Supplementary-Figures

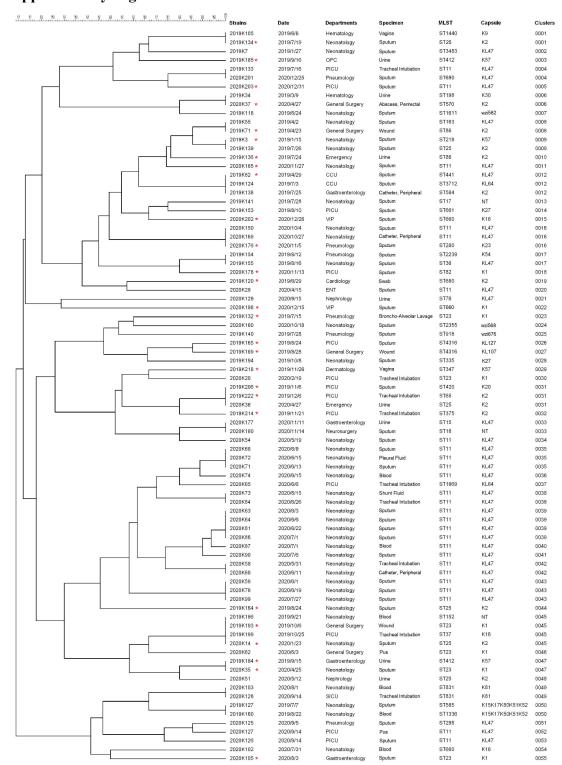


FIGURE S1 Phylogenetic tree of hypervirulence genes positive *K. pneumoniae* (hgKp) isolates (n = 83). The evolutionary analysis for finger printing profiles of Intergenic Consensus-Polymerase Chain Reaction (ERIC-PCR) was performed by BioNumerics software. Strains marked red "*" were hypervirulent *K. pneumoniae*.

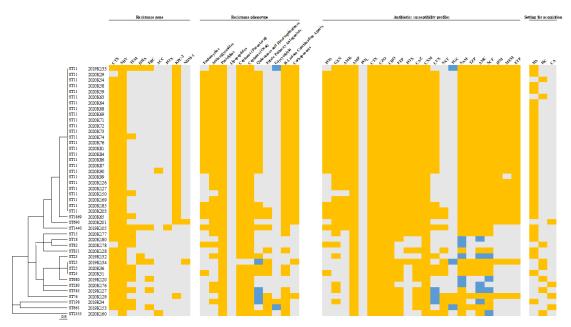


FIGURE S2 Characteristics of MDR-hgKp isolates (n = 44). Resistance gene (left), predicted phenotype (middle), and antibiotics susceptibility profiles (right) of ESBLs-producing isolates (n = 44) (from top to bottom are isolates in the phylogenetic relationship analyzed by Phyloviz 2.0 software using the hierarchical clustering algorithm based on the complete-linkage method of hamming distance between STs). Yellow filling means resistant, blue means intermediate, and grey means susceptible. FOS, fosfomycin; GEN, gentamicin; AMK, amikacin; AMP, ampicillin; POL, polymyxin; CTX, cefotaxime; CZO, cefazolin; CRO, ceftriaxone; FEP, cefepime; FOX, cefoxitin; CAZ, ceftazidime; CXM, cefuroxime; LVX, levofloxacin; SXT, trimethoprim-sulfamethoxazole; TGC, tigecycline; SAM, ampicillin-sulbactam; TZP, piperacillin-tazobactam; AMC, amoxicillin-clavulanic acid; SCF, cefperazone-sulbactam; IPM, imipenem; MEM, meropenem; ETP, ertapenem; HA, hospital-associated infection; HC, healthcare- associated infection; CA, community- associated infection.

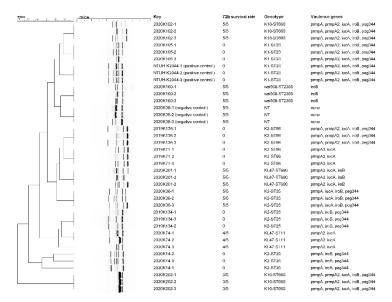


FIGURE S3 Homology of randomly selected strains (n = 11) used to build murine sepsis model. Strains-1, strains before mice injection; Strains-2 and Strains-3, strains recovered from a separate portion of the harvested livers of the injected mice. Fresh livers were grinded in paraformaldehyde-free PBS. Bacteria in supernatant were cultured on blood agar plate at 37 °C overnight, and identified by MALDI-TOF mass spectrometry. The evolutionary analysis for finger printing profiles of Intergenic Consensus-Polymerase Chain Reaction (ERIC-PCR) was performed by BioNumerics software.

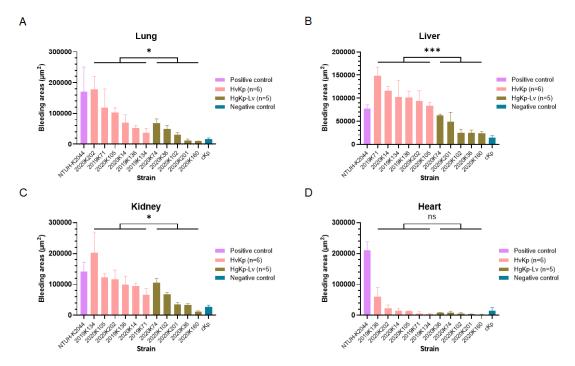


FIGURE S4 Damage of hvKp infection to mice. Data of organs bleeding areas were expressed as means \pm SDs, P < 0.05 (*), P < 0.001 (***) and P > 0.05 (ns). Between hvKp and hgKp-Lv isolates infected mice, significant differences were observed in the bleeding areas of lung (t = 2.33, P = 0.0446, 95% confidence interval [CI] = 42018 to 98612), of liver (t = 5.62, P = 0.0003, 95% CI = 1776.2 to 116974), of kidney (t = 2.58, P = 0.0298, 95% CI = 8126.2 to 124402), but not of heart (t = 1.66, P = 0.1558, 95% CI = -7219 to 35917) using independent-samples t-test.

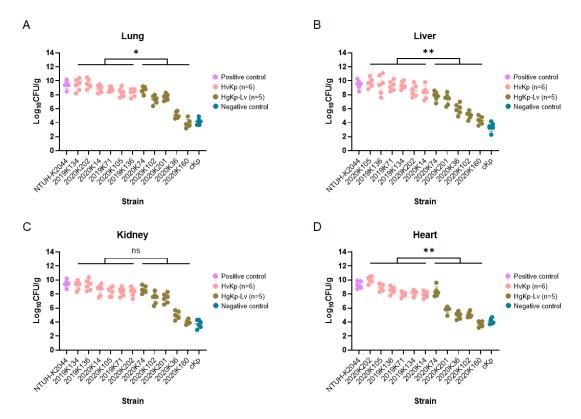


FIGURE S5 Bacterial burdens in the mice organs. Data shown are means \pm SDs, P < 0.05 (*), P < 0.01 (**) and P > 0.05 (ns). Between hvKp and hgKp-Lv isolates infected mice, significant differences were observed in bacterial CFU of lung (t = 2.81, P = 0.0205, 95% confidence interval [CI] = 6.6 to 9), of liver (t = 4.64, P = 0.0012, 95% CI = 6.5 to 9), of heart (t = 3.87, P = 0.0038, 95% CI = 5.9 to 8.5), and a slight difference was observed of kidney (t = 2.53, P = 0.0596, 95% CI = 6.5 to 8.8) using independent-samples t-test.