To assess the genetic variation of different SARS-CoV-2 strains, the 2019 Novel Coronavirus Resource of China National Center for Bioinformation aligned 77,801 genome sequences of SARS-CoV-2 detected globally and identified a total of 15,018 mutations, including 14,824 single-nucleotide polymorphisms (SNG) (BIGD)[31]. In the S protein, four amino acid alterations, V483A, L455I, F456V and G476S, are located near the binding interface in the RBD, but their effects on binding to the host receptor are unknown. The alteration D614G in the S1 subunit was found more frequently than other S variant sites, and it is the marker of a major subclade of SARS-CoV-2 (clade G). Since March 2020, SARS-CoV-2 variants with G614 in the S protein have replaced the original D614 variants and become the dominant form circulating globally. Compared with the D614 variant, higher viral loads were found in patients infected with the G614 variant, but clinical data suggested no significant link between the D614G alteration and disease severity[32]. Pseudotyped viruses carrying the S protein with G614 generated higher infectious titers than viruses carrying the S protein with D614, suggesting the alteration may have increased the infectivity of SARS-CoV-2 (REF.[32]). However, the results of in vitro experiments based on pseudovirus models may not exactly reflect natural infection. This preliminary finding should be validated by more studies using wild-type SARS-CoV-2 variants to test different target cells and animal models. Whether this amino acid change enhanced virus transmissibility is still to be determined. Another marker mutation for SARS-CoV-2 evolution is the single-nucleotide