

## Supplementary materials

Figure S1. Diagram showing the genetic elements harbouring *bla*<sub>KPC-2</sub> and *bla*<sub>KPC-3</sub> in *K. pneumoniae* isolates.

Figure S2. Phylogenetic relationships among global *K. quasipneumoniae* subsp. *quasipneumoniae* ST196 and ST1416 isolates based on core genome SNPs.

Table S1. A list of isolates with metadata, AMR genes and virulence phenotypes determined by Kleborate, Resfinder and Plasmidfinder (isolates of newly assigned ST are highlighted in red).

Table S2. Pairwise differences (SNPs) among *Klebsiella* species and isolates from core genome alignment generated from Parsnp.

Table S3. The accession numbers of publicly available genomes/raw reads of ST383 strains used for comparative genomic

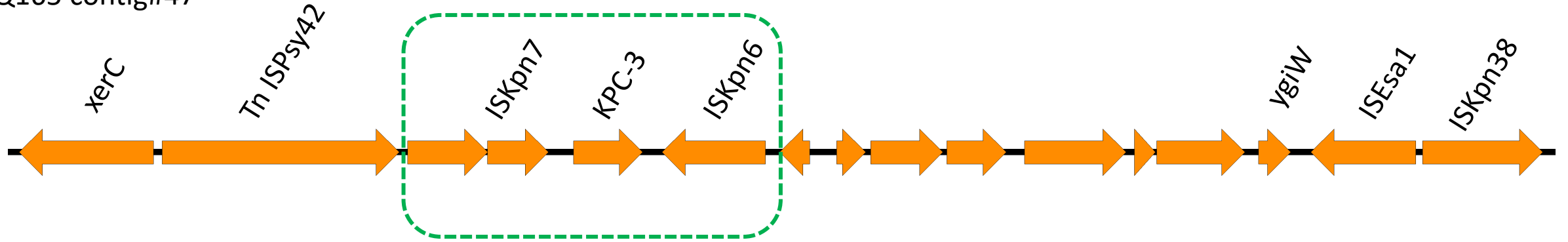
Table S4. Clinical and epidemiological information of six prevalent *K. pneumoniae* ST isolates.

Table S5. The accession numbers of publicly available genomes of *K. quasipneumoniae* subsp. *quasipneumoniae* ST1416 and ST196 strains.

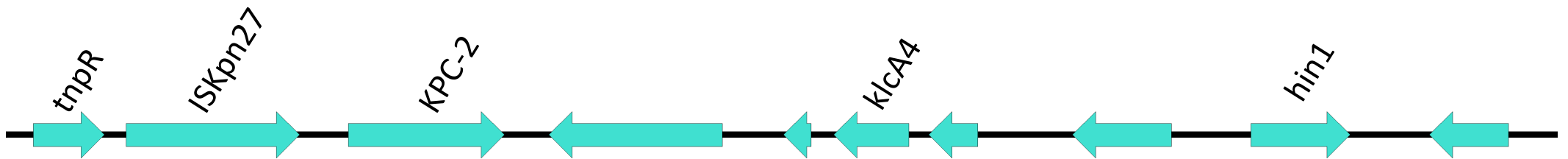
Fig. S1

*bla*<sub>KPC-3</sub> in sample FQ156 and FQ165 was sandwiched between ISKpn6 and ISKpn7 and located on a traditional Tn4401a mobile element

FQ165 contig#47



*bla*<sub>KPC-2</sub> in sample FQ26, FQ34, FQ139 also located on Tn4401 like genetic elements



FQ26 contig#71

Fig. S2. Phylogenetic relationships among local and global *K. quasipneumoniae* ST196 and ST1416 isolates.

