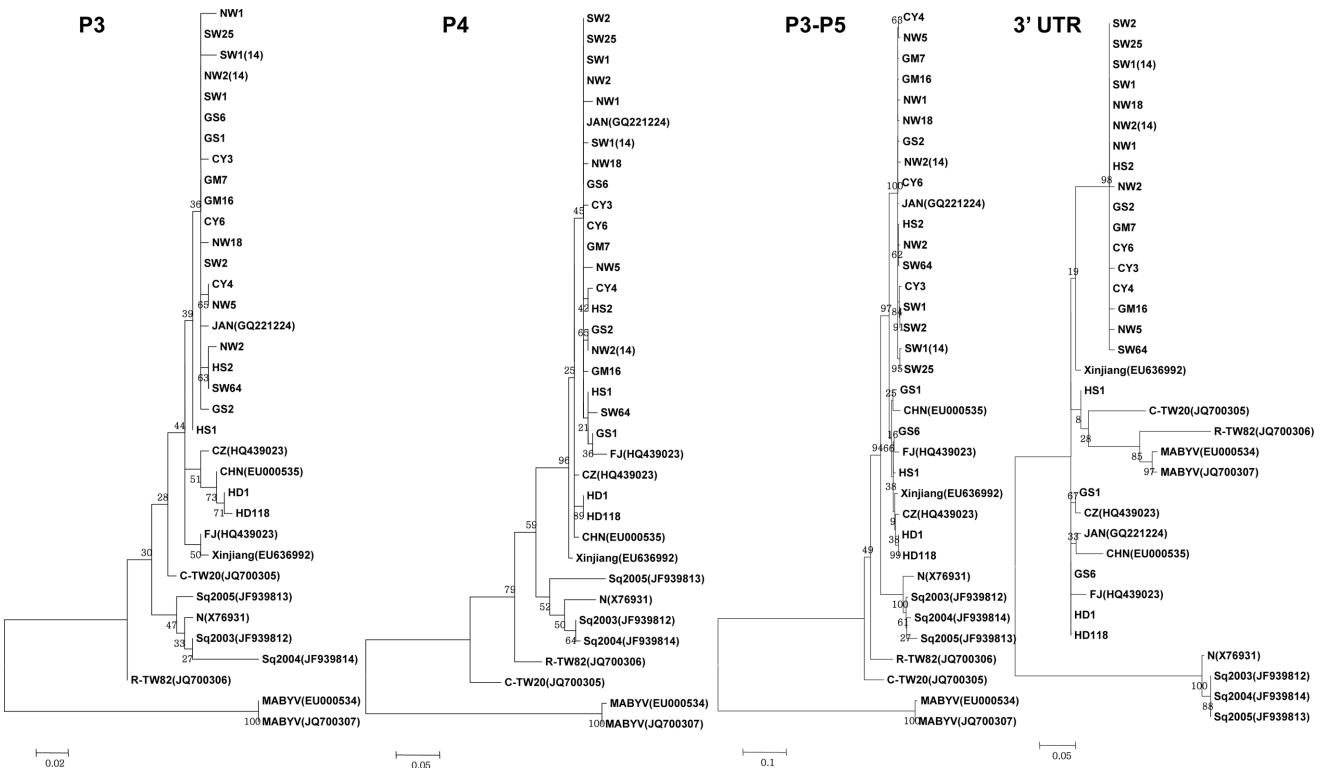**Supplementary Fig. 1.** Phylogenetic trees reconstructed using amino acid sequences of the 5' proximal proteins (P0, P1, and P1-P2) and nucleotide sequences of the IR region. Phylogenetic trees were reconstructed using maximum likelihood in MEGA 6.

Supplementary Fig. 2. Phylogenetic trees reconstructed using amino acid sequences of the 3' proximal proteins (P3, P4, and P3-P5) and nucleotide sequences of the 3' UTR region. Phylogenetic trees were reconstructed using maximum likelihood in MEGA 6.