

Supplemental Figure 4. Temporal distribution of co-infection samples and measures of genetic diversity for the countries with the largest numbers of co-infection samples (United States and United Kingdom). The top panels depict the number of samples in the CoVEO database collected each week from the appropriate country. The second panels show the collection date of co-infection samples identified in the given country. The third panels demonstrate the country-wise weekly prevalence curves of variants in the GISAID database that were included in the study. Coloured curves correspond to the most abundant variants in the whole set of detected co-infection samples (Delta, Omicron (BA.1), Alpha, Iota, Epsilon, 20E), while different shades of grey demonstrate the remaining lineages. On the bottom panel, various measures (the number of concurrently circulating lineages, the cumulative number of lineages and information entropy) of genetic diversity are plotted based on GISAID data from the given country.

