

Supplementary Figure 4. Weekly co-infection rate in the function of genetic diversity. Weekly co-infection rate was calculated as the percentage of co-infection samples out of all good-quality samples in the given country, in the given week. Genetic diversity was either defined as the number of lineages concurrently present in the given country in the given week in GISAID data (left panels) or the information entropy (right panels, see Methods). Only lineages investigated by the present study were considered. Weeks for which the number of good-quality samples in the CoVEO database did not reach 10 were discarded. Each marker represents the data for a single week. Marker size corresponds to the number of good-quality samples available. “R” and “p” indicate Pearson-correlation coefficients and respective two-sided t-test p-values (non-significant ($p \geq 0.05$) results are not displayed).

