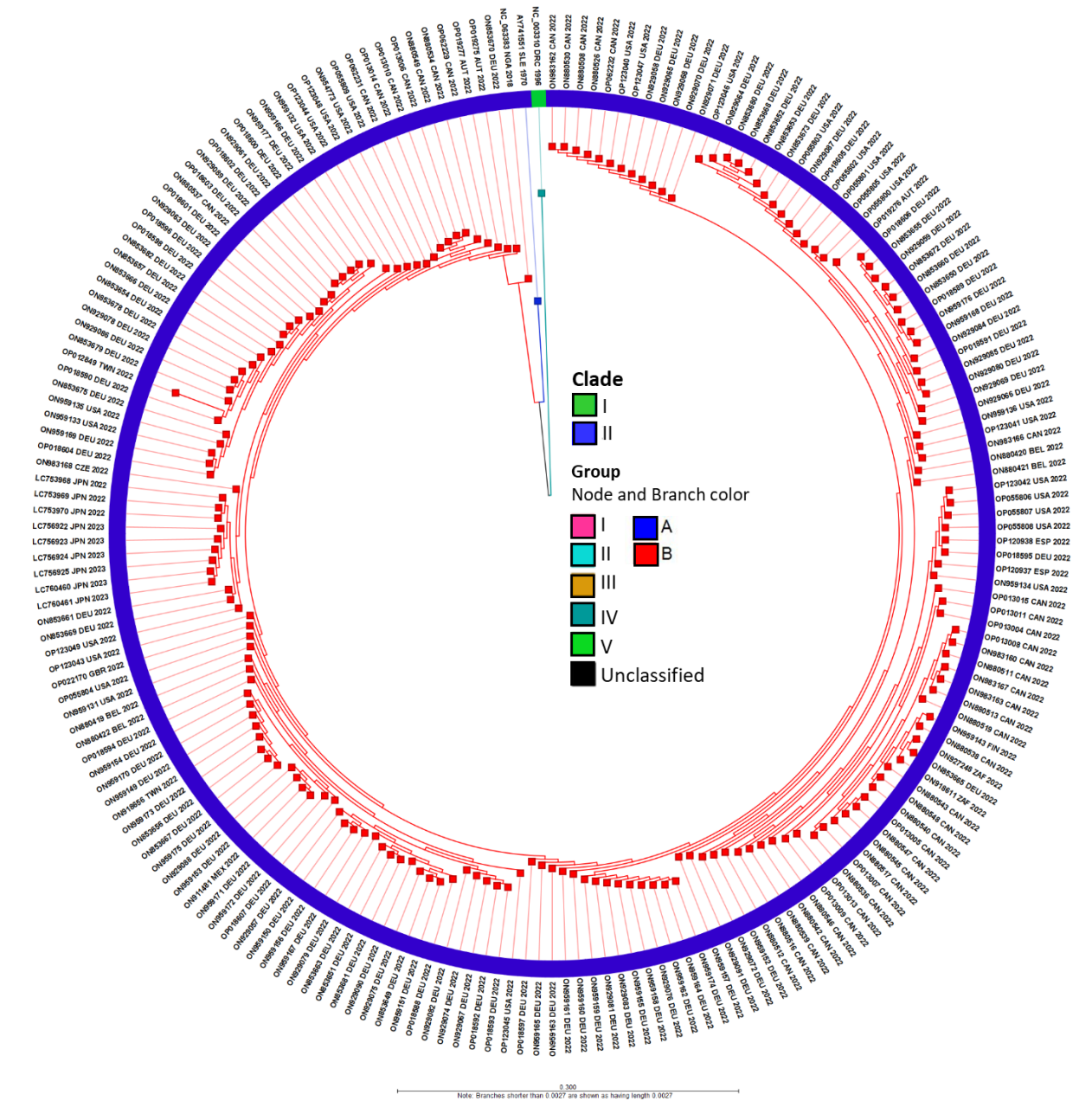
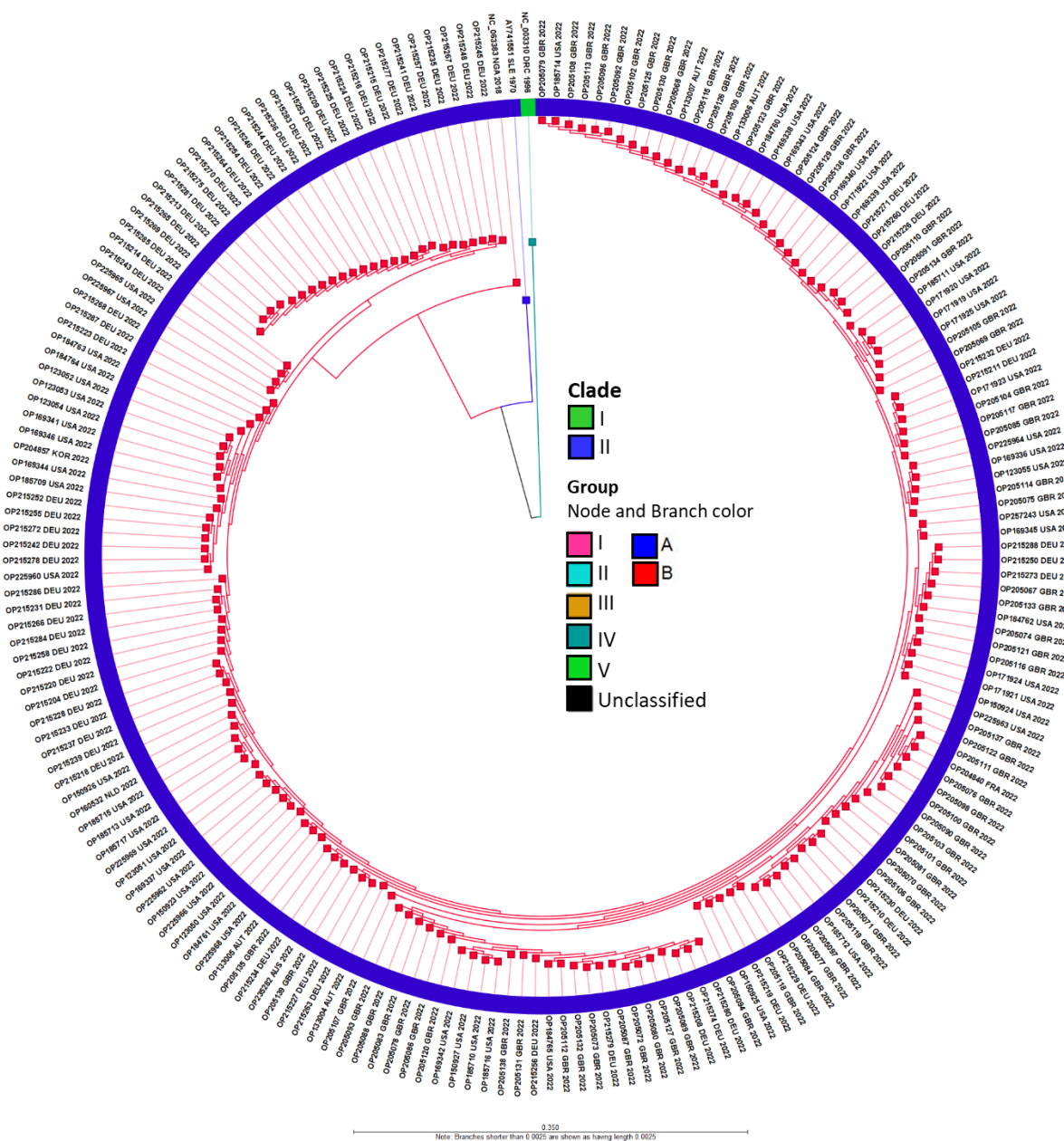


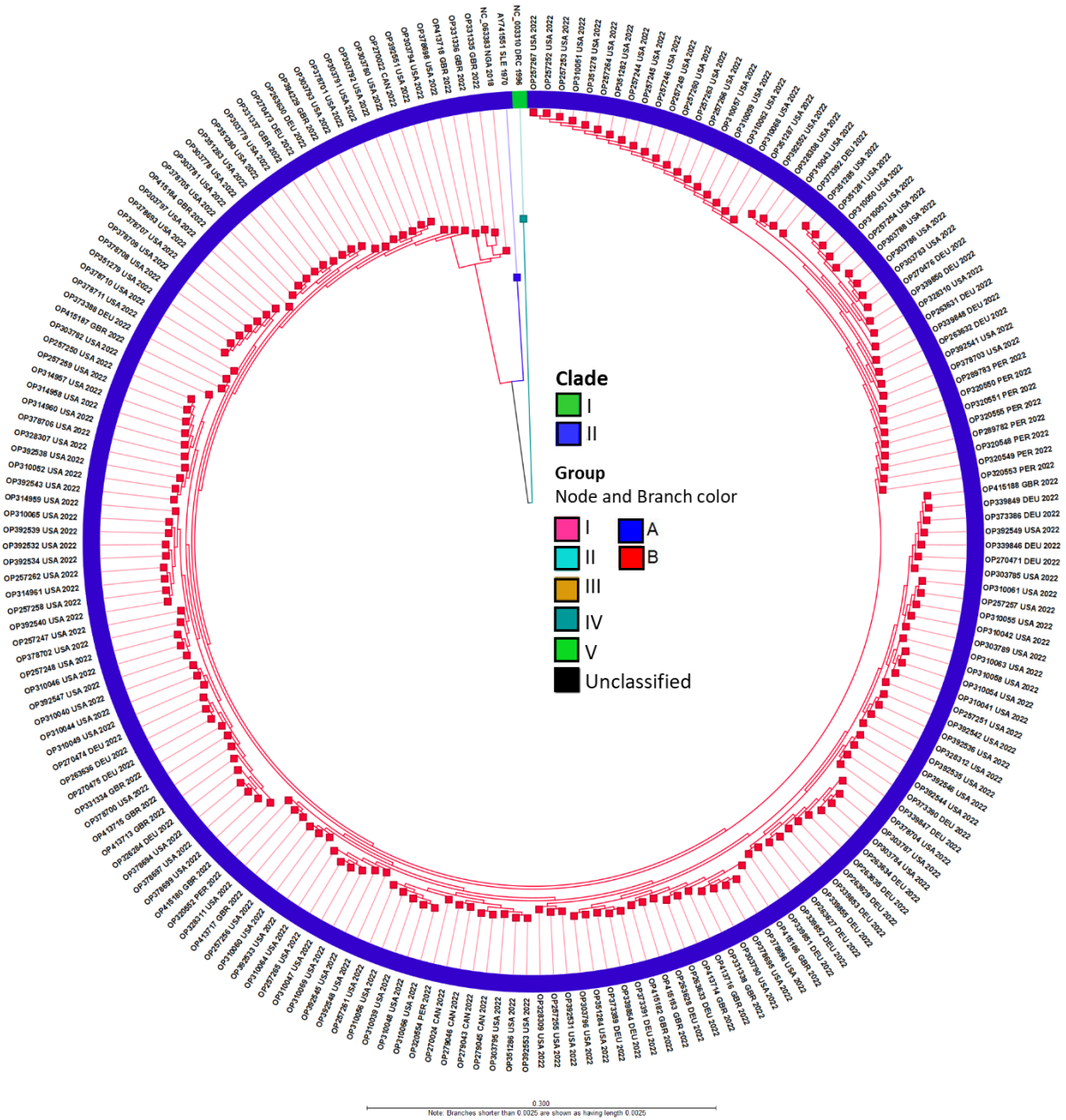
A



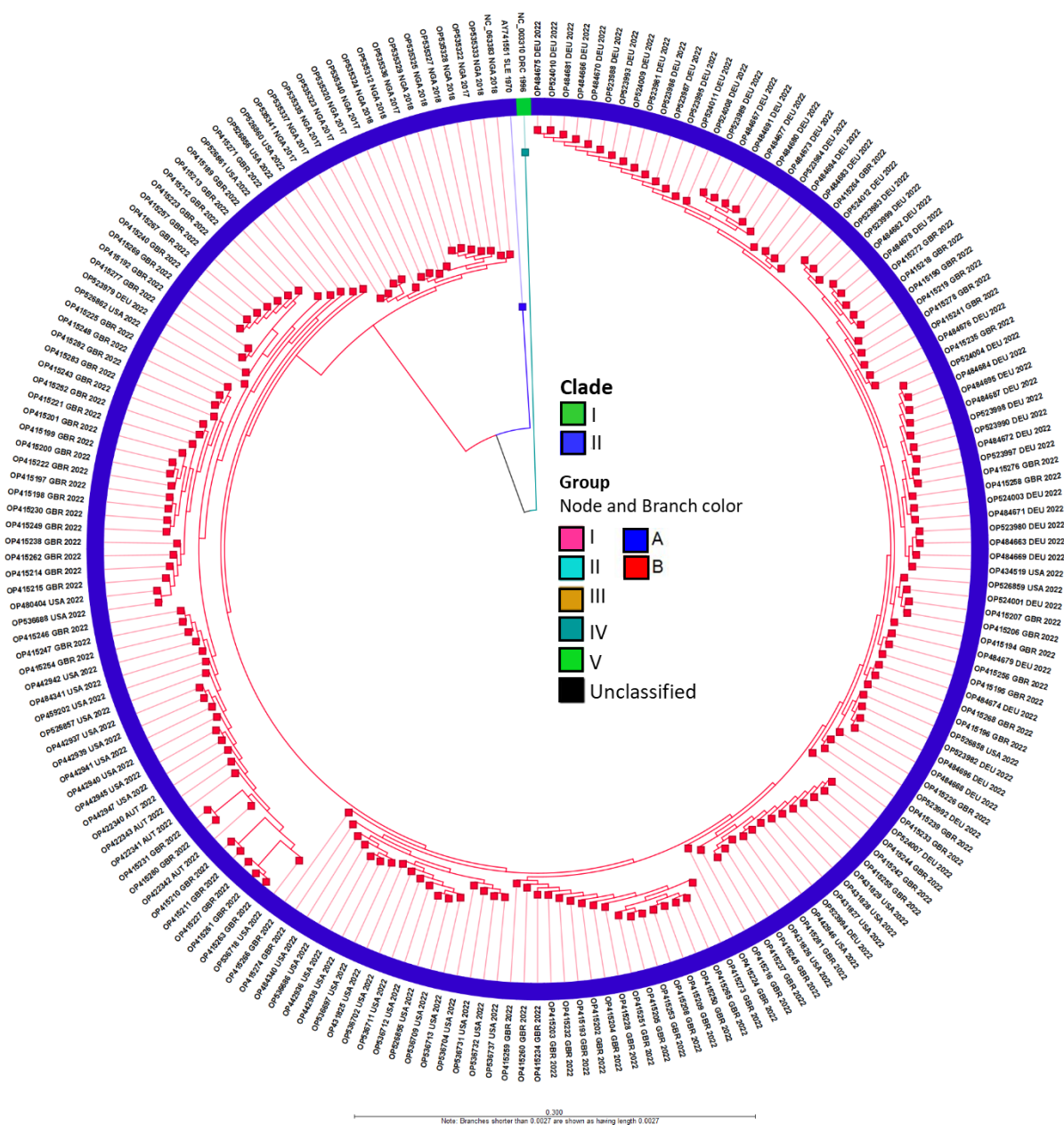
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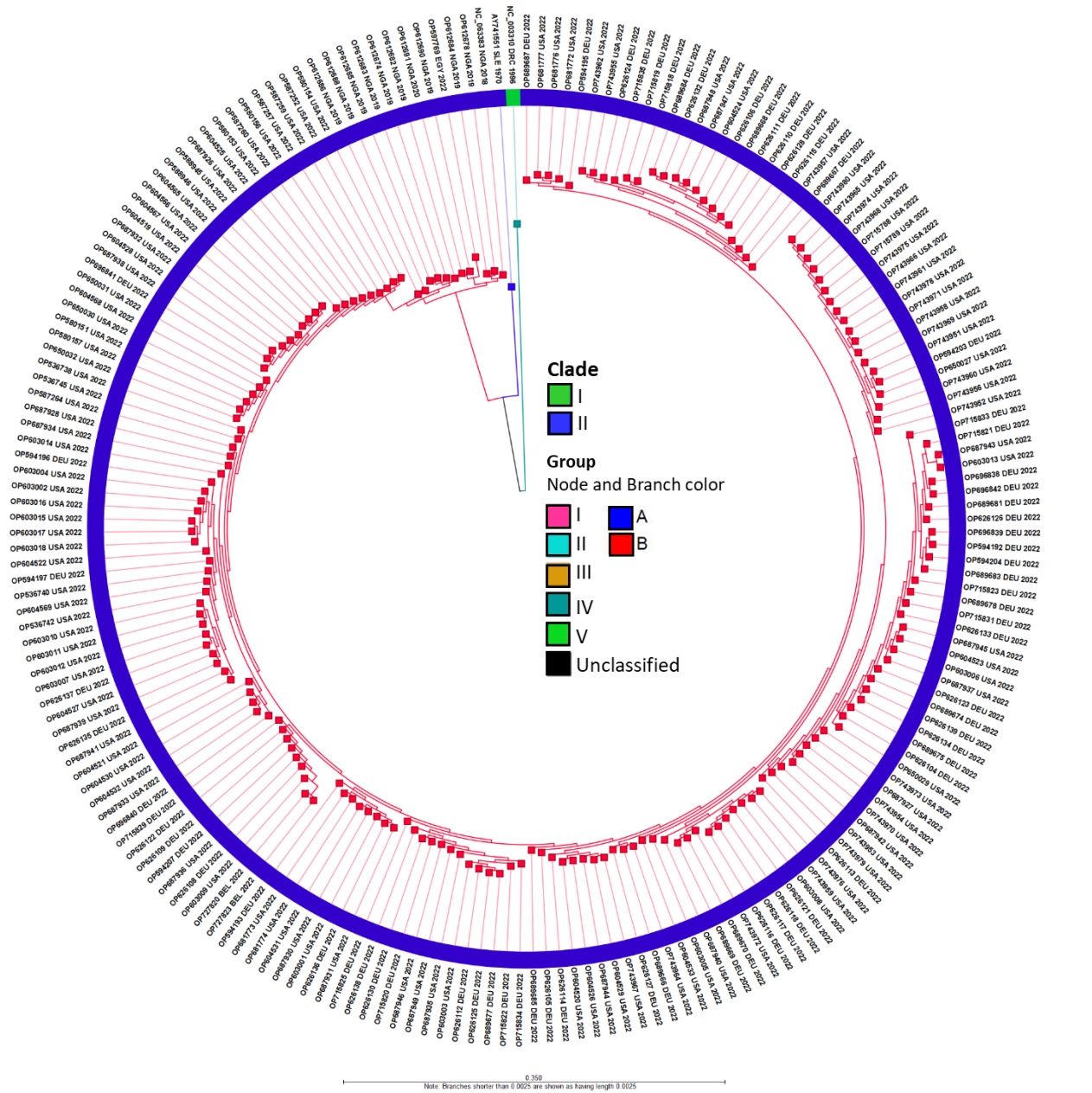
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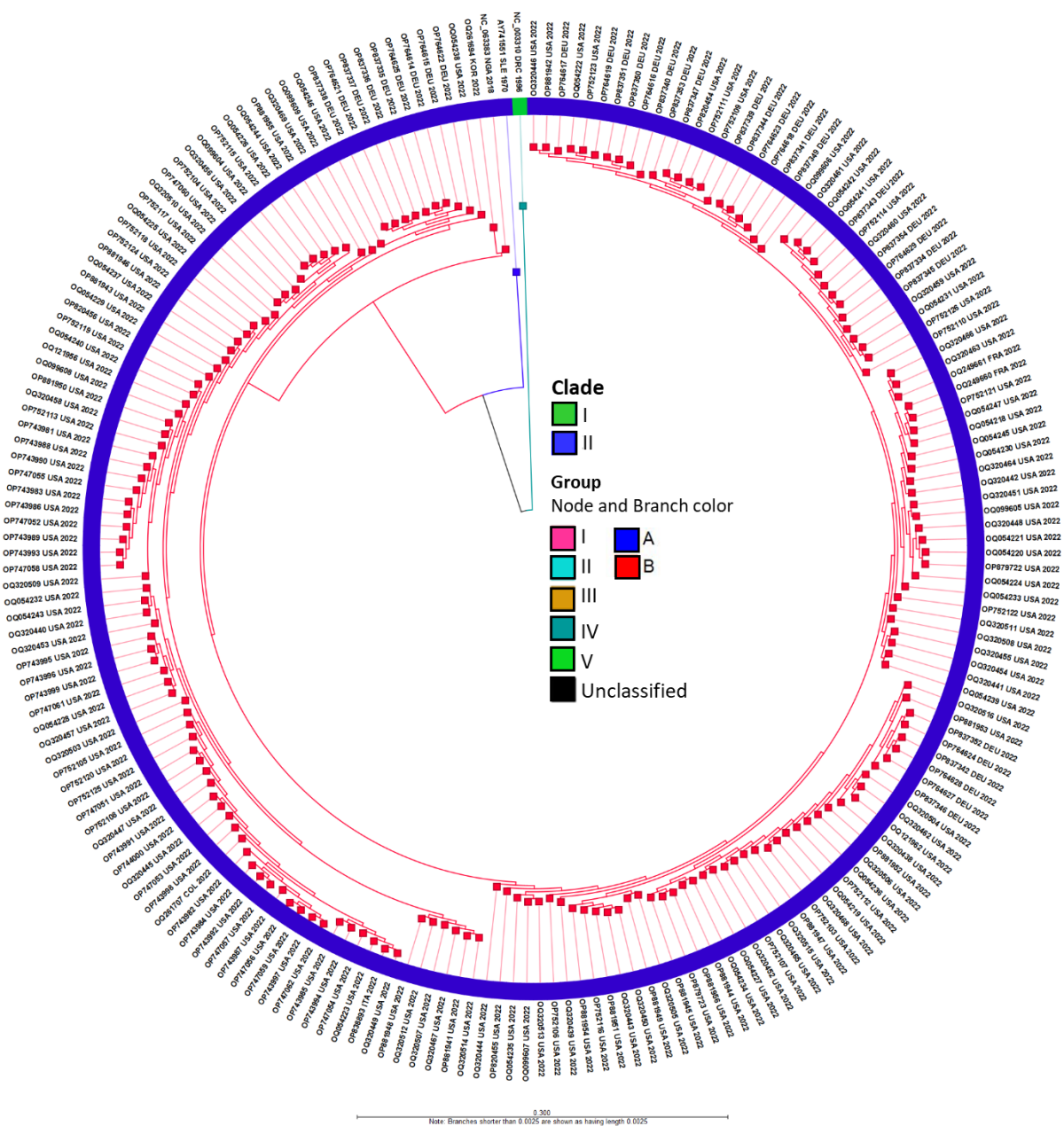
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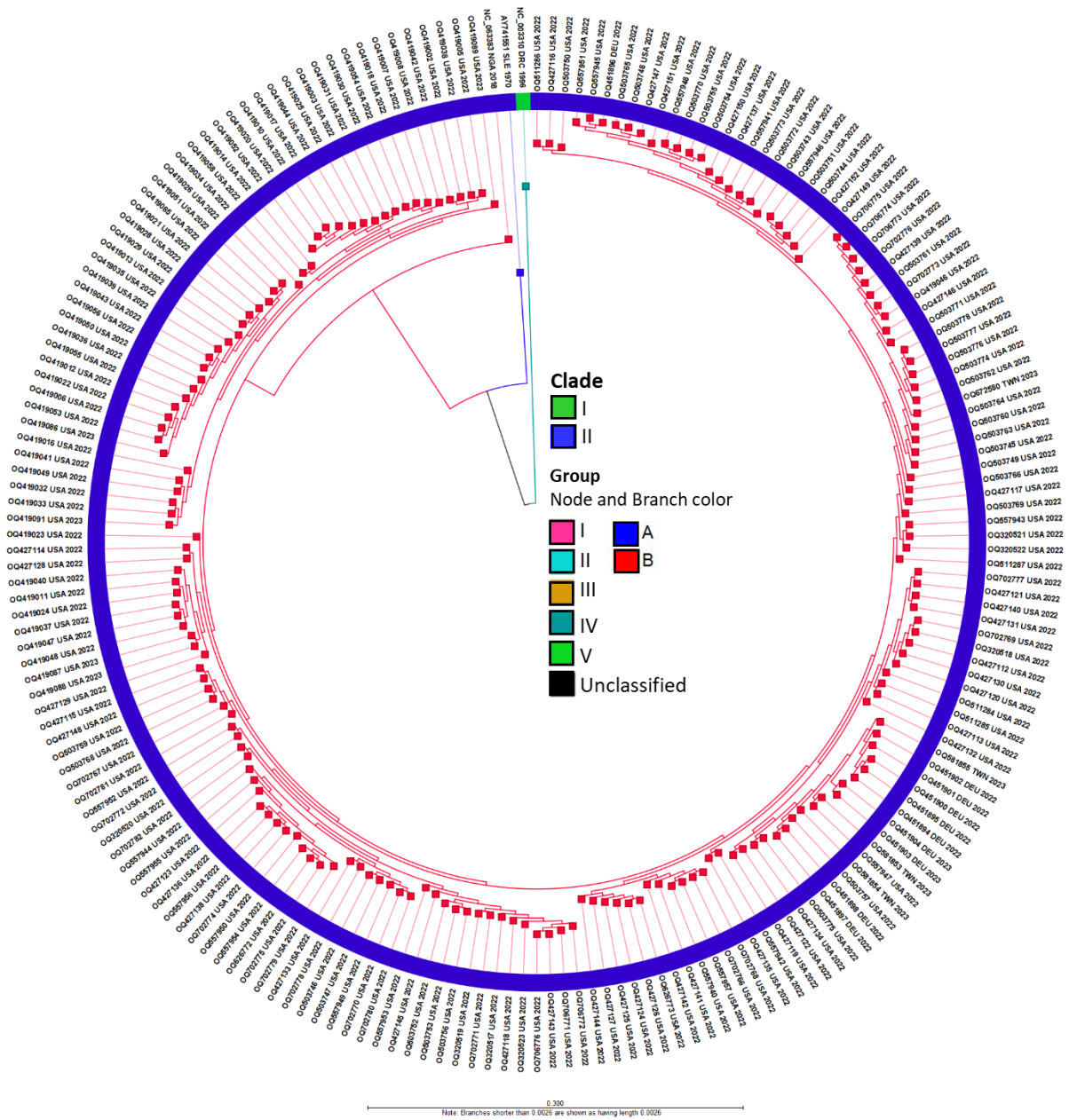
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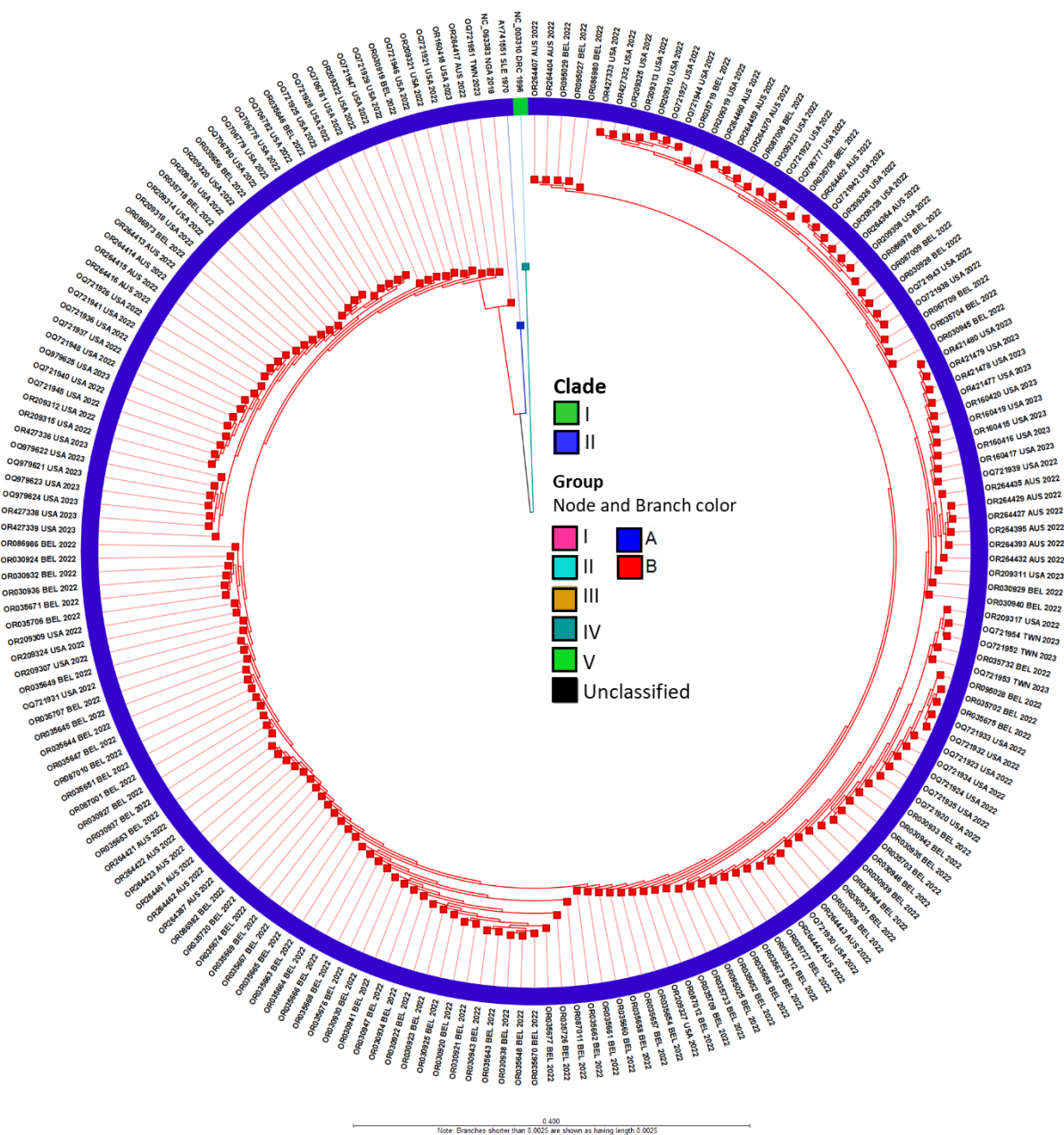
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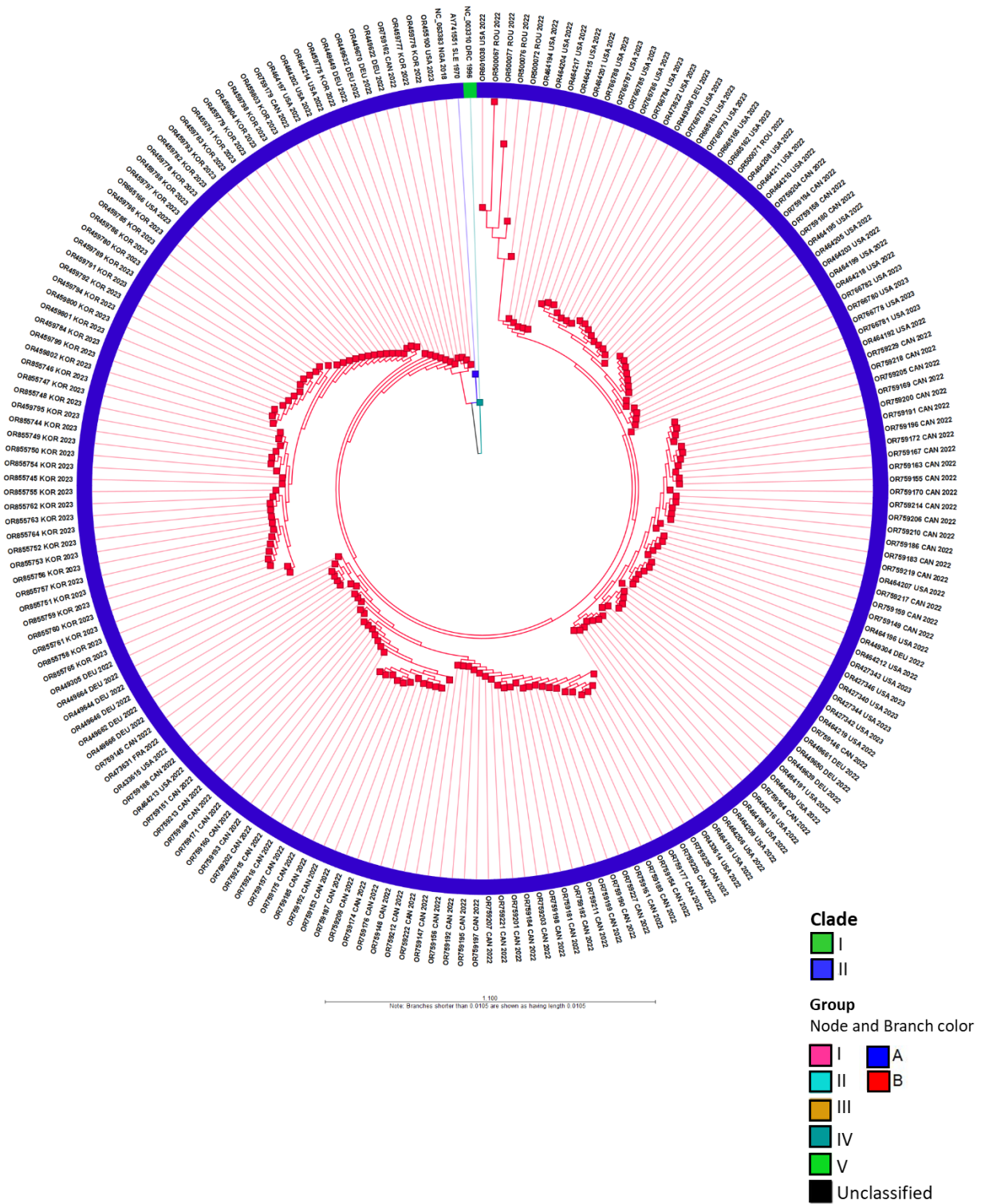


G

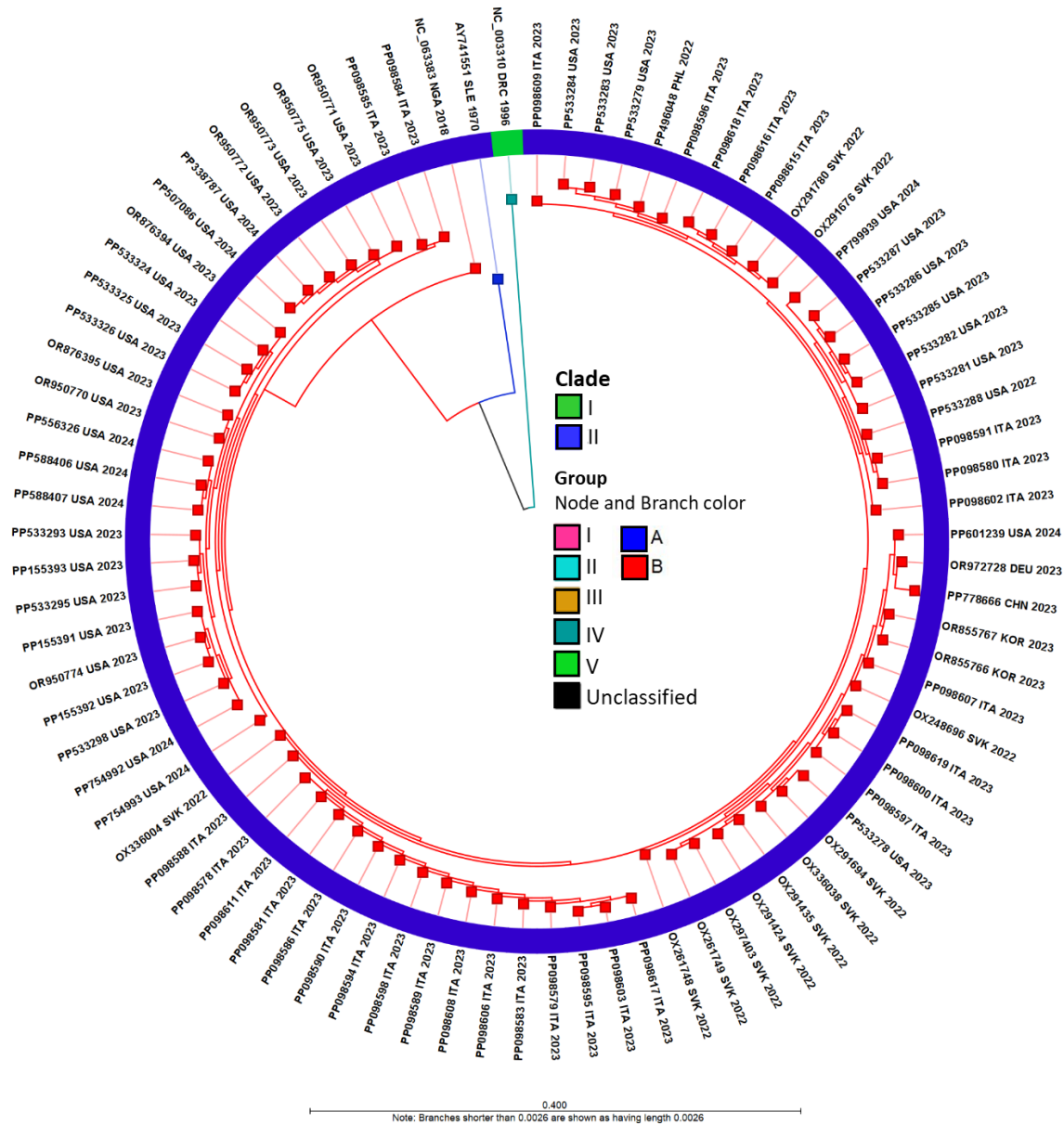


H





J



Supplementary Figure S2. Circular phylograms of 1,878 MPXV genomes clustering with Clade IIB. Three attributes of each genome (sequence accession number, 3-letter country code, and year collected) are displayed as the outermost ring for providing geo-temporal and evolutionary relationships. The MPXV reference genomes used in the alignments were from Clades I (NC_003310), IIA (AY741551), and IIB (NC_063383). (A) Phylogram of 199 genomes from LC753968_JPN_2022 to OP123049_USA_2022, (B) Phylogram of 200 genomes from OP123050_USA_2022 to OP257243_USA_2022, (C) Phylogram of 200 genomes from OP257244_USA_2022 to OP415188_GBR_2022, (D) Phylogram of 199 genomes from OP415189_GBR_2022 to OP536737_USA_2022, (E) Phylogram of 200 genomes from OP536738_USA_2022 to OP743980_USA_2022, (F) Phylogram of 200 genomes from OP743981_USA_2022 to OQ320516_USA_2022, (G) Phylogram of 199 genomes from OQ320517_USA_2022 to

OQ706776_USA_2022, **(H)** Phylogram of 199 genomes from OQ706777_USA_2022 to OR427339_USA_2023, **(I)** Phylogram of 200 genomes from OR427340_USA_2023 to OR855765_KOR_2023, **(J)** Phylogram of 82 genomes from OR855766_KOR_2023 to PP799939_USA_2024. Genome accession numbers (alphanumeric) are listed in ascending order for (A-J). The ANI NJ unrooted trees were constructed from the pairwise comparison tables.