

Supplementary Figure S2. The maximum likelihood consensus tree of the norovirus and nairovirus polymerase (A: 2,588 amino acids) and nucleocapsid (B: 526 amino acids) sequences. The trees are constructed using 1,000 replicates. Branches achieving $\geq 95\%$ bootstrap support are annotated with red dots. Noroviruses other than Beiji nairovirus are marked. Viruses are indicated by GenBank accession, name and isolate identifier where available. Sequences detected in the study are indicated by sample ID and country of detection.

