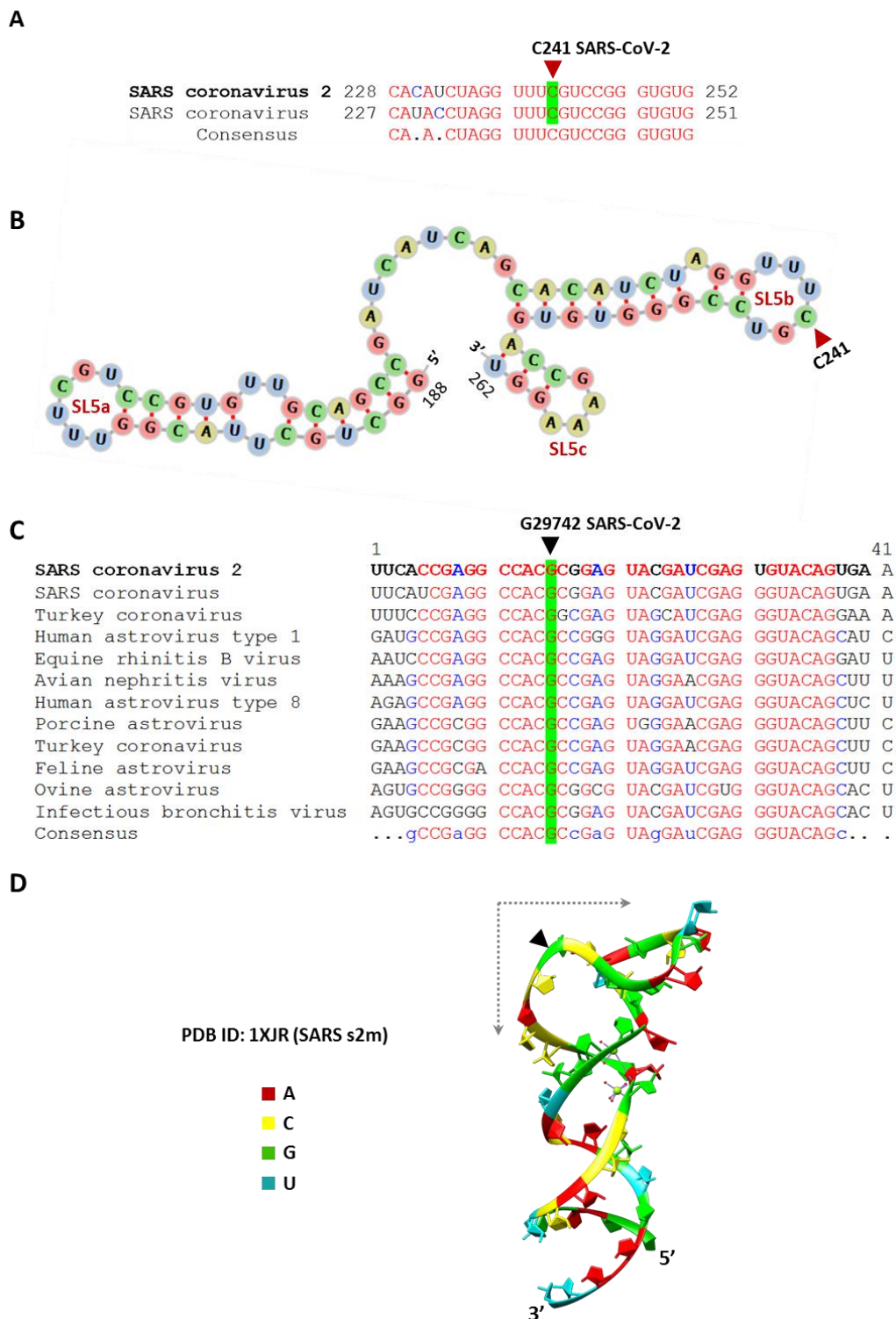


Supplementary Figure S1



Supplementary Figure S1. Structural elements in the SARS-CoV-2 UTRs and nucleotide substitutions. **A.** Alignment of the 5' UTR SL5a stem-loop region from SARS-CoV and SARS-CoV2 genomes showing the conserved loop residue – C241 in SARS-CoV-2 mutated to T in 34.8% of genomes analysed. **B.** The 5' UTR stem-loops SL5a, SL5b and SL5c from SARS-CoV-2 depicting the position of C241 residue in the hexameric loop of SL5b. **C.** Multiple alignment of stem-loop II-like motif (s2m) in the 3' UTR of coronaviruses with the G29742 mutation hotspot in SARS-CoV-2 highlighted. The SARS-CoV and SARS-CoV-2 sequences are nearly identical. **D.** The crystal structure of SARS-CoV s2m (PDB ID: 1XJR) showing the crucial position of the conserved G residue in the right-angle bent region of the stem-loop.