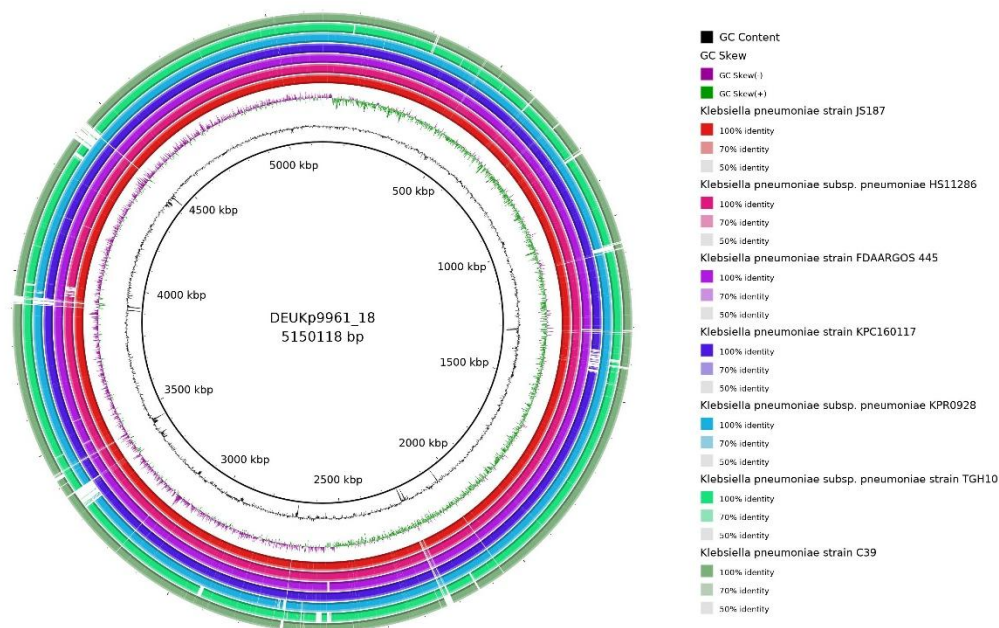
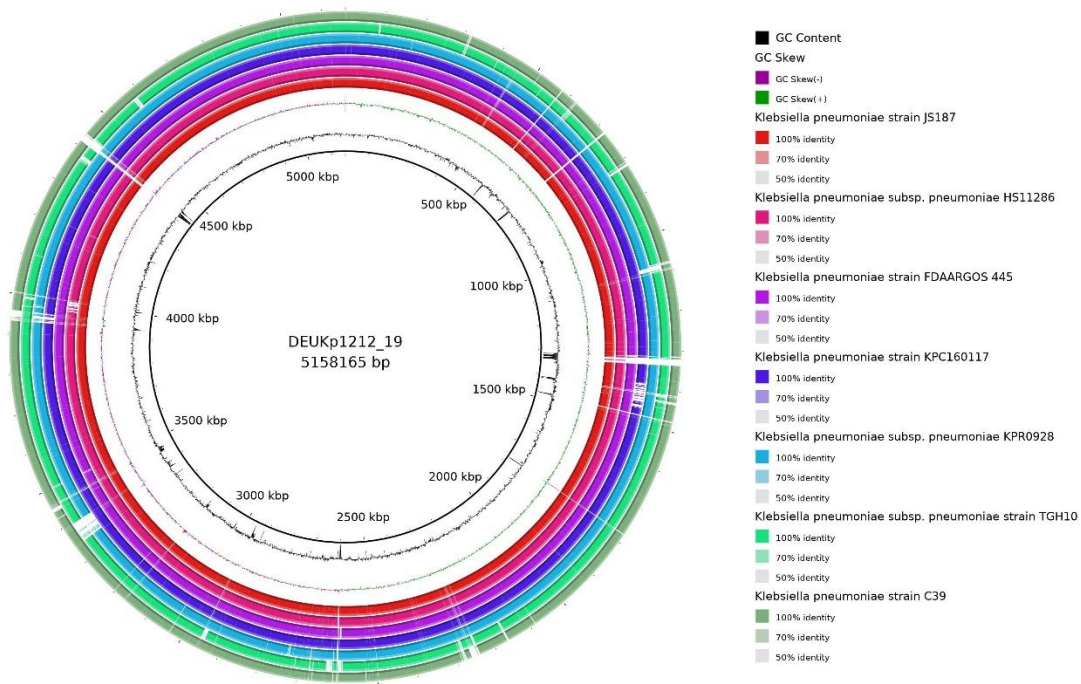


Supplementary Figure 2a-e. Schematic representation of GC content of all samples and comparison with other genomes of *K. pneumoniae*

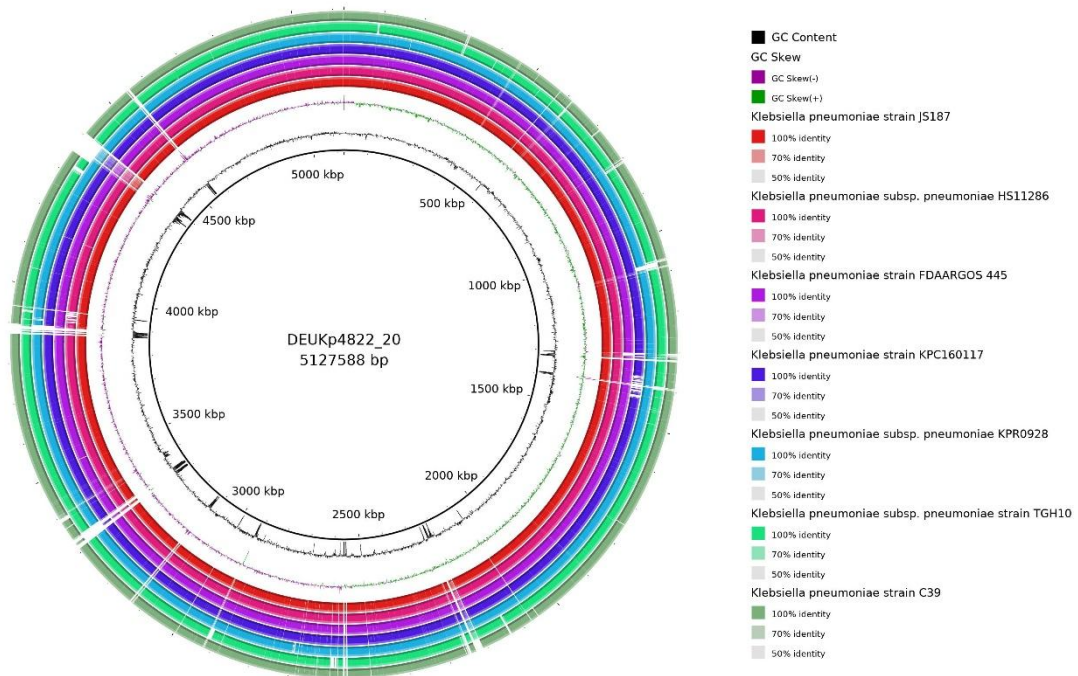
The comparative genomic analysis of the 5 *K. pneumoniae* clinical isolates was performed against several reference strains, including *K. pneumoniae* JS187, HS11286, FDAARGOS 445, KPC160117, KPR0928, TGH10, and C39. The circular genome map, as shown in **Supplementary Figure 2**, illustrates the genomic architecture of the isolates, highlighting the conserved regions, sequence identity, GC content, and GC skew. These results demonstrate that the clinical isolates exhibit high sequence similarity with the compared reference strains across the majority of the genome, consistent with the characteristic genomic structure of *K. pneumoniae*. Variations in the alignment rings across the different isolates indicate specific regions of genomic plasticity, which are essential for understanding the evolutionary adaptation and the presence of unique mobile genetic elements or virulence determinants within these strains.

(a)

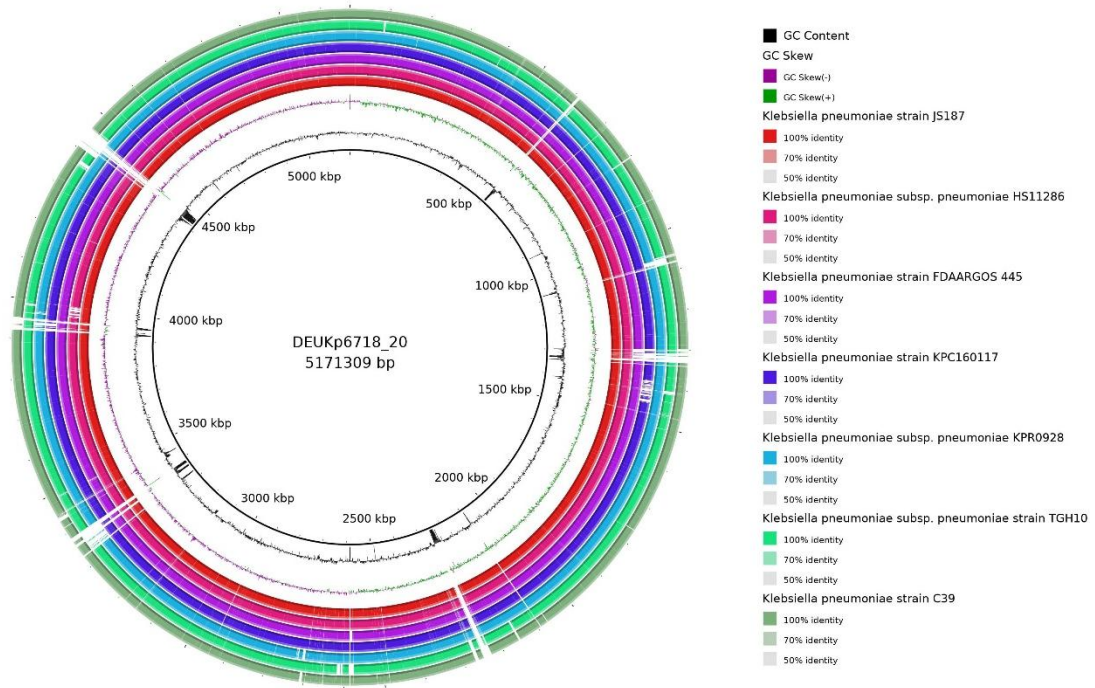




(c)



(d)



(e)

