



Supplementary Fig. 1. Supplementary data are available at <https://doi.org/10.14405/kjvr.20230005>.

A phylogenetic tree based on the 5'-untranslated region was generated using MEGAX and the maximum likelihood method; the numbers over branches indicate the bootstrap values (1,000 replicates) as percentages, supporting each phylogenetic branch. The sequence identified in this study is shown in boldface. BVDV, bovine viral diarrhea virus.