**Supplementary Figure S1. PhyML tree analysis of MERS-CoV Spike gene sequences.**

Maximum likelihood tree of 97 MERS-CoV Spike gene sequences, generated using PhyML. The trees

include sequences from the 2013--2014 UAE clusters as well as camel-derived viruses sequenced in this

study and representative sequences from GenBank. The lineages described in Sabir et al. are indicated.

The clusters described in the paper are highlighted in the colored boxes.