

***Bradyrhizobium altum* sp. nov., *Bradyrhizobium oropedii* sp. nov. and *Bradyrhizobium acaciae* sp. nov. from South Africa show locally restricted and pantropical *nodA* phylogeographic patterns**

Supplementary material: Supplementary figures

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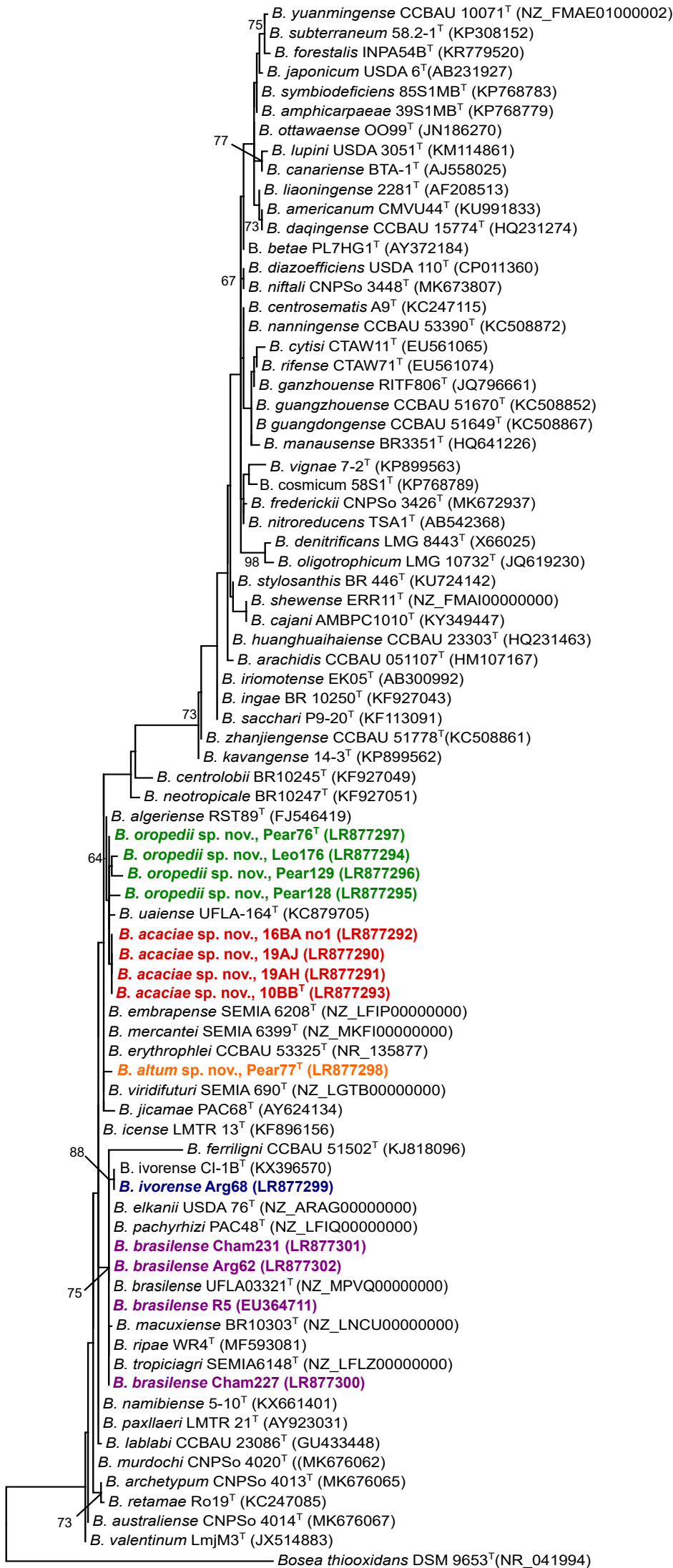
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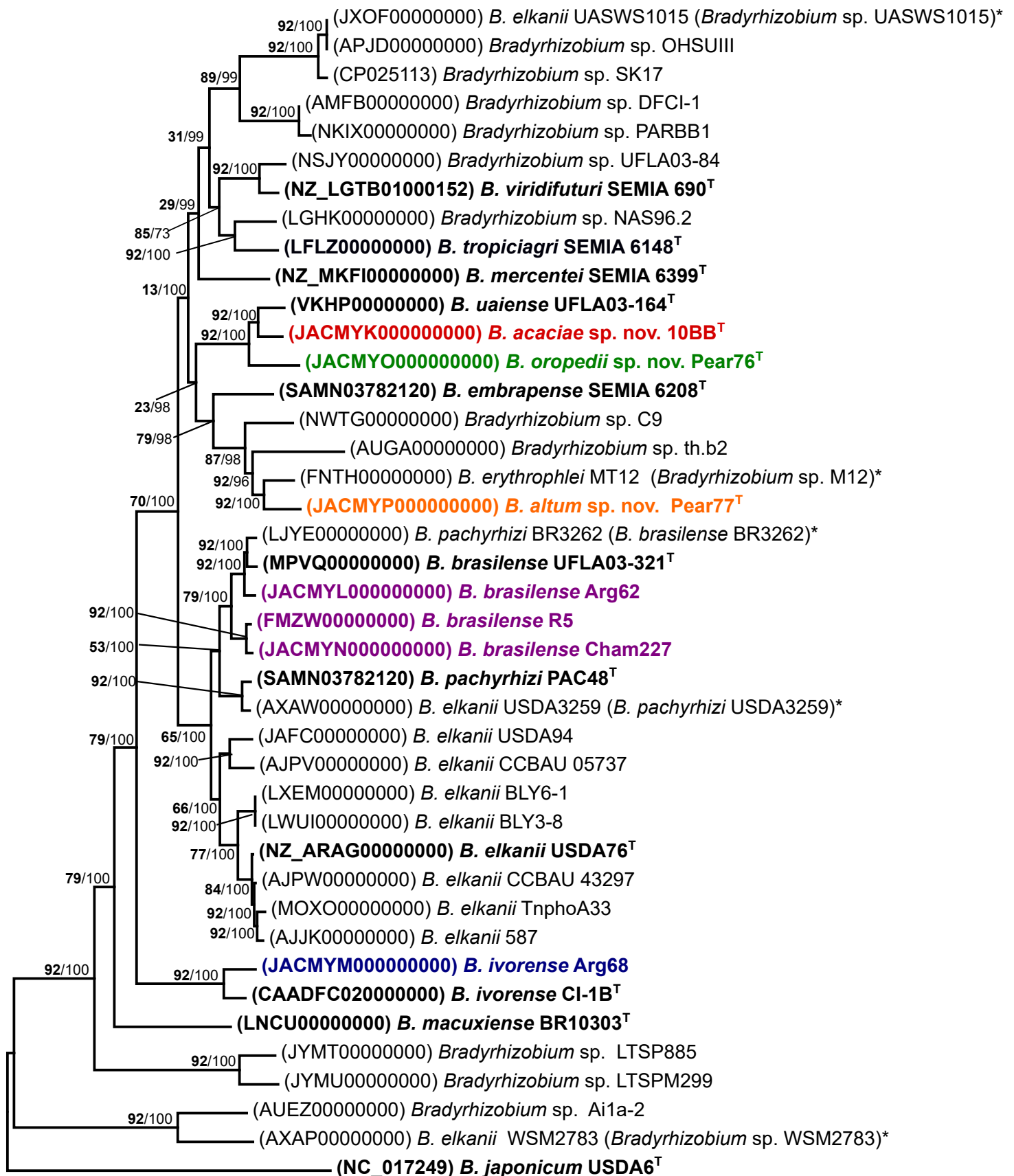
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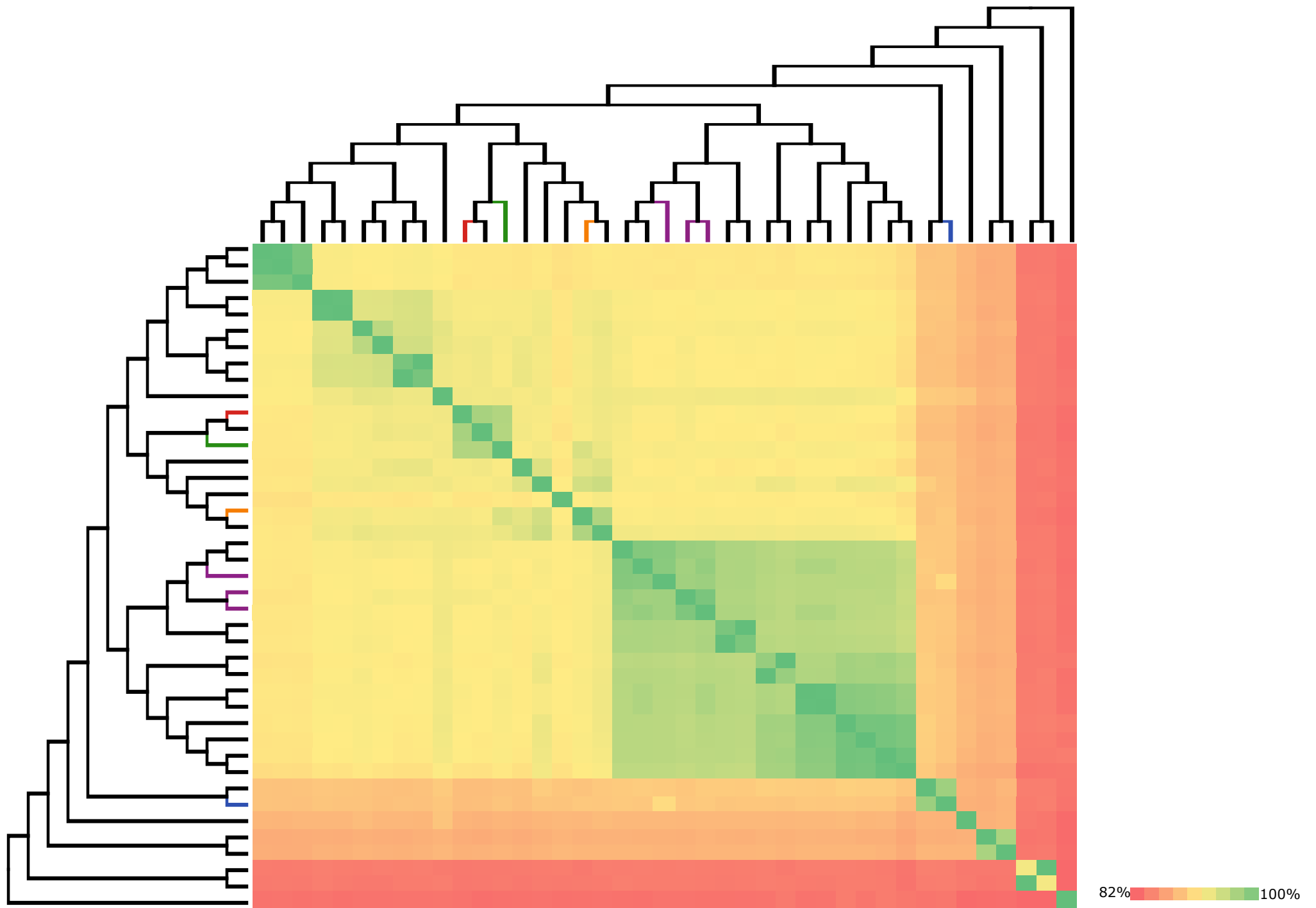


Supplementary Figure S1: Maximum-likelihood phylogeny based on a total of 80 16S rRNA gene sequences were used for this phylogeny, including all described *Bradyrhizobium* type strains (until August 2020), strains investigated in this study and outgroup. *Bosea thiooxidans* DSM9653^T was used as the outgroup. GenBank accession numbers are indicated in brackets and the strains investigated in this study are shown in color. Bootstrap values were inferred from 1000 replicates and only the support values greater than 60% are shown on the nodes. The scale bar indicates the nucleotide substitutions per site. The taxa included all partial 16S rRNA sequences available for *Bradyrhizobium* type strains described to date (August 2020).



0.01

Supplementary Figure S2: Maximum-likelihood phylogeny of 92 protein-coding genes identified and extracted using the UBCG pipeline (Na et al., 2018). This phylogeny includes all the strains within the *B. elkanii* supergroup with genome sequences (listed in brackets) available as per Avontuur et al. 2019. *Bradyrhizobium japonicum* USDA 6^T was used as an outgroup. Only strains of the proposed novel species for which a genome sequence is available was included in the phylogeny and is indicated in color. Incorrect species names are rectified and indicated in brackets with an asterisk. Names are corrected according to the Genome Taxonomy Database (Parks et al., 2018). *Bradyrhizobium* type strains are shown in bold. Nodal support values include gsi (Gene Support Index) shown in bold, followed by the bootstrap support. The scale bar represents the number of nucleotide changes per site.



Supplementary Figure S3: A heatmap showing fast alignment-free computation of whole-genome Average Nucleotide Identity (FastANI) similarity values relative to the intra-generic relationships of *Bradyrhizobium elkanii* supergroup based on the maximum-likelihood topology (Supplementary Figure 1). FastANI values were calculated utilizing the Mashmap algorithm (Jain et al., 2018).

Supplementary Figure S4: Maximum likelihood phylogeny of the genus *Bradyrhizobium* based on *nodA* gene sequences used in Beukes et al., (2016) study. *Methylobacterium nodulans* ORS2060^T was used as an outgroup. Strains of novel species are shown in their respective colours. Bootstrap support values are inferred from 1000 replicates and values greater than 60% are indicated at the nodes. The scale bar indicates the number of nucleotide changes per site.