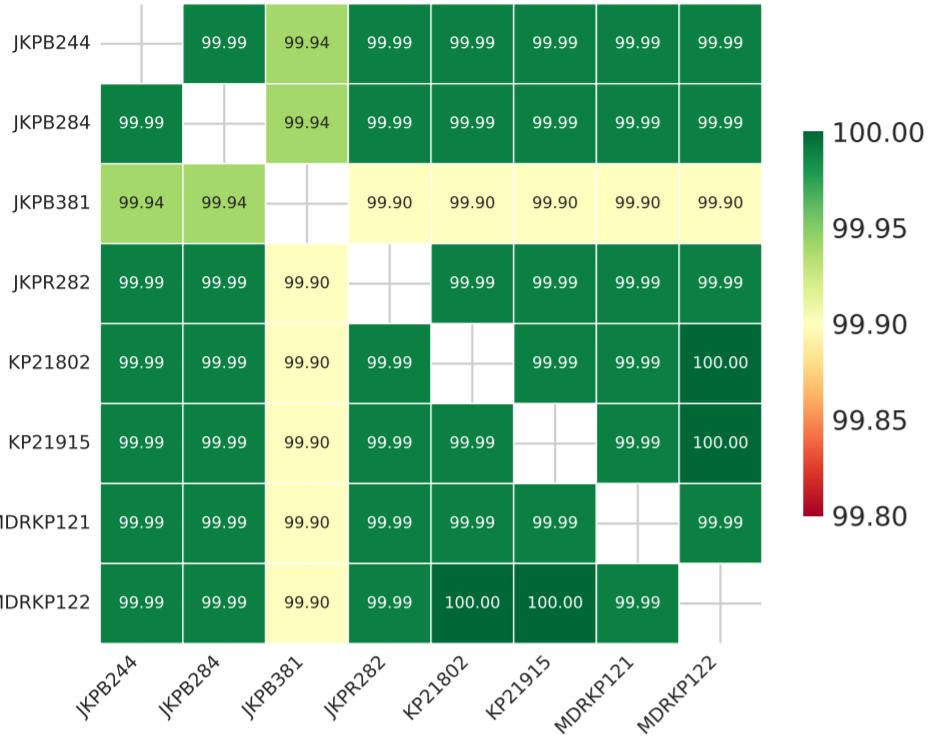


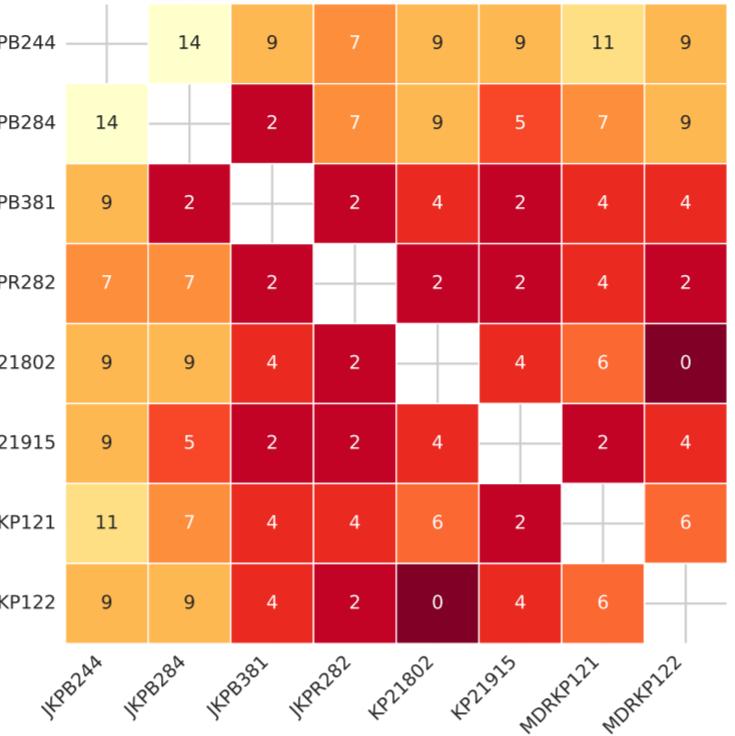
# Whole-Plasmid Comparison: KPC-2 Carrying IncFII+IncR Plasmids

## 8 ST11 *K. pneumoniae* (Saudi Arabia) vs 10 Global References

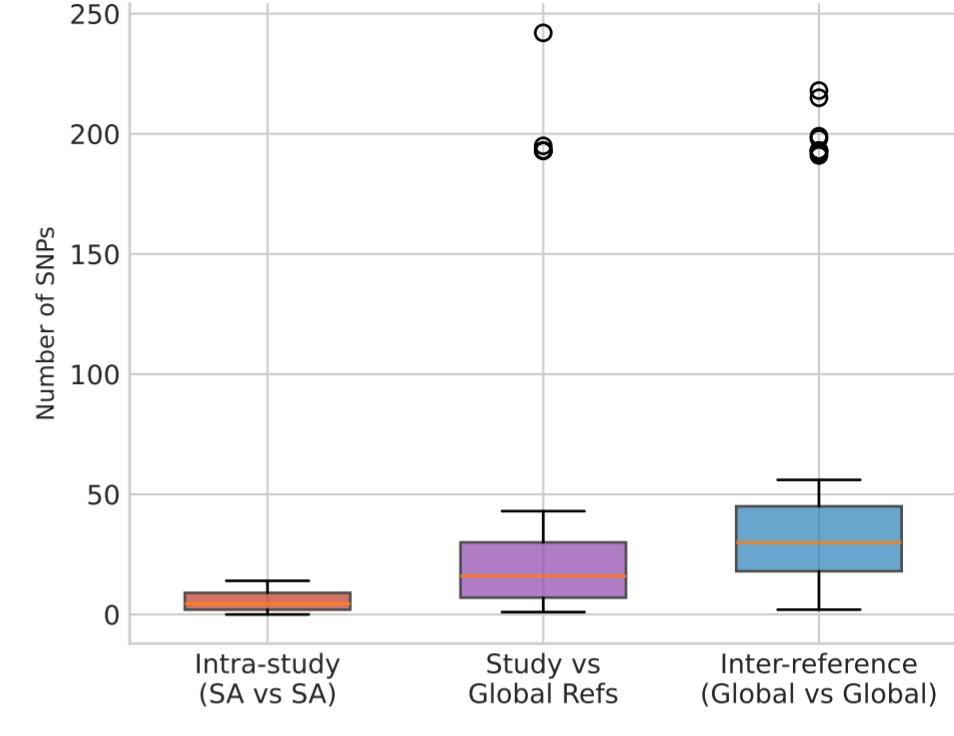
**A. Intra-study ANI (%)**



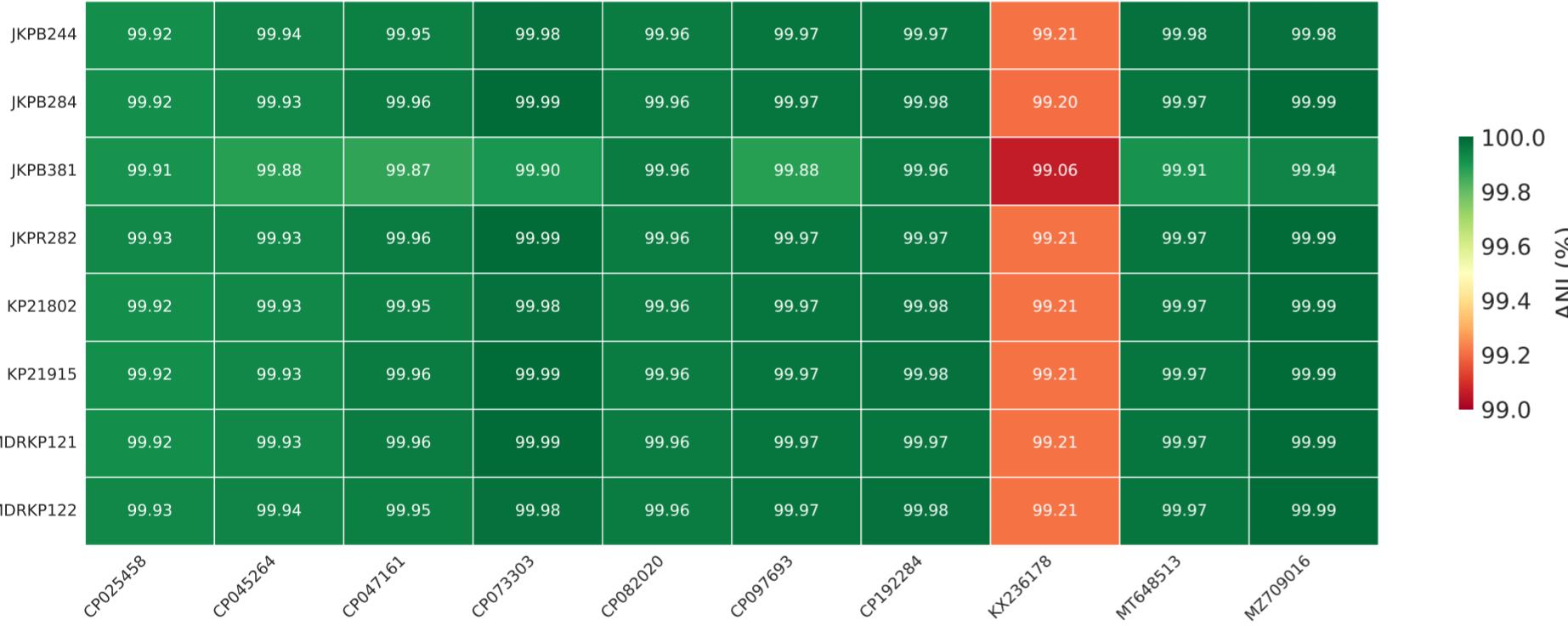
**B. Intra-study SNPs**



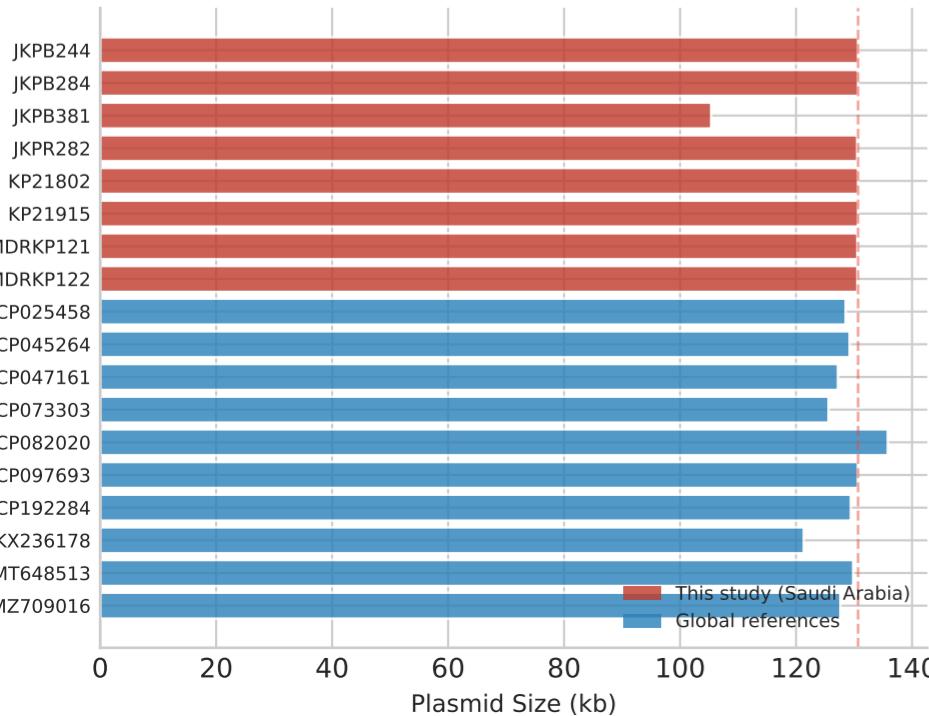
**C. SNP Distribution by Comparison Group**



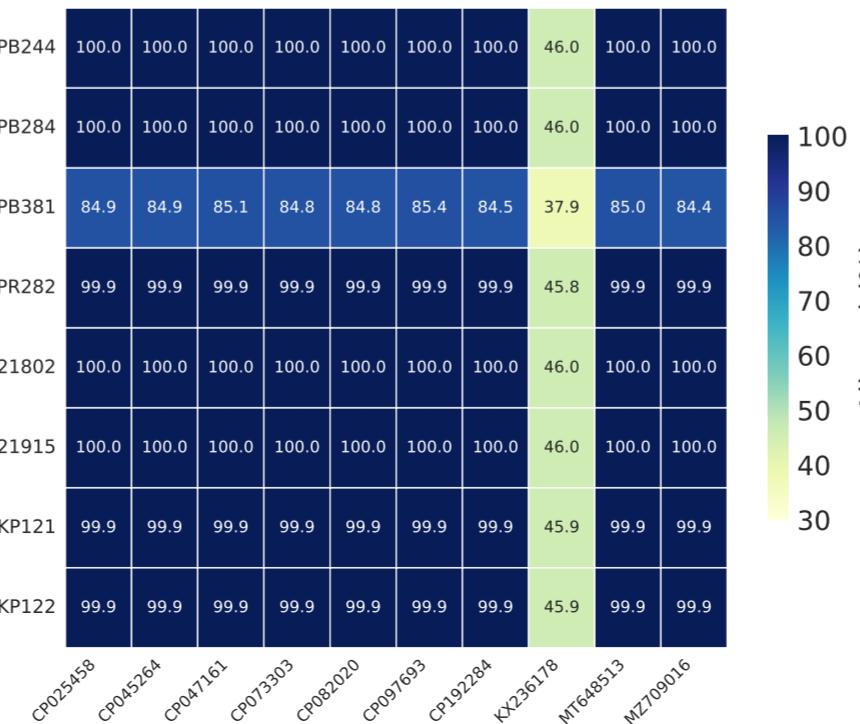
**D. Study vs Global Reference ANI (%)**



**F. Plasmid Sizes**



**G. Aligned Coverage (Study vs Refs)**



**H. Summary**

KEY FINDINGS	
INTRA-STUDY COMPARISON:	
• 6/8 plasmids nearly identical (0-14 SNPs, >99.9% ANI)	
• JKPB381: truncated variant (105 kb)	
• JKPR282: different backbone	
STUDY vs GLOBAL REFERENCES:	
• ANI: 99.06-99.99%	
• Mean SNPs: 34.9	
• Highest similarity to CP097693 (China, 130.7 kb, same size)	
CORE AMR MODULE (6/8 isolates):	
blaKPC-2 + blaCTX-M-65 + blaSHV-12	
+ blaTEM-1 + fosA3 + rmtB1 + catA2	
CONCLUSION:	
The IncFII(pHN7A8)+IncR KPC-2 plasmid in Saudi Arabia is part of a globally conserved plasmid lineage circulating in ST11 <i>K. pneumoniae</i> , with highest similarity to Chinese isolates, suggesting intercontinental plasmid transfer.	