

Midpoint rooted phylogeny of the *Amarillovirales* **NS5 gene.** Sequences in the tree were aligned with MAFFT v.7.490, and the tree was inferred using IQ-TREE v.1.6.12 with Model Finder limited to LG. Branches are scaled by amino acid substitutions. The red dots indicate the placement of the novel tunicate-associated virus fragmented identified in this study. The blue dot indicates the placement of Chowder bay tunicate-associated flavi-like virus.