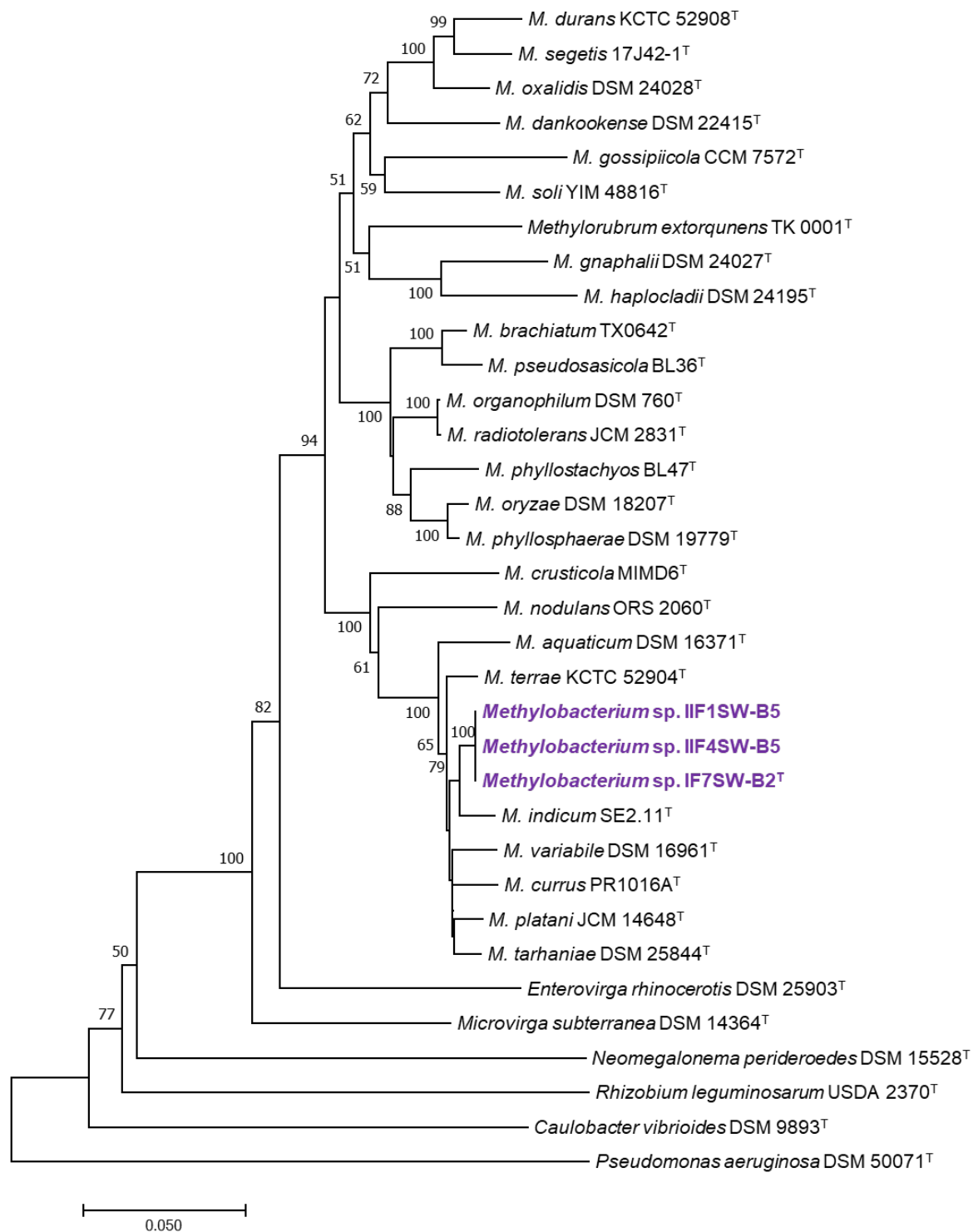
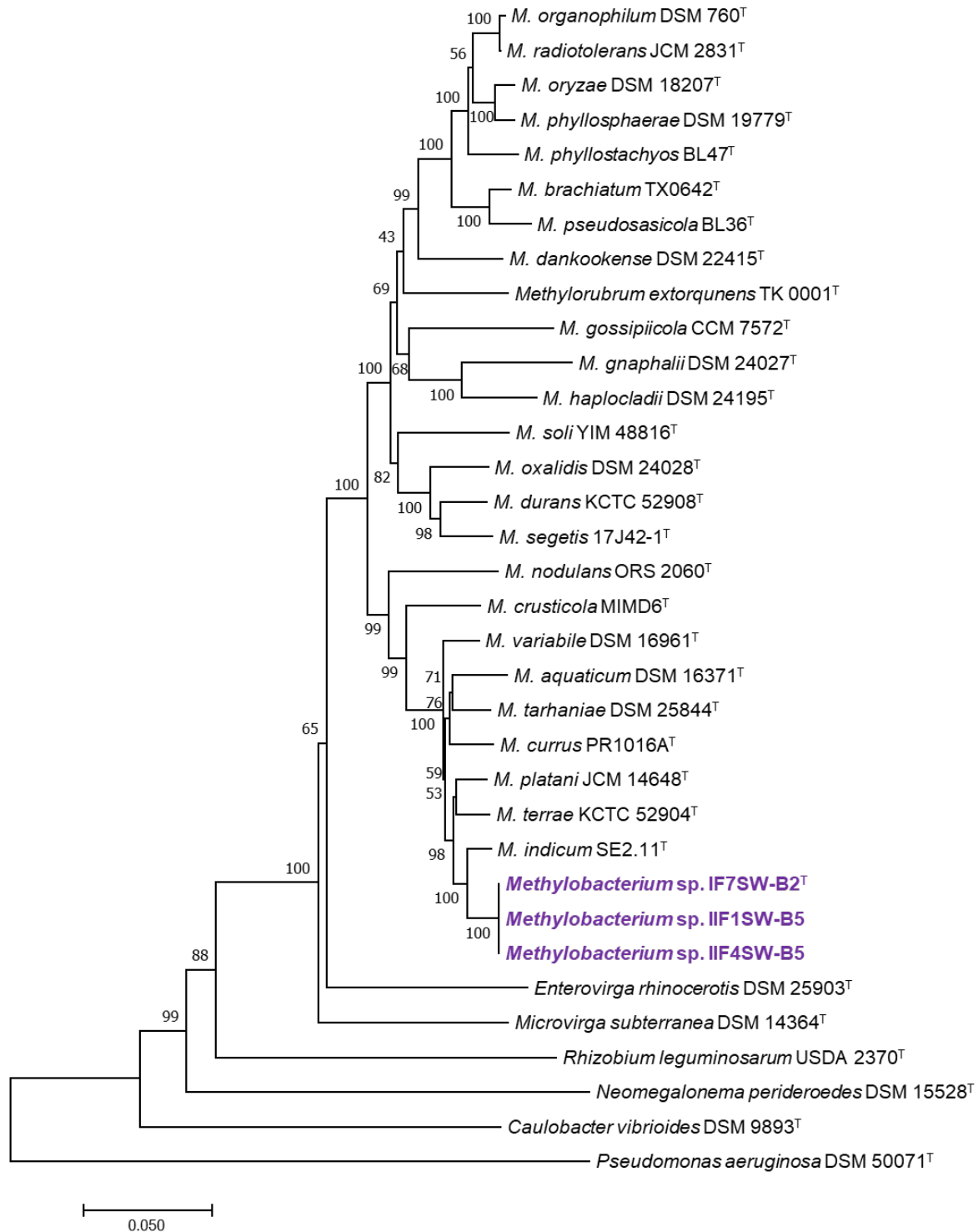


**Supplementary Figure S1.** Phylogenetic tree generated by the neighbor-joining method, based on ATP synthase F1 (*atpD*) beta subunit sequence, showing the phylogenetic relationship of *Methylobacterium* sp. nov. with members of the family *Methylobacteriaceae*. Bootstrap values from 1000 replications are shown at branch points. Bar, 0.05 substitution per site.

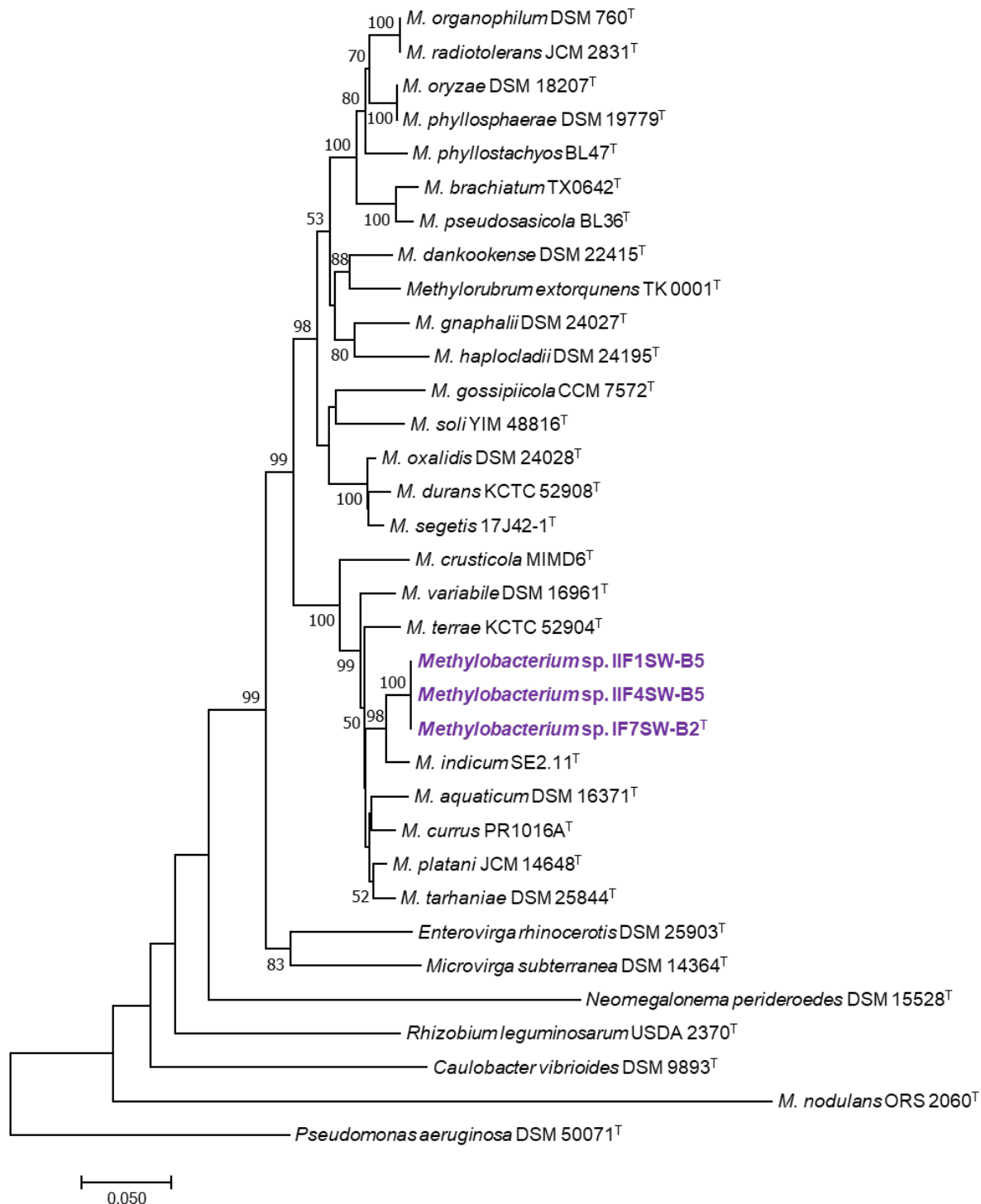




**Supplementary Figure S3.** Phylogenetic tree generated by the neighbor-joining method, based on chaperone gene (*dnaK*) sequence, showing the phylogenetic relationship of *Methylobacterium* sp. nov. with members of the family *Methylobacteriaceae*. Bootstrap values from 1000 replications are shown at branch points. Bar, 0.05 substitution per site.

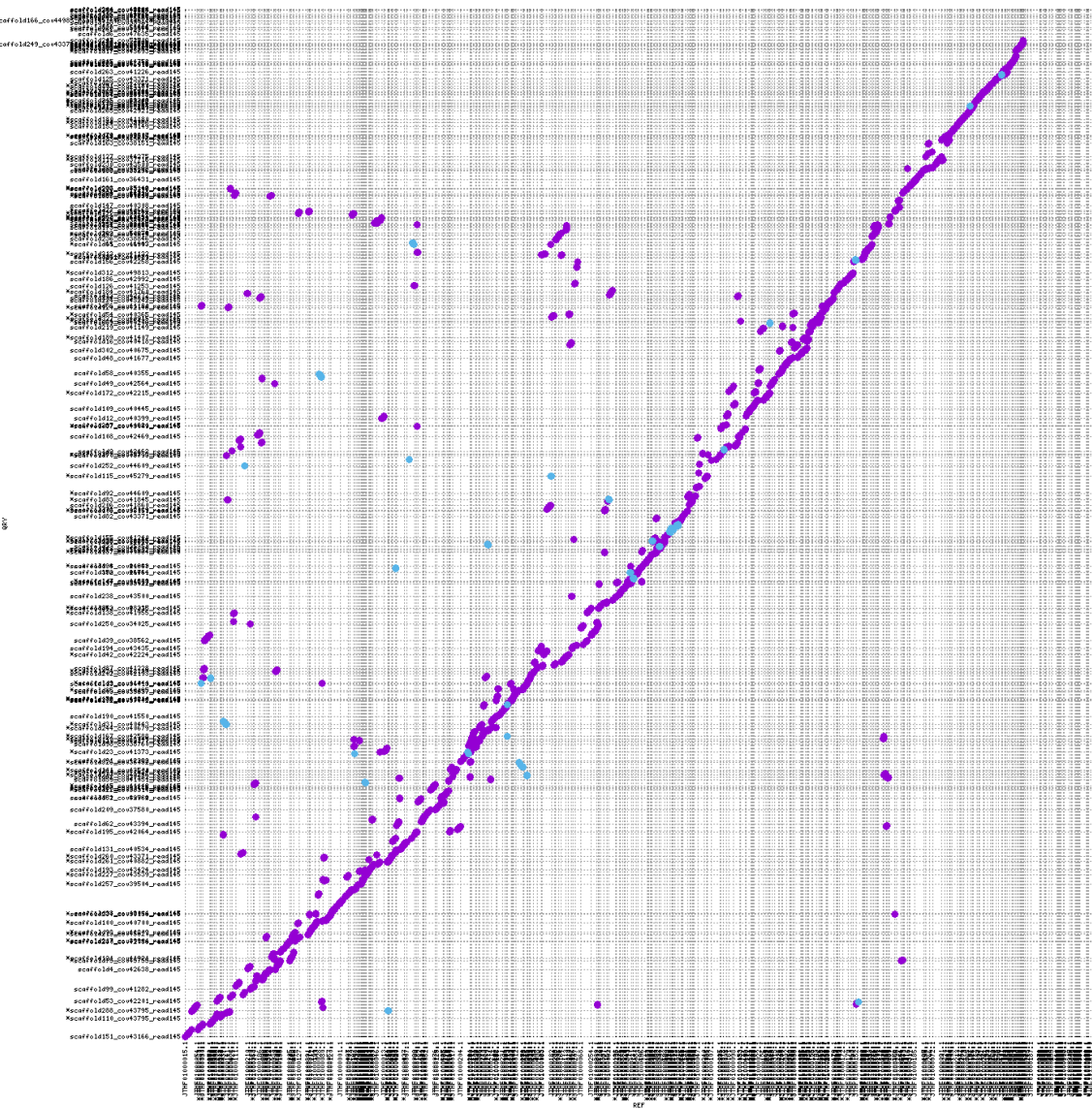


**Supplementary Figure S4.** Phylogenetic tree generated by the neighbor-joining method, based on DNA-directed RNA polymerase (*rpoB*) beta subunit sequence, showing the phylogenetic relationship of *Methylobacterium* sp. nov. with members of the family *Methylobacteriaceae*. Bootstrap values from 1000 replications are shown at branch points. Bar, 0.05 substitution per site.

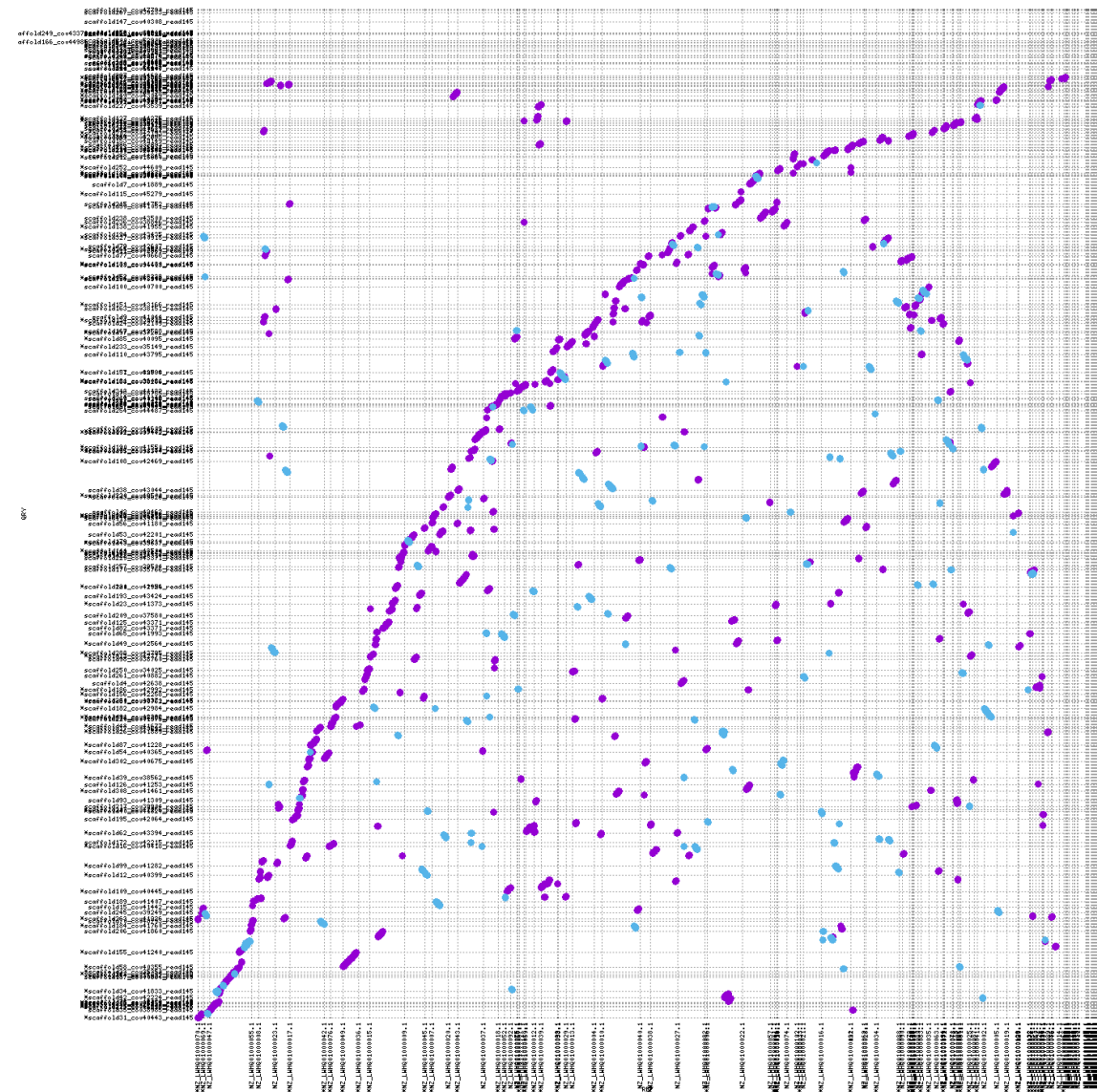


**Supplementary Figure S5.** Phylogenetic tree generated by the neighbor-joining method, based on glutamine synthetase type I gene (*glnI*) sequence, showing the phylogenetic relationship of *Methylobacterium* sp. nov. with members of the family *Methylobacteriaceae*. Bootstrap values from 1000 replications are shown at branch points. Bar, 0.05 substitution per site.

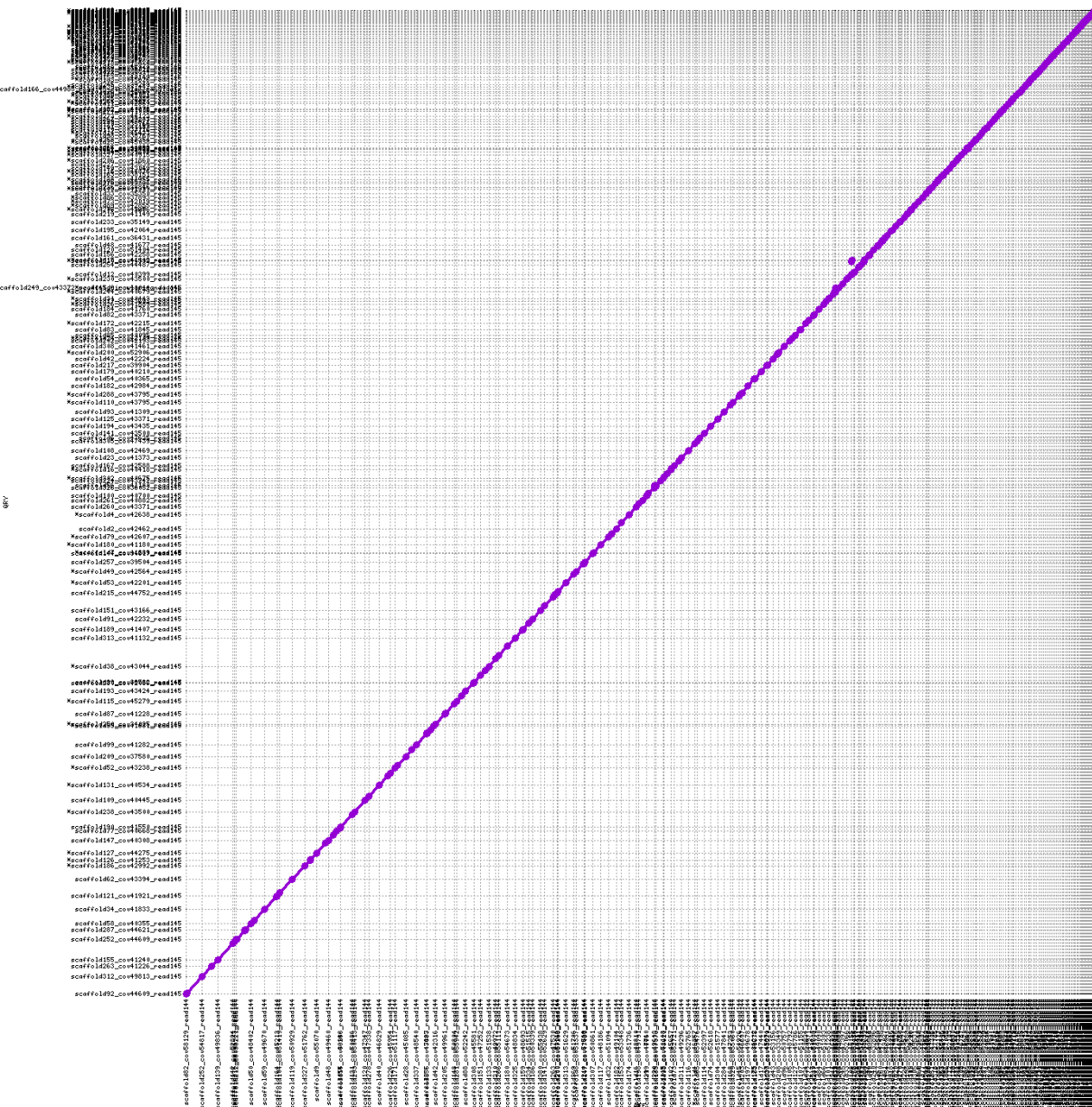




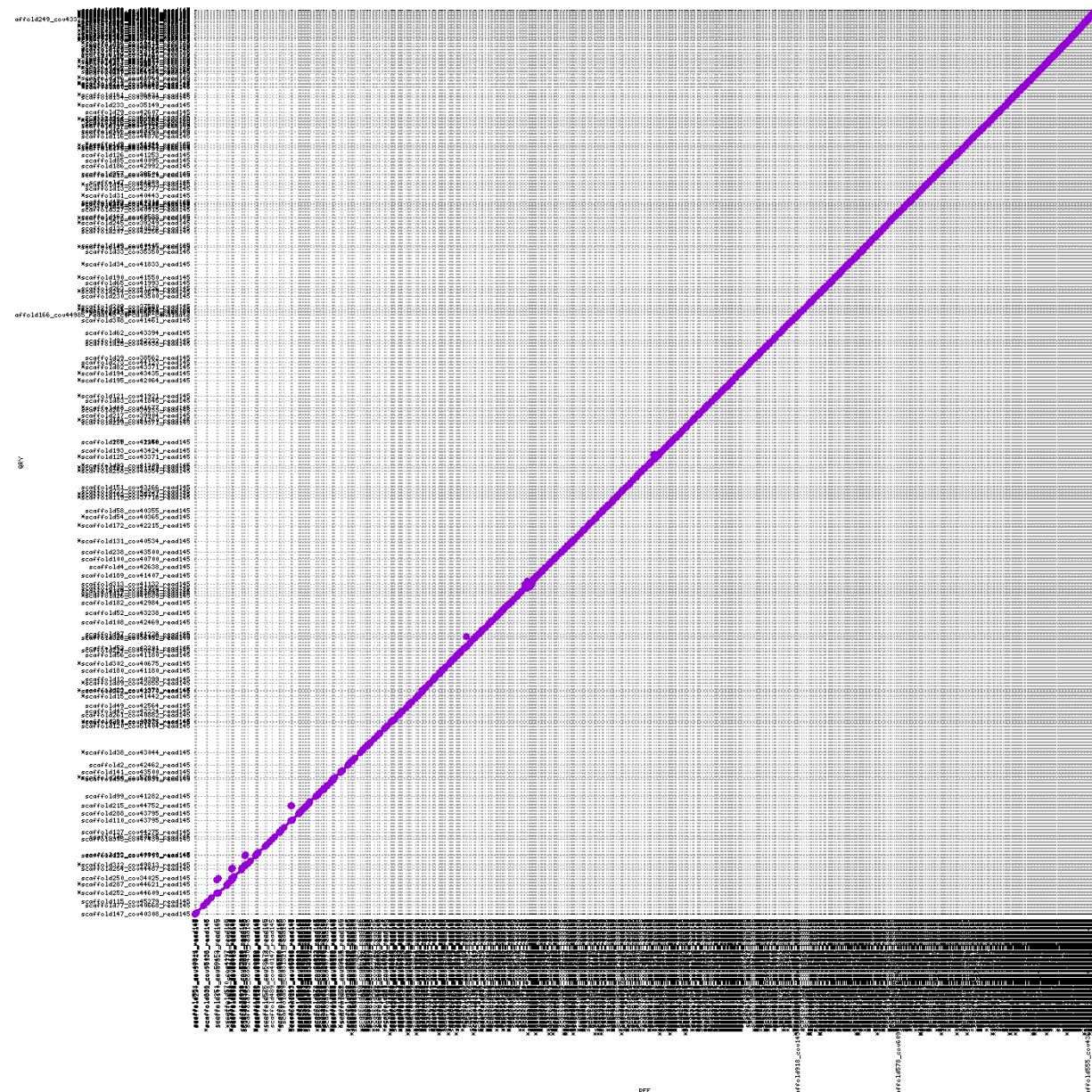
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Ref: *Methylobacterium platani*\_PMB02  
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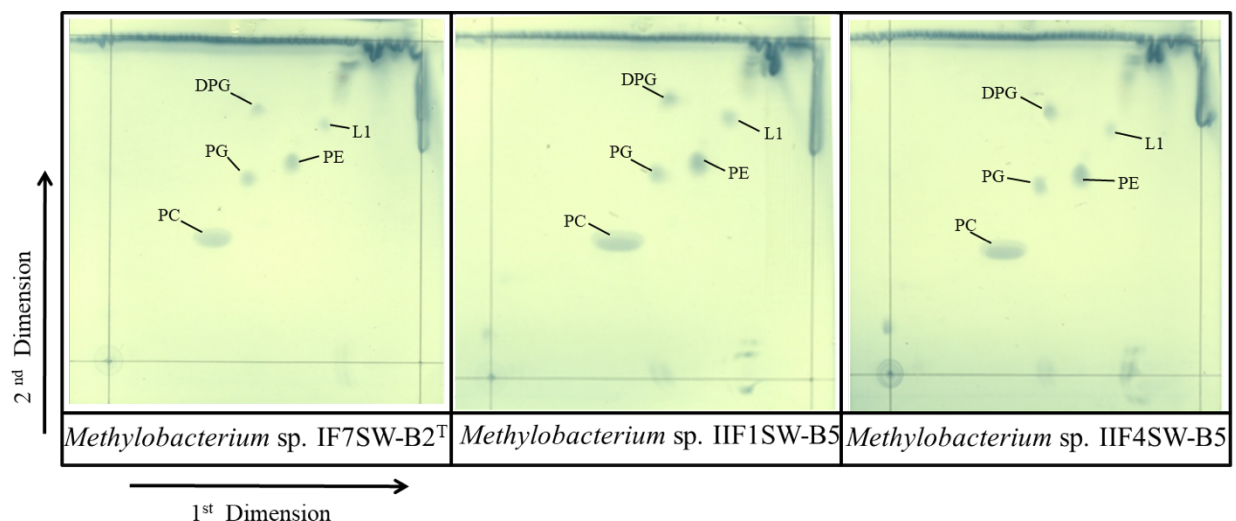
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Query: Methylobacterium\_sp.\_IF7SW-B2



Ref: Methylobacterium\_sp.\_IIF4SW-B5  
Query: Methylobacterium\_sp.\_IF7SW-B2



**Supplementary Figure S6.** MUMmer plot alignment of the entire genomes of three ISS strains, *M. indicum* SE2.11, and *M. platani* PMB02 to detect their divergence and similarity.



**Supplementary Figure S7.** Two-dimensional thin-layer chromatogram of whole cell lipid extracts of *Methylobacterium* sp. IF7SW-B2<sup>T</sup>, *Methylobacterium* sp. IIF1SW-B5 and *Methylobacterium* sp. IIF4SW-B5. The first direction was developed in CHCl<sub>3</sub>:CH<sub>3</sub>OH:H<sub>2</sub>O (65:25:4 v/v) and the second in CHCl<sub>3</sub>:CH<sub>3</sub>OH:CH<sub>3</sub>COOH:H<sub>2</sub>O (80:12:15:4 v/v). Total **polar lipids** were stained with 5% ethanolic molybdophosphoric acid. PE, phosphatidylethanolamine; DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PC, phosphatidylcholine and L1, unidentified lipid.



[illegible]