



Figure 1 Phylogenetic analysis
A) Scattered distribution of sequences obtained in this study among other 2484 publicly available SARS-CoV-2 sequences, indicating widespread circulation in the community. Sequences derived from patients in blue and from health-care workers in red. **B)** Close-up of cluster 2 of 2 HCW I05 and I09 with most likely transmission from patient P32. **C)** Close-up of HCW I02 with most-likely transmission from the community. **D)** Close-up of cluster 1 with 6 HCW without a direct link to a specific patient.