

Figure S1 (A) Diagram of Type IV-A CRISPR system structure. (B) Distribution of Type IV-A system across MLST in *Klebsiella pneumoniae*. The purple lines denote the presence of Type IV-A system in strains. Large and short lines represent intact and degenerated CRISPR system, respectively. The major STs are highlighted in different colors.

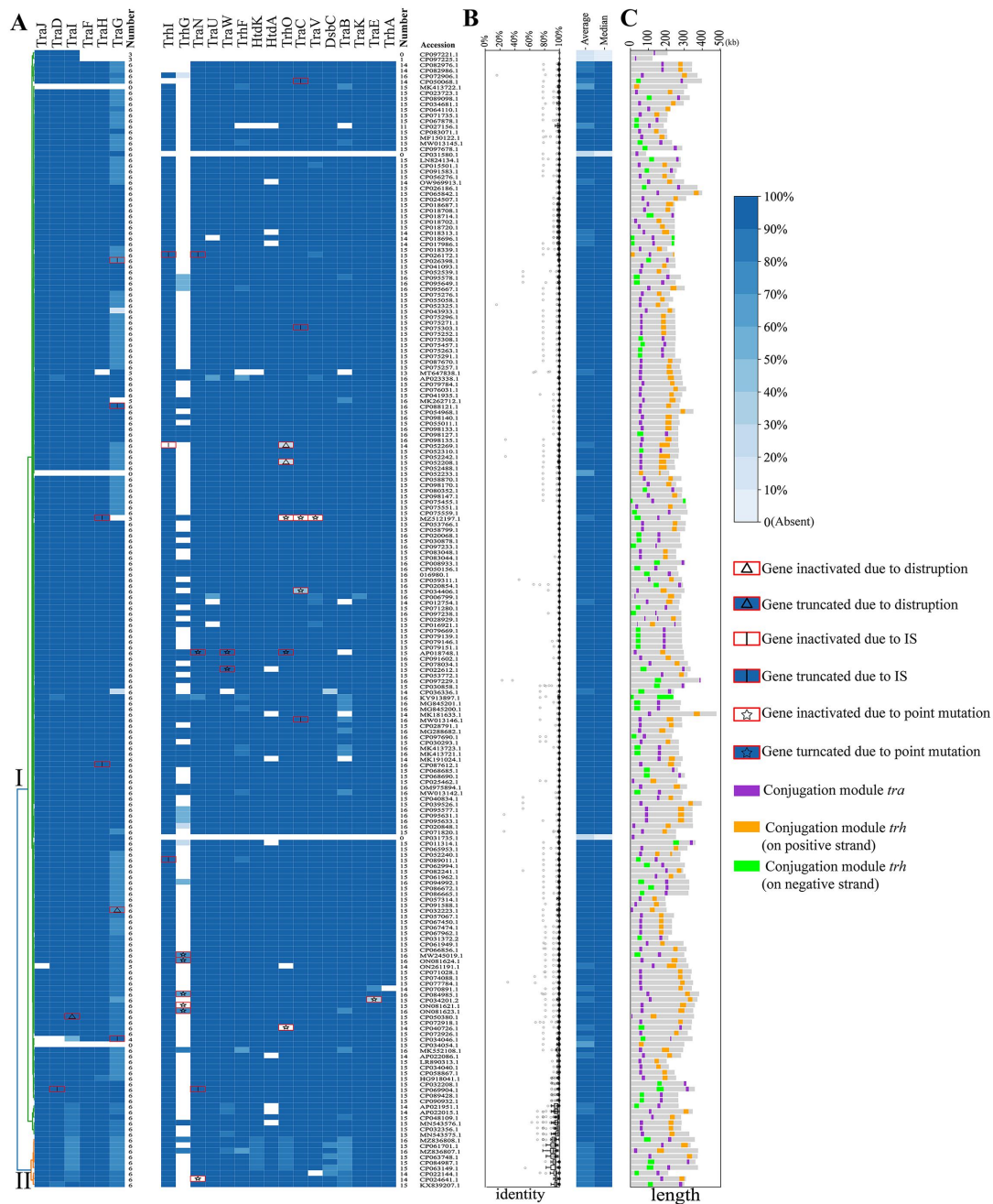


Figure S2 Comparison of the conjugation transfer proteins of CRISPR-harboring plasmids.

(A) Homology matrix of the conjugation transfer proteins. The color gradient represents identities at the amino acid level to pNDM-MAR conjugation proteins. Genbank accession number for each plasmid is marked on the left. (B) Box plot of the identity distribution of each conjugation protein. The corresponding median and average values are shown at the right, using the same color gradient scheme. (C) Positions of the conjugation modules. The *Tra2* cluster orientations are colored in orange or green. The *TraI* region are colored in purple, regardless of orientation.

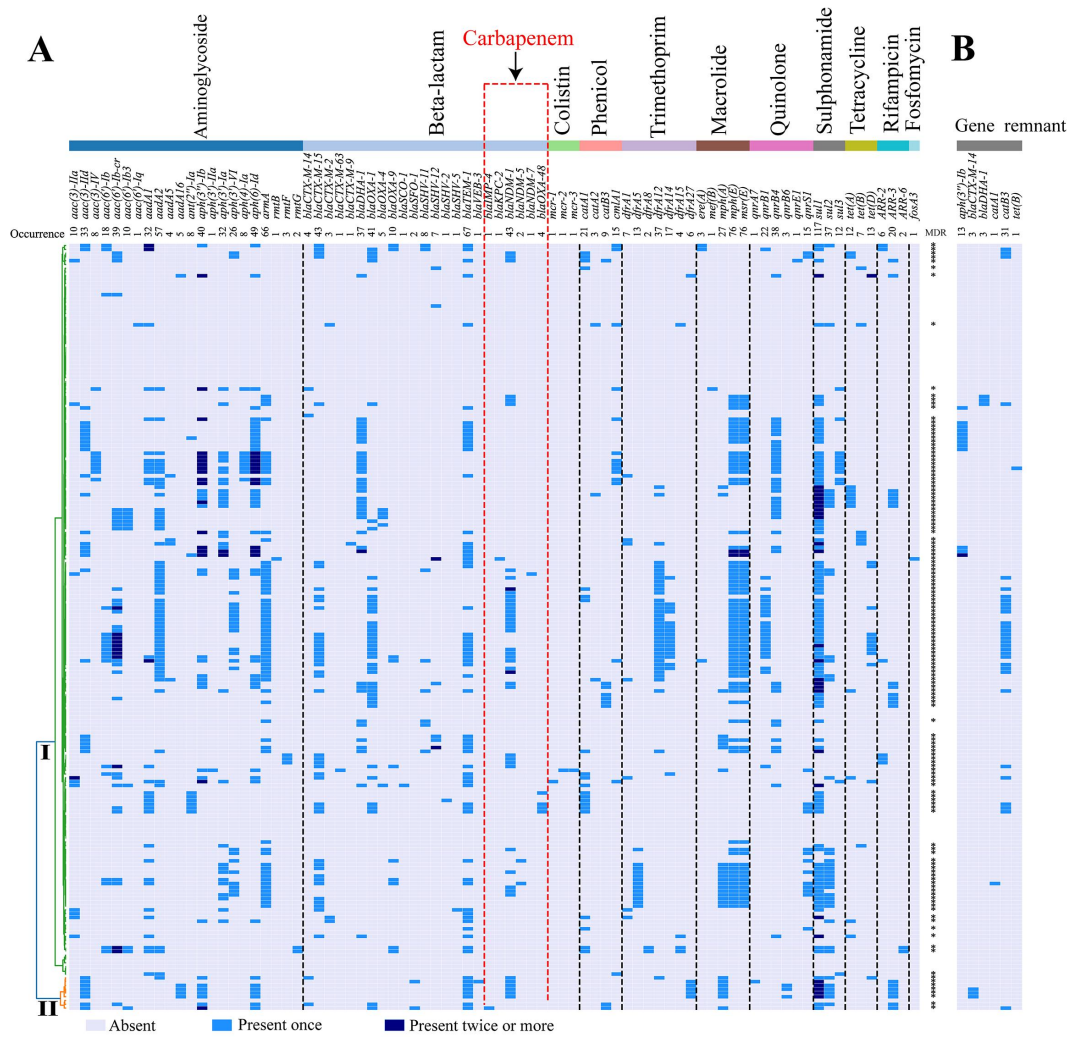


Figure S3 ARG profiles of all 203 CRISPR-positive plasmids. (A) Profiles of intact ARGs. The antibiotic classes of ARGs are denoted by different colors. The MDR plasmids are indicated by an asterisk. The occurrences of each ARG among these plasmids are shown. (B) Profiles of truncated ARGs.

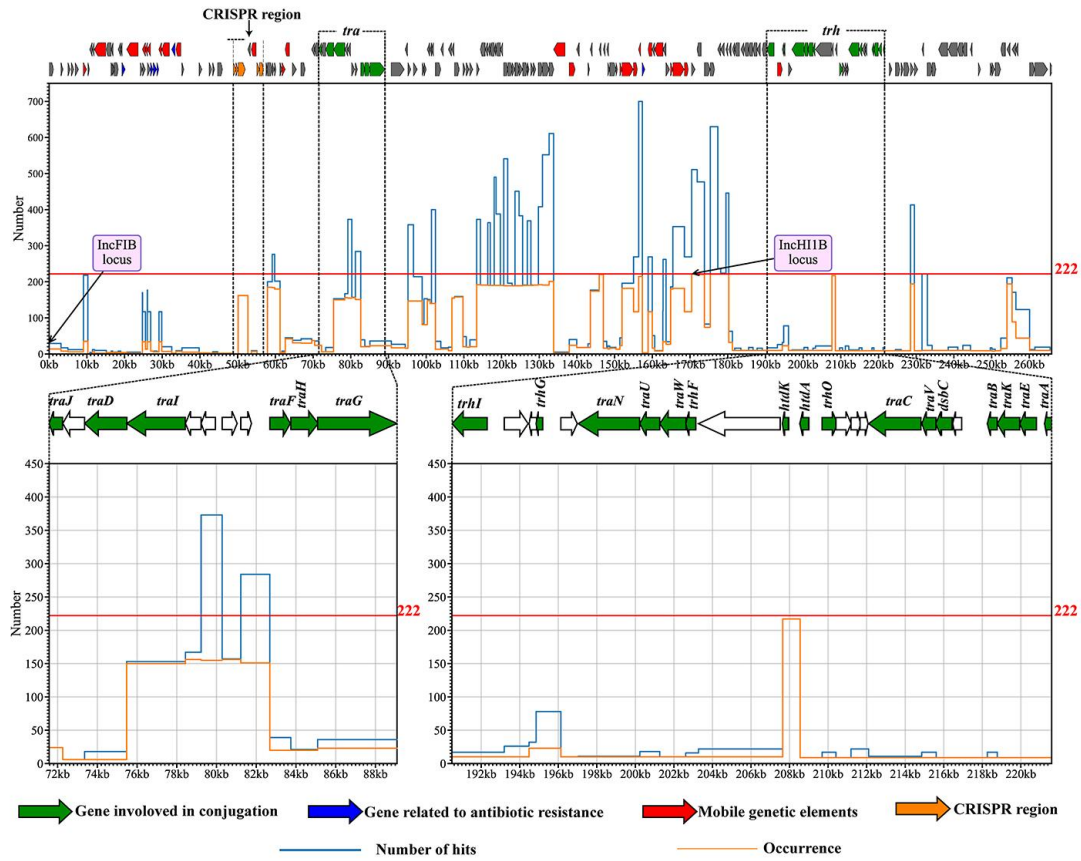


Figure S4 Alignment plot of CRISPR-negative plasmids against plasmid pNDM-MAR. The description of the chart is similar to Figure 3.