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.