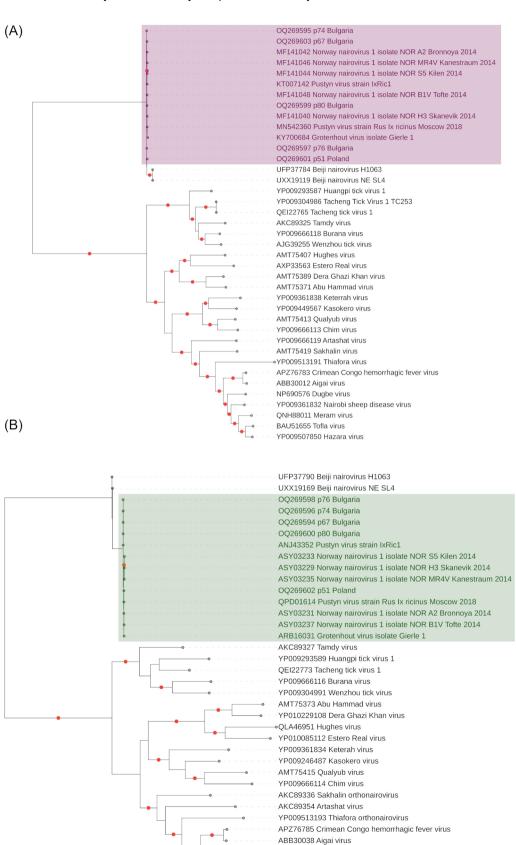
Supplementary Figure S2. The maximum likelihood consensus tree of the norwavirus and nairovirus polymerase (A: 2,588 amino acids) and nucleocapsid (B: 526 amino acids) sequences. The trees are constructed using 1,000 replicates. Branches achieving ≥95% bootstrap support are annotated with red dots. Norwaviruses 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.



QNH88013 Meram virus YP009227120 Tofla virus YP009507852 Hazara virus

NP690574 Dugbe virus

YP009361831 Nairobi sheep disease virus