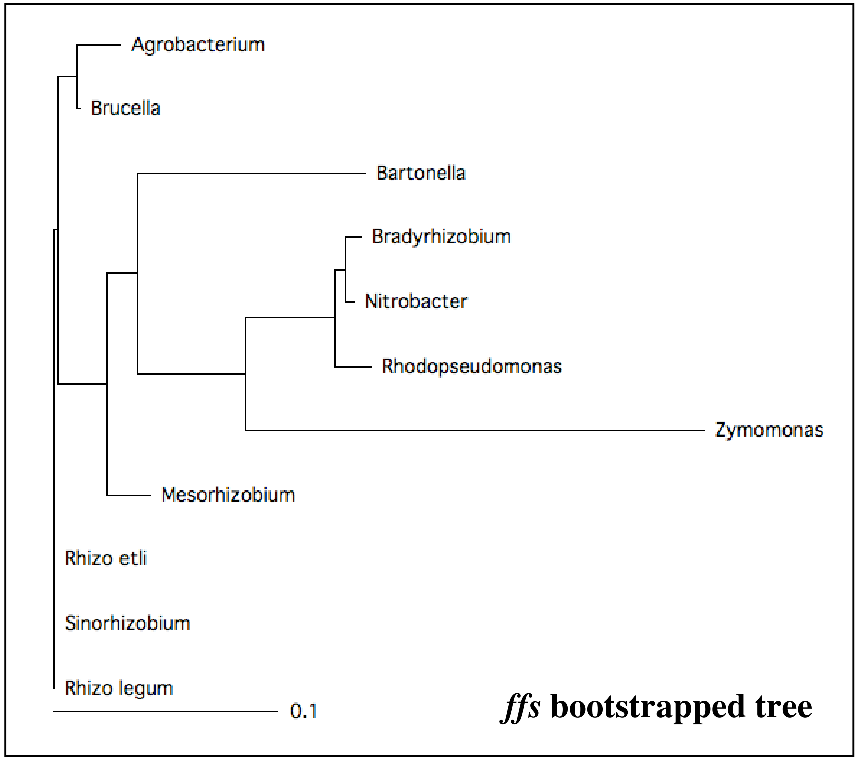

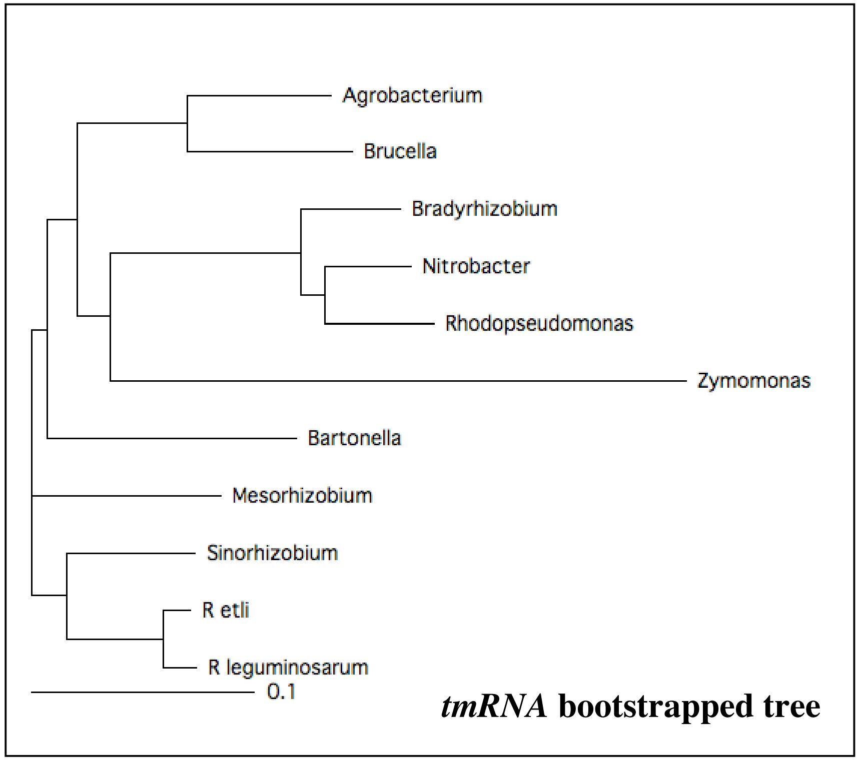

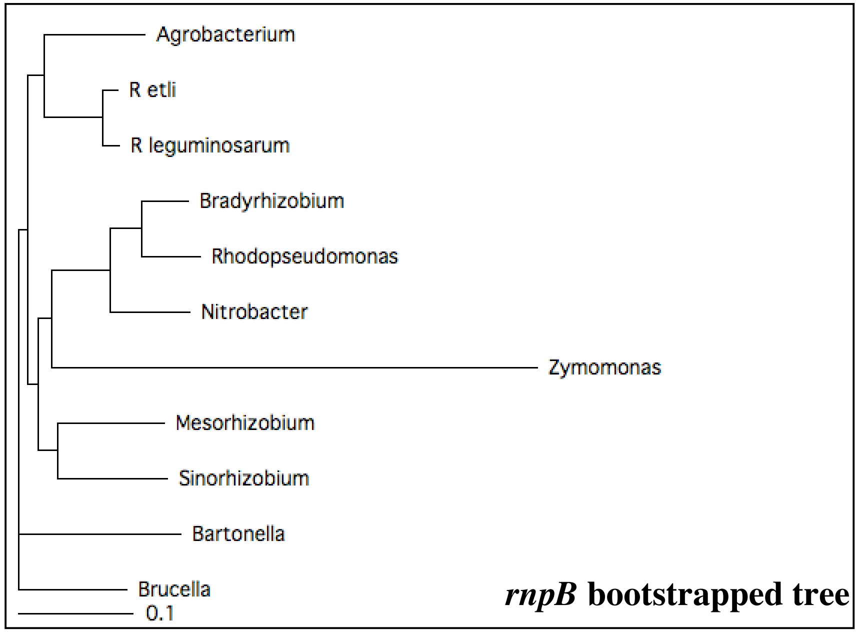

Phylogenetic maximum likehood trees based on *ffs*, *rnpB* and *tmRNA* in the subgroup-2 alphaproteobacteria.

These unrooted tree derived from the comparison of the complete predicted sequences of *ffs*, *tmRNA* and *rnpB* small RNAs [ref] from closely related alpha-proteobacteria. The analysis used Neighbourg joining method. Bootstrap values (1000).