**Table S1** Methanotroph species, phylogenetic group and accession numbers of methane monooxygenase used in the sequence similarity and phylogenetic analysis, and the percentage identities with *Bathymodiolus platifrons* endosymbiont pmoA, pmoB and pmoC amino acids.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Protein** | **Methanotroph species** | **Phylogenetic group** | **Accession number** | ***Bathymodiolus* *platifrons* endosymbiont** |
| **pmoA I%** | **pmoB I%** | **pmoC I%** |
| pmoA | *Methylomonas methanica*  | Type I | WP\_013817026 | 93.7 | 16.1 | 46 |
|  | *Methylomonas koyamae*  | Type I | WP\_064041206 | 92.7 | 16.1 | 45.6 |
|  | *Methylobacter luteus*  | Type I | WP\_027159170 | 92.9 | 17.5 | 46.4 |
|  | *Methylobacter whittenburyi*  | Type I | WP\_036297036 | 92.7 | 18.1 | 46.8 |
|  | *Methylomicrobium buryatense* | Type I | WP\_017841993 | 91.1 | 17.1 | 46.2 |
|  | *Methylomicrobium alcaliphilum* 20Z | Type I | CCE22213 | 90.9 | 17.3 | 46.6 |
|  | *Methylococcus capsulatus* (Bath) | Type X | AAB49821 | 87.3 | 16.5 | 47.4 |
|  | *Methylocaldum szegediense* | Type X | WP\_026609851 | 85.5 | 16.1 | 46.6 |
|  | *Methylocaldum* sp. T025  | Type X | BAF49650 | 85.5 | 16.1 | 46.6 |
|  | *Methylocaldum* sp. 14B  | Type X | WP\_077732836 | 85.3 | 16.3 | 46.6 |
|  | *Methylocystis parvus*  | Type II | WP\_016921576 | 77.8 | 16.9 | 45.6 |
|  | *Methylosinus* sp. LW4  | Type II | WP\_018265987 | 78.2 | 17.5 | 45.4 |
|  | *Methylocystis* sp. SC2  | Type II | CAE48352 | 77.2 | 16.9 | 45.8 |
| pmoB | *Methylomonas methanica*  | Type I | WP\_013817027 | 16.7 | 86.3 | 11.7 |
|  | *Methylomonas koyamae*  | Type I | WP\_064041205 | 16.9 | 85.3 | 11.3 |
|  | *Methylobacter luteus*  | Type I | WP\_027159171 | 16.7 | 87.1 | 12.1 |
|  | *Methylobacter whittenburyi*  | Type I | WP\_036297856 | 16.7 | 88.5 | 12.3 |
|  | *Methylomicrobium buryatense*  | Type I | WP\_017841994 | 15.9 | 84.5 | 12.3 |
|  | *Methylomicrobium alcaliphilum* 20Z | Type I | CCE22214 | 16.1 | 84.7 | 11.7 |
|  | *Methylococcus capsulatus* (Bath) | Type X | AAB49822 | 15.1 | 75.4 | 11.9 |
|  | *Methylocaldum szegediense* | Type X | WP\_026609851 | 15.3 | 74.4 | 11.3 |
|  | *Methylocaldum* sp. T025  | Type X | BAF49661 | 14.5 | 71.2 | 10.5 |
|  | *Methylocaldum* sp. 14B  | Type X | WP\_077732837 | 24.4 | 66.9 | 21.2 |
|  | *Methylocystis parvus*  | Type II | WP\_016921577 | 14.3 | 52.2 | 8.9 |
|  | *Methylosinus* sp. LW4  | Type II | WP\_018265986 | 13.9 | 52.4 | 7.9 |
|  | *Methylocystis* sp. SC2  | Type II | CAE48353 | 13.9 | 52.6 | 7.7 |
| pmoC | *Methylomonas methanica*  | Type I | WP\_013817025 | 46.8 | 11.3 | 93.8 |
|  | *Methylomonas koyamae*  | Type I | WP\_064041207 | 46.4 | 11.5 | 93.7 |
|  | *Methylobacter luteus*  | Type I | WP\_027159169 | 46.4 | 11.5 | 93.1 |
|  | *Methylobacter whittenburyi*  | Type I | WP\_036297034 | 46.2 | 11.1 | 93.8 |
|  | *Methylomicrobium buryatense*  | Type I | WP\_017841992 | 46.2 | 11.9 | 93.1 |
|  | *Methylomicrobium alcaliphilum* 20Z | Type I | CCE22212 | 46.2 | 11.5 | 92.9 |
|  | *Methylococcus capsulatus* (Bath) | Type X | AAB49820 | 44.2 | 12.5 | 84.7 |
|  | *Methylocaldum szegediense* | Type X | WP\_026609851 | 43.8 | 10.9 | 83.5 |
|  | *Methylocaldum* sp. T025  | Type X | BAF49659 | 43.8 | 10.9 | 83.5 |
|  | *Methylocaldum* sp. 14B  | Type X | WP\_077732835 | 44 | 11.3 | 83.9 |
|  | *Methylocystis parvus*  | Type II | WP\_016921575 | 46.4 | 12.1 | 77 |
|  | *Methylosinus* sp. LW4  | Type II | WP\_018265988 | 45.8 | 11.9 | 76.4 |
|  | *Methylocystis* sp. SC2  | Type II | CAE48351 | 45.6 | 12.3 | 77.2 |

I%: percentage identity, calculated by clustal W methods in MegAlign software of DNAstar.