

residues for receptor binding<sup>40</sup> (FIG. 3b). In comparison with the Guangdong strains, pangolin coronaviruses reported from Guangxi are less similar to SARS-CoV-2, with 85.5% genome sequence identity<sup>39</sup>. The repeated occurrence of SARS-CoV-2-related coronavirus infections in pangolins from different smuggling events suggests that these animals are possible hosts of the viruses. However, unlike bats, which carry coronaviruses healthily, the infected pangolins showed clinical signs and histopathological changes, including interstitial pneumonia and inflammatory cell infiltration in diverse organs<sup>40</sup>. These abnormalities suggest that pangolins are unlikely to be the reservoir of these coronaviruses but more likely acquired the viruses after spillover from the natural hosts.

An intermediate host usually plays an important role in the outbreak of bat-derived emerging coronaviruses; for example, palm civets for SARS-CoV and dromedary camels for MERS-CoV. The virus strains carried by these two intermediate hosts were almost genetically identical to the corresponding viruses in humans (more than 99% genome sequence identity)<sup>1</sup>. Despite an RBD that is virtually identical to that of SARS-CoV-2, the pangolin coronaviruses known to date have no more than 92% genome identity with SARS-CoV-2 (REF.<sup>42</sup>). The available data are insufficient to interpret pangolins as the intermediate host of SARS-CoV-2. So far, no evidence has shown that pangolins were directly involved in the emergence of SARS-CoV-2.