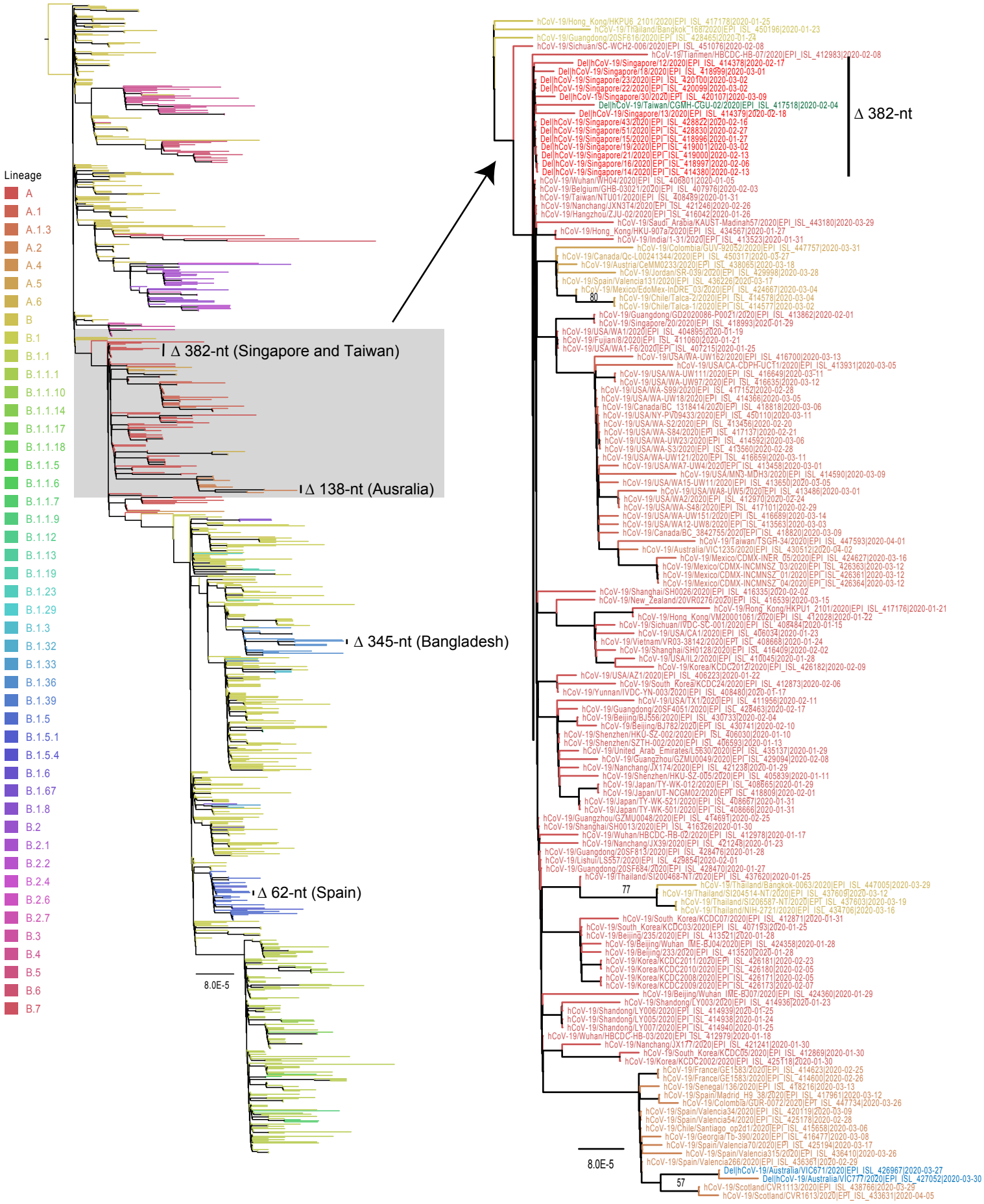

Fig. S3. Maximum-likelihood tree of SARS-CoV-2 genomes (n=1,038) reconstructed using RAxML with bootstrap values >50 indicated at branch nodes.