

Phylogenetic tree showing the relationships between various GCA sequences. The tree is rooted at the bottom left. Bootstrap values are shown in black at the nodes, and posterior probabilities are shown in red. The sequences are labeled on the right side of the tree. The scale bar at the bottom left indicates 250 units.

Sequences and their associated values (Bootstrap/Posterior Probability):

- GCA_000500565.1 (0.0694/0.079)
- GCA_002843115.1 (0.921/0.31)
- GCA_013307185.1 (1.93/0.49)
- GCA_020075925.1 (0.669/0.55)
- GCA_001306395.1 (2.54/0.61)
- GCA_019449955.1 (2.12/0.8)
- GCA_001008015.1 (5.1/1)
- GCA_002846075.1 (241/17.7)
- GCA_000971665.1 (95.3/0.96)
- GCA_000014485.1 (17.2/1)
- GCA_020076365.1 (2.44/0.9)
- GCA_020076105.1 (15.6/0.9)
- GCA_020075945.1 (6.32/0.9)
- GCA_002914925.1 (0.0859/0.772)
- GCA_020076115.1 (0.914/0.71)
- GCA_020076065.1 (0.855/0.528)
- GCA_020076145.1 (1.15/0.54)
- GCA_020076045.1 (2.47/0.36)
- GCA_020075965.1 (0.0193/0.27)
- GCA_019450095.1 (2.97/0.51)
- Root (0/0)