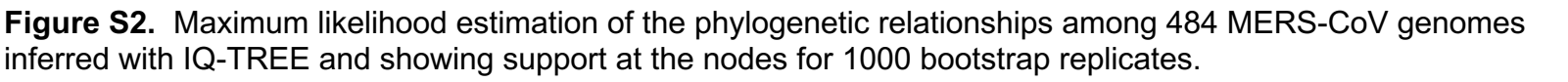
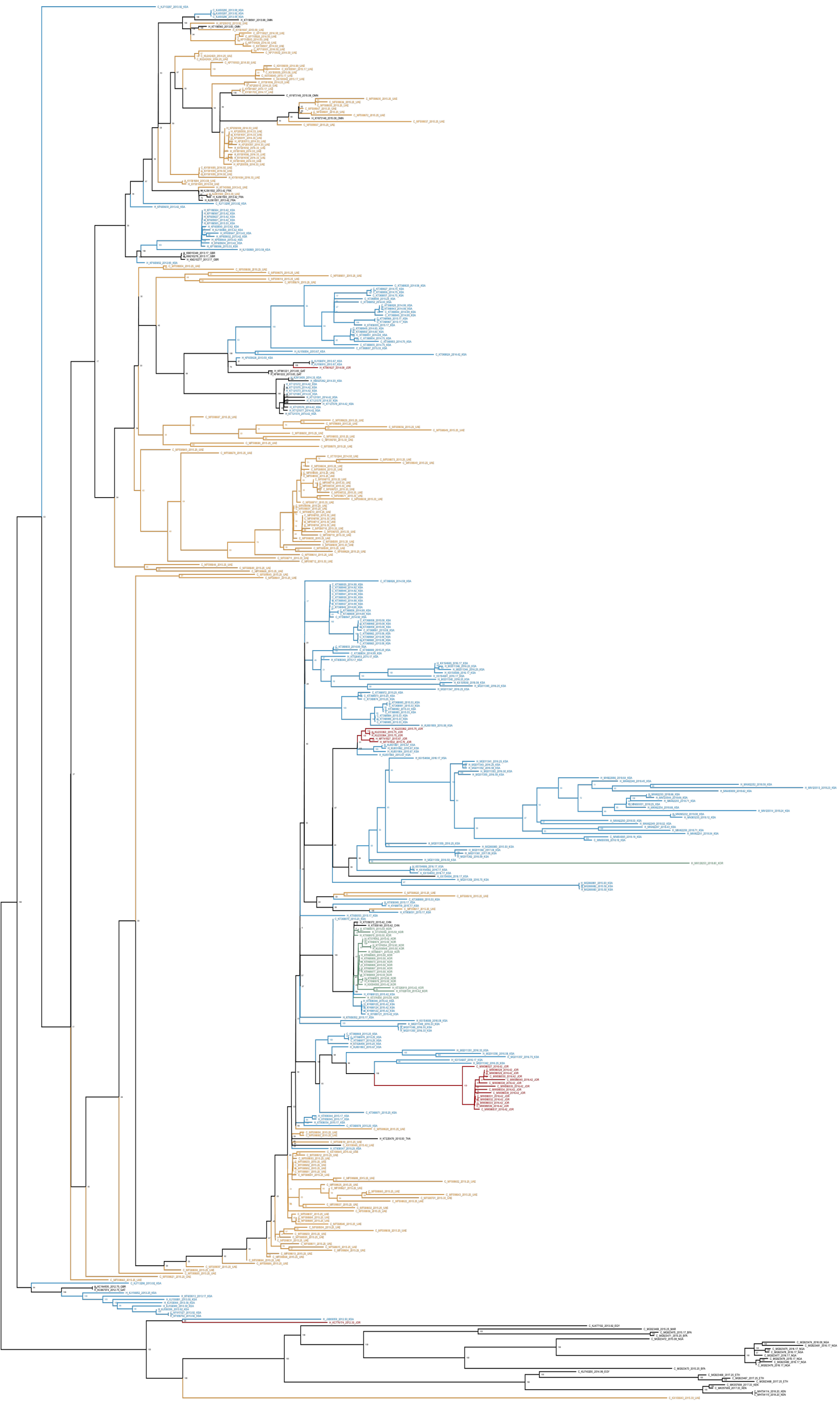


**Figure S1.** Sensitivity of the LRPCR assay when amplifying the MERS-CoV genome field collected camel nasal swabs. TCID<sub>50</sub> equivalent per swab for each sample is shown on the y-axis as determined by qRT-PCR in van Doremalen et al. 2017 [5]. Number of LRPCR amplicons successfully recovered for each sample on the x-axis with 5 amplicons indicating recovery of more than 99% of the genome.





**Figure S3.** Maximum likelihood estimation of the phylogenetic relationships among 425 MERS-CoV genomes with recombinant sequences stripped. ML tree inferred with IQ-TREE and showing support at the nodes for 1000 bootstrap replicates.