

tunicate-associated hepe-like virus 4



Midpoint rooted phylogeny of the *Hepelivirales*. Sequences 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 dots indicate the placement of novel tunicate-associated viruses.