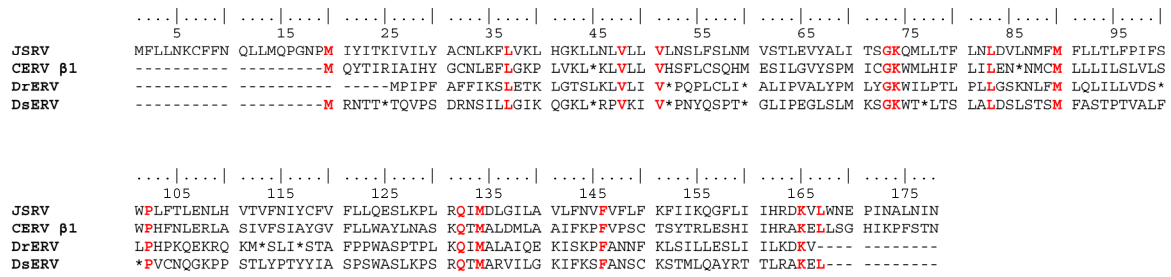

gag
gag
pro
pro
pol



Figure S1. The complete nucleotide sequence of the CERV β1 genome with deduced amino acid sequences of the ORFs for the *gag*, *pro*, *pol* and *env* genes. The stop codons are indicated as *. The major homology region is marked with a red box.



JSRV: Jaagsiekte sheep retrovirus, AF105220; CERV β1: cervid endogenous betaretrovirus 1, OL547611; DrERV: *Desmodus rotundus* (bat)endogenous retrovirus, KP175520; DsERV: *Dasypus novemcinctus* (armadillo) endogenous retrovirus, NW004490279.

Figure S2. Orf-x alignment. Alignment of the predicted amino acid sequence of orf-x from betaretrovirus detected in armadillo, bat, deer, and sheep. Gaps in alignment are shown by dashes; * indicates stop codons and letter highlighted in red represents identity.

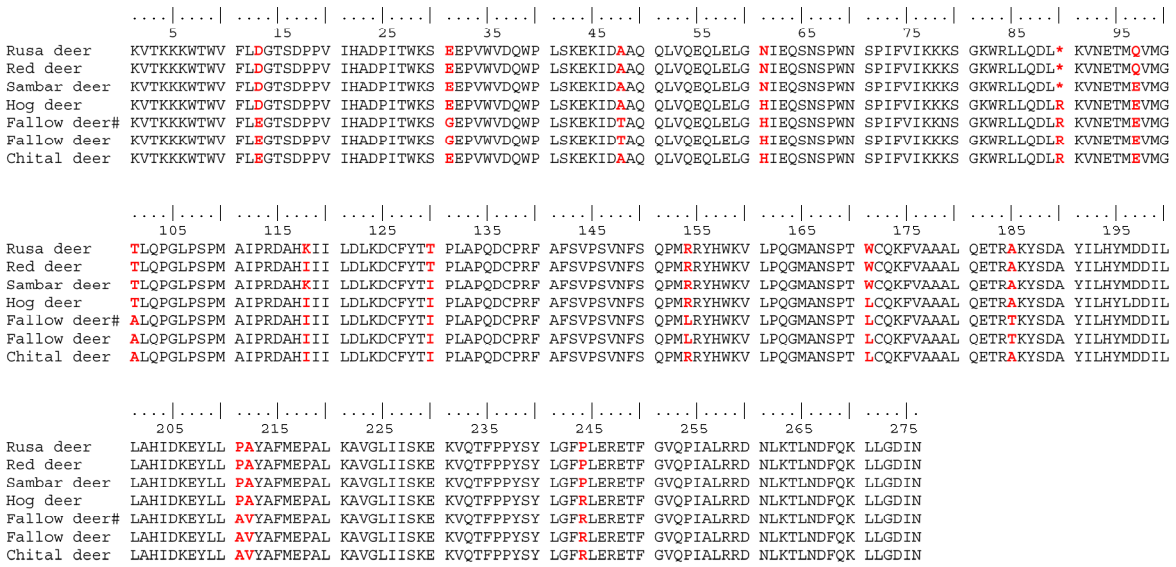


Figure S3. Alignment of *pol* gene aa sequences obtained in this study. Numbers indicate nucleotide positions. '*' denotes a stop codon. Variable regions are highlighted in red. # indicates sequence OL547611 obtained by next-generation sequencing.