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.

Figure S1A. *Acidobacteria* Phylogenetic tree

Figure S1B. *Actinobacteria* Phylogenetic tree

Figure S1C. *Alphaproteobacteria* Phylogenetic Tree

Figure S1D. *Bacilli* Phylogenetic Tree (excluding *Lactobacillus* species)

Figure S1E. *Bacteroidota (Bacteriodales)* Phylogenetic Tree

Figure S1F. *Bacteroidota* Phylogenetic Tree (excluding *Bacteroidales*)

Figure S1G. *Clostridiales* Phylogenetic Tree

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

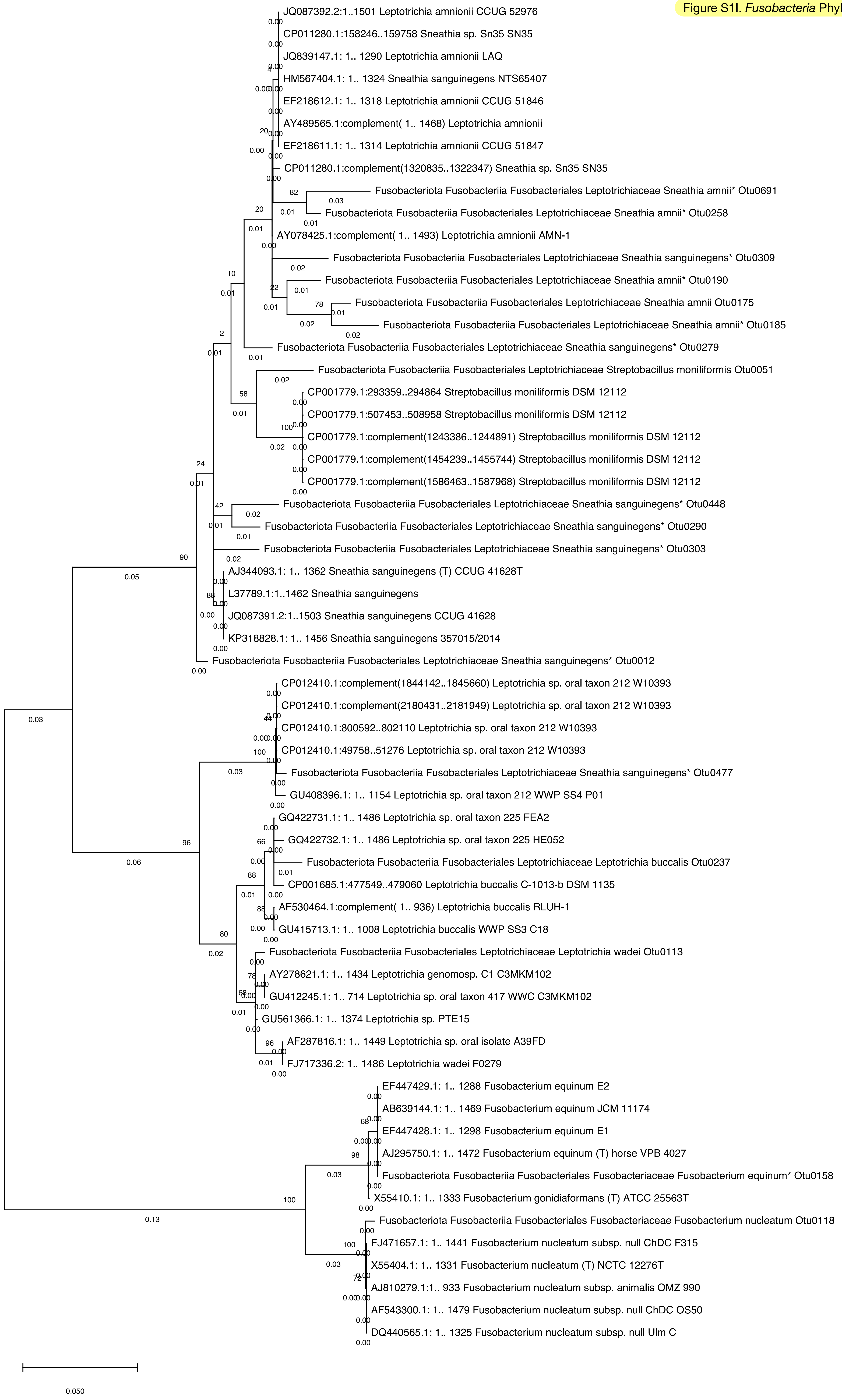
Figure S1I. *Fusobacteria* Phylogenetic Tree

Figure S1J. *Gardnerella* Phylogenetic Tree

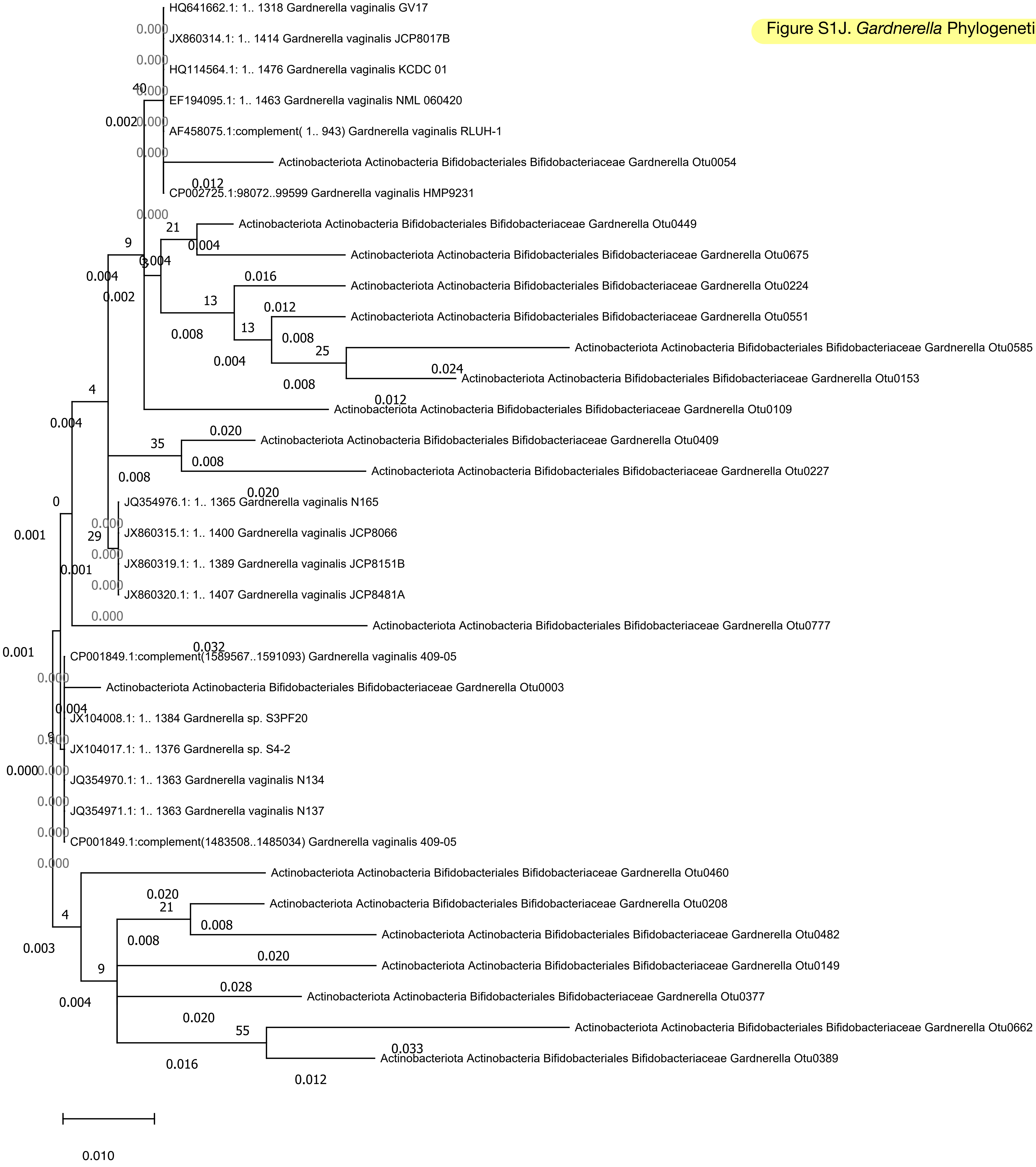

Figure S1K. *Lachnospiraceae* phylogenetic tree

Figure S1L. *Lactobacillus* Phylogenetic Tree

Figure S1M. Miscellaneous Phylogenetic Tree


Figure S1N. *Negativicutes* Phylogenetic Tree

Figure S1O. *Peptostreptococcus* Phylogenetic Tree

Figure S1P. *Proteobacteria* Phylogenetic Tree (excluding *Alphaproteobacteria* specie)