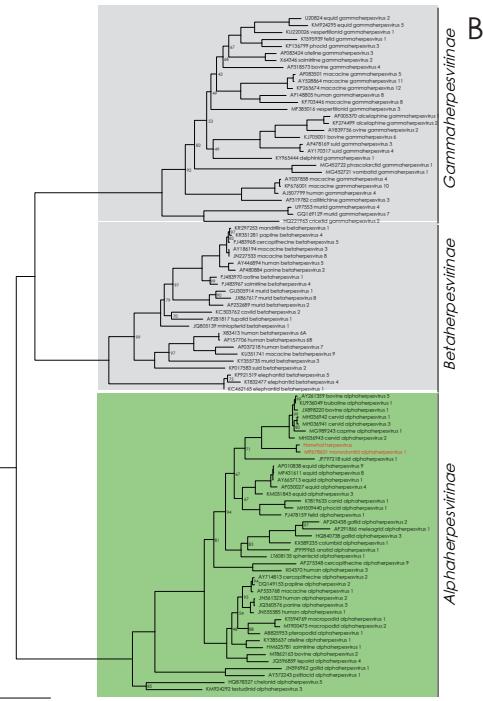
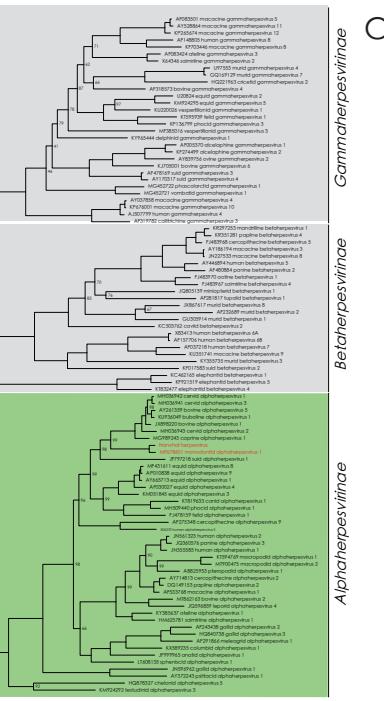


**Fig. S1:** Phylogram depicting the relationship of the narwhal herpesvirus (NHV) to other members of the family *Orthoherpesviridae*, based on the individual amino acid sequence alignment of the (A) DNA packaging terminase subunit 1, (B) DNA polymerase catalytic subunit, (C) envelope glycoprotein B, (D) helicase-primase helicase subunit, (E) major capsid protein, (F) uracil-DNA glycosylase. Maximum Likelihood trees were generated using 1000 bootstraps and branch lengths are based on the number of inferred substitutions, as indicated by the scale. Virus GenBank accession numbers are listed, followed by the virus names. NHV and monodontid alphaherpesvirus 1 are highlighted in red. All nodes are supported by 100% bootstrap values except the nodes labelled with bootstrap values.

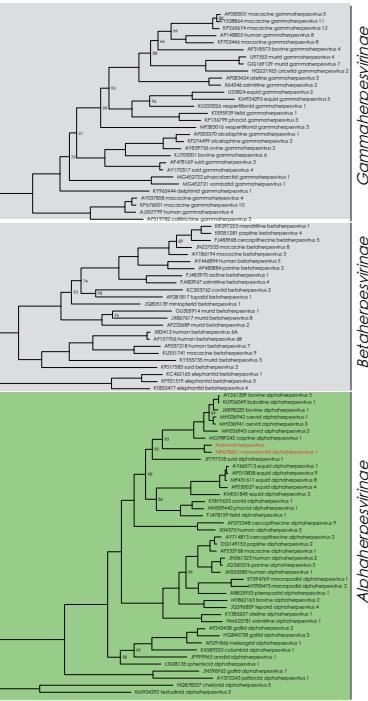
A)



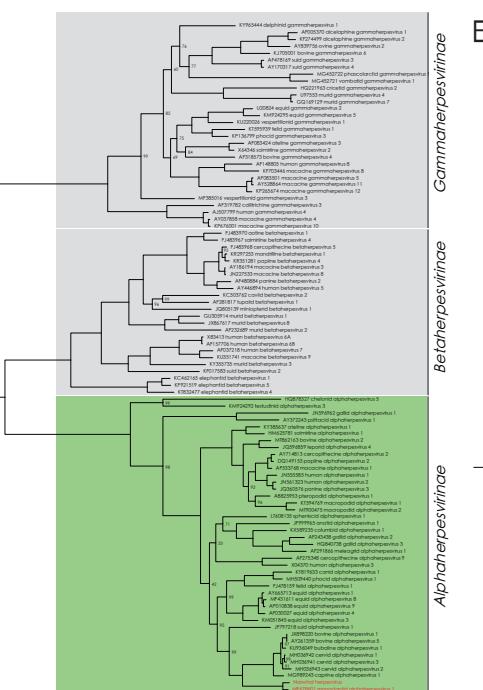
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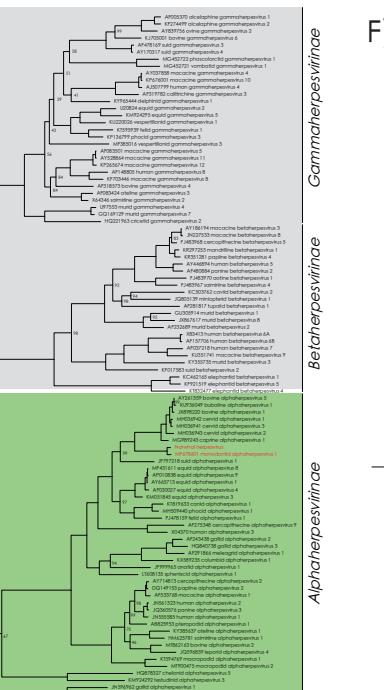
C)



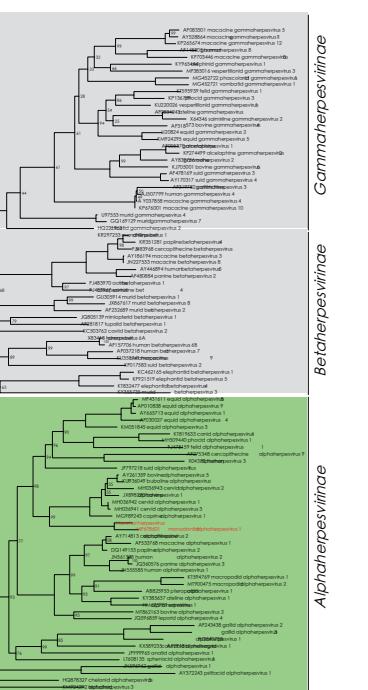
D)



E)



F)



Gammaherpesvirinae

Betaherpesvirinae

Alphaherpesvirinae

Gammaherpesvirinae

Betaherpesvirinae

Alphaherpesvirinae