



**Figure S1.** Evolutionary history inferred using Maximum Likelihood based on the General Reverse Transcriptase model. The tree topology with the highest log likelihood (-994.90) is shown, with branch lengths measured in the number of substitutions per site. The analysis involved 37 amino acid sequences, and all positions containing gaps and missing data were eliminated. There was a total of 102 positions in the final dataset, and phylogeny was tested using 100 bootstrap replicates. Evolutionary analyses were conducted in MEGA7.