



Location

- Africa
- Argentina
- Australia
- Austria
- Bangladesh
- Belgium
- Brazil
- Cambodia
- Canada
- Chile
- China
- Colombia
- Costa_Rica
- Czech_Republic
- Denmark
- England
- Finland
- France
- Georgia
- Germany
- Greece
- Guam
- Hong_Kong
- Hungary
- Iceland
- India
- Indonesia
- Iran
- Ireland
- Israel
- Italy
- Jamaica
- Japan
- Jordan
- Kazakhstan
- Korea
- Kuwait
- Latvia
- Lebanon
- Luxembourg
- Malaysia
- Mexico
- Nepal
- Netherlands
- New_Zealand
- Northern_Ireland
- Norway
- Poland
- Portugal
- Puerto_Rico
- Qatar
- Romania
- Russia
- Saudi_Arabia
- Scotland
- Singapore
- Slovakia
- South_Korea
- Spain
- Sweden
- Switzerland
- Taiwan
- Thailand
- Turkey
- USA
- United_Arab_Emirates
- Vietnam
- Wales

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.