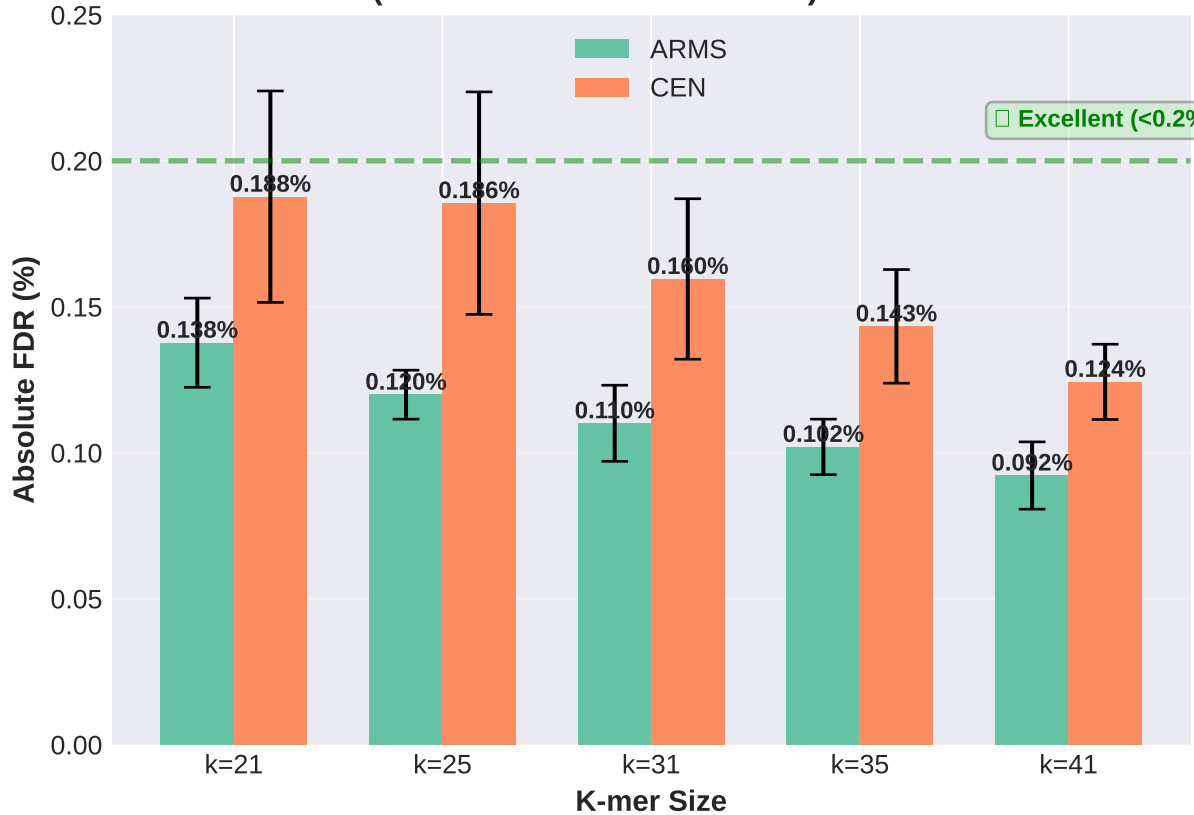
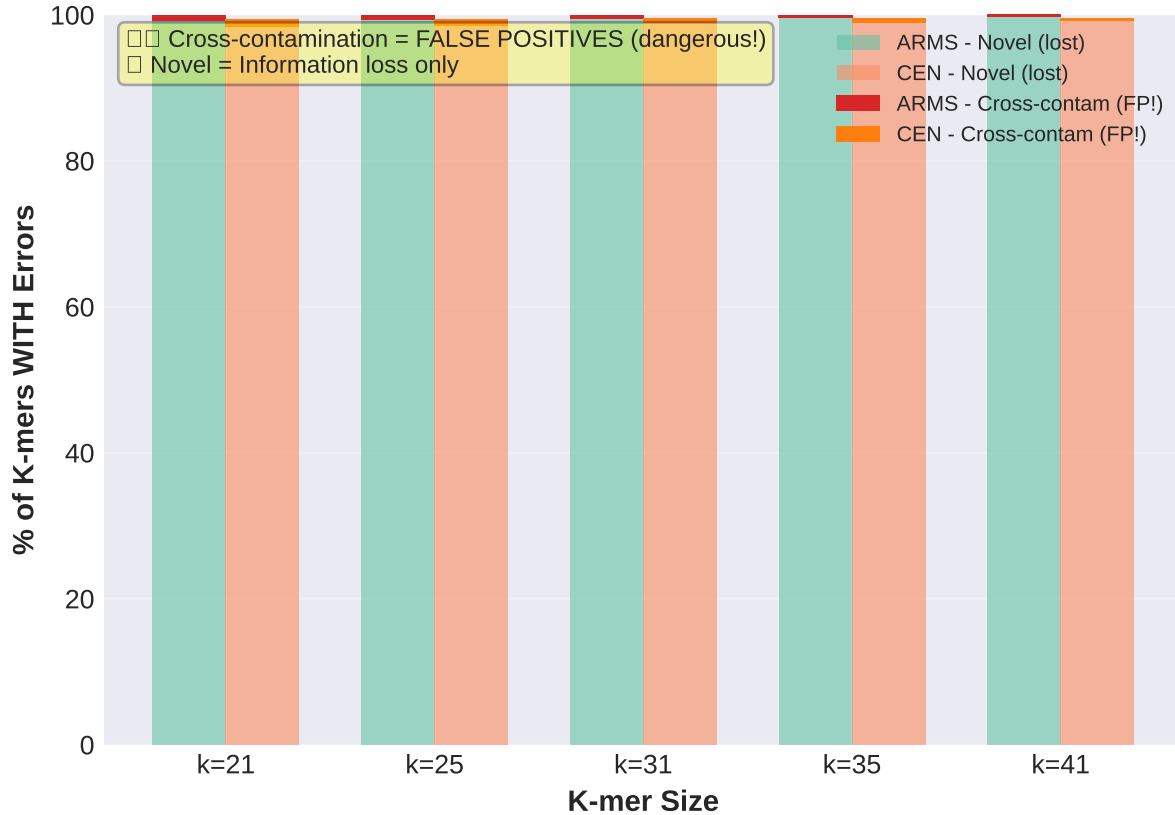


Cross-Contamination Risk from Sequencing Errors  
(1% per-base error rate, ONT-like)

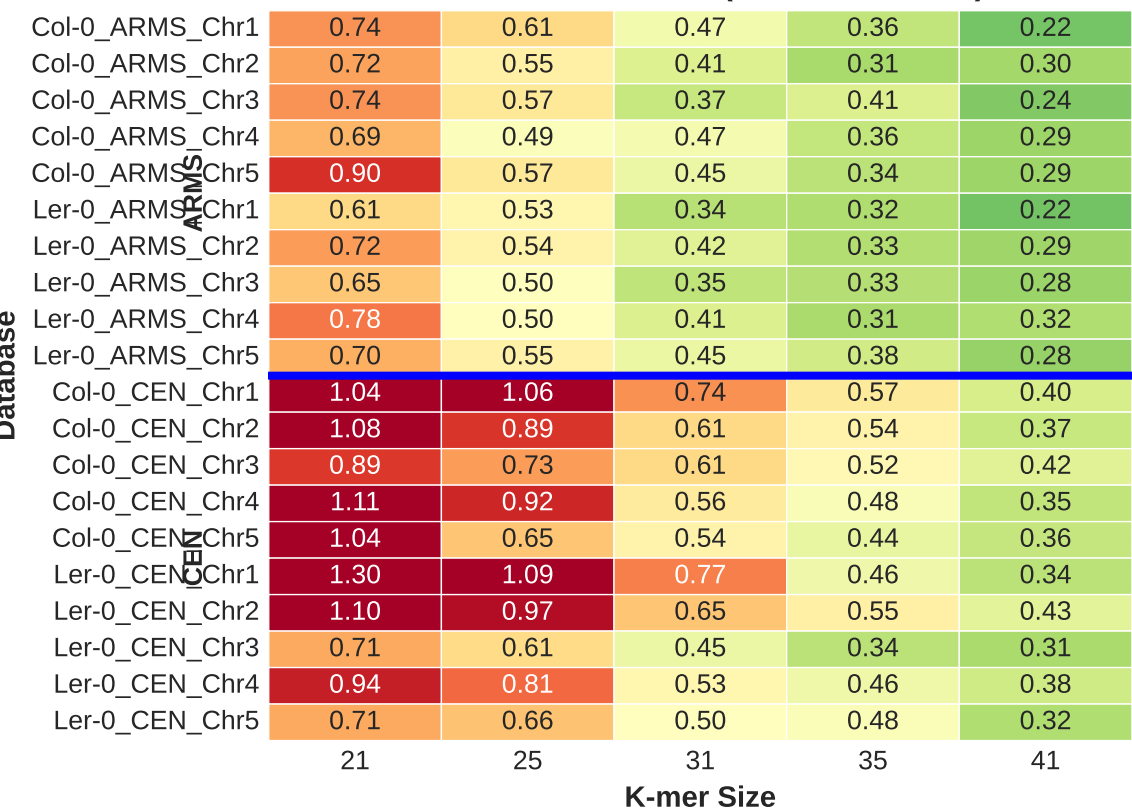
A. Absolute FDR (% of ALL k-mers that are FP)



B. Error Fate: Novel vs Cross-Contamination



C. Cross-Contamination Rate (False Positives!)



D. Database False Positive Risk Ranking  
(averaged across k-sizes)

