

1 **Supplemental materials**

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3 **Physiological characterization of soil DNRA bacteria isolated via a colorimetric screening method**  
4 **implies involvement of NO<sub>3</sub><sup>-</sup> in ecophysiological regulation of DNRA activity**

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13 **Running Title:** Physiological characterization of soil DNRA bacteria

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17 **Supplemental methods and materials**

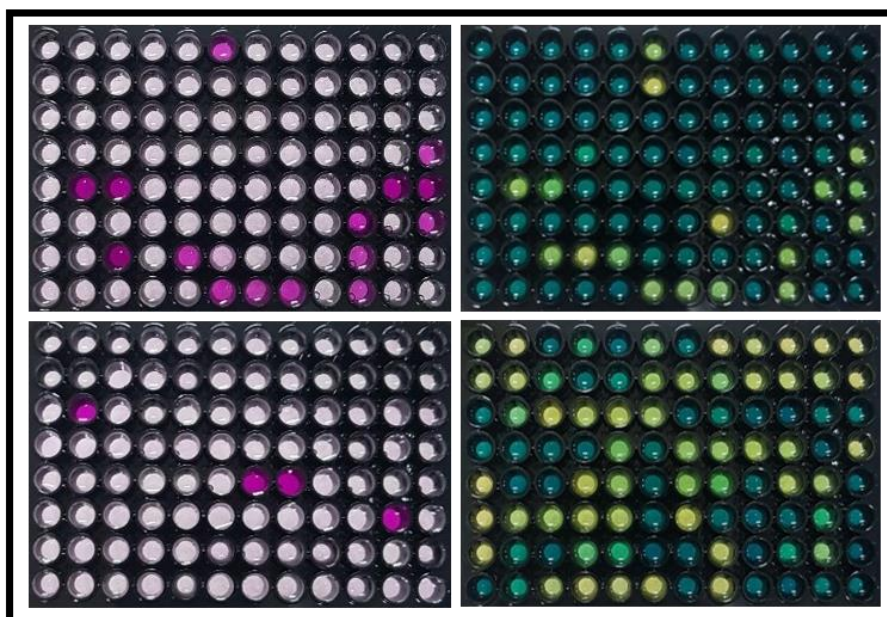
18 **Reverse transcription quantitative PCR (RT-qPCR)**

19 Samples for transcription analysis were treated with RNAprotect™ Bacteria Reagent (Qiagen, Hilden,  
20 Germany) immediately after extraction from the culture vessels and stored as pellets in 1.5-mL Eppendorf  
21 tubes at -80°C. After thawing the cell pellets on ice, 0.35 mL buffer RLT carrying 3.5 µL of 2-  
22 mercaptoethanol was added along with 50 mg acid-washed 0.1 mm glass beads (BioSpec Products, Inc.,  
23 Bartlesville, OK). The cell pellets were mechanically disrupted with using Bead Ruptor 12 Bead Mill  
24 Homogenizer (Omni International, Inc., Kennesaw, GA) at the maximum speed for 5-minutes and  
25 immediately cooled on ice. Total RNA was extracted with RNeasy™ Mini Kit (Qiagen) according to the  
26 instruction provided by the manufacturer. After digesting with RNase-free DNase set (Qiagen), the RNA  
27 solution was purified with RNeasy™ MinElute Cleanup Kit (Qiagen). The purity and concentration of the  
28 eluted samples were checked using a NanoDrop™ 2000 spectrophotometer and 2 µL of (Thermo  
29 Scientific, Waltham, MA). Reverse transcription of the total RNA to first strand cDNA was performed in  
30 20-µL reactions using SuperScript™ reverse transcriptase (Invitrogen, Carlsbad, CA) according to the  
31 instructions provided by the manufacturer. The cDNA samples were treated with RNaseH (Invitrogen) to  
32 digest remnant RNA and stored for -20 °C until use.

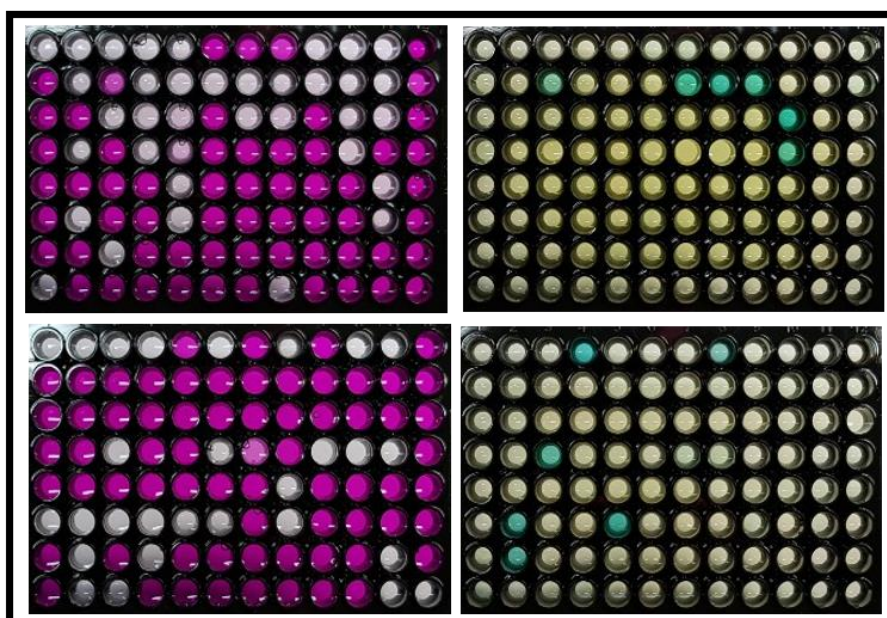
33  
34 The primer sets for quantitative PCR (qPCR) targeting the *nrfA*, *nirB*, and *recA* genes of *Citrobacter* sp.  
35 DNRA2 and the *nirB* and *recA* genes of *Enterobacter* sp. DNRA5 were designed using Primer3Plus  
36 software v2.4.2 (1). The specificity of each primer set to the intended target sequence was checked using  
37 Primer-BLAST (2). Ten-fold serial dilutions of the PCR2.1® TOPO vector (Invitrogen) with the PCR  
38 amplicons inserted were prepared for construction of qPCR calibration curves. Quantitative PCR was  
39 performed with a QuantStudio™ 3 Real-Time PCR system (Thermo Fisher Scientific) using SYBR Green  
40 chemistry. The transcript (cDNA) copy numbers were calculated with the C<sub>t</sub> values and the  
41 preconstructed calibration curves. The *nrfA* and/or *nirB* transcript copy numbers were then normalized

42 with the transcript copy numbers of the single-copy housekeeping gene *recA* (3). Biological replicates  
43 ( $n=3$ ) were processed in parallel through the entire extraction, purification, and reverse transcription  
44 processes and qPCR assays.

Lactate



Glucose

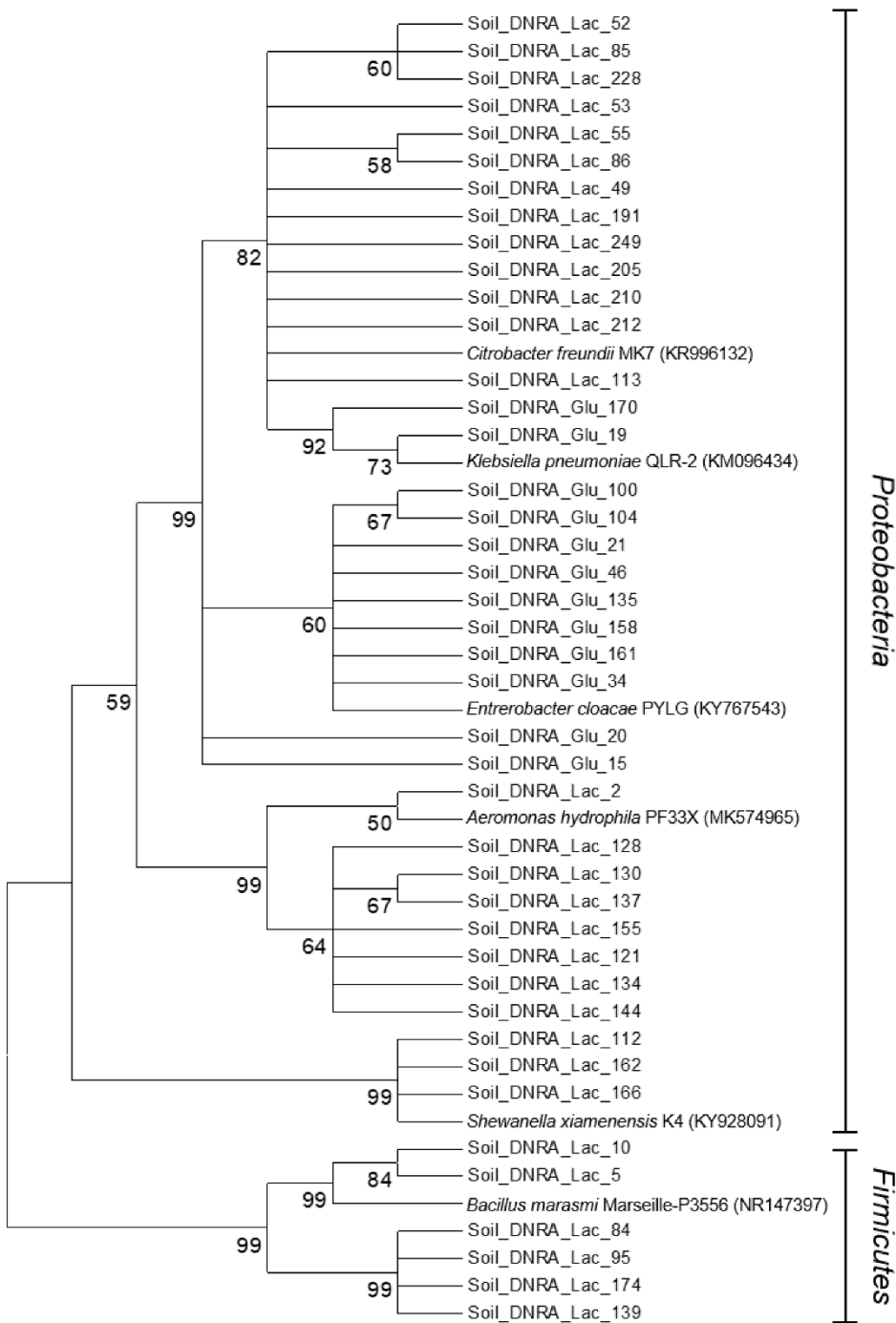


Nitrate assay

Ammonium assay

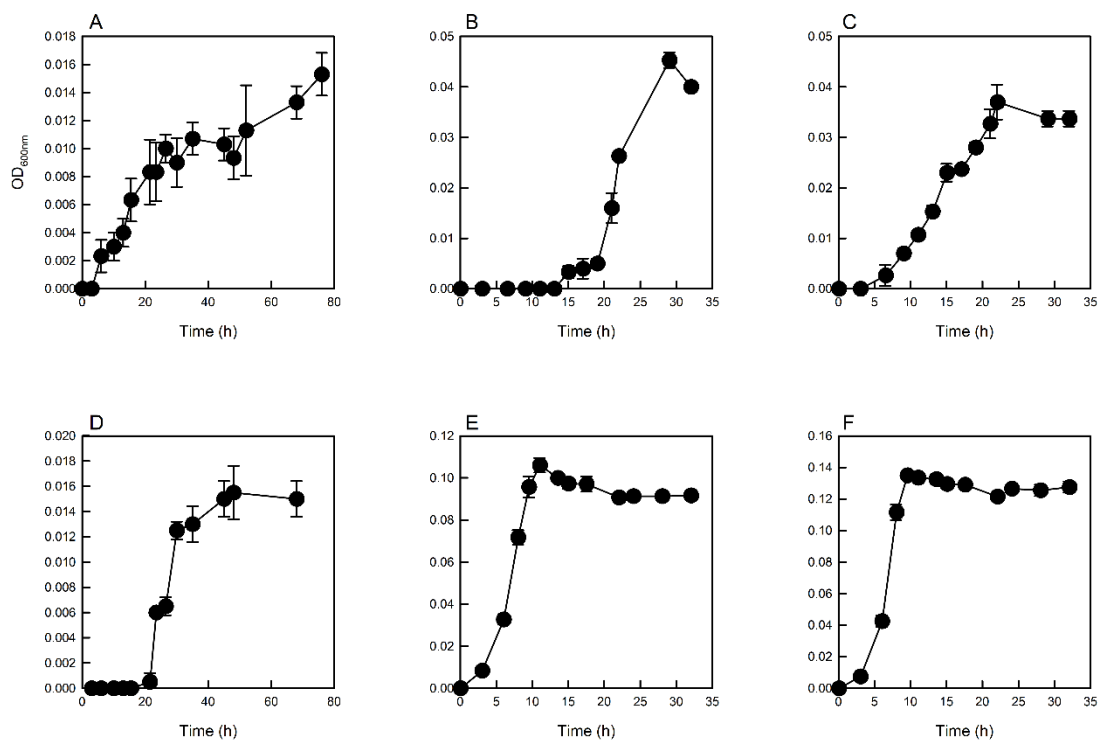
45

46 **Fig. S1.** Results of the duplicate 96-well microplate tests for high-throughput screening of DNRA-  
47 positive isolates from (a) lactate- or (b) glucose-grown colonies. A total of 192 colonies were tested for  
48 each carbon source. The plates on the left were used for measuring  $\text{NO}_3^-$  and  $\text{NO}_2^-$  concentrations using  
49 the Griess method (the pictures as shown were taken after  $\text{VCl}_3$  treatment). The plates on the right were  
50 used for measuring  $\text{NH}_4^+$  concentrations with the salicylate method. The criteria for DNRA-positive wells  
51 were absence of  $\text{NO}_3^-/\text{NO}_2^-$  and  $\text{NH}_4^+$  concentration higher than 0.8 mM.



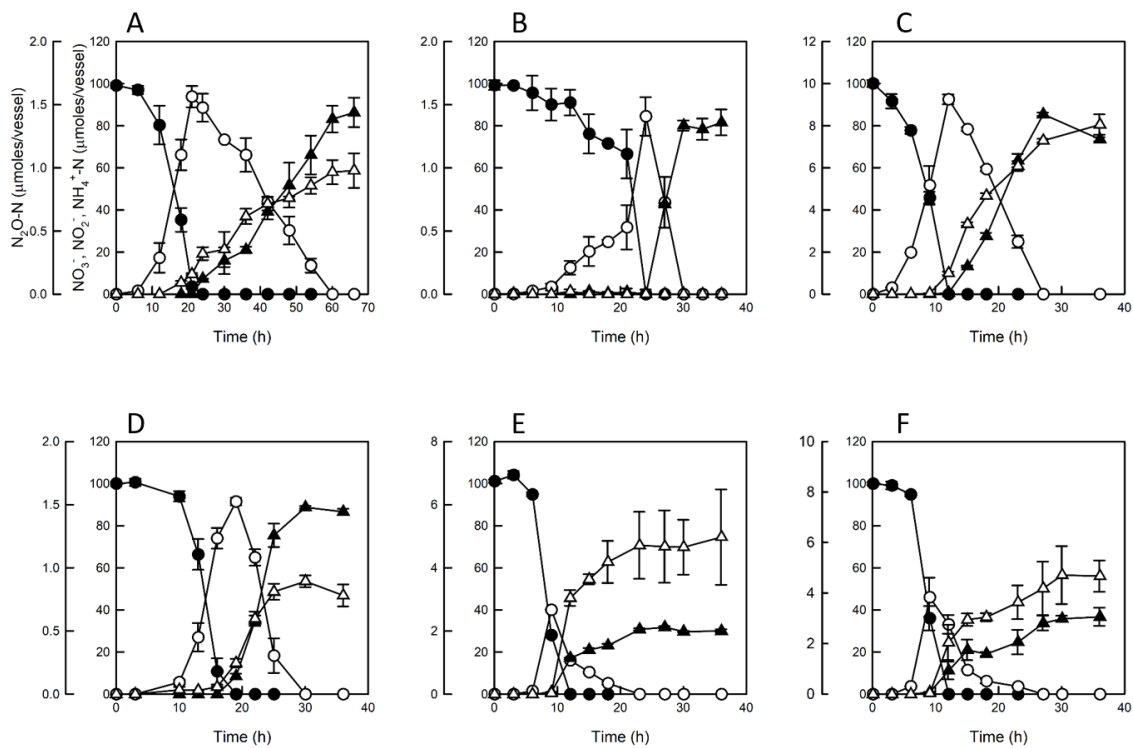
52

53 **Fig. S2.** Phylogenetic tree (50% bootstrap cut-off value) constructed with the partial 16S rRNA gene  
 54 sequences (amplified with the 27F/1492R primer set) of the soil isolates. The tree was constructed with  
 55 MEGA v10.0.5 using the maximum likelihood algorithm. The numbers at the bifurcation points indicate  
 56 the bootstrap values computed with 1000 bootstrap replicates.



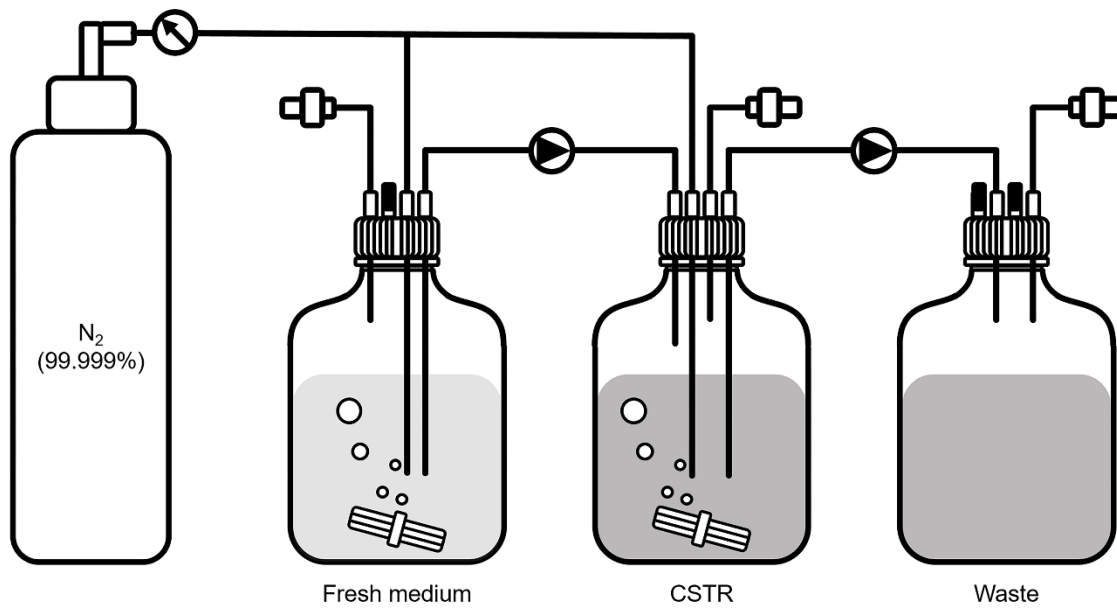
57

58 **Fig. S3.** Microbial growth monitored in the batch cultures of the six DNRA-catalyzing organisms. The  
 59 panels A-F correspond to the panels A-F of Figure 2, showing transformation of nitrogen species in the  
 60 same cultures.



61

62 **Fig. S4.**  $\text{NO}_3^-$  reduction monitored in 100-mL batch cultures (prepared in sealed 160-mL serum bottles  
 63 with  $\text{N}_2$  headspace without  $\text{C}_2\text{H}_2$ ) of (A) *Aeromonas* sp. DNRA1, (B) *Bacillus* sp. DNRA2, (C)  
 64 *Citrobacter* sp. DNRA3, (D) *Shewanella* sp. DNRA4, (E) *Enterobacter* sp. DNRA5, and (F) *Klebsiella*  
 65 sp. DNRA6. The averages of biological replicates ( $n=3$ ) are presented with the error bars representing  
 66 their standard deviations ( $\text{NO}_3^-$ : ●,  $\text{NO}_2^-$ : ○,  $\text{NH}_4^+$ : ▲,  $\text{N}_2\text{O-N}$ : △).



67

68 **Fig. S5.** A schematic diagram of the continuous-stirred tank reactor (CSTR) system used for establishing  
 69 steady-state continuous cultures of *Citrobacter* sp. DNRA2 and *Enterobacter* sp. DNRA5 at two different  
 70 C-to-N ratios.



71 **Table S1.** The physico-chemical properties of the rice paddy soil used as the inoculum. The numbers in the parentheses are standard deviation  
72 of triplicate measurements  
73

<b>TC</b> <b>(g kg<sup>-1</sup>)</b>	<b>TOC</b> <b>(g kg<sup>-1</sup>)</b>	<b>OM</b> <b>(g kg<sup>-1</sup>)</b>	<b>TN</b> <b>(%)</b>	<b>CEC</b> <b>(cmol<sub>c</sub> kg<sup>-1</sup>)</b>	<b>pH</b>	<b>NO<sub>3</sub><sup>-</sup>-N</b> <b>(mg kg<sup>-1</sup>)</b>	<b>NH<sub>4</sub><sup>+</sup>-N</b> <b>(mg kg<sup>-1</sup>)</b>	<b>Sand</b> <b>(%)</b>	<b>Silt</b> <b>(%)</b>	<b>Clay</b> <b>(%)</b>
8.2 (0.5)	7.4 (0.2)	13.5 (0.4)	0.21 (0.02)	5.3 (0.3)	6.9 (0.1)	39.6 (4.3)	12.4 (1.1)	35.0 (1.5)	45.0 (1.4)	20.0 (0.7)

74

75 **Table S2.** Draft genome statistics

<b>Organism</b>	<b>Sequencing platform</b>	<b>Assembly and annotation tool</b>	<b>Average coverage (x)</b>	<b>Size (Mb)</b>	<b>Number of CDS</b>	<b>GC content (%)</b>	<b>Completeness</b>	<b>Contamination</b>
<i>Aeromonas</i> sp. strain DNRA1	Illumina Hiseq 4000	SPAdes v3.14.0 NCBI's PGAP	797.31	4.77	4293	61.24	99.97	0.0
<i>Bacillus</i> sp. strain DNRA2	Illumina Hiseq 4000	SPAdes v3.14.0 NCBI's PGAP	764.87	4.40	4311	38.80	98.33	3.0
<i>Citrobacter</i> sp. strain DNRA3	Illumina Hiseq 4000	SPAdes v3.14.0 NCBI's PGAP	477.48	4.99	4632	51.92	99.87	0.31
<i>Shewanella</i> sp. strain DNRA4	Illumina Hiseq 4000	SPAdes v3.14.0 NCBI's PGAP	798.86	4.67	4051	46.09	99.84	0.29
<i>Enterobacter</i> sp. strain DNRA5	Illumina Hiseq 4000	SPAdes v3.14.0 NCBI's PGAP	662.72	4.53	4198	55.78	99.97	0.33
<i>Klebsiella</i> sp. strain DNRA6	Illumina Hiseq 4000	SPAdes v3.14.0 NCBI's PGAP	540.65	5.99	5774	55.30	100.0	0.47

76

77 **Table S3.** Genes recovered from the draft genomes putatively involved in N metabolism and regulation.

Gene annotation	Gene name	Locus_tag	Organism	Amino acid identity (%)	Accession number	
<b><i>Aeromonas</i> sp. DNRA1</b>						
$\text{NO}_3^- \rightarrow \text{NO}_2^-$	<b><i>napA</i> and its accessory genes</b>					
	ferredoxin-type protein NapF	<i>napF</i>	HG555_02380	<i>Aeromonas hydrophila</i>	99.41	WP_045529749
	chaperone NapD	<i>napD</i>	HG555_02375	<i>Aeromonas</i> spp.	100.00	WP_024943776
	nitrate reductase catalytic subunit NapA	<i>napA</i>	HG555_02370	<i>Aeromonas</i> spp.	100.00	WP_076359931
	ferredoxin-type protein NapG	<i>napG</i>	HG555_02365	<i>Aeromonas</i> spp.	98.77	WP_005299334
	quinol dehydrogenase ferredoxin subunit NapH	<i>napH</i>	HG555_02360	<i>Aeromonas</i> spp.	99.31	WP_011705483
	nitrate reductase cytochrome c-type subunit	<i>napB</i>	HG555_02355	<i>Aeromonas</i> spp.	100.00	WP_005299342
	cytochrome c-type protein NapC	<i>napC</i>	HG555_02350	<i>Aeromonas</i> spp.	100.00	WP_011705485
$\text{NO}_2^- \rightarrow \text{NH}_4^+$	<b><i>nirB</i> and its accessory genes</b>					
	nitrite reductase large subunit	<i>nirB</i>	HG555_18685	<i>Aeromonas hydrophila</i>	99.41	WP_139705000
	nitrite reductase small subunit NirD	<i>nirD</i>	HG555_18680	<i>Aeromonas</i> spp.	100.00	WP_016352322
	nitrite transporter NirC	<i>nirC</i>	HG555_18675	<i>Aeromonas dhakensis</i>	97.78	WP_124249490
$\text{NO}_2^- \rightarrow \text{NH}_4^+$	<b><i>nrfA</i> and its accessory genes</b>					
	ammonia-forming nitrite reductase cytochrome c552 subunit	<i>nrfA</i>	HG555_00360	<i>Aeromonas hydrophila</i>	99.17	WP_016350546
	cytochrome c nitrite reductase pentaheme subunit	<i>nrfB</i>	HG555_00365 HG555_09795	<i>Aeromonas hydrophila</i>	99.51	WP_043122582

	4Fe-4S dicluster domain-containing protein	<i>nrfC</i>	HG555_00370 HG555_09800	<i>Aeromonas</i> spp.	99.57	WP_076360881
	cytochrome c nitrite reductase subunit NrfD	<i>nrfD</i>	HG555_00375 HG555_09805	<i>Aeromonas hydrophila</i>	99.37	WP_102988884
	heme lyase NrfEFG subunit NrfE	<i>nrfE</i>	HG555_00380	<i>Aeromonas caviae</i>	97.40	WP_167826358
	heme lyase NrfEFG subunit NrfF	<i>nrfF</i>	HG555_00390	<i>Aeromonas hydrophila</i>	99.24	WP_017409585
NO → N <sub>2</sub> O	NO-inducible flavohemoprotein	<i>hmpA</i>	HG555_17580	<i>Aeromonas</i> spp.	98.99	WP_076361509
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> sensor	nitrate/nitrite two-component system sensor histidine kinase NarQ	<i>narQ</i>	HG555_02390	<i>Aeromonas</i> spp.	99.82	WP_076359937
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> response regulator	two-component system response regulator NarL	<i>narL</i>	HG555_02395	<i>Aeromonas</i> spp.	100.00	WP_017410431
<b><i>Bacillus</i> sp. DNRA2</b>						
NO <sub>3</sub> <sup>-</sup> → NO <sub>2</sub> <sup>-</sup>	nitrate reductase catalytic subunit NapA	<i>napA</i>	HHO41_19260	<i>Bacillus marasmi</i>	93.77	WP_147533058
N <sub>2</sub> O → N <sub>2</sub>	<b><i>nosZ</i> and its accessory genes</b>					
	Sec-dependent nitrous-oxide reductase	<i>nosZ</i>	HHO41_18885	<i>Bacillus marasmi</i>	93.57	WP_147535054
	nitrous oxide reductase family maturation protein NosD	<i>nosD</i>	HHO41_18895	<i>Bacillus marasmi</i>	83.26	WP_147535056
	ATP-binding cassette domain-containing protein	<i>nosF</i>	HHO41_18905	<i>Bacillus marasmi</i>	85.02	WP_147535058
NO <sub>2</sub> <sup>-</sup> → NH <sub>4</sub> <sup>+</sup>	<b><i>nrfA</i> and its accessory genes</b>					
	ammonia-forming cytochrome c nitrite reductase subunit c552	<i>nrfA</i>	HHO41_19235	<i>Bacillus marasmi</i>	92.54	WP_147532674
	cytochrome c nitrite reductase, small subunit	<i>nrfH</i>	HHO41_19240	<i>Bacillus marasmi</i>	89.08	WP_147532675

NO → N <sub>2</sub> O	<b><i>norB</i> and its accessory genes</b>					
	nitric oxide reductase large subunit, quinol-dependent	<i>norB</i>	HHO41_00170	<i>Bacillus</i> sp. MM2020_4	83.76	WP_166244948
	nitric oxide reductase activation protein NorD	<i>norD</i>	HHO41_15485	<i>Bacillus tuaregi</i>	80.13	WP_071396319
NO → N <sub>2</sub> O	NO-inducible flavohemoprotein	<i>hmpA</i>	HHO41_03255	<i>Bacillus marasmi</i>	81.36	WP_147534311
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> sensor	nitrate/nitrite two-component system sensor histidine kinase NarQ	<i>narQ</i>	HHO41_17565	<i>Bacillus marasmi</i>	85.77	WP_147535080
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> response regulator	two-component system response regulator NarL	<i>narL</i>	HHO41_17560	<i>Bacillus marasmi</i>	88.69	WP_147535082
<b><i>Citrobacter</i> sp. DNRA3</b>						
NO <sub>3</sub> <sup>-</sup> → NO <sub>2</sub> <sup>-</sup>	<b><i>napA</i> and its accessory genes</b>					
	ferredoxin-type protein NapF	<i>napF</i>	HG548_01625	<i>Citrobacter</i> spp.	100.00	WP_003027564
	chaperone NapD	<i>napD</i>	HG548_01630	<i>Citrobacter freundii</i>	97.70	WP_138828737
	nitrate reductase catalytic subunit NapA	<i>napA</i>	HG548_01635	<i>Citrobacter</i> spp.	100.00	WP_008785300
	ferredoxin-type protein NapG	<i>napG</i>	HG548_01640	<i>Citrobacter</i> sp. wls714	99.57	WP_137398035
	quinol dehydrogenase ferredoxin subunit NapH	<i>napH</i>	HG548_01645	<i>Citrobacter portucalensis</i>	99.65	WP_148361724
	nitrate reductase cytochrome c-type subunit	<i>napB</i>	HG548_01650	<i>Citrobacter</i> spp.	100.00	WP_048215889
	cytochrome c-type protein NapC	<i>napC</i>	HG548_01655	<i>Citrobacter freundii</i>	99.50	WP_141875442
NO <sub>3</sub> <sup>-</sup> → NO <sub>2</sub> <sup>-</sup>	<b><i>narG</i> and its accessory genes</b>					
	nitrate reductase subunit alpha	<i>narG</i>	HG548_04140 HG548_05245	<i>Citrobacter</i> spp.	100.00	WP_048224041

	nitrate reductase subunit beta	<i>narH</i>	HG548_04145 HG548_05240	<i>Citrobacter braakii</i>	99.80	WP_151222616
	nitrate reductase molybdenum cofactor assembly chaperone	<i>narJ</i>	HG548_04150 HG548_05235	<i>Citrobacter</i> spp.	100.00	WP_003833387
	respiratory nitrate reductase subunit gamma	<i>narI</i>	HG548_04155 HG548_05230	<i>Citrobacter</i> spp.	99.56	WP_047410761
$\text{NO}_2^- \rightarrow \text{NH}_4^+$	<b><i>nirB</i> and its accessory genes</b>					
	NADPH-nitrite reductase large subunit	<i>nirB</i>	HG548_14725	<i>Citrobacter</i> spp.	100.00	WP_008786307
	nitrite reductase small subunit NirD	<i>nirD</i>	HG548_14730	<i>Citrobacter freundii</i>	99.07	WP_119174616
	nitrite transporter NirC	<i>nirC</i>	HG548_14735	<i>Citrobacter</i> spp.	100.00	WP_008786308
$\text{NO}_2^- \rightarrow \text{NH}_4^+$	<b><i>nrfA</i> and its accessory genes</b>					
	ammonia-forming nitrite reductase cytochrome c552 subunit	<i>nrfA</i>	HG548_21145	<i>Citrobacter</i> spp.	100.00	WP_128316992
	cytochrome c nitrite reductase pentaheme subunit	<i>nrfB</i>	HG548_21140	<i>Citrobacter</i> spp.	100.00	WP_003826649
	cytochrome c nitrite reductase Fe-S protein	<i>nrfC</i>	HG548_21135	<i>Citrobacter portucalensis</i>	99.55	WP_008786934
	cytochrome c nitrite reductase subunit NrfD	<i>nrfD</i>	HG548_21130	<i>Citrobacter</i> spp.	100.00	WP_032942109
	heme lyase subunit NrfE	<i>nrfE</i>	HG548_01685 HG548_21125	<i>Citrobacter portucalensis</i>	99.48	WP_071692188
	heme lyase NrfEFG subunit NrfF	<i>nrfF</i>	HG548_21120	<i>Citrobacter</i> spp.	100.00	WP_048227480
	heme lyase NrfEFG subunit NrfG	<i>nrfG</i>	HG548_21115	<i>Citrobacter</i> spp.	100.00	WP_003826658
$\text{NO} \rightarrow \text{N}_2\text{O}$	<b><i>norV</i> and its accessory genes</b>					
	anaerobic nitric oxide reductase flavorubredoxin	<i>norV</i>	HG548_20600	<i>Citrobacter</i> spp.	100.00	WP_048225258

	NADH:flavorubredoxin reductase NorW	<i>norW</i>	HG548_20605	<i>Citrobacter</i> spp.	99.73	WP_048215690
NO → N <sub>2</sub> O	NO-inducible flavohemoprotein	<i>hmpA</i>	HG548_00200	<i>Citrobacter</i> spp.	99.75	WP_016150774
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> sensor	nitrate/nitrite two-component system sensor histidine kinase NarQ	<i>narQ</i>	HG548_00620	<i>Citrobacter</i> spp.	100.00	WP_048215801
	nitrate/nitrite two-component system sensor histidine kinase NarX	<i>narX</i>	HG548_04130	<i>Citrobacter portucalensis</i>	99.83	WP_060682118
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> response regulator	two-component system response regulator NarL	<i>narL</i>	HG548_04125	<i>Citrobacter</i> sp. SNU WT2	99.07	WP_135322090
	nitrate/nitrite response regulator protein NarP	<i>narP</i>	HG548_01700	<i>Citrobacter</i> sp. MH181794	99.07	WP_123267584
<b><i>Shewanella</i> sp. DNRA4</b>						
NO <sub>3</sub> <sup>-</sup> → NO <sub>2</sub> <sup>-</sup>	<b><i>napA</i> and its accessory genes</b>					
	ferredoxin-type protein NapF	<i>napF</i>	HG547_00545	<i>Shewanella</i> spp.	100.00	WP_037416811
	nitrate reductase	<i>napE</i>	HG547_11880	<i>Shewanella</i> spp.	100.00	WP_011716898
	chaperone NapD	<i>napD</i>	HG547_11885 HG547_15745	<i>Shewanella</i> spp.	100.00	WP_037418275
	nitrate reductase catalytic subunit NapA	<i>napA</i>	HG547_11890 HG547_15750	<i>Shewanella xiamenensis</i>	99.76	WP_099457969
	ferredoxin-type protein NapG	<i>napG</i>	HG547_15755	<i>Shewanella</i> spp.	100.00	WP_144376391
	quinol dehydrogenase ferredoxin subunit NapH	<i>napH</i>	HG547_15760	<i>Shewanella xiamenensis</i>	99.69	WP_144376392
	nitrate reductase cytochrome c-type subunit	<i>napB</i>	HG547_11895 HG547_15765	<i>Shewanella xiamenensis</i>	98.76	WP_069454825
	cytochrome c3 family protein	<i>napC</i>	HG547_11900	<i>Shewanella</i> spp.	99.48	WP_037418266

N <sub>2</sub> O → N <sub>2</sub>	<b>Accessory genes of <i>nosZ</i> (lacking <i>nosZ</i>)</b>					
	nitrous oxide reductase family maturation protein NosD	<i>nosD</i>	HG547_07965	<i>Shewanella xiamenensis</i>	98.82	WP_144345893
	nitrous oxide reductase accessory protein NosL	<i>nosL</i>	HG547_07970	<i>Shewanella</i> spp.	100.00	WP_037413896
NO <sub>2</sub> <sup>-</sup> → NH <sub>4</sub> <sup>+</sup>	<b><i>nrfA</i> and its accessory genes</b>					
	ammonia-forming nitrite reductase cytochrome c552 subunit	<i>nrfA</i>	HG547_03945	<i>Shewanella</i> spp.	100.00	WP_037421983
	cytochrome c nitrite reductase pentaheme subunit	<i>nrfB</i>	HG547_05485	<i>Shewanella</i> spp.	100.00	WP_037423605
	cytochrome c nitrite reductase, Fe-S protein	<i>nrfC</i>	HG547_05480	<i>Shewanella</i> spp.	99.56	WP_047537960
	cytochrome c nitrite reductase subunit NrfD	<i>nrfD</i>	HG547_05475	<i>Shewanella</i> spp.	100.00	WP_037423597
	cytochrome c nitrate reductase biogenesis protein NrfE	<i>nrfE</i>	HG547_08005 HG547_20195	<i>Shewanella xiamenensis</i>	99.12	WP_172587517
	cytochrome c nitrite reductase, accessory protein NrfF	<i>nrfF</i>	HG547_20185	<i>Shewanella</i> spp.	100.00	WP_037422794
	formate-dependent nitrite reductase complex subunit NrfG	<i>nrfG</i>	HG547_07985	<i>Shewanella</i> spp.	99.55	WP_037413889
NO → N <sub>2</sub> O	nitric oxide reductase large subunit, quinol-dependent	<i>norB</i>	HG547_05045	<i>Shewanella xiamenensis</i>	99.74	WP_144374961
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> sensor	nitrate/nitrite two-component system sensor histidine kinase NarQ	<i>narQ</i>	HG547_03940	<i>Shewanella</i> spp.	99.67	WP_037430125
NO <sub>3</sub> <sup>-</sup> /NO <sub>2</sub> <sup>-</sup> response regulator	two-component system response regulator NarL	<i>narL</i>	HG547_03935	<i>Shewanella</i> spp.	100.00	WP_037421976



<b><i>Enterobacter</i> sp. DNRA5</b>						
$\text{NO}_3^- \rightarrow \text{NO}_2^-$	nitrate reductase catalytic subunit NapA	<i>napA</i>	HG551_08085	<i>Enterobacter asburiae</i>	100.00	WP_163353898
$\text{NO}_3^- \rightarrow \text{NO}_2^-$	<b><i>narG</i> and its accessory genes</b>					
	nitrate reductase subunit alpha	<i>narG</i>	HG551_08060	<i>Enterobacter</i> spp.	100.00	WP_163353897
	nitrate reductase subunit beta	<i>narH</i>	HG551_08055	<i>Enterobacter</i> spp.	100.00	WP_023312109
	nitrate reductase molybdenum cofactor assembly chaperone	<i>narJ</i>	HG551_08050	<i>Enterobacter</i> spp.	100.00	WP_126786824
	respiratory nitrate reductase subunit gamma	<i>narI</i>	HG551_08045	<i>Enterobacter asburiae</i>	99.86	WP_087822739
$\text{NO}_2^- \rightarrow \text{NH}_4^+$	<b><i>nirB</i> and its accessory genes</b>					
	nitrite reductase large subunit	<i>nirB</i>	HG551_19495	<i>Enterobacter</i> spp.	100.00	WP_047173936
	nitrite reductase small subunit NirD	<i>nirD</i>	HG551_19490	<i>Enterobacter</i> spp.	100.00	WP_163354624
$\text{NO} \rightarrow \text{N}_2\text{O}$	<b><i>norV</i> and its accessory genes</b>					
	anaerobic nitric oxide reductase flavorubredoxin	<i>norV</i>	HG551_15850	<i>Enterobacter</i> spp.	100.00	WP_126303027
	NADH:flavorubredoxin reductase NorW	<i>norW</i>	HG551_15845	<i>Enterobacter</i> spp.	100.00	WP_163354226
$\text{NO} \rightarrow \text{N}_2\text{O}$	NO-inducible flavohemoprotein	<i>hmpA</i>	HG551_11810	<i>Enterobacter</i> spp.	100.00	WP_163354077
$\text{NO}_3^-/\text{NO}_2^-$ sensor	nitrate/nitrite two-component system sensor histidine kinase NarQ	<i>narQ</i>	HG551_11370	<i>Enterobacter</i> spp.	100.00	WP_045399789
	nitrate/nitrite two-component system sensor histidine kinase NarX	<i>narX</i>	HG551_08070	<i>Enterobacter</i> spp.	100.00	WP_023312112

$\text{NO}_3^-/\text{NO}_2^-$ response regulator	two-component system response regulator NarL	<i>narL</i>	HG551_08075	<i>Enterobacter hormaechei</i>	100.00	WP_059295271
<b><i>Klebsiella</i> strain DNRA6</b>						
$\text{NO}_3^- \rightarrow \text{NO}_2^-$	nitrate reductase	<i>napA</i>	HG597_05520	<i>Klebsiella</i> spp.	99.88	WP_049112896
$\text{NO}_3^- \rightarrow \text{NO}_2^-$	<b><i>narG</i> and its accessory genes</b>					
	nitrate reductase subunit alpha	<i>narG</i>	HG597_02245 HG597_05495	<i>Klebsiella</i> spp.	100.00	WP_112165142
	nitrate reductase subunit beta	<i>narH</i>	HG597_02240 HG597_05490	<i>Klebsiella</i> spp.	100.00	WP_004120666
	nitrate reductase molybdenum cofactor assembly chaperone	<i>narJ</i>	HG597_02235 HG597_05485	<i>Klebsiella</i> spp.	100.00	WP_004120668
	respiratory nitrate reductase subunit gamma	<i>narI</i>	HG597_02230 HG597_05480	<i>Klebsiella</i> spp.	100.00	WP_004120670
$\text{NO}_2^- \rightarrow \text{NH}_4^+$	<b><i>nirB</i> and its accessory genes</b>					
	NADPH-nitrite reductase large subunit	<i>nirB</i>	HG597_17540	<i>Klebsiella</i> spp.	100.00	WP_004125996
	nitrite reductase small subunit NirD	<i>nirD</i>	HG597_05525 HG597_17535	<i>Klebsiella</i> spp.	99.07	WP_004126000
	nitrite transporter NirC	<i>nirC</i>	HG597_17530	<i>Klebsiella</i> spp.	100.00	WP_004126003
$\text{NO} \rightarrow \text{N}_2\text{O}$	<b><i>norV</i> and its accessory genes</b>					
	anaerobic nitric oxide reductase flavorubredoxin	<i>norV</i>	HG597_18120	<i>Klebsiella</i> spp.	100.00	WP_004124052
	NADH:flavorubredoxin reductase NorW	<i>norW</i>	HG597_18125	<i>Klebsiella</i> spp.	99.73	WP_004124056
$\text{NO} \rightarrow \text{N}_2\text{O}$	NO-inducible flavoheмоprotein	<i>hmpA</i>	HG597_13065	<i>Klebsiella</i> spp.	98.99	WP_049112992
$\text{NO}_3^-/\text{NO}_2^-$ sensor	nitrate/nitrite two- component system sensor histidine kinase NarX	<i>narX</i>	HG597_05505	<i>Klebsiella</i> spp.	100.00	WP_004121755
$\text{NO}_3^-/\text{NO}_2^-$ response regulator	two-component system response regulator NarL	<i>narL</i>	HG597_05510	<i>Klebsiella</i> spp.	100.00	WP_004121757

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