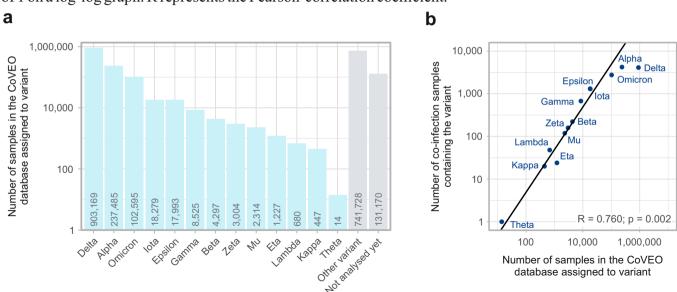
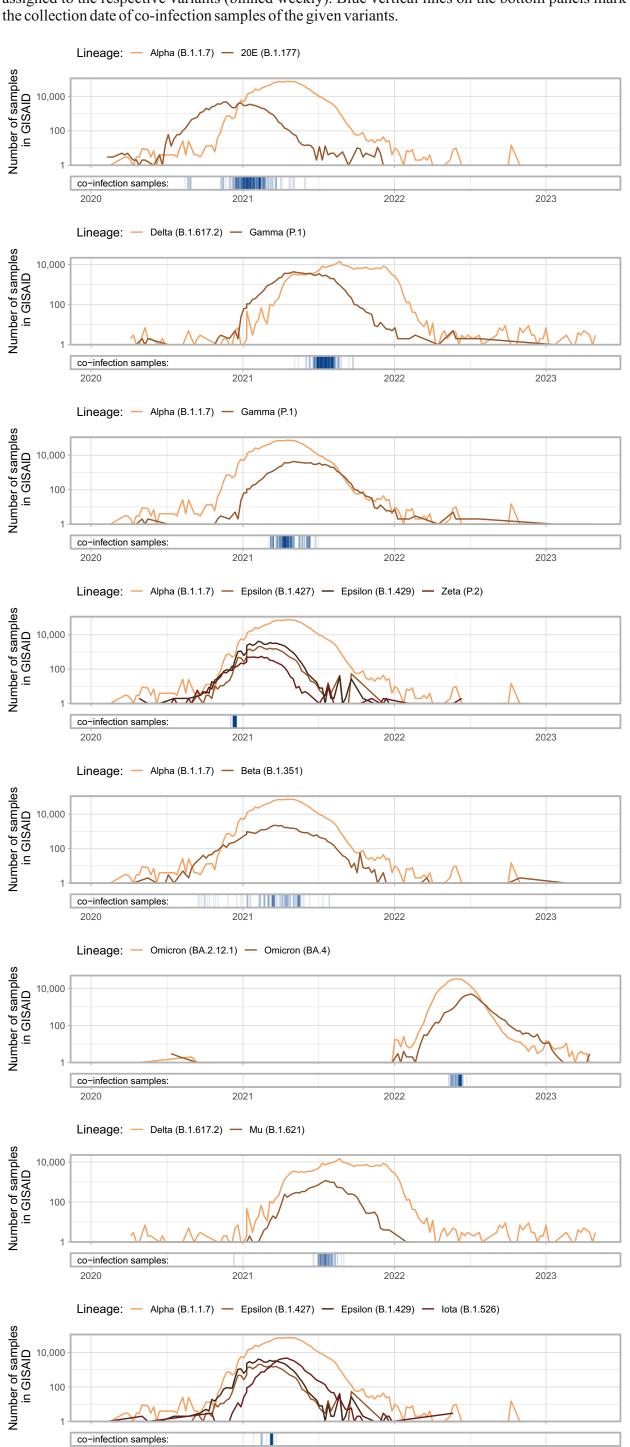
SARS-CoV-2 samples with a human host assigned to different variants in the CoVEO database. **b.** The relationship between the total number of samples assigned to a specific variant and the number of coinfection samples containing the variant. The straight black line represents a linear dependence with a slope of 1 on a log-log graph. R represents the Pearson-correlation coefficient.

Supplementary Figure 1. The number of samples in the CoVEO database. a. The number of good-quality



Supplementary Figure 2. Temporal distribution of co-infection samples for variant combinations with more than 50 samples. (The same figures for the top 4 most abundant combinations are shown in Figure 1C of the main manuscript.) Prevalence curves indicate the number of GISAID samples assigned to the respective variants (binned weekly). Blue vertical lines on the bottom panels mark the collection date of co-infection samples of the given variants.



co–infection samples (N = 4):

Kappa (B.1.617.1) - - B.1.1.318

Omicron (BA.2.12.1) - Omicron (BA.5) - Omicron (BA.4)

GISAID

2023

- - Mu (B.1.621)

- - B.1.617.3

2022

– Theta (P.3)

- - Omicron (BA.3) - - Eta (B.1.525)

- - B.1.623

collection date

– Lambda (C.37)– A.23.1

-- Beta (B.1.351) -- Gamma (P.1) -- AV.1

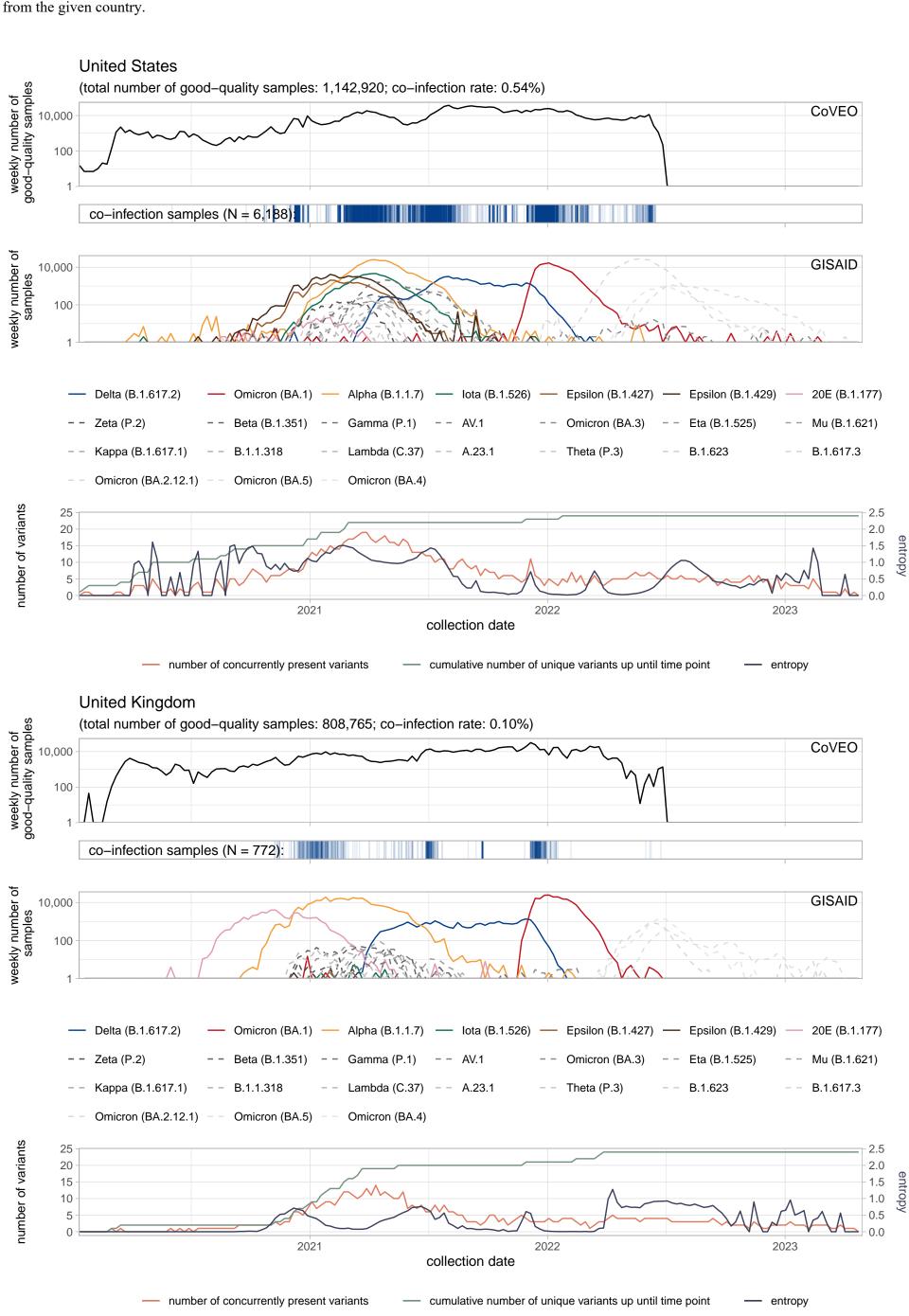
weekly number of samples

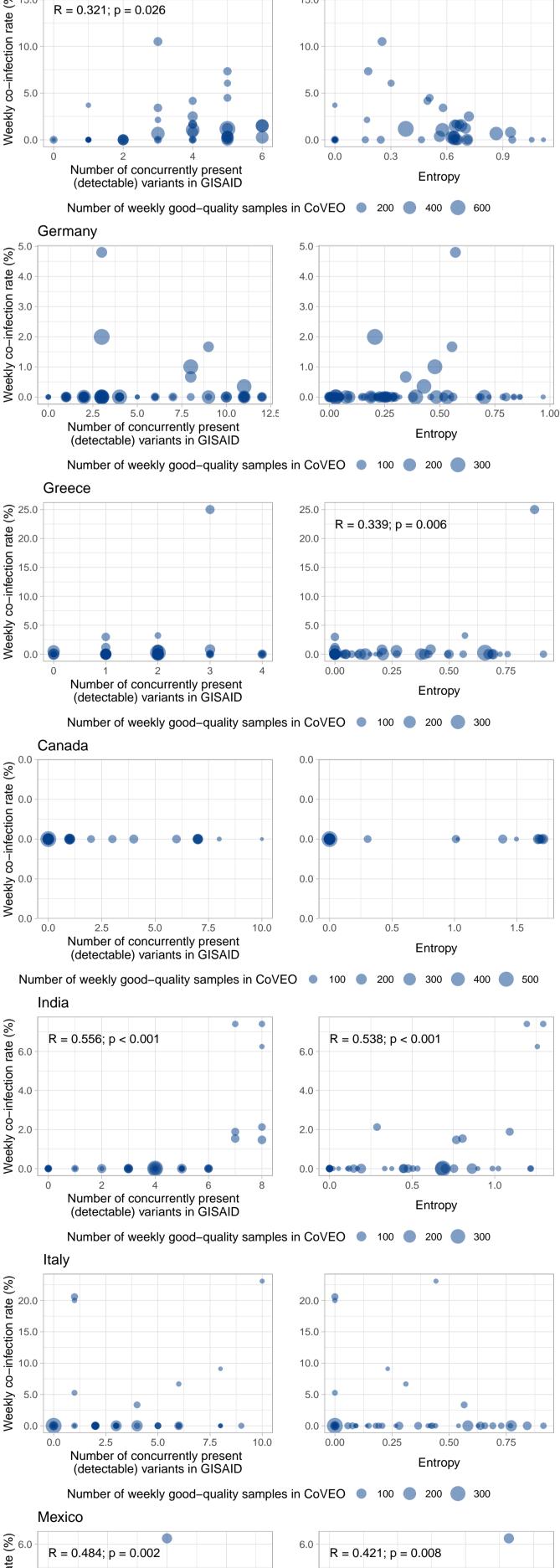
1,000

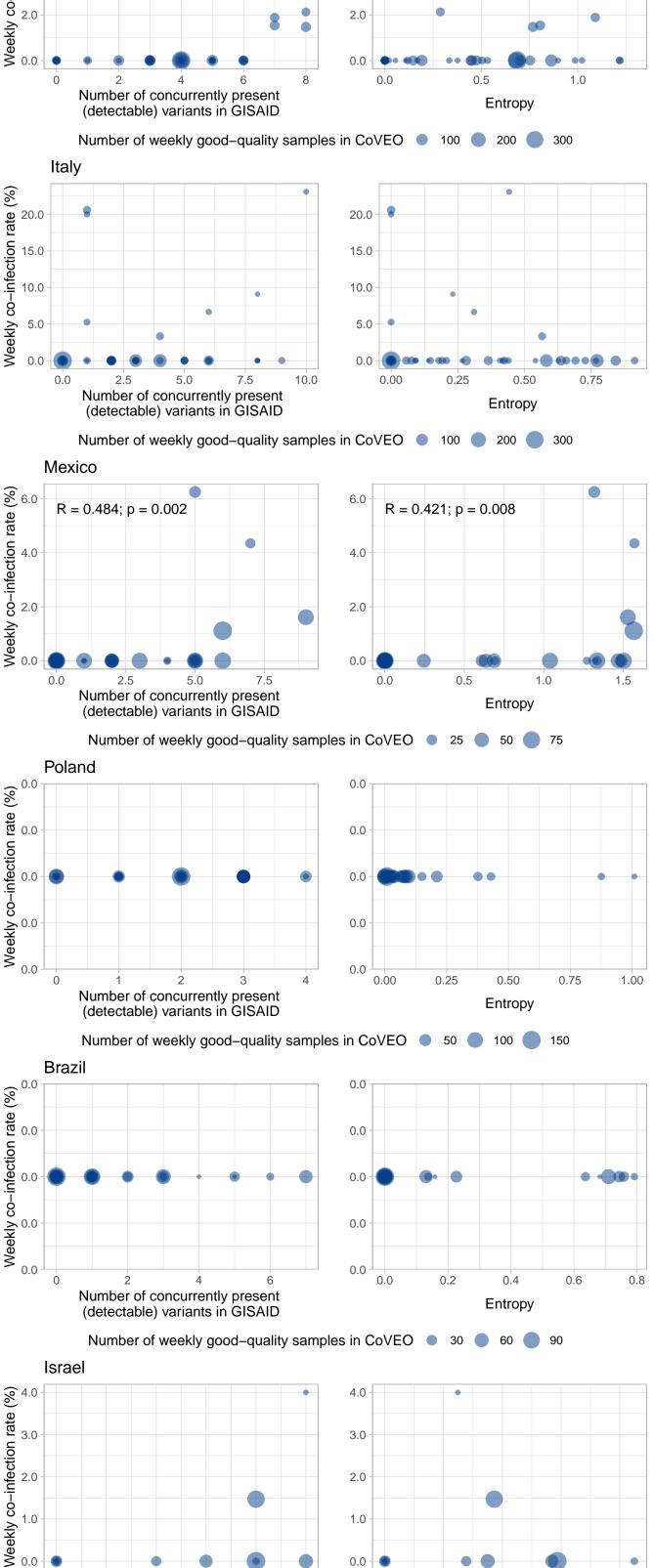
100

10

– Zeta (P.2)







0.0

0.1

50

0.2

100

Entropy

0.3

0.4

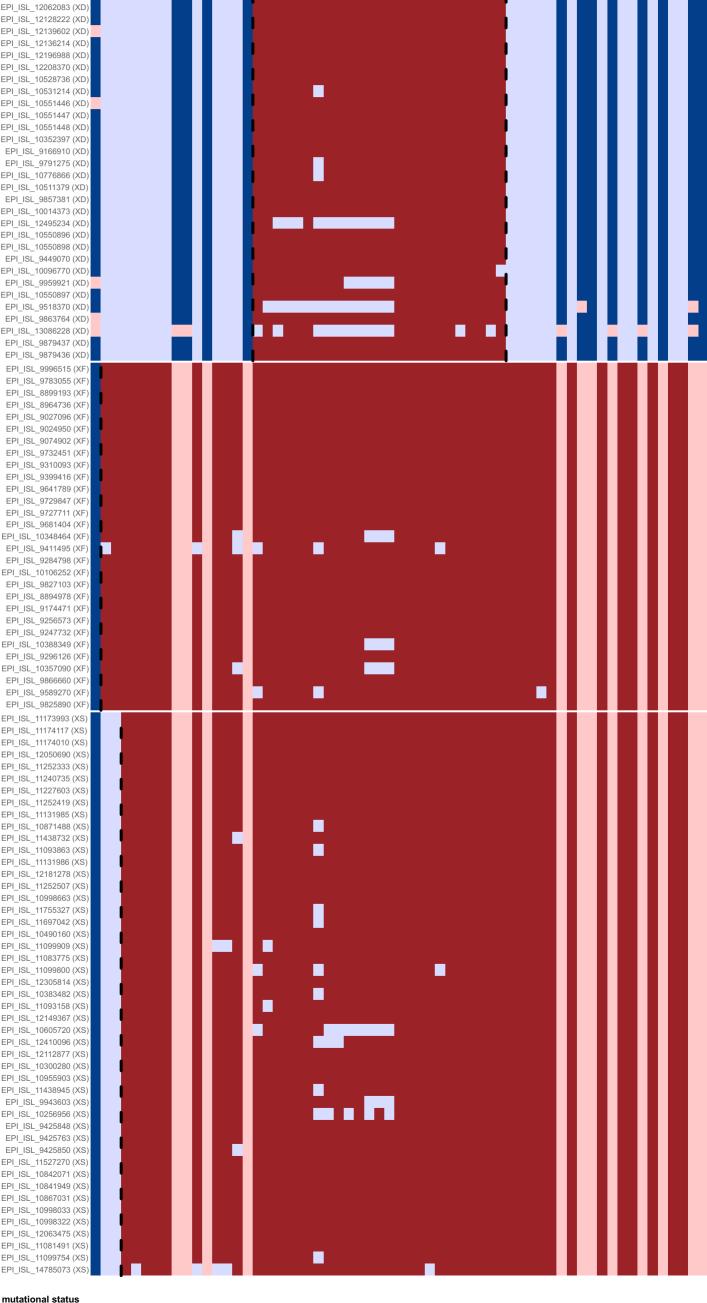
0

Number of concurrently present

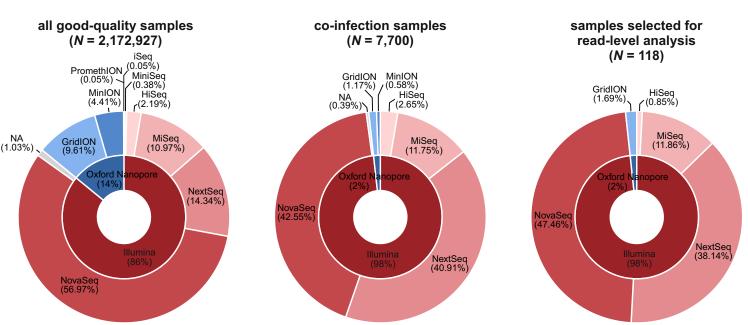
(detectable) variants in GISAID

Number of weekly good–quality samples in CoVEO •

Supplementary Figure 6. Disjunct defining mutations in GISAID samples assigned to the XD, XF and XS 'Deltacron' (recombinant Delta and Omicron) lineages. Samples (rows) are listed by their GISAID ID, with their Pango lineage indicated in brackets. Defining mutations (columns) are colored by their respective variant (blue for Delta and red for Omicron). Heatmap colors show whether the given sample contains the given mutation or not (dark blue: present Delta-mutation; light blue: missing Omicron-mutation; dark red: present Omicronmutation; light red: missing Delta-mutation). Dashed vertical lines mark the recombination breakpoint range(s) for each lineage. (The same genomic regions are indicated with red shaded areas in Figure 4 of the main manuscript.) 10449: C > A 1182: AGTTTGTCG > A 1186: T > C 15240: C > T 15451: G > A 14666: C > T 18163: A > G 21762: C > T 18163: A > G 21764: T > C 22178: G > A 22193: AMTD > A 22193: AMTD > A 22193: AMTD > A 22674: C > T 22674: C > A 22673: T > C 22674: C > T 22674: C > A 22674: C > A 22674: C > A 22675: T > C 23006: A > G 23040: C > A 23055: C > A 23065: A > C 23065: A > C 23065: A > C 23060: C > T 23070: C > A 2460: C > A 2460: C > A 2460: C > A 2460: C > A 25584: C > T 2560: C > T 2570: C > T 2570: C > T 2570: C > T 2750: C > T 2770: C > T EPI ISL 10819657 (XD) EPI_ISL_10210832 (XD) EPI_ISL_10207240 (XD) EPI_ISL_12062083 (XD) EPI_ISL_12128222 (XD) EPI_ISL_12139602 (XD) EPI_ISL_12136214 (XD) EPI_ISL_12196988 (XD) EPI_ISL_12208370 (XD) EPI_ISL_10528736 (XD) EPI_ISL_10531214 (XD) EPI_ISL_10551446 (XD) EPI_ISL_10551447 (XD) EPI_ISL_10551448 (XD) EPI ISL 10352397 (XD) EPI_ISL_9166910 (XD) EPI ISL 9791275 (XD) EPI_ISL_10776866 (XD) EPI ISL 10511379 (XD) EPI ISL 9857381 (XD) EPI_ISL_10014373 (XD) EPI_ISL_12495234 (XD) EPI_ISL_10550896 (XD) EPI_ISL_10550898 (XD) EPI_ISL_9449070 (XD) EPI_ISL_10096770 (XD) EPI_ISL_9959921 (XD) EPI_ISL_10550897 (XD) EPI ISL 9518370 (XD) EPI_ISL_9863764 (XD) EPI_ISL_13086228 (XD) EPI ISL 9879437 (XD) EPI ISL 9879436 (XD) EPI_ISL_9996515 (XF) EPI_ISL_9783055 (XF) EPI_ISL_8899193 (XF) EPI_ISL_8964736 (XF) EPI_ISL_9027096 (XF) EPI_ISL_9024950 (XF) EPI_ISL_9074902 (XF) EPI_ISL_9732451 (XF) EPI_ISL_9310093 (XF) EPI_ISL_9399416 (XF) EPI_ISL_9641789 (XF) EPI_ISL_9729847 (XF) EPI_ISL_9727711 (XF) EPI_ISL_9681404 (XF) EPI_ISL_10348464 (XF) EPI_ISL_9411495 (XF) EPI_ISL_9284798 (XF) EPI_ISL_10106252 (XF) EPI_ISL_9827103 (XF) EPI_ISL_8894978 (XF) EPI_ISL_9174471 (XF) EPI_ISL_9256573 (XF) EPI_ISL_9247732 (XF) EPI_ISL_10388349 (XF) EPI_ISL_9296126 (XF) EPI_ISL_10357090 (XF) EPI_ISL_9866660 (XF) EPI_ISL_9589270 (XF) EPI_ISL_9825890 (XF) EPI_ISL_11173993 (XS) EPI_ISL_11174117 (XS) EPI_ISL_11174010 (XS) EPI_ISL_12050690 (XS) EPI_ISL_11252333 (XS) EPI_ISL_11240735 (XS) EPI_ISL_11227603 (XS) EPI_ISL_11252419 (XS) EPI_ISL_11131985 (XS) EPI_ISL_10871488 (XS) EPI_ISL_11438732 (XS) EPI_ISL_11093863 (XS) EPI_ISL_11131986 (XS) EPI_ISL_12181278 (XS)



Supplementary Figure 7. Distribution of sequencing platforms and instruments within all good-quality samples included in the study, for co-infection samples and for samples selected for downstream read-level analysis.



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 platform coverage

Supplementary Figure 8. Schematic diagram of the workflow used to produce the data analysed in the study. Only those steps of the VEO variant calling pipeline (github.com/enasequence/covid-sequence-analysis-workflow) and features of the COVID-19



