Supplementary Table 1: The functions of non-structural proteins in a typical coronavirus and SARS-CoV-2 (predicted by bioinformatics tools).

Non-Structural proteins	Functions of a typical CoV	SARS-CoV-2 (predicted by bioinformatics tools)
nsp1	Cellular mRNA degradation, inhibiting IFN signaling	Suppress antiviral host response
nsp2	Unknown	Unknown
nsp3	PLP, polypeptides cleaving, blocking host innate immune response, promoting cytokine expression	Putative PL-pro domain
nsp4	DMV (double-membrane vesicle) formation	Complex with nsp3 and 6: DMV formation
nsp5	3CLpro, Mpro, polypeptides cleaving, inhibiting IFN signaling	3CL-pro domain
nsp6	Restricting autophagosome expansion, DMV formation	Complex with nsp3 and 4: DMV formation
nsp7	Cofactor with nsp8 and nsp12	Complex with nsp8: primase
nsp8	Cofactor with nsp7 and nsp12, primase	Complex with nsp7: primase
nsp9	Dimerization and RNA binding	RNA/DNA binding activity
nsp10	Scaffold protein for nsp14 and nsp16	Complex with nsp14: replication fidelity
nsp11	Unknown	Short peptide at the end of orf1a (2019-nCoV HKU-SZ-005b)
nsp12	Primer dependent RdRp	RNA-dependent RNA polymerase
nsp13	RNA helicase, 5′triphosphatase	Helicase
nsp14	Exoribonuclease, N7-MTase	ExoN: 3′–5′ exonuclease
nsp15	Endoribonuclease, evasion of dsRNA sensors	XendoU: poly(U)-specific endoribonuclease
nsp16	2′-O-MTase; avoiding MDA5 recognition, negatively regulating innate immunity	2′-O-MT: 2′-O-ribose methyltransferase