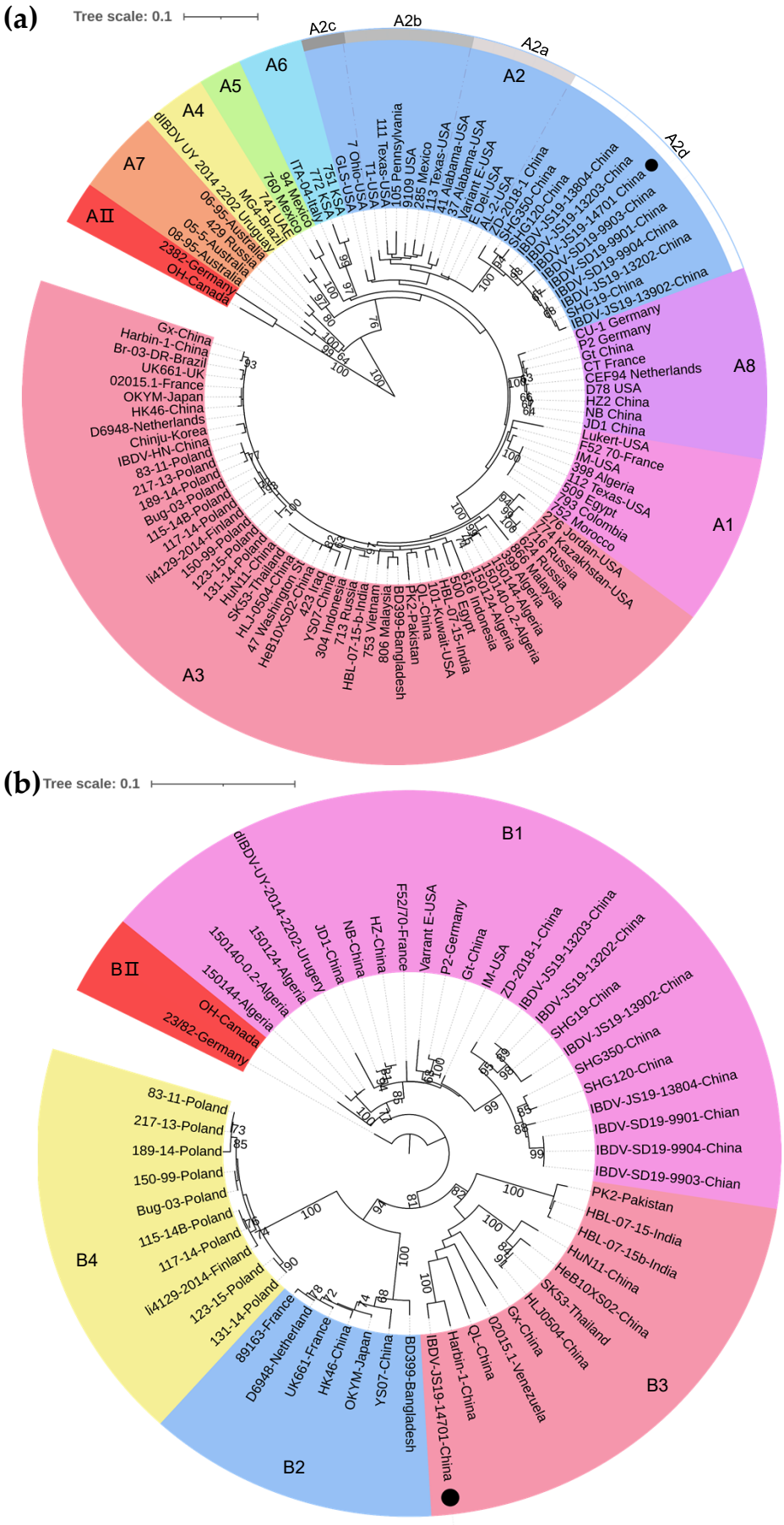


Figure S1. Phylogenetic analysis of the nucleotide sequences encoding the HVR of VP2 (a) and B-marker of VP1 (b). The trees were generated by the Maximum-likelihood method with MEGA6 software. Trees were drawn to scale, with branch lengths measured in the number of substitutions per site. Only branches supported by a bootstrap value above 60% were displayed. The genogroup for each branch was marked. The segment-reassortant strain detected in this study (IBDV-JS19-14701) was highlighted with a solid circle.