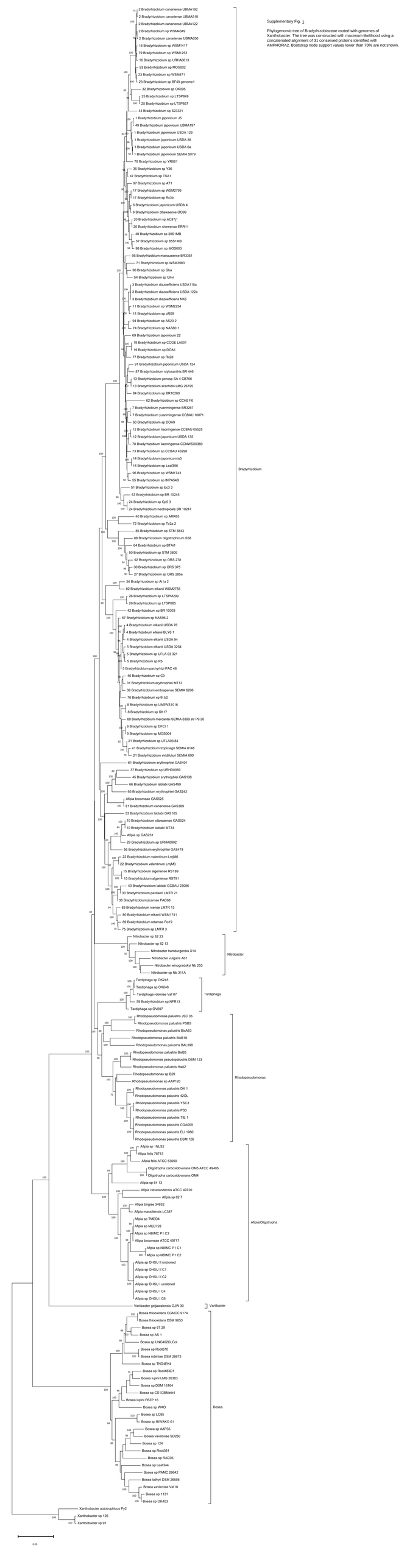

Supplementary Fig. 1

Phylogenomic tree of Bradyrhizobiaceae rooted with genomes of Xanthobacter. The tree was constructed with maximum likelihood using a concatenated alignment of 31 conserved proteins identified with AMPHORA2. Bootstrap node support values lower than 70% are not shown.