

A genomic survey of Reb homologues suggests widespread occurrence of R-bodies in Proteobacteria

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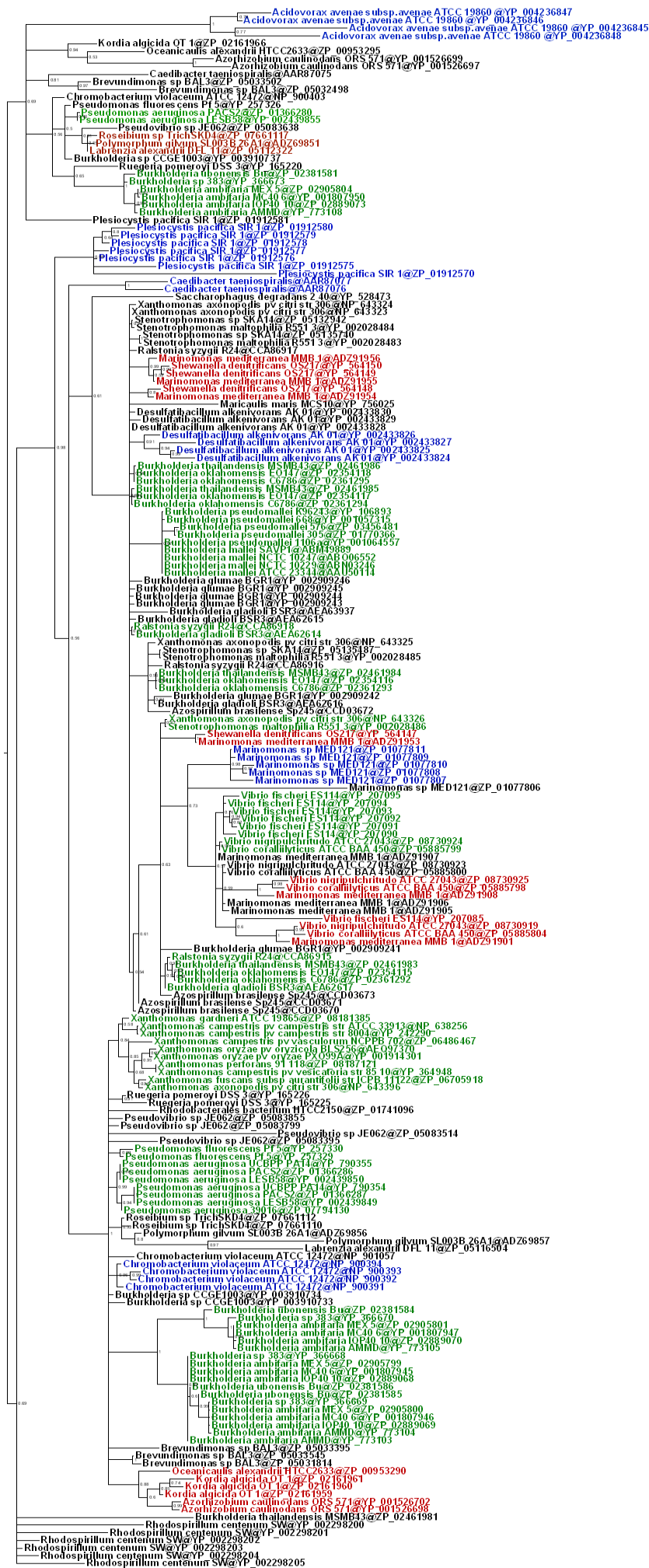


Figure S1 Phylogeny of Reb homologues. Unrooted Bayesian phylogenetic tree of 203 Reb homologues. The tree was obtained by using Phylobayes 3.3 with the LG model of amino acid substitution and a discrete gamma distribution with four categories to take into account among-site rate variation. Note that the tree is not fully resolved due to the small number of positions that could be used for analysis (73 amino acids). Numbers at nodes represent posterior probabilities. The scale bar represents the average number of substitutions per site. Colored taxa correspond to the rebs represented in Figure 5.