

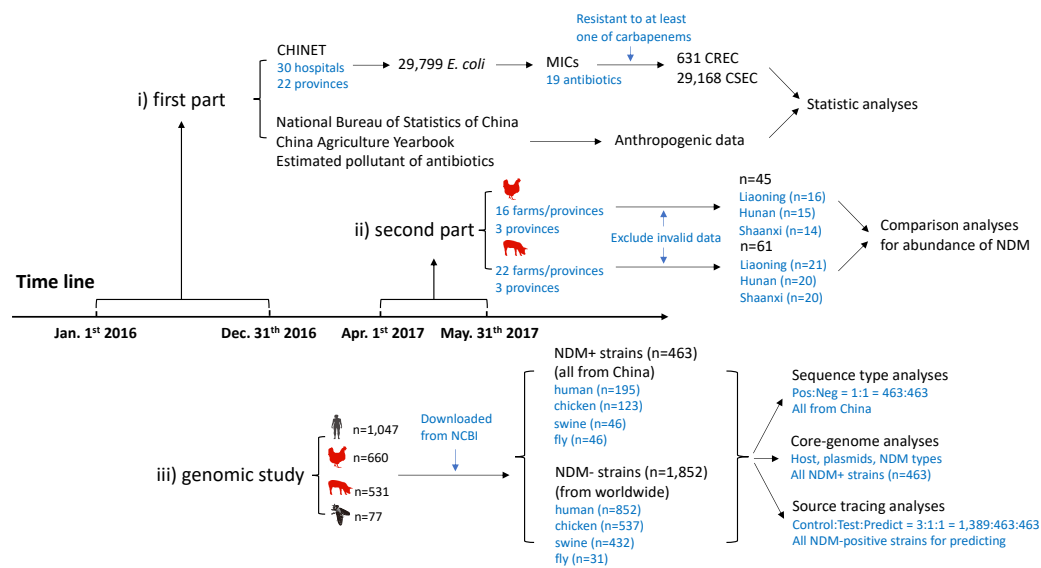


Figure S1. Flowchart of data sources and study process. CHINET: China Antimicrobial Surveillance Network; MIC: minimum inhibitory concentration; CREC: carbapenem-resistant *Escherichia coli*; CSEC: carbapenem-susceptible *Escherichia coli*; NDM+: NDM positive; NDM–: NDM negative; Pos: positive; Neg: negative.

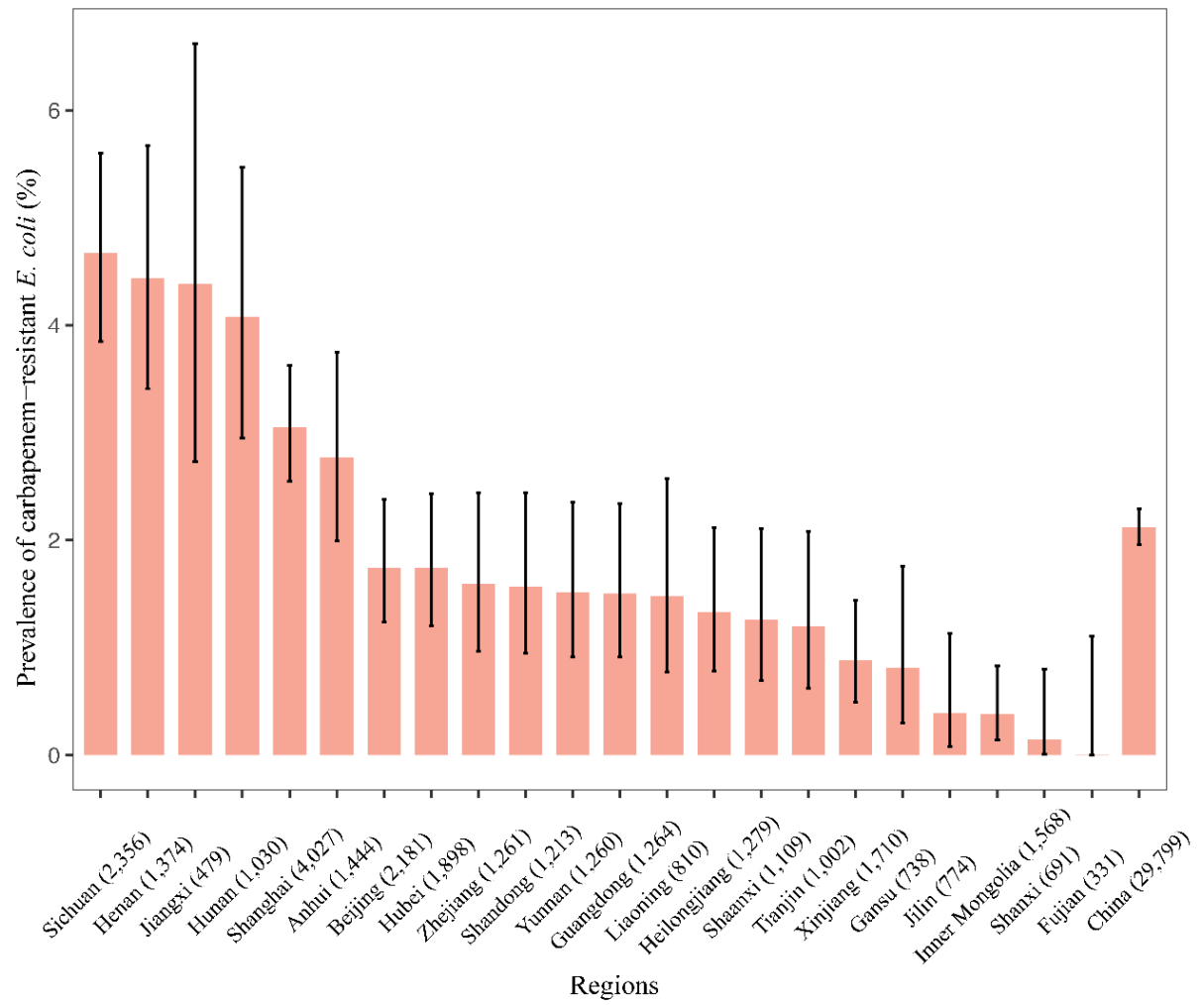


Figure S2. Prevalence of carbapenem-resistant *E. coli* in 22 Chinese provinces.
Bars indicate 95% confidence intervals.

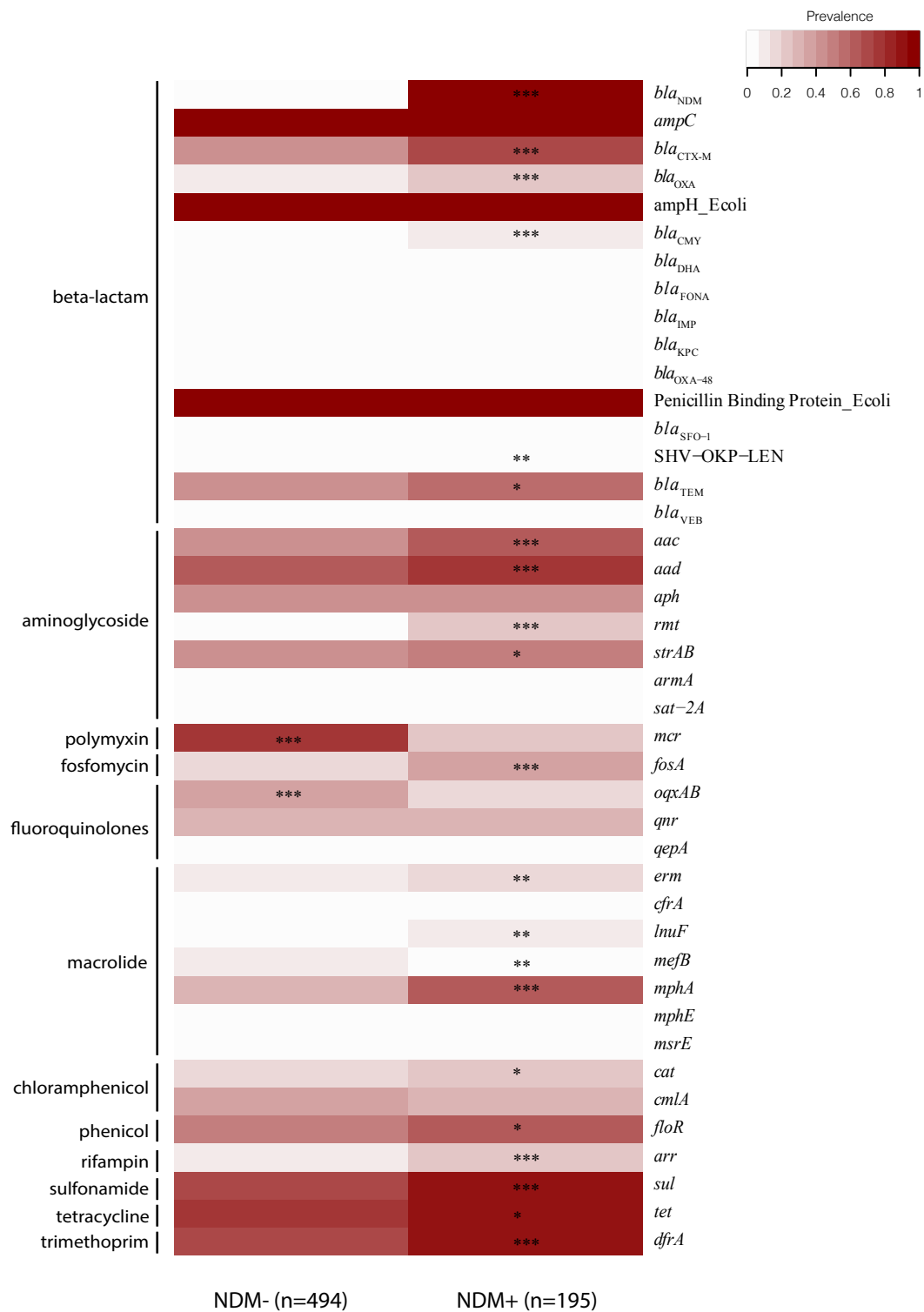


Figure S3. Heatmap of resistance genes in NDM-positive and negative strains of clinical origin. The significant difference of prevalence was indicated with asterisk, including *, **, and * representing P -value less than 0.05, 0.01, and 0.001, respectively. The statistical analysis was using χ^2 or Fisher's Exact test.**

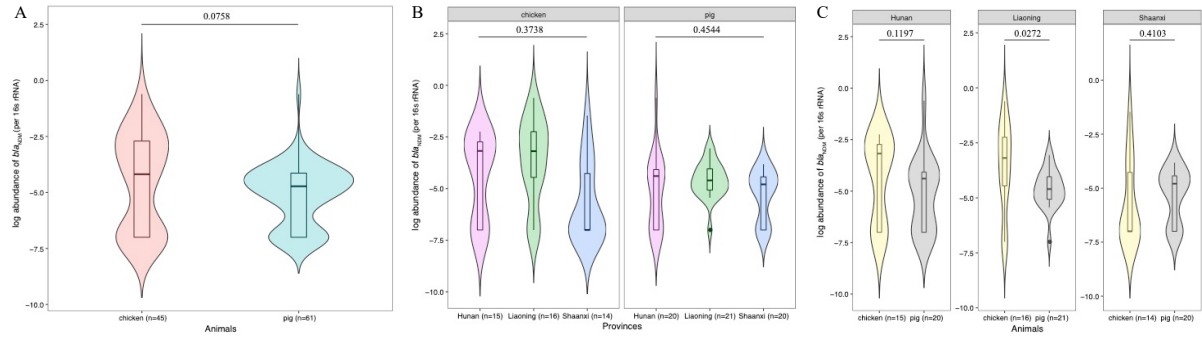


Figure S4. Relative abundance of blaNDM in samples from (A) chickens and pigs, (B) individual provinces, and (C) each type of animal by province. The number of farms is shown in parentheses. Log relative abundance ($\log_{10}$) is shown on the y-axis of the box plots. The horizontal box lines from top to bottom represent the first quartile, median, and third quartile, respectively. Whiskers denote the range of points within the first quartile, minus $1.5 \times$ the interquartile range, and the third quartile, $1.5 \times$ the interquartile range. A Mann-Whitney U-test or a Kruskal-Wallis *H*-test was used to estimate differences between and among groups, with exact p-values shown at the top of each diagram.

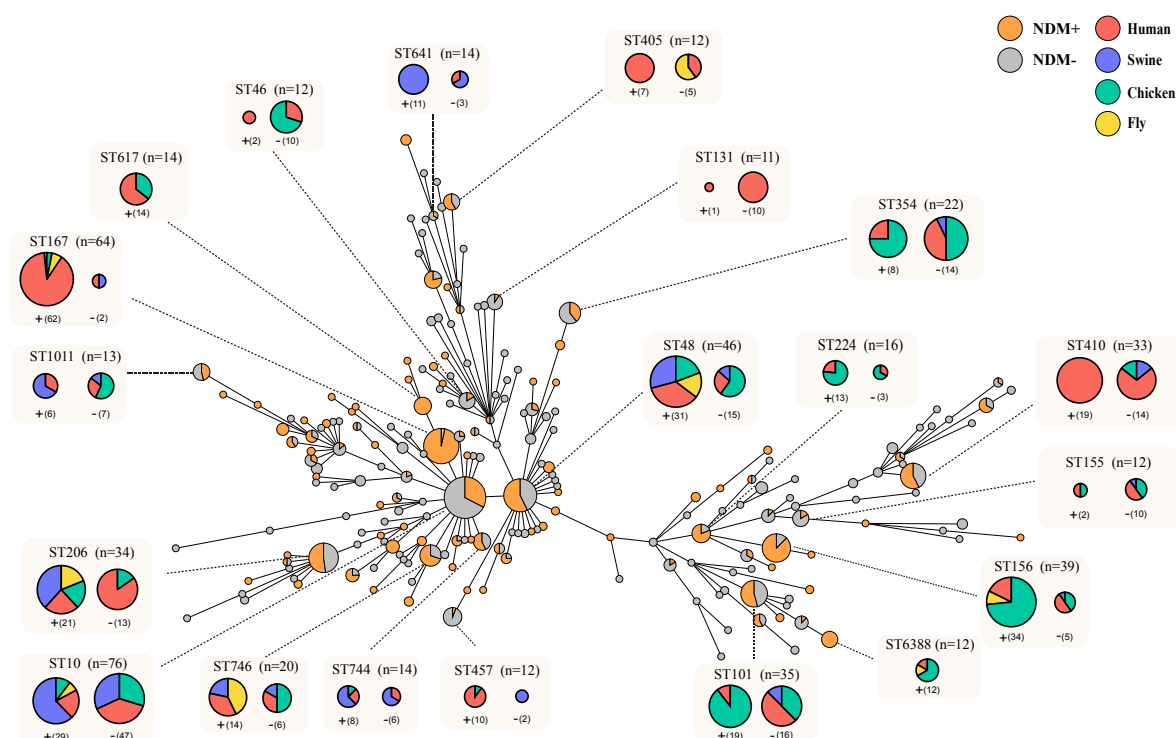


Figure S5. Minimum spanning tree of all NDM-positive isolates based on multi-locus sequence typing data. Each node within the tree represents a single sequence type (ST). The size of the circle indicates the number of isolates belonging to the corresponding ST. The branch length between each node is proportional to the number of nucleotide differences in seven housekeep genes between linked nodes. Nodes with more than ten isolates are labeled with the corresponding ST, number of isolates (including NDM-positive (+) and -negative (-) isolates; listed in parentheses after the ST, and the distribution of corresponding hosts.

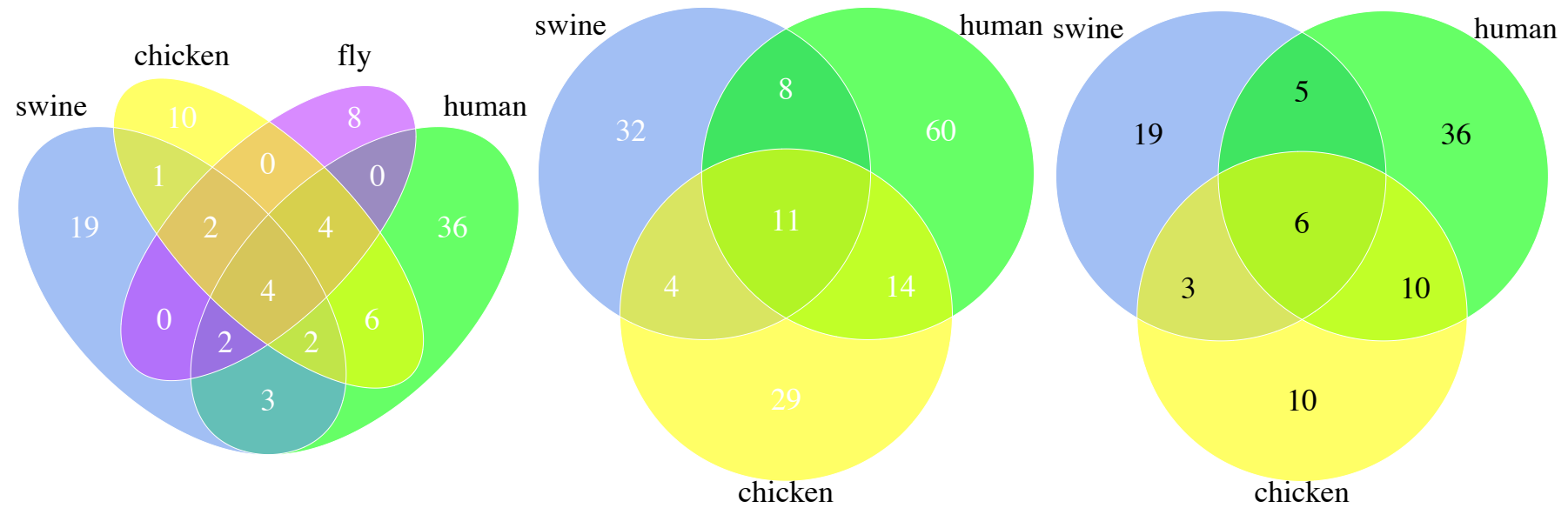


Figure S6. Venn diagram of shared STs by origin. NDM-positive isolates are shown on the left, NDM-negative isolates are in the center, and NDM-positive isolates minus those derived from flies are shown on the right.