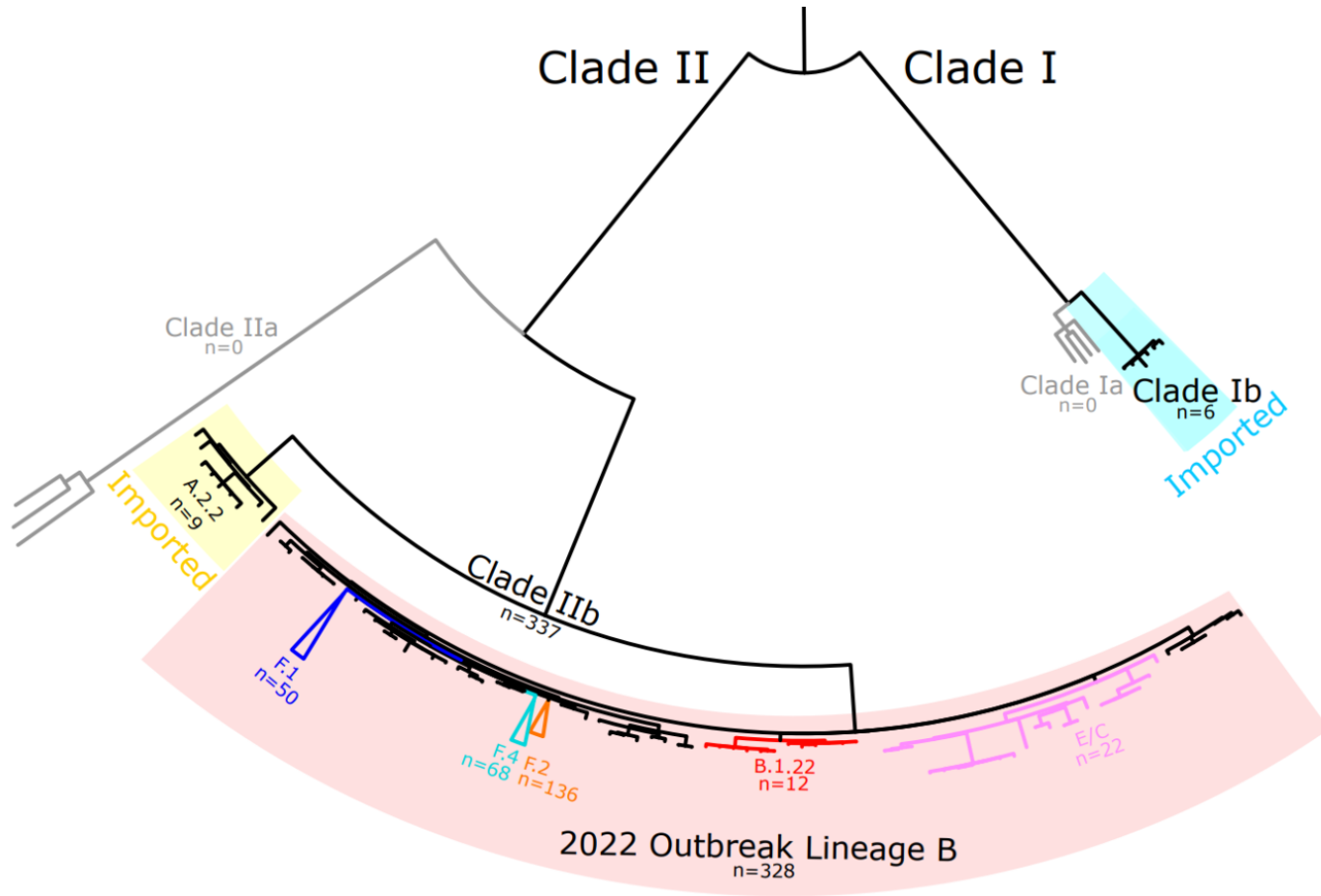


SUPPLEMENTARY FIGURE. Phylogenetic tree of *monkeypox virus* sequences* — United States, 2024–2025



Abbreviation: MPXV = *monkeypox virus*.

* Among 343 sequences with collection dates of January 1, 2024–December 31, 2025, 337 belonged to clade IIb, six belonged to clade Ib, and nine to lineage A.2.2. Two additional clade Ib and three additional clade IIb lineage A.2.2 MPXV sequences were identified but not included in phylogenetic analysis because of low quality, and one 2025 clade Ib case was excluded because sample collection occurred in 2026. Overall, 328 sequences were descended from the global 2022 outbreak lineage B MPXV. Sublineages that contained >10 sequences are highlighted with colored branches. Sublineages containing ≥50 sequences were collapsed into triangles for ease of viewing. Genomes were aligned using mafft (version 7.490; Kazutaka Katoh) using algorithm FFT-NS-1; reference genomes from MPXV clade Ia and IIa were included in the alignment since no MPXV sequences from the United States during 2024–2025 fell into these subclades. Phylogenetic analysis was performed using raxml-ng v2.0.0; all branches had >70% support based on 1,000 bootstrap replicates.