Supplementary Material

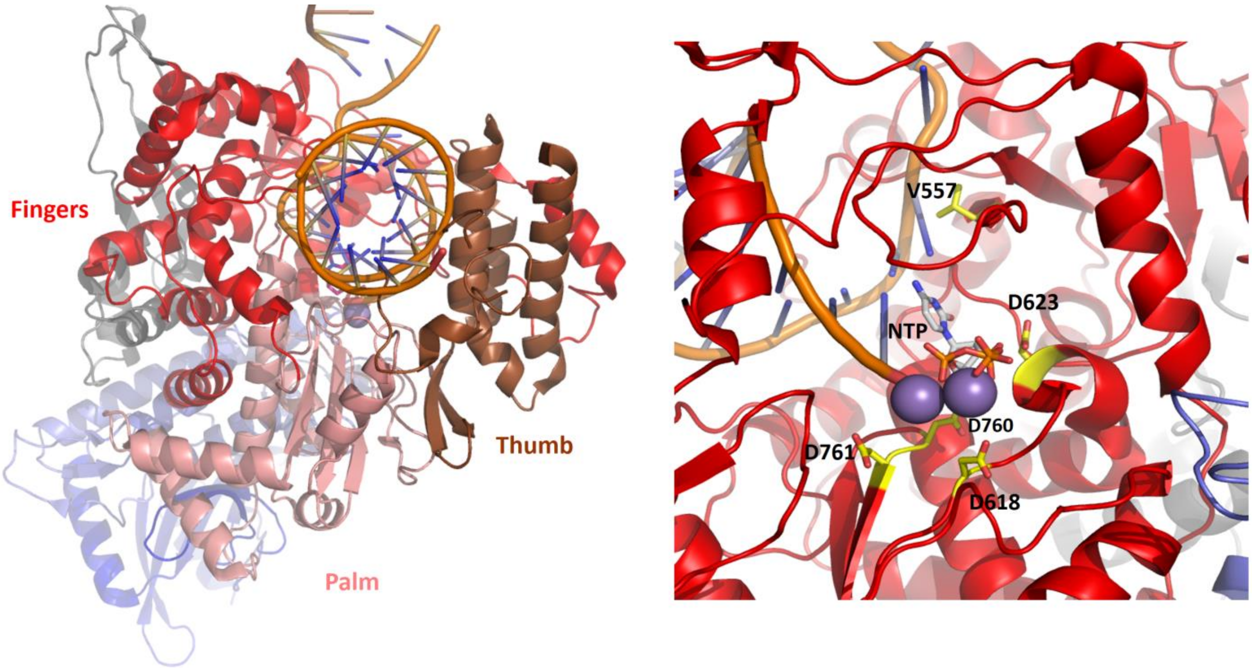

Figure S1. Model of SARS-CoV-2 elongation complex; The positions of the RNA template and primer were obtained from the structural alignment of SARS-CoV-2 Nsp12 with the elongation complex of poliovirus (PDB code 3OL6). The position of Mg^{2+} ions was taken from the structure of norovirus (PDB code 3H5Y). The three subdomains of the polymerase domain, fingers (residues 366-581 and 621-679), palm (residues 582-620 and 680-815), and the thumb (residues 816-920) are shown in red, salmon and brown, respectively. Right) A zoom of the catalytic site showing the position of the incoming NTP and divalent cations (grey). The conserved Asp residues playing a key role in the NTP and divalent cations binding and Val557 (involved in Remdesivir resistance) are shown as yellow sticks.

Table S1. Sequence identities of SARS-CoV2 Nsps with homologous proteins. Identities are reported with homologs from SARS-CoV and MHV. The binary alignments were performed using Lalign Server tool.

SARS-CoV-2	SARS-CoV	MHV
Nsp7	98.8	43.5
Nsp8	97.5	45.3
Nsp9	97.3	46.9
Nsp10	97.1	52.5
Nsp12	96.4	66.3
Nsp13	99.8	67.3
Nsp14	95.1	82.5
Nsp15	88.7	44.9
Nsp16	93.3	63.9