±	$9.13\cdot10^{-1}$
unknown d: *Bacteria*	2.04	$5.90\cdot10^{-1}$	$3.67\cdot10^{-1}$	$4.44\cdot10^{-1}$	$6.92\cdot10^{-1}$	$6.59\cdot10^{-1}$	N.D.[d]	$6.84\cdot10^{-1}$	±	$6.41\cdot10^{-1}$
Azonexus	$1.48\cdot10^{-1}$	1.25	$6.52\cdot10^{-1}$	$3.30\cdot10^{-1}$	$3.75\cdot10^{-1}$	$4.68\cdot10^{-1}$	N.D.[d]	$4.60\cdot10^{-1}$	±	$4.06\cdot10^{-1}$
Ferrimicrobium	1.50	$2.63\cdot10^{-1}$	$4.66\cdot10^{-1}$	$3.89\cdot10^{-1}$	$1.36\cdot10^{-2}$	$2.93\cdot10^{-2}$	N.D.[d]	$3.81\cdot10^{-1}$	±	$5.29\cdot10^{-1}$

Table S91. Moscow WRRF genus-level PAO results summary continued.

Genus[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	±	SD[c]
Bdellovibrio	1.31	$4.18\cdot10^{-1}$	$8.77\cdot10^{-2}$	$1.10\cdot10^{-1}$	$3.89\cdot10^{-1}$	$2.54\cdot10^{-1}$	N.D.[d]	$3.67\cdot10^{-1}$	±	$4.45\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[f] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S92. Summary of genus-level relative abundance by operational day of the 16S rRNA gene sequencing results with the PAO primer set.

Genus[a,b]	S-EBPR (S87)			V-EBPR (S88)			G-EBPR (S89)			R-EBPR (S90)			Moscow WRRF (S91)		
	Average	± %	SD[c]	Average	± %	SD[c]	Average	± %	SD[c]	Average	± %	SD[c]	Average	± %	SD[c]
Dechloromonas	$2.56\cdot10^{-2}$	±	$3.02\cdot10^{-2}$	1.90	±	1.52	2.26	±	3.33	63.8	±	7.86	6.96	±	5.42
unknown f: *Rhodocyclaceae*	7.40	±	6.10	12.3	±	11.4	1.03	±	$5.35\cdot10^{-1}$	5.39	±	6.85	51.2	±	14.0
Propionivibrio	44.3	±	37.8	31.4	±	35.6	47.7	±	39.3	6.52	±	8.82	22.5	±	3.94
Azospira	41.8	±	38.1	$3.86\cdot10^{-1}$	±	$7.26\cdot10^{-1}$	$6.00\cdot10^{-1}$	±	$8.22\cdot10^{-1}$	$1.05\cdot10^{-1}$	±	$1.19\cdot10^{-1}$	$3.46\cdot10^{-1}$	±	$2.72\cdot10^{-1}$
unknown d: *Bacteria*	$7.43\cdot10^{-1}$	±	1.21	17.6	±	17.9	7.08	±	7.33	1.41	±	$7.51\cdot10^{-1}$	$6.84\cdot10^{-1}$	±	$6.41\cdot10^{-1}$
unknown c: *Betaproteobacteria*	$5.96\cdot10^{-2}$	±	$7.58\cdot10^{-2}$	$8.13\cdot10^{-2}$	±	$6.31\cdot10^{-2}$	$3.69\cdot10^{-1}$	±	$4.23\cdot10^{-1}$	14.7	±	11.1	8.78	±	8.10
Azonexus	$2.44\cdot10^{-2}$	±	$3.06\cdot10^{-2}$	8.74	±	17.2	1.85	±	2.76	$9.34\cdot10^{-1}$	±	1.24	$4.60\cdot10^{-1}$	±	$4.06\cdot10^{-1}$
Ferrimicrobium	$5.52\cdot10^{-3}$	±	$5.77\cdot10^{-3}$	2.97	±	5.12	7.85	±	13.6	$7.50\cdot10^{-1}$	±	1.55	$3.81\cdot10^{-1}$	±	$5.29\cdot10^{-1}$
unknown c: *Gammaproteobacteria*	$1.19\cdot10^{-1}$	±	$1.63\cdot10^{-1}$	2.60	±	2.48	7.72	±	9.04	$2.30\cdot10^{-2}$	±	$1.22\cdot10^{-2}$	$2.36\cdot10^{-1}$	±	$3.29\cdot10^{-1}$
Bdellovibrio	$4.53\cdot10^{-2}$	±	$4.66\cdot10^{-2}$	5.22	±	9.32	7.58	±	10.4	3.14	±	1.86	$3.67\cdot10^{-1}$	±	$4.45\cdot10^{-1}$
unknown p: *Proteobacteria*	4.41	±	7.39	1.68	±	1.85	$4.31\cdot10^{-1}$	±	$3.72\cdot10^{-1}$	$1.77\cdot10^{-1}$	±	$1.74\cdot10^{-1}$	$6.77\cdot10^{-2}$	±	$9.21\cdot10^{-2}$
Ilumatobacter	$1.81\cdot10^{-3}$	±	$2.47\cdot10^{-3}$	4.29	±	8.01	3.53	±	6.44	$2.18\cdot10^{-1}$	±	$4.43\cdot10^{-1}$	$1.27\cdot10^{-2}$	±	$2.74\cdot10^{-2}$
unknown c: *Actinobacteria*	$2.77\cdot10^{-3}$	±	$3.74\cdot10^{-3}$	1.91	±	3.03	3.00	±	4.23	$7.56\cdot10^{-2}$	±	$6.99\cdot10^{-2}$	$5.39\cdot10^{-2}$	±	$7.10\cdot10^{-2}$
unknown f: *Xanthomonadaceae*	$2.42\cdot10^{-1}$	±	$2.94\cdot10^{-1}$	2.21	±	2.51	1.26	±	1.12	$5.54\cdot10^{-1}$	±	$7.21\cdot10^{-1}$	$7.90\cdot10^{-1}$	±	$9.13\cdot10^{-1}$
unknown o: *Acidimicrobiales*	$1.54\cdot10^{-2}$	±	$1.58\cdot10^{-2}$	$8.06\cdot10^{-1}$	±	1.25	1.25	±	2.00	$1.26\cdot10^{-1}$	±	$1.83\cdot10^{-1}$	2.08	±	2.29
Rhodocyclus	$2.24\cdot10^{-2}$	±	$3.18\cdot10^{-2}$	$2.49\cdot10^{-1}$	±	$1.54\cdot10^{-1}$	$1.06\cdot10^{-1}$	±	$9.96\cdot10^{-2}$	$1.43\cdot10^{-1}$	±	$1.76\cdot10^{-1}$	1.95	±	2.86
Parachlamydia	$1.03\cdot10^{-2}$	±	$2.73\cdot10^{-2}$	1.73	±	1.70	1.36	±	3.28	$2.03\cdot10^{-1}$	±	$2.68\cdot10^{-1}$	$4.44\cdot10^{-2}$	±	$3.55\cdot10^{-2}$

Table S92. Summary of genus-level PAO results continued.

Genus[a,b]	S-EBPR (S87)			V-EBPR (S88)			G-EBPR (S89)			R-EBPR (S90)			Moscow WRRF (S91)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%			%			%			%			%	
unknown f: *Verrucomicrobiaceae*	$2.32{\cdot}10^{-2}$	±	$4.13{\cdot}10^{-2}$	$8.41{\cdot}10^{-1}$	±	$8.64{\cdot}10^{-1}$	1.62	±	2.61	$3.21{\cdot}10^{-1}$	±	$4.54{\cdot}10^{-1}$	$1.23{\cdot}10^{-1}$	±	$1.19{\cdot}10^{-1}$
Parcubacteria_genera_inc._sed.[d]	N.D.[e]			$8.91{\cdot}10^{-2}$	±	$9.80{\cdot}10^{-2}$	$1.01{\cdot}10^{-1}$	±	$1.14{\cdot}10^{-1}$	$1.04{\cdot}10^{-1}$	±	$1.18{\cdot}10^{-1}$	1.40	±	1.14
Minor phylotypes (224)[f]	$2.85{\cdot}10^{-1}$	±	$2.40{\cdot}10^{-1}$	1.26	±	$9.26{\cdot}10^{-1}$	$9.34{\cdot}10^{-1}$	±	$7.86{\cdot}10^{-1}$	$9.67{\cdot}10^{-1}$	±	$2.66{\cdot}10^{-1}$	$7.13{\cdot}10^{-1}$	±	$3.93{\cdot}10^{-1}$
unknown f: *Acidimicrobiaceae*	$1.16{\cdot}10^{-2}$	±	$2.45{\cdot}10^{-2}$	$4.65{\cdot}10^{-1}$	±	$6.99{\cdot}10^{-1}$	1.12	±	1.84	$2.95{\cdot}10^{-2}$	±	$3.71{\cdot}10^{-2}$	$1.52{\cdot}10^{-2}$	±	$2.54{\cdot}10^{-2}$
Bacteriovorax	$4.16{\cdot}10^{-2}$	±	$1.01{\cdot}10^{-1}$	$4.32{\cdot}10^{-1}$	±	$8.86{\cdot}10^{-1}$	$4.34{\cdot}10^{-1}$	±	$3.01{\cdot}10^{-1}$	$9.81{\cdot}10^{-2}$	±	$9.79{\cdot}10^{-2}$	$8.08{\cdot}10^{-1}$	±	1.97
unknown c: *Deltaproteobacteria*	$4.57{\cdot}10^{-1}$	±	$6.65{\cdot}10^{-1}$	$4.43{\cdot}10^{-1}$	±	$5.40{\cdot}10^{-1}$	$4.97{\cdot}10^{-1}$	±	1.24	$1.61{\cdot}10^{-1}$	±	$1.02{\cdot}10^{-1}$	$1.45{\cdot}10^{-2}$	±	$1.24{\cdot}10^{-2}$
unknown o: *Clostridiales*	$1.76{\cdot}10^{-3}$	±	$4.66{\cdot}10^{-3}$	$3.29{\cdot}10^{-1}$	±	$5.91{\cdot}10^{-1}$	$5.54{\cdot}10^{-2}$	±	$6.17{\cdot}10^{-2}$	$1.15{\cdot}10^{-3}$	±	$2.09{\cdot}10^{-3}$	$1.70{\cdot}10^{-2}$	±	$1.50{\cdot}10^{-2}$
unknown c: *Alphaproteobacteria*	$1.44{\cdot}10^{-3}$	±	$2.76{\cdot}10^{-3}$	$7.66{\cdot}10^{-2}$	±	$1.15{\cdot}10^{-1}$	$2.66{\cdot}10^{-1}$	±	$4.20{\cdot}10^{-1}$	$5.94{\cdot}10^{-2}$	±	$8.35{\cdot}10^{-2}$	$9.05{\cdot}10^{-3}$	±	$1.36{\cdot}10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] To conserve space, "*incertae sedis*" has been abbreviated "*inc. sed.*" with the original capitalization and interceding characters preserved.

[e] N.D. = Not detected.

[f] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

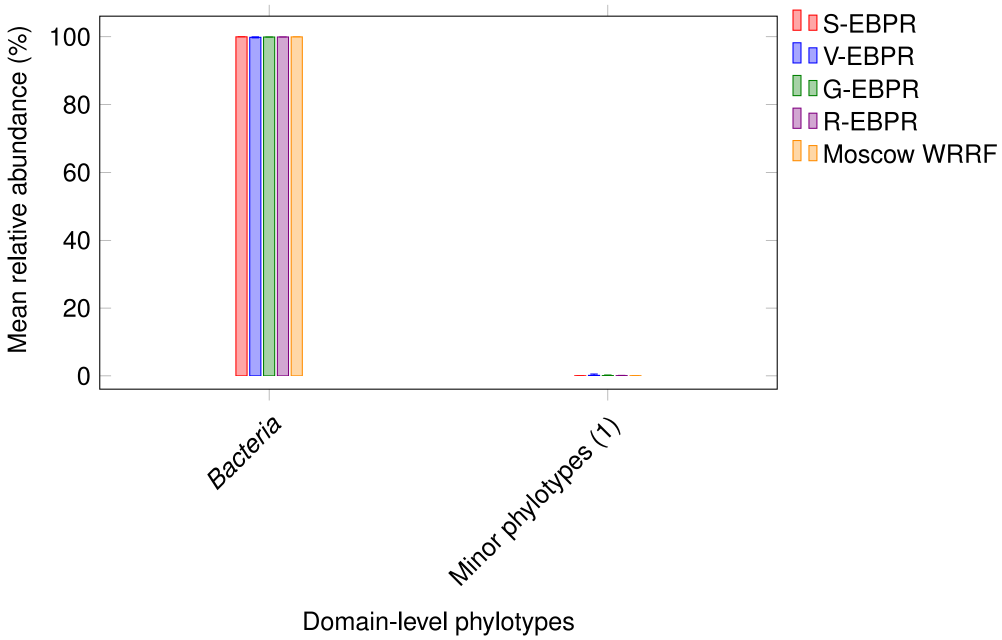

Figure S124. Mean relative abundance for phylotypes identified using the PAO primer set at the domain level (see Tables S57 to S61). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the domain level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

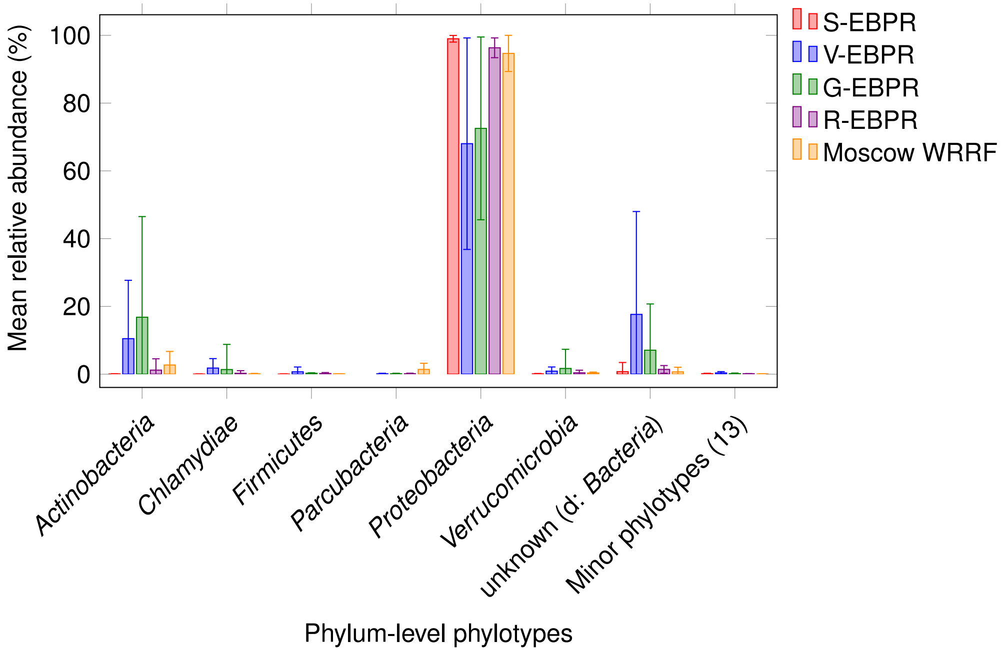

Figure S125. Mean relative abundance for phylotypes identified using the PAO primer set at the phylum level (see Tables S63 to S67). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the phylum level are indicated by "unknown" followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

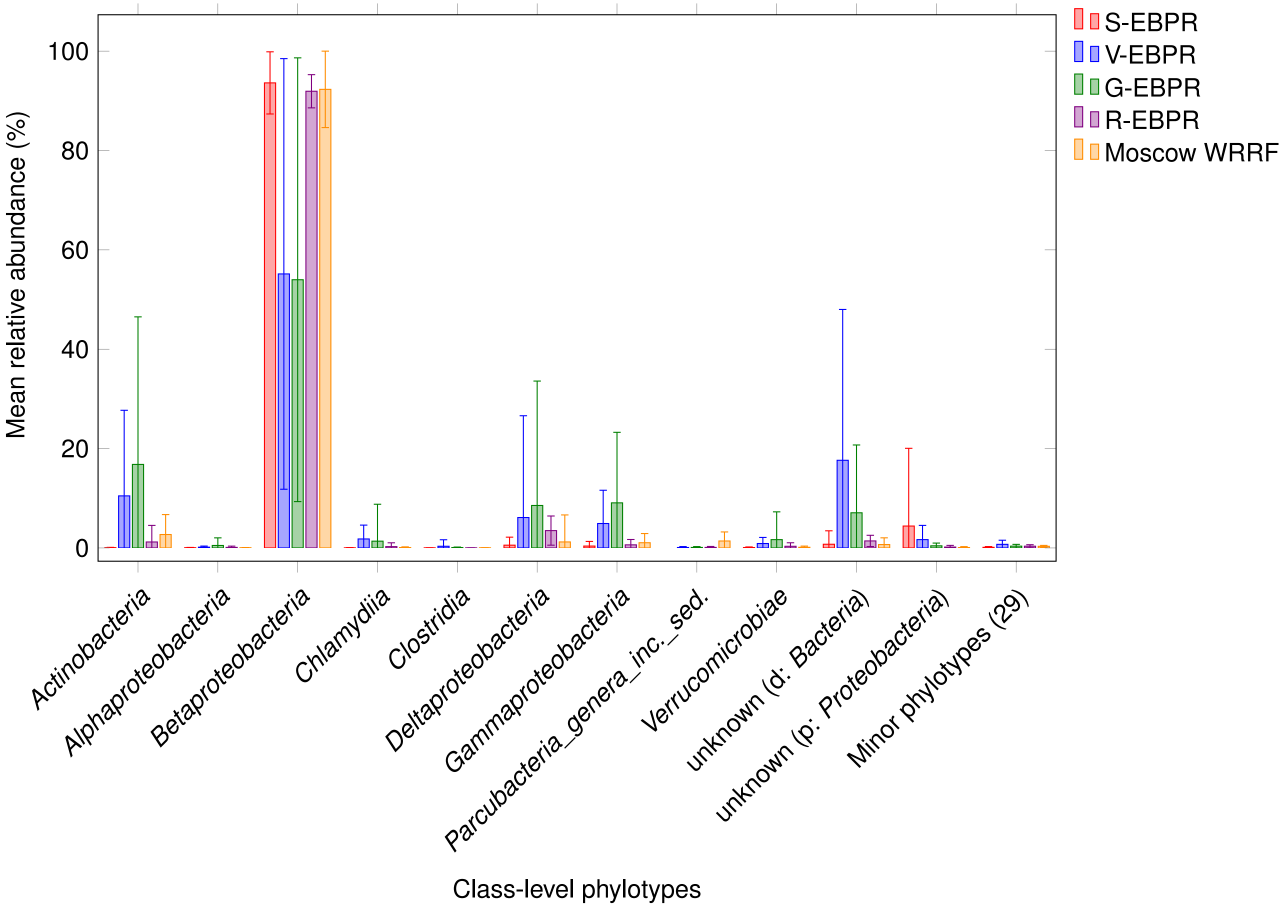

Figure S126. Mean relative abundance for phylotypes identified using the PAO primer set at the class level (see Tables S69 to S73). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the class level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

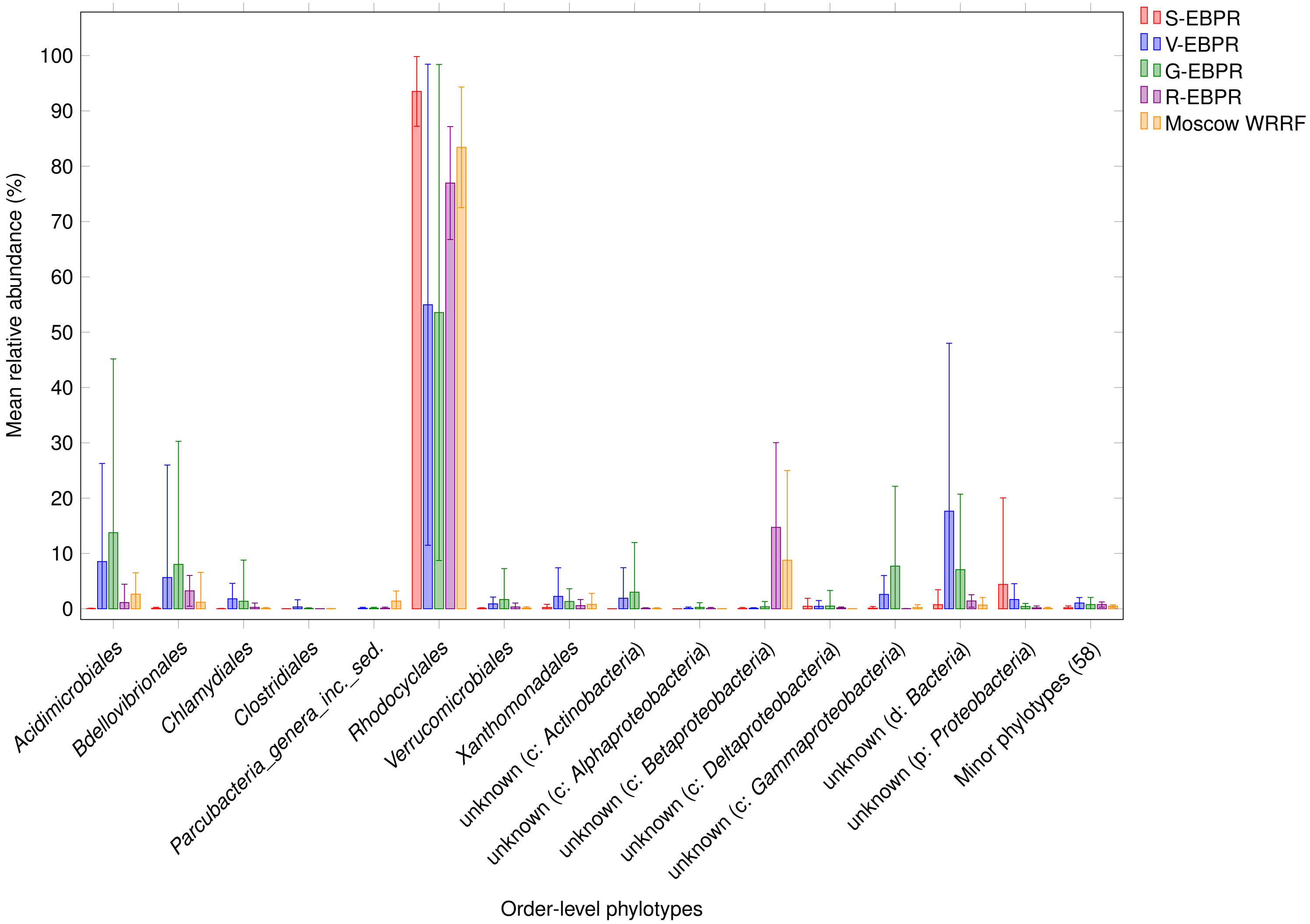

Figure S127. Mean relative abundance for phylotypes identified using the PAO primer set at the order level (see Tables S75 to S79). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the order level are indicated by "unknown" followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

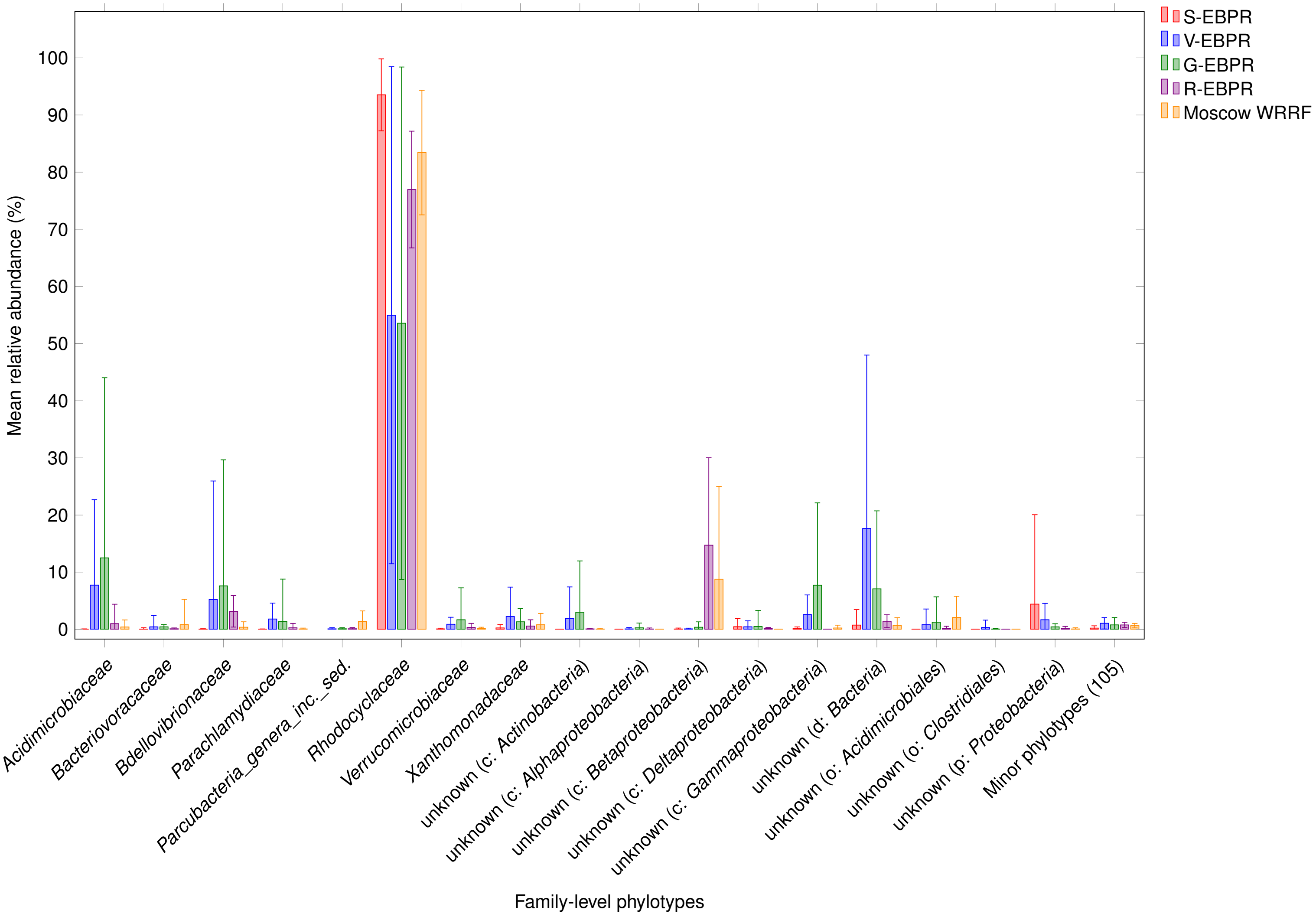

Figure S128. Mean relative abundance for phylotypes identified using the PAO primer set at the family level (see Tables S81 to S85). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the family level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

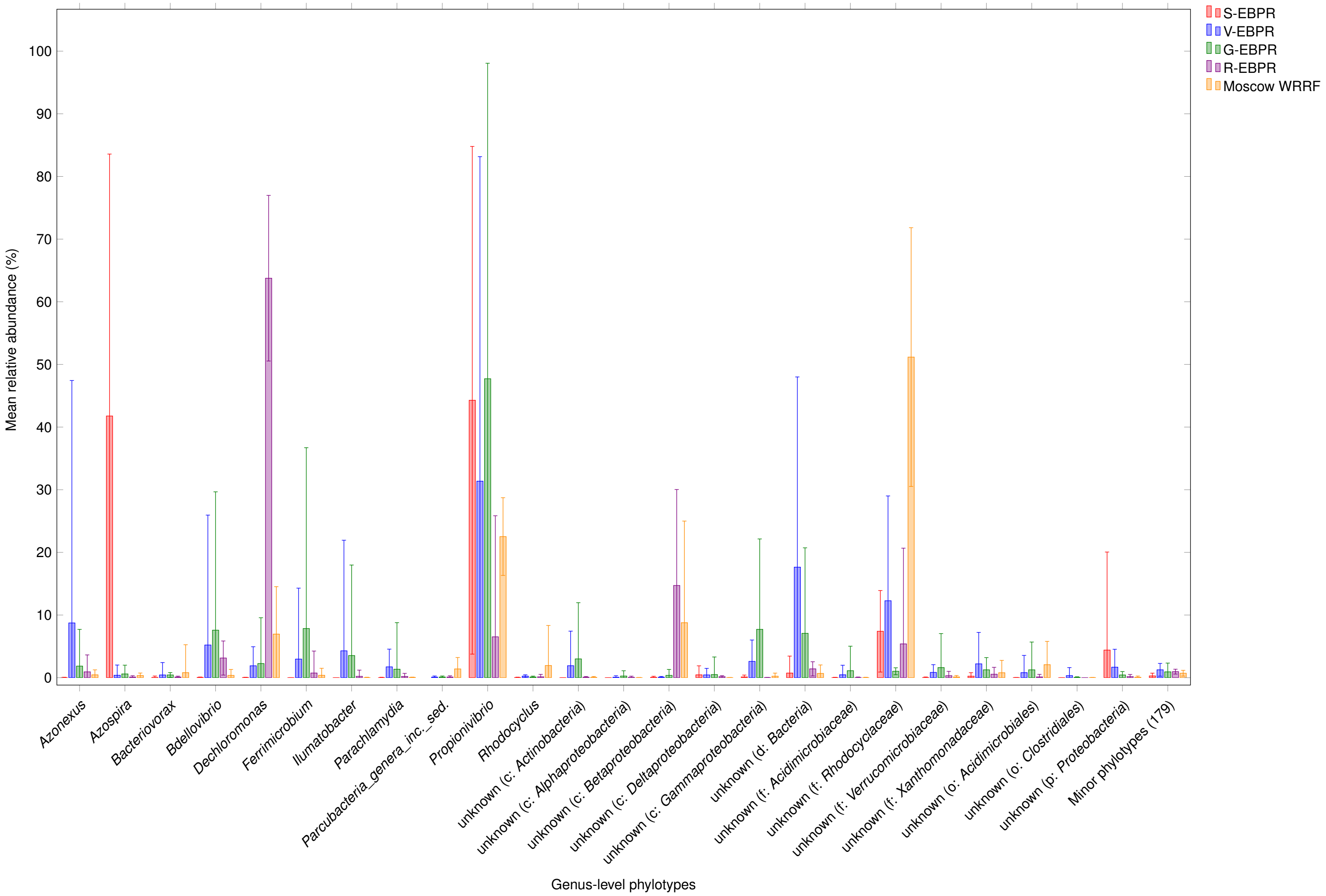

Figure S129. Mean relative abundance for phylotypes identified using the PAO primer set at the genus level (see Tables S87 to S91). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the genus level are indicated by "unknown" followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

Heatmaps

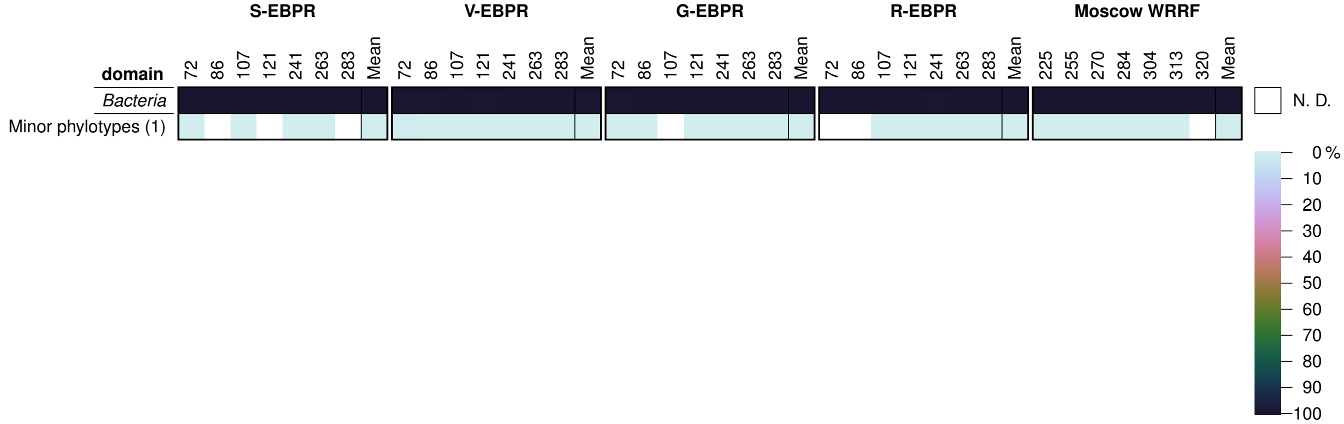

Figure S130. Heat map showing the relative abundance of phylotypes identified at the domain level using the PAO primer set (see Tables S57 to S61). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

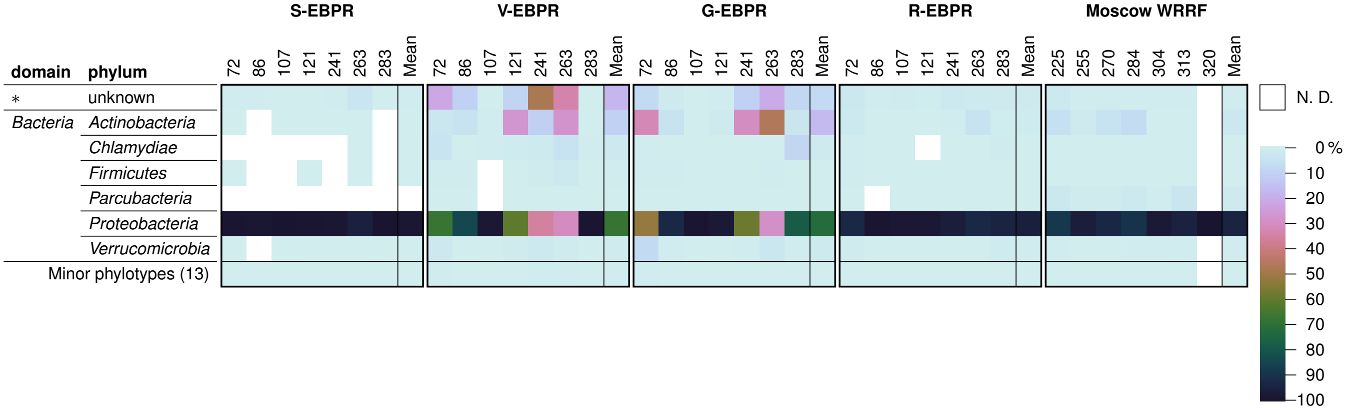

Figure S131. Heat map showing the relative abundance of phylotypes identified at the phylum level using the PAO primer set (see Tables S63 to S67). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

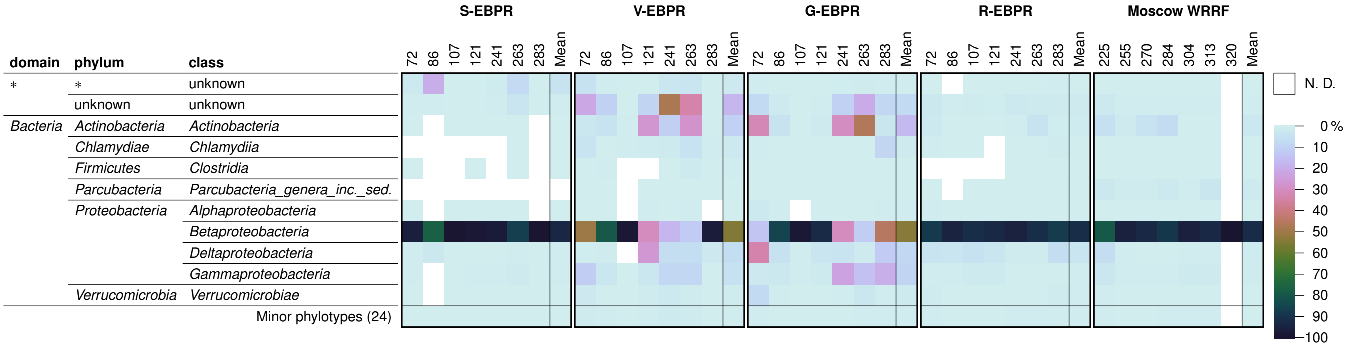

Figure S132. Heat map showing the relative abundance of phylotypes identified at the class level using the PAO primer set (see Tables S69 to S73). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

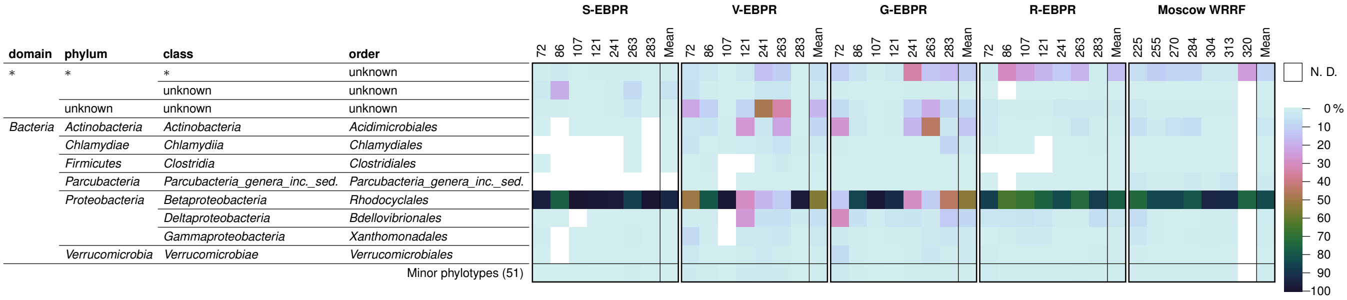

Figure S133. Heat map showing the relative abundance of phylotypes identified at the order level using the PAO primer set (see Tables S75 to S79). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

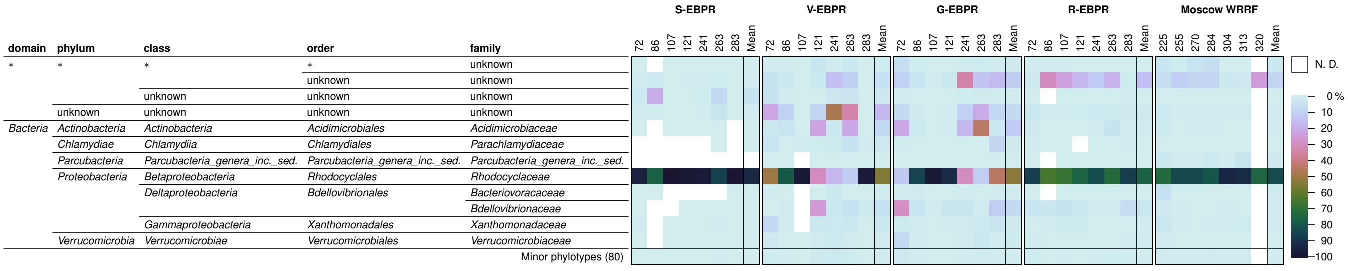

Figure S134. Heat map showing the relative abundance of phylotypes identified at the family level using the PAO primer set (see Tables S81 to S85). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

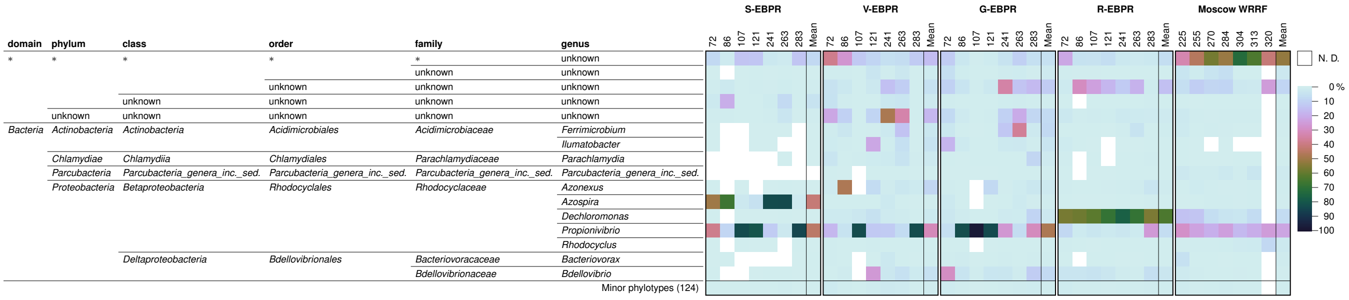

Figure S135. Heat map showing the relative abundance of phylotypes identified at the genus level using the PAO primer set (see Tables S87 to S91). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

GAO primer set

Diversity metrics

Table S93. Sample diversity and evenness indices and richness estimates using the GAO primer set.

Operational day	Total reads	Total phylotypes	Major[a] phylotypes	Minor[b] phylotypes	H'[c]	R[d]	D[e]	S_{Chao1}[f]
S-EBPR								
72	1 663	10	4	6	0.41	0.18	0.16	16.00
86	2 752	11	4	7	0.40	0.17	0.15	11.33
107	3 900	10	4	6	0.36	0.16	0.14	16.00
121	226	7	4	3	0.56	0.29	0.23	7.00
241	2 344	12	6	6	0.76	0.31	0.32	12.00
263	7 809	13	4	9	0.38	0.15	0.15	19.00
283	1 651	11	5	6	0.60	0.25	0.25	11.33
V-EBPR								
72	5 349	19	3	16	0.43	0.15	0.14	20.50
86	1 748	12	3	9	0.37	0.15	0.12	18.00
107	934	15	5	10	0.91	0.34	0.36	18.00
121	512	10	3	7	0.77	0.33	0.38	10.33
241	12 267	18	1	17	0.25	0.09	0.08	18.50
263	6 516	17	4	13	0.39	0.14	0.13	17.50
283	2 400	13	2	11	0.26	0.10	0.08	19.00
G-EBPR								
72	666	13	5	8	0.54	0.21	0.19	22.98
86	1 919	16	5	11	0.58	0.21	0.21	16.60
107	3 024	18	4	14	0.60	0.21	0.22	18.75
121	3 780	15	3	12	0.44	0.16	0.15	15.50
241	16 130	17	2	15	0.20	0.07	0.06	32.00
263	10 840	18	2	16	0.20	0.07	0.06	39.00
283	6 739	18	3	15	0.30	0.10	0.10	19.50
R-EBPR								
72	2 036	20	5	15	0.68	0.23	0.24	22.00
86	1 099	21	7	14	1.38	0.45	0.58	21.25
107	1 136	23	7	16	1.50	0.48	0.66	28.25
121	16	6	6	0	1.49	0.83	0.72	7.41
241	178	13	8	5	1.66	0.65	0.73	22.94
263	575	17	5	12	1.30	0.46	0.61	20.33
283	633	13	6	7	1.13	0.44	0.57	16.00
Moscow WRRF								
225	1 744	17	7	10	0.92	0.32	0.38	22.00
255	2 475	14	4	10	0.56	0.21	0.20	15.00
270	3 070	20	5	15	0.69	0.23	0.25	34.00
284	3 130	17	6	11	0.85	0.30	0.35	17.25
304	883	19	8	11	1.10	0.38	0.43	23.99
313	1 353	22	7	15	1.12	0.36	0.43	49.98

Table S93. Sample diversity and evenness indices and richness estimates using the GAO primer set continued.

Operational day	Total reads	Total phylotypes	Major[a] phylotypes	Minor[b] phylotypes	H'[c]	R[d]	D[e]	S_{Chao1}[f]
320	1 292	19	8	11	1.20	0.41	0.48	28.99

[a] Major phylotypes constitute at least 1% of the total relative abundance.

[b] Minor phylotypes constitute less than 1% of the total relative abundance.

[c] Shannon diversity index, given by $H' = -\sum_{i=1}^{S} \left(p_i \cdot \ln p_i\right)$ where S is the total number of phylotypes and p_i is the relative abundance of the i-th phylotype (Shannon, 1948).

[d] Pielou evenness index, given by $R = \frac{H'}{\ln S}$ where H' is the Shannon diversity index and S is the total number of phylotypes.

[e] Simpson's diversity index, given by $D = 1 - \sum_{i=1}^{S} p_i^2$ where S is the total number of phylotypes and p_i is the relative abundance of the i-th phylotype (Simpson, 1949).

[f] Bias-corrected Chao1 richness estimate, given by $S_{\text{Chao1}} = S + \frac{n+1}{n} \cdot \frac{F_1 \cdot (F_1 - 1)}{2 \cdot (F_2 + 1)}$ where S is the total number of phylotypes, n is the total number of sequences, F_1 is the total number of phylotypes to which only one sequence was assigned, and F_2 is the total number of phylotypes to which only two sequences were assigned.

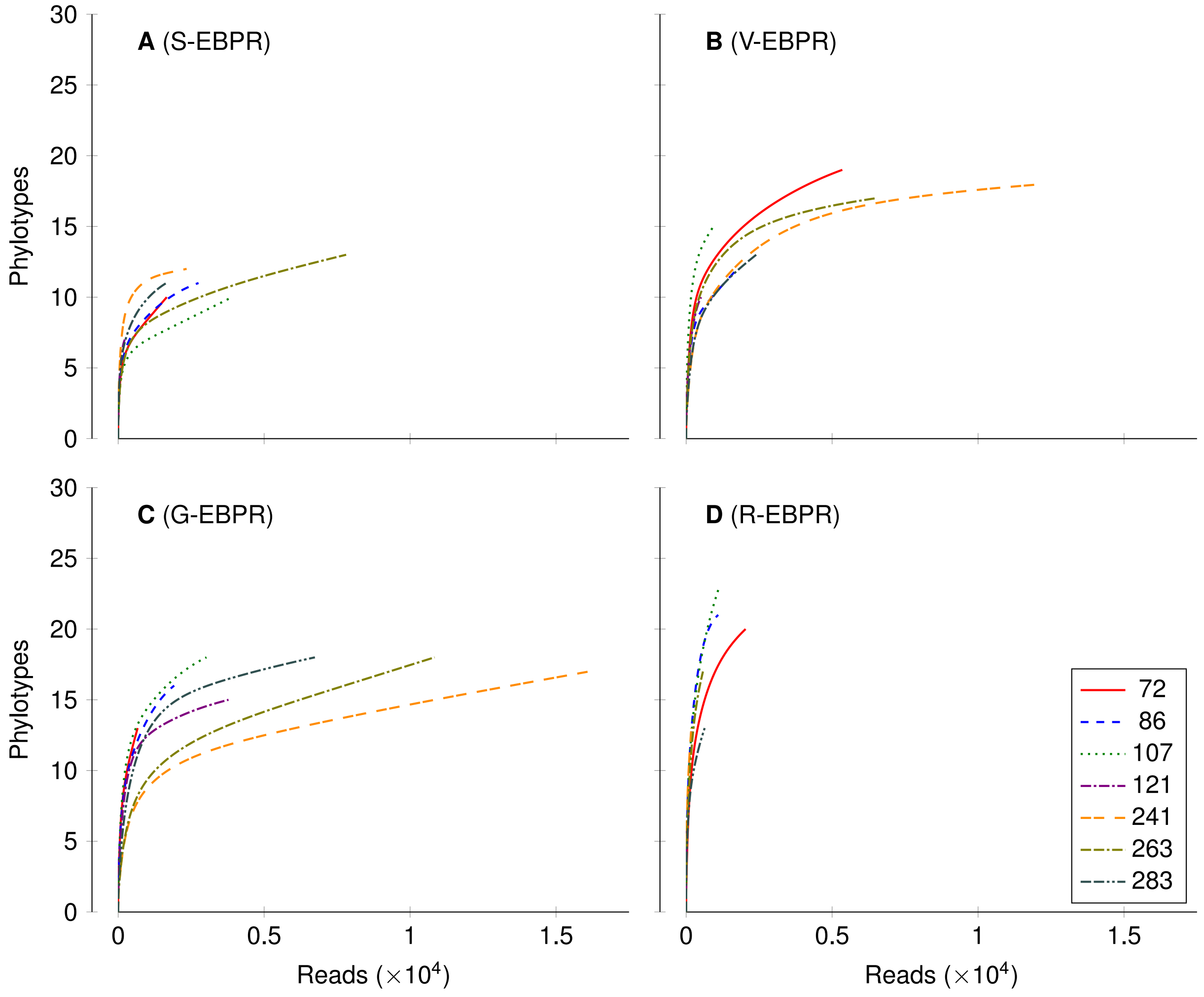

Figure S136. Rarefaction curves for the GAO primer set results for each lab-scale EBPR reactor.

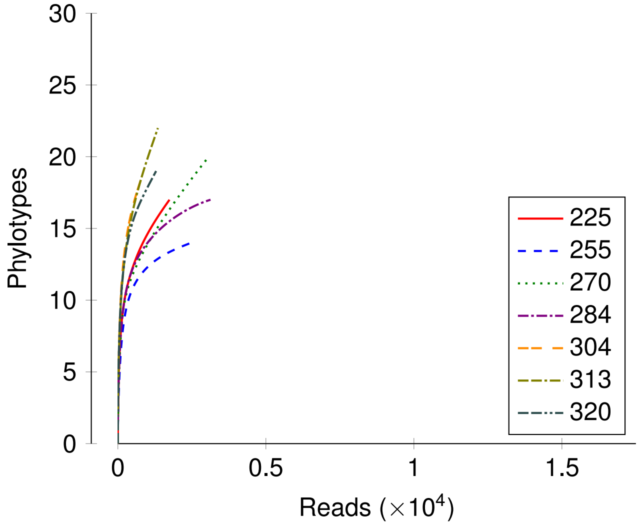

Figure S137. Rarefaction curves for the GAO primer set results for the Moscow WRRF.

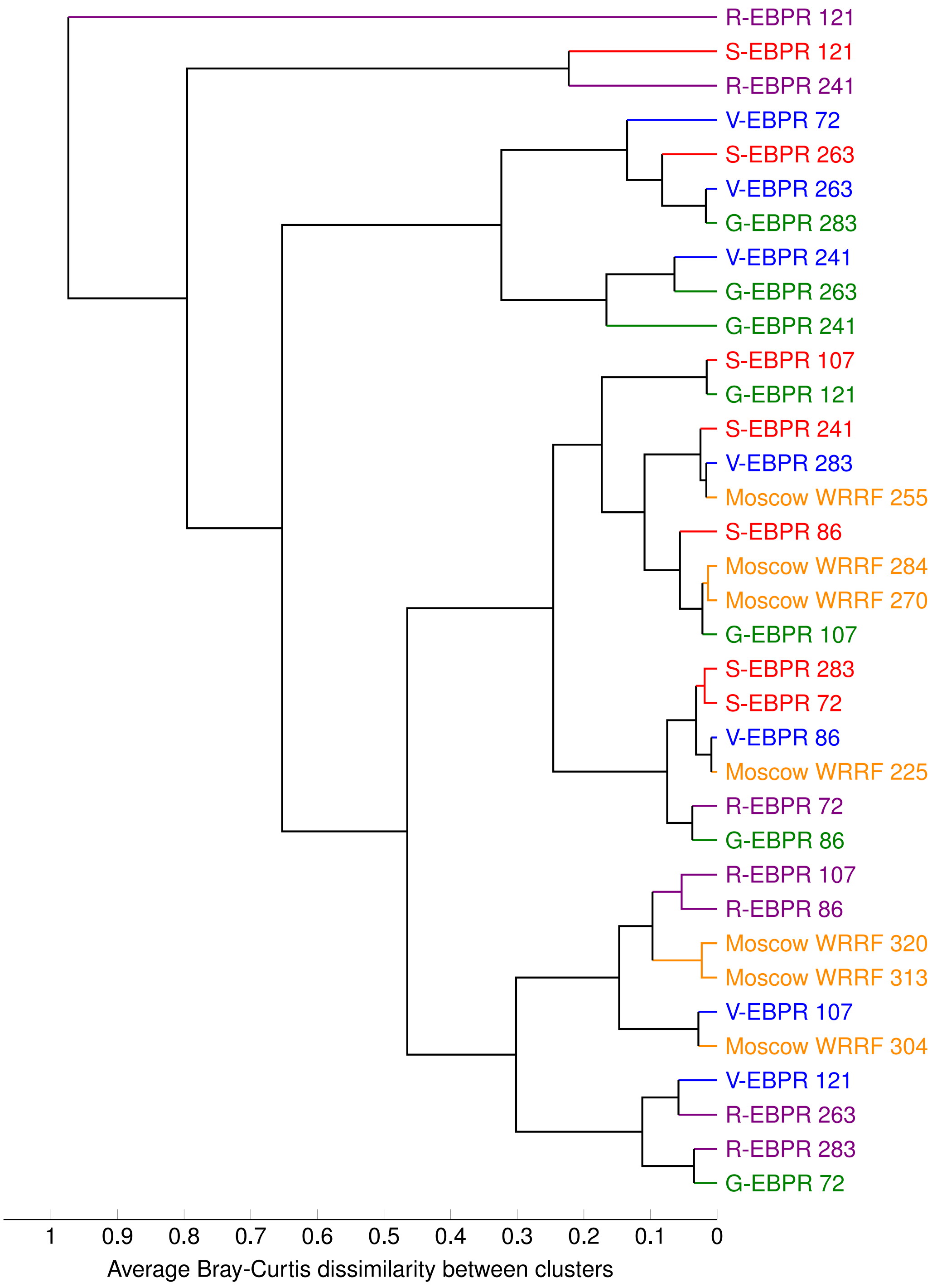

Figure S138. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the GAO primer set at the domain level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

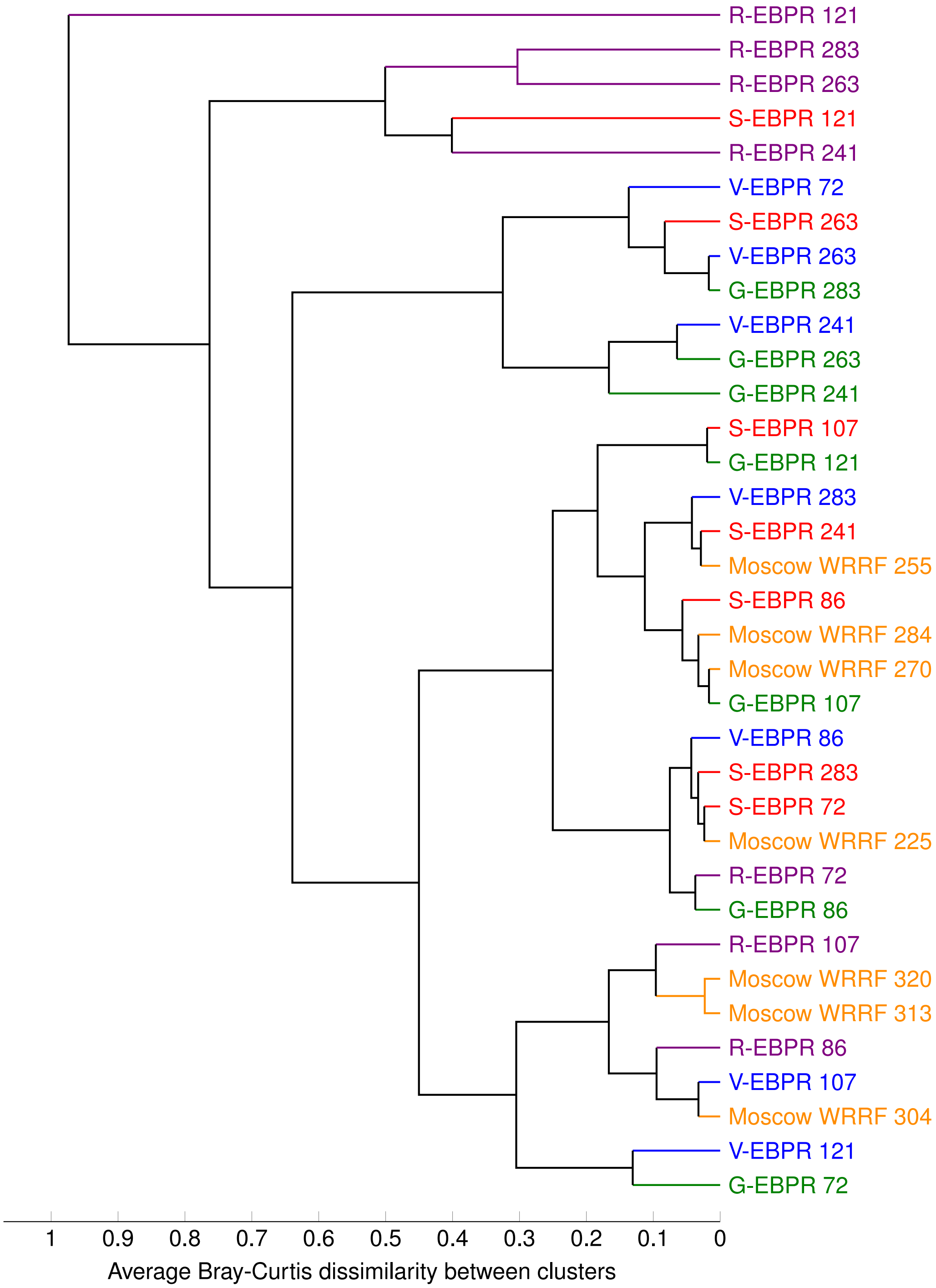

Figure S139. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the GAO primer set at the phylum level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

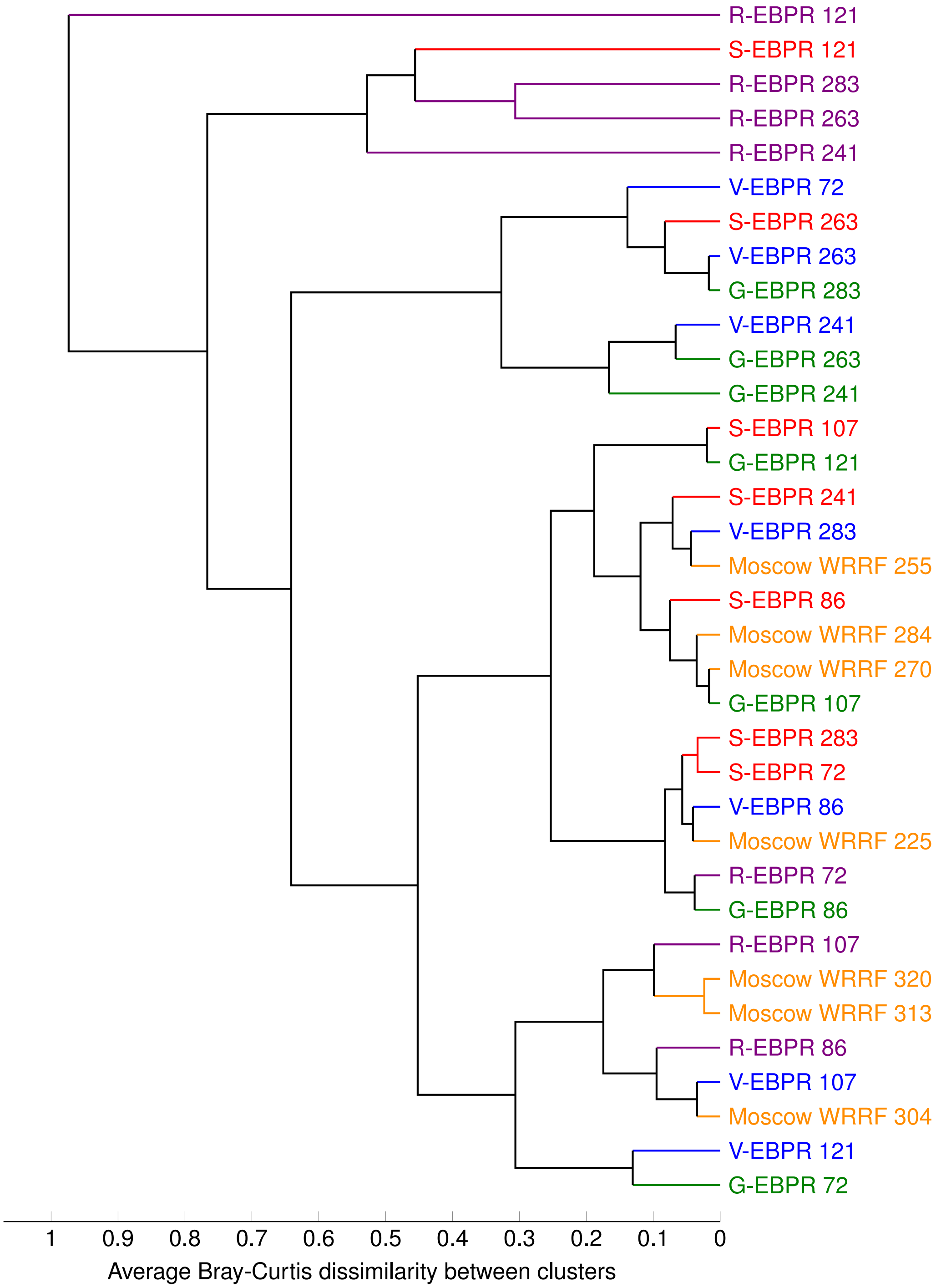

Figure S140. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the GAO primer set at the class level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

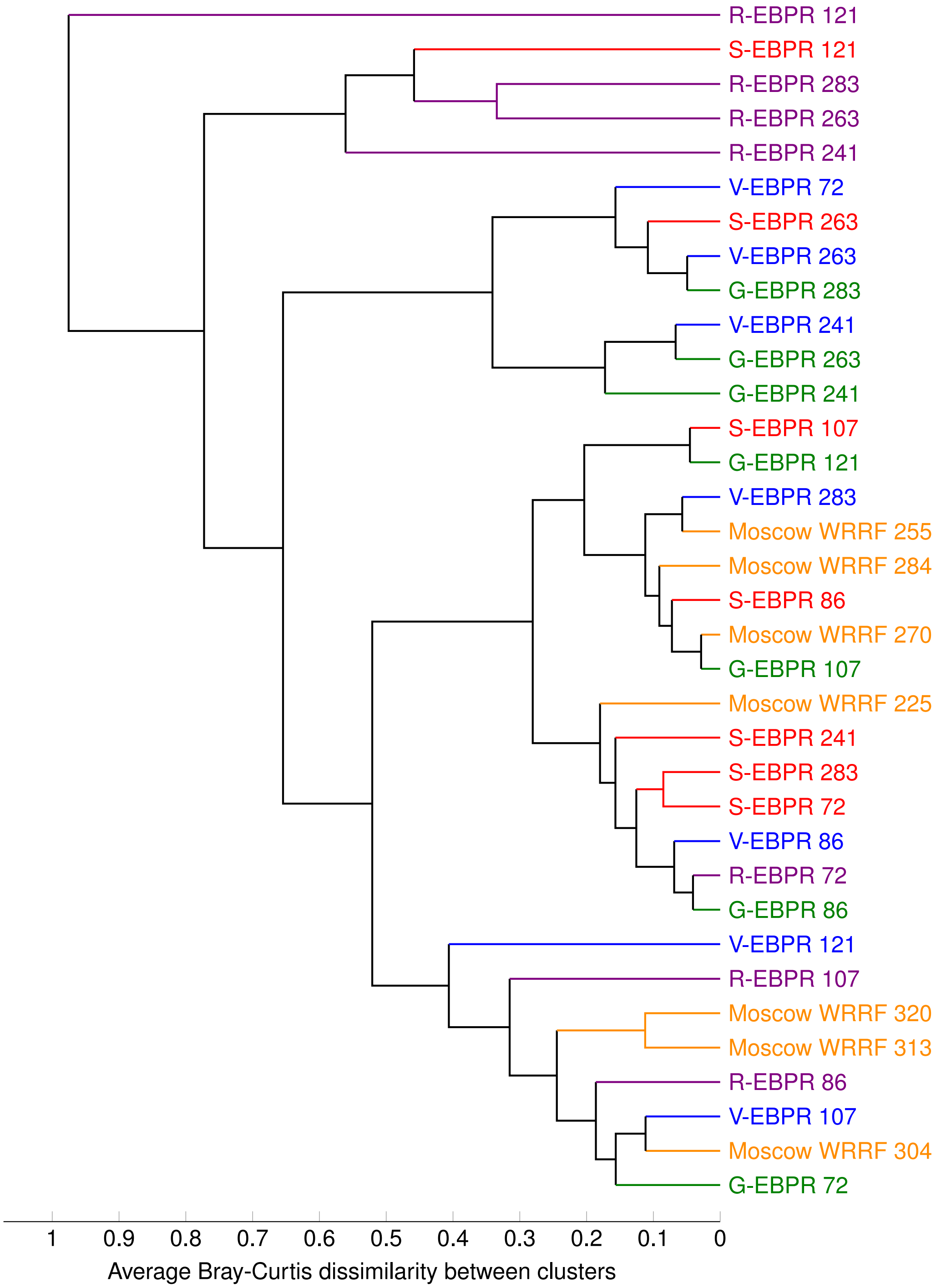

Figure S141. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the GAO primer set at the order level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

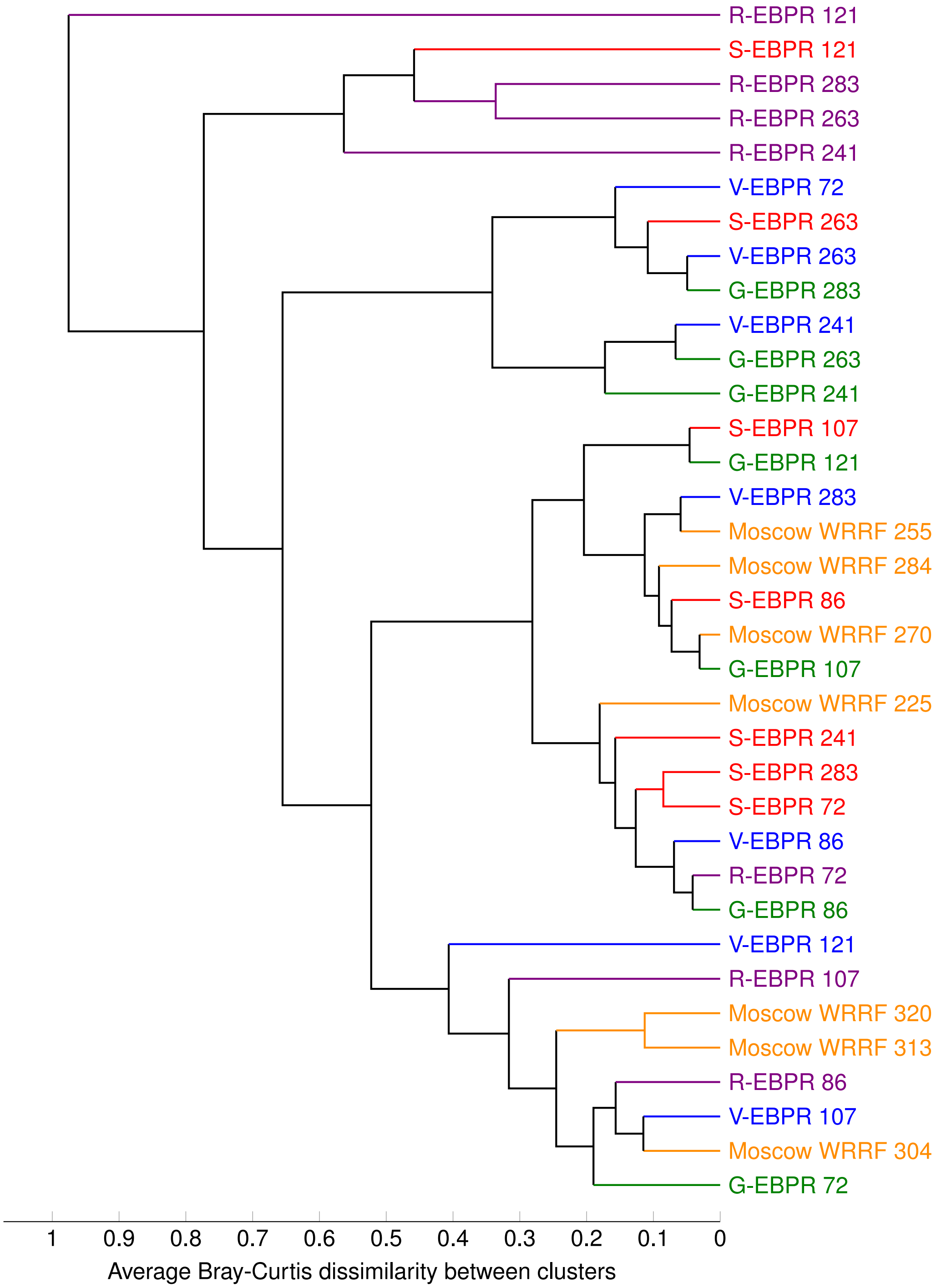

Figure S142. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the GAO primer set at the family level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

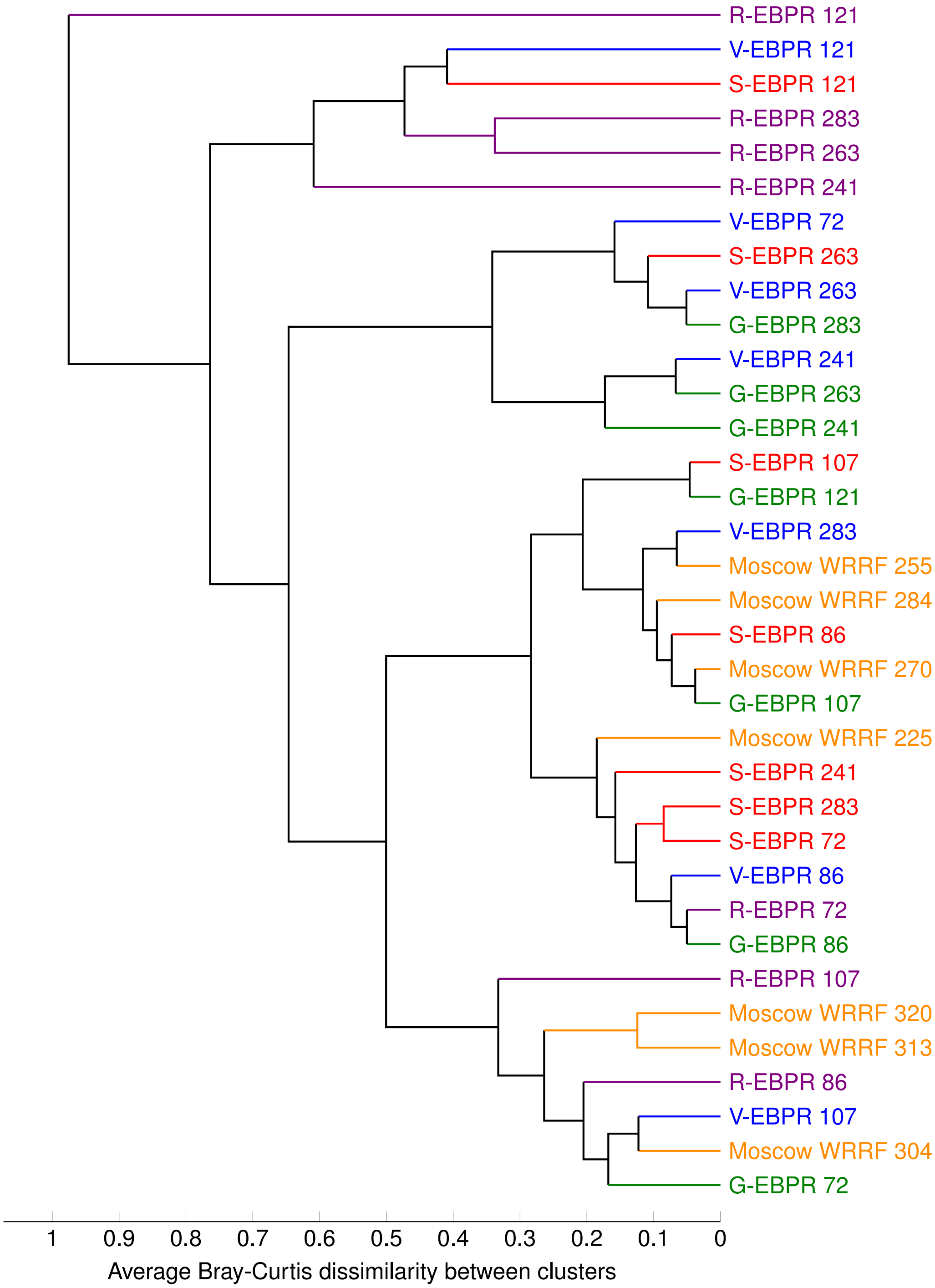

Figure S143. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the GAO primer set at the genus level. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). The average linkage method was used to define the dissimilarity between clusters.

Table S94. Dissimilarity matrix for samples with phylotypes identified using the GAO primer set at the domain level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	25	0																																	
	107	40	18	0																																
	121	76	85	89	0																															
	241	18	19	33	82	0																														
	263	65	48	34	94	54	0																													
	283	9	30	43	76	18	65	0																												
V-EBPR	72	53	33	18	92	46	22	56	0																											
	86	8	25	40	77	18	65	13	51	0																										
	107	39	55	66	61	48	80	35	73	41	0																									
	121	62	75	81	41	71	90	62	86	63	42	0																								
	241	76	64	53	96	72	26	78	40	75	87	93	0																							
	263	60	42	28	93	54	13	63	11	58	78	86	32	0																						
	283	23	9	25	83	17	54	28	38	17	53	71	67	46	0																					
G-EBPR	72	46	62	72	50	57	85	45	78	46	18	30	90	82	58	0																				
	86	11	23	38	79	14	62	14	49	5	38	66	74	57	17	49	0																			
	107	31	7	19	86	22	47	34	31	27	55	76	62	40	12	64	23	0																		
	121	40	17	5	89	33	36	44	19	37	64	79	53	28	22	70	35	15	0																	
	241	81	71	61	97	77	37	82	52	81	90	95	15	44	74	92	79	69	62	0																
	263	74	60	48	96	68	20	75	36	72	85	93	7	27	64	88	71	58	49	20	0															
	283	61	42	28	94	54	9	63	14	59	76	88	30	5	48	82	57	40	29	41	24	0														
R-EBPR	72	13	21	37	80	11	61	16	47	9	40	67	73	56	17	52	5	22	34	78	70	55	0													
	86	45	59	69	66	51	81	42	74	48	18	48	88	80	58	26	44	55	67	90	86	78	43	0												
	107	56	67	74	68	60	85	54	79	58	29	38	90	81	66	32	55	65	72	92	89	81	54	35	0											
	121	98	99	99	89	99	100	98	99	98	97	94	100	100	99	96	98	99	99	100	100	100	99	97	97	0										
	241	87	89	93	54	87	96	83	94	89	70	72	98	96	92	70	85	89	92	98	97	95	85	73	74	85	0									
	263	66	75	82	44	69	89	62	85	69	38	36	93	89	76	39	62	71	80	94	92	87	62	32	44	95	55	0								
	283	79	83	88	48	79	93	75	90	80	57	61	95	93	85	62	75	80	87	96	95	91	74	51	60	95	62	34	0							
Moscow WRRF	225	16	35	48	77	27	69	14	56	17	36	63	78	63	31	46	18	36	45	83	76	64	19	43	53	98	83	62	74	0						
	255	22	11	27	83	13	54	26	39	19	49	72	68	48	7	58	15	12	24	74	64	48	13	52	60	99	87	68	78	26	0					
	270	30	7	19	86	20	47	33	31	28	56	77	62	41	13	65	25	4	17	69	59	41	21	57	66	99	89	72	81	34	11	0				
	284	31	9	24	87	23	50	35	34	29	57	76	64	43	14	65	26	10	21	71	61	44	23	59	66	99	90	75	83	29	13	9	0			
	304	43	58	68	60	50	82	39	74	45	12	38	88	79	56	16	43	57	65	90	86	78	43	18	29	96	68	37	58	38	51	58	58	0		
	313	28	45	57	72	37	75	25	64	30	22	48	83	69	42	35	28	43	54	86	81	70	28	27	36	98	77	47	64	23	35	43	45	23	0	
	320	33	49	60	70	42	77	30	66	34	20	50	84	72	46	33	33	48	57	87	82	72	33	29	39	98	77	51	66	21	41	47	44	21	12	0

Table S95. Dissimilarity matrix for samples with phylotypes identified using the GAO primer set at the phylum level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	25	0																																	
	107	40	18	0																																
	121	76	85	89	0																															
	241	18	19	33	82	0																														
	263	65	48	34	94	54	0																													
	283	9	30	43	76	18	65	0																												
V-EBPR	72	53	33	18	92	46	22	56	0																											
	86	8	25	40	77	18	65	13	51	0																										
	107	39	55	66	61	48	80	35	73	41	0																									
	121	62	75	81	41	71	90	62	86	63	42	0																								
	241	76	64	53	96	72	26	78	40	75	87	93	0																							
	263	60	42	28	93	54	13	63	11	58	78	86	32	0																						
	283	23	9	25	83	17	54	28	38	17	53	71	67	46	0																					
G-EBPR	72	46	62	72	50	57	85	45	78	46	18	30	90	82	58	0																				
	86	11	23	38	79	14	62	14	49	5	38	66	74	57	17	49	0																			
	107	31	7	19	86	22	47	34	31	27	55	76	62	40	12	64	23	0																		
	121	40	17	5	89	33	36	44	19	37	64	79	53	28	22	70	35	15	0																	
	241	81	71	61	97	77	37	82	52	81	90	95	15	44	74	92	79	69	62	0																
	263	74	60	48	96	68	20	75	36	72	85	93	7	27	64	88	71	58	49	20	0															
	283	61	42	28	94	54	9	63	14	59	76	88	30	5	48	82	57	40	29	41	24	0														
R-EBPR	72	13	21	37	80	11	61	16	47	9	40	67	73	56	17	52	5	22	34	78	70	55	0													
	86	45	59	69	66	51	81	42	74	48	18	48	88	80	58	26	44	55	67	90	86	78	43	0												
	107	56	67	74	68	60	85	54	79	58	29	38	90	81	66	32	55	65	72	92	89	81	54	35	0											
	121	98	99	99	89	99	100	98	99	98	97	94	100	100	99	96	98	99	99	100	100	100	99	97	97	0										
	241	87	89	93	54	87	96	83	94	89	70	72	98	96	92	70	85	89	92	98	97	95	85	73	74	85	0									
	263	66	75	82	44	69	89	62	85	69	38	36	93	89	76	39	62	71	80	94	92	87	62	32	44	95	55	0								
	283	79	83	88	48	79	93	75	90	80	57	61	95	93	85	62	75	80	87	96	95	91	74	51	60	95	62	34	0							
Moscow WRRF	225	16	35	48	77	27	69	14	56	17	36	63	78	63	31	46	18	36	45	83	76	64	19	43	53	98	83	62	74	0						
	255	22	11	27	83	13	54	26	39	19	49	72	68	48	7	58	15	12	24	74	64	48	13	52	60	99	87	68	78	26	0					
	270	30	7	19	86	20	47	33	31	28	56	77	62	41	13	65	25	4	17	69	59	41	21	57	66	99	89	72	81	34	11	0				
	284	31	9	24	87	23	50	35	34	29	57	76	64	43	14	65	26	10	21	71	61	44	23	59	66	99	90	75	83	29	13	9	0			
	304	43	58	68	60	50	82	39	74	45	12	38	88	79	56	16	43	57	65	90	86	78	43	18	29	96	68	37	58	38	51	58	58	0		
	313	28	45	57	72	37	75	25	64	30	22	48	83	69	42	35	28	43	54	86	81	70	28	27	36	98	77	47	64	23	35	43	45	23	0	
	320	33	49	60	70	42	77	30	66	34	20	50	84	72	46	33	33	48	57	87	82	72	33	29	39	98	77	51	66	21	41	47	44	21	12	0

Table S96. Dissimilarity matrix for samples with phylotypes identified using the GAO primer set at the class level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	25	0																																	
	107	40	18	0																																
	121	76	85	89	0																															
	241	18	19	33	82	0																														
	263	65	48	34	94	54	0																													
	283	9	30	43	76	18	65	0																												
V-EBPR	72	53	33	18	92	46	22	56	0																											
	86	8	25	40	77	18	65	13	51	0																										
	107	39	55	66	61	48	80	35	73	41	0																									
	121	62	75	81	41	71	90	62	86	63	42	0																								
	241	76	64	53	96	72	26	78	40	75	87	93	0																							
	263	60	42	28	93	54	13	63	11	58	78	86	32	0																						
	283	23	9	25	83	17	54	28	38	17	53	71	67	46	0																					
G-EBPR	72	46	62	72	50	57	85	45	78	46	18	30	90	82	58	0																				
	86	11	23	38	79	14	62	14	49	5	38	66	74	57	17	49	0																			
	107	31	7	19	86	22	47	34	31	27	55	76	62	40	12	64	23	0																		
	121	40	17	5	89	33	36	44	19	37	64	79	53	28	22	70	35	15	0																	
	241	81	71	61	97	77	37	82	52	81	90	95	15	44	74	92	79	69	62	0																
	263	74	60	48	96	68	20	75	36	72	85	93	7	27	64	88	71	58	49	20	0															
	283	61	42	28	94	54	9	63	14	59	76	88	30	5	48	82	57	40	29	41	24	0														
R-EBPR	72	13	21	37	80	11	61	16	47	9	40	67	73	56	17	52	5	22	34	78	70	55	0													
	86	45	59	69	66	51	81	42	74	48	18	48	88	80	58	26	44	55	67	90	86	78	43	0												
	107	56	67	74	68	60	85	54	79	58	29	38	90	81	66	32	55	65	72	92	89	81	54	35	0											
	121	98	99	99	89	99	100	98	99	98	97	94	100	100	99	96	98	99	99	100	100	100	99	97	97	0										
	241	87	89	93	54	87	96	83	94	89	70	72	98	96	92	70	85	89	92	98	97	95	85	73	74	85	0									
	263	66	75	82	44	69	89	62	85	69	38	36	93	89	76	39	62	71	80	94	92	87	62	32	44	95	55	0								
	283	79	83	88	48	79	93	75	90	80	57	61	95	93	85	62	75	80	87	96	95	91	74	51	60	95	62	34	0							
Moscow WRRF	225	16	35	48	77	27	69	14	56	17	36	63	78	63	31	46	18	36	45	83	76	64	19	43	53	98	83	62	74	0						
	255	22	11	27	83	13	54	26	39	19	49	72	68	48	7	58	15	12	24	74	64	48	13	52	60	99	87	68	78	26	0					
	270	30	7	19	86	20	47	33	31	28	56	77	62	41	13	65	25	4	17	69	59	41	21	57	66	99	89	72	81	34	11	0				
	284	31	9	24	87	23	50	35	34	29	57	76	64	43	14	65	26	10	21	71	61	44	23	59	66	99	90	75	83	29	13	9	0			
	304	43	58	68	60	50	82	39	74	45	12	38	88	79	56	16	43	57	65	90	86	78	43	18	29	96	68	37	58	38	51	58	58	0		
	313	28	45	57	72	37	75	25	64	30	22	48	83	69	42	35	28	43	54	86	81	70	28	27	36	98	77	47	64	23	35	43	45	23	0	
	320	33	49	60	70	42	77	30	66	34	20	50	84	72	46	33	33	48	57	87	82	72	33	29	39	98	77	51	66	21	41	47	44	21	12	0

Table S97. Dissimilarity matrix for samples with phylotypes identified using the GAO primer set at the order level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	25	0																																	
	107	40	18	0																																
	121	76	85	89	0																															
	241	18	19	33	82	0																														
	263	65	48	34	94	54	0																													
	283	9	30	43	76	18	65	0																												
V-EBPR	72	53	33	18	92	46	22	56	0																											
	86	8	25	40	77	18	65	13	51	0																										
	107	39	55	66	61	48	80	35	73	41	0																									
	121	62	75	81	41	71	90	62	86	63	42	0																								
	241	76	64	53	96	72	26	78	40	75	87	93	0																							
	263	60	42	28	93	54	13	63	11	58	78	86	32	0																						
	283	23	9	25	83	17	54	28	38	17	53	71	67	46	0																					
G-EBPR	72	46	62	72	50	57	85	45	78	46	18	30	90	82	58	0																				
	86	11	23	38	79	14	62	14	49	5	38	66	74	57	17	49	0																			
	107	31	7	19	86	22	47	34	31	27	55	76	62	40	12	64	23	0																		
	121	40	17	5	89	33	36	44	19	37	64	79	53	28	22	70	35	15	0																	
	241	81	71	61	97	77	37	82	52	81	90	95	15	44	74	92	79	69	62	0																
	263	74	60	48	96	68	20	75	36	72	85	93	7	27	64	88	71	58	49	20	0															
	283	61	42	28	94	54	9	63	14	59	76	88	30	5	48	82	57	40	29	41	24	0														
R-EBPR	72	13	21	37	80	11	61	16	47	9	40	67	73	56	17	52	5	22	34	78	70	55	0													
	86	45	59	69	66	51	81	42	74	48	18	48	88	80	58	26	44	55	67	90	86	78	43	0												
	107	56	67	74	68	60	85	54	79	58	29	38	90	81	66	32	55	65	72	92	89	81	54	35	0											
	121	98	99	99	89	99	100	98	99	98	97	94	100	100	99	96	98	99	99	100	100	100	99	97	97	0										
	241	87	89	93	54	87	96	83	94	89	70	72	98	96	92	70	85	89	92	98	97	95	85	73	74	85	0									
	263	66	75	82	44	69	89	62	85	69	38	36	93	89	76	39	62	71	80	94	92	87	62	32	44	95	55	0								
	283	79	83	88	48	79	93	75	90	80	57	61	95	93	85	62	75	80	87	96	95	91	74	51	60	95	62	34	0							
Moscow WRRF	225	16	35	48	77	27	69	14	56	17	36	63	78	63	31	46	18	36	45	83	76	64	19	43	53	98	83	62	74	0						
	255	22	11	27	83	13	54	26	39	19	49	72	68	48	7	58	15	12	24	74	64	48	13	52	60	99	87	68	78	26	0					
	270	30	7	19	86	20	47	33	31	28	56	77	62	41	13	65	25	4	17	69	59	41	21	57	66	99	89	72	81	34	11	0				
	284	31	9	24	87	23	50	35	34	29	57	76	64	43	14	65	26	10	21	71	61	44	23	59	66	99	90	75	83	29	13	9	0			
	304	43	58	68	60	50	82	39	74	45	12	38	88	79	56	16	43	57	65	90	86	78	43	18	29	96	68	37	58	38	51	58	58	0		
	313	28	45	57	72	37	75	25	64	30	22	48	83	69	42	35	28	43	54	86	81	70	28	27	36	98	77	47	64	23	35	43	45	23	0	
	320	33	49	60	70	42	77	30	66	34	20	50	84	72	46	33	33	48	57	87	82	72	33	29	39	98	77	51	66	21	41	47	44	21	12	0

Table S98. Dissimilarity matrix for samples with phylotypes identified using the GAO primer set at the family level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	25	0																																	
	107	40	18	0																																
	121	76	85	89	0																															
	241	18	19	33	82	0																														
	263	65	48	34	94	54	0																													
	283	9	30	43	76	18	65	0																												
V-EBPR	72	53	33	18	92	46	22	56	0																											
	86	8	25	40	77	18	65	13	51	0																										
	107	39	55	66	61	48	80	35	73	41	0																									
	121	62	75	81	41	71	90	62	86	63	42	0																								
	241	76	64	53	96	72	26	78	40	75	87	93	0																							
	263	60	42	28	93	54	13	63	11	58	78	86	32	0																						
	283	23	9	25	83	17	54	28	38	17	53	71	67	46	0																					
G-EBPR	72	46	62	72	50	57	85	45	78	46	18	30	90	82	58	0																				
	86	11	23	38	79	14	62	14	49	5	38	66	74	57	17	49	0																			
	107	31	7	19	86	22	47	34	31	27	55	76	62	40	12	64	23	0																		
	121	40	17	5	89	33	36	44	19	37	64	79	53	28	22	70	35	15	0																	
	241	81	71	61	97	77	37	82	52	81	90	95	15	44	74	92	79	69	62	0																
	263	74	60	48	96	68	20	75	36	72	85	93	7	27	64	88	71	58	49	20	0															
	283	61	42	28	94	54	9	63	14	59	76	88	30	5	48	82	57	40	29	41	24	0														
R-EBPR	72	13	21	37	80	11	61	16	47	9	40	67	73	56	17	52	5	22	34	78	70	55	0													
	86	45	59	69	66	51	81	42	74	48	18	48	88	80	58	26	44	55	67	90	86	78	43	0												
	107	56	67	74	68	60	85	54	79	58	29	38	90	81	66	32	55	65	72	92	89	81	54	35	0											
	121	98	99	99	89	99	100	98	99	98	97	94	100	100	99	96	98	99	99	100	100	100	99	97	97	0										
	241	87	89	93	54	87	96	83	94	89	70	72	98	96	92	70	85	89	92	98	97	95	85	73	74	85	0									
	263	66	75	82	44	69	89	62	85	69	38	36	93	89	76	39	62	71	80	94	92	87	62	32	44	95	55	0								
	283	79	83	88	48	79	93	75	90	80	57	61	95	93	85	62	75	80	87	96	95	91	74	51	60	95	62	34	0							
Moscow WRRF	225	16	35	48	77	27	69	14	56	17	36	63	78	63	31	46	18	36	45	83	76	64	19	43	53	98	83	62	74	0						
	255	22	11	27	83	13	54	26	39	19	49	72	68	48	7	58	15	12	24	74	64	48	13	52	60	99	87	68	78	26	0					
	270	30	7	19	86	20	47	33	31	28	56	77	62	41	13	65	25	4	17	69	59	41	21	57	66	99	89	72	81	34	11	0				
	284	31	9	24	87	23	50	35	34	29	57	76	64	43	14	65	26	10	21	71	61	44	23	59	66	99	90	75	83	29	13	9	0			
	304	43	58	68	60	50	82	39	74	45	12	38	88	79	56	16	43	57	65	90	86	78	43	18	29	96	68	37	58	38	51	58	58	0		
	313	28	45	57	72	37	75	25	64	30	22	48	83	69	42	35	28	43	54	86	81	70	28	27	36	98	77	47	64	23	35	43	45	23	0	
	320	33	49	60	70	42	77	30	66	34	20	50	84	72	46	33	33	48	57	87	82	72	33	29	39	98	77	51	66	21	41	47	44	21	12	0

Table S99. Dissimilarity matrix for samples with phylotypes identified using the GAO primer set at the genus level, grouped by reactor and operational day. Sample dissimilarity was quantified according to Bray-Curtis (given by $1-2\cdot\frac{\sum_{i=0}^{n}\min(A_i,B_i)}{\sum_{i=0}^{n}A_i+B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, respectively, and n is the total number of phylotypes; Bray and Curtis, 1957). Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		S-EBPR							V-EBPR							G-EBPR							R-EBPR							Moscow WRRF						
		72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	72	86	107	121	241	263	283	225	255	270	284	304	313	320
S-EBPR	72	0																																		
	86	25	0																																	
	107	40	18	0																																
	121	76	85	89	0																															
	241	18	19	33	82	0																														
	263	65	48	34	94	54	0																													
	283	9	30	43	76	18	65	0																												
V-EBPR	72	53	33	18	92	46	22	56	0																											
	86	8	25	40	77	18	65	13	51	0																										
	107	39	55	66	61	48	80	35	73	41	0																									
	121	62	75	81	41	71	90	62	86	63	42	0																								
	241	76	64	53	96	72	26	78	40	75	87	93	0																							
	263	60	42	28	93	54	13	63	11	58	78	86	32	0																						
	283	23	9	25	83	17	54	28	38	17	53	71	67	46	0																					
G-EBPR	72	46	62	72	50	57	85	45	78	46	18	30	90	82	58	0																				
	86	11	23	38	79	14	62	14	49	5	38	66	74	57	17	49	0																			
	107	31	7	19	86	22	47	34	31	27	55	76	62	40	12	64	23	0																		
	121	40	17	5	89	33	36	44	19	37	64	79	53	28	22	70	35	15	0																	
	241	81	71	61	97	77	37	82	52	81	90	95	15	44	74	92	79	69	62	0																
	263	74	60	48	96	68	20	75	36	72	85	93	7	27	64	88	71	58	49	20	0															
	283	61	42	28	94	54	9	63	14	59	76	88	30	5	48	82	57	40	29	41	24	0														
R-EBPR	72	13	21	37	80	11	61	16	47	9	40	67	73	56	17	52	5	22	34	78	70	55	0													
	86	45	59	69	66	51	81	42	74	48	18	48	88	80	58	26	44	55	67	90	86	78	43	0												
	107	56	67	74	68	60	85	54	79	58	29	38	90	81	66	32	55	65	72	92	89	81	54	35	0											
	121	98	99	99	89	99	100	98	99	98	97	94	100	100	99	96	98	99	99	100	100	100	99	97	97	0										
	241	87	89	93	54	87	96	83	94	89	70	72	98	96	92	70	85	89	92	98	97	95	85	73	74	85	0									
	263	66	75	82	44	69	89	62	85	69	38	36	93	89	76	39	62	71	80	94	92	87	62	32	44	95	55	0								
	283	79	83	88	48	79	93	75	90	80	57	61	95	93	85	62	75	80	87	96	95	91	74	51	60	95	62	34	0							
Moscow WRRF	225	16	35	48	77	27	69	14	56	17	36	63	78	63	31	46	18	36	45	83	76	64	19	43	53	98	83	62	74	0						
	255	22	11	27	83	13	54	26	39	19	49	72	68	48	7	58	15	12	24	74	64	48	13	52	60	99	87	68	78	26	0					
	270	30	7	19	86	20	47	33	31	28	56	77	62	41	13	65	25	4	17	69	59	41	21	57	66	99	89	72	81	34	11	0				
	284	31	9	24	87	23	50	35	34	29	57	76	64	43	14	65	26	10	21	71	61	44	23	59	66	99	90	75	83	29	13	9	0			
	304	43	58	68	60	50	82	39	74	45	12	38	88	79	56	16	43	57	65	90	86	78	43	18	29	96	68	37	58	38	51	58	58	0		
	313	28	45	57	72	37	75	25	64	30	22	48	83	69	42	35	28	43	54	86	81	70	28	27	36	98	77	47	64	23	35	43	45	23	0	
	320	33	49	60	70	42	77	30	66	34	20	50	84	72	46	33	33	48	57	87	82	72	33	29	39	98	77	51	66	21	41	47	44	21	12	0

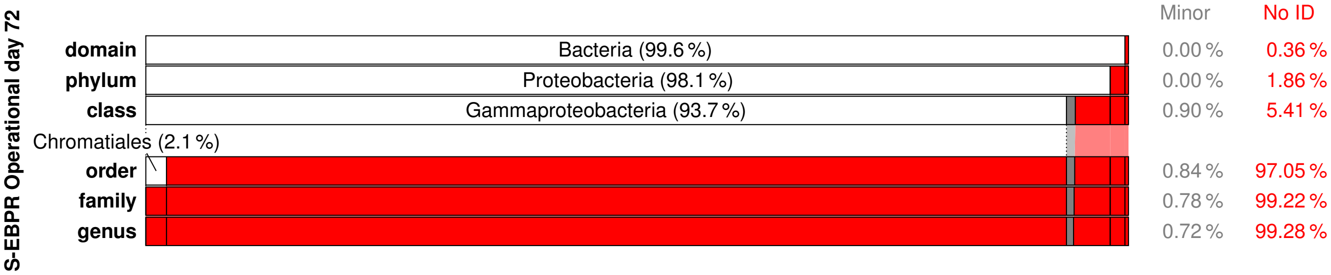

Figure S144. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

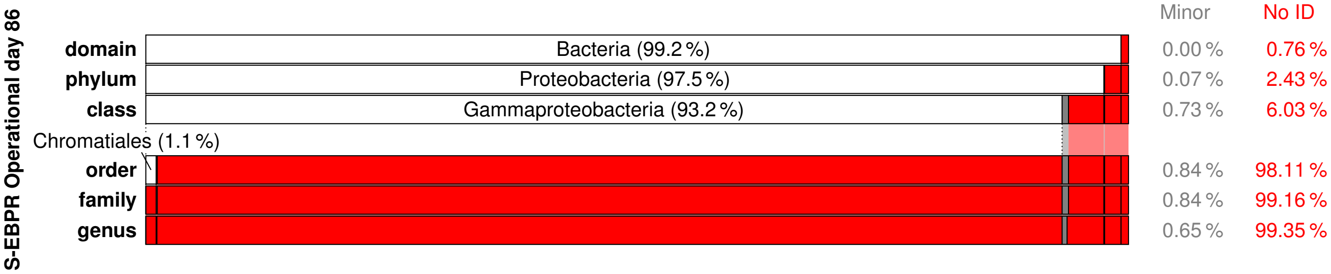

Figure S145. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

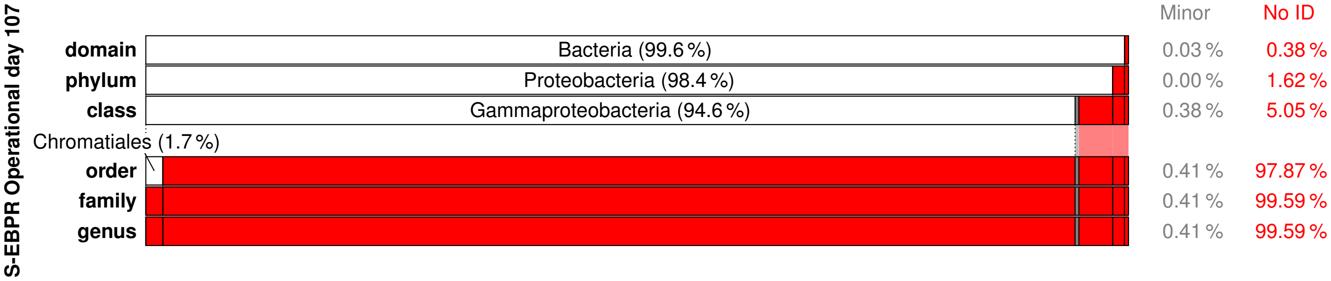

Figure S146. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

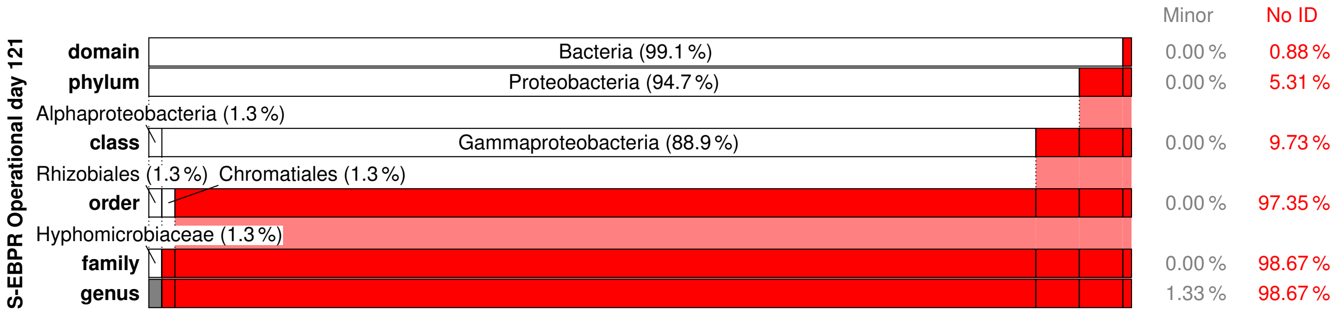

Figure S147. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

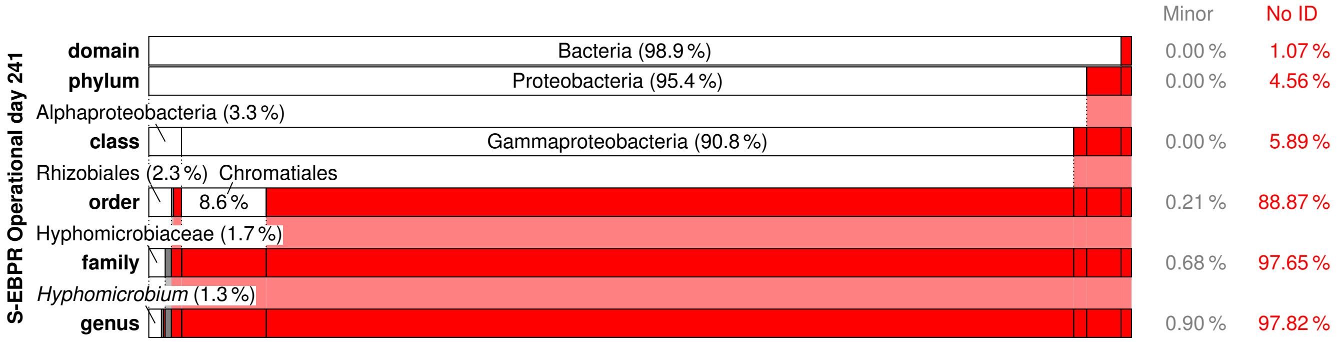

Figure S148. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

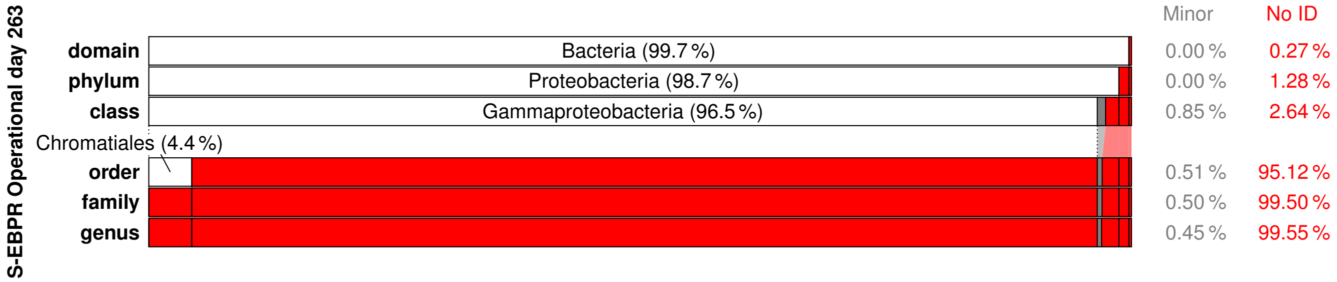

Figure S149. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

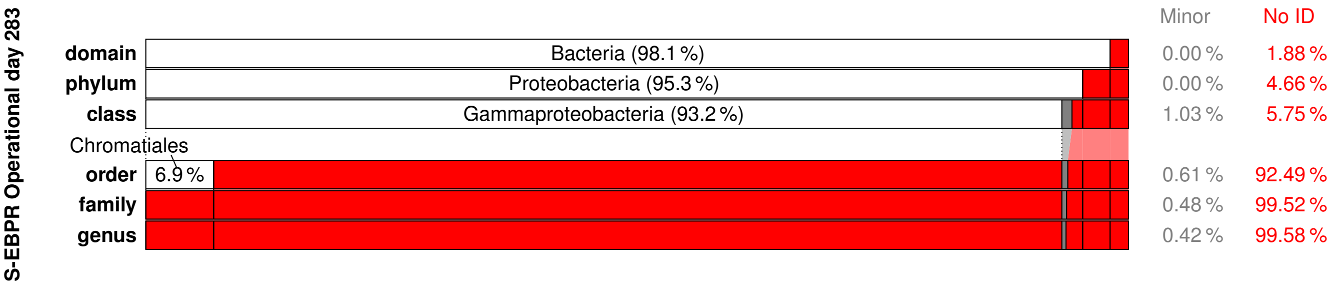

Figure S150. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

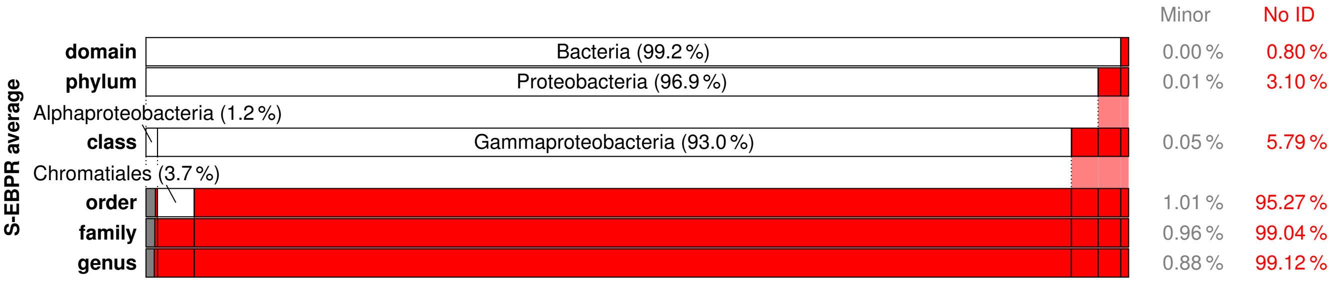

Figure S151. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for S-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

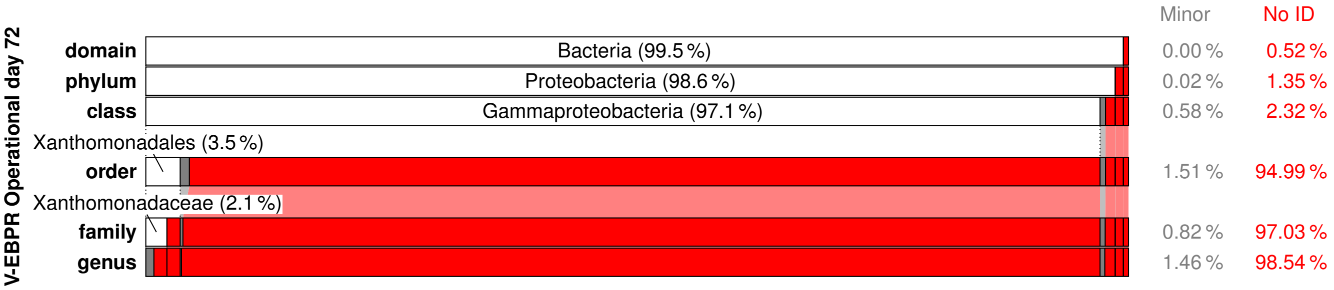

Figure S152. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

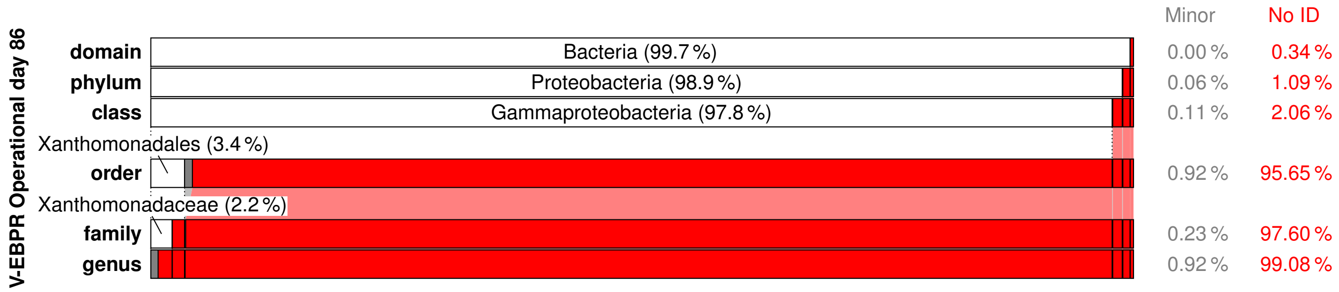

Figure S153. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

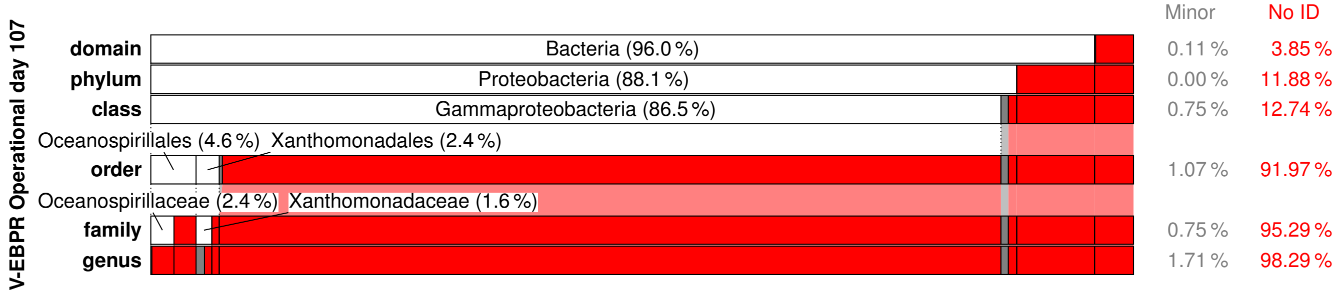

Figure S154. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

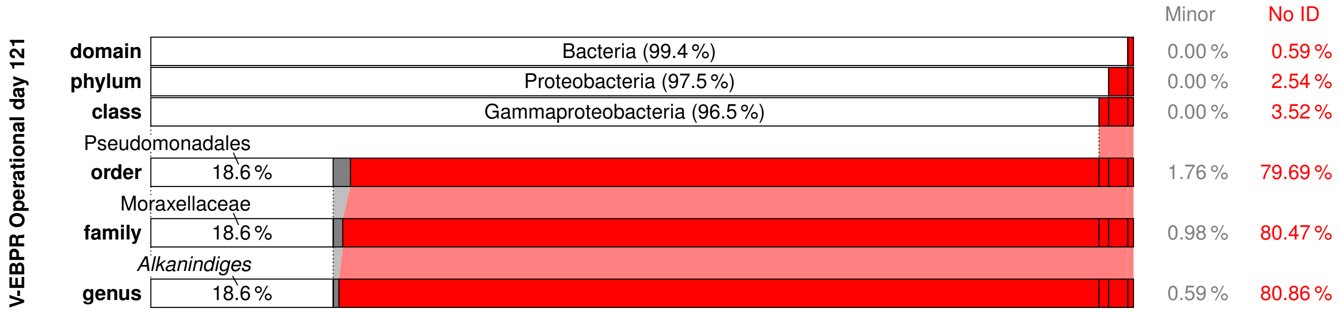

Figure S155. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

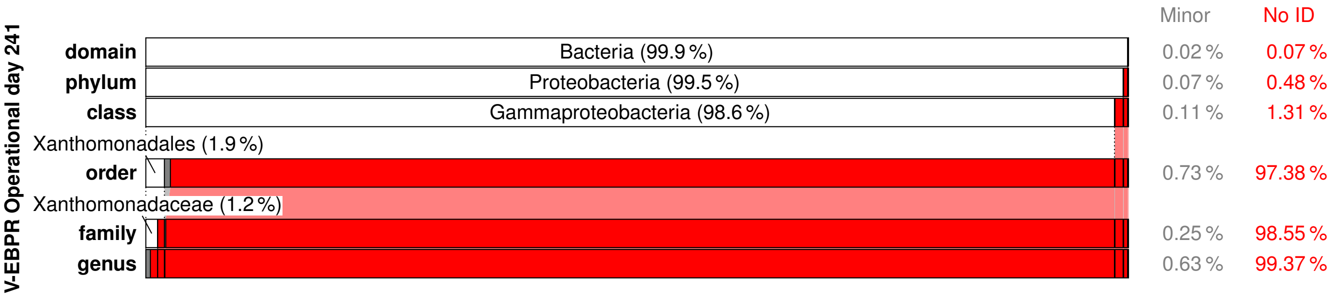

Figure S156. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

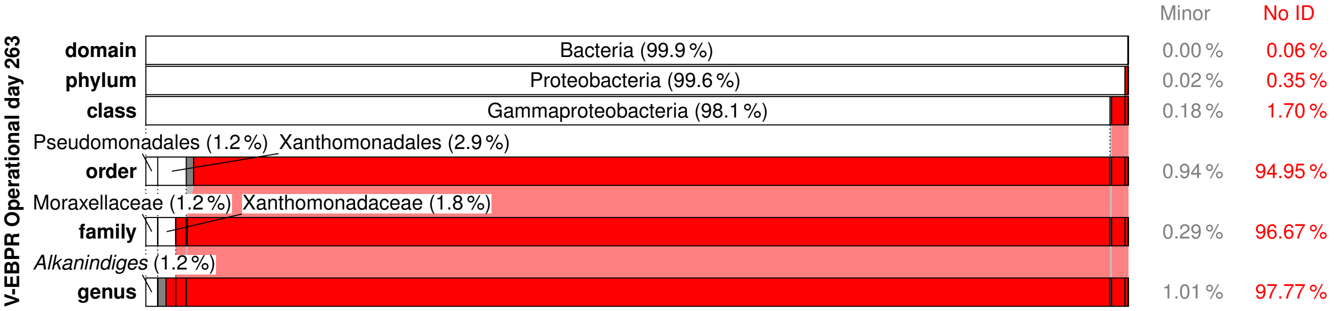

Figure S157. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

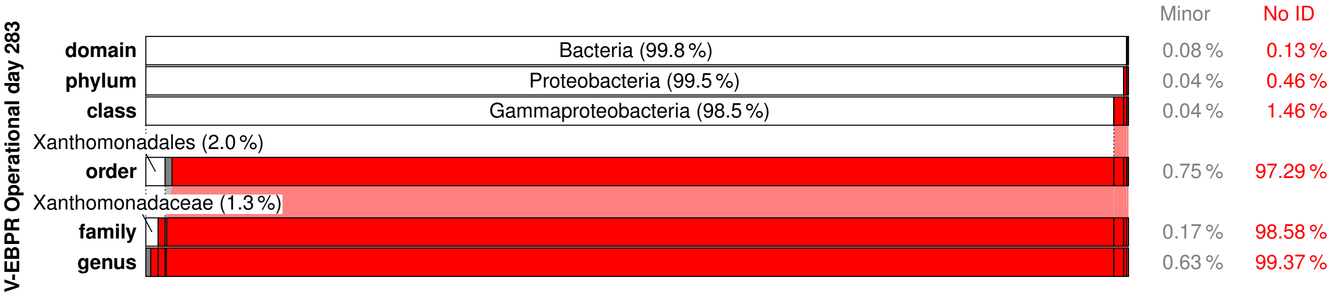

Figure S158. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

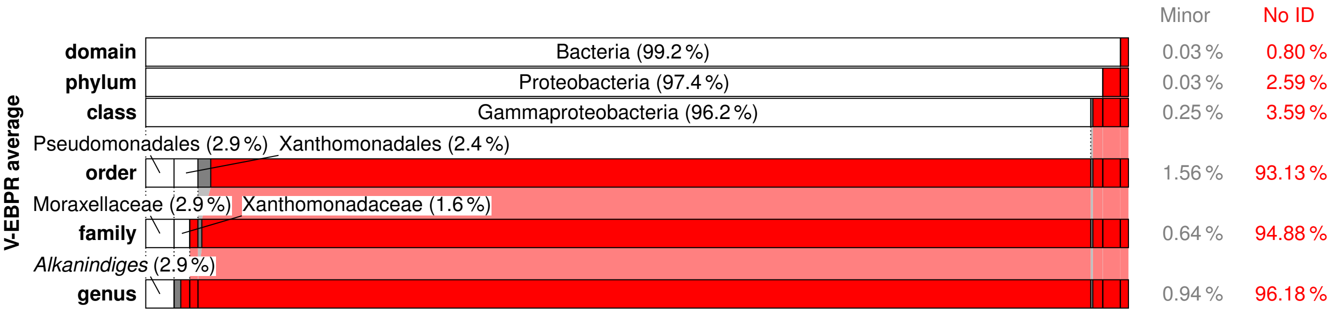

Figure S159. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for V-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

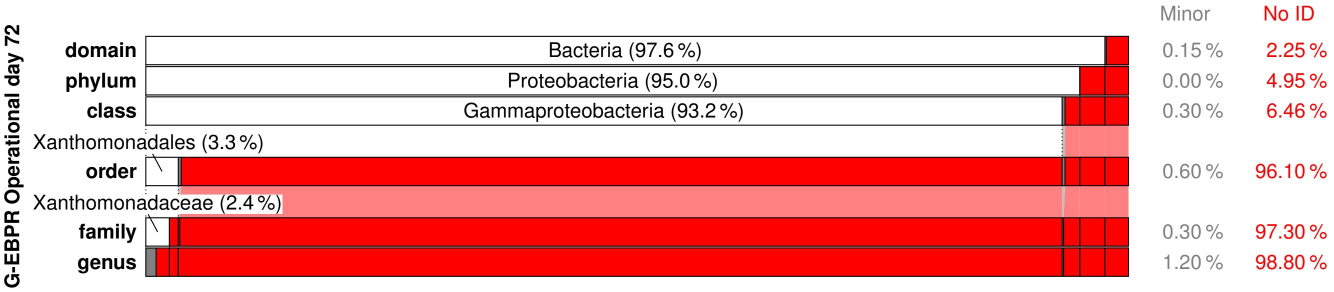

Figure S160. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

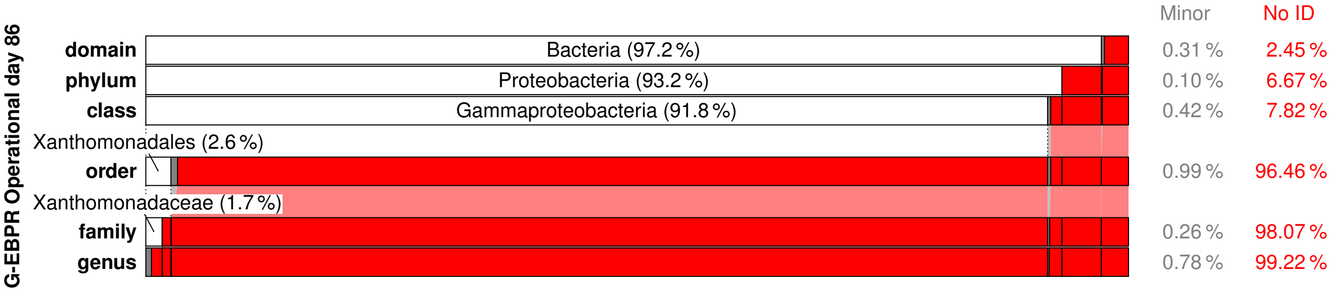

Figure S161. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted “No ID”, and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted “Minor”, and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved.

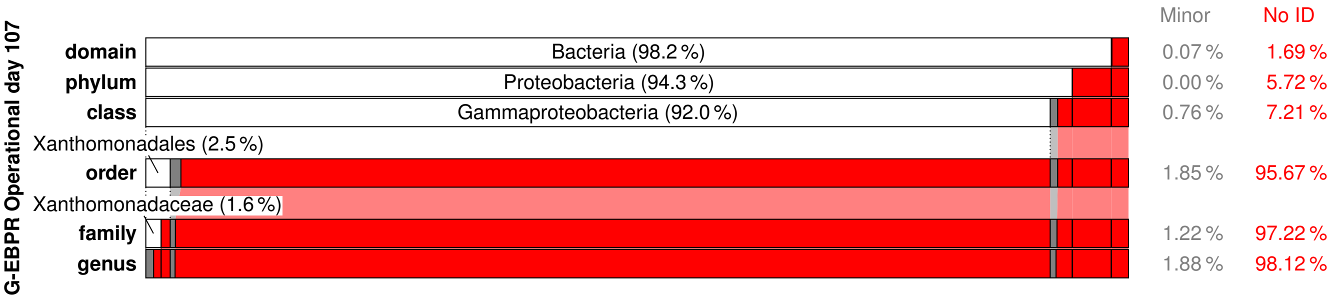

Figure S162. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

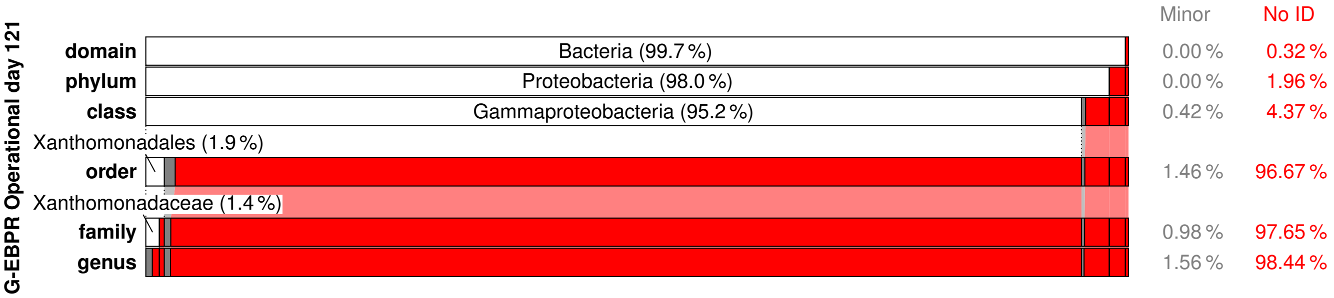

Figure S163. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

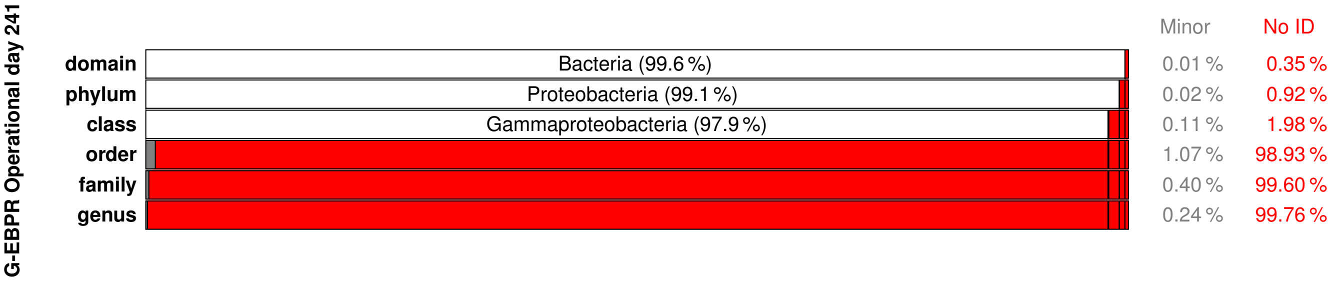

Figure S164. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

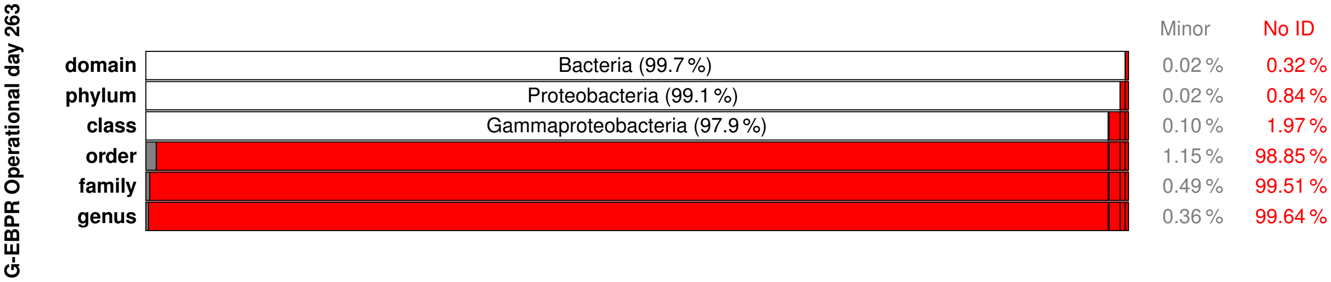

Figure S165. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

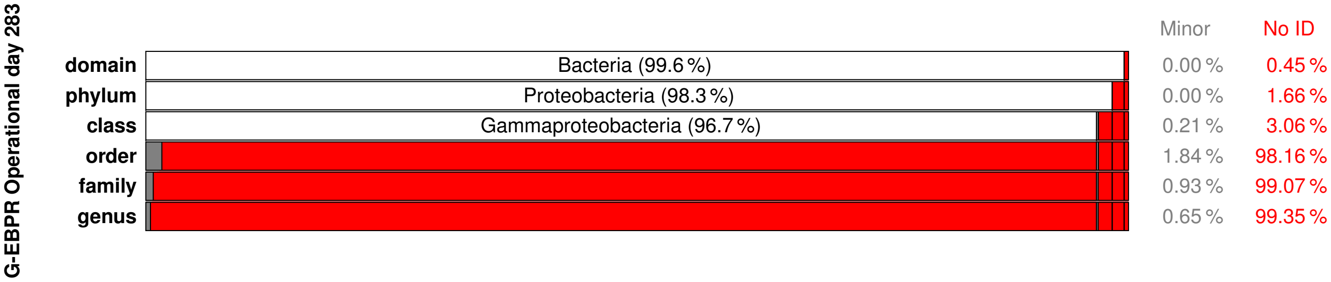

Figure S166. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

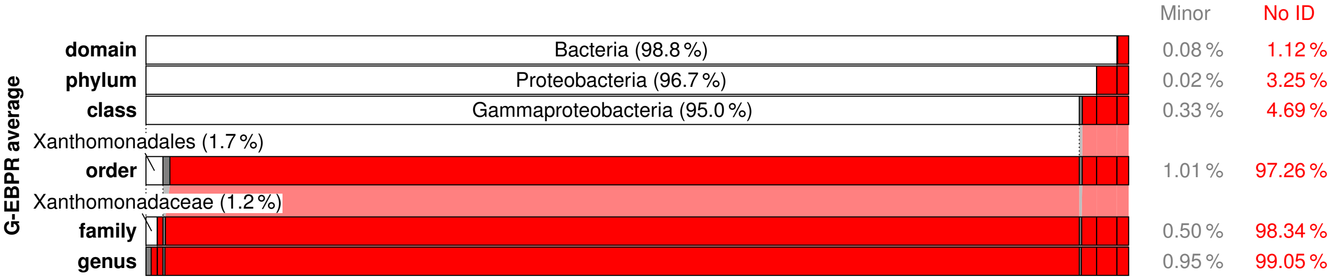

Figure S167. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for G-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

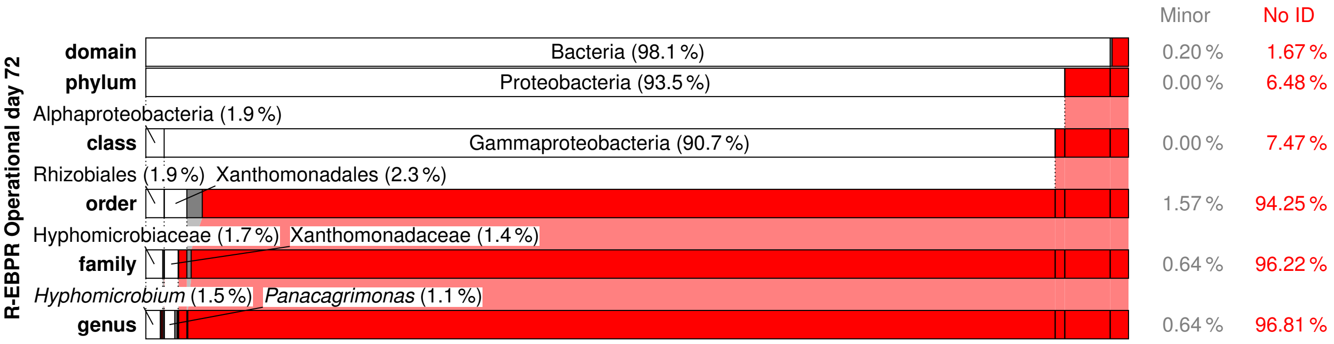

Figure S168. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR operational day 72. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

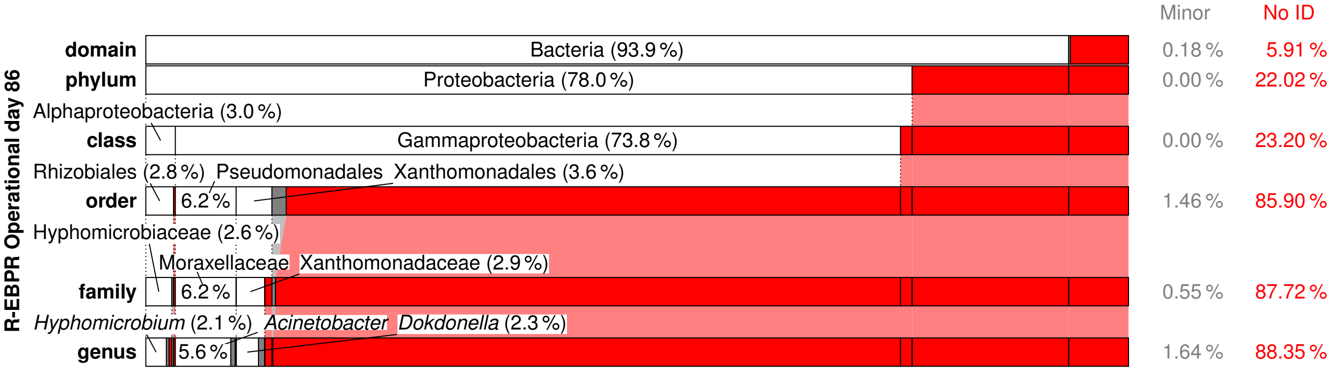

Figure S169. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR operational day 86. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

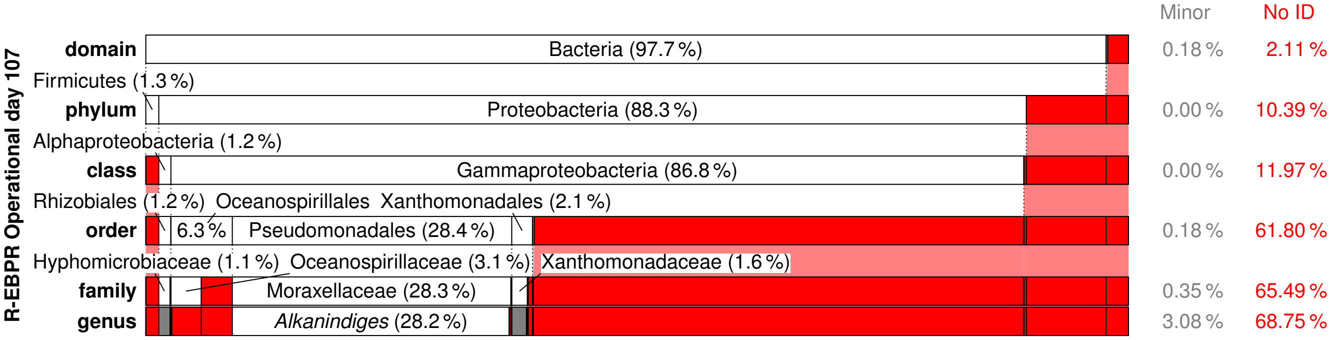

Figure S170. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR operational day 107. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

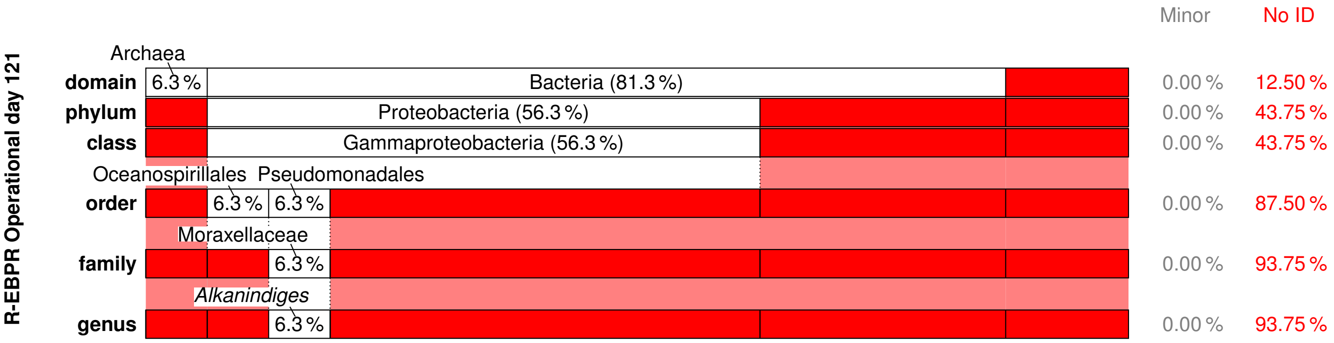

Figure S171. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR operational day 121. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

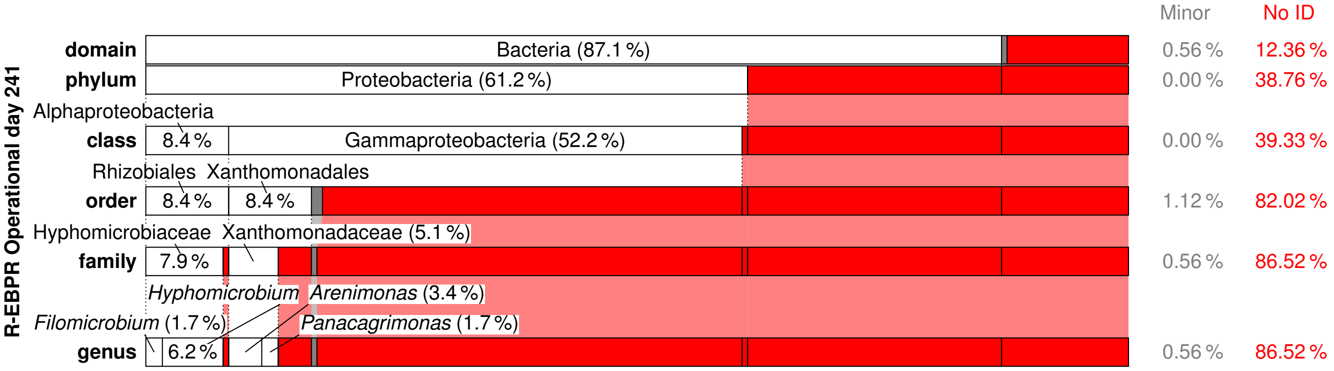

Figure S172. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR operational day 241. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

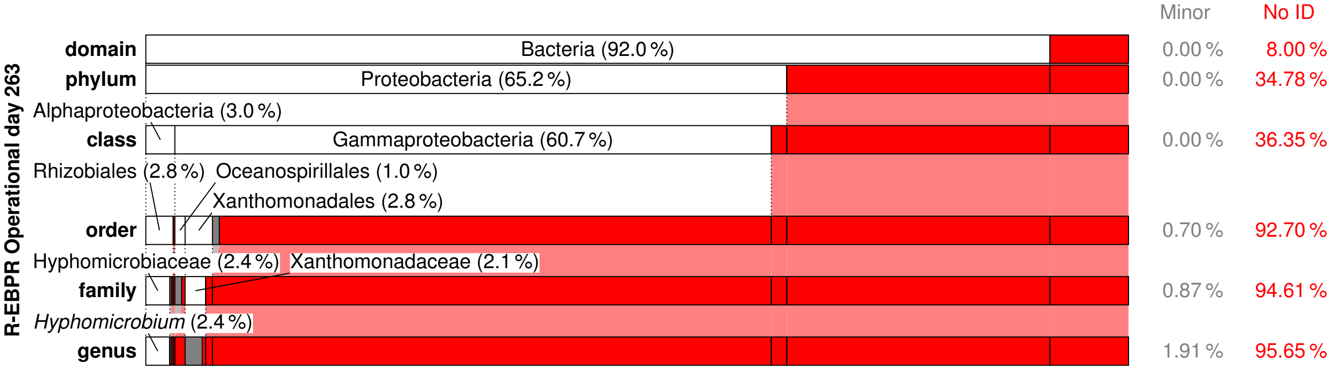

Figure S173. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR operational day 263. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

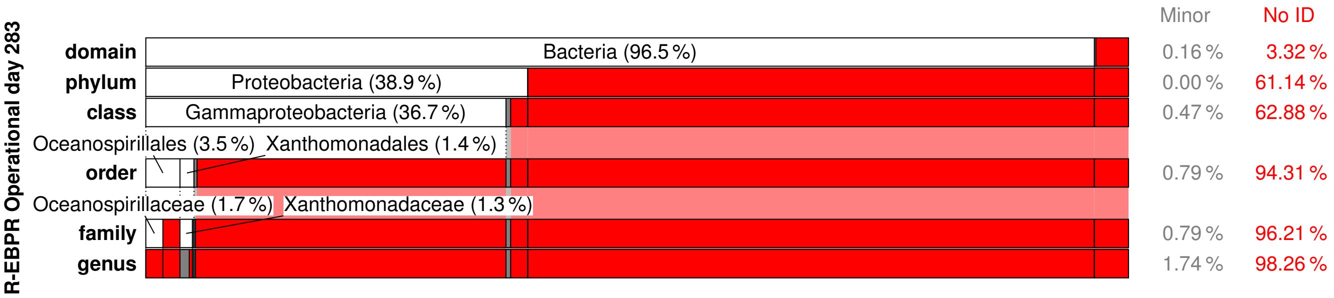

Figure S174. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR operational day 283. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

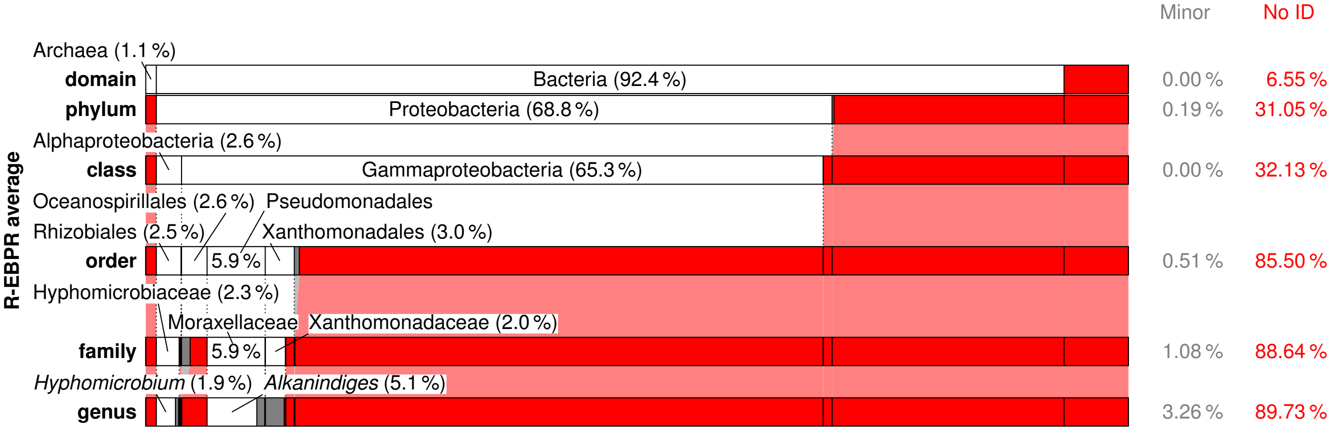

Figure S175. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for R-EBPR. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

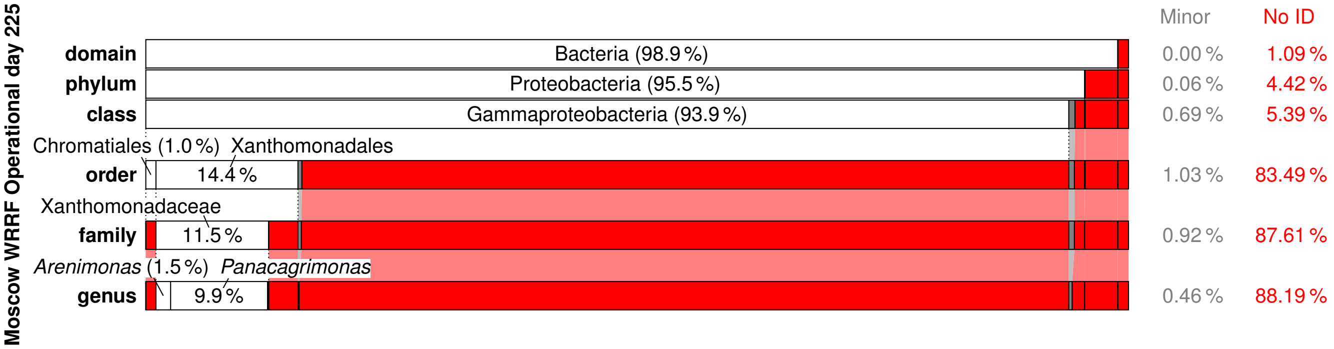

Figure S176. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF operational day 225. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

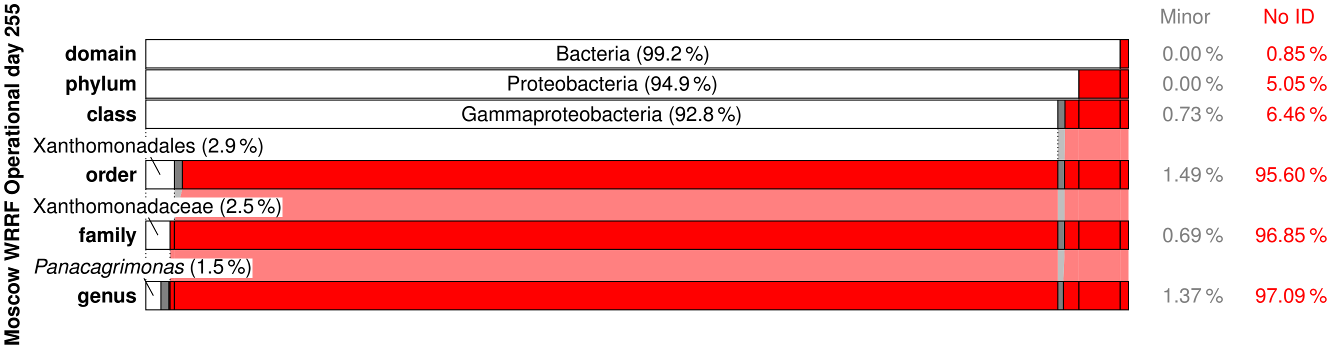

Figure S177. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF operational day 255. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

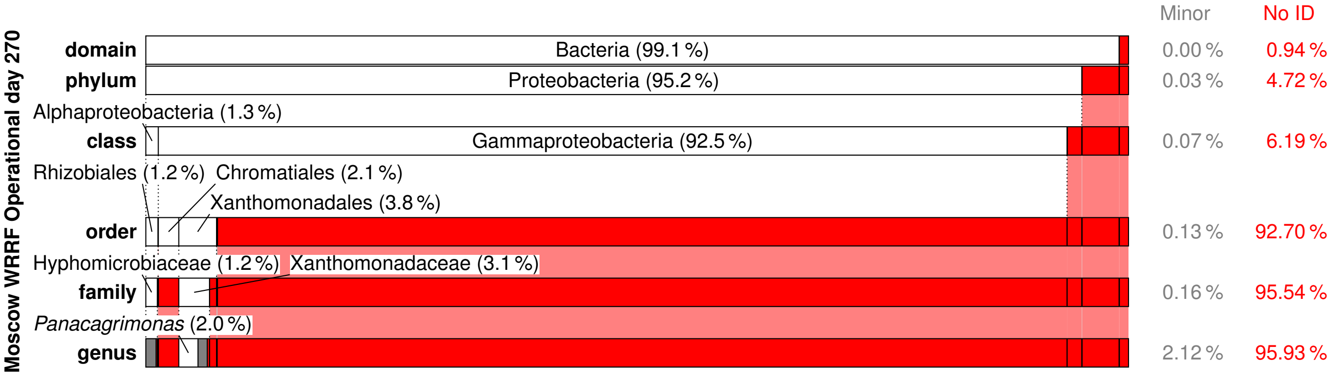

Figure S178. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF operational day 270. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

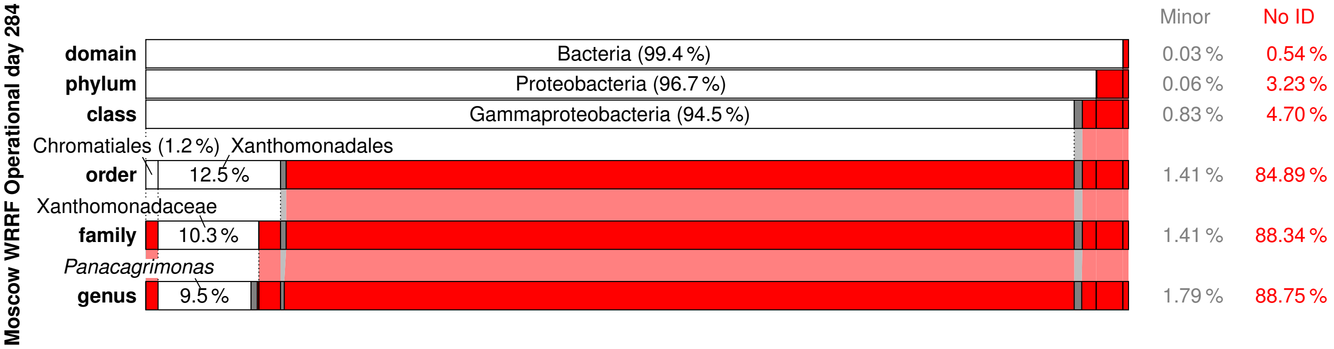

Figure S179. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF operational day 284. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

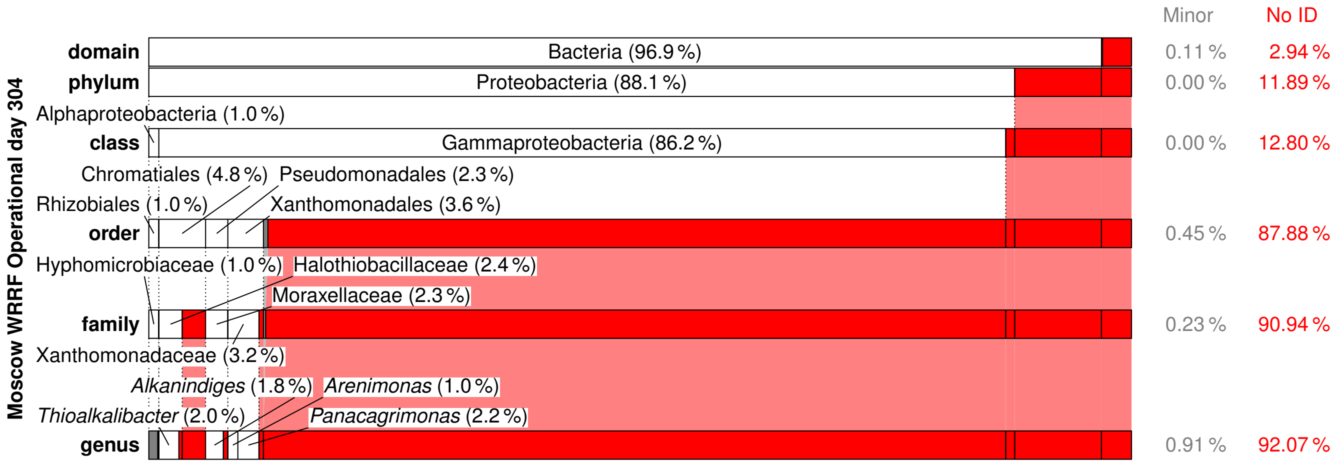

Figure S180. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF operational day 304. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

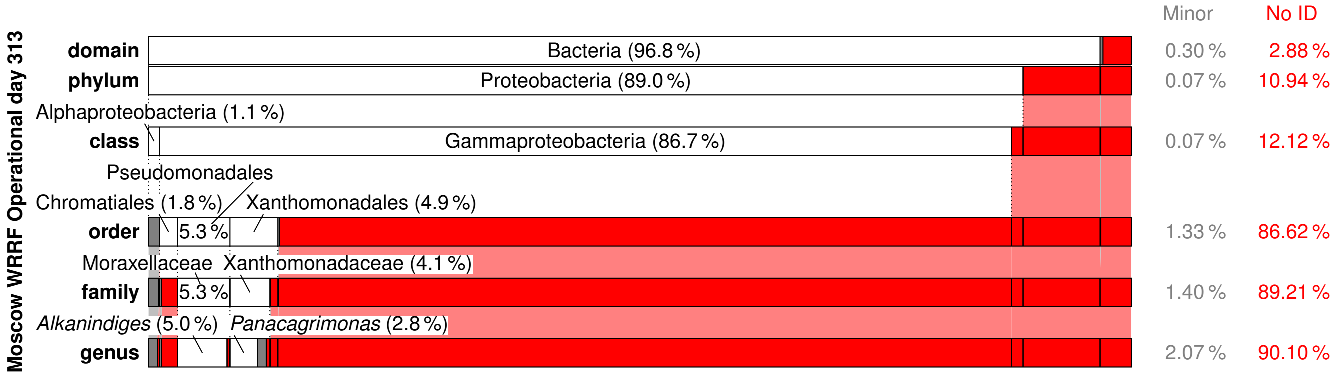

Figure S181. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF operational day 313. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

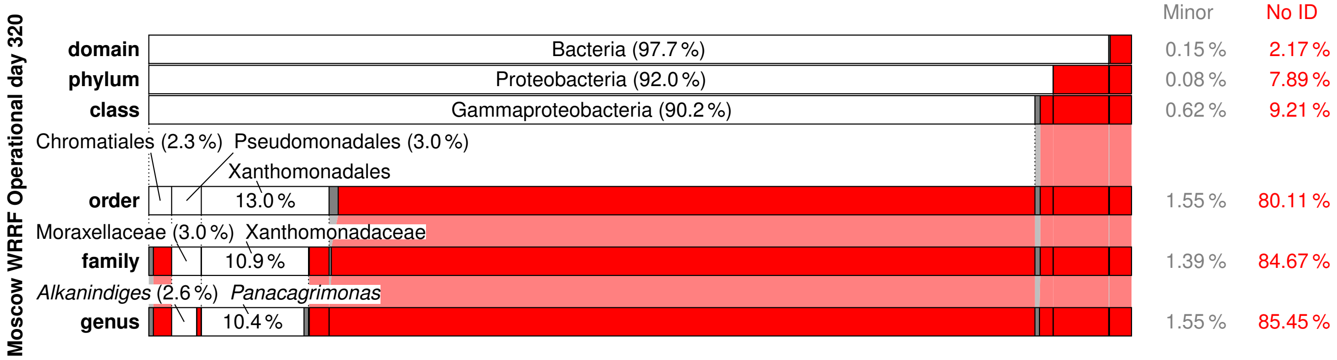

Figure S182. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF operational day 320. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes with less than 1 % of the total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

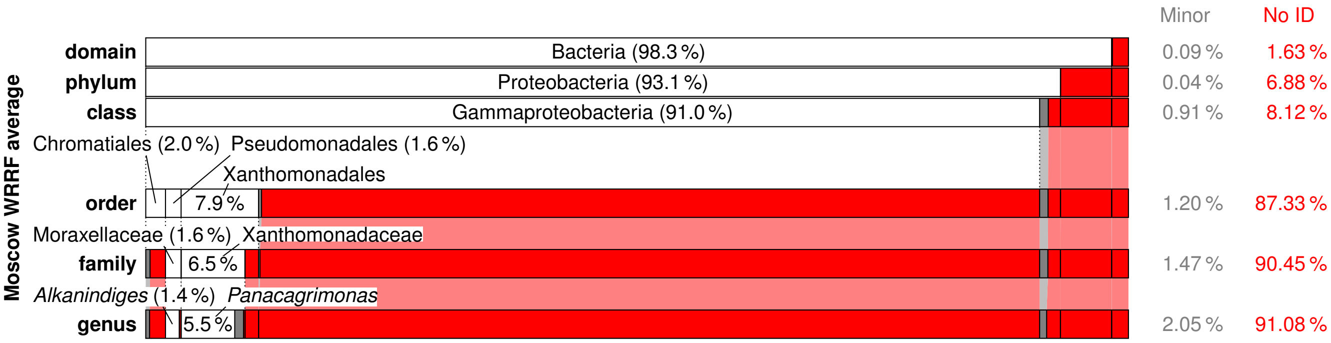

Figure S183. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing GAO primer set results for Moscow WRRF. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", and depicted in red. Identified phylotypes less than 1 % of the average total relative abundance were aggregated, denoted "Minor", and depicted in gray. Phylotypes with at least 1 % average relative abundance are labeled. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved.

Table S100. S-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.6	99.2	99.6	99.1	98.9	99.7	98.1	99.2	$\pm 5.58\cdot10^{-1}$
unknown	$3.61\cdot10^{-1}$	$7.63\cdot10^{-1}$	$3.85\cdot10^{-1}$	$8.85\cdot10^{-1}$	1.07	$2.69\cdot10^{-1}$	1.88	$8.01\cdot10^{-1}$	$\pm 5.61\cdot10^{-1}$
Minor phylotypes (1)[d]	N.D.[e]	N.D.[e]	$2.56\cdot10^{-2}$	N.D.[e]	N.D.[e]	N.D.[e]	N.D.[e]	$3.66\cdot10^{-3}$	$\pm 9.69\cdot10^{-3}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S101. V-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	99.5	99.7	96.0	99.4	99.9	99.9	99.8	99.2	± 1.40
unknown	$5.23\cdot10^{-1}$	$3.43\cdot10^{-1}$	3.85	$5.86\cdot10^{-1}$	$7.34\cdot10^{-2}$	$6.14\cdot10^{-2}$	$1.25\cdot10^{-1}$	$7.95\cdot10^{-1}$	± 1.37
Minor phylotypes (1)[d]	N.D.[e]	N.D.[e]	$1.07\cdot10^{-1}$	N.D.[e]	$1.63\cdot10^{-2}$	N.D.[e]	$8.33\cdot10^{-2}$	$2.95\cdot10^{-2}$	$\pm 4.58\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S102. G-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Domain[a,b]	72	86	107	121	241	263	283	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Bacteria	97.6	97.2	98.2	99.7	99.6	99.7	99.6	98.8	± 1.08
unknown	2.25	2.45	1.69	$3.17\cdot10^{-1}$	$3.53\cdot10^{-1}$	$3.23\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.12	$\pm 9.74\cdot10^{-1}$

Table S102. G-EBPR domain-level GAO results summary continued.

Domain[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Minor phylotypes (1)[d]	$1.50\cdot10^{-1}$	$3.13\cdot10^{-1}$	$6.61\cdot10^{-2}$	N.D.[e]	$1.24\cdot10^{-2}$	$1.85\cdot10^{-2}$	N.D.[e]	$8.00\cdot10^{-2} \pm 1.16\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.
[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.
[e] N.D. = Not detected.

Table S103. R-EBPR domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Domain[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Bacteria	98.1	93.9	97.7	81.3	87.1	92.0	96.5	92.4 ± 6.23
unknown	1.67	5.91	2.11	12.5	12.4	8.00	3.32	6.55 ± 4.58
Archaea	$1.96\cdot10^{-1}$	$1.82\cdot10^{-1}$	$1.76\cdot10^{-1}$	6.25	$5.62\cdot10^{-1}$	N.D.[d]	$1.58\cdot10^{-1}$	1.07 ± 2.29

[a] Phylotypes were sorted in descending order of the mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.
[d] N.D. = Not detected.

Table S104. Moscow WRRF domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Domain[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average ± SD[c] %
Bacteria	98.9	99.2	99.1	99.4	96.9	96.8	97.7	98.3 ± 1.11
unknown	1.09	$8.48\cdot10^{-1}$	$9.45\cdot10^{-1}$	$5.43\cdot10^{-1}$	2.94	2.88	2.17	1.63 ± 1.01
Minor phylotypes (1)[d]	N.D.[e]	N.D.[e]	N.D.[e]	$3.19\cdot10^{-2}$	$1.13\cdot10^{-1}$	$2.96\cdot10^{-1}$	$1.55\cdot10^{-1}$	$8.51\cdot10^{-2} \pm 1.11\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.
[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.
[e] N.D. = Not detected.

Table S105. Summary of domain-level relative abundance by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Domain[a,b]	S-EBPR (S100)		V-EBPR (S101)		G-EBPR (S102)		R-EBPR (S103)		Moscow WRRF (S104)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
Bacteria	99.2	$\pm 5.58{\cdot}10^{-1}$	99.2	± 1.40	98.8	± 1.08	92.4	± 6.23	98.3	± 1.11
unknown	$8.01{\cdot}10^{-1}$	$\pm 5.61{\cdot}10^{-1}$	$7.95{\cdot}10^{-1}$	± 1.37	1.12	$\pm 9.74{\cdot}10^{-1}$	6.55	± 4.58	1.63	± 1.01
Archaea	$3.66{\cdot}10^{-3}$	$\pm 9.69{\cdot}10^{-3}$	$2.95{\cdot}10^{-2}$	$\pm 4.58{\cdot}10^{-2}$	$8.00{\cdot}10^{-2}$	$\pm 1.16{\cdot}10^{-1}$	1.07	± 2.29	$8.51{\cdot}10^{-2}$	$\pm 1.11{\cdot}10^{-1}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.

Table S106. S-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Proteobacteria	98.1	97.5	98.4	94.7	95.4	98.7	95.3	96.9	± 1.68
unknown	1.50	1.67	1.21	4.42	3.50	1.01	2.79	2.30	± 1.30
d: *Bacteria*									
unknown	$3.61{\cdot}10^{-1}$	$7.63{\cdot}10^{-1}$	$3.85{\cdot}10^{-1}$	$8.85{\cdot}10^{-1}$	1.07	$2.69{\cdot}10^{-1}$	1.88	$8.01{\cdot}10^{-1}$	$\pm 5.61{\cdot}10^{-1}$
Minor phylotypes (9)[d]	N.D.[e]	$7.27{\cdot}10^{-2}$	$2.56{\cdot}10^{-2}$	N.D.[e]	N.D.[e]	N.D.[e]	N.D.[e]	$1.40{\cdot}10^{-2}$	$\pm 2.76{\cdot}10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.
[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.
[e] N.D. = Not detected.

Table S107. V-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Proteobacteria	98.6	98.9	88.1	97.5	99.5	99.6	99.5	97.4	± 4.15
unknown	$8.23{\cdot}10^{-1}$	$7.44{\cdot}10^{-1}$	7.92	1.95	$4.08{\cdot}10^{-1}$	$2.92{\cdot}10^{-1}$	$2.92{\cdot}10^{-1}$	1.78	± 2.77
d: *Bacteria*									
unknown	$5.23{\cdot}10^{-1}$	$3.43{\cdot}10^{-1}$	3.85	$5.86{\cdot}10^{-1}$	$7.34{\cdot}10^{-2}$	$6.14{\cdot}10^{-2}$	$1.25{\cdot}10^{-1}$	$7.95{\cdot}10^{-1}$	± 1.37

Table S107. V-EBPR phylum-level GAO results summary continued.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
Minor phylotypes (9)[d]	$1.87\cdot10^{-2}$	$5.72\cdot10^{-2}$	$1.07\cdot10^{-1}$	N.D.[e]	$6.52\cdot10^{-2}$	$1.53\cdot10^{-2}$	$8.33\cdot10^{-2}$	$4.96\cdot10^{-2}$	$\pm3.94\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S108. G-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
Proteobacteria	95.0	93.2	94.3	98.0	99.1	99.1	98.3	96.7	± 2.47
unknown d: *Bacteria*	2.55	4.01	3.97	1.64	$5.70\cdot10^{-1}$	$5.17\cdot10^{-1}$	1.22	2.07	± 1.48
unknown	2.25	2.45	1.69	$3.17\cdot10^{-1}$	$3.53\cdot10^{-1}$	$3.23\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.12	$\pm9.74\cdot10^{-1}$
Minor phylotypes (9)[d]	$1.50\cdot10^{-1}$	$3.13\cdot10^{-1}$	$6.61\cdot10^{-2}$	N.D.[e]	$1.86\cdot10^{-2}$	$1.85\cdot10^{-2}$	N.D.[e]	$8.09\cdot10^{-2}$	$\pm1.15\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S109. R-EBPR phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c] %
Proteobacteria	93.5	78.0	88.3	56.3	61.2	65.2	38.9	68.8	± 19.1
unknown d: *Bacteria*	4.62	15.9	8.10	25.0	25.8	26.8	57.7	23.4	± 17.5
unknown	1.67	5.91	2.11	12.5	12.4	8.00	3.32	6.55	± 4.58
unknown d: *Archaea*	$1.96\cdot10^{-1}$	$1.82\cdot10^{-1}$	$1.76\cdot10^{-1}$	6.25	$5.62\cdot10^{-1}$	N.D.[d]	$1.58\cdot10^{-1}$	1.07	± 2.29
Firmicutes	N.D.[d]	N.D.[d]	1.32	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	$1.89\cdot10^{-1}$	$\pm\ 4.99\cdot10^{-1}$

Table S109. R-EBPR phylum-level GAO results summary continued.

Phylum[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average ± SD[c] %
Minor phylotypes (7)[e]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]

[a] Phylotypes were sorted in descending order of the mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.
[d] N.D. = Not detected.
[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S110. Moscow WRRF phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Phylum[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Proteobacteria	95.5	94.9	95.2	96.7	88.1	89.0	92.0	93.1	± 3.41
unknown d: *Bacteria*	3.33	4.20	3.78	2.65	8.83	7.83	5.65	5.18	± 2.36
unknown	1.09	$8.48\cdot10^{-1}$	$9.45\cdot10^{-1}$	$5.43\cdot10^{-1}$	2.94	2.88	2.17	1.63	± 1.01
Minor phylotypes (9)[d]	$5.73\cdot10^{-2}$	N.D.[e]	$3.26\cdot10^{-2}$	$9.58\cdot10^{-2}$	$1.13\cdot10^{-1}$	$2.96\cdot10^{-1}$	$1.55\cdot10^{-1}$	$1.07\cdot10^{-1}$	$\pm 9.79\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.
[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.
[e] N.D. = Not detected.

Table S111. Summary of phylum-level relative abundance by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Phylum[a,b]	S-EBPR (S106)		V-EBPR (S107)		G-EBPR (S108)		R-EBPR (S109)		Moscow WRRF (S110)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
Proteobacteria	96.9	± 1.68	97.4	± 4.15	96.7	± 2.47	68.8	± 19.1	93.1	± 3.41
unknown d: *Bacteria*	2.30	± 1.30	1.78	± 2.77	2.07	± 1.48	23.4	± 17.5	5.18	± 2.36
unknown	$8.01\cdot10^{-1}$	$\pm 5.61\cdot10^{-1}$	$7.95\cdot10^{-1}$	± 1.37	1.12	$\pm 9.74\cdot10^{-1}$	6.55	± 4.58	1.63	± 1.01
unknown d: *Archaea*	$3.66\cdot10^{-3}$	$\pm 9.69\cdot10^{-3}$	$2.12\cdot10^{-2}$	$\pm 4.09\cdot10^{-2}$	$6.07\cdot10^{-2}$	$\pm 8.62\cdot10^{-2}$	1.07	± 2.29	$6.35\cdot10^{-2}$	$\pm 8.25\cdot10^{-2}$
Firmicutes	N.D.[d]		$4.86\cdot10^{-3}$	$\pm 8.36\cdot10^{-3}$	N.D.[d]		$1.89\cdot10^{-1}$	$\pm 4.99\cdot10^{-1}$	$9.13\cdot10^{-3}$	$\pm 2.42\cdot10^{-2}$

Table S111. Summary of phylum-level GAO results continued.

Phylum[a,b]	S-EBPR (S106) Average ± SD[c] %	V-EBPR (S107) Average ± SD[c] %	G-EBPR (S108) Average ± SD[c] %	R-EBPR (S109) Average ± SD[c] %	Moscow WRRF (S110) Average ± SD[c] %
Minor phylotypes (7)[e]	$1.04\cdot10^{-2}$ $\pm 2.75\cdot10^{-2}$	$2.34\cdot10^{-2}$ $\pm 3.00\cdot10^{-2}$	$2.02\cdot10^{-2}$ $\pm 3.81\cdot10^{-2}$	N.D.[d]	$3.45\cdot10^{-2}$ $\pm 3.53\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S112. S-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Gammaproteobacteria	93.7	93.2	94.6	88.9	90.8	96.5	93.2	93.0	± 2.48
unknown p: *Proteobacteria*	3.55	3.60	3.44	4.42	1.32	1.36	1.09	2.68	± 1.37
unknown d: *Bacteria*	1.50	1.67	1.21	4.42	3.50	1.01	2.79	2.30	± 1.30
Alphaproteobacteria	$9.02\cdot10^{-1}$	$6.54\cdot10^{-1}$	$3.85\cdot10^{-1}$	1.33	3.33	$8.32\cdot10^{-1}$	$7.87\cdot10^{-1}$	1.17	$\pm 9.91\cdot10^{-1}$
unknown	$3.61\cdot10^{-1}$	$7.63\cdot10^{-1}$	$3.85\cdot10^{-1}$	$8.85\cdot10^{-1}$	1.07	$2.69\cdot10^{-1}$	1.88	$8.01\cdot10^{-1}$	$\pm 5.61\cdot10^{-1}$
Minor phylotypes (12)[d]	N.D.[e]	$7.27\cdot10^{-2}$	$2.56\cdot10^{-2}$	N.D.[e]	N.D.[e]	$1.28\cdot10^{-2}$	$2.42\cdot10^{-1}$	$5.05\cdot10^{-2}$	$\pm 8.85\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S113. V-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Gammaproteobacteria	97.1	97.8	86.5	96.5	98.6	98.1	98.5	96.2	± 4.32
unknown d: *Bacteria*	$8.23\cdot10^{-1}$	$7.44\cdot10^{-1}$	7.92	1.95	$4.08\cdot10^{-1}$	$2.92\cdot10^{-1}$	$2.92\cdot10^{-1}$	1.78	± 2.77
unknown p: *Proteobacteria*	$9.72\cdot10^{-1}$	$9.73\cdot10^{-1}$	$8.57\cdot10^{-1}$	$9.77\cdot10^{-1}$	$8.31\cdot10^{-1}$	1.35	1.00	$9.94\cdot10^{-1}$	$\pm 1.70\cdot10^{-1}$

Table S113. V-EBPR class-level GAO results summary continued.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown	$5.23\cdot10^{-1}$	$3.43\cdot10^{-1}$	3.85	$5.86\cdot10^{-1}$	$7.34\cdot10^{-2}$	$6.14\cdot10^{-2}$	$1.25\cdot10^{-1}$	$7.95\cdot10^{-1}$	±1.37
Minor phylotypes (13)[d]	$5.80\cdot10^{-1}$	$1.14\cdot10^{-1}$	$8.57\cdot10^{-1}$	N.D.[e]	$1.14\cdot10^{-1}$	$1.84\cdot10^{-1}$	$8.33\cdot10^{-2}$	$2.76\cdot10^{-1}$	$\pm 3.17\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S114. G-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Gammaproteobacteria	93.2	91.8	92.0	95.2	97.9	97.9	96.7	95.0	±2.66
unknown d: *Bacteria*	2.55	4.01	3.97	1.64	$5.70\cdot10^{-1}$	$5.17\cdot10^{-1}$	1.22	2.07	±1.48
unknown p: *Proteobacteria*	1.50	1.15	1.49	2.41	1.06	1.13	1.39	1.45	$\pm 4.60\cdot10^{-1}$
unknown	2.25	2.45	1.69	$3.17\cdot10^{-1}$	$3.53\cdot10^{-1}$	$3.23\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.12	$\pm 9.74\cdot10^{-1}$
Minor phylotypes (13)[d]	$4.50\cdot10^{-1}$	$6.25\cdot10^{-1}$	$8.27\cdot10^{-1}$	$4.23\cdot10^{-1}$	$1.05\cdot10^{-1}$	$1.01\cdot10^{-1}$	$2.08\cdot10^{-1}$	$3.91\cdot10^{-1}$	$\pm 2.73\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S115. R-EBPR class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Gammaproteobacteria	90.7	73.8	86.8	56.3	52.2	60.7	36.7	65.3	±19.5
unknown d: *Bacteria*	4.62	15.9	8.10	25.0	25.8	26.8	57.7	23.4	±17.5
unknown	1.67	5.91	2.11	12.5	12.4	8.00	3.32	6.55	± 4.58
Alphaproteobacteria	1.87	3.00	1.23	N.D.[d]	8.43	2.96	$4.74\cdot10^{-1}$	2.57	± 2.83
unknown d: *Archaea*	$1.96\cdot10^{-1}$	$1.82\cdot10^{-1}$	$1.76\cdot10^{-1}$	6.25	$5.62\cdot10^{-1}$	N.D.[d]	$1.58\cdot10^{-1}$	1.07	± 2.29

Table S115. R-EBPR class-level GAO results summary continued.

Class[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average	±	SD[c]
								%		
unknown p: *Proteobacteria*	$9.82 \cdot 10^{-1}$	1.18	$2.64 \cdot 10^{-1}$	N.D.[d]	$5.62 \cdot 10^{-1}$	1.57	1.74	$8.99 \cdot 10^{-1}$	±	$6.53 \cdot 10^{-1}$
unknown p: *Firmicutes*	N.D.[d]	N.D.[d]	1.32	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	$1.89 \cdot 10^{-1}$	±	$4.99 \cdot 10^{-1}$
Minor phylotypes (10)[e]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]		

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S116. Moscow WRRF class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Class[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average	± SD[c]
								%	
Gammaproteobacteria	93.9	92.8	92.5	94.5	86.2	86.7	90.2	91.0	± 3.38
unknown d: *Bacteria*	3.33	4.20	3.78	2.65	8.83	7.83	5.65	5.18	± 2.36
unknown	1.09	$8.48 \cdot 10^{-1}$	$9.45 \cdot 10^{-1}$	$5.43 \cdot 10^{-1}$	2.94	2.88	2.17	1.63	± 1.01
unknown p: *Proteobacteria*	$9.75 \cdot 10^{-1}$	1.41	1.47	1.41	$9.06 \cdot 10^{-1}$	1.18	1.32	1.24	$\pm 2.23 \cdot 10^{-1}$
Alphaproteobacteria	$6.31 \cdot 10^{-1}$	$7.27 \cdot 10^{-1}$	1.27	$8.31 \cdot 10^{-1}$	1.02	1.11	$5.42 \cdot 10^{-1}$	$8.76 \cdot 10^{-1}$	$\pm 2.67 \cdot 10^{-1}$
Minor phylotypes (12)[d]	$5.73 \cdot 10^{-2}$	N.D.[e]	$6.51 \cdot 10^{-2}$	$9.58 \cdot 10^{-2}$	$1.13 \cdot 10^{-1}$	$2.96 \cdot 10^{-1}$	$1.55 \cdot 10^{-1}$	$1.12 \cdot 10^{-1}$	$\pm 9.45 \cdot 10^{-2}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S117. Summary of class-level relative abundance by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Class[a,b]	S-EBPR (S112) Average	± SD[c]	V-EBPR (S113) Average	± SD[c]	G-EBPR (S114) Average	± SD[c]	R-EBPR (S115) Average	± SD[c]	Moscow WRRF (S116) Average	± SD[c]
	%		%		%		%		%	
Gammaproteobacteria	93.0	± 2.48	96.2	± 4.32	95.0	± 2.66	65.3	± 19.5	91.0	± 3.38

Table S117. Summary of class-level GAO results continued.

Class[a,b]	S-EBPR (S112)		V-EBPR (S113)		G-EBPR (S114)		R-EBPR (S115)		Moscow WRRF (S116)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
unknown d: *Bacteria*	2.30	± 1.30	1.78	± 2.77	2.07	± 1.48	23.4	± 17.5	5.18	± 2.36
unknown	$8.01\cdot10^{-1}$	± $5.61\cdot10^{-1}$	$7.95\cdot10^{-1}$	± 1.37	1.12	± $9.74\cdot10^{-1}$	6.55	± 4.58	1.63	± 1.01
unknown p: *Proteobacteria*	2.68	± 1.37	$9.94\cdot10^{-1}$	± $1.70\cdot10^{-1}$	1.45	± $4.60\cdot10^{-1}$	$8.99\cdot10^{-1}$	± $6.53\cdot10^{-1}$	1.24	± $2.23\cdot10^{-1}$
Alphaproteobacteria	1.17	± $9.91\cdot10^{-1}$	$2.26\cdot10^{-1}$	± $3.03\cdot10^{-1}$	$3.11\cdot10^{-1}$	± $2.34\cdot10^{-1}$	2.57	± 2.83	$8.76\cdot10^{-1}$	± $2.67\cdot10^{-1}$
unknown d: *Archaea*	$3.66\cdot10^{-3}$	± $9.69\cdot10^{-3}$	$2.12\cdot10^{-2}$	± $4.09\cdot10^{-2}$	$6.07\cdot10^{-2}$	± $8.62\cdot10^{-2}$	1.07	± 2.29	$6.35\cdot10^{-2}$	± $8.25\cdot10^{-2}$
unknown p: *Firmicutes*	N.D.[d]		N.D.[d]		N.D.[d]		$1.89\cdot10^{-1}$	± $4.99\cdot10^{-1}$	$9.13\cdot10^{-3}$	± $2.42\cdot10^{-2}$
Minor phylotypes (10)[e]	$4.68\cdot10^{-2}$	± $9.02\cdot10^{-2}$	$2.83\cdot10^{-2}$	± $2.66\cdot10^{-2}$	$2.02\cdot10^{-2}$	± $3.81\cdot10^{-2}$	N.D.[d]		$3.91\cdot10^{-2}$	± $3.71\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S118. S-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	91.6	92.1	92.8	87.6	82.2	92.1	86.3	89.2	± 4.00
Chromatiales	2.10	1.05	1.72	1.33	8.62	4.37	6.90	3.73	± 3.00
unknown p: *Proteobacteria*	3.55	3.60	3.44	4.42	1.32	1.36	1.09	2.68	± 1.37
unknown d: *Bacteria*	1.50	1.67	1.21	4.42	3.50	1.01	2.79	2.30	± 1.30
Rhizobiales	$8.42\cdot10^{-1}$	$6.54\cdot10^{-1}$	$3.59\cdot10^{-1}$	1.33	2.30	$4.74\cdot10^{-1}$	$3.63\cdot10^{-1}$	$9.03\cdot10^{-1}$	± $7.05\cdot10^{-1}$
unknown	$3.61\cdot10^{-1}$	$7.63\cdot10^{-1}$	$3.85\cdot10^{-1}$	$8.85\cdot10^{-1}$	1.07	$2.69\cdot10^{-1}$	1.88	$8.01\cdot10^{-1}$	± $5.61\cdot10^{-1}$
Minor phylotypes (28)[d]	$6.01\cdot10^{-2}$	$1.82\cdot10^{-1}$	$7.69\cdot10^{-2}$	N.D.[e]	1.02	$3.84\cdot10^{-1}$	$6.66\cdot10^{-1}$	$3.42\cdot10^{-1}$	± $3.80\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S119. V-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Order[a,b]	72	86	107	121	241	263	283	Average ±	SD[c]
	%	%	%	%	%	%	%	%	
unknown c: *Gammaproteobacteria*	92.7	93.6	79.2	76.2	96.1	93.2	95.8	89.5	±8.24
Pseudomonadales	$1.31\cdot10^{-1}$	$5.72\cdot10^{-2}$	N.D.[d]	18.6	$5.71\cdot10^{-2}$	1.21	$1.25\cdot10^{-1}$	2.88	±6.93
Xanthomonadales	3.50	3.43	2.36	$9.77\cdot10^{-1}$	1.89	2.90	1.96	2.43	$\pm9.12\cdot10^{-1}$
unknown d: *Bacteria*	$8.23\cdot10^{-1}$	$7.44\cdot10^{-1}$	7.92	1.95	$4.08\cdot10^{-1}$	$2.92\cdot10^{-1}$	$2.92\cdot10^{-1}$	1.78	±2.77
unknown p: *Proteobacteria*	$9.72\cdot10^{-1}$	$9.73\cdot10^{-1}$	$8.57\cdot10^{-1}$	$9.77\cdot10^{-1}$	$8.31\cdot10^{-1}$	1.35	1.00	$9.94\cdot10^{-1}$	$\pm1.70\cdot10^{-1}$
Minor phylotypes (27)[e]	1.23	$8.58\cdot10^{-1}$	1.18	$5.86\cdot10^{-1}$	$5.46\cdot10^{-1}$	$7.06\cdot10^{-1}$	$5.83\cdot10^{-1}$	$8.13\cdot10^{-1}$	$\pm2.88\cdot10^{-1}$
unknown	$5.23\cdot10^{-1}$	$3.43\cdot10^{-1}$	3.85	$5.86\cdot10^{-1}$	$7.34\cdot10^{-2}$	$6.14\cdot10^{-2}$	$1.25\cdot10^{-1}$	$7.95\cdot10^{-1}$	±1.37
Oceanospirillales	$1.50\cdot10^{-1}$	N.D.[d]	4.60	$1.95\cdot10^{-1}$	$1.22\cdot10^{-1}$	$2.30\cdot10^{-1}$	$8.33\cdot10^{-2}$	$7.69\cdot10^{-1}$	±1.69

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S120. G-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Order[a,b]	72	86	107	121	241	263	283	Average ±	SD[c]
	%	%	%	%	%	%	%	%	
unknown c: *Gammaproteobacteria*	89.6	88.5	88.5	92.2	96.9	96.9	95.1	92.5	±3.78
unknown d: *Bacteria*	2.55	4.01	3.97	1.64	$5.70\cdot10^{-1}$	$5.17\cdot10^{-1}$	1.22	2.07	±1.48
Xanthomonadales	3.30	2.55	2.48	1.88	$4.71\cdot10^{-1}$	$6.09\cdot10^{-1}$	$7.86\cdot10^{-1}$	1.73	±1.12
unknown p: *Proteobacteria*	1.50	1.15	1.49	2.41	1.06	1.13	1.39	1.45	$\pm4.60\cdot10^{-1}$
unknown	2.25	2.45	1.69	$3.17\cdot10^{-1}$	$3.53\cdot10^{-1}$	$3.23\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.12	$\pm9.74\cdot10^{-1}$
Minor phylotypes (29)[d]	$7.51\cdot10^{-1}$	1.30	1.92	1.53	$6.01\cdot10^{-1}$	$5.54\cdot10^{-1}$	1.05	1.10	$\pm5.12\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S121. R-EBPR order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Order[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	86.8	62.5	49.8	43.8	42.7	56.2	31.4	53.3	± 17.8
unknown d: *Bacteria*	4.62	15.9	8.10	25.0	25.8	26.8	57.7	23.4	± 17.5
unknown	1.67	5.91	2.11	12.5	12.4	8.00	3.32	6.55	± 4.58
Pseudomonadales	N.D.[d]	6.19	28.4	6.25	$5.62\cdot10^{-1}$	N.D.[d]	N.D.[d]	5.92	± 10.3
Xanthomonadales	2.31	3.64	2.11	N.D.[d]	8.43	2.78	1.42	2.96	± 2.67
Oceanospirillales	$6.39\cdot10^{-1}$	$5.46\cdot10^{-1}$	6.25	6.25	N.D.[d]	1.04	3.48	2.60	± 2.73
Rhizobiales	1.87	2.82	1.23	N.D.[d]	8.43	2.78	$4.74\cdot10^{-1}$	2.51	± 2.82
unknown d: *Archaea*	$1.96\cdot10^{-1}$	$1.82\cdot10^{-1}$	$1.76\cdot10^{-1}$	6.25	$5.62\cdot10^{-1}$	N.D.[d]	$1.58\cdot10^{-1}$	1.07	± 2.29
unknown p: *Proteobacteria*	$9.82\cdot10^{-1}$	1.18	$2.64\cdot10^{-1}$	N.D.[d]	$5.62\cdot10^{-1}$	1.57	1.74	$8.99\cdot10^{-1}$	± $6.53\cdot10^{-1}$
Minor phylotypes (24)[e]	$9.33\cdot10^{-1}$	1.09	$1.76\cdot10^{-1}$	N.D.[d]	$5.62\cdot10^{-1}$	$8.70\cdot10^{-1}$	$3.16\cdot10^{-1}$	$5.64\cdot10^{-1}$	± $4.16\cdot10^{-1}$
unknown p: *Firmicutes*	N.D.[d]	N.D.[d]	1.32	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	$1.89\cdot10^{-1}$	± $4.99\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.
[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.
[c] Sample standard deviation.
[d] N.D. = Not detected.
[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S122. Moscow WRRF order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Order[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	78.0	89.1	86.4	80.2	75.1	74.5	70.9	79.2	± 6.59
Xanthomonadales	14.4	2.91	3.84	12.5	3.62	4.88	13.0	7.88	± 5.14
unknown d: *Bacteria*	3.33	4.20	3.78	2.65	8.83	7.83	5.65	5.18	± 2.36
Chromatiales	1.03	$7.68\cdot10^{-1}$	2.08	1.25	4.76	1.85	2.32	2.01	± 1.34
unknown	1.09	$8.48\cdot10^{-1}$	$9.45\cdot10^{-1}$	$5.43\cdot10^{-1}$	2.94	2.88	2.17	1.63	± 1.01
Pseudomonadales	$5.73\cdot10^{-2}$	N.D.[d]	$6.51\cdot10^{-2}$	$3.83\cdot10^{-1}$	2.27	5.32	3.02	1.59	± 2.04
unknown p: *Proteobacteria*	$9.75\cdot10^{-1}$	1.41	1.47	1.41	$9.06\cdot10^{-1}$	1.18	1.32	1.24	± $2.23\cdot10^{-1}$
Rhizobiales	$5.73\cdot10^{-1}$	$6.87\cdot10^{-1}$	1.24	$8.31\cdot10^{-1}$	1.02	$8.87\cdot10^{-1}$	$5.42\cdot10^{-1}$	$8.25\cdot10^{-1}$	± $2.50\cdot10^{-1}$

Table S122. Moscow WRRF order-level GAO results summary continued.

Order[a,b]	225	255	270	284	304	313	320	Average	± SD[c]
	%	%	%	%	%	%	%	%	
Minor phylotypes (26)[e]	$4.59\cdot10^{-1}$	$8.08\cdot10^{-2}$	$1.30\cdot10^{-1}$	$2.88\cdot10^{-1}$	$5.66\cdot10^{-1}$	$6.65\cdot10^{-1}$	1.08	$4.67\cdot10^{-1}$	$\pm3.47\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S123. Summary of order-level relative abundance by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Order[a,b]	S-EBPR (S118)		V-EBPR (S119)		G-EBPR (S120)		R-EBPR (S121)		Moscow WRRF (S122)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
unknown c: *Gammaproteobacteria*	89.2	±4.00	89.5	±8.24	92.5	±3.78	53.3	±17.8	79.2	±6.59
unknown d: *Bacteria*	2.30	±1.30	1.78	±2.77	2.07	±1.48	23.4	±17.5	5.18	±2.36
Xanthomonadales	$2.11\cdot10^{-2}$	$\pm4.00\cdot10^{-2}$	2.43	$\pm9.12\cdot10^{-1}$	1.73	±1.12	2.96	± 2.67	7.88	±5.14
unknown	$8.01\cdot10^{-1}$	$\pm5.61\cdot10^{-1}$	$7.95\cdot10^{-1}$	±1.37	1.12	$\pm9.74\cdot10^{-1}$	6.55	± 4.58	1.63	±1.01
Pseudomonadales	N.D.[d]		2.88	±6.93	$2.07\cdot10^{-1}$	$\pm2.51\cdot10^{-1}$	5.92	±10.3	1.59	±2.04
Chromatiales	3.73	±3.00	$5.37\cdot10^{-1}$	$\pm1.40\cdot10^{-1}$	$4.47\cdot10^{-1}$	$\pm1.12\cdot10^{-1}$	$4.58\cdot10^{-1}$	$\pm3.69\cdot10^{-1}$	2.01	±1.34
unknown p: *Proteobacteria*	2.68	±1.37	$9.94\cdot10^{-1}$	$\pm1.70\cdot10^{-1}$	1.45	$\pm4.60\cdot10^{-1}$	$8.99\cdot10^{-1}$	$\pm6.53\cdot10^{-1}$	1.24	$\pm2.23\cdot10^{-1}$
Oceanospirillales	N.D.[d]		$7.69\cdot10^{-1}$	±1.69	$5.73\cdot10^{-2}$	$\pm1.26\cdot10^{-1}$	2.60	± 2.73	$2.81\cdot10^{-1}$	$\pm3.08\cdot10^{-1}$
Rhizobiales	$9.03\cdot10^{-1}$	$\pm7.05\cdot10^{-1}$	$2.24\cdot10^{-1}$	$\pm3.00\cdot10^{-1}$	$2.67\cdot10^{-1}$	$\pm2.11\cdot10^{-1}$	2.51	± 2.82	$8.25\cdot10^{-1}$	$\pm2.50\cdot10^{-1}$
unknown d: *Archaea*	$3.66\cdot10^{-3}$	$\pm9.69\cdot10^{-3}$	$2.12\cdot10^{-2}$	$\pm4.09\cdot10^{-2}$	$6.07\cdot10^{-2}$	$\pm8.62\cdot10^{-2}$	1.07	± 2.29	$6.35\cdot10^{-2}$	$\pm8.25\cdot10^{-2}$
Minor phylotypes (23)[e]	$3.17\cdot10^{-1}$	$\pm3.95\cdot10^{-1}$	$3.10\cdot10^{-2}$	$\pm2.64\cdot10^{-2}$	$6.40\cdot10^{-2}$	$\pm7.30\cdot10^{-2}$	$1.06\cdot10^{-1}$	$\pm1.01\cdot10^{-1}$	$1.14\cdot10^{-1}$	$\pm9.69\cdot10^{-2}$
unknown p: *Firmicutes*	N.D.[d]		N.D.[d]		N.D.[d]		$1.89\cdot10^{-1}$	$\pm4.99\cdot10^{-1}$	$9.13\cdot10^{-3}$	$\pm2.42\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S124. S-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	91.6	92.1	92.8	87.6	82.2	92.1	86.3	89.2	± 4.00
unknown o: *Chromatiales*	2.10	1.05	1.72	1.33	8.58	4.37	6.90	3.72	± 2.99
unknown p: *Proteobacteria*	3.55	3.60	3.44	4.42	1.32	1.36	1.09	2.68	± 1.37
unknown d: *Bacteria*	1.50	1.67	1.21	4.42	3.50	1.01	2.79	2.30	± 1.30
unknown	$3.61\cdot10^{-1}$	$7.63\cdot10^{-1}$	$3.85\cdot10^{-1}$	$8.85\cdot10^{-1}$	1.07	$2.69\cdot10^{-1}$	1.88	$8.01\cdot10^{-1}$	$\pm 5.61\cdot10^{-1}$
Hyphomicrobiaceae	$6.61\cdot10^{-1}$	$5.45\cdot10^{-1}$	$3.59\cdot10^{-1}$	1.33	1.66	$4.23\cdot10^{-1}$	$3.63\cdot10^{-1}$	$7.63\cdot10^{-1}$	$\pm 5.21\cdot10^{-1}$
Minor phylotypes (44)[d]	$2.41\cdot10^{-1}$	$2.91\cdot10^{-1}$	$7.69\cdot10^{-2}$	N.D.[e]	1.71	$4.35\cdot10^{-1}$	$6.66\cdot10^{-1}$	$4.88\cdot10^{-1}$	$\pm 5.81\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S125. V-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	92.7	93.6	79.2	76.2	96.1	93.2	95.8	89.5	± 8.24
Moraxellaceae	$1.31\cdot10^{-1}$	$5.72\cdot10^{-2}$	N.D.[d]	18.6	$4.89\cdot10^{-2}$	1.21	$1.25\cdot10^{-1}$	2.88	± 6.93
unknown d: *Bacteria*	$8.23\cdot10^{-1}$	$7.44\cdot10^{-1}$	7.92	1.95	$4.08\cdot10^{-1}$	$2.92\cdot10^{-1}$	$2.92\cdot10^{-1}$	1.78	± 2.77
Xanthomonadaceae	2.15	2.17	1.61	$9.77\cdot10^{-1}$	1.20	1.83	1.25	1.60	$\pm 4.75\cdot10^{-1}$
unknown p: *Proteobacteria*	$9.72\cdot10^{-1}$	$9.73\cdot10^{-1}$	$8.57\cdot10^{-1}$	$9.77\cdot10^{-1}$	$8.31\cdot10^{-1}$	1.35	1.00	$9.94\cdot10^{-1}$	$\pm 1.70\cdot10^{-1}$
unknown o: *Xanthomonadales*	1.35	1.26	$7.49\cdot10^{-1}$	N.D.[d]	$6.93\cdot10^{-1}$	1.07	$7.08\cdot10^{-1}$	$8.33\cdot10^{-1}$	$\pm 4.54\cdot10^{-1}$
Minor phylotypes (41)[e]	1.23	$8.58\cdot10^{-1}$	1.18	$5.86\cdot10^{-1}$	$5.54\cdot10^{-1}$	$7.06\cdot10^{-1}$	$5.83\cdot10^{-1}$	$8.14\cdot10^{-1}$	$\pm 2.87\cdot10^{-1}$
unknown	$5.23\cdot10^{-1}$	$3.43\cdot10^{-1}$	3.85	$5.86\cdot10^{-1}$	$7.34\cdot10^{-2}$	$6.14\cdot10^{-2}$	$1.25\cdot10^{-1}$	$7.95\cdot10^{-1}$	± 1.37
unknown o: *Oceanospirillales*	$3.74\cdot10^{-2}$	N.D.[d]	2.25	$1.95\cdot10^{-1}$	$4.08\cdot10^{-2}$	$1.38\cdot10^{-1}$	$4.17\cdot10^{-2}$	$3.86\cdot10^{-1}$	$\pm 8.24\cdot10^{-1}$

Table S125. V-EBPR family-level GAO results summary continued.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Oceanospirillaceae	$1.12\cdot10^{-1}$	N.D.[d]	2.36	N.D.[d]	$8.15\cdot10^{-2}$	$9.21\cdot10^{-2}$	$4.17\cdot10^{-2}$	$3.83\cdot10^{-1}$	$\pm 8.71\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S126. G-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	89.6	88.5	88.5	92.2	96.9	96.9	95.1	92.5	± 3.78
unknown d: *Bacteria*	2.55	4.01	3.97	1.64	$5.70\cdot10^{-1}$	$5.17\cdot10^{-1}$	1.22	2.07	± 1.48
Minor phylotypes (45)[d]	1.65	2.19	2.84	2.04	$8.37\cdot10^{-1}$	$8.30\cdot10^{-1}$	1.34	1.67	$\pm 7.41\cdot10^{-1}$
unknown p: *Proteobacteria*	1.50	1.15	1.49	2.41	1.06	1.13	1.39	1.45	$\pm 4.60\cdot10^{-1}$
Xanthomonadaceae	2.40	1.67	1.55	1.38	$2.36\cdot10^{-1}$	$3.32\cdot10^{-1}$	$5.05\cdot10^{-1}$	1.15	$\pm 8.14\cdot10^{-1}$
unknown	2.25	2.45	1.69	$3.17\cdot10^{-1}$	$3.53\cdot10^{-1}$	$3.23\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.12	$\pm 9.74\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S127. R-EBPR family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Family[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	86.8	62.5	49.8	43.8	42.7	56.2	31.4	53.3	± 17.8
unknown d: *Bacteria*	4.62	15.9	8.10	25.0	25.8	26.8	57.7	23.4	± 17.5
unknown	1.67	5.91	2.11	12.5	12.4	8.00	3.32	6.55	± 4.58
Moraxellaceae	N.D.[d]	6.19	28.3	6.25	$5.62\cdot10^{-1}$	N.D.[d]	N.D.[d]	5.91	± 10.3

Table S127. R-EBPR family-level GAO results summary continued.

Family[a,b]	72	86	107	121	241	263	283	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
Hyphomicrobiaceae	1.72	2.64	1.14	N.D.[d]	7.87	2.43	$4.74{\cdot}10^{-1}$	2.33	±	2.63
Xanthomonadaceae	1.42	2.91	1.58	N.D.[d]	5.06	2.09	1.26	2.05	±	1.59
unknown o: *Oceanospirillales*	$2.95{\cdot}10^{-1}$	$2.73{\cdot}10^{-1}$	3.17	6.25	N.D.[d]	$3.48{\cdot}10^{-1}$	1.74	1.72	±	2.29
unknown d: *Archaea*	$1.96{\cdot}10^{-1}$	$1.82{\cdot}10^{-1}$	$1.76{\cdot}10^{-1}$	6.25	$5.62{\cdot}10^{-1}$	N.D.[d]	$1.58{\cdot}10^{-1}$	1.07	±	2.29
unknown p: *Proteobacteria*	$9.82{\cdot}10^{-1}$	1.18	$2.64{\cdot}10^{-1}$	N.D.[d]	$5.62{\cdot}10^{-1}$	1.57	1.74	$8.99{\cdot}10^{-1}$	±	$6.53{\cdot}10^{-1}$
Oceanospirillaceae	$3.44{\cdot}10^{-1}$	$2.73{\cdot}10^{-1}$	3.08	N.D.[d]	N.D.[d]	$6.96{\cdot}10^{-1}$	1.74	$8.76{\cdot}10^{-1}$	±	1.14
unknown o: *Xanthomonadales*	$8.35{\cdot}10^{-1}$	$7.28{\cdot}10^{-1}$	$4.40{\cdot}10^{-1}$	N.D.[d]	3.37	$6.96{\cdot}10^{-1}$	N.D.[d]	$8.67{\cdot}10^{-1}$	±	1.16
Minor phylotypes (38)[e]	1.13	1.27	$4.40{\cdot}10^{-1}$	N.D.[d]	1.12	1.22	$4.74{\cdot}10^{-1}$	$8.08{\cdot}10^{-1}$	±	$4.98{\cdot}10^{-1}$
unknown p: *Firmicutes*	N.D.[d]	N.D.[d]	1.32	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	$1.89{\cdot}10^{-1}$	±	$4.99{\cdot}10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S128. Moscow WRRF family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Family[a,b]	225	255	270	284	304	313	320	Average	±	SD[c]
	%	%	%	%	%	%	%		%	
unknown c: *Gammaproteobacteria*	78.0	89.1	86.4	80.2	75.1	74.5	70.9	79.2	±	6.59
Xanthomonadaceae	11.5	2.46	3.13	10.3	3.17	4.07	10.9	6.49	±	4.14
unknown d: *Bacteria*	3.33	4.20	3.78	2.65	8.83	7.83	5.65	5.18	±	2.36
unknown	1.09	$8.48{\cdot}10^{-1}$	$9.45{\cdot}10^{-1}$	$5.43{\cdot}10^{-1}$	2.94	2.88	2.17	1.63	±	1.01
Moraxellaceae	$5.73{\cdot}10^{-2}$	N.D.[d]	$6.51{\cdot}10^{-2}$	$3.83{\cdot}10^{-1}$	2.27	5.32	3.02	1.59	±	2.04
unknown o: *Chromatiales*	1.03	$7.68{\cdot}10^{-1}$	2.08	1.25	2.38	1.63	1.86	1.57	±	$5.83{\cdot}10^{-1}$
unknown o: *Xanthomonadales*	2.98	$4.44{\cdot}10^{-1}$	$7.17{\cdot}10^{-1}$	2.20	$4.53{\cdot}10^{-1}$	$7.39{\cdot}10^{-1}$	2.01	1.36	±	1.02
unknown p: *Proteobacteria*	$9.75{\cdot}10^{-1}$	1.41	1.47	1.41	$9.06{\cdot}10^{-1}$	1.18	1.32	1.24	±	$2.23{\cdot}10^{-1}$
Hyphomicrobiaceae	$5.73{\cdot}10^{-1}$	$6.87{\cdot}10^{-1}$	1.17	$8.31{\cdot}10^{-1}$	1.02	$8.13{\cdot}10^{-1}$	$5.42{\cdot}10^{-1}$	$8.05{\cdot}10^{-1}$	±	$2.30{\cdot}10^{-1}$

Table S128. Moscow WRRF family-level GAO results summary continued.

Family[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
Minor phylotypes (40)[e]	$4.59\cdot10^{-1}$	$8.08\cdot10^{-2}$	$1.95\cdot10^{-1}$	$2.88\cdot10^{-1}$	$5.66\cdot10^{-1}$	$8.13\cdot10^{-1}$	1.16	$5.09\cdot10^{-1}$	$\pm 3.77\cdot10^{-1}$
Halothiobacillaceae	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	2.38	$2.22\cdot10^{-1}$	$4.64\cdot10^{-1}$	$4.38\cdot10^{-1}$	$\pm 8.74\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S129. Summary of family-level relative abundance by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Family[a,b]	S-EBPR (S124)		V-EBPR (S125)		G-EBPR (S126)		R-EBPR (S127)		Moscow WRRF (S128)	
	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	89.2	± 4.00	89.5	± 8.24	92.5	± 3.78	53.3	± 17.8	79.2	± 6.59
unknown d: *Bacteria*	2.30	± 1.30	1.78	± 2.77	2.07	± 1.48	23.4	± 17.5	5.18	± 2.36
unknown	$8.01\cdot10^{-1}$	$\pm 5.61\cdot10^{-1}$	$7.95\cdot10^{-1}$	± 1.37	1.12	$\pm 9.74\cdot10^{-1}$	6.55	± 4.58	1.63	± 1.01
Xanthomonadaceae	$2.11\cdot10^{-2}$	$\pm 4.00\cdot10^{-2}$	1.60	$\pm 4.75\cdot10^{-1}$	1.15	$\pm 8.14\cdot10^{-1}$	2.05	± 1.59	6.49	± 4.14
Moraxellaceae	N.D.[d]		2.88	± 6.93	$2.07\cdot10^{-1}$	$\pm 2.51\cdot10^{-1}$	5.91	± 10.3	1.59	± 2.04
unknown o: *Chromatiales*	3.72	± 2.99	$5.21\cdot10^{-1}$	$\pm 1.22\cdot10^{-1}$	$4.24\cdot10^{-1}$	$\pm 1.52\cdot10^{-1}$	$4.51\cdot10^{-1}$	$\pm 3.60\cdot10^{-1}$	1.57	$\pm 5.83\cdot10^{-1}$
unknown p: *Proteobacteria*	2.68	± 1.37	$9.94\cdot10^{-1}$	$\pm 1.70\cdot10^{-1}$	1.45	$\pm 4.60\cdot10^{-1}$	$8.99\cdot10^{-1}$	$\pm 6.53\cdot10^{-1}$	1.24	$\pm 2.23\cdot10^{-1}$
Hyphomicrobiaceae	$7.63\cdot10^{-1}$	$\pm 5.21\cdot10^{-1}$	$2.04\cdot10^{-1}$	$\pm 2.81\cdot10^{-1}$	$2.02\cdot10^{-1}$	$\pm 2.03\cdot10^{-1}$	2.33	± 2.63	$8.05\cdot10^{-1}$	$\pm 2.30\cdot10^{-1}$
unknown o: *Oceanospirillales*	N.D.[d]		$3.86\cdot10^{-1}$	$\pm 8.24\cdot10^{-1}$	$3.18\cdot10^{-2}$	$\pm 8.41\cdot10^{-2}$	1.72	± 2.29	$1.56\cdot10^{-1}$	$\pm 2.50\cdot10^{-1}$
unknown o: *Xanthomonadales*	N.D.[d]		$8.33\cdot10^{-1}$	$\pm 4.54\cdot10^{-1}$	$5.73\cdot10^{-1}$	$\pm 3.22\cdot10^{-1}$	$8.67\cdot10^{-1}$	± 1.16	1.36	± 1.02
unknown d: *Archaea*	$3.66\cdot10^{-3}$	$\pm 9.69\cdot10^{-3}$	$2.12\cdot10^{-2}$	$\pm 4.09\cdot10^{-2}$	$6.07\cdot10^{-2}$	$\pm 8.62\cdot10^{-2}$	1.07	± 2.29	$6.35\cdot10^{-2}$	$\pm 8.25\cdot10^{-2}$
Oceanospirillaceae	N.D.[d]		$3.83\cdot10^{-1}$	$\pm 8.71\cdot10^{-1}$	$2.55\cdot10^{-2}$	$\pm 4.35\cdot10^{-2}$	$8.76\cdot10^{-1}$	± 1.14	$1.25\cdot10^{-1}$	$\pm 9.46\cdot10^{-2}$
Minor phylotypes (36)[e]	$4.57\cdot10^{-1}$	$\pm 5.80\cdot10^{-1}$	$6.77\cdot10^{-2}$	$\pm 7.37\cdot10^{-2}$	$1.52\cdot10^{-1}$	$\pm 1.34\cdot10^{-1}$	$3.57\cdot10^{-1}$	$\pm 1.88\cdot10^{-1}$	$1.55\cdot10^{-1}$	$\pm 1.43\cdot10^{-1}$
Halothiobacillaceae	$6.09\cdot10^{-3}$	$\pm 1.61\cdot10^{-2}$	N.D.[d]		N.D.[d]		N.D.[d]		$4.38\cdot10^{-1}$	$\pm 8.74\cdot10^{-1}$

Table S129. Summary of family-level GAO results continued.

Family[a,b]	S-EBPR (S124) Average ± SD[c] %	V-EBPR (S125) Average ± SD[c] %	G-EBPR (S126) Average ± SD[c] %	R-EBPR (S127) Average ± SD[c] %	Moscow WRRF (S128) Average ± SD[c] %
unknown p: *Firmicutes*	N.D.[d]	N.D.[d]	N.D.[d]	$1.89\cdot10^{-1}$ ± $4.99\cdot10^{-1}$	$9.13\cdot10^{-3}$ ± $2.42\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S130. S-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	91.6	92.1	92.8	87.6	82.2	92.1	86.3	89.2	± 4.00
unknown o: *Chromatiales*	2.10	1.05	1.72	1.33	8.58	4.37	6.90	3.72	± 2.99
unknown p: *Proteobacteria*	3.55	3.60	3.44	4.42	1.32	1.36	1.09	2.68	± 1.37
unknown d: *Bacteria*	1.50	1.67	1.21	4.42	3.50	1.01	2.79	2.30	± 1.30
unknown	$3.61\cdot10^{-1}$	$7.63\cdot10^{-1}$	$3.85\cdot10^{-1}$	$8.85\cdot10^{-1}$	1.07	$2.69\cdot10^{-1}$	1.88	$8.01\cdot10^{-1}$	± $5.61\cdot10^{-1}$
Hyphomicrobium	$6.61\cdot10^{-1}$	$5.09\cdot10^{-1}$	$3.33\cdot10^{-1}$	$8.85\cdot10^{-1}$	1.28	$3.71\cdot10^{-1}$	$3.63\cdot10^{-1}$	$6.29\cdot10^{-1}$	± $3.49\cdot10^{-1}$
Minor phylotypes (62)[d]	$2.41\cdot10^{-1}$	$3.27\cdot10^{-1}$	$1.03\cdot10^{-1}$	$4.42\cdot10^{-1}$	2.09	$4.87\cdot10^{-1}$	$6.66\cdot10^{-1}$	$6.22\cdot10^{-1}$	± $6.72\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S131. V-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	92.7	93.6	79.2	76.2	96.1	93.2	95.8	89.5	± 8.24

Table S131. V-EBPR genus-level GAO results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
Alkanindiges	$1.31\cdot10^{-1}$	$5.72\cdot10^{-2}$	N.D.[d]	18.6	$4.89\cdot10^{-2}$	1.21	$1.25\cdot10^{-1}$	2.88	±6.93
unknown d: *Bacteria*	$8.23\cdot10^{-1}$	$7.44\cdot10^{-1}$	7.92	1.95	$4.08\cdot10^{-1}$	$2.92\cdot10^{-1}$	$2.92\cdot10^{-1}$	1.78	±2.77
Minor phylotypes (59)[e]	2.06	1.60	2.14	1.17	1.02	1.55	1.08	1.52	$\pm4.55\cdot10^{-1}$
unknown p: *Proteobacteria*	$9.72\cdot10^{-1}$	$9.73\cdot10^{-1}$	$8.57\cdot10^{-1}$	$9.77\cdot10^{-1}$	$8.31\cdot10^{-1}$	1.35	1.00	$9.94\cdot10^{-1}$	$\pm1.70\cdot10^{-1}$
unknown f: *Xanthomonadaceae*	1.33	1.43	$7.49\cdot10^{-1}$	$3.91\cdot10^{-1}$	$7.34\cdot10^{-1}$	$9.82\cdot10^{-1}$	$7.50\cdot10^{-1}$	$9.09\cdot10^{-1}$	$\pm3.66\cdot10^{-1}$
unknown o: *Xanthomonadales*	1.35	1.26	$7.49\cdot10^{-1}$	N.D.[d]	$6.93\cdot10^{-1}$	1.07	$7.08\cdot10^{-1}$	$8.33\cdot10^{-1}$	$\pm4.54\cdot10^{-1}$
unknown	$5.23\cdot10^{-1}$	$3.43\cdot10^{-1}$	3.85	$5.86\cdot10^{-1}$	$7.34\cdot10^{-2}$	$6.14\cdot10^{-2}$	$1.25\cdot10^{-1}$	$7.95\cdot10^{-1}$	±1.37
unknown o: *Oceanospirillales*	$3.74\cdot10^{-2}$	N.D.[d]	2.25	$1.95\cdot10^{-1}$	$4.08\cdot10^{-2}$	$1.38\cdot10^{-1}$	$4.17\cdot10^{-2}$	$3.86\cdot10^{-1}$	$\pm8.24\cdot10^{-1}$
unknown f: *Oceanospirillaceae*	$1.12\cdot10^{-1}$	N.D.[d]	2.25	N.D.[d]	$8.15\cdot10^{-2}$	$9.21\cdot10^{-2}$	$4.17\cdot10^{-2}$	$3.68\cdot10^{-1}$	$\pm8.30\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S132. G-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	89.6	88.5	88.5	92.2	96.9	96.9	95.1	92.5	±3.78
Minor phylotypes (63)[d]	2.70	2.76	3.64	2.70	$9.30\cdot10^{-1}$	1.04	1.68	2.21	±1.01
unknown d: *Bacteria*	2.55	4.01	3.97	1.64	$5.70\cdot10^{-1}$	$5.17\cdot10^{-1}$	1.22	2.07	±1.48
unknown p: *Proteobacteria*	1.50	1.15	1.49	2.41	1.06	1.13	1.39	1.45	$\pm4.60\cdot10^{-1}$
unknown	2.25	2.45	1.69	$3.17\cdot10^{-1}$	$3.53\cdot10^{-1}$	$3.23\cdot10^{-1}$	$4.45\cdot10^{-1}$	1.12	$\pm9.74\cdot10^{-1}$

Table S132. G-EBPR genus-level GAO results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown f: *Xanthomonadaceae*	1.35	1.09	$7.61\cdot10^{-1}$	$7.14\cdot10^{-1}$	$1.43\cdot10^{-1}$	$1.20\cdot10^{-1}$	$1.63\cdot10^{-1}$	$6.21\cdot10^{-1}$	±	$4.96\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S133. R-EBPR genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown c: *Gammaproteobacteria*	86.8	62.5	49.8	43.8	42.7	56.2	31.4	53.3	±	17.8
unknown d: *Bacteria*	4.62	15.9	8.10	25.0	25.8	26.8	57.7	23.4	±	17.5
unknown	1.67	5.91	2.11	12.5	12.4	8.00	3.32	6.55	±	4.58
Alkanindiges	N.D.[d]	$4.55\cdot10^{-1}$	28.2	6.25	$5.62\cdot10^{-1}$	N.D.[d]	N.D.[d]	5.06	±	10.4
Hyphomicrobium	1.47	2.09	$9.68\cdot10^{-1}$	N.D.[d]	6.18	2.43	$4.74\cdot10^{-1}$	1.95	±	2.05
unknown o: *Oceanospirillales*	$2.95\cdot10^{-1}$	$2.73\cdot10^{-1}$	3.17	6.25	N.D.[d]	$3.48\cdot10^{-1}$	1.74	1.72	±	2.29
unknown d: *Archaea*	$1.96\cdot10^{-1}$	$1.82\cdot10^{-1}$	$1.76\cdot10^{-1}$	6.25	$5.62\cdot10^{-1}$	N.D.[d]	$1.58\cdot10^{-1}$	1.07	±	2.29
Minor phylotypes (52)[e]	1.38	1.64	$7.92\cdot10^{-1}$	N.D.[d]	1.12	1.74	$7.90\cdot10^{-1}$	1.07	±	$6.01\cdot10^{-1}$
unknown p: *Proteobacteria*	$9.82\cdot10^{-1}$	1.18	$2.64\cdot10^{-1}$	N.D.[d]	$5.62\cdot10^{-1}$	1.57	1.74	$8.99\cdot10^{-1}$	±	$6.53\cdot10^{-1}$
unknown o: *Xanthomonadales*	$8.35\cdot10^{-1}$	$7.28\cdot10^{-1}$	$4.40\cdot10^{-1}$	N.D.[d]	3.37	$6.96\cdot10^{-1}$	N.D.[d]	$8.67\cdot10^{-1}$	±	1.16
unknown f: *Oceanospirillaceae*	$3.44\cdot10^{-1}$	$2.73\cdot10^{-1}$	2.99	N.D.[d]	N.D.[d]	$6.96\cdot10^{-1}$	1.74	$8.63\cdot10^{-1}$	±	1.11
Arenimonas	$4.91\cdot10^{-2}$	$3.64\cdot10^{-1}$	$4.40\cdot10^{-1}$	N.D.[d]	3.37	$8.70\cdot10^{-1}$	$9.48\cdot10^{-1}$	$8.63\cdot10^{-1}$	±	1.16
Acinetobacter	N.D.[d]	5.64	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	$8.06\cdot10^{-1}$	±	2.13
Panacagrimonas	1.08	$2.73\cdot10^{-1}$	$7.04\cdot10^{-1}$	N.D.[d]	1.69	$1.74\cdot10^{-1}$	N.D.[d]	$5.60\cdot10^{-1}$	±	$6.35\cdot10^{-1}$
Dokdonella	$1.96\cdot10^{-1}$	2.27	$3.52\cdot10^{-1}$	N.D.[d]	N.D.[d]	$5.22\cdot10^{-1}$	N.D.[d]	$4.78\cdot10^{-1}$	±	$8.18\cdot10^{-1}$
Filomicrobium	$9.82\cdot10^{-2}$	$2.73\cdot10^{-1}$	$1.76\cdot10^{-1}$	N.D.[d]	1.69	N.D.[d]	N.D.[d]	$3.19\cdot10^{-1}$	±	$6.12\cdot10^{-1}$

Table S133. R-EBPR genus-level GAO results summary continued.

Genus[a,b]	72 %	86 %	107 %	121 %	241 %	263 %	283 %	Average %	±	SD[c]
unknown p: *Firmicutes*	N.D.[d]	N.D.[d]	1.32	N.D.[d]	N.D.[d]	N.D.[d]	N.D.[d]	$1.89\cdot10^{-1}$	±	$4.99\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

Table S134. Moscow WRRF genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Genus[a,b]	225 %	255 %	270 %	284 %	304 %	313 %	320 %	Average %	± SD[c]
unknown c: *Gammaproteobacteria*	78.0	89.1	86.4	80.2	75.1	74.5	70.9	79.2	± 6.59
Panacagrimonas	9.86	1.54	1.95	9.46	2.15	2.81	10.4	5.46	± 4.20
unknown d: *Bacteria*	3.33	4.20	3.78	2.65	8.83	7.83	5.65	5.18	± 2.36
Minor phylotypes (58)[d]	1.15	$8.89\cdot10^{-1}$	1.63	1.31	2.38	2.29	2.17	1.69	± $5.98\cdot10^{-1}$
unknown	1.09	$8.48\cdot10^{-1}$	$9.45\cdot10^{-1}$	$5.43\cdot10^{-1}$	2.94	2.88	2.17	1.63	± 1.01
unknown o: *Chromatiales*	1.03	$7.68\cdot10^{-1}$	2.08	1.25	2.38	1.63	1.86	1.57	± $5.83\cdot10^{-1}$
Alkanindiges	$5.73\cdot10^{-2}$	N.D.[e]	$3.26\cdot10^{-2}$	$3.83\cdot10^{-1}$	1.81	5.03	2.55	1.41	± 1.88
unknown o: *Xanthomonadales*	2.98	$4.44\cdot10^{-1}$	$7.17\cdot10^{-1}$	2.20	$4.53\cdot10^{-1}$	$7.39\cdot10^{-1}$	2.01	1.36	± 1.02
unknown p: *Proteobacteria*	$9.75\cdot10^{-1}$	1.41	1.47	1.41	$9.06\cdot10^{-1}$	1.18	1.32	1.24	± $2.23\cdot10^{-1}$
Arenimonas	1.49	$8.08\cdot10^{-1}$	$9.45\cdot10^{-1}$	$6.07\cdot10^{-1}$	1.02	$8.87\cdot10^{-1}$	$4.64\cdot10^{-1}$	$8.89\cdot10^{-1}$	± $3.29\cdot10^{-1}$
Thioalkalibacter	N.D.[e]	N.D.[e]	N.D.[e]	N.D.[e]	2.04	$2.22\cdot10^{-1}$	$4.64\cdot10^{-1}$	$3.89\cdot10^{-1}$	± $7.48\cdot10^{-1}$

[a] Phylotypes were sorted in descending order of the mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

[e] N.D. = Not detected.

Table S135. Summary of genus-level relative abundance by operational day of the 16S rRNA gene sequencing results with the GAO primer set.

Genus[a,b]	S-EBPR (S130)		V-EBPR (S131)		G-EBPR (S132)		R-EBPR (S133)		Moscow WRRF (S134)	
	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]	Average	± SD[c]
	%		%		%		%		%	
unknown c: *Gammaproteobacteria*	89.2	± 4.00	89.5	± 8.24	92.5	± 3.78	53.3	± 17.8	79.2	± 6.59
unknown d: *Bacteria*	2.30	± 1.30	1.78	± 2.77	2.07	± 1.48	23.4	± 17.5	5.18	± 2.36
unknown	$8.01\cdot10^{-1}$	$\pm 5.61\cdot10^{-1}$	$7.95\cdot10^{-1}$	± 1.37	1.12	$\pm 9.74\cdot10^{-1}$	6.55	± 4.58	1.63	± 1.01
Panacagrimonas	$1.83\cdot10^{-3}$	$\pm 4.84\cdot10^{-3}$	$5.81\cdot10^{-1}$	$\pm 1.66\cdot10^{-1}$	$2.77\cdot10^{-1}$	$\pm 1.68\cdot10^{-1}$	$5.60\cdot10^{-1}$	$\pm 6.35\cdot10^{-1}$	5.46	± 4.20
Alkanindiges	N.D.[d]		2.88	± 6.93	$2.02\cdot10^{-1}$	$\pm 2.53\cdot10^{-1}$	5.06	± 10.4	1.41	± 1.88
unknown o: *Chromatiales*	3.72	± 2.99	$5.21\cdot10^{-1}$	$\pm 1.22\cdot10^{-1}$	$4.24\cdot10^{-1}$	$\pm 1.52\cdot10^{-1}$	$4.51\cdot10^{-1}$	$\pm 3.60\cdot10^{-1}$	1.57	$\pm 5.83\cdot10^{-1}$
unknown p: *Proteobacteria*	2.68	± 1.37	$9.94\cdot10^{-1}$	$\pm 1.70\cdot10^{-1}$	1.45	$\pm 4.60\cdot10^{-1}$	$8.99\cdot10^{-1}$	$\pm 6.53\cdot10^{-1}$	1.24	$\pm 2.23\cdot10^{-1}$
Hyphomicrobium	$6.29\cdot10^{-1}$	$\pm 3.49\cdot10^{-1}$	$1.84\cdot10^{-1}$	$\pm 2.48\cdot10^{-1}$	$1.74\cdot10^{-1}$	$\pm 1.49\cdot10^{-1}$	1.95	± 2.05	$6.26\cdot10^{-1}$	$\pm 2.57\cdot10^{-1}$
unknown o: *Oceanospirillales*	N.D.[d]		$3.86\cdot10^{-1}$	$\pm 8.24\cdot10^{-1}$	$3.18\cdot10^{-2}$	$\pm 8.41\cdot10^{-2}$	1.72	± 2.29	$1.56\cdot10^{-1}$	$\pm 2.50\cdot10^{-1}$
unknown o: *Xanthomonadales*	N.D.[d]		$8.33\cdot10^{-1}$	$\pm 4.54\cdot10^{-1}$	$5.73\cdot10^{-1}$	$\pm 3.22\cdot10^{-1}$	$8.67\cdot10^{-1}$	± 1.16	1.36	± 1.02
unknown d: *Archaea*	$3.66\cdot10^{-3}$	$\pm 9.69\cdot10^{-3}$	$2.12\cdot10^{-2}$	$\pm 4.09\cdot10^{-2}$	$6.07\cdot10^{-2}$	$\pm 8.62\cdot10^{-2}$	1.07	± 2.29	$6.35\cdot10^{-2}$	$\pm 8.25\cdot10^{-2}$
unknown f: *Xanthomonadaceae*	$5.19\cdot10^{-3}$	$\pm 1.37\cdot10^{-2}$	$9.09\cdot10^{-1}$	$\pm 3.66\cdot10^{-1}$	$6.21\cdot10^{-1}$	$\pm 4.96\cdot10^{-1}$	$1.21\cdot10^{-1}$	$\pm 1.50\cdot10^{-1}$	$1.42\cdot10^{-1}$	$\pm 1.30\cdot10^{-1}$
Arenimonas	$1.04\cdot10^{-2}$	$\pm 2.75\cdot10^{-2}$	$9.76\cdot10^{-2}$	$\pm 1.21\cdot10^{-1}$	$2.28\cdot10^{-1}$	$\pm 2.25\cdot10^{-1}$	$8.63\cdot10^{-1}$	± 1.16	$8.89\cdot10^{-1}$	$\pm 3.29\cdot10^{-1}$
unknown f: *Oceanospirillaceae*	N.D.[d]		$3.68\cdot10^{-1}$	$\pm 8.30\cdot10^{-1}$	$2.55\cdot10^{-2}$	$\pm 4.35\cdot10^{-2}$	$8.63\cdot10^{-1}$	± 1.11	$1.25\cdot10^{-1}$	$\pm 9.46\cdot10^{-2}$
Acinetobacter	N.D.[d]		N.D.[d]		$4.24\cdot10^{-3}$	$\pm 1.12\cdot10^{-2}$	$8.06\cdot10^{-1}$	± 2.13	$4.65\cdot10^{-3}$	$\pm 1.23\cdot10^{-2}$
Minor phylotypes (49)[e]	$4.96\cdot10^{-1}$	$\pm 6.34\cdot10^{-1}$	$8.30\cdot10^{-2}$	$\pm 6.82\cdot10^{-2}$	$1.59\cdot10^{-1}$	$\pm 1.32\cdot10^{-1}$	$4.93\cdot10^{-1}$	$\pm 2.72\cdot10^{-1}$	$4.82\cdot10^{-1}$	$\pm 3.47\cdot10^{-1}$
Dokdonella	N.D.[d]		$1.01\cdot10^{-2}$	$\pm 1.83\cdot10^{-2}$	$2.59\cdot10^{-2}$	$\pm 5.54\cdot10^{-2}$	$4.78\cdot10^{-1}$	$\pm 8.18\cdot10^{-1}$	$4.56\cdot10^{-3}$	$\pm 1.21\cdot10^{-2}$
Thioalkalibacter	$6.09\cdot10^{-3}$	$\pm 1.61\cdot10^{-2}$	N.D.[d]		N.D.[d]		N.D.[d]		$3.89\cdot10^{-1}$	$\pm 7.48\cdot10^{-1}$
Filomicrobium	$9.92\cdot10^{-2}$	$\pm 1.70\cdot10^{-1}$	$1.97\cdot10^{-2}$	$\pm 4.02\cdot10^{-2}$	$2.23\cdot10^{-2}$	$\pm 4.88\cdot10^{-2}$	$3.19\cdot10^{-1}$	$\pm 6.12\cdot10^{-1}$	$7.45\cdot10^{-2}$	$\pm 6.96\cdot10^{-2}$
unknown p: *Firmicutes*	N.D.[d]		N.D.[d]		N.D.[d]		$1.89\cdot10^{-1}$	$\pm 4.99\cdot10^{-1}$	$9.13\cdot10^{-3}$	$\pm 2.42\cdot10^{-2}$

[a] Phylotypes were sorted in descending order of the maximum mean relative abundance.

[b] Unknown phylotypes are differentiated based on their classification at superior taxonomic levels. Where available, the most specific taxonomic level and taxon assigned to the phylotype are included under the unknown. Taxonomic levels are abbreviated as d: domain, p: phylum, c: class, o: order, and f: family.

[c] Sample standard deviation.

[d] N.D. = Not detected.

[e] "Minor phylotypes" is the aggregation of the phylotypes individually constituting less than 1 % of the total relative abundance for all of the operational days shown; the number of included phylotypes is indicated in parentheses.

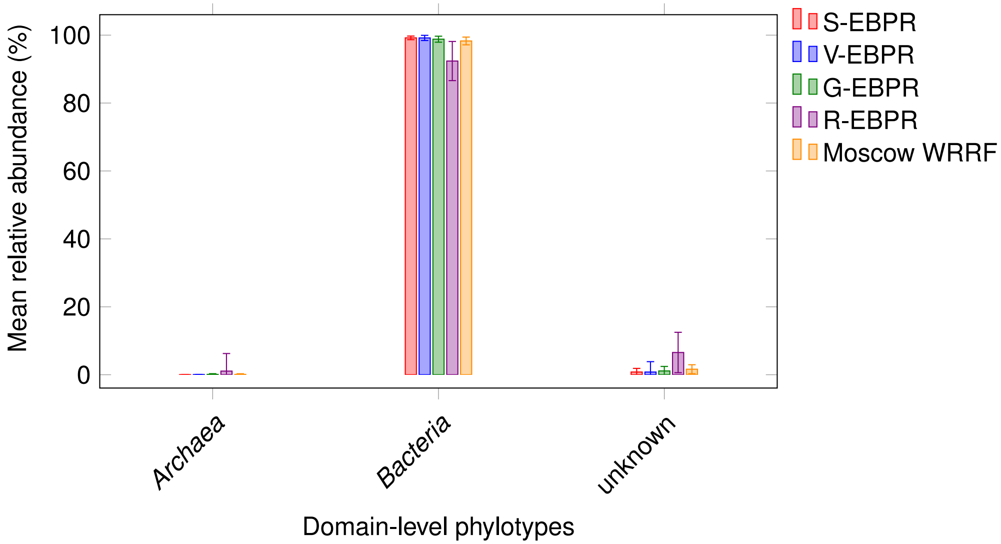

Figure S184. Mean relative abundance for phylotypes identified using the GAO primer set at the domain level (see Tables S100 to S104). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the domain level are indicated by "unknown" followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

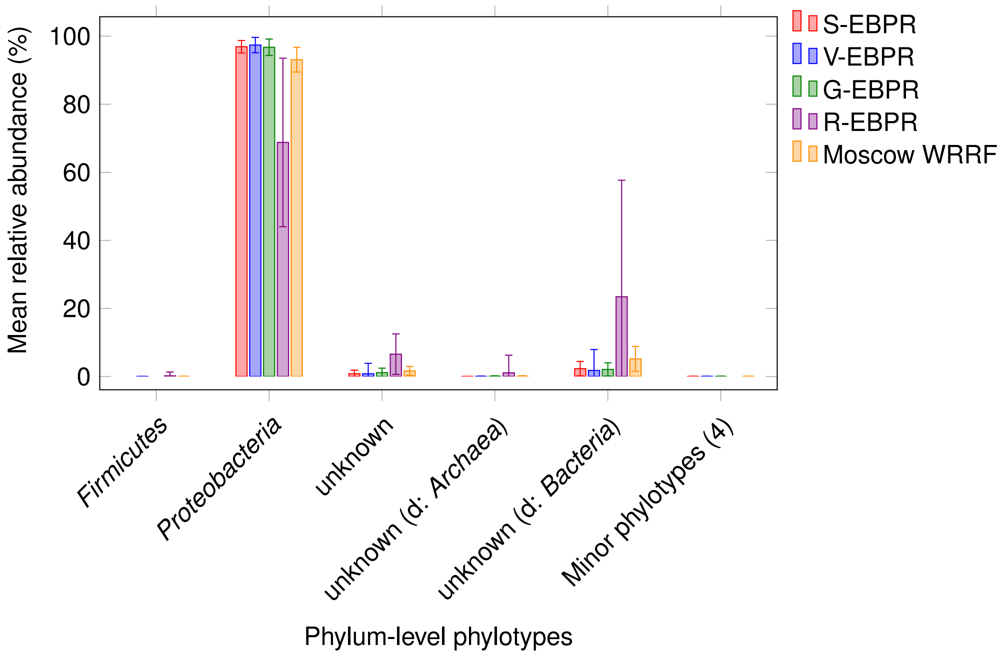

Figure S185. Mean relative abundance for phylotypes identified using the GAO primer set at the phylum level (see Tables S106 to S110). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the phylum level are indicated by "unknown" followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

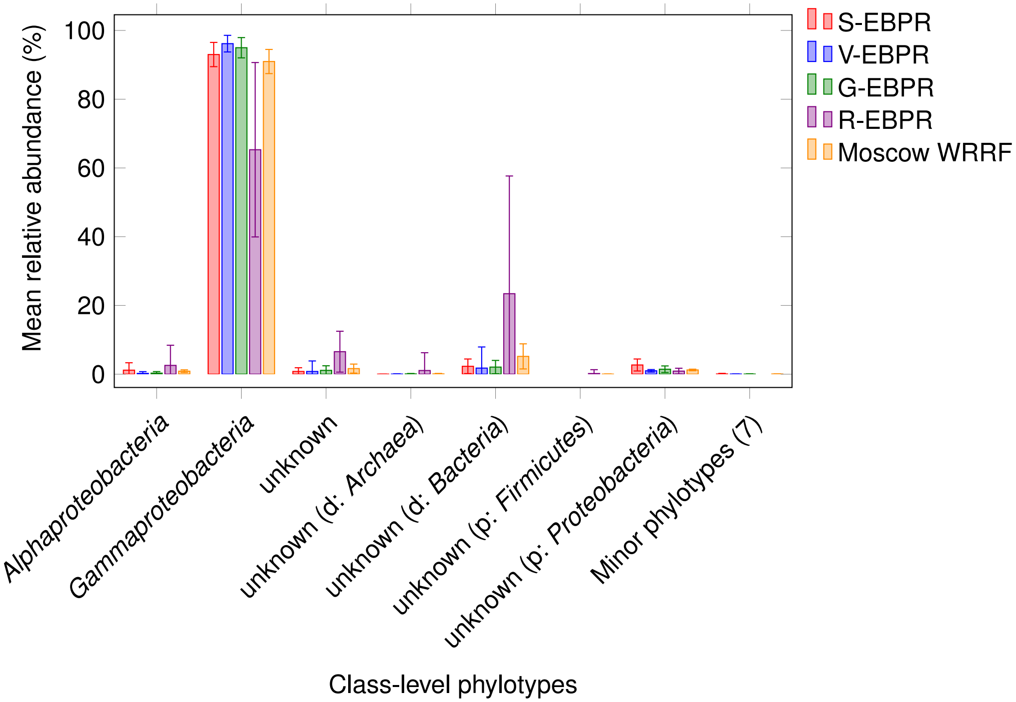

Figure S186. Mean relative abundance for phylotypes identified using the GAO primer set at the class level (see Tables S112 to S116). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the class level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

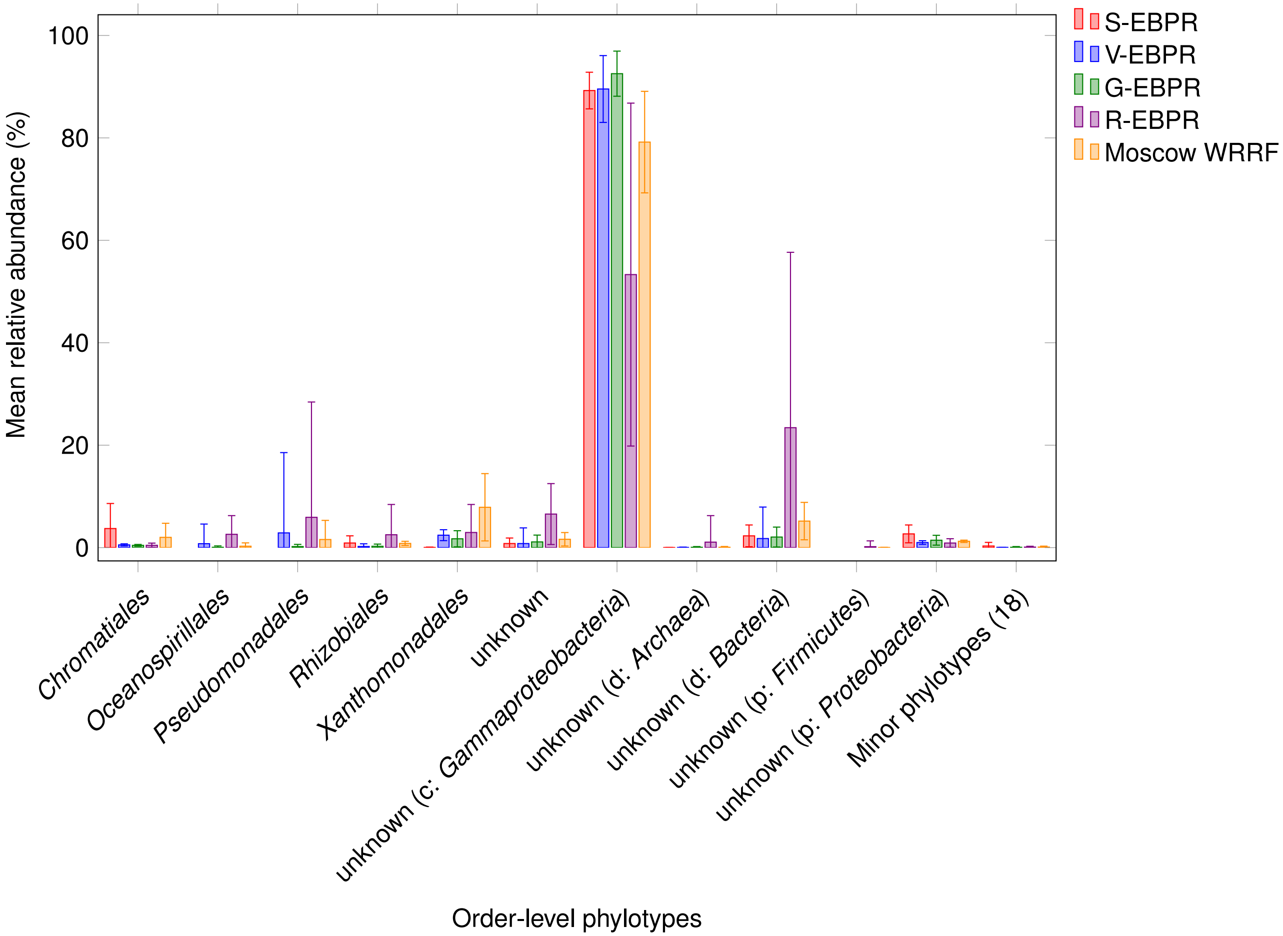

Figure S187. Mean relative abundance for phylotypes identified using the GAO primer set at the order level (see Tables S118 to S122). Phylotypes with less than 1 % in all of the samples were lumped into “Minor phylotypes” at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the order level are indicated by “unknown” followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

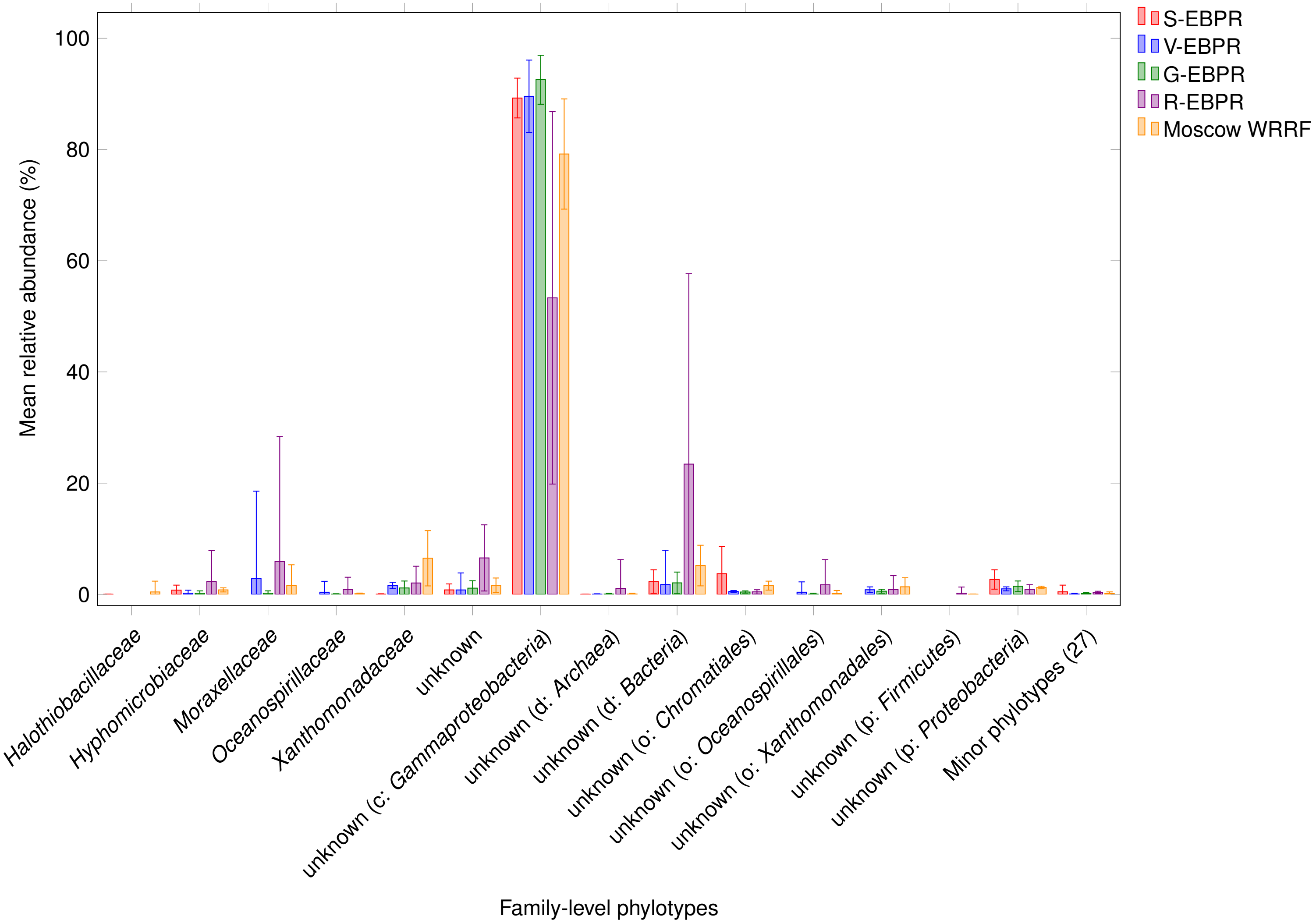

Figure S188. Mean relative abundance for phylotypes identified using the GAO primer set at the family level (see Tables S124 to S128). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the family level are indicated by "unknown" followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

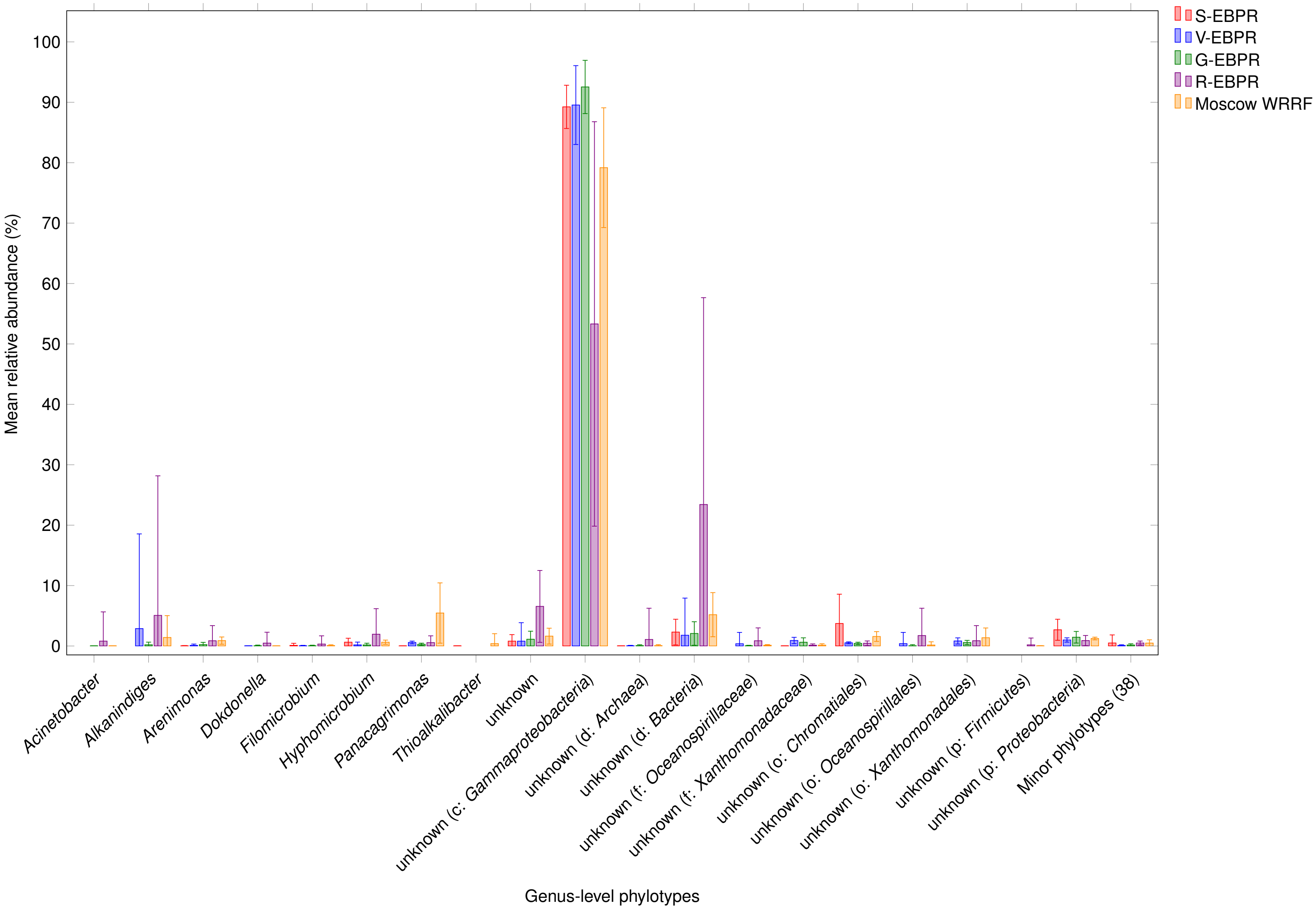

Figure S189. Mean relative abundance for phylotypes identified using the GAO primer set at the genus level (see Tables S130 to S134). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the category has been omitted. Non-minor phylotypes which were not identified at the genus level are indicated by "unknown" followed by the most specific identified taxonomic level (if available) in parenthesis (where d: domain, p: phylum, c: class, o: order, f: family). Note that the bars for phylotypes which were not detected in a given reactor (i.e., 0 % relative abundance in all of the associated samples) are omitted. Error bars indicate the sample standard deviation.

Heatmaps

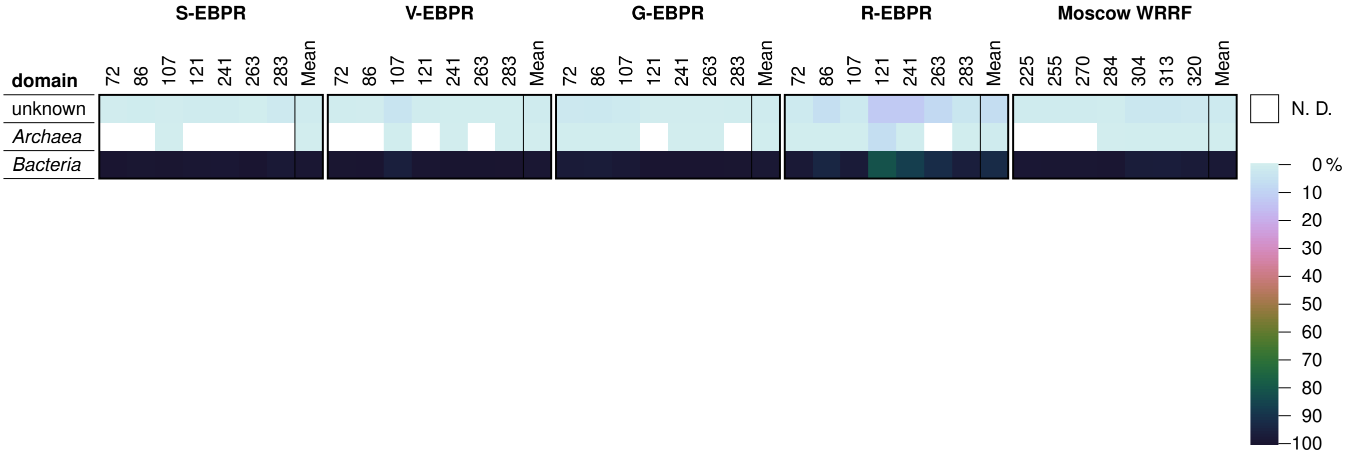

Figure S190. Heat map showing the relative abundance of phylotypes identified at the domain level using the GAO primer set (see Tables S100 to S104). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as “unknown”) were aggregated by the most specific taxonomic level at which they were identified (the “*” is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted “Minor phylotypes” at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the line has been omitted.

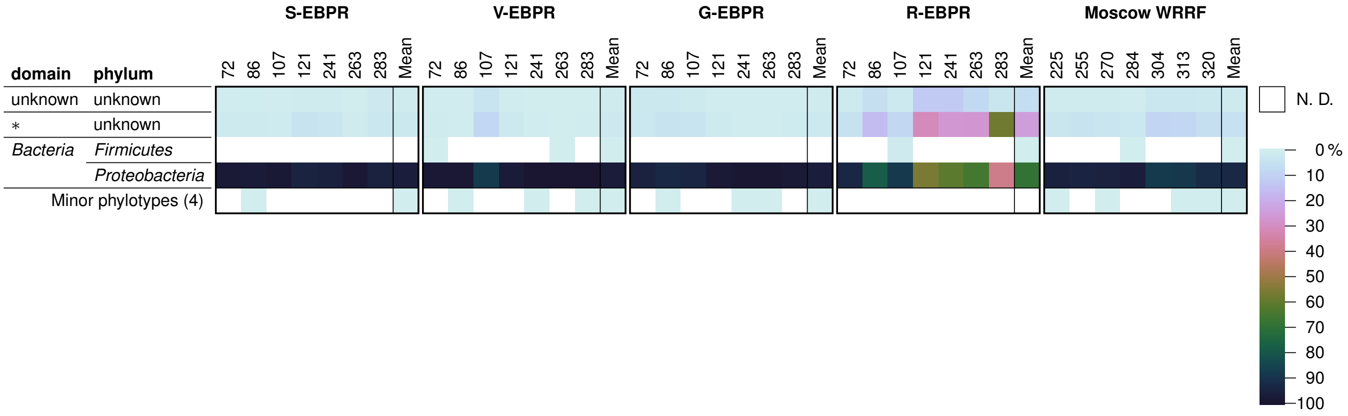

Figure S191. Heat map showing the relative abundance of phylotypes identified at the phylum level using the GAO primer set (see Tables S106 to S110). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as “unknown”) were aggregated by the most specific taxonomic level at which they were identified (the “*” is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, “*incertae sedis*”, when present in taxon names, has been abbreviated as “*inc. sed.*” with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted “Minor phylotypes” at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following “Minor phylotypes”. If no phylotypes were so categorized, the line has been omitted.

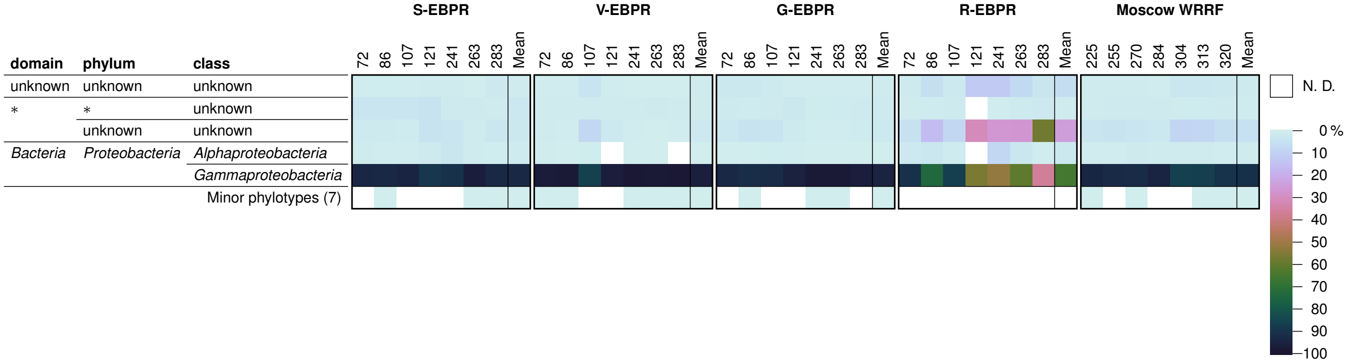

Figure S192. Heat map showing the relative abundance of phylotypes identified at the class level using the GAO primer set (see Tables S112 to S116). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

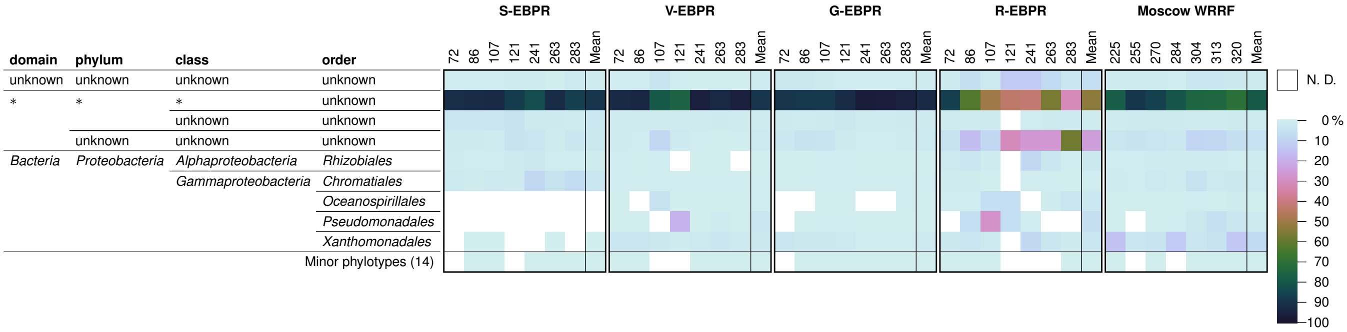

Figure S193. Heat map showing the relative abundance of phylotypes identified at the order level using the GAO primer set (see Tables S118 to S122). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

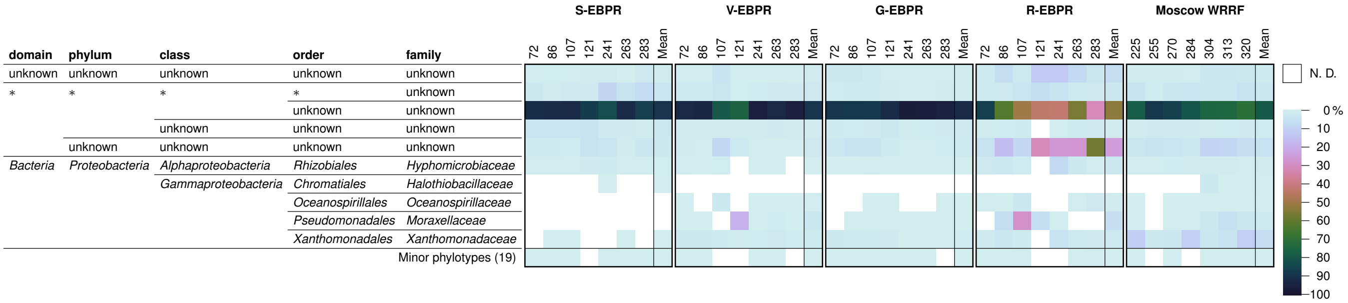

Figure S194. Heat map showing the relative abundance of phylotypes identified at the family level using the GAO primer set (see Tables S124 to S128). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

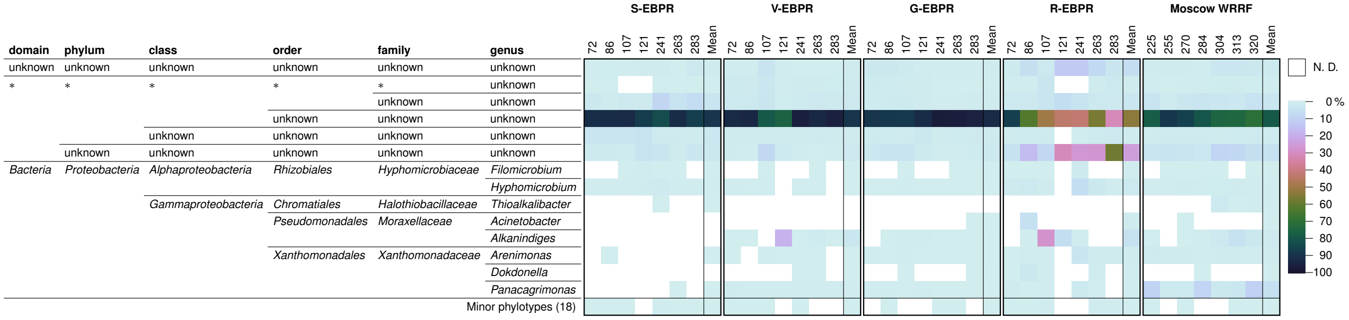

Figure S195. Heat map showing the relative abundance of phylotypes identified at the genus level using the GAO primer set (see Tables S130 to S134). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted as "unknown") were aggregated by the most specific taxonomic level at which they were identified (the "*" is used to indicate any identified taxon name). Note that the adopted color scheme (based on Green (2011)) is nonlinear at 0 % relative abundance to differentiate phylotypes which were not detected (N. D.) in a sample from those that were. To conserve space, "*incertae sedis*", when present in taxon names, has been abbreviated as "*inc. sed.*" with the original capitalization and interceding characters preserved. Any identified phylotypes with less than 1 % relative abundance in all samples were aggregated and denoted "Minor phylotypes" at the bottom of the heat map. The number of phylotypes categorized accordingly is indicated in the parenthesis following "Minor phylotypes". If no phylotypes were so categorized, the line has been omitted.

Section S4. BLASTN results

Table S136. *Candidatus* Accumulibacter phosphatis reference sequence summary.[a] Extra super duper long table caption to test if the landscape option is atuomaticallay changed fwith fithe deteks thes options.

NCBI GenBank Accession	Category[b]	Length (bp)	Source citation	RDP Nïve Bayesian Classifier Results[c]					
				Order	Score	Family	Score	Genus	Score
AF204244.1	I	1460	Crocetti et al. (2000)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	71
AF255641.1	I	1433	Liu et al. (2001)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	63
AF502224.1	I	1460	McMahon et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	71
AF502225.1	I	1461	McMahon et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	78
AJ224937.1	I	1322	Hesselmann et al. (1999)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	79
AY064178.1	I	1496	Zilles et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	94
AY064179.1	I	1397	Zilles et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	70
EF565148.1	I	2193	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Rhodocyclus	57
AF204247.1	IIA	1459	Crocetti et al. (2000)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	89
AF502227.1	IIA	1460	McMahon et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	73
AF502229.1	IIA	1459	McMahon et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	70
AF502230.1	IIA	1459	McMahon et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	78
AF502231.1	IIA	1459	McMahon et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	70
EF565147.1	IIA	2178	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	50
EF565153.1	IIA	2115	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Rhodocyclus	37
EF565155.1	IIA	2177	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Rhodocyclus	41
EF565156.1	IIA	2177	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Rhodocyclus	40
EF565149.1	IIB	2211	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Ferribacterium	34
EF565150.1	IIB	1914	He et al. (2007)	Rhodocyclales	90	Rhodocyclaceae	90	Ferribacterium	51
EF565152.1	IIB	2153	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	75
EF565157.1	IIB	2213	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Ferribacterium	38
AY062125.1	IIC (and IID)	1499	Zilles et al. (2002)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	98
EF565151.1	IIC (and IID)	2179	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	72
EF565158.1	IIC (and IID)	2203	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Rhodocyclus	77
EF565159.1	IIC (and IID)	2205	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Rhodocyclus	70
EF565160.1	IIC (and IID)	2197	He et al. (2007)	Rhodocyclales	100	Rhodocyclaceae	100	Propionivibrio	74
EF565161.1	IIC (and IID)	1752	He et al. (2007)	Rhodocyclales	94	Rhodocyclaceae	94	Rhodocyclus	30

[a] Sequences selected following the approach of Mao et al. (2015).

[b] Type and clade as assigned by He et al. (2007).

[c] The classification and scores for all higher taxonomic levels were shared across the sequences (i.e., each was classified as belonging to the *Bacteria* domain with a score of 100 %, the *Proteobacteria* phylum with a score of 100 %, and the *Betaproteobacteria* class with a score of 100 %).

Table S137. Summary of `blastn` analysis for *Candidatus* Accumulibacter phosphatis (CAP) of the joined sequences from the EUB primer set categorized as *Rhodocyclaceae* by `RDP`.

Operational	Number of sequences			Relative abundance (%)			CAP % of
day or date	Total	*Rhodocyclaceae*	CAP	*Rhodocyclaceae*	CAP	qPCR	*Rhodocyclaceae*
S-EBPR							
72	40 801	4107	84	10.07	0.21	4.17	2.05
86	74 359	5822	2	7.83	0.0	4.48	0.03
107	57 770	14 919	2329	25.82	4.03	4.09	15.61
121	55 175	14 962	84	27.12	0.15	2.92	0.56
241	104 835	10 554	22	10.07	0.02	5.42	0.21
263	88 684	1952	3	2.2	0.0	0.61	0.15
283	81 841	24 860	17 556	30.38	21.45	15.14	70.62
V-EBPR							
72	60 230	368	28	0.61	0.05	0.67	7.61
86	66 185	4920	22	7.43	0.03	0.4	0.45
107	67 995	11 720	829	17.24	1.22	0.12	7.07
121	76 395	15 119	4	19.79	0.01	0.24	0.03
241	101 373	4135	0	4.08	0.0	0.21	0.0
263	6428	548	0	8.53	0.0	0.42	0.0
283	37 887	743	0	1.96	0.0	2.6	0.0
G-EBPR							
72	67 027	520	2	0.78	0.0	0.4	0.38
86	70 389	4718	2	6.7	0.0	0.27	0.04
107	61 488	14 591	1	23.73	0.0	0.26	0.01
121	72 010	10 926	0	15.17	0.0	0.32	0.0
241	99 125	6471	0	6.53	0.0	0.42	0.0
263	75 414	2381	0	3.16	0.0	0.79	0.0
283	1208	61	0	5.05	0.0	0.82	0.0
R-EBPR							
72	44 916	666	9	1.48	0.02	0.52	1.35
86	57 159	2776	4	4.86	0.01	1.14	0.14
107	59 757	5091	1	8.52	0.0	0.62	0.02
121	56 336	11 391	3	20.22	0.01	0.17	0.03
241	79 844	4971	2	6.23	0.0	0.16	0.04
263	67 562	3573	3	5.29	0.0	0.11	0.08
283	74 690	200	0	0.27	0.0	0.33	0.0
Moscow WRRF							
225	80 207	4003	233	4.99	0.29	3.97	5.82
255	116 631	2831	359	2.43	0.31	7.23	12.68
270	85 256	2137	280	2.51	0.33	5.33	13.1
284	78 823	2348	268	2.98	0.34	17.54	11.41
304	91 185	6054	914	6.64	1.0	9.09	15.1
313	85 041	5612	921	6.6	1.08	10.13	16.41
320	90 397	5348	950	5.92	1.05	4.52	17.76

Table S138. Summary of `blastn` analysis for *Candidatus* Accumulibacter phosphatis (CAP) of the joined sequences from the PAO primer set categorized as *Rhodocyclaceae* by `RDP`.

Operational	Number of sequences			Relative abundance (%)		CAP % of
day or date	Total	*Rhodocyclaceae*	CAP	*Rhodocyclaceae*	CAP	*Rhodocyclaceae*
S-EBPR						
72	16 215	15 569	7303	96.02	45.04	46.91
86	369	284	29	76.96	7.86	10.21
107	23 425	23 305	22 652	99.49	96.7	97.2
121	26 988	26 574	24 919	98.47	92.33	93.77
241	35 474	34 567	4810	97.44	13.56	13.92
263	27 666	23 939	726	86.53	2.62	3.03
283	71 580	71 459	70 149	99.83	98.0	98.17
V-EBPR						
72	5839	2942	2456	50.39	42.06	83.48
86	3426	2717	909	79.31	26.53	33.46
107	1995	1964	1894	98.45	94.94	96.44
121	7872	2367	865	30.07	10.99	36.54
241	17 583	3104	245	17.65	1.39	7.89
263	24 784	2904	28	11.72	0.11	0.96
283	58 510	56 850	55 341	97.16	94.58	97.35
G-EBPR						
72	5710	714	77	12.5	1.35	10.78
86	6146	5249	76	85.41	1.24	1.45
107	17 296	17 019	6	98.4	0.03	0.04
121	30 553	28 201	21	92.3	0.07	0.07
241	31 675	9477	44	29.92	0.14	0.46
263	14 827	1673	13	11.28	0.09	0.78
283	35 031	15 802	298	45.11	0.85	1.89
R-EBPR						
72	4126	3595	852	87.13	20.65	23.7
86	4265	2752	137	64.53	3.21	4.98
107	10 587	7189	197	67.9	1.86	2.74
121	20 560	15 591	546	75.83	2.66	3.5
241	35 230	29 309	624	83.19	1.77	2.13
263	26 514	19 347	255	72.97	0.96	1.32
283	19 082	16 634	1018	87.17	5.33	6.12
Moscow WRRF						
225	31 029	22 813	8353	73.52	26.92	36.62
255	28 463	23 947	11 790	84.13	41.42	49.23
270	18 238	15 381	9424	84.33	51.67	61.27
284	25 431	20 416	10 844	80.28	42.64	53.12
304	22 117	20 863	14 807	94.33	66.95	70.97
313	20 495	18 940	11 476	92.41	55.99	60.59
320	12	9	7	75.0	58.33	77.78

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