Figure S1. Antibody neutralisation of PV entry into HeLa ACE2 and HEK 293T cells. Neutralisation of the stated PV by a reference convalescent serum (20/130) and mouse anti-RBD mAbs 12443 and 12444. Each plot provides neutralisation values from HeLa ACE2 and HEK 293T cells. Data points represent the mean of n=3 independent experiments. Error bars indicate standard error of the mean. Curve fitting performed in GraphPad Prism, the curves on each plot (i.e. HeLa ACE2 and HEK 293T) were determined to be statistically indistinguishable.
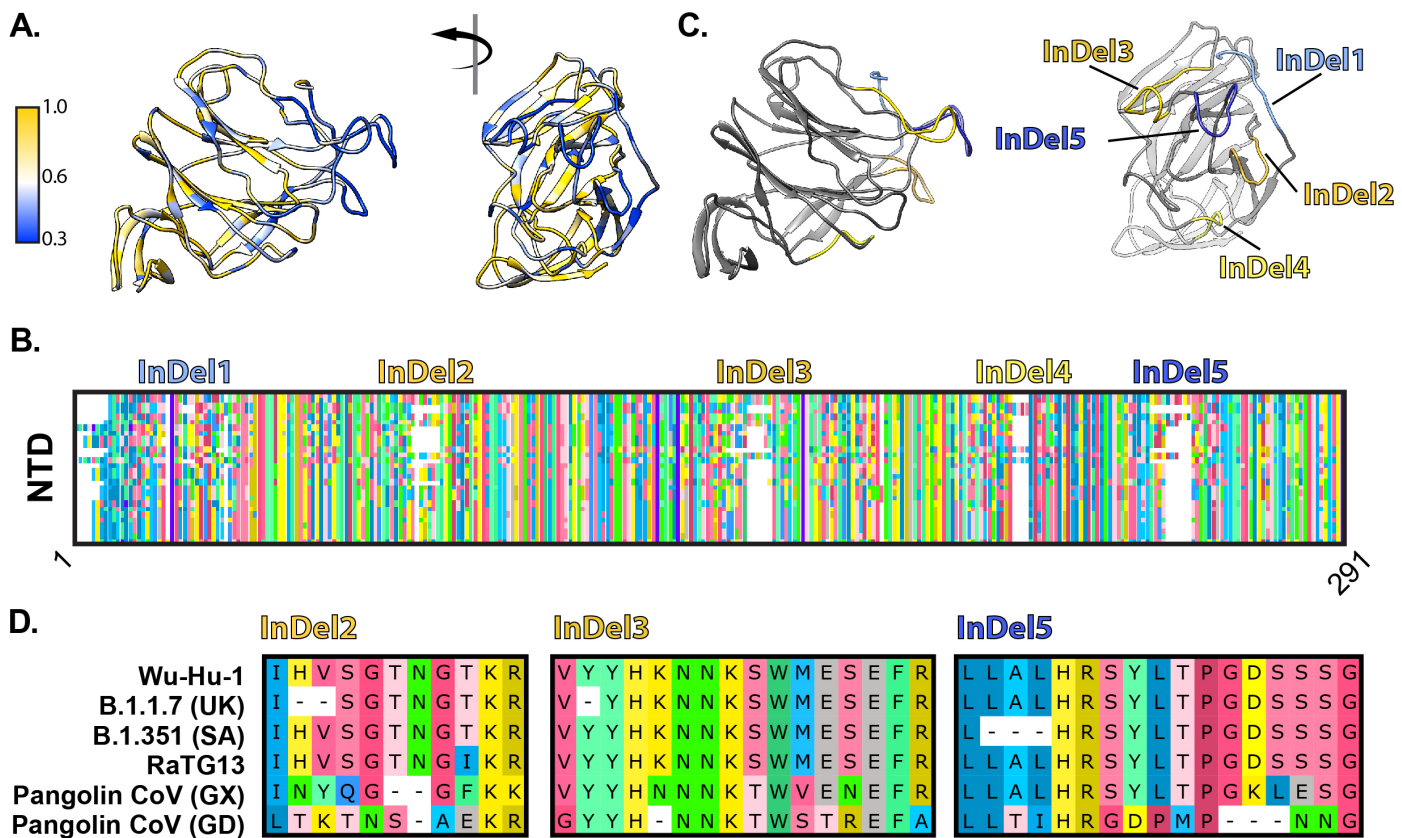
Figure S2. Sarbecovirus spike N-terminal domain contains InDel regions map to outwardly facing loops. A. Cartoon representation of a single N-terminal domain, shown from the side and en face, color coded for conservation, as denoted on the scale. **B.** Overview protein alignment of the spike N-terminal domain (residues 1-291 of SARS-CoV-2) from 28 diverse sarbecoviruses, residues color coded by amino acid identity. Annotations show the location of five regions of insertion/deletion (InDel), as defined by Garry et. al.. **D.** InDel regions map to outwardly facing loops on the NTD. **E.** Protein alignments demonstrating that current SARS-CoV-2 variants of concern and, closely related, Pangolin CoVs have deletions within InDel regions 2,3 and 5.