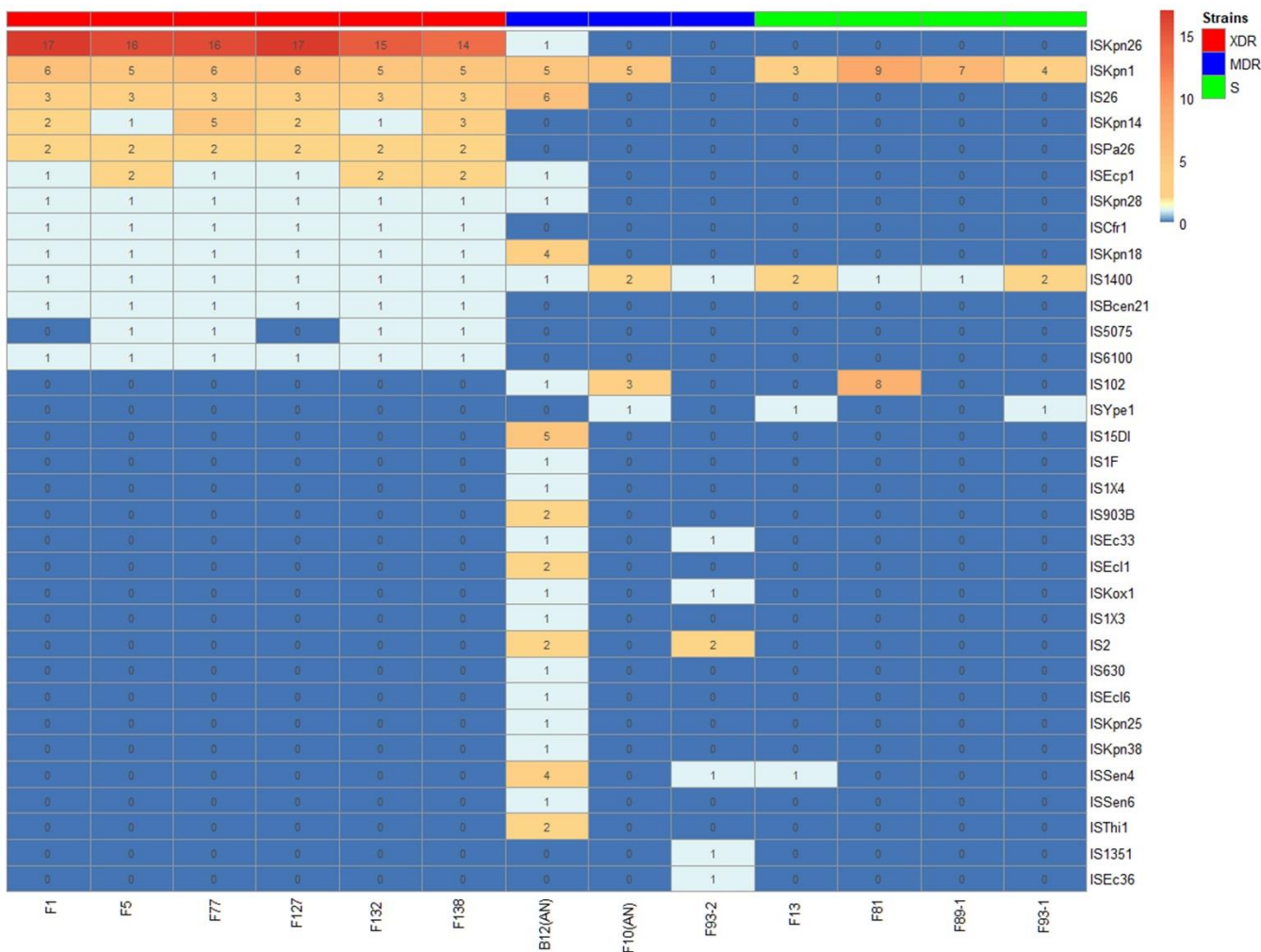


Supplementary Figure 1: Insertion sequences and transposases within the 13 *Klebsiella pneumoniae* strains were detected using the online platform ISfinder. The average number of insertion sequences in the XDR, MDR, and S strains decreased progressively, and the number of the insertion sequences in the XDR group *e.g.*, ISKpn26, IS26, or ISKpn14, is apparently larger than in the MDR and S groups. XDR: Extensively drug resistant; MDR: Multidrug-resistant.



Supplementary Figure 2: Core SNPs between each pair of the six ST11 carbapenemase-producing *Klebsiella pneumoniae* (CP-Kp) strains were called using kSNP. The numbers of core SNPs between each pair of the six ST11 CP-Kp XDR strains ranged from 4-55. Furthermore, there were 7 core SNPs between F1 and F127 and 4-14 core SNPs among F5, F77, F132, and F138, while there were 50-55 core SNPs differentiating the strains of F1 and F127 from the strains of F5, F77, F132, and F138. SNPs: Single-nucleotide polymorphisms.

F1	F1					
F5	52	F5				
F77	50	6	F77			
F127	7	55	53	F127		
F132	50	6	4	53	F132	
F138	52	14	12	55	12	F138

Supplementary Figure 3: Distribution of Clusters of Orthologous Groups (COG) functional categories among the 13 *Klebsiella pneumoniae* strains. All predicted proteins in the 13 strains genomes were aligned against the COG database. The distributions of the functional genes in the 13 genomes were similar.

