

S1 Fig. Phylogenetic Trees of 16 individual phylum

Evolutionary analysis by Maximum Likelihood method

The evolutionary history was inferred by using the Maximum Likelihood method and Tamura-Nei model [1]. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Tamura-Nei model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). All positions with less than 95% site coverage were eliminated, i.e., fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option). Evolutionary analyses were conducted in MEGA X [2]

1. Tamura K. and Nei M. (1993). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* 10:512-526.
2. Kumar S., Stecher G., Li M., Knyaz C., and Tamura K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35:1547-1549.

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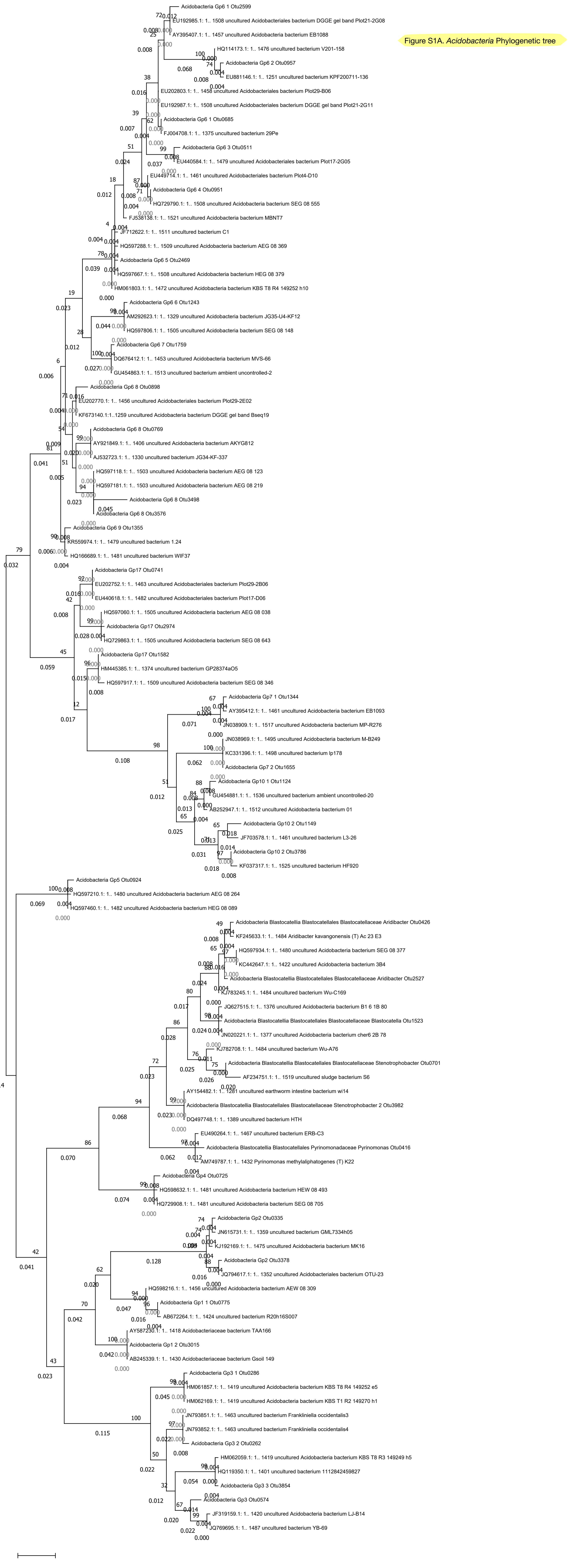
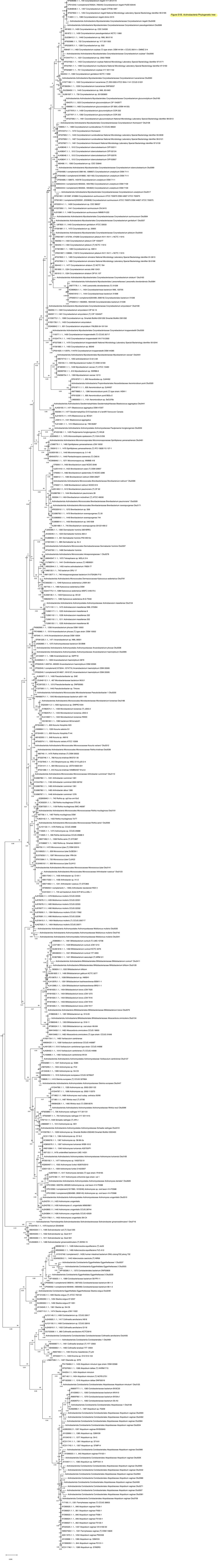
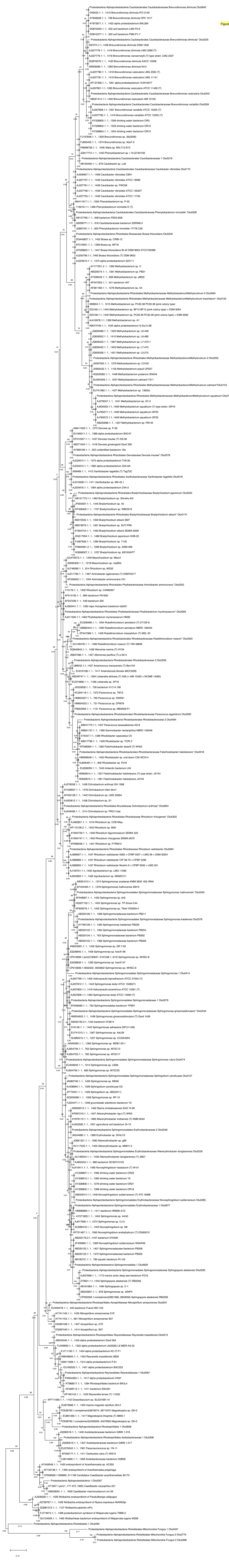


Figure S1A. *Acidobacteria* Phylogenetic tree





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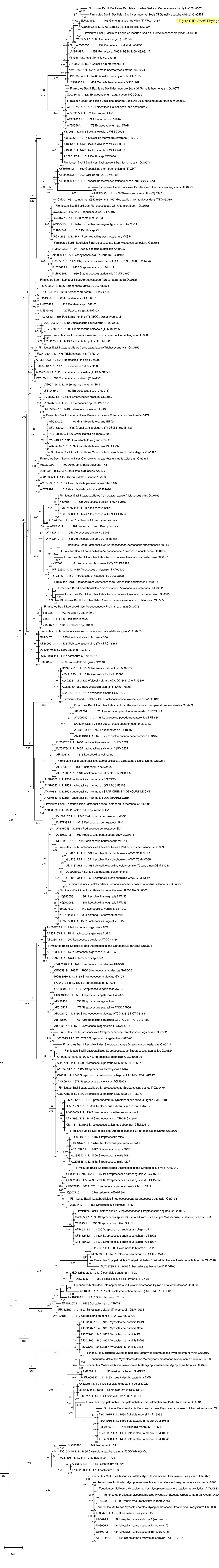


Figure S1E. Bacteroida (Bacteroidales) Phylogenetic Tree

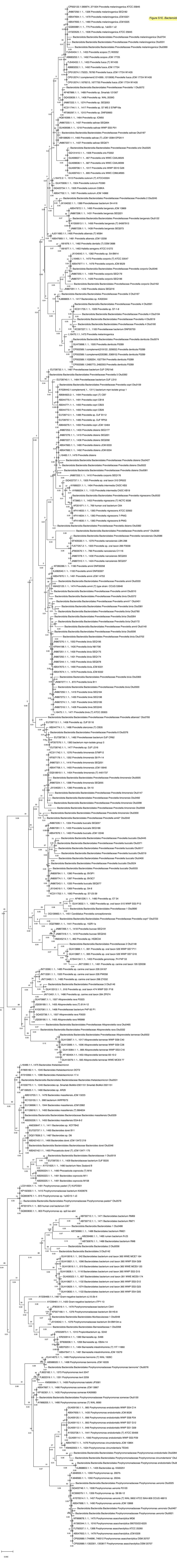


Figure S1F. Bacteroidota Phylogenetic Tree (excluding Bacteroidales)



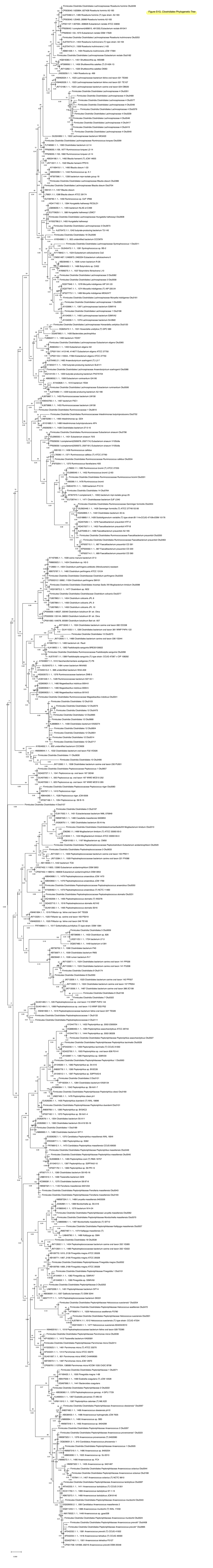


Figure S1H. Clostridiales Phylogenetic Tree (excluding Peptococcus species and Lachnospiraceae species)

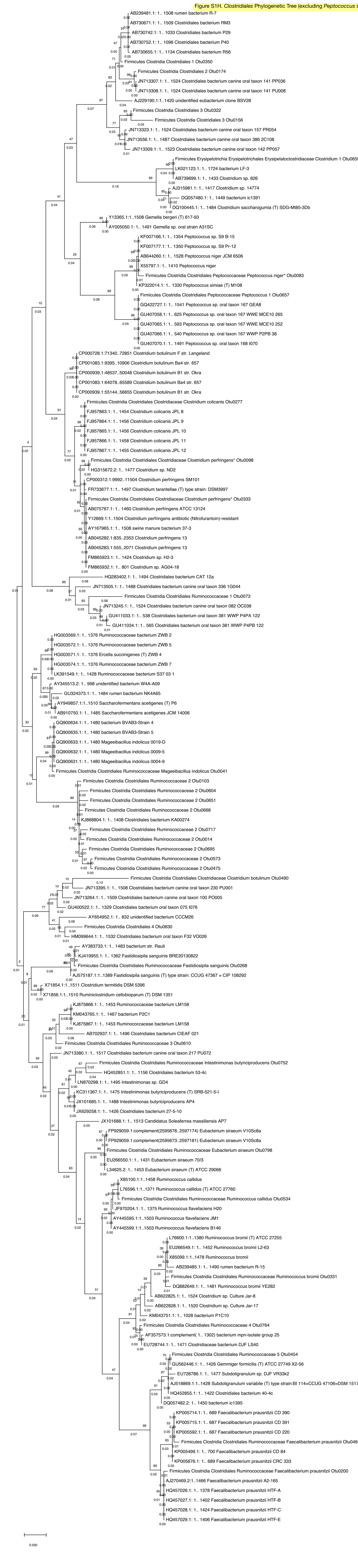


Figure S11. *Fusobacteria* Phylogenetic Tree

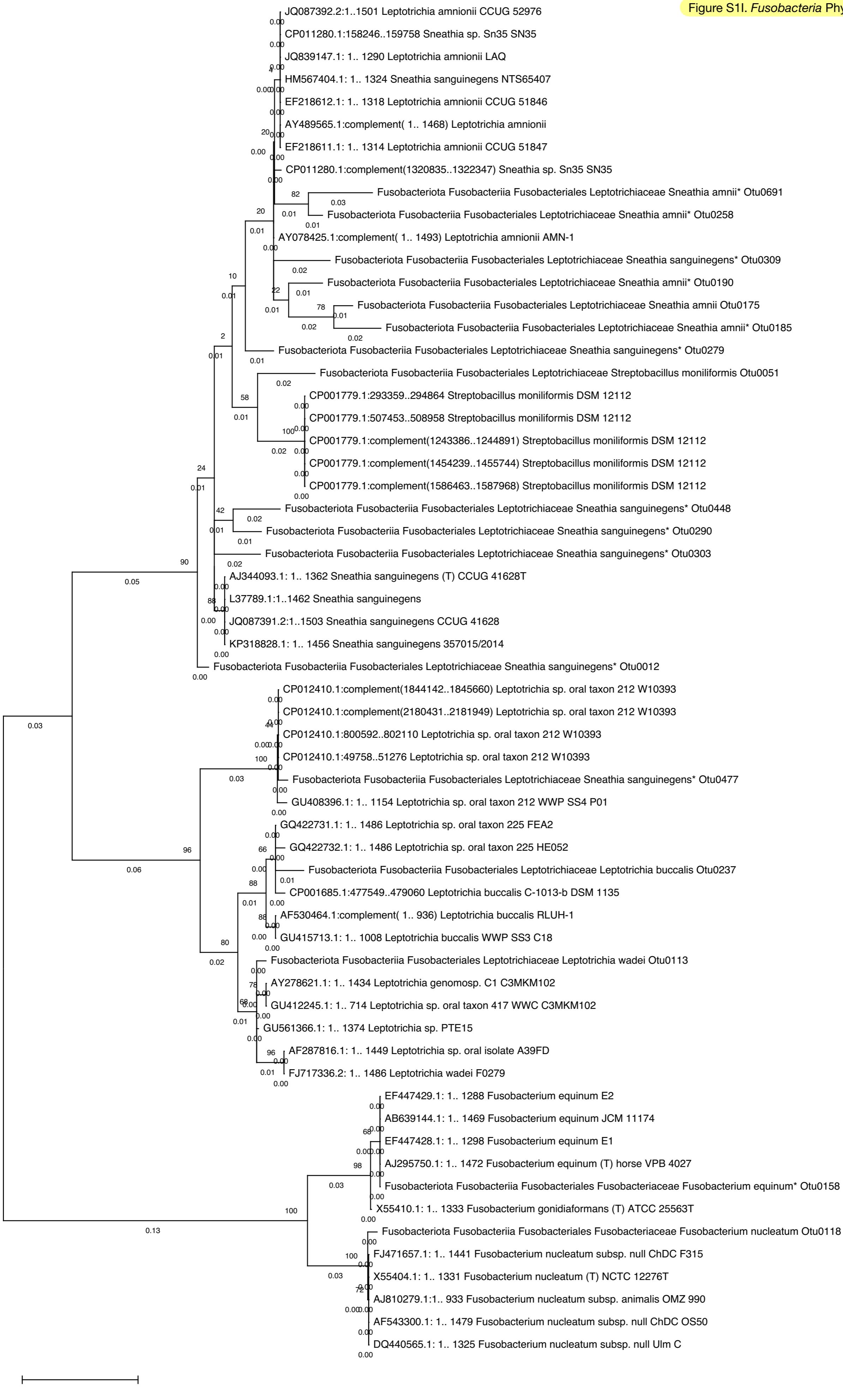


Figure S1J. *Gardnerella* Phylogenetic Tree

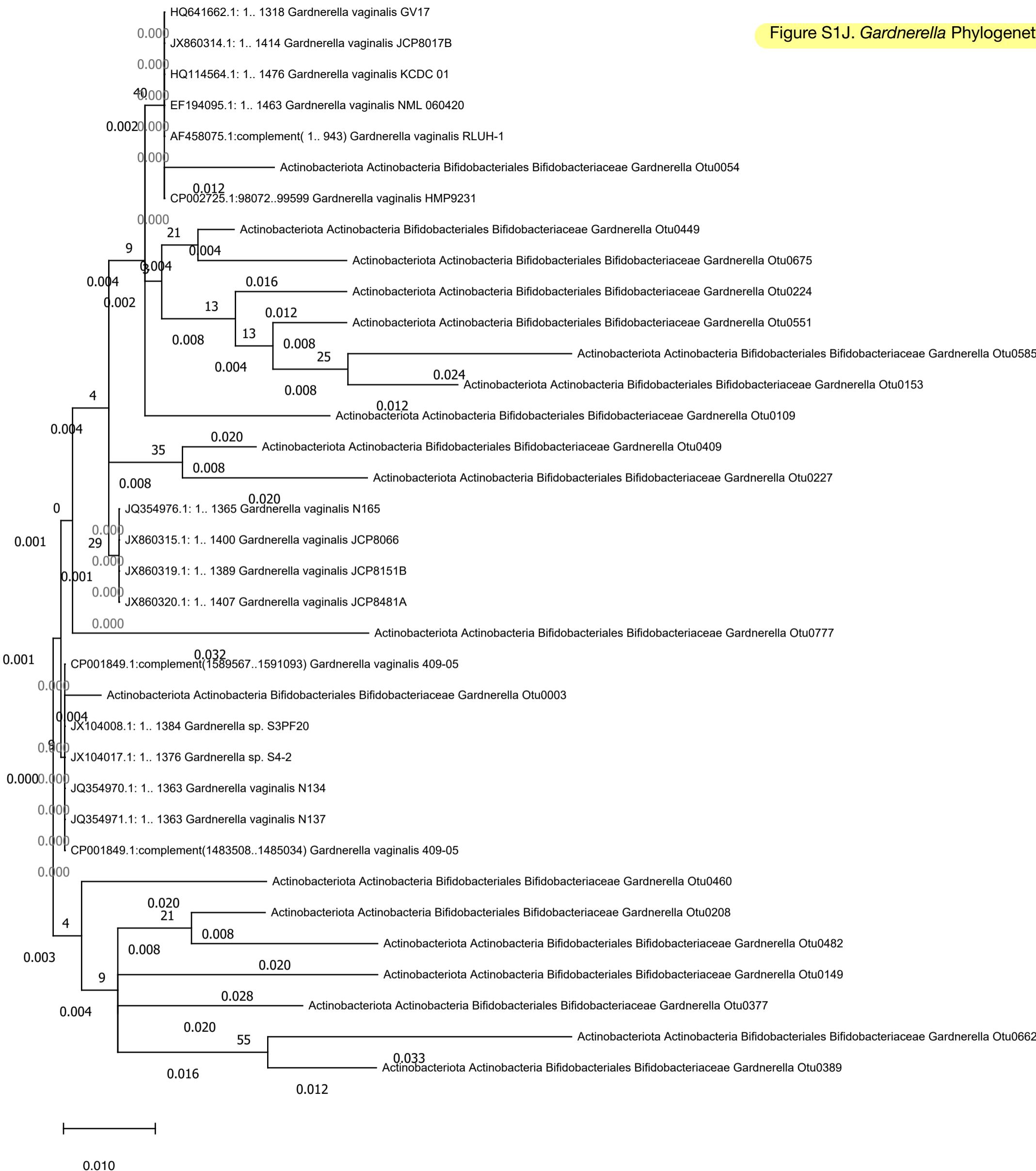


Figure S1K. Lachnospiraceae phylogenetic tree

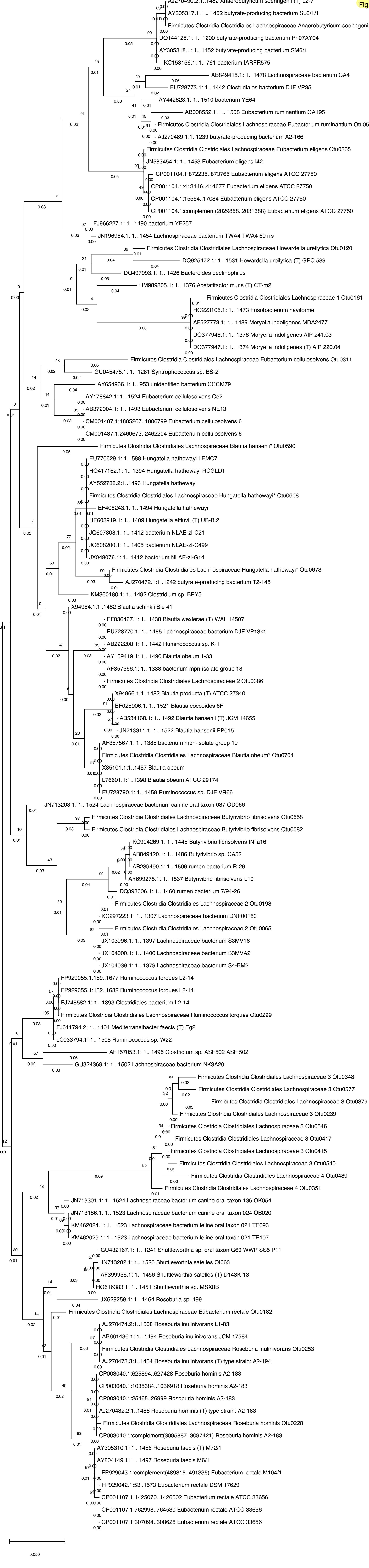


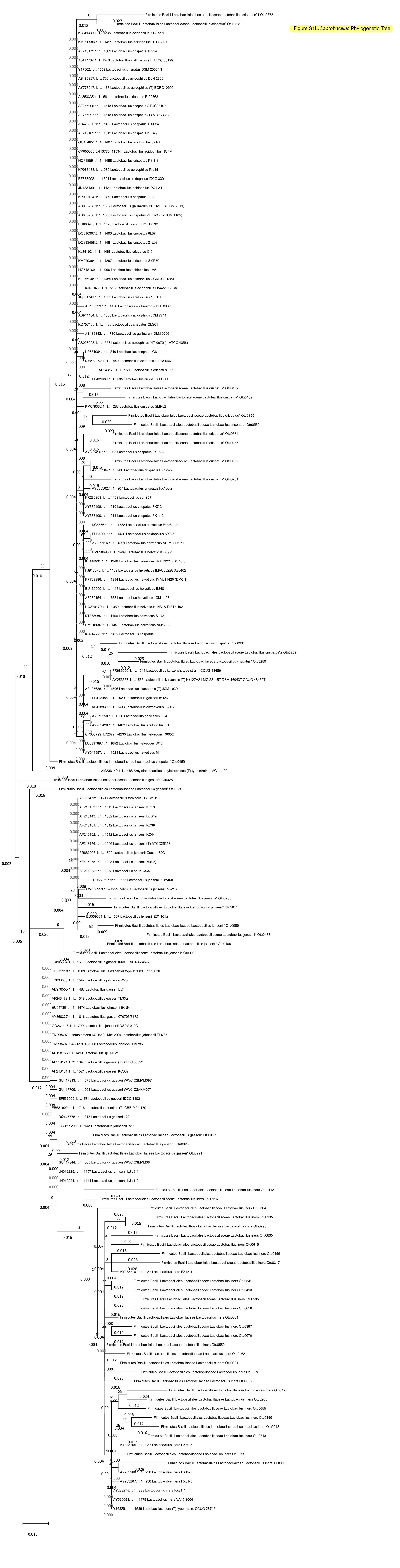
Figure S1L. *Lactobacillus* Phylogenetic Tree

Figure S1M. Miscellaneous Phylogenetic Tree

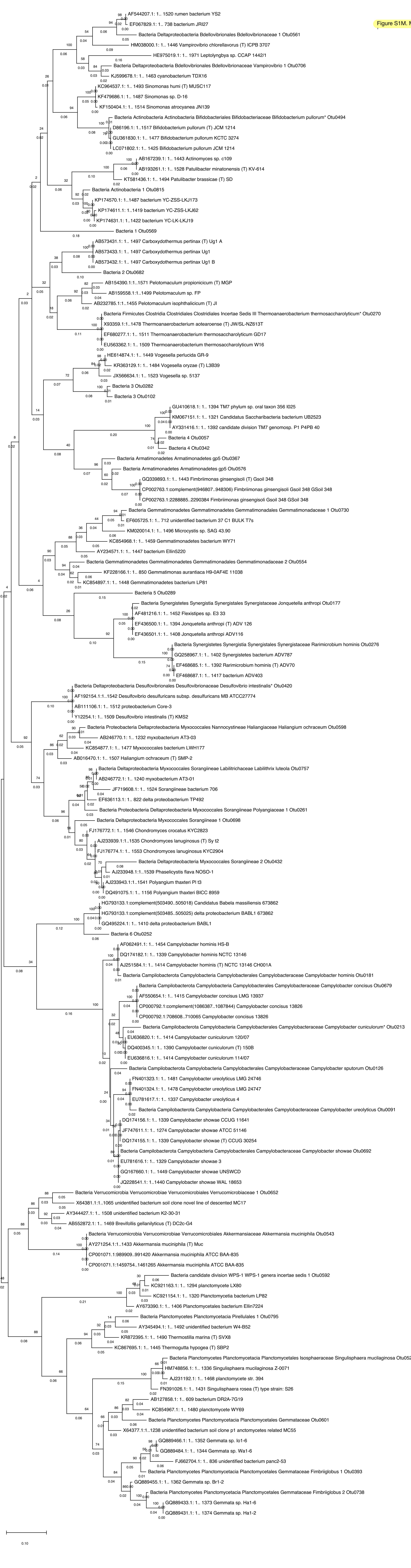


Figure S1N. *Negativicutes* Phylogenetic Tree

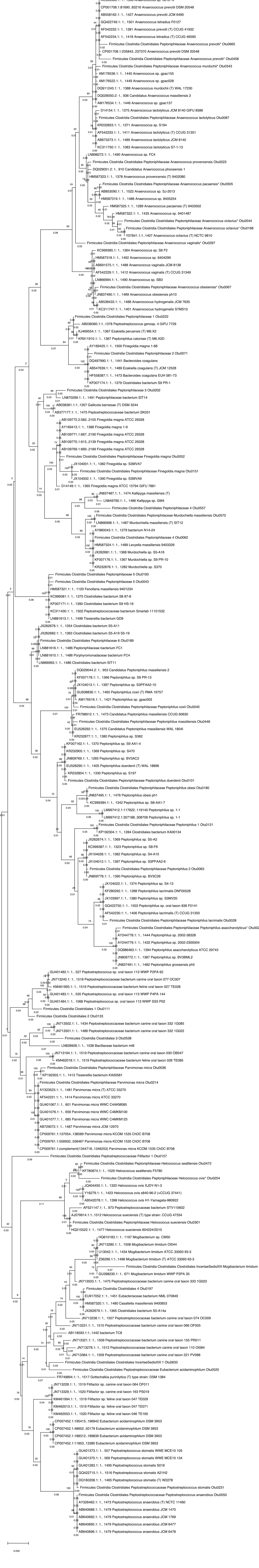
Figure S10. *Peptostreptococcus* Phylogenetic Tree

Figure S17. *Proteobacteria* Phylogenetic Tree (excluding *Alphaproteobacteria* species)