

Legends: Supporting material: Sequence comparisons in **Figures S1 to S13** have been submitted online alongside this manuscript. These alignments can be scrolled along their entire lengths.

Figure S1: *SARS-CoV-2 Wuhan-Hu-1 & HERV-E*; **Figure S2:** *SARS-CoV-2 Wuhan-Hu-1* and human chromosome 1, start position 11,783,698; **Figure S3 :** *SARS-CoV-2 Wuhan-Hu-1* and human chromosome 13, start position 34,882,059; **Figure S4 :** *SARS-CoV-2 Wuhan-Hu-1* and *Oryza sativa, chromosome 1*; **Figure S5:** *Bombus pascuorum* chromosome 14 vs. *Oryza sativa* chromosome 11; **Figure S6:** *Homo sapiens* mitochondrion, complete genome vs. *Latimeria chalumnae* mitochondrion; **Figure S7** *Mus musculus* strain C57BL/6J chromosome 19 vs. *Triticum aestivum* cultivar Chinese Spring chromosome 6D; **Figure S8:** *Mycobacterium tuberculosis* vs. *Oryza sativa* chromosome 8; **Figure S9:** *SARS-CoV-2 Wuhan-Hu-1 & Fig badnavirus*; **Figure S10:** *SARS-CoV-2 Wuhan-Hu-1 & Fig badnavirus 2*; **Figure S11:** *SARS-CoV-2 Omicron BA.1* different isolates; **Figure S12:** *Homo sapiens* chromosome 17 vs. *Lycium barbarum* isolate Lr01 chromosome 6; **Figure S13:** *SARS-CoV-2* vs. *Adenovirus type 12 (Ad12)* – See Graphical Abstract and manuscript page 35; **Figures S14 and S15:** In these experiments, shuffled SARS-CoV-2 sequences were aligned to certain unaltered sequences on human chromosomes 1 and 13, respectively. Details and the actual results of comparative sequence alignments have been presented in **Table 2**.

By scrolling through the alignments, the high degree of sequence identities in patchy patterns will be apparent. Further alignments of the *SARS-CoV-2* sequence with nucleotide sequences of additional species are available from the authors.