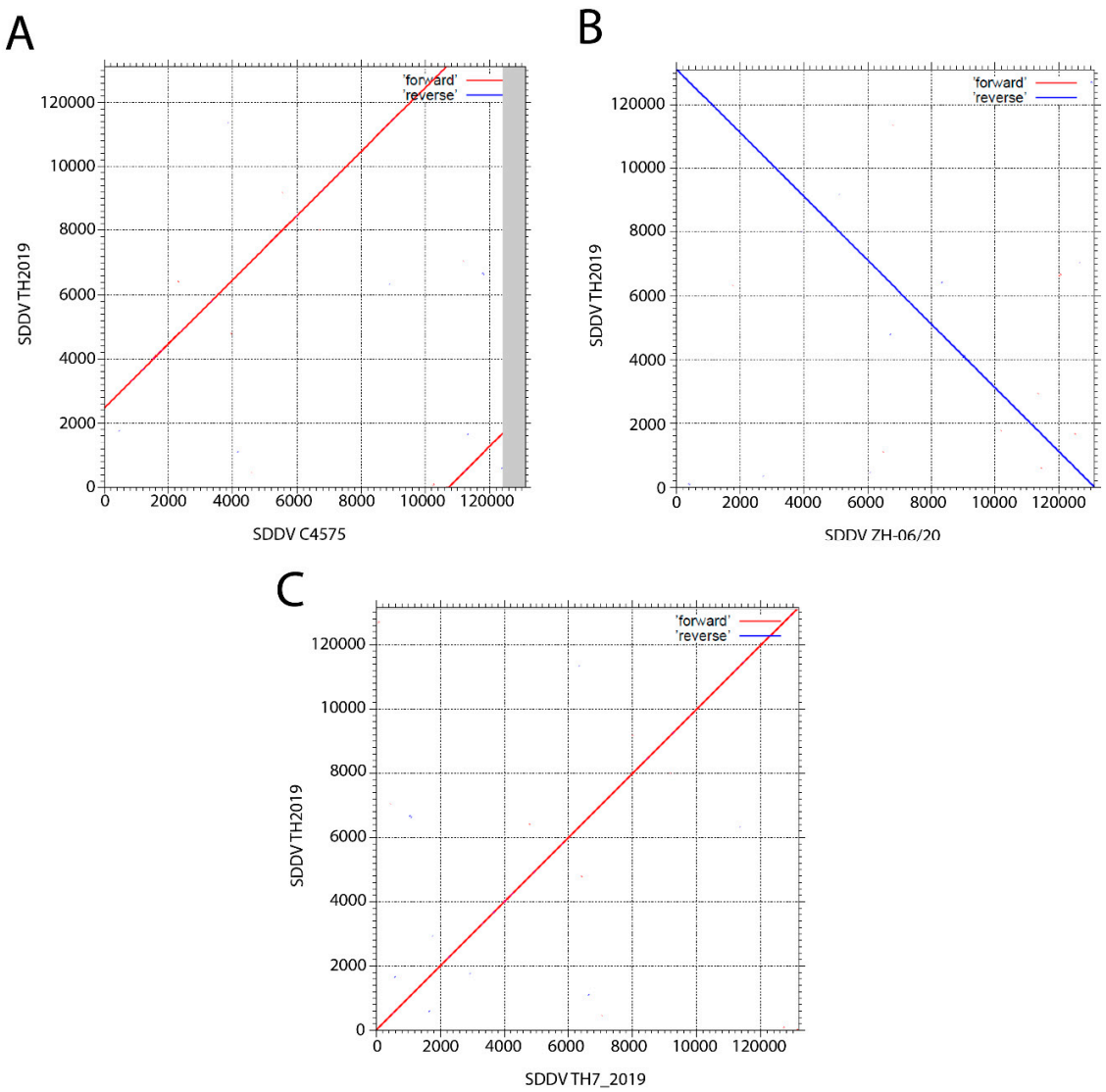


Figure S1. Dot plot of whole genome sequence alignment between the reference genome (SDDV TH2019) and SDDV (A) C4575, (B) ZH-06/20, and (C) TH7_2019.

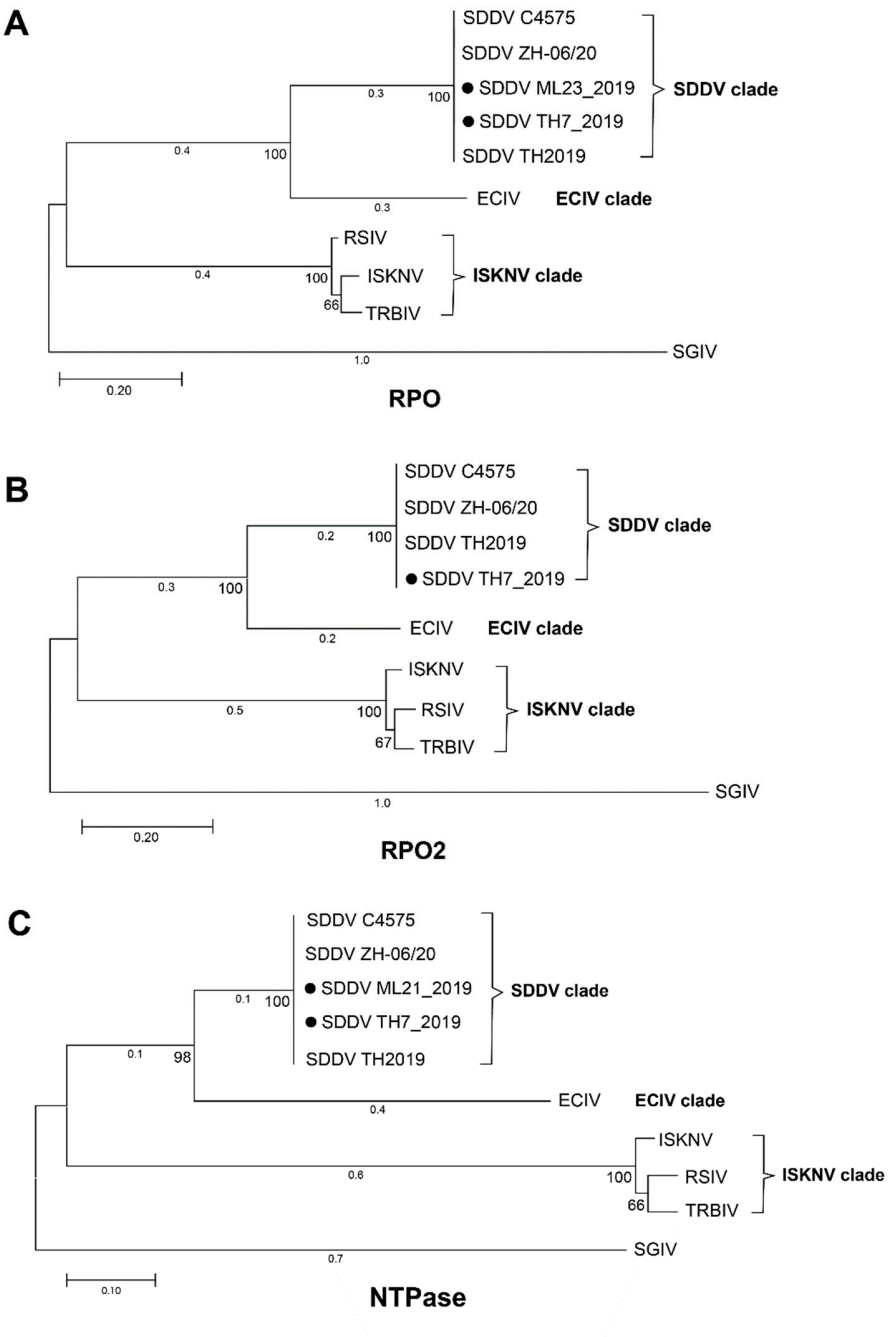


Figure S2. Maximum-likelihood tree based on (A) DNA-dependent RNA polymerase II alpha subunit (RPO), (B) DNA-dependent RNA polymerase II beta subunit (RPO2), and (C) NTPase gene constructed using MEGA X software with K2 + G nucleotide substitution model and 1,000 replications. Scale bar represents nucleotide substitution per site. Solid black circle represents SDDV strains from this study. SGIV, belonging to the genus *Ranavirus*, was used as an outgroup. Bootstrap support values in percentage are shown at the tree node.

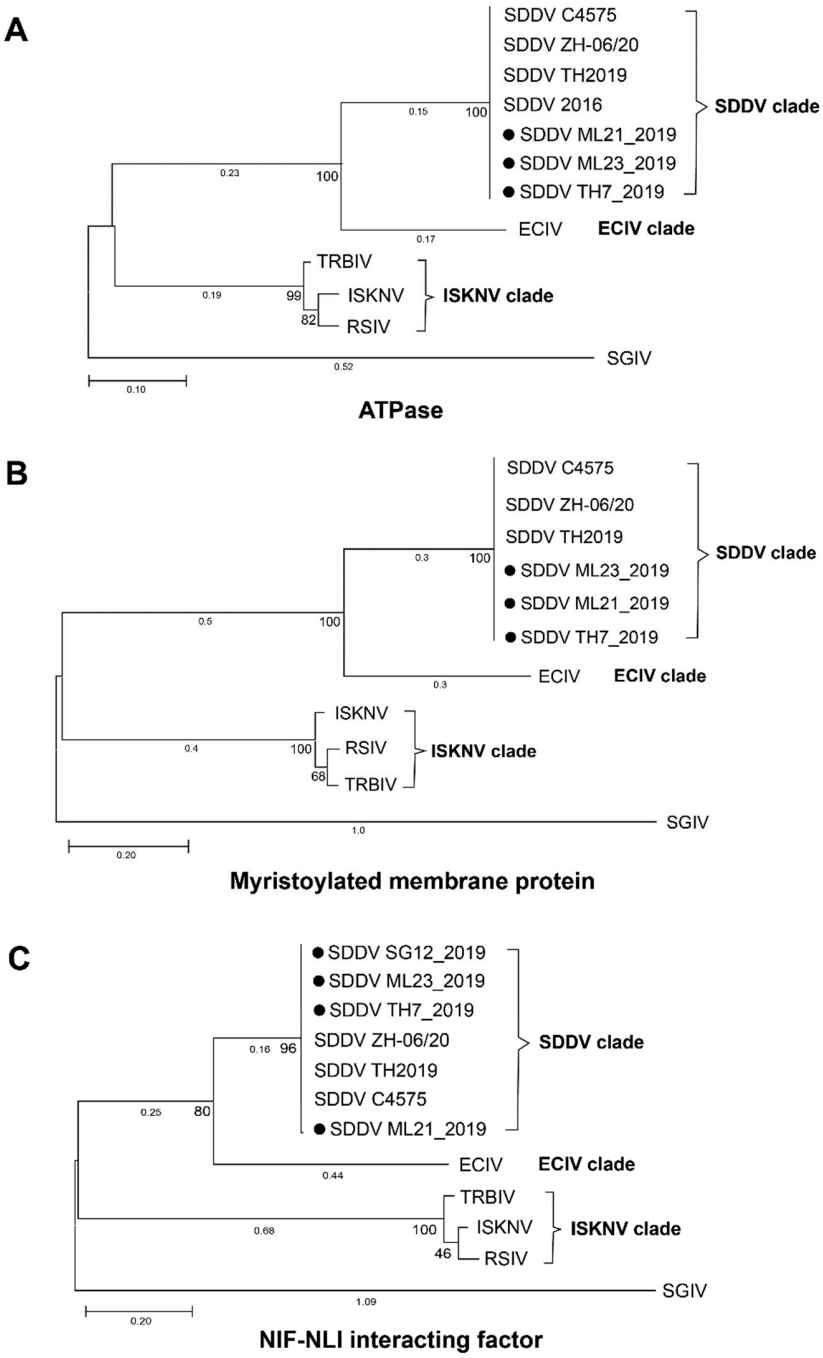


Figure S3. Maximum-likelihood tree based on (A) ATPase, (B) myristoylated membrane protein, and (C) NIF-NLI interacting factor gene constructed using MEGA X software with K2 + G nucleotide substitution model and 1,000 replications. Scale bar represents nucleotide substitution per site. Solid black circle represents SDDV strains from this study. SGIV, belonging to the genus *Ranavirus*, was used as an outgroup. Bootstrap support values in percentage are shown at the tree node.

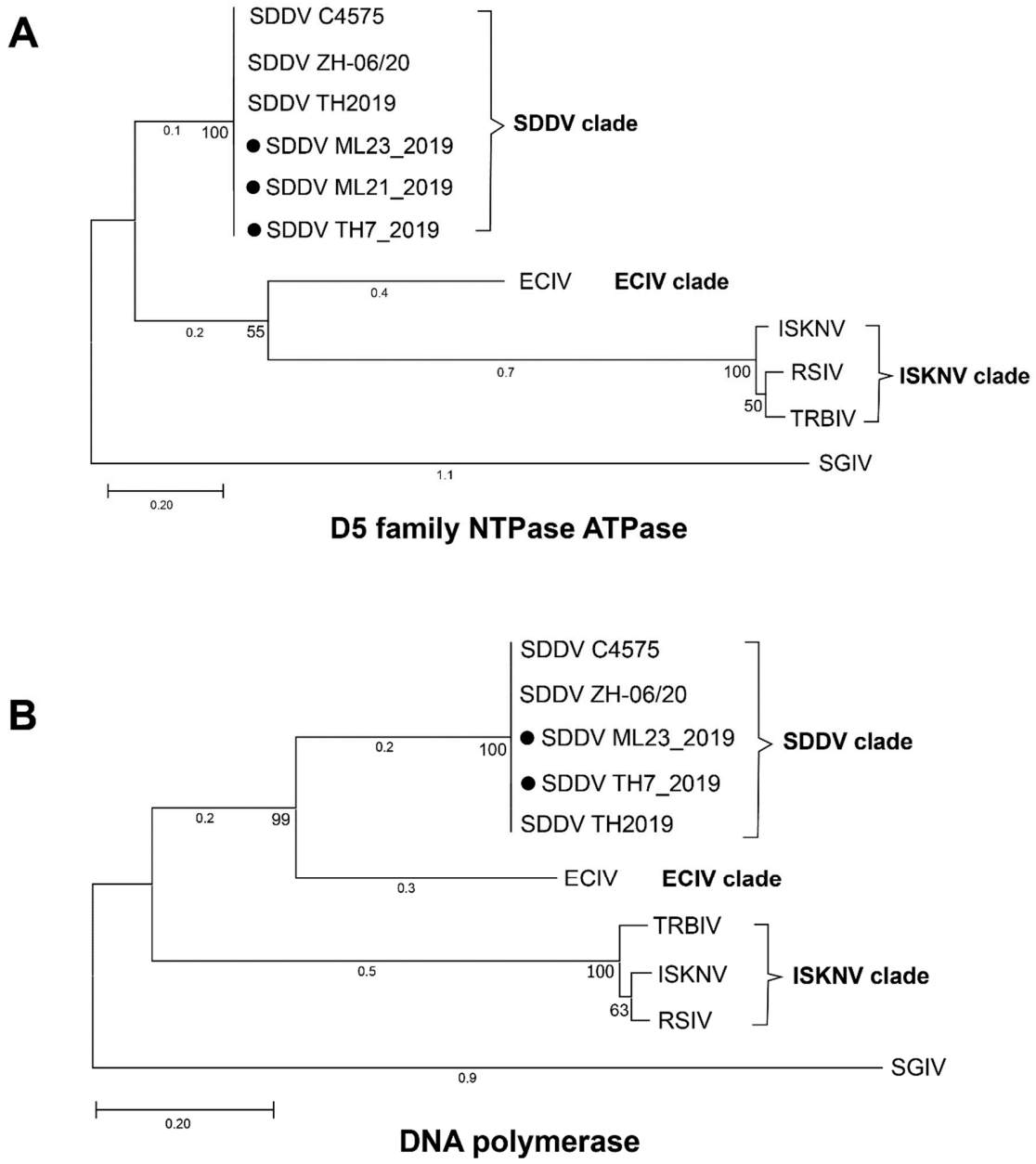


Figure S4. Maximum-likelihood tree based on (A) D5 family NTPase ATPase and (B) DNA polymerase gene constructed using MEGA X software with GTR + G nucleotide substitution model and 1,000 replications. Scale bar represents nucleotide substitution per site. Solid black circle represents SDDV strains from this study. SGIV, belonging to the genus *Ranavirus*, was used as an outgroup. Bootstrap support values in percentage are shown at the tree node.

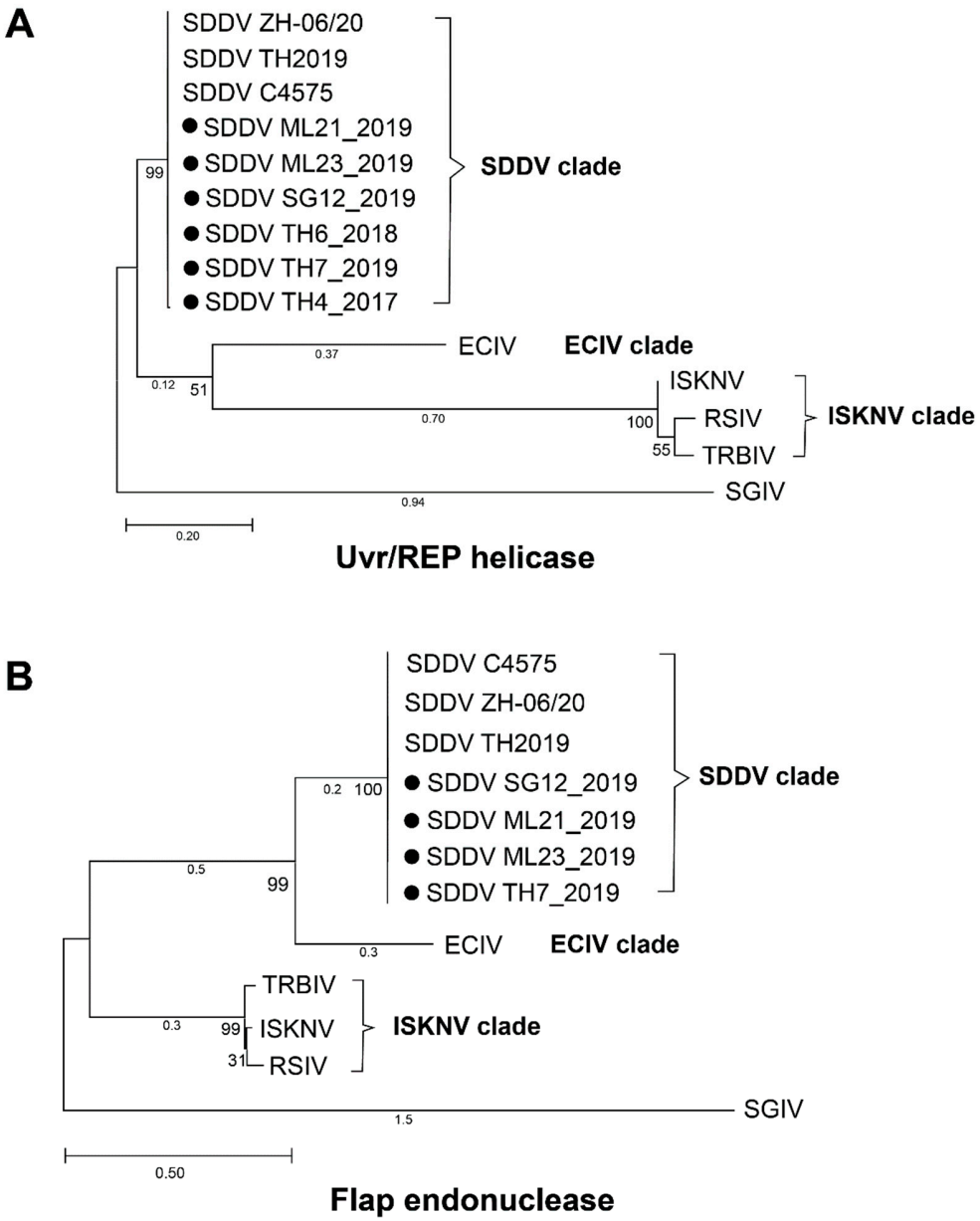


Figure S5. Maximum-likelihood tree based on (A) Uvr/REP helicase and (B) flap endonuclease gene constructed using MEGA X software with K2 + G + I nucleotide substitution model and 1,000 replications. Scale bar represents nucleotide substitution per site. Solid black circle represents SDDV strains from this study. SGIV, belonging to the genus *Ranavirus*, was used as an outgroup. Bootstrap support values in percentage are shown at the tree node.