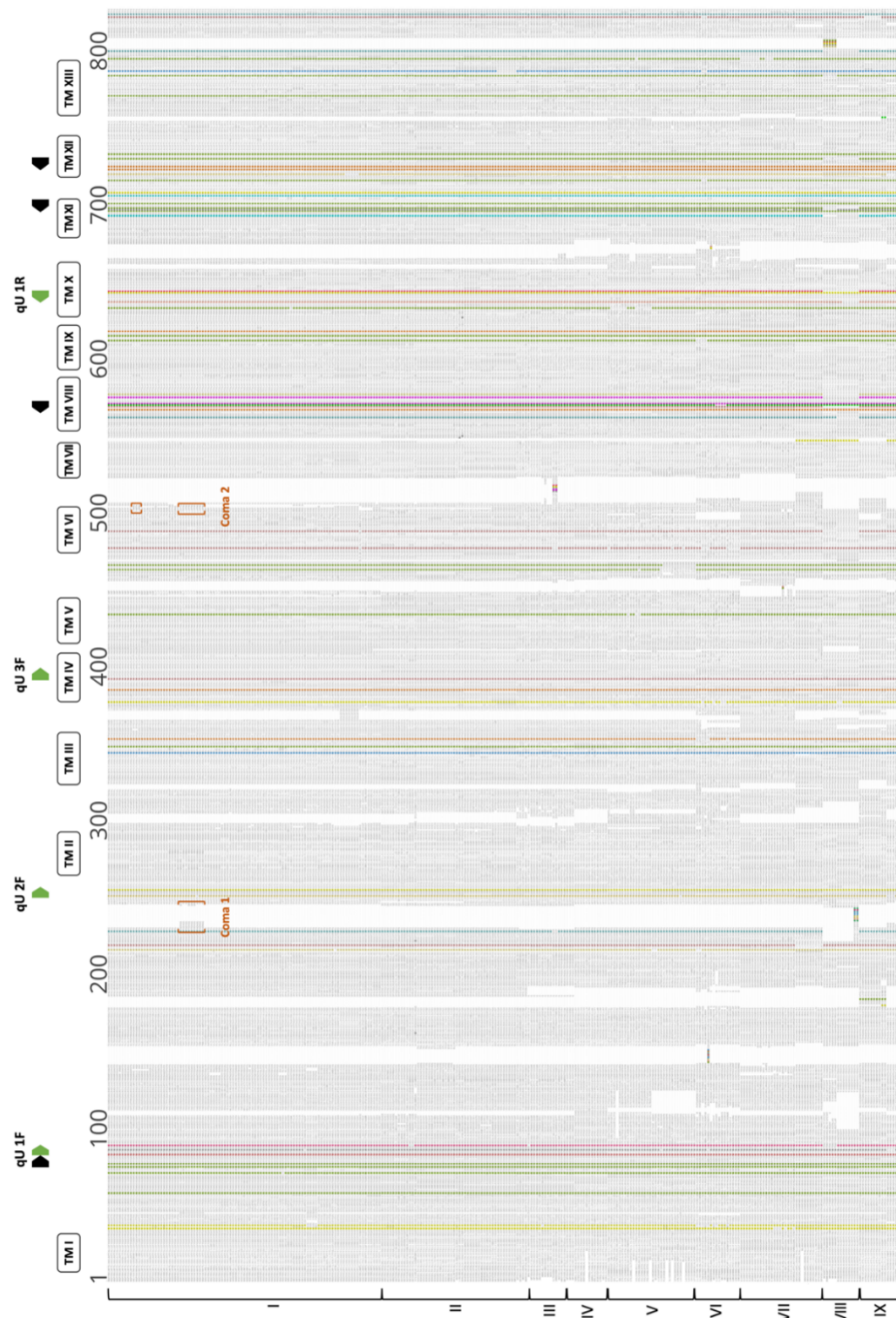
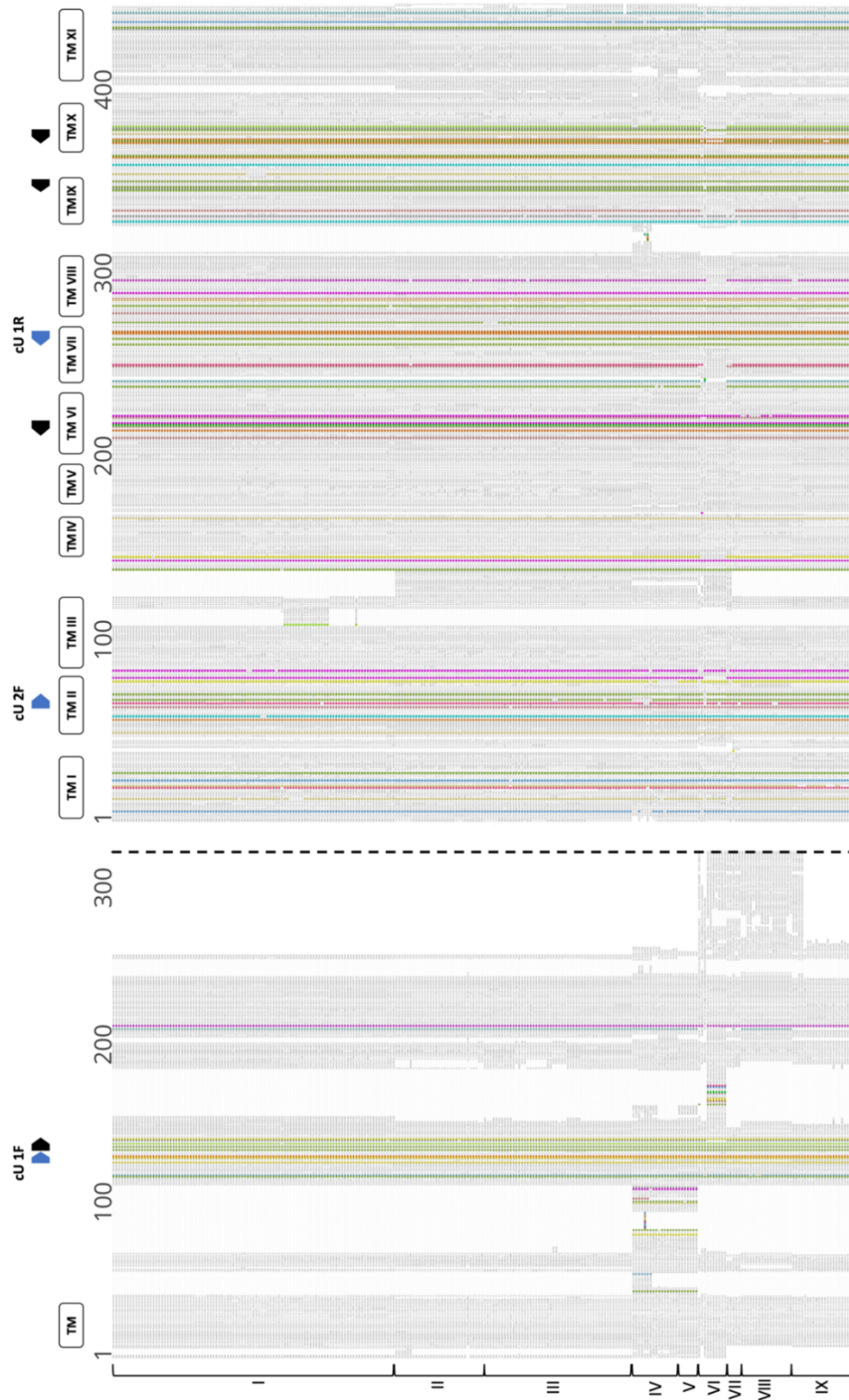


## Supporting Materials



**Fig. S1 Amino acid sequence alignment of 289 QNOR.** The colored amino acid positions represent 95% conserved amino acids across all 289 QNOR sequences. Primers for *qnor* + *cnor* and *qnor* are shown in black and green. Corresponding *qnor* clades and transmembrane domain assignments are shown on the left and top, respectively.



**Fig. S2 Amino acid sequence alignment of 259 CNORC and CNORB.** The colored amino acid positions represent 95% conserved amino acids across all 259 CNORC and CNORB sequences. Primers for *qnor* + *cnor* and *cnor* are shown in black and blue. Corresponding *cnor* clades and transmembrane domain assignments are shown on the left and top, respectively.

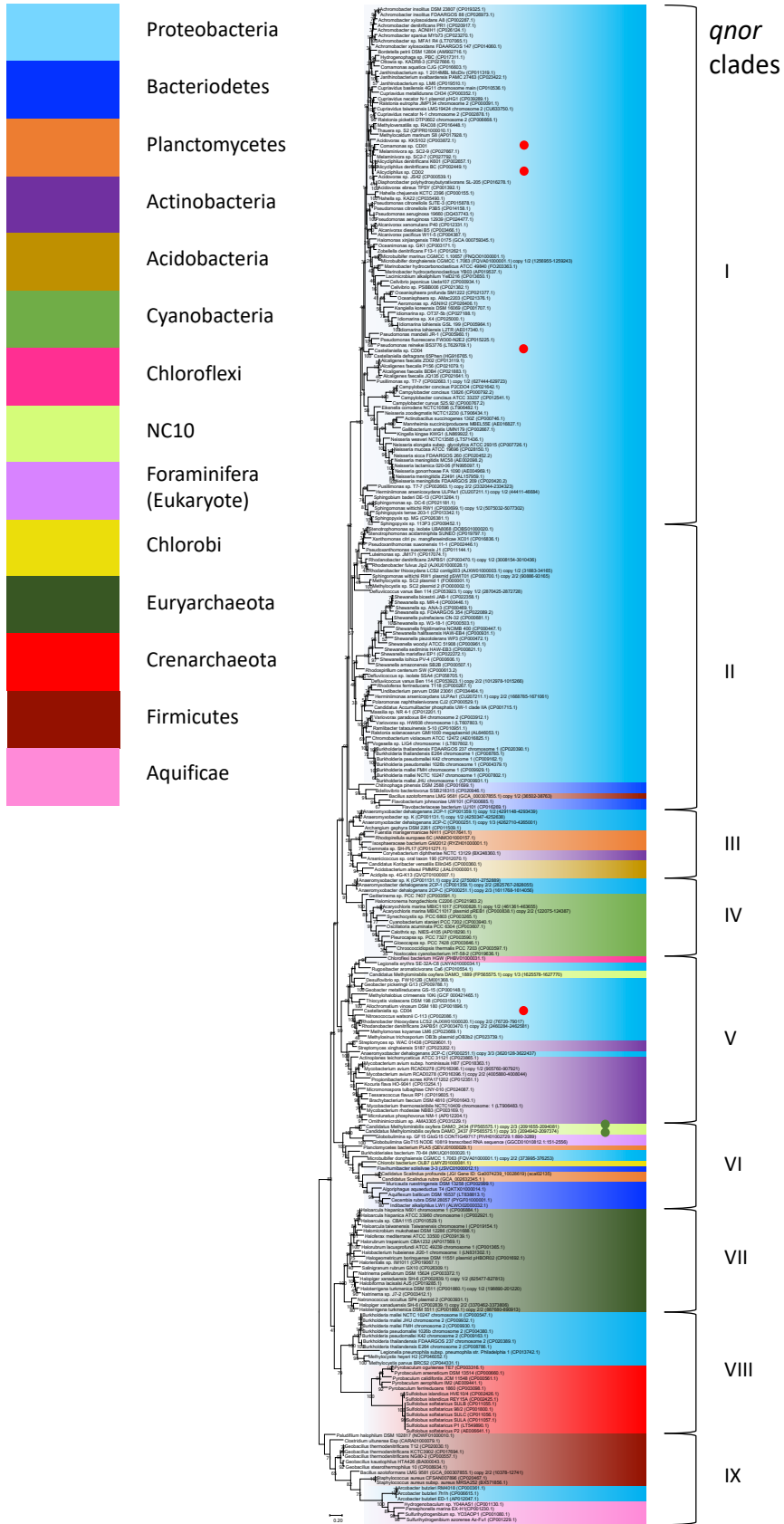


Fig. S3 Phylogenetic tree of 289 *qnor* using the maximum likelihood method.

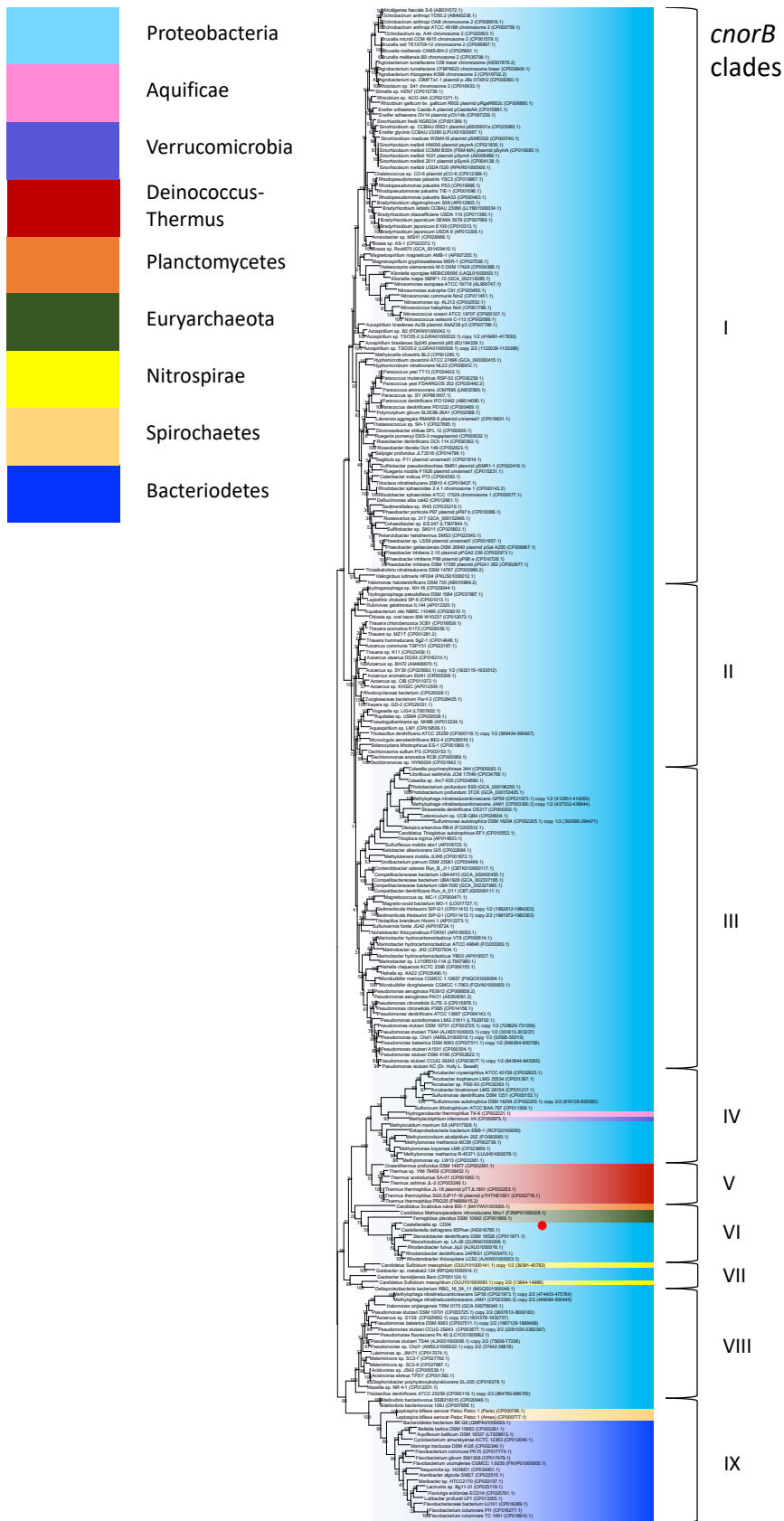
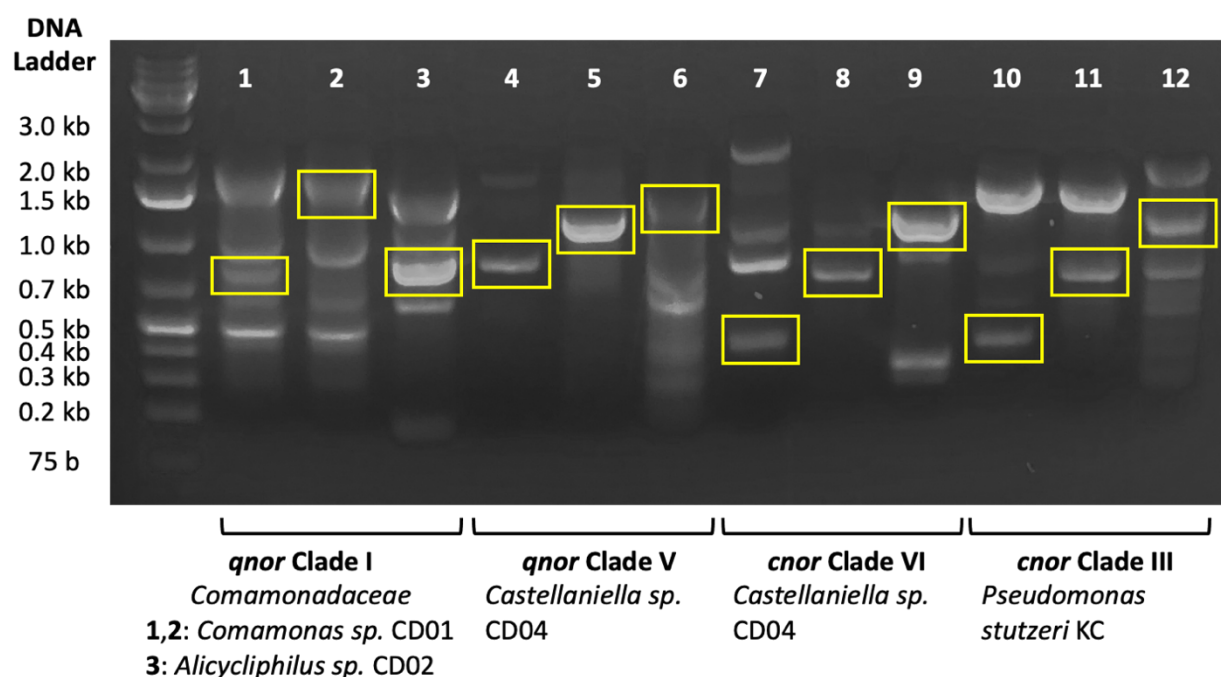


Fig. S4 Phylogenetic tree of 259 *cnorB* using the maximum likelihood method.



**Fig. S5 Primer testing results with a DNA ladder (O'GeneRuler 1 kb Plus DNA Ladder, Thermo Scientific™, MA, USA).** The following Clade-specific or *nor*-universal primers were used for 12 PCR; 1: qU 2F (Clade I) + qcU 1R, 2: qU 2F (Clade I) + qcU 3R, 3: qU 2F (Clade I) + qS Coma R, 4: qU 2F (Clade V) + qcU 1R, 5: qU 2F (Clade V) + qcU 2R, 6: qcU 1F + qU 1R (Clade V), 7: cU 2F (Clade VI) + qcU 1R, 8: cU 2F (Clade VI) + qcU 2R, 9: qcU 1F + cU 1R (Clade VI), 10: cU 2F (Clade III) + qcU 1R, 11: cU 2F (Clade III) + qcU 2R, 12: qcU 1F + cU 1R (Clade III).

**Table S1 Conserved amino acids and primer sets for *qnor* (*qnor*-universal, qU) designed in this study.** See Table 1 for key to amino acids.

Primer name	Primer direction	Primer sequence (5'-3')	Amino acid number	Nucleotide sequence (5'-3')	Amino acid type	Amino acid (%)
qU 1F	Forward	GAYTDBWSNGCNGANKVNYT	1	GAY	D	100
			2	TDB	W	62.6
					Y	22.1
			3	WSN	T	75.8
					S	20.4
			4	GCN	A	97.6
			5	GAN	D	70.9
					E	16.6
			6	KVN	W	57.4
				A	16.3	

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					Y	11.4
			7	YT	L	97.2
qU 2F	Forward	TAYACNAAYAAAYTKBCCNYAN	1	TAY	Y	92.0
			2	ACN	T	98.3
			3	AAAY	N	74.7
			4	AAAY	N	88.6
			5	TKB	W	87.2
					F	12.8
			6	CCN	P	100
			7	YAN	H	49.8
					Y	27.3
qU 3F	Forward	ATHGCNACNGSNTKBBTN	1	ATH	I	88.6
			2	GCN	A	89.3
			3	ACN	T	74.7
			4	GSN	A	36.0
					G	33.9
			5	TKB	W	54.7
					F	39.8
			6	BTN	L	80.6
					V	10.4
qU 1R	Reverse	ARNGGNANNACYTCNARNGYNSW	1	WSN	S	97.9
			2	RCN	A	76.5
					T	13.8
			3	YTN	L	87.2
			4	GAR	E	94.5
			5	GTN	V	89.6
			6	NTN	V	75.4
					I	13.5
					L	10.0
			7	CCN	P	100
			8	YT	L	95.5

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**Table S2 Conserved amino acids and primer sets for *cnor* (*cnor*-universal, cU) designed in this study. See Table 1 for key to amino acids.**

Primer name	Primer direction	Primer sequence (5'-3')	Amino acid number	Nucleotide sequence (5'-3')	Amino acid type	Amino acid (%)			
cU 1F	Forward	TGYRTNRANTGYCAYWSNHT	1	TGY	C	99.6			
			2	RTN	I	61.0			
					M	19.7			
					V	12.0			
			3	RAN	N	47.9			
					G	43.6			
			4	TGY	C	99.6			
			5	CAY	H	99.6			
			6	WSN	T	80.7			
					S	17.8			
			7	HT	L	72.6			
					I	25.9			
			cU 2F	Forward	YTNYTNHYNGGNTTYWTB	1	YTN	L	81.1
						2	YTN	L	96.9
3	HYN	F				32.4			
		L				19.3			
		M				17.0			
		T				11.6			
4	GGN	G				95.8			
5	TTY	F				93.4			
6	WTB	M				70.7			
		F				21.2			
cU 1R	Reverse	RTGRTGNSCNGTNCNADNAD				1	HTN	I	79.2
								L	15.1
			2	HTN	L	68.3			
					I	28.2			
			3	GGN	G	100			
			4	ACN	T	85.7			
			5	GSN	G	90.0			
					A	10.0			
			6	CAY	H	100			
			7	CAY	H	100			

**Table S3** A reverse primer specific for *Comamonadaceae*. Degeneracies were added to wobble positions as per the IUPAC code: R = A or G; Y = C or T; S = G or C; W = A or T; K = G or T; M = A or C; B = C or G or T; D = A or G or T; H = A or C or T; V = A or C or G.

Primer name	Reverse primer sequence (5'-3') in the Coma-specific region 2	Nucleotide sequence for <i>Comamonadaceae</i> family in the Coma-specific regions 2
qnor Coma-specific	VYYRBTGSGVBYSARCAG	CTGYTSRVBCSCAVYRRB

**Table S4** Nucleotide sequences of *Comamonadaceae* microorganisms in the Coma-specific region 2.

Microorganism name	Nucleotide sequence (5'-3') in the Coma-specific region 2
<i>Hydrogenophaga</i> sp. PBC	CTGTTGCGCGCAACGGG
<i>Ottowia</i> sp. KADR8-3	CTGTTGCCCCGCACCAAG
<i>Comamonas aquatica</i> CJG	CTGCTGGCCCCGCAATGGT
<i>Comamonas</i> sp. CD01	CTGCTCAAGCCCAGCGGC
<i>Melaminivora</i> sp. SC2-9	CTGTTCAAGCCCCAACGGC
<i>Melaminivora</i> sp. SC2-7	CTGCTGGCCCCCAACGGC
<i>Alicyclophilus denitrificans</i> K601	CTGCTGGCCCCCAACGGC
<i>Alicyclophilus denitrificans</i> BC	CTGCTGGCCCCCAACGGC
<i>Alicyclophilus</i> sp. CD02	CTGCTGGCCCCCAACGGC
<i>Diaphorobacter polyhydroxybutyratorans</i> SL-205	CTGCTGGCTCCCAACGGC
<i>Acidovorax ebreus</i> TPSY	CTGCTGGCCCCCAACGGC

**Table S5** *nod*-specific primers were designed using the *nor*-universal primers (qcU). Primer sequences were based on two *nod* sequences from *Candidatus Methyloirabilis oxyfera* DAMO2434 and DAMO2437. Reduction in nucleotide numbers in *nod* primers compared to the *nor*-universal primers is due to GC content considerations. See Table S3 for key to the IUPAC code of degeneracies.

Primer name	Primer direction	Primer sequence (5'-3')	Amino acid number	Sequence for DAMO 2434 and DAMO 2437 (5'-3')	Nucleotide sequence of DAMO 2434	Nucleotide sequence of DAMO 2437
nod qcU 1F	Forward	GGWGACGGCGSWGARCGC	1	GGW	GGA	GGT
			2	GAC	GAC	GAC
			3	GGC	GGC	GGC
			4	GSW	GGT	GCA
			5	GAR	GAA	GAG
			6	CGC	CGC	CGC
nod qcU 1R	Reverse	ACCTCAACCCACATGTGAATGTT	1	AAC	AAC	AAC
			2	ATT	ATT	ATT
			3	CAC	CAC	CAC
			4	ATG	ATG	ATG
			5	TGG	TGG	TGG
			6	GTT	GTT	GTT
			7	GAG	GAG	GAG
			8	GT	GT	GT
nod qcU 2R	Reverse	CGAGCCSAWGACACCCSGCRCC	1	GGY	GGC	GGT
			2	GCS	GCG	GCC
			3	GGT	GGT	GGT
			4	GTC	GTC	GTC
			5	WTS	TTC	ATG
			6	GGC	GGC	GGC
			7	TCG	TCG	TCG
nod qcU 3R	Reverse	AACATGGCGSCATGGGCATG	1	CAT	CAT	CAT
			2	GCC	GCC	GCC
			3	CAT	CAT	CAT
			4	GSC	GCC	GGC
			5	GCC	GCC	GCC
			6	ATG	ATG	ATG
			7	TT	TT	TT

**Table S6 Examples of *qnor* Clade-specific primers.** Primers for each Clade were designed based on a representative strain in that Clade using qU2F and qU1R.

Position	Clade-specific primers	Primer sequence
qU2F	<i>qnor</i> Clade I ( <i>Comamonas</i> sp. CD01)	TAC ACC AAC AAC TGG CCG CA
	<i>qnor</i> Clade II ( <i>Defluviicoccus</i> sp. SSA4)	TAC ACC ATG AAC TGG CCG CA
	<i>qnor</i> Clade III ( <i>Gemmata</i> sp. SH-PL17)	TAC ACC CAC AAC TGG CCG TA
	<i>qnor</i> Clade IV ( <i>Synechocystis</i> sp. PCC 6803)	TAT ACA GCC AAC TGG CCC CA
	<i>qnor</i> Clade V ( <i>Castellaniella</i> sp. CD04)	TAC ACC AAC AAC TTC CCC TA
	<i>qnor</i> Clade VI ( <i>Flavihumibacter solisilvae</i> 3-3)	TAT ACG CAC AAC TGG CCC TA
	<i>qnor</i> Clade VII ( <i>Haloferax mediterranei</i> ATCC 33500)	TAC ACG AAC GAC TGG CCG TA
	<i>qnor</i> Clade VIII ( <i>Pyrobaculum aerophilum</i> IM2)	TAC ATG CCT GGC ATT CT
	<i>qnor</i> Clade IX ( <i>Geobacillus stearothermophilus</i> 10)	TAC ACC AAC AAC TGG CCG TA
qU1R	<i>qnor</i> Clade I ( <i>Comamonas</i> sp. CD01)	AGC GGC ACC ACT TCC AGC GCG CT
	<i>qnor</i> Clade II ( <i>Defluviicoccus</i> sp. SSA4)	AGC GGC ACC ACT TCC AGC GCC GA
	<i>qnor</i> Clade III ( <i>Gemmata</i> sp. SH-PL17)	AGC GGC ACG ACC TCC AGG GCG CT
	<i>qnor</i> Clade IV ( <i>Synechocystis</i> sp. PCC 6803)	AAA GGA ACC ACT TCC AGA GCG GA
	<i>qnor</i> Clade V ( <i>Castellaniella</i> sp. CD04)	AGC GGG ACG ACT TCA AGC ACC GA
	<i>qnor</i> Clade VI ( <i>Flavihumibacter solisilvae</i> 3-3)	AAC GGG ATA ACC TGC AAA GTC GA
	<i>qnor</i> Clade VII ( <i>Haloferax mediterranei</i> ATCC 33500)	AGC GGG ATG AGT TCG AGC GTC GA
	<i>qnor</i> Clade VIII ( <i>Pyrobaculum aerophilum</i> IM2)	ATT GGG AGC ACT TCT AAA GTG GA
	<i>qnor</i> Clade IX ( <i>Geobacillus stearothermophilus</i> 10)	AGT GGA ATT ACT TCT AAT GCT GA

**Table S7 Examples of *cnor* Clade-specific primers.** Primers for each Clade were designed based on a representative strain in that Clade using cU2F and of cU1R.

Position	Clade-specific primers	Primer sequence
cU2F	<i>cnor</i> Clade I ( <i>Paracoccus denitrificans</i> PD1222)	CTG CTC CTG GGC TTT TTC
	<i>cnor</i> Clade II ( <i>Thauera chlorobenzoica</i> 3CB1)	CTG CTG TTC GGC TTC ATG
	<i>cnor</i> Clade III ( <i>Pseudomonas stutzeri</i> KC)	CTG CTG TTT GGC TTC ATG
	<i>cnor</i> Clade IV ( <i>Methylobacterium methanica</i> MC09)	ATG TTG TAT GGC TTT ATC
	<i>cnor</i> Clade V ( <i>Thermus thermophilus</i> PRQ25)	CTCCTTTTGGGCTTCATG
	<i>cnor</i> Clade VI ( <i>Castellaniella</i> sp. CD04)	ATT CTC TGC GGC TTC ATT
	<i>cnor</i> Clade VII ( <i>Geobacter</i> sp. metabat2.124)	CTT CTC TCC GGC TTC ATG
	<i>cnor</i> Clade VIII ( <i>Pseudomonas fluorescens</i> Ps 40)	GTA CTG ACC GGC TTC ATG
	<i>cnor</i> Clade IX ( <i>Flavobacterium gilvum</i> EM1308)	TTG TTG ACC GGT TTT ATG
cU1R	<i>cnor</i> Clade I ( <i>Paracoccus denitrificans</i> PD1222)	ATG GTG CCC GGT GCC CAG GAT
	<i>cnor</i> Clade II ( <i>Thauera chlorobenzoica</i> 3CB1)	GTG GTG ACC GGT ACC GAT CAG
	<i>cnor</i> Clade III ( <i>Pseudomonas stutzeri</i> KC)	GTG GTG ACC CGT ACC GAT GAT
	<i>cnor</i> Clade IV ( <i>Methylobacterium methanica</i> MC09)	ATG ATG TCC CAG CCC TAA AAT
	<i>cnor</i> Clade V ( <i>Thermus thermophilus</i> PRQ25)	GTG GTG GCC GAG GCC CAG GAT
	<i>cnor</i> Clade VI ( <i>Castellaniella</i> sp. CD04)	GTG GTG GGC GTT GCC GAT GAG

<i>cnor</i> Clade VII ( <i>Geobacter</i> sp. metabat2.124)	GTG GTG ACC GGT GCC GAG TAT
<i>cnor</i> Clade VIII ( <i>Pseudomonas fluorescens</i> Ps 40)	GTG GTG CGC GGT ACC GAT AAT
<i>cnor</i> Clade IX ( <i>Flavobacterium gilvum</i> EM1308)	ATG GTG TCC TGT TCC CAA AAC

**Table S8** Overlapping regions between *nor*-universal primers and pre-existing primers. For the pre-existing primers, qnorB5R, qnorB7R, cnorB6R, and cnorB7R are from (Braker and Tiedje, 2003), cnorB3 Reverse and cnorB6 Reverse from (Casciotti and Ward, 2005), and nod 2015R from (Zhu et al., 2017). The overlapping nucleotides are in bold and underlined.

<i>nor</i> -universal primers in this study	Pre-existing primers	Overlapping nucleotide
qcU1R CCYTCNACCCANARRTGNAYNAY	qnorB5R	<u>ACCCANAGRTGNACNACCCACCA</u>
	cnorB3 Reverse	<u>CCYTCVACCCAGASATGCAC</u>
qcU2R RAANCCNMRNANNCCNGCNCC	qnorB7R	GGNTTCDTGAT <u>DAARCCNCC</u>
	cnorB6R	<u>GAANCCCCANACNCCNGC</u>
	cnorB6 Reverse	TGCAK <u>SARRCCCCABACBCC</u>
qcU3R CCVHWNADNGCNVNRTGNSCRTG	cnorB7R	<u>TGNCCRTG</u> NGCNGCNGT
	nod 2015R	ATGTTACCYTTKAC <u>ACCGAAC</u>

#### Text S1 Phylogeny of *qnor* and *nod*

Clade I of *qnor* contains three *qnor* genes from the N<sub>2</sub>O-producing CANDO isolates (*Comamonas* sp. CD01, *Alicycliphilus* sp. CD02, and *Castellaniella* sp. CD04 - WP\_066454372.1) and multiple heterotrophic denitrifying bacteria within the families *Burkholderiaceae* (*Ralstonia*, *Cupriavidus*), *Comamonadaceae* (*Comamonas*, *Alicycliphilus*, *Acidovorax*, *Diaphorobacter*, *Ottowia*, *Hydrogenophaga*, *Melaminivora*) and *Alcaligenaceae* (*Bordetella*, *Achromobacter*, *Castellaniella*, *Alcaligenes*). Possibly pathogenic *Neisseria* strains are also present in Clade I.

Clade II of *qnor* consists of *qnor* genes from *Xanthomonadaceae* (*Xanthomonas*, *Pseudoxanthomonas*, *Stenotrophomonas*), *Shewanella*, and *Burkholderia*. Clade II also contains sequences from *Comamonadaceae* (*Rhodoferrax*, *Polaromonas*, *Variovorax*, *Ramlibacter*) that differ from those of Clade I *Comamonadaceae*. Clade II also includes two *qnor* genes from two separate plasmids within an  $\alpha$ -proteobacterial methanotroph (*Methylocystis* sp. SC2) and one *qnor* gene from a phosphate-accumulating organism (*Candidatus Accumulibacter phosphatis* UW-1

clade IIA). Clade II also contains four *qnor* genes from *Bacterioidetes* (*Chitinophaga*, *Bdellovibrio*, *Flavobacterium*, *Flavobacteriaceae*), and one of two *qnor* genes detected in *Bacillus azotoformans* LMG 9581 (*Firmicutes*).

Clade III contains three *qnor* genes from *Actinobacteria* (*Archangium*, *Corynebacterium* and *Arsenicococcus*), four from *Planctomycetes* (*Fuerstia*, *Rhodopirellula*, *Isosphaeraceae* and *Gemmata*), and three from *Acidobacteria* (*Koribacter*, *Acidobacterium*, *Acidipila*), including the first copy of *qnor* from *Anaeromyxobacter dehalogenans* 2CP-C.

Clade IV contains a second copy of *qnor* from *Anaeromyxobacter dehalogenans* 2CP-C and *qnor* from Cyanobacterial strains (*Geitlerinema*, *Chroococciopsis*, *Nostocales*, *Pleurocapsa*, *Acaryochloris*, *Synechocystis*, *Arthrospira*, *Cyanobacterium*, *Fischerella*, *Gloeocapsa*, *Oscillatoria*, *Halomicronema*, *Calothrix*).

Clade V contains mostly Actinobacterial *qnor* genes in *Streptomyces*, *Actinoplanes*, *Mycobacterium*, *Propionibacterium*, *Kocuria*, *Micromonospora*, *Tessaracoccus*, *Brachybacterium*, *Microtholunatus*, and *Ornithinimicrobium* with a second copy of *qnor* in *Castellaniella* sp. CD04 (WP\_084386783.1) and a third copy in *Anaeromyxobacter dehalogenans* 2CP-C. Clade V also includes *qnor* genes from numerous *Geobacter* strains, an  $\alpha$ -proteobacterium (Type II) methanotroph (*Methylosinus trichosporium* OB3b), a  $\gamma$ -proteobacterium (Type I) halophilic methanotroph (*Methylohalobius crimeensis* 10Ki), two purple sulfur bacterial strains (*Thiocystis*, *Allochromatium*) and *qnor* genes in *Candidatus Methyloirabilis oxyfera* (DAMO1889), *Chloroflexi*, *Legionella*, and *Rugosibacter*.

Clade VI contains *qnor* from *Bacterioidetes* strains (*Flaviumibacter*, *Muricauda*, *Algoriphagus*, *Cecembia*, *Indibacter*, *Aquiflexum*) and two anammox strains (*Candidatus Scalindua profunda* and *Candidatus Scalindua rubra*). It also contains two *nod* genes in *Candidatus Methyloirabilis oxyfera* (DAMO2434 and DAMO2437) adjacent to *qnor* from *Foraminifera*.

Clade VII contains mostly halophilic *Euryarchaeota* (*Haloarcula*, *Halorubrum*, *Halogeometricum*, *Halobacterium*, *Salinigranum*, *Halorientalis*, *Natrinema*, *Haloterrigena*, *Halopiger*, *Halobiforma*, *Natronococcus*, and *Haloterrigena*). Clade VIII contains *qnor* genes in *Creanarchaeota* (*Sulfolobus* and *Pyrobaculum*). One Crenarchaeal strain, *Sulfolobus solfataricus* P2, has an extraordinarily lengthy *qnor* sequence (AE006641.1) due to the extra amino acids in the N-terminal region of qNOR. Clade VIII also has second copies of *qnor* from numerous *Burkholderia* strains and *qnor* from two *Methylocystis* strains, both  $\alpha$ -proteobacteria methanotrophs.

Clade IX contains *qnor* genes from extremophiles such as *Aquificae* (*Hydrogenobaculum*, *Persephonella*, *Sulfurihydrogenibium*) and Gram-positive *Firmicutes* (*Geobacillus*, *Bacillus*, *Staphylococcus*, *Paludifilum*) with multiple Proteobacterial *Arcobacter* strains. Clade IX includes *Bacillus azotoformans* LMG 9581 with a second copy of *qnor*.

## Text S2 Phylogeny of *cnor*

Clade I of the *cnor* tree contains many rhizosphere  $\alpha$ -proteobacteria or plant pathogens within the *Rhizobiales* order such as *Ochrobactrum*, *Rhizobium*, *Sinorhizobium*, *Bradyrhizobium*, *Shinella*, *Ensifer*, *Bosea*, *Aminobacter*, *Agrobacterium*, *Hyphomicrobium*, *Breoghania*, *Cohaesibacter*, and *Rhodopseudomonas*. Clade I also contains multiple strains in the *Rhodospirillales* order, such as the *Rhodospirillaceae* family (*Azospirillum* and *Magnetospirillum*, *Thalassospira*) and the *Rhodobacteraceae* family (*Paracoccus*, *Thalassococcus*, *Dinoroseobacter*, *Labrenzia*, *Ruegeria*, *Roseobacter*, *Roseobacter*, *Thiobacimonas*, *Salipiger*, *Sagittula*, *Sulfitobacter*, *Leisingera*, *Celeribacter*, *Thioclava*, *Defluviimonas*, *Sulfitobacter*, *Sedimentitalea*, *Roseovaris*, *Antarctobacter*, *Phaeobacter*). Also included within *cnor* Clade I are Ammonia-oxidizing bacteria such as *Nitrosomonas* and *Nitrosococcus* strains and halophiles (*Thioalkalivibrio*, *Halioglobus*, *Halomonas*).

Clade II contains *Thauera* and *Azoarcus* strains within the *Zoogloeaceae* family and some strains within the *Comamonadaceae* family (*Hydrogenophaga*, *Leptothrix*, *Aquabacterium*, *Ottowia*). Clade II *cnor* is also found within the orders *Neisseriales* (*Vogesella*, *Aquitalea*, *Pseudogulbenkiania*, *Aquaspirillum*, *Microvirgula*, *Sideroxydans*) and *Rhodocyclales* (*Dechlorosoma*, *Dechloromonas*).

Clade III contains *cnor* from glycogen-accumulating organisms (GAOs), such as *Contendobacter* and *Competibacter*, and multiple *Pseudomonas* strains, such as *P. stutzeri* KC, and other  $\gamma$ -proteobacteria.

Clade IV contains *Verrucomicrobia* (*Methylacidiphilum infernorum* V4), *Aquificae* (*Hydrogenobacter thermophilus* TK-6) and proteobacterial strains, such as  $\gamma$ -proteobacteria methanotrophs (*Methylomonas*, *Methylomicrobium* and *Methylocaldum*), sulfur-oxidizing bacteria (*Sulfurovum* and *Sulfurimonas*), and potential animal pathogens (*Arcobacter*).

Clade V contains *Deinococcus-Thermus* strains (*Thermus* and *Oceanithermus*). Clade VI contains *cnor* genes from *Castellaniella* and *Rhodanobacter* that also harbor *qnor*. *Candidatus Scalindua rubra*, an anammox *Plantomycetes* strain in *qnor* Clade VI, also possesses a Clade VI *cnor*. *Euryarchaeota* strains (*Ferroglobus*, *Candidatus Methanoperedens nitroreducens*) also cluster in Clade VI.

Clade VII has two copies of *cnor* from *Candidatus Sulfohobium mesophilum* (*Nitrospirae*), two *cnor* from two *Geobacter* strains and one from *Deltaproteobacteria* bacterium RBG\_16\_54\_11. Clade VIII contains  $\beta$ -proteobacteria that harbor both *qnor* and *cnor* such as *Halomonas*, *Luteimonas*, *Massilia*, *Acidovorax*, *Melaminivora*, and *Diaphorobacter*. Most *Pseudomonas* strains in Clade VIII have an additional copy of *cnor* in Clade III. The majority of Clade IX comprises *Bacteroidetes* strains (*Belliella*, *Aquiflexum*, *Cyclobacterium*, *Marivirga*, *Flavobacterium*, *Aequorivita*, *Arenibacter*, *Maribacter*, *Lacinutrix*, *Flavivirga*, *Lutibacter*) with two *cnor* from two *Spirochaetes* strains.

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