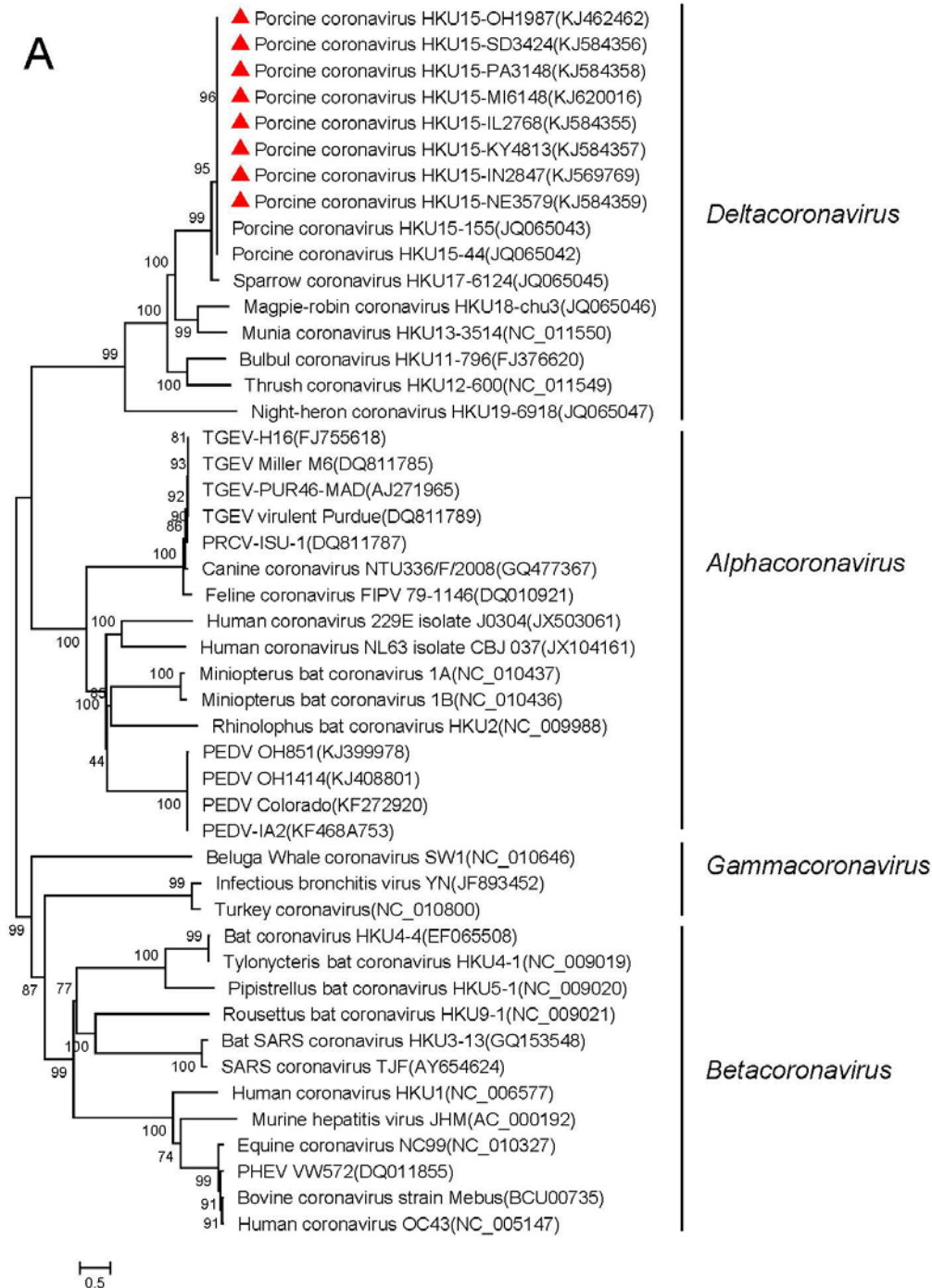
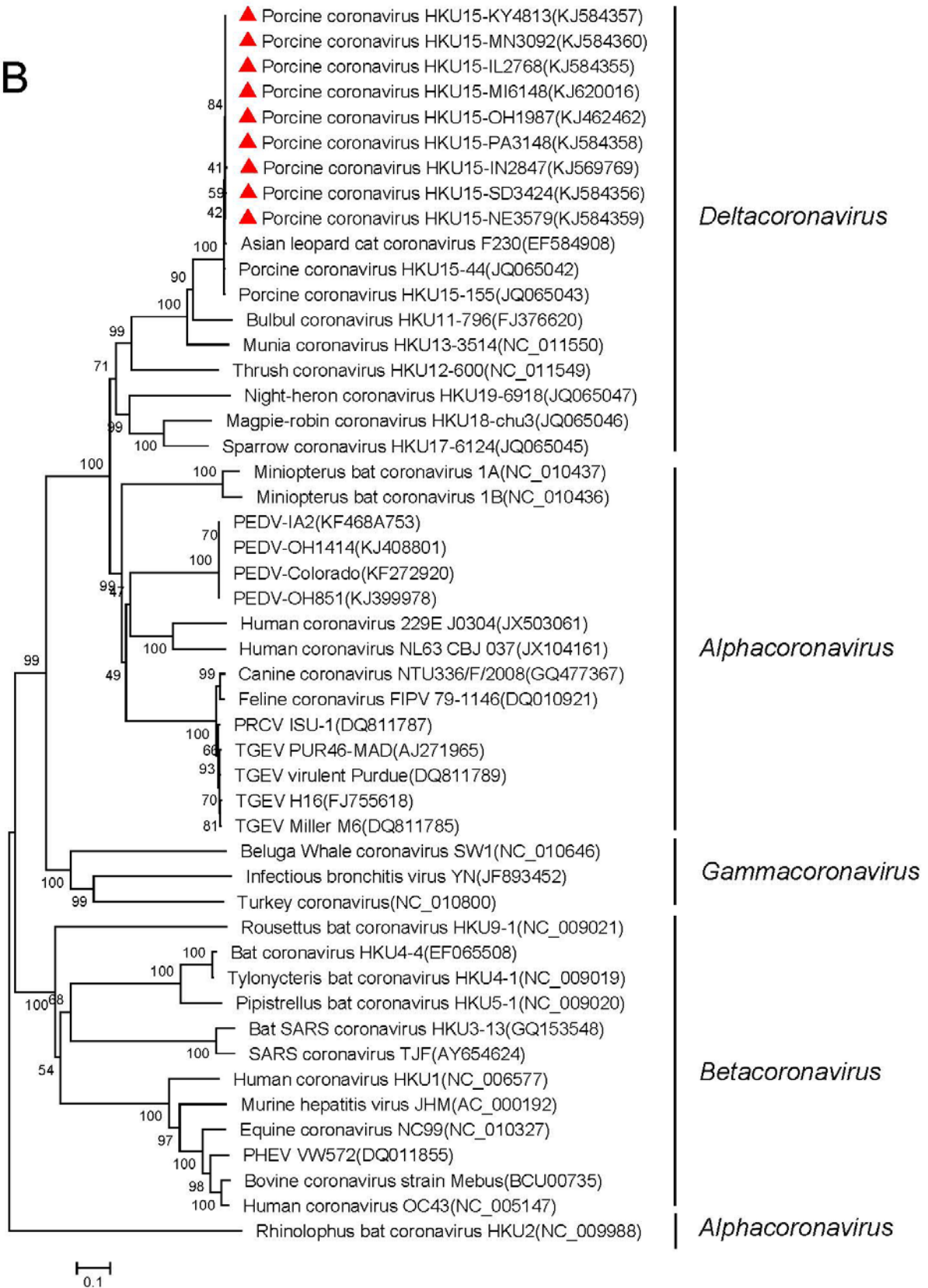
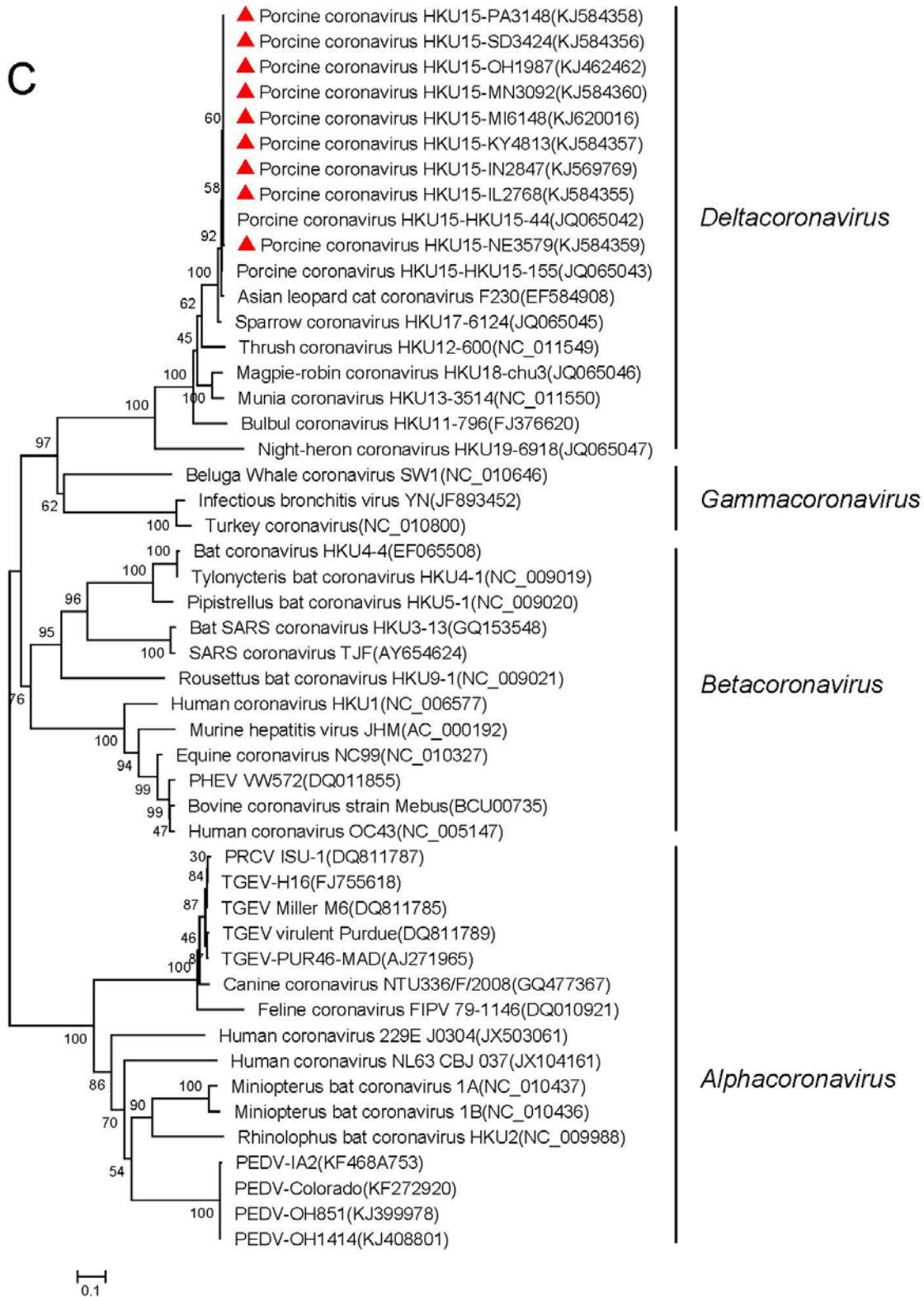


Porcine Coronavirus HKU15 Detected in 9 US States, 2014

Technical Appendix



B



Technical Appendix Figure. Phylogenetic tree constructed on the basis of the whole genome sequences (A), spike protein (B) and nucleocapsid protein (C) of 4 genera of coronaviruses (*Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus*, and *Deltacoronavirus*), including the 9 US strains of porcine coronavirus HKU15 (indicated by red triangle). The dendrogram was constructed by using the neighbor-joining method in the MEGA software package, version 6.05 (<http://www.megasoftware.net>). Bootstrap resampling (1,000 replications) was performed, and bootstrap values are indicated for each node. Reference sequences obtained from GenBank are indicated by strain name and accession number. Scale bar represents 0.5 nt (A) or 0.1 aa (B, C) substitutions per site. PEDV, porcine epidemic diarrhea virus; PHEV, porcine hemagglutinating encephalomyelitis virus; PRCV, porcine respiratory coronavirus; TGEV, transmissible gastroenteritis coronavirus; SARS, severe acute respiratory syndrome.