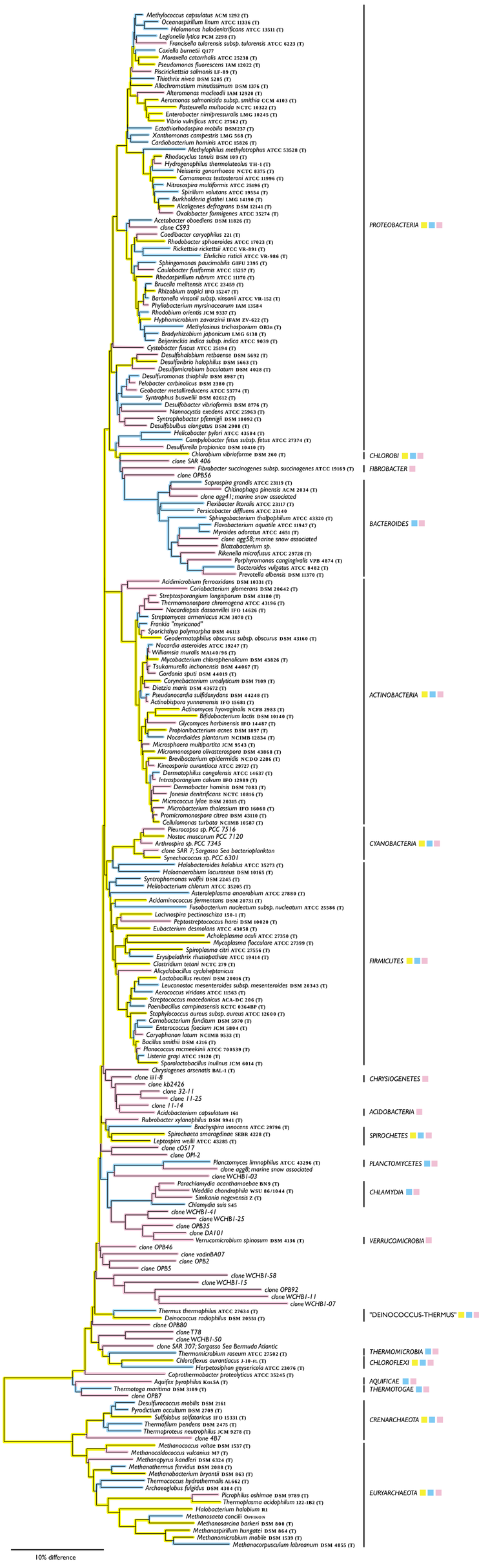

The RDP-II Backbone Tree for Release 8.0. The tree was inferred from a distance matrix generated in PAUP® with the Weighbor (weighted neighbor joining) algorithm. The 217 sequences represent about 187 of the 203 taxonomic families (20 of the 25 phyla) in the forthcoming edition of Bergey's Manual of Systematic Bacteriology as well as uncultured diversity in the form of the 30 "clone" sequences that were amplified from the environment. The represented Bergey's phyla are shown on the right. Yellow taxa were first subject to phylogenetic analysis based on 16S rDNA sequence in 1980. Yellow and blue taxa were included in the first RDP tree in 1992.