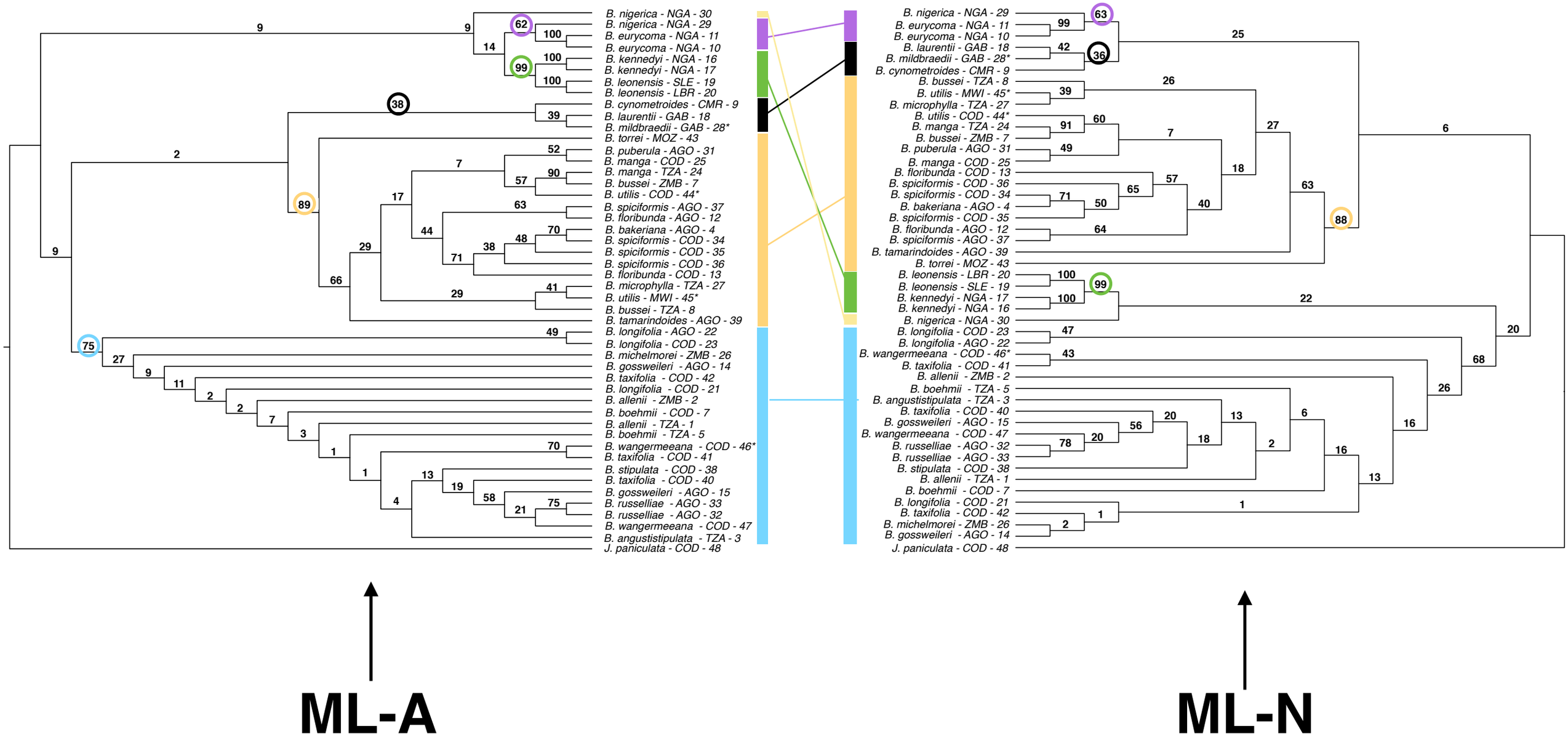

Figure S1. Comparison between Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using rDNA sequences and two different coding schemes. Cladograms were produced using RAxML-NG software (Kozlov et al., 2019) and intra-individual site polymorphisms (2ISPs) were coded either following the IUPAC nomenclature and considered as ambiguous (ML-A) or coded as missing data (ML-N). Most of the branches have low bootstraps (BS) supports regardless of the coding schemes.

ML-N

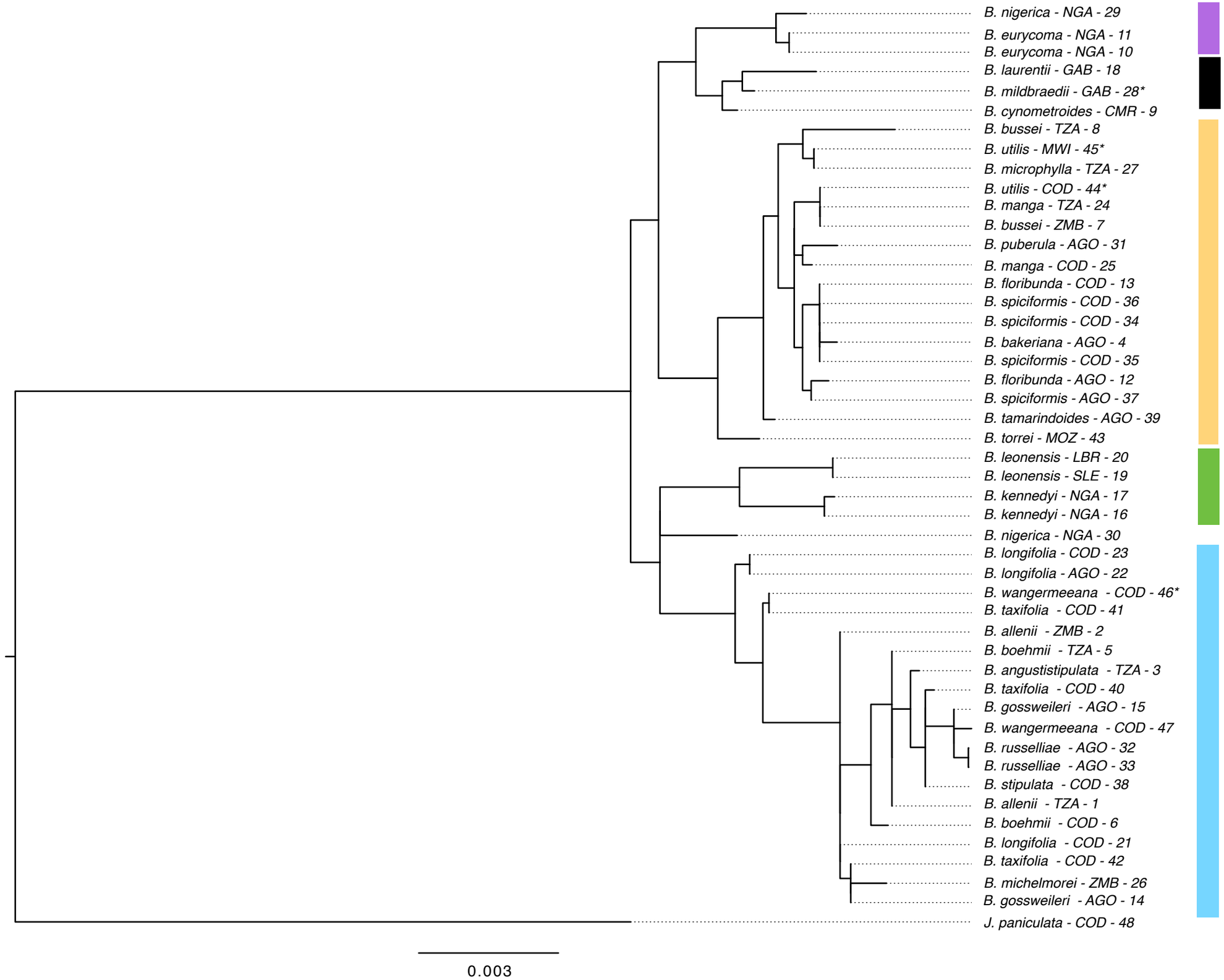

Figure S2. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Intra-individual site polymorphisms (2ISPs) were coded as missing data (i.e. N).

ML-A

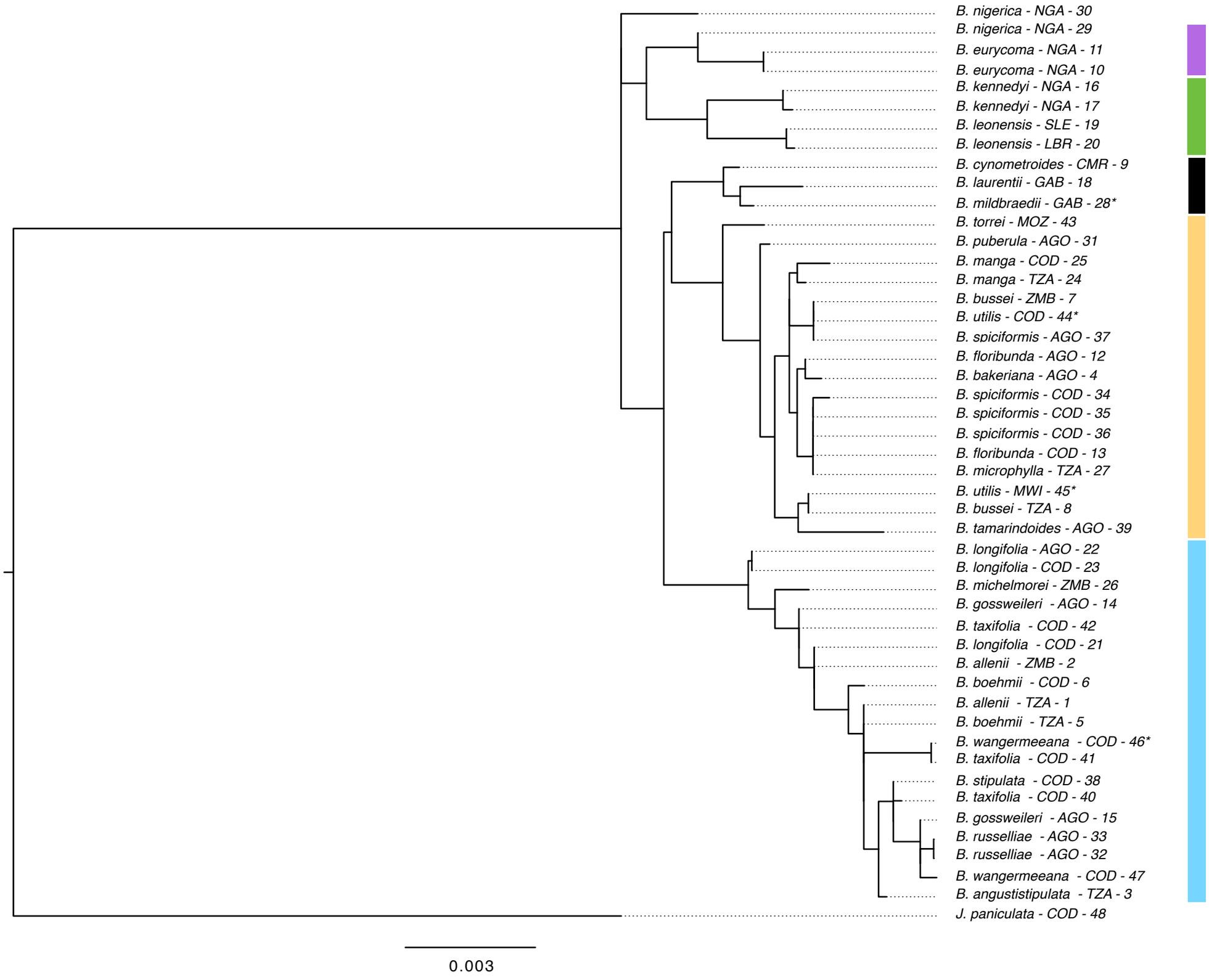

Figure S3. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as ambiguous (ML-A).

ML-I

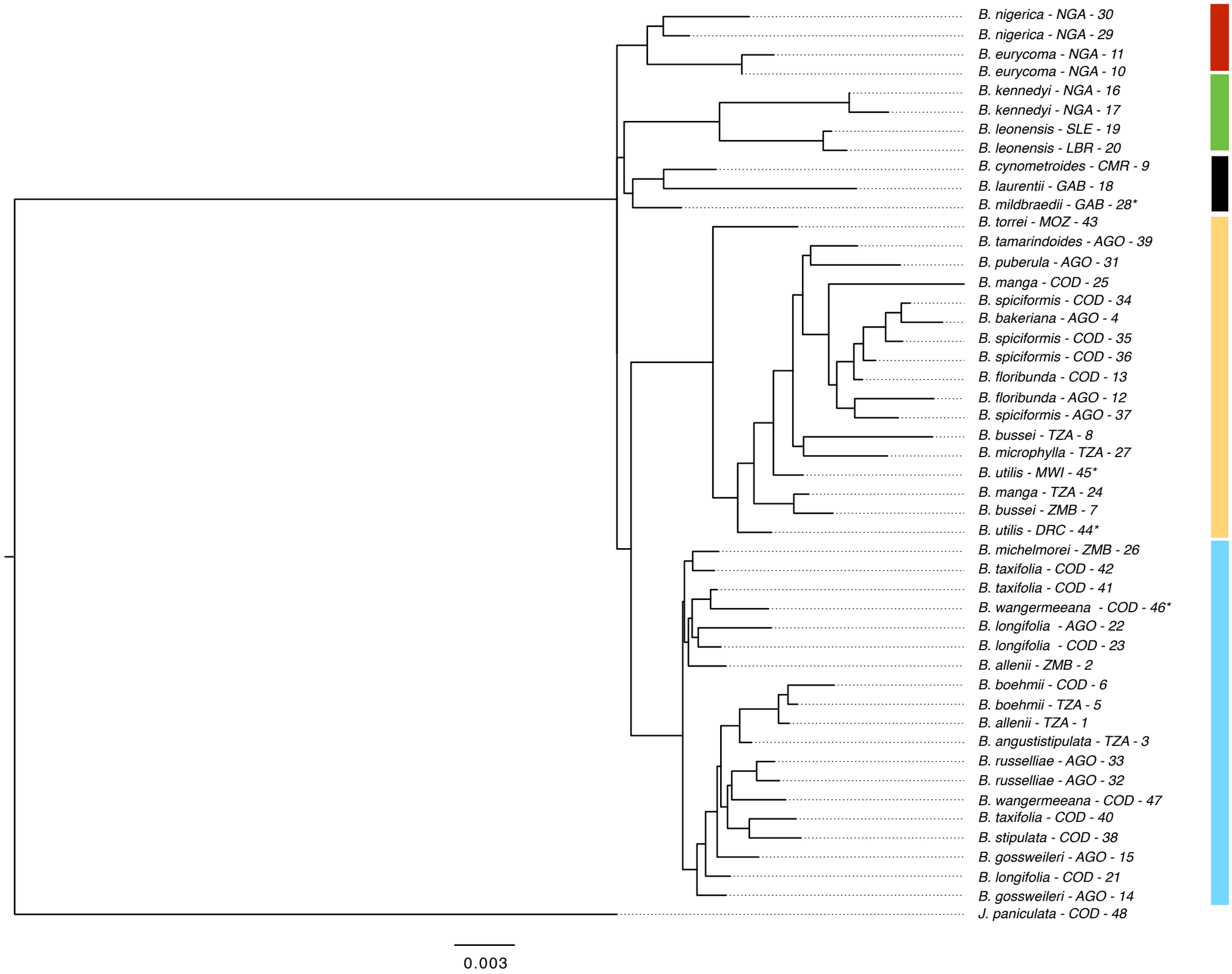

Figure S4. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as informative (ML-I).

ML-N (two partitions)

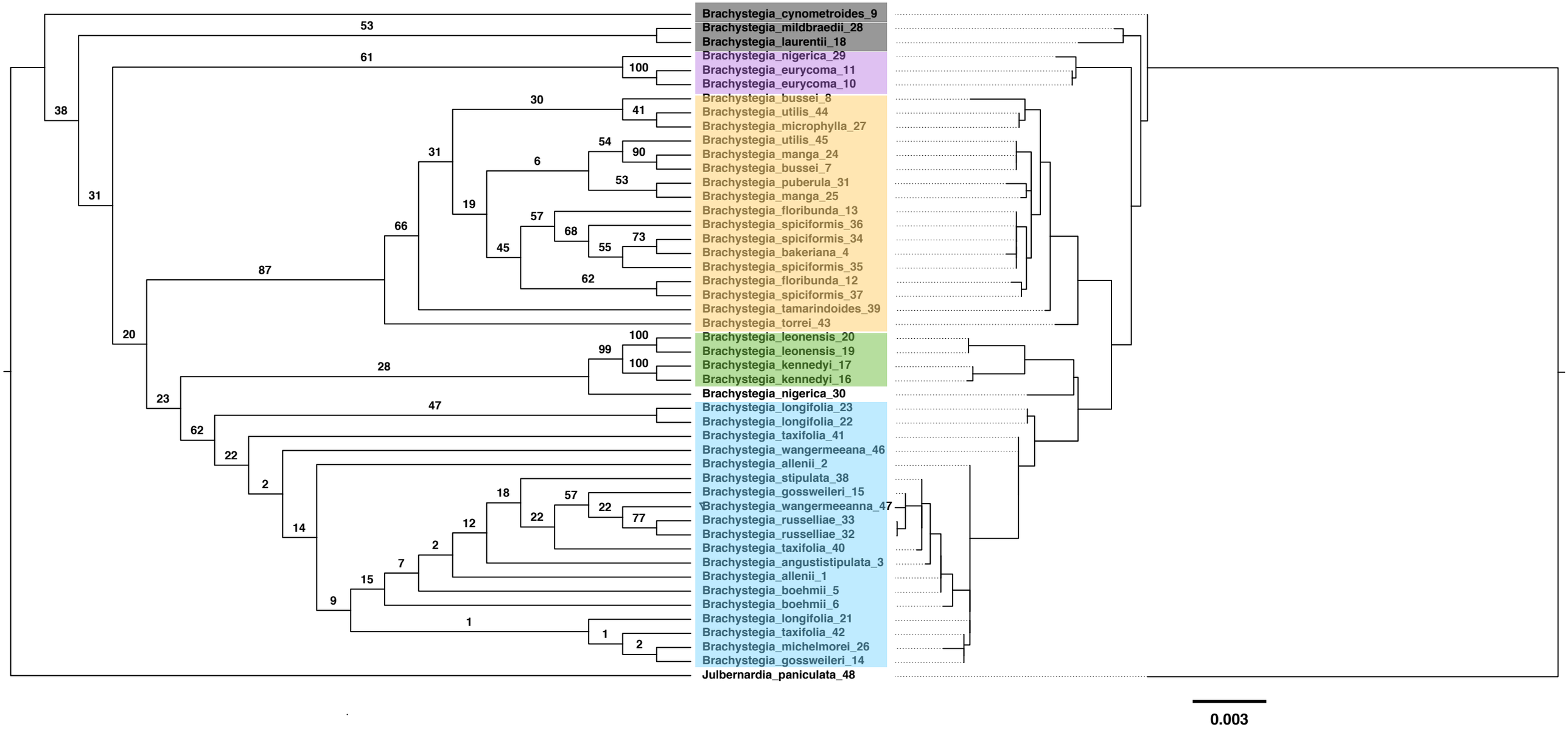

Figure S5. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Cladogram (left) and its corresponding phylogram (right) are both provided. Intra-individual site polymorphisms (2ISPs) were coded as missing data (i.e. N). ML inference was conducted using two partitions (ITS1+ ITS2 vs all rRNA genes; GTR+I+G model for each partition).

ML-A (two partitions)

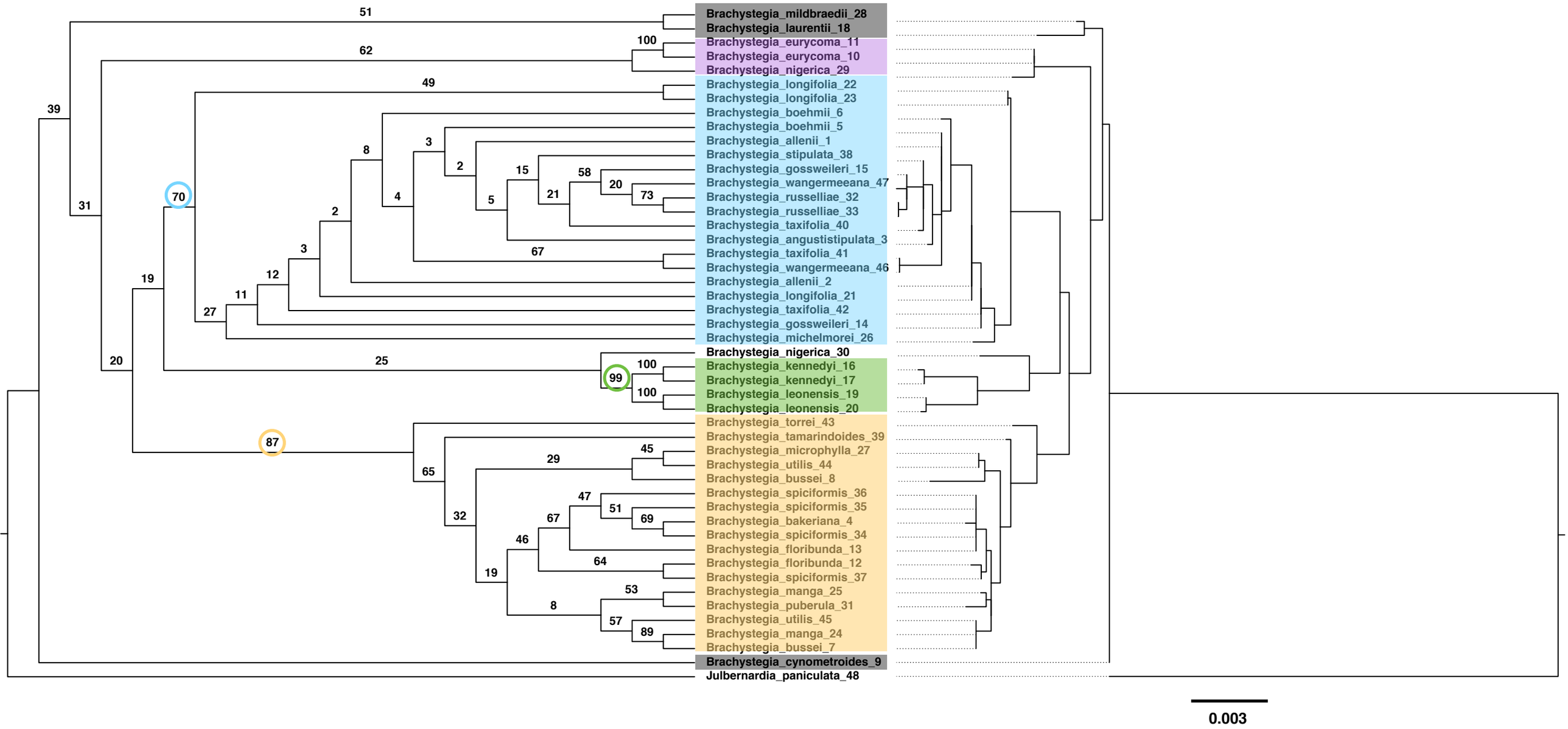

Figure S6. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Cladogram (left) and its corresponding phylogram (right) are both provided. Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as ambiguous (ML-A). ML inference was conducted using two partitions (ITS1+ ITS2 vs all rRNA genes; GTR+I+G model for each partition).

ML-I (two partitions)

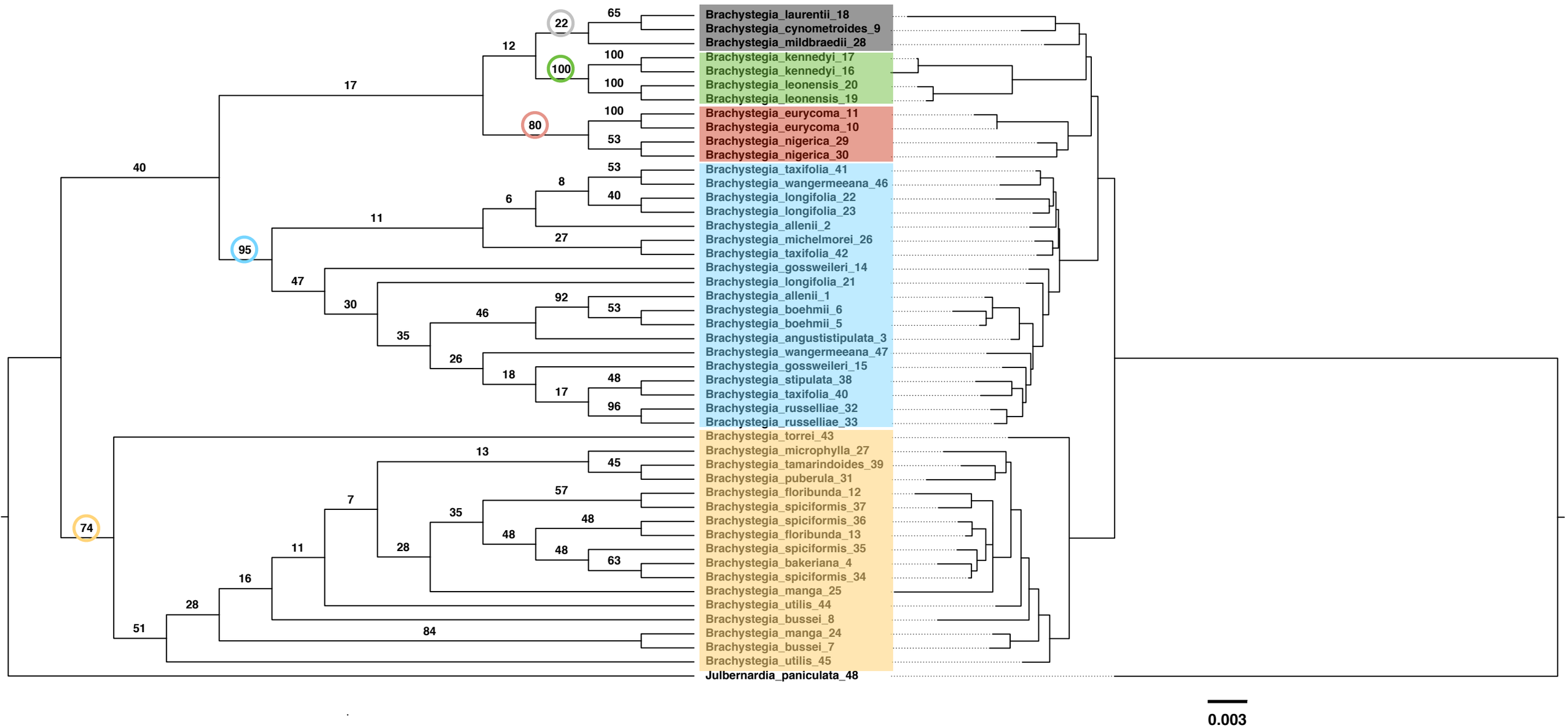

Figure S7. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Cladogram (left) and its corresponding phylogram (right) are both provided. Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as as informative (ML-I). ML inference was conducted using two partitions (ITS1+ ITS2 vs all rRNA genes).

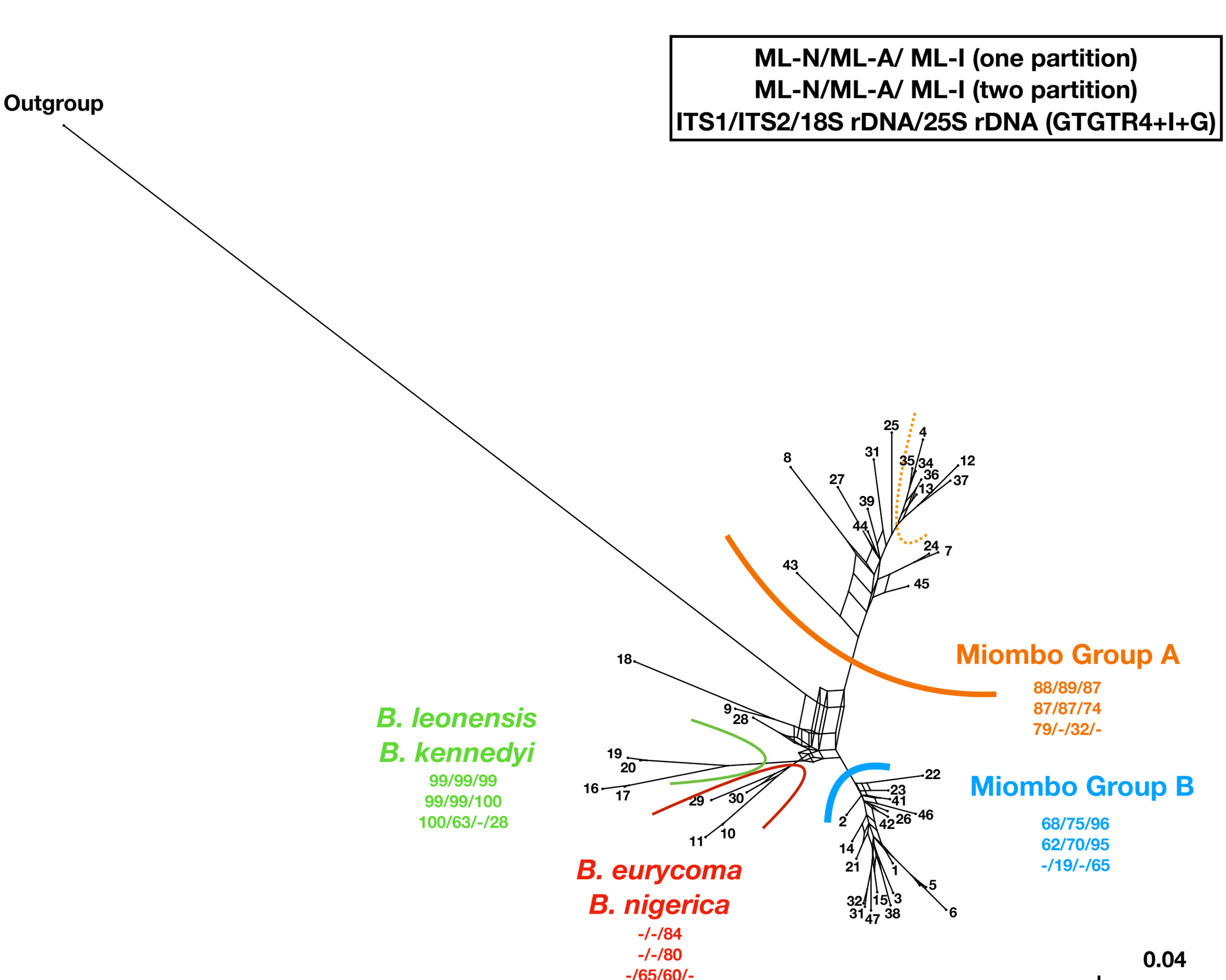

Figure S8. Bootsrap consensus network. The four main clades identified in the different Maximum-Likelihood (ML) phylogenetic inferences are delineated with thick coloured lines. The BS support values for these clades are given according to the different ML analyses (ML-N, ML-A, ML-I; one and two partitions; ML-I for ITS1, ITS2, 18S and 25S). In Miombo A, the specimens of *B. bakeriana*, *B. floribunda* and *B. spiciformis* are clustered together (delineate with the dotted orange line).

18S

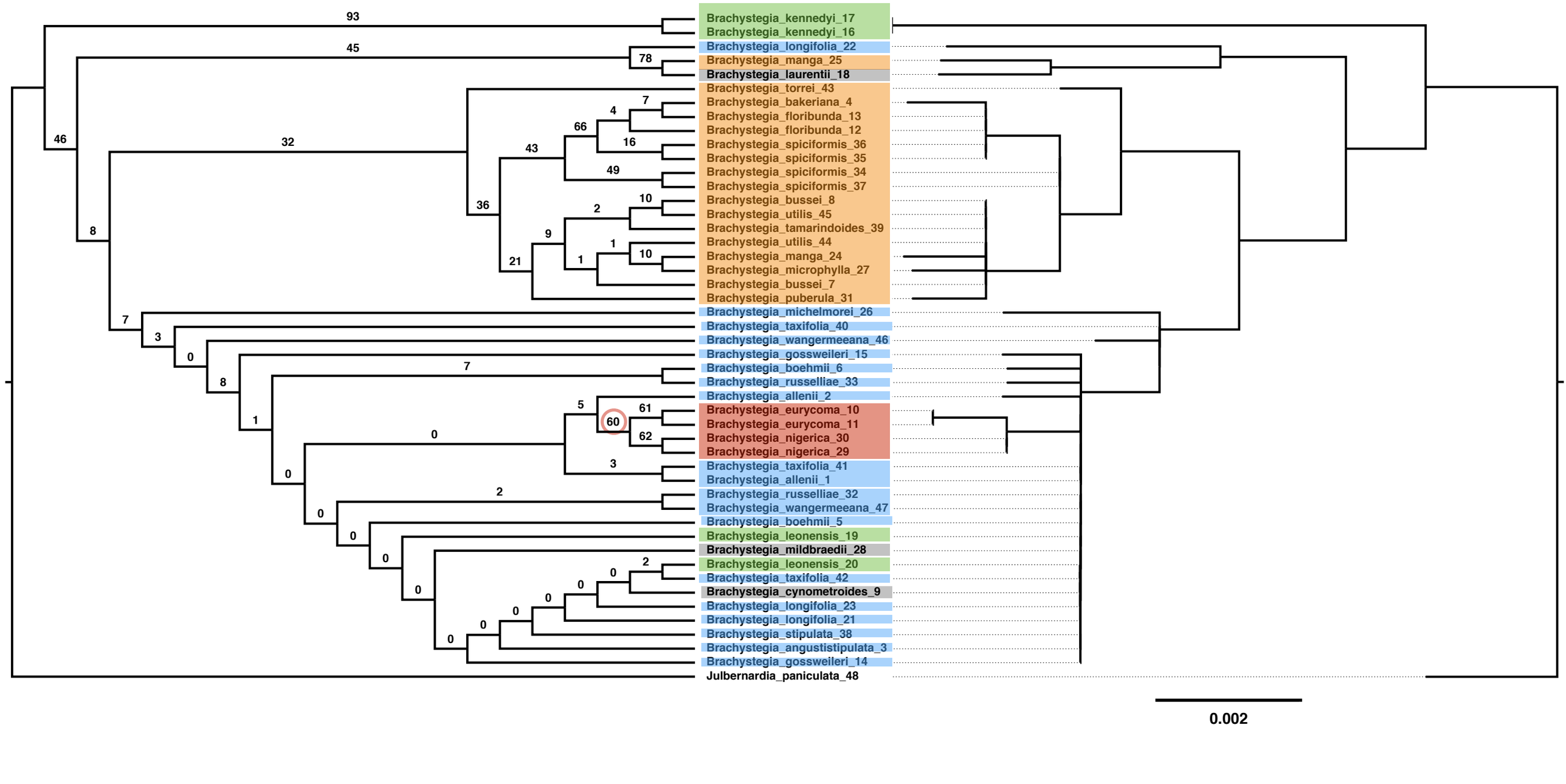

Figure S9. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using the 18S rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Cladogram (left) and its corresponding phylogram (right) are both provided. Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as as informative (ML-I)

25S

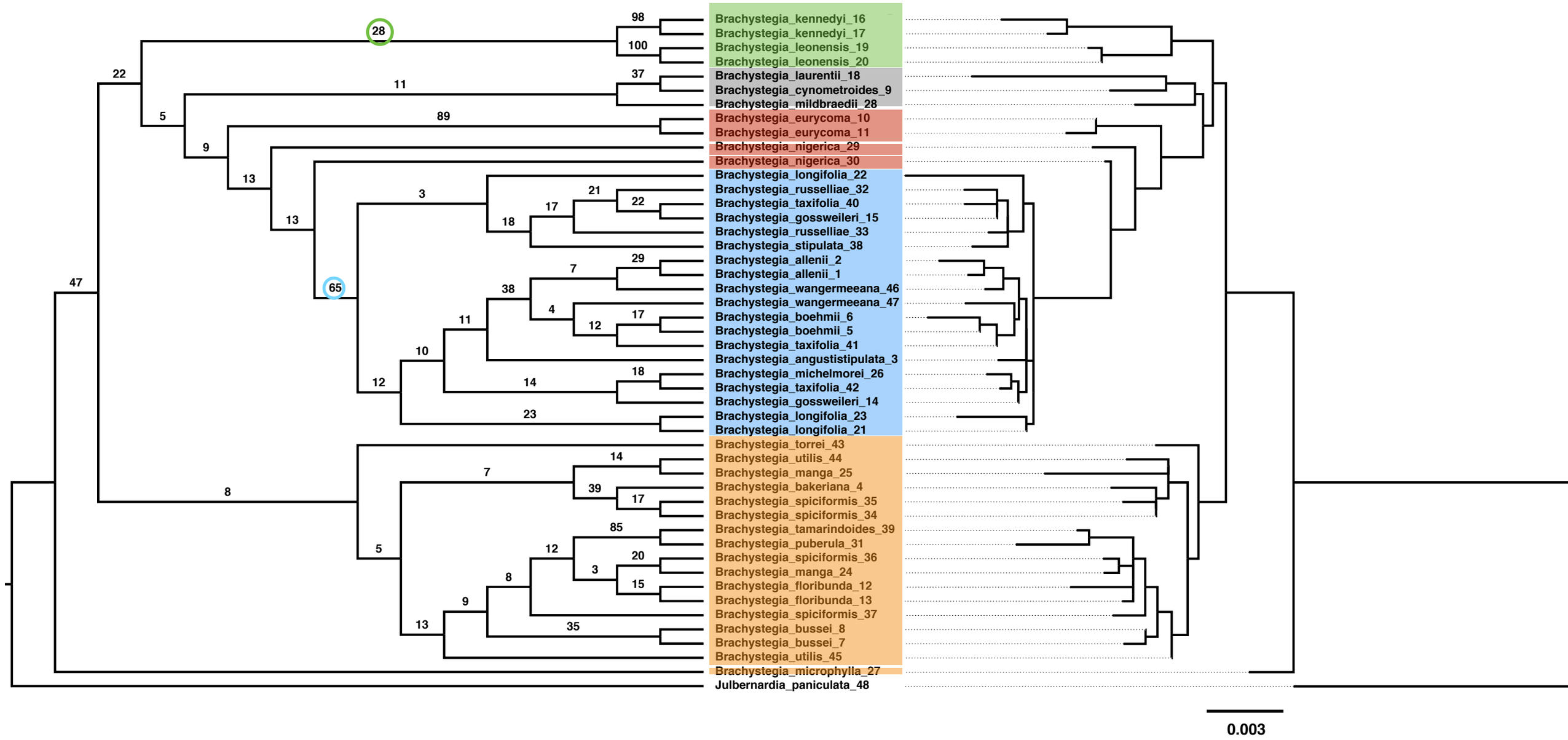

Figure S10. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using the 18S rDNA sequences and produced using RAxML-NG software (Kozlov et al., 2019). Cladogram (left) and its corresponding phylogram (right) are both provided. Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as as informative (ML-I)

ITS1

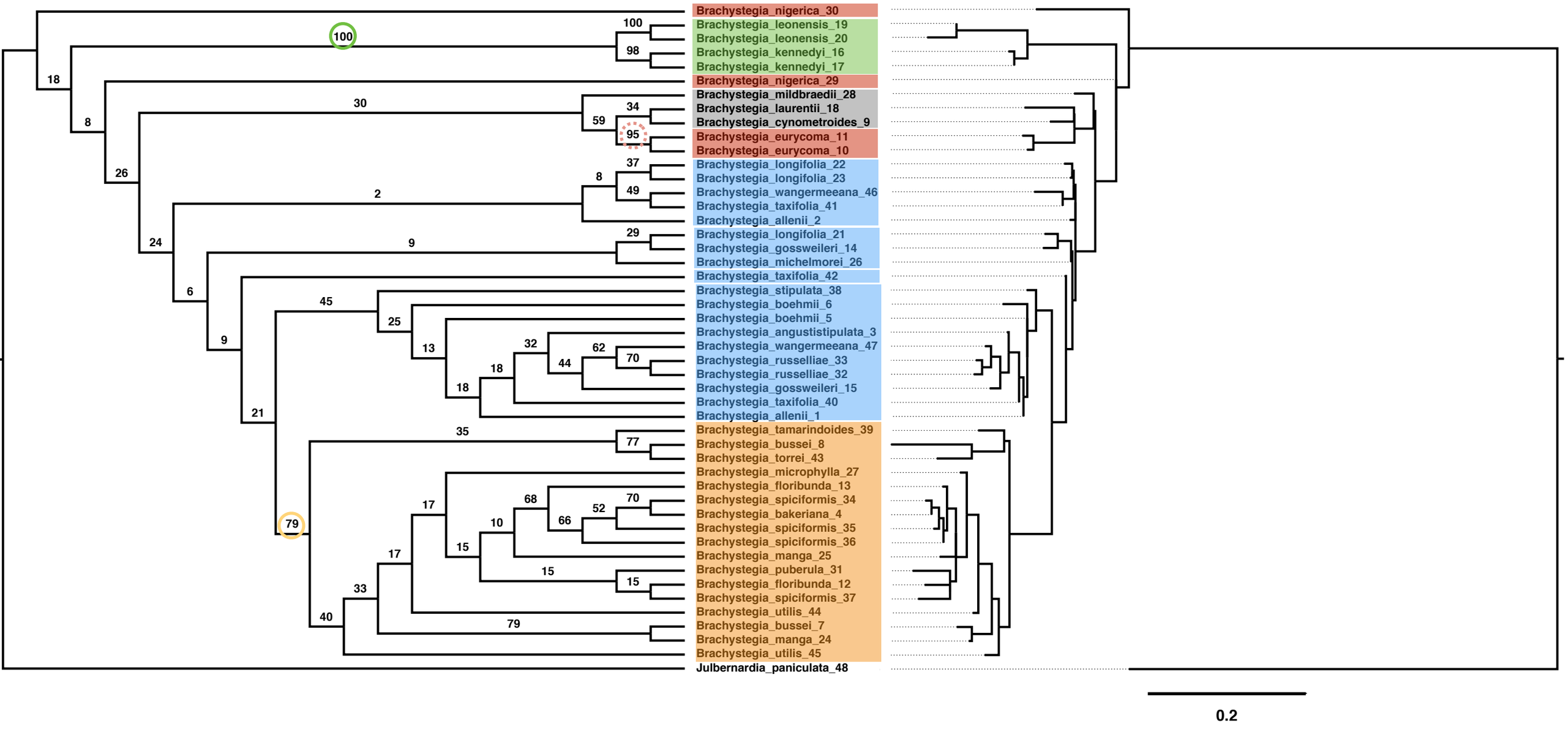

Figure S10. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using the internal transcribed spacer 1 (ITS1) sequences and produced using RAxML-NG software (Kozlov et al., 2019). Cladogram (left) and its corresponding phylogram (right) are both provided. Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as as informative (ML-I)

ITS2

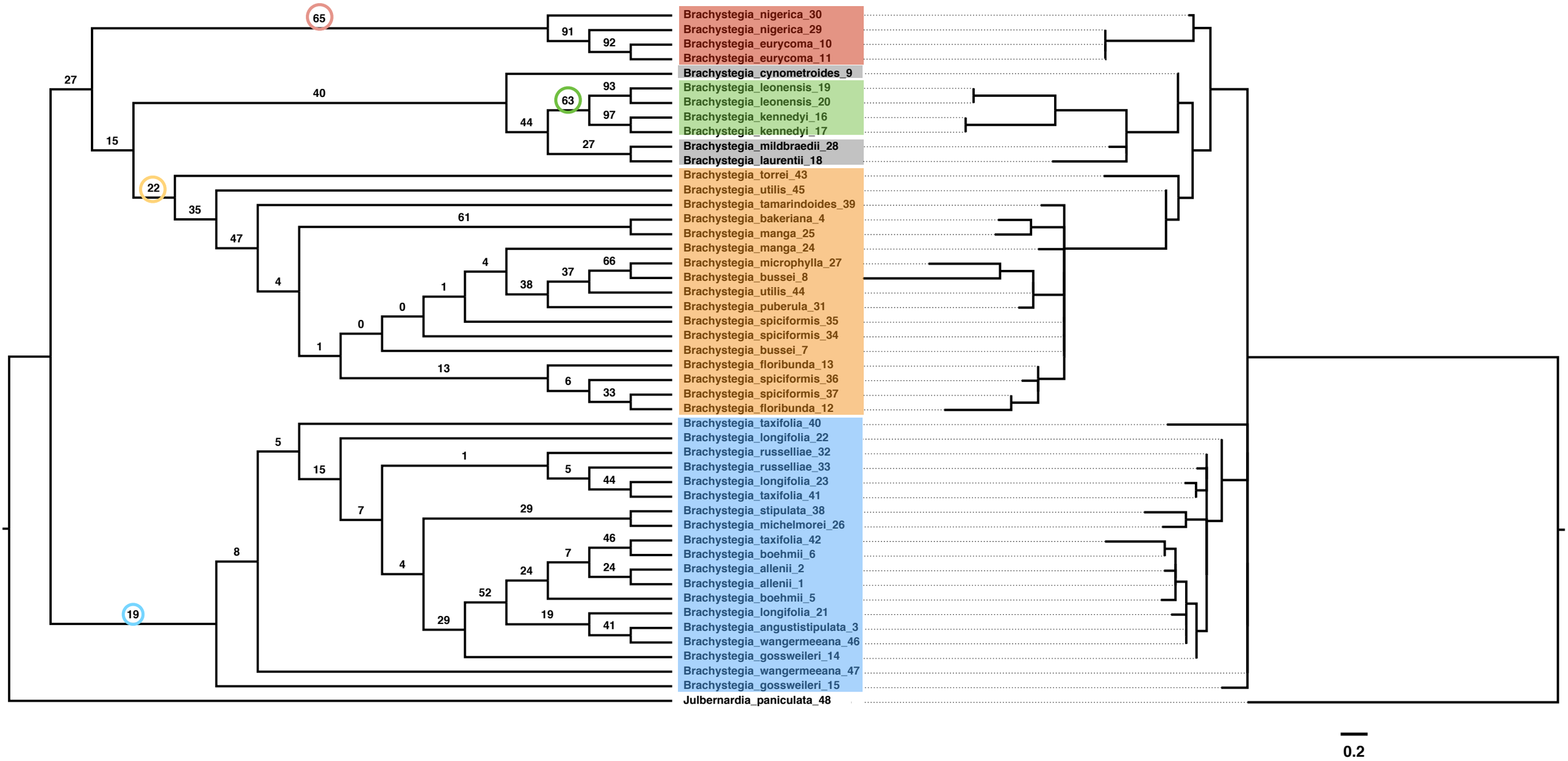

Figure S12. Maximum-Likelihood phylogenetic inferences of *Brachystegia* species using the internal transcribed spacer 2 (ITS2) sequences and produced using RAxML-NG software (Kozlov et al., 2019). Cladogram (left) and its corresponding phylogram (right) are both provided. Intra-individual site polymorphisms (2ISPs) were coded following the IUPAC nomenclature and considered as as informative (ML-I)