

Midpoint rooted phylogeny of the *Amarillovirales* **NS3 gene.** Sequences in the tree were aligned with MAFFT v7.490, and the tree was inferred using IQ-TREE v1.6.12 with Model Finder limited to LG. Branches are scaled by amino acid substitutions. The red dot indicates the placement of the novel tunicate-associated virus fragmented identified in this study.