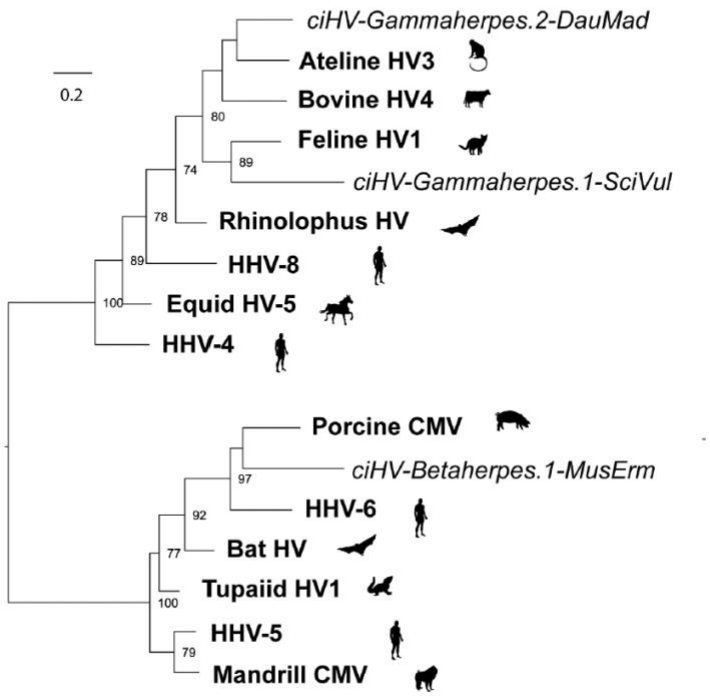
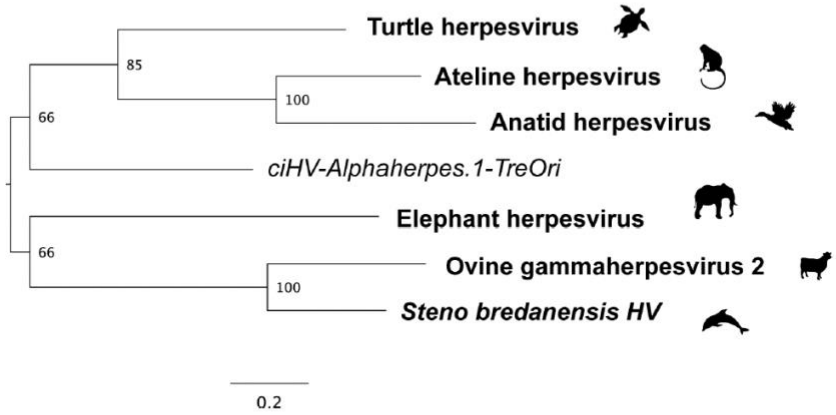
Herpesvirus *terminase*

a)



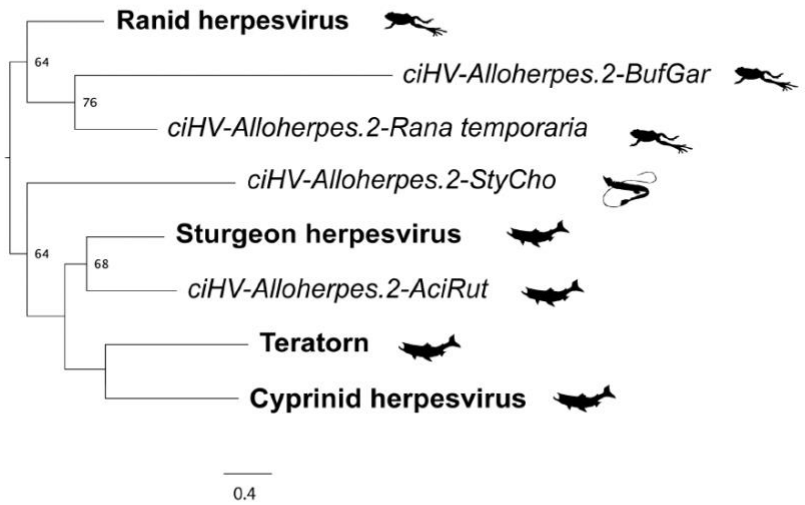
Herpesvirus *glycoprotein B*

b)



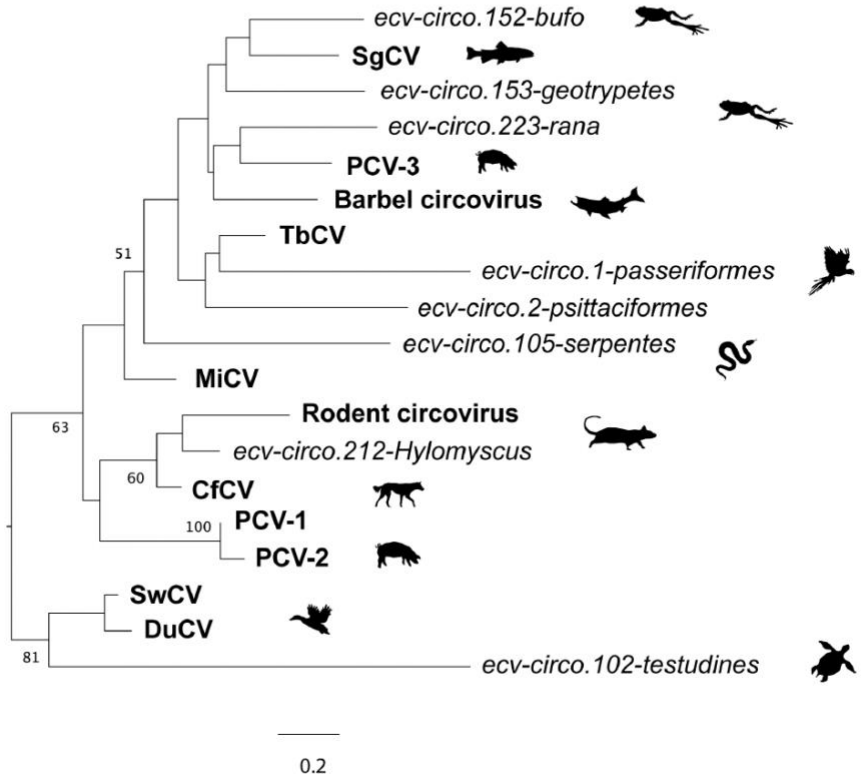
Alloherpesvirus *terminase*

c)

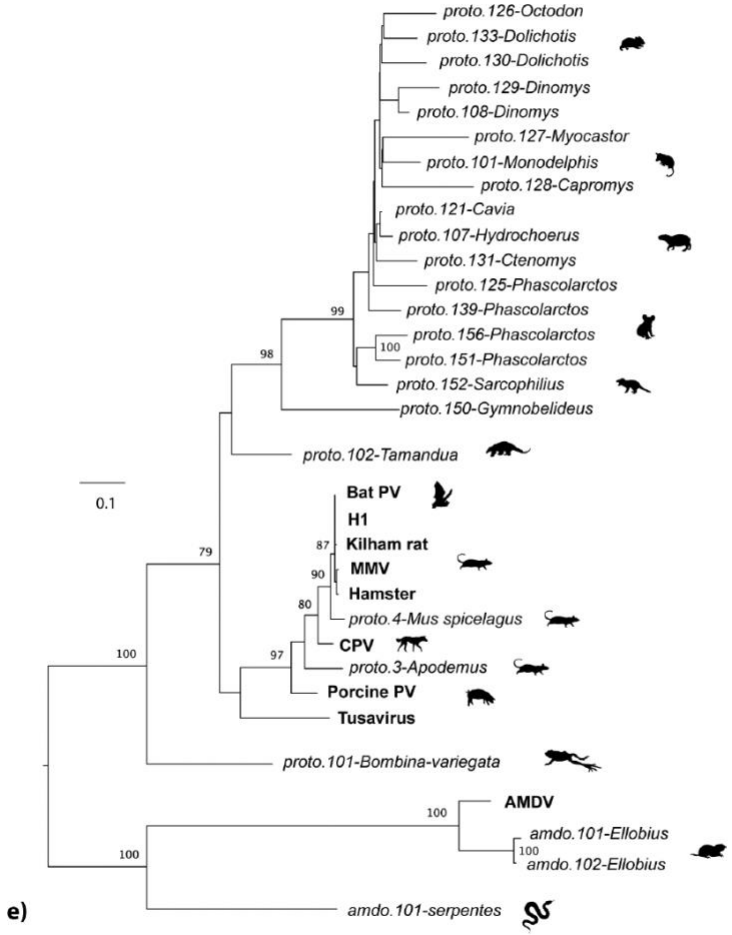


Circovirus *rep*

d)



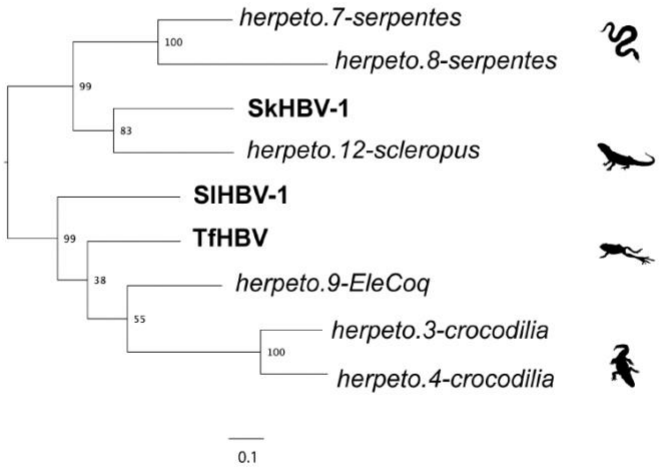
Parvovirus *rep*



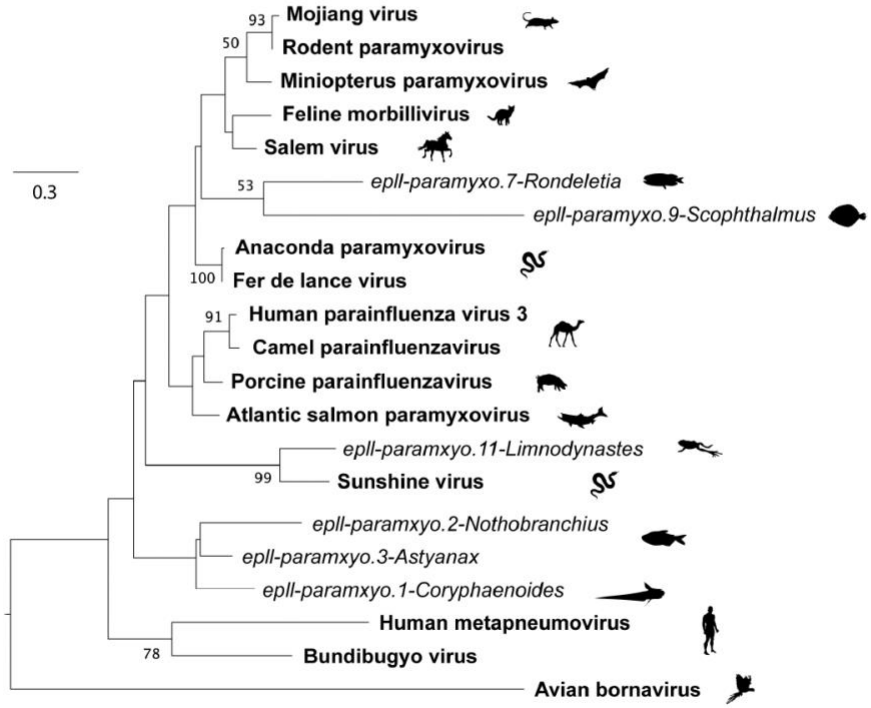
e)

Hepadnavirus *pol*

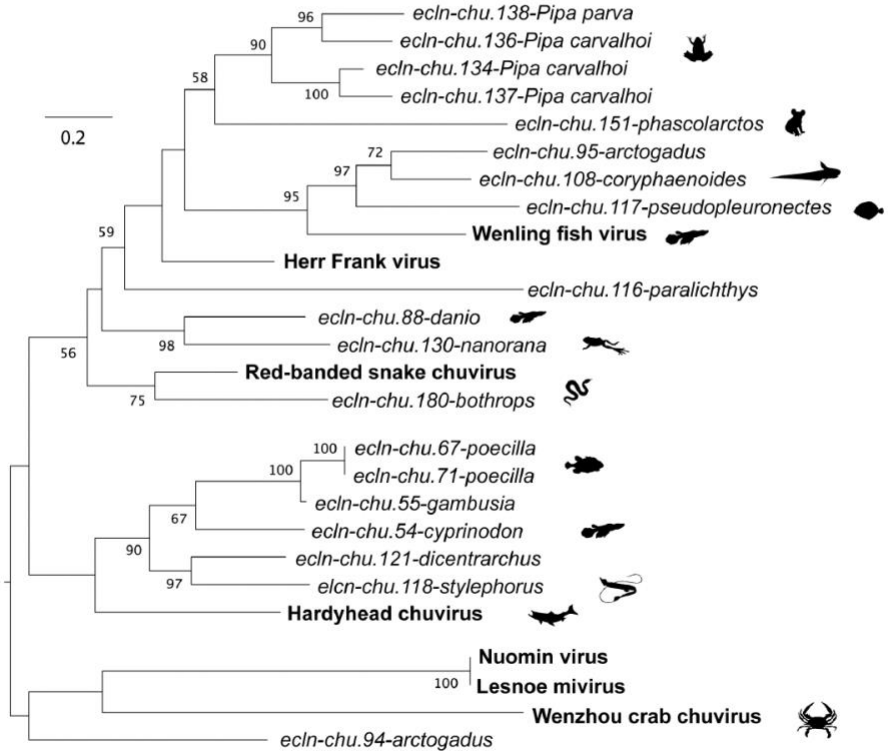
f)



g) **Paramyxovirus *L-polymerase***



h) **Chuvirus *nucleoprotein***



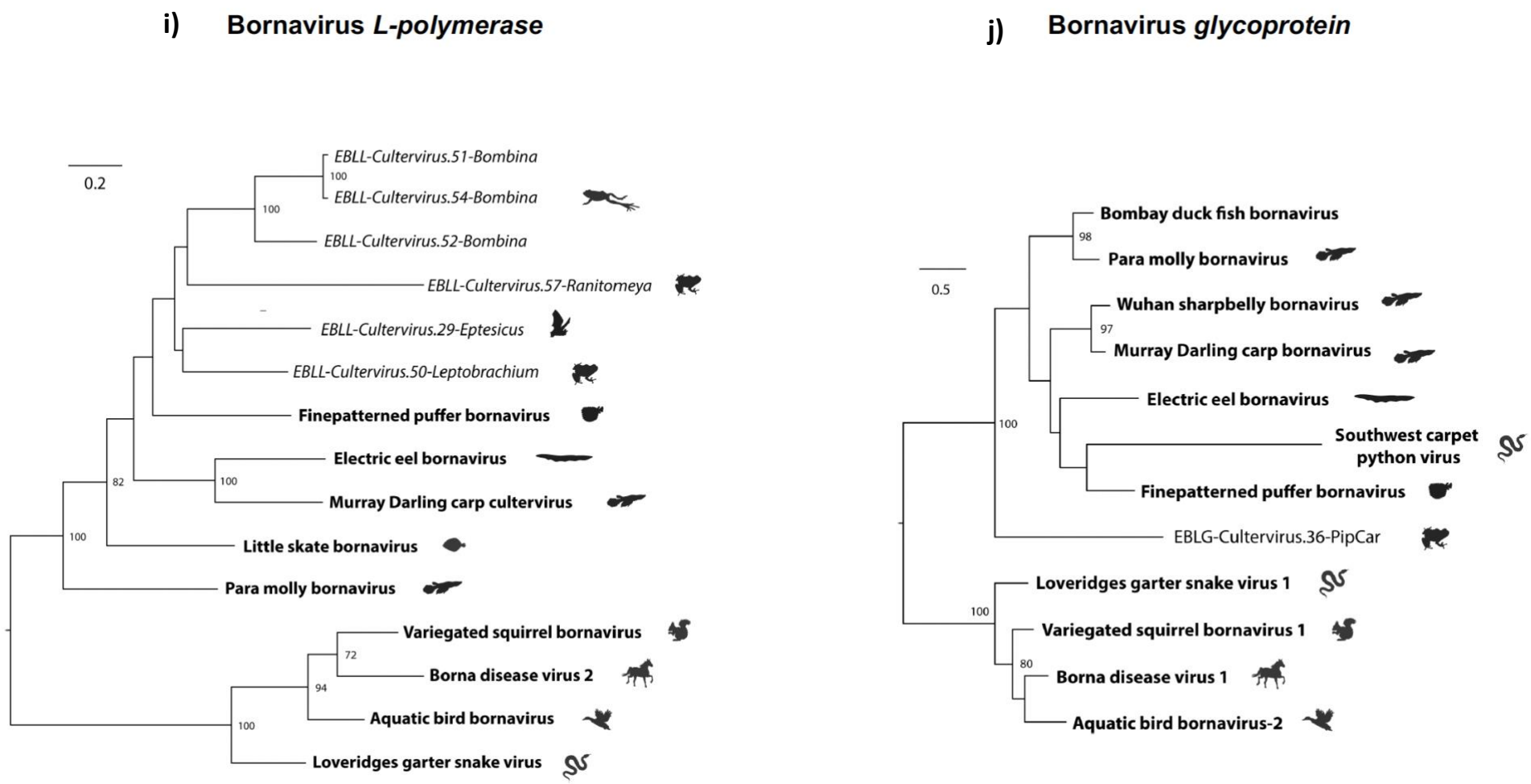


Figure S7. Evolutionary relationships of vertebrate EVEs and viruses.
Bootstrapped maximum likelihood trees showing the reconstructed evolutionary relationships between vertebrate EVEs and related viruses. **(a)** Gammaherpesvirus *terminase*; **(b)** Alphaherpesvirus *glycoprotein B*; **(c)** Alloherpesvirus *terminase*; **(d)** Circovirus *rep*; **(e)** Parvovirus *rep*; **(f)** Hepadnavirus *pol*; **(g)** Paramyxovirus *L polymerase*; **(h)** Chuvirus *nucleoprotein*; **(i)** Bornavirus *L polymerase*; **(j)** Bornavirus *glycoprotein*. Numbers on nodes indicate bootstrap

support (100 bootstrap replicates). All trees were constructed from nucleotide level alignments using the General Time Reversible (GTR) model of nucleotide substitution. Scale bars show evolutionary distance in substitutions per site. Taxon names are shown in bold for viruses, italics for EVEs. Where EVE sequences occurred in >1 host species (indicated by a host group rather than a species name in the EVE identifier), consensus sequences were analysed. Where EVE sequences were identified in a single species, the species name is shown using a three letter abbreviation (e.g. 'DauMad' for *Daubentonia madagascariensis*).