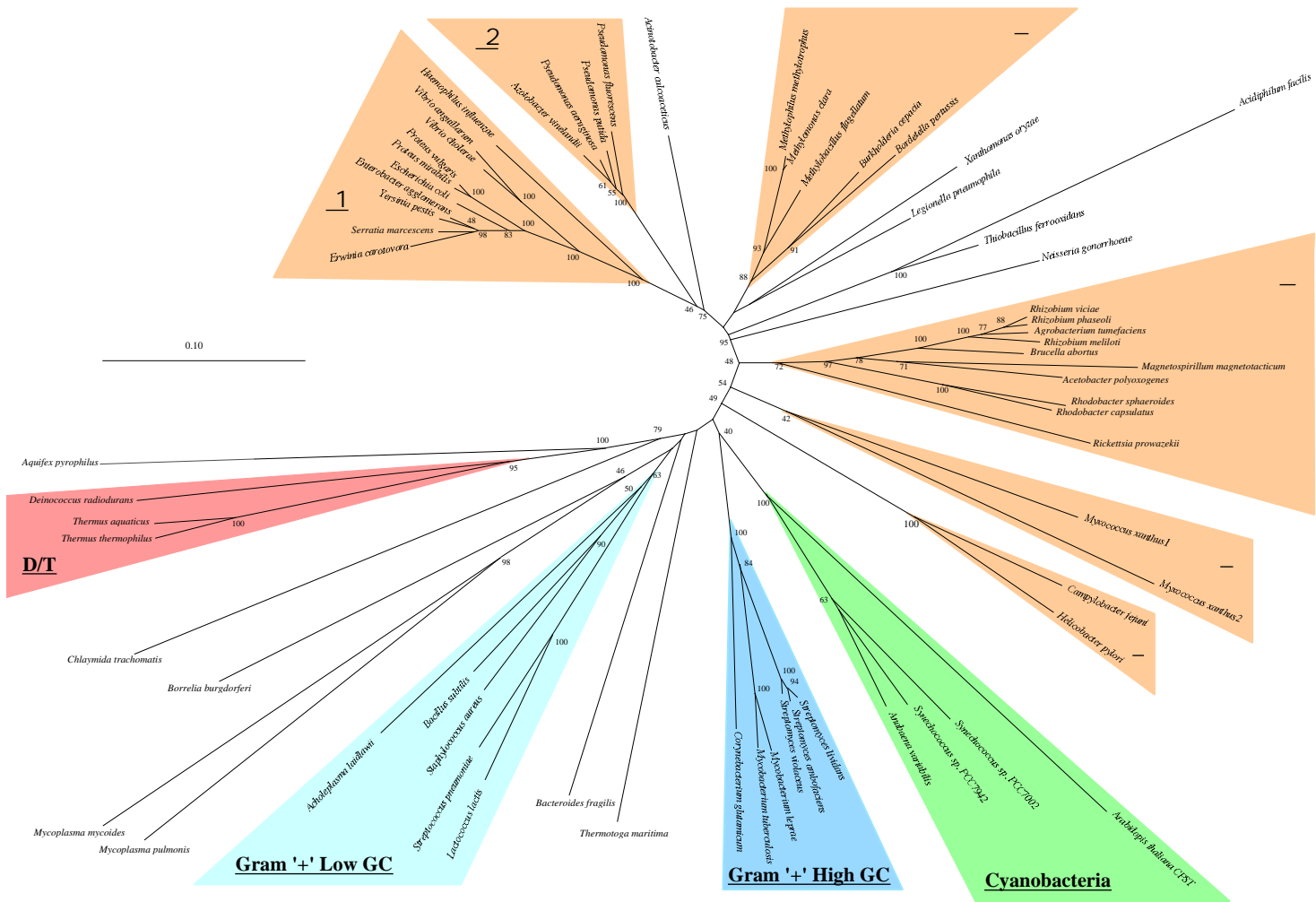


**A.**



[illegible]

Figure 3. Fitch-Margoliash trees for RecA (A) and SS-rRNA (B).

Trees were generated from the multiple sequence alignments by the method of Fitch and Margoliash. Regions of ambiguous alignment and indels were excluded from the analysis (see Methods). For the RecA tree, distances were calculated using the *protdist* program of PHYLIP with a PAM-matrix based distance correction. For the SS-rRNA tree, distances were calculated using the *dnadist* program of PHYLIP and the Kimura-2-parameter distance correction. Consensus clades representing groups found in all phylogenetic methods are highlighted. Branch lengths and scale bars correspond to estimated evolutionary distance. Bootstrap values when over 40 are indicated.