Electronic Supplementary Information

Insights Gained into Activated Sludge Nitrification through Structural and Functional Profiling of Microbial Community Response to Starvation Stress

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Nitrospira reference sequences and OTUs of interest

N. moscoviensis 16S rRNA gene (GenBank: X82558.1 base pairs 521-773):
TACGAAGGTGGCAAGCGTTGTTCGGATTCACTGGGCGTACAGGGAGCGTAGG
CGGTTGGGTAAGCCCTCCGTGAAATCTCCGGGCCTAACCCGGAAAGTGCAGA
GGGGACTGCTCGGCTTGAGGATGGGAGAGGAGCGCGGAATTCCCGGTGTAGC
GGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTCT
GGAACATTTCTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

N. defluvii 16S rRNA gene (GenBank: DQ059545.1 base pairs 522-774):
TACGAAGGTGGCAAGCGTTGTTCGGATTCACTGGGCGTACAGGGTGTGTAGG
CGGTTTGGTAAGCCTTCTGTTAAAGCTTCGGGCCCAACCCGGAAAGCGCAGA
GGGTACTGCCAGGCTAGAGGGTGGGAGAGGAGCGCGGAATTCCCGGTGTAG
CGGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACATACCTGACGCTGAGACACGAAAGCGTGGGGAGCAAACAGG

N. marina 16S rRNA gene (GenBank: X82559.1 base pairs 522-774):
TACGAAGGTGGCAAGCGTTGTTCGGATTTACTGGGCGTAAAGAGCACGTAGG
CGGTTGGGAAAGCCTTTTGGGAAATCTCCCGGCTTAACCGGGAAAGGTCGAG
AGGAACTATTCAGCTAGAGGACGGGAGAGGAGCGCGGAATTCCCGGTGTAG
CGGTGAAATGCGTAGATATCGGGAAGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACGTACCTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGG

N. backiana 16S rRNA gene (GenBank: EU084879.1 base pairs 524-776):
TACGAAGGTGGCAAGCGTTGTTCGGATTTACTGGGCGTAAAGGGAGCGTAGG
CGGTTCGGTAAGACCGATGGGAAATCCCGGAGCTTAACTTCGGAAGGTCATC
GGTGACTGCCGGGCTAGAGGACGGGAGAGGAGCGCGGAATTCCCGGTGTAG
CGGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACGTTCCTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

N. calida 16S rRNA gene (GenBank: HM485589.1 base pairs 522-774):
TACGAAGGTGGCAAGCGTTGTTCGGATTTACTGGGCGTACAGGGTGCGTAGG
CGGTTCGGTAAGCCCTTCGGGAAAGCTCCGGGCTTAACCCGGAAAGGTCGGA
GGGGACTGCCGAGCTAGAGGACGGGAGAGGAGCGCGGAATTCCCGGTGTAG

CGGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACGTTTCTGATGCTGAGGCACGAAAGCGTGGGGAGCAAACAGG

N. nitrosa 16S rRNA gene (European Nucleotide Archive: CZQA01000015.1 base pairs 522-774):

TACGAAGGTGGCAAGCGTTGTTCGGATTTACTGGGCGTACAGGGAGCGTAGG
CGGTTGGGTAAGCCCTCCGTGAAATCTCCGGGCCTAACCCGGAAAGTGCGGA
GGGGACTGCTCGGCTAGAGGATGGGAGAGGAGCGCGGAATTCCCGGTGTAG
CGGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACATTTCTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

N. inopinata 16S rRNA gene (European Nucleotide Archive: LN885086.1 base pairs 522-774):

TACGAAGGTGGCAAGCGTTGTTCGGATTTACTGGGCGTACAGGGAGCGTAGG
CGGTTGGGTAAGCCCTCCGTGAAATCTCCGGGCCTAACCCGGAAAGTGCGGA
GGGGACTGCTTGGCTAGAGGATGGGAGAGGAGCGCGGAATTCCCGGTGTAG
CGGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACATTTCTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

Leptospirillum ferroadiazotrophum 16S rRNA gene (GenBank: KT834983 base pairs 507-759):

GACAGGGGTGGCAAGCGTTGTTCGGAGTGACTGGGCGTAAAGGGTCTGTAGG
TGGTTTTTCAAGTCTTTGGTAAAAAGCCGTGGCTTAACCATGGTGAGGCCAAG
GAGACTGGGAGACTCGAGGCTGGGAGAGGGAAGCGGAATTTCTGGTGTAGC
GGTGAAATGCGTAGAGATCAGAAAGAAGGCCGGTGGCGAAGGCGGCTTCCT
GGAACAGACCTGACACTGAGAGACGAAAGCGTGGGGAGCAAACAGG

Nitrospira OTU A:

TACGAAGGTGGCAAGCGTTGTTCGGATTCACTGGGCGTACAGGGTGTGTAGG
CGGTTTGGTAAGCCTTCTGTTAAAGCTTCGGGCCCAACCCGGAAAGCGCAGA
GGGTACTGCCAGGCTAGAGGGTGGGAGAGGAGCGCGGAATTCCCGGTGTAG
CGGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACATACCTGACGCTGAGACACGAAAGCGTGGGGAGCAAACAGG

Nitrospira OTU B:

TACGAAGGTGGCAAGCGTTGTTCGGATTTACTGGGCGTACAGGGAGCGTAGG
CGGTTGGGTAAGCCCTCCGTGAAATCTCCGGGCCTAACCCGGAAAGTGCGGA
GGGGACTGCTCGGCTAGAGGATGGGAGAGGAGCGCGGAATTCCCGGTGTAG
CGGTGAAATGCGTAGAGATCGGGAGGAAGGCCGGTGGCGAAGGCGGCGCTC
TGGAACATTTCTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

Supplementary Tables

Table S1 Seed sludge collection dates, temperatures and sampling details

Trial	Experimental Temp (°C)	Date of Collection	Collection Temp (°C)	Frequency of NPR tests	Samples selected for 16S rRNA amplicon sequencing
14 °C Trial 1	14	4/7/2014	15.17	Days 2, 3, 5, 8, 11, 14, 18	Days 2, 3, 5, 8, 11, 14, 18
20 °C Trial 1	20	12/2/2013	18.38	Days 2, 3, 5, 7, 10, 14, 18	Days 2, 3, 5, 7, 10, 14, 18
30 °C Trial 1	30	2/19/2014	15.17	Days 2, 3, 5, 7, 9, 12, 16	Days 2, 3, 5, 7, 9, 12, 16
14 °C Trial 2	14	3/20/2015	14.36	Days 2, 3, 5, 7, 10, 14, 18 Recovery for 6hr, 12hr, 24hr, 36hr, 48hr	INF, Days 0, 2, 7, 18, Recovery for 12hr, 48hr
20 °C Trial 2	20	5/11/2015	20.49	Days 2, 3, 5, 7, 10, 14, 18 Recovery for 6hr, 12hr, 24hr, 36hr, 48hr	INF, Days 0, 2, 7, 18, Recovery for 12hr, 48hr
27 °C Trial 1	27	6/23/2015	23.72	Days 2, 3, 5, 7, 10, 14, 18 Recovery for 6hr, 12hr, 24hr, 36hr, 48hr	INF, Days 0, 2, 7, 18, Recovery for 12hr, 48hr
Note: INF- sample taken at influent of DC Water nitrification basin, “Fed for” samples are those taken after Starvation Reactor was dosed with ammonia					

Supplementary Figures

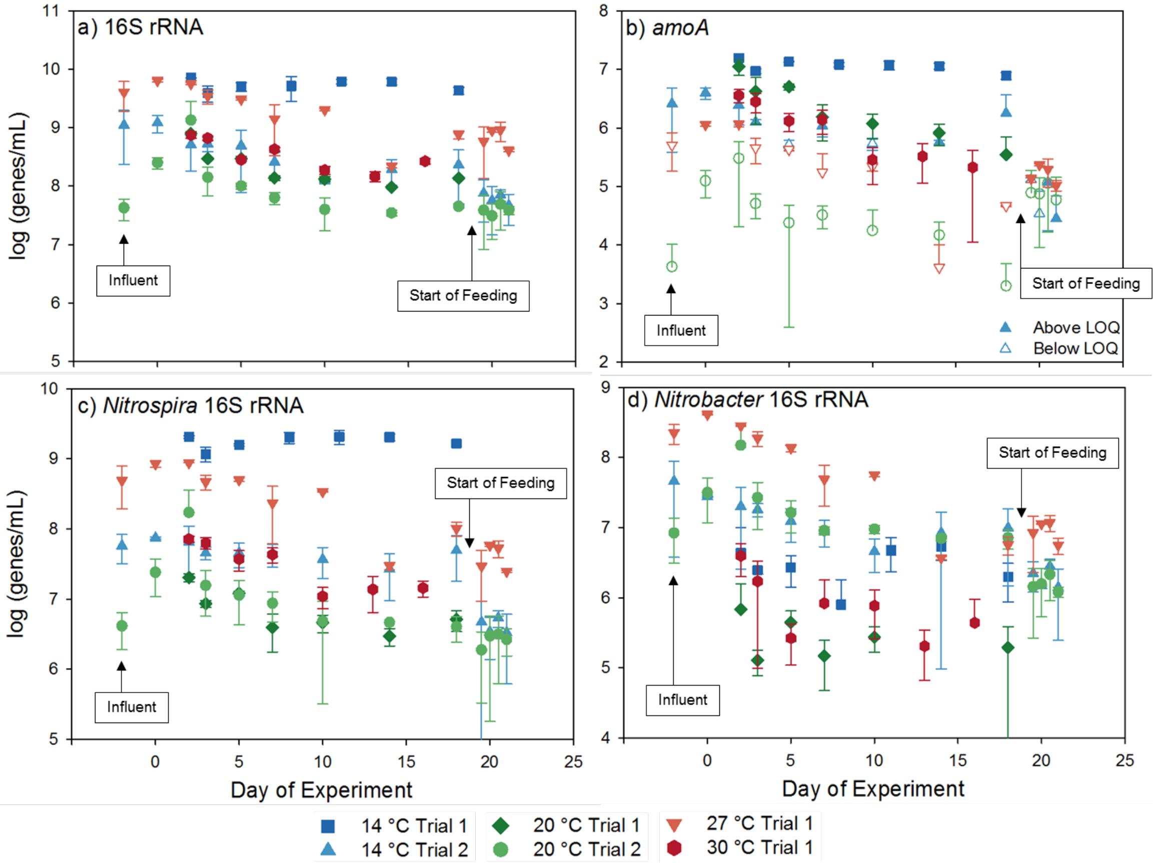


Figure S1 Gene concentrations quantified in DNA extracted from MLSS samples throughout all trials using qPCR of a) total 16S rRNA genes using universal primers b) *amoA* gene encoding the ammonia monooxygenase enzyme used by bacteria for oxidizing ammonia (AOBs) c) *Nitrospira* 16S rRNA targeting only *Nitrospira* species and d) *Nitrobacter* 16S rRNA targeting only *Nitrobacter* species.

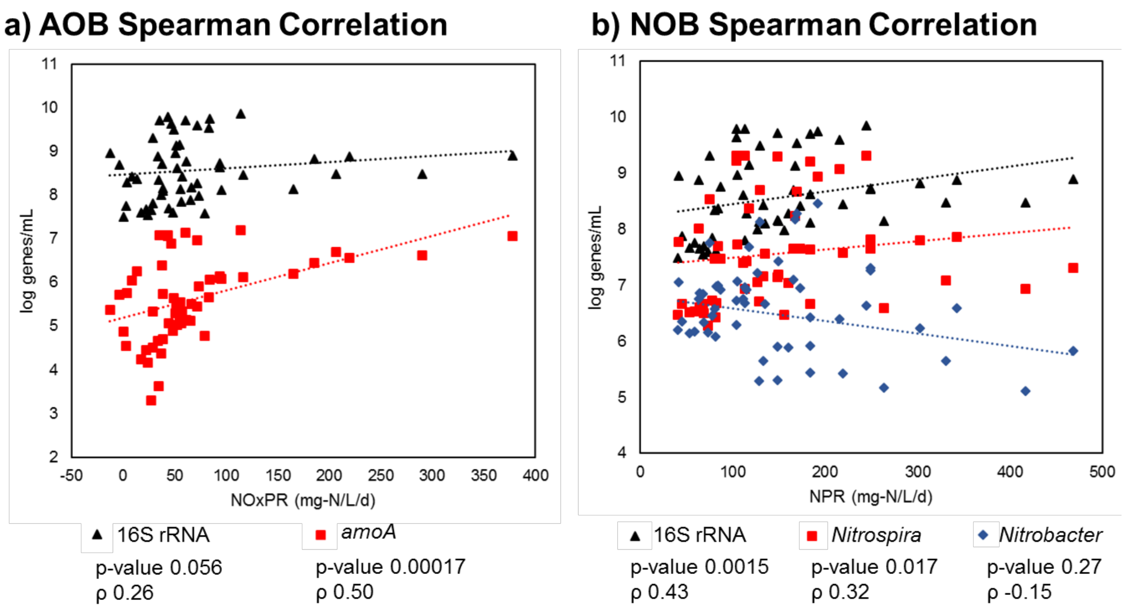


Figure S2 Correlation analysis between metabolic activity (NO_xPR and NPR) and concentration of associated genes via qPCR. Statistical values are indicated in the legend with significant p-values <0.05 and Spearman correlation coefficient (ρ) with a value of 1 indicating perfect positive correlation and -1 indicating perfect negative correlation.

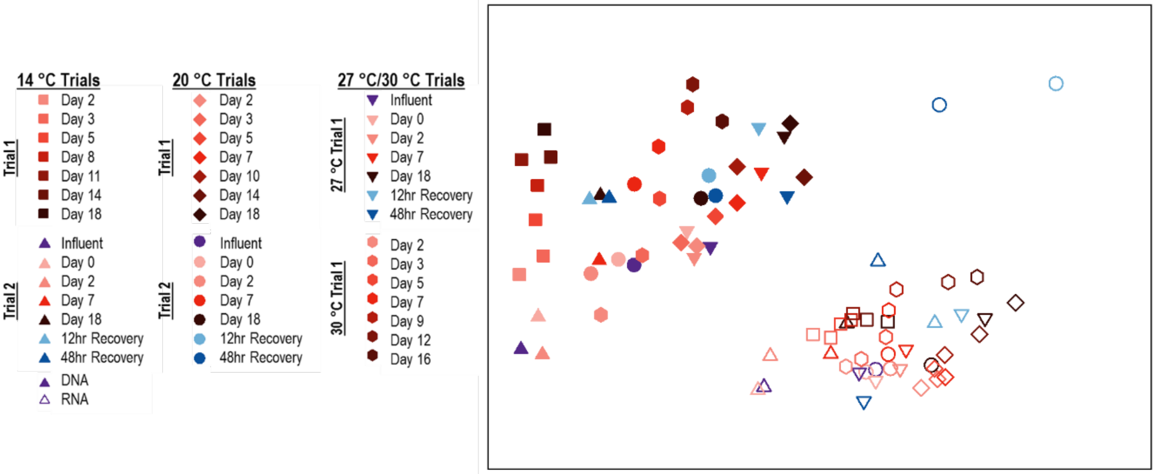
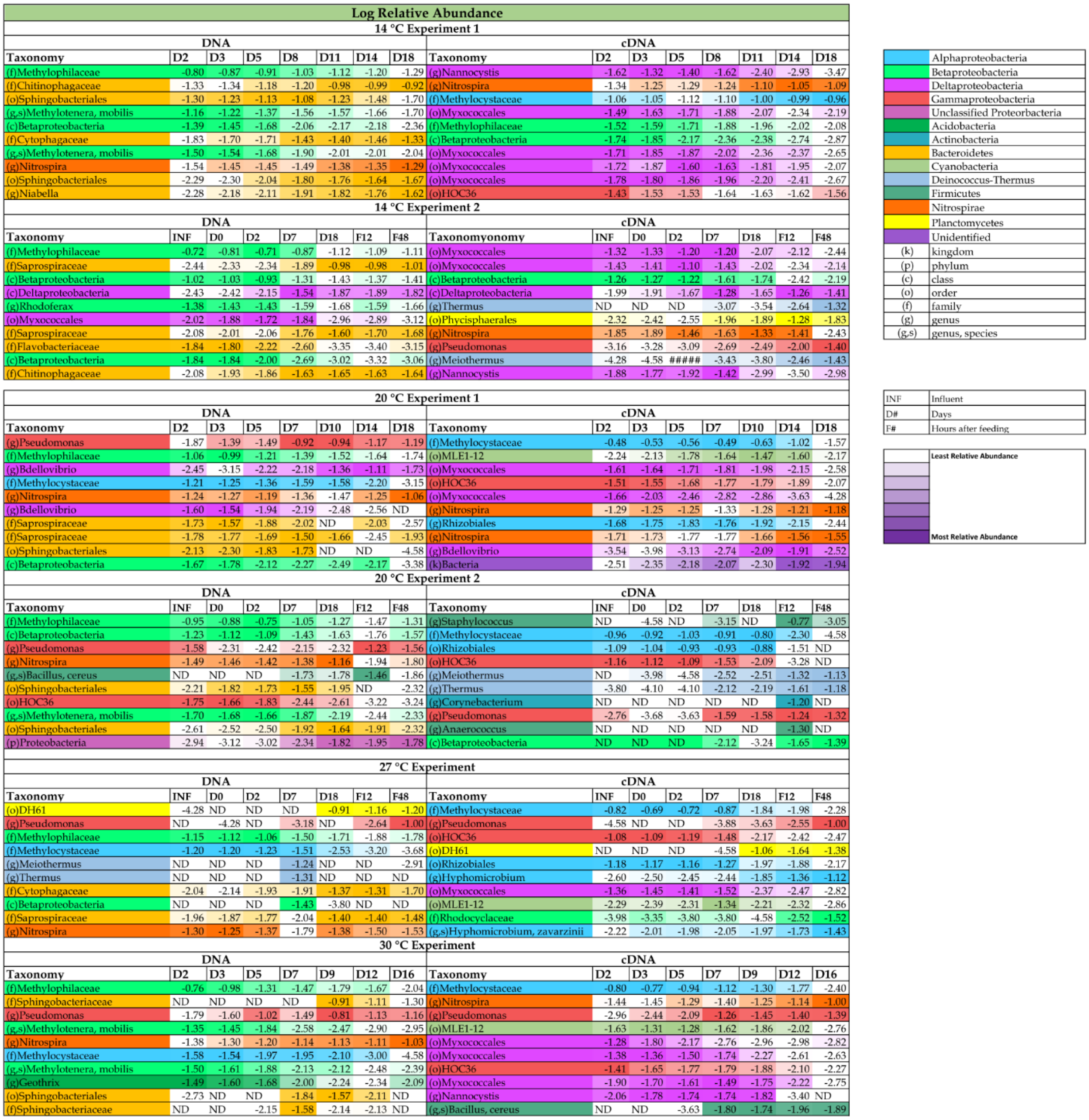


Figure S3 Comparison of microbial community composition of all conditions and trials applied across this study. MDS ordination of unifrac distance matrix of OTU table rarefied to lowest sample sequencing depth (38,000 sequences). Intensity of red shading increases with time in Starvation Reactor, purple points indicate samples taken from the influent of the DC Water nitrification basin sampled after mixing of return activated sludge, blue points represent samples collected during the "recovery" phase, after feeding of ammonium to the Starvation Reactor.



Log Relative Abundance

14 °C Experiment 1

DNA								cDNA							
Taxonomy	**D2**	**D3**	**D5**	**D8**	**D11**	**D14**	**D18**	**Taxonomy**	**D2**	**D3**	**D5**	**D8**	**D11**	**D14**	**D18**
(f)Methylophilaceae	-0.80	-0.87	-0.91	-1.03	-1.12	-1.20	-1.29	(g)Nannocystis	-1.62	-1.32	-1.40	-1.62	-2.40	-2.93	-3.47
(f)Chitinophagaceae	-1.33	-1.34	-1.18	-1.20	-0.98	-0.99	-0.92	(g)Nitrospira	-1.34	-1.25	-1.29	-1.24	-1.10	-1.05	-1.09
(o)Sphingobacteriales	-1.30	-1.23	-1.13	-1.08	-1.23	-1.48	-1.70	(f)Methylocystaceae	-1.06	-1.05	-1.12	-1.10	-1.00	-0.99	-0.96
(g,s)Methylotenera, mobilis	-1.16	-1.22	-1.37	-1.56	-1.57	-1.66	-1.70	(o)Myxococcales	-1.49	-1.63	-1.71	-1.88	-2.07	-2.34	-2.19
(c)Betaproteobacteria	-1.39	-1.45	-1.68	-2.06	-2.17	-2.18	-2.36	(f)Methylophilaceae	-1.52	-1.59	-1.71	-1.88	-1.96	-2.02	-2.08
(f)Cytophagaceae	-1.83	-1.70	-1.71	-1.43	-1.40	-1.46	-1.33	(c)Betaproteobacteria	-1.74	-1.85	-2.17	-2.36	-2.38	-2.74	-2.87
(g,s)Methylotenera, mobilis	-1.50	-1.54	-1.68	-1.90	-2.01	-2.01	-2.04	(o)Myxococcales	-1.71	-1.85	-1.87	-2.02	-2.36	-2.37	-2.65
(g)Nitrospira	-1.54	-1.45	-1.45	-1.49	-1.38	-1.35	-1.29	(o)Myxococcales	-1.72	-1.87	-1.60	-1.63	-1.81	-1.95	-2.07
(o)Sphingobacteriales	-2.29	-2.30	-2.04	-1.80	-1.76	-1.64	-1.67	(o)Myxococcales	-1.78	-1.80	-1.86	-1.96	-2.20	-2.41	-2.67
(g)Niabella	-2.28	-2.18	-2.11	-1.91	-1.82	-1.76	-1.62	(o)HOC36	-1.43	-1.53	-1.53	-1.64	-1.63	-1.62	-1.56

14 °C Experiment 2

DNA								cDNA							
Taxonomy	**INF**	**D0**	**D2**	**D7**	**D18**	**F12**	**F48**	**Taxonomyonomy**	**INF**	**D0**	**D2**	**D7**	**D18**	**F12**	**F48**
(f)Methylophilaceae	-0.72	-0.81	-0.71	-0.87	-1.12	-1.09	-1.11	(o)Myxococcales	-1.32	-1.33	-1.20	-1.20	-2.07	-2.12	-2.44
(f)Saprospiraceae	-2.44	-2.33	-2.34	-1.89	-0.98	-0.98	-1.01	(o)Myxococcales	-1.43	-1.41	-1.10	-1.43	-2.02	-2.34	-2.14
(c)Betaproteobacteria	-1.02	-1.03	-0.93	-1.31	-1.43	-1.37	-1.41	(c)Betaproteobacteria	-1.26	-1.27	-1.22	-1.61	-1.74	-2.42	-2.19
(c)Deltaproteobacteria	-2.43	-2.42	-2.15	-1.54	-1.87	-1.89	-1.82	(c)Deltaproteobacteria	-1.99	-1.91	-1.67	-1.28	-1.65	-1.26	-1.41
(g)Rhodoferax	-1.38	-1.43	-1.43	-1.59	-1.68	-1.59	-1.66	(g)Thermus	ND	ND	ND	-3.07	-3.54	-2.64	-1.32
(o)Myxococcales	-2.02	-1.88	-1.72	-1.84	-2.96	-2.89	-3.12	(o)Phycisphaerales	-2.32	-2.42	-2.55	-1.96	-1.89	-1.28	-1.83
(f)Saprospiraceae	-2.08	-2.01	-2.06	-1.76	-1.60	-1.70	-1.68	(g)Nitrospira	-1.85	-1.89	-1.46	-1.63	-1.33	-1.41	-2.43
(f)Flavobacteriaceae	-1.84	-1.80	-2.22	-2.60	-3.35	-3.40	-3.15	(g)Pseudomonas	-3.16	-3.28	-3.09	-2.69	-2.49	-2.00	-1.40
(c)Betaproteobacteria	-1.84	-1.84	-2.00	-2.69	-3.02	-3.32	-3.06	(g)Meiothermus	-4.28	-4.58	#####	-3.43	-3.80	-2.46	-1.43
(f)Chitinophagaceae	-2.08	-1.93	-1.86	-1.63	-1.65	-1.63	-1.64	(g)Nannocystis	-1.88	-1.77	-1.92	-1.42	-2.99	-3.50	-2.98

🟦	Alphaproteobacteria
🟩	Betaproteobacteria
🟪	Deltaproteobacteria
🟥	Gammaproteobacteria
🟪	Unclassified Proteorbacteria
🟩	Acidobacteria
🟦	Actinobacteria
🟧	Bacteroidetes
🟩	Cyanobacteria
🟦	Deinococcus-Thermus
🟩	Firmicutes
🟧	Nitrospirae
🟨	Planctomycetes
🟪	Unidentified
(k)	kingdom
(p)	phylum
(c)	class
(o)	order
(f)	family
(g)	genus
(g,s)	genus, species

20 °C Experiment 1

DNA								cDNA							
Taxonomy	**D2**	**D3**	**D5**	**D7**	**D10**	**D14**	**D18**	**Taxonomy**	**D2**	**D3**	**D5**	**D7**	**D10**	**D14**	**D18**
(g)Pseudomonas	-1.87	-1.39	-1.49	-0.92	-0.94	-1.17	-1.19	(f)Methylocystaceae	-0.48	-0.53	-0.56	-0.49	-0.63	-1.02	-1.57
(f)Methylophilaceae	-1.06	-0.99	-1.21	-1.39	-1.52	-1.64	-1.74	(o)MLE1-12	-2.24	-2.13	-1.78	-1.64	-1.47	-1.60	-2.17
(g)Bdellovibrio	-2.45	-3.15	-2.22	-2.18	-1.36	-1.11	-1.73	(o)Myxococcales	-1.61	-1.64	-1.71	-1.81	-1.98	-2.15	-2.58
(f)Methylocystaceae	-1.21	-1.25	-1.36	-1.59	-1.58	-2.20	-3.15	(o)HOC36	-1.51	-1.55	-1.68	-1.77	-1.79	-1.89	-2.07
(g)Nitrospira	-1.24	-1.27	-1.19	-1.36	-1.47	-1.25	-1.06	(o)Myxococcales	-1.66	-2.03	-2.46	-2.82	-2.86	-3.63	-4.28
(g)Bdellovibrio	-1.60	-1.54	-1.94	-2.19	-2.48	-2.56	ND	(g)Nitrospira	-1.29	-1.25	-1.25	-1.33	-1.28	-1.21	-1.18
(f)Saprospiraceae	-1.73	-1.57	-1.88	-2.02	ND	-2.03	-2.57	(g)Rhizobiales	-1.68	-1.75	-1.83	-1.76	-1.92	-2.15	-2.44
(f)Saprospiraceae	-1.78	-1.77	-1.69	-1.50	-1.66	-2.45	-1.93	(g)Nitrospira	-1.71	-1.73	-1.77	-1.77	-1.66	-1.56	-1.55
(o)Sphingobacteriales	-2.13	-2.30	-1.83	-1.73	ND	ND	-4.58	(g)Bdellovibrio	-3.54	-3.98	-3.13	-2.74	-2.09	-1.91	-2.52
(c)Betaproteobacteria	-1.67	-1.78	-2.12	-2.27	-2.49	-2.17	-3.38	(k)Bacteria	-2.51	-2.35	-2.18	-2.07	-2.30	-1.92	-1.94

INF	Influent
D#	Days
F#	Hours after feeding

⬜	**Least Relative Abundance**
🟪	
🟪	
🟪	
🟪	
🟪	
🟪	**Most Relative Abundance**

20 °C Experiment 2

DNA								cDNA							
Taxonomy	**INF**	**D0**	**D2**	**D7**	**D18**	**F12**	**F48**	**Taxonomy**	**INF**	**D0**	**D2**	**D7**	**D18**	**F12**	**F48**
(f)Methylophilaceae	-0.95	-0.88	-0.75	-1.05	-1.27	-1.47	-1.31	(g)Staphylococcus	ND	-4.58	ND	-3.15	ND	-0.77	-3.05
(c)Betaproteobacteria	-1.23	-1.12	-1.09	-1.43	-1.63	-1.76	-1.57	(f)Methylocystaceae	-0.96	-0.92	-1.03	-0.91	-0.80	-2.30	-4.58
(g)Pseudomonas	-1.58	-2.31	-2.42	-2.15	-2.32	-1.23	-1.56	(o)Rhizobiales	-1.09	-1.04	-0.93	-0.93	-0.88	-1.51	ND
(g)Nitrospira	-1.49	-1.46	-1.42	-1.38	-1.16	-1.94	-1.80	(o)HOC36	-1.16	-1.12	-1.09	-1.53	-2.09	-3.28	ND
(g,s)Bacillus, cereus	ND	ND	ND	-1.73	-1.78	-1.46	-1.86	(g)Meiothermus	ND	-3.98	-4.58	-2.52	-2.51	-1.32	-1.13
(o)Sphingobacteriales	-2.21	-1.82	-1.73	-1.55	-1.95	ND	-2.32	(g)Thermus	-3.80	-4.10	-4.10	-2.12	-2.19	-1.61	-1.18
(o)HOC36	-1.75	-1.66	-1.83	-2.44	-2.61	-3.22	-3.24	(g)Corynebacterium	ND	ND	ND	ND	ND	-1.20	ND
(g,s)Methylotenera, mobilis	-1.70	-1.68	-1.66	-1.87	-2.19	-2.44	-2.33	(g)Pseudomonas	-2.76	-3.68	-3.63	-1.59	-1.58	-1.24	-1.32
(o)Sphingobacteriales	-2.61	-2.52	-2.50	-1.92	-1.64	-1.91	-2.32	(g)Anaerococcus	ND	ND	ND	ND	ND	-1.30	ND
(p)Proteobacteria	-2.94	-3.12	-3.02	-2.34	-1.82	-1.95	-1.78	(c)Betaproteobacteria	ND	ND	ND	-2.12	-3.24	-1.65	-1.39

27 °C Experiment

DNA								cDNA							
Taxonomy	**INF**	**D0**	**D2**	**D7**	**D18**	**F12**	**F48**	**Taxonomy**	**INF**	**D0**	**D2**	**D7**	**D18**	**F12**	**F48**
(o)DH61	-4.28	ND	ND	ND	-0.91	-1.16	-1.20	(f)Methylocystaceae	-0.82	-0.69	-0.72	-0.87	-1.84	-1.98	-2.28
(g)Pseudomonas	ND	-4.28	ND	-3.18	ND	-2.64	-1.00	(g)Pseudomonas	-4.58	ND	ND	-3.88	-3.63	-2.55	-1.00
(f)Methylophilaceae	-1.15	-1.12	-1.06	-1.50	-1.71	-1.88	-1.78	(o)HOC36	-1.08	-1.09	-1.19	-1.48	-2.17	-2.42	-2.47
(f)Methylocystaceae	-1.20	-1.20	-1.23	-1.51	-2.53	-3.20	-3.68	(o)DH61	ND	ND	ND	-4.58	-1.06	-1.64	-1.38
(g)Meiothermus	ND	ND	ND	-1.24	ND	ND	-2.91	(o)Rhizobiales	-1.18	-1.17	-1.16	-1.27	-1.97	-1.88	-2.17
(g)Thermus	ND	ND	ND	-1.31	ND	ND	ND	(g)Hyphomicrobium	-2.60	-2.50	-2.45	-2.44	-1.85	-1.36	-1.12
(f)Cytophagaceae	-2.04	-2.14	-1.93	-1.91	-1.37	-1.31	-1.70	(o)Myxococcales	-1.36	-1.45	-1.41	-1.52	-2.37	-2.47	-2.82
(c)Betaproteobacteria	ND	ND	ND	-1.43	-3.80	ND	ND	(o)MLE1-12	-2.29	-2.39	-2.31	-1.34	-2.21	-2.32	-2.86
(f)Saprospiraceae	-1.96	-1.87	-1.77	-2.04	-1.40	-1.40	-1.48	(f)Rhodocyclaceae	-3.98	-3.35	-3.80	-3.80	-4.58	-2.52	-1.52
(g)Nitrospira	-1.30	-1.25	-1.37	-1.79	-1.38	-1.50	-1.53	(g,s)Hyphomicrobium, zavarzinii	-2.22	-2.01	-1.98	-2.05	-1.97	-1.73	-1.43

30 °C Experiment

DNA								cDNA							
Taxonomy	**D2**	**D3**	**D5**	**D7**	**D9**	**D12**	**D16**	**Taxonomy**	**D2**	**D3**	**D5**	**D7**	**D9**	**D12**	**D16**
(f)Methylophilaceae	-0.76	-0.98	-1.31	-1.47	-1.79	-1.67	-2.04	(f)Methylocystaceae	-0.80	-0.77	-0.94	-1.12	-1.30	-1.77	-2.40
(f)Sphingobacteriaceae	ND	ND	ND	ND	-0.91	-1.11	-1.30	(g)Nitrospira	-1.44	-1.45	-1.29	-1.40	-1.25	-1.14	-1.00
(g)Pseudomonas	-1.79	-1.60	-1.02	-1.49	-0.81	-1.13	-1.16	(g)Pseudomonas	-2.96	-2.44	-2.09	-1.26	-1.45	-1.40	-1.39
(g,s)Methylotenera, mobilis	-1.35	-1.45	-1.84	-2.58	-2.47	-2.90	-2.95	(o)MLE1-12	-1.63	-1.31	-1.28	-1.62	-1.86	-2.02	-2.76
(g)Nitrospira	-1.38	-1.30	-1.20	-1.14	-1.13	-1.11	-1.03	(o)Myxococcales	-1.28	-1.80	-2.17	-2.76	-2.96	-2.98	-2.82
(f)Methylocystaceae	-1.58	-1.54	-1.97	-1.95	-2.10	-3.00	-4.58	(o)Myxococcales	-1.38	-1.36	-1.50	-1.74	-2.27	-2.61	-2.63
(g,s)Methylotenera, mobilis	-1.50	-1.61	-1.88	-2.13	-2.12	-2.48	-2.39	(o)HOC36	-1.41	-1.65	-1.77	-1.79	-1.88	-2.10	-2.27
(g)Geothrix	-1.49	-1.60	-1.68	-2.00	-2.24	-2.34	-2.09	(o)Myxococcales	-1.90	-1.70	-1.61	-1.49	-1.75	-2.22	-2.75
(o)Sphingobacteriales	-2.73	ND	ND	-1.84	-1.57	-2.11	ND	(g)Nannocystis	-2.06	-1.78	-1.74	-1.74	-1.82	-3.40	ND
(f)Sphingobacteriaceae	ND	ND	-2.15	-1.58	-2.14	-2.13	ND	(g,s)Bacillus, cereus	ND	ND	-3.63	-1.80	-1.74	-1.96	-1.89

Figure S4 Ten most variable OTUs in each trial and nucleic acid type (DNA or cDNA). Values are log relative abundance (normalized to sequencing depth (38,000)). Heat mapping for each OTU indicates behavior of OTU in that trial (intensity of color corresponds to relative abundance).