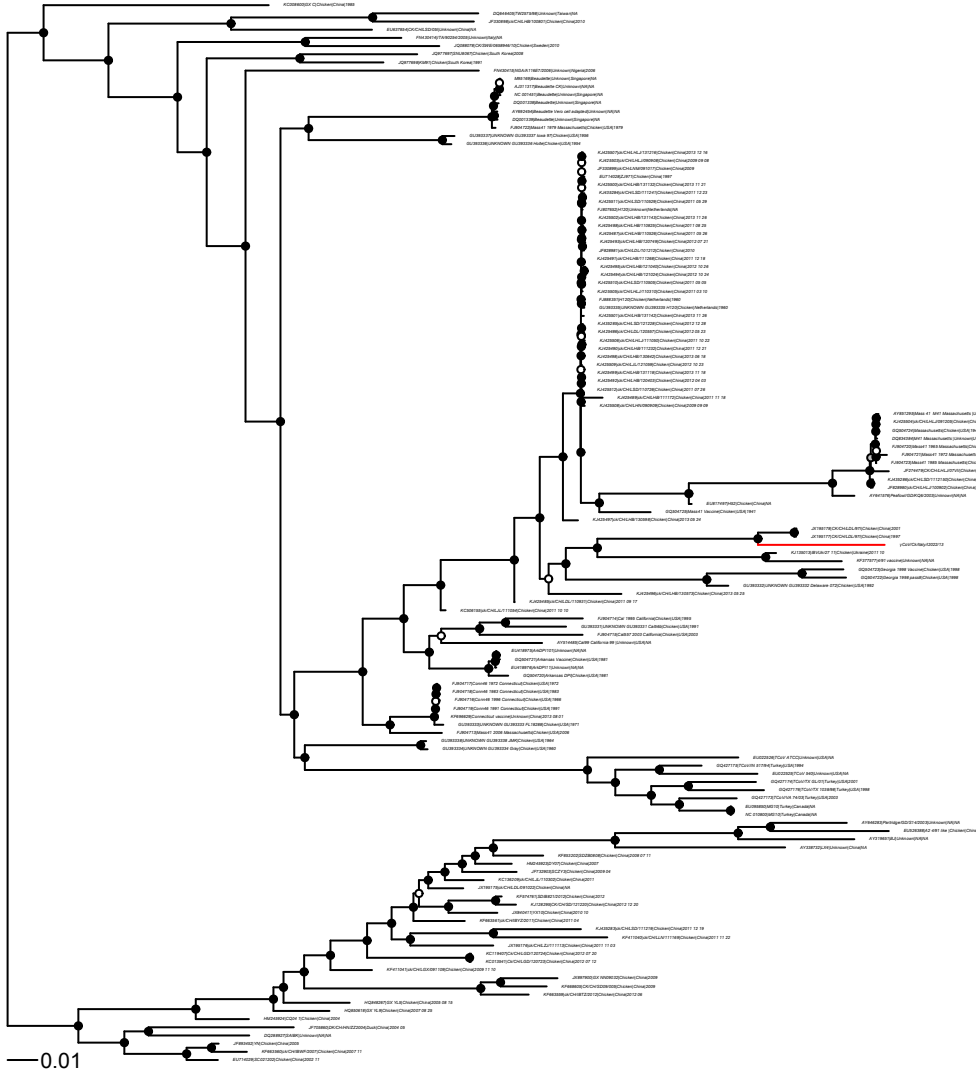

Supplementary figure 1. Maximum likelyhood phylogenetic tree based on 130 complete genome sequences. Branch corresponding to strain γCoV/Ck/Italy/I2022/13 is colored in red. Nodes displaying a bootstrap support higher that 70%, between 70 and 50% and lower than 50% are represented as black, grey and white circles, respectively.It is possible to zoom in to appreciate further details and tip labels