

Figure S1. Antibiotic resistance prevalence of meat-source *Klebsiella pneumoniae* isolates. The antibiotics tested were: ampicillin (AMP), ampicillin-sulbactam (SAM), cefazolin (CFZ), cefoxitin (FOX), ceftriaxone (CRO), ceftazidime (CAZ), cefotaxime (CTX), ciprofloxacin (CIP), gentamicin (GEN), nalidixic acid (NAL), tetracycline (TET), trimethoprim-sulfamethoxazole (SXT). Multidrug resistance (MDR) was defined as resistance to three or more classes of antibiotics. None of the isolates were resistant to amikacin or imipenem (not shown). (** P < 0.01, ***P < 0.001)

Figure S2. Minimum spanning tree of meat-source and clinical isolates based on multilocus sequence typing profiles. Each circle represents a unique sequence-type (ST). The size of the circle is proportional to the number of isolates. Single-locus variants are connected by solid black lines, dotted lines connect STs with two or more allelic differences, and darker dotted lines indicate more shared alleles. There were 60 unique STs among the 82 study isolates. The minimum spanning tree was generated using the computer program PHYLOViZ [37].



