Supplementary material

Table S1. Overview of the pathways modules and reference profiles within nitrogen metabolism used to calculate the predicted relative abundance of genes within each pathway. All data was extracted from the Kyoto Encyclopaedia for Genes and Genomes (KEGG) database www.genome.jp/kegg/.

Pathway	Overview	Module	KEGG Ortholog reference profile (KO)
Nitrogen fixation	Nitrogen => ammonia	M00175	K02588 + K02586 + K02591 - K00531
Nitrification	Ammonia => nitrite	M00528	K10944+K10945+K10946 K10535
Denitrification	Nitrate => nitrogen	M00529	(K00370+K00371+K00374+K00373, K02567+K02568) (K00368,K15864) (K04561+K02305,K15877) K00376
Dissimilatory nitrate reduction	Nitrate => ammonia	M00530	(K00370+K00371+K00374+K00373, K02567+K02568) (K00362+K00363,K03385+K15876)
Assimilatory nitrate reduction	Nitrate => ammonia	M00531	(K00367,K10534,K00372-K00360) (K00366,K17877)
Complete nitrification	Ammonia => nitrite => nitrate	M00804	K10944+K10945+K10946 K10535 K00370+K00371

Fig. S1. Nitrogen metabolism pathway map 00910 downloaded from the Kyoto Encyclopaedia for Genes and Genomes (KEGG) database. In the upper part of the diagram, the numbers in the boxes are Enzyme Commission (EC numbers) for enzymes and the chemical reactions they catalyse. In the lower part of the diagram, the enzyme numbers are replaced by the codes for the gene that code for each enzyme. Arrows indicate the direction and pathway of the reactions: arrows pointing to the right indicate reduction reactions and arrows pointing to the left indicate oxidation reactions. The circles indicate the different inorganic forms of nitrogen.