

Phylogenetic tree showing the relationships between various SARS-CoV-2 sequences. The tree is rooted at the bottom left. The sequences are labeled as follows:

- SARS-CoV-2 (100)
- Laos, Yunnan BANAL (100)
- Laos BANAL (100)
- EPI\_ISI\_430264530-Cov-19:laosLaosBANAL\_103/2020 (100)
- PCV19 (100)
- Yunnan SARS-CoV-2-like (100)
- SARS-like (100)
- Subeicovirus spp. (100)
- novel/RHGB02 (100)
- novel/RHGB03 (100)
- novel/RHGB04 (100)
- novel/RHGB01 (100)
- MW1719567.1[Subeicovirus\_RHGB01]\_complete\_genome (100)
- MZ1190138[laos\_SARS-like coronavirus\_Xhobsta-2\_strain\_BiCiCv/Xhobsta-2/RhRussia2020]\_complete\_genome (100)
- Subeicovirus spp. (100)
- KH36452.1[Bat\_Hu-betacoronavirus\_Zhejiang2013]\_complete\_genome (99)
- NC\_025171[Bat\_Hu-betacoronavirus\_Zhejiang2013]\_complete\_genome (98)
- Batbetacoronavirus (root) (97)