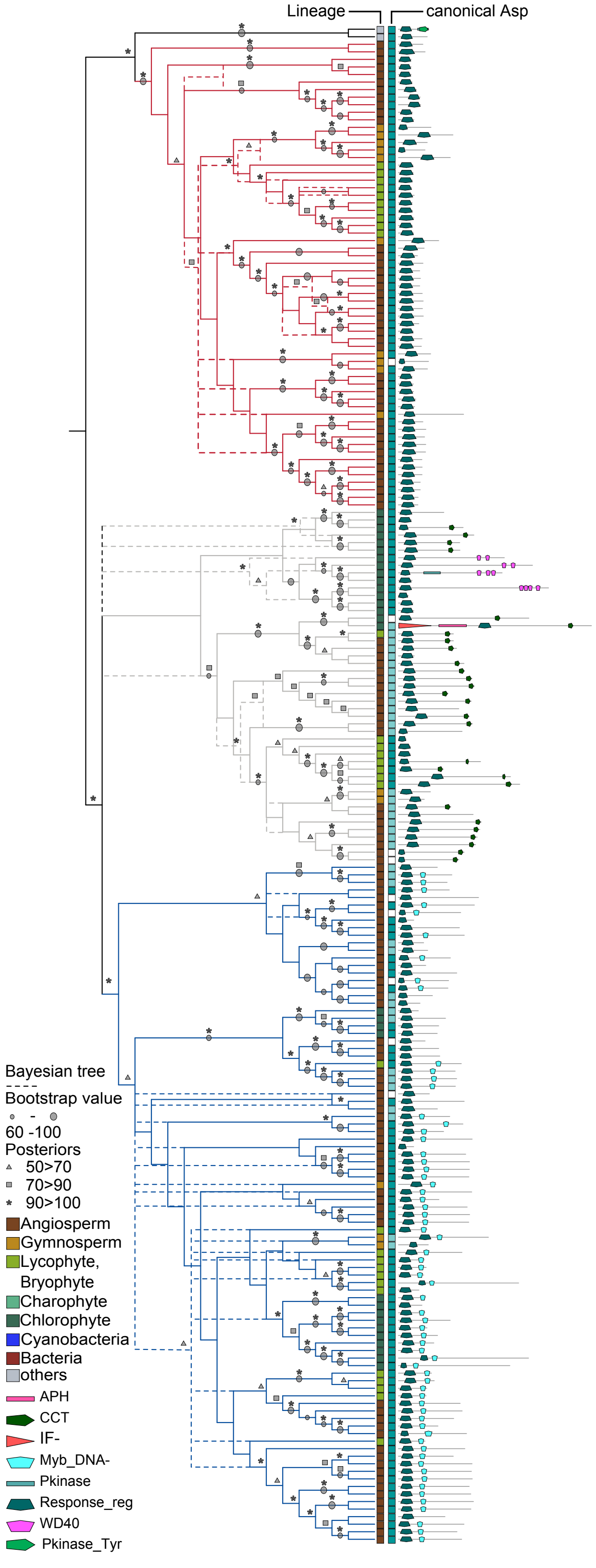

Supplemental Figure S4. Phylogenetic relationship of type-A, type-B and pseudo response regulators. The phylogenetic tree for the sub clades of the RRA, RRB and PRRs generated using a Maximum likelihood algorithm (shown in Fig. 6) is compared to a tree calculated using Bayesian interference. The results for Maximum Likelihood approach is represented by straight lines, the Bayesian interference tree is represented by dashed lines. Bootstrap and posterior values are given.