Table S4. Taxonomic assignments of *nos* transcripts based on metatranscriptomic analysis.

| Sample | Accession No. | NCBI-nr annotation | Organism | Phylum/Proteobacterial class | Identity(%) | Similarity(%) | Bit score | E-value |
|---|---|---|---|---|---|---|---|---|
| 1 | CUT00741.1 | nitrous oxide reductase apoprotein | Candidatus Kryptobacter tengchongensis | Candidaus Kryptonia | 85% | 91% | 124 | 2.10E-30 |
| | CUU07937.1 | nitrous oxide reductase apoprotein | Candidatus Kryptobacter tengchongensis | Candidatus Kryptonia | 84% | 93% | 116 | 5.10E-28 |
| | KJU81867.1 | nitrous-oxide reductase | Candidatus Magnetobacterium bavaricum | Nitrospirae | 77% | 88% | 108 | 6.10E-25 |
| | KXK07378.1 | nitrous-oxide reductase | Acidobacteria bacterium OLB17 | Acidobacteria | 73% | 84% | 92.4 | 2.10E-19 |
| | OFW07091.1 | nitrous-oxide reductase | Acidobacteria bacterium RIFCSPLOWO2 | Acidobacteria | 93% | 100% | 163 | 1.10E-44 |
| | OGO48016.1 | cytochrome C, partial | Chloroflexi bacterium | Chloroflexi | 96% | 100% | 99.8 | 3.10E-22 |
| | OIP06540.1 | cytochrome C | Betaproteobacteria bacterium | Betaproteobacteria | 92% | 97% | 212 | 1.00E-61 |
| | WP_011984568.1 | nitrous-oxide reductase | Anaeromyxobacter sp. Fw109-5 | Deltaproteobacteria | 87% | 97% | 143 | 2.10E-37 |
| | WP_040335623.1 | TAT-dependent nitrous-oxide reductase | Candidatus Magnetobacterium casensis | Nitrospirae | 77% | 88% | 115 | 2.10E-27 |
| | WP_093189600.1 | cytochrome C | Thiocapsa sp. KS1 | Gammaproteobacteria | 77% | 91% | 90.1 | 1.10E-18 |
| 2 | AHG92568.1 | Nitrous-oxide reductase, Sec-dependent (plasmid) | Gemmatirosa kalamazoonesis | Gemmatimonadetes | 78% | 91% | 173 | 1.10E-47 |
| | WP_066155737.1 | MULTISPECIES: nitrous-oxide reductase | Hydrogenophaga | Betaproteobacteria | 82% | 93% | 170 | 4.10E-46 |
| 3 | KJU81616.1 | nitrous-oxide reductase, partial | Candidatus Magnetobacterium bavaricum | Nitrospirae | 66% | 79% | 99.4 | 3.10E-24 |
| | KJU81616.1 | nitrous-oxide reductase, partial | Candidatus Magnetobacterium bavaricum | Nitrospirae | 66% | 79% | 99.4 | 3.10E-24 |
| | OGU35993.1 | nitrous oxide reductase | Ignavibacteria bacterium | Chlorobi | 71% | 84% | 117 | 5.10E-28 |
| | OQY84612.1 | cytochrome C | Chloroflexi bacterium UTCFX4 | Chloroflexi | 80% | 88% | 139 | 1.10E-35 |
| | WP_011984568.1 | nitrous-oxide reductase | Anaeromyxobacter sp. Fw109-5 | Deltaproteobacteria | 94% | 97% | 157 | 3.00E-43 |