



Supplementary Figure S1. Schematic Workflow of the experimental study. The study can be divided into four major parts. The first part is the temporal mutation of nsp7 and nsp8 for 2022-2023 from global sequence data. The second part is the conserved domain database analysis which identified critical interaction residues. The third part is the computational alanine scan of the viral replication protein complex. The first three parts are then subjected to the fourth part of the study which is on protein modeling and mutational effects prediction.