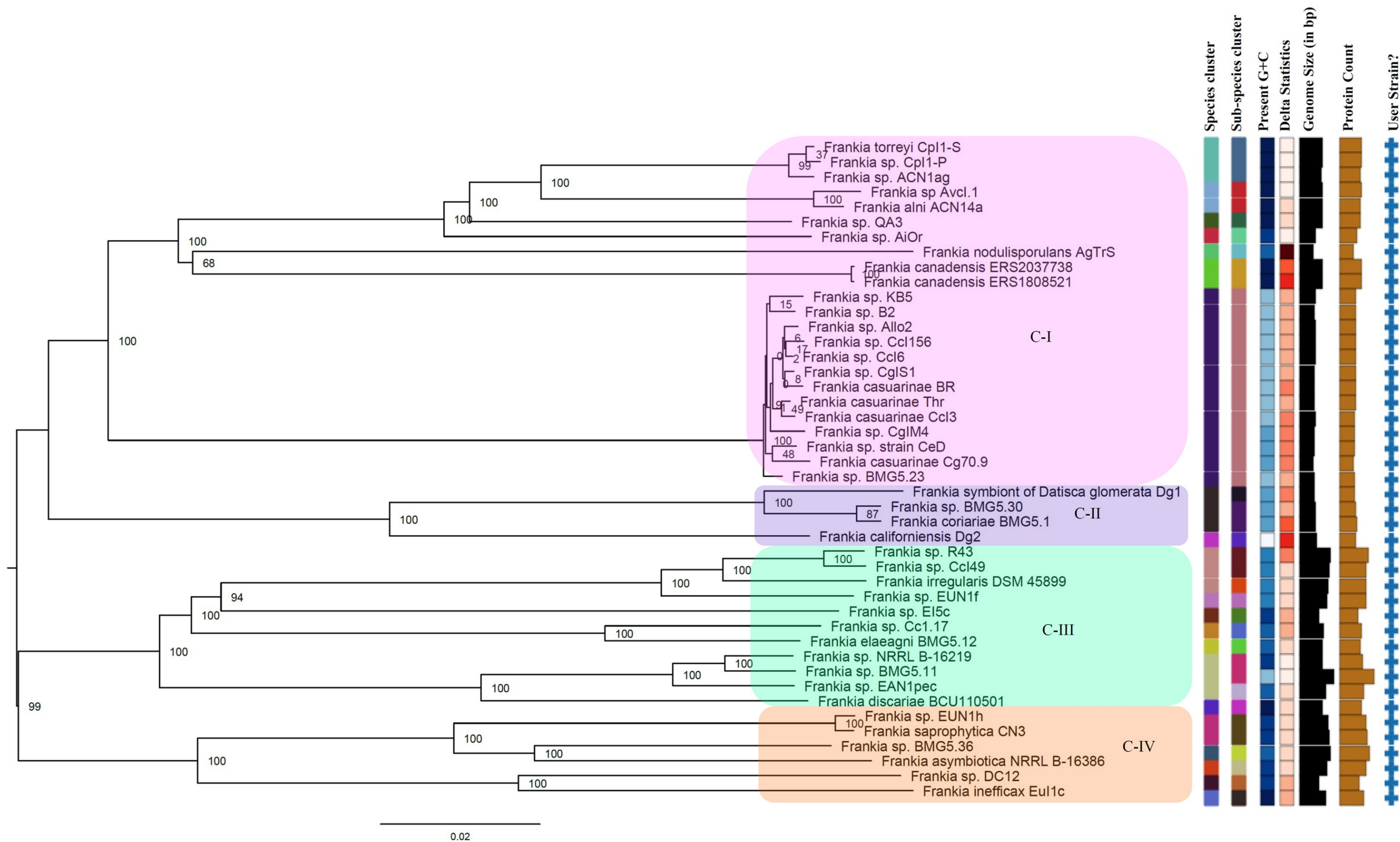




Supplementary figure 2: Whole genome based phylogeny of Frankia. Type (Strain) Genome Server was used for generating the tree. TYGS sub-divided the whole genome based phylogeny generation into pair-wise comparison of genome sequences using Genome Blast Distance Phylogeny (GBDP) and accurate intergenomic distances calculation by 'trimming' and distance formula. 100 distance replicates were used for that analysis. Digital DNA-DNA Hybridization (DDH) scores and confidence intervals were calculated through GGDC2.1 server. Intergenomic distance based phylogeny was generated through a balanced minimum evolution tree with branch support via FASTME 2.1.6.1. Branch point support was inferred from 100 pseudo-bootstrap replicates per branch. The phylogeny was generated using the default parameters. Heatmaps with species cluster, sub-species cluster, G+C amount, delta statistics, the genome size (bp) and protein content were generated through the TYGS server using default parameters.