**Table 2** Contribution of different taxonomic groups to counts of marker genes involved in carbon, nitrogen and sulfur conversions.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Taxon | Calvin cycle | *prkB* | Respiration | Fermentation | rTCA | WL | CO oxidation | AAnP | N fixation | NO reduction | N2O reduction | DNRA | *hao* | N mineralization | NO3- assimilation | N assimilation | DSR | S oxidation | S asssimilation | S mineralization | DMSO reduction |
| *Acidobacteria* | 0 | 0 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.07 | 0 | 0.08 | 0 | 0 | 0.03 | 1.03 | 0 |
| *Actinobacteria* | 0 | 0 | 0.64 | 0.23 | 0 | 0 | 0.08 | 0 | 0 | 0 | 0 | 0.03 | 0 | 0.32 | 0 | 5.41 | 0 | 0 | 0.15 | 0 | 0 |
| *Alphaproteobacteria* | 0.05 | 0 | 4.84 | 0 | 0 | 0 | **6.74** | **6.98** | 0.01 | 0.12 | 0 | 0 | 0 | **6.39** | 5.49 | 49.4 | 0 | 2.05 | 0.85 | 11.7 | 0 |
| *Aquificae* | 0 | 0 | 0.06 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.26 | 0 | 0 | 0 | 0 | 0.06 | 0 | 0 | 0 | 0 | 0 |
| *Bacteroidetes* | 0 | 0 | 3.42 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 3.00 | **0.27** | 0 | 3.90 | 0.03 | 15.5 | 0 | 0 | 5.06 | 0.20 | 0 |
| *Betaproteobacteria* | 0.04 | 0.06 | 0.07 | 0.09 | 0 | 0 | 0.22 | 0 | 0 | 0.03 | 0 | 0 | 0 | 0.06 | 0.41 | 19.2 | 0 | 1.09 | 2.07 | 0.69 | 0 |
| *Chlorobi* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 | 0 | 0 | 0 | 0 | 0.2 | 0 | 0.31 | 0 | 0 | 0.03 | 0.15 | 0 |
| *Chloroflexi* | 0 | 0 | 0.02 | 0 | 0 | 0 | 0.07 | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 | 0 | 0.03 | 0 | 0 | 0 | 0.30 | 0 |
| *Chrysiogenetes* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.01 | 0 | 0.06 | 0 | 0 | 0.01 | 0 | 0 |
| *Cyanobacteria* | 0.09 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.29 | 0 | 0.10 | 0 | 0 | 0.13 | 0.05 | 0 |
| *Deferribacteres* | 0 | 0 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Deinococcus-Thermus* | 0.01 | 0 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.01 | 0 | 0.11 | 0 | 0 | 0 | 0.09 | 0 |
| *Deltaproteobacteria* | 0 | 0 | 0.09 | 0 | 0 | **0.06** | 0.21 | 0 | 0.04 | 0.01 | 0 | 0.07 | **0.22** | 0.23 | 0 | 0.58 | **0.19** | 0 | 0.56 | 0.20 | 0.03 |
| *Epsilonproteobacteria* | 0 | 0 | 0 | 0 | **0.28** | 0 | 0 | 0 | **0.32** | 0 | 0 | 0 | 0 | 0.05 | 0 | 1.49 | 0 | 0.03 | 0.13 | 0 | 0 |
| *Firmicutes* | 0.01 | 0 | 0.01 | **4.90** | 0 | 0.02 | 0.15 | 0 | 0.03 | 0 | 0 | 0.03 | 0 | 0.70 | 0 | 3.16 | 0 | 0 | 0.22 | 0.09 | **0.36** |
| *Fornicata* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.02 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Fusobacteria* | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.04 | 0 | 0 | 0.03 | 0.13 | 0 |
| *Gammaproteobacteria* | 0.05 | **12.1** | **9.86** | 1.03 | 0 | 0 | 0.06 | 0.04 | 0 | **3.91** | **8.28** | 0 | 0 | 4.75 | **14.1** | **50.6** | 0 | **2.64** | **22.4** | **14.0** | 0 |
| *Nitrospirae* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 | 0 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Planctomycetes* | 0 | 0 | 0.02 | 0.08 | 0 | 0 | 0 | 0 | 0 | 0.01 | 0 | 0.16 | 0 | 0 | 0 | 0.26 | 0 | 0 | 0.03 | 0 | 0 |
| *Spirochaetes* | 0 | 0 | 0 | 0.03 | 0 | 0 | 0.16 | 0 | 0 | 0.01 | 0 | 0 | 0 | 0.11 | 0 | 0.15 | 0 | 0 | 0 | 0.03 | 0.12 |
| *Thermobaculum* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.10 | 0 | 0 | 0 | 0 | 0 | 0.08 | 0 |
| *Thermotogae* | 0.01 | 0 | 0 | 0 | 0 | 0 | 0.17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.01 | 0 | 0 |
| *Verrucomicrobia* | 0 | 0 | 0.13 | 0.05 | 0 | 0 | 0 | 0 | 0 | 0 | 0.17 | 0.03 | 0 | 0.25 | 0 | 0.82 | 0 | 0 | 0.18 | 0 | 0 |
| *Crenarchaeota* | 0 | 0 | 0 | 0 | 0 | 0 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0.02 | 0 | 0 | 0.02 | 0 | 0 | 0 | 0 |
| *Euryarchaeota* | 0.04 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.12 | 0.09 | 0.10 | 0 | 0 | 0.02 | 0.12 | 0 |
| *Alveolata* | 0 | 0 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.18 | 0 | 0.03 | 0 | 0 | 0 | 0 | 0 |
| *Euglenozoa* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 | 0 |
| *Opistokonta* | 0 | 0 | 0.16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.15 | 0 | 0.13 | 0 | 0 | 0.11 | 0.03 | 0 |
| *Rhodophyta* | 0.16 | 0 | 0.03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.02 | 0 | 0 | 0 | 0 | 0 |
| *Stramenopiles* | 0.34 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 | 0 | 0.15 | 0 | 0 | 0 | 0 | 0 |
| *Viridiplantae* | **3.10** | 0.06 | 1.10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.03 | 0 | 0.35 | 0 | 0 | 0.03 | 0.15 | 0 |

The values shown for each taxon are the average number of matches from all samples to marker genes for a process expressed per 100 Mbp of metagenomic sequence. Counts from the taxonomic group with the greatest contribution to each process is shown in bold. Genes used as markers for each process are the same as described in Figure 4.