

is 93.3% identical to SARS-CoV-2 across the genome. In the long lab gene, it exhibits 97.2% identity to SARS-CoV-2, which is even higher than for RaTG13 (REF). In addition to RaTG13 and RmYN02, phylogenetic analysis shows that bat coronaviruses ZC45 and ZXC21 previously detected in *Rhinolophus pusillus* bats from eastern China also fall into the SARS-CoV-2 lineage of the subgenus Sarbecovirus" (FIG. 2). The discovery of diverse bat coronaviruses closely related to SARS-CoV-2 suggests that bats are possible reservoirs of SARS-CoV-2 (REF.\*). Nevertheless, on the basis of current findings, the divergence between SARS-CoV-2 and related bat coronaviruses likely represents more than 20 years of sequence evolution, suggesting that these bat coronaviruses can be regarded only as the likely evolutionary precursor of SARS-CoV-2 but not as the direct progenitor of SARS-CoV-2 (REF.\*). Beyond bats, pangolins are another wildlife host probably linked with SARS-CoV-2. Multiple SARS-CoV-2-related viruses have been identified in tissues of Malayan pangolins smuggled from Southeast Asia into southern China from 2017 to 2019. These viruses from pangolins independently seized by Guangxi and Guangdong provincial customs belong to two distinct sublineages\*-\*". The Guangdong strains, which were isolated or sequenced by different research groups from smuggled pangolins, have 99.8% sequence identity with each other". They are very closely related to SARS-CoV-2, exhibiting 92.4% sequence similarity. Notably, the RBD of Guangdong pangolin coronaviruses is highly similar to that of SARS-CoV-2. The receptor-binding motif (RBM; which is part of the RBD) of these viruses has only one amino acid variation from SARS-CoV-2, and it is identical to that of SARS-CoV-2 in all five critical