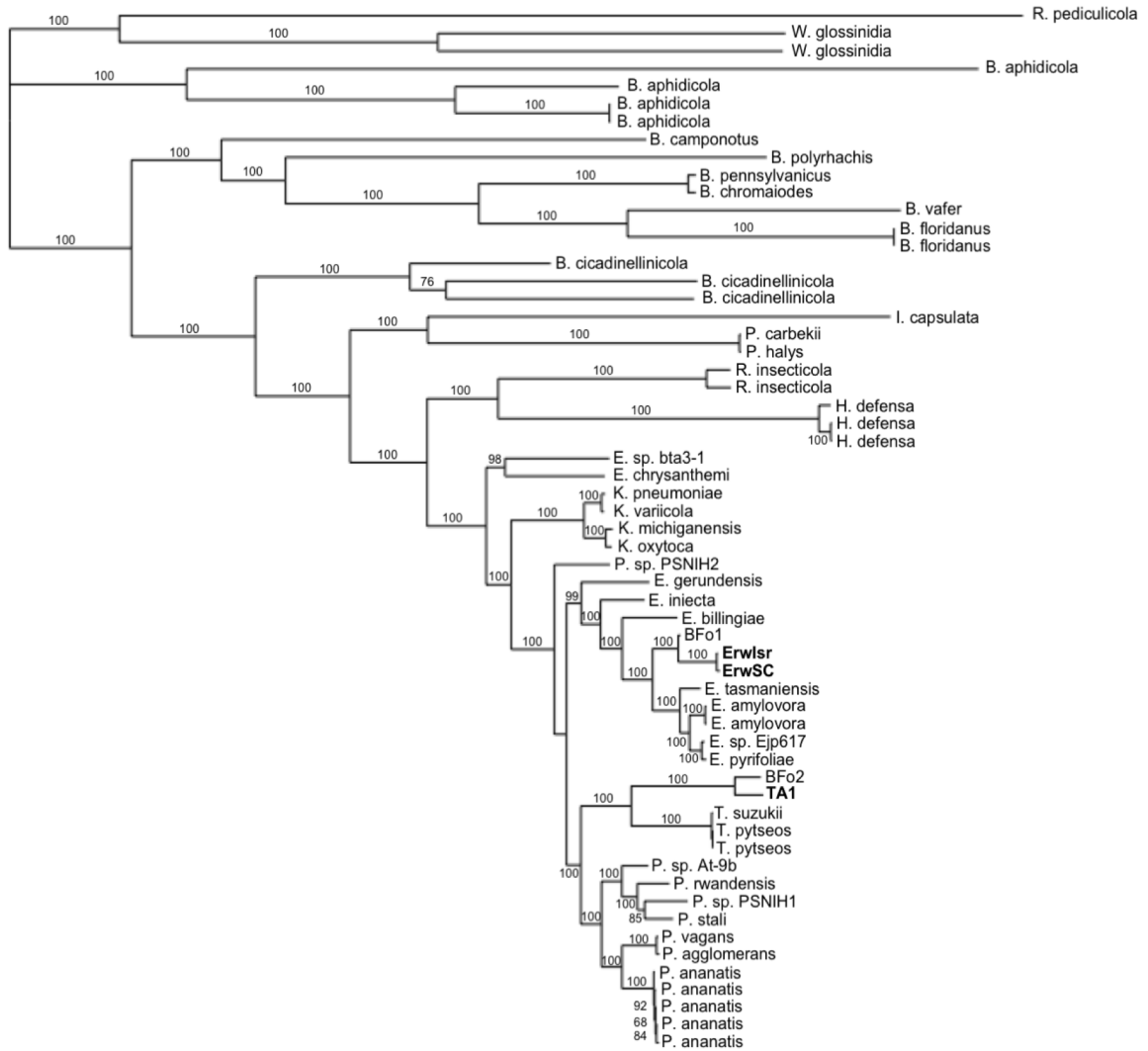


**PhD Thesis Erratum** – Frances Blow, 2017

**Page 62** An incorrect version of the phylogenetic tree was inserted in the published thesis. Please see the correct figure below, which was constructed using the ortholog set and methods described in the Materials and Methods section for this chapter.



**Figure 3.2** | Maximum-Likelihood phylogeny of 59 free-living and insect symbiotic members of the Gammaproteobacteria. Taxa were included in the analysis based on their phylogenetic proximity according to analysis of the 16S rRNA marker gene. The tree was inferred from a concatenated alignment of 81 orthologous clusters that were generated from an OrthoMCL analysis of complete or draft genomes and were present for all taxa included in the tree.