

Supplemental Table S1. Summary of primers used to detect denitrification functional genes.

Primer <sup>a</sup>	Primer sequence (5'-3')	Organism <sup>b</sup>	Size of the PCR fragment (bp)	Annealing temperature (°C)	Reference
<i>napA</i> -F1	CTGGACIATGGGYTTIAACCA	<i>Escherichia coli</i> O6	492	52°C	46
<i>napA</i> -R1	CCTTCYTTYTCIACCCACAT				
<i>narG</i> -F1	ACICAYGGIGTIAACTGYAC	<i>Pseudomonas stutzeri</i> ATCC 17588	523	52°C	46
<i>narG</i> -R1	TCGSMRTACCAGTCRTARAA				
<i>nirS</i> 1F	CCTAYTGCCGCCRCART	<i>Pseudomonas aeruginosa</i> ATCC 27853	890	Touchdown 56-51°C	28
<i>nirS</i> 6R	CGTTGAACTTRCCGGT				
<i>nirK</i> F	TCATGGTCCTGCCGCGYGACGG	<i>Alcaligenes faecalis</i> ATCC 8750	329	Touchdown 63-53°C	32
<i>nirK</i> R	GAACCTGCCGGTNGCCAGAC				
<i>cnorB</i> 2F	GACAAGNNNTACTGGTGGT	<i>Pseudomonas aeruginosa</i> ATCC 27853	389	Touchdown 57-52.5°C	26
<i>cnorB</i> 6R	GAANCCCCANACNCCNGC				
<i>qnorB</i> 2F	GGNCAYCARGGNTAYGA	<i>Alcaligenes faecalis</i> ATCC 8750	637	Touchdown 57-52.5°C	26
<i>qnorB</i> 7R	GGNGGRTTDATCADGAANCC				
<i>nosZ</i> -F-1181	CGCTGTTCTCGACAGYCAG	<i>Pseudomonas stutzeri</i> ATCC 17588	680	56°C	67
<i>nosZ</i> -R-1880	ATGTGCAKIGCRTGGCAGAA				

<sup>a</sup>Forward and reverse primers are indicated by F and R as the last letter, respectively.

<sup>b</sup> Strains used for PCR positive control.

Supplemental Table S2. Site, site type, dilution origin, and phenotype, for 75 strains.

Strain #	Site	Site type	Dilution Origin <sup>a</sup>	Phenotype <sup>b</sup>
1	G7	Brine/oil	10 <sup>-3</sup>	DN
2	G7	Brine/oil	10 <sup>-3</sup>	DN
3	G7	Brine/oil	10 <sup>-3</sup>	NR
<b>4</b>	<b>G7</b>	<b>Brine/oil</b>	<b>10<sup>-4</sup></b>	<b>DN</b>
5	G7	Brine/oil	10 <sup>-3</sup>	NR
6	G7	Brine/oil	10 <sup>-3</sup>	NR
<b>7</b>	<b>G7</b>	<b>Brine/oil</b>	<b>10<sup>-4</sup></b>	<b>None</b>
<b>8</b>	<b>G7</b>	<b>Brine/oil</b>	<b>10<sup>-4</sup></b>	<b>None</b>
<b>9</b>	<b>G7</b>	<b>Brine/oil</b>	<b>10<sup>-5</sup></b>	<b>None</b>
<b>10</b>	<b>G7</b>	<b>Brine/oil</b>	<b>10<sup>-5</sup></b>	<b>NR</b>
11	G5	Brine/oil	10 <sup>-2</sup>	NR
12	G5	Brine/oil	10 <sup>-3</sup>	NR
<b>13</b>	<b>G5</b>	<b>Brine/oil</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
14	G5	Brine/oil	10 <sup>-2</sup>	NR
15	G5	Brine/oil	10 <sup>-3</sup>	NR
16	G5	Brine/oil	10 <sup>-2</sup>	NR
17	G5	Brine/oil	10 <sup>-2</sup>	NR
18	G5	Brine/oil	10 <sup>-2</sup>	NR
19	G5	Brine/oil	10 <sup>-2</sup>	NR
20	G5	Brine/oil	10 <sup>-2</sup>	NR
21	LF	Oil	10 <sup>-3</sup>	NR
22	LF	Oil	10 <sup>-3</sup>	NR
23	LF	Oil	10 <sup>-3</sup>	NR
<b>24</b>	<b>LF</b>	<b>Oil</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
<b>25</b>	<b>LF</b>	<b>Oil</b>	<b>10<sup>-5</sup></b>	<b>NR</b>
26	J6-NF	Oil	10 <sup>-2</sup>	None
27	J6-NF	Oil	10 <sup>-3</sup>	None
<b>28</b>	<b>J6-NF</b>	<b>Oil</b>	<b>10<sup>-4</sup></b>	<b>None</b>
29	J6-F	Oil	10 <sup>-2</sup>	NR
30	J6-F	Oil	10 <sup>-2</sup>	NR
31	J6-F	Oil	10 <sup>-3</sup>	NR
32	J6-F	Oil	10 <sup>-3</sup>	NR
33	G5P	Prairie	10 <sup>-2</sup>	NR
34	G5P	Prairie	10 <sup>-2</sup>	NR
35	G5P	Prairie	10 <sup>-2</sup>	NR
36	G5P	Prairie	10 <sup>-2</sup>	NR
37	G5P	Prairie	10 <sup>-2</sup>	NR
38	G5P	Prairie	10 <sup>-2</sup>	NR
39	G5P	Prairie	10 <sup>-2</sup>	NR
40	G5P	Prairie	10 <sup>-2</sup>	NR
41	G5P	Prairie	10 <sup>-3</sup>	NR
<b>42</b>	<b>G5P</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
43	J6P	Prairie	10 <sup>-2</sup>	NR
44	J6P	Prairie	10 <sup>-2</sup>	None
45	J6P	Prairie	10 <sup>-2</sup>	NR

46	J6P	Prairie	10 <sup>-3</sup>	NR
47	J6P	Prairie	10 <sup>-3</sup>	None
<b>48</b>	<b>J6P</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>None</b>
49	G7P	Prairie	10 <sup>-2</sup>	NR
50	G7P	Prairie	10 <sup>-2</sup>	None
51	G7P	Prairie	10 <sup>-2</sup>	None
52	G7P	Prairie	10 <sup>-2</sup>	None
<b>53</b>	<b>G7P</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
54	G7P	Prairie	10 <sup>-3</sup>	NR
<b>55</b>	<b>G7P</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>None</b>
<b>56</b>	<b>G7P</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
57	G7P	Prairie	10 <sup>-2</sup>	DN
58	G7P	Prairie	10 <sup>-2</sup>	None
59	G7P	Prairie	10 <sup>-3</sup>	NR
60	G7P	Prairie	10 <sup>-3</sup>	None
61	LFP	Prairie	10 <sup>-2</sup>	NR
62	LFP	Prairie	10 <sup>-2</sup>	None
63	LFP	Prairie	10 <sup>-2</sup>	None
64	LFP	Prairie	10 <sup>-2</sup>	None
65	LFP	Prairie	10 <sup>-3</sup>	DN
66	LFP	Prairie	10 <sup>-3</sup>	None
<b>67</b>	<b>LFP</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
<b>68</b>	<b>LFP</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
69	LFP	Prairie	10 <sup>-2</sup>	DN
70	LFP	Prairie	10 <sup>-2</sup>	NR
71	LFP	Prairie	10 <sup>-3</sup>	None
72	LFP	Prairie	10 <sup>-3</sup>	None
<b>73</b>	<b>LFP</b>	<b>Prairie</b>	<b>10<sup>-4</sup></b>	<b>NR</b>
74	LFP	Prairie	10 <sup>-2</sup>	NR
75	LFP	Prairie	10 <sup>-3</sup>	NR

\*The highly abundant strains (e.g. originated from wells with 10<sup>-4</sup> or 10<sup>-5</sup> dilution) are indicated in bold letters.

Site Type:

Brine/oil: contaminated by a spill containing both oil-field brine (salt water) and crude oil (G5 and G7), at approximately 10:1 brine to oil ratio (vol/vol).

Oil: contaminated by a spill of crude oil (LF, J6-NF and J6-F).

Prairie: Uncontaminated (G5P, G7P, J6P, LFP)

<sup>a</sup> Dilution corresponded to microtiter plate-wells from which strains were originated, e.g.  $10^{-3}$  corresponds to a 1:1000 final dilution of soil: saline dilutant into nitrate broth. See materials and methods for more information

<sup>b</sup> Phenotype: NR: nitrate reduction, DN: nitrite reduction/denitrification, None: no reduction of nitrate or nitrite.

Supplemental Table S3. Genbank accession numbers for 16S rRNA gene sequence and functional genes for nitrate reducing and denitrifying genes.

Isolate #/ Phenotype (e.g. NR, DN, or None)	Isolate name (16S rRNA Accession #)	Genus [% similarity] <sup>1</sup> (Class/subclass)	Closest GenBank match accession # (% similarity)	<i>napA</i>	<i>narG</i>	<i>nirS</i>	<i>nirK</i>	<i>cnorB</i>	<i>nosZ</i>
<b>1</b> DN	<b>G7-101B3B</b> <b>(JQ917765)</b>	<b><i>Pseudomonas</i></b> <b>[100%] (γ)</b>	<b>KU977117</b> <b>(99.86%)</b>	<b>++*</b>	<b>+</b>	<b>++*</b>		<b>+</b>	<b>+</b>
<b>2</b> DN	<b>G7-105B12A</b> <b>(JQ917766)</b>	<b><i>Pseudomonas</i></b> <b>[100%] (γ)</b>	<b>MG754443</b> <b>(100%)</b>	<b>+</b>	<b>+</b>	<b>++*</b>		<b>+</b>	<b>+</b>
<b>3</b> NR	<b>G7-129B8B</b> <b>(JQ917767)</b>	<b><i>Pseudomonas</i></b> <b>[100%] (γ)</b>	<b>MN208153</b> <b>(99.57%)</b>						
<b>4</b> DN	<b>G7-135C4</b> <b>(JQ917768)</b>	<b><i>Ensifer</i></b> <b>[99%] (α)</b>	<b>KU877644</b> <b>(100%)</b>					<b>++*</b>	
<b>5</b> NR	<b>G7-221B10A</b> <b>(JQ917769)</b>	<b><i>Achromobacter</i></b> <b>[99%] (β)</b>	<b>MK789752</b> <b>(99.86%)</b>		<b>+</b>				<b>+</b>
<b>6</b> NR	<b>G7-221B10B</b> <b>(JQ917770)</b>	<b><i>Aeromonas</i></b> <b>[100%] (γ)</b>	<b>KJ157321</b> <b>(100%)</b>	<b>+</b>					<b>+</b>
<b>7</b> None	<b>G7-305C11A1</b> <b>(JQ917771)</b>	<b><i>Bosea</i></b> <b>[100%] (α)</b>	<b>MG775032</b> <b>(99.85%)</b>	<b>++*</b>					
<b>8</b> None	<b>G7-305C11B</b> <b>(JQ917772)</b>	<b><i>Bosea</i></b> <b>[100%] (α)</b>	<b>ON698112</b> <b>(99.71%)</b>	<b>++*</b>					
<b>9</b> None	<b>G7-325D2</b> <b>(JQ917773)</b>	<b><i>Arthrobacter</i></b> <b>[100%] (Actino)</b>	<b>KM817229</b> <b>(99.93%)</b>						
<b>10</b> NR	<b>G7-401D6</b> <b>(JQ917774)</b>	<b><i>Phenylobacterium</i></b> <b>[100%] (α)</b>	<b>FJ605405</b> <b>(99.93%)</b>						
<b>11</b> NR	<b>G5NA3A</b> <b>(JQ917775)</b>	<b><i>Stenotrophomonas</i></b> <b>[100%] (γ)</b>	<b>MK475029</b> <b>(99.71%)</b>						

12 NR	G5NB3B (JQ917776)	<i>Pseudomonas</i> [95%] (γ)	MH703445 (98.83%)	+					
13 NR	G5NC6A2 (JQ917777)	<i>Stenotrophomonas</i> [100%] (γ)	KY820657 (99.93%)						
14 NR	G5MA8 (JQ917778)	<i>Brevibacillus</i> [100%] (Bacilli)	MW736872 (99.49%)						
15 NR	G5MB8A (JQ917779)	<i>Bacillus</i> [100%] (Bacilli)	GU568201 (99.93%)						
16 NR	G5MA9A2 (JQ917780)	<i>Brevibacillus</i> [100%] (Bacilli)	KT363753 (99.63%)						
17 NR	G5MA10B (JQ917781)	<i>Paenibacillus</i> [100%] (Bacilli)	KT719740 (99.35%)						
18 NR	G5SA2A1 (JQ917782)	<i>Stenotrophomonas</i> [100%] (γ)	ON556407 (99.79%)		+				
19 NR	G5SA3A (JQ917783)	<i>Brevibacillus</i> [100%] (Bacilli)	MT427642 (99.64%)						
20 NR	G5SA5A (JQ917784)	<i>Bacillus</i> [100%] (Bacilli)	MK592620 (99.42%)						
21 NR	LF-521B12 (JQ917785)	<i>Stenotrophomonas</i> [100%] (γ)	JN867123 (100%)						
22 NR	LF-617B2A1A (JQ917786)	<i>Chryseobacterium</i> [100%] (Flavo)	JN208181 (99.71%)						
23 NR	LF-617B2A1B (JQ917787)	<i>Stenotrophomonas</i> [100%] (γ)	HQ670707 (99.29%)						
24 NR	LF-821C8A1 (JQ917788)	<i>Serratia</i> [100%] (γ)	MT538443 (99.93%)		+				
25 NR	LF-825D4 (JQ917789)	<i>Enterobacter</i> [99%] (γ)	HM854373 (99.86%)		+		+		

26	J6N-NFA4A None (JQ917790)	<i>Stenotrophomonas</i> [100%] (γ)	MG905299 (99.28%)						
27	J6N- NFB4B1 None (JQ917791)	<i>Stenotrophomonas</i> [100%] (γ)	MN181024 (99.14%)						
28	J6N- NFC6A2 None (JQ917792)	<i>Stenotrophomonas</i> [100%] (γ)	MG905288 (99.93%)		+				
29	J6N-FA10A NR (JQ917793)	<i>Microbacterium</i> [100%] (Actino)	MH168999 (100%)						
30	J6N-FA10C NR (JQ917794)	<i>Pseudomonas</i> [100%] (γ)	AB621834 (100%)						
31	J6N-FB11B NR (JQ917795)	<i>Enterobacter</i> [92%] (γ)	MT102735 (99.27%)		+				
32	J6N-FB11C NR (JQ917796)	<i>Enterobacter</i> [100%] (γ)	MN181146 (99.64%)		+				
33	G5PA8B1 NR (JQ917797)	<i>Lysinibacillus</i> [100%] (Bacilli)	MT507231 (99.86%)						
34	G5PA8B2 NR (JQ917798)	<i>Stenotrophomonas</i> [100%] (γ)	KY849353 (99.21%)		+				
35	G5PA9A1 NR (JQ917799)	<i>Stenotrophomonas</i> [100%] (γ)	MT543133 (99.50%)		+				
36	G5PA9A2 NR (JQ917800)	<i>Stenotrophomonas</i> [100%] (γ)	MH429813 (99.86%)						
37	G5PA9B NR (JQ917801)	<i>Stenotrophomonas</i> [100%] (γ)	MW695215 (99.86%)		+				+
38	G5PA10A1 NR (JQ917802)	<i>Stenotrophomonas</i> [100%] (γ)	HQ185400 (99.64%)		+				
39	G5PA10A2 NR (JQ917803)	<i>Stenotrophomonas</i> [100%] (γ)	MN372320 (99.64%)		++*				
40	G5PA10B NR (JQ917804)	<i>Stenotrophomonas</i> [100%] (γ)	ON357999 (99.36%)		+				

41 NR	G5PB12A1 (JQ917805)	<i>Stenotrophomonas</i> [100%] (γ)	ON357998 (99.43%)		+				
42 NR	G5PC11 (JQ917806)	<i>Stenotrophomonas</i> [100%] (γ)	MH788995 (99.28%)		++*				
43 NR	J6PA9A (JQ917807)	<i>Achromobacter</i> [100%] (β)	ON831558 (99.78%)						
44 None	J6PA9B2 (JQ917808)	<i>Lysinibacillus</i> [100%] (Bacilli)	MK789730 (99.37%)						
45 NR	J6PA12A (JQ917809)	<i>Achromobacter</i> [100%] (β)	MH773230 (95.68%)						
46 NR	J6PB8A (JQ917810)	<i>Brevibacillus</i> [100%] (Bacilli)	KU500374 (99.56%)						
47 None	J6PB8B (JQ917811)	<i>Brevibacillus</i> [100%] (Bacilli)	MW736860 (99.79%)						
48 None	J6PC12A (JQ917812)	<i>Rhodococcus</i> [100%] (Actino)	KT380589 (97.65%)						
49 NR	G7P1A3A1 (JQ917813)	<i>Achromobacter</i> [100%] (β)	KY206819 (99.93%)	++*	+		+		+
50 None	G7P1A3A2 (JQ917814)	<i>Stenotrophomonas</i> [100%] (γ)	OQ968958 (99.43%)						
51 None	G7P1A3B1 (JQ917815)	<i>Stenotrophomonas</i> [100%] (γ)	ON448385 (99.28%)						
52 None	G7P1A3B2 (JQ917816)	<i>Stenotrophomonas</i> [100%] (γ)	KU551125 (99.86%)						
53 NR	G7P1C4 (JQ917817)	<i>Brevibacillus</i> [100%] (Bacilli)	KX170837 (99.93%)						
54 NR	G7P1B2 (JQ917818)	<i>Brevibacillus</i> [100%] (Bacilli)	MT052647 (99.55%)						
55 None	G7P2C6A (JQ917819)	<i>Acinetobacter</i> [100%] (γ)	MH671640 (98.90%)						
56 NR	G7P2C6B (JQ917820)	<i>Acinetobacter</i> [100%] (γ)	MN733120 (100%)						



57 DN	G7P2A3A (JQ917821)	<i>Stenotrophomonas</i> [100%] (γ)	KF737383 (99.49%)						
58 None	G7P2A3B (JQ917822)	<i>Acinetobacter</i> [100%] (γ)	MH130300 (98.04%)						
59 NR	G7P2B3A (JQ917823)	<i>Brevibacillus</i> [100%] (Bacilli)	KT363755 (99.64%)						
60 None	G7P2B3B (JQ917824)	<i>Bacillus</i> [100%] (Bacilli)	MT605503 (99.90%)		+				
<b>61 NR</b>	<b>LFP1A9A1 (JQ917825)</b>	<b><i>Stenotrophomonas</i> [100%] (γ)</b>	<b>LC506130 (100%)</b>						
62 None	LFP1A9A2 (JQ917826)	<i>Stenotrophomonas</i> [100%] (γ)	MG833394 (99.50%)						
63 None	LFP1A9B1 (JQ917827)	<i>Stenotrophomonas</i> [100%] (γ)	MK612128 (99.43%)						
64 None	LFP1A9B2 (JQ917828)	<i>Stenotrophomonas</i> [100%] (γ)	KT580582 (99.93%)						
<b>65 DN</b>	<b>LFP1B10A (JQ917829)</b>	<b><i>Pseudomonas</i> [100%] (γ)</b>	<b>KC207086 (99.93%)</b>		+			++*	++*
66 None	LFP1B10B (JQ917830)	<i>Burkholderia</i> [100%] (β)	KF788042 (99.35%)						
<b>67 NR</b>	<b>LFP1C12A (JQ917831)</b>	<b><i>Pseudomonas</i> [100%] (γ)</b>	<b>AY623928 (99.93%)</b>	++*					
<b>68 NR</b>	<b>LFP1C12B (JQ917832)</b>	<b><i>Pseudomonas</i> [100%] (γ)</b>	<b>OR358908 (99.50%)</b>	++*					
69 DN	LFP2A8A2 (JQ917833)	<i>Ensifer</i> [100%] (α)	MT431909 (100%)	++*					
<b>70 NR</b>	<b>LFP2A8B (JQ917834)</b>	<b><i>Acinetobacter</i> [100%] (γ)</b>	<b>MN696228 (100%)</b>						
71 None	LFP2B10A (JQ917835)	<i>Stenotrophomonas</i> [100%] (γ)	MN889390 (99.43%)						
72 None	LFP2B10B1 (JQ917836)	<i>Acinetobacter</i> [100%] (γ)	MN082060 (100%)						

73 NR	<b>LFP2C11</b> (JQ917837)	<i>Pseudomonas</i> [100%] (γ)	<b>MT539779</b> (99.86%)	+					
74 NR	LFP2A8A1 (JQ917838)	<i>Stenotrophomonas</i> [100%] (γ)	JQ675547 (99.93%)						
75 NR	<b>LFP2B10B2</b> (JQ917839)	<i>Kocuria</i> [100%] (Actino)	<b>MK205170</b> (100%)						

Isolate name: internal description of strain.

<sup>1</sup>Threshold level of similarity as determined by The Ribosomal Database Project (RDP)

Classifier program.

NR: nitrate reduction.

DN: nitrite reduction/denitrification.

None: no reduction of nitrate or nitrite.

+: PCR amplification product obtained

++\*: Sequencing of PCR product confirmed identity

The 33 selected strains are indicated in bold letters.

*napA*: periplasmic nitrate reductase.

*narG*: membrane-bound nitrate reductase.

*nirS*: cytochrome cd1-nitrite reductase.

*nirK*: copper nitrite reductase

*cnorB*: cytochrome bc-type complex nitric oxide reductase gene.

*nosZ*: nitrous oxide reductase gene.

Note: no amplification products were obtained using the *qnorB* primers.

Supplemental Table S4. Summary of nitrate reducing/denitrification genes from isolates (Accession number “in bold”/ Closest GenBank match accession # (% similarity))

Isolate #/ NR/DN	<i>napA</i> / Accession #	<i>narG</i> / Accession #	<i>nirS</i> / Accession #	<i>cnorB</i> / Accession #	<i>nosZ</i> / Accession #
1 DN	<b>OR416962</b> / <i>Pseudomonas frederiksborgensis</i> strain AS1 CP018319, 98%		<b>OR416971</b> / <i>Pseudomonas frederiksborgensis</i> strain AS1 CP018319, 99%		
2 DN			<b>OR416972</b> / <i>Pseudomonas frederiksborgensis</i> strain AS1 CP018319, 98%		
4 DN				<b>OR416960</b> <i>Ensifer adhaerens</i> strain NER9 CP101518, 96%	
7 None	<b>OR416963</b> / <i>Bosea beijingensis</i> strain REN20 CP132359, 91%				
8 None	<b>OR416964</b> / <i>Bosea beijingensis</i> strain REN20 CP132359, 91%				
39 NR		<b>OR416969</b> / <i>Stenotrophomonas geniculata</i> strain BR23 CP134450, 99.61%			
42 NR		<b>OR416970</b> / <i>Stenotrophomonas geniculata</i> strain BR23 CP134450, 99.61%			
49 NR	<b>OR416965</b> / <i>Achromobacter pestifer</i> strain FDAARGOS_79 CP053985, 95.85%				
65 DN				<b>OR416961</b> / Pseudomonadaceae bacterium isolate f13e6c2e-50f2- 4c75-b4f3- 64e691971528 , OY763427 , 89.21%	<b>OR416973</b> / <i>Pseudomonas</i> sp. P9_35, CP125373, 97.35%

67 NR	<b>OR416966/</b> <i>Pseudomonas</i> <i>umsongensis</i> strain BS3657 LT629767, 98%				
68 NR	<b>OR416967</b> <i>Pseudomonas</i> <i>umsongensis</i> strain BS3657 LT629767, 98%				
69 DN	<b>OR416968/</b> <i>Ensifer adhaerens</i> strain Corn53 CP030262, 98.76%				

NR: nitrate reduction

DN: nitrite reduction/denitrification

None: no reduction of nitrate or nitrite.

\*% similarity of isolate sequence to that of closest GenBank match, excluding uncultured or environmental sample sequences.

*napA*: periplasmic nitrate reductase.

*narG*: membrane-bound nitrate reductase.

*nirS*: cytochrome cd1-nitrite reductase.

*cnorB*: cytochrome bc-type complex nitric oxide reductase gene.

*nosZ*: nitrous oxide reductase gene.