



**Supplemental Figure 6:** Phylogenies of conserved replicase subunits of representative nidoviruses. Unrooted Bayesian phylogenies based on multiple sequence alignments of indicated conserved regions of replicase polyproteins. At select nodes, Bayesian posterior probabilities are indicated. The five major nidovirus families and subfamilies are indicated as are select genera and the currently uncategorized BPNV and possum nidovirus taxa. Known host phyla are indicated in parentheses. The branch leading to BPNV is highlighted red for emphasis.