Additional materials

**Table S1** Phylogenetic classification of the 16S rRNA gene sequences (relative abundance >1%) in methanotrophic–heterotrophic communities.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Cycle** | **BLASTs** | | **Phylogenetic classification of the 16S rRNA gene sequences** | | | | | | | **%Relative abundance** | | | | | |
| **Top match** | **%Similarity** | | **Phylum** | **Class** | **Order** | **Family** | **Genus** | **Cycle 103** | | **Cycle 113** | | **Cycle 156** | |
| OTU\_1 | *Methylosinus* | 100 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Methylocystaceae* | *Methylosinus* | 8.3 | | 4.6 | | 51.5 | |
| OTU\_10 | *Methylosinus* | 97 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Methylocystaceae* | *Methylosinus* | 0.0 | | 0.0 | | 1.6 | |
| OTU\_11 | *Ferrovibrio* | 98 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhodospirillales* | *Rhodospirillaceae* | *Phaeospirillum* | 0.0 | | 1.9 | | 1.4 | |
| OTU\_12 | *Methylosinus* | 98 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Methylocystaceae* | *Methylosinus* | 1.2 | | 0.0 | | 1.3 | |
| OTU\_13 | *Hyphomicrobium* | 99 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Hyphomicrobiaceae* | *Hyphomicrobium* | 6.4 | | 2.8 | | 1.3 | |
| OTU\_14 | *Brevundimonas* | 100 | | *Proteobacteria* | *Alphaproteobacteria* | *Caulobacterales* | *Caulobacteraceae* | *-* | 0.0 | | 0.0 | | 1.2 | |
| OTU\_15 | *Methylosinus* | 94 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Methylocystaceae* | *Methylosinus* | 0.0 | | 0.0 | | 1.1 | |
| OTU\_16 | *Hyphomicrobium* | 99 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Hyphomicrobiaceae* | *Hyphomicrobium* | 11.5 | | 5.1 | | 0.0 | |
| OTU\_17 | *Hyphomicrobium* | 99 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Hyphomicrobiaceae* | *Hyphomicrobium* | 1.1 | | 0.0 | | 0.0 | |
| OTU\_18 | *Methylomonas* | 100 | | *Proteobacteria* | *Gammaproteobacteria* | *Methylococcales* | *Methylococcaceae* | *Methylomonas* | 0.0 | | 1.8 | | 0.0 | |
| OTU\_19 | *Burkholderia* | 100 | | *Proteobacteria* | *Betaproteobacteria* | *Burkholderiales* | *Burkholderiaceae* | *Burkholderia* | 2.9 | | 0.0 | | 0.0 | |
| OTU\_2 | *Methylophilus* | 100 | | *Proteobacteria* | *Betaproteobacteria* | *Methylophilales* | *Methylophilaceae* | *Methylophilus* | 0.0 | | 0.0 | | 10.6 | |
| OTU\_20 | *Methylocystis* | 99 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Methylocystaceae* | *Methylosinus* | 1.2 | | 0.0 | | 0.0 | |
| OTU\_21 | *Terrimonas* | 100 | | *Bacteroidetes* | *[Saprospirae]* | *[Saprospirales]* | *Chitinophagaceae* | *-* | 1.0 | | 1.9 | | 0.0 | |
| OTU\_22 | *Pseudomonas* | 100 | | *Proteobacteria* | *Gammaproteobacteria* | *Pseudomonadales* | *Pseudomonadaceae* | *Pseudomonas* | 0.0 | | 1.4 | | 0.0 | |
| OTU\_23 | *Hyphomicrobium* | 99 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Hyphomicrobiaceae* | *Hyphomicrobium* | 1.9 | | 3.4 | | 0.0 | |
| OTU\_24 | *Methylocystis* | 96 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Methylocystaceae* | *Methylosinus* | 1.2 | | 0.0 | | 0.0 | |
| OTU\_25 | *Hyphomicrobium* | 99 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Hyphomicrobiaceae* | *Hyphomicrobium* | 2.9 | | 1.3 | | 0.0 | |
| OTU\_3 | *Comamonas* | 100 | | *Proteobacteria* | *Betaproteobacteria* | *Burkholderiales* | *Comamonadaceae* | *-* | 0.0 | | 0.0 | | 6.6 | |
| OTU\_4 | *Caulobacter* | 98 | | *Proteobacteria* | *Alphaproteobacteria* | *Caulobacterales* | *Caulobacteraceae* | *-* | 0.0 | | 0.0 | | 3.4 | |
| OTU\_5 | *Methylosinus* | 100 | | *Proteobacteria* | *Alphaproteobacteria* | *Rhizobiales* | *Methylocystaceae* | *Methylosinus* | 40.4 | | 55.7 | | 3.3 | |
| OTU\_6 | *Rhodanobacter* | 100 | | *Proteobacteria* | *Gammaproteobacteria* | *Xanthomonadales* | *Xanthomonadaceae* | *Rhodanobacter* | 5.5 | | 3.4 | | 2.5 | |
| OTU\_7 | *Methylophilus* | 96 | | *Proteobacteria* | *Betaproteobacteria* | *Methylophilales* | *Methylophilaceae* | *Methylophilus* | 0.0 | | 0.0 | | 2.3 | |
| OTU\_8 | *Pigmentiphaga* | 100 | | *Proteobacteria* | *Betaproteobacteria* | *Burkholderiales* | *Alcaligenaceae* | *Pigmentiphaga* | 0.0 | | 0.0 | | 2.2 | |
| OTU\_9 | *Chryseobacterium* | 99 | | *Bacteroidetes* | *Flavobacteriia* | *Flavobacteriales* | *-* | *-* | 1.2 | | 3.4 | | 1.7 | |
| Other | | | | | | | | | | 14.6 | | 16.8 | | 9.8 | |