

Supplementary

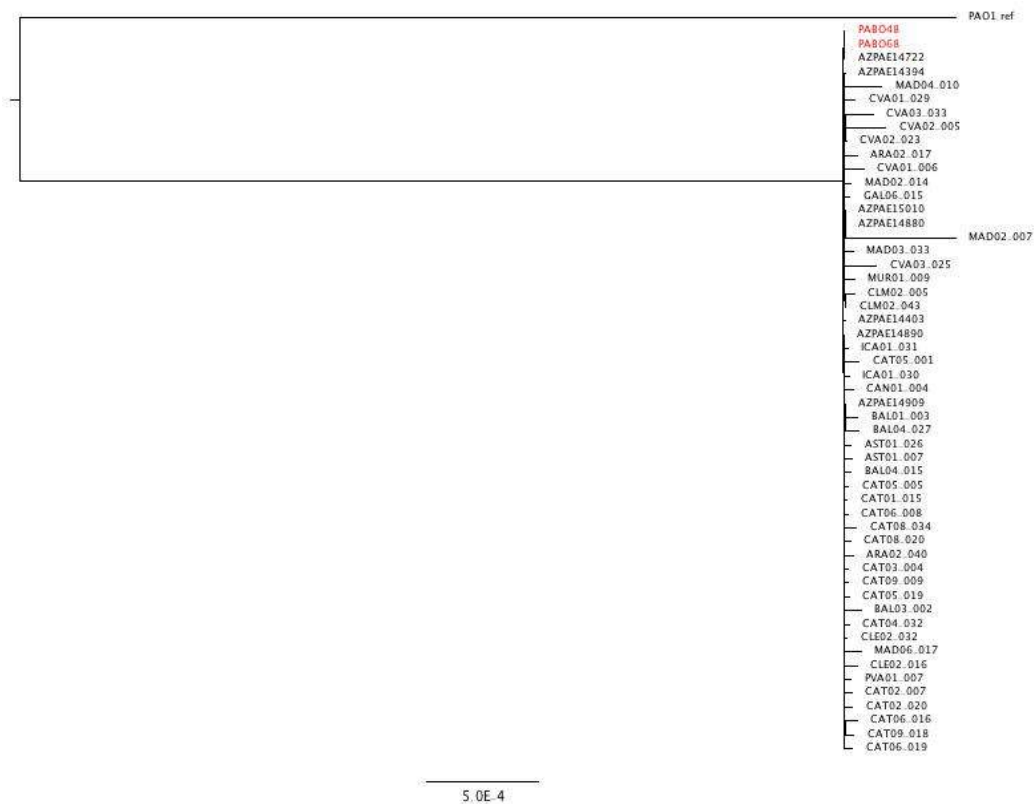


Figure S1. Maximum likelihood phylogenetic tree based on the SNPs in the core genomes of ST175 *Pseudomonas aeruginosa* clinical strains. Strains associated with transmission event described in this study are highlighted in red.

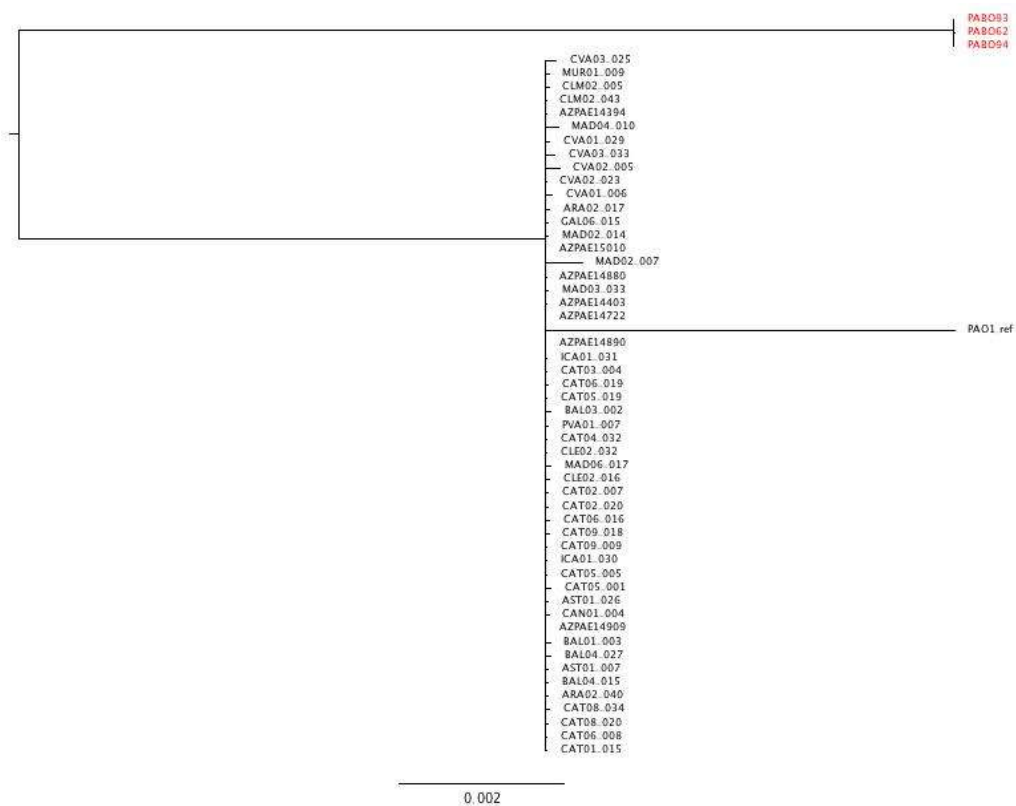


Figure S2. Maximum likelihood phylogenetic tree based on the SNPs in the core genomes of ST235 *Pseudomonas aeruginosa* environmental strains. Strains associated with transmission event described in this study are highlighted in red.