Supplemental Materials

Table S1. Statistics of metagenome sequencing and quality control for the samples used in this study.

Table S2. List of reference genomes of *K. pneumoniae* species complex used in this study.

Table S3. Summary of gene family presence and absence in the *K. pneumoniae* pangenome of 30 metagenome-reconstructed strains.

Table S4. Summary of COG-based functional classification of *K. pneumoniae* pangenome gene families.

Table S5. Distribution of antimicrobial resistance genes in the metagenome-reconstructed strains of *K. pneumoniae*.

Table S6. Distribution of virulence-associated genes in the metagenome-reconstructed strains of *K. pneumoniae*. 