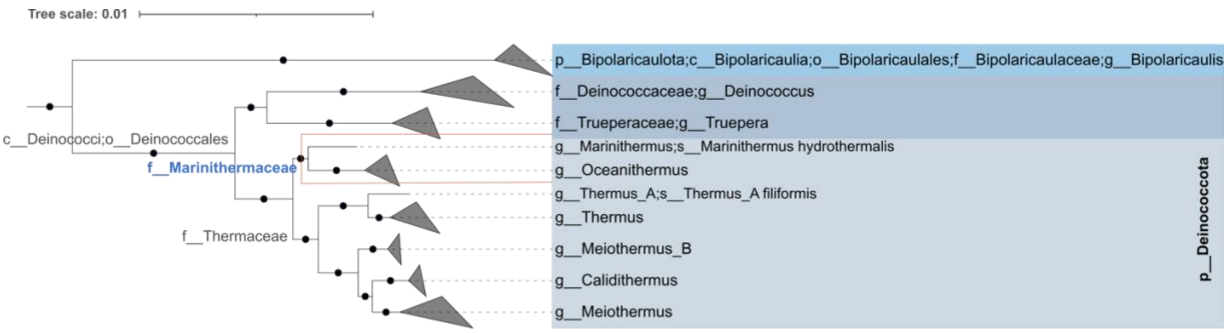
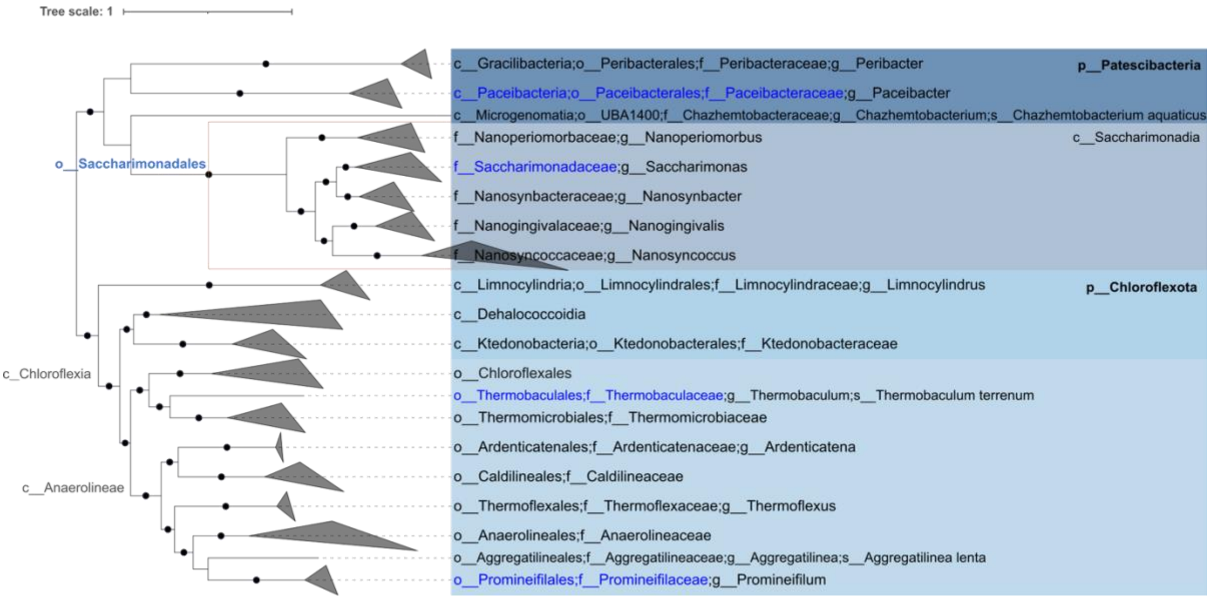
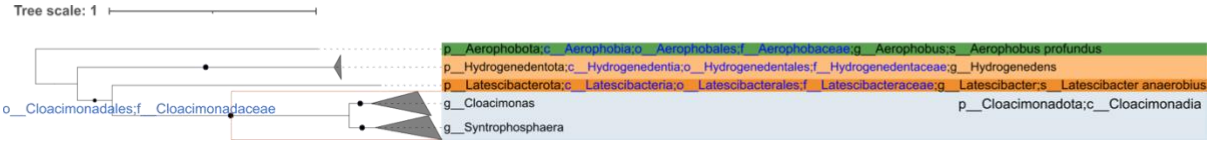
Supplementary figures



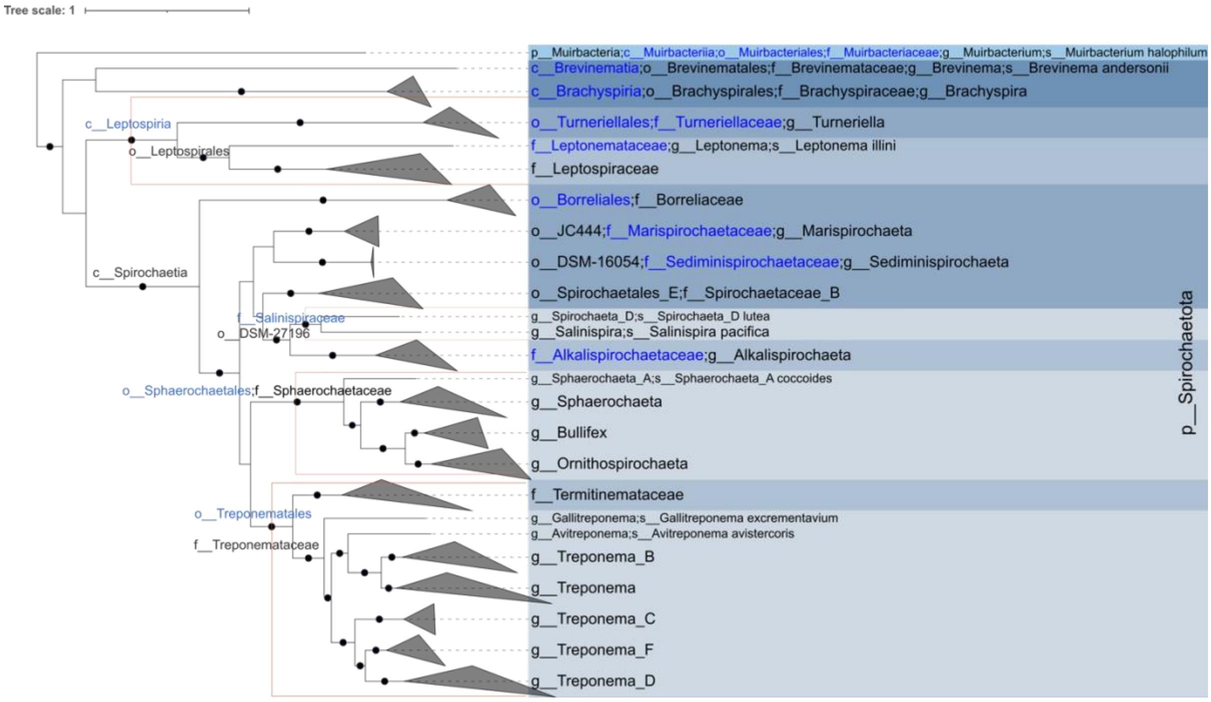
Supplemental Figure 1. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



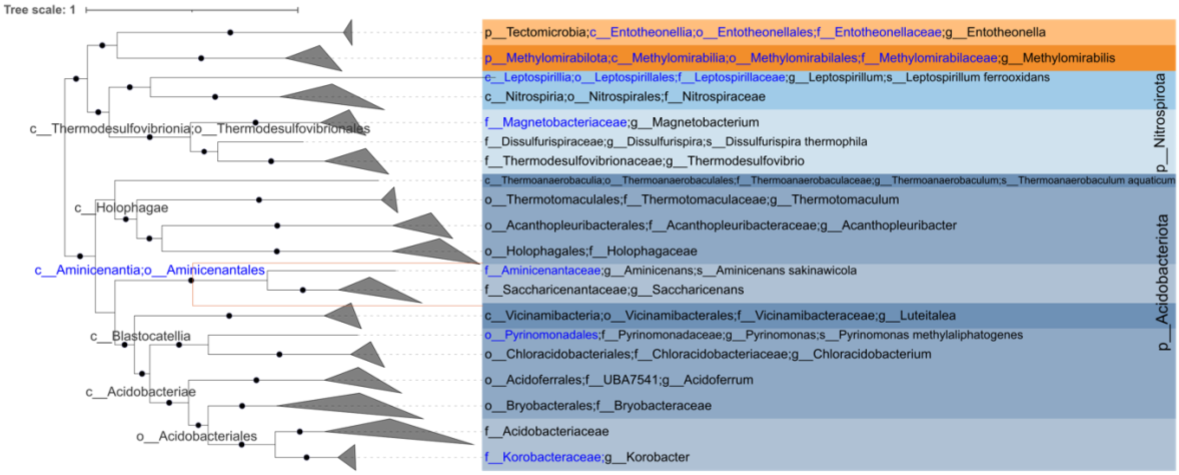
Supplemental Figure 2 Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



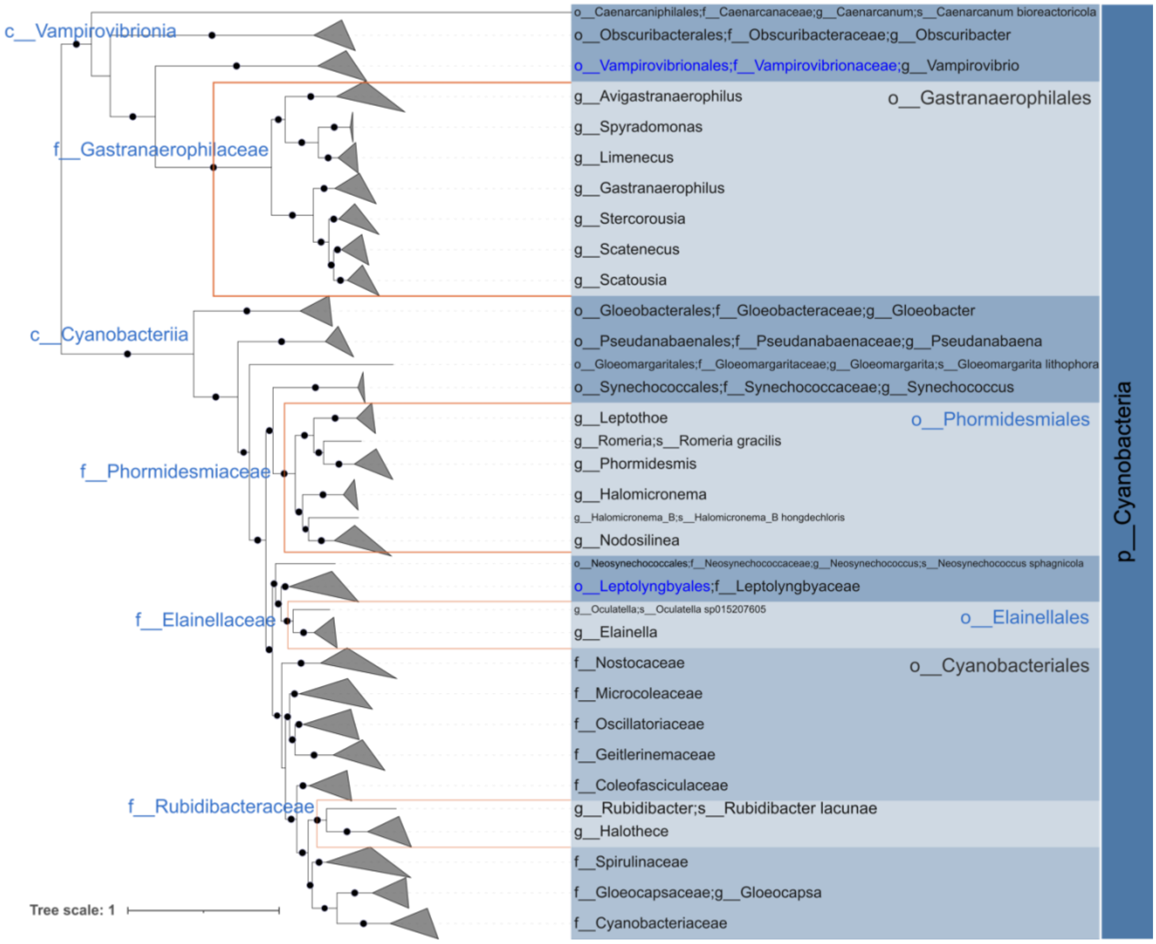
Supplemental Figure 3. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



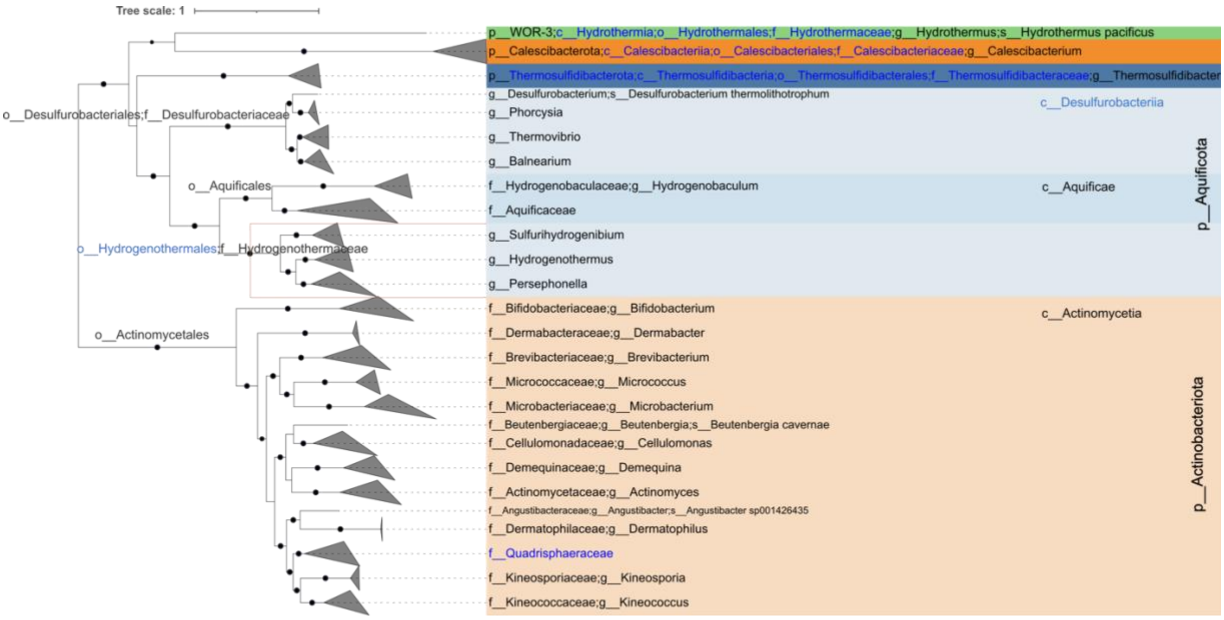
Supplemental Figure 4. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



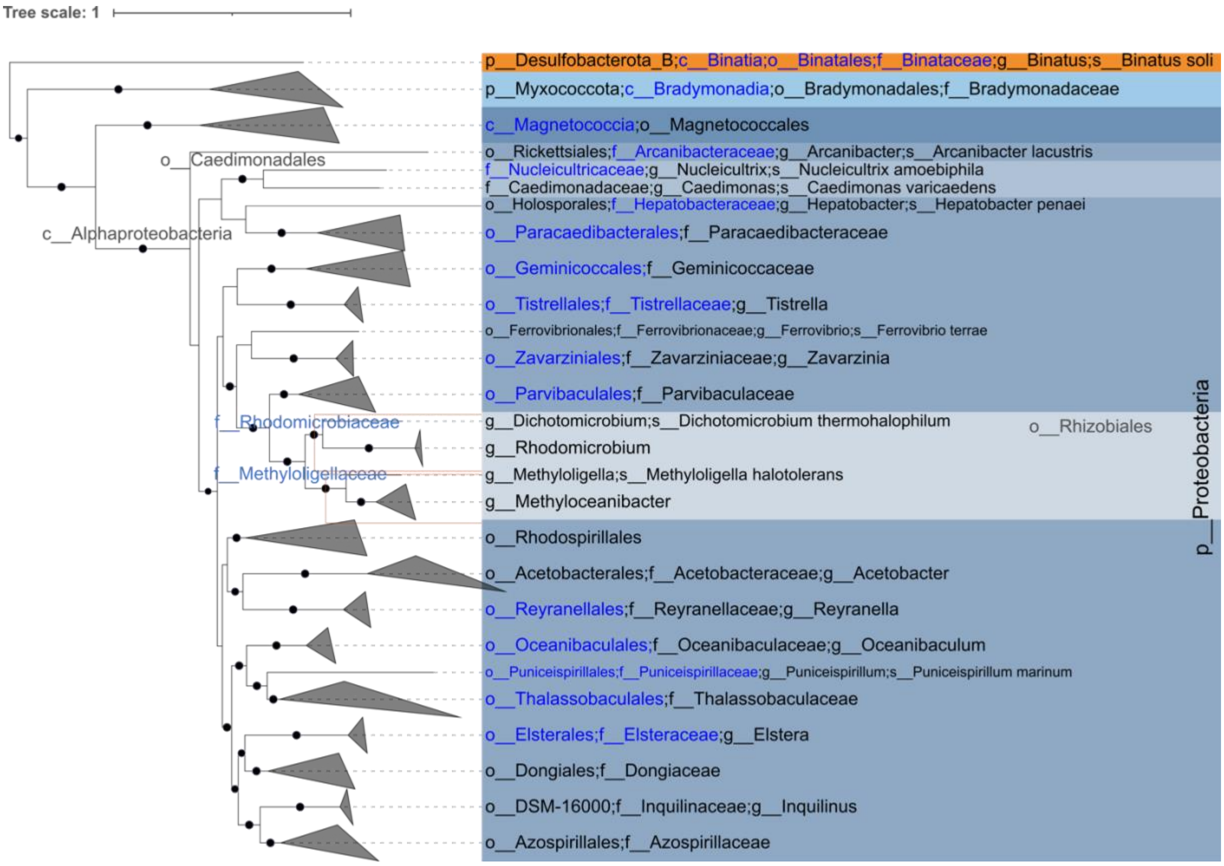
Supplemental Figure 5. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



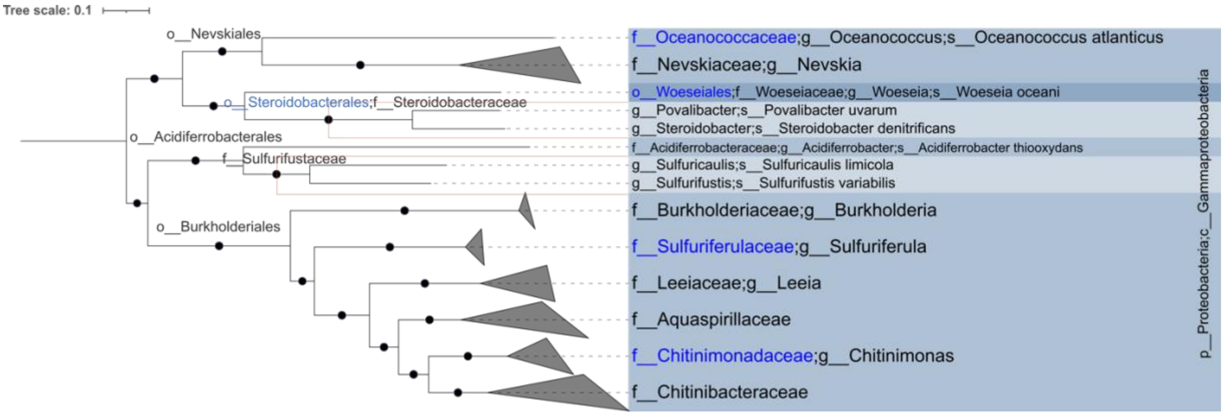
Supplemental Figure 6. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



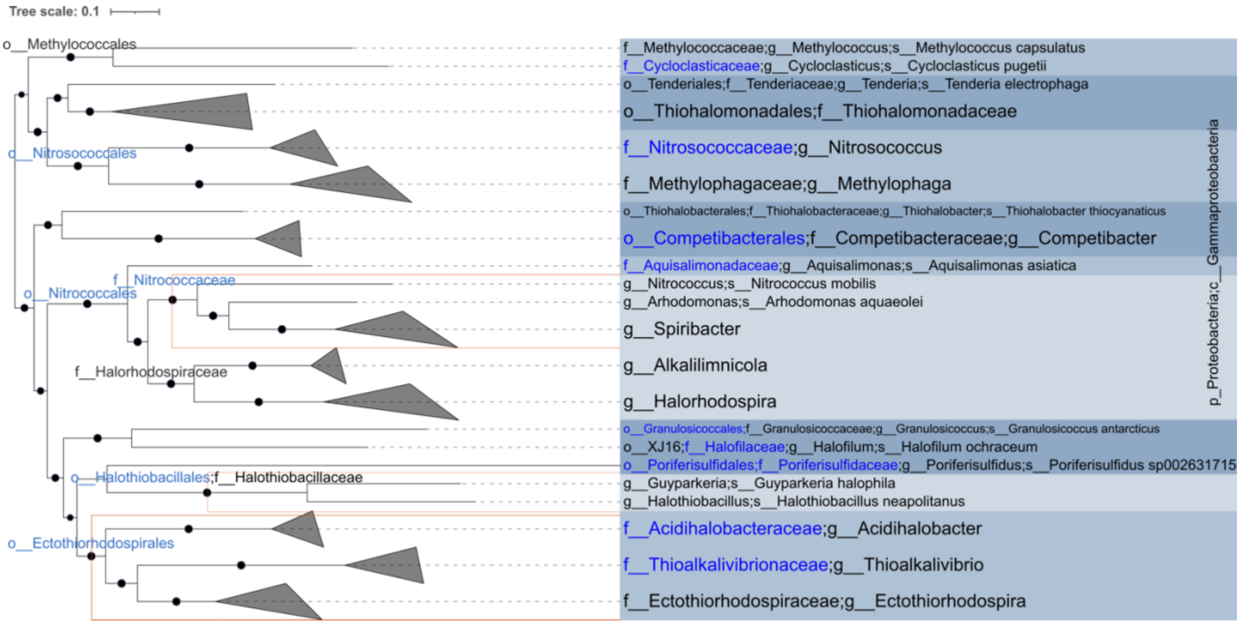
Supplemental Figure 7. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



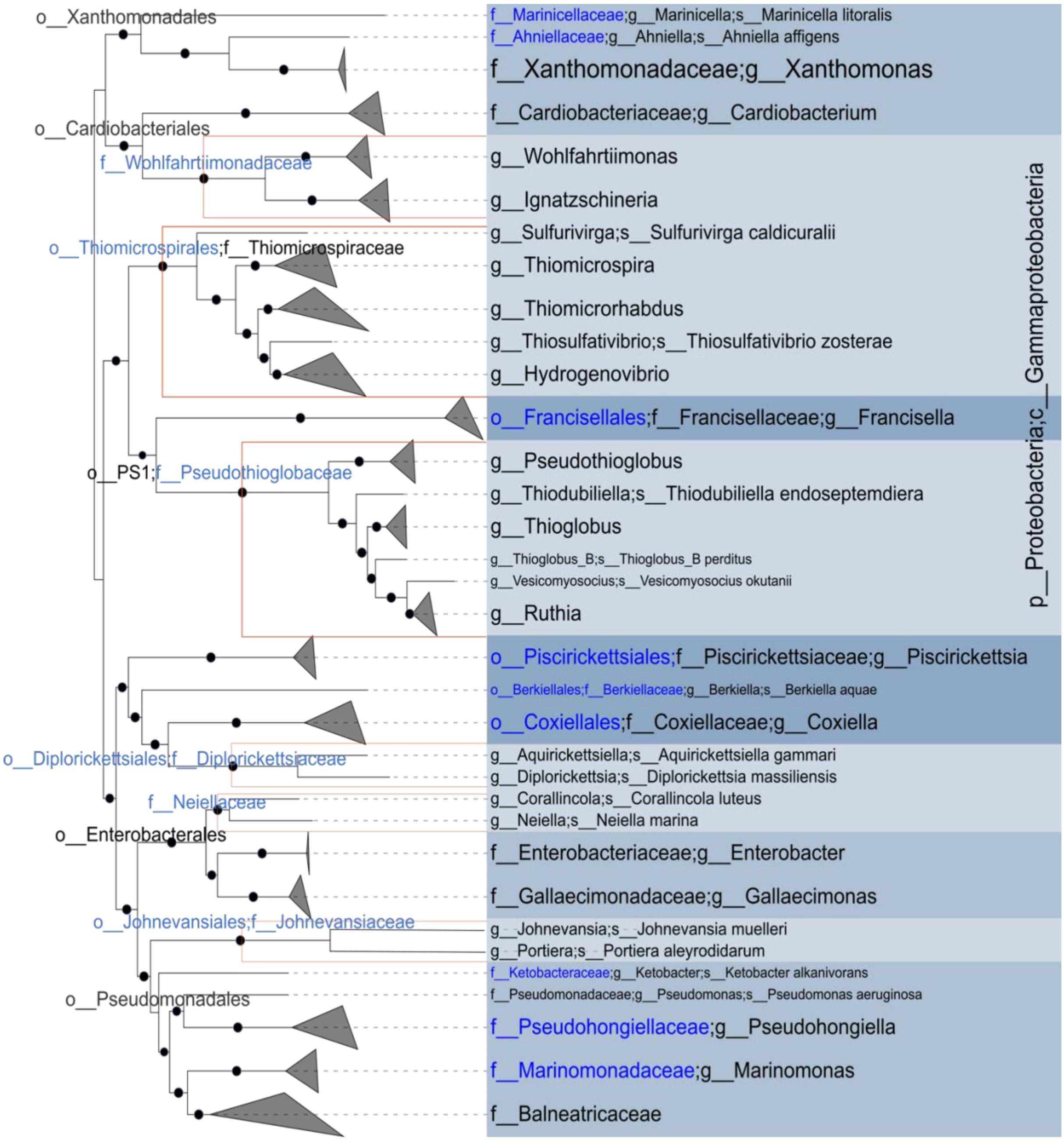
Supplemental Figure 8. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



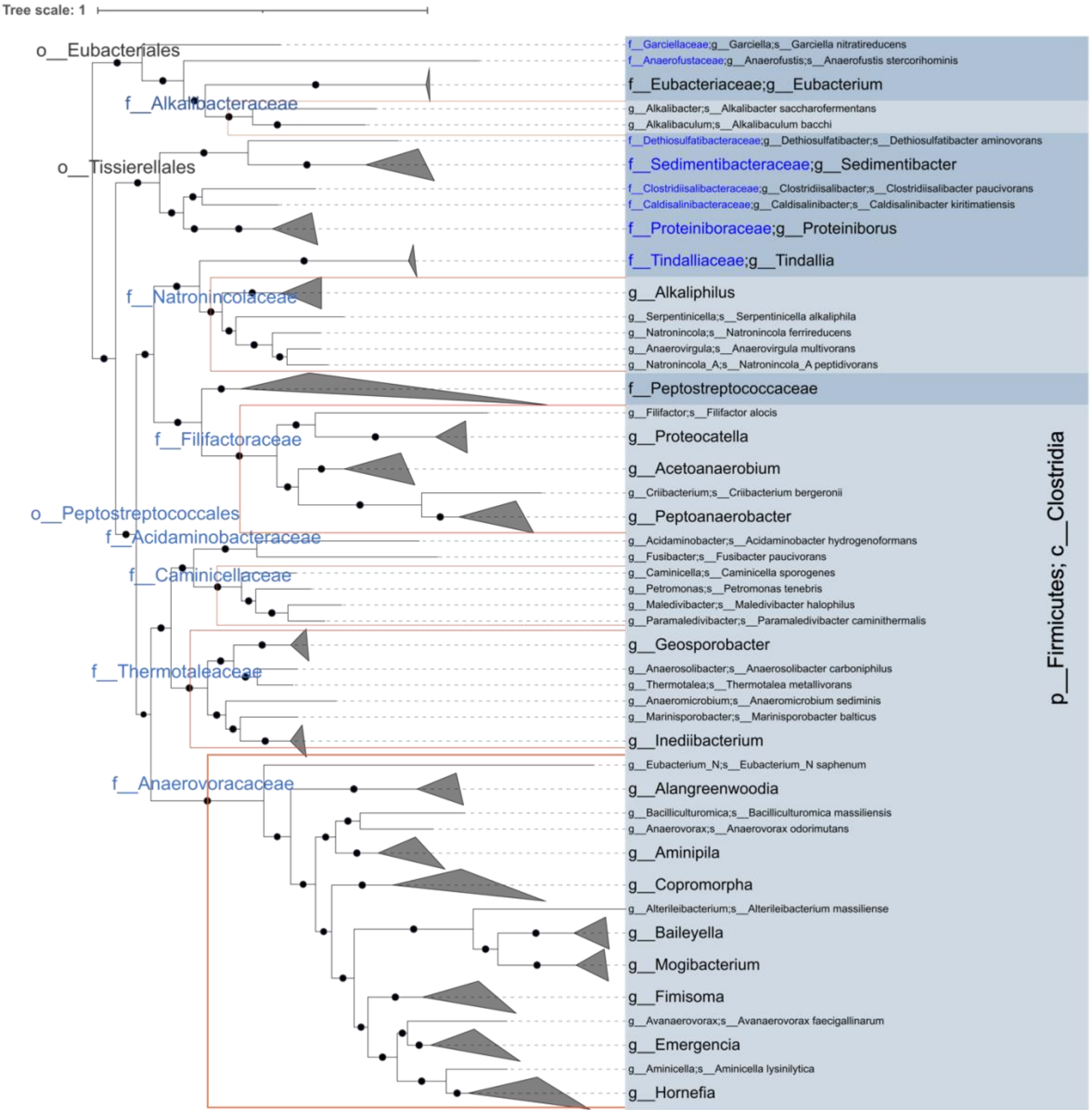
Supplemental Figure 9. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



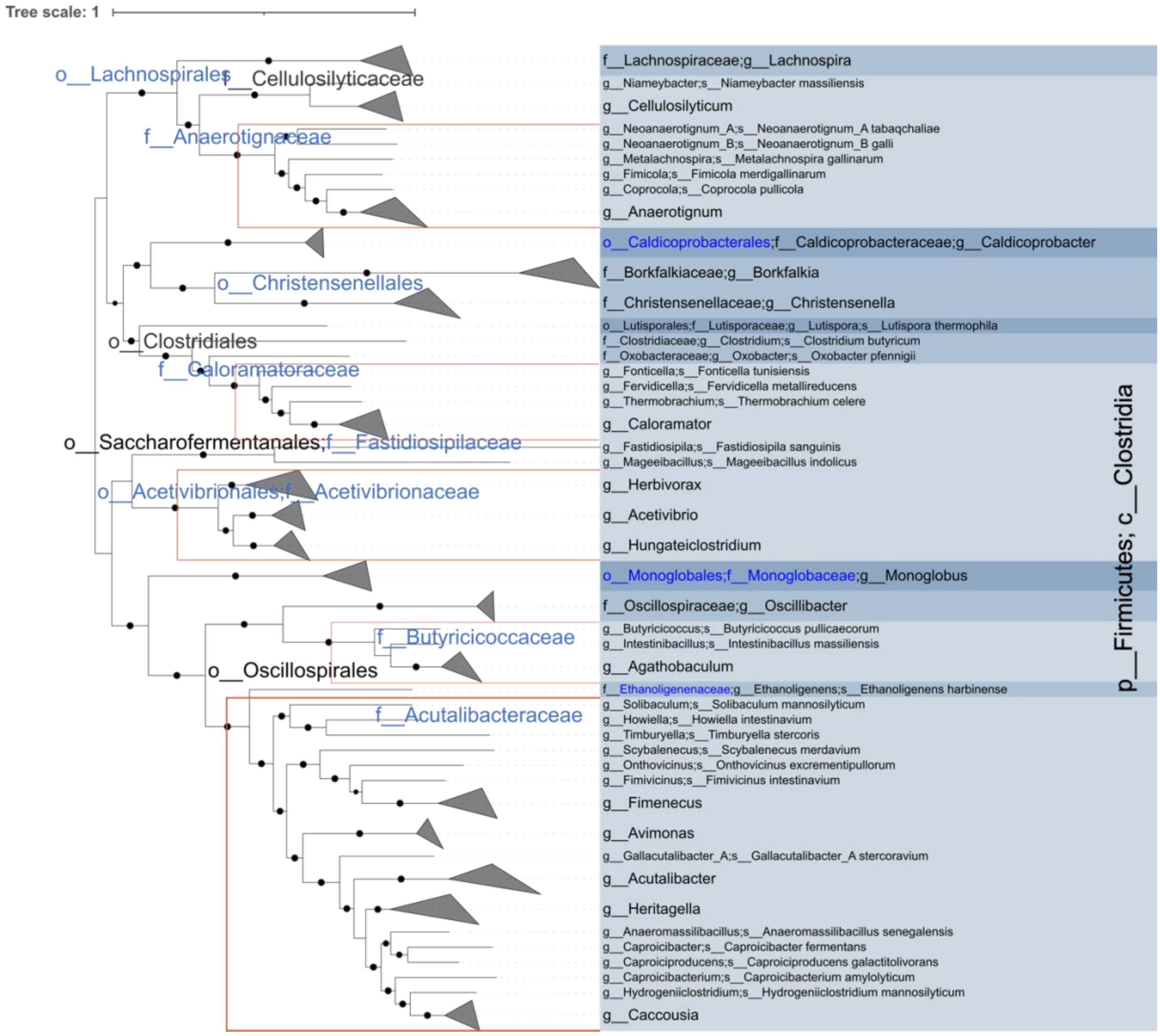
Supplemental Figure 10. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



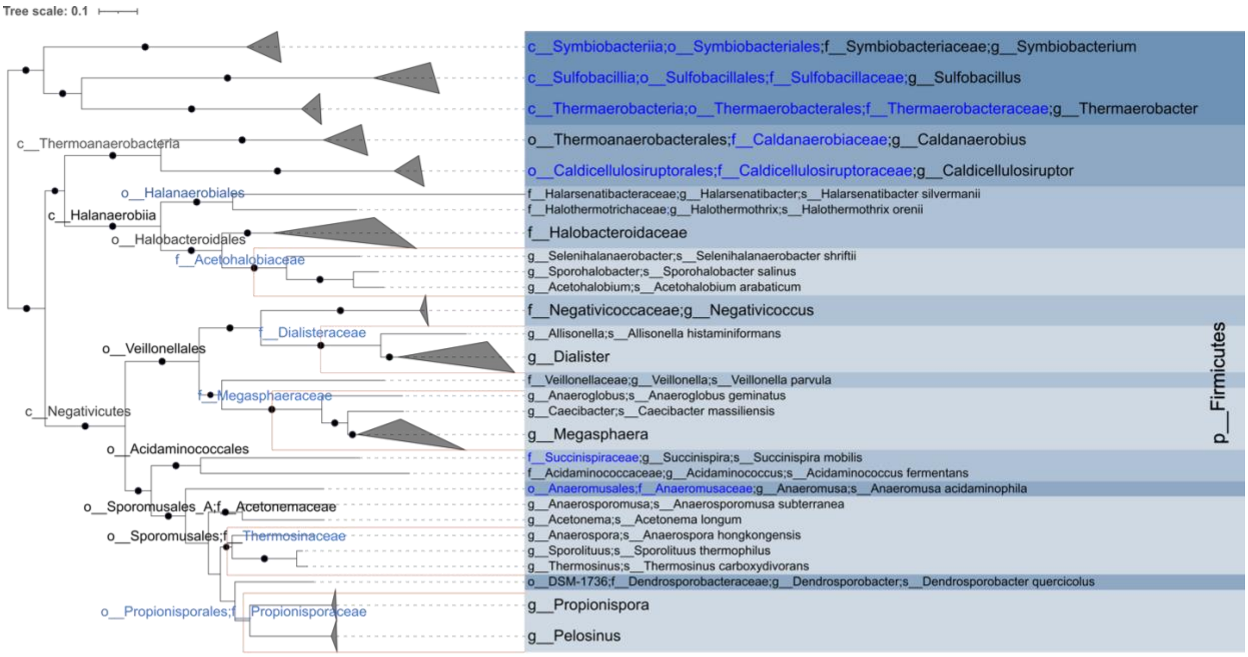
Supplemental Figure 11. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



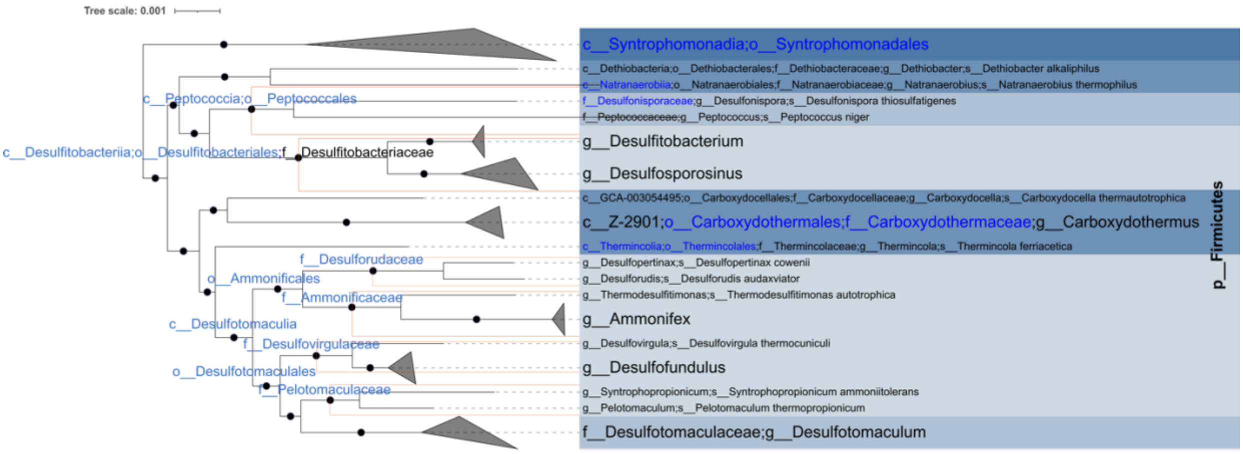
Supplemental Figure 12. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



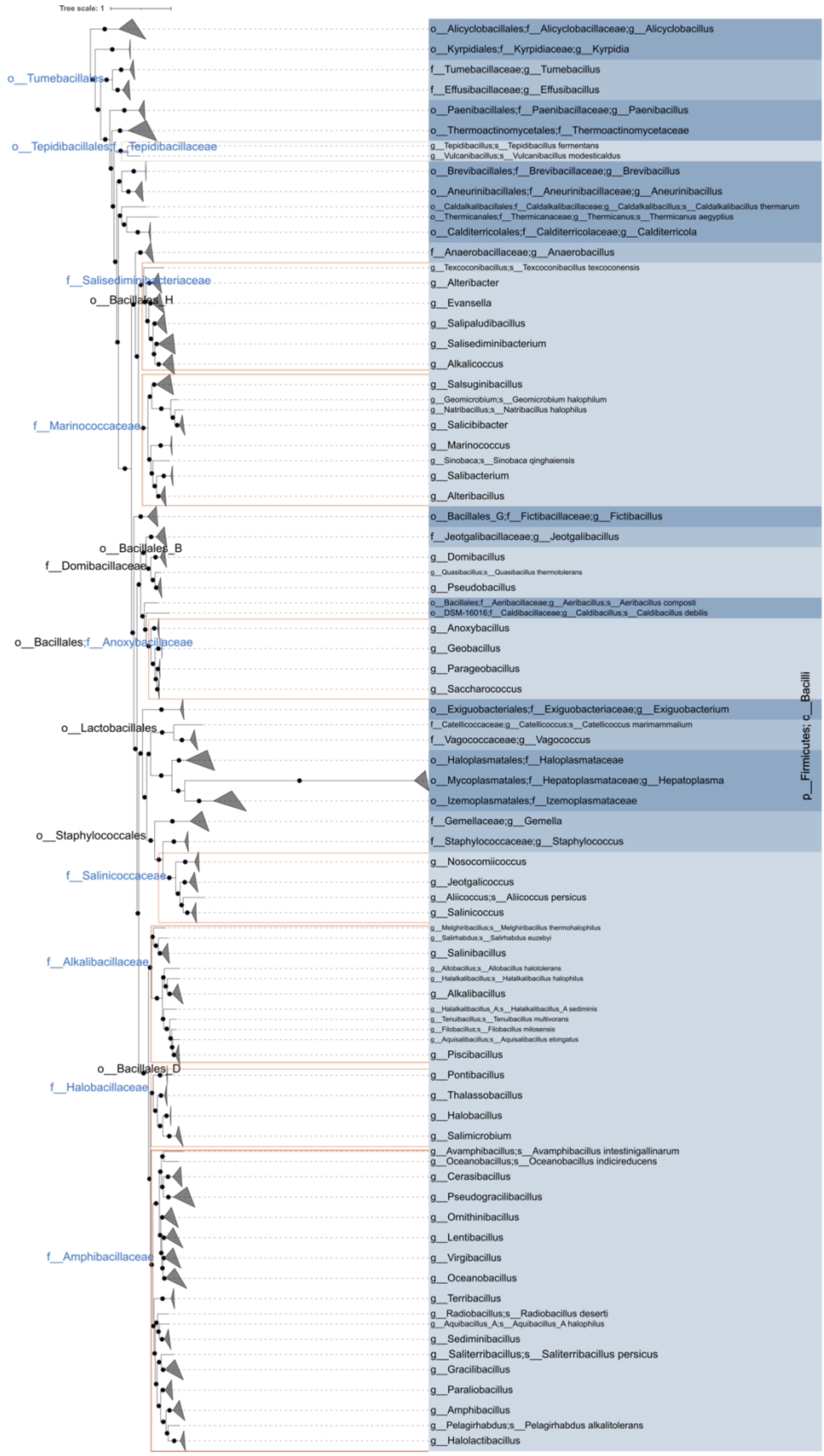
Supplemental Figure 13. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



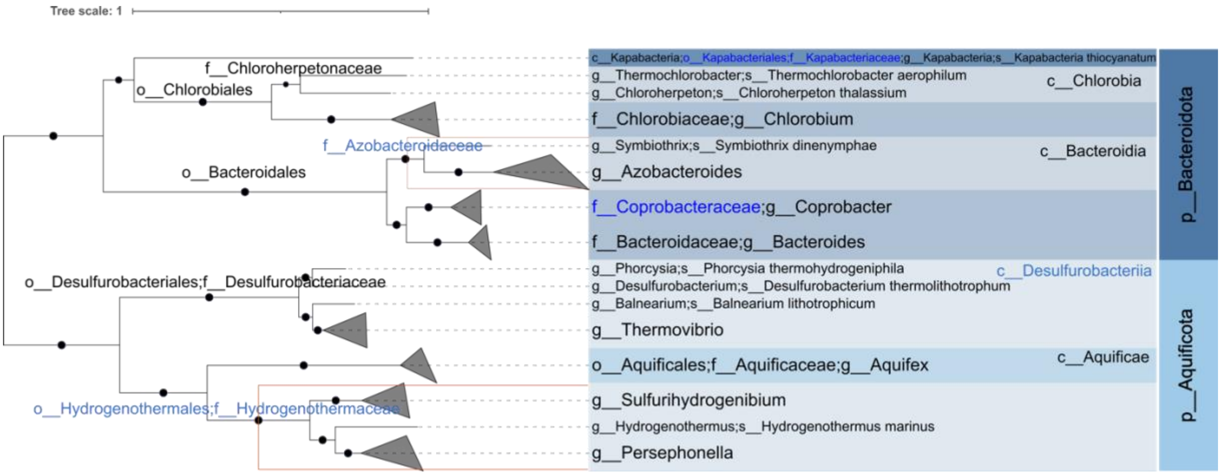
Supplemental Figure 14. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



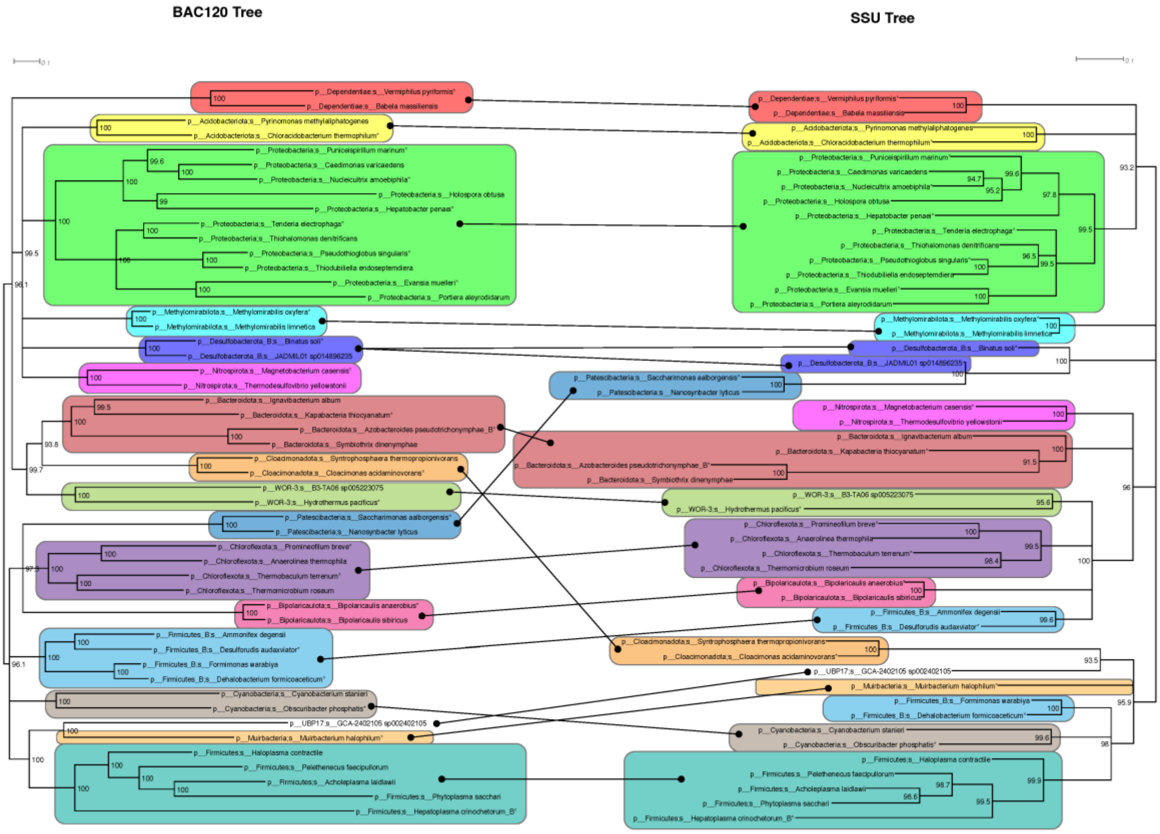
Supplemental Figure 15. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



Supplemental Figure 16. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



Supplemental Figure 17. Maximum likelihood phylogenetic inference of 120 concatenated protein markers using IQ-TREE under the LG matrix. Shading reflects rank-level grouping, with black circles indicating >90% support. Names of taxa defined in GTDB are coloured in blue.



Supplemental Figure 18. Species-level phylogenies illustrating congruences between 16S rRNA gene and bac120 marker set taxonomies. Coloured boxes reflect phylum-level grouping and names applied to type species proposed under the SeqCode indicated with asterisk.