Water Research

Supplementary Material for:

Polyhydroxyalkanoate Synthesis by Mixed Microbial Consortia Cultured on Fermented Dairy Manure: Effect of Oxygen Mass Transfer on Process Rates/Yields and the Associated Microbial Ecology

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Section S1. Genus-level Illumina sequencing results

EUB primer set

Diversity metrics

Table S1. 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]
			AE4					
29	116 215	514	19	495	3.80	0.61	0.91	574.38
52	78 914	502	22	480	4.24	0.68	0.97	601.11
271	105 066	490	17	473	3.66	0.59	0.94	593.33
			AE8					
29	120 133	550	26	524	4.22	0.67	0.96	659.44
52	77 834	550	20	530	4.34	0.69	0.96	725.52
271	104 742	542	17	525	3.98	0.63	0.95	675.22
			AE12					
29	99 663	467	20	447	3.98	0.65	0.95	644.22
52	29 583	332	19	313	3.53	0.61	0.88	448.90
271	88 463	531	19	512	3.71	0.59	0.92	614.39
			AE20					
29	80 065	421	16	405	3.59	0.59	0.91	529.78
52	68 933	479	21	458	4.26	0.69	0.96	568.07
271	68 926	520	22	498	4.41	0.71	0.98	631.62

[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

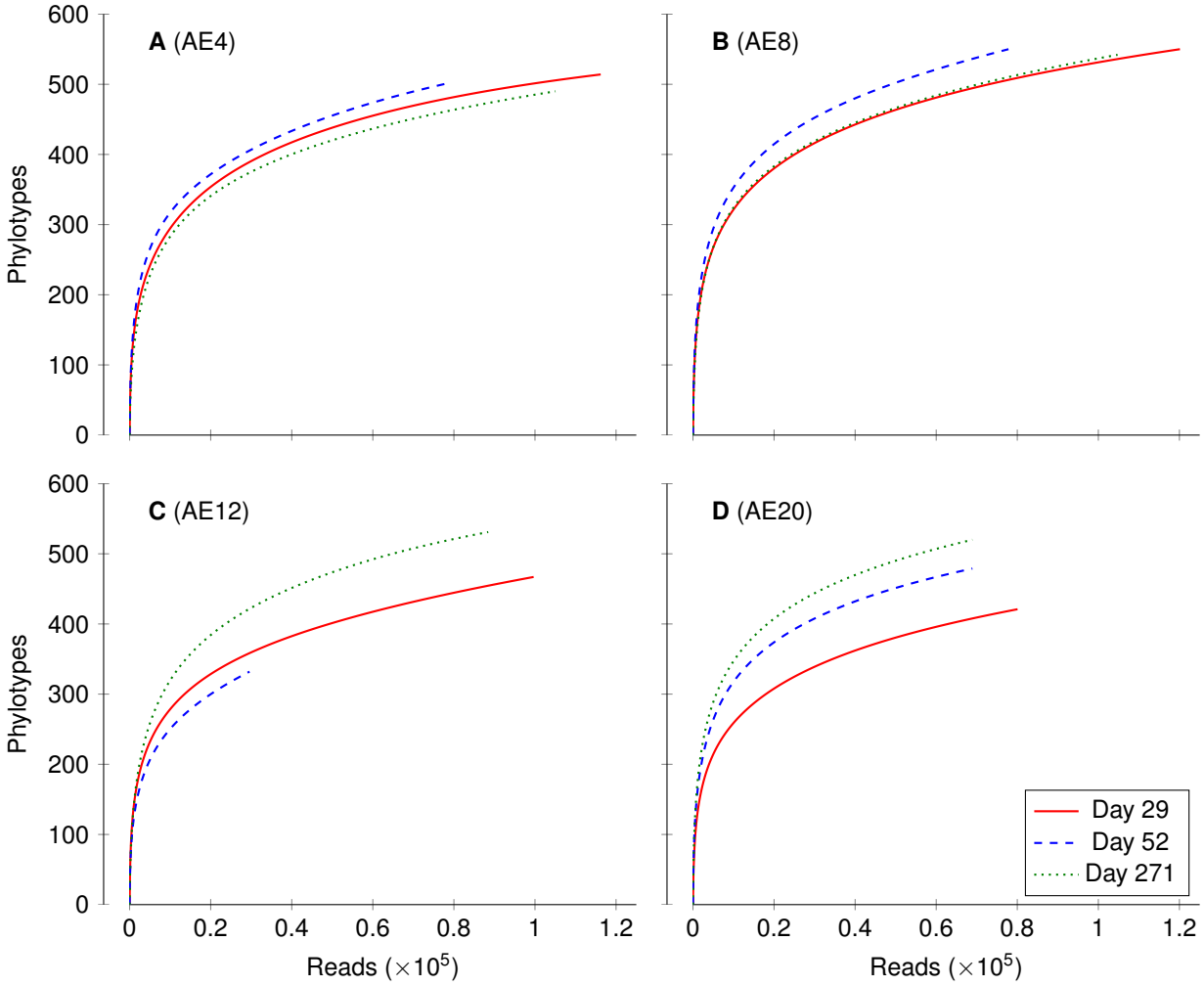

Figure S1. Rarefaction curves for the EUB primer.

Cluster analysis

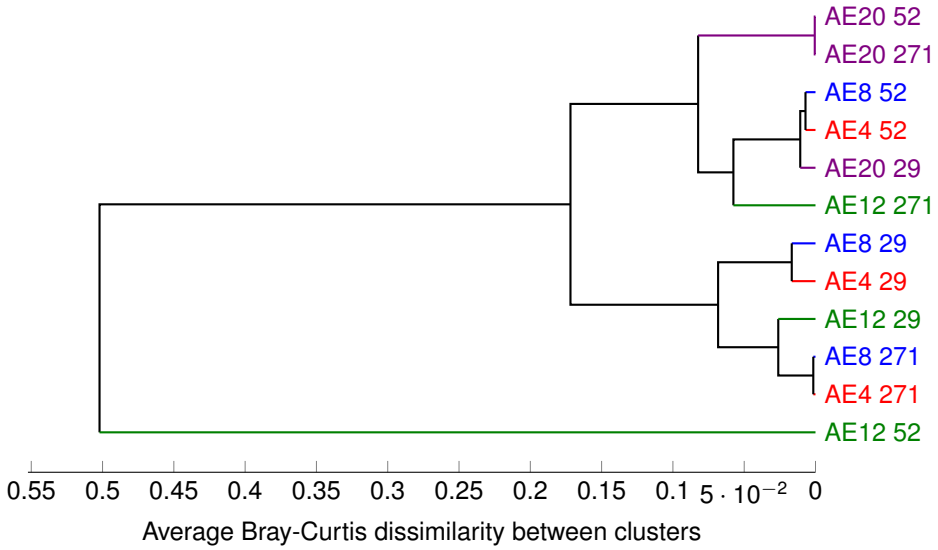

Figure S2. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the domain level. Sample dissimiliarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, repsectively, 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 S2. Bray-Curtis dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the domain level, grouped by reactor and operational day. Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		AE4			AE8			AE12			AE20		
		29	52	271	29	52	271	29	52	271	29	52	271
AE4	29	0											
	52	53	0										
	271	70	65	0									
AE8	29	24	51	69	0								
	52	41	39	73	41	0							
	271	63	55	20	61	63	0						
AE12	29	29	48	70	27	39	62	0					
	52	65	54	82	66	49	73	63	0				
	271	71	55	33	68	63	33	69	72	0			
AE20	29	35	50	78	41	43	68	36	55	69	0		
	52	46	44	79	46	29	68	42	45	68	42	0	
	271	64	56	51	62	57	42	62	68	43	65	59	0

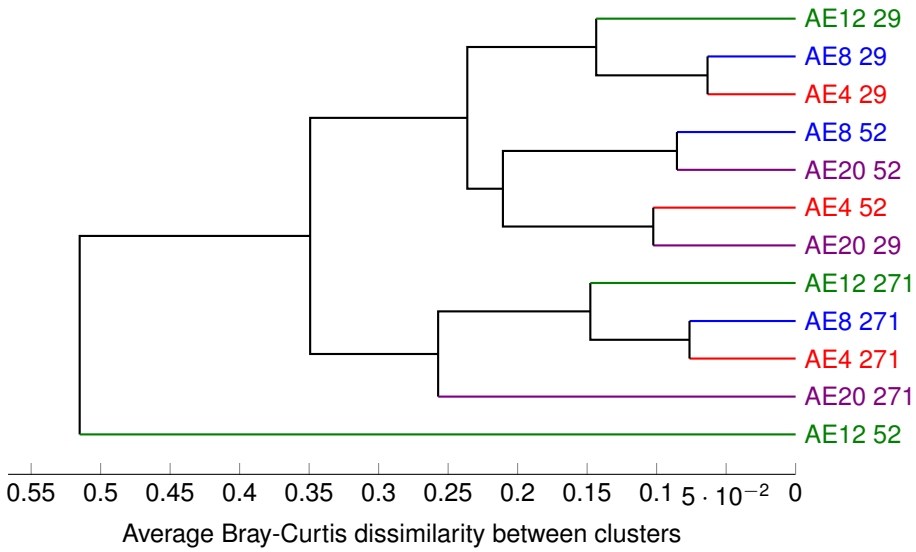

Figure S3. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the phylum level. Sample dissimiliarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, repsectively, 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 S3. Bray-Curtis dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the phylum level, grouped by reactor and operational day. Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		AE4			AE8			AE12			AE20		
		29	52	271	29	52	271	29	52	271	29	52	271
AE4	29	0											
	52	53	0										
	271	70	65	0									
AE8	29	24	51	69	0								
	52	41	39	73	41	0							
	271	63	55	20	61	63	0						
AE12	29	29	48	70	27	39	62	0					
	52	65	54	82	66	49	73	63	0				
	271	71	55	33	68	63	33	69	72	0			
AE20	29	35	50	78	41	43	68	36	55	69	0		
	52	46	44	79	46	29	68	42	45	68	42	0	
	271	64	56	51	62	57	42	62	68	43	65	59	0

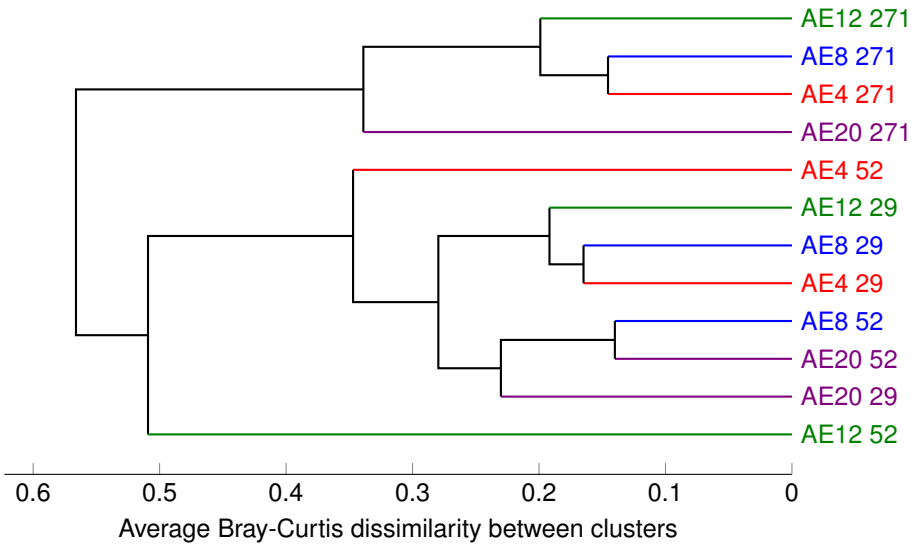

Figure S4. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the class level. Sample dissimiliarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, repsectively, 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 S4. Bray-Curtis dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the class level, grouped by reactor and operational day. Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		AE4			AE8			AE12			AE20		
		29	52	271	29	52	271	29	52	271	29	52	271
AE4	29	0											
	52	53	0										
	271	70	65	0									
AE8	29	24	51	69	0								
	52	41	39	73	41	0							
	271	63	55	20	61	63	0						
AE12	29	29	48	70	27	39	62	0					
	52	65	54	82	66	49	73	63	0				
	271	71	55	33	68	63	33	69	72	0			
AE20	29	35	50	78	41	43	68	36	55	69	0		
	52	46	44	79	46	29	68	42	45	68	42	0	
	271	64	56	51	62	57	42	62	68	43	65	59	0

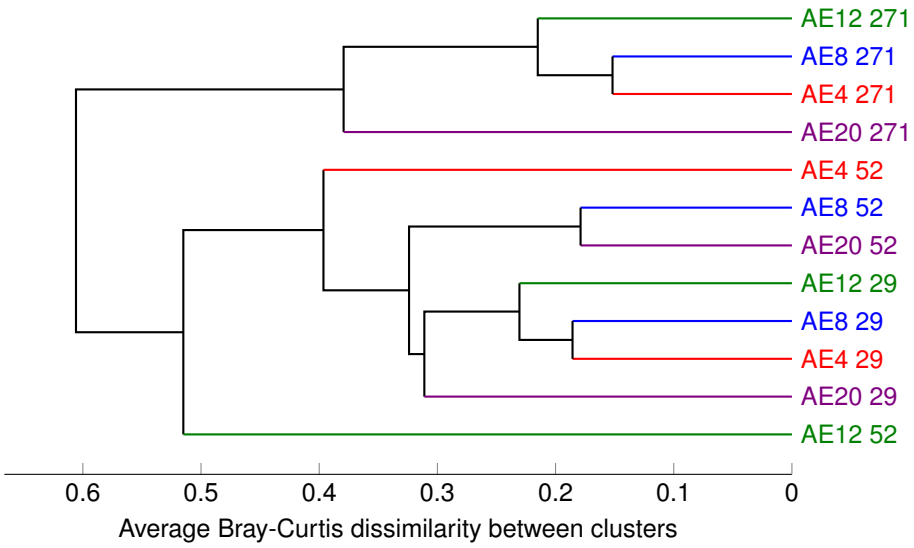

Figure S5. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the order level. Sample dissimiliarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, repsectively, 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 S5. Bray-Curtis dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the order level, grouped by reactor and operational day. Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		AE4			AE8			AE12			AE20		
		29	52	271	29	52	271	29	52	271	29	52	271
AE4	29	0											
	52	53	0										
	271	70	65	0									
AE8	29	24	51	69	0								
	52	41	39	73	41	0							
	271	63	55	20	61	63	0						
AE12	29	29	48	70	27	39	62	0					
	52	65	54	82	66	49	73	63	0				
	271	71	55	33	68	63	33	69	72	0			
AE20	29	35	50	78	41	43	68	36	55	69	0		
	52	46	44	79	46	29	68	42	45	68	42	0	
	271	64	56	51	62	57	42	62	68	43	65	59	0

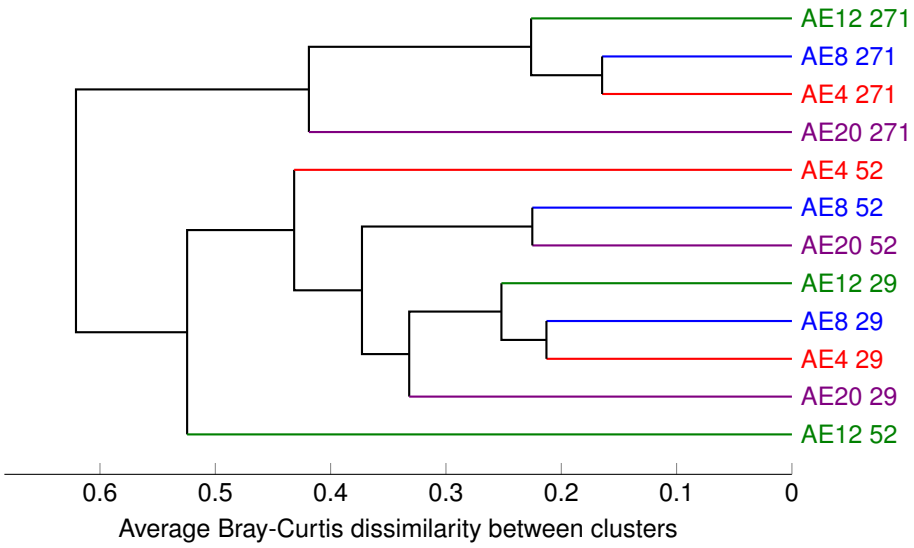

Figure S6. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the family level. Sample dissimiliarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, repsectively, 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 S6. Bray-Curtis dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the family level, grouped by reactor and operational day. Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		AE4			AE8			AE12			AE20		
		29	52	271	29	52	271	29	52	271	29	52	271
AE4	29	0											
	52	53	0										
	271	70	65	0									
AE8	29	24	51	69	0								
	52	41	39	73	41	0							
	271	63	55	20	61	63	0						
AE12	29	29	48	70	27	39	62	0					
	52	65	54	82	66	49	73	63	0				
	271	71	55	33	68	63	33	69	72	0			
AE20	29	35	50	78	41	43	68	36	55	69	0		
	52	46	44	79	46	29	68	42	45	68	42	0	
	271	64	56	51	62	57	42	62	68	43	65	59	0

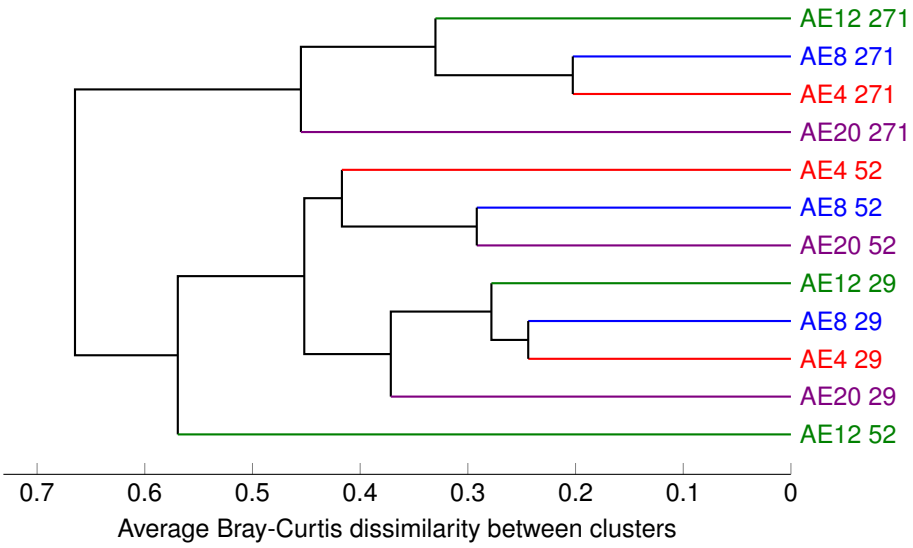

Figure S7. Hierarchical agglomerative cluster analysis of the samples with phylotypes identified using the EUB primer set at the genus level. Sample dissimiliarity was quantified according to Bray-Curtis (given by $1 - 2 \cdot \frac{\sum_{i=0}^{n} \min(A_i, B_i)}{\sum_{i=0}^{n} A_i + B_i}$ where A_i and B_i are the number of joined sequences assigned to phylotype i in samples A and B, repsectively, 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 S7. Bray-Curtis dissimilarity matrix for samples with phylotypes identified using the EUB primer set at the genus level, grouped by reactor and operational day. Dissimilarity values have been multiplied by 100 to yield the percent dissimilarity.

		AE4			AE8			AE12			AE20		
		29	52	271	29	52	271	29	52	271	29	52	271
AE4	29	0											
	52	53	0										
	271	70	65	0									
AE8	29	24	51	69	0								
	52	41	39	73	41	0							
	271	63	55	20	61	63	0						
AE12	29	29	48	70	27	39	62	0					
	52	65	54	82	66	49	73	63	0				
	271	71	55	33	68	63	33	69	72	0			
AE20	29	35	50	78	41	43	68	36	55	69	0		
	52	46	44	79	46	29	68	42	45	68	42	0	
	271	64	56	51	62	57	42	62	68	43	65	59	0

Taxonomic hierarchy with relative abundance

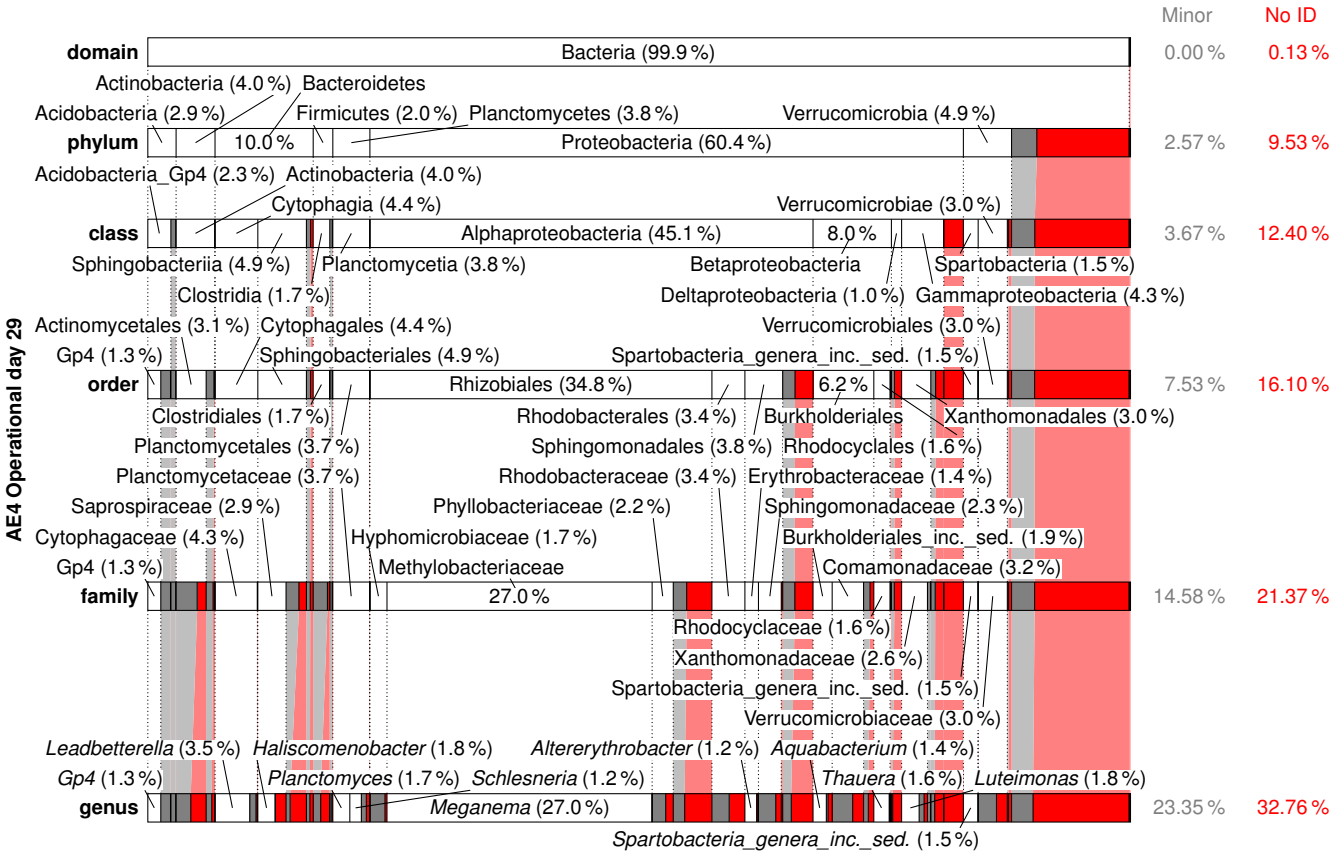

Figure S8. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE4 operational day 29. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

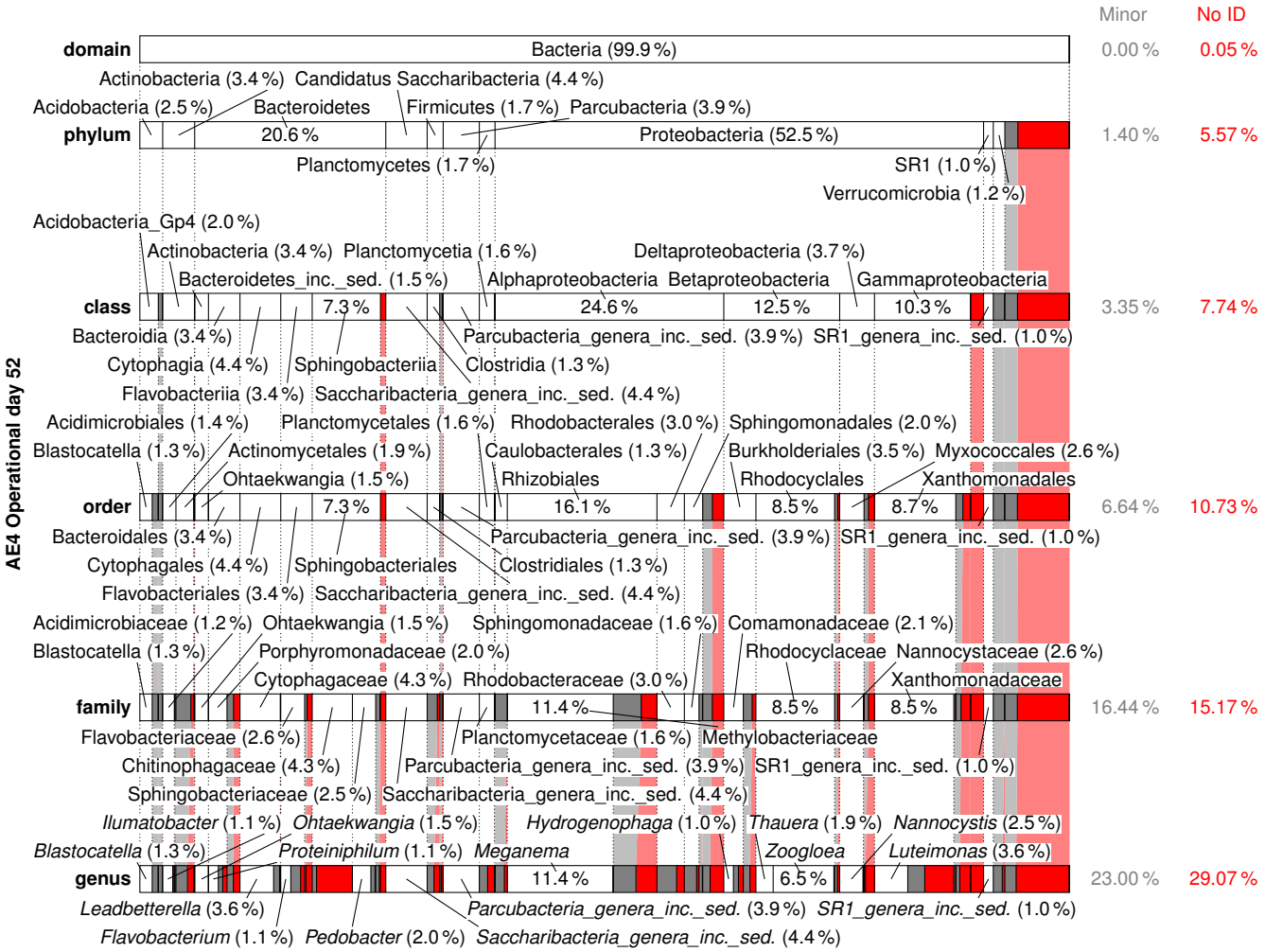

Figure S9. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE4 operational day 52. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

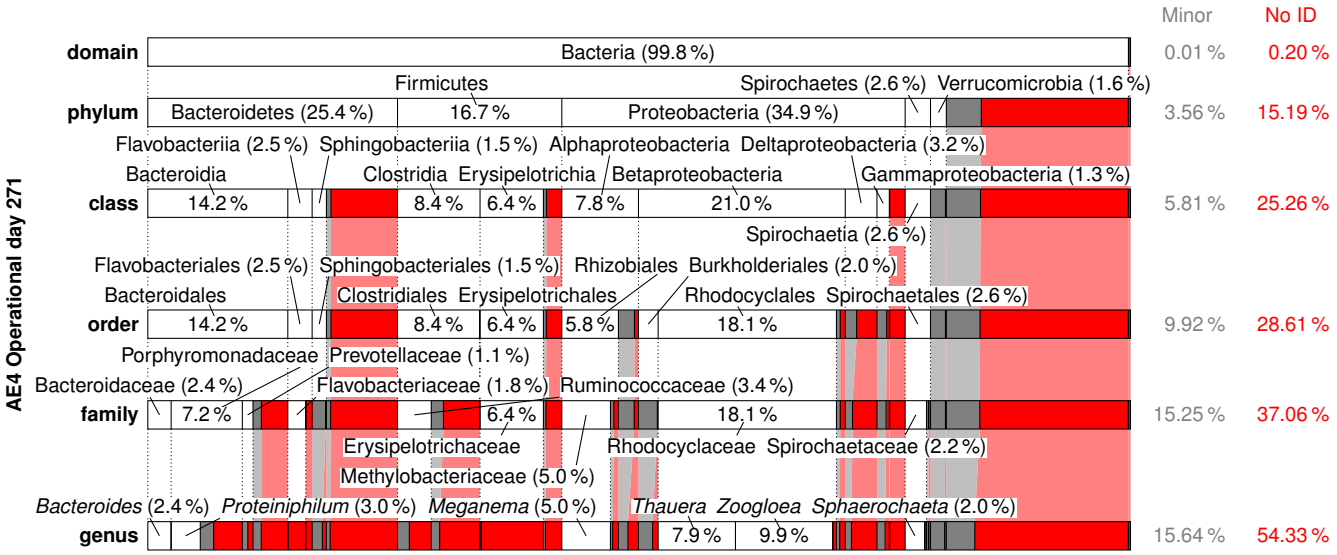

Figure S10. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE4 operational day 271. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

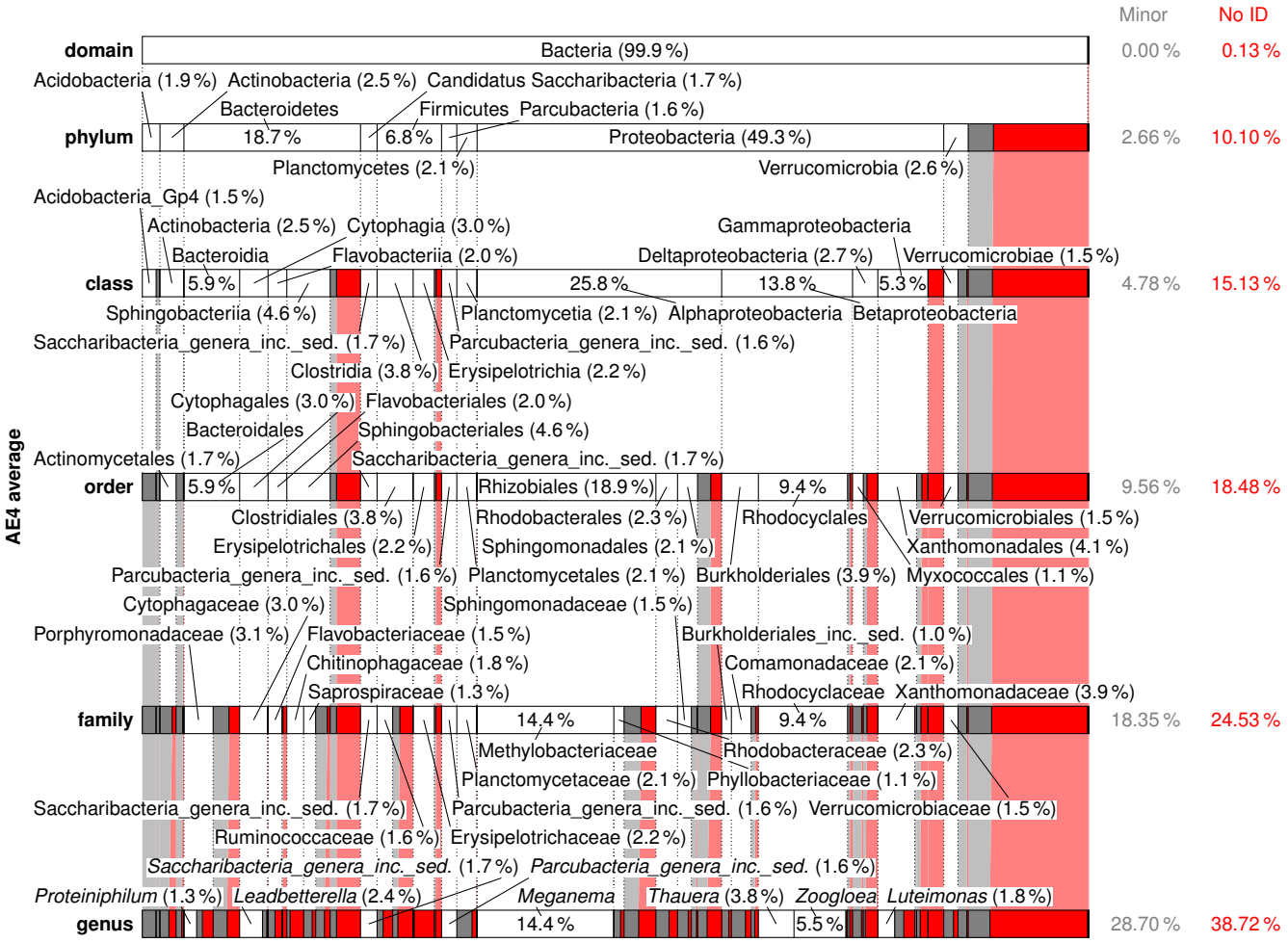

Figure S11. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE4. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", 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.

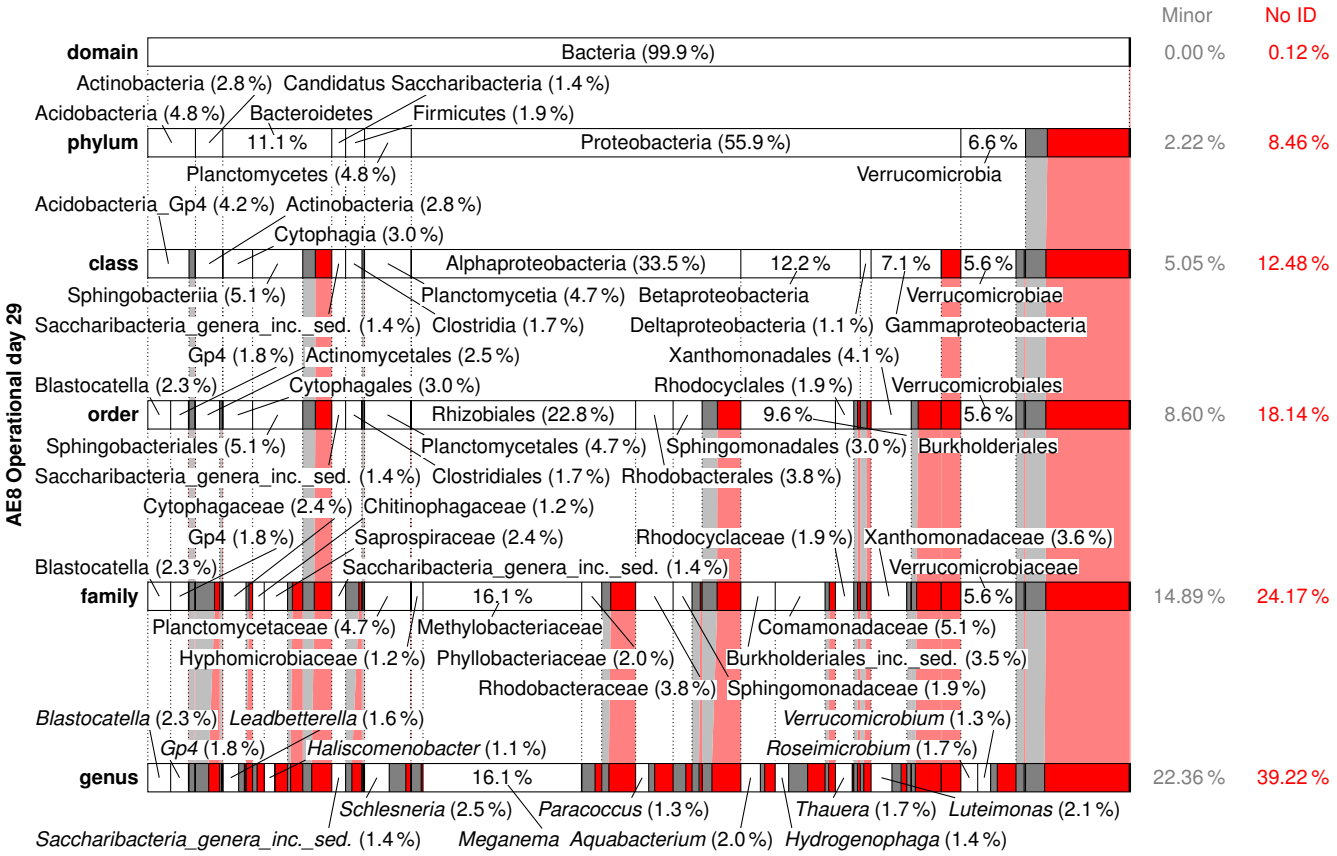

Figure S12. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE8 operational day 29. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

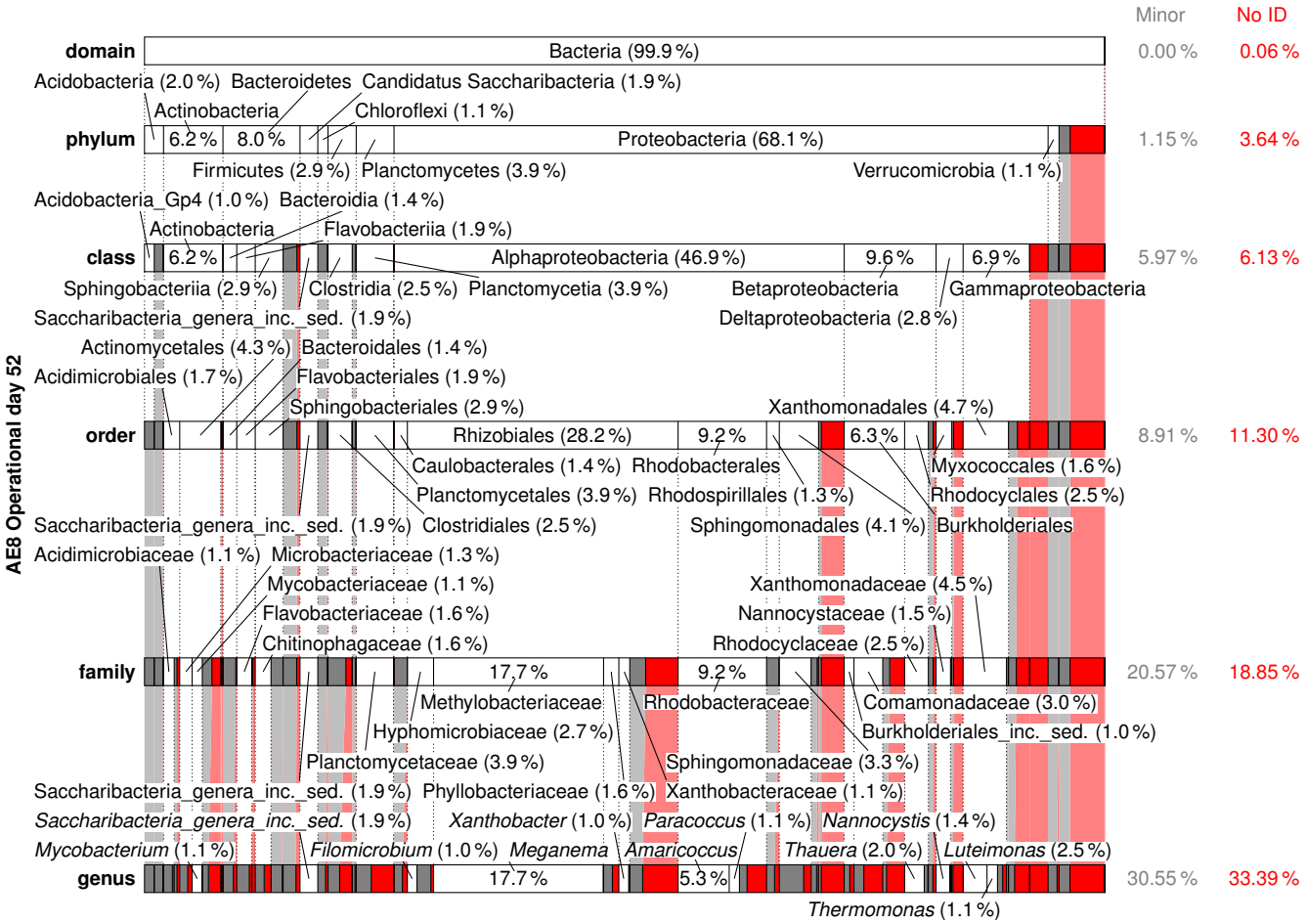

Figure S13. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE8 operational day 52. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

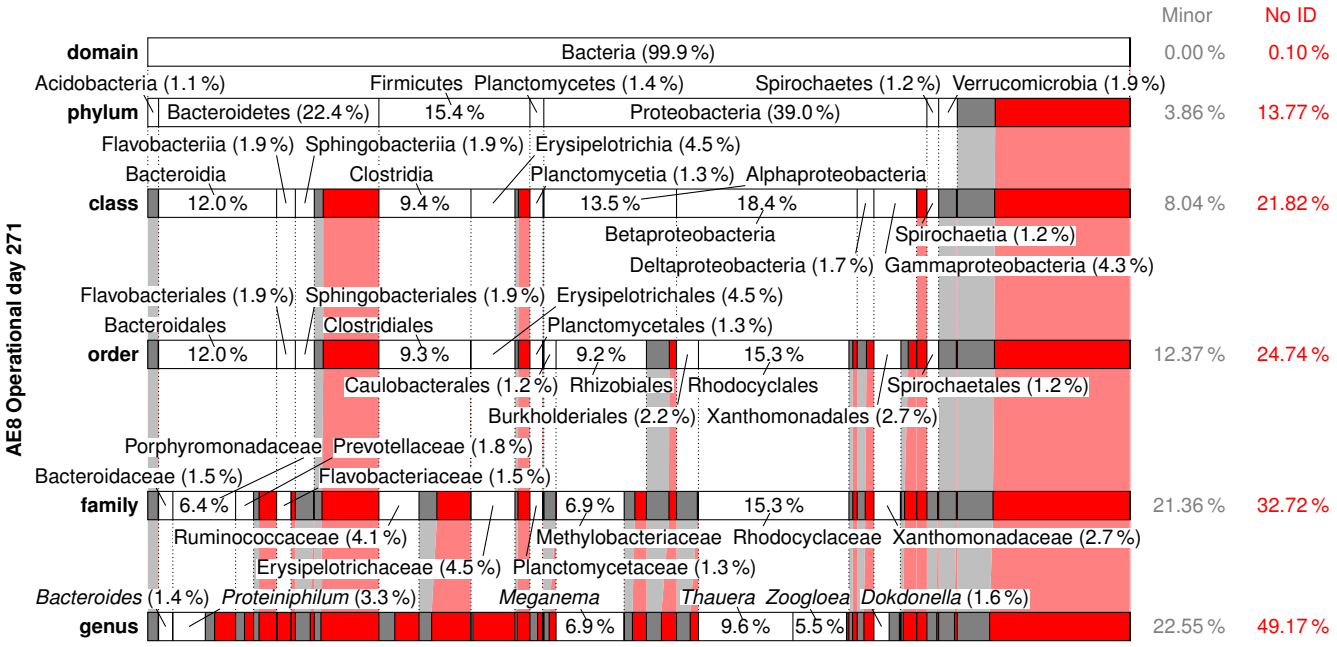

Figure S14. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE8 operational day 271. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

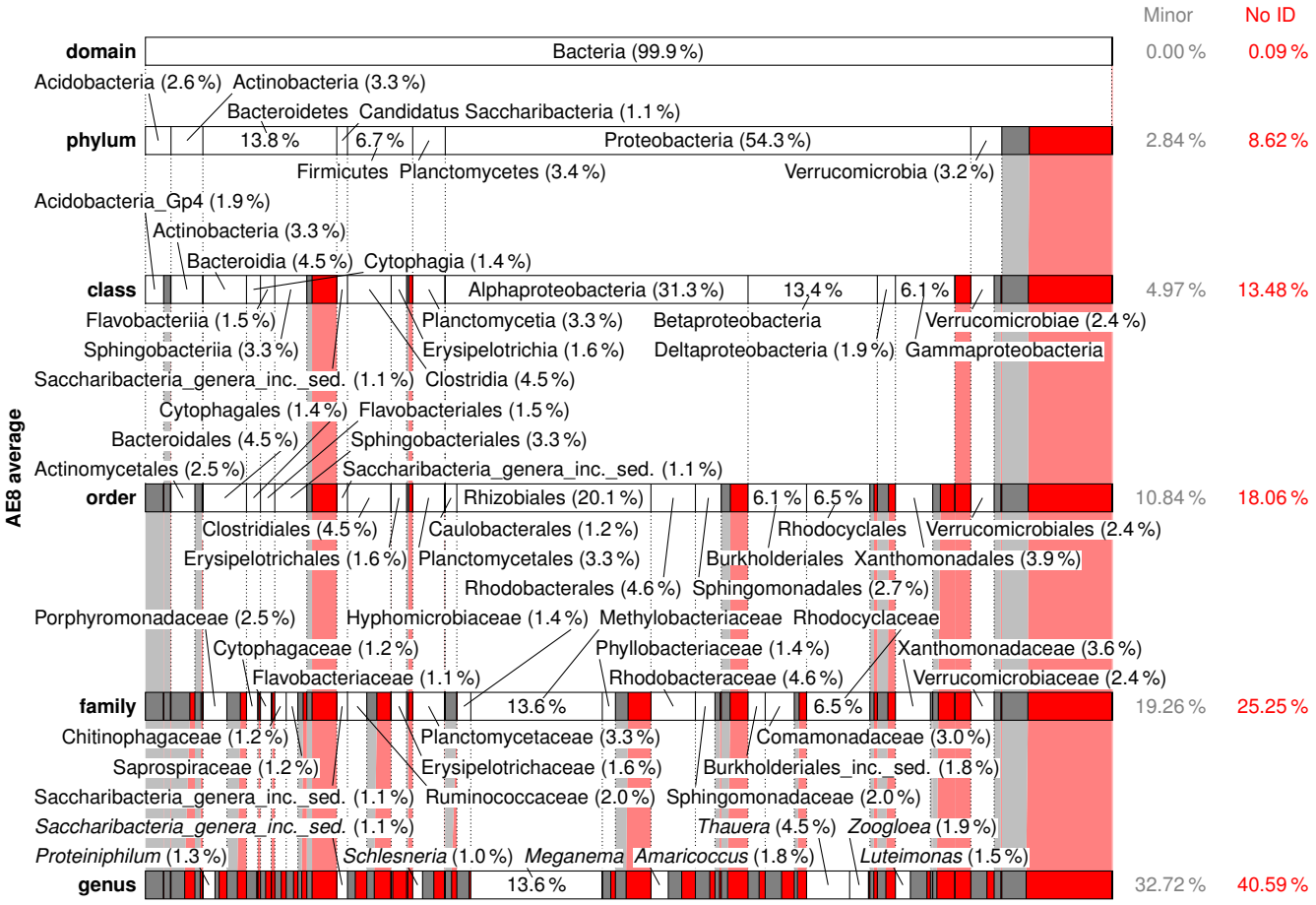

Figure S15. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE8. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", 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.

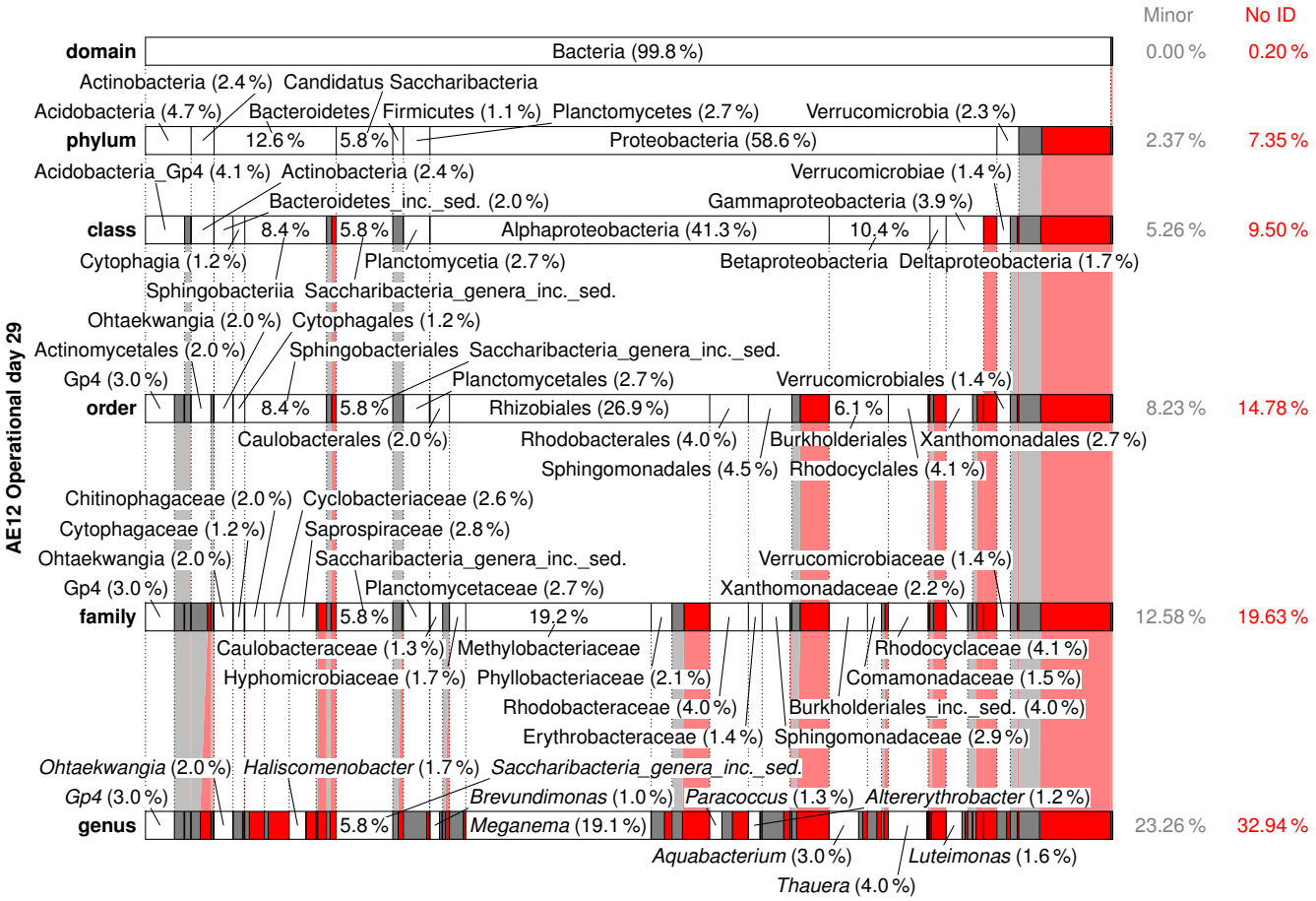

Figure S16. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE12 operational day 29. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

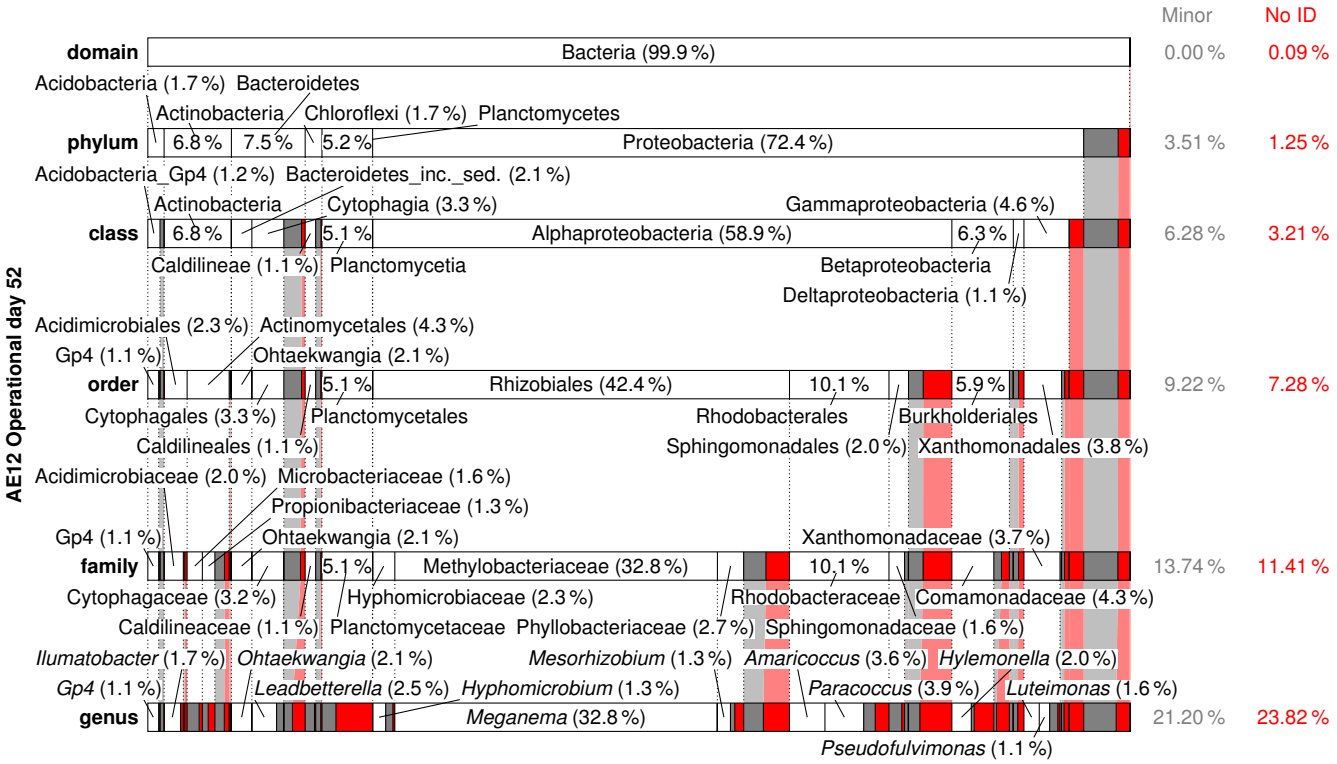

Figure S17. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE12 operational day 52. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

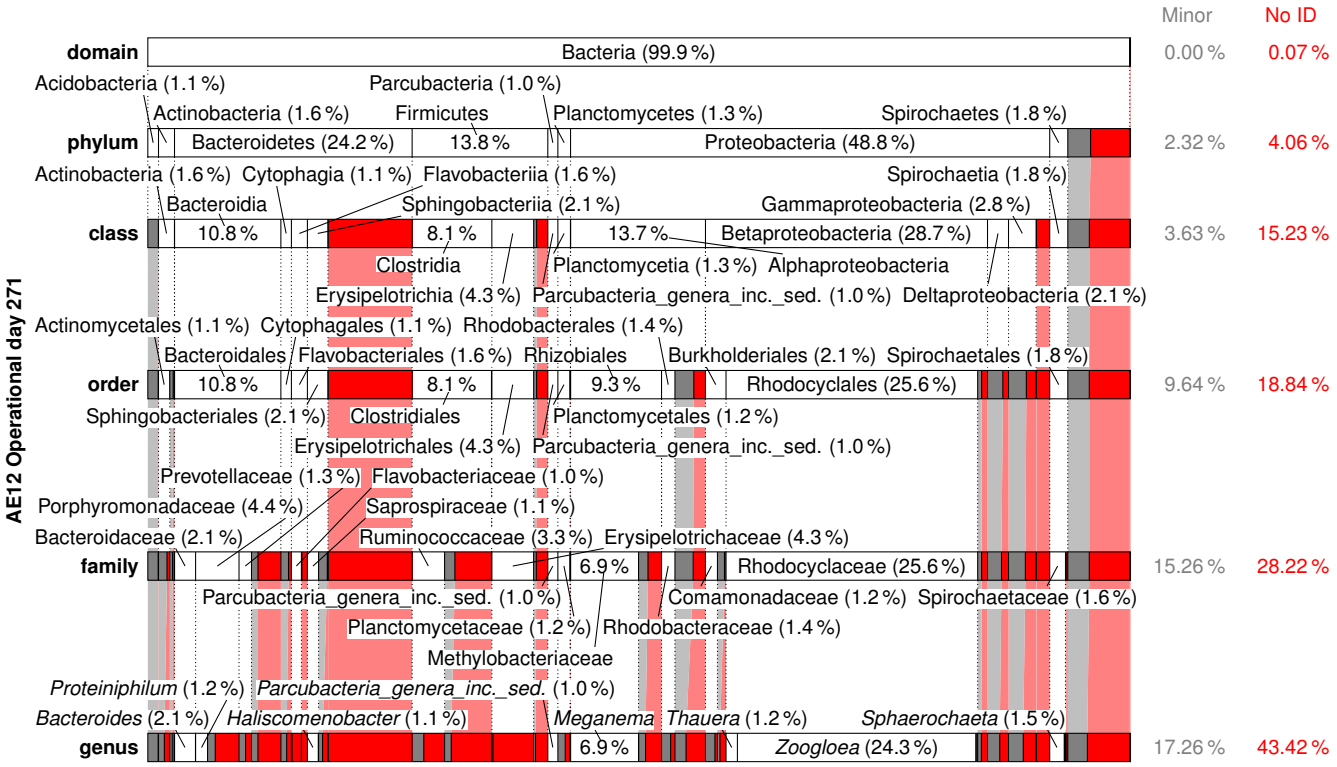

Figure S18. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE12 operational day 271. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

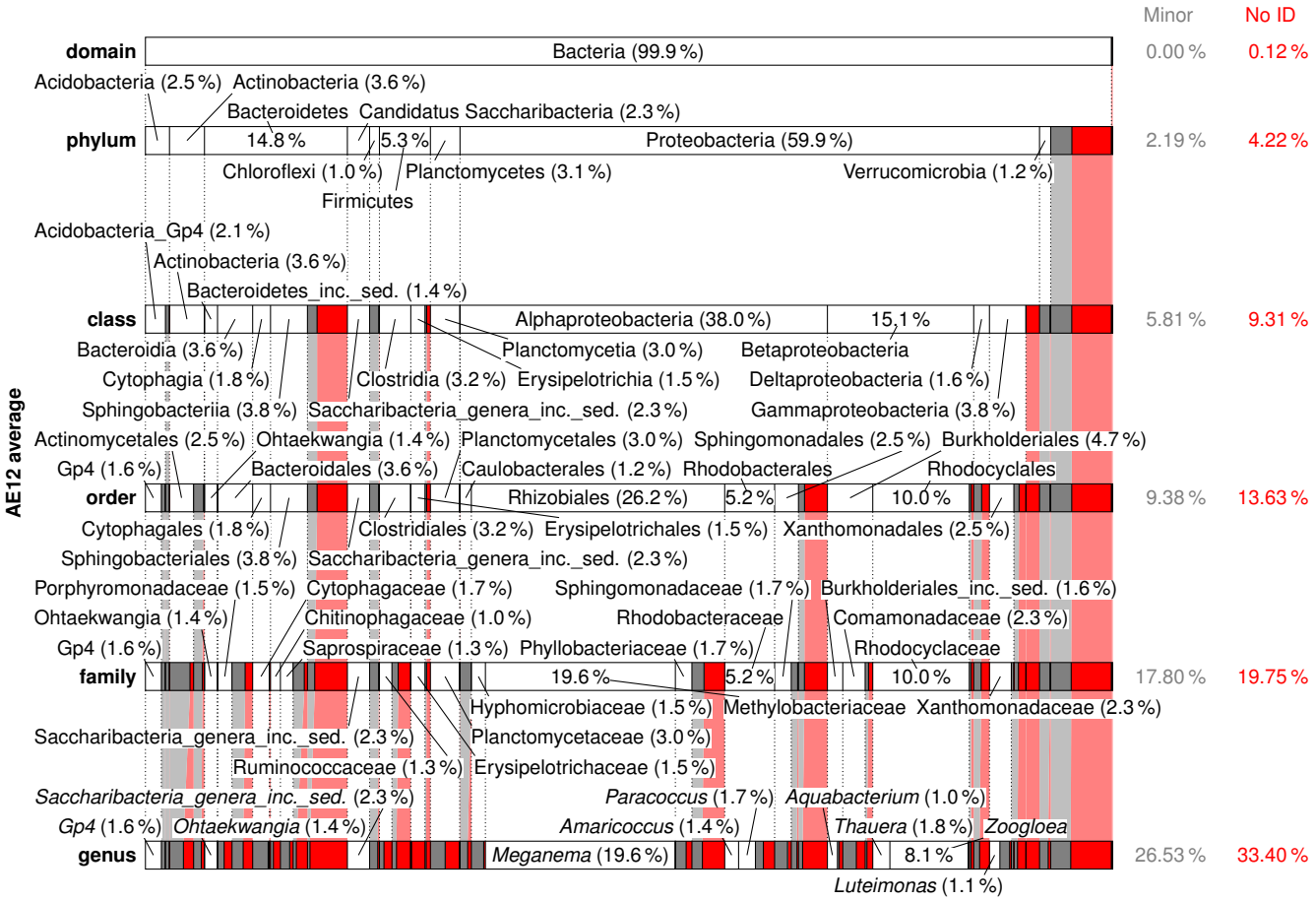

Figure S19. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE12. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", 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.

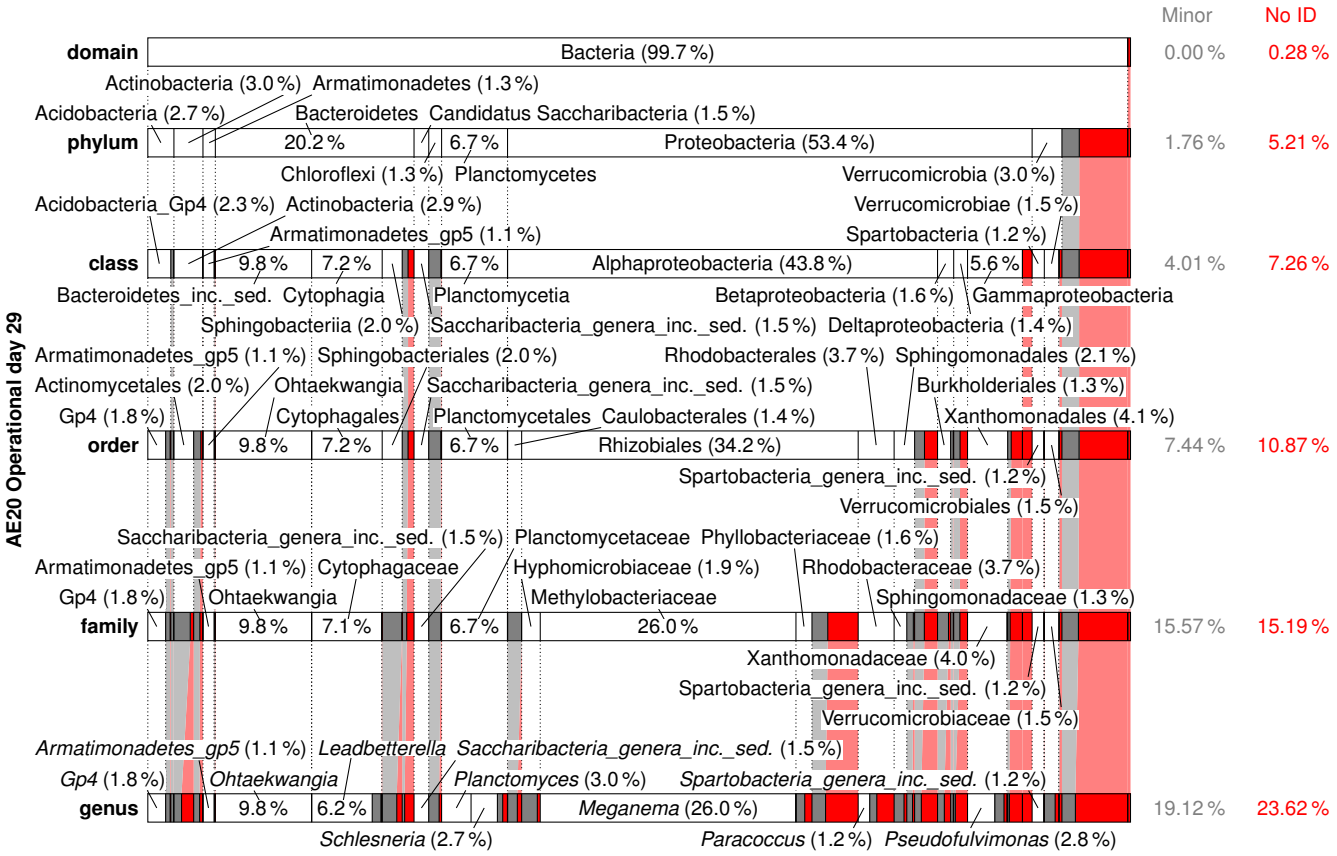

Figure S20. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE20 operational day 29. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

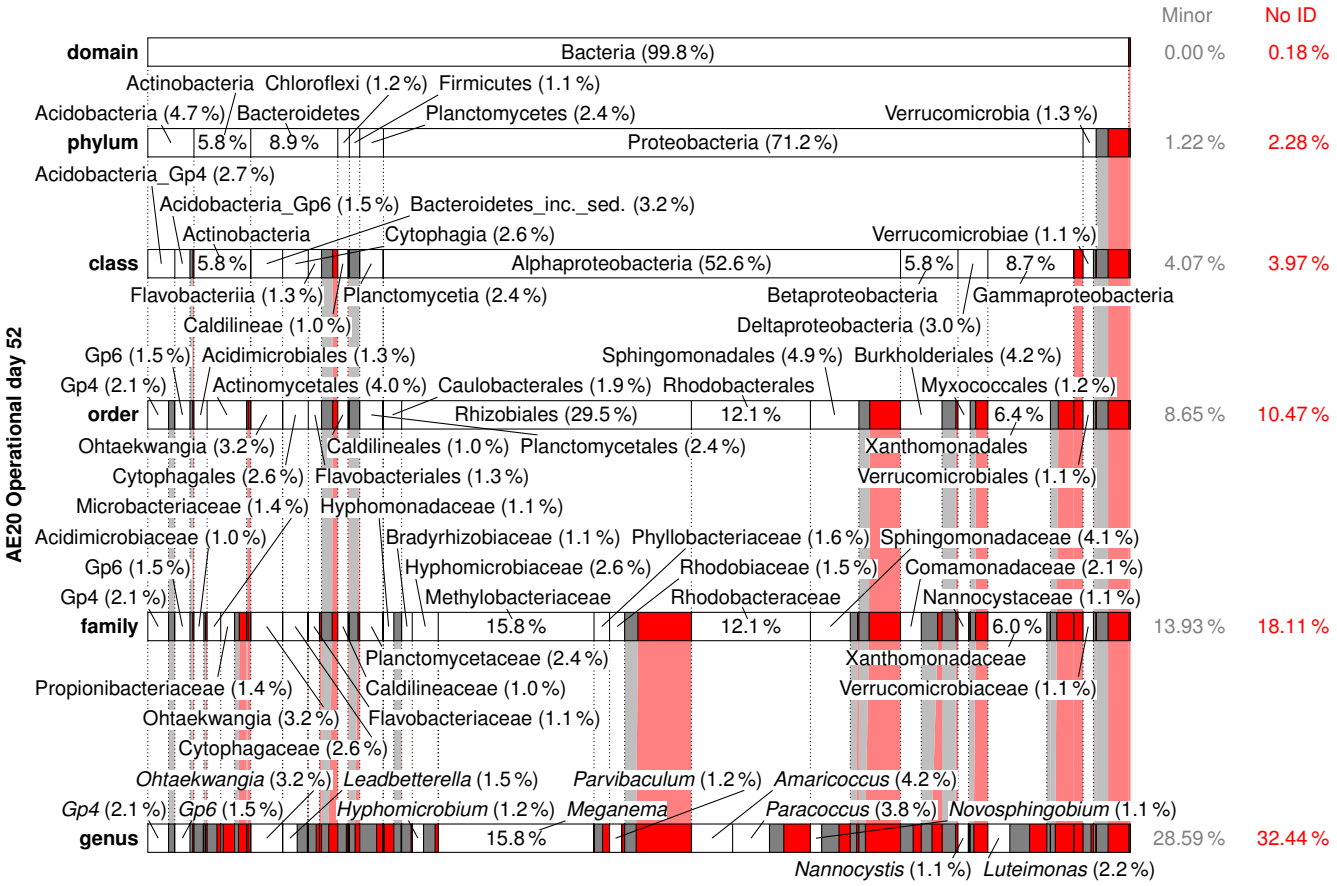

Figure S21. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE20 operational day 52. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

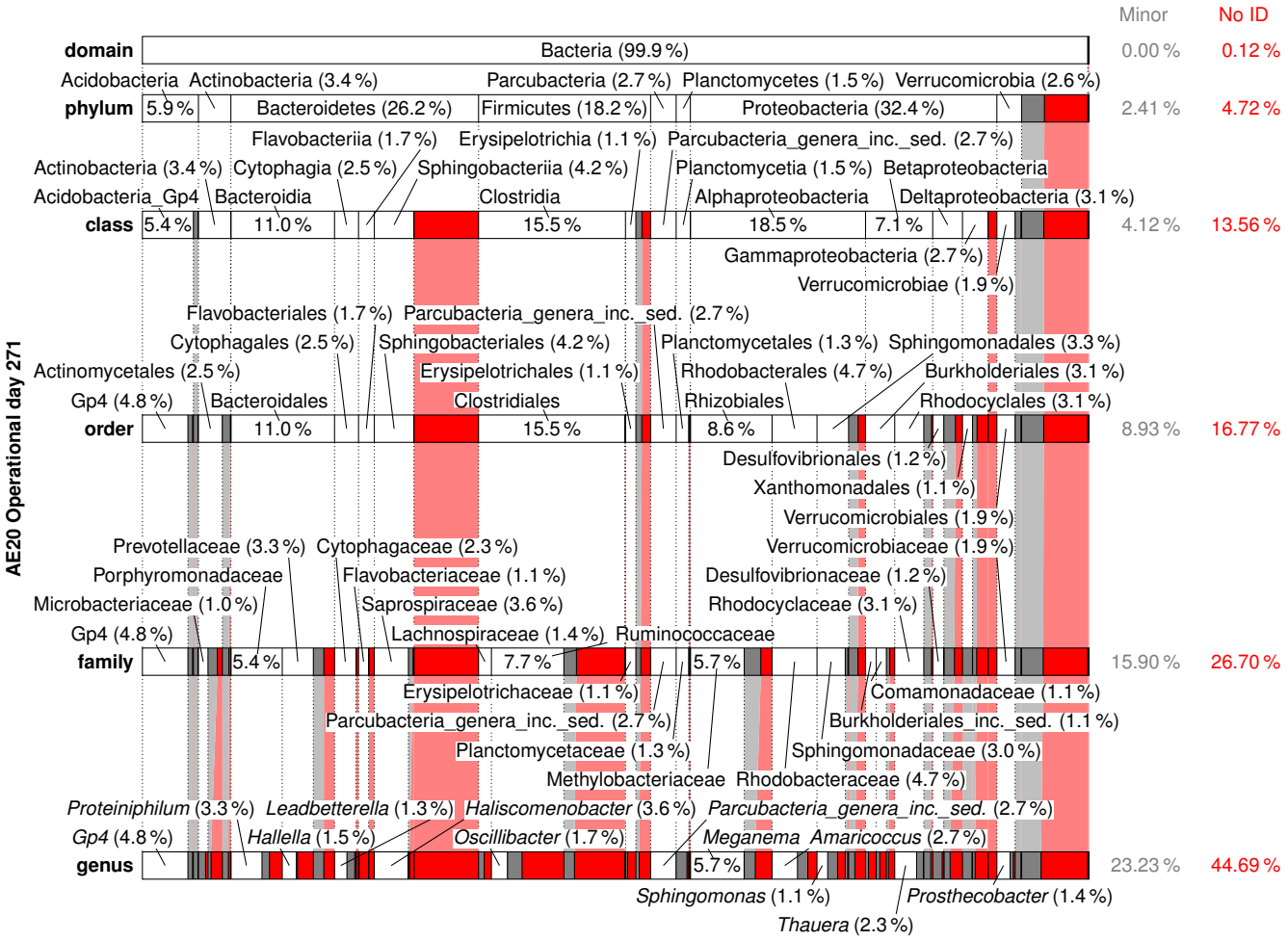

Figure S22. Relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE20 operational day 271. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "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.

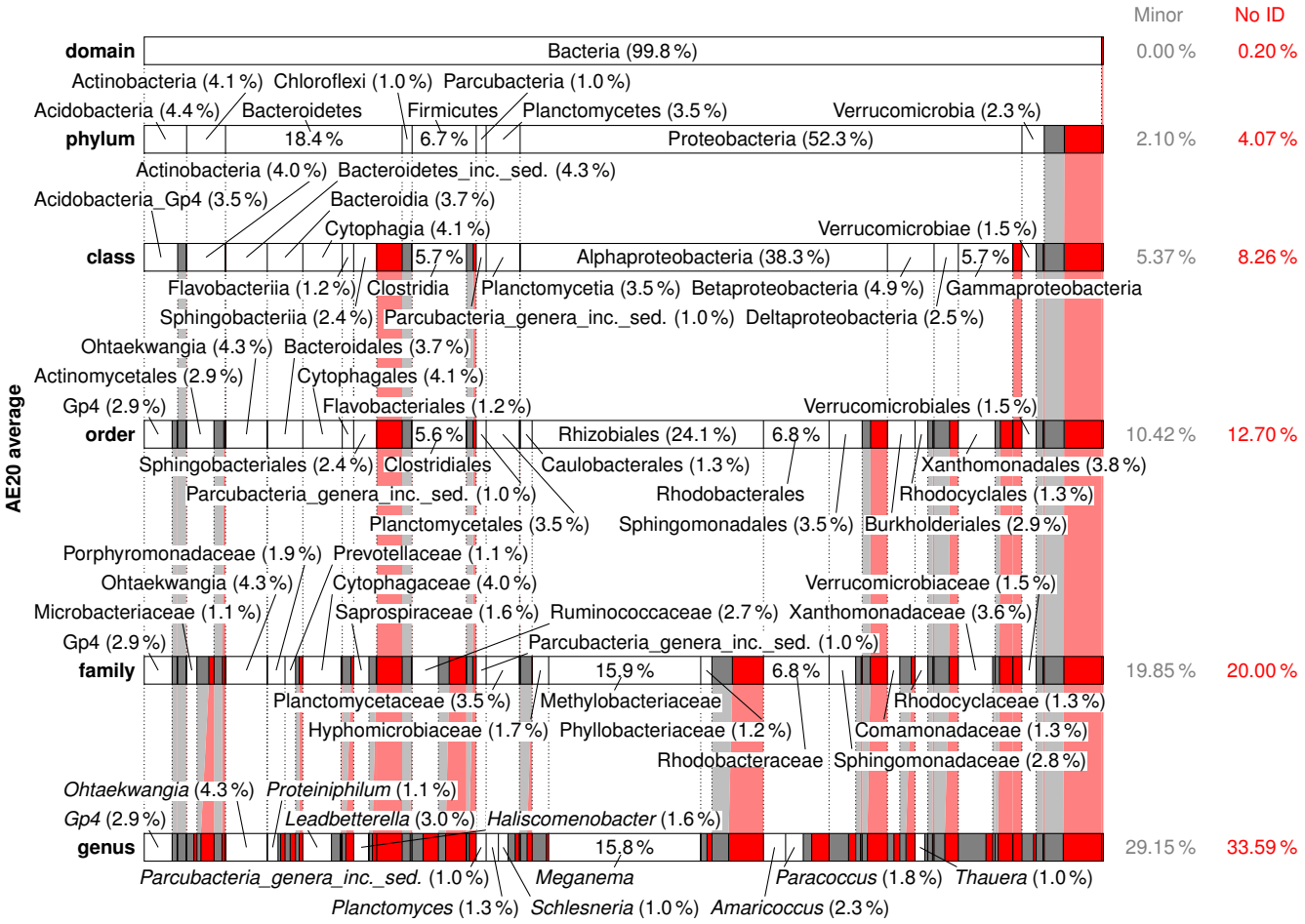

Figure S23. Average relative abundance and taxonomic classification of the 16S rRNA gene sequencing EUB primer set results for AE20. Phylotypes which were not identified or those whose identification at a specific taxonomic level did not exceed the bootstrap threshold were aggregated, denoted "No ID", 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 S8. AE4 domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Bacteria	99.9	99.9	99.8	99.9	$\pm 8.01 \cdot 10^{-2}$
Minor phylotypes (2)[e]	$1.32 \cdot 10^{-1}$	$5.20 \cdot 10^{-2}$	$2.12 \cdot 10^{-1}$	$1.32 \cdot 10^{-1}$	$\pm 8.01 \cdot 10^{-2}$

[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] 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 S9. AE4 phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Proteobacteria	60.4	52.5	34.9	49.3	± 13.0
Bacteroidetes	9.99	20.6	25.4	18.7	± 7.88
unknown	9.40	5.51	15.0	9.96	± 4.75
d: *Bacteria*					
Firmicutes	2.00	1.72	16.7	6.81	± 8.58
Verrucomicrobia	4.90	1.24	1.61	2.59	± 2.02
Actinobacteria	3.96	3.44	$1.98 \cdot 10^{-1}$	2.53	± 2.04
Planctomycetes	3.77	1.69	$9.66 \cdot 10^{-1}$	2.14	± 1.46
Acidobacteria	2.88	2.46	$2.51 \cdot 10^{-1}$	1.86	± 1.41
Candidatus Saccharibacteria	$7.65 \cdot 10^{-1}$	4.45	$3.52 \cdot 10^{-2}$	1.75	± 2.37
Parcubacteria	$8.43 \cdot 10^{-2}$	3.89	$8.59 \cdot 10^{-1}$	1.61	± 2.01
Minor phylotypes (35)[e]	1.70	1.28	1.46	1.48	$\pm 2.10 \cdot 10^{-1}$
Spirochaetes	$1.51 \cdot 10^{-1}$	$1.72 \cdot 10^{-1}$	2.58	$9.68 \cdot 10^{-1}$	± 1.40
SR1	$3.44 \cdot 10^{-3}$	1.04	N. D.	$3.49 \cdot 10^{-1}$	$\pm 6.02 \cdot 10^{-1}$

[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 S10. AE4 class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Alphaproteobacteria	45.1	24.6	7.80	25.8	± 18.7
Betaproteobacteria	7.98	12.5	21.0	13.8	± 6.64
unknown d: *Bacteria*	9.40	5.51	15.0	9.96	± 4.75
Bacteroidia	$2.15 \cdot 10^{-2}$	3.39	14.2	5.88	± 7.43
Gammaproteobacteria	4.29	10.3	1.26	5.29	± 4.62
Sphingobacteriia	4.94	7.34	1.45	4.58	± 2.96
Clostridia	1.69	1.35	8.40	3.81	± 3.98
Cytophagia	4.36	4.39	$2.57 \cdot 10^{-1}$	3.00	± 2.38
Deltaproteobacteria	1.04	3.74	3.23	2.67	± 1.44
Minor phylotypes (80)[e]	2.78	2.33	2.74	2.62	± $2.50 \cdot 10^{-1}$
unknown p: *Bacteroidetes*	$2.71 \cdot 10^{-1}$	$5.75 \cdot 10^{-1}$	6.77	2.54	± 3.67
Actinobacteria	3.95	3.43	$1.97 \cdot 10^{-1}$	2.52	± 2.03
Erysipelotrichia	$1.45 \cdot 10^{-1}$	$1.14 \cdot 10^{-1}$	6.45	2.24	± 3.65
Planctomycetia	3.77	1.65	$9.51 \cdot 10^{-1}$	2.12	± 1.47
Flavobacteriia	$8.60 \cdot 10^{-2}$	3.38	2.48	1.98	± 1.70
Saccharibacteria_genera_inc._sed.[f]	$7.65 \cdot 10^{-1}$	4.45	$3.52 \cdot 10^{-2}$	1.75	± 2.37
unknown p: *Proteobacteria*	1.99	1.39	1.57	1.65	± $3.06 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$8.43 \cdot 10^{-2}$	3.89	$8.59 \cdot 10^{-1}$	1.61	± 2.01
Verrucomicrobiae	2.97	$6.79 \cdot 10^{-1}$	$8.69 \cdot 10^{-1}$	1.51	± 1.27
Acidobacteria_Gp4	2.35	1.98	$4.19 \cdot 10^{-2}$	1.46	± 1.24
Spirochaetia	$1.51 \cdot 10^{-1}$	$1.72 \cdot 10^{-1}$	2.58	$9.68 \cdot 10^{-1}$	± 1.40
Bacteroidetes_inc._sed.[f]	$3.11 \cdot 10^{-1}$	1.48	$2.11 \cdot 10^{-1}$	$6.68 \cdot 10^{-1}$	± $7.07 \cdot 10^{-1}$
Spartobacteria	1.50	$2.04 \cdot 10^{-1}$	$2.86 \cdot 10^{-2}$	$5.79 \cdot 10^{-1}$	± $8.07 \cdot 10^{-1}$
unknown p: *Firmicutes*	$5.33 \cdot 10^{-2}$	$9.88 \cdot 10^{-2}$	1.57	$5.73 \cdot 10^{-1}$	± $8.61 \cdot 10^{-1}$
SR1_genera_inc._sed.[f]	$3.44 \cdot 10^{-3}$	1.04	N. D.	$3.49 \cdot 10^{-1}$	± $6.02 \cdot 10^{-1}$

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

Table S11. AE4 order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Rhizobiales	34.8	16.1	5.76	18.9	± 14.7
unknown d: *Bacteria*	9.40	5.51	15.0	9.96	± 4.75
Rhodocyclales	1.65	8.46	18.1	9.42	± 8.29
Bacteroidales	$2.15 \cdot 10^{-2}$	3.39	14.2	5.88	± 7.43
Minor phylotypes (174)[e]	5.32	6.12	5.17	5.54	± $5.07 \cdot 10^{-1}$
Sphingobacteriales	4.94	7.34	1.45	4.58	± 2.96
Xanthomonadales	2.97	8.74	$5.79 \cdot 10^{-1}$	4.10	± 4.20
Burkholderiales	6.19	3.46	2.00	3.88	± 2.13
Clostridiales	1.68	1.35	8.36	3.80	± 3.96
Cytophagales	4.36	4.39	$2.57 \cdot 10^{-1}$	3.00	± 2.38
unknown p: *Bacteroidetes*	$2.71 \cdot 10^{-1}$	$5.75 \cdot 10^{-1}$	6.77	2.54	± 3.67
Rhodobacterales	3.36	2.95	$5.59 \cdot 10^{-1}$	2.29	± 1.51
Erysipelotrichales	$1.45 \cdot 10^{-1}$	$1.14 \cdot 10^{-1}$	6.45	2.24	± 3.65
Sphingomonadales	3.85	1.98	$5.16 \cdot 10^{-1}$	2.11	± 1.67
Planctomycetales	3.74	1.63	$9.25 \cdot 10^{-1}$	2.10	± 1.46
Flavobacteriales	$8.60 \cdot 10^{-2}$	3.38	2.48	1.98	± 1.70
Saccharibacteria_genera_inc._sed.[f]	$7.65 \cdot 10^{-1}$	4.45	$3.52 \cdot 10^{-2}$	1.75	± 2.37
Actinomycetales	3.06	1.91	$1.34 \cdot 10^{-1}$	1.70	± 1.47
unknown p: *Proteobacteria*	1.99	1.39	1.57	1.65	± $3.06 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$8.43 \cdot 10^{-2}$	3.89	$8.59 \cdot 10^{-1}$	1.61	± 2.01
Verrucomicrobiales	2.97	$6.79 \cdot 10^{-1}$	$8.69 \cdot 10^{-1}$	1.51	± 1.27
unknown c: *Alphaproteobacteria*	1.83	1.22	$4.09 \cdot 10^{-1}$	1.15	± $7.14 \cdot 10^{-1}$
unknown c: *Deltaproteobacteria*	$7.23 \cdot 10^{-1}$	$6.44 \cdot 10^{-1}$	2.07	1.15	± $8.01 \cdot 10^{-1}$
Myxococcales	$6.37 \cdot 10^{-2}$	2.62	$7.20 \cdot 10^{-1}$	1.13	± 1.33
Spirochaetales	$1.51 \cdot 10^{-1}$	$1.72 \cdot 10^{-1}$	2.58	$9.68 \cdot 10^{-1}$	± 1.40
Blastocatella	$9.90 \cdot 10^{-1}$	1.33	$1.90 \cdot 10^{-3}$	$7.74 \cdot 10^{-1}$	± $6.90 \cdot 10^{-1}$
Caulobacterales	$6.88 \cdot 10^{-1}$	1.32	$2.32 \cdot 10^{-1}$	$7.47 \cdot 10^{-1}$	± $5.46 \cdot 10^{-1}$
Acidimicrobiales	$7.34 \cdot 10^{-1}$	1.42	$3.14 \cdot 10^{-2}$	$7.30 \cdot 10^{-1}$	± $6.96 \cdot 10^{-1}$
Ohtaekwangia	$3.11 \cdot 10^{-1}$	1.48	$2.09 \cdot 10^{-1}$	$6.68 \cdot 10^{-1}$	± $7.07 \cdot 10^{-1}$
Gp4	1.32	$6.40 \cdot 10^{-1}$	$4.00 \cdot 10^{-2}$	$6.67 \cdot 10^{-1}$	± $6.40 \cdot 10^{-1}$
Spartobacteria_genera_inc._sed.[f]	1.49	$2.01 \cdot 10^{-1}$	$2.76 \cdot 10^{-2}$	$5.74 \cdot 10^{-1}$	± $8.00 \cdot 10^{-1}$
unknown p: *Firmicutes*	$5.33 \cdot 10^{-2}$	$9.88 \cdot 10^{-2}$	1.57	$5.73 \cdot 10^{-1}$	± $8.61 \cdot 10^{-1}$

Table S11. AE4 order-level EUB results summary continued.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
SR1_genera_inc._sed.[f]	$3.44 \cdot 10^{-3}$	1.04	N. D.	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$

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

Table S12. AE4 family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
Methylobacteriaceae	27.0	11.4	4.95	14.4	±	11.3
Minor phylotypes (370)[e]	14.5	13.5	9.97	12.6	±	2.36
unknown	9.40	5.51	15.0	9.96	±	4.75
d: *Bacteria*						
Rhodocyclaceae	1.65	8.46	18.1	9.42	±	8.29
Xanthomonadaceae	2.63	8.53	$5.56 \cdot 10^{-1}$	3.91	±	4.14
Porphyromonadaceae	$1.12 \cdot 10^{-2}$	1.99	7.24	3.08	±	3.74
Cytophagaceae	4.31	4.34	$1.99 \cdot 10^{-1}$	2.95	±	2.38
unknown	$2.71 \cdot 10^{-1}$	$5.75 \cdot 10^{-1}$	6.77	2.54	±	3.67
p: *Bacteroidetes*						
Rhodobacteraceae	3.36	2.95	$5.59 \cdot 10^{-1}$	2.29	±	1.51
Erysipelotrichaceae	$1.45 \cdot 10^{-1}$	$1.14 \cdot 10^{-1}$	6.45	2.24	±	3.65
Planctomycetaceae	3.74	1.63	$9.25 \cdot 10^{-1}$	2.10	±	1.46
Comamonadaceae	3.20	2.10	$9.49 \cdot 10^{-1}$	2.08	±	1.12
Chitinophagaceae	$5.89 \cdot 10^{-1}$	4.32	$4.18 \cdot 10^{-1}$	1.78	±	2.21
Saccharibacteria_genera_inc._sed.[f]	$7.65 \cdot 10^{-1}$	4.45	$3.52 \cdot 10^{-2}$	1.75	±	2.37
unknown	1.99	1.39	1.57	1.65	±	$3.06 \cdot 10^{-1}$
p: *Proteobacteria*						
Ruminococcaceae	$8.48 \cdot 10^{-1}$	$6.61 \cdot 10^{-1}$	3.43	1.65	±	1.55
Parcubacteria_genera_inc._sed.[f]	$8.43 \cdot 10^{-2}$	3.89	$8.59 \cdot 10^{-1}$	1.61	±	2.01
unknown	2.57	1.69	$4.65 \cdot 10^{-1}$	1.58	±	1.06
o: *Rhizobiales*						
Verrucomicrobiaceae	2.97	$6.79 \cdot 10^{-1}$	$8.69 \cdot 10^{-1}$	1.51	±	1.27
Flavobacteriaceae	$3.10 \cdot 10^{-2}$	2.57	1.83	1.48	±	1.31

Table S12. AE4 family-level EUB results summary continued.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
Sphingomonadaceae	2.32	1.58	$4.77 \cdot 10^{-1}$	1.46	±	$9.27 \cdot 10^{-1}$
unknown	$2.31 \cdot 10^{-1}$	$2.57 \cdot 10^{-1}$	3.69	1.39	±	1.99
o: *Clostridiales*						
Saprospiraceae	2.87	$3.84 \cdot 10^{-1}$	$5.64 \cdot 10^{-1}$	1.27	±	1.39
unknown	1.83	1.22	$4.09 \cdot 10^{-1}$	1.15	±	$7.14 \cdot 10^{-1}$
c: *Alphaproteobacteria*						
unknown	$7.23 \cdot 10^{-1}$	$6.44 \cdot 10^{-1}$	2.07	1.15	±	$8.01 \cdot 10^{-1}$
c: *Deltaproteobacteria*						
unknown	$5.16 \cdot 10^{-3}$	$6.89 \cdot 10^{-1}$	2.69	1.13	±	1.40
o: *Bacteroidales*						
Phyllobacteriaceae	2.15	$9.57 \cdot 10^{-1}$	$1.36 \cdot 10^{-1}$	1.08	±	1.01
Burkholderiales_inc._sed.[f]	1.95	$3.46 \cdot 10^{-1}$	$7.93 \cdot 10^{-1}$	1.03	±	$8.27 \cdot 10^{-1}$
Bacteroidaceae	$4.30 \cdot 10^{-3}$	$5.98 \cdot 10^{-1}$	2.37	$9.92 \cdot 10^{-1}$	±	1.23
Nannocystaceae	$8.60 \cdot 10^{-4}$	2.56	$2.31 \cdot 10^{-1}$	$9.31 \cdot 10^{-1}$	±	1.42
Sphingobacteriaceae	$1.14 \cdot 10^{-1}$	2.51	$1.39 \cdot 10^{-1}$	$9.19 \cdot 10^{-1}$	±	1.37
Hyphomicrobiaceae	1.74	$9.12 \cdot 10^{-1}$	$1.04 \cdot 10^{-1}$	$9.18 \cdot 10^{-1}$	±	$8.18 \cdot 10^{-1}$
Blastocatella	$9.90 \cdot 10^{-1}$	1.33	$1.90 \cdot 10^{-3}$	$7.74 \cdot 10^{-1}$	±	$6.90 \cdot 10^{-1}$
Spirochaetaceae	N. D.	$1.08 \cdot 10^{-1}$	2.17	$7.61 \cdot 10^{-1}$	±	1.23
Ohtaekwangia	$3.11 \cdot 10^{-1}$	1.48	$2.09 \cdot 10^{-1}$	$6.68 \cdot 10^{-1}$	±	$7.07 \cdot 10^{-1}$
Gp4	1.32	$6.40 \cdot 10^{-1}$	$4.00 \cdot 10^{-2}$	$6.67 \cdot 10^{-1}$	±	$6.40 \cdot 10^{-1}$
Erythrobacteraceae	1.38	$3.78 \cdot 10^{-1}$	$2.86 \cdot 10^{-2}$	$5.95 \cdot 10^{-1}$	±	$7.02 \cdot 10^{-1}$
Acidimicrobiaceae	$5.08 \cdot 10^{-1}$	1.25	$1.33 \cdot 10^{-2}$	$5.90 \cdot 10^{-1}$	±	$6.22 \cdot 10^{-1}$
Spartobacteria_genera_inc._sed.[f]	1.49	$2.01 \cdot 10^{-1}$	$2.76 \cdot 10^{-2}$	$5.74 \cdot 10^{-1}$	±	$8.00 \cdot 10^{-1}$
unknown	$5.33 \cdot 10^{-2}$	$9.88 \cdot 10^{-2}$	1.57	$5.73 \cdot 10^{-1}$	±	$8.61 \cdot 10^{-1}$
p: *Firmicutes*						
Prevotellaceae	N. D.	$8.87 \cdot 10^{-2}$	1.09	$3.91 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$
SR1_genera_inc._sed.[f]	$3.44 \cdot 10^{-3}$	1.04	N. D.	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$

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

Table S13. AE4 genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average ± %[d]	SD[c]
Minor phylotypes (1445)[e]	29.7	27.3	18.8	25.3	± 5.71
Meganema	27.0	11.4	4.95	14.4	± 11.3
unknown d: *Bacteria*	9.40	5.51	15.0	9.96	± 4.75
Zoogloea	$6.02 \cdot 10^{-3}$	6.54	9.90	5.48	± 5.03
Thauera	1.56	1.86	7.87	3.76	± 3.56
unknown p: *Bacteroidetes*	$2.71 \cdot 10^{-1}$	$5.75 \cdot 10^{-1}$	6.77	2.54	± 3.67
Leadbetterella	3.54	3.62	$8.38 \cdot 10^{-2}$	2.42	± 2.02
unknown f: *Erysipelotrichaceae*	$2.07 \cdot 10^{-2}$	$2.15 \cdot 10^{-2}$	6.32	2.12	± 3.64
Luteimonas	1.78	3.58	$9.52 \cdot 10^{-4}$	1.79	± 1.79
Saccharibacteria_genera_inc._sed.[f]	$7.65 \cdot 10^{-1}$	4.45	$3.52 \cdot 10^{-2}$	1.75	± 2.37
unknown p: *Proteobacteria*	1.99	1.39	1.57	1.65	± $3.06 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$8.43 \cdot 10^{-2}$	3.89	$8.59 \cdot 10^{-1}$	1.61	± 2.01
unknown o: *Rhizobiales*	2.57	1.69	$4.65 \cdot 10^{-1}$	1.58	± 1.06
unknown f: *Chitinophagaceae*	$4.07 \cdot 10^{-1}$	3.86	$4.47 \cdot 10^{-2}$	1.44	± 2.11
unknown o: *Clostridiales*	$2.31 \cdot 10^{-1}$	$2.57 \cdot 10^{-1}$	3.69	1.39	± 1.99
Proteiniphilum	$7.74 \cdot 10^{-3}$	1.05	2.96	1.34	± 1.50
unknown f: *Xanthomonadaceae*	$3.41 \cdot 10^{-1}$	3.12	$3.33 \cdot 10^{-2}$	1.17	± 1.70
unknown c: *Alphaproteobacteria*	1.83	1.22	$4.09 \cdot 10^{-1}$	1.15	± $7.14 \cdot 10^{-1}$
unknown c: *Deltaproteobacteria*	$7.23 \cdot 10^{-1}$	$6.44 \cdot 10^{-1}$	2.07	1.15	± $8.01 \cdot 10^{-1}$
unknown o: *Bacteroidales*	$5.16 \cdot 10^{-3}$	$6.89 \cdot 10^{-1}$	2.69	1.13	± 1.40
unknown f: *Porphyromonadaceae*	N. D.	$4.69 \cdot 10^{-1}$	2.92	1.13	± 1.57
unknown f: *Ruminococcaceae*	$5.13 \cdot 10^{-1}$	$2.86 \cdot 10^{-1}$	2.23	1.01	± 1.07
Bacteroides	$2.58 \cdot 10^{-3}$	$5.96 \cdot 10^{-1}$	2.36	$9.85 \cdot 10^{-1}$	± 1.22
Nannocystis	$8.60 \cdot 10^{-4}$	2.52	$2.21 \cdot 10^{-1}$	$9.15 \cdot 10^{-1}$	± 1.40
unknown f: *Rhodobacteraceae*	1.60	$8.33 \cdot 10^{-1}$	$2.80 \cdot 10^{-1}$	$9.04 \cdot 10^{-1}$	± $6.63 \cdot 10^{-1}$
Haliscomenobacter	1.77	$3.76 \cdot 10^{-1}$	$5.60 \cdot 10^{-1}$	$9.01 \cdot 10^{-1}$	± $7.55 \cdot 10^{-1}$

Table S13. AE4 genus-level EUB results summary continued.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
Blastocatella	$9.90 \cdot 10^{-1}$	1.33	$1.90 \cdot 10^{-3}$	$7.74 \cdot 10^{-1}$	±	$6.90 \cdot 10^{-1}$
unknown f: *Flavobacteriaceae*	$6.02 \cdot 10^{-3}$	$4.32 \cdot 10^{-1}$	1.79	$7.43 \cdot 10^{-1}$	±	$9.32 \cdot 10^{-1}$
Planctomyces	1.73	$3.36 \cdot 10^{-1}$	$1.28 \cdot 10^{-1}$	$7.32 \cdot 10^{-1}$	±	$8.71 \cdot 10^{-1}$
Pedobacter	$6.11 \cdot 10^{-2}$	1.99	$8.19 \cdot 10^{-2}$	$7.10 \cdot 10^{-1}$	±	1.11
Sphaerochaeta	N. D.	$9.88 \cdot 10^{-2}$	1.98	$6.93 \cdot 10^{-1}$	±	1.12
Ohtaekwangia	$3.11 \cdot 10^{-1}$	1.48	$2.09 \cdot 10^{-1}$	$6.68 \cdot 10^{-1}$	±	$7.07 \cdot 10^{-1}$
Gp4	1.32	$6.40 \cdot 10^{-1}$	$4.00 \cdot 10^{-2}$	$6.67 \cdot 10^{-1}$	±	$6.40 \cdot 10^{-1}$
Aquabacterium	1.35	$9.00 \cdot 10^{-2}$	$4.42 \cdot 10^{-1}$	$6.28 \cdot 10^{-1}$	±	$6.52 \cdot 10^{-1}$
unknown f: *Comamonadaceae*	1.11	$5.23 \cdot 10^{-1}$	$1.66 \cdot 10^{-1}$	$5.99 \cdot 10^{-1}$	±	$4.75 \cdot 10^{-1}$
Spartobacteria_genera_inc._sed.[f]	1.49	$2.01 \cdot 10^{-1}$	$2.76 \cdot 10^{-2}$	$5.74 \cdot 10^{-1}$	±	$8.00 \cdot 10^{-1}$
unknown p: *Firmicutes*	$5.33 \cdot 10^{-2}$	$9.88 \cdot 10^{-2}$	1.57	$5.73 \cdot 10^{-1}$	±	$8.61 \cdot 10^{-1}$
Hydrogenophaga	$4.65 \cdot 10^{-1}$	1.04	$1.53 \cdot 10^{-1}$	$5.51 \cdot 10^{-1}$	±	$4.48 \cdot 10^{-1}$
Altererythrobacter	1.20	$3.50 \cdot 10^{-1}$	$2.57 \cdot 10^{-2}$	$5.26 \cdot 10^{-1}$	±	$6.09 \cdot 10^{-1}$
Schlesneria	1.17	$2.33 \cdot 10^{-1}$	$1.50 \cdot 10^{-1}$	$5.19 \cdot 10^{-1}$	±	$5.67 \cdot 10^{-1}$
Ilumatobacter	$3.85 \cdot 10^{-1}$	1.09	$1.24 \cdot 10^{-2}$	$4.94 \cdot 10^{-1}$	±	$5.45 \cdot 10^{-1}$
unknown f: *Verrucomicrobiaceae*	1.11	$2.43 \cdot 10^{-1}$	$8.28 \cdot 10^{-2}$	$4.77 \cdot 10^{-1}$	±	$5.50 \cdot 10^{-1}$
unknown f: *Saprospiraceae*	1.11	$7.60 \cdot 10^{-3}$	$3.81 \cdot 10^{-3}$	$3.73 \cdot 10^{-1}$	±	$6.36 \cdot 10^{-1}$
Flavobacterium	$1.12 \cdot 10^{-2}$	1.08	$2.09 \cdot 10^{-2}$	$3.70 \cdot 10^{-1}$	±	$6.13 \cdot 10^{-1}$
SR1_genera_inc._sed.[f]	$3.44 \cdot 10^{-3}$	1.04	N. D.	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$

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

Table S14. AE8 domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
Bacteria	99.9	99.9	99.9	99.9	±	$2.78 \cdot 10^{-2}$

Table S14. AE8 domain-level EUB results summary continued.

Domain[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Minor phylotypes (2)[e]	$1.21 \cdot 10^{-1}$	$6.55 \cdot 10^{-2}$	$9.93 \cdot 10^{-2}$	$9.52 \cdot 10^{-2}$	$\pm 2.78 \cdot 10^{-2}$

[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] 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 S15. AE8 phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Proteobacteria	55.9	68.1	39.0	54.3	± 14.6
Bacteroidetes	11.1	8.02	22.4	13.8	± 7.59
unknown	8.34	3.58	13.7	8.53	± 5.05
d: *Bacteria*					
Firmicutes	1.93	2.93	15.4	6.74	± 7.49
Planctomycetes	4.76	3.94	1.41	3.37	± 1.74
Actinobacteria	2.78	6.18	$9.25 \cdot 10^{-1}$	3.30	± 2.67
Verrucomicrobia	6.58	1.14	1.90	3.21	± 2.95
Acidobacteria	4.85	1.98	1.10	2.64	± 1.96
Minor phylotypes (36)[e]	1.40	1.14	2.52	1.69	$\pm 7.37 \cdot 10^{-1}$
Candidatus Saccharibacteria	1.41	1.86	$5.54 \cdot 10^{-2}$	1.11	$\pm 9.38 \cdot 10^{-1}$
Chloroflexi	$6.82 \cdot 10^{-1}$	1.06	$4.53 \cdot 10^{-1}$	$7.32 \cdot 10^{-1}$	$\pm 3.08 \cdot 10^{-1}$
Spirochaetes	$2.62 \cdot 10^{-1}$	$8.22 \cdot 10^{-2}$	1.20	$5.14 \cdot 10^{-1}$	$\pm 5.99 \cdot 10^{-1}$

[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 S16. AE8 class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Alphaproteobacteria	33.5	46.9	13.5	31.3	± 16.8
Betaproteobacteria	12.2	9.56	18.4	13.4	± 4.53
unknown d: *Bacteria*	8.34	3.58	13.7	8.53	± 5.05
Gammaproteobacteria	7.15	6.92	4.34	6.14	± 1.56
Minor phylotypes (84)[e]	4.42	4.65	5.27	4.78	± $4.43 \cdot 10^{-1}$
Clostridia	1.67	2.52	9.37	4.52	± 4.22
Bacteroidia	$7.57 \cdot 10^{-2}$	1.44	12.0	4.51	± 6.53
Planctomycetia	4.74	3.90	1.33	3.33	± 1.78
Sphingobacteriia	5.10	2.90	1.93	3.31	± 1.63
Actinobacteria	2.78	6.18	$9.23 \cdot 10^{-1}$	3.29	± 2.66
unknown p: *Bacteroidetes*	1.67	$3.20 \cdot 10^{-1}$	5.67	2.55	± 2.78
Verrucomicrobiae	5.61	$6.54 \cdot 10^{-1}$	$9.74 \cdot 10^{-1}$	2.41	± 2.77
Acidobacteria_Gp4	4.19	1.02	$4.42 \cdot 10^{-1}$	1.88	± 2.02
Deltaproteobacteria	1.10	2.82	1.70	1.87	± $8.72 \cdot 10^{-1}$
unknown p: *Proteobacteria*	1.99	1.92	1.03	1.65	± $5.33 \cdot 10^{-1}$
Erysipelotrichia	$1.12 \cdot 10^{-1}$	$1.91 \cdot 10^{-1}$	4.48	1.59	± 2.50
Flavobacteriia	$6.18 \cdot 10^{-1}$	1.92	1.91	1.48	± $7.49 \cdot 10^{-1}$
Cytophagia	3.03	$6.59 \cdot 10^{-1}$	$6.41 \cdot 10^{-1}$	1.44	± 1.38
Saccharibacteria_genera_inc._sed.[f]	1.41	1.86	$5.54 \cdot 10^{-2}$	1.11	± $9.38 \cdot 10^{-1}$
Spirochaetia	$2.62 \cdot 10^{-1}$	$8.22 \cdot 10^{-2}$	1.20	$5.14 \cdot 10^{-1}$	± $5.99 \cdot 10^{-1}$
unknown p: *Firmicutes*	$3.91 \cdot 10^{-2}$	$5.14 \cdot 10^{-2}$	1.18	$4.23 \cdot 10^{-1}$	± $6.54 \cdot 10^{-1}$

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

Table S17. AE8 order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Rhizobiales	22.8	28.2	9.20	20.1	± 9.79
unknown	8.34	3.58	13.7	8.53	± 5.05
d: *Bacteria*					
Minor phylotypes (177)[e]	6.83	8.09	8.50	7.81	$\pm 8.69 \cdot 10^{-1}$
Rhodocyclales	1.86	2.47	15.3	6.55	± 7.59
Burkholderiales	9.63	6.29	2.23	6.05	± 3.70
Rhodobacterales	3.81	9.21	$7.61 \cdot 10^{-1}$	4.60	± 4.28
Bacteroidales	$7.57 \cdot 10^{-2}$	1.44	12.0	4.51	± 6.53
Clostridiales	1.65	2.51	9.33	4.50	± 4.21
Xanthomonadales	4.09	4.73	2.75	3.85	± 1.01
Sphingobacteriales	5.10	2.90	1.93	3.31	± 1.63
Planctomycetales	4.68	3.89	1.30	3.29	± 1.77
Sphingomonadales	2.95	4.09	$9.89 \cdot 10^{-1}$	2.68	± 1.57
unknown	1.67	$3.20 \cdot 10^{-1}$	5.67	2.55	± 2.78
p: *Bacteroidetes*					
Actinomycetales	2.47	4.28	$6.70 \cdot 10^{-1}$	2.47	± 1.80
Verrucomicrobiales	5.61	$6.54 \cdot 10^{-1}$	$9.74 \cdot 10^{-1}$	2.41	± 2.77
unknown	2.38	2.38	$7.31 \cdot 10^{-1}$	1.83	$\pm 9.53 \cdot 10^{-1}$
c: *Alphaproteobacteria*					
unknown	1.99	1.92	1.03	1.65	$\pm 5.33 \cdot 10^{-1}$
p: *Proteobacteria*					
Erysipelotrichales	$1.12 \cdot 10^{-1}$	$1.91 \cdot 10^{-1}$	4.48	1.59	± 2.50
unknown	2.35	1.28	$8.51 \cdot 10^{-1}$	1.49	$\pm 7.71 \cdot 10^{-1}$
c: *Gammaproteobacteria*					
Flavobacteriales	$6.18 \cdot 10^{-1}$	1.92	1.91	1.48	$\pm 7.49 \cdot 10^{-1}$
Cytophagales	3.03	$6.59 \cdot 10^{-1}$	$6.41 \cdot 10^{-1}$	1.44	± 1.38
Caulobacterales	$9.46 \cdot 10^{-1}$	1.39	1.25	1.19	$\pm 2.26 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	1.41	1.86	$5.54 \cdot 10^{-2}$	1.11	$\pm 9.38 \cdot 10^{-1}$
Blastocatella	2.32	$5.82 \cdot 10^{-1}$	$1.91 \cdot 10^{-2}$	$9.75 \cdot 10^{-1}$	± 1.20
Gp4	1.81	$4.23 \cdot 10^{-1}$	$4.17 \cdot 10^{-1}$	$8.83 \cdot 10^{-1}$	$\pm 8.02 \cdot 10^{-1}$
Rhodospirillales	$5.22 \cdot 10^{-1}$	1.33	$5.25 \cdot 10^{-1}$	$7.91 \cdot 10^{-1}$	$\pm 4.63 \cdot 10^{-1}$
Myxococcales	$3.79 \cdot 10^{-1}$	1.63	$2.51 \cdot 10^{-1}$	$7.55 \cdot 10^{-1}$	$\pm 7.64 \cdot 10^{-1}$
Acidimicrobiales	$2.16 \cdot 10^{-1}$	1.68	$1.88 \cdot 10^{-1}$	$6.95 \cdot 10^{-1}$	$\pm 8.54 \cdot 10^{-1}$
Spirochaetales	$2.62 \cdot 10^{-1}$	$8.22 \cdot 10^{-2}$	1.20	$5.14 \cdot 10^{-1}$	$\pm 5.99 \cdot 10^{-1}$

Table S17. AE8 order-level EUB results summary continued.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
unknown p: *Firmicutes*	$3.91 \cdot 10^{-2}$	$5.14 \cdot 10^{-2}$	1.18	$4.23 \cdot 10^{-1}$	$\pm 6.54 \cdot 10^{-1}$

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

Table S18. AE8 family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Minor phylotypes (372)[e]	15.4	19.1	16.0	16.9	± 1.99
Methylobacteriaceae	16.1	17.7	6.93	13.6	± 5.82
unknown d: *Bacteria*	8.34	3.58	13.7	8.53	± 5.05
Rhodocyclaceae	1.86	2.47	15.3	6.55	± 7.59
Rhodobacteraceae	3.81	9.21	$7.61 \cdot 10^{-1}$	4.60	± 4.28
Xanthomonadaceae	3.63	4.51	2.69	3.61	$\pm 9.10 \cdot 10^{-1}$
Planctomycetaceae	4.68	3.89	1.30	3.29	± 1.77
Comamonadaceae	5.07	3.00	$9.43 \cdot 10^{-1}$	3.00	± 2.06
unknown p: *Bacteroidetes*	1.67	$3.20 \cdot 10^{-1}$	5.67	2.55	± 2.78
Porphyromonadaceae	$5.41 \cdot 10^{-2}$	1.00	6.39	2.48	± 3.42
Verrucomicrobiaceae	5.61	$6.54 \cdot 10^{-1}$	$9.74 \cdot 10^{-1}$	2.41	± 2.77
unknown o: *Rhizobiales*	2.54	3.37	1.18	2.36	± 1.11
Sphingomonadaceae	1.93	3.31	$8.35 \cdot 10^{-1}$	2.02	± 1.24
Ruminococcaceae	$9.98 \cdot 10^{-1}$	$9.08 \cdot 10^{-1}$	4.08	2.00	± 1.81
unknown c: *Alphaproteobacteria*	2.38	2.38	$7.31 \cdot 10^{-1}$	1.83	$\pm 9.53 \cdot 10^{-1}$
Burkholderiales_inc._sed.[f]	3.50	1.02	$8.10 \cdot 10^{-1}$	1.78	± 1.50
unknown p: *Proteobacteria*	1.99	1.92	1.03	1.65	$\pm 5.33 \cdot 10^{-1}$
Erysipelotrichaceae	$1.12 \cdot 10^{-1}$	$1.91 \cdot 10^{-1}$	4.48	1.59	± 2.50

Table S18. AE8 family-level EUB results summary continued.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
unknown c: *Gammaproteobacteria*	2.35	1.28	$8.51 \cdot 10^{-1}$	1.49	$\pm 7.71 \cdot 10^{-1}$
unknown o: *Clostridiales*	$3.08 \cdot 10^{-1}$	$6.54 \cdot 10^{-1}$	3.44	1.47	± 1.72
Hyphomicrobiaceae	1.19	2.73	$4.12 \cdot 10^{-1}$	1.44	± 1.18
Phyllobacteriaceae	2.03	1.59	$4.61 \cdot 10^{-1}$	1.36	$\pm 8.10 \cdot 10^{-1}$
Saprospiraceae	2.38	$3.70 \cdot 10^{-1}$	$8.78 \cdot 10^{-1}$	1.21	± 1.04
Chitinophagaceae	1.18	1.64	$7.11 \cdot 10^{-1}$	1.18	$\pm 4.66 \cdot 10^{-1}$
Cytophagaceae	2.36	$6.26 \cdot 10^{-1}$	$5.04 \cdot 10^{-1}$	1.16	± 1.04
Flavobacteriaceae	$3.09 \cdot 10^{-1}$	1.55	1.47	1.11	$\pm 6.94 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	1.41	1.86	$5.54 \cdot 10^{-2}$	1.11	$\pm 9.38 \cdot 10^{-1}$
Blastocatella	2.32	$5.82 \cdot 10^{-1}$	$1.91 \cdot 10^{-2}$	$9.75 \cdot 10^{-1}$	± 1.20
Gp4	1.81	$4.23 \cdot 10^{-1}$	$4.17 \cdot 10^{-1}$	$8.83 \cdot 10^{-1}$	$\pm 8.02 \cdot 10^{-1}$
unknown o: *Burkholderiales*	$6.28 \cdot 10^{-1}$	1.55	$1.21 \cdot 10^{-1}$	$7.67 \cdot 10^{-1}$	$\pm 7.26 \cdot 10^{-1}$
Microbacteriaceae	$5.82 \cdot 10^{-1}$	1.30	$3.51 \cdot 10^{-1}$	$7.43 \cdot 10^{-1}$	$\pm 4.92 \cdot 10^{-1}$
unknown o: *Bacteroidales*	$1.08 \cdot 10^{-2}$	$1.04 \cdot 10^{-1}$	1.79	$6.33 \cdot 10^{-1}$	$\pm 9.99 \cdot 10^{-1}$
Prevotellaceae	$8.32 \cdot 10^{-4}$	$3.98 \cdot 10^{-2}$	1.83	$6.23 \cdot 10^{-1}$	± 1.04
Bacteroidaceae	$4.16 \cdot 10^{-3}$	$2.78 \cdot 10^{-1}$	1.45	$5.78 \cdot 10^{-1}$	$\pm 7.69 \cdot 10^{-1}$
Nannocystaceae	$4.16 \cdot 10^{-3}$	1.50	$2.39 \cdot 10^{-2}$	$5.11 \cdot 10^{-1}$	$\pm 8.61 \cdot 10^{-1}$
Acidimicrobiaceae	$1.42 \cdot 10^{-1}$	1.11	$1.36 \cdot 10^{-1}$	$4.62 \cdot 10^{-1}$	$\pm 5.59 \cdot 10^{-1}$
unknown p: *Firmicutes*	$3.91 \cdot 10^{-2}$	$5.14 \cdot 10^{-2}$	1.18	$4.23 \cdot 10^{-1}$	$\pm 6.54 \cdot 10^{-1}$
Mycobacteriaceae	$1.02 \cdot 10^{-1}$	1.06	$4.58 \cdot 10^{-2}$	$4.02 \cdot 10^{-1}$	$\pm 5.69 \cdot 10^{-1}$
Xanthobacteraceae	$1.17 \cdot 10^{-2}$	1.14	$2.48 \cdot 10^{-2}$	$3.91 \cdot 10^{-1}$	$\pm 6.45 \cdot 10^{-1}$
unknown o: *Sphingobacteriales*	1.05	$1.03 \cdot 10^{-2}$	$7.26 \cdot 10^{-2}$	$3.79 \cdot 10^{-1}$	$\pm 5.85 \cdot 10^{-1}$

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

Table S19. AE8 genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Minor phylotypes (1444)[e]	30.6	36.8	27.8	31.7	± 4.61
Meganema	16.1	17.7	6.93	13.6	± 5.80
unknown d: *Bacteria*	8.34	3.58	13.7	8.53	± 5.05
Thauera	1.70	2.04	9.61	4.45	± 4.47
unknown p: *Bacteroidetes*	1.67	$3.20 \cdot 10^{-1}$	5.67	2.55	± 2.78
unknown o: *Rhizobiales*	2.54	3.37	1.18	2.36	± 1.11
Zoogloea	$1.83 \cdot 10^{-2}$	$3.60 \cdot 10^{-1}$	5.45	1.94	± 3.04
unknown c: *Alphaproteobacteria*	2.38	2.38	$7.31 \cdot 10^{-1}$	1.83	$\pm 9.53 \cdot 10^{-1}$
Amaricoccus	$2.41 \cdot 10^{-2}$	5.32	$2.20 \cdot 10^{-2}$	1.79	± 3.06
unknown p: *Proteobacteria*	1.99	1.92	1.03	1.65	$\pm 5.33 \cdot 10^{-1}$
Luteimonas	2.12	2.49	$2.29 \cdot 10^{-2}$	1.54	± 1.33
unknown c: *Gammaproteobacteria*	2.35	1.28	$8.51 \cdot 10^{-1}$	1.49	$\pm 7.71 \cdot 10^{-1}$
unknown o: *Clostridiales*	$3.08 \cdot 10^{-1}$	$6.54 \cdot 10^{-1}$	3.44	1.47	± 1.72
unknown f: *Erysipelotrichaceae*	$2.16 \cdot 10^{-2}$	$1.03 \cdot 10^{-2}$	4.27	1.43	± 2.45
unknown f: *Rhodobacteraceae*	1.88	2.03	$3.48 \cdot 10^{-1}$	1.42	$\pm 9.30 \cdot 10^{-1}$
unknown f: *Comamonadaceae*	1.77	1.97	$1.93 \cdot 10^{-1}$	1.31	$\pm 9.73 \cdot 10^{-1}$
Proteiniphilum	$2.91 \cdot 10^{-2}$	$4.32 \cdot 10^{-1}$	3.30	1.25	± 1.78
unknown f: *Ruminococcaceae*	$6.06 \cdot 10^{-1}$	$4.95 \cdot 10^{-1}$	2.47	1.19	± 1.11
Saccharibacteria_genera_inc._sed.[f]	1.41	1.86	$5.54 \cdot 10^{-2}$	1.11	$\pm 9.38 \cdot 10^{-1}$
unknown f: *Planctomycetaceae*	$4.83 \cdot 10^{-1}$	2.32	$5.15 \cdot 10^{-1}$	1.11	± 1.05
Schlesneria	2.51	$5.31 \cdot 10^{-1}$	$1.62 \cdot 10^{-2}$	1.02	± 1.32
Blastocatella	2.32	$5.82 \cdot 10^{-1}$	$1.91 \cdot 10^{-2}$	$9.75 \cdot 10^{-1}$	± 1.20
Gp4	1.81	$4.23 \cdot 10^{-1}$	$4.17 \cdot 10^{-1}$	$8.83 \cdot 10^{-1}$	$\pm 8.02 \cdot 10^{-1}$
Aquabacterium	1.99	$2.11 \cdot 10^{-1}$	$3.80 \cdot 10^{-1}$	$8.59 \cdot 10^{-1}$	$\pm 9.80 \cdot 10^{-1}$
Paracoccus	1.33	1.07	$5.92 \cdot 10^{-2}$	$8.19 \cdot 10^{-1}$	$\pm 6.71 \cdot 10^{-1}$
unknown f: *Porphyromonadaceae*	$2.08 \cdot 10^{-2}$	$2.45 \cdot 10^{-1}$	2.13	$8.00 \cdot 10^{-1}$	± 1.16

Table S19. AE8 genus-level EUB results summary continued.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average ± SD[c] %[d]
unknown	$6.28 \cdot 10^{-1}$	1.55	$1.21 \cdot 10^{-1}$	$7.67 \cdot 10^{-1} \pm 7.26 \cdot 10^{-1}$
o: *Burkholderiales*				
Haliscomenobacter	1.09	$3.62 \cdot 10^{-1}$	$8.24 \cdot 10^{-1}$	$7.59 \cdot 10^{-1} \pm 3.68 \cdot 10^{-1}$
unknown	1.90	$1.55 \cdot 10^{-1}$	$1.82 \cdot 10^{-1}$	$7.47 \cdot 10^{-1} \pm 1.00$
f: *Verrucomicrobiaceae*				
Hydrogenophaga	1.36	$4.70 \cdot 10^{-1}$	$2.79 \cdot 10^{-1}$	$7.04 \cdot 10^{-1} \pm 5.79 \cdot 10^{-1}$
unknown	$1.08 \cdot 10^{-2}$	$1.04 \cdot 10^{-1}$	1.79	$6.33 \cdot 10^{-1} \pm 9.99 \cdot 10^{-1}$
o: *Bacteroidales*				
unknown	1.07	$4.33 \cdot 10^{-1}$	$3.89 \cdot 10^{-1}$	$6.32 \cdot 10^{-1} \pm 3.84 \cdot 10^{-1}$
f: *Burkholderiales_inc._sed.*[f]				
Leadbetterella	1.61	$2.17 \cdot 10^{-1}$	N. D.	$6.09 \cdot 10^{-1} \pm 8.74 \cdot 10^{-1}$
Roseimicrobium	1.71	$2.18 \cdot 10^{-2}$	$2.77 \cdot 10^{-2}$	$5.88 \cdot 10^{-1} \pm 9.75 \cdot 10^{-1}$
unknown	$9.49 \cdot 10^{-2}$	$2.48 \cdot 10^{-1}$	1.38	$5.74 \cdot 10^{-1} \pm 7.02 \cdot 10^{-1}$
f: *Flavobacteriaceae*				
Bacteroides	$8.32 \cdot 10^{-4}$	$2.76 \cdot 10^{-1}$	1.44	$5.71 \cdot 10^{-1} \pm 7.62 \cdot 10^{-1}$
Dokdonella	$1.66 \cdot 10^{-3}$	$1.07 \cdot 10^{-1}$	1.55	$5.54 \cdot 10^{-1} \pm 8.67 \cdot 10^{-1}$
Nannocystis	$3.33 \cdot 10^{-3}$	1.44	$2.39 \cdot 10^{-2}$	$4.90 \cdot 10^{-1} \pm 8.26 \cdot 10^{-1}$
Thermomonas	$3.14 \cdot 10^{-1}$	1.09	$4.96 \cdot 10^{-2}$	$4.86 \cdot 10^{-1} \pm 5.43 \cdot 10^{-1}$
Verrucomicrobium	1.32	$3.08 \cdot 10^{-2}$	$2.10 \cdot 10^{-2}$	$4.57 \cdot 10^{-1} \pm 7.46 \cdot 10^{-1}$
unknown	1.29	$7.71 \cdot 10^{-3}$	$5.44 \cdot 10^{-2}$	$4.50 \cdot 10^{-1} \pm 7.25 \cdot 10^{-1}$
f: *Saprospiraceae*				
unknown	$3.91 \cdot 10^{-2}$	$5.14 \cdot 10^{-2}$	1.18	$4.23 \cdot 10^{-1} \pm 6.54 \cdot 10^{-1}$
p: *Firmicutes*				
Mycobacterium	$9.99 \cdot 10^{-2}$	1.05	$4.58 \cdot 10^{-2}$	$4.00 \cdot 10^{-1} \pm 5.68 \cdot 10^{-1}$
unknown	1.05	$1.03 \cdot 10^{-2}$	$7.26 \cdot 10^{-2}$	$3.79 \cdot 10^{-1} \pm 5.85 \cdot 10^{-1}$
o: *Sphingobacteriales*				
Xanthobacter	$7.49 \cdot 10^{-3}$	1.03	$2.39 \cdot 10^{-2}$	$3.52 \cdot 10^{-1} \pm 5.83 \cdot 10^{-1}$
Filomicrobium	$4.16 \cdot 10^{-3}$	1.00	$1.43 \cdot 10^{-2}$	$3.40 \cdot 10^{-1} \pm 5.73 \cdot 10^{-1}$

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

Table S20. AE12 domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Bacteria	99.8	99.9	99.9	99.9	$\pm 7.16 \cdot 10^{-2}$
Minor phylotypes (2)[e]	$2.05 \cdot 10^{-1}$	$9.13 \cdot 10^{-2}$	$7.23 \cdot 10^{-2}$	$1.23 \cdot 10^{-1}$	$\pm 7.16 \cdot 10^{-2}$

[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] 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 S21. AE12 phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Proteobacteria	58.6	72.4	48.8	59.9	± 11.9
Bacteroidetes	12.6	7.51	24.2	14.8	± 8.54
Firmicutes	1.10	$9.03 \cdot 10^{-1}$	13.8	5.27	± 7.39
unknown	7.14	1.16	3.99	4.10	± 2.99
d: *Bacteria*					
Actinobacteria	2.37	6.85	1.63	3.62	± 2.82
Planctomycetes	2.74	5.15	1.29	3.06	± 1.95
Acidobacteria	4.72	1.66	1.09	2.49	± 1.95
Candidatus Saccharibacteria	5.85	$9.74 \cdot 10^{-1}$	$7.35 \cdot 10^{-2}$	2.30	± 3.11
Verrucomicrobia	2.26	$2.70 \cdot 10^{-1}$	$9.33 \cdot 10^{-1}$	1.16	± 1.02
Minor phylotypes (35)[e]	1.11	1.14	$9.24 \cdot 10^{-1}$	1.06	$\pm 1.18 \cdot 10^{-1}$
Chloroflexi	$8.80 \cdot 10^{-1}$	1.71	$4.63 \cdot 10^{-1}$	1.02	$\pm 6.35 \cdot 10^{-1}$
Parcubacteria	$5.45 \cdot 10^{-1}$	$3.14 \cdot 10^{-1}$	1.02	$6.27 \cdot 10^{-1}$	$\pm 3.61 \cdot 10^{-1}$
Spirochaetes	$3.21 \cdot 10^{-2}$	$3.38 \cdot 10^{-3}$	1.84	$6.25 \cdot 10^{-1}$	± 1.05

[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 S22. AE12 class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Alphaproteobacteria	41.3	58.9	13.7	38.0	± 22.8
Betaproteobacteria	10.4	6.25	28.7	15.1	± 11.9
unknown d: *Bacteria*	7.14	1.16	3.99	4.10	± 2.99
Sphingobacteriia	8.45	$9.09 \cdot 10^{-1}$	2.10	3.82	± 4.05
Gammaproteobacteria	3.89	4.60	2.81	3.77	± $9.02 \cdot 10^{-1}$
Bacteroidia	$3.11 \cdot 10^{-2}$	$3.72 \cdot 10^{-2}$	10.8	3.63	± 6.23
Actinobacteria	2.36	6.84	1.63	3.61	± 2.82
Clostridia	$8.85 \cdot 10^{-1}$	$7.27 \cdot 10^{-1}$	8.11	3.24	± 4.22
unknown p: *Bacteroidetes*	$4.76 \cdot 10^{-1}$	$3.68 \cdot 10^{-1}$	8.55	3.13	± 4.69
Planctomycetia	2.72	5.15	1.28	3.05	± 1.96
Minor phylotypes (81)[e]	2.98	2.42	2.14	2.51	± $4.32 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	5.85	$9.74 \cdot 10^{-1}$	$7.35 \cdot 10^{-2}$	2.30	± 3.11
Acidobacteria_Gp4	4.05	1.24	$9.16 \cdot 10^{-1}$	2.07	± 1.72
Cytophagia	1.22	3.25	1.07	1.85	± 1.22
Deltaproteobacteria	1.67	1.08	2.14	1.63	± $5.28 \cdot 10^{-1}$
Erysipelotrichia	$5.92 \cdot 10^{-2}$	$8.45 \cdot 10^{-2}$	4.25	1.47	± 2.42
unknown p: *Proteobacteria*	1.37	1.48	1.35	1.40	± $7.00 \cdot 10^{-2}$
Bacteroidetes_inc._sed.[f]	1.96	2.08	$1.36 \cdot 10^{-2}$	1.35	± 1.16
Flavobacteriia	$5.01 \cdot 10^{-1}$	$8.59 \cdot 10^{-1}$	1.63	$9.96 \cdot 10^{-1}$	± $5.76 \cdot 10^{-1}$
Caldilineae	$7.20 \cdot 10^{-1}$	1.07	$3.71 \cdot 10^{-1}$	$7.21 \cdot 10^{-1}$	± $3.50 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$5.45 \cdot 10^{-1}$	$3.14 \cdot 10^{-1}$	1.02	$6.27 \cdot 10^{-1}$	± $3.61 \cdot 10^{-1}$
Verrucomicrobiae	1.39	$1.55 \cdot 10^{-1}$	$3.36 \cdot 10^{-1}$	$6.26 \cdot 10^{-1}$	± $6.66 \cdot 10^{-1}$
Spirochaetia	$3.21 \cdot 10^{-2}$	$3.38 \cdot 10^{-3}$	1.84	$6.25 \cdot 10^{-1}$	± 1.05
unknown p: *Firmicutes*	$1.71 \cdot 10^{-2}$	N. D.	1.14	$3.85 \cdot 10^{-1}$	± $6.52 \cdot 10^{-1}$

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

Table S23. AE12 order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average ± SD[c] %[d]
Rhizobiales	26.9	42.4	9.26	26.2 ± 16.6
Rhodocyclales	4.11	$2.13 \cdot 10^{-1}$	25.6	9.98 ± 13.7
Minor phylotypes (177)[e]	6.72	5.04	7.06	6.27 ± 1.08
Rhodobacterales	4.00	10.1	1.36	5.16 ± 4.49
Burkholderiales	6.12	5.85	2.09	4.69 ± 2.25
unknown	7.14	1.16	3.99	4.10 ± 2.99
d: *Bacteria*				
Sphingobacteriales	8.45	$9.09 \cdot 10^{-1}$	2.10	3.82 ± 4.05
Bacteroidales	$3.11 \cdot 10^{-2}$	$3.72 \cdot 10^{-2}$	10.8	3.63 ± 6.23
Clostridiales	$8.82 \cdot 10^{-1}$	$7.27 \cdot 10^{-1}$	8.08	3.23 ± 4.20
unknown	$4.76 \cdot 10^{-1}$	$3.68 \cdot 10^{-1}$	8.55	3.13 ± 4.69
p: *Bacteroidetes*				
Planctomycetales	2.70	5.15	1.24	3.03 ± 1.98
Xanthomonadales	2.74	3.83	$9.98 \cdot 10^{-1}$	2.52 ± 1.43
Actinomycetales	2.05	4.28	1.15	2.49 ± 1.61
Sphingomonadales	4.50	1.99	$9.13 \cdot 10^{-1}$	2.47 ± 1.84
unknown	3.00	2.91	1.19	2.37 ± 1.02
c: *Alphaproteobacteria*				
Saccharibacteria_genera_inc._sed.[f]	5.85	$9.74 \cdot 10^{-1}$	$7.35 \cdot 10^{-2}$	2.30 ± 3.11
Cytophagales	1.22	3.25	1.07	1.85 ± 1.22
Gp4	2.99	1.11	$8.41 \cdot 10^{-1}$	1.65 ± 1.17
Erysipelotrichales	$5.92 \cdot 10^{-2}$	$8.45 \cdot 10^{-2}$	4.25	1.47 ± 2.42
unknown	1.37	1.48	1.35	1.40 ± $7.00 \cdot 10^{-2}$
p: *Proteobacteria*				
Ohtaekwangia	1.96	2.08	$1.13 \cdot 10^{-2}$	1.35 ± 1.16
Caulobacterales	2.02	$7.10 \cdot 10^{-1}$	$7.75 \cdot 10^{-1}$	1.17 ± $7.41 \cdot 10^{-1}$
Flavobacteriales	$5.01 \cdot 10^{-1}$	$8.59 \cdot 10^{-1}$	1.63	$9.96 \cdot 10^{-1}$ ± $5.76 \cdot 10^{-1}$
Acidimicrobiales	$2.20 \cdot 10^{-1}$	2.34	$3.13 \cdot 10^{-1}$	$9.58 \cdot 10^{-1}$ ± 1.20
unknown	1.30	$5.48 \cdot 10^{-1}$	$5.79 \cdot 10^{-1}$	$8.09 \cdot 10^{-1}$ ± $4.25 \cdot 10^{-1}$
c: *Deltaproteobacteria*				
Caldilineales	$7.20 \cdot 10^{-1}$	1.07	$3.71 \cdot 10^{-1}$	$7.21 \cdot 10^{-1}$ ± $3.50 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$5.45 \cdot 10^{-1}$	$3.14 \cdot 10^{-1}$	1.02	$6.27 \cdot 10^{-1}$ ± $3.61 \cdot 10^{-1}$
Verrucomicrobiales	1.39	$1.55 \cdot 10^{-1}$	$3.36 \cdot 10^{-1}$	$6.26 \cdot 10^{-1}$ ± $6.66 \cdot 10^{-1}$
Spirochaetales	$3.21 \cdot 10^{-2}$	$3.38 \cdot 10^{-3}$	1.84	$6.25 \cdot 10^{-1}$ ± 1.05

Table S23. AE12 order-level EUB results summary continued.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
unknown p: *Firmicutes*	$1.71 \cdot 10^{-2}$	N. D.	1.14	$3.85 \cdot 10^{-1}$	± $6.52 \cdot 10^{-1}$

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

Table S24. AE12 family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Methylobacteriaceae	19.2	32.8	6.92	19.6	± 13.0
Minor phylotypes (370)[e]	12.4	12.1	12.0	12.2	± $2.39 \cdot 10^{-1}$
Rhodocyclaceae	4.11	$2.13 \cdot 10^{-1}$	25.6	9.98	± 13.7
Rhodobacteraceae	4.00	10.1	1.36	5.16	± 4.49
unknown d: *Bacteria*	7.14	1.16	3.99	4.10	± 2.99
unknown p: *Bacteroidetes*	$4.76 \cdot 10^{-1}$	$3.68 \cdot 10^{-1}$	8.55	3.13	± 4.69
Planctomycetaceae	2.70	5.15	1.24	3.03	± 1.98
unknown c: *Alphaproteobacteria*	3.00	2.91	1.19	2.37	± 1.02
Comamonadaceae	1.45	4.27	1.22	2.31	± 1.70
Saccharibacteria_genera_inc._sed.[f]	5.85	$9.74 \cdot 10^{-1}$	$7.35 \cdot 10^{-2}$	2.30	± 3.11
Xanthomonadaceae	2.23	3.67	$8.75 \cdot 10^{-1}$	2.26	± 1.40
unknown o: *Rhizobiales*	2.65	2.39	1.38	2.14	± $6.72 \cdot 10^{-1}$
Cytophagaceae	1.17	3.25	$7.44 \cdot 10^{-1}$	1.72	± 1.34
Sphingomonadaceae	2.87	1.59	$6.87 \cdot 10^{-1}$	1.72	± 1.10
Phyllobacteriaceae	2.15	2.67	$3.11 \cdot 10^{-1}$	1.71	± 1.24
Gp4	2.99	1.11	$8.41 \cdot 10^{-1}$	1.65	± 1.17
Burkholderiales_inc._sed.[f]	3.96	$3.08 \cdot 10^{-1}$	$5.00 \cdot 10^{-1}$	1.59	± 2.06
Porphyromonadaceae	$2.51 \cdot 10^{-2}$	$3.72 \cdot 10^{-2}$	4.42	1.49	± 2.53
Erysipelotrichaceae	$5.92 \cdot 10^{-2}$	$8.45 \cdot 10^{-2}$	4.25	1.47	± 2.42

Table S24. AE12 family-level EUB results summary continued.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
Hyphomicrobiaceae	1.68	2.26	$4.26 \cdot 10^{-1}$	1.46	±	$9.37 \cdot 10^{-1}$
unknown	1.37	1.48	1.35	1.40	±	$7.00 \cdot 10^{-2}$
p: *Proteobacteria*						
Ohtaekwangia	1.96	2.08	$1.13 \cdot 10^{-2}$	1.35	±	1.16
Saprospiraceae	2.78	$2.03 \cdot 10^{-2}$	1.14	1.31	±	1.39
unknown	$1.31 \cdot 10^{-1}$	$1.69 \cdot 10^{-2}$	3.73	1.29	±	2.11
o: *Clostridiales*						
Ruminococcaceae	$4.80 \cdot 10^{-1}$	$8.79 \cdot 10^{-2}$	3.30	1.29	±	1.75
Chitinophagaceae	2.03	$4.33 \cdot 10^{-1}$	$5.98 \cdot 10^{-1}$	1.02	±	$8.81 \cdot 10^{-1}$
Cyclobacteriaceae	2.56	$1.69 \cdot 10^{-2}$	$2.50 \cdot 10^{-1}$	$9.42 \cdot 10^{-1}$	±	1.41
Microbacteriaceae	$9.10 \cdot 10^{-1}$	1.55	$3.30 \cdot 10^{-1}$	$9.31 \cdot 10^{-1}$	±	$6.11 \cdot 10^{-1}$
unknown	1.30	$5.48 \cdot 10^{-1}$	$5.79 \cdot 10^{-1}$	$8.09 \cdot 10^{-1}$	±	$4.25 \cdot 10^{-1}$
c: *Deltaproteobacteria*						
unknown	$3.01 \cdot 10^{-3}$	N. D.	2.33	$7.78 \cdot 10^{-1}$	±	1.34
o: *Bacteroidales*						
Acidimicrobiaceae	$1.22 \cdot 10^{-1}$	1.96	$2.26 \cdot 10^{-1}$	$7.69 \cdot 10^{-1}$	±	1.03
Flavobacteriaceae	$4.14 \cdot 10^{-1}$	$7.34 \cdot 10^{-1}$	1.02	$7.21 \cdot 10^{-1}$	±	$3.01 \cdot 10^{-1}$
Caldilineaceae	$7.20 \cdot 10^{-1}$	1.07	$3.71 \cdot 10^{-1}$	$7.21 \cdot 10^{-1}$	±	$3.50 \cdot 10^{-1}$
Bacteroidaceae	$1.00 \cdot 10^{-3}$	N. D.	2.15	$7.16 \cdot 10^{-1}$	±	1.24
Propionibacteriaceae	$4.08 \cdot 10^{-1}$	1.27	$3.91 \cdot 10^{-1}$	$6.91 \cdot 10^{-1}$	±	$5.05 \cdot 10^{-1}$
Erythrobacteraceae	1.42	$3.79 \cdot 10^{-1}$	$1.87 \cdot 10^{-1}$	$6.63 \cdot 10^{-1}$	±	$6.66 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$5.45 \cdot 10^{-1}$	$3.14 \cdot 10^{-1}$	1.02	$6.27 \cdot 10^{-1}$	±	$3.61 \cdot 10^{-1}$
Verrucomicrobiaceae	1.39	$1.55 \cdot 10^{-1}$	$3.36 \cdot 10^{-1}$	$6.26 \cdot 10^{-1}$	±	$6.66 \cdot 10^{-1}$
Caulobacteraceae	1.32	$4.09 \cdot 10^{-1}$	$1.19 \cdot 10^{-1}$	$6.14 \cdot 10^{-1}$	±	$6.24 \cdot 10^{-1}$
Spirochaetaceae	N. D.	N. D.	1.61	$5.35 \cdot 10^{-1}$	±	$9.27 \cdot 10^{-1}$
Prevotellaceae	N. D.	N. D.	1.27	$4.24 \cdot 10^{-1}$	±	$7.34 \cdot 10^{-1}$
unknown	$1.71 \cdot 10^{-2}$	N. D.	1.14	$3.85 \cdot 10^{-1}$	±	$6.52 \cdot 10^{-1}$
p: *Firmicutes*						

[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 S25. AE12 genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Minor phylotypes (1448)[e]	30.3	26.3	23.3	26.6	± 3.52
Meganema	19.1	32.8	6.92	19.6	± 12.9
Zoogloea	N. D.	$2.37 \cdot 10^{-2}$	24.3	8.10	± 14.0
unknown d: *Bacteria*	7.14	1.16	3.99	4.10	± 2.99
unknown p: *Bacteroidetes*	$4.76 \cdot 10^{-1}$	$3.68 \cdot 10^{-1}$	8.55	3.13	± 4.69
unknown c: *Alphaproteobacteria*	3.00	2.91	1.19	2.37	± 1.02
Saccharibacteria_genera_inc._sed.[f]	5.85	$9.74 \cdot 10^{-1}$	$7.35 \cdot 10^{-2}$	2.30	± 3.11
unknown o: *Rhizobiales*	2.65	2.39	1.38	2.14	± $6.72 \cdot 10^{-1}$
Thauera	3.98	$1.76 \cdot 10^{-1}$	1.16	1.77	± 1.97
Paracoccus	1.27	3.95	$6.78 \cdot 10^{-3}$	1.74	± 2.01
Gp4	2.99	1.11	$8.41 \cdot 10^{-1}$	1.65	± 1.17
unknown f: *Planctomycetaceae*	$2.86 \cdot 10^{-1}$	3.73	$4.91 \cdot 10^{-1}$	1.50	± 1.93
Amaricoccus	$9.03 \cdot 10^{-3}$	3.61	$6.96 \cdot 10^{-1}$	1.44	± 1.91
unknown p: *Proteobacteria*	1.37	1.48	1.35	1.40	± $7.00 \cdot 10^{-2}$
unknown f: *Erysipelotrichaceae*	$3.01 \cdot 10^{-3}$	N. D.	4.15	1.38	± 2.39
Ohtaekwangia	1.96	2.08	$1.13 \cdot 10^{-2}$	1.35	± 1.16
unknown o: *Clostridiales*	$1.31 \cdot 10^{-1}$	$1.69 \cdot 10^{-2}$	3.73	1.29	± 2.11
unknown f: *Rhodobacteraceae*	1.65	1.40	$4.37 \cdot 10^{-1}$	1.16	± $6.41 \cdot 10^{-1}$
Luteimonas	1.65	1.56	$1.92 \cdot 10^{-2}$	1.08	± $9.16 \cdot 10^{-1}$
Aquabacterium	3.05	$6.76 \cdot 10^{-3}$	$5.54 \cdot 10^{-2}$	1.04	± 1.74
Haliscomenobacter	1.73	$1.69 \cdot 10^{-2}$	1.12	$9.57 \cdot 10^{-1}$	± $8.70 \cdot 10^{-1}$
unknown f: *Comamonadaceae*	$4.82 \cdot 10^{-1}$	2.00	$2.55 \cdot 10^{-1}$	$9.12 \cdot 10^{-1}$	± $9.47 \cdot 10^{-1}$
Leadbetterella	$4.52 \cdot 10^{-2}$	2.51	$3.39 \cdot 10^{-2}$	$8.65 \cdot 10^{-1}$	± 1.43
unknown f: *Ruminococcaceae*	$3.01 \cdot 10^{-1}$	$4.39 \cdot 10^{-2}$	2.12	$8.21 \cdot 10^{-1}$	± 1.13
unknown f: *Cyclobacteriaceae*	2.19	$1.69 \cdot 10^{-2}$	$2.33 \cdot 10^{-1}$	$8.12 \cdot 10^{-1}$	± 1.19
unknown f: *Porphyromonadaceae*	$8.03 \cdot 10^{-3}$	$3.38 \cdot 10^{-3}$	2.42	$8.10 \cdot 10^{-1}$	± 1.39

Table S25. AE12 genus-level EUB results summary continued.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
unknown	1.30	$5.48 \cdot 10^{-1}$	$5.79 \cdot 10^{-1}$	$8.09 \cdot 10^{-1}$	±	$4.25 \cdot 10^{-1}$
c: *Deltaproteobacteria*						
unknown	$3.01 \cdot 10^{-3}$	N. D.	2.33	$7.78 \cdot 10^{-1}$	±	1.34
o: *Bacteroidales*						
Mesorhizobium	$8.79 \cdot 10^{-1}$	1.33	$1.16 \cdot 10^{-1}$	$7.73 \cdot 10^{-1}$	±	$6.11 \cdot 10^{-1}$
Hyphomicrobium	$6.73 \cdot 10^{-1}$	1.33	$1.98 \cdot 10^{-1}$	$7.34 \cdot 10^{-1}$	±	$5.69 \cdot 10^{-1}$
unknown	1.57	$3.65 \cdot 10^{-1}$	$2.39 \cdot 10^{-1}$	$7.23 \cdot 10^{-1}$	±	$7.32 \cdot 10^{-1}$
f: *Chitinophagaceae*						
Bacteroides	$1.00 \cdot 10^{-3}$	N. D.	2.13	$7.11 \cdot 10^{-1}$	±	1.23
Hylemonella	$1.30 \cdot 10^{-2}$	1.97	$1.24 \cdot 10^{-2}$	$6.67 \cdot 10^{-1}$	±	1.13
Ilumatobacter	$1.01 \cdot 10^{-1}$	1.68	$2.11 \cdot 10^{-1}$	$6.63 \cdot 10^{-1}$	±	$8.79 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$5.45 \cdot 10^{-1}$	$3.14 \cdot 10^{-1}$	1.02	$6.27 \cdot 10^{-1}$	±	$3.61 \cdot 10^{-1}$
Altererythrobacter	1.18	$3.52 \cdot 10^{-1}$	$1.55 \cdot 10^{-1}$	$5.63 \cdot 10^{-1}$	±	$5.46 \cdot 10^{-1}$
Sphaerochaeta	N. D.	N. D.	1.48	$4.93 \cdot 10^{-1}$	±	$8.54 \cdot 10^{-1}$
Pseudofulvimonas	$2.61 \cdot 10^{-2}$	1.06	$3.66 \cdot 10^{-1}$	$4.85 \cdot 10^{-1}$	±	$5.28 \cdot 10^{-1}$
Brevundimonas	1.00	$3.62 \cdot 10^{-1}$	$5.43 \cdot 10^{-2}$	$4.72 \cdot 10^{-1}$	±	$4.83 \cdot 10^{-1}$
Proteiniphilum	$9.03 \cdot 10^{-3}$	$2.70 \cdot 10^{-2}$	1.22	$4.17 \cdot 10^{-1}$	±	$6.91 \cdot 10^{-1}$
unknown	$1.71 \cdot 10^{-2}$	N. D.	1.14	$3.85 \cdot 10^{-1}$	±	$6.52 \cdot 10^{-1}$
p: *Firmicutes*						
unknown	1.05	$3.38 \cdot 10^{-3}$	$1.81 \cdot 10^{-2}$	$3.57 \cdot 10^{-1}$	±	$6.00 \cdot 10^{-1}$
f: *Saprospiraceae*						

[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 S26. AE20 domain-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Bacteria	99.7	99.8	99.9	99.8	$\pm 7.85 \cdot 10^{-2}$

Table S26. AE20 domain-level EUB results summary continued.

Domain[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Minor phylotypes (2)[e]	$2.81 \cdot 10^{-1}$	$1.81 \cdot 10^{-1}$	$1.26 \cdot 10^{-1}$	$1.96 \cdot 10^{-1}$	$\pm 7.85 \cdot 10^{-2}$

[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] 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 S27. AE20 phylum-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Proteobacteria	53.4	71.2	32.4	52.3	± 19.4
Bacteroidetes	20.2	8.85	26.2	18.4	± 8.79
Firmicutes	$8.08 \cdot 10^{-1}$	1.05	18.2	6.68	± 9.96
Acidobacteria	2.66	4.70	5.92	4.42	± 1.65
Actinobacteria	2.96	5.78	3.43	4.05	± 1.51
unknown d: *Bacteria*	4.93	2.10	4.59	3.87	± 1.55
Planctomycetes	6.71	2.41	1.50	3.54	± 2.78
Verrucomicrobia	3.03	1.33	2.61	2.33	± $8.86 \cdot 10^{-1}$
Minor phylotypes (35)[e]	$8.37 \cdot 10^{-1}$	$8.02 \cdot 10^{-1}$	1.56	1.06	± $4.25 \cdot 10^{-1}$
Chloroflexi	1.31	1.18	$6.34 \cdot 10^{-1}$	1.04	± $3.58 \cdot 10^{-1}$
Parcubacteria	$4.01 \cdot 10^{-1}$	$1.89 \cdot 10^{-2}$	2.69	1.04	± 1.45
Candidatus Saccharibacteria	1.50	$5.29 \cdot 10^{-1}$	$2.77 \cdot 10^{-1}$	$7.68 \cdot 10^{-1}$	± $6.44 \cdot 10^{-1}$
Armatimonadetes	1.26	$4.79 \cdot 10^{-2}$	$7.11 \cdot 10^{-2}$	$4.60 \cdot 10^{-1}$	± $6.93 \cdot 10^{-1}$

[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 S28. AE20 class-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average ± %[d]	SD[c]
Alphaproteobacteria	43.8	52.6	18.5	38.3	± 17.7
Gammaproteobacteria	5.59	8.74	2.70	5.68	± 3.02
Clostridia	$6.12 \cdot 10^{-1}$	$8.65 \cdot 10^{-1}$	15.5	5.67	± 8.53
Betaproteobacteria	1.64	5.84	7.10	4.86	± 2.86
Bacteroidetes_inc._sed.[e]	9.80	3.24	$5.80 \cdot 10^{-3}$	4.35	± 4.99
Cytophagia	7.18	2.61	2.53	4.11	± 2.66
Actinobacteria	2.95	5.77	3.42	4.04	± 1.51
unknown d: *Bacteria*	4.93	2.10	4.59	3.87	± 1.55
Bacteroidia	$3.25 \cdot 10^{-2}$	$1.44 \cdot 10^{-1}$	11.0	3.71	± 6.27
Minor phylotypes (81)[f]	2.93	2.73	5.13	3.60	± 1.33
Planctomycetia	6.71	2.36	1.50	3.52	± 2.79
Acidobacteria_Gp4	2.34	2.75	5.38	3.49	± 1.65
unknown p: *Bacteroidetes*	$6.08 \cdot 10^{-1}$	$5.24 \cdot 10^{-1}$	6.82	2.65	± 3.61
Deltaproteobacteria	1.41	3.04	3.14	2.53	± $9.73 \cdot 10^{-1}$
Sphingobacteriia	2.04	$9.86 \cdot 10^{-1}$	4.18	2.40	± 1.63
Verrucomicrobiae	1.46	1.06	1.93	1.48	± $4.34 \cdot 10^{-1}$
Flavobacteriia	$5.63 \cdot 10^{-1}$	1.35	1.67	1.19	± $5.68 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[e]	$4.01 \cdot 10^{-1}$	$1.89 \cdot 10^{-2}$	2.69	1.04	± 1.45
Caldilineae	$8.83 \cdot 10^{-1}$	1.03	$5.47 \cdot 10^{-1}$	$8.21 \cdot 10^{-1}$	± $2.49 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	1.50	$5.29 \cdot 10^{-1}$	$2.77 \cdot 10^{-1}$	$7.68 \cdot 10^{-1}$	± $6.44 \cdot 10^{-1}$
Acidobacteria_Gp6	$2.41 \cdot 10^{-1}$	1.54	$2.68 \cdot 10^{-1}$	$6.83 \cdot 10^{-1}$	± $7.43 \cdot 10^{-1}$
Spartobacteria	1.24	$5.37 \cdot 10^{-2}$	$5.80 \cdot 10^{-3}$	$4.34 \cdot 10^{-1}$	± $7.00 \cdot 10^{-1}$
Erysipelotrichia	$6.49 \cdot 10^{-2}$	$6.09 \cdot 10^{-2}$	1.10	$4.08 \cdot 10^{-1}$	± $5.98 \cdot 10^{-1}$
Armatimonadetes_gp5	1.13	$3.19 \cdot 10^{-2}$	$3.19 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$	± $6.33 \cdot 10^{-1}$

[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] 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 S29. AE20 order-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average ± %[d]	SD[c]
Rhizobiales	34.2	29.5	8.63	24.1	± 13.6
Minor phylotypes (174)[e]	5.45	7.12	8.45	7.00	± 1.50
Rhodobacterales	3.66	12.1	4.74	6.84	± 4.60
Clostridiales	$6.11 \cdot 10^{-1}$	$8.63 \cdot 10^{-1}$	15.5	5.65	± 8.51
Ohtaekwangia	9.80	3.24	$5.80 \cdot 10^{-3}$	4.35	± 4.99
Cytophagales	7.18	2.61	2.53	4.11	± 2.66
unknown	4.93	2.10	4.59	3.87	± 1.55
d: *Bacteria*					
Xanthomonadales	4.09	6.37	1.06	3.84	± 2.66
Bacteroidales	$3.25 \cdot 10^{-2}$	$1.44 \cdot 10^{-1}$	11.0	3.71	± 6.27
Planctomycetales	6.71	2.36	1.34	3.47	± 2.85
Sphingomonadales	2.09	4.93	3.34	3.45	± 1.43
Gp4	1.82	2.11	4.81	2.91	± 1.65
Burkholderiales	1.34	4.22	3.08	2.88	± 1.45
Actinomycetales	2.01	4.02	2.53	2.85	± 1.04
unknown	$6.08 \cdot 10^{-1}$	$5.24 \cdot 10^{-1}$	6.82	2.65	± 3.61
p: *Bacteroidetes*					
Sphingobacteriales	2.04	$9.86 \cdot 10^{-1}$	4.18	2.40	± 1.63
unknown	1.33	3.15	$7.86 \cdot 10^{-1}$	1.75	± 1.24
c: *Alphaproteobacteria*					
Verrucomicrobiales	1.46	1.06	1.93	1.48	± $4.34 \cdot 10^{-1}$
Rhodocyclales	$2.55 \cdot 10^{-1}$	$6.69 \cdot 10^{-1}$	3.07	1.33	± 1.52
unknown	1.14	1.57	1.16	1.29	± $2.42 \cdot 10^{-1}$
c: *Gammaproteobacteria*					
Caulobacterales	1.44	1.85	$4.69 \cdot 10^{-1}$	1.25	± $7.10 \cdot 10^{-1}$
Flavobacteriales	$5.63 \cdot 10^{-1}$	1.35	1.67	1.19	± $5.68 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$4.01 \cdot 10^{-1}$	$1.89 \cdot 10^{-2}$	2.69	1.04	± 1.45
Acidimicrobiales	$6.86 \cdot 10^{-1}$	1.34	$7.31 \cdot 10^{-1}$	$9.19 \cdot 10^{-1}$	± $3.65 \cdot 10^{-1}$
unknown	$7.62 \cdot 10^{-1}$	1.24	$7.41 \cdot 10^{-1}$	$9.14 \cdot 10^{-1}$	± $2.82 \cdot 10^{-1}$
c: *Deltaproteobacteria*					
Caldilineales	$8.83 \cdot 10^{-1}$	1.03	$5.47 \cdot 10^{-1}$	$8.21 \cdot 10^{-1}$	± $2.49 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	1.50	$5.29 \cdot 10^{-1}$	$2.77 \cdot 10^{-1}$	$7.68 \cdot 10^{-1}$	± $6.44 \cdot 10^{-1}$
Myxococcales	$6.37 \cdot 10^{-2}$	1.24	$8.12 \cdot 10^{-1}$	$7.06 \cdot 10^{-1}$	± $5.97 \cdot 10^{-1}$
Gp6	$2.41 \cdot 10^{-1}$	1.54	$2.68 \cdot 10^{-1}$	$6.83 \cdot 10^{-1}$	± $7.43 \cdot 10^{-1}$
Desulfovibrionales	$2.89 \cdot 10^{-1}$	$6.96 \cdot 10^{-2}$	1.17	$5.10 \cdot 10^{-1}$	± $5.84 \cdot 10^{-1}$
Spartobacteria_genera_inc._sed.[f]	1.20	$5.08 \cdot 10^{-2}$	$5.80 \cdot 10^{-3}$	$4.20 \cdot 10^{-1}$	± $6.78 \cdot 10^{-1}$
Erysipelotrichales	$6.49 \cdot 10^{-2}$	$6.09 \cdot 10^{-2}$	1.10	$4.08 \cdot 10^{-1}$	± $5.98 \cdot 10^{-1}$

Table S29. AE20 order-level EUB results summary continued.

Order[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Armatimonadetes_gp5	1.13	$3.19 \cdot 10^{-2}$	$3.19 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$	± $6.33 \cdot 10^{-1}$

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

Table S30. AE20 family-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Methylobacteriaceae	26.0	15.8	5.69	15.9	± 10.2
Minor phylotypes (368)[e]	11.3	14.9	16.2	14.1	± 2.52
Rhodobacteraceae	3.66	12.1	4.74	6.84	± 4.60
Ohtaekwangia	9.80	3.24	$5.80 \cdot 10^{-3}$	4.35	± 4.99
Cytophagaceae	7.14	2.55	2.27	3.99	± 2.73
unknown	4.93	2.10	4.59	3.87	± 1.55
d: *Bacteria*					
Xanthomonadaceae	4.00	6.00	$7.46 \cdot 10^{-1}$	3.58	± 2.65
Planctomycetaceae	6.71	2.36	1.34	3.47	± 2.85
unknown	3.09	5.44	1.19	3.24	± 2.13
o: *Rhizobiales*					
Gp4	1.82	2.11	4.81	2.91	± 1.65
Sphingomonadaceae	1.29	4.05	2.99	2.78	± 1.39
Ruminococcaceae	$2.56 \cdot 10^{-1}$	$3.08 \cdot 10^{-1}$	7.65	2.74	± 4.26
unknown	$6.08 \cdot 10^{-1}$	$5.24 \cdot 10^{-1}$	6.82	2.65	± 3.61
p: *Bacteroidetes*					
Porphyromonadaceae	$2.37 \cdot 10^{-2}$	$1.09 \cdot 10^{-1}$	5.43	1.85	± 3.09
unknown	$6.24 \cdot 10^{-2}$	$1.52 \cdot 10^{-1}$	5.13	1.78	± 2.90
o: *Clostridiales*					
unknown	1.33	3.15	$7.86 \cdot 10^{-1}$	1.75	± 1.24
c: *Alphaproteobacteria*					
Hyphomicrobiaceae	1.89	2.65	$6.37 \cdot 10^{-1}$	1.73	± 1.02
Saprospiraceae	$9.77 \cdot 10^{-1}$	$1.94 \cdot 10^{-1}$	3.60	1.59	± 1.78
Verrucomicrobiaceae	1.46	1.06	1.93	1.48	± $4.34 \cdot 10^{-1}$
Rhodocyclaceae	$2.55 \cdot 10^{-1}$	$6.69 \cdot 10^{-1}$	3.07	1.33	± 1.52

Table S30. AE20 family-level EUB results summary continued.

Family[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	±	SD[c]
unknown	1.14	1.57	1.16	1.29	±	$2.42 \cdot 10^{-1}$
c: *Gammaproteobacteria*						
Comamonadaceae	$6.83 \cdot 10^{-1}$	2.11	1.07	1.29	±	$7.38 \cdot 10^{-1}$
Phyllobacteriaceae	1.63	1.58	$2.95 \cdot 10^{-1}$	1.17	±	$7.58 \cdot 10^{-1}$
Prevotellaceae	$1.25 \cdot 10^{-3}$	N. D.	3.29	1.10	±	1.90
Microbacteriaceae	$8.18 \cdot 10^{-1}$	1.38	1.01	1.07	±	$2.88 \cdot 10^{-1}$
Parcubacteria_genera_inc._sed.[f]	$4.01 \cdot 10^{-1}$	$1.89 \cdot 10^{-2}$	2.69	1.04	±	1.45
unknown	$7.62 \cdot 10^{-1}$	1.24	$7.41 \cdot 10^{-1}$	$9.14 \cdot 10^{-1}$	±	$2.82 \cdot 10^{-1}$
c: *Deltaproteobacteria*						
Propionibacteriaceae	$6.33 \cdot 10^{-1}$	1.41	$6.47 \cdot 10^{-1}$	$8.97 \cdot 10^{-1}$	±	$4.45 \cdot 10^{-1}$
Flavobacteriaceae	$3.86 \cdot 10^{-1}$	1.13	1.06	$8.61 \cdot 10^{-1}$	±	$4.13 \cdot 10^{-1}$
Caldilineaceae	$8.83 \cdot 10^{-1}$	1.03	$5.47 \cdot 10^{-1}$	$8.21 \cdot 10^{-1}$	±	$2.49 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	1.50	$5.29 \cdot 10^{-1}$	$2.77 \cdot 10^{-1}$	$7.68 \cdot 10^{-1}$	±	$6.44 \cdot 10^{-1}$
Burkholderiales_inc._sed.[f]	$1.36 \cdot 10^{-1}$	$8.43 \cdot 10^{-1}$	1.13	$7.03 \cdot 10^{-1}$	±	$5.12 \cdot 10^{-1}$
Gp6	$2.41 \cdot 10^{-1}$	1.54	$2.68 \cdot 10^{-1}$	$6.83 \cdot 10^{-1}$	±	$7.43 \cdot 10^{-1}$
Bradyrhizobiaceae	$3.78 \cdot 10^{-1}$	1.08	$5.46 \cdot 10^{-1}$	$6.67 \cdot 10^{-1}$	±	$3.65 \cdot 10^{-1}$
Hyphomonadaceae	$4.41 \cdot 10^{-1}$	1.05	$3.10 \cdot 10^{-1}$	$6.02 \cdot 10^{-1}$	±	$3.97 \cdot 10^{-1}$
Rhodobiaceae	$1.17 \cdot 10^{-1}$	1.54	$4.50 \cdot 10^{-2}$	$5.68 \cdot 10^{-1}$	±	$8.43 \cdot 10^{-1}$
Nannocystaceae	$5.37 \cdot 10^{-2}$	1.09	$4.66 \cdot 10^{-1}$	$5.37 \cdot 10^{-1}$	±	$5.22 \cdot 10^{-1}$
Desulfovibrionaceae	$2.86 \cdot 10^{-1}$	$6.96 \cdot 10^{-2}$	1.17	$5.09 \cdot 10^{-1}$	±	$5.84 \cdot 10^{-1}$
Acidimicrobiaceae	$4.35 \cdot 10^{-1}$	1.01	$6.96 \cdot 10^{-2}$	$5.04 \cdot 10^{-1}$	±	$4.72 \cdot 10^{-1}$
Lachnospiraceae	$4.50 \cdot 10^{-2}$	$4.93 \cdot 10^{-2}$	1.36	$4.85 \cdot 10^{-1}$	±	$7.58 \cdot 10^{-1}$
Spartobacteria_genera_inc._sed.[f]	1.20	$5.08 \cdot 10^{-2}$	$5.80 \cdot 10^{-3}$	$4.20 \cdot 10^{-1}$	±	$6.78 \cdot 10^{-1}$
Erysipelotrichaceae	$6.49 \cdot 10^{-2}$	$6.09 \cdot 10^{-2}$	1.10	$4.08 \cdot 10^{-1}$	±	$5.98 \cdot 10^{-1}$
Armatimonadetes_gp5	1.13	$3.19 \cdot 10^{-2}$	$3.19 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$	±	$6.33 \cdot 10^{-1}$
unknown	$1.25 \cdot 10^{-3}$	$1.16 \cdot 10^{-2}$	1.13	$3.80 \cdot 10^{-1}$	±	$6.46 \cdot 10^{-1}$
o: *Bacteroidales*						

[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 S31. AE20 genus-level relative abundance summary by operational day of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average %[d]	± SD[c]
Minor phylotypes (1447)[e]	23.5	36.4	33.3	31.1	± 6.74
Meganema	26.0	15.8	5.68	15.8	± 10.2
Ohtaekwangia	9.80	3.24	$5.80 \cdot 10^{-3}$	4.35	± 4.99
unknown d: *Bacteria*	4.93	2.10	4.59	3.87	± 1.55
unknown o: *Rhizobiales*	3.09	5.44	1.19	3.24	± 2.13
Leadbetterella	6.16	1.48	1.31	2.99	± 2.75
Gp4	1.82	2.11	4.81	2.91	± 1.65
unknown p: *Bacteroidetes*	$6.08 \cdot 10^{-1}$	$5.24 \cdot 10^{-1}$	6.82	2.65	± 3.61
Amaricoccus	$4.25 \cdot 10^{-2}$	4.20	2.68	2.31	± 2.10
Paracoccus	1.18	3.75	$5.88 \cdot 10^{-1}$	1.84	± 1.68
unknown f: *Rhodobacteraceae*	1.76	2.71	$9.71 \cdot 10^{-1}$	1.81	± $8.70 \cdot 10^{-1}$
unknown o: *Clostridiales*	$6.24 \cdot 10^{-2}$	$1.52 \cdot 10^{-1}$	5.13	1.78	± 2.90
unknown c: *Alphaproteobacteria*	1.33	3.15	$7.86 \cdot 10^{-1}$	1.75	± 1.24
unknown f: *Ruminococcaceae*	$1.71 \cdot 10^{-1}$	$2.05 \cdot 10^{-1}$	4.42	1.60	± 2.44
Haliscomenobacter	$9.69 \cdot 10^{-1}$	$1.61 \cdot 10^{-1}$	3.58	1.57	± 1.79
unknown c: *Gammaproteobacteria*	1.14	1.57	1.16	1.29	± $2.42 \cdot 10^{-1}$
Planctomyces	3.00	$4.09 \cdot 10^{-1}$	$4.28 \cdot 10^{-1}$	1.28	± 1.49
Proteiniphilum	$1.25 \cdot 10^{-2}$	$6.24 \cdot 10^{-2}$	3.28	1.12	± 1.87
Parcubacteria_genera_inc._sed.[f]	$4.01 \cdot 10^{-1}$	$1.89 \cdot 10^{-2}$	2.69	1.04	± 1.45
Thauera	$2.49 \cdot 10^{-1}$	$4.99 \cdot 10^{-1}$	2.31	1.02	± 1.13
Schlesneria	2.68	$2.32 \cdot 10^{-1}$	$9.72 \cdot 10^{-2}$	1.00	± 1.45
Pseudofulvimonas	2.78	$1.10 \cdot 10^{-1}$	N. D.	$9.64 \cdot 10^{-1}$	± 1.58
Luteimonas	$6.07 \cdot 10^{-1}$	2.24	$2.90 \cdot 10^{-2}$	$9.57 \cdot 10^{-1}$	± 1.14
unknown c: *Deltaproteobacteria*	$7.62 \cdot 10^{-1}$	1.24	$7.41 \cdot 10^{-1}$	$9.14 \cdot 10^{-1}$	± $2.82 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[f]	1.50	$5.29 \cdot 10^{-1}$	$2.77 \cdot 10^{-1}$	$7.68 \cdot 10^{-1}$	± $6.44 \cdot 10^{-1}$
unknown f: *Propionibacteriaceae*	$5.47 \cdot 10^{-1}$	1.16	$5.89 \cdot 10^{-1}$	$7.65 \cdot 10^{-1}$	± $3.42 \cdot 10^{-1}$
Hyphomicrobium	$8.28 \cdot 10^{-1}$	1.15	$2.93 \cdot 10^{-1}$	$7.58 \cdot 10^{-1}$	± $4.34 \cdot 10^{-1}$
unknown f: *Sphingomonadaceae*	$2.82 \cdot 10^{-1}$	1.14	$8.14 \cdot 10^{-1}$	$7.46 \cdot 10^{-1}$	± $4.34 \cdot 10^{-1}$

Table S31. AE20 genus-level EUB results summary continued.

Genus[a,b]	Day 29 %[d]	Day 52 %[d]	Day 271 %[d]	Average ± %[d]	SD[c]
unknown	$2.92 \cdot 10^{-1}$	1.76	$5.22 \cdot 10^{-2}$	$7.01 \cdot 10^{-1}$ ±	$9.24 \cdot 10^{-1}$
f: *Xanthomonadaceae*					
Prosthecobacter	$1.82 \cdot 10^{-1}$	$4.92 \cdot 10^{-1}$	1.40	$6.90 \cdot 10^{-1}$ ±	$6.30 \cdot 10^{-1}$
Gp6	$2.41 \cdot 10^{-1}$	1.54	$2.68 \cdot 10^{-1}$	$6.83 \cdot 10^{-1}$ ±	$7.43 \cdot 10^{-1}$
Oscillibacter	$3.25 \cdot 10^{-2}$	$2.18 \cdot 10^{-2}$	1.70	$5.85 \cdot 10^{-1}$ ±	$9.66 \cdot 10^{-1}$
Sphingomonas	$1.27 \cdot 10^{-1}$	$4.87 \cdot 10^{-1}$	1.13	$5.82 \cdot 10^{-1}$ ±	$5.08 \cdot 10^{-1}$
unknown	N. D.	N. D.	1.67	$5.56 \cdot 10^{-1}$ ±	$9.62 \cdot 10^{-1}$
f: *Prevotellaceae*					
Novosphingobium	$3.38 \cdot 10^{-1}$	1.15	$1.62 \cdot 10^{-1}$	$5.50 \cdot 10^{-1}$ ±	$5.26 \cdot 10^{-1}$
unknown	$1.71 \cdot 10^{-1}$	$3.26 \cdot 10^{-1}$	1.01	$5.01 \cdot 10^{-1}$ ±	$4.45 \cdot 10^{-1}$
f: *Flavobacteriaceae*					
Hallella	$1.25 \cdot 10^{-3}$	N. D.	1.49	$4.98 \cdot 10^{-1}$ ±	$8.61 \cdot 10^{-1}$
unknown	$3.75 \cdot 10^{-3}$	$2.18 \cdot 10^{-2}$	1.35	$4.59 \cdot 10^{-1}$ ±	$7.73 \cdot 10^{-1}$
f: *Porphyromonadaceae*					
Spartobacteria_genera_inc._sed.[f]	1.20	$5.08 \cdot 10^{-2}$	$5.80 \cdot 10^{-3}$	$4.20 \cdot 10^{-1}$ ±	$6.78 \cdot 10^{-1}$
Parvibaculum	N. D.	1.23	$1.45 \cdot 10^{-3}$	$4.09 \cdot 10^{-1}$ ±	$7.07 \cdot 10^{-1}$
Armatimonadetes_gp5	1.13	$3.19 \cdot 10^{-2}$	$3.19 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$ ±	$6.33 \cdot 10^{-1}$
unknown	$1.25 \cdot 10^{-3}$	$1.16 \cdot 10^{-2}$	1.13	$3.80 \cdot 10^{-1}$ ±	$6.46 \cdot 10^{-1}$
o: *Bacteroidales*					
Nannocystis	$4.87 \cdot 10^{-2}$	1.06	$2.18 \cdot 10^{-2}$	$3.76 \cdot 10^{-1}$ ±	$5.91 \cdot 10^{-1}$

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

Table S32. Summary of domain-level relative abundance by reactor of the 16S rRNA gene sequencing results with the EUB primer set.

Domain[a,b]	AE4 (S8)		AE8 (S14)		AE12 (S20)		AE20 (S26)	
	Average ± %[d]	SD[c]	Average ± %[d]	SD[c]	Average ± %[d]	SD[c]	Average ± %[d]	SD[c]
Bacteria	99.9	$\pm 8.01 \cdot 10^{-2}$	99.9	$\pm 2.78 \cdot 10^{-2}$	99.9	$\pm 7.16 \cdot 10^{-2}$	99.8	$\pm 7.85 \cdot 10^{-2}$

Table S32. Summary of domain-level EUB results continued.

Domain[a,b]	AE4 (S8)			AE8 (S14)			AE12 (S20)			AE20 (S26)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Minor phylotypes (2)[e]	$1.32 \cdot 10^{-1}$	±	$8.01 \cdot 10^{-2}$	$9.52 \cdot 10^{-2}$	±	$2.78 \cdot 10^{-2}$	$1.23 \cdot 10^{-1}$	±	$7.16 \cdot 10^{-2}$	$1.96 \cdot 10^{-1}$	±	$7.85 \cdot 10^{-2}$

[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 S33. Summary of phylum-level relative abundance by reactor of the 16S rRNA gene sequencing results with the EUB primer set.

Phylum[a,b]	AE4 (S9)			AE8 (S15)			AE12 (S21)			AE20 (S27)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Proteobacteria	49.3	±	13.0	54.3	±	14.6	59.9	±	11.9	52.3	±	19.4
Bacteroidetes	18.7	±	7.88	13.8	±	7.59	14.8	±	8.54	18.4	±	8.79
unknown d: *Bacteria*	9.96	±	4.75	8.53	±	5.05	4.10	±	2.99	3.87	±	1.55
Firmicutes	6.81	±	8.58	6.74	±	7.49	5.27	±	7.39	6.68	±	9.96
Acidobacteria	1.86	±	1.41	2.64	±	1.96	2.49	±	1.95	4.42	±	1.65
Actinobacteria	2.53	±	2.04	3.30	±	2.67	3.62	±	2.82	4.05	±	1.51
Planctomycetes	2.14	±	1.46	3.37	±	1.74	3.06	±	1.95	3.54	±	2.78
Verrucomicrobia	2.59	±	2.02	3.21	±	2.95	1.16	±	1.02	2.33	±	$8.86 \cdot 10^{-1}$
Candidatus Saccharibacteria	1.75	±	2.37	1.11	±	$9.38 \cdot 10^{-1}$	2.30	±	3.11	$7.68 \cdot 10^{-1}$	±	$6.44 \cdot 10^{-1}$
Parcubacteria	1.61	±	2.01	$4.74 \cdot 10^{-1}$	±	$4.16 \cdot 10^{-1}$	$6.27 \cdot 10^{-1}$	±	$3.61 \cdot 10^{-1}$	1.04	±	1.45
Chloroflexi	$7.02 \cdot 10^{-1}$	±	$3.76 \cdot 10^{-1}$	$7.32 \cdot 10^{-1}$	±	$3.08 \cdot 10^{-1}$	1.02	±	$6.35 \cdot 10^{-1}$	1.04	±	$3.58 \cdot 10^{-1}$
Spirochaetes	$9.68 \cdot 10^{-1}$	±	1.40	$5.14 \cdot 10^{-1}$	±	$5.99 \cdot 10^{-1}$	$6.25 \cdot 10^{-1}$	±	1.05	$2.32 \cdot 10^{-1}$	±	$3.84 \cdot 10^{-1}$
Minor phylotypes (33)[e]	$7.57 \cdot 10^{-1}$	±	$3.98 \cdot 10^{-1}$	$8.77 \cdot 10^{-1}$	±	$1.48 \cdot 10^{-1}$	$7.29 \cdot 10^{-1}$	±	$4.50 \cdot 10^{-1}$	$8.31 \cdot 10^{-1}$	±	$4.72 \cdot 10^{-2}$
Armatimonadetes	$1.96 \cdot 10^{-2}$	±	$1.56 \cdot 10^{-2}$	$7.45 \cdot 10^{-2}$	±	$3.94 \cdot 10^{-2}$	$6.31 \cdot 10^{-2}$	±	$4.83 \cdot 10^{-2}$	$4.60 \cdot 10^{-1}$	±	$6.93 \cdot 10^{-1}$
SR1	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$	$2.60 \cdot 10^{-1}$	±	$4.13 \cdot 10^{-1}$	$2.67 \cdot 10^{-1}$	±	$4.60 \cdot 10^{-1}$	$1.25 \cdot 10^{-3}$	±	$2.16 \cdot 10^{-3}$

[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] 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 S34. Summary of class-level relative abundance by reactor of the 16S rRNA gene sequencing results with the EUB primer set.

Class[a,b]	AE4 (S10)			AE8 (S16)			AE12 (S22)			AE20 (S28)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Alphaproteobacteria	25.8	±	18.7	31.3	±	16.8	38.0	±	22.8	38.3	±	17.7
Betaproteobacteria	13.8	±	6.64	13.4	±	4.53	15.1	±	11.9	4.86	±	2.86
unknown	9.96	±	4.75	8.53	±	5.05	4.10	±	2.99	3.87	±	1.55
d: *Bacteria*												
Gammaproteobacteria	5.29	±	4.62	6.14	±	1.56	3.77	±	$9.02 \cdot 10^{-1}$	5.68	±	3.02
Bacteroidia	5.88	±	7.43	4.51	±	6.53	3.63	±	6.23	3.71	±	6.27
Clostridia	3.81	±	3.98	4.52	±	4.22	3.24	±	4.22	5.67	±	8.53
Sphingobacteriia	4.58	±	2.96	3.31	±	1.63	3.82	±	4.05	2.40	±	1.63
Bacteroidetes_inc._sed.[e]	$6.68 \cdot 10^{-1}$	±	$7.07 \cdot 10^{-1}$	$5.44 \cdot 10^{-1}$	±	$2.58 \cdot 10^{-1}$	1.35	±	1.16	4.35	±	4.99
Cytophagia	3.00	±	2.38	1.44	±	1.38	1.85	±	1.22	4.11	±	2.66
Actinobacteria	2.52	±	2.03	3.29	±	2.66	3.61	±	2.82	4.04	±	1.51
Planctomycetia	2.12	±	1.47	3.33	±	1.78	3.05	±	1.96	3.52	±	2.79
Acidobacteria_Gp4	1.46	±	1.24	1.88	±	2.02	2.07	±	1.72	3.49	±	1.65
unknown	2.54	±	3.67	2.55	±	2.78	3.13	±	4.69	2.65	±	3.61
p: *Bacteroidetes*												
Deltaproteobacteria	2.67	±	1.44	1.87	±	$8.72 \cdot 10^{-1}$	1.63	±	$5.28 \cdot 10^{-1}$	2.53	±	$9.73 \cdot 10^{-1}$
Verrucomicrobiae	1.51	±	1.27	2.41	±	2.77	$6.26 \cdot 10^{-1}$	±	$6.66 \cdot 10^{-1}$	1.48	±	$4.34 \cdot 10^{-1}$
Saccharibacteria_genera_inc._sed.[e]	1.75	±	2.37	1.11	±	$9.38 \cdot 10^{-1}$	2.30	±	3.11	$7.68 \cdot 10^{-1}$	±	$6.44 \cdot 10^{-1}$
Erysipelotrichia	2.24	±	3.65	1.59	±	2.50	1.47	±	2.42	$4.08 \cdot 10^{-1}$	±	$5.98 \cdot 10^{-1}$
Minor phylotypes (77)[f]	1.93	±	$4.67 \cdot 10^{-1}$	2.22	±	$2.30 \cdot 10^{-1}$	1.75	±	$5.44 \cdot 10^{-1}$	2.10	±	$4.49 \cdot 10^{-1}$
Flavobacteriia	1.98	±	1.70	1.48	±	$7.49 \cdot 10^{-1}$	$9.96 \cdot 10^{-1}$	±	$5.76 \cdot 10^{-1}$	1.19	±	$5.68 \cdot 10^{-1}$
unknown	1.65	±	$3.06 \cdot 10^{-1}$	1.65	±	$5.33 \cdot 10^{-1}$	1.40	±	$7.00 \cdot 10^{-2}$	$9.51 \cdot 10^{-1}$	±	$2.99 \cdot 10^{-2}$
p: *Proteobacteria*												
Parcubacteria_genera_inc._sed.[e]	1.61	±	2.01	$4.74 \cdot 10^{-1}$	±	$4.16 \cdot 10^{-1}$	$6.27 \cdot 10^{-1}$	±	$3.61 \cdot 10^{-1}$	1.04	±	1.45
Spirochaetia	$9.68 \cdot 10^{-1}$	±	1.40	$5.14 \cdot 10^{-1}$	±	$5.99 \cdot 10^{-1}$	$6.25 \cdot 10^{-1}$	±	1.05	$2.32 \cdot 10^{-1}$	±	$3.84 \cdot 10^{-1}$
Caldilineae	$4.44 \cdot 10^{-1}$	±	$1.66 \cdot 10^{-1}$	$5.42 \cdot 10^{-1}$	±	$1.83 \cdot 10^{-1}$	$7.21 \cdot 10^{-1}$	±	$3.50 \cdot 10^{-1}$	$8.21 \cdot 10^{-1}$	±	$2.49 \cdot 10^{-1}$
Acidobacteria_Gp6	$2.39 \cdot 10^{-1}$	±	$1.59 \cdot 10^{-1}$	$3.80 \cdot 10^{-1}$	±	$2.24 \cdot 10^{-1}$	$2.35 \cdot 10^{-1}$	±	$1.73 \cdot 10^{-1}$	$6.83 \cdot 10^{-1}$	±	$7.43 \cdot 10^{-1}$
Spartobacteria	$5.79 \cdot 10^{-1}$	±	$8.07 \cdot 10^{-1}$	$3.16 \cdot 10^{-1}$	±	$1.83 \cdot 10^{-1}$	$2.10 \cdot 10^{-1}$	±	$3.05 \cdot 10^{-1}$	$4.34 \cdot 10^{-1}$	±	$7.00 \cdot 10^{-1}$
unknown	$5.73 \cdot 10^{-1}$	±	$8.61 \cdot 10^{-1}$	$4.23 \cdot 10^{-1}$	±	$6.54 \cdot 10^{-1}$	$3.85 \cdot 10^{-1}$	±	$6.52 \cdot 10^{-1}$	$3.15 \cdot 10^{-1}$	±	$5.24 \cdot 10^{-1}$
p: *Firmicutes*												
Armatimonadetes_gp5	$6.31 \cdot 10^{-3}$	±	$6.07 \cdot 10^{-3}$	$4.38 \cdot 10^{-2}$	±	$2.47 \cdot 10^{-2}$	$4.89 \cdot 10^{-2}$	±	$5.43 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$	±	$6.33 \cdot 10^{-1}$
SR1_genera_inc._sed.[e]	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$	$2.60 \cdot 10^{-1}$	±	$4.13 \cdot 10^{-1}$	$2.67 \cdot 10^{-1}$	±	$4.60 \cdot 10^{-1}$	$1.25 \cdot 10^{-3}$	±	$2.16 \cdot 10^{-3}$

[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] 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 S35. Summary of order-level relative abundance by reactor of the 16S rRNA gene sequencing results with the EUB primer set.

Order[a,b]	AE4 (S11)			AE8 (S17)			AE12 (S23)			AE20 (S29)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Rhizobiales	18.9	±	14.7	20.1	±	9.79	26.2	±	16.6	24.1	±	13.6
Rhodocyclales	9.42	±	8.29	6.55	±	7.59	9.98	±	13.7	1.33	±	1.52
unknown	9.96	±	4.75	8.53	±	5.05	4.10	±	2.99	3.87	±	1.55
d: *Bacteria*												
Rhodobacterales	2.29	±	1.51	4.60	±	4.28	5.16	±	4.49	6.84	±	4.60
Burkholderiales	3.88	±	2.13	6.05	±	3.70	4.69	±	2.25	2.88	±	1.45
Bacteroidales	5.88	±	7.43	4.51	±	6.53	3.63	±	6.23	3.71	±	6.27
Clostridiales	3.80	±	3.96	4.50	±	4.21	3.23	±	4.20	5.65	±	8.51
Sphingobacteriales	4.58	±	2.96	3.31	±	1.63	3.82	±	4.05	2.40	±	1.63
Ohtaekwangia	$6.68\cdot10^{-1}$	±	$7.07\cdot10^{-1}$	$5.43\cdot10^{-1}$	±	$2.58\cdot10^{-1}$	1.35	±	1.16	4.35	±	4.99
Minor phylotypes (168)[e]	3.46	±	$5.17\cdot10^{-1}$	4.31	±	$1.26\cdot10^{-1}$	3.17	±	1.10	4.16	±	1.02
Cytophagales	3.00	±	2.38	1.44	±	1.38	1.85	±	1.22	4.11	±	2.66
Xanthomonadales	4.10	±	4.20	3.85	±	1.01	2.52	±	1.43	3.84	±	2.66
Planctomycetales	2.10	±	1.46	3.29	±	1.77	3.03	±	1.98	3.47	±	2.85
Sphingomonadales	2.11	±	1.67	2.68	±	1.57	2.47	±	1.84	3.45	±	1.43
unknown	2.54	±	3.67	2.55	±	2.78	3.13	±	4.69	2.65	±	3.61
p: *Bacteroidetes*												
Gp4	$6.67\cdot10^{-1}$	±	$6.40\cdot10^{-1}$	$8.83\cdot10^{-1}$	±	$8.02\cdot10^{-1}$	1.65	±	1.17	2.91	±	1.65
Actinomycetales	1.70	±	1.47	2.47	±	1.80	2.49	±	1.61	2.85	±	1.04
Verrucomicrobiales	1.51	±	1.27	2.41	±	2.77	$6.26\cdot10^{-1}$	±	$6.66\cdot10^{-1}$	1.48	±	$4.34\cdot10^{-1}$
unknown	1.15	±	$7.14\cdot10^{-1}$	1.83	±	$9.53\cdot10^{-1}$	2.37	±	1.02	1.75	±	1.24
c: *Alphaproteobacteria*												
Saccharibacteria_genera_inc._sed.[f]	1.75	±	2.37	1.11	±	$9.38\cdot10^{-1}$	2.30	±	3.11	$7.68\cdot10^{-1}$	±	$6.44\cdot10^{-1}$
Erysipelotrichales	2.24	±	3.65	1.59	±	2.50	1.47	±	2.42	$4.08\cdot10^{-1}$	±	$5.98\cdot10^{-1}$
Flavobacteriales	1.98	±	1.70	1.48	±	$7.49\cdot10^{-1}$	$9.96\cdot10^{-1}$	±	$5.76\cdot10^{-1}$	1.19	±	$5.68\cdot10^{-1}$
unknown	1.65	±	$3.06\cdot10^{-1}$	1.65	±	$5.33\cdot10^{-1}$	1.40	±	$7.00\cdot10^{-2}$	$9.51\cdot10^{-1}$	±	$2.99\cdot10^{-2}$
p: *Proteobacteria*												
Parcubacteria_genera_inc._sed.[f]	1.61	±	2.01	$4.74\cdot10^{-1}$	±	$4.16\cdot10^{-1}$	$6.27\cdot10^{-1}$	±	$3.61\cdot10^{-1}$	1.04	±	1.45
unknown	$6.42\cdot10^{-1}$	±	$3.22\cdot10^{-1}$	1.49	±	$7.71\cdot10^{-1}$	$7.06\cdot10^{-1}$	±	$2.74\cdot10^{-1}$	1.29	±	$2.42\cdot10^{-1}$
c: *Gammaproteobacteria*												
Caulobacterales	$7.47\cdot10^{-1}$	±	$5.46\cdot10^{-1}$	1.19	±	$2.26\cdot10^{-1}$	1.17	±	$7.41\cdot10^{-1}$	1.25	±	$7.10\cdot10^{-1}$
unknown	1.15	±	$8.01\cdot10^{-1}$	$7.18\cdot10^{-1}$	±	$2.95\cdot10^{-1}$	$8.09\cdot10^{-1}$	±	$4.25\cdot10^{-1}$	$9.14\cdot10^{-1}$	±	$2.82\cdot10^{-1}$
c: *Deltaproteobacteria*												
Myxococcales	1.13	±	1.33	$7.55\cdot10^{-1}$	±	$7.64\cdot10^{-1}$	$4.30\cdot10^{-1}$	±	$4.52\cdot10^{-1}$	$7.06\cdot10^{-1}$	±	$5.97\cdot10^{-1}$
Blastocatella	$7.74\cdot10^{-1}$	±	$6.90\cdot10^{-1}$	$9.75\cdot10^{-1}$	±	1.20	$3.96\cdot10^{-1}$	±	$5.22\cdot10^{-1}$	$5.16\cdot10^{-1}$	±	$7.85\cdot10^{-2}$
Spirochaetales	$9.68\cdot10^{-1}$	±	1.40	$5.14\cdot10^{-1}$	±	$5.99\cdot10^{-1}$	$6.25\cdot10^{-1}$	±	1.05	$2.32\cdot10^{-1}$	±	$3.84\cdot10^{-1}$
Acidimicrobiales	$7.30\cdot10^{-1}$	±	$6.96\cdot10^{-1}$	$6.95\cdot10^{-1}$	±	$8.54\cdot10^{-1}$	$9.58\cdot10^{-1}$	±	1.20	$9.19\cdot10^{-1}$	±	$3.65\cdot10^{-1}$
Rhodospirillales	$5.54\cdot10^{-1}$	±	$2.61\cdot10^{-1}$	$7.91\cdot10^{-1}$	±	$4.63\cdot10^{-1}$	$5.82\cdot10^{-1}$	±	$3.08\cdot10^{-1}$	$8.33\cdot10^{-1}$	±	$2.63\cdot10^{-1}$
Caldilineales	$4.44\cdot10^{-1}$	±	$1.66\cdot10^{-1}$	$5.42\cdot10^{-1}$	±	$1.83\cdot10^{-1}$	$7.21\cdot10^{-1}$	±	$3.50\cdot10^{-1}$	$8.21\cdot10^{-1}$	±	$2.49\cdot10^{-1}$

Table S35. Summary of order-level EUB results continued.

Order[a,b]	AE4 (S11)			AE8 (S17)			AE12 (S23)			AE20 (S29)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Gp6	$2.39 \cdot 10^{-1}$	±	$1.59 \cdot 10^{-1}$	$3.80 \cdot 10^{-1}$	±	$2.24 \cdot 10^{-1}$	$2.35 \cdot 10^{-1}$	±	$1.73 \cdot 10^{-1}$	$6.83 \cdot 10^{-1}$	±	$7.43 \cdot 10^{-1}$
Spartobacteria_genera_inc._sed.[f]	$5.74 \cdot 10^{-1}$	±	$8.00 \cdot 10^{-1}$	$3.10 \cdot 10^{-1}$	±	$1.84 \cdot 10^{-1}$	$2.07 \cdot 10^{-1}$	±	$3.03 \cdot 10^{-1}$	$4.20 \cdot 10^{-1}$	±	$6.78 \cdot 10^{-1}$
unknown	$5.73 \cdot 10^{-1}$	±	$8.61 \cdot 10^{-1}$	$4.23 \cdot 10^{-1}$	±	$6.54 \cdot 10^{-1}$	$3.85 \cdot 10^{-1}$	±	$6.52 \cdot 10^{-1}$	$3.15 \cdot 10^{-1}$	±	$5.24 \cdot 10^{-1}$
p: *Firmicutes*												
Desulfovibrionales	$1.89 \cdot 10^{-1}$	±	$2.14 \cdot 10^{-1}$	$2.28 \cdot 10^{-1}$	±	$3.39 \cdot 10^{-1}$	$2.31 \cdot 10^{-1}$	±	$2.34 \cdot 10^{-1}$	$5.10 \cdot 10^{-1}$	±	$5.84 \cdot 10^{-1}$
Armatimonadetes_gp5	$6.31 \cdot 10^{-3}$	±	$6.07 \cdot 10^{-3}$	$4.38 \cdot 10^{-2}$	±	$2.47 \cdot 10^{-2}$	$4.89 \cdot 10^{-2}$	±	$5.43 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$	±	$6.33 \cdot 10^{-1}$
SR1_genera_inc._sed.[f]	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$	$2.60 \cdot 10^{-1}$	±	$4.13 \cdot 10^{-1}$	$2.67 \cdot 10^{-1}$	±	$4.60 \cdot 10^{-1}$	$1.25 \cdot 10^{-3}$	±	$2.16 \cdot 10^{-3}$

[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] 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 S36. Summary of family-level relative abundance by reactor of the 16S rRNA gene sequencing results with the EUB primer set.

Family[a,b]	AE4 (S12)			AE8 (S18)			AE12 (S24)			AE20 (S30)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Methylobacteriaceae	14.4	±	11.3	13.6	±	5.82	19.6	±	13.0	15.9	±	10.2
Rhodocyclaceae	9.42	±	8.29	6.55	±	7.59	9.98	±	13.7	1.33	±	1.52
unknown	9.96	±	4.75	8.53	±	5.05	4.10	±	2.99	3.87	±	1.55
d: *Bacteria*												
Minor phylotypes (353)[e]	7.71	±	$8.28 \cdot 10^{-2}$	9.79	±	1.32	7.06	±	1.01	9.20	±	2.15
Rhodobacteraceae	2.29	±	1.51	4.60	±	4.28	5.16	±	4.49	6.84	±	4.60
Ohtaekwangia	$6.68 \cdot 10^{-1}$	±	$7.07 \cdot 10^{-1}$	$5.43 \cdot 10^{-1}$	±	$2.58 \cdot 10^{-1}$	1.35	±	1.16	4.35	±	4.99
Cytophagaceae	2.95	±	2.38	1.16	±	1.04	1.72	±	1.34	3.99	±	2.73
Xanthomonadaceae	3.91	±	4.14	3.61	±	$9.10 \cdot 10^{-1}$	2.26	±	1.40	3.58	±	2.65
Planctomycetaceae	2.10	±	1.46	3.29	±	1.77	3.03	±	1.98	3.47	±	2.85
unknown	1.58	±	1.06	2.36	±	1.11	2.14	±	$6.72 \cdot 10^{-1}$	3.24	±	2.13
o: *Rhizobiales*												
unknown	2.54	±	3.67	2.55	±	2.78	3.13	±	4.69	2.65	±	3.61
p: *Bacteroidetes*												
Porphyromonadaceae	3.08	±	3.74	2.48	±	3.42	1.49	±	2.53	1.85	±	3.09
Comamonadaceae	2.08	±	1.12	3.00	±	2.06	2.31	±	1.70	1.29	±	$7.38 \cdot 10^{-1}$
Gp4	$6.67 \cdot 10^{-1}$	±	$6.40 \cdot 10^{-1}$	$8.83 \cdot 10^{-1}$	±	$8.02 \cdot 10^{-1}$	1.65	±	1.17	2.91	±	1.65
Sphingomonadaceae	1.46	±	$9.27 \cdot 10^{-1}$	2.02	±	1.24	1.72	±	1.10	2.78	±	1.39

Table S36. Summary of family-level EUB results continued.

Family[a,b]	AE4 (S12)			AE8 (S18)			AE12 (S24)			AE20 (S30)		
	Average	±	SD[c] %[d]	Average	±	SD[c] %[d]	Average	±	SD[c] %[d]	Average	±	SD[c] %[d]
Ruminococcaceae	1.65	±	1.55	2.00	±	1.81	1.29	±	1.75	2.74	±	4.26
Verrucomicrobiaceae	1.51	±	1.27	2.41	±	2.77	$6.26\cdot10^{-1}$	±	$6.66\cdot10^{-1}$	1.48	±	$4.34\cdot10^{-1}$
unknown	1.15	±	$7.14\cdot10^{-1}$	1.83	±	$9.53\cdot10^{-1}$	2.37	±	1.02	1.75	±	1.24
c: *Alphaproteobacteria*												
Saccharibacteria_genera_inc._sed.[f]	1.75	±	2.37	1.11	±	$9.38\cdot10^{-1}$	2.30	±	3.11	$7.68\cdot10^{-1}$	±	$6.44\cdot10^{-1}$
Erysipelotrichaceae	2.24	±	3.65	1.59	±	2.50	1.47	±	2.42	$4.08\cdot10^{-1}$	±	$5.98\cdot10^{-1}$
unknown	1.39	±	1.99	1.47	±	1.72	1.29	±	2.11	1.78	±	2.90
o: *Clostridiales*												
Chitinophagaceae	1.78	±	2.21	1.18	±	$4.66\cdot10^{-1}$	1.02	±	$8.81\cdot10^{-1}$	$4.67\cdot10^{-1}$	±	$1.46\cdot10^{-1}$
Burkholderiales_inc._sed.[f]	1.03	±	$8.27\cdot10^{-1}$	1.78	±	1.50	1.59	±	2.06	$7.03\cdot10^{-1}$	±	$5.12\cdot10^{-1}$
Hyphomicrobiaceae	$9.18\cdot10^{-1}$	±	$8.18\cdot10^{-1}$	1.44	±	1.18	1.46	±	$9.37\cdot10^{-1}$	1.73	±	1.02
Phyllobacteriaceae	1.08	±	1.01	1.36	±	$8.10\cdot10^{-1}$	1.71	±	1.24	1.17	±	$7.58\cdot10^{-1}$
unknown	1.65	±	$3.06\cdot10^{-1}$	1.65	±	$5.33\cdot10^{-1}$	1.40	±	$7.00\cdot10^{-2}$	$9.51\cdot10^{-1}$	±	$2.99\cdot10^{-2}$
p: *Proteobacteria*												
Parcubacteria_genera_inc._sed.[f]	1.61	±	2.01	$4.74\cdot10^{-1}$	±	$4.16\cdot10^{-1}$	$6.27\cdot10^{-1}$	±	$3.61\cdot10^{-1}$	1.04	±	1.45
Saprospiraceae	1.27	±	1.39	1.21	±	1.04	1.31	±	1.39	1.59	±	1.78
unknown	$6.42\cdot10^{-1}$	±	$3.22\cdot10^{-1}$	1.49	±	$7.71\cdot10^{-1}$	$7.06\cdot10^{-1}$	±	$2.74\cdot10^{-1}$	1.29	±	$2.42\cdot10^{-1}$
c: *Gammaproteobacteria*												
Flavobacteriaceae	1.48	±	1.31	1.11	±	$6.94\cdot10^{-1}$	$7.21\cdot10^{-1}$	±	$3.01\cdot10^{-1}$	$8.61\cdot10^{-1}$	±	$4.13\cdot10^{-1}$
unknown	1.15	±	$8.01\cdot10^{-1}$	$7.18\cdot10^{-1}$	±	$2.95\cdot10^{-1}$	$8.09\cdot10^{-1}$	±	$4.25\cdot10^{-1}$	$9.14\cdot10^{-1}$	±	$2.82\cdot10^{-1}$
c: *Deltaproteobacteria*												
unknown	1.13	±	1.40	$6.33\cdot10^{-1}$	±	$9.99\cdot10^{-1}$	$7.78\cdot10^{-1}$	±	1.34	$3.80\cdot10^{-1}$	±	$6.46\cdot10^{-1}$
o: *Bacteroidales*												
Prevotellaceae	$3.91\cdot10^{-1}$	±	$6.02\cdot10^{-1}$	$6.23\cdot10^{-1}$	±	1.04	$4.24\cdot10^{-1}$	±	$7.34\cdot10^{-1}$	1.10	±	1.90
Microbacteriaceae	$6.50\cdot10^{-1}$	±	$5.21\cdot10^{-1}$	$7.43\cdot10^{-1}$	±	$4.92\cdot10^{-1}$	$9.31\cdot10^{-1}$	±	$6.11\cdot10^{-1}$	1.07	±	$2.88\cdot10^{-1}$
Bacteroidaceae	$9.92\cdot10^{-1}$	±	1.23	$5.78\cdot10^{-1}$	±	$7.69\cdot10^{-1}$	$7.16\cdot10^{-1}$	±	1.24	$2.82\cdot10^{-1}$	±	$4.63\cdot10^{-1}$
Blastocatella	$7.74\cdot10^{-1}$	±	$6.90\cdot10^{-1}$	$9.75\cdot10^{-1}$	±	1.20	$3.96\cdot10^{-1}$	±	$5.22\cdot10^{-1}$	$5.16\cdot10^{-1}$	±	$7.85\cdot10^{-2}$
Cyclobacteriaceae	$3.10\cdot10^{-1}$	±	$2.69\cdot10^{-1}$	$1.75\cdot10^{-1}$	±	$1.56\cdot10^{-1}$	$9.42\cdot10^{-1}$	±	1.41	$1.81\cdot10^{-1}$	±	$1.41\cdot10^{-1}$
Nannocystaceae	$9.31\cdot10^{-1}$	±	1.42	$5.11\cdot10^{-1}$	±	$8.61\cdot10^{-1}$	$3.56\cdot10^{-1}$	±	$3.74\cdot10^{-1}$	$5.37\cdot10^{-1}$	±	$5.22\cdot10^{-1}$
Sphingobacteriaceae	$9.19\cdot10^{-1}$	±	1.37	$3.69\cdot10^{-1}$	±	$4.24\cdot10^{-1}$	$2.14\cdot10^{-1}$	±	$2.01\cdot10^{-1}$	$1.11\cdot10^{-1}$	±	$1.51\cdot10^{-1}$
Propionibacteriaceae	$2.53\cdot10^{-1}$	±	$2.95\cdot10^{-1}$	$3.01\cdot10^{-1}$	±	$2.43\cdot10^{-1}$	$6.91\cdot10^{-1}$	±	$5.05\cdot10^{-1}$	$8.97\cdot10^{-1}$	±	$4.45\cdot10^{-1}$
Caldilineaceae	$4.44\cdot10^{-1}$	±	$1.66\cdot10^{-1}$	$5.42\cdot10^{-1}$	±	$1.83\cdot10^{-1}$	$7.21\cdot10^{-1}$	±	$3.50\cdot10^{-1}$	$8.21\cdot10^{-1}$	±	$2.49\cdot10^{-1}$
Acidimicrobiaceae	$5.90\cdot10^{-1}$	±	$6.22\cdot10^{-1}$	$4.62\cdot10^{-1}$	±	$5.59\cdot10^{-1}$	$7.69\cdot10^{-1}$	±	1.03	$5.04\cdot10^{-1}$	±	$4.72\cdot10^{-1}$
unknown	$2.89\cdot10^{-1}$	±	$1.81\cdot10^{-1}$	$7.67\cdot10^{-1}$	±	$7.26\cdot10^{-1}$	$4.39\cdot10^{-1}$	±	$3.34\cdot10^{-1}$	$3.95\cdot10^{-1}$	±	$1.55\cdot10^{-1}$
o: *Burkholderiales*												
Spirochaetaceae	$7.61\cdot10^{-1}$	±	1.23	$3.40\cdot10^{-1}$	±	$5.57\cdot10^{-1}$	$5.35\cdot10^{-1}$	±	$9.27\cdot10^{-1}$	$1.62\cdot10^{-1}$	±	$2.78\cdot10^{-1}$
Gp6	$2.39\cdot10^{-1}$	±	$1.59\cdot10^{-1}$	$3.80\cdot10^{-1}$	±	$2.24\cdot10^{-1}$	$2.35\cdot10^{-1}$	±	$1.73\cdot10^{-1}$	$6.83\cdot10^{-1}$	±	$7.43\cdot10^{-1}$
Bradyrhizobiaceae	$3.16\cdot10^{-1}$	±	$2.62\cdot10^{-1}$	$3.31\cdot10^{-1}$	±	$3.25\cdot10^{-1}$	$3.56\cdot10^{-1}$	±	$2.73\cdot10^{-1}$	$6.67\cdot10^{-1}$	±	$3.65\cdot10^{-1}$
Erythrobacteraceae	$5.95\cdot10^{-1}$	±	$7.02\cdot10^{-1}$	$5.29\cdot10^{-1}$	±	$3.70\cdot10^{-1}$	$6.63\cdot10^{-1}$	±	$6.66\cdot10^{-1}$	$5.64\cdot10^{-1}$	±	$2.49\cdot10^{-1}$

Table S36. Summary of family-level EUB results continued.

Family[a,b]	AE4 (S12)			AE8 (S18)			AE12 (S24)			AE20 (S30)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Caulobacteraceae	$4.61 \cdot 10^{-1}$	±	$4.41 \cdot 10^{-1}$	$6.15 \cdot 10^{-1}$	±	$1.91 \cdot 10^{-1}$	$6.14 \cdot 10^{-1}$	±	$6.24 \cdot 10^{-1}$	$6.41 \cdot 10^{-1}$	±	$4.34 \cdot 10^{-1}$
Hyphomonadaceae	$2.81 \cdot 10^{-1}$	±	$1.11 \cdot 10^{-1}$	$5.70 \cdot 10^{-1}$	±	$1.09 \cdot 10^{-1}$	$5.46 \cdot 10^{-1}$	±	$2.14 \cdot 10^{-1}$	$6.02 \cdot 10^{-1}$	±	$3.97 \cdot 10^{-1}$
Spartobacteria_genera_inc._sed.[f]	$5.74 \cdot 10^{-1}$	±	$8.00 \cdot 10^{-1}$	$3.10 \cdot 10^{-1}$	±	$1.84 \cdot 10^{-1}$	$2.07 \cdot 10^{-1}$	±	$3.03 \cdot 10^{-1}$	$4.20 \cdot 10^{-1}$	±	$6.78 \cdot 10^{-1}$
unknown	$5.73 \cdot 10^{-1}$	±	$8.61 \cdot 10^{-1}$	$4.23 \cdot 10^{-1}$	±	$6.54 \cdot 10^{-1}$	$3.85 \cdot 10^{-1}$	±	$6.52 \cdot 10^{-1}$	$3.15 \cdot 10^{-1}$	±	$5.24 \cdot 10^{-1}$
p: *Firmicutes*												
Rhodobiaceae	$7.99 \cdot 10^{-2}$	±	$9.55 \cdot 10^{-2}$	$5.86 \cdot 10^{-2}$	±	$4.51 \cdot 10^{-2}$	$4.80 \cdot 10^{-2}$	±	$2.79 \cdot 10^{-2}$	$5.68 \cdot 10^{-1}$	±	$8.43 \cdot 10^{-1}$
Desulfovibrionaceae	$1.89 \cdot 10^{-1}$	±	$2.14 \cdot 10^{-1}$	$2.28 \cdot 10^{-1}$	±	$3.39 \cdot 10^{-1}$	$2.31 \cdot 10^{-1}$	±	$2.34 \cdot 10^{-1}$	$5.09 \cdot 10^{-1}$	±	$5.84 \cdot 10^{-1}$
Lachnospiraceae	$2.07 \cdot 10^{-1}$	±	$1.95 \cdot 10^{-1}$	$2.73 \cdot 10^{-1}$	±	$2.90 \cdot 10^{-1}$	$1.85 \cdot 10^{-1}$	±	$2.40 \cdot 10^{-1}$	$4.85 \cdot 10^{-1}$	±	$7.58 \cdot 10^{-1}$
Mycobacteriaceae	$2.18 \cdot 10^{-1}$	±	$1.79 \cdot 10^{-1}$	$4.02 \cdot 10^{-1}$	±	$5.69 \cdot 10^{-1}$	$2.89 \cdot 10^{-1}$	±	$4.17 \cdot 10^{-1}$	$1.20 \cdot 10^{-1}$	±	$5.67 \cdot 10^{-2}$
Armatimonadetes_gp5	$6.31 \cdot 10^{-3}$	±	$6.07 \cdot 10^{-3}$	$4.38 \cdot 10^{-2}$	±	$2.47 \cdot 10^{-2}$	$4.89 \cdot 10^{-2}$	±	$5.43 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$	±	$6.33 \cdot 10^{-1}$
Xanthobacteraceae	$3.98 \cdot 10^{-2}$	±	$4.68 \cdot 10^{-2}$	$3.91 \cdot 10^{-1}$	±	$6.45 \cdot 10^{-1}$	$2.69 \cdot 10^{-1}$	±	$4.41 \cdot 10^{-1}$	$1.75 \cdot 10^{-1}$	±	$2.51 \cdot 10^{-1}$
unknown	$3.00 \cdot 10^{-1}$	±	$4.02 \cdot 10^{-1}$	$3.79 \cdot 10^{-1}$	±	$5.85 \cdot 10^{-1}$	$3.26 \cdot 10^{-1}$	±	$4.97 \cdot 10^{-1}$	$5.33 \cdot 10^{-2}$	±	$3.05 \cdot 10^{-2}$
o: *Sphingobacteriales*												
SR1_genera_inc._sed.[f]	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$	$2.60 \cdot 10^{-1}$	±	$4.13 \cdot 10^{-1}$	$2.67 \cdot 10^{-1}$	±	$4.60 \cdot 10^{-1}$	$1.25 \cdot 10^{-3}$	±	$2.16 \cdot 10^{-3}$

[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] 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 S37. Summary of genus-level relative abundance by reactor of the 16S rRNA gene sequencing results with the EUB primer set.

Genus[a,b]	AE4 (S13)			AE8 (S19)			AE12 (S25)			AE20 (S31)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Minor phylotypes (1414)[e]	18.0	±	2.58	21.8	±	3.70	18.1	±	2.34	22.6	±	5.05
Meganema	14.4	±	11.3	13.6	±	5.80	19.6	±	12.9	15.8	±	10.2
unknown	9.96	±	4.75	8.53	±	5.05	4.10	±	2.99	3.87	±	1.55
d: *Bacteria*												
Zoogloea	5.48	±	5.03	1.94	±	3.04	8.10	±	14.0	$2.87 \cdot 10^{-1}$	±	$3.74 \cdot 10^{-1}$
Thauera	3.76	±	3.56	4.45	±	4.47	1.77	±	1.97	1.02	±	1.13
Ohtaekwangia	$6.68 \cdot 10^{-1}$	±	$7.07 \cdot 10^{-1}$	$5.43 \cdot 10^{-1}$	±	$2.58 \cdot 10^{-1}$	1.35	±	1.16	4.35	±	4.99
unknown	1.58	±	1.06	2.36	±	1.11	2.14	±	$6.72 \cdot 10^{-1}$	3.24	±	2.13
o: *Rhizobiales*												
unknown	2.54	±	3.67	2.55	±	2.78	3.13	±	4.69	2.65	±	3.61
p: *Bacteroidetes*												
Leadbetterella	2.42	±	2.02	$6.09 \cdot 10^{-1}$	±	$8.74 \cdot 10^{-1}$	$8.65 \cdot 10^{-1}$	±	1.43	2.99	±	2.75

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

Genus[a,b]	AE4 (S13)			AE8 (S19)			AE12 (S25)			AE20 (S31)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Gp4	$6.67 \cdot 10^{-1}$	±	$6.40 \cdot 10^{-1}$	$8.83 \cdot 10^{-1}$	±	$8.02 \cdot 10^{-1}$	1.65	±	1.17	2.91	±	1.65
unknown	1.15	±	$7.14 \cdot 10^{-1}$	1.83	±	$9.53 \cdot 10^{-1}$	2.37	±	1.02	1.75	±	1.24
c: *Alphaproteobacteria*												
Amaricoccus	$2.73 \cdot 10^{-1}$	±	$4.58 \cdot 10^{-1}$	1.79	±	3.06	1.44	±	1.91	2.31	±	2.10
Saccharibacteria_genera_inc._sed.[f]	1.75	±	2.37	1.11	±	$9.38 \cdot 10^{-1}$	2.30	±	3.11	$7.68 \cdot 10^{-1}$	±	$6.44 \cdot 10^{-1}$
unknown	2.12	±	3.64	1.43	±	2.45	1.38	±	2.39	$2.98 \cdot 10^{-1}$	±	$5.10 \cdot 10^{-1}$
f: *Erysipelotrichaceae*												
Paracoccus	$4.26 \cdot 10^{-1}$	±	$4.07 \cdot 10^{-1}$	$8.19 \cdot 10^{-1}$	±	$6.71 \cdot 10^{-1}$	1.74	±	2.01	1.84	±	1.68
unknown	$9.04 \cdot 10^{-1}$	±	$6.63 \cdot 10^{-1}$	1.42	±	$9.30 \cdot 10^{-1}$	1.16	±	$6.41 \cdot 10^{-1}$	1.81	±	$8.70 \cdot 10^{-1}$
f: *Rhodobacteraceae*												
Luteimonas	1.79	±	1.79	1.54	±	1.33	1.08	±	$9.16 \cdot 10^{-1}$	$9.57 \cdot 10^{-1}$	±	1.14
unknown	1.39	±	1.99	1.47	±	1.72	1.29	±	2.11	1.78	±	2.90
o: *Clostridiales*												
unknown	1.65	±	$3.06 \cdot 10^{-1}$	1.65	±	$5.33 \cdot 10^{-1}$	1.40	±	$7.00 \cdot 10^{-2}$	$9.51 \cdot 10^{-1}$	±	$2.99 \cdot 10^{-2}$
p: *Proteobacteria*												
Parcubacteria_genera_inc._sed.[f]	1.61	±	2.01	$4.74 \cdot 10^{-1}$	±	$4.16 \cdot 10^{-1}$	$6.27 \cdot 10^{-1}$	±	$3.61 \cdot 10^{-1}$	1.04	±	1.45
unknown	1.01	±	1.07	1.19	±	1.11	$8.21 \cdot 10^{-1}$	±	1.13	1.60	±	2.44
f: *Ruminococcaceae*												
Haliscomenobacter	$9.01 \cdot 10^{-1}$	±	$7.55 \cdot 10^{-1}$	$7.59 \cdot 10^{-1}$	±	$3.68 \cdot 10^{-1}$	$9.57 \cdot 10^{-1}$	±	$8.70 \cdot 10^{-1}$	1.57	±	1.79
unknown	$4.91 \cdot 10^{-1}$	±	$2.19 \cdot 10^{-1}$	1.11	±	1.05	1.50	±	1.93	$4.43 \cdot 10^{-1}$	±	$2.25 \cdot 10^{-1}$
f: *Planctomycetaceae*												
unknown	$6.42 \cdot 10^{-1}$	±	$3.22 \cdot 10^{-1}$	1.49	±	$7.71 \cdot 10^{-1}$	$7.06 \cdot 10^{-1}$	±	$2.74 \cdot 10^{-1}$	1.29	±	$2.42 \cdot 10^{-1}$
c: *Gammaproteobacteria*												
unknown	1.44	±	2.11	$5.16 \cdot 10^{-1}$	±	$3.54 \cdot 10^{-1}$	$7.23 \cdot 10^{-1}$	±	$7.32 \cdot 10^{-1}$	$2.51 \cdot 10^{-1}$	±	$4.94 \cdot 10^{-2}$
f: *Chitinophagaceae*												
Proteiniphilum	1.34	±	1.50	1.25	±	1.78	$4.17 \cdot 10^{-1}$	±	$6.91 \cdot 10^{-1}$	1.12	±	1.87
unknown	$5.99 \cdot 10^{-1}$	±	$4.75 \cdot 10^{-1}$	1.31	±	$9.73 \cdot 10^{-1}$	$9.12 \cdot 10^{-1}$	±	$9.47 \cdot 10^{-1}$	$6.11 \cdot 10^{-1}$	±	$2.69 \cdot 10^{-1}$
f: *Comamonadaceae*												
Planctomyces	$7.32 \cdot 10^{-1}$	±	$8.71 \cdot 10^{-1}$	$4.24 \cdot 10^{-1}$	±	$2.05 \cdot 10^{-1}$	$3.92 \cdot 10^{-1}$	±	$1.94 \cdot 10^{-1}$	1.28	±	1.49
unknown	1.17	±	1.70	$3.58 \cdot 10^{-1}$	±	$2.38 \cdot 10^{-1}$	$1.75 \cdot 10^{-1}$	±	$1.23 \cdot 10^{-1}$	$7.01 \cdot 10^{-1}$	±	$9.24 \cdot 10^{-1}$
f: *Xanthomonadaceae*												
unknown	1.15	±	$8.01 \cdot 10^{-1}$	$7.18 \cdot 10^{-1}$	±	$2.95 \cdot 10^{-1}$	$8.09 \cdot 10^{-1}$	±	$4.25 \cdot 10^{-1}$	$9.14 \cdot 10^{-1}$	±	$2.82 \cdot 10^{-1}$
c: *Deltaproteobacteria*												
unknown	1.13	±	1.40	$6.33 \cdot 10^{-1}$	±	$9.99 \cdot 10^{-1}$	$7.78 \cdot 10^{-1}$	±	1.34	$3.80 \cdot 10^{-1}$	±	$6.46 \cdot 10^{-1}$
o: *Bacteroidales*												
unknown	1.13	±	1.57	$8.00 \cdot 10^{-1}$	±	1.16	$8.10 \cdot 10^{-1}$	±	1.39	$4.59 \cdot 10^{-1}$	±	$7.73 \cdot 10^{-1}$
f: *Porphyromonadaceae*												
Aquabacterium	$6.28 \cdot 10^{-1}$	±	$6.52 \cdot 10^{-1}$	$8.59 \cdot 10^{-1}$	±	$9.80 \cdot 10^{-1}$	1.04	±	1.74	$7.65 \cdot 10^{-2}$	±	$8.47 \cdot 10^{-2}$
Schlesneria	$5.19 \cdot 10^{-1}$	±	$5.67 \cdot 10^{-1}$	1.02	±	1.32	$4.13 \cdot 10^{-1}$	±	$3.63 \cdot 10^{-1}$	1.00	±	1.45

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

Genus[a,b]	AE4 (S13)			AE8 (S19)			AE12 (S25)			AE20 (S31)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Bacteroides	$9.85\cdot10^{-1}$	±	1.22	$5.71\cdot10^{-1}$	±	$7.62\cdot10^{-1}$	$7.11\cdot10^{-1}$	±	1.23	$2.75\cdot10^{-1}$	±	$4.52\cdot10^{-1}$
Blastocatella	$7.74\cdot10^{-1}$	±	$6.90\cdot10^{-1}$	$9.75\cdot10^{-1}$	±	1.20	$3.96\cdot10^{-1}$	±	$5.22\cdot10^{-1}$	$5.16\cdot10^{-1}$	±	$7.85\cdot10^{-2}$
Pseudofulvimonas	$9.69\cdot10^{-2}$	±	$7.83\cdot10^{-2}$	$1.49\cdot10^{-1}$	±	$2.45\cdot10^{-1}$	$4.85\cdot10^{-1}$	±	$5.28\cdot10^{-1}$	$9.64\cdot10^{-1}$	±	1.58
Nannocystis	$9.15\cdot10^{-1}$	±	1.40	$4.90\cdot10^{-1}$	±	$8.26\cdot10^{-1}$	$3.39\cdot10^{-1}$	±	$3.47\cdot10^{-1}$	$3.76\cdot10^{-1}$	±	$5.91\cdot10^{-1}$
unknown	$2.58\cdot10^{-1}$	±	$2.01\cdot10^{-1}$	$1.12\cdot10^{-1}$	±	$8.92\cdot10^{-2}$	$8.12\cdot10^{-1}$	±	1.19	$1.40\cdot10^{-1}$	±	$9.25\cdot10^{-2}$
f: *Cyclobacteriaceae*												
Mesorhizobium	$4.19\cdot10^{-1}$	±	$3.78\cdot10^{-1}$	$4.62\cdot10^{-1}$	±	$1.70\cdot10^{-1}$	$7.73\cdot10^{-1}$	±	$6.11\cdot10^{-1}$	$3.15\cdot10^{-1}$	±	$1.93\cdot10^{-1}$
unknown	$2.89\cdot10^{-1}$	±	$1.81\cdot10^{-1}$	$7.67\cdot10^{-1}$	±	$7.26\cdot10^{-1}$	$4.39\cdot10^{-1}$	±	$3.34\cdot10^{-1}$	$3.95\cdot10^{-1}$	±	$1.55\cdot10^{-1}$
o: *Burkholderiales*												
unknown	$1.31\cdot10^{-1}$	±	$1.24\cdot10^{-1}$	$1.90\cdot10^{-1}$	±	$1.29\cdot10^{-1}$	$3.94\cdot10^{-1}$	±	$2.70\cdot10^{-1}$	$7.65\cdot10^{-1}$	±	$3.42\cdot10^{-1}$
f: *Propionibacteriaceae*												
Hyphomicrobium	$4.12\cdot10^{-1}$	±	$3.55\cdot10^{-1}$	$4.66\cdot10^{-1}$	±	$2.41\cdot10^{-1}$	$7.34\cdot10^{-1}$	±	$5.69\cdot10^{-1}$	$7.58\cdot10^{-1}$	±	$4.34\cdot10^{-1}$
unknown	$4.77\cdot10^{-1}$	±	$5.50\cdot10^{-1}$	$7.47\cdot10^{-1}$	±	1.00	$1.82\cdot10^{-1}$	±	$1.77\cdot10^{-1}$	$2.68\cdot10^{-1}$	±	$8.63\cdot10^{-2}$
f: *Verrucomicrobiaceae*												
unknown	$3.26\cdot10^{-1}$	±	$2.05\cdot10^{-1}$	$5.41\cdot10^{-1}$	±	$2.87\cdot10^{-1}$	$3.88\cdot10^{-1}$	±	$2.28\cdot10^{-1}$	$7.46\cdot10^{-1}$	±	$4.34\cdot10^{-1}$
f: *Sphingomonadaceae*												
unknown	$7.43\cdot10^{-1}$	±	$9.32\cdot10^{-1}$	$5.74\cdot10^{-1}$	±	$7.02\cdot10^{-1}$	$4.68\cdot10^{-1}$	±	$4.40\cdot10^{-1}$	$5.01\cdot10^{-1}$	±	$4.45\cdot10^{-1}$
f: *Flavobacteriaceae*												
Pedobacter	$7.10\cdot10^{-1}$	±	1.11	$2.43\cdot10^{-1}$	±	$2.92\cdot10^{-1}$	$9.77\cdot10^{-2}$	±	$1.18\cdot10^{-1}$	$1.88\cdot10^{-2}$	±	$2.31\cdot10^{-2}$
Hydrogenophaga	$5.51\cdot10^{-1}$	±	$4.48\cdot10^{-1}$	$7.04\cdot10^{-1}$	±	$5.79\cdot10^{-1}$	$2.80\cdot10^{-1}$	±	$1.17\cdot10^{-1}$	$3.23\cdot10^{-1}$	±	$2.39\cdot10^{-1}$
Sphaerochaeta	$6.93\cdot10^{-1}$	±	1.12	$3.08\cdot10^{-1}$	±	$5.04\cdot10^{-1}$	$4.93\cdot10^{-1}$	±	$8.54\cdot10^{-1}$	$1.47\cdot10^{-1}$	±	$2.51\cdot10^{-1}$
Prosthecobacter	$2.33\cdot10^{-1}$	±	$8.48\cdot10^{-2}$	$3.84\cdot10^{-1}$	±	$1.49\cdot10^{-1}$	$1.10\cdot10^{-1}$	±	$3.61\cdot10^{-2}$	$6.90\cdot10^{-1}$	±	$6.30\cdot10^{-1}$
Gp6	$2.39\cdot10^{-1}$	±	$1.59\cdot10^{-1}$	$3.80\cdot10^{-1}$	±	$2.24\cdot10^{-1}$	$2.35\cdot10^{-1}$	±	$1.73\cdot10^{-1}$	$6.83\cdot10^{-1}$	±	$7.43\cdot10^{-1}$
Hylemonella	$9.44\cdot10^{-3}$	±	$1.49\cdot10^{-2}$	$6.01\cdot10^{-2}$	±	$1.03\cdot10^{-1}$	$6.67\cdot10^{-1}$	±	1.13	$3.79\cdot10^{-2}$	±	$3.03\cdot10^{-2}$
Ilumatobacter	$4.94\cdot10^{-1}$	±	$5.45\cdot10^{-1}$	$3.86\cdot10^{-1}$	±	$4.60\cdot10^{-1}$	$6.63\cdot10^{-1}$	±	$8.79\cdot10^{-1}$	$4.76\cdot10^{-1}$	±	$4.44\cdot10^{-1}$
unknown	$2.77\cdot10^{-1}$	±	$1.34\cdot10^{-1}$	$6.32\cdot10^{-1}$	±	$3.84\cdot10^{-1}$	$3.59\cdot10^{-1}$	±	$1.47\cdot10^{-1}$	$4.27\cdot10^{-1}$	±	$3.72\cdot10^{-1}$
f: *Burkholderiales_inc._sed.*[f]												
Roseimicrobium	$3.03\cdot10^{-1}$	±	$4.97\cdot10^{-1}$	$5.88\cdot10^{-1}$	±	$9.75\cdot10^{-1}$	$7.62\cdot10^{-2}$	±	$1.10\cdot10^{-1}$	$1.64\cdot10^{-1}$	±	$1.50\cdot10^{-1}$
Oscillibacter	$3.59\cdot10^{-1}$	±	$2.71\cdot10^{-1}$	$3.91\cdot10^{-1}$	±	$3.71\cdot10^{-1}$	$2.16\cdot10^{-1}$	±	$3.18\cdot10^{-1}$	$5.85\cdot10^{-1}$	±	$9.66\cdot10^{-1}$
Sphingomonas	$1.38\cdot10^{-1}$	±	$1.13\cdot10^{-1}$	$1.43\cdot10^{-1}$	±	$8.97\cdot10^{-2}$	$1.73\cdot10^{-1}$	±	$1.10\cdot10^{-1}$	$5.82\cdot10^{-1}$	±	$5.08\cdot10^{-1}$
Spartobacteria_genera_inc._sed.[f]	$5.74\cdot10^{-1}$	±	$8.00\cdot10^{-1}$	$3.10\cdot10^{-1}$	±	$1.84\cdot10^{-1}$	$2.07\cdot10^{-1}$	±	$3.03\cdot10^{-1}$	$4.20\cdot10^{-1}$	±	$6.78\cdot10^{-1}$
unknown	$5.73\cdot10^{-1}$	±	$8.61\cdot10^{-1}$	$4.23\cdot10^{-1}$	±	$6.54\cdot10^{-1}$	$3.85\cdot10^{-1}$	±	$6.52\cdot10^{-1}$	$3.15\cdot10^{-1}$	±	$5.24\cdot10^{-1}$
p: *Firmicutes*												
Altererythrobacter	$5.26\cdot10^{-1}$	±	$6.09\cdot10^{-1}$	$4.42\cdot10^{-1}$	±	$2.97\cdot10^{-1}$	$5.63\cdot10^{-1}$	±	$5.46\cdot10^{-1}$	$4.83\cdot10^{-1}$	±	$2.07\cdot10^{-1}$
unknown	$1.81\cdot10^{-1}$	±	$2.98\cdot10^{-1}$	$3.08\cdot10^{-1}$	±	$5.31\cdot10^{-1}$	$2.01\cdot10^{-1}$	±	$3.48\cdot10^{-1}$	$5.56\cdot10^{-1}$	±	$9.62\cdot10^{-1}$
f: *Prevotellaceae*												
Dokdonella	$6.25\cdot10^{-3}$	±	$5.46\cdot10^{-3}$	$5.54\cdot10^{-1}$	±	$8.67\cdot10^{-1}$	$2.33\cdot10^{-1}$	±	$3.81\cdot10^{-1}$	$2.44\cdot10^{-2}$	±	$2.15\cdot10^{-2}$
Novosphingobium	$4.53\cdot10^{-1}$	±	$2.94\cdot10^{-1}$	$4.67\cdot10^{-1}$	±	$3.66\cdot10^{-1}$	$4.69\cdot10^{-1}$	±	$3.30\cdot10^{-1}$	$5.50\cdot10^{-1}$	±	$5.26\cdot10^{-1}$
Brevundimonas	$3.14\cdot10^{-1}$	±	$3.86\cdot10^{-1}$	$3.68\cdot10^{-1}$	±	$1.59\cdot10^{-1}$	$4.72\cdot10^{-1}$	±	$4.83\cdot10^{-1}$	$5.01\cdot10^{-1}$	±	$3.94\cdot10^{-1}$
Hallella	$1.41\cdot10^{-1}$	±	$2.29\cdot10^{-1}$	$2.69\cdot10^{-1}$	±	$4.42\cdot10^{-1}$	$1.64\cdot10^{-1}$	±	$2.84\cdot10^{-1}$	$4.98\cdot10^{-1}$	±	$8.61\cdot10^{-1}$

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

Genus[a,b]	AE4 (S13)			AE8 (S19)			AE12 (S25)			AE20 (S31)		
	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]	Average	±	SD[c]
		%[d]			%[d]			%[d]			%[d]	
Thermomonas	$1.68 \cdot 10^{-1}$	±	$2.45 \cdot 10^{-1}$	$4.86 \cdot 10^{-1}$	±	$5.43 \cdot 10^{-1}$	$4.68 \cdot 10^{-2}$	±	$4.25 \cdot 10^{-2}$	$6.85 \cdot 10^{-2}$	±	$1.14 \cdot 10^{-1}$
Verrucomicrobium	$1.43 \cdot 10^{-1}$	±	$2.21 \cdot 10^{-1}$	$4.57 \cdot 10^{-1}$	±	$7.46 \cdot 10^{-1}$	$3.32 \cdot 10^{-2}$	±	$3.40 \cdot 10^{-2}$	$3.53 \cdot 10^{-2}$	±	$7.92 \cdot 10^{-3}$
unknown	$3.73 \cdot 10^{-1}$	±	$6.36 \cdot 10^{-1}$	$4.50 \cdot 10^{-1}$	±	$7.25 \cdot 10^{-1}$	$3.57 \cdot 10^{-1}$	±	$6.00 \cdot 10^{-1}$	$1.90 \cdot 10^{-2}$	±	$1.36 \cdot 10^{-2}$
f: *Saprospiraceae*												
Parvibaculum	$3.34 \cdot 10^{-2}$	±	$5.78 \cdot 10^{-2}$	$8.57 \cdot 10^{-4}$	±	$1.48 \cdot 10^{-3}$	$1.13 \cdot 10^{-3}$	±	$1.95 \cdot 10^{-3}$	$4.09 \cdot 10^{-1}$	±	$7.07 \cdot 10^{-1}$
Mycobacterium	$2.17 \cdot 10^{-1}$	±	$1.78 \cdot 10^{-1}$	$4.00 \cdot 10^{-1}$	±	$5.68 \cdot 10^{-1}$	$2.88 \cdot 10^{-1}$	±	$4.15 \cdot 10^{-1}$	$1.20 \cdot 10^{-1}$	±	$5.67 \cdot 10^{-2}$
Armatimonadetes_gp5	$6.31 \cdot 10^{-3}$	±	$6.07 \cdot 10^{-3}$	$4.38 \cdot 10^{-2}$	±	$2.47 \cdot 10^{-2}$	$4.89 \cdot 10^{-2}$	±	$5.43 \cdot 10^{-2}$	$3.97 \cdot 10^{-1}$	±	$6.33 \cdot 10^{-1}$
unknown	$3.00 \cdot 10^{-1}$	±	$4.02 \cdot 10^{-1}$	$3.79 \cdot 10^{-1}$	±	$5.85 \cdot 10^{-1}$	$3.26 \cdot 10^{-1}$	±	$4.97 \cdot 10^{-1}$	$5.33 \cdot 10^{-2}$	±	$3.05 \cdot 10^{-2}$
o: *Sphingobacteriales*												
Flavobacterium	$3.70 \cdot 10^{-1}$	±	$6.13 \cdot 10^{-1}$	$2.22 \cdot 10^{-1}$	±	$2.44 \cdot 10^{-1}$	$1.23 \cdot 10^{-1}$	±	$1.14 \cdot 10^{-1}$	$2.69 \cdot 10^{-1}$	±	$3.81 \cdot 10^{-1}$
Xanthobacter	$2.17 \cdot 10^{-2}$	±	$3.39 \cdot 10^{-2}$	$3.52 \cdot 10^{-1}$	±	$5.83 \cdot 10^{-1}$	$2.60 \cdot 10^{-1}$	±	$4.34 \cdot 10^{-1}$	$1.61 \cdot 10^{-1}$	±	$2.48 \cdot 10^{-1}$
SR1_genera_inc._sed.[f]	$3.49 \cdot 10^{-1}$	±	$6.02 \cdot 10^{-1}$	$2.60 \cdot 10^{-1}$	±	$4.13 \cdot 10^{-1}$	$2.67 \cdot 10^{-1}$	±	$4.60 \cdot 10^{-1}$	$1.25 \cdot 10^{-3}$	±	$2.16 \cdot 10^{-3}$
Filomicrobium	$5.33 \cdot 10^{-3}$	±	$3.16 \cdot 10^{-3}$	$3.40 \cdot 10^{-1}$	±	$5.73 \cdot 10^{-1}$	$9.37 \cdot 10^{-3}$	±	$2.34 \cdot 10^{-3}$	$1.40 \cdot 10^{-2}$	±	$9.36 \cdot 10^{-3}$

[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] 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.

Bar plots

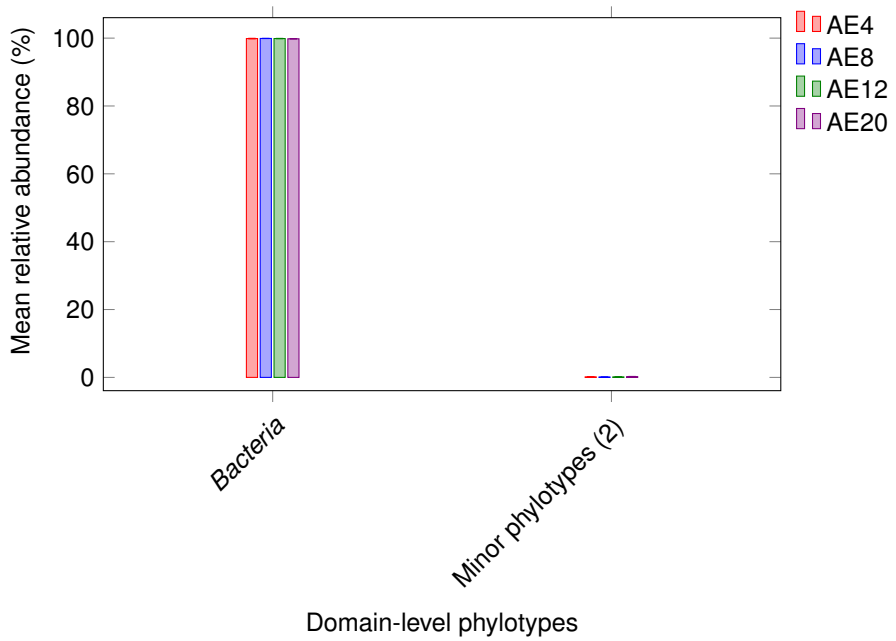

Figure S24. Mean relative abundance for phylotypes identified using the EUB primer set at the domain level (see Table S32). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated 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.

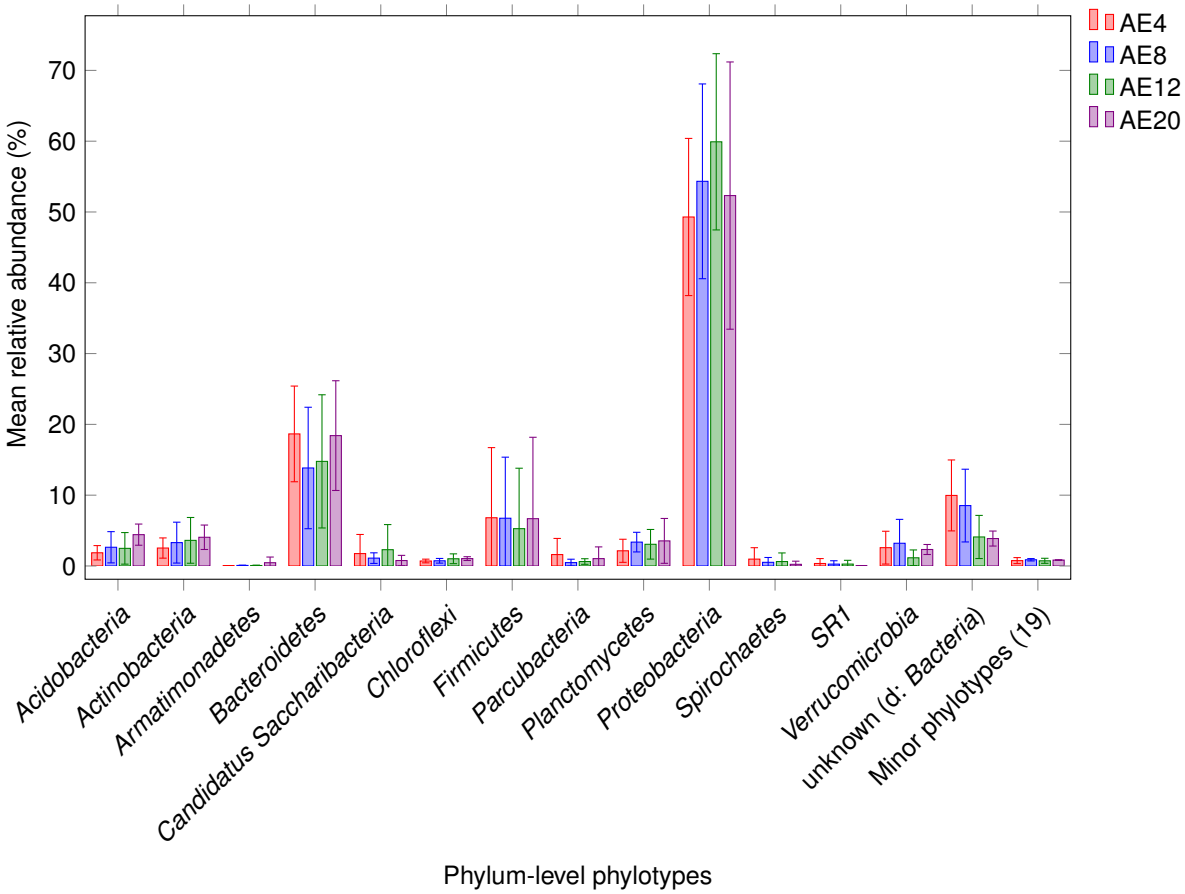

Figure S25. Mean relative abundance for phylotypes identified using the EUB primer set at the phylum level (see Table S33). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated 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.

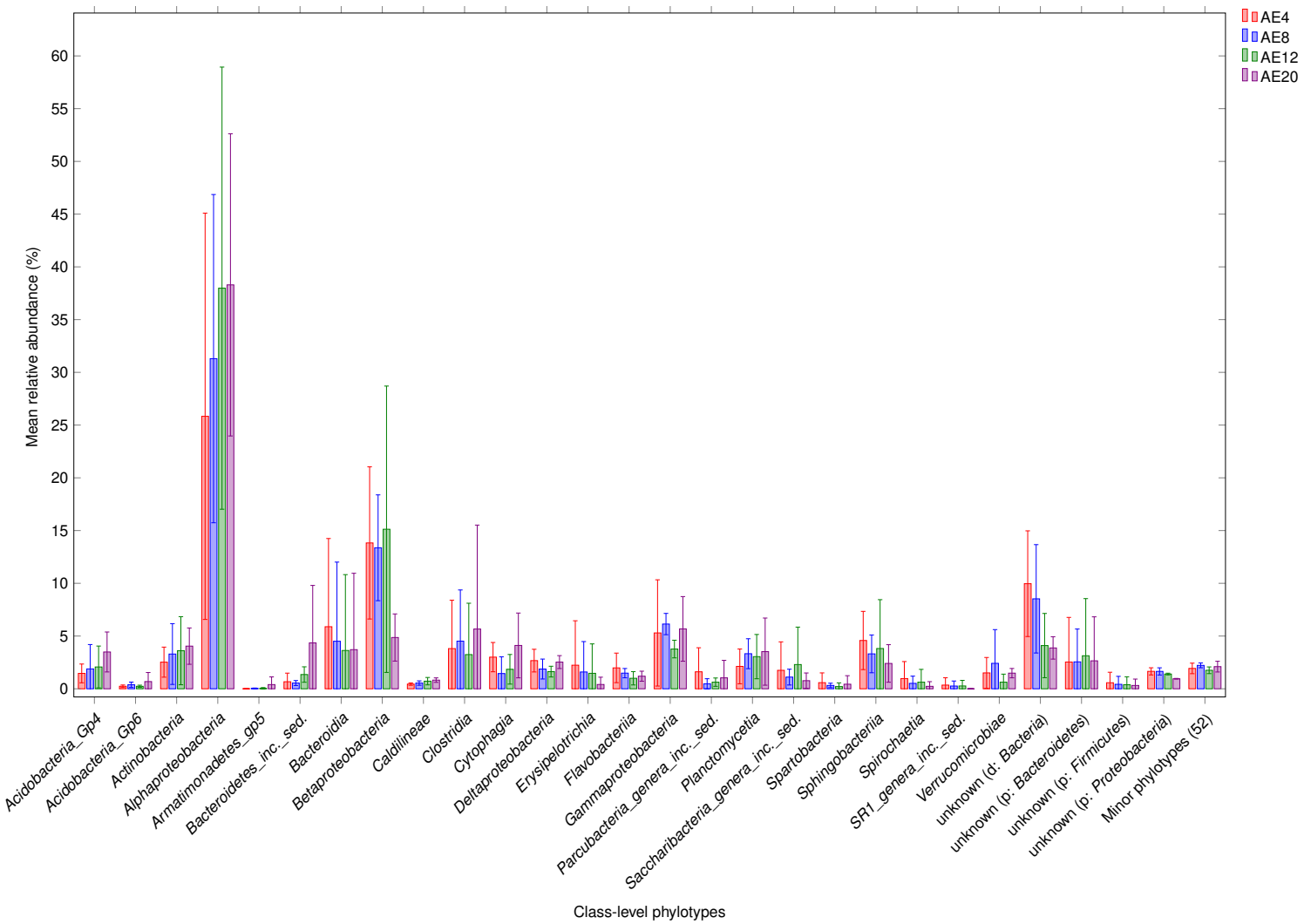

Figure S26. Mean relative abundance for phylotypes identified using the EUB primer set at the class level (see Table S34). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated 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.

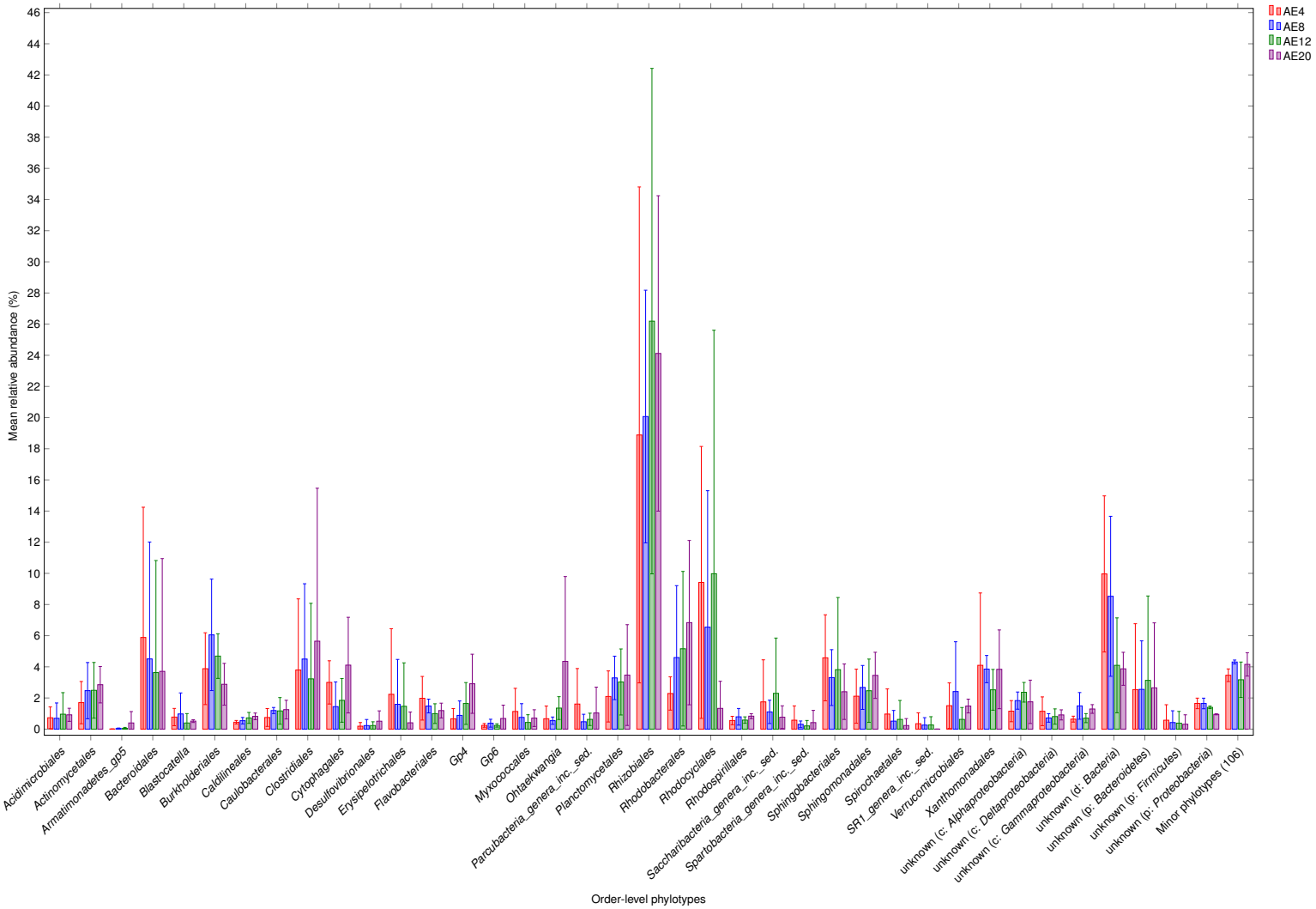

Figure S27. Mean relative abundance for phylotypes identified using the EUB primer set at the order level (see Table S35). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated 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.

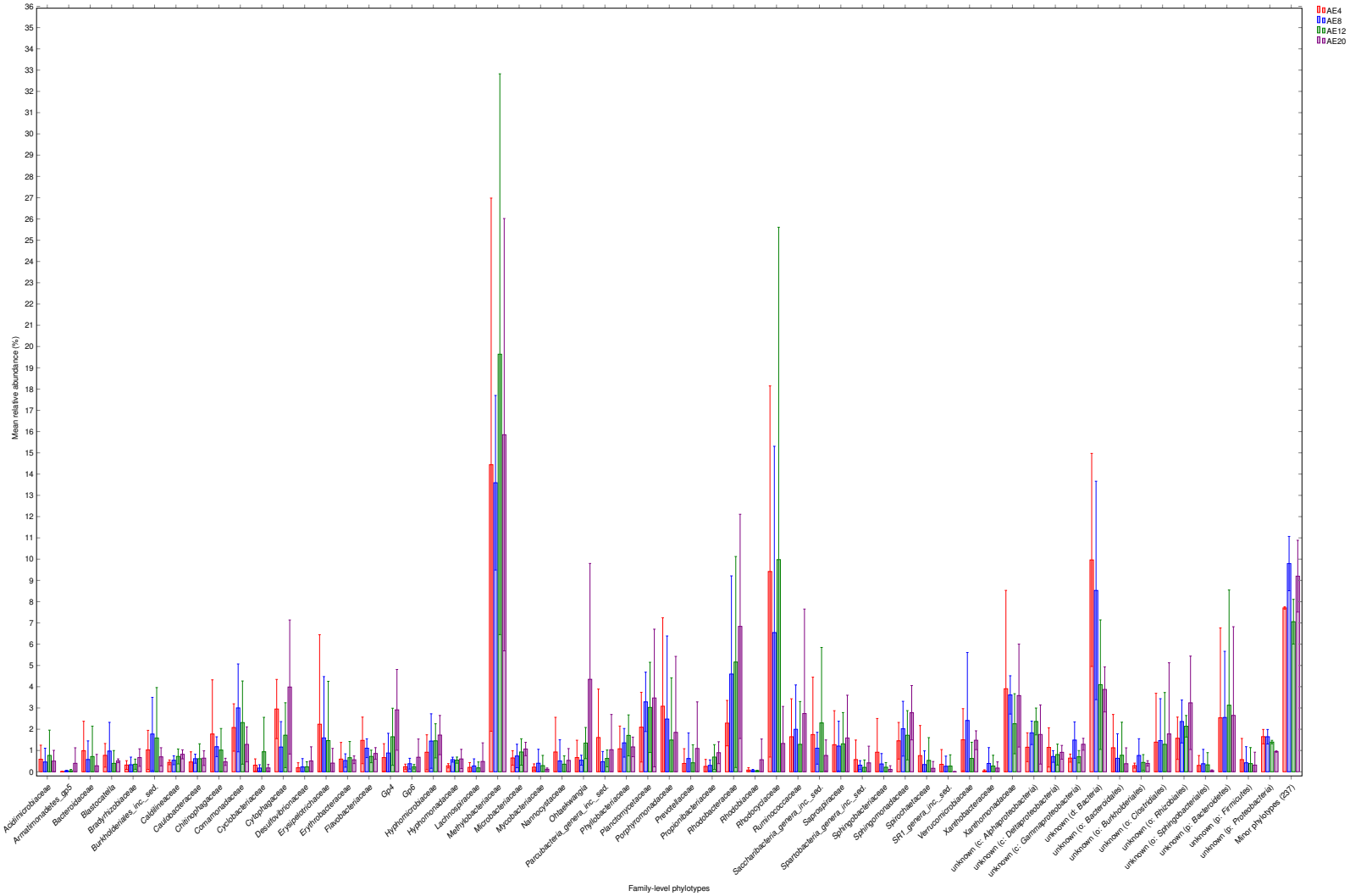

Figure S28. Mean relative abundance for phylotypes identified using the EUB primer set at the family level (see Table S36). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated 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 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.

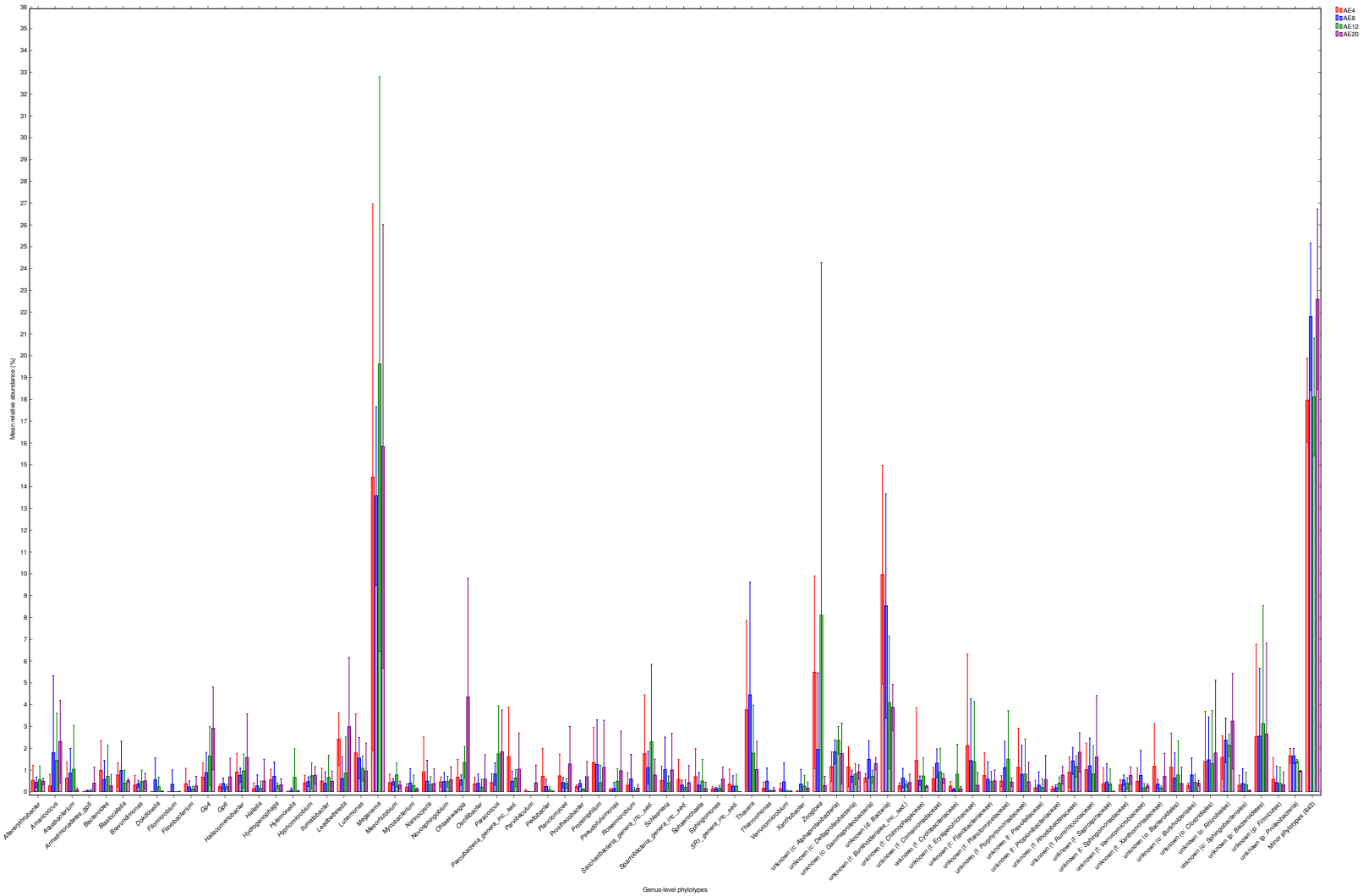

Figure S29. Mean relative abundance for phylotypes identified using the EUB primer set at the genus level (see Table S37). Phylotypes with less than 1 % in all of the samples were lumped into "Minor phylotypes" at the right hand side of the plot. The number of phylotypes categorized accordingly is indicated 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

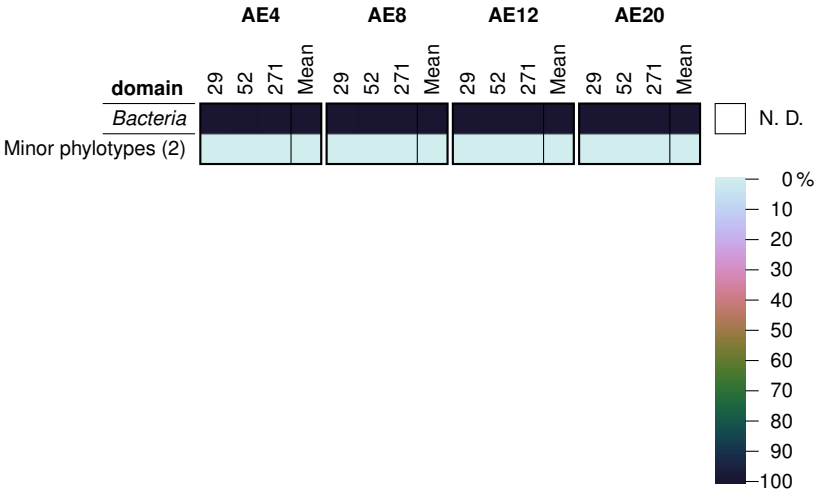

Figure S30. Heat map showing the relative abundance of phylotypes identified at the domain level using the EUB primer set (see Tables S8, S14, S20, and S26). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted 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.

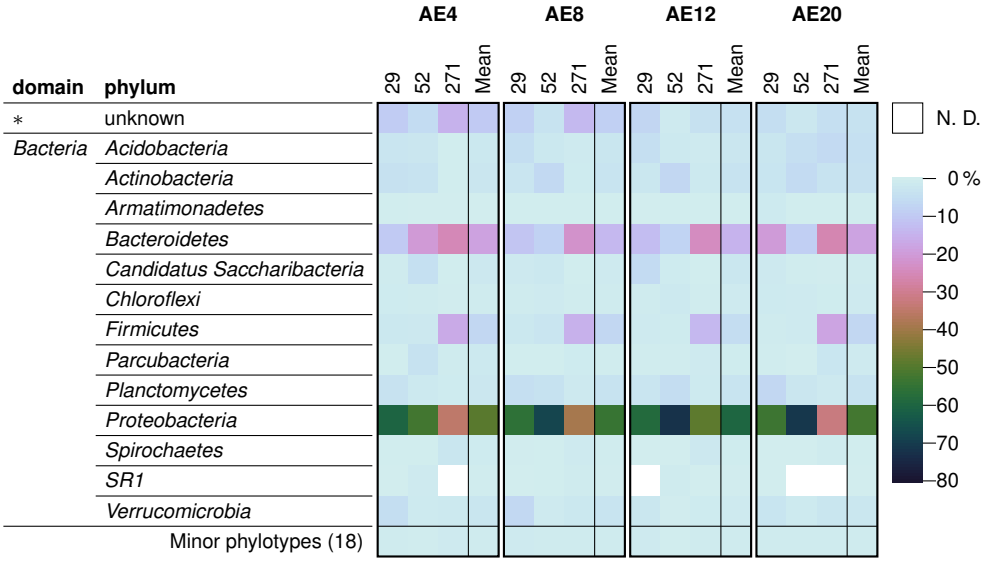

Figure S31. Heat map showing the relative abundance of phylotypes identified at the phylum level using the EUB primer set (see Tables S9, S15, S21, and S27). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted 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.

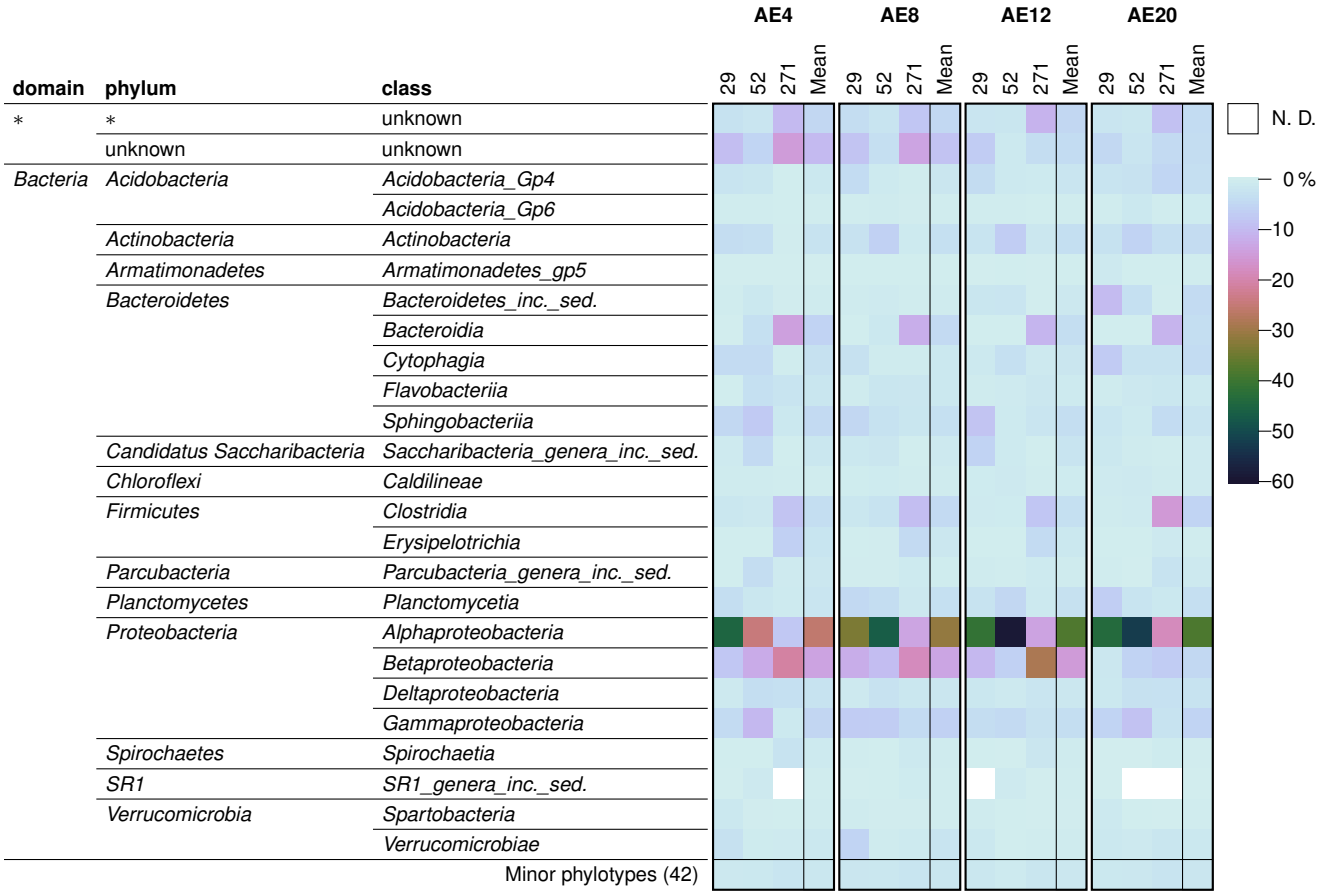

Figure S32. Heat map showing the relative abundance of phylotypes identified at the class level using the EUB primer set (see Tables S10, S16, S22, and S28). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted 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.

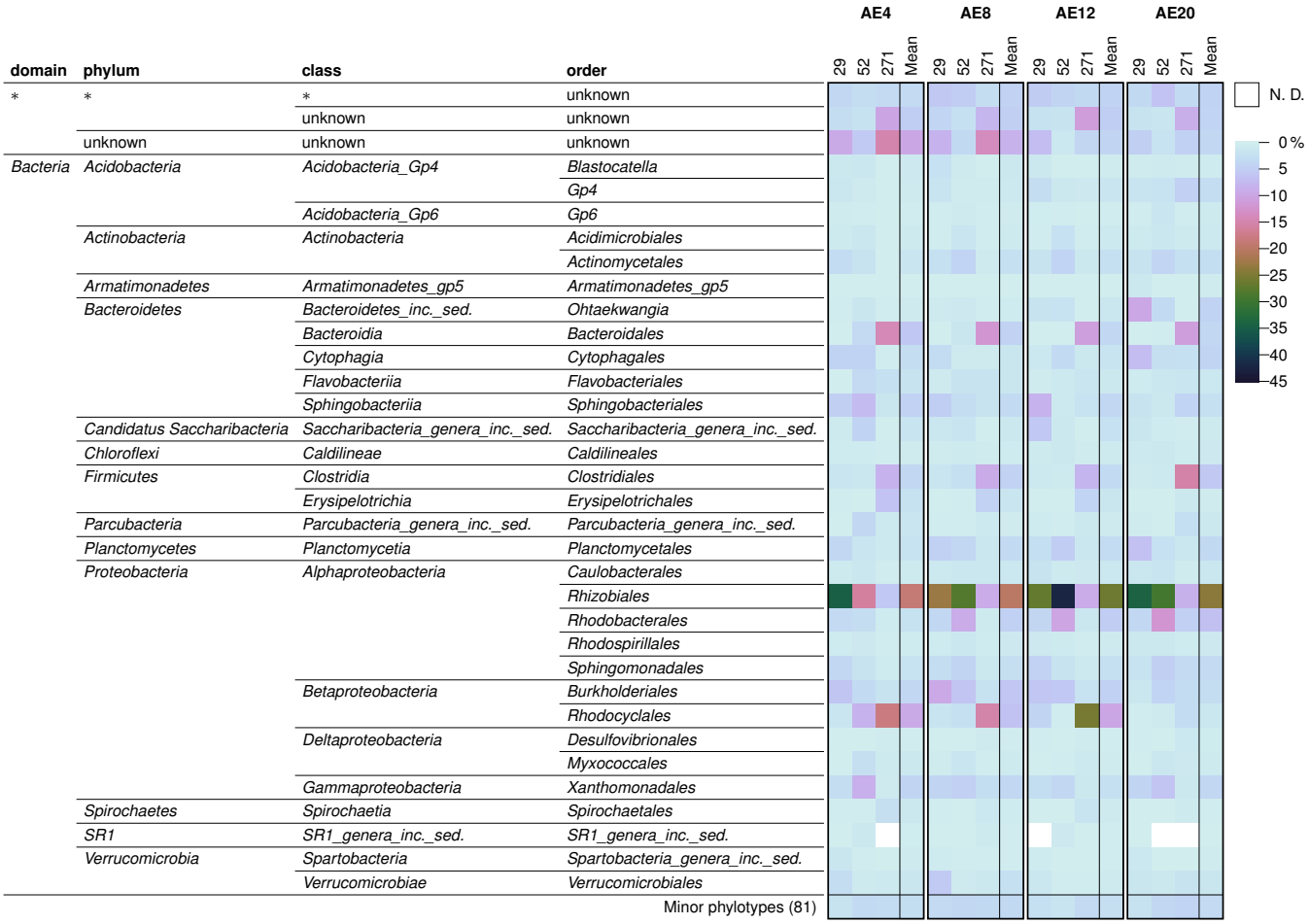

Figure S33. Heat map showing the relative abundance of phylotypes identified at the order level using the EUB primer set (see Tables S11, S17, S23, and S29). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted 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.

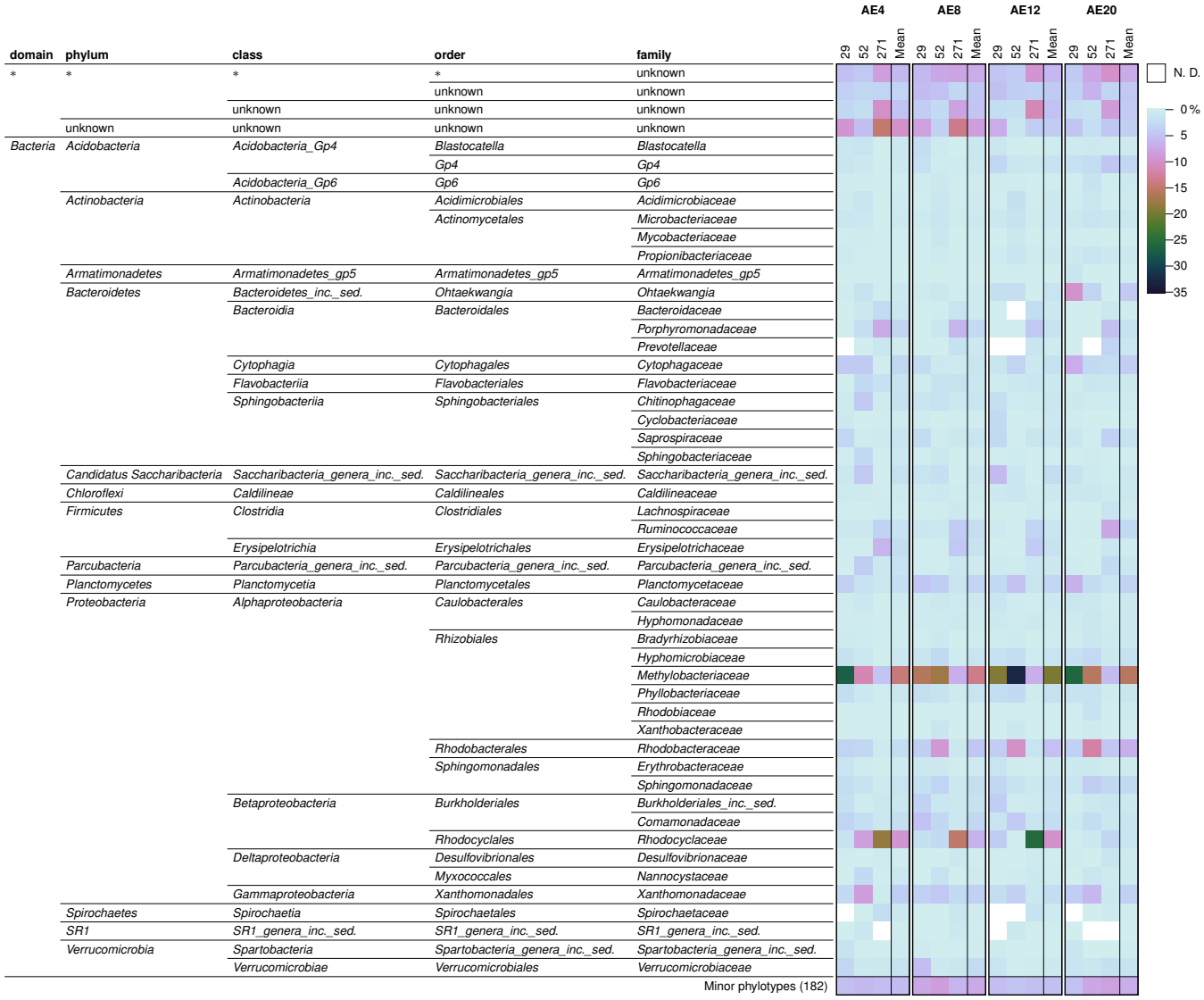

Figure S34. Heat map showing the relative abundance of phylotypes identified at the family level using the EUB primer set (see Tables S12, S18, S24, and S30). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted 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.

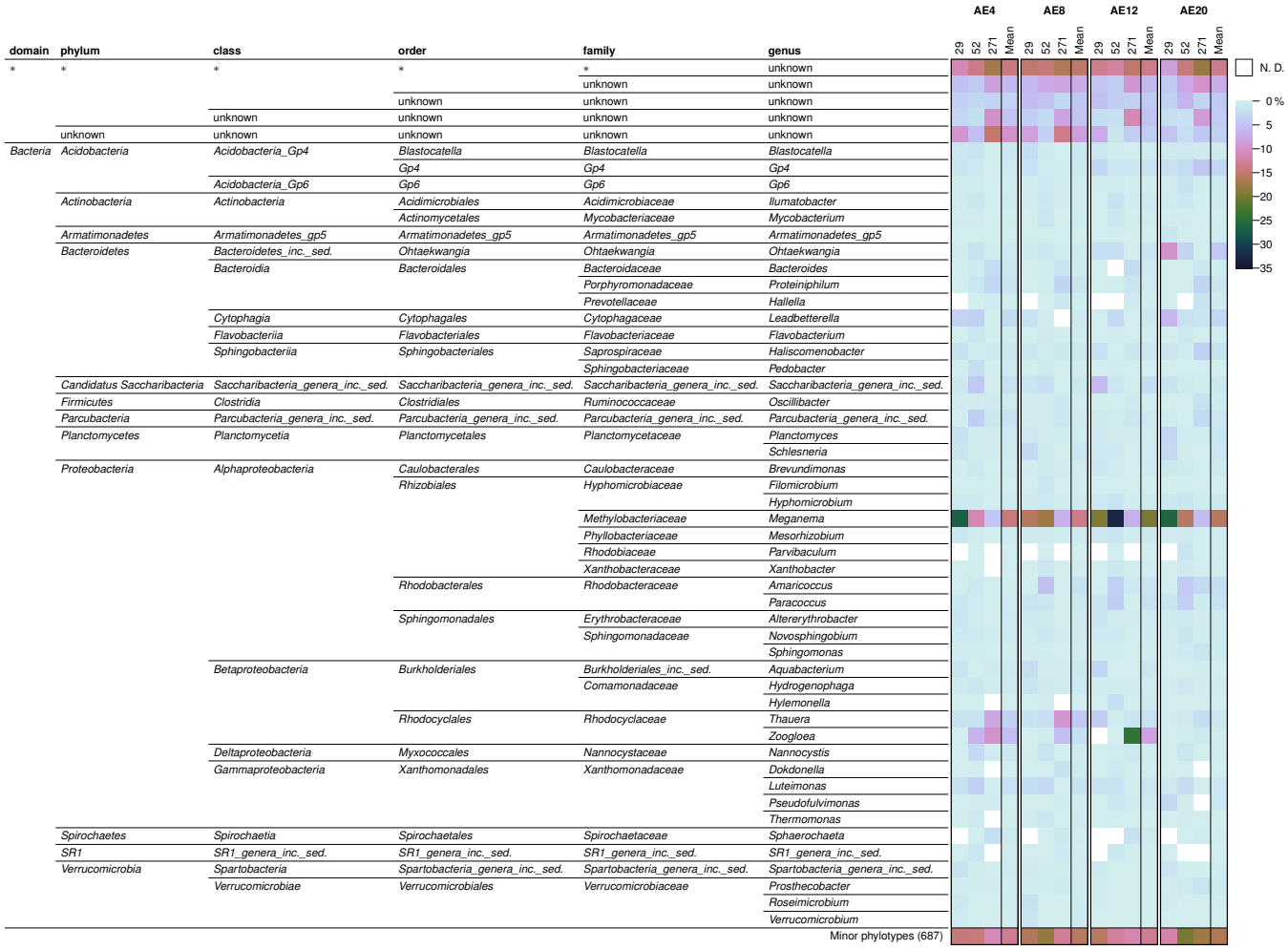

Figure S35. Heat map showing the relative abundance of phylotypes identified at the genus level using the EUB primer set (see Tables S13, S19, S25, and S31). Samples are organized by reactor and operational day and the phylotypes sorted according to taxonomic hierarchy. Unidentified phylotypes (denoted 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 S2. References

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