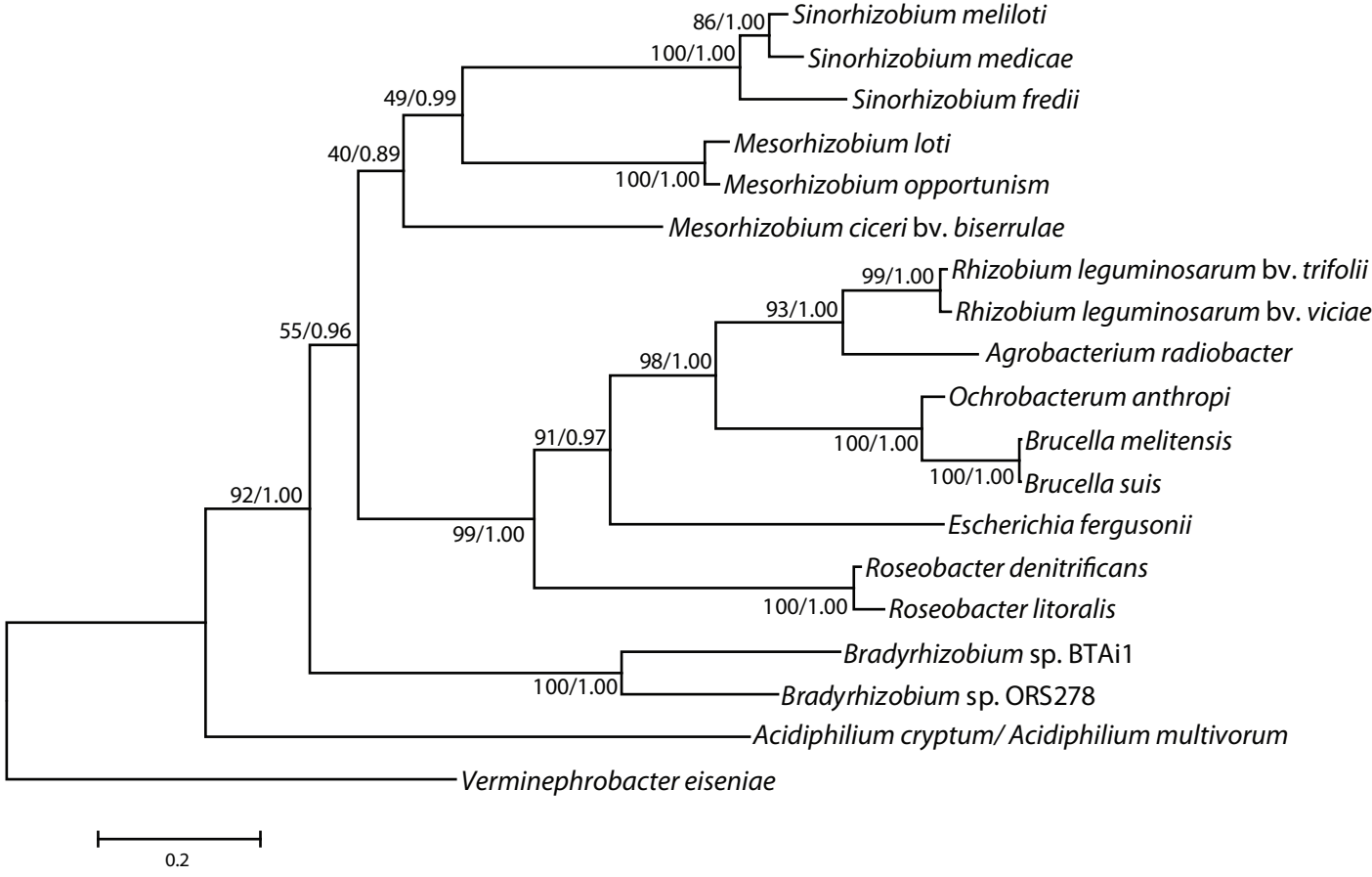

Figure S1. EryA distance tree

EryA phylogenetic tree was constructed using ML and Bayesian analysis. Support for each clade is expressed as a percentage (Bayesian/ML, ie. posterior probability and bootstrap values respectively) adjacent to the nodes that supports the monophyly of various clades. The branch lengths are based on ML analysis and are proportional to the number of substitutions per site. This phylogenetic tree was used in the mirror tree in Figure 2 without branch lengths due to space restrictions.