

Supplementary information II

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13 **Table S1: Accession numbers/gene identifiers for all sequences used for phylogenetic analysis of**
 14 **pOCC/eHao/NrfA genes (Fig. S4).**

Species Name	Gene identifier [IMG/NCBI ID]
Candidatus Electronema sp. GS	TAA75457.1
Candidatus Electrothrix aarhusiensis MCF	RWX43088.1
Candidatus Electrothrix marina A5	RWX50766.1
Actinobacillus pleuropneumoniae S8	2552278133
Actinobacillus succinogenes 130Z	640807619
Actinobacillus ureae ATCC 25976	650340686
Ammonifex degensii KC4	646359879
Anaerococcus prevotii ACS-065-V-Col13	2529738369
Anaerolinea thermophila UNI-1	649906650
Bacillus sp. 1NLA3E	2506744287
Bacteroidetes bacterium GWA2_31_9	2721822901
Beggiatoa sp. "Orange Guaymas"	2502838749
Caldilinea aerophila STL-6-01, DSM 14535	2513225030
Calditrichaeota bacterium	RMH60699.1
Caminiobacter mediatlanticus	WP_007473950.1
Campylobacter curvus	WP_011992073.1
Campylobacter fetus	WP_002849252.1
Campylobacter hominis ATCC BAA-381	640869848
Campylobacter jejuni jejuni NCTC 11168	637040891
Candidatus Cloacimonetes bacterium	PCJ16198.1
Candidatus Magnetoovum chiemensis	KJR43854.1
Candidatus Thiomargarita nelsonii S10	KHD11702.2
Candidatus Thioglobus autotrophicus	WP_053951924.1
Candidatus Thioglobus sp. EF1	ALE52942.1
Capnocytophaga gingivalis JCVIHMP016	644450706
Citrobacter koseri ATCC BAA-895	640917778
Comamonadaceae bacterium EBPR	2619975620
Corynebacterium pseudotuberculosis CCUG 27541	2628297476
Delisea pulchra	2617265124
Delta proteobacterium MLMS-1	EAT04113.1
Desulfosporosinus meridiei S10	2510242216
Desulfovibrio desulfuricans ATCC 27774	643580866
Desulfovibrio salexigens DSM 2638	644838886
Desulfovibrio vulgaris Hildenborough	637121843
Desulfurispirillum indicum S5	649844489
Desulfurivibrio alkaliphilus AHT2	ADH84778.1
endosymbiont of Riftia pachyptila	EGV52177.1
Escherichia coli HS	640923413
Gallibacterium anatis DSM 16844	2514917813

Geobacter uraniumreducens Rf4	WP_011940785.1
Grimontia hollisae CIP 101886	647235545
Haemophilus influenzae 2019	2630849089
Lentisphaerae bacterium RIFOXYB12_FULLL_65_16	2716626204
Marivirga tractuosa DSM 4126	649787403
Meiothermus silvanus DSM 9946	646843608
Myxococcus xanthus DK 1622	638023578
Nautilia profundicola	WP_015902282.1
Nitrospiraceae bacterium	RJR18741.1
Nitrospirae bacterium JdFR-81	2730372430
Oceanospirillales bacterium SCGC AD-311-B11v3	2701081706
Omnitrophica WOR_2 bacterium GWA2_45_18	2721786119
Opiritatus terrae PB90-1	641694276
Pelobacter carbinolicus DSM 2380	637752476
Photobacterium profundum SS9	637585967
Planctomycetes bacterium	RKY19412.1
Planctomyces brasiliensis DSM 5305	649980400
Planctomyces maris DSM 8797	641112668
Porphyromonas gingivalis W83	637150428
Prevotella marshii DSM 16973	648809557
Propionivibrio dicarboxylicus DSM 5885	SDI64766.1
Providencia alcalifaciens DSM 30120	643148102
Riemerella anatipestifer DSM 15868	649778058
Selenomonas sputigena ATCC 35185	646081185
Shewanella oneidensis MR-1	637345732
Shewanella sediminis HAW-EB3	WP_012144695.1
Sulfurospirillum deleyianum DSM 6946	646423959
Thioalkalivibrio nitratireducens DSM 14787	2521963319
Thioalkalivibrio paradoxus ARh 1	2513007479
Thioalkalivibrio thiocyanoxidans ARh 4	2506728454
Vibrio fischeri ES114	637636232
Vibrio fluvialis I21563	2546700336
Vibrio harveyi ATCC 25919	2583678091
Wolinella succinogenes DSM 1740	637456212
Yersinia enterocolitica YEA	2611555138
Aeromonas hydrophila ATCC 7966	639715039
Bacillus subtilis	KOS70037.1

17 **Table S2: Accession numbers/gene identifiers for all sequences used for phylogenetic analysis of NapA genes**
 18 **(Fig. S1).**

Species Name	Gene identifier [IMG/NCBI ID]
Candidatus Electronema sp. GS	2729874203
Aggregatibacter actinomycetemcomitans DSM 8324	2515250942
Anaeromyxobacter dehalogenans 2CP-C	ABC80683.1
Azospirillum brasilense sp7	2599104047
Azospirillum brasilense sp7	2599101664
Bordetella bronchiseptica RB50	CAE33292.1
Bordetella parapertussis 12822	Q7W733.1
Bradyrhizobium japonicum USDA 110	637374628
Burkholderia xenovorans LB400	637953004
Campylobacter jejuni jejuni NCTC 11168	YP_002344187.1
Candidatus Desulfuromonas soudanensis WTL	2609285564
Cupriavidus necator pHG1	640427642
Cystobacter violaceus Cb vi76	2592593039
Dechloromonas aromatica RCB	637681987
Desulfitobacterium hafniense DCB-2	ACL19345.1
Desulfobulbus japonicus DSM 18378	WP_028579228.1
Desulfobulbus mediterraneus	WP_028585221.1
Desulfobulbus propionicus DSM 2032	ADW17542.1
Desulfocapsa sulfexigens DSM 10523	AGF79815.1
Desulfocapsa sulfexigens	WP_015405499.1
Desulfovibrio desulfuricans ATCC 27774	ACL48525.1
Desulfurivibrio alkaliphilus AHT2	646847134
Dissulfuribacter thermophilus S69	OCC14250.1
Escherichia coli DH1	646935360
Geobacter lovleyi SZ	ACD94779.1
Geobacter pickeringii G13	AJE02263.1
Haemophilus ducreyi ATCC 33940	2599173274
Haemophilus influenzae F3047	649868883
Helicobacter hepaticus ATCC 51449	Q7VJT5.1
Kryptonium sp. JGI-4	2599799712
Kryptonium sp. JGI-6	2600397245
Kryptonium sp. JGI-23	2601849902
Magnetospirillum magneticum AMB-1	637821302
Paracoccus denitrificans PD1222	ABL72782.1
Paracoccus pantotrophus DSM 1403	SFY43853.1
Pasteurella multocida 36950	2512391891
Photobacterium profundum SS9	637585562
Photobacterium profundum SS9	637586736

<i>Pseudomonas aeruginosa</i> PAO1	637051567
<i>Pseudomonas</i> sp. G-179	AAD46689.1
<i>Ralstonia eutropha</i> JMP134	637694190
<i>Ralstonia metallidurans</i> CH34	637979487
<i>Rhizobium</i> sp. CF142	WP_007818974.1
<i>Rhodobacter sphaeroides</i> 2.4.1	ABA81591.1
<i>Salmonella enterica enterica</i> sv. Choleraesuis SC-B67	637641152
<i>Salmonella typhimurium</i> LT2	637212978
<i>Sedimenticola selenatireducens</i> AK4OH1	2513982609
<i>Sinorhizobium meliloti</i>	AIM03004.1
<i>Shewanella frigidimarina</i> NCIMB 400	ABI70414.1
<i>Shewanella oneidensis</i> MR-1	AAN53924.1
<i>Shigella flexneri</i> CCH060	2531700739
<i>Sinorhizobium meliloti</i> RMO17	2598504540
<i>Sorangium cellulosum</i> 'So ce 56'	641348992
<i>Sulfurospirillum barnesii</i> SES-3	2507135060
<i>Symbiobacterium thermophilum</i> IAM 14863	BAD39902.1
<i>Thermosulfurimonas dismutans</i>	OAQ21381.1
<i>Vibrio vulnificus</i> ATCC 43382	2662388500
<i>Wolinella succinogenes</i> DSM 1740	637456405
<i>Bacillus subtilis</i>	WP_124073427.1
<i>Synechococcus elongatus</i> PCC 7942	CAA52675.1

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21 **Table S3: Accession numbers/gene identifiers for all sequences used for phylogenetic analysis of NapD genes**
 22 **(Fig. S2).**

Species Name	Gene identifier [IMG/NCBI ID]
Candidatus Electronema sp. GS	2729874204
Candidatus Electronema sp. GS	2729874205
Desulfurivibrio alkaliphilus AHT2	646847137
Aggregatibacter actinomycetemcomitans DSM 8324	2515250943
Anaeromyxobacter dehalogenans 2CP-C	ABC80682.1
Azospirillum brasilense sp7	2599104048
Azospirillum brasilense sp7	2599101665
Bordetella bronchiseptica RB50	CAE33291.1
Bordetella parapertussis 12822	637109774
Bradyrhizobium japonicum USDA 110	637374627
Burkholderia xenovorans LB400	637953003
Campylobacter jejuni jejuni NCTC 11168	CAL34913.1
Candidatus Desulfuromonas soudanensis WTL	2609285565
Cupriavidus necator pHG1	640427641
Dechloromonas aromatica RCB	637681988
Desulfitobacterium hafniense DCB-2	643561198
Desulfobulbus japonicus DSM 18378	WP_028579227.1
Desulfobulbus propionicus DSM 2032	ADW17543.1
Desulfocapsa sulfexigens DSM 10523	AGF78837.1
Desulfovibrio desulfuricans ATCC 27774	ACL48526.1
Desulfurivibrio alkaliphilus AHT2	646847137
Escherichia coli DH1	646935359
Geobacter lovleyi SZ	ACD94778.1
Geobacter pickeringii G13	AJE02262.1
Haemophilus ducreyi ATCC 33940	2599173275
Haemophilus influenzae F3047	649868884
Helicobacter hepaticus ATCC 51449	637431176
Kryptonium sp. JGI-4	2599799715
Kryptonium sp. JGI-6	2600397248
Magnetospirillum magneticum AMB-1	BAE51495.1
Paracoccus denitrificans PD1222	ABL72781.1
Paracoccus pantotrophus	SFY43855.1
Pasteurella multocida 36950	2512391890
Photobacterium profundum SS9	637585561
Pseudomonas aeruginosa PAO1	637051568
Pseudomonas sp. G-179	AAD46688.1
Ralstonia metallidurans CH34	637979488
Rhizobium sp. CF142	EJJ28403.1

Rhodobacter sphaeroides 2.4.1	640069464
Salmonella enterica enterica sv. Choleraesuis SC-B67	637641153
Salmonella typhimurium LT2	637212979
Sedimenticola selenatireducens AK4OH1	2513982608
Shewanella frigidimarina NCIMB 400	ABI72396.1
Shewanella oneidensis MR-1	AAN53925.1
Shigella flexneri CCH060	2531700738
Sinorhizobium meliloti RMO17	2598504539
Sulfurospirillum barnesii SES-3	2507135066
Symbiobacterium thermophilum IAM 14863	637537430
Wolinella succinogenes DSM 1740	637456399

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25 **Table S4: Accession numbers/gene identifiers for all sequences used for phylogenetic analysis of NapF genes**
 26 **(Fig. S3).**

Species Name	Gene identifier [IMG/NCBI ID]
Candidatus Electronema sp. GS	2729874206
Candidatus Electrothrix aarhusiensis MCF	2608444788
Candidatus Electrothrix marina A3	2609183527
Aggregatibacter segnis	WP_109859830.1
Arcobacter sp. CECT 8986	WP_128990985.1
Avibacterium avium	WP_115250139.1
Azospirillum brasilense sp7	2599104049
Azovibrio restrictus	WP_026685580.1
Beggiatoa sp. 4572	OQY57412.1
Candidatus Accumulibacter sp.	TLD45631.1
Denitromonas halophilus	WP_144176374.1
Enterovibrio coralii	WP_067418395.1
Escherichia coli DH1	646935358
Haemophilus ducreyi ATCC 33940	2599173276
Haemophilus influenzae F3047	649868885
Hydrogenimonas thermophila	WP_092910301.1
Magnetospira sp. QH-2	WP_046020781.1
Magnetospirillum magneticum AMB-1	637821304
Pasteurella multocida 36950	2512391889
Pectobacterium peruvienne	WP_048259758.1
Pectobacterium zantedeschiae	WP_129706134.1
Photobacterium profundum SS9	637585560
Pseudomonas aeruginosa PAO1	637051569
Pseudomonas sp. G-179	AAD46687.1
Rhizobium sp. CF142	WP_007818978.1
Rhodocyclaceae bacterium	TXG88186.1
Rodentibacter ratti	WP_077497317.1
Salmonella typhimurium LT2	637212980
Sedimenticola selenatireducens AK4OH1	2513982607
Shewanella frigidimarina NCIMB 400	ABI71179.1
Shewanella oneidensis MR-1	AAN54718.1
Shigella flexneri CCH060	2531700737
Sinorhizobium meliloti RMO17	2598504538
Solemya elarraichensis gill symbiont	WP_078476978.1
Sulfuricella denitrificans	WP_148290815.1
Sulfurospirillum barnesii SES-3	2507135064
Vibrio vulnificus ATCC 43382	2662388498
Wolinella succinogenes DSM 1740	637456401

27 **Table S5: Transcript levels (RPKM) and differential transcription (DESeq2) of the 100 most highly**
 28 **expressed genes of Ca. Electronema sp. GS. DNRA genes are highlighted.**

Rank	IMG Gene ID	Locus Tag	Gene Product Name	Average RPKM under nitrate-reducing conditions	log2 fold Change between oxic control and nitrate amendme nt	Adj. p value
1	2729874347	Ga0183576_10762	PilA	107488	-1.12	1.00
2	2729875496	Ga0183576_13321	hypothetical protein	37779	0.81	1.00
3	2729875974	Ga0183576_16010	cytochrome c	36783	0.41	1.00
4	2729875937	Ga0183576_1578	hypothetical protein	35366	1.52	0.96
5	2729874243	Ga0183576_10656	hypothetical protein	29243	-2.78	0.65
6	2729874606	Ga0183576_1117	hypothetical protein	25514	0.34	1.00
7	2729874008	Ga0183576_10443	Putative peptidoglycan binding domain-containing protein	19765	0.29	1.00
8	2729875690	Ga0183576_14111	hypothetical protein	19659	-0.11	1.00
9	2729875544	Ga0183576_13513	hypothetical protein	16289	-0.58	1.00
10	2729873391	Ga0183576_10111	cold-shock DNA-binding protein family	16178	0.66	1.00
11	2729873390	Ga0183576_10110	cold-shock DNA-binding protein family	13896	-0.57	1.00
12	2729874498	Ga0183576_10928	hypothetical protein	12838	0.37	1.00
13	2729875691	Ga0183576_14112	hypothetical protein	12251	-2.02	0.98
14	2729875791	Ga0183576_14613	hypothetical protein	11553	-0.14	1.00
15	2729874205	Ga0183576_10618	periplasmic nitrate reductase chaperone NapD	11247	2.16	0.97
16	2729874203	Ga0183576_10616	periplasmic nitrate reductase subunit NapA apoprotein	11063	1.09	1.00
17	2729875033	Ga0183576_11921	tRNA 2-thiouridine synthesizing protein E	11022	0.95	1.00
18	2729874199	Ga0183576_10612	pOCC	10387	0.76	1.00
19	2729874502	Ga0183576_10932	hypothetical protein	10266	0.11	1.00
20	2729874460	Ga0183576_10883	hypothetical protein	9917	1.68	0.76
21	2729874759	Ga0183576_11353	Opacity protein	9686	0.78	1.00
22	2729873817	Ga0183576_102205	cold-shock DNA-binding protein family	9540	1.78	0.76
23	2729874596	Ga0183576_11052	hypothetical protein	9508	-0.84	1.00
24	2729875792	Ga0183576_14614	4Fe-4S dicluster domain-containing protein	9457	0.35	1.00
25	2729874206	Ga0183576_10619	periplasmic nitrate reductase maturation protein NapF	8988	1.83	1.00
26	2729875357	Ga0183576_12812	hypothetical protein	8953	-0.22	1.00
27	2729875626	Ga0183576_1392	pyrroloquinoline quinone biosynthesis protein D	8725	-0.74	1.00
28	2729874566	Ga0183576_11022	protein of unknown function (DUF4360)	8432	1.85	0.89
29	2729873552	Ga0183576_101173	hypothetical protein	8273	-0.90	1.00
30	2729873752	Ga0183576_102140	LSU ribosomal protein L10P	8041	0.86	1.00
31	2729874198	Ga0183576_10611	hypothetical protein	7954	-1.03	1.00
32	2729875893	Ga0183576_1535	hypothetical protein	7912	0.13	1.00
33	2729873736	Ga0183576_102124	dissimilatory adenylylsulfate reductase beta subunit	7383	0.04	1.00
34	2729873441	Ga0183576_10161	Dissimilatory sulfite reductase D (DsrD)	7310	0.44	1.00
35	2729874204	Ga0183576_10617	periplasmic nitrate reductase chaperone NapD	7118	2.22	0.98
36	2729873786	Ga0183576_102174	SSU ribosomal protein S4P	7036	0.55	1.00
37	2729874424	Ga0183576_10847	integration host factor subunit beta	6979	0.16	1.00
38	2729873757	Ga0183576_102145	SSU ribosomal protein S7P	6792	-0.04	1.00
39	2729874342	Ga0183576_10757	type IV pilus assembly protein PilW	6786	-0.03	1.00
40	2729874202	Ga0183576_10615	ferredoxin-type protein NapG	6696	0.97	1.00
41	2729873774	Ga0183576_102162	small subunit ribosomal protein S14	6654	0.14	1.00
42	2729873784	Ga0183576_102172	small subunit ribosomal protein S13	6594	-0.22	1.00
43	2729875627	Ga0183576_1393	hypothetical protein	6565	-0.52	1.00
44	2729876010	Ga0183576_1637	protein refolding chaperone Spy/CpxP family	6469	1.51	1.00
45	2729875938	Ga0183576_1579	conserved repeat domain-containing protein	6393	0.52	1.00
46	2729873766	Ga0183576_102154	LSU ribosomal protein L22P	6281	0.40	1.00
47	2729873765	Ga0183576_102153	SSU ribosomal protein S19P	6153	-0.37	1.00
48	2729873773	Ga0183576_102161	LSU ribosomal protein L5P	6105	0.11	1.00
49	2729873761	Ga0183576_102149	LSU ribosomal protein L3P	5695	0.41	1.00
50	2729875790	Ga0183576_14612	hypothetical protein	5618	0.95	1.00
51	2729875517	Ga0183576_13418	Chemoreceptor zinc-binding domain-containing protein	5599	-0.80	1.00
52	2729875936	Ga0183576_1577	hypothetical protein	5557	-1.23	NA
53	2729873737	Ga0183576_102125	dissimilatory adenylylsulfate reductase alpha subunit precursor	5542	0.16	1.00

54	2729873628	Ga0183576_10216	hypothetical protein	5520	-1.23	1.00
55	2729873772	Ga0183576_102160	large subunit ribosomal protein L24	5453	0.26	1.00
56	2729873767	Ga0183576_102155	SSU ribosomal protein S3P	5255	0.45	1.00
57	2729876009	Ga0183576_1636	protein of unknown function (DUF4405)	5130	1.29	1.00
58	2729874874	Ga0183576_1164	hypothetical protein	5022	0.12	1.00
59	2729875244	Ga0183576_12431	Protein of unknown function (DUF3106)	4929	-1.13	1.00
60	2729873775	Ga0183576_102163	SSU ribosomal protein S8P	4912	-0.12	1.00
61	2729873763	Ga0183576_102151	LSU ribosomal protein L23P	4874	0.64	1.00
62	2729873994	Ga0183576_10429	hypothetical protein	4783	-0.83	1.00
63	2729874712	Ga0183576_1136	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6)	4742	1.36	1.00
64	2729874102	Ga0183576_10531	transcriptional regulator, MucR family	4710	-0.20	1.00
65	2729874459	Ga0183576_10882	hypothetical protein	4699	1.64	0.92
66	2729874605	Ga0183576_1116	hypothetical protein	4621	-0.40	1.00
67	2729874340	Ga0183576_10755	PilX N-terminal	4597	0.89	1.00
68	2729875483	Ga0183576_1338	SSU ribosomal protein S21P	4589	0.77	1.00
69	2729873785	Ga0183576_102173	SSU ribosomal protein S11P	4513	0.62	1.00
70	2729874200	Ga0183576_10613	periplasmic nitrate reductase subunit NapB	4490	0.45	1.00
71	2729875622	Ga0183576_13819	mRNA interferase YafQ	4465	-2.08	0.92
72	2729874323	Ga0183576_10738	hypothetical protein	4441	0.31	1.00
73	2729873985	Ga0183576_10420	integration host factor subunit alpha	4329	-0.62	1.00
74	2729873758	Ga0183576_102146	translation elongation factor 2 (EF-2/EF-G)	4263	-0.01	1.00
75	2729875693	Ga0183576_14114	hypothetical protein	4176	-0.45	1.00
76	2729873987	Ga0183576_10422	hypothetical protein	4138	1.08	1.00
77	2729873776	Ga0183576_102164	large subunit ribosomal protein L6	4109	-0.07	1.00
78	2729873787	Ga0183576_102175	DNA-directed RNA polymerase subunit alpha	3881	0.51	1.00
79	2729875722	Ga0183576_14220	manganese-dependent inorganic pyrophosphatase	3820	-0.13	1.00
80	2729873751	Ga0183576_102139	LSU ribosomal protein L1P	3793	0.07	1.00
81	2729873778	Ga0183576_102166	SSU ribosomal protein S5P	3776	0.13	1.00
82	2729874463	Ga0183576_10886	Uncharacterized conserved protein YkwD, contains CAP (CSP/antigen 5/PR1) domain	3756	-0.22	1.00
83	2729873745	Ga0183576_102133	translation elongation factor 1A (EF-1A/EF-Tu)	3705	0.13	1.00
84	2729873993	Ga0183576_10428	hypothetical protein	3643	-1.36	0.98
85	2729875666	Ga0183576_14017	LSU ribosomal protein L13P	3639	0.71	1.00
86	2729874304	Ga0183576_10719	hemoglobin	3634	0.83	1.00
87	2729875208	Ga0183576_12331	Putative beta-barrel porin 2	3624	-0.78	1.00
88	2729875284	Ga0183576_12610	chaperonin GroES	3578	1.20	0.62
89	2729875916	Ga0183576_1555	outer membrane protein	3530	-1.55	1.00
90	2729875283	Ga0183576_1269	chaperonin GroEL	3508	0.86	1.00
91	2729873762	Ga0183576_102150	LSU ribosomal protein L4P	3507	-0.08	1.00
92	2729873749	Ga0183576_102137	transcription antitermination protein nusG	3503	-0.22	1.00
93	2729873753	Ga0183576_102141	LSU ribosomal protein L12P	3413	0.79	1.00
94	2729873764	Ga0183576_102152	LSU ribosomal protein L2P	3403	0.39	1.00
95	2729875667	Ga0183576_14018	SSU ribosomal protein S9P	3354	0.55	1.00
96	2729874201	Ga0183576_10614	ferredoxin-type protein NapH	3235	1.88	0.96
97	2729873760	Ga0183576_102148	SSU ribosomal protein S10P	3192	0.40	1.00
98	2729874739	Ga0183576_11333	hypothetical protein	3147	0.23	1.00
99	2729873783	Ga0183576_102171	bacterial translation initiation factor 1 (bIF-1)	3113	0.65	1.00
100	2729874509	Ga0183576_10939	SSU ribosomal protein S1P	3073	0.12	1.00

30 **Table S6. Number of reads mapped to each of the 40 *nrfA* gene fragments and to the pOCC gene identified**
 31 **in the metatranscriptome assembly. For each fragment, the assembly length (bp) and best BLAST hit with**
 32 **accession number for identification are shown.**

Assembly	Length (bp)	Reads	Best BLAST Hit	Identity	Accession Nr.
2729874199 ^a	1455	21010	<i>Candidatus</i> Electronema sp. GS	-	TAA75457.1
NODE_1035	1059	6476	Ignavibacteria bacterium GWA2_35_8	50.42%	OGU15306.1
NODE_1697	843	1525	Bacteroidales bacterium	63.70%	RPH32637.1
NODE_5700	471	504	Bacterium BRH_c32	80.38%	KUO63373.1
NODE_6090	423	345	Ignavibacteriae bacterium HGW-1	71.01%	PKL86473.1
NODE_5479	480	304	Ignavibacteriales bacterium	60.26%	RJP63828.1
NODE_8548	390	245	Chloroflexi bacterium	71.32%	KAA0272499.1
NODE_22774	243	157	<i>Draconibacterium orientale</i>	76.54%	WP_038561595.1
NODE_12207	330	148	<i>Desulfosporosinus</i> sp. OL	86.36%	WP_075365416.1
NODE_22783	243	145	Ignavibacteriae bacterium	71.60%	MAT57261.1
NODE_9233	378	145	Bacteroidales bacterium 6E	76.19%	WP_062081844.1
NODE_10525	354	123	Ignavibacteriales bacterium	76.67%	KAB2881609.1
NODE_48342	174	115	Ignavibacteria bacterium	81.03%	HFI71567.1
NODE_23662	240	109	Anaerolineaceae bacterium	85.00%	RJP51273.1
NODE_17382	279	86	Anaerolineaceae bacterium	90.32%	RJP51273.1
NODE_16670	285	77	Deltaproteobacteria bacterium	93.68%	TSA47763.1
NODE_18587	270	75	<i>Bacteroides thetaiotaomicron</i>	73.33%	WP_128832607.1
NODE_59156	156	73	Anaerolineaceae bacterium	92.31%	RJP51273.1
NODE_56775	162	72	Bacteroidetes bacterium HGW-14	88.89%	PKP38169.1
NODE_48499	171	65	Bacteroidetes bacterium HGW-20	67.86%	PKP19544.1
NODE_18190	273	64	Geobacteraceae bacterium GWC2	92.22%	OGU02519.1
NODE_20849	255	61	<i>Nitrospira</i> sp. ND1	74.12%	WP_080880016.1
NODE_59250	156	54	Anaerolineaceae bacterium	66.67%	RJP50667.1
NODE_30190	216	49	Desulfovibrionaceae bacterium CG1	90.28%	OIO01983.1
NODE_72988	144	49	<i>Mariniphaga anaerophila</i>	75.00%	WP_073001158.1
NODE_20195	261	47	<i>Desulfobacula</i> sp.	98.85%	NJM01957.1
NODE_42133	183	44	Armatimonadetes bacterium	77.05%	HAZ64043.1
NODE_103826	120	44	Verrucomicrobia bacterium	75.00%	HGZ03587.1
NODE_48665	174	41	Chloroflexi bacterium	87.72%	KAA0284799.1
NODE_76761	138	40	Bacteroidetes bacterium GWF2_40_14	95.65%	OFY43517.1
NODE_48080	171	36	Bacteroidetes bacterium GWF2_49_14	87.72%	OFY56707.1
NODE_48149	174	33	Bacteroidetes bacterium HGW-14	81.03%	PKP38169.1
NODE_80762	135	33	Holophagaceae bacterium	93.33%	HCZ34028.1
NODE_43798	180	25	<i>Mariniphaga anaerophila</i>	86.67%	HDR50005.1
NODE_85269	135	23	Bacteroidetes bacterium GWF2_49_14	80.00%	OFY56707.1
NODE_96491	129	20	<i>Desulfobulbus elongatus</i>	86.05%	WP_028318537.1
NODE_72356	144	18	<i>Parabacteroides chartae</i>	89.58%	WP_079683478.1

NODE_77293	141	17	Prolixibacteraceae bacterium	91.30%	HAX97138.1
NODE_52928	165	17	Anaerolineaceae bacterium	90.91%	RJP51273.1
NODE_109263	117	16	<i>Sedimentibacter saalensis</i>	97.44%	WP_145083802.1
NODE_78515	138	16	Holophagaceae bacterium	80.43%	HCZ34028.1

33 ^a The *nrfA*-HMM did not identify the octaheme cytochrome (pOCC) encoded in *Ca. Electronema* sp. GS as *nrfA*
34 in the metatranscriptome assembly. The number of reads was therefore taken from mapping the transcriptome to
35 the pOCC in the full genome of *Ca. Electronema* sp. GS.

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Table S7. Number of reads mapped to each of the 16 *nirK* gene fragments identified in the metatranscriptome assembly. For each fragment, the assembly length (bp) and best BLAST hit with accession number for identification are shown.

Assembly	Length (bp)	Reads	Best BLAST Hit	Identity	Accession Nr.
NODE_543	1440	2087	Bacteroidetes bacterium	70.35%	HCR49498.1
NODE_5286	486	506	<i>Pseudomonas aeruginosa</i>	99.37%	WP_134611211.1
NODE_13019	255	261	<i>Turneriella parva</i>	84.51%	WP_157210629.1
NODE_10281	357	181	<i>Methylothermobacter mobilis</i>	94.12%	WP_019898664.1
NODE_16623	285	171	<i>Turneriella parva</i>	92.63%	WP_157210629.1
NODE_9189	378	102	<i>Candidatus Nitrotoga</i> sp. SPKER	97.62%	RFC32878.1
NODE_123633	108	52	<i>Methylothermobacter mobilis</i>	100.00%	WP_019898664.1
NODE_43088	183	50	Bacteroidetes bacterium	93.44%	KAF0128322.1
NODE_40578	144	45	<i>Nitrosomonas</i> sp.	100.00%	TXI16409.1
NODE_69784	147	40	Chloroflexi bacterium	93.88%	RPI92707.1
NODE_101121	123	40	<i>Candidatus Nitrotoga</i> sp. LAW	97.56%	RFC35445.1
NODE_111589	117	39	<i>Candidatus Nitrotoga fabula</i>	97.44%	SPS04597.1
NODE_72142	144	35	<i>Nitrosomonas</i> sp.	100.00%	WP_110340319.1
NODE_96242	126	33	<i>Methylothermobacter mobilis</i>	97.62%	WP_019898664.1
NODE_125899	108	31	<i>Turneriella parva</i> DSM 21527	100.00%	AFM12745.1
NODE_85775	132	16	Chloroflexi bacterium	95.45%	KAA0276016.1

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44 **Table S8. Number of reads mapped to each of the 63 *nirS* gene fragments identified in the**
 45 **metatranscriptome assembly. For each fragment, the assembly length (bp) and best BLAST hit with**
 46 **accession number for identification are shown.**

Assembly	Length (bp)	Reads	Best BLAST Hit	Identity	Accession nr.
NODE_249	1659	14524	Rhodocyclaceae bacterium	79.14%	KAB2931495.1
NODE_1159	1008	11681	<i>Magnetospirillum</i> sp. XM-1	98.21%	WP_068432955.1
NODE_3104	531	8195	<i>Magnetospirillum</i> sp. XM-1	98.86%	WP_068432955.1
NODE_580	1380	5929	<i>Sulfurimonas</i> sp. rificsphingho	98.26%	OHD96676.1
NODE_709	1272	5193	<i>Sulfurimonas</i> sp. RIFOXYB12	97.64%	OHE03859.1
NODE_389	1644	4673	<i>Sulfuricella denitrificans</i>	86.73%	WP_009206840.1
NODE_536	1344	4408	Bacteroidetes bacterium	65.22%	HGZ30921.1
NODE_3454	573	2518	Rhodospirillaceae bacterium	86.84%	KAF0222361.1
NODE_363	1726	2491	<i>Sulfuricella denitrificans</i>	87.45%	WP_009206840.1
NODE_9353	372	2241	<i>Sulfuricella</i> sp. T08	87.10%	WP_059423846.1
NODE_1325	924	2192	<i>Sulfurimonas</i> sp. RIFCSPHIGHO2	98.38%	OHD96676.1
NODE_116143	111	2078	Rhodocyclaceae bacterium UTPRO2	91.89%	OQY75115.1
NODE_2019	775	1752	<i>Sulfurimonas</i> sp. RIFCSPHIGHO2	98.51%	OHD96676.1
NODE_1206	987	1649	Gallionellaceae bacterium	89.67%	TXT25620.1
NODE_9592	369	1615	<i>Sulfurimonas</i> sp. RIFCSPHIGHO2	97.56%	OHE03859.1
NODE_5013	498	1512	Nitrosomonadales bacterium skT11	91.57%	BCB27672.1
NODE_1811	816	1487	<i>Sulfurimonas</i> sp. RIFCSPHIGHO2	100.00%	OHE03859.1
NODE_3274	609	1357	Rhodocyclaceae bacterium UTPRO2	87.19%	OQY75115.1
NODE_482	1521	1271	<i>Sulfuricella denitrificans</i>	87.84%	WP_009206840.1
NODE_993	600	1125	<i>Sulfurimonas</i> sp. RIFCSPHIGHO2	98.50%	OHD96676.1
NODE_740	603	1121	<i>Sulfurimonas</i> sp. RIFCSPHIGHO2	98.51%	OHD96676.1
NODE_2511	696	1083	Rhodocyclaceae bacterium UTPRO2	88.36%	OQY75115.1
NODE_18486	255	904	Gallionellaceae bacterium	97.62%	TNC95217.1
NODE_3126	624	654	<i>Ideonella</i> sp. A 288	93.75%	WP_088280822.1
NODE_3293	606	612	Gallionellaceae bacterium	96.04%	TNC95217.1
NODE_3112	600	566	<i>Sulfurimonas</i> sp. RIFOXYB12	96.00%	OHE03859.1
NODE_4772	513	560	Gallionellaceae bacterium	97.66%	TNC95217.1
NODE_980	1101	493	<i>Sulfuricella denitrificans</i>	84.32%	WP_009206840.1
NODE_5258	327	492	<i>Gallionella</i> sp.	90.74%	TAN85400.1
NODE_4190	543	448	Gallionellaceae bacterium	90.61%	TNC95217.1
NODE_14620	303	441	Rhodocyclaceae bacterium UTPRO2	94.06%	OQY75115.1
NODE_2435	615	424	<i>Sulfuricurvum kujiense</i>	76.47%	WP_013461204.1
NODE_51574	165	405	<i>Magnetospirillum</i> sp. ME-1	83.64%	WP_085374872.1
NODE_10008	315	379	Rhodocyclaceae bacterium	93.27%	KAB2931495.1

NODE_17055	282	378	<i>Extensimonas perlucida</i>	89.36%	WP_144735445.1
NODE_1315	459	363	<i>Sulfurimonas</i> sp. RIFOXYB12	94.77%	OHE03859.1
NODE_3039	459	357	<i>Sulfurimonas</i> sp. RIFOXYB12	94.77%	OHE03859.2
NODE_978	459	350	<i>Sulfurimonas</i> sp. RIFOXYB12	94.77%	OHE03859.3
NODE_80248	138	235	uncultured bacterium	100.00%	ANQ68160.1
NODE_16986	240	130	<i>Curvibacter delicatus</i>	76.25%	WP_066710706.1
NODE_60746	153	113	<i>Sphaerotilus hippiei</i>	100.00%	WP_110402103.1
NODE_59881	156	111	<i>Sulfuricella</i> sp. T08	84.62%	WP_059423846.1
NODE_27254	225	101	uncultured bacterium	84.00%	AWJ69776.1
NODE_66350	150	93	uncultured bacterium	100.00%	ALE65713.1
NODE_49032	171	91	Rhodocyclales bacterium GWA2	100.00%	OHC64126.1
NODE_40843	186	81	Rhodocyclales bacterium	93.55%	PWB40471.1
NODE_102220	120	74	Gallionellaceae bacterium CG1	100.00%	OIO75741.1
NODE_89030	129	69	Rhodocyclaceae bacterium UTPRO2	93.02%	OQY75115.1
NODE_44058	180	69	Nitrosomonadales bacterium skT11	91.67%	BCB27672.1
NODE_65734	150	69	<i>Magnetospirillum</i> sp. ME-1	92.00%	WP_085374872.1
NODE_2798	132	63	Rhodocyclaceae bacterium UTPRO2]	86.13%	OQY75115.1
NODE_58464	159	59	<i>Dechloromonas</i> sp. H13	96.23%	WP_153145771.1
NODE_43211	180	49	uncultured bacterium	100.00%	AHZ56195.1
NODE_76577	141	49	uncultured bacterium	91.49%	AHZ56205.1
NODE_100448	123	43	Nitrosomonadales bacterium skT11	95.74%	BCB27672.1
NODE_76804	141	38	<i>Sulfuricella</i> sp. T08	95.74%	WP_059423846.1
NODE_79472	138	33	<i>Magnetospirillum magneticum</i> AMB-1	95.65%	BAE52969.1
NODE_82237	138	32	uncultured bacterium	93.48%	BAD37160.1
NODE_53350	141	32	<i>Magnetospirillum magneticum</i>	100.00%	WP_148207685.1
NODE_2441	141	30	<i>Batrachochytrium dendrobatidis</i> JAM81	83.33%	XP_006681176.1
NODE_59724	159	21	Betaproteobacteria bacterium	84.91%	TAK41309.1
NODE_122668	108	21	Deltaproteobacteria bacterium HGW	94.44%	PKN14918.1
NODE_65216	153	12	uncultured organism	80.39%	AAN60890.1