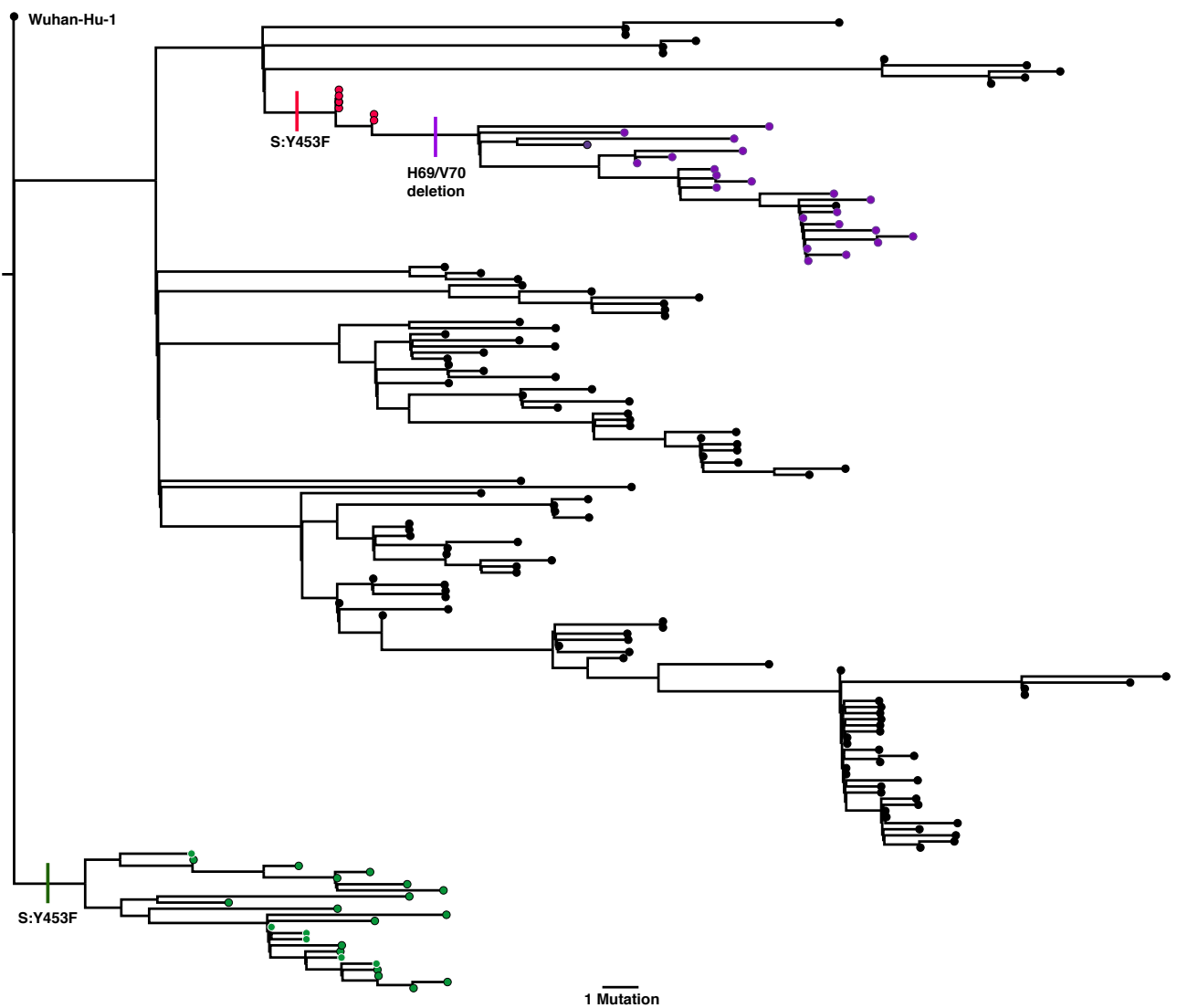
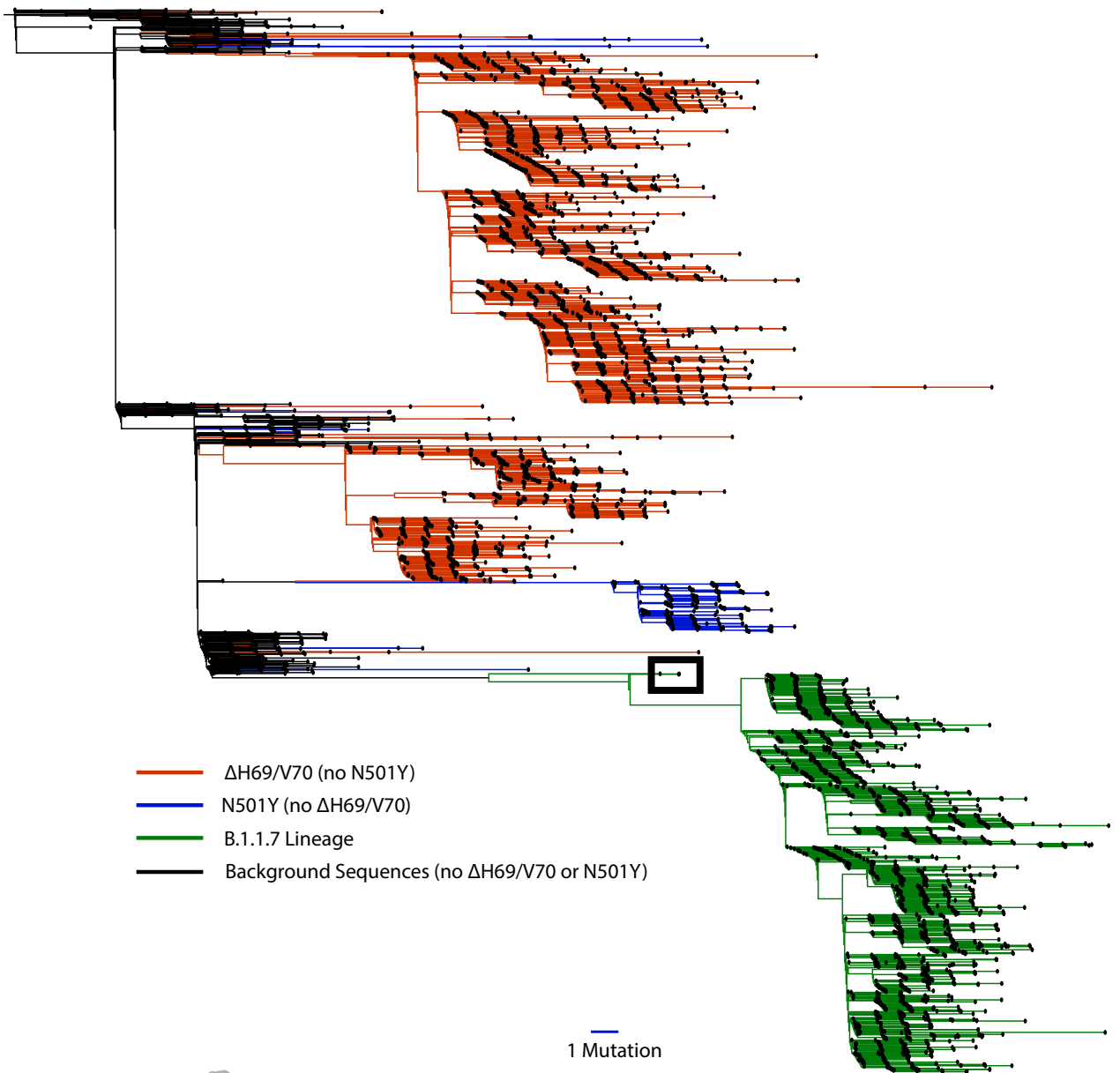


**Supplementary Figure 1. Circularised maximum likelihood phylogeny of global sequences carrying Spike mutant 439K.** All sequences in the GISAID database containing S:439K (3820 sequences, 26th November 2020) were realigned to Wuhan-Hu-1 using MAFFT. Viruses carrying the Spike double deletion  $\Delta$ H69/V70 (red) emerged and expanded from viruses with S:439K (black).

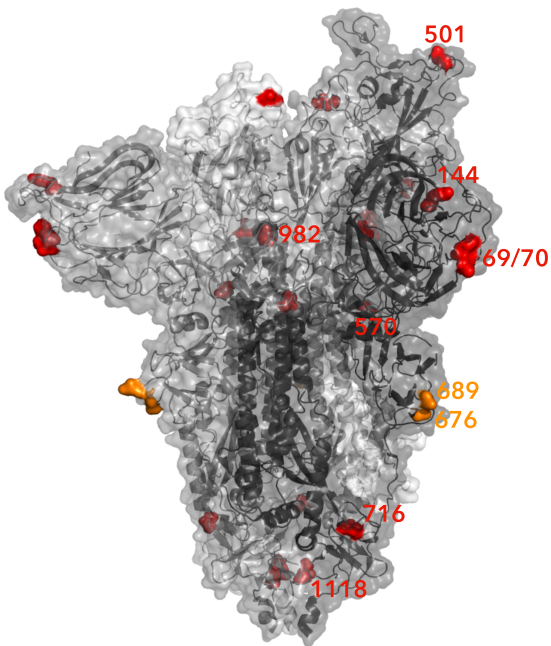


**Supplementary Figure 2. Maximum likelihood phylogenetic phylogeny of mink-origin SARS-CoV-2 sequences.** All 753 sequences in the GISAID database (accessed 14<sup>th</sup> December 2020) were downloaded and realigned to Wuhan-Hu-1 using MAFFT. Two distinct lineages carrying the mink-associated Spike Y453F mutations can be seen in Danish (red) sequences, with a separate lineage isolated only in Netherlands (green). After acquiring the Y453F mutation, Danish mink also appeared to acquire the Spike deletion  $\Delta$ H69/V70 (purple).

A



B



**Supplementary Figure 3. A. Lineages bearing Spike N501Y and  $\Delta$ H69/V70 mutations:** A sub-sampled global phylogeny of SARS-CoV-2 sequences bearing either the  $\Delta$ H69/V70 or N501Y mutations. Duplicate sequences were removed, and 200 randomly sub-sampled background sequences (without either mutation) were included to create a representative sub-sample of sequences. Distinct sub-lineages of the  $\Delta$ H69/V70 mutation are currently circulating, predominantly in the UK. The novel UK variant VOC 202012/01 (Lineage B.1.1.7, green) is also shown and in black box a related sequence carrying N501Y,  $\Delta$ H69/V70 and D1118H. **B. Surface representation of spike homotrimer in open conformation** with one upright RBD overlaid with ribbon representation (PDB: 6ZGG, Wrobel et al., 2020), with different monomers shown in shades of grey. The deleted residues H69 and V70 and the residues involved in amino acid substitutions (501, 570, 716, 982 and 1118) and the deletion at position 144 are coloured red on each monomer and labelled on the monomer with an upright RBD. The location of an exposed loop containing the furin cleavage site and including residue 681 is absent from the structure, though modelled residues either side of this loop, 676 and 689, are coloured orange.