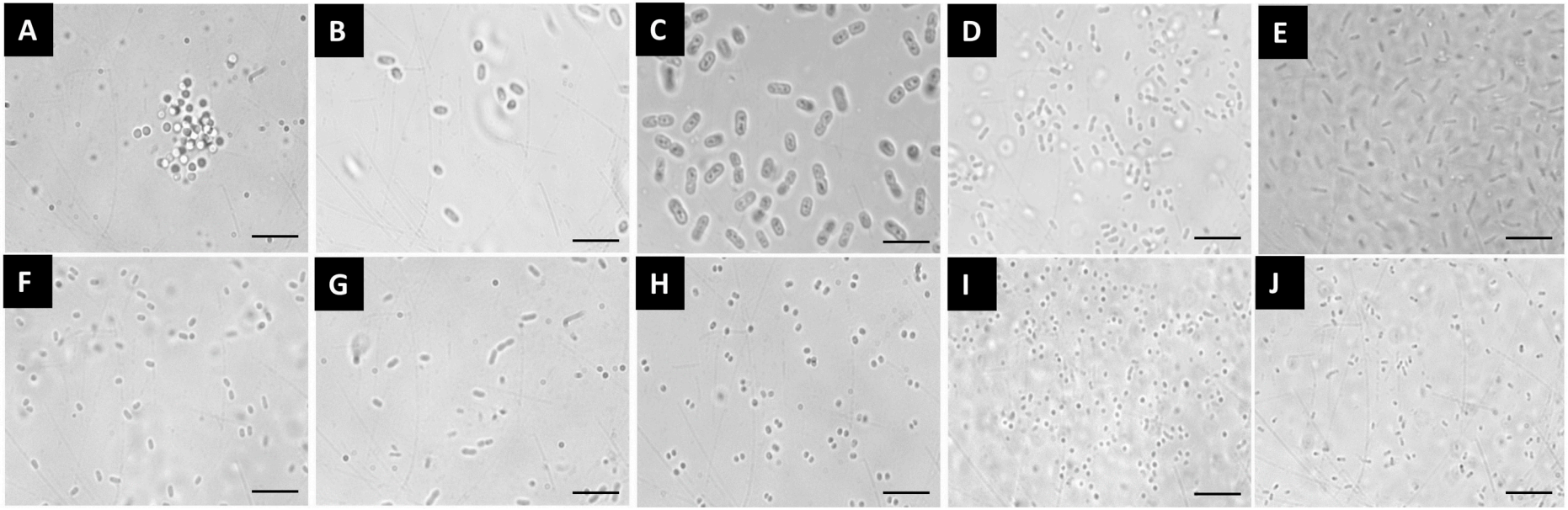
Supplementary Table S1: Presence of genes with potential for conferring PGP traits in methanotrophs strains

Strain name → **PGPR genes ↓**	***Methylocucumis oryzae* BM10**	***Ca.* Methylobacter coli BlB1**	***Methylomonas sp.* Kb3**	***Methylosinus trichosporium* KRF10**	***Methylomonas sp.* WWC4**	***Methylocystis sp*. SnCys**	***Ca.* Methylobacter oryzae KRF1**	***Methylolobus aquaticus* FWC3**	***Methylosinus sporium* KRF6**	***Methylomagnum ishizawai* (strain 175)**
Nitrogen fixation operon	NifHDK operon	NifHDK operon	NifHDK operon	NifHDK operon	NifHDK operon	NifHDK operon	NifHDK and VnfDKGH	NifHDK operon	NifHDK operon	NifHDK operon
Phosphate solubilization (PQQ, glucose dehydrogenase gene homolog, pstA, B, C)	+	+	+	+	+	+	+	+	+	+
Cellulose degradation (Glycoside hydrolase)	+	+	+	+	+	+	+	+	+	+
Alkaline phosphatase	+	+	+	+	+	+	-	+	+	+
Trehalose metabolism	-	-	-	+	-	-	+	+	+	-

Supplementary Table S2: Summary of methanotrophs used in defined consortia in this study

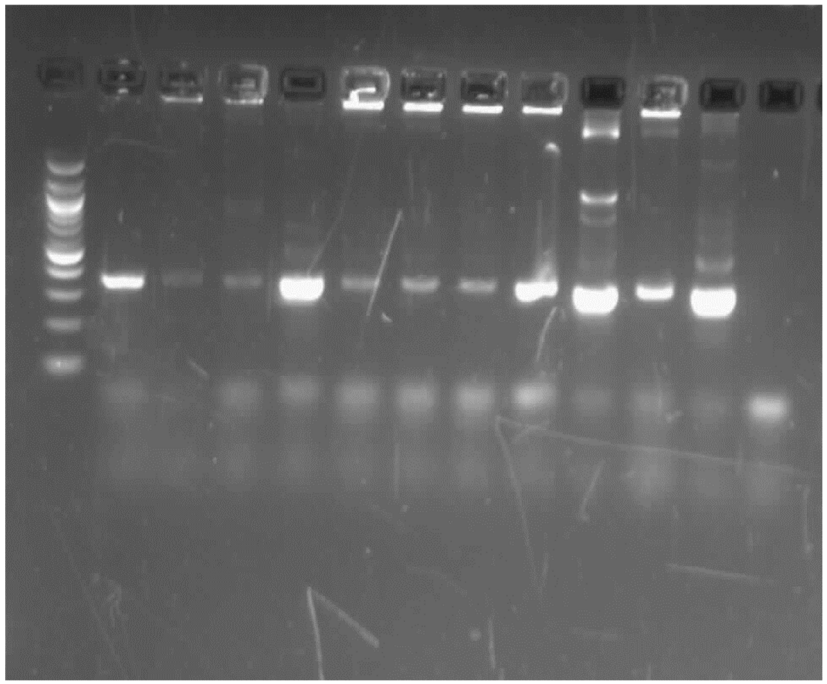
Name of the organism		Identification using *pmoA* gene		Identification using 16S rRNA gene		Presence of nitrogen fixation genes
	Strain name	Nearest match (with type strain)	% Similarity	Nearest match (with type strain)	% Similarity	
Methylomonas koyamae	BM6	*Methylomonas koyamae* Fw12E-Y	99.2	*Methylomonas koyamae* Fw12E-Y	100	+
Methylomonas koyamae	KRF3	*Methylomonas koyamae* Fw12E-Y	96.8	*Methylomonas koyamae* Fw12E-Y	99.32	+
Methylomonas koyamae	IS1	*Methylomonas koyamae* Fw12E-Y	94.19	*Methylomonas koyamae* Fw12E-Y	100	+
Methylomonas sp.	DMS2	*Methylomonas koyamae* Fw12E-Y	94.3	*Methylomonas koyamae* Fw12E-Y	96.3	+
Methylosinus sporium	KRF7	*Methylosinus sporium* NCIMB 11126	98.39	*Methylosinus sporium* NCIMB 11126	98.29	+
Methylosinus sporium	KRF8	*Methylosinus sporium* NCIMB 11126	98.33	*Methylosinus sporium* NCIMB 11126	98.43	+
Methylosinus sporium	KRF9	*Methylosinus sporium* NCIMB 11126	98.33	*Methylosinus sporium* NCIMB 11126	98.39	+
Methylosinus trichosporium	KRF10	*Methylosinus trichosporium* OB3b	96.42	*Methylosinus trichosporium* OB3b	98.72	+
Methylosinus iwaonis	SnCys	*Methylosinus iwaonis* SS37A-Re	99.34	*Methylocystis iwaonis* SS37A-Re	99.93	+
Methylomagnum ishizawai	KRF4	*Methylomagnum ishizawai* RS11-D	99.80	*Methylomagnum ishizawai* RS11-D	99.85	+

SUPPL FIG 1



Supplementary Figure S1: Microscopic features of live cells of type I and type II methanotrophs observed under 100X (oil immersion) magnification phase-contrast microscope (Nikon 80i, Japan microscope with a camera) **A**. *Ca*. Methylobacter coli strain BlB1, **B**. *Methylocucumis oryzae* strain BM10, C. *Methylomagnum ishizawai* strain KRF4, D. *Methylomonas sp. strain* Kb3, **E**. *Methylosinus trichosporium* strain KRF10, **F**. *Methylomonas sp.* strain WWC4, **G**. *Ca.* Methylobacter oryzae strain KRF1, **H.** *Methylolobus aquaticus* strain FWC3, **I.** *Methylosinus sporium* strain KRF6, **J**. *Methylosinus sp.* SnCys

SUPPL FIG 2



Supplementary Figure S2: Gel electrophoresis image of *nifH* PCR products checked for the methanotrophic strains used in defined consortia (type I *Methylomonas* and type II *Methylocystis-Methylosinus* consortia), and *Methylomagnum ishizawai* strain KRF4 with positive and negative controls.

nifH gene amplification products (362 bp) Lane 1: 100bp ladder, Lane 2: *Methylomonas koyamae* BM6, Lane 3: *Methylomonas koyamae* KRF3, Lane 4*: Methylomonas koyamae* IS1, Lane 5: *Methylomonas sp.* DMS2, Lane 6*: Methylosinus sporium* KRF7, Lane 7: *Methylosinus sporium* KRF8, Lane 8: *Methylosinus sporium* KRF9, Lane 9: *Methylosinus trichosporium* KRF10, Lane 10: *Methylosinus iwaonis* Sn-Cys*,* Lane 11: *Methylomagnum ishizawai* KRF4, Lane 12: Positive control, Lane 13: Negative control

Supplementary Methods:

DNA extraction of biomass was carried out using a modified Gram-negative process of GenElute™ Bacterial Genomic DNA Kit Protocol (Sigma Aldrich, USA) (https://www.sigmaaldrich.com/IN/en/product/sigma/na2110). The genomes were sequenced in Medgenome laboratories, in Bangalore. The genomic comparison of NCBI-submitted genomes of isolated methanotrophs with their closest members was analyzed to calculate the average nucleotide identity (ANIb-G, http://jspecies.ribohost.com/jspeciesws/#analyse), digital DNA–DNA hybridization (dDDH, http://ggdc.dsmz.de/) and the average amino-acid identity (AAI, http://enve-omics.ce.gatech.edu/aai/).

Genome sequencing: The genomes were sequenced by Medgenome, Bangalore, using Illumina sequencing technology, which produced paired-end reads. After low-quality bases and adapter sequence filtration, the high-quality paired-end reads were retained using Trimmomatic (v 0.35) and cutadapt (v 1.18). The assembly was optimized using an SSPACE-basic assembler to obtain high-quality genome assembly. High-quality reads were assembled using the Soapdenovo-127mer assembler (v 2.04). Scaffolds were constructed with an N_{50}. Genes were annotated using blastX.

Genome annotation:

NCBI (National Centre for Biological Information): NCBI Prokaryotic Genome Annotation Pipeline (PGAP) was used for genome annotation that combines alignment-based methods with methods of predicting protein-coding and RNA genes and other functional elements directly from the sequence (https://submit.ncbi.nlm.nih.gov/).

RAST: RAST (Rapid Annotation using Subsystem Technology) server was used for annotating complete or nearly complete bacterial and archaeal genomes (https://rast.nmpdr.org/). It provides high-quality genome annotations for these genomes across the whole phylogenetic tree. The annotation provides the mapping of genes to subsystems and metabolic reconstruction.

KEGG web server: The metabolic pathways were constructed using the KEGG 2.2 webserver (https://www.kegg.jp/blastkoala/) using the amino acids FASTA file as an input. The pathway can also be reconstructed using KEGG Mapper (https://www.genome.jp/kegg/mapper/reconstruct.html) using the KEGG-annotation file. Pathways for genes responsible for plant growth promotion, including nitrogen fixation, were retrieved from the KEGG mapper.

***nifH* gene amplification:**

The functional *nifH* gene was amplified from the single colonies of cultures of strains belonging to the genus *Methylomonas*, *Methylocystis*, *Methylosinus*, and *Methylomagnum ishizawai* strain KRF4 using the functional *nifH* primer pair [26]. All amplifications were carried out in 25-µl total volume in ABI thermal cycler (Veriti) using Takara® PCR Master Mix. The PCR program for 30 cycles was set as, denaturation at 94℃ for 30s, annealing at 53℃ for 1min, and extension at 72℃ for 1min. After amplification was done, the gel electrophoresis was carried out and confirmed the results for the presence of the *nifH* gene and the product is 362 bp.

Growth in nitrogen-free medium:

The strains were cultured in 65 ml or 125 ml serum bottles with NMS medium which was devoid of potassium nitrate or any other nitrogen source. The serum bottles with 15 ml of nitrogen-free NMS medium were first gassed with nitrogen and then autoclaved. After cooling down and

inoculation, 40% of the gas phase was replaced with 20% methane and 20% air to achieve micro-aerophilic conditions of 4-5% oxygen in the headspace. The bottles were incubated under static conditions. Positive controls were kept where a modified NMS medium (with 1g KNO_3 per l of medium was used). The growth was noted in terms of visible turbidity or pellicle formation.