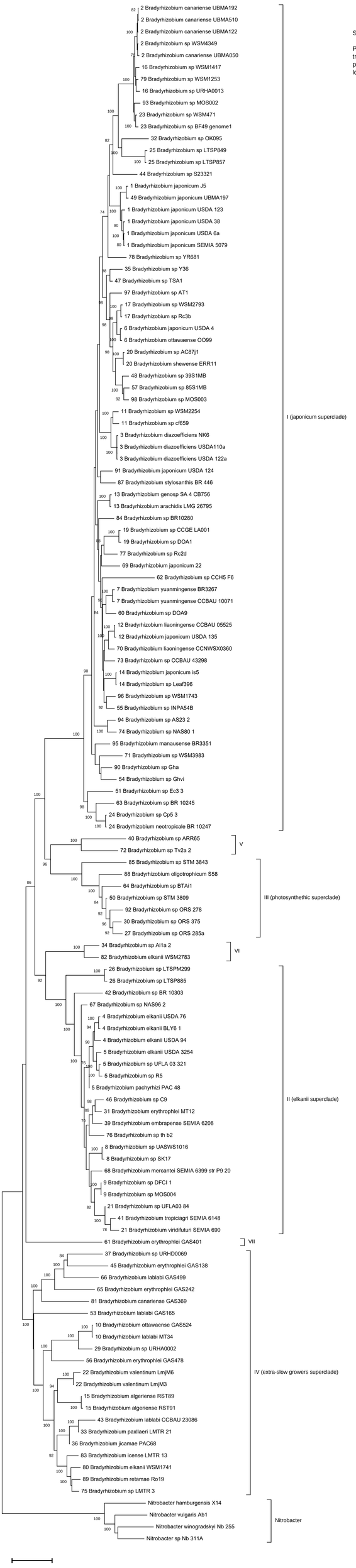

Supplementary Figure 2

Phylogenomic tree of Bradyrhizobium. Superclades are indicated with Roman numerals. The tree was constructed with maximum likelihood using a concatenated alignment of 31 conserved proteins identified with AMPHORA2 (7672 aa alignment length). Bootstrap node support values lower than 70% are not shown.