



Supplementary Figure 5. Amino acid changes in the spike (S) protein between the Omicron BA.1 and the Delta isolate used in this study. The S protein is shown from two different angles. Sequence variants located in the receptor binding domain are highlighted in magenta. Changes to residue bonding were visualised using Pymol (<https://pymol.org/2/>) using Protein Databank in Europe (PDBe) structure 7fg3.