Supplementary figures

Immagine che contiene schermata, testo, linea, Policromia

Descrizione generata automaticamente

**Supplementary figure 1:** Schematic representation of SARS-CoV-2 (color filled) and SARS-CoV-1 (striped) genomic sequences carrying ORF7a, ORF7b and/or ORF8 deletions.

In the enlargment are shown sequences carrying big deletions compared to Wuhan strain and our 426del.  From top to bottom, are represented: the reference sequence NC\_045512.2; 426 nt deletion found in this study; 382 nt deletion found in Singapore in 2020; 138 nt deletion found in Australian samples in 2020; 345 nt deletion found in Bangladesh samples in 2020; 62 nt deletion found in Spanish samples in 2020; 872 nt deletion found in Poland in 2021; 415 nt deletion found in SARS-CoV-1 in 2023. In yellow are shown the TRS. In sky-blue is represented ORF6 gene, in blue, ORF7a gene, in brown ORF7b gene, in pink is shown ORF8 gene and in green N gene. Deletions are represented as line: the 426 deletion here described is in red while others SARS-CoV-2 deletions are in blue. The last genome here represented is SARS-CoV-1 genome with a 415 nt deletion spanning between ORF7b and ORF8.

Immagine che contiene testo, schermata, diagramma, modello

Descrizione generata automaticamente

**Supplementary figure 2:** Protter predictions. (A) Prediction of Orf7b protein; (B) the hybrid peptide product resulting from the Orf7b and Orf8 426 deletion. Interestingly, the conformation of the peptide has predicted to be in an inverse configuration, with the N-terminal inside the membrane.