

Supplemental Figures

to

PathoSPOT genomic epidemiology reveals under-the-radar nosocomial outbreaks

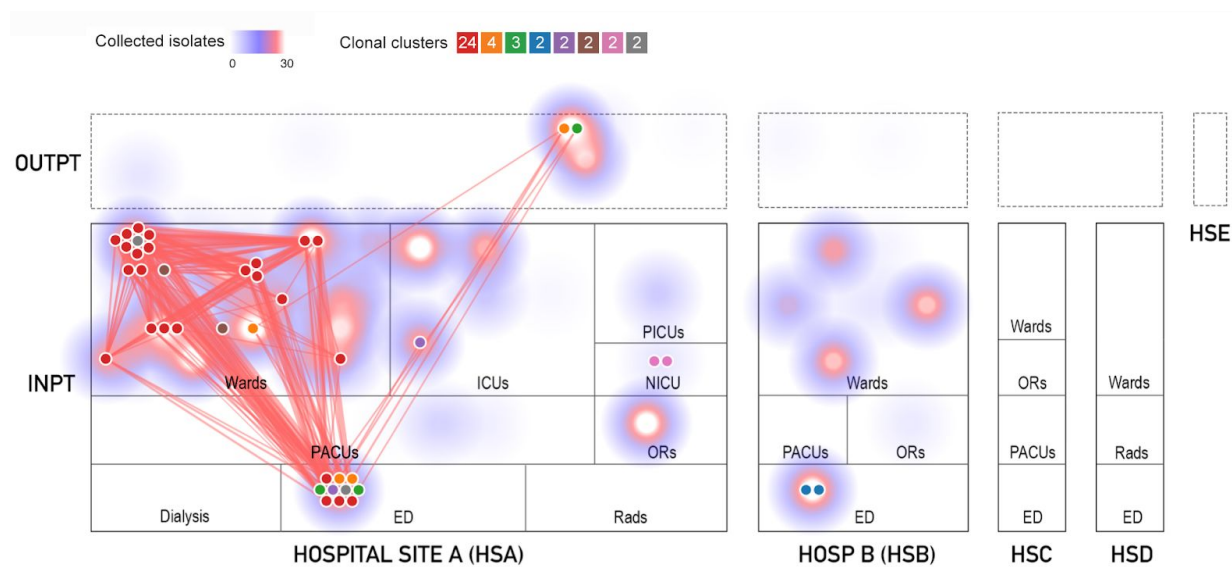


Fig. S1. Network layout view of clonal clusters

The PathoSPOT network layout shows spatial relationships among patients in each of the 8 clusters, using the threshold of ≤ 15 SNVs across the entire 24 months of the dataset, and only the first related isolate from each patient. Nodes are colored by clonal cluster, as indicated in the legend at top center, which also lists the numbers of nodes in each cluster. Nodes are laid out spatially by hospital and ward where the patient was sampled, with ward types grouped together (labeled boxes), and nodes from the same ward placed adjacent to one another (the position of each anonymized ward within the box is arbitrary). Genomic links underneath the threshold are depicted as red lines, with many clusters spread across different wards and ward types. Underneath the network map, the total number of positive cultures collected from each location is depicted as a shaded density plot, with the color scale depicted at top left; this highlights heavily sampled locations. An interactive version of this figure is available at <https://pathospot.org/?fig=S1>.

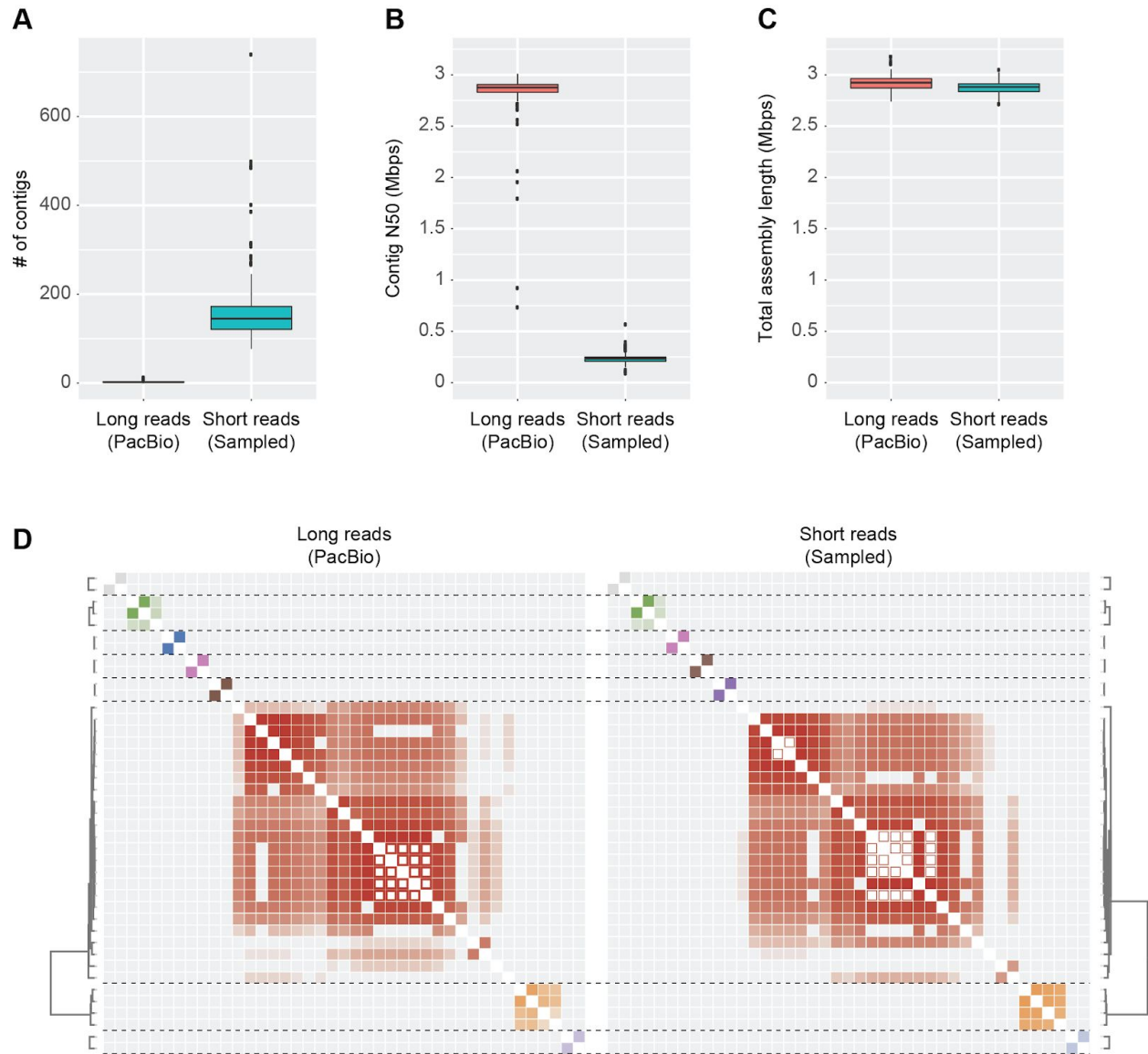
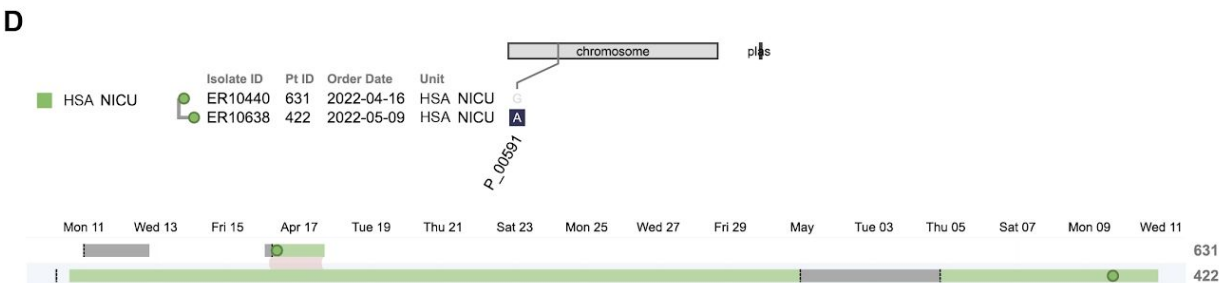
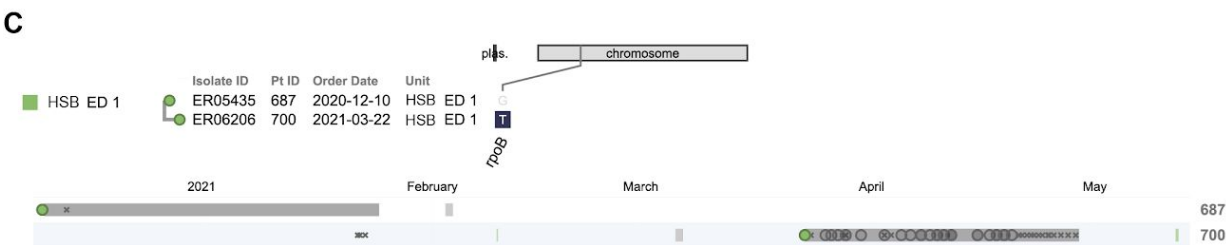
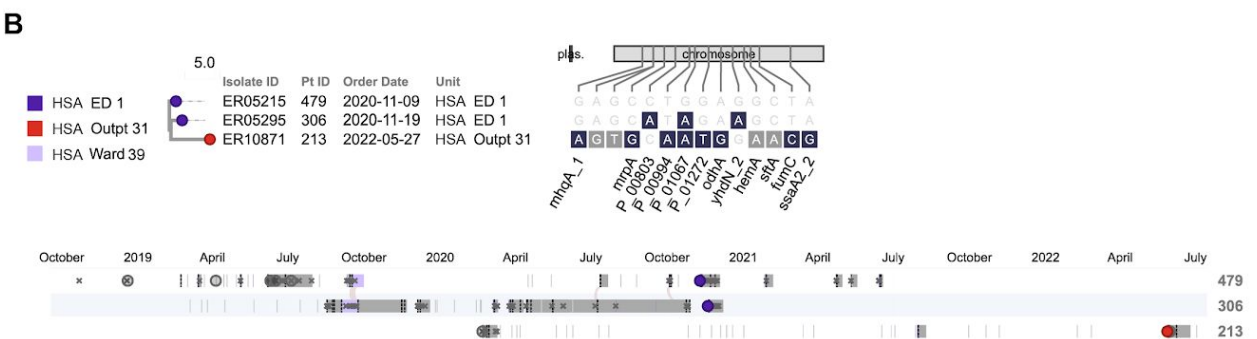
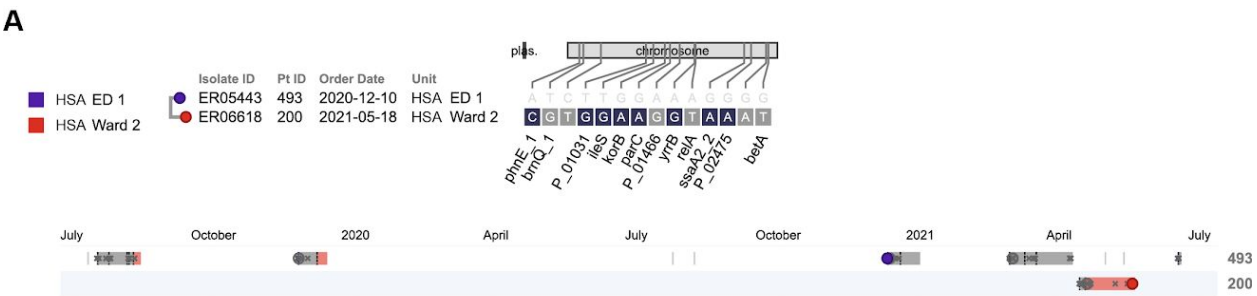


Fig. S2. Comparison of PathoSPOT analysis of long-read and short-read assemblies

Box plots comparing the total number of assembled contigs **(A)**, the contig N50 **(B)** and the total assembly lengths **(C)** for PacBio long read and sampled paired-end short-read assemblies for all study isolates. **(D)** Heatmaps of pairwise core genome SNP distances between clustered isolates based on complete long-read assemblies (left) vs. fragmented short-read assemblies (right). Horizontal dashed lines demarcate cluster boundaries at a maximum pairwise distance of 15 SNVs and show that the same clonal clusters are obtained for PathoSPOT analyses of long- and short-read assemblies (note that different colors are assigned to the same cluster in each analysis due to differences in the order of assignments).



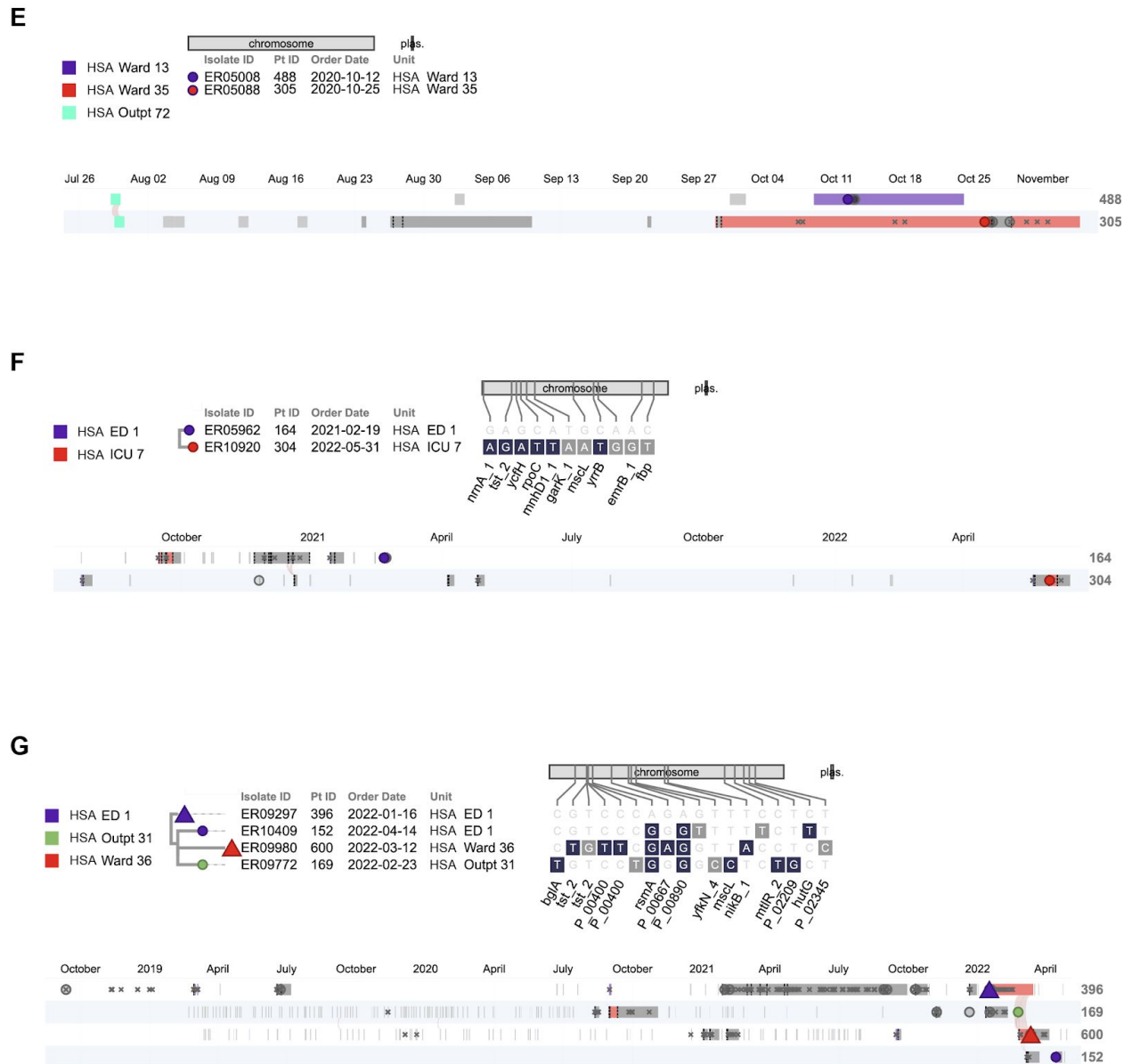


Fig. S3. Other clonal clusters identified by PathoSPOT analysis

Phylogenetic trees of core genomes and epidemiologic timelines created by the “dendro-timeline” visualization in PathSPOT for the seven smaller clonal clusters identified in our study (**A-G**). Layout and drawing conventions are as in Figures 3A and B. All date information in this figure was recoded to protect health information. Each of the clusters presented in this figure can be explored via links from the cluster legend (next to “8 clusters detected”) at <https://pathospot.org/?fig=2>.