

Supplemental Figure 2. Maximum-likelihood phylogenetic tree constructed with sequences from index cases (n=38), partners (n=34), and reference sequences sampled in North Carolina (n=1672). Index cases are indicated by red circles at tips, partners are indicated by squares at tips, and reference sequences have no tip shape. Numbers at tips indicate year of sequence sampling. For clades involving index cases with high branch support (>90%) are labeled. Transmission clusters involving index cases are shaded and labeled (A-M). Clades involving only reference sequences are collapsed.

