Table S1. Genome statistics of the obtained metagenome-assembled genomes (MAGs) affiliated to methanotrophs.

MAGs	Assemble method	Binning method	Completeness	Contamination	Classification by GTDBkit
Bin.025	IDBA	MetaBAT2	92.54	2.28	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Methylococcales;f__Methylococcaceae;g__Methylomagnum;s__
Bin.053	IDBA	MetaBAT2	98.28	0.75	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__;s__
Bin.078	MEGAHIT	MetaBAT2	95.31	2.28	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Methylococcales;f__Methylococcaceae;g__Methylomagnum;s__
Bin.006	MetaSPAdes	MaxBin2	98.59	2.63	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__;s__
Bin.016	MetaSPAdes	MetaBAT2	93.27	0.63	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Methylosinus;s__Methylosinus sporium
Bin.033	MetaSPAdes	MetaBAT2	98.59	0.75	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__;s__
Bin.035	MetaSPAdes	MetaBAT2	98.79	2.45	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Methylococcales;f__Methylococcaceae;g__Methylomagnum;s__

Table S2. Gene features of Bin.033 predicted by prokka v1.14.5. This table has been provided as a separate Excel file.

Table S3. Gene features of Bin.033 annotated by RAST tool kit. This table has been provided as a separate Excel file.

Table S4. Gene functions of Bin.033 annotated by BlastKOALA through against the Kyoto Encyclopedia of Genes and Genomes database. This table has been provided as a separate Excel file.

Table S5. Length of *pmoA*-like genes in genomes of currently known aerobic methanotrophs. This table has been provided as a separate Excel file.

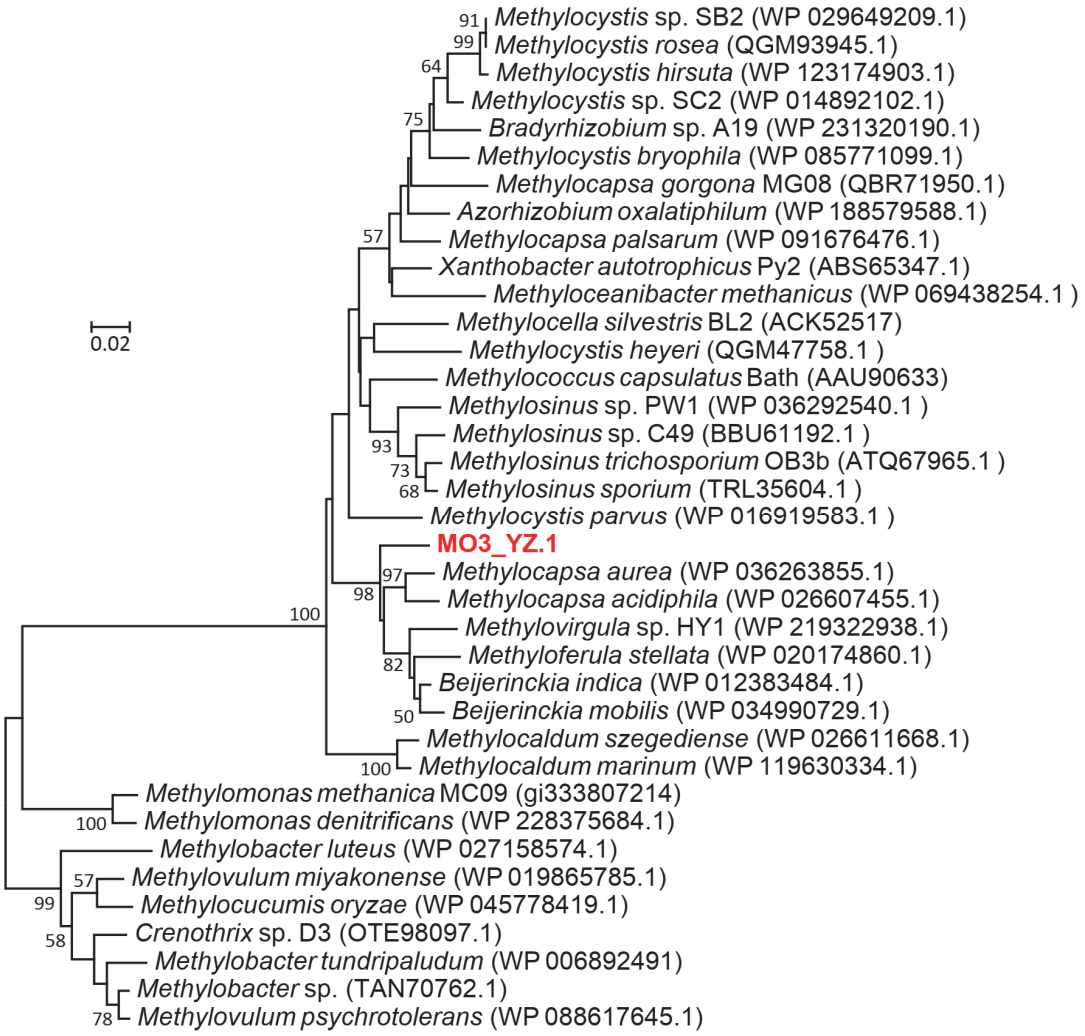


Figure S1. Neighbour-joining phylogenetic tree of the *nifH* gene from MO3_YZ.1. The tree based on 290 amino acid positions is constructed using MEGA software (version 6.06) and evaluated with 1000 bootstraps. Bootstrap values higher than 50% are given at the branch nodes. Scale bar indicates 2% amino acid sequence divergence.

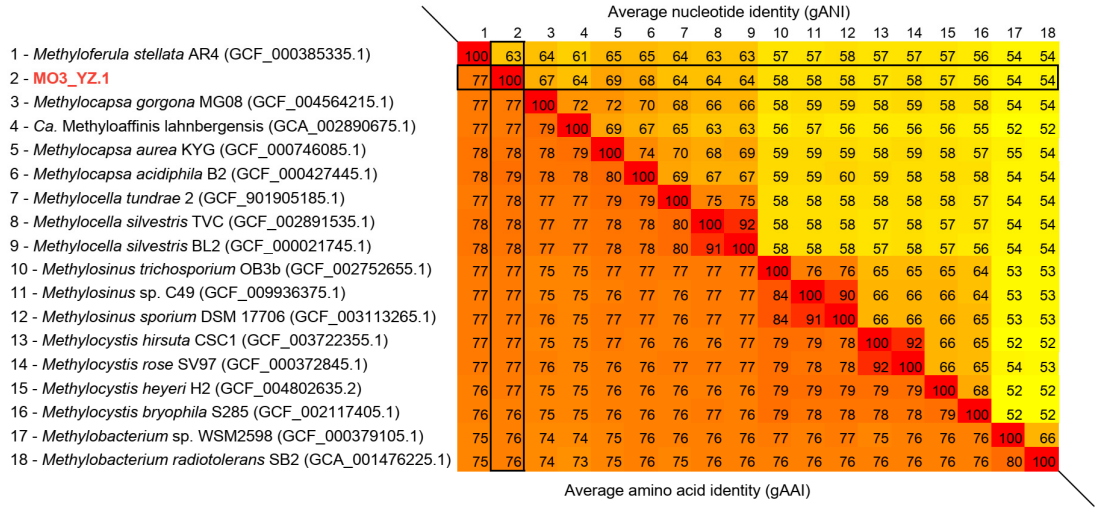


Figure S2. Matrix of pairwise genomic average nucleotide identity (gANI) and genomic average amino acid identity (gAAI) values of MO3_YZ.1 and its relatives. The genomes sequences were ordered as in Figure 4. The gANI was presented in the lower left triangle and the gAAI was presented in the upper right triangle. Bothe of gANI and gAAI in this figure were calculated by tools of Kostas lab.



Figure S3. Alignments of amino acid sequences of PmoA subunit from methanotrophs. The amino acids that form the tricopper cluster site are shown in blue.