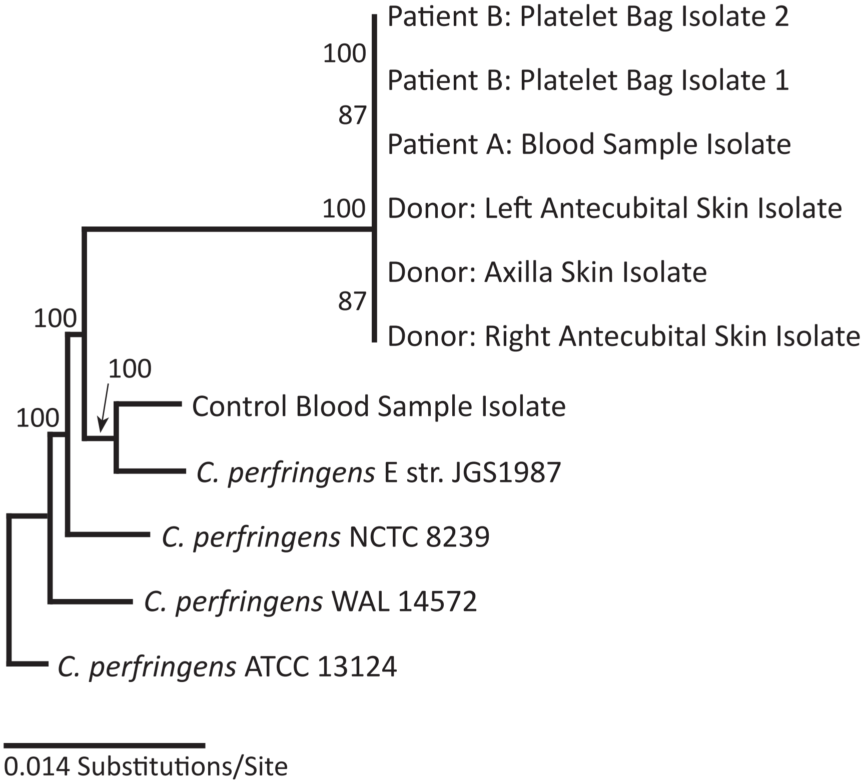
SUPPLEMENTARY FIGURE 1. Maximum likelihood phylogenetic tree of *Clostridium perfringens* isolates — Utah, August 2017



Note: Maximum likelihood phylogenetic tree was generated using 2,016 concatenated shared homologous protein coding genes. The figure includes four *C. perfringens* strains named E str. JGS1978, NCTCX 8239, WAL 14572, and ATCC 13124 which are unrelated to the outbreak and are used to root the phylogenetic tree and give context to the outbreak isolates.