Figures for Feasibility and Data:

Figure 1:

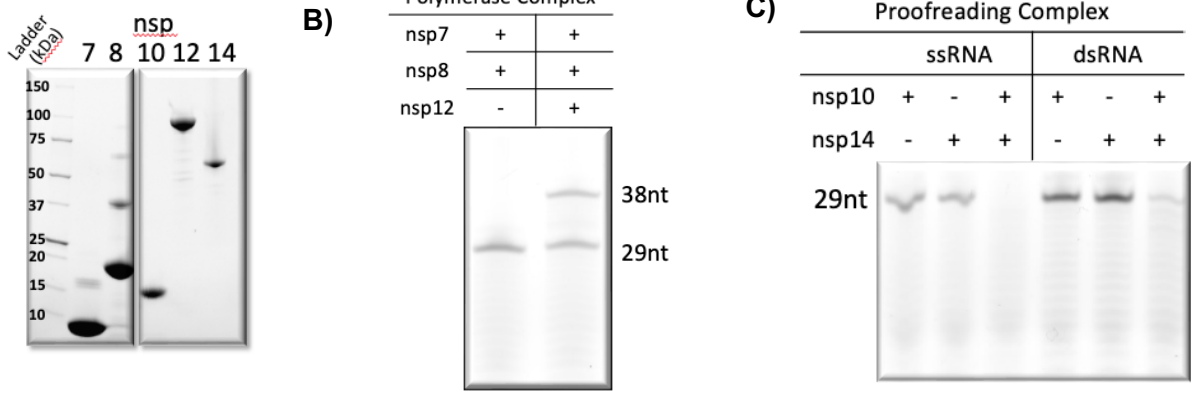

Figure 1: Active SARS-CoV-2 polymerase and proofreading complexes. **A)** Expression and pufication of of SARS-CoV-2 non-structural proteins: *nsp7 (*9kDa), *nsp8 (*22kDa), *nsp10 (*15kDa), *nsp14 (*60kDa), *nsp12 (*110kDa). **B)** The nsp12 polymerase extends RNA primers (29nt) in the presence of nsp7 and nsp8 to a full length product (38nt) **C)** The proofreading complex degrades both single and double-stranded RNA. The proofreading complex is of 3'-5' exoribonuclease nsp14 and cofactor nsp10.

Figure 2:

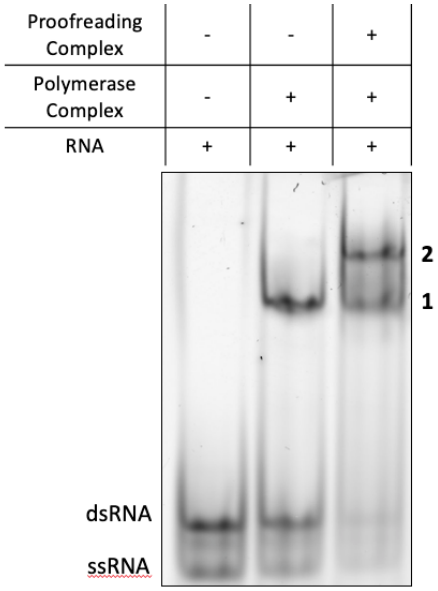

Figure 2: Assembly of a polymerase + proofreading complex. Primer-template pairs labeled with a fluorophore bind the polymerase complex causing a reduced gel mobility by native-PAGE. Addition of the proofreading complex results in a further shift. Complex formation of the RNA+polymerase is indicated by the number 1, while formation of a RNA+polymerase+proofreading complex is indicated by the number 2.

Figure 3:

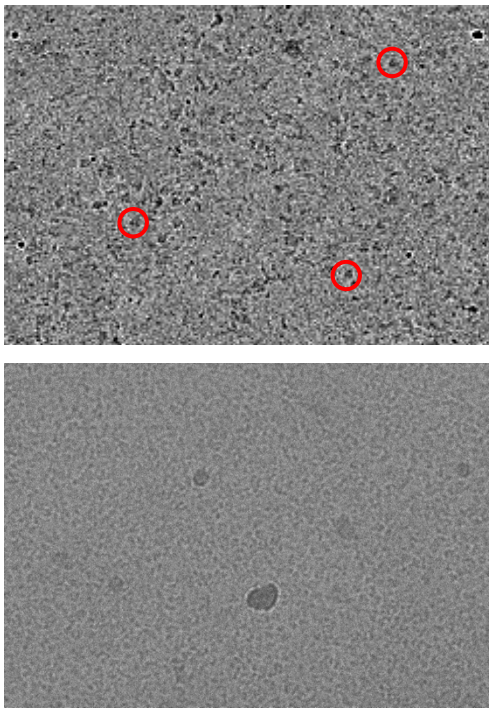

Figure 3: Disassembly of polymerase+proofreading complexes during blot-plunge vitrification. Samples of either coronavirus polymerase (**A**) or polymerase+proofreading (**B**) complexes prepared at 1mg/mL, frozen using blot-plunge vitrification and imaged using a 200kV Talos Arctica cryo-electron microscope under similar protocols. Polymerase complexes present as defined puncta in the EM images (red circles) and allow the determination of high-resolution structures. Polymerase+proofreading complexes display as ill-defined and likely disassembled complexes and/or denatured proteins.