**Appendix Figures S1-S6: (Extended) Maximum likelihood phylogenetic trees**

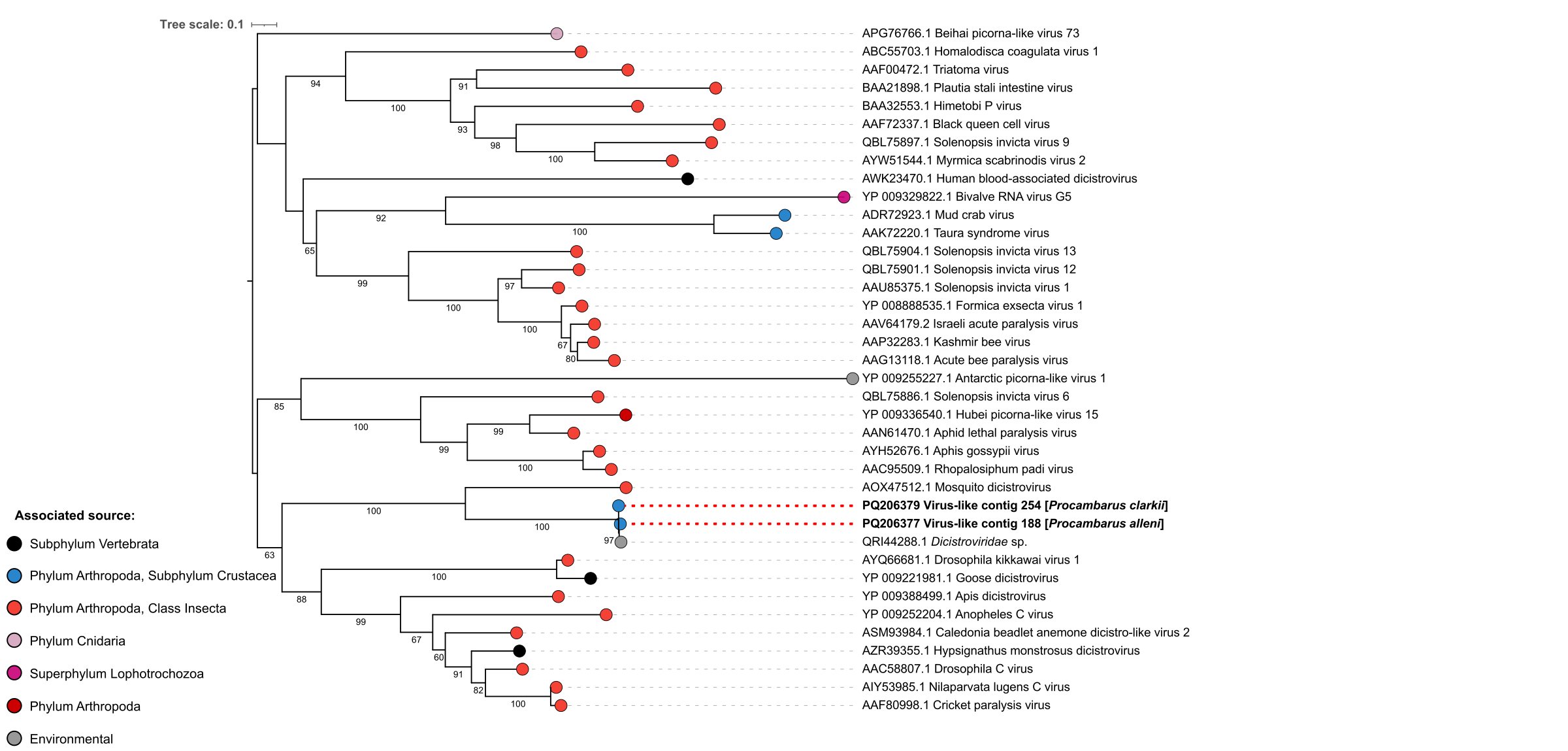
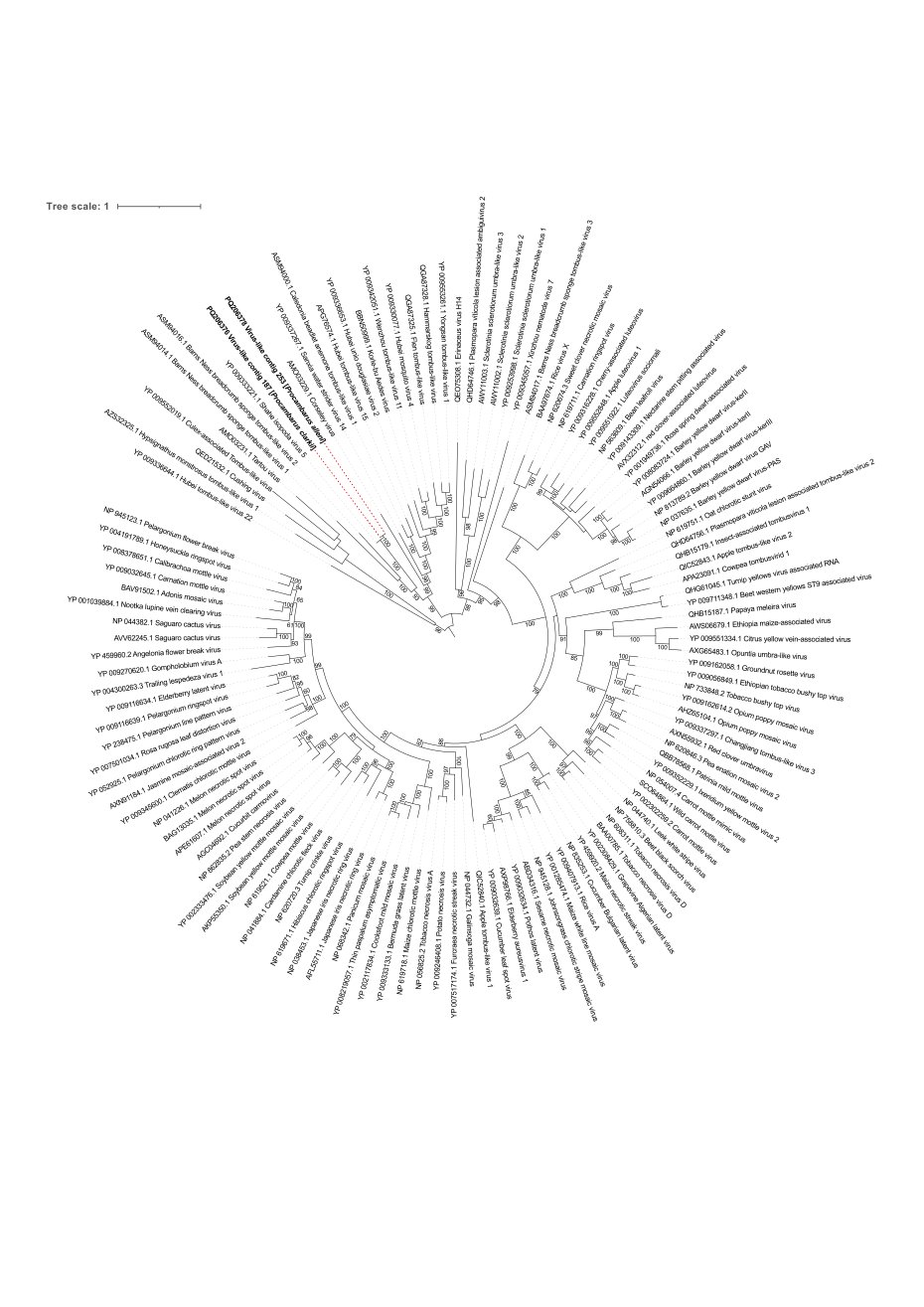
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Figure S1: Maximum likelihood phylogenetic analysis of the RdRp amino acid sequences of *Dicistroviridae* sp. virus-like sequences (Virus-like contig 188 and Virus-like contig 254) obtained from pooled samples of *P. alleni* and *P. clarkii* and related members of *Dicistroviridae* family. Tree is rooted at mid-point Values next to the branches represent bootstrap (%) support values (those higher than 60 % are shown), while the branch length represents the average number of amino acid substitutions per site. Tip labels are color coded according to the associated source samples as shown in the legend. The dotted line connecting the leaf corresponding to viral sequence from this study and its label is shown in red. In labels, NCBI Genbank accessions are given in front of contig or virus names.



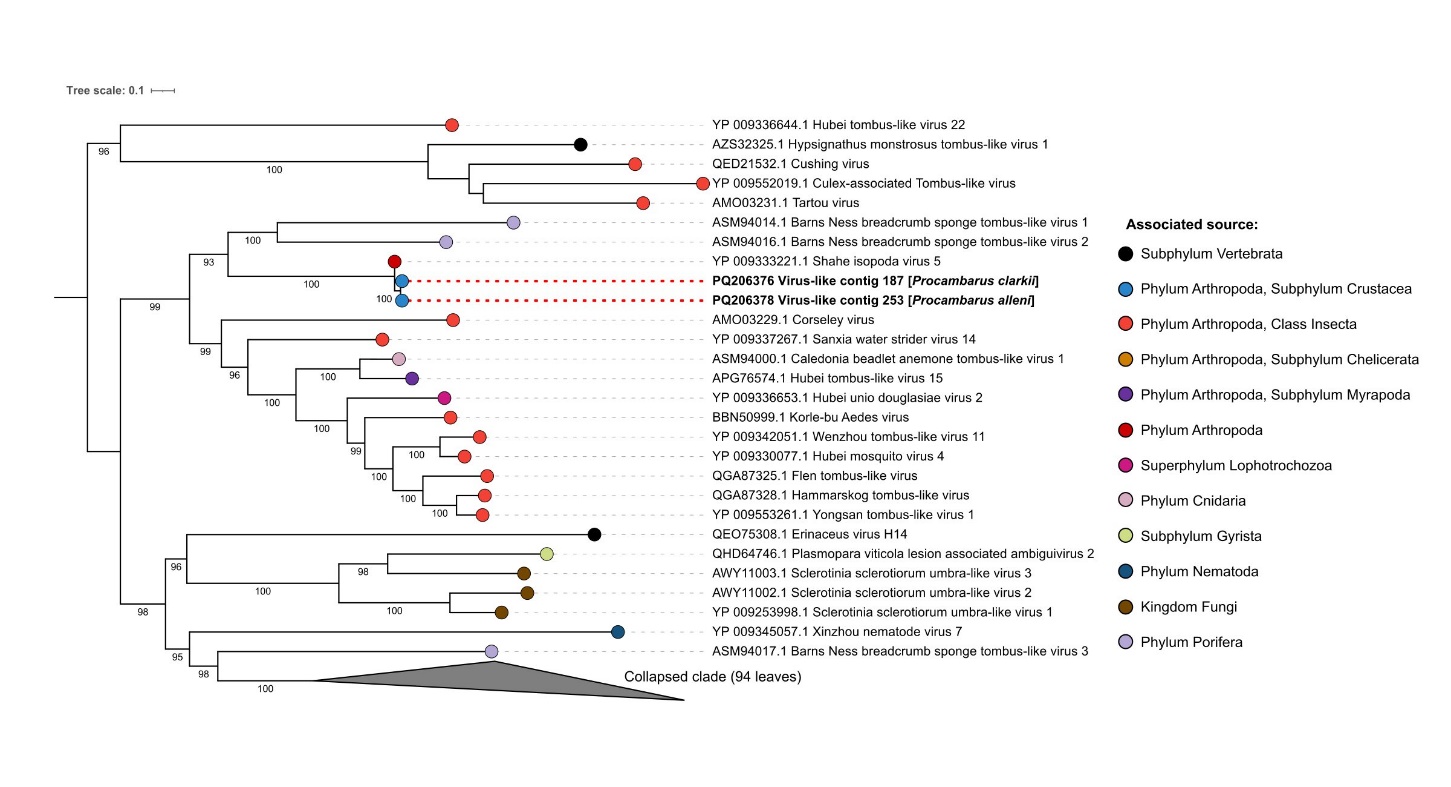


Figure S2: (Up) Maximum likelihood phylogenetic analysis of the RdRp amino acid sequences of Virus-like contig 253 obtained from pooled samples of *P. alleni* and Virus-like contig 187 obtained from pooled samples of *P. clarkii* and members related to *Tombusviridae* family according to RVMT global RNA virus phylogenetic analysis (Neri et al., 2022). Tree is rooted at mid-point. Values next to the branches represent bootstrap (%) support values (those higher than 60 % are shown), while the branch length represents the average number of amino acid substitutions per site. Tip labels are color coded according to the associated source samples as shown in the legend. The dotted line connecting the leaf corresponding to viral sequence from this study and its label is shown in red. In labels, NCBI Genbank accessions are given in front of contig or virus names. (Down) Collapsed phylogenetic tree.

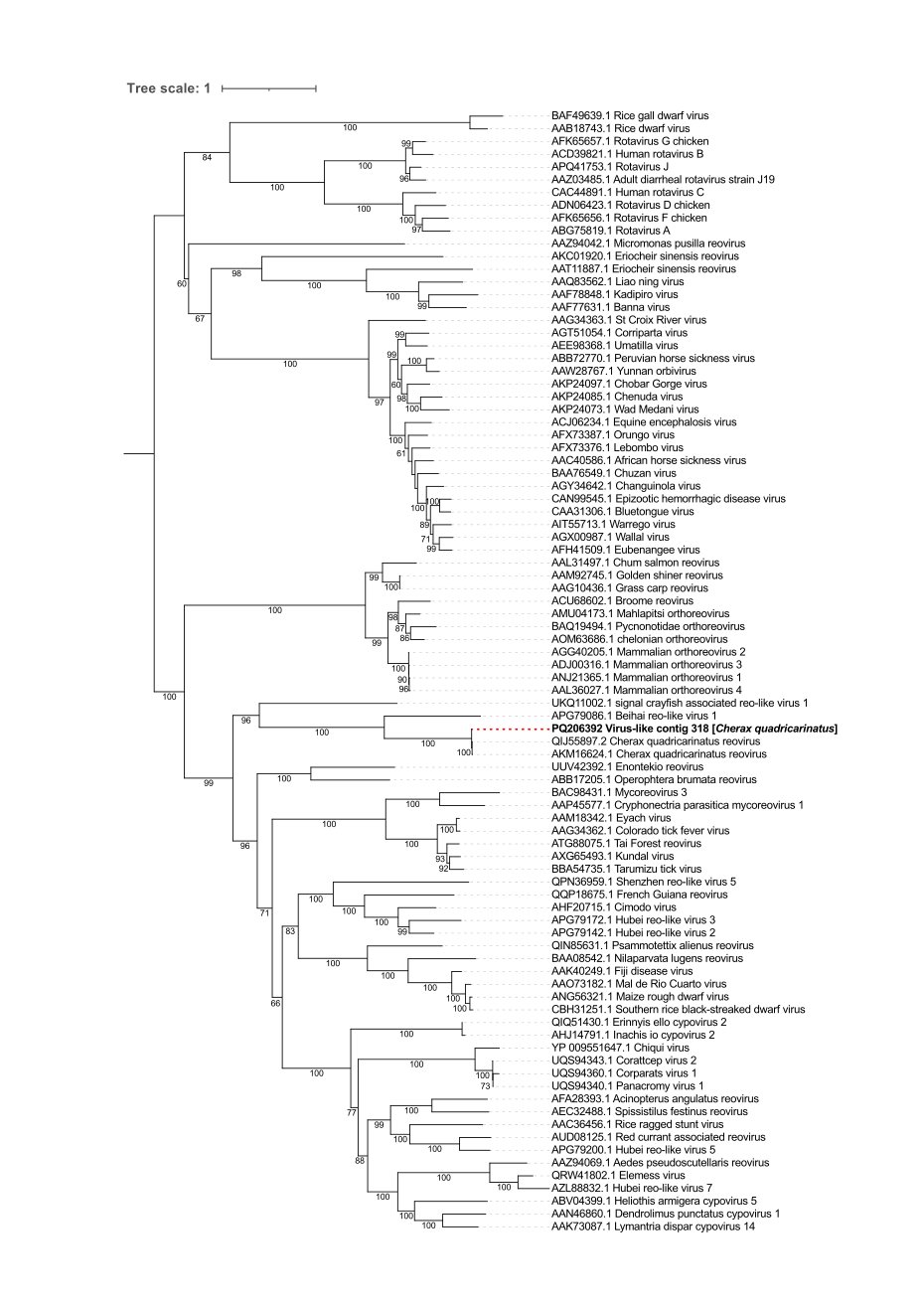


Figure S3: Maximum likelihood phylogenetic analysis of the RdRp amino acid sequences of Cherax quadricarinatus reovirus (Virus-like contig 318) obtained from pooled samples of *C. quadricarinatus* and related members of order *Reovirales*. Tree is rooted at mid-point. Values next to the branches represent bootstrap (%) support values (those higher than 60 % are shown), while the branch length represents the average number of amino acid substitutions per site. The dotted line connecting the leaf corresponding to viral sequence from this study and its label is shown in red. In labels, NCBI Genbank accessions are given in front of contig or virus names.

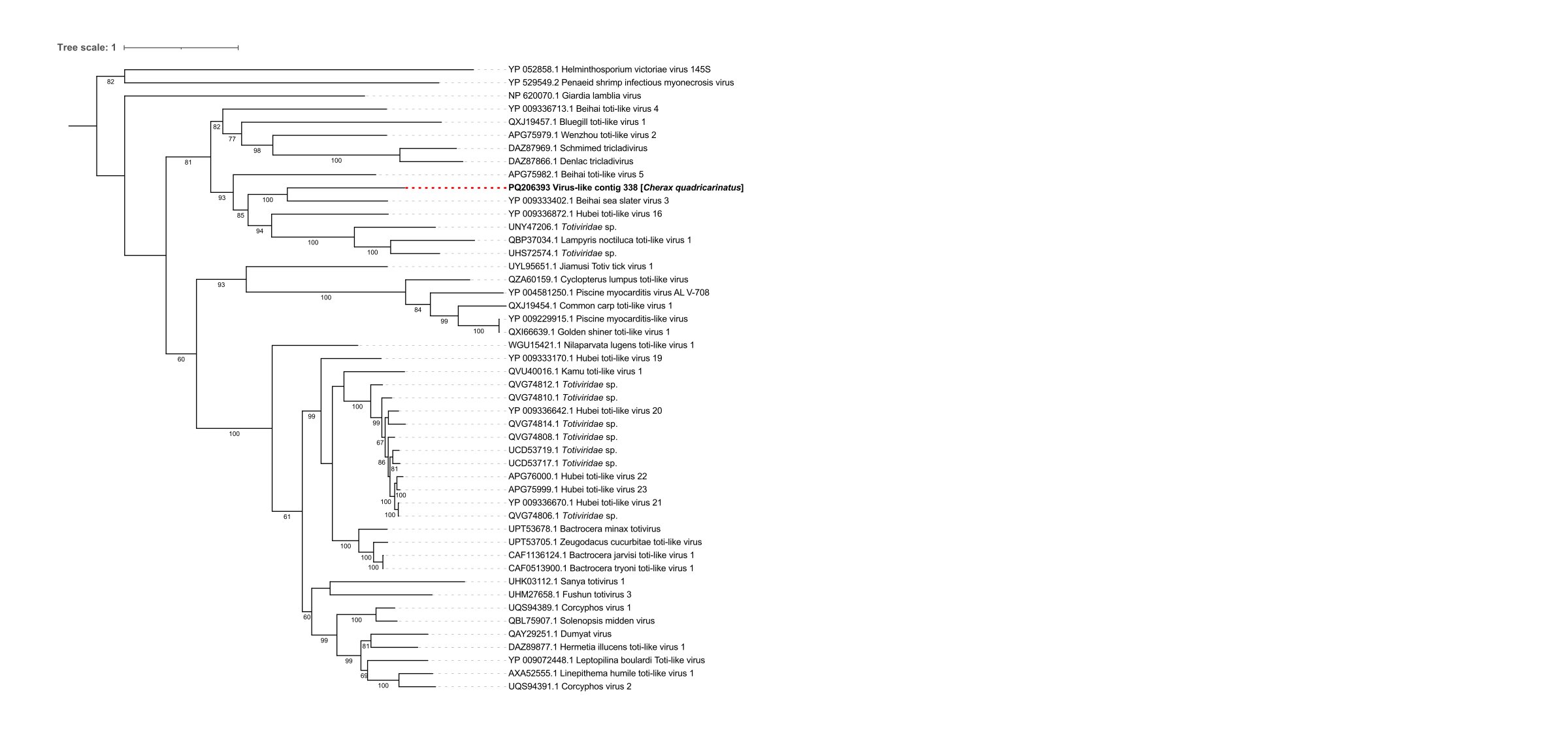
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Figure S4: Maximum likelihood phylogenetic analysis of the RdRp amino acid sequences of Virus-like contig 338 obtained from pooled samples of *C. quadricarinatus* related members of *Ghabrivirales* order. Tree is rooted at mid-point. Values next to the branches represent bootstrap (%) support values (those higher than 60 % are shown), while the branch length represents the average number of amino acid substitutions per site. The dotted line connecting the leaf corresponding to viral sequence from this study and its label is shown in red. In labels, NCBI Genbank accessions are given in front of contig or virus names.

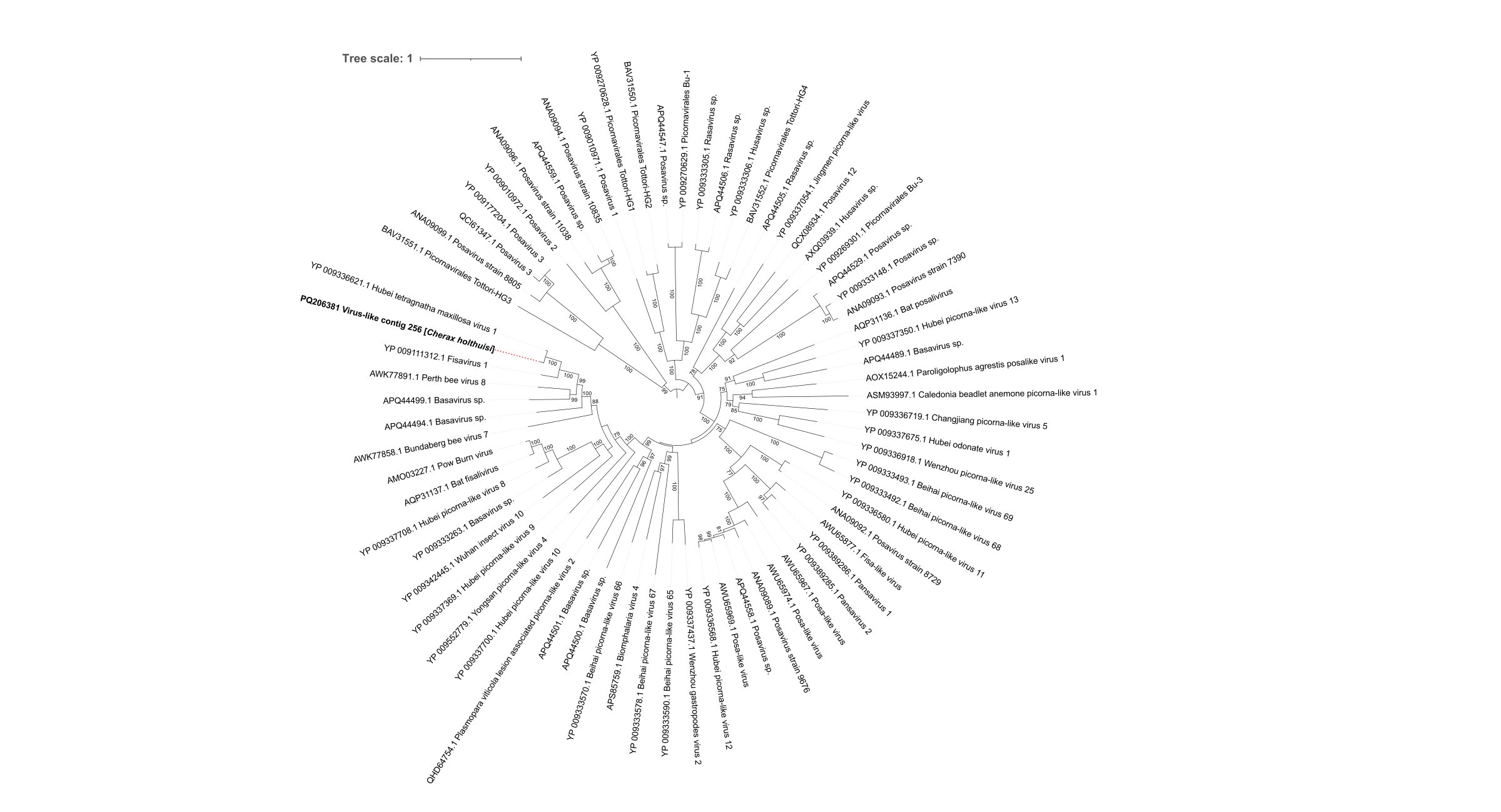
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Figure S5: Maximum likelihood phylogenetic analysis of the RdRp amino acid sequences of Virus-like contig 256 from pooled samples of *C. holthuisi* and related members of *Picornavirales* f.0035 clade (Neri et al., 2022). Tree is rooted at mid-point Values next to the branches represent bootstrap (%) support values (those higher than 60 % are shown), while the branch length represents the average number of amino acid substitutions per site. The branch leading to leaf corresponding to viral sequence from this study is shown in red.

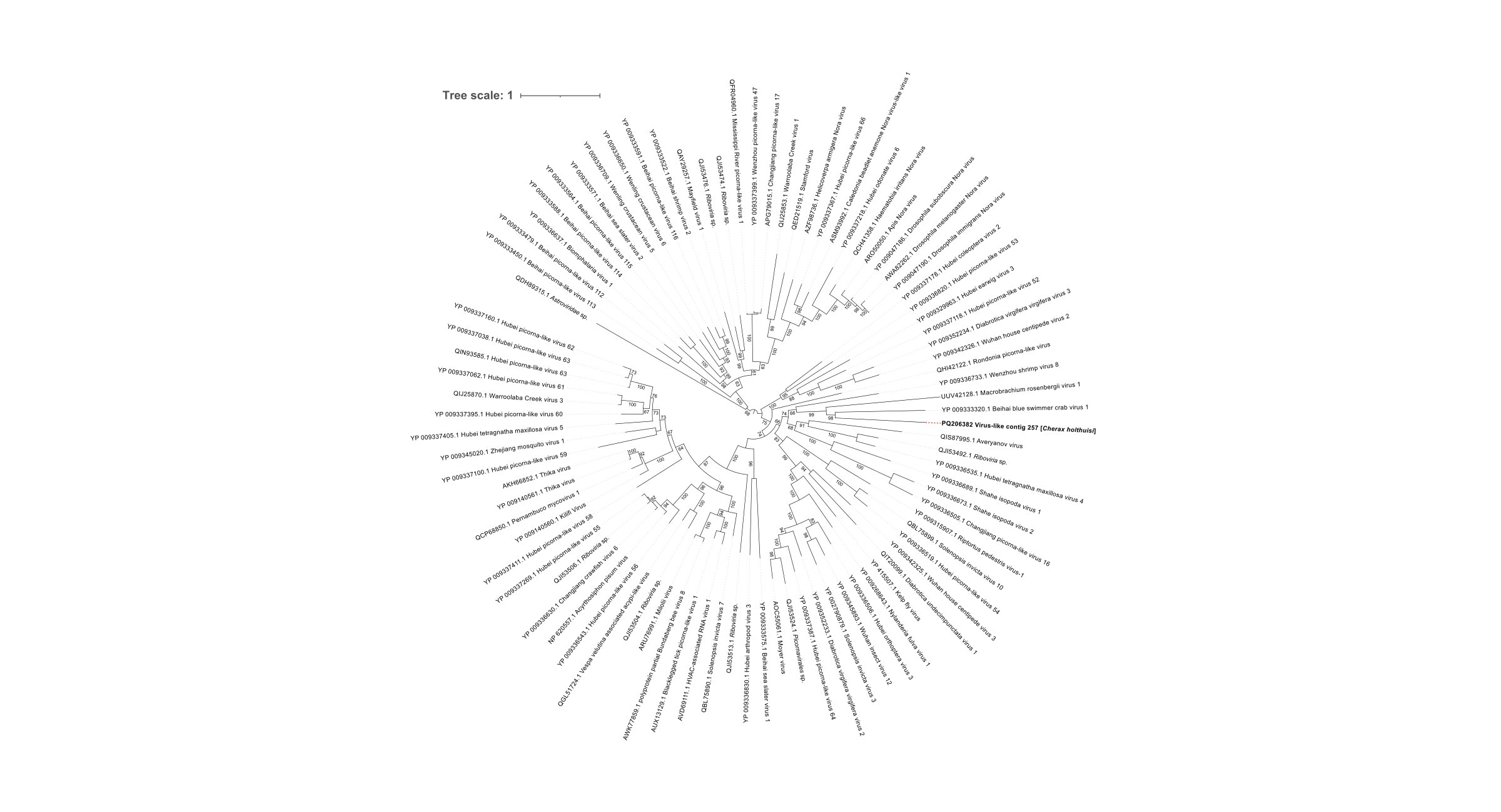
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Figure S6: Maximum likelihood phylogenetic analysis of the RdRp amino acid sequences of Virus-like contig 257 from pooled samples of *C. holthuisi* and members of *Solinviviridae* family (Neri et al., 2022). Tree is rooted at mid-point. Values next to the branches represent bootstrap (%) support values (those higher than 60 % are shown), while the branch length represents the average number of amino acid substitutions per site. The dotted line connecting the leaf corresponding to viral sequence from this study and its label is shown in red. In labels, NCBI Genbank accessions are given in front of contig or virus names.