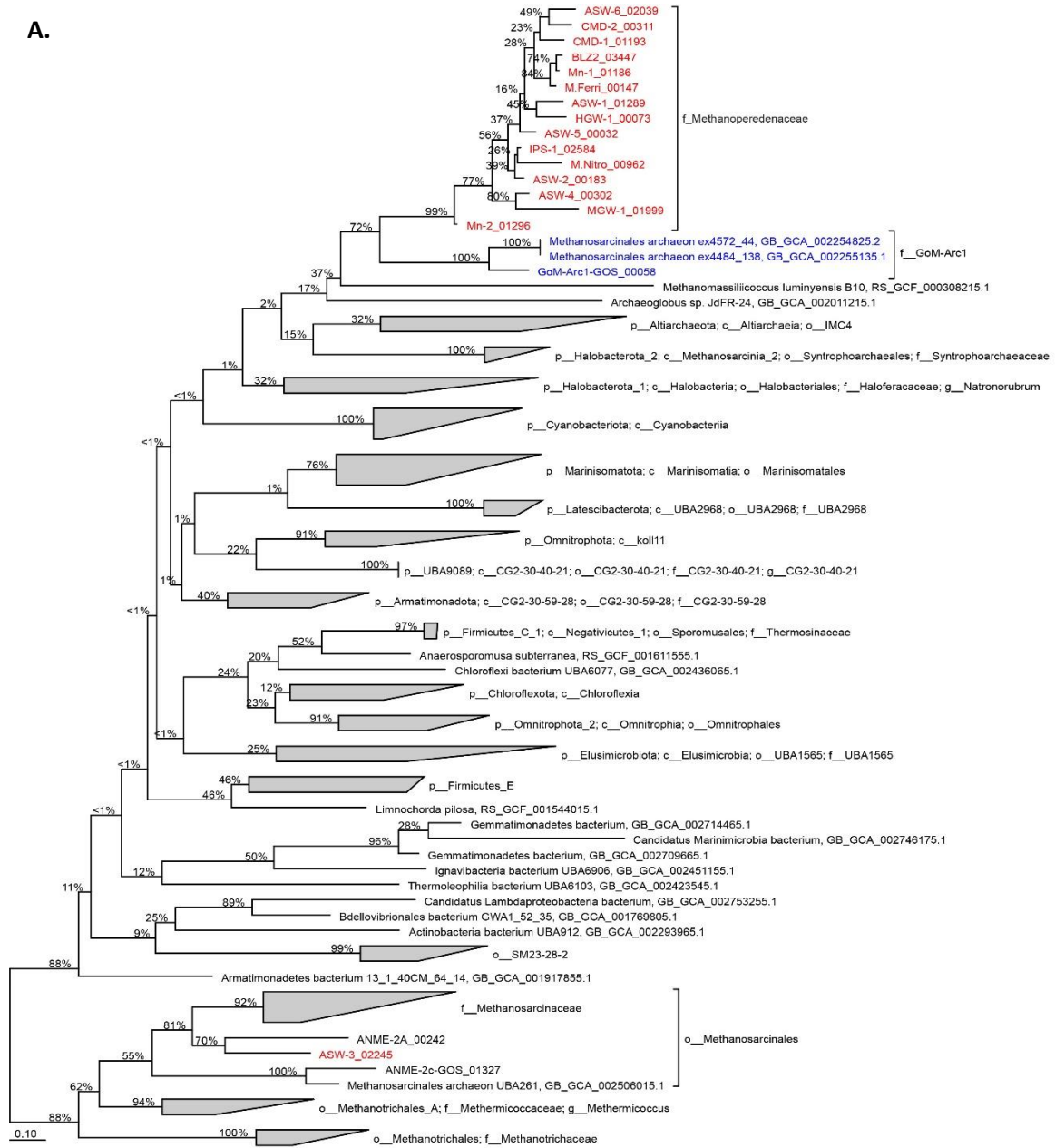
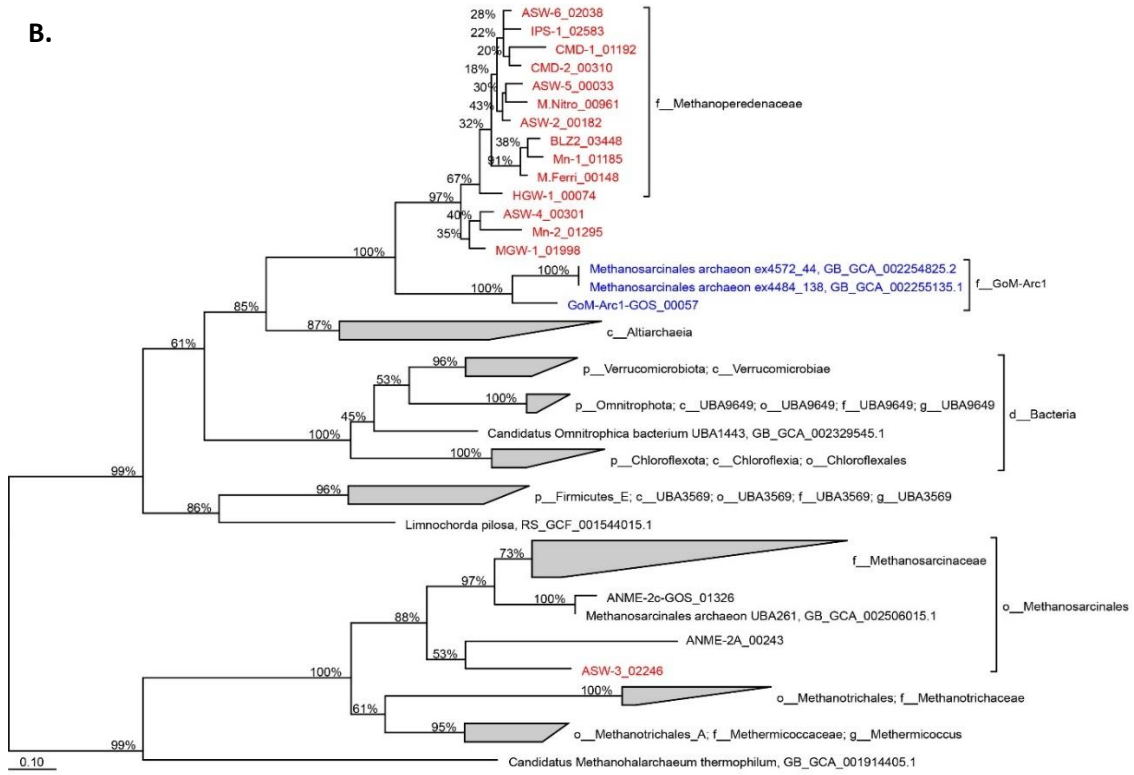


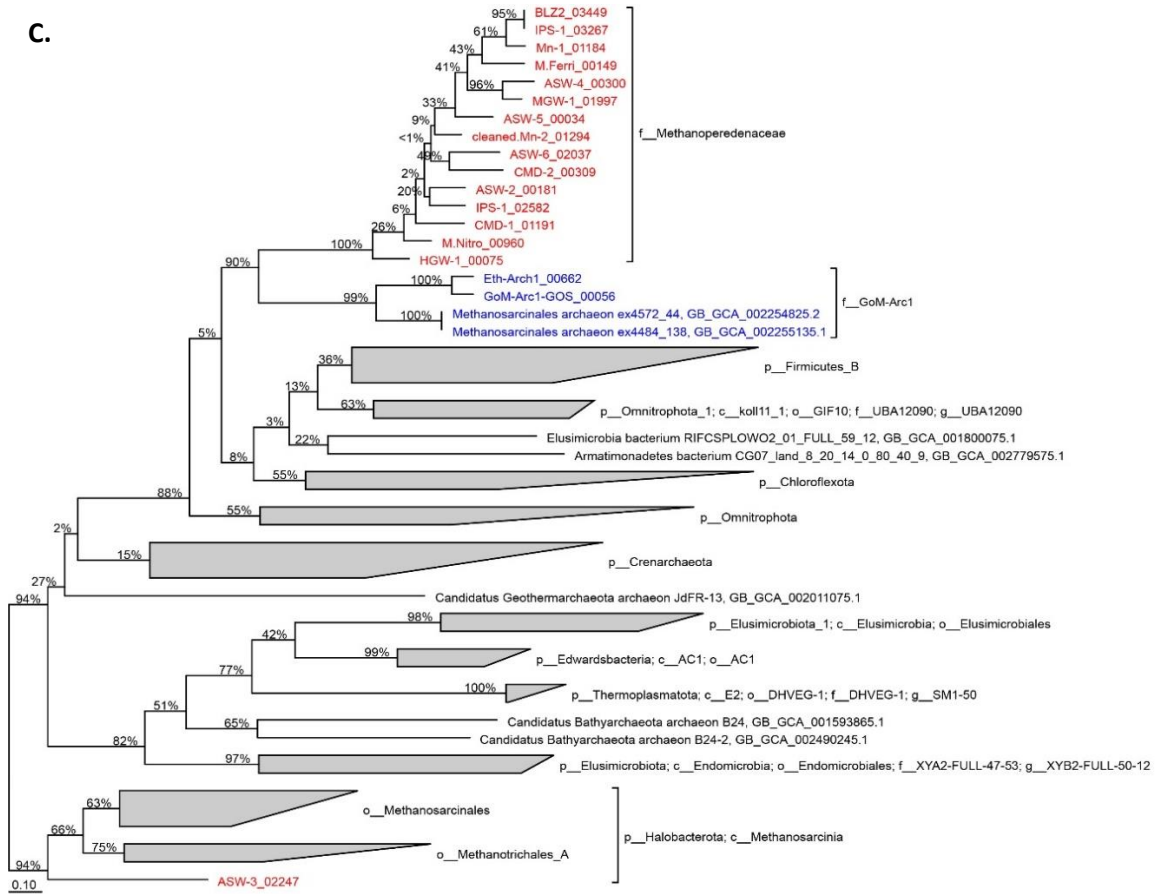
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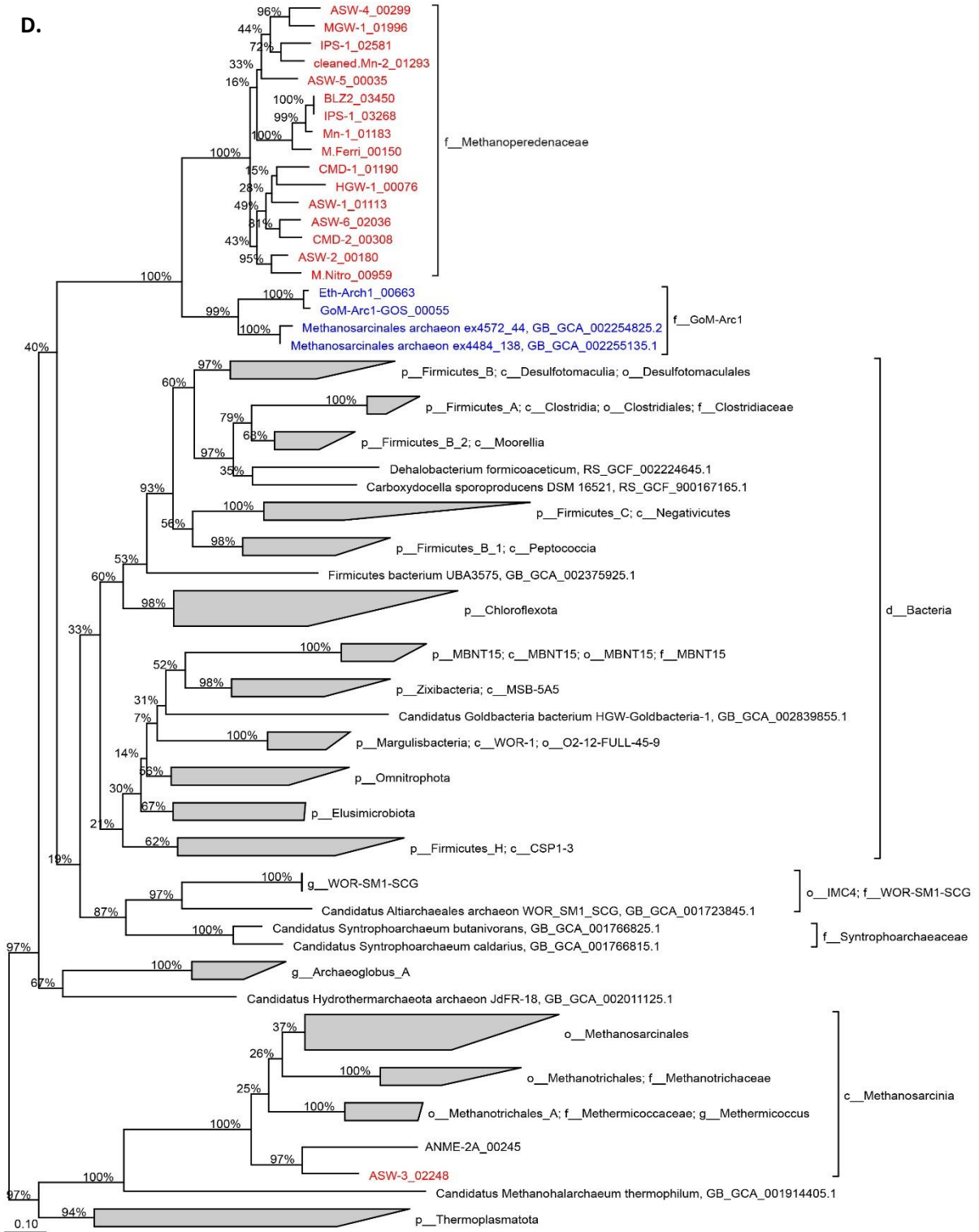
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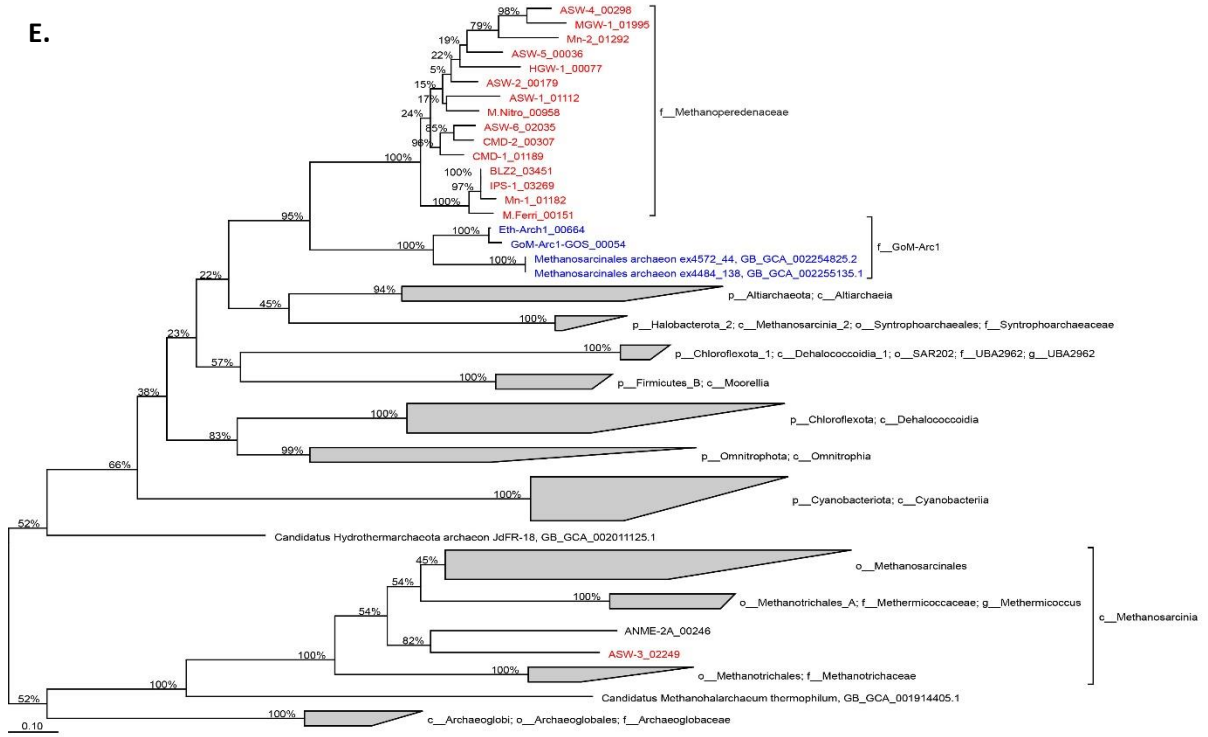
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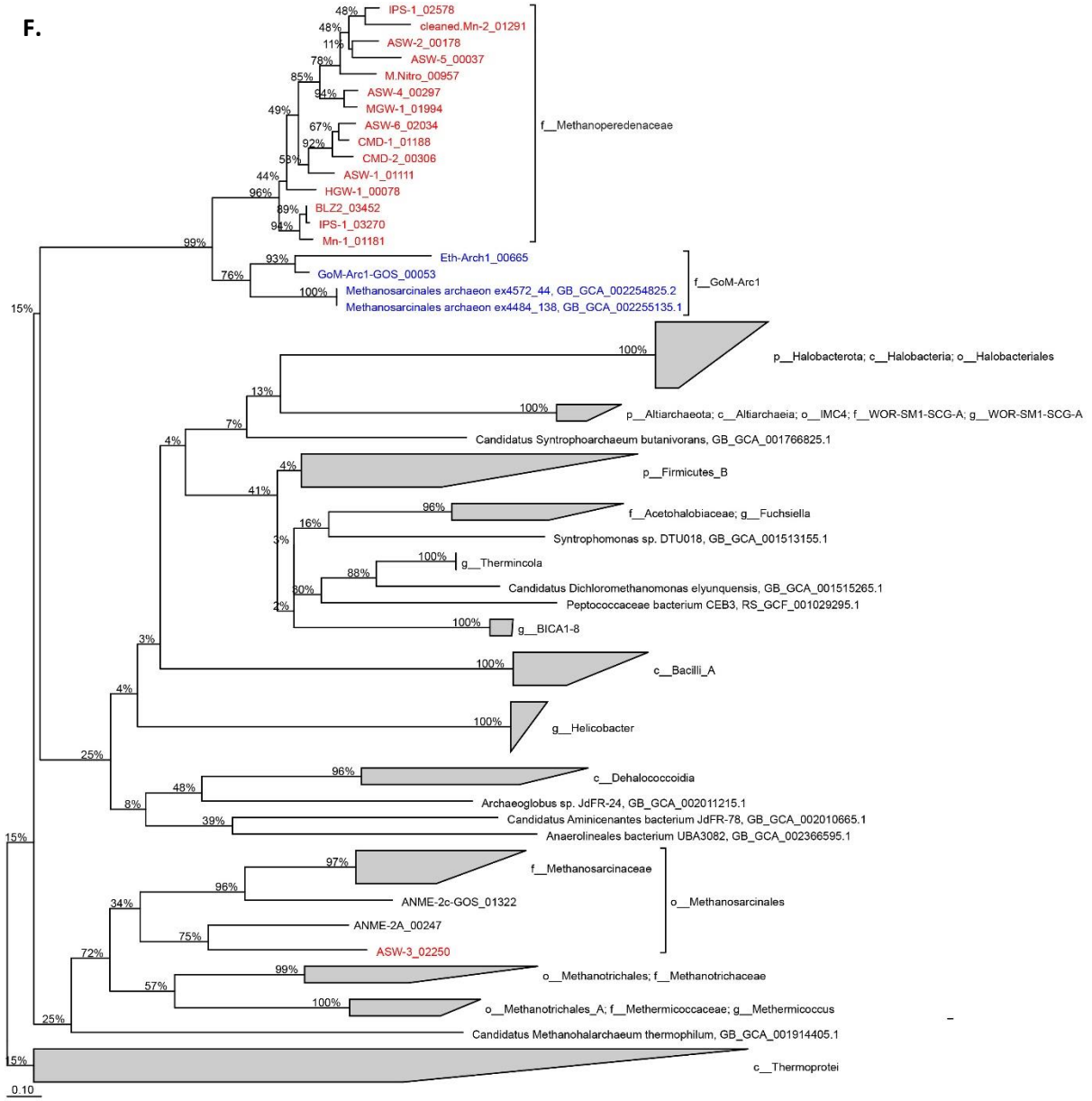
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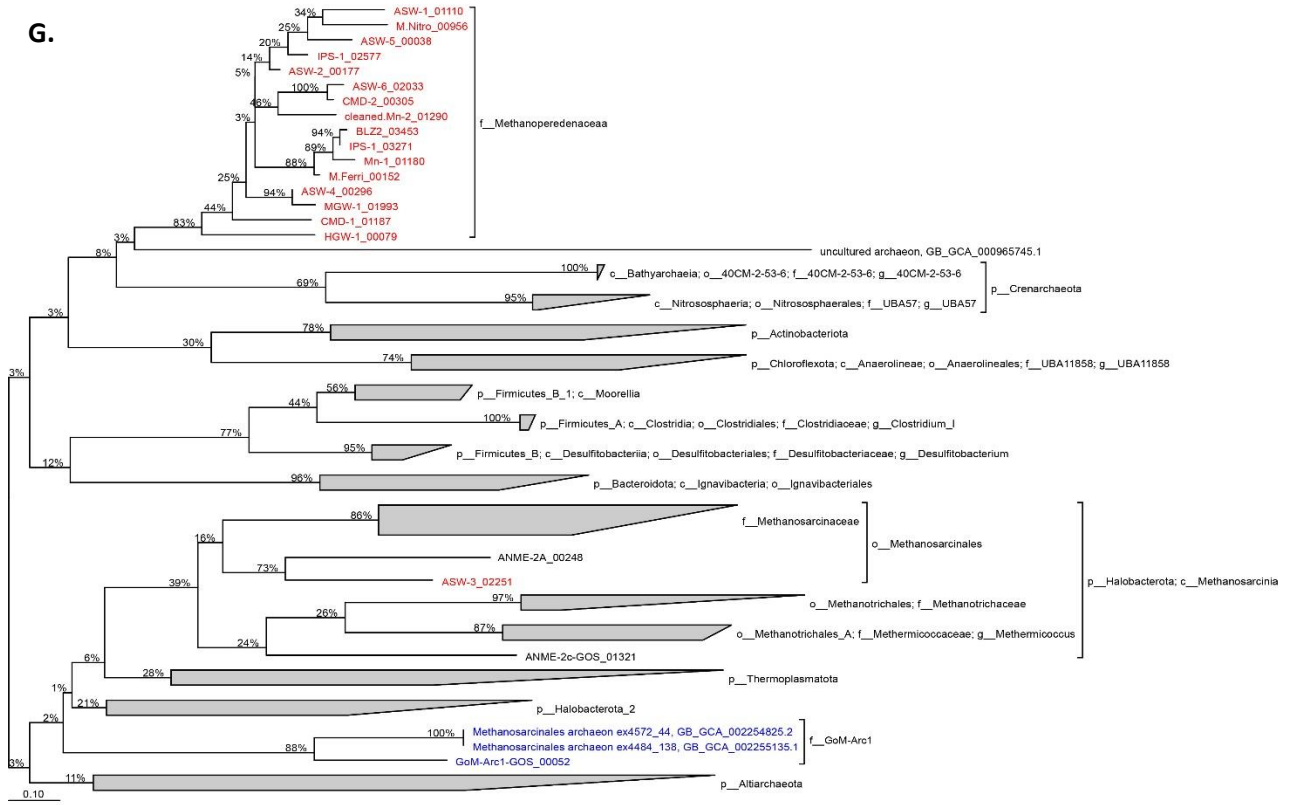
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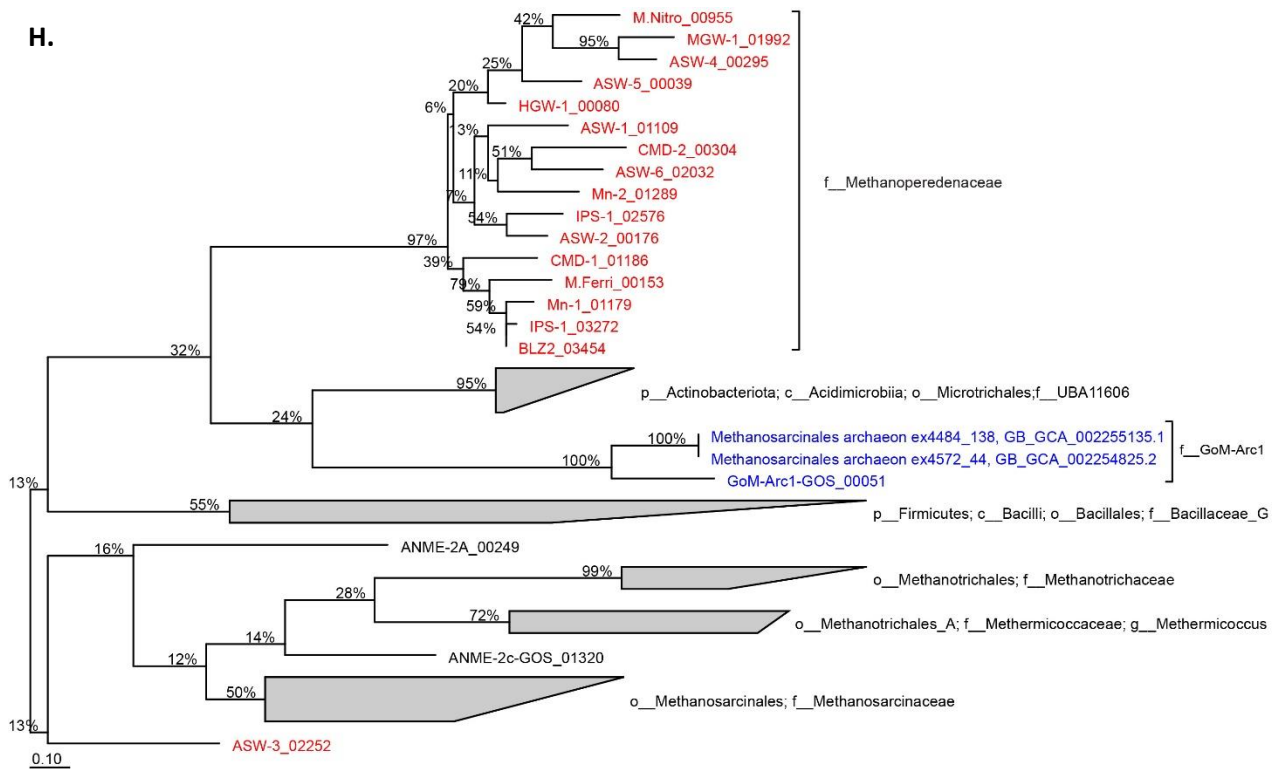
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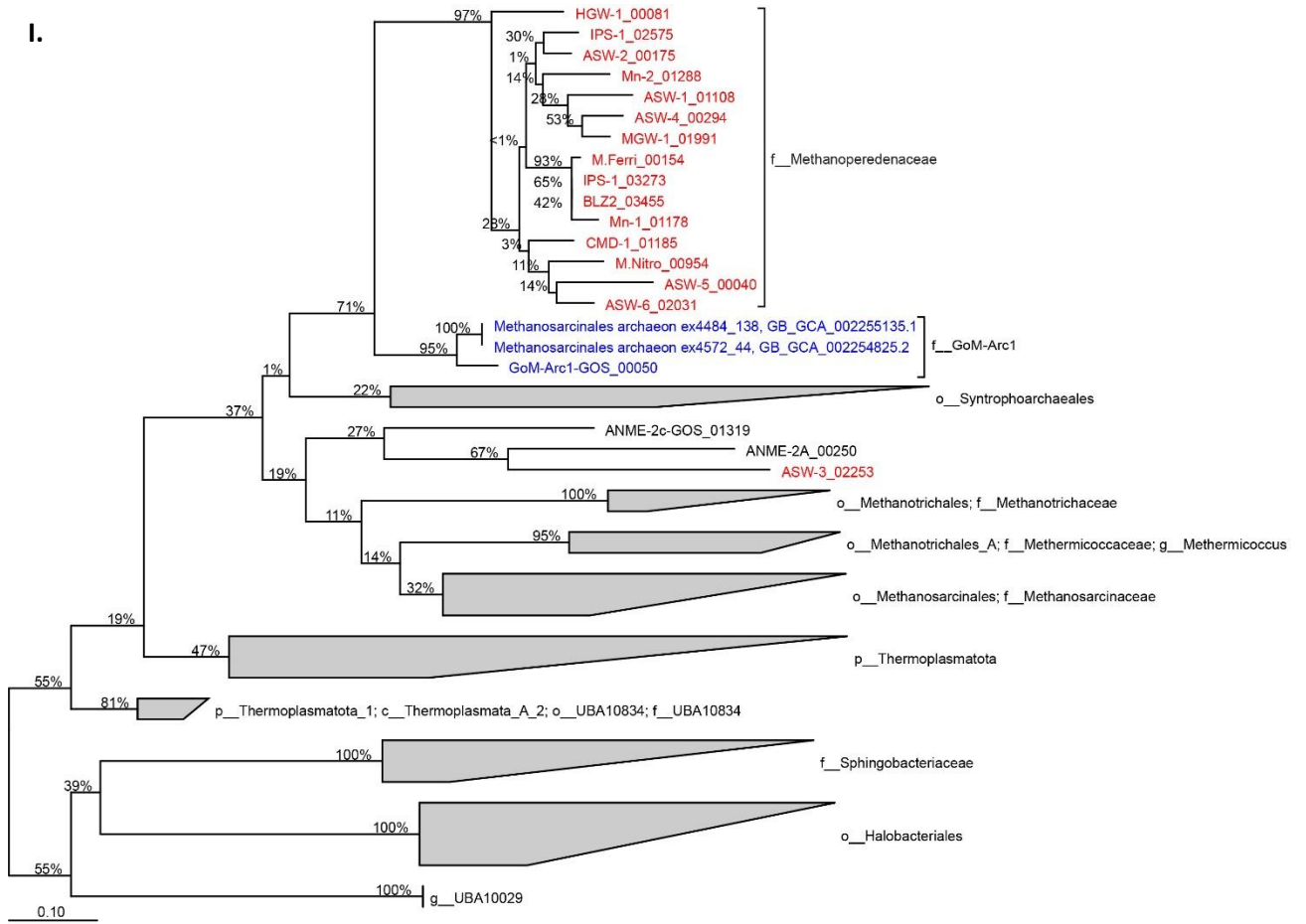
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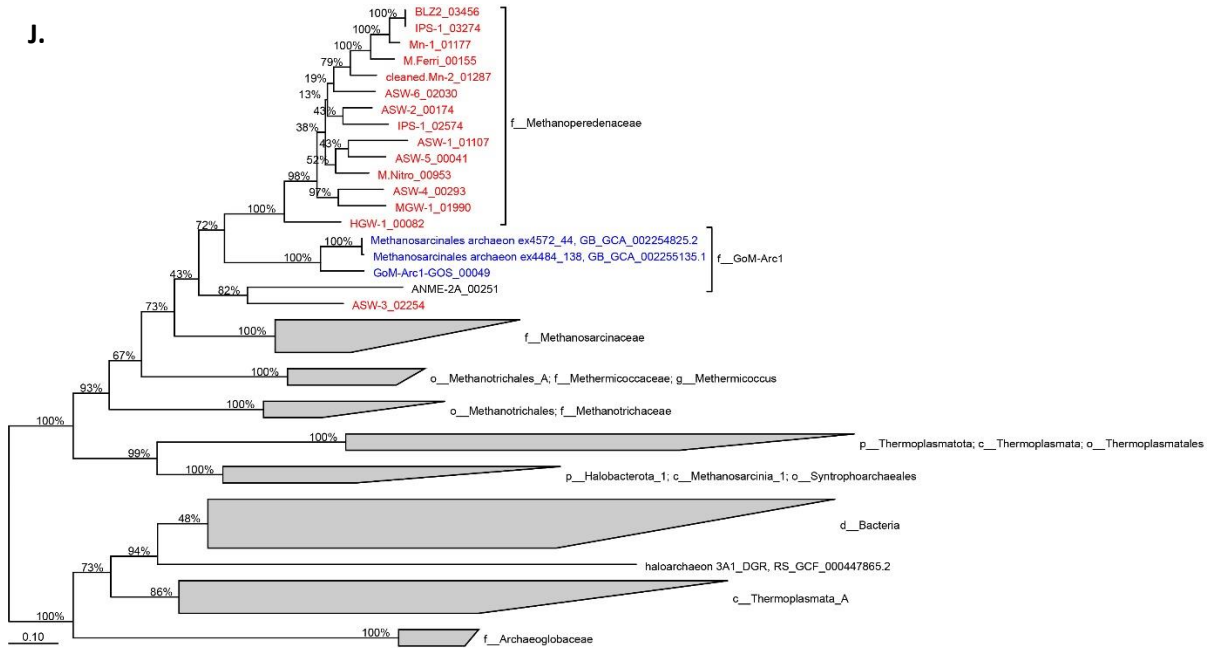
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I.

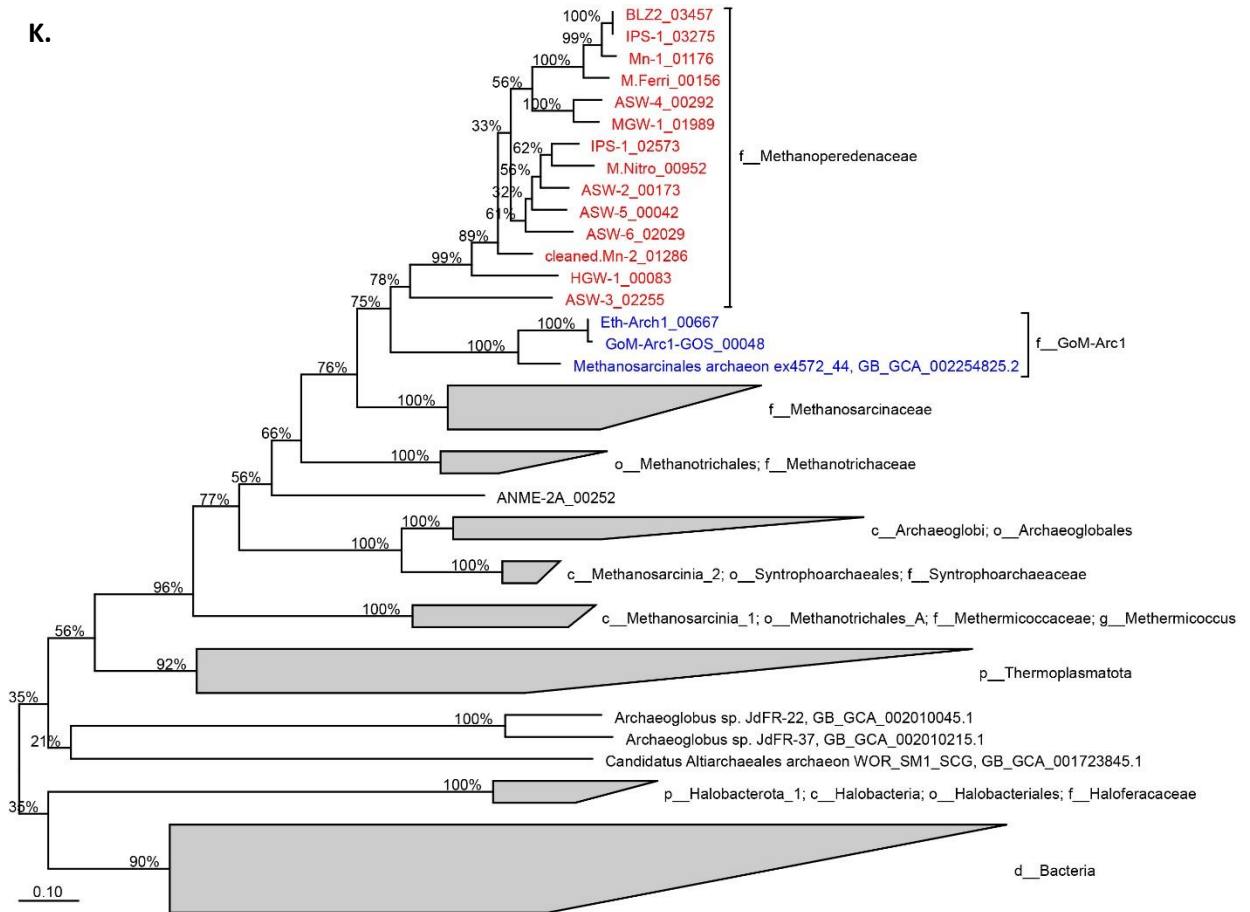


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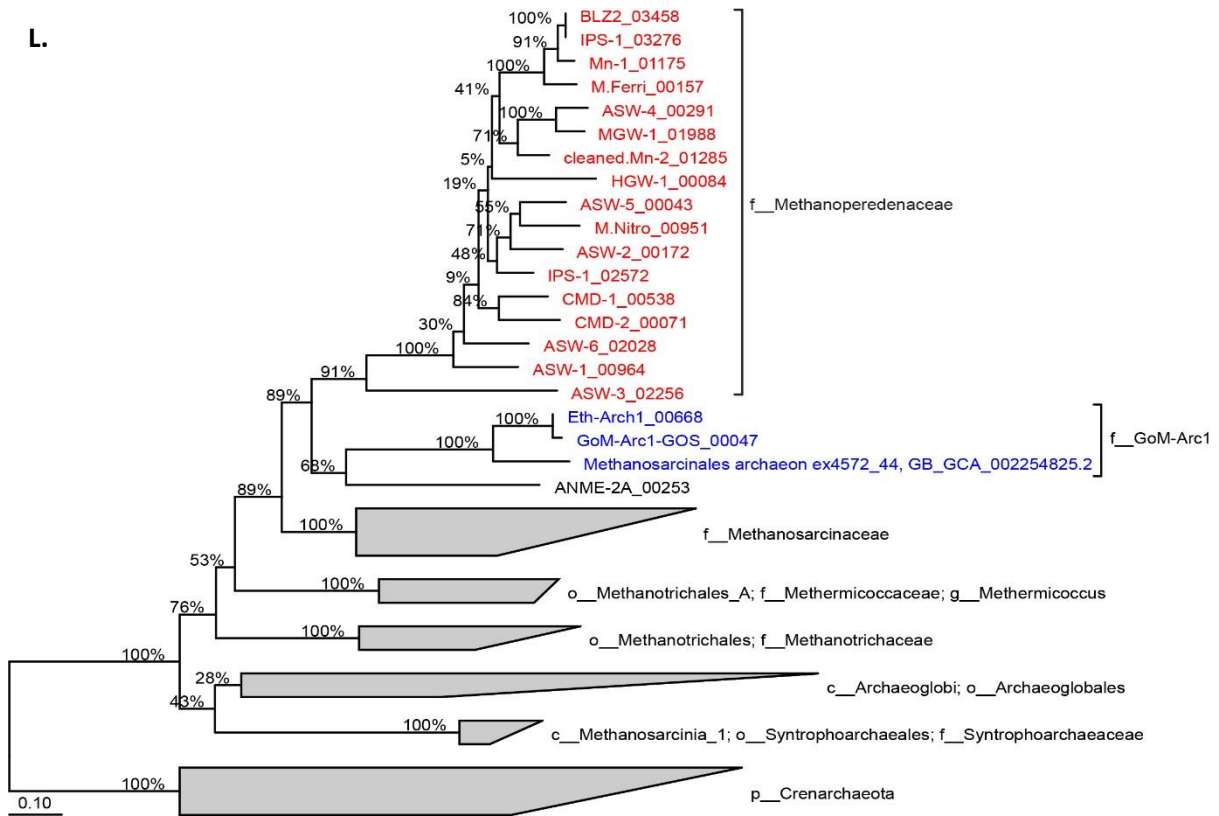


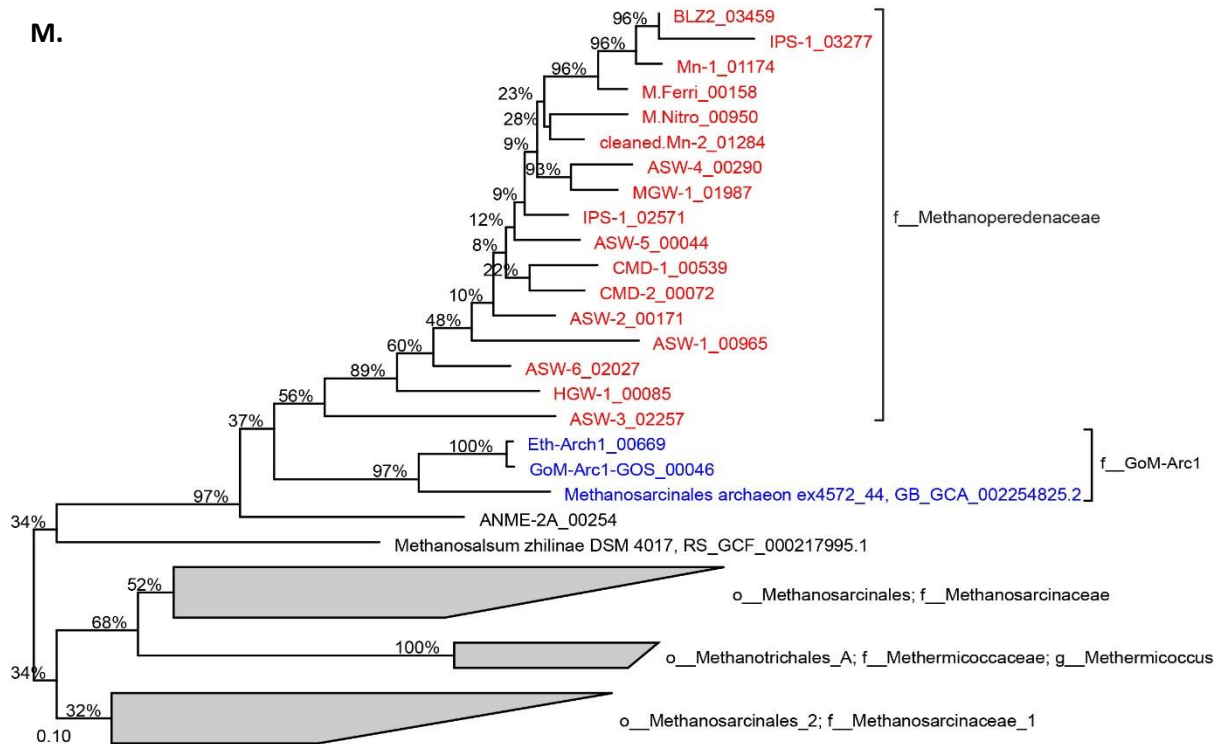


K.



L.





**Figure S6. Phylogenetic analysis of the Fpo subunits annotated in the *Methanoperedenaceae* genomes. A. FpoA B. FpoB C. FpoC D. FpoD E. FpoH F. FpoI G. FpoJ<sub>1</sub> H. FpoJ<sub>2</sub> I. FpoK J. FpoL K. FpoM L. FpoN M. FpoO.** Putative genes recovered from the *Methanoperedenaceae* are highlighted in red. The gene trees were inferred using maximum likelihood and support values calculated via non-parametric bootstrapping. Reference genes and the taxonomy are from the GTDB v83 database (D.H. Parks, M. Chuvochina, D. W. Waite, C. Rinke, A. Skarshewski, P.-A. Chaumeil and P. Hugenholtz, Nat Biotechnol 36: 996-1004, 2018, <https://doi.org/10.1038/nbt.4229>).