Supplemental Materials

Nitrogen Cycle Evaluation (NiCE) Chip for the Simultaneous Analysis of Multiple N-Cycle Associated Genes

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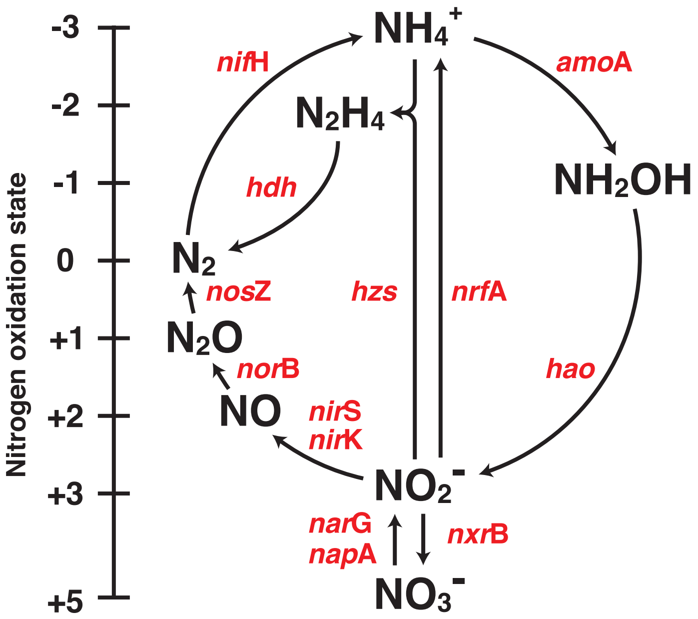
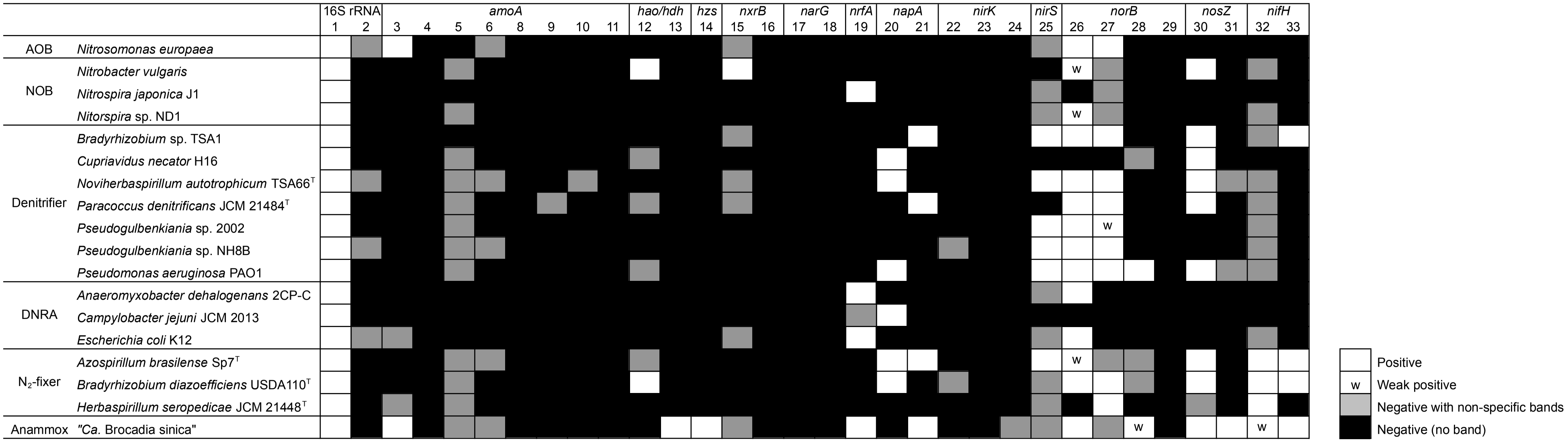


Figure S1. Nitrogen cycle and the associated functional genes.



		16S rRNA		amoA								hao/hdh		hzs	nxrB		narG		nrfA	napA		nirK			nirS	norB				nosZ		nifH	
		1	2	3	4	5	6	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33
AOB	*Nitrosomonas europaea*	☐	▨	☐	■	■	▨	■	■	■	■	■	■	■	▨	■	■	■	■	■	■	■	■	■	▨	☐	☐	■	■	■	■	■	■
NOB	*Nitrobacter vulgaris*	☐	■	■	■	▨	■	■	■	■	■	☐	■	■	☐	■	■	■	■	■	■	■	■	■	■	w	▨	■	■	☐	■	▨	■
	Nitrospira japonica J1	☐	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	☐	■	■	■	■	■	▨	■	▨	■	■	■	■	■	■
	Nitorspira sp. ND1	☐	■	■	■	▨	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	▨	w	▨	■	■	■	■	▨	■
Denitrifier	*Bradyrhizobium* sp. TSA1	☐	■	■	■	■	■	■	■	■	■	■	■	■	▨	■	■	■	■	■	☐	■	■	■	☐	☐	☐	■	■	☐	■	▨	☐
	Cupriavidus necator H16	☐	■	■	■	▨	■	■	■	■	■	▨	■	■	■	■	■	■	■	☐	■	■	■	■	■	■	■	▨	■	☐	■	■	■
	Noviherbaspirillum autotrophicum TSA66^T	☐	▨	■	■	▨	▨	■	■	▨	■	■	■	■	▨	■	■	■	■	☐	■	■	■	■	☐	☐	☐	■	■	☐	▨	▨	■
	Paracoccus denitrificans JCM 21484^T	☐	■	■	■	▨	■	■	▨	■	■	▨	■	■	▨	■	■	■	■	■	☐	■	■	■	■	☐	☐	■	■	☐	■	▨	■
	Pseudogulbenkiania sp. 2002	☐	■	■	■	▨	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	☐	☐	w	■	■	■	■	▨	■
	Pseudogulbenkiania sp. NH8B	☐	▨	■	■	▨	▨	■	■	■	■	■	■	■	■	■	■	■	■	■	■	▨	■	■	☐	☐	☐	■	■	■	■	▨	■
	Pseudomonas aeruginosa PAO1	☐	■	■	■	▨	■	■	■	■	■	▨	■	■	■	■	■	■	■	☐	■	■	■	■	☐	☐	☐	☐	■	☐	▨	▨	■
DNRA	*Anaeromyxobacter dehalogenans* 2CP-C	☐	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	☐	■	■	■	■	■	▨	☐	■	■	■	■	■	■	■
	Campylobacter jejuni JCM 2013	☐	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	▨	☐	■	■	■	■	■	■	■	■	■	■	■	■	■
	Escherichia coli K12	☐	▨	▨	■	■	■	■	■	■	■	■	■	■	▨	■	■	■	☐	■	■	■	■	■	▨	☐	■	■	■	■	■	▨	■
N_2-fixer	*Azospirillum brasilense* Sp7^T	☐	■	■	■	▨	▨	■	■	■	■	▨	■	■	■	■	■	■	■	☐	☐	■	■	■	☐	w	▨	▨	■	☐	■	☐	☐
	Bradyrhizobium diazoefficiens USDA110^T	☐	■	■	■	▨	■	■	■	■	■	☐	■	■	■	■	■	■	■	☐	■	▨	■	■	▨	☐	☐	▨	■	☐	■	☐	☐
	Herbaspirillum seropedicae JCM 21448^T	☐	■	▨	■	▨	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	▨	■	☐	■	■	▨	■	☐	■
Anammox	*"Ca.* Brocadia sinica"	☐	■	☐	■	▨	▨	■	■	■	■	■	☐	☐	▨	■	■	■	☐	■	☐	■	■	▨	▨	☐	▨	w	■	☐	☐	w	☐

☐	Positive
w	Weak positive
▨	Negative with non-specific bands
■	Negative (no band)

Figure S2. PCR amplification of the 16S rRNA gene and the N cycle functional by conventional PCR assays. Legend: 1, 341F and 805R primers; 2, Archaea-F KO and Archaea-R KO primers; 3, amoA_1F and amoA_2R primers; 4, amoA_1F and amoA_F1_R2 primers; 5, Gamo172 F1 and Gamo172 F1_R1 primers; 6, Gamo172 F1 and Gamo172 F1_R2 primers; 7, Gamo172 F2 and Gamo172 F2_R1 primers; 8, Arch-amoAF and Arch-amoAR primers; 9, Arch-amoAFA and Arch-amoAR primers; 10, Arch-amoAFB and Arch-amoAR primers; 11, Arch-amoA-for and Arch-amoA-rev primers; 12, hzocl1F1 and hzocl1R2 primers; 13, haoF4 and haoR2 primers; 14, hzsA_1597F and hzsA1857R primers; 15, NxrB 1F and NxrB 1R primers; 16, nxrB169f and nxrB638r primers; 17, W9F and T38R primers; 18, narG1960f and narG2650r primers; 19, nrfAF2aw and nrfAR1 primers; 20, V66 and V67 primers; 21, V17m and napA4r primers; 22, FlaCu and R3Cu primers; 23, nirK876 and nirK1040 primers; 24, nirK_166F and NxrB 1F primers; 25, nirSCd3aF and nirSR3cd primers; 26, norB2 and norB6 primers; 27, cnorB-2F and cnorB-6R primers; 28, qnorB2F and qnorB7R primers; 29, qnorB2F and qnorB5R primers; 30, nosZ1F and nosZ1R primers; 31, nosZ-II-F and nosZ-II-R primers; 32, nifHF and nifHR primers; 33, IGK3 and DVV primers.

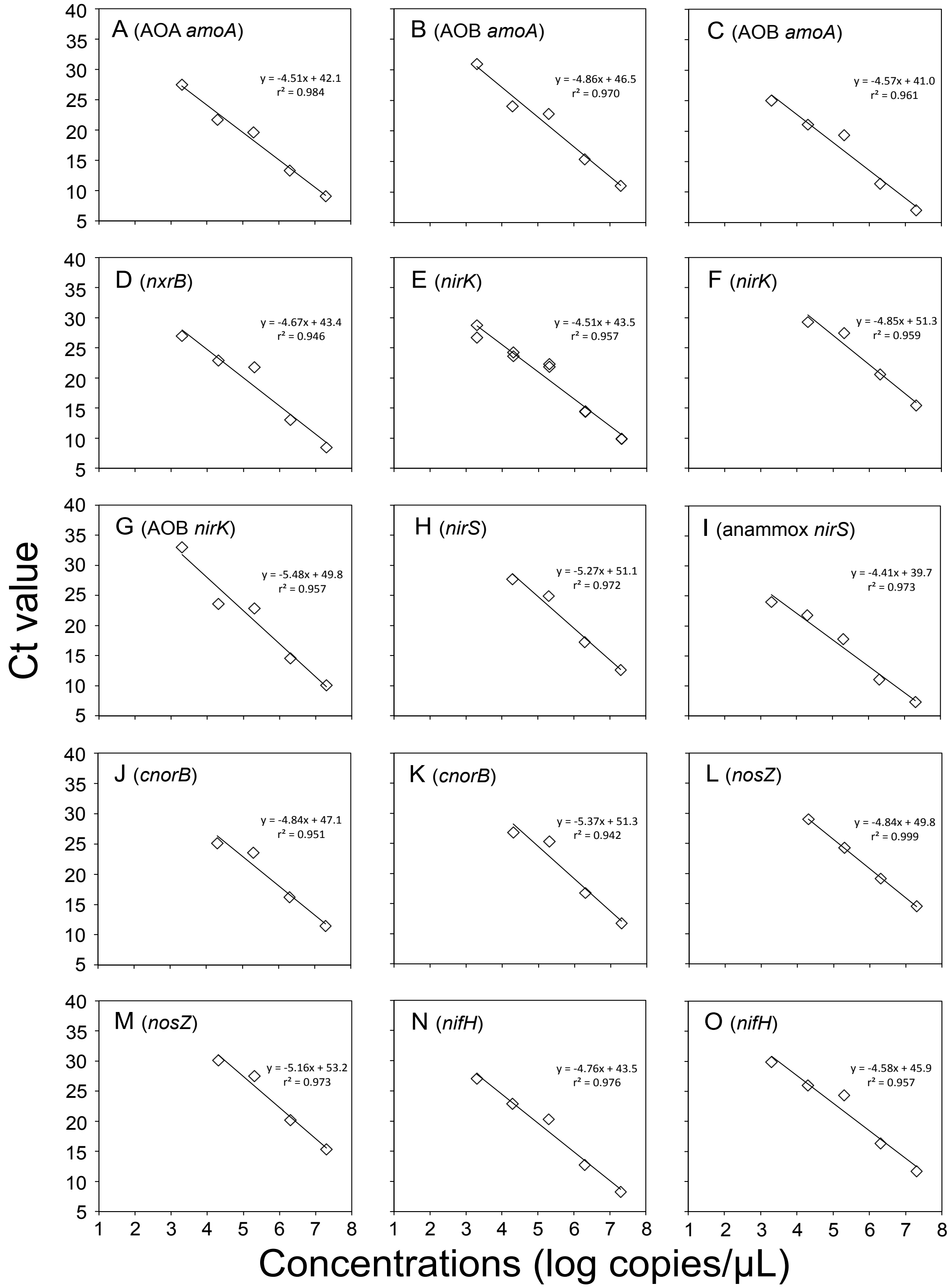


Figure S3. Standard curves generated based on the results of the NiCE chip assays. Legend: A, AOA *amoA* amplified using Arch-amoA-for and Arch-amoA-rev primers; B, AOB *amoA* amplified using amoA_F1 and amoA_F1_R2 primers; C, AOB *amoA* amplified using amoA_F1 and amoA_2R primers; D, *nxrB* amplified using nxrB169f and nxrB638r primers; E, *nirK* amplified using FlaCu and R3Cu primers; F, *nirK* amplified using nirK876 and nirK1040 primers; G, *N. europaea*- and *N. eutropha*-specific *nirK* amplified using nirK_166F and nirK_665R primers; H, *nirS* amplified using nirSCd3aF and nirSR3cd primers; I, Anammox *nirS* amplified using Scnir372F and Scnir845R primers; J, *cnorB* amplified using norB2 and norB6 primers; K, *cnorB* amplified using cnorB-2F and cnorB-6R primers; L, *nosZ* amplified using nosZ1F and nosZ1R primers; M, *nosZ* amplified using nosZ2F and nosZ2R primers; N, *nifH* amplified using nifHF and nifHR primers; O, *nifH* amplified using IGK3 and DVV primers.

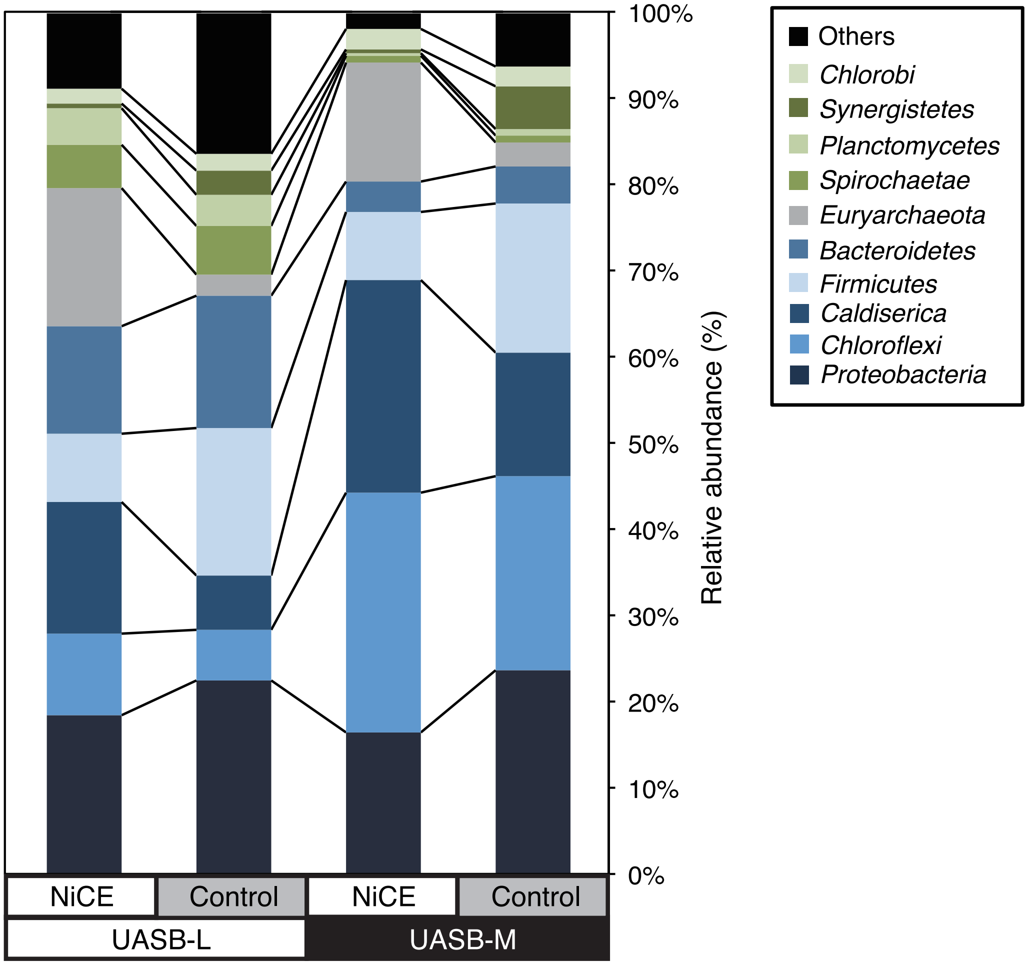


Figure S4. Microbial community structures in UASB-L and UASB-M samples as assessed by the 16S rRNA gene sequencing. The PCR amplification was done by using the NiCE chip (designated as NiCE) and by conventional PCR (control). Phylogenetic affiliations the 16S rRNA gene sequences were identified using a blastn search against reference sequences into bacterial and archaeal phyla.

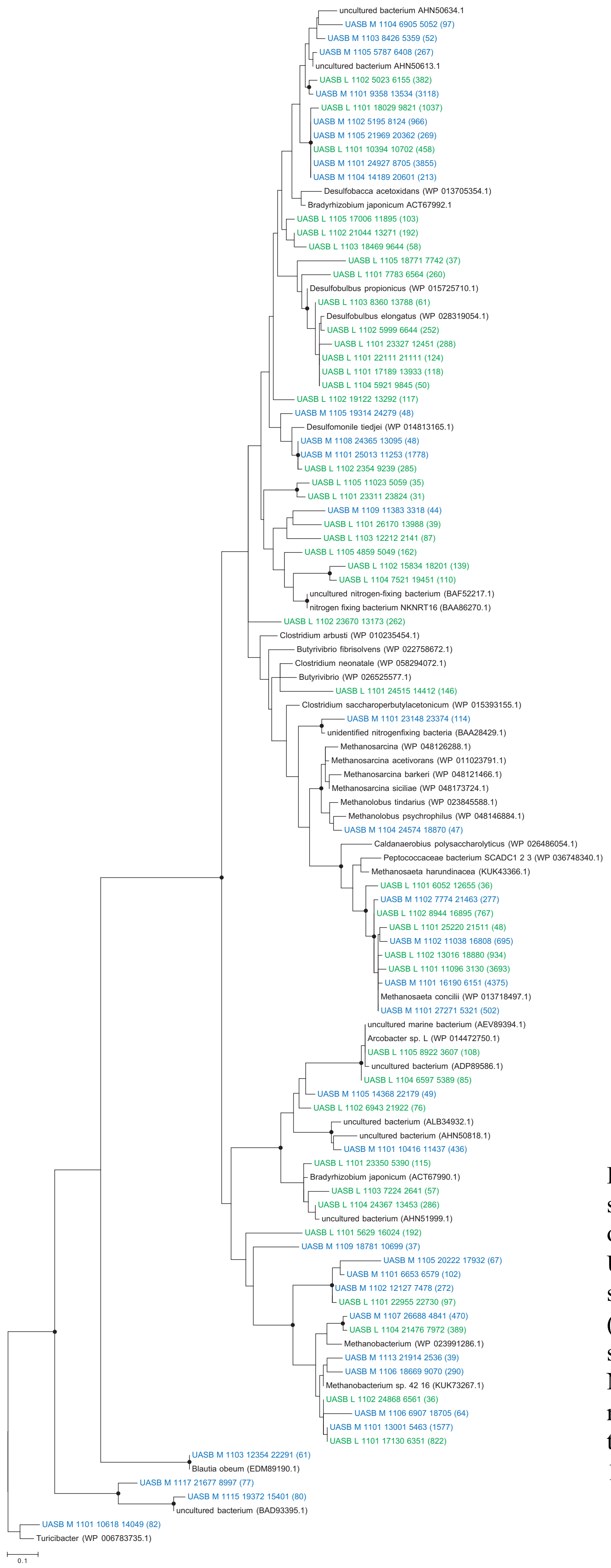


Figure S5. Maximum-likelihood tree showing the phylogenetic affiliation of the *nifH* sequences obtained from UASB-M (blue) and UASB-L (green) samples. Operational taxonomic units (OTUs) determined based on 95% sequence similarity are shown. Numbers in parentheses indicate the number of sequence reads affiliated to the OTU. The scale bar represents 10% sequence divergence.

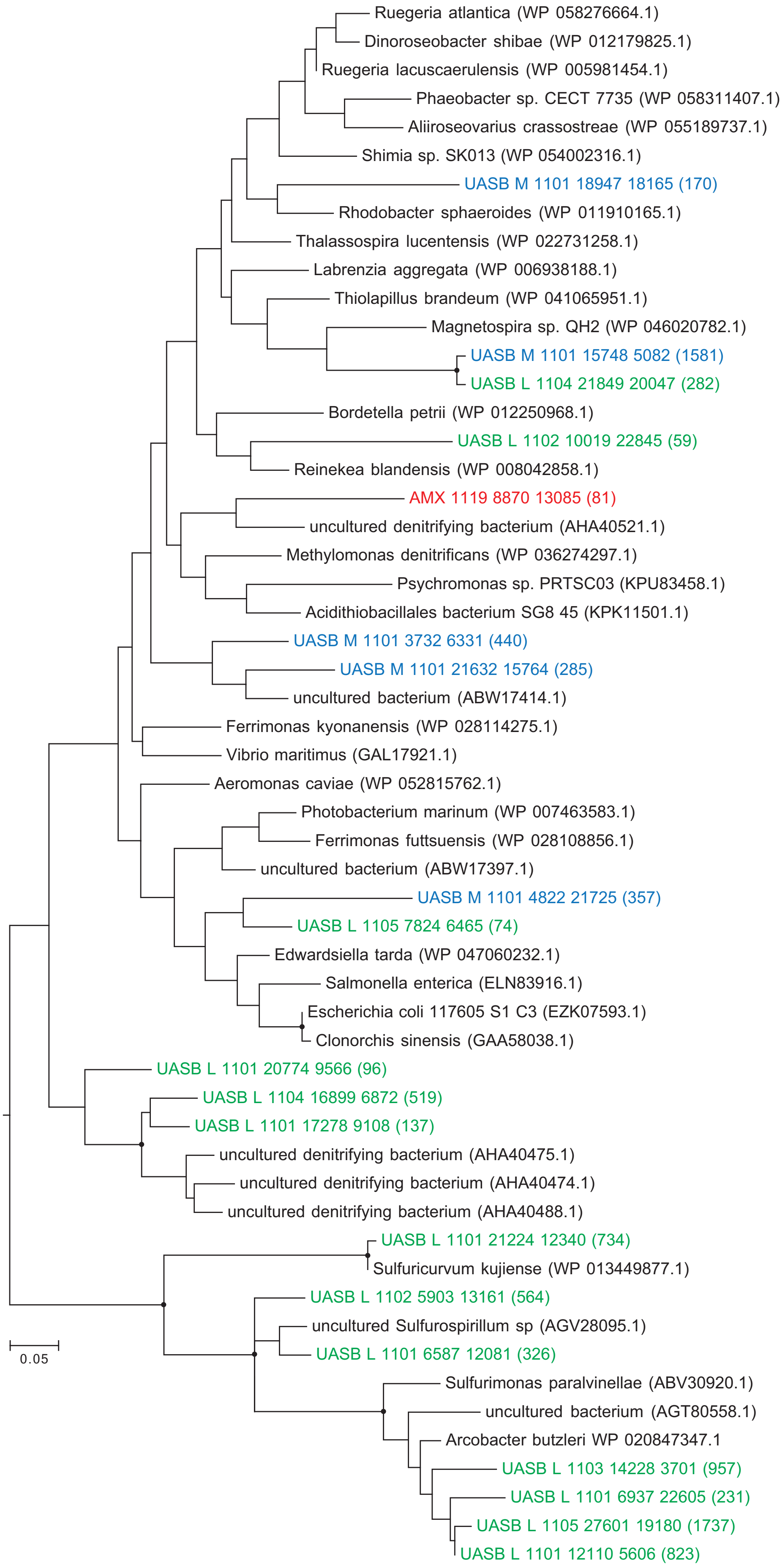


Figure S6. Maximum-likelihood tree showing the phylogenetic affiliation of the *napA* sequences obtained from UASB-M (blue) and UASB-L (green) samples. Operational taxonomic units (OTUs) determined based on 95% sequence similarity are shown. Numbers in parentheses indicate the number of sequence reads affiliated to the OTU. The scale bar represents 5% sequence divergence.

Table S1. Oligonucleotide primers used in this study.

Target	Forward primer		Reverse primer		Size*	Ref.
	Name	Sequence (5' - 3')	Name	Sequence (5' - 3')	(bp)	
16S rRNA gene						
Bacteria	341F	CCTACGGGNGGCWGCAG	805R	GACTACHVGGGTATCTAATCC	333	1
Archaea	Archaea-F KO	CCCTAYGGGGYGCASCAGGC	Archaea-R KO	GCYCYCCCGCCAATTCMTTTA	554	2
*amo*A						
AOB	amoA_1F	GGGGTTTCTACTGGTGGT	amoA_2R	CCCCTCKGSAAAGCCTTCTTC	490	3
	amoA_F1	GGGGHTTYTACTGGTGGT	amoA_F1_R2	TTTGATCCCCTCTGGAAACCCTTC	490	3†
	Gamo172 F1	GGBGACTGGGAYTTCTGG	Gamo172 F1_R1	AAARCCCGAGAAGAAMGC	542	This study
	Gamo172 F1	GGBGACTGGGAYTTCTGG	Gamo172 F1_R2	AAAACCCGCAAAAAAGGC	542	This study
	Gamo172 F2	TGGGATTTCTGGATGGAC	Gamo172 F2_R1	TGATACGAACGCAGAGAA	542	This study
AOA	Arch-amoAF	STAATGGTCTGGCTTAGACG	Arch-amoAR	GCGGCCATCCATCTGTATGT	649	4
	Arch-amoAFA	ACACCAGTTTGGYTACCWTCDGC	Arch-amoAR	GCGGCCATCCATCTGTATGT	354	5
	Arch-amoAFB	CATCCRATGTGGATTCCATCDTG	Arch-amoAR	GCGGCCATCCATCTGTATGT	354	5
	Arch-amoA-for	CTGAYTGGGCYTGGACATC	Arch-amoA-rev	TTCTTCTTTGTTGCCCAGTA	255	6
hao/*hdh*						
Anammox	hzocl1F1	TGYAAGACYTGYCAYTGG	hzocl1R2	ACTCCAGATRTGCTGACC	470	7
AOB	haoF4	AYCTKCGCTCRATGGG	haoR2	GGTTGGTYTTCTGKCCGG	738	8
hzs						
Anammox	hzsA_1597F	WTYGGKTATCARTATGTAG	hzsA1857R	AAABGGYGAATCATARTGGC	263	9†
nxrB						
Nitrobacter	NxrB 1F	ACGTGGAGACCAAGCCGGG	NxrB 1R	CCGTGCTGTTGAYCTCGTTGA	380	10
Nitrospira	nxrB169f	TACATGTGGTGGAACA	nxrB638r	CGGTTCTGGTCRATCA	485	11

Target	Forward primer		Reverse primer		Size[*] (bp)	Ref.
	Name	Sequence (5' - 3')	Name	Sequence (5' - 3')		
narG						
Bacteria	W9F	MGNGGNTGYCCNMGNGGNGC	T38R	ACRTCNGTYTGYTCNCCCCA	500	12
	narG1960f	AYGTSGGSCARGARAA	narG2650r	TYTCRTACCABGTBGC	650	13
nrfA						
DNRA	nrfAF2aw	CARTGYCAYGTBGARTA	nrfAR1	TWNGGCATRTGRCARTC	269	14
napA						
Bacteria	V66	TAYTTYYTNHSNAARATHATGTAYGG	V67	DATNGGRTGCATYTCNGCCATRTT	400	15
	V17m	TGGACVATGGGYTTYAAYC	napA4r	ACYTCRCGHGCVGTRCCRCA	152	16
nirS						
Denitrifiers	nirSCd3aF	AACGYSAAGGARACSGG	nirSR3cd	GASTTCGGRTGSGTCTTSAYGAA	339	17
Anammox	Scnir372F	TGTRGCCAGYATTGTWGCGT	Scnir845R	TCAAGCCAGACCCATTTRCT	473	18[†]
nirK						
Denitrifiers	FlaCu	ATCATGGTSCTGCCGCG	R3Cu	GCCTCGATCAGRTTGTGGTT	472	19
	nirK876	ATYGGCGGVAYGGCGA	nirK1040	GCCTCGATCAGRTTRTGGTT	164	20
AOB	nirK_166F	GTWCCSGGTCCGGTYGTRCG	nirK_665R	TCRTTGGGWCCRGCRTTGAC	499	21
norB						
Denitrifiers	norB2	GACAARHWVTAYTGGTGGT	norB6	TGCAKSARRCCCCABACBCC	394	22
	cnorB-2F	GACAAGNNNTACTGGTGGT	cnorB-6R	GAANCCCCANACNCCNGC	372	23
Bacteria	qnorB2F	GGNCAYCARGGNTAYGA	qnorB5R	ACCCANAGRTGNACNACCCACCA	240	23
	qnorB2F	GGNCAYCARGGNTAYGA	qnorB7R	GGNGGRTTDATCADGAANCC	618	23
nosZ						
Denitrifiers	nosZ1F	WCSYTGTTCMTCGACAGCCAG	nosZ1R	ATGTCGATCARCTGVKCRTTYTC	259	24
	nosZ-II-F	CTIGGICCIYTKCAYAC	nosZ-II-R	GCIGARCARAAITCBGTRC	745	25

Target	Forward primer		Reverse primer		Size*	Ref.
	Name	Sequence (5' - 3')	Name	Sequence (5' - 3')	(bp)	
nifH						
N_2-fixers	nifHF	AAAGGYGGWATCGGYAARTCCACCAC	nifHR	TTGTTSGCSGCRTACATSGCCATCAT	457	26
	IGK3	GCIWTHTAYGGIAARGGIGGIATHGGIAA	DVV	ATIGCRAAICCICCRCAIACIACRTC	394	27

*Amplicon size without illumina tag sequences, sample-unique index and illumina adaptor (about 150 bp).

†Original sequence was modified to improve coverage.

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Table S2. Blastx results of the MiSeq sequence reads retrieved from pure bacterial strains and enrichment culture samples.

Query			Highest Blastx Hit				
Sample[a]	Gene	Sequence ID[b]	E value	Identity	Description	Organisms	Accession
1	*nxrB*	AC602:1:1101:18190:4325	3.00E-82	98%	Nitrite oxidoreductase	*Nitrobacter vulgaris*	CAL09964.1
2	*nxrB*	AC602:1:1106:22855:14231	5.00E-55	93%	Nitrite oxidoreductase beta subunit	*Ca*. Nitrospira bockiana	AHA36496.1
3	*nxrB*	AC602:1:1101:13350:6363	8.00E-104	100%	Nitrate oxidoreductase subunit beta	*Ca*. Nitrospira defluvii	WP_013249748
4	*amoA*	AC602:1:1101:20016:2363	6.00E-28	99%	Ammonia monooxygenase, partial	*Ca*. Nitrosocosmicus franklandus	AMH87091.1
4	*nirK*	AC602:1:1101:20028:5606	9.00E-90	90%	Nitrite reductase, copper-containing	*Bradyrhizobium* sp. Ai1a-2	WP_027578884
5	*hzs*	AC602:1:1101:22101:3624	4.00E-41	97%	Hydrazine synthase subunit A	*Ca*. Brocadia sinica	KXK32732.1
5	*hao/hdh*	AC602:1:1101:7970:2276	2.00E-94	97%	Hydroxylamine oxidoreductase-like protein	*Ca*. Brocadia sinica	KXK32736.1
5	*nxrB*	AC602:1:1101:3318:11095	1.00E-88	99%	Nitrate oxidoreductase subunit beta	*Ca*. Brocadia sinica	WP_052565644
5	*nrfA*	AC602:1:1101:13715:2414	2.00E-38	100%	Nitrite reductase	*Ca*. Brocadia sinica	WP_052565197

[a] 1, *Nitrobacter vulgaris*; 2, *Nitrospira japonica* J1; 3, *Nitrospira sp*. ND1; 4, Enrichment culture of ammonia-oxidizing archaeon; 5, Enrichment culture of "*Ca.* Brocadia sinica"

[b] Complete sequence ID comes after the instrument ID of "M01935:46:000000000-".

Table S3. Proportions of sequence reads sorted to each target gene bin. Proportions of non-target sequences and the number of sequence reads for each sample are also shown.

Sample		Total number of reads	Proportion of sequence reads (%)													
			narG	*nxrB*	*nirK*	*nirS*	*nifH*	*amoA*	*nrfA*	*napA*	*hzs*	*hao*	*nosZ*	*norB*	16S rRNA gene	Non-target
AOB	*Nitrosomonas europaea*	180,774	7.9	3.6	6.4	7.2	8.8	13.6	2.9	2.4	0.0	0.5	14.7	5.7	1.5	24.9
NOB	*Nitrobacter vulgaris*	237,322	5.3	11.0	10.2	3.2	6.6	0.6	0.4	5.9	0.0	0.0	31.9	14.4	6.5	4.1
	Nitrospira japonica J1	271,482	7.7	9.6	2.3	8.2	4.8	1.2	3.2	4.6	0.0	0.0	16.7	9.1	6.0	26.6
	Nitorspira sp. ND1	246,579	5.8	10.0	12.9	3.5	3.4	3.0	10.6	7.4	0.0	0.0	1.3	10.9	9.3	22.1
Denitrifier	*Bradyrhizobium* sp. TSA1	488,063	4.6	5.0	9.6	6.9	2.3	2.5	0.7	17.5	0.0	0.0	18.9	15.1	6.3	10.5
	Cupriavidus necator H16	347,475	8.6	3.6	4.9	8.0	2.6	1.5	2.0	27.0	0.0	0.0	19.5	15.1	0.0	7.2
	Noviherbaspirillum autotrophicum TSA66^{T}	461,991	6.8	10.6	4.7	4.5	4.4	2.8	3.0	11.6	0.0	0.0	13.0	17.4	5.0	16.2
	Paracoccus denitrificans JCM 21484^{T}	364,057	3.2	3.8	1.6	6.9	5.8	0.1	2.5	24.6	0.0	0.0	23.0	12.5	7.0	9.0
	Pseudogulbenkiania sp. 2002	250,883	3.5	12.5	8.0	19.3	1.7	1.3	0.3	1.8	0.0	0.2	13.4	17.4	9.5	11.1
	Pseudogulbenkiania sp. NH8B	317,279	6.8	1.8	15.6	0.3	12.2	1.5	16.6	8.2	0.0	0.0	2.8	6.7	7.8	19.8
	Pseudomonas aeruginosa PAO1	176,670	4.9	6.5	13.2	14.9	2.7	0.1	1.0	13.9	0.0	0.1	16.0	19.4	12.3	0.0
DNRA	*Anaeromyxobacter dehalogenans* 2CP-C	228,433	0.8	0.4	0.9	0.2	5.7	0.0	37.7	6.2	0.0	0.0	0.7	29.9	16.4	1.1
	Campylobacter jejuni JCM 2013	200,681	0.3	0.0	25.8	2.0	0.0	0.0	31.7	29.7	0.0	0.0	0.1	0.1	0.0	10.1
	Escherichia coli K12	341,214	5.7	2.5	0.7	1.0	6.1	5.3	28.8	19.7	0.0	0.0	4.6	4.5	7.7	13.5
N_2-fixer	*Azospirillum brasilense* Sp7^{T}	86,227	8.1	10.0	1.8	11.9	8.4	10.3	1.7	19.9	0.0	0.0	11.6	7.3	10.4	0.0
	Bradyrhizobium diazoefficiens USDA110^{T}	401,541	8.0	4.2	6.4	4.4	17.2	0.1	4.0	17.2	0.0	0.0	17.3	14.7	5.3	1.2
	Herbaspirillum seropedicae JCM 21448^{T}	316,359	10.1	1.4	1.6	8.0	15.0	5.4	9.8	4.6	0.0	0.0	9.4	14.9	2.9	17.2
Anammox	"*Ca.* Brocadia sinica"	55,162	5.8	9.2	3.9	4.3	1.5	4.6	13.2	7.0	7.0	10.5	7.9	4.8	4.7	15.8
Environ-mental	UASB-M	531,131	5.7	0.5	4.3	2.4	7.6	1.5	12.4	7.6	0.0	0.0	4.9	8.9	3.6	40.5
	UASB-L	661,458	4.7	1.9	2.4	1.6	3.7	1.1	8.5	3.4	0.0	0.2	5.3	5.6	2.7	58.8

Table S4. Closest relatives of the operational taxonomic units (OTUs) identified from (a) UASB-L and (b) UASB-M samples. Demultiplexed sequence reads obtained by the NiCE chip-amplicon sequencing were assembled and then sorted to the N cycle functional gene bin by blastn. Reads in each bin were grouped into OTU based on sequence similarities at ≥95%. Relative abundance of each OTU in total sequence reads in the sample is also shown. Same data are used to generate Fig. 4.

a) UASB-L

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nxrB	M01935:46:000000000-AC602:1:1101:22605:9690 (LC256820)	8.2%	nxrB;AP012337;location.2281235..2282458.;Caldilinea.aerophila.DSM.14535...NBRC.104270.definition.nitrate.reductase.beta.subunit	2E-12
nxrB	M01935:46:000000000-AC602:1:1103:15164:3056 (LC230433)	1.1%	nxrB;AP012337;location.2281235..2282458.;Caldilinea.aerophila.DSM.14535...NBRC.104270.definition.nitrate.reductase.beta.subunit	1E-28
nirK	M01935:46:000000000-AC602:1:1101:27787:8721 (LC230434)	1.5%	nirK;EU285337;location.<1.515.;uncultured.bacterium.definition.copper-containing.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1101:18495:9284 (LC230435)	1.4%	nirK;HM116353;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1102:10172:14390 (LC230436)	0.78%	nirK;AB162332;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1101:12816:19525 (LC230437)	0.75%	nirK;AB162937;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1102:28478:14751 (LC230438)	0.50%	nirK;HQ916682;location.<1.360.;uncultured.bacterium.definition.NirK	3E-162
nirK	M01935:46:000000000-AC602:1:1102:19553:20134 (LC256821)	0.36%	nirK;DQ182205;location.<1.473.;uncultured.bacterium.definition.putative.nitrite.reductase	1E-81

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nirK	M01935:46:000000000-AC602:1:1102:11590:5036 (LC230439)	0.30%	nirK;AB453443;location.<1.436.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1105:7370:19214 (LC230440)	0.25%	nirK;FJ204572;location.<1.541.;uncultured.bacterium.definition.nitrite.reductase	2E-123
nirK	M01935:46:000000000-AC602:1:1103:6449:23430 (LC230441)	0.19%	nirK;DQ304337;location.<1.473.;uncultured.bacterium.definition.putative.nitrite.reductase	9E-73
nirK	M01935:46:000000000-AC602:1:1105:12008:13301 (LC230442)	0.17%	nirK;FR774851;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	2E-135
nirS	M01935:46:000000000-AC602:1:1101:23782:4351 (LC230443)	0.82%	nirS;AB773624;location.<1..>nirS;374.;uncultured.bacterium.definition.nitrite.reductase	2E-52
nirS	M01935:46:000000000-AC602:1:1104:10868:20080 (LC230444)	0.29%	nirS;FR865832;location.<1..>nirS;408.;uncultured.bacterium.definition.cd1-containing.nitrite.reductase	2E-48
nirS	M01935:46:000000000-AC602:1:1104:13414:18089 (LC230445)	0.22%	nirS;HM438818;location.<1..>nirS;873.;uncultured.organism.definition.cytochrome.cd1-containing.nitrite.reductase	2E-60
nirS	M01935:46:000000000-AC602:1:1101:19733:14440 (LC230446)	0.21%	nirS;JQ582714;location.<1..>nirS;337.;Zoogloea.sp..AR30.definition.cytochrome.cd1.nitrite.reductase	4E-148
nirS	M01935:46:000000000-AC602:1:1101:14366:22991 (LC230447)	0.098%	nirS;GQ443950;location.<1..>nirS;402.;uncultured.bacterium.definition.nitrite.reductase	2E-106
nirS	M01935:46:000000000-AC602:1:1103:22874:4209 (LC230448)	0.096%	nirS;DQ337877;location.<1..>nirS;425.;uncultured.bacterium.definition.NirS	4E-68

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nifH	M01935:46:000000000-AC602:1:1101:11096:3130 (LC230449)	8.8%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	2E-141
nifH	M01935:46:000000000-AC602:1:1101:18029:9821 (LC230450)	2.5%	nifH;FN555079;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	2E-58
nifH	M01935:46:000000000-AC602:1:1102:13016:18880 (LC230451)	2.2%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	0
nifH	M01935:46:000000000-AC602:1:1101:17130:6351 (LC230452)	2.0%	nifH;X56071;location.132..959.;Methanobacterium.ivanovii.definition.nitrogenase.Mo-Fe.protein	2E-57
nifH	M01935:46:000000000-AC602:1:1102:8944:16895 (LC230453)	1.8%	nifH;DQ098182;location.<1..>nifH;353.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	8E-101
nifH	M01935:46:000000000-AC602:1:1101:10394:10702 (LC230454)	1.1%	nifH;FN555079;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	8E-64
nifH	M01935:46:000000000-AC602:1:1104:21476:7972 (LC230455)	0.93%	nifH;CP000867;location.complement(1694838..1695665).;Methanococcus.maripaludis.C6.definition.nitrogenase.iron.protein	5E-28
nifH	M01935:46:000000000-AC602:1:1102:5023:6155 (LC230456)	0.91%	nifH;FN555078;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	5E-56
nifH	M01935:46:000000000-AC602:1:1101:23327:12451 (LC230457)	0.69%	nifH;CP002364;location.3518933..3519760.;Desulfobulbus.propionicus.DSM.2032.definition.Mo-nitrogenase.iron.protein.subunit.NifH	1E-99
nifH	M01935:46:000000000-AC602:1:1104:24367:13453 (LC230458)	0.68%	nifH;AY601051;location.<1..>nifH;461.;uncultured.bacterium.definition.dinitrogenase.reductase	6E-117
nifH	M01935:46:000000000-AC602:1:1102	0.68%	nifH;HQ660907;location.<1..>nifH;328.;uncultured.bacterium.defin	4E-161

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
	:2354:9239 (LC230459)		ition.dinitrogenase.reductase	
nifH	M01935:46:000000000-AC602:1:1102 :23670:13173 (LC230460)	0.63%	nifH;EF196648;location.<1..>nifH;362.;uncultured.nitrogen-fixing. bacterium.definition.dinitrogenase.reductase	2E-27
nifH	M01935:46:000000000-AC602:1:1101 :7783:6564 (LC230461)	0.62%	nifH;CP002431;location.1151267..1152094.;Desulfovibrio.aespoeensis.Aspo-2.definition.nitrogenase.iron.protein	3E-143
nifH	M01935:46:000000000-AC602:1:1102 :5999:6644 (LC230462)	0.60%	nifH;CP002364;location.3518933..3519760.;Desulfobulbus.propionicus.DSM.2032.definition.Mo-nitrogenase.iron.protein.subunit.NifH	4E-81
nifH	M01935:46:000000000-AC602:1:1102 :21044:13271 (LC230463)	0.46%	nifH;HM219783;location.<1..>nifH;328.;uncultured.bacterium.definition.dinitrogenase.reductase	6E-40
nifH	M01935:46:000000000-AC602:1:1101 :5629:16024 (LC230464)	0.46%	nifH;AY224038;location.<1..>nifH;324.;uncultured.bacterium.definition.dinitrogenase.reductase.Fe.protein	8E-29
nifH	M01935:46:000000000-AC602:1:1105 :4859:5049 (LC230465)	0.39%	nifH;GU193915;location.<1..>nifH;359.;uncultured.bacterium.definition.nitrogenase	6E-80
nifH	M01935:46:000000000-AC602:1:1101 :24515:14412 (LC230466)	0.35%	nifH;AB184945;location.<1..>nifH;387.;uncultured.bacterium.definition.dinitrogenase.reductase	1E-24
nifH	M01935:46:000000000-AC602:1:1102 :15834:18201 (LC230467)	0.33%	nifH;CP002403;location.complement(2743508..2744365).;Ruminococcus.albus.7.definition.nitrogenase.iron.protein	3E-23
nifH	M01935:46:000000000-AC602:1:1101 :22111:21111 (LC230468)	0.30%	nifH;EU915064;location.<1..>nifH;360.;uncultured.Antarctic.bacterium.definition.dinitrogenase.reductase	2E-132
nifH	M01935:46:000000000-AC602:1:1101 :17189:13933 (LC230469)	0.28%	nifH;EU915064;location.<1..>nifH;360.;uncultured.Antarctic.bacterium.definition.dinitrogenase.reductase	3E-125

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nifH	M01935:46:000000000-AC602:1:1102:19122:13292 (LC230470)	0.28%	nifH;AJ313259;location.<1..>nifH;333.;uncultured.bacterium.definition.nitrogenase.Fe.protein	3E-57
nifH	M01935:46:000000000-AC602:1:1101:23350:5390 (LC230471)	0.27%	nifH;GQ289580;location.complement(<1..>nifH;461).;Bradyrhizobium.japonicum.definition.NifH	2E-101
nifH	M01935:46:000000000-AC602:1:1104:7521:19451 (LC230472)	0.26%	nifH;AM746581;location.<1..>nifH;322.;uncultured.bacterium.definition.dinitrogenase.reductase	2E-17
nifH	M01935:46:000000000-AC602:1:1105:8922:3607 (LC230473)	0.26%	nifH;HQ455837;location.<1..>nifH;398.;uncultured.marine.bacterium.definition.dinitrogenase.reductase	2E-150
nifH	M01935:46:000000000-AC602:1:1105:17006:11895 (LC230474)	0.25%	nifH;AY137237;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	4E-41
nifH	M01935:46:000000000-AC602:1:1101:22955:22730 (LC230475)	0.23%	nifH;AY231492;location.<1..>nifH;324.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	3E-53
nifH	M01935:46:000000000-AC602:1:1103:12212:2141 (LC230476)	0.21%	nifH;GQ289569;location.complement(<1..>nifH;458).;Bradyrhizobium.japonicum.definition.NifH	2E-33
nifH	M01935:46:000000000-AC602:1:1104:6597:5389 (LC230477)	0.20%	nifH;HM852967;location.<1..>nifH;409.;uncultured.bacterium.definition.dinitrogenase.iron.protein	1E-160
nifH	M01935:46:000000000-AC602:1:1102:6943:21922 (LC230478)	0.18%	nifH;U97118;location.<1..>nifH;411.;Azoarcus.indigens.definition.nitrogenase.iron.protein	1E-133
nifH	M01935:46:000000000-AC602:1:1103:8360:13788 (LC230479)	0.15%	nifH;HQ190142;location.<1..>nifH;426.;uncultured.bacterium.definition.nitrogenase.component.II	6E-120

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nifH	M01935:46:000000000-AC602:1:1103:18469:9644 (LC230480)	0.14%	nifH;DQ402888;location.<1..>nifH;417.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	9E-42
nifH	M01935:46:000000000-AC602:1:1103:7224:2641 (LC230481)	0.14%	nifH;CP000142;location.2447668..2448546.;Pelobacter.carbinolicus.DSM.2380.definition.nitrogenase.iron.protein	6E-157
nifH	M01935:46:000000000-AC602:1:1104:5921:9845 (LC230482)	0.12%	nifH;CP002364;location.3518933..3519760.;Desulfobulbus.propionicus.DSM.2032.definition.Mo-nitrogenase.iron.protein.subunit.NifH	3E-109
nifH	M01935:46:000000000-AC602:1:1101:25220:21511 (LC230483)	0.11%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	1E-167
nifH	M01935:46:000000000-AC602:1:1101:26170:13988 (LC230484)	0.093%	nifH;JN162497;location.<1..>nifH;381.;uncultured.bacterium.definition.dinitrogenase.reductase	2E-49
nifH	M01935:46:000000000-AC602:1:1105:18771:7742 (LC230485)	0.088%	nifH;HM113557;location.<1..>nifH;324.;uncultured.organism.definition.NifH	3E-48
nifH	M01935:46:000000000-AC602:1:1101:6052:12655 (LC230486)	0.086%	nifH;DQ098176;location.<1..>nifH;354.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	2E-79
nifH	M01935:46:000000000-AC602:1:1102:24868:6561 (LC230487)	0.086%	nifH;X56071;location.132..959.;Methanobacterium.ivanovii.definition.nitrogenase.Mo-Fe.protein	8E-63
nifH	M01935:46:000000000-AC602:1:1105:11023:5059 (LC230488)	0.084%	nifH;HQ455838;location.<1..>nifH;362.;uncultured.marine.bacterium.definition.dinitrogenase.reductase	3E-28
nifH	M01935:46:000000000-AC602:1:1101:23311:23824 (LC230489)	0.074%	nifH;HQ455838;location.<1..>nifH;362.;uncultured.marine.bacterium.definition.dinitrogenase.reductase	1E-34

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nifH	M01935:46:000000000-AC602:1:1103:18699:11981 (LC230490)	0.062%	nifH;CP002364;location.3518933..3519760.;Desulfobulbus.propionicus.DSM.2032.definition.Mo-nitrogenase.iron.protein.subunit.NifH	6E-117
nifH	M01935:46:000000000-AC602:1:1105:12116:13177 (LC230491)	0.060%	nifH;HQ605987;location.<1..>nifH;360.;uncultured.organism.definition.nitrogenase	6E-33
nifH	M01935:46:000000000-AC602:1:1103:10865:14544 (LC230492)	0.055%	nifH;EF208185;location.<1..>nifH;366.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	3E-118
nifH	M01935:46:000000000-AC602:1:1101:13391:23414 (LC230493)	0.053%	nifH;EU915064;location.<1..>nifH;360.;uncultured.Antarctic.bacterium.definition.dinitrogenase.reductase	1E-127
nifH	M01935:46:000000000-AC602:1:1103:16207:22916 (LC230494)	0.053%	nifH;HQ455838;location.<1..>nifH;362.;uncultured.marine.bacterium.definition.dinitrogenase.reductase	4E-37
nifH	M01935:46:000000000-AC602:1:1101:8663:8116 (LC230495)	0.043%	nifH;GQ452751;location.<1..>nifH;389.;uncultured.microorganism.definition.NifH	1E-33
nifH	M01935:46:000000000-AC602:1:1105:15257:19300 (LC230496)	0.041%	nifH;EU978418;location.<1..>nifH;368.;uncultured.microorganism.definition.NifH	5E-173
nifH	M01935:46:000000000-AC602:1:1101:3430:9045 (LC230497)	0.038%	nifH;AY224045;location.<1..>nifH;318.;uncultured.bacterium.definition.dinitrogenase.reductase.Fe.protein	1E-129
nifH	M01935:46:000000000-AC602:1:1105:18096:13479 (LC230498)	0.036%	nifH;HQ010120;location.<1..>nifH;383.;uncultured.bacterium.definition.dinitrogenase.reductase	3E-47
nifH	M01935:46:000000000-AC602:1:1102:12994:16340 (LC230499)	0.026%	nifH;HQ190142;location.<1..>nifH;426.;uncultured.bacterium.definition.nitrogenase.component.II	2E-76
nifH	M01935:46:000000000-AC602:1:1105	0.024%	nifH;AY221783;location.<1..>nifH;327.;uncultured.bacterium.defin	2E-30

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
	:15667:18766 (LC230500)		ition.dinitrogenase.reductase	
nifH	M01935:46:000000000-AC602:1:1103:7208:10246 (LC230501)	0.022%	nifH;CP002364;location.3518933..3519760.;Desulfobulbus.propionicus.DSM.2032.definition.Mo-nitrogenase.iron.protein.subunit.NifH	5E-136
nifH	M01935:46:000000000-AC602:1:1105:19141:8859 (LC230502)	0.022%	nifH;HQ660907;location.<1..>nifH;328.;uncultured.bacterium.definition.dinitrogenase.reductase	9E-113
nifH	M01935:46:000000000-AC602:1:1103:7423:18121 (LC230503)	0.019%	nifH;GQ289566;location.complement(<1..>nifH;461).;Bradyrhizobium.japonicum.definition.NifH	1E-62
nifH	M01935:46:000000000-AC602:1:1103:12593:19020 (LC230504)	0.019%	nifH;AY787557;location.<1..>nifH;362.;uncultured.bacterium.definition.nitrogenase.iron.protein	9E-113
nifH	M01935:46:000000000-AC602:1:1103:10270:23798 (LC230505)	0.017%	nifH;CP002364;location.3518933..3519760.;Desulfobulbus.propionicus.DSM.2032.definition.Mo-nitrogenase.iron.protein.subunit.NifH	2E-107
nifH	M01935:46:000000000-AC602:1:1103:3174:9055 (LC256822)	0.014%	nifH;AF325795;location.<1..>nifH;430.;Spirochaeta.zuelzerae.definition.dinitrogenase.reductase	5E-34
nifH	M01935:46:000000000-AC602:1:1101:22085:20046 (LC230506)	0.012%	nifH;EU915064;location.<1..>nifH;360.;uncultured.Antarctic.bacterium.definition.dinitrogenase.reductase	5E-108
nifH	M01935:46:000000000-AC602:1:1102:10683:3544 (LC230507)	0.010%	nifH;HQ190142;location.<1..>nifH;426.;uncultured.bacterium.definition.nitrogenase.component.II	1E-102
nifH	M01935:46:000000000-AC602:1:1102:17995:11039 (LC230508)	0.010%	nifH;AEXQ01000094;location.2098..2847.;Turicibacter.sp..HGF1.definition.putative.nitrogenase.iron.protein	5E-24
nifH	M01935:46:000000000-AC602:1:1102:15573:13629 (LC230509)	0.007%	nifH;FN555078;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	2E-55

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nifH	M01935:46:000000000-AC602:1:1104:13324:21448 (LC230510)	0.007%	nifH;CP002431;location.1151267..1152094.;Desulfovibrio.aespoeensis.Aspo-2.definition.nitrogenase.iron.protein	6E-111
nifH	M01935:46:000000000-AC602:1:1104:18604:4894 (LC230511)	0.007%	nifH;EF626685;location.<1..>nifH;338.;Azonexus.hydrophilus.definition.dinitrogenase.reductase.subunit	7E-95
nifH	M01935:46:000000000-AC602:1:1104:27401:10065 (LC230512)	0.005%	nifH;GQ289580;location.complement(<1..>nifH;461).;Bradyrhizobium.japonicum.definition.NifH	2E-95
nifH	M01935:46:000000000-AC602:1:1103:14080:19047 (LC230513)	0.005%	nifH;CP002364;location.3518933..3519760.;Desulfobulbus.propionicus.DSM.2032.definition.Mo-nitrogenase.iron.protein.subunit.NifH	9E-110
nifH	M01935:46:000000000-AC602:1:1105:18166:17719 (LC230514)	0.005%	nifH;CP003220;location.complement(1437333..1438160).;Desulfovibrio.desulfuricans.ND132.definition.nitrogenase.iron.protein	6E-86
nifH	M01935:46:000000000-AC602:1:1102:16976:12646 (LC230515)	0.005%	nifH;EU693408;location.<1..>nifH;379.;uncultured.bacterium.definition.NifH	1E-74
nifH	M01935:46:000000000-AC602:1:1102:10312:3339 (LC230516)	0.005%	nifH;DQ098166;location.<1..>nifH;362.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	8E-104
nifH	M01935:46:000000000-AC602:1:1103:12047:5532 (LC230517)	0.005%	nifH;CP002431;location.1151267..1152094.;Desulfovibrio.aespoeensis.Aspo-2.definition.nitrogenase.iron.protein	5E-68
nifH	M01935:46:000000000-AC602:1:1101:11265:19548 (LC230518)	0.005%	nifH;DQ078018;location.<1..>nifH;362.;uncultured.bacterium.definition.NifH	3E-48
nifH	M01935:46:000000000-AC602:1:1105:4161:11000 (LC230519)	0.002%	nifH;AP012320;location.4587848..4588729.;Rubrivivax.gelatinosus.IL144.definition.nitrogenase.iron.protein.NifH	5E-105

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nifH	M01935:46:000000000-AC602:1:1105:15134:11708 (LC230520)	0.002%	nifH;CP003220;location.complement(1437333..1438160).;Desulfovibrio.desulfuricans.ND132.definition.nitrogenase.iron.protein	9E-110
nifH	M01935:46:000000000-AC602:1:1104:25188:6207 (LC230521)	0.002%	nifH;CP003220;location.complement(1437333..1438160).;Desulfovibrio.desulfuricans.ND132.definition.nitrogenase.iron.protein	1E-90
nifH	M01935:46:000000000-AC602:1:1103:8230:24325 (LC230522)	0.002%	nifH;DQ402833;location.<1..>nifH;417.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	4E-53
nifH	M01935:46:000000000-AC602:1:1102:2101:15056 (LC256823)	0.002%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	2E-107
nifH	M01935:46:000000000-AC602:1:1102:17994:10710 (LC230523)	0.002%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	2E-79
nifH	M01935:46:000000000-AC602:1:1104:13381:16038 (LC230524)	0.002%	nifH;CP002431;location.1151267..1152094.;Desulfovibrio.aespoeensis.Aspo-2.definition.nitrogenase.iron.protein	4E-115
nifH	M01935:46:000000000-AC602:1:1104:18612:16660 (LC230525)	0.002%	nifH;DQ480966;location.<1..>nifH;329.;uncultured.bacterium.definition.dinitrogenase.reductase	2E-70
nifH	M01935:46:000000000-AC602:1:1104:8719:11883 (LC230526)	0.002%	nifH;DQ098182;location.<1..>nifH;353.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	9E-73
nifH	M01935:46:000000000-AC602:1:1101:20348:21323 (LC230527)	0.002%	nifH;DQ520543;location.<1..>nifH;361.;uncultured.bacterium.definition.nitrogenase.iron.protein	6E-74
nifH	M01935:46:000000000-AC602:1:1102:21633:7759 (LC230528)	0.002%	nifH;CP002431;location.1151267..1152094.;Desulfovibrio.aespoeensis.Aspo-2.definition.nitrogenase.iron.protein	2E-83

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nifH	M01935:46:000000000-AC602:1:1101:25728:10177 (LC230529)	0.002%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	7E-95
nrfA	M01935:46:000000000-AC602:1:1104:14081:15521 (LC230530)	1.1%	nrfA_Welsh;AJ697846;location.<1..>nrfA_Welsh;487.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	1E-20
nrfA	M01935:46:000000000-AC602:1:1101:4384:20473 (LC256824)	1.03%	nrfA_Welsh;AMFJ01033964;location.30683..32173.;uncultured.bacterium.definition.hypothetical.protein	2E-22
nrfA	M01935:46:000000000-AC602:1:1101:19338:19060 (LC230531)	0.79%	nrfA_Welsh;AJ697839;location.<1..>nrfA_Welsh;478.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	2E-13
nrfA	M01935:46:000000000-AC602:1:1104:20179:8852 (LC230532)	0.41%	nrfA_Welsh;AJ697838;location.<2..>nrfA_Welsh;493.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	5E-17
nrfA	M01935:46:000000000-AC602:1:1103:22550:21221 (LC230533)	0.20%	nrfA_Welsh;AJ697846;location.<1..>nrfA_Welsh;487.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	9E-25
nrfA	M01935:46:000000000-AC602:1:1101:6607:14800 (LC230534)	0.18%	nrfA_Welsh;JX293781;location.<1..>nrfA_Welsh;236.;uncultured.bacterium.definition.nitrite.reductase	3E-15
nrfA	M01935:46:000000000-AC602:1:1103:28627:7853 (LC230535)	0.15%	nrfA_Welsh;CP006772;location.complement(2473277..2474770).;Bacteroidales.bacterium.CF.definition.Cytochrome.c-552	9E-99
nrfA	M01935:46:000000000-AC602:1:1103:3265:19429 (LC230536)	0.13%	nrfA_Welsh;AJ697839;location.<1..>nrfA_Welsh;478.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	7E-13
nrfA	M01935:46:000000000-AC602:1:1103:13912:18378 (LC230537)	0.12%	nrfA_Welsh;FJ810664;location.<1..>nrfA_Welsh;463.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	2E-62

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nrfA	M01935:46:000000000-AC602:1:1101:13953:20862 (LC230538)	0.10%	nrfA_Welsh;JX293802;location.<1..>nrfA_Welsh;236.;uncultured.bacterium.definition.nitrite.reductase	9E-28
nrfA	M01935:46:000000000-AC602:1:1102:10149:9239 (LC230539)	0.072%	nrfA_Welsh;CP001816;location.704163..705710.;Sulfurospirillum.deleyianum.DSM.6946.definition.Nitrite.reductase.(cytochrome;.ammonia-forming)	1E-21
nrfA	M01935:46:000000000-AC602:1:1101:15550:6901 (LC256825)	0.060%	nrfA_Welsh;AMFJ01031605;location.2141..3637.;uncultured.bacterium.definition.hypothetical.protein	2E-14
nrfA	M01935:46:000000000-AC602:1:1101:21481:8185 (LC230540)	0.053%	nrfA_Welsh;FJ810667;location.<1..>nrfA_Welsh;463.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	6E-66
nrfA	M01935:46:000000000-AC602:1:1102:19252:21428 (LC230541)	0.038%	nrfA_Welsh;FJ810664;location.<1..>nrfA_Welsh;463.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	6E-66
nrfA	M01935:46:000000000-AC602:1:1104:18496:9666 (LC230542)	0.026%	nrfA_Welsh;JX293749;location.<1..>nrfA_Welsh;236.;uncultured.bacterium.definition.nitrite.reductase	8E-13
nrfA	M01935:46:000000000-AC602:1:1101:22540:13504 (LC230543)	0.017%	nrfA_Welsh;JX293802;location.<1..>nrfA_Welsh;236.;uncultured.bacterium.definition.nitrite.reductase	6E-35
nrfA	M01935:46:000000000-AC602:1:1105:25807:14075 (LC230544)	0.010%	nrfA_Welsh;CP000251;location.complement(1053180..1054652).;Anaeromyxobacter.dehalogenans.2CP-C.definition.respiratory.nitrite.reductase.(cytochrome;.ammonia-forming).precursor	4E-33

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nrfA	M01935:46:000000000-AC602:1:1102:19552:21255 (LC230545)	0.002%	nrfA_Welsh;FJ810666;location.<1..>nrfA_Welsh;463.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	2E-63
napA	M01935:46:000000000-AC602:1:1105:27601:19180 (LC230546)	4.1%	napA;AP012048;location.complement(476588..479398).;Arcobacter.sp..L.definition.nitrate.reductase.catalytic.subunit	2E-110
napA	M01935:46:000000000-AC602:1:1101:17212:15418 (LC230547)	3.5%	napA;EU495680;location.<1..>napA;495.;uncultured.bacterium.definition.NapA	1E-19
napA	M01935:46:000000000-AC602:1:1103:14228:3701 (LC230548)	2.3%	napA;CP006615;location.complement(357757..360567).;Arcobacter.butzleri.7h1h.definition.periplasmic.nitrate.reductase..large.subunit	7E-101
napA	M01935:46:000000000-AC602:1:1101:12110:5606 (LC230549)	2.0%	napA;CP006615;location.complement(357757..360567).;Arcobacter.butzleri.7h1h.definition.periplasmic.nitrate.reductase..large.subunit	1E-124
napA	M01935:46:000000000-AC602:1:1102:27788:19549 (LC230550)	1.9%	napA;AM406670;location.complement(4318452..4320995).;Azoarcus.sp..BH72.definition.probable.nitrate.reductase	4E-84
napA	M01935:46:000000000-AC602:1:1101:21224:12340 (LC230551)	1.8%	napA;CP002356;location.57110..59896.;Sulfuricurvum.kujiense.DSM.16994.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	0
napA	M01935:46:000000000-AC602:1:1101:7711:20933 (LC230177)	1.7%	napA;CP002356;location.57110..59896.;Sulfuricurvum.kujiense.DSM.16994.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	1E-50
napA	M01935:46:000000000-AC602:1:1102:5903:13161 (LC230552)	1.3%	napA;KF056876;location.<1..>napA;399.;uncultured.Sulfurospirillum.sp..definition.periplasmic.nitrate.reductase.subunit.A	3E-78

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
napA	M01935:46:000000000-AC602:1:1104:16899:6872 (LC230553)	1.2%	napA;CP000089;location.complement(3764048..3766561).;Dechloromonas.aromatica.RCB.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	4E-65
napA	M01935:46:000000000-AC602:1:1101:6587:12081 (LC230554)	0.78%	napA;KF056876;location.<1..>napA;399.;uncultured.Sulfurospirillum.sp..definition.periplasmic.nitrate.reductase.subunit.A	5E-80
napA	M01935:46:000000000-AC602:1:1102:23549:14921 (LC230555)	0.77%	napA;CP003153;location.511069..513594.;Dechlorosoma.suillum.PS.definition.periplasmic.nitrate.reductase..large.subunit	3E-29
napA	M01935:46:000000000-AC602:1:1104:21849:20047 (LC230556)	0.67%	napA;EU125408;location.<1..>napA;414.;uncultured.bacterium.definition.periplasmic.nitrate.reductase	4E-59
napA	M01935:46:000000000-AC602:1:1101:9603:10281 (LC256826)	0.66%	napA;KF056876;location.<1..>napA;399.;uncultured.Sulfurospirillum.sp..definition.periplasmic.nitrate.reductase.subunit.A	2E-55
napA	M01935:46:000000000-AC602:1:1101:14839:5298 (LC230557)	0.62%	napA;EU526312;location.<1..>napA;1845.;Sulfurospirillum.arsenophilum.definition.periplasmic.nitrate.reductase.catalytic.subunit	2E-24
napA	M01935:46:000000000-AC602:1:1104:22760:20925 (LC230558)	0.59%	napA;HQ727705;location.<1..>napA;462.;uncultured.Thauera.sp..definition.periplasmic.nitrate.reductase.subunit	8E-33
napA	M01935:46:000000000-AC602:1:1101:4947:6387 (LC230559)	0.59%	napA;EU495669;location.<1..>napA;493.;uncultured.bacterium.definition.NapA	5E-34
napA	M01935:46:000000000-AC602:1:1101:6937:22605 (LC230560)	0.55%	napA;CP006615;location.complement(357757..360567).;Arcobacter.butzleri.7h1h.definition.periplasmic.nitrate.reductase..large.subunit	2E-113
napA	M01935:46:000000000-AC602:1:1101:13141:8748 (LC230561)	0.52%	napA;FQ311870;location.739528..742020.;Azospirillum.lipoferum.4B.definition.periplasmic.nitrate.reductase..large.subunit	3E-32

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
napA	M01935:46:000000000-AC602:1:1104:26652:4645 (LC230562)	0.51%	napA;CP003153;location.511069..513594.;Dechlorosoma.suillum.PS.definition.periplasmic.nitrate.reductase..large.subunit	2E-27
napA	M01935:46:000000000-AC602:1:1101:17278:9108 (LC230563)	0.33%	napA;CP000089;location.complement(3764048..3766561).;Dechloromonas.aromatica.RCB.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	3E-75
napA	M01935:46:000000000-AC602:1:1104:2537:17138 (LC230564)	0.27%	napA;CP003153;location.511069..513594.;Dechlorosoma.suillum.PS.definition.periplasmic.nitrate.reductase..large.subunit	1E-19
napA	M01935:46:000000000-AC602:1:1101:20774:9566 (LC230565)	0.23%	napA;AJXE01000032;location.25416..27920.;Pseudomonas.stutzeri.TS44.definition.nitrate.reductase.catalytic.subunit	9E-88
napA	M01935:46:000000000-AC602:1:1105:7824:6465 (LC230566)	0.18%	napA;AJ004933;location.739..>napA;2415.;Rhodopseudomonas.sp..definition.periplasmic.nitrate.reductase..large.subunit	3E-72
napA	M01935:46:000000000-AC602:1:1103:19275:11498 (LC230567)	0.15%	napA;HQ727705;location.<1..>napA;462.;uncultured.Thauera.sp..definition.periplasmic.nitrate.reductase.subunit	2E-30
napA	M01935:46:000000000-AC602:1:1102:4767:6662 (LC230568)	0.15%	napA;CP000491;location.207310..209805.;Paracoccus.denitrificans.PD1222.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	1E-37
napA	M01935:46:000000000-AC602:1:1102:10019:22845 (LC230569)	0.14%	napA;AFOT01000197;location.48043..50526.;Vibrio.cholerae.HC-02A1.definition.periplasmic.nitrate.reductase..large.subunit	5E-34
napA	M01935:46:000000000-AC602:1:1104:23572:20725 (LC230570)	0.065%	napA;AP010946;location.complement(299590..302091).;Azospirillum.sp..B510.definition.periplasmic.nitrate.reductase	9E-88

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
napA	M01935:46:000000000-AC602:1:1102:18841:4177 (LC230571)	0.060%	napA;CP003153;location.511069..513594.;Dechlorosoma.suillum.PS.definition.periplasmic.nitrate.reductase..large.subunit	1E-28
napA	M01935:46:000000000-AC602:1:1103:20939:6727 (LC230572)	0.057%	napA;KF056876;location.<1..>napA;399.;uncultured.Sulfurospirillum.sp..definition.periplasmic.nitrate.reductase.subunit.A	2E-95
napA	M01935:46:000000000-AC602:1:1103:5606:18171 (LC230573)	0.002%	napA;CP006615;location.complement(357757..360567).;Arcobacter.butzleri.7h1h.definition.periplasmic.nitrate.reductase..large.subunit	2E-125
napA	M01935:46:000000000-AC602:1:1103:14783:6540 (LC230574)	0.002%	napA;AM406670;location.complement(4318452..4320995).;Azoarcus.sp..BH72.definition.probable.nitrate.reductase	6E-83
napA	M01935:46:000000000-AC602:1:1102:14370:21111 (LC230575)	0.002%	napA;CP000089;location.complement(3764048..3766561).;Dechloromonas.aromatica.RCB.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	7E-24
nosZ	M01935:46:000000000-AC602:1:1101:23159:2892 (LC230576)	1.4%	nosZ;AB545690;location.<1.660.;Azospirillum.sp..TSO32-4.definition.nitrous.oxide.reductase	4E-70
nosZ	M01935:46:000000000-AC602:1:1101:18615:3185 (LC230577)	1.4%	nosZ;HQ625260;location.<1.702.;uncultured.bacterium.definition.nitrous.oxide.reductase	2E-102
nosZ	M01935:46:000000000-AC602:1:1101:9809:9444 (LC230578)	1.4%	nosZ;EU083520;location.complement(<1.1090).;uncultured.bacterium.definition.nitrous.oxide.reductase	9E-59
nosZ	M01935:46:000000000-AC602:1:1101:10329:4022 (LC230579)	0.76%	nosZ;HQ625260;location.<1.702.;uncultured.bacterium.definition.nitrous.oxide.reductase	5E-91
nosZ	M01935:46:000000000-AC602:1:1103:6645:15238 (LC230580)	0.75%	nosZ;JQ038958;location.<1.423.;uncultured.bacterium.definition.putative.nitrous.oxide.reductase	2E-53

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nosZ	M01935:46:000000000-AC602:1:1103:12120:20219 (LC230581)	0.70%	nosZ;EU053040;location.<1.673.;uncultured.bacterium.definition.nitrous.oxide.reductase	8E-121
nosZ	M01935:46:000000000-AC602:1:1102:8124:16077 (LC230582)	0.66%	nosZ;EU053057;location.<1.673.;uncultured.bacterium.definition.nitrous.oxide.reductase	3E-108
nosZ	M01935:46:000000000-AC602:1:1103:22216:8472 (LC230583)	0.45%	nosZ;GU362730;location.<1.455.;uncultured.bacterium.definition.nitrous.oxide.reductase	1E-76
nosZ	M01935:46:000000000-AC602:1:1104:10465:20668 (LC230584)	0.38%	nosZ;AY577569;location.<1.454.;uncultured.bacterium.definition.nitrous.oxide.reductase	4E-95
nosZ	M01935:46:000000000-AC602:1:1102:19787:5810 (LC230585)	0.37%	nosZ;HQ625260;location.<1.702.;uncultured.bacterium.definition.nitrous.oxide.reductase	4E-51
nosZ	M01935:46:000000000-AC602:1:1101:14046:14670 (LC230586)	0.32%	nosZ;AY913224;location.<1.645.;uncultured.forest.soil.bacterium.definition.nitrous.oxide.reductase	1E-98
nosZ	M01935:46:000000000-AC602:1:1101:18723:15921 (LC230587)	0.32%	nosZ;EU192075;location.<1.710.;Paracoccus.sp..BW001.definition.nitrous.oxide.reductase	6E-100
nosZ	M01935:46:000000000-AC602:1:1103:19765:19753 (LC256827)	0.31%	nosZ;EU083518;location.complement(<1.1093).;uncultured.bacterium.definition.nitrous.oxide.reductase	1E-104
nosZ	M01935:46:000000000-AC602:1:1102:7815:12954 (LC230588)	0.30%	nosZ;AY425164;location.<1.457.;uncultured.bacterium.definition.nitrous.oxide.reductase	2E-47
nosZ	M01935:46:000000000-AC602:1:1102:12182:17030 (LC230589)	0.24%	nosZ;JF509086;location.<1.707.;uncultured.bacterium.definition.nitrous.oxide.reductase	1E-48

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
nosZ	M01935:46:000000000-AC602:1:1102:15775:21101 (LC230590)	0.20%	nosZ;AY325700;location.<1.663.;uncultured.bacterium.definition.putative.nitrous.oxide.reductase	7E-38
nosZ	M01935:46:000000000-AC602:1:1102:27348:14691 (LC230591)	0.11%	nosZ;FN868506;location.<1.387.;uncultured.bacterium.definition.nitrous-oxide.reductase	1E-94
nosZ	M01935:46:000000000-AC602:1:1104:17010:13433 (LC230592)	0.033%	nosZ;KC936777;location.<1.267.;uncultured.bacterium.definition.nitrous.oxide.reductase	2E-44
nosZ	M01935:46:000000000-AC602:1:1103:23064:10017 (LC230593)	0.029%	nosZ;AY913111;location.<1.672.;uncultured.forest.soil.bacterium.definition.nitrous.oxide.reductase	1E-38
norB	M01935:46:000000000-AC602:1:1101:24190:9926 (LC230214)	4.2%	norB;HQ615313;location.<1..>norB;646.;uncultured.bacterium.definition.putative.nitric.oxide.reductase	6E-26
norB	M01935:46:000000000-AC602:1:1101:17679:2202 (LC230594)	1.5%	norB;HF936747;location.<1..>norB;453.;uncultured.bacterium.definition.nitric.oxide.reductase	5E-71
norB	M01935:46:000000000-AC602:1:1104:26137:6035 (LC230215)	1.1%	norB;CP000478;location.complement(3622744..3625020).;Syntrophobacter.fumaroxidans.MPOB.definition.cytochrome.b.subunit.of.nitric.oxide.reductase	1E-101
norB	M01935:46:000000000-AC602:1:1101:27731:6386 (LC230595)	1.0%	norB;AP007255;location.complement(3147718..3149037).;Magnetospirillum.magneticum.AMB-1.definition.Nitric.oxide.reductase.large.subunit	1E-83
norB	M01935:46:000000000-AC602:1:1101:22677:8842 (LC230596)	0.83%	norB;CU459003;location.1460427..1461764.;Magnetospirillum.gryphiswaldense.MSR-1.definition.Nitric-oxide.reductase.subunit.B	4E-53

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
norB	M01935:46:000000000-AC602:1:1103:4240:13149 (LC230597)	0.31%	norB;AM284362;location.<1..>norB;419.;Paracoccus.sp..R-28244.definition.nitric.oxide.reductase.CnorB	1E-145
norB	M01935:46:000000000-AC602:1:1103:8592:14229 (LC230598)	0.27%	norB;AM284368;location.<1..>norB;433.;Acidovorax.sp..R-24667.definition.nitric.oxide.reductase.CnorB	2E-122
norB	M01935:46:000000000-AC602:1:1105:16314:15577 (LC230599)	0.25%	norB;AM284370;location.<1..>norB;436.;Azovibrio.sp..R-25062.definition.nitric.oxide.reductase.CnorB	2E-79
norB	M01935:46:000000000-AC602:1:1104:12454:16930 (LC230600)	0.24%	norB;AM284381;location.<1..>norB;420.;Dechloromonas.sp..R-28401.definition.nitric.oxide.reductase.CnorB	3E-155
norB	M01935:46:000000000-AC602:1:1102:15074:20849 (LC230601)	0.22%	norB;CP000830;location.3347463..3348842.;Dinoroseobacter.shibae.DFL.12...DSM.16493.definition.nitric.oxide.reductase.subunit.B	8E-57
norB	M01935:46:000000000-AC602:1:1104:25631:18240 (LC230602)	0.22%	norB;CP001280;location.1637157..1638512.;Methylocella.silvestris.BL2.definition.Nitric-oxide.reductase	1E-46
norB	M01935:46:000000000-AC602:1:1103:10975:24561 (LC230603)	0.17%	norB;HF936748;location.<1..>norB;455.;uncultured.bacterium.definition.nitric.oxide.reductase	9E-51
norB	M01935:46:000000000-AC602:1:1101:12655:8400 (LC230604)	0.16%	norB;AB014090;location.3757..5145.;Paracoccus.denitrificans.definition.NorB	1E-62
norB	M01935:46:000000000-AC602:1:1105:25461:20470 (LC230605)	0.11%	norB;FN600628;location.<1..>norB;353.;Bradyrhizobium.sp..GSM-467.definition.cytochrome.c.dependent.nitric.oxide.reductase	2E-138
norB	M01935:46:000000000-AC602:1:1103:6275:8938 (LC230606)	0.050%	norB;CP002083;location.611075..612424.;Hyphomicrobium.denitrificans.ATCC.51888.definition.Nitric-oxide.reductase	9E-51

Gene	OTU (accession number)	Abundance	blast hit	*e*-value
norB	M01935:46:000000000-AC602:1:1104:16297:14009 (LC230607)	0.048%	norB;CU459003;location.1460427..1461764.;Magnetospirillum.gryphiswaldense.MSR-1.definition.Nitric-oxide.reductase.subunit.B	2E-67
norB	M01935:46:000000000-AC602:1:1102:9076:10984 (LC230608)	0.033%	norB;CU459003;location.1460427..1461764.;Magnetospirillum.gryphiswaldense.MSR-1.definition.Nitric-oxide.reductase.subunit.B	4E-53
norB	M01935:46:000000000-AC602:1:1103:9533:13647 (LC230609)	0.014%	norB;CP002083;location.611075..612424.;Hyphomicrobium.denitrificans.ATCC.51888.definition.Nitric-oxide.reductase	4E-65
norB	M01935:46:000000000-AC602:1:1101:18901:5898 (LC256828)	0.010%	norB;AM284340;location.<1..>norB;435.;Rhizobium.sp..R-24658.definition.nitric.oxide.reductase.CnorB	1E-145

b) UASB M

Gene	OTU (accession number)	abundance	blast hit	*e*-value
nxrB	M01935:46:000000000-AC602:1:1102:6087:15587 (LC230262)	0.69%	nxrB;AM286333;location.<1..>nxrB;371.;Nitrobacter.sp..263.definition.nitrite.oxidoreductase	6E-160
nirK	M01935:46:000000000-AC602:1:1105:26379:6299 (LC230267)	2.0%	nirK;AB162934;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	9E-64
nirK	M01935:46:000000000-AC602:1:1101:10691:8522 (LC230268)	1.7%	nirK;DQ232405;location.<1.480.;uncultured.bacterium.definition.NirK	0
nirK	M01935:46:000000000-AC602:1:1102:7924:14095 (LC230269)	1.7%	nirK;HQ162043;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	4E-143
nirK	M01935:46:000000000-AC602:1:1103:28415:18155 (LC256813)	1.3%	nirK;HM116323;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	4E-35
nirK	M01935:46:000000000-AC602:1:1103:24593:14554 (LC230270)	1.3%	nirK;AB162323;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1102:8263:11887 (LC230271)	1.1%	nirK;JN255536;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	2E-111
nirK	M01935:46:000000000-AC602:1:1101:24059:22435 (LC230272)	0.85%	nirK;HM116353;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1101:11639:17149 (LC230273)	0.79%	nirK;AB162328;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1107:21964:11331 (LC230274)	0.70%	nirK;GQ496041;location.<1.474.;uncultured.bacterium.definition.copper.dependent.nitrite.reductase	0

nirK	M01935:46:000000000-AC602:1:1102:13287:18127 (LC230275)	0.64%	nirK;HM628827;location.<1.474.;uncultured.bacterium.definition.copper-containing.nitrite.reductase	3E-42
nirK	M01935:46:000000000-AC602:1:1102:11114:6529 (LC230276)	0.52%	nirK;AB453564;location.<1.436.;uncultured.bacterium.definition.nitrite.reductase	5E-90
nirK	M01935:46:000000000-AC602:1:1101:13050:10679 (LC230277)	0.51%	nirK;DQ996546;location.<1.503.;uncultured.bacterium.definition.NirK	0
nirK	M01935:46:000000000-AC602:1:1102:17212:18683 (LC230278)	0.49%	nirK;AY583400;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	2E-178
nirK	M01935:46:000000000-AC602:1:1103:15359:9073 (LC230279)	0.49%	nirK;AM230886;location.<1.447.;Paracoccus.sp..R-28242.definition.nitrite.reductase	2E-138
nirK	M01935:46:000000000-AC602:1:1102:7799:12742 (LC230280)	0.45%	nirK;AB684572;location.<1.433.;uncultured.bacterium.definition.nitrite.reductase	3E-51
nirK	M01935:46:000000000-AC602:1:1102:25955:5682 (LC230281)	0.35%	nirK;HM116353;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	3E-171
nirK	M01935:46:000000000-AC602:1:1107:4024:20652 (LC230282)	0.31%	nirK;AB162933;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1111:10607:6193 (LC230283)	0.31%	nirK;AB453443;location.<1.436.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1104:8543:10716 (LC230284)	0.31%	nirK;HM116322;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1109:14967:6558 (LC230285)	0.25%	nirK;AB118903;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	8E-138
nirK	M01935:46:000000000-AC602:1:1103	0.25%	nirK;DQ182205;location.<1.473.;uncultured.bacterium.definition.p	1E-81

	:8524:6041 (LC230286)		utative.nitrite.reductase	
nirK	M01935:46:000000000-AC602:1:1102:12556:5997 (LC230287)	0.17%	nirK;DQ182218;location.<1.473.;uncultured.bacterium.definition.putative.nitrite.reductase	1E-118
nirK	M01935:46:000000000-AC602:1:1115:6902:20649 (LC230288)	0.15%	nirK;AM419528;location.<1.480.;uncultured.organism.definition.putative.copper.containing.dissimilatory.nitrite.reductase	2E-80
nirK	M01935:46:000000000-AC602:1:1103:23631:20146 (LC230289)	0.12%	nirK;DQ182164;location.<1.473.;uncultured.bacterium.definition.putative.nitrite.reductase	9E-73
nirK	M01935:46:000000000-AC602:1:1107:7046:8626 (LC230290)	0.098%	nirK;HM628847;location.<1.474.;uncultured.bacterium.definition.copper-containing.nitrite.reductase	6E-31
nirK	M01935:46:000000000-AC602:1:1107:20725:17395 (LC230291)	0.095%	nirK;AY121544;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	8E-101
nirK	M01935:46:000000000-AC602:1:1104:4435:20523 (LC230292)	0.088%	nirK;HQ162043;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	2E-138
nirK	M01935:46:000000000-AC602:1:1105:17478:9459 (LC230293)	0.084%	nirK;AY583400;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	8E-166
nirK	M01935:46:000000000-AC602:1:1110:4706:5004 (LC230294)	0.070%	nirK;EF615323;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	3E-128
nirK	M01935:46:000000000-AC602:1:1115:14147:4820 (LC230295)	0.059%	nirK;DQ304381;location.<1.473.;uncultured.bacterium.definition.putative.nitrite.reductase	3E-45
nirK	M01935:46:000000000-AC602:1:1101:18441:11502 (LC230296)	0.052%	nirK;HQ162043;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	2E-36
nirK	M01935:46:000000000-AC602:1:1115:4545:21439 (LC230297)	0.038%	nirK;HM116343;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	0

nirK	M01935:46:000000000-AC602:1:1111:15768:19409 (LC230298)	0.023%	nirK;GQ496041;location.<1.474.;uncultured.bacterium.definition.copper.dependent.nitrite.reductase	3E-159
nirK	M01935:46:000000000-AC602:1:1115:7958:15004 (LC230299)	0.016%	nirK;GU270500;location.complement(<1.515).;uncultured.bacterium.definition.nitrite.reductase	4E-84
nirK	M01935:46:000000000-AC602:1:1110:15732:14096 (LC230300)	0.015%	nirK;HM116307;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1111:14957:20954 (LC230301)	0.013%	nirK;DQ783969;location.<1.473.;uncultured.bacterium.definition.NirK	2E-77
nirK	M01935:46:000000000-AC602:1:1113:13050:4564 (LC230302)	0.011%	nirK;HQ162042;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	5E-124
nirK	M01935:46:000000000-AC602:1:1117:15492:12356 (LC230303)	0.007%	nirK;HQ162043;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	7E-157
nirK	M01935:46:000000000-AC602:1:1110:26248:18058 (LC230304)	0.005%	nirK;GU136453;location.<1.515.;uncultured.Ochrobactrum.sp..definition.NirK	8E-135
nirK	M01935:46:000000000-AC602:1:1106:18524:15519 (LC230305)	0.003%	nirK;AY583400;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	4E-121
nirK	M01935:46:000000000-AC602:1:1109:10841:21968 (LC230306)	0.003%	nirK;HM116315;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	2E-86
nirK	M01935:46:000000000-AC602:1:1109:12222:13732 (LC230307)	0.003%	nirK;HM116315;location.<1.473.;uncultured.bacterium.definition.nitrite.reductase	1E-81
nirK	M01935:46:000000000-AC602:1:1110:27005:17944 (LC230308)	0.003%	nirK;AB379562;location.<1.436.;uncultured.bacterium.definition.copper-containing.nitrate.reductase	6E-37
nirK	M01935:46:000000000-AC602:1:1113	0.002%	nirK;AB453443;location.<1.436.;uncultured.bacterium.definition.ni	1E-136

	:18417:6883 (LC230309)		trite.reductase	
nirK	M01935:46:000000000-AC602:1:1113:29296:11543 (LC230310)	0.002%	nirK;HM116353;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	0
nirK	M01935:46:000000000-AC602:1:1109:15422:17888 (LC230311)	0.002%	nirK;HQ162041;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	9E-107
nirK	M01935:46:000000000-AC602:1:1107:17666:4684 (LC230312)	0.002%	nirK;HM116322;location.<1.474.;uncultured.bacterium.definition.nitrite.reductase	1E-164
nirK	M01935:46:000000000-AC602:1:1106:21629:2183 (LC230313)	0.002%	nirK;AB162323;location.<1.515.;uncultured.bacterium.definition.nitrite.reductase	1E-145
nirS	M01935:46:000000000-AC602:1:1101:24724:7294 (LC230314)	2.3%	nirS;AF549050;location.<1..>nirS;750.;uncultured.organism.definition.nitrite.reductase	5E-37
nirS	M01935:46:000000000-AC602:1:1105:5158:15834 (LC230315)	0.76%	nirS;AY583452;location.<1..>nirS;414.;uncultured.bacterium.definition.nitrite.reductase	3E-41
nirS	M01935:46:000000000-AC602:1:1113:20844:4087 (LC230316)	0.50%	nirS;JN179356;location.<1..>nirS;660.;uncultured.bacterium.definition.nitrite.reductase	2E-76
nirS	M01935:46:000000000-AC602:1:1106:11576:21706 (LC230317)	0.48%	nirS;KC412684;location.<1..>nirS;894.;uncultured.bacterium.definition.cytochrome.cd1-containing.nitrite.reductase	6E-113
nirS	M01935:46:000000000-AC602:1:1103:11066:6052 (LC230318)	0.36%	nirS;FR865832;location.<1..>nirS;408.;uncultured.bacterium.definition.cd1-containing.nitrite.reductase	1E-96
nirS	M01935:46:000000000-AC602:1:1106:28549:12054 (LC230319)	0.34%	nirS;EF558502;location.<1..>nirS;885.;uncultured.bacterium.definition.dissimilatory.nitrite.reductase	8E-60
nirS	M01935:46:000000000-AC602:1:1102:12861:8008 (LC230320)	0.28%	nirS;JX941766;location.<1..>nirS;411.;uncultured.bacterium.definition.nitrite.reductase	2E-29

nirS	M01935:46:000000000-AC602:1:1117:24605:15061 (LC230321)	0.19%	nirS;HE616604;location.<1..>nirS;413.;uncultured.bacterium.definition.nitrite.reductase.(cytochrome.cd1-containing)	8E-91
nirS	M01935:46:000000000-AC602:1:1108:10365:12720 (LC256814)	0.062%	nirS;EF558414;location.<1..>nirS;888.;uncultured.bacterium.definition.dissimilatory.nitrite.reductase	3E-75
nirS	M01935:46:000000000-AC602:1:1107:12360:2600 (LC230322)	0.031%	nirS;HM116273;location.<1..>nirS;411.;uncultured.bacterium.definition.nitrite.reductase	2E-156
nifH	M01935:46:000000000-AC602:1:1101:16190:6151 (LC230323)	7.2%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	1E-136
nifH	M01935:46:000000000-AC602:1:1101:24927:8705 (LC230324)	6.3%	nifH;FJ381614;location.<1..>nifH;363.;uncultured.bacterium.definition.dinitrogenase.reductase	3E-66
nifH	M01935:46:000000000-AC602:1:1101:9358:13534 (LC256815)	5.1%	nifH;FN555078;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	2E-55
nifH	M01935:46:000000000-AC602:1:1101:25013:11253 (LC230325)	2.9%	nifH;HQ660907;location.<1..>nifH;328.;uncultured.bacterium.definition.dinitrogenase.reductase	4E-161
nifH	M01935:46:000000000-AC602:1:1101:13001:5463 (LC230326)	2.6%	nifH;X56071;location.132..959.;Methanobacterium.ivanovii.definition.nitrogenase.Mo-Fe.protein	2E-60
nifH	M01935:46:000000000-AC602:1:1102:5195:8124 (LC230327)	1.6%	nifH;JN122952;location.<1..>nifH;369.;uncultured.bacterium.definition.nitrogenase	2E-52
nifH	M01935:46:000000000-AC602:1:1102:11038:16808 (LC230328)	1.1%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	3E-165
nifH	M01935:46:000000000-AC602:1:1101:27271:5321 (LC230329)	0.82%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	2E-153

nifH	M01935:46:000000000-AC602:1:1105:9041:17489 (LC256816)	0.77%	nifH;CP000867;location.complement(1694838..1695665).;Methanococcus.maripaludis.C6.definition.nitrogenase.iron.protein	1E-15
nifH	M01935:46:000000000-AC602:1:1101:10416:11437 (LC230330)	0.71%	nifH;FJ977296;location.<1..>nifH;606.;uncultured.Frankia.sp..definition.dinitrogenase.reductase	1E-102
nifH	M01935:46:000000000-AC602:1:1106:18669:9070 (LC230331)	0.48%	nifH;X56071;location.132..959.;Methanobacterium.ivanovii.definition.nitrogenase.Mo-Fe.protein	6E-39
nifH	M01935:46:000000000-AC602:1:1102:7774:21463 (LC230332)	0.45%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	1E-148
nifH	M01935:46:000000000-AC602:1:1102:12127:7478 (LC230333)	0.45%	nifH;AY231492;location.<1..>nifH;324.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	7E-51
nifH	M01935:46:000000000-AC602:1:1105:21969:20362 (LC230334)	0.44%	nifH;FN555079;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	1E-53
nifH	M01935:46:000000000-AC602:1:1105:5787:6408 (LC230335)	0.44%	nifH;HM750561;location.<1..>nifH;417.;uncultured.bacterium.definition.dinitrogenase.reductase	1E-62
nifH	M01935:46:000000000-AC602:1:1104:14189:20601 (LC230336)	0.35%	nifH;JN122952;location.<1..>nifH;369.;uncultured.bacterium.definition.nitrogenase	2E-61
nifH	M01935:46:000000000-AC602:1:1101:23148:23374 (LC230337)	0.19%	nifH;DQ520489;location.<1..>nifH;355.;uncultured.bacterium.definition.nitrogenase.iron.protein	5E-18
nifH	M01935:46:000000000-AC602:1:1101:6653:6579 (LC230338)	0.17%	nifH;AY231493;location.<1..>nifH;324.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	7E-73
nifH	M01935:46:000000000-AC602:1:1104:6905:5052 (LC230339)	0.16%	nifH;FN555079;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	7E-58

nifH	M01935:46:000000000-AC602:1:1101:10618:14049 (LC230340)	0.13%	nifH;AEXQ01000094;location.2098..2847.;Turicibacter.sp..HGF1.definition.putative.nitrogenase.iron.protein	5E-24
nifH	M01935:46:000000000-AC602:1:1115:19372:15401 (LC230341)	0.13%	nifH;AB184899;location.<1..>nifH;384.;uncultured.bacterium.definition.dinitrogenase.reductase	6E-39
nifH	M01935:46:000000000-AC602:1:1117:21677:8997 (LC230342)	0.13%	nifH;AJ010290;location.<1..>nifH;383.;uncultured.microorganism.SN-33.definition.dinitrogenase.reductase	3E-47
nifH	M01935:46:000000000-AC602:1:1105:20222:17932 (LC230343)	0.11%	nifH;AY196426;location.<1..>nifH;368.;uncultured.nitrogen-fixing.bacterium.definition.nitrogenase.iron.protein	2E-66
nifH	M01935:46:000000000-AC602:1:1106:6907:18705 (LC230344)	0.10%	nifH;X56071;location.132..959.;Methanobacterium.ivanovii.definition.nitrogenase.Mo-Fe.protein	3E-56
nifH	M01935:46:000000000-AC602:1:1103:12354:22291 (LC230345)	0.10%	nifH;AAVO02000001;location.complement(285652..286431).;Ruminococcus.obeum.ATCC.29174.definition.putative.nitrogenase.iron.protein	6E-144
nifH	M01935:46:000000000-AC602:1:1103:8426:5359 (LC230346)	0.085%	nifH;FJ502311;location.<1..>nifH;321.;uncultured.bacterium.definition.NifH	3E-106
nifH	M01935:46:000000000-AC602:1:1105:14368:22179 (LC230347)	0.080%	nifH;EF199951;location.<1..>nifH;449.;Halorhodospira.halophila.definition.nitrogenase.iron.protein	3E-122
nifH	M01935:46:000000000-AC602:1:1108:24365:13095 (LC230348)	0.079%	nifH;HQ660907;location.<1..>nifH;328.;uncultured.bacterium.definition.dinitrogenase.reductase	2E-129
nifH	M01935:46:000000000-AC602:1:1105:19314:24279 (LC230349)	0.079%	nifH;EF196656;location.<1..>nifH;362.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	3E-28

nifH	M01935:46:000000000-AC602:1:1104:24574:18870 (LC230350)	0.077%	nifH;GQ452751;location.<1..>nifH;389.;uncultured.microorganism.definition.NifH	8E-29
nifH	M01935:46:000000000-AC602:1:1109:11383:3318 (LC230351)	0.072%	nifH;HM750617;location.<1..>nifH;414.;uncultured.bacterium.definition.dinitrogenase.reductase	1E-99
nifH	M01935:46:000000000-AC602:1:1113:21914:2536 (LC230352)	0.064%	nifH;X56071;location.132..959.;Methanobacterium.ivanovii.definition.nitrogenase.Mo-Fe.protein	1E-27
nifH	M01935:46:000000000-AC602:1:1109:18781:10699 (LC230353)	0.061%	nifH;AB208369;location.<1..>nifH;390.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	2E-147
nifH	M01935:46:000000000-AC602:1:1102:8258:12248 (LC230354)	0.049%	nifH;AY224010;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase.Fe.protein	2E-45
nifH	M01935:46:000000000-AC602:1:1108:19579:17918 (LC230355)	0.048%	nifH;FN555079;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	7E-52
nifH	M01935:46:000000000-AC602:1:1106:5678:18961 (LC230356)	0.034%	nifH;FN555078;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	1E-59
nifH	M01935:46:000000000-AC602:1:1115:22276:4483 (LC230357)	0.029%	nifH;AB208267;location.<1..>nifH;387.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	3E-66
nifH	M01935:46:000000000-AC602:1:1109:19568:11923 (LC230358)	0.029%	nifH;FP929036;location.1082045..1082920.;Butyrivibrio.fibrisolvens.16/4.definition.Nitrogenase.subunit.NifH.(ATPase)	7E-11
nifH	M01935:46:000000000-AC602:1:1106:11970:17017 (LC230359)	0.023%	nifH;DQ402773;location.<1..>nifH;417.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	2E-52
nifH	M01935:46:000000000-AC602:1:1104	0.023%	nifH;DQ485356;location.<1..>nifH;350.;uncultured.bacterium.defin	5E-56

	:4417:16177 (LC230360)		ition.dinitrogenase.reductase	
nifH	M01935:46:000000000-AC602:1:1106:13345:12687 (LC230361)	0.020%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	1E-124
nifH	M01935:46:000000000-AC602:1:1103:9770:15882 (LC230362)	0.020%	nifH;AB273420;location.<1..>nifH;424.;uncultured.nitrogen-fixing.bacterium.definition.dinitrogenase.reductase	3E-28
nifH	M01935:46:000000000-AC602:1:1105:11861:7056 (LC230363)	0.018%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	1E-136
nifH	M01935:46:000000000-AC602:1:1107:5940:10149 (LC230364)	0.018%	nifH;FN555078;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	5E-62
nifH	M01935:46:000000000-AC602:1:1106:4650:11617 (LC230365)	0.013%	nifH;JN122953;location.<1..>nifH;369.;uncultured.bacterium.definition.nitrogenase	4E-84
nifH	M01935:46:000000000-AC602:1:1105:18226:12399 (LC230366)	0.010%	nifH;FJ686519;location.<1..>nifH;362.;uncultured.bacterium.definition.nitrogenase.reductase	1E-31
nifH	M01935:46:000000000-AC602:1:1114:21401:6976 (LC230367)	0.008%	nifH;EF568543;location.<1..>nifH;354.;uncultured.microorganism.definition.dinitrogenase.reductase	4E-118
nifH	M01935:46:000000000-AC602:1:1113:11048:19010 (LC230368)	0.003%	nifH;HQ190142;location.<1..>nifH;426.;uncultured.bacterium.definition.nitrogenase.component.II	4E-75
nifH	M01935:46:000000000-AC602:1:1107:20034:12348 (LC230369)	0.002%	nifH;HQ190167;location.<1..>nifH;421.;uncultured.bacterium.definition.nitrogenase.component.II	8E-101
nifH	M01935:46:000000000-AC602:1:1108:14155:15018 (LC230370)	0.002%	nifH;HM750576;location.<1..>nifH;417.;uncultured.bacterium.definition.dinitrogenase.reductase	4E-87
nifH	M01935:46:000000000-AC602:1:1114	0.002%	nifH;FJ381614;location.<1..>nifH;363.;uncultured.bacterium.definit	6E-80

	:15613:19473 (LC230371)		ion.dinitrogenase.reductase	
nifH	M01935:46:000000000-AC602:1:1115:17279:24278 (LC230372)	0.002%	nifH;FN555078;location.<1..>nifH;327.;uncultured.bacterium.definition.dinitrogenase.reductase	5E-65
nifH	M01935:46:000000000-AC602:1:1115:14272:21189 (LC256817)	0.002%	nifH;AM286444;location.<1..>nifH;290.;uncultured.bacterium.definition.nifH.protein	2E-48
nrfA	M01935:46:000000000-AC602:1:1102:8996:23918 (LC230373)	2.0%	nrfA_Welsh;AJ697846;location.<1..>nrfA_Welsh;487.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	5E-23
nrfA	M01935:46:000000000-AC602:1:1107:9274:13398 (LC230374)	1.7%	nrfA_Welsh;AJ697839;location.<1..>nrfA_Welsh;478.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	2E-13
nrfA	M01935:46:000000000-AC602:1:1101:9732:7732 (LC230375)	0.36%	nrfA_Welsh;AJ697846;location.<1..>nrfA_Welsh;487.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	9E-25
nrfA	M01935:46:000000000-AC602:1:1105:22832:13746 (LC230376)	0.24%	nrfA_Welsh;CP006772;location.complement(2473277..2474770).;Bacteroidales.bacterium.CF.definition.Cytochrome.c-552	9E-99
nrfA	M01935:46:000000000-AC602:1:1106:22847:18398 (LC230377)	0.17%	nrfA_Welsh;AJ697848;location.<1..>nrfA_Welsh;496.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	5E-17
nrfA	M01935:46:000000000-AC602:1:1109:21340:15917 (LC230378)	0.14%	nrfA_Welsh;FJ810664;location.<1..>nrfA_Welsh;463.;uncultured.bacterium.definition.cytochrome.c.nitrite.reductase	2E-10
napA	M01935:46:000000000-AC602:1:1101:20732:2948 (LC230379)	6.8%	napA;EU495680;location.<1..>napA;495.;uncultured.bacterium.definition.NapA	1E-19
napA	M01935:46:000000000-AC602:1:1101:15748:5082 (LC230380)	2.6%	napA;EU125408;location.<1..>napA;414.;uncultured.bacterium.definition.periplasmic.nitrate.reductase	2E-58
napA	M01935:46:000000000-AC602:1:1101:16494:2829 (LC230381)	2.0%	napA;EU495669;location.<1..>napA;493.;uncultured.bacterium.definition.NapA	5E-34

napA	M01935:46:000000000-AC602:1:1104:28318:12525 (LC230382)	0.97%	napA;EU495669;location.<1..>napA;493.;uncultured.bacterium.definition.NapA	8E-27
napA	M01935:46:000000000-AC602:1:1103:3549:6969 (LC230383)	0.92%	napA;CP000662;location.complement(85399..87885).;Rhodobacter.sphaeroides.ATCC.17025.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	8E-27
napA	M01935:46:000000000-AC602:1:1104:19935:17842 (LC230384)	0.89%	napA;CP001715;location.4467228..4469753.;Candidatus.Accumulibacter.phosphatis.clade.IIA.str..UW-1.definition.periplasmic.nitrate.reductase..large.subunit	1E-19
napA	M01935:46:000000000-AC602:1:1103:6404:3165 (LC230385)	0.82%	napA;EU495666;location.<1..>napA;493.;uncultured.bacterium.definition.NapA	1E-19
napA	M01935:46:000000000-AC602:1:1101:3732:6331 (LC230386)	0.72%	napA;AMXD01000089;location.4823..7369.;Thauera.aminoaromatica.S2.definition.nitrate.reductase.catalytic.subunit	6E-83
napA	M01935:46:000000000-AC602:1:1101:4822:21725 (LC230387)	0.58%	napA;AY305378;location.228154..230649.;Ralstonia.eutropha.H16.definition.periplasmic.nitrate.reductase.large.subunit	5E-37
napA	M01935:46:000000000-AC602:1:1110:10677:11574 (LC230388)	0.55%	napA;EF217122;location.<1..>napA;152.;uncultured.bacterium.definition.putitative.periplasmic.nitrate.reductase.large.subunit	8E-27
napA	M01935:46:000000000-AC602:1:1101:21632:15764 (LC230389)	0.47%	napA;AMXD01000089;location.4823..7369.;Thauera.aminoaromatica.S2.definition.nitrate.reductase.catalytic.subunit	2E-52
napA	M01935:46:000000000-AC602:1:1101:18947:18165 (LC230390)	0.28%	napA;FQ311870;location.739528..742020.;Azospirillum.lipoferum.4B.definition.periplasmic.nitrate.reductase..large.subunit	1E-62
napA	M01935:46:000000000-AC602:1:1103:22060:4743 (LC230391)	0.26%	napA;CP003153;location.511069..513594.;Dechlorosoma.suillum.PS.definition.periplasmic.nitrate.reductase..large.subunit	1E-31

napA	M01935:46:000000000-AC602:1:1104:19152:21780 (LC230392)	0.24%	napA;EF217098;location.<1..>napA;152.;uncultured.bacterium.definition.putitative.periplasmic.nitrate.reductase.large.subunit	2E-27
napA	M01935:46:000000000-AC602:1:1115:23228:14875 (LC230393)	0.18%	napA;CP001715;location.4467228..4469753.;Candidatus.Accumulibacter.phosphatis.clade.IIA.str..UW-1.definition.periplasmic.nitrate.reductase..large.subunit	2E-24
napA	M01935:46:000000000-AC602:1:1103:25061:21605 (LC230394)	0.16%	napA;EU495673;location.<1..>napA;493.;uncultured.bacterium.definition.NapA	8E-30
napA	M01935:46:000000000-AC602:1:1101:26952:13033 (LC230395)	0.090%	napA;CP000491;location.207310..209805.;Paracoccus.denitrificans.PD1222.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	9E-39
napA	M01935:46:000000000-AC602:1:1107:5471:22626 (LC230396)	0.008%	napA;CP000491;location.207310..209805.;Paracoccus.denitrificans.PD1222.definition.periplasmic.nitrate.reductase.subunit.NapA.apoprotein	1E-28
napA	M01935:46:000000000-AC602:1:1102:23410:16905 (LC230397)	0.002%	napA;EF217094;location.<1..>napA;152.;uncultured.bacterium.definition.putitative.periplasmic.nitrate.reductase.large.subunit	5E-34
nosZ	M01935:46:000000000-AC602:1:1101:13149:6248 (LC230398)	2.6%	nosZ;HQ625260;location.<1.702.;uncultured.bacterium.definition.nitrous.oxide.reductase	2E-102
nosZ	M01935:46:000000000-AC602:1:1106:10553:11894 (LC230399)	1.9%	nosZ;EU271710;location.<1.436.;uncultured.bacterium.definition.NosZ	4E-64
nosZ	M01935:46:000000000-AC602:1:1105:16674:22851 (LC230400)	1.2%	nosZ;HQ625260;location.<1.702.;uncultured.bacterium.definition.nitrous.oxide.reductase	3E-80
nosZ	M01935:46:000000000-AC602:1:1101:4510:15814 (LC230401)	0.84%	nosZ;HQ625260;location.<1.702.;uncultured.bacterium.definition.nitrous.oxide.reductase	2E-87

nosZ	M01935:46:000000000-AC602:1:1101:2029:11036 (LC230402)	0.68%	nosZ;AY425164;location.<1.457.;uncultured.bacterium.definition.nitrous.oxide.reductase	2E-47
nosZ	M01935:46:000000000-AC602:1:1113:16612:15928 (LC230403)	0.30%	nosZ;FN600636;location.<1.662.;Mesorhizobium.sp..4FB11.definition.nitrous.oxide.reductase	3E-74
nosZ	M01935:46:000000000-AC602:1:1111:19311:7597 (LC230404)	0.18%	nosZ;AY325676;location.<1.663.;uncultured.bacterium.definition.putative.nitrous.oxide.reductase	4E-61
nosZ	M01935:46:000000000-AC602:1:1101:10554:6069 (LC230405)	0.16%	nosZ;EF644923;location.<1.660.;uncultured.bacterium.definition.putative.nitrous.oxide.reductase	2E-87
nosZ	M01935:46:000000000-AC602:1:1111:22540:13853 (LC230406)	0.13%	nosZ;FJ209375;location.<1.754.;uncultured.bacterium.definition.putative.nitrous.oxide.reductase	3E-74
nosZ	M01935:46:000000000-AC602:1:1114:7872:15369 (LC230407)	0.092%	nosZ;GU362715;location.<1.460.;uncultured.bacterium.definition.nitrous.oxide.reductase	4E-61
nosZ	M01935:46:000000000-AC602:1:1103:12820:19830 (LC230408)	0.075%	nosZ;HQ836615;location.<1.363.;uncultured.bacterium.definition.nitrous.oxide.reductase	5E-57
nosZ	M01935:46:000000000-AC602:1:1108:10820:24695 (LC230409)	0.057%	nosZ;EU083524;location.complement(<1.1093).;uncultured.bacterium.definition.nitrous.oxide.reductase	4E-95
nosZ	M01935:46:000000000-AC602:1:1102:9843:17147 (LC230410)	0.049%	nosZ;DQ238554;location.<1.646.;uncultured.bacterium.definition.nitrous.oxide.reductase	8E-41
nosZ	M01935:46:000000000-AC602:1:1111:14366:15330 (LC230411)	0.033%	nosZ;JF310511;location.<1.699.;uncultured.bacterium.definition.nitrous.oxide.reductase	2E-44
nosZ	M01935:46:000000000-AC602:1:1103:14963:7888 (LC256818)	0.029%	nosZ;FN859724;location.<1.700.;uncultured.bacterium.definition.nitrous.oxide.reductase	5E-88

norB	M01935:46:000000000-AC602:1:1101:18586:4510 (LC230412)	3.2%	norB;AP007255;location.complement(3147718..3149037).;Magnetospirillum.magneticum.AMB-1.definition.Nitric.oxide.reductase.large.subunit	1E-83
norB	M01935:46:000000000-AC602:1:1102:10116:18103 (LC230209)	3.1%	norB;CP000478;location.complement(3622744..3625020).;Syntrophobacter.fumaroxidans.MPOB.definition.cytochrome.b.subunit.of.nitric.oxide.reductase	1E-101
norB	M01935:46:000000000-AC602:1:1105:15356:2835 (LC230413)	0.79%	norB;HF936747;location.<1..>norB;453.;uncultured.bacterium.definition.nitric.oxide.reductase	7E-64
norB	M01935:46:000000000-AC602:1:1105:9854:23331 (LC230414)	0.48%	norB;AM284363;location.<1..>norB;432.;Paracoccus.sp..R-28245.definition.nitric.oxide.reductase.CnorB	0
norB	M01935:46:000000000-AC602:1:1105:22748:10730 (LC230415)	0.32%	norB;CP002083;location.611075..612424.;Hyphomicrobium.denitrificans.ATCC.51888.definition.Nitric-oxide.reductase	2E-64
norB	M01935:46:000000000-AC602:1:1103:13425:11348 (LC230416)	0.32%	norB;JQ480611;location.<1..>norB;342.;Bosea.sp..AR3.definition.nitric.oxide.reductase	4E-161
norB	M01935:46:000000000-AC602:1:1109:18593:3458 (LC230210)	0.30%	norB;HQ615190;location.<1..>norB;640.;uncultured.bacterium.definition.putative.nitric.oxide.reductase	3E-25
norB	M01935:46:000000000-AC602:1:1114:26962:18991 (LC230417)	0.29%	norB;AJ132911;location.769..2115.;Bradyrhizobium.japonicum.definition.nitric.oxide.reductase.subunit.B	3E-137
norB	M01935:46:000000000-AC602:1:1111:7212:9580 (LC230418)	0.27%	norB;AP007255;location.complement(3147718..3149037).;Magnetospirillum.magneticum.AMB-1.definition.Nitric.oxide.reductase.large.subunit	8E-73
norB	M01935:46:000000000-AC602:1:1103:7386:8150 (LC230419)	0.25%	norB;AFER01000001;location.complement(1455544..1456884).;Rhodobacter.sphaeroides.WS8N.definition.nitric-oxide.reductase.subu	7E-67

			nit.B	
norB	M01935:46:000000000-AC602:1:1109:20760:11693 (LC230420)	0.25%	norB;ACYY01000001;location.complement(156706..158070).;Rhodobacter.sp..SW2.definition.Nitric-oxide.reductase	3E-78
norB	M01935:46:000000000-AC602:1:1103:8005:13370 (LC230421)	0.24%	norB;CU459003;location.1460427..1461764.;Magnetospirillum.gryphiswaldense.MSR-1.definition.Nitric-oxide.reductase.subunit.B	2E-51
norB	M01935:46:000000000-AC602:1:1105:21789:14751 (LC256819)	0.19%	norB;HF936749;location.<1..>norB;455.;uncultured.bacterium.definition.putative.nitric.oxide.reductase	1E-52
norB	M01935:46:000000000-AC602:1:1104:6502:3578 (LC230422)	0.18%	norB;CP001280;location.1637157..1638512.;Methylocella.silvestris.BL2.definition.Nitric-oxide.reductase	3E-57
norB	M01935:46:000000000-AC602:1:1104:19278:19332 (LC230423)	0.16%	norB;AM284362;location.<1..>norB;419.;Paracoccus.sp..R-28244.definition.nitric.oxide.reductase.CnorB	5E-148
norB	M01935:46:000000000-AC602:1:1111:5549:19887 (LC230424)	0.11%	norB;AM284340;location.<1..>norB;435.;Rhizobium.sp..R-24658.definition.nitric.oxide.reductase.CnorB	1E-148
norB	M01935:46:000000000-AC602:1:1105:19012:3089 (LC230425)	0.098%	norB;CU459003;location.1460427..1461764.;Magnetospirillum.gryphiswaldense.MSR-1.definition.Nitric-oxide.reductase.subunit.B	4E-65
norB	M01935:46:000000000-AC602:1:1106:23904:23963 (LC230426)	0.095%	norB;CP002568;location.610943..612313.;Polymorphum.gilvum.SL003B-26A1.definition.Nitric.oxide.reductase..large.subunit	1E-34
norB	M01935:46:000000000-AC602:1:1106:23192:14439 (LC230211)	0.087%	norB;HQ615174;location.<1..>norB;640.;uncultured.bacterium.definition.putative.nitric.oxide.reductase	1E-21
norB	M01935:46:000000000-AC602:1:1103:14543:16054 (LC230427)	0.079%	norB;CP000830;location.3347463..3348842.;Dinoroseobacter.shibae.DFL.12...DSM.16493.definition.nitric.oxide.reductase.subunit.B	3E-84

norB	M01935:46:000000000-AC602:1:1104:16255:23311 (LC230212)	0.054%	norB;AFUR01000001;location.complement(1629221..1631563).;Actinomyces.sp..oral.taxon.175.str..F0384.definition.putative.nitric.oxide.reductase..NorZ	1E-14
norB	M01935:46:000000000-AC602:1:1106:12993:20326 (LC230428)	0.044%	norB;CU459003;location.1460427..1461764.;Magnetospirillum.gryphiswaldense.MSR-1.definition.Nitric-oxide.reductase.subunit.B	1E-65
norB	M01935:46:000000000-AC602:1:1113:6087:11288 (LC230429)	0.029%	norB;CP000032;location.complement(237713..239080).;Ruegeria.pomeroyi.DSS-3.definition.nitric.oxide.reductase..large.subunit	4E-87
norB	M01935:46:000000000-AC602:1:1106:14975:7626 (LC230213)	0.013%	norB;AKCV01000022;location.complement(196457..198748).;Ralstonia.sp..PBA.definition.nitric.oxide.reductase.-like.protein	3E-28
norB	M01935:46:000000000-AC602:1:1114:14906:13531 (LC230430)	0.007%	norB;FQ311871;location.complement(85091..86440).;Azospirillum.lipoferum.4B.definition.Nitric.oxide.reductase.(NOR)..large.subunit	1E-89
norB	M01935:46:000000000-AC602:1:1114:11798:15260 (LC230431)	0.003%	norB;HE616890;location.1000304..1001650.;Sinorhizobium.fredii.HH103.definition.cytochrome.c.oxidase..subunit.I	2E-91
norB	M01935:46:000000000-AC602:1:1103:12143:7193 (LC230432)	0.002%	norB;CU459003;location.1460427..1461764.;Magnetospirillum.gryphiswaldense.MSR-1.definition.Nitric-oxide.reductase.subunit.B	1E-89

Table S5. Shannon (*H*') and inverse Simpson (1/*D*) indices calculated for each the N cycle functional genes found in anaerobic granular sludge (UASB-L and UASB-M) samples. ND; gene not detected.

	UASB-L		UASB-M	
	H'	1/*D*	*H*'	1/*D*
nxrB	0.36	1.26	ND	ND
nirK	1.85	9.64	3.07	16.5
nirS	1.24	8.65	1.79	4.15
nifH	2.91	9.95	2.56	8.23
nrfA	2.16	6.28	1.30	2.97
napA	2.90	13.8	2.19	5.53
nosZ	2.64	11.6	1.95	5.25
norB	2.08	4.95	2.28	5.60
narG	0.53	1.54	ND	ND

Table S6. Correlations between transcript quantities measured by the NiCE chip and those measured by conventional qPCR. Numbers shown below each target gene indicate assay ID used in Fig. 2.

Test methods	*nirS*		*cnorB*		*amoA*		*nirK*		*nosZ* clade I	
	25		26		3		24		30	
Pearson's product-moment correlation	0.88	***	0.79	***	0.38	*	0.13	ns	0.81	***
Spearman's rank correlation	0.83	***	0.80	***	0.49	**	0.23	ns	0.85	***
Kendall's rank correlation	0.69	***	0.64	***	0.36	**	0.16	ns	0.66	***

p values: *, <0.05; **, <0.01; ***, <0.001; ns, not significant (>0.05)