Supplementary Material

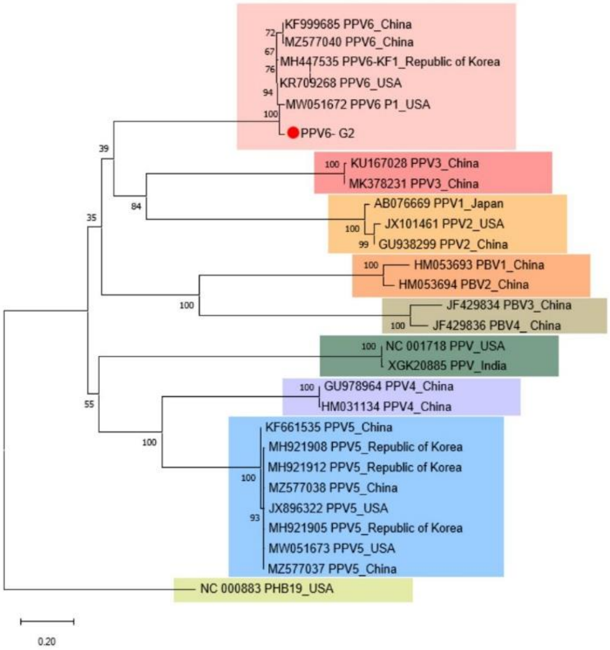

Figure S1: Genetic characterization of PPV. Phylogenetic analysis of the complete PPV6 genome, identified in Group 2, inferred with the maximum likelihood method, Kimura-2 model parameter. All analyses were performed with 1000 bootstrap replicates. The sequence obtained in this study is indicated by the red dot. (GenBank access: PX092311).

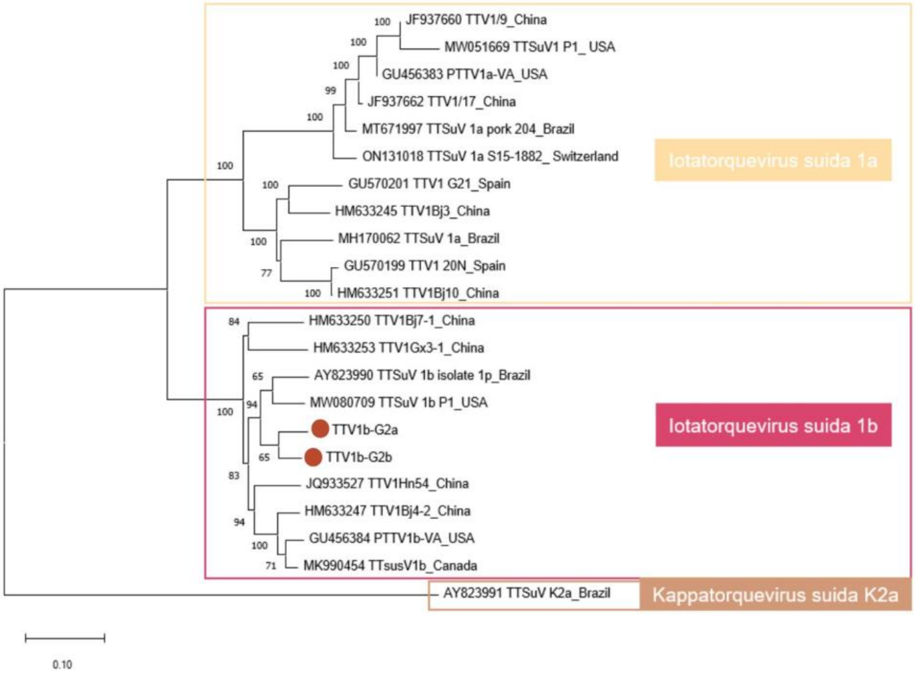

Figure S2: Phylogenetic analysis of the complete TTSuV genome was inferred using the maximum likelihood method, Tamura-3 model parameter. All analyses were performed with 1000 bootstrap replicates. The TTV1b_G2a and TTV1b_G2b sequences are grouped into the Iotatorquevirus suida1b cluster. The sequences obtained in this study are indicated by the red dots (GenBank access: PX092309; PX092310).

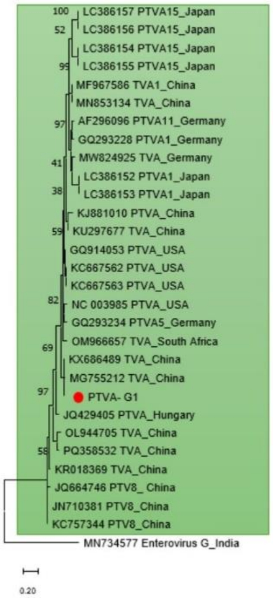

Figure S3: Phylogenetic analysis of PTV, found in Group 1, was inferred using the maximum likelihood method, Kimura-2 model parameter. All analyses were performed with 1000 bootstrap replicates. The sequence obtained in this study is indicated by the red dot (b) (GenBank access: PX101488).