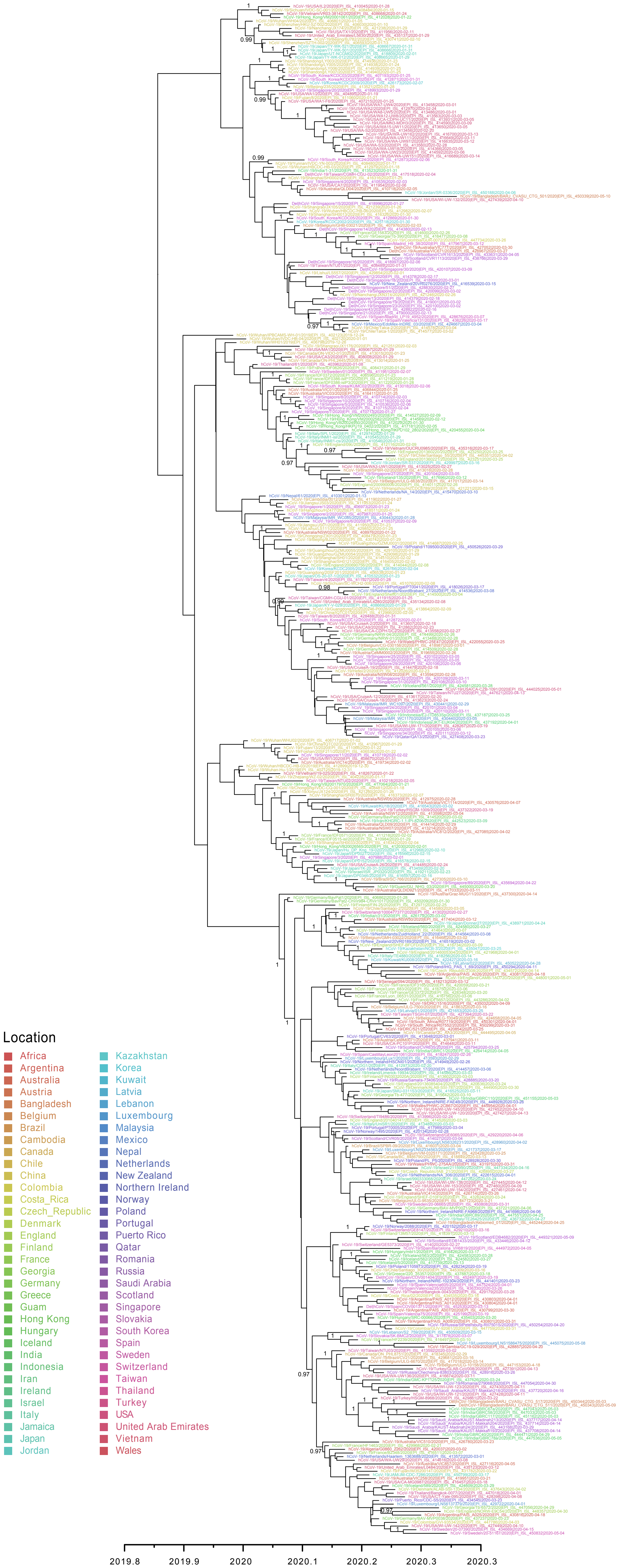

Fig. S4. Evolutionary relationships of human SARS-CoV-2 and SARS-CoV-2 Δ382. Temporal phylogeny of 419 complete genomes inferred using an uncorrelated lognormal relaxed clock model in BEAST. Coloured virus names represent different geographic locations. Bayesian posterior probabilities of ≥0.95 are indicated at nodes. Scale bar represents time in years.