Table X. KEGG orthologs involved in N cycling and the linked microbial taxa. NB. Genes that originate from taxa not detected in Organic Lake by SSU sequence marked with an asterisk.

|  |  |  |  |
| --- | --- | --- | --- |
| gene | KO | taxon | relative abundance |
| **Nitrogen fixation** | | | |
| nitrogenase (*nif*D) | K02586 | *Arcobacter*  *Desulfatibacillum*  *Clostridium*  *Chlorobaculum* \*  *Chlorobium \** |  |
| nitrogenase (*nif*H) | K02588 | *Arcobacter* |  |
| nitrogenase (*nif*K) | K02591 | *Arcobacter*  *Geobacter*  *Xanthobacter* |  |
| **Denitrification** | | | |
| nitric oxide reductase (*nor*C) | K02305 |  |  |
| nitric oxide reductase (*nor*B) | K04561 |  |  |
| nitrous oxide reductase (*nos*Z) | K00376 |  |  |
| **Dissimilatory nitrate reduction to ammonia (DNRA)** | | | |
| cytochrome C nitrite reductase  (*nrf*A) | K03385 |  |  |
| **Anammox** | | | |
| hydroxylamine oxidase (HAO) | K10535 | Desulfatibacillum  Desulfohalobium  Desulfococcus |  |
| **Mineralization/uptake** | | | |
| glutamate dehydrogenase (*gdh*A) | K00260 | Bacillus  Thermosediminibacter  Staphylococcus  Thermoanaerobacter  Macrococcus |  |
| glutamate dehydrogenase (*gdh*A) | K00261 |  |  |
| glutamate dehydrogenase (*gdh*A) | K00262 |  |  |
| **Assimilation** | | | |
| assimilatory nitrate reductase | K00360 | Azorhizobium (1)  Herminiimonas\*  Nitrobacter (15)  Spirosoma (1) | Alphaproteobacteria  Betaproteobacteria?  Alphaproteobacteria  Cytophagia |
| glutamine synthetase (*gln*A) | K01915 |  |  |
| glutamate synthase (*glt*B) | K00265 |  |  |
| glutamate synthase (*glt*S) | K00284 |  |  |