

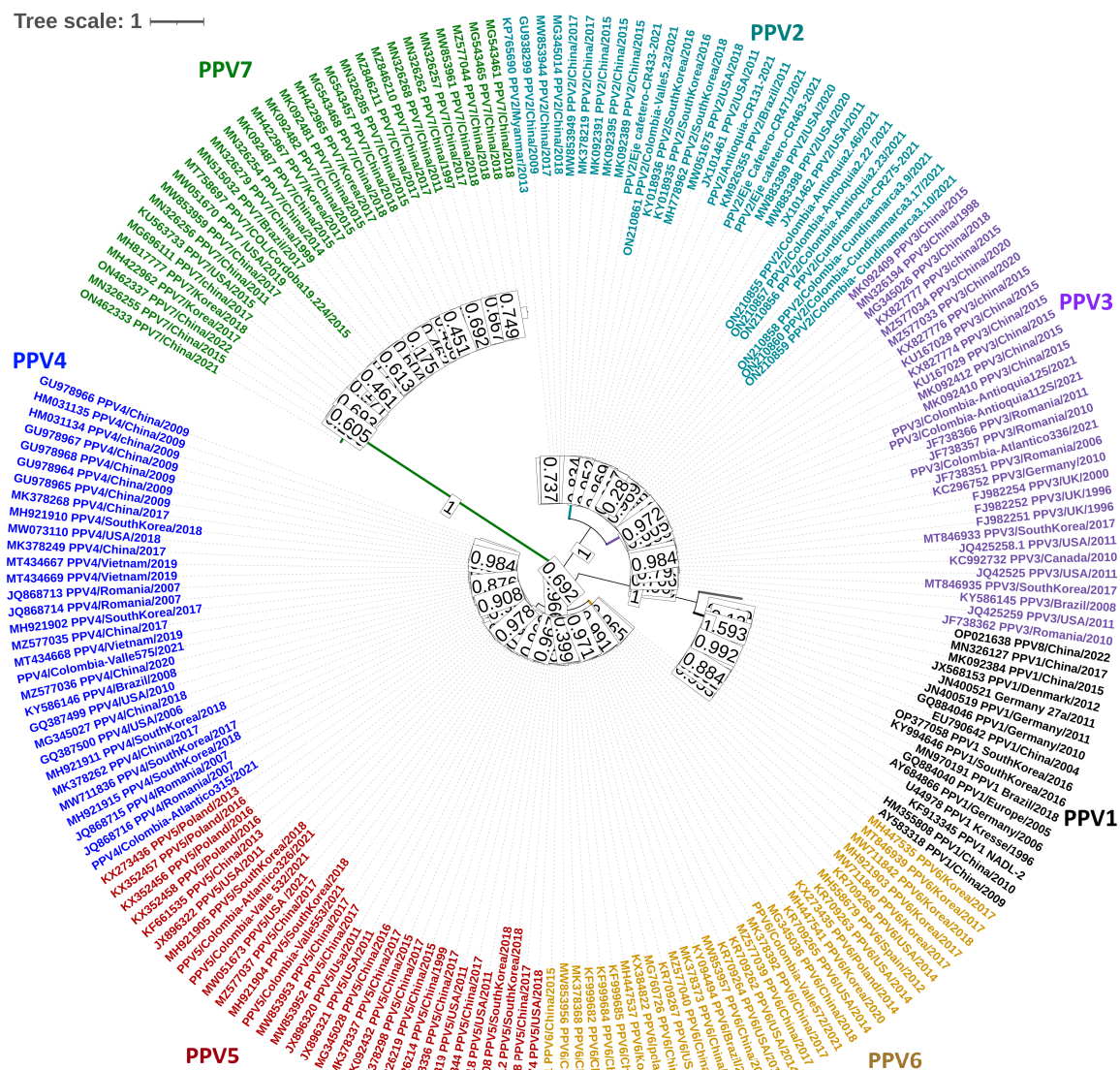


Figure S2. Phylogenetic distribution of porcine parvoviruses (PPV1 through PPV8). This distribution was determined by aligning 200 representatives nonstructural (NS) gene sequences retrieved from the NCBI GenBank nucleotide database. The phylogenetic tree was constructed using the Neighbor-joining method with the p-distance model. Bootstrap values are indicated by grey circles. The analysis was performed using MEGA - version 11.0 [49]. Bootstrap values are indicated on the branches.

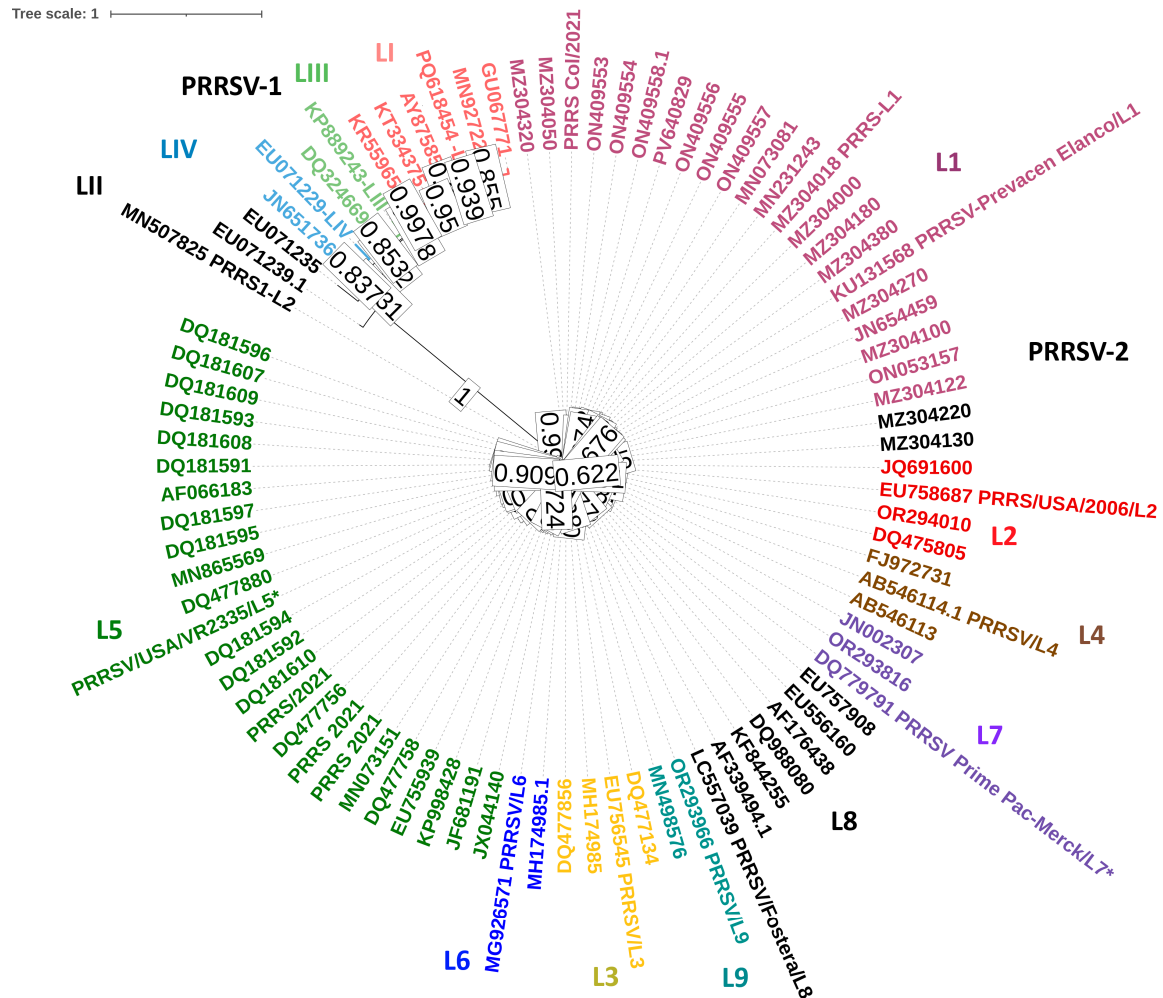


Figure S3. Phylogenetic distribution of porcine reproductive and respiratory syndrome virus (PRRSV). This analysis is based on the alignment of 80 representative ORF5 nucleotide (nt) sequences from PRRSV-1 and PRRSV-2, which are available in the NCBI GenBank nt database. The phylogenetic tree was constructed using the Neighbor-joining method along with the K2+G+I model. Bootstrap values are indicated on the branches. The analysis was performed using MEGA - version 11.0 [49].