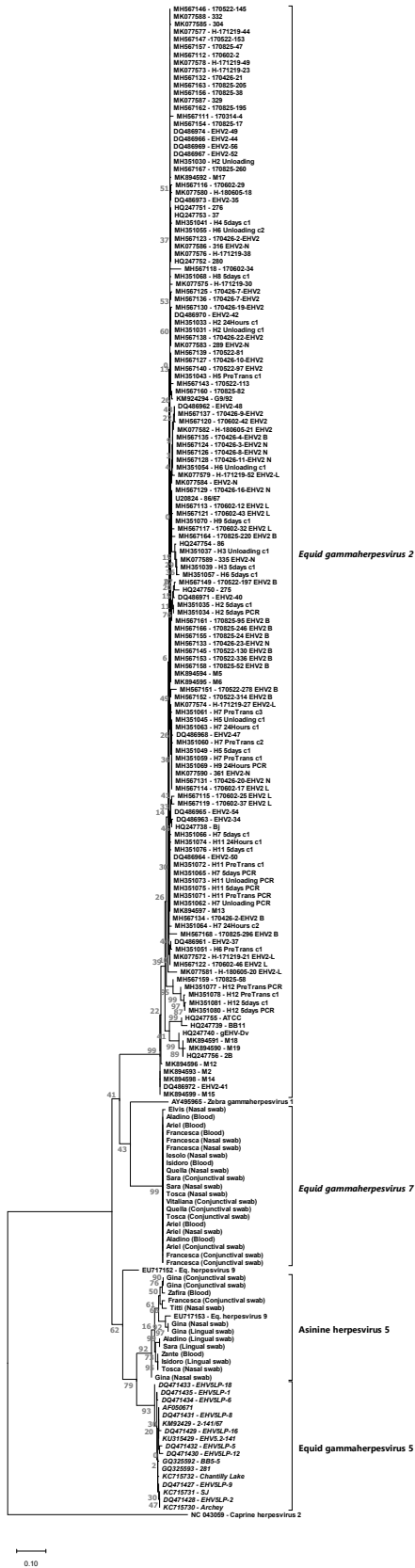


Supplementary Figure S1. Phylogenetic trees of gammaherpesviruses identified in donkeys. Maximum likelihood trees based on the glycoprotein B (gB), terminase (ter), and DNA polymerase (DPOL) genes are shown. The trees were built with MEGAX with partial nucleotide sequences (gB: 405nt, ter: 356nt, DPOL: 182nt) using the maximum likelihood approach with Kimura 2 parameters (gB) or Tamura 3 parameters (DPOL and ter) models, identified as the best fitting models using the modeltest analysis implemented in MEGAX. A discrete Gamma distribution was used to model evolutionary rate differences among sites (+G = 0.4575 for gB, +G = 1.0948 for DPOL, +G = 0.5394 for ter) and branch robustness was evaluated through 1000 bootstrap replicates. Species official (*italics*) or provisory names are indicated when available and sequences obtained in this study are indicated by the name of the donkey while the type of sample is specified in parenthesis.

gB



DPOL



ter

