

Clonal background and routes of plasmid transmission underlie antimicrobial resistance features of bloodstream *Klebsiella pneumoniae*

Odion O. Ikimiukor, Nicole I. Zac Solingo, Ifeoluwa J. Akintayo, Michael M. Marcovici, Stephanie S. R. Souza, Adrienne Workman, Isabella W. Martin, Cheryl P. Andam

Supplementary Information

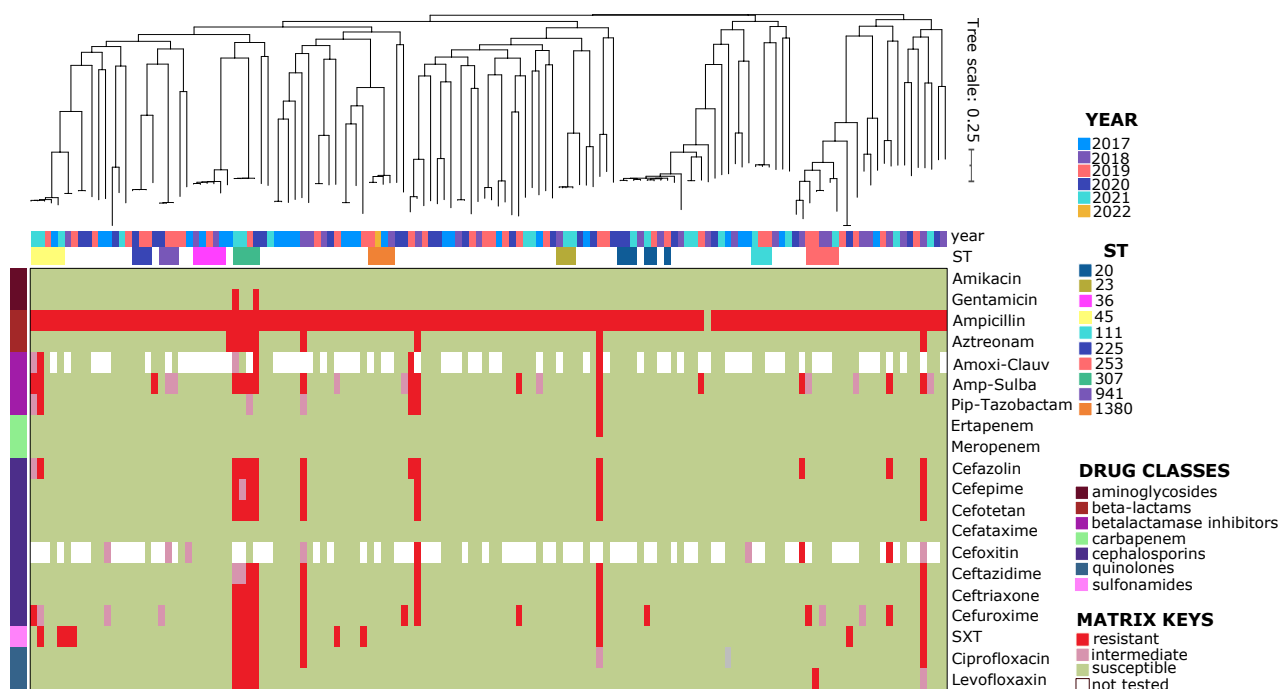


Figure S1. Matrix showing drug susceptibility profiles of *K. pneumoniae* strains in this study. Antimicrobial susceptibility profiles are reported as resistant, susceptible, or intermediate using interpretative breakpoints from CLSI (Clinical and Laboratory Standards Institute, 2021). Horizontal bars show year of isolation and sequence types (ST) represented by 3 or more isolates. Vertical bars show drug classes of antimicrobials tested.

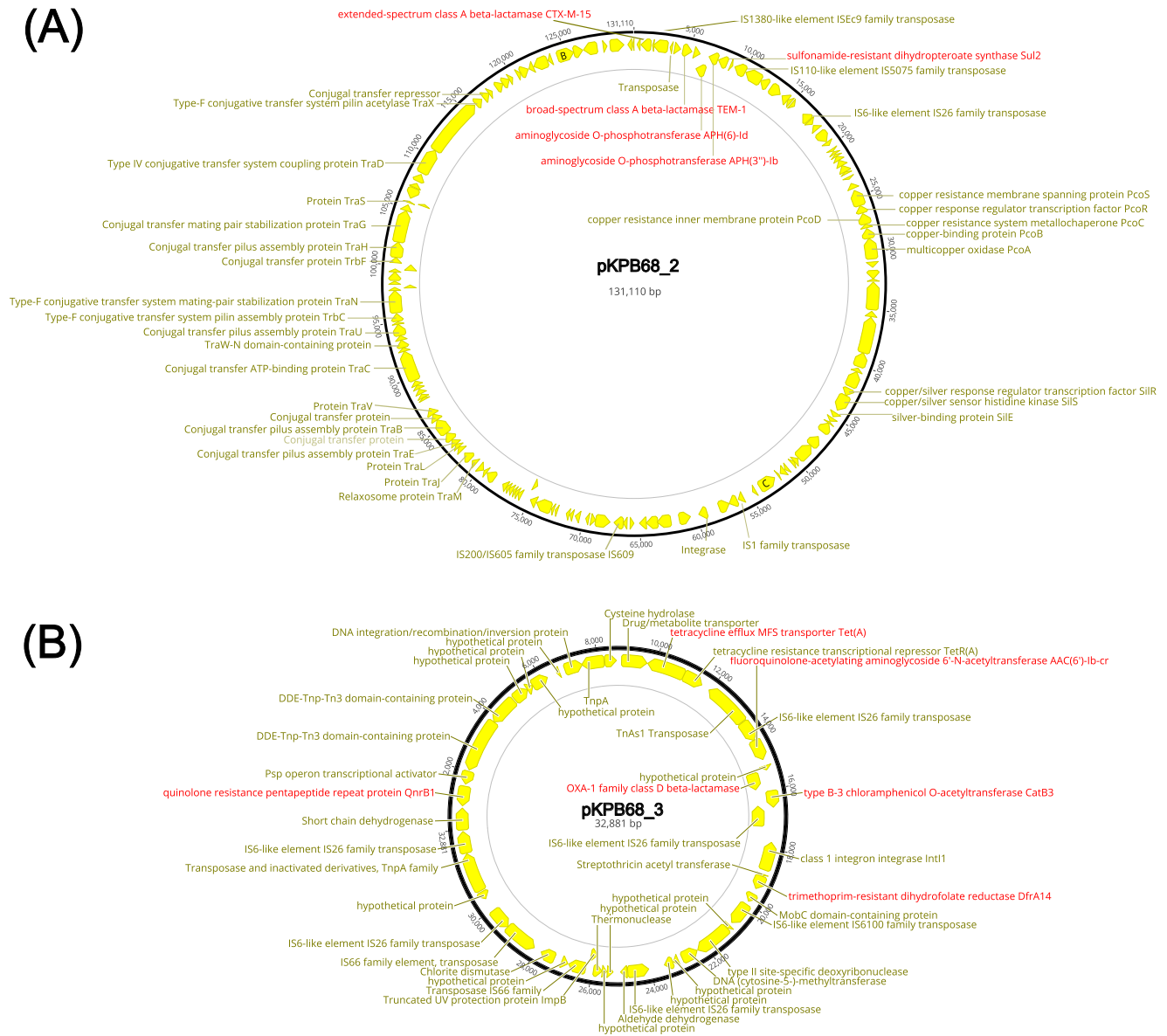


Figure S2. Annotation of the multidrug resistance plasmids. (A) pKPB62_2 and (B) pKPB68_3. Antimicrobial resistance genes are shown in red text and other genes in black text. The plasmids were sequenced using Oxford Nanopore Technologies GridION.

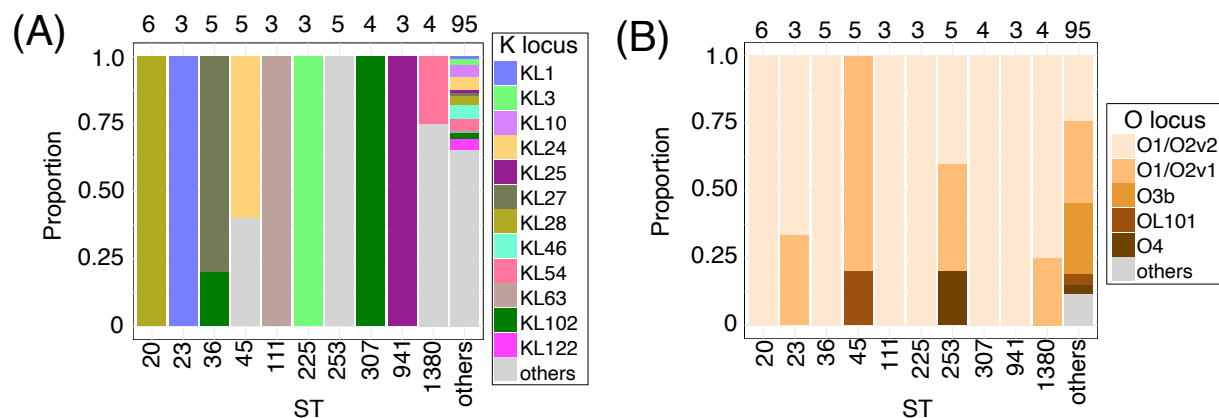


Figure S3. Distribution of the surface polysaccharide capsule (KL) and lipopolysaccharide (O) that determine the antigenic serotypes. (A) Distribution of KL types by sequence type (ST) in bloodstream *K. pneumoniae* in this study. (B) Distribution of O types by ST in bloodstream *K. pneumoniae* in this study. Less common types are grouped together in the category “others”.

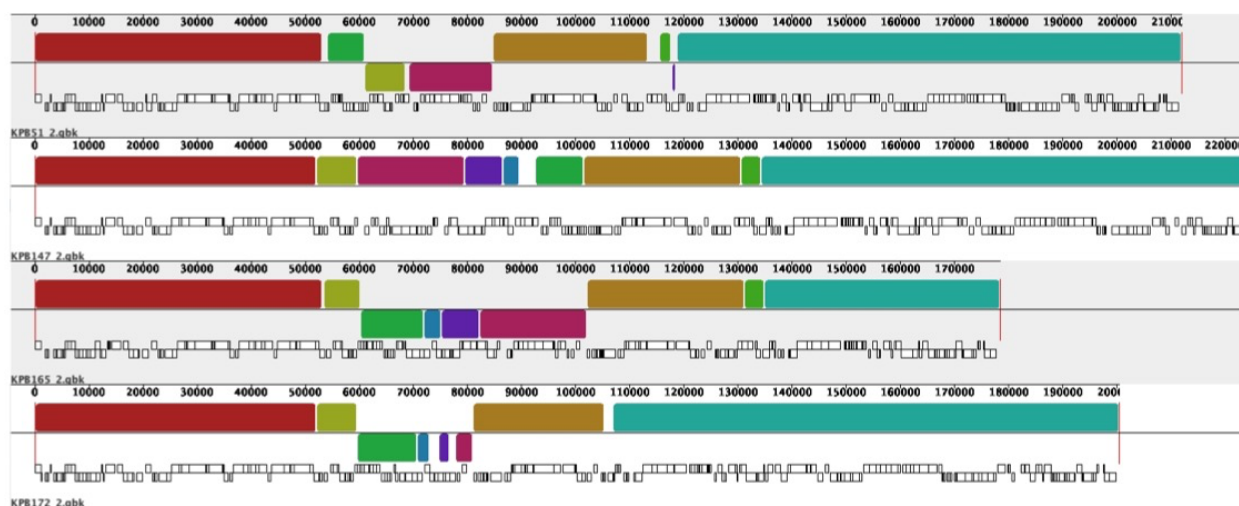


Figure S4. MAUVE generated map of the four hypervirulence *K. pneumoniae* plasmids in this study. Colored block shows homology that exists between plasmid genomes. The plasmids were sequenced using Oxford Nanopore Technologies GridION.

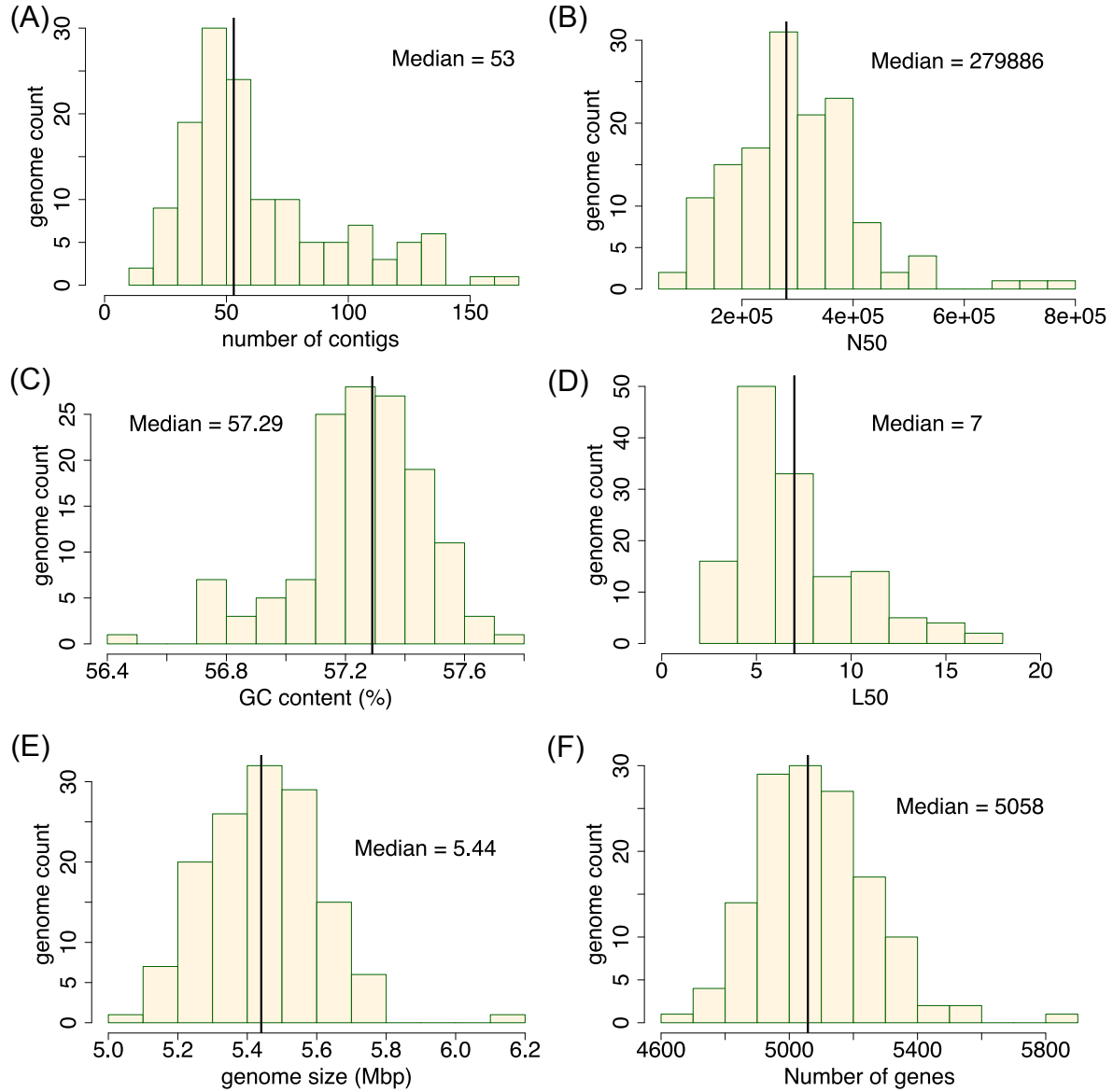


Figure S5. Genome quality metrics of 136 Illumina-sequenced *K. pneumoniae* genomes in this study. (A) number of contigs, (B) N50, (C) G+C content, (D) L50, (E) genome size, (F) number of genes.

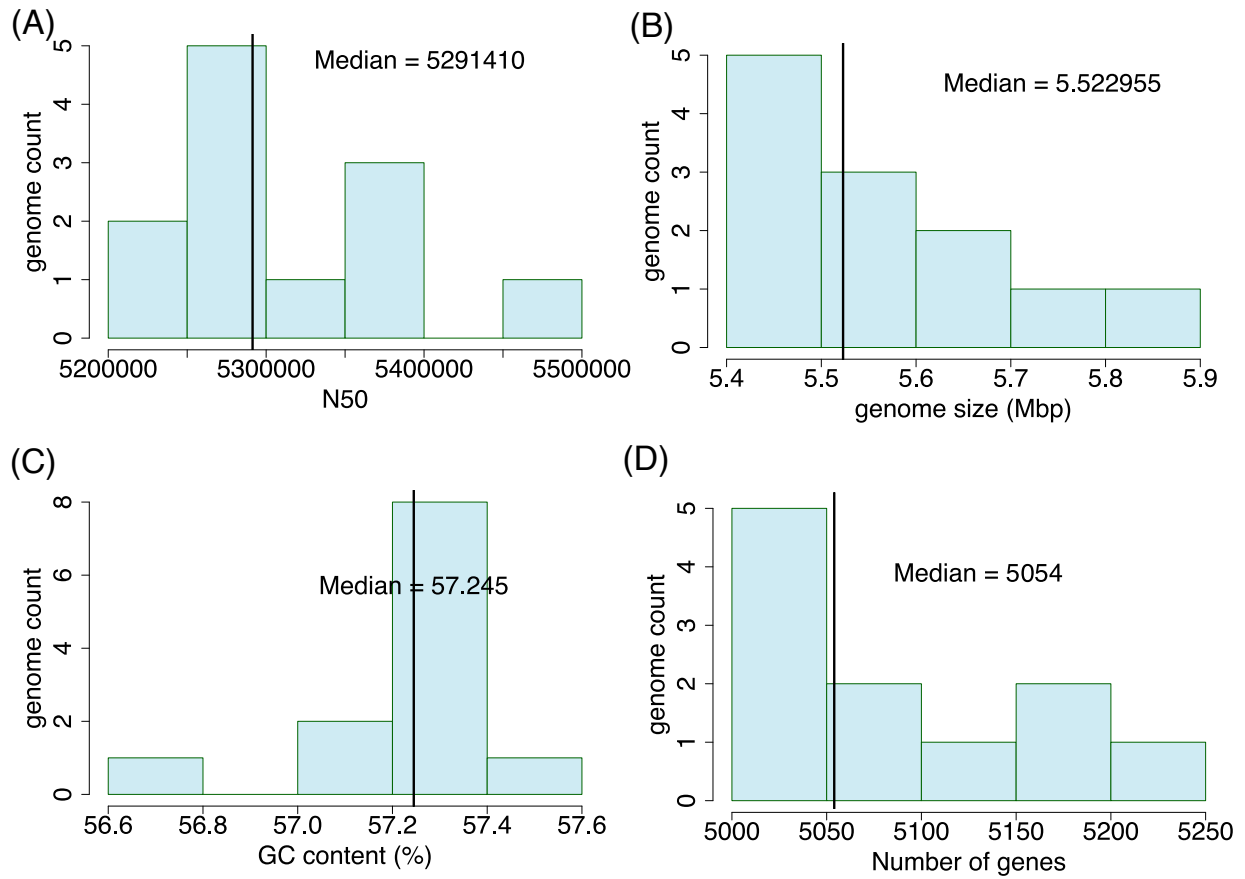


Figure S6. Genome quality metrics of 12 *K. pneumoniae* genomes sequenced using Oxford Nanopore Technologies GridION in this study. (A) N50, (B) genome size, (C) G+C content, (D) number of genes