**Supplementary Fig. 1.** All 32 patient cases in a SARS-CoV-2 hospital ward outbreak. Individual case numbers and letters indicating shared room are seen on the y-axis, and timeline of the outbreak period (days) seen on the x-axis. Bars show day of admission until discharge from the affected ward. Colors represent duration of shared room with another case and viral clade. Dots indicate time-point for sampling and stars represent symptom onset.

**Supplementary Fig. 2a-b.** Phylogenetic trees of SARS-CoV-2 sequences from a hospital ward outbreak with regional context. Trees were constructed using Neighbour-joining clustering and distances calculated using Jukes-Cantor with bootstrap 1000 in CLC Genomics Workbench. Colors indicate viral clades and sequence origin. a: Tree of viral sequences obtained by whole-genome sequencing (WGS) of 42 outbreak samples from 28 patients (blue dots), 14 health care workers (HCW; red dots) and 84 patients simultaneously sampled in regional primary health care centers (community; black dots). b: Detailed tree of viral sequences from the outbreak of 28 patients (blue dots) and 14 HCWs (red dots), indicated by their individual outbreak case numbers. Bootstrap values are represented by numbers on tree branches.