Figure S3. Divergence tree and zoom into additional sequence clusters, which did not result in large community spread. A. Isolates from Basel area cohort in global context. B. A small clade assigned to B.1.5 consists of two clusters with an accumulation of samples from Basel. C. Cluster within lineage B.1.8 with two Basel samples without known epidemiological link. D. Two family cluster within lineage B.2 that did not spread further into the Basel community.