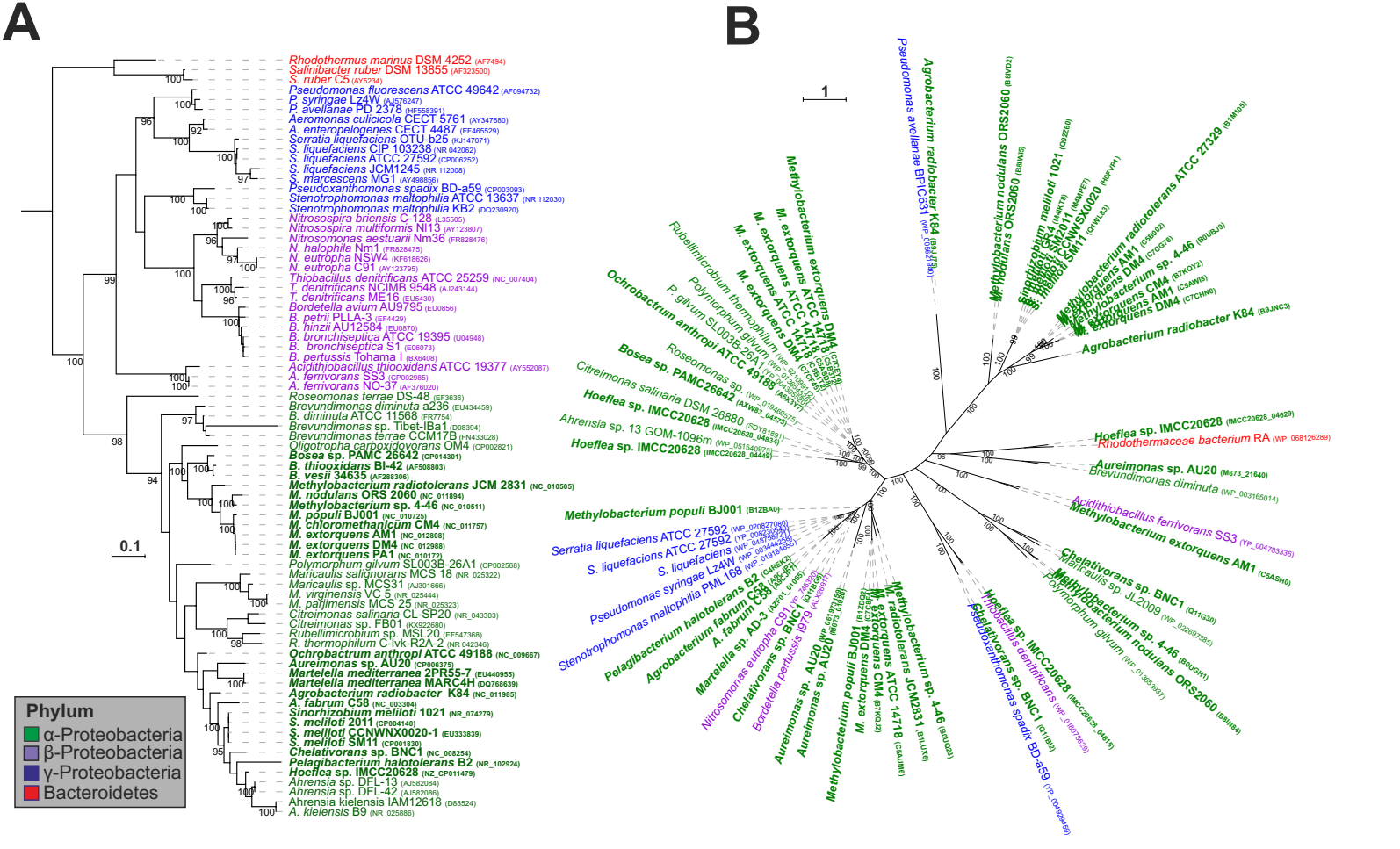

Figure S6. Exchange of Cu-ATPases among several α-, β- and γ- Proteobacteria and Bacteroidetes species. The foreign origin of 30 putative recently transferred genes coding for Cu-ATPases identified in members of *Rhizobiales* order (see text) was tested with a phylogenetic approach comparing the species' phylogeny, inferred from 16S rRNA genes (A) with the phylogeny inferred from homologous Cu^{+}-ATPase coding genes (B). The incongruent phylogenetic relationship amog Cu-ATPases (B) support the hypothesis that those genes have been exchanged among distantly related species. The branch support value (Bootstrap) of each phylogenetic group is indicated at the nodes. The scale bars for *16S rDNA* gene and CopA phylogenies indicate 0.1 and 0.3 expected changes per nucleotide or amino acid under the applied model, respectively.