Supplementary Figure 7 . Schematic diagram of the workflow used to produce the data analysed in the study. Only thos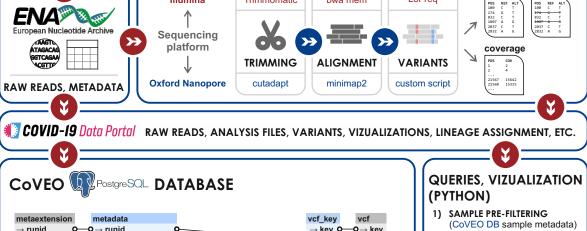e steps of the VEO variant calling pipeline (github.com/enasequence/covid-sequence-analysis-workflow) and features of the COVID-19 Data Portal (https://www.covid19dataportal.org/) are shown that are relevant to the current analysis. More details on both can be found in Rahman et al. (2023). For the CoVEO database, only those tables and fields are displayed that were queried during data processing. Queries, codes, data files and vizualizations are uploaded to the csabaiBio/SARSCoV2-coinf github repository.