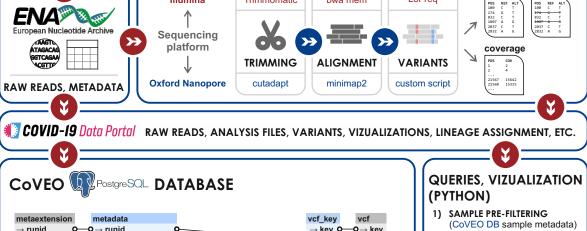
(github.com/enasequence/covid-sequence-analysis-workflow) and features of the COVID-19 Data Portal (https://www.covid19dataportal.org/) are shown that are relevant to the current analysis. More details on both can be found in Rahman et al. (2023). For the CoVEO database, only those tables and fields are displayed that were queried during data processing. Queries, codes, data files and vizualizations are uploaded to the csabaiBio/SARSCoV2-coinf github repository. UNIFIED VARIANT CALLING WORKFLOW VCF filtered VCF LoFrea **Trimmomatic** Illumina bwa mem POS 100 174 832 1807 ean Nucleotide Archive Sequencing

Supplementary Figure 7. Schematic diagram of the workflow used to produce the data analysed in the study. Only those steps of the VEO variant calling pipeline



→ runid O → runid → key O-O → kev description sample accession Orunid dp 2) CO-INFECTION SAMPLES first created experiment accession pos (CoVEO DB mutations) base_count study_accession ref collection date INTRA-HOST RECOMBINATION country n content collection date valid (CoVEO DB mutations (af) & \rightarrow id $b \rightarrow \text{runid}$ ocountry id **VARIANTS** raw reads from the COVID-19 country name estimated n content host id Data Portal) instrument id host instrument → id0 bi ← Ø csabaiBio/SARSCoV2-coinf host SAMPLE METADATA instrument platform instrument model