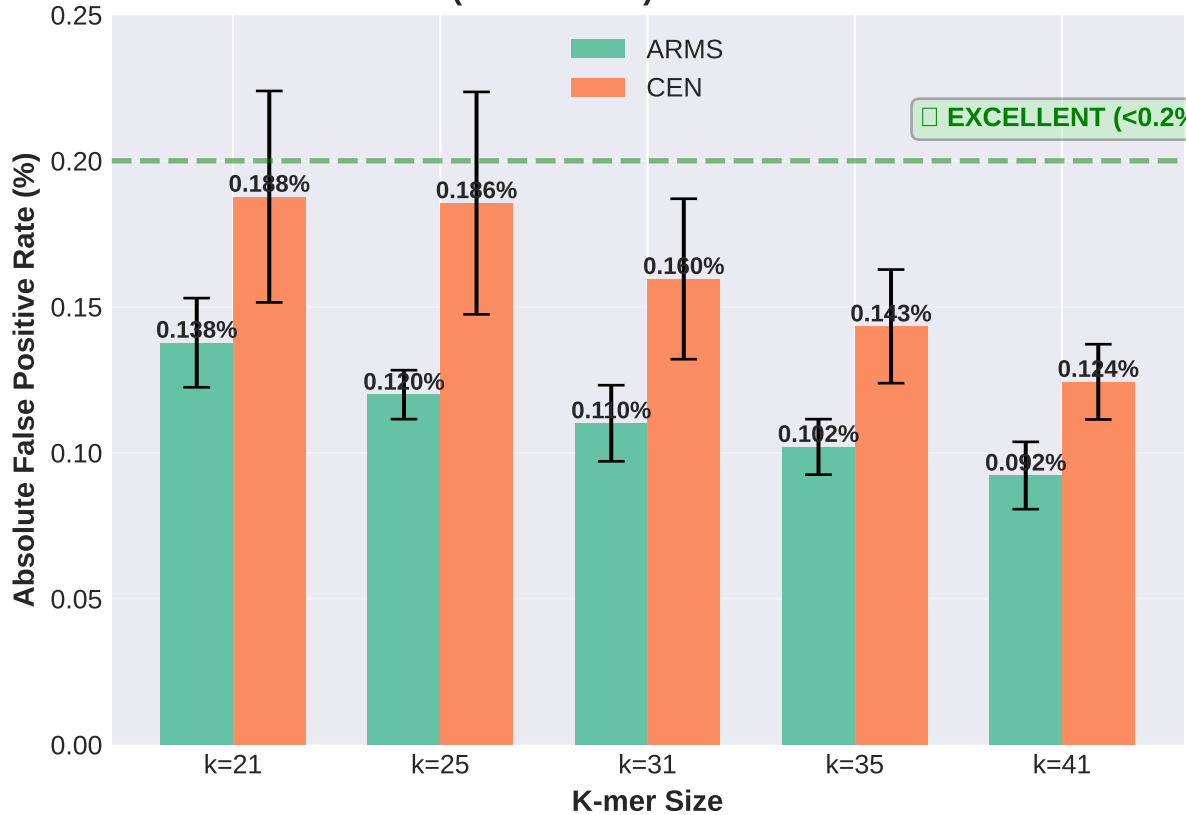
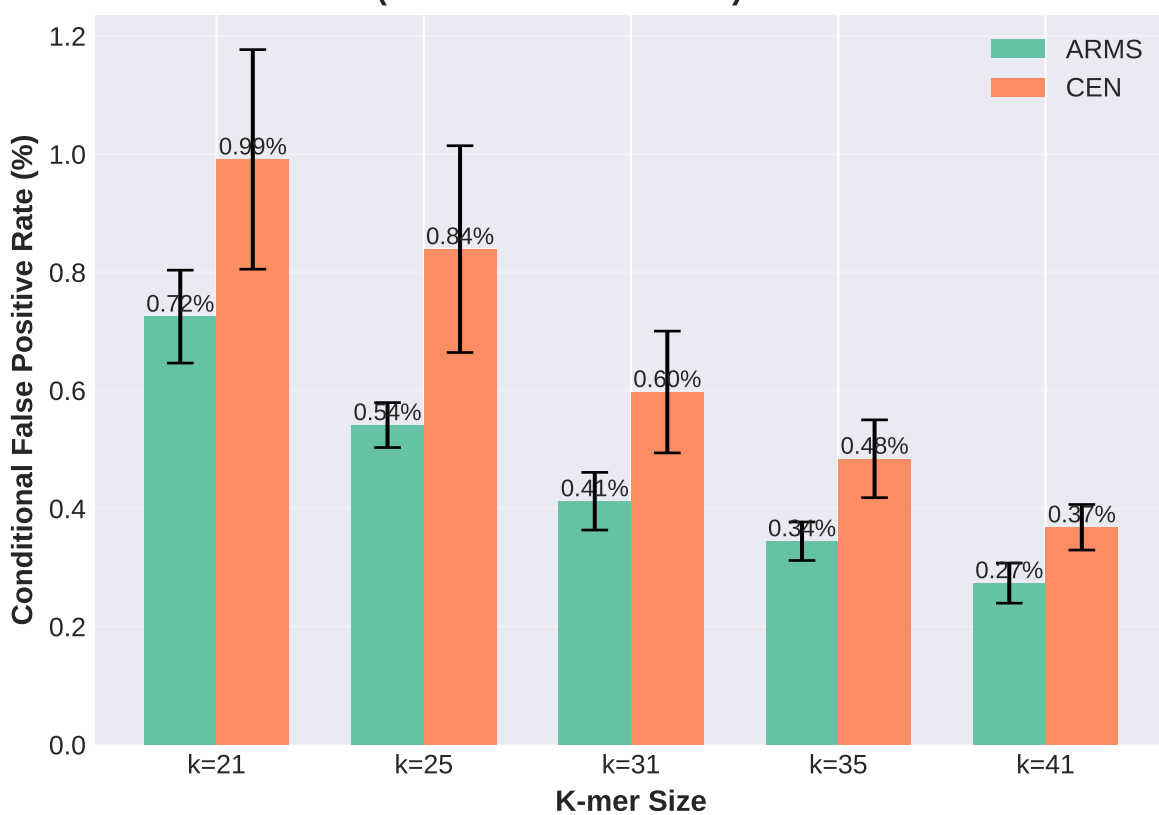


Cross-Contamination Risk from Sequencing Errors
(1% per-base error rate, ONT-like)

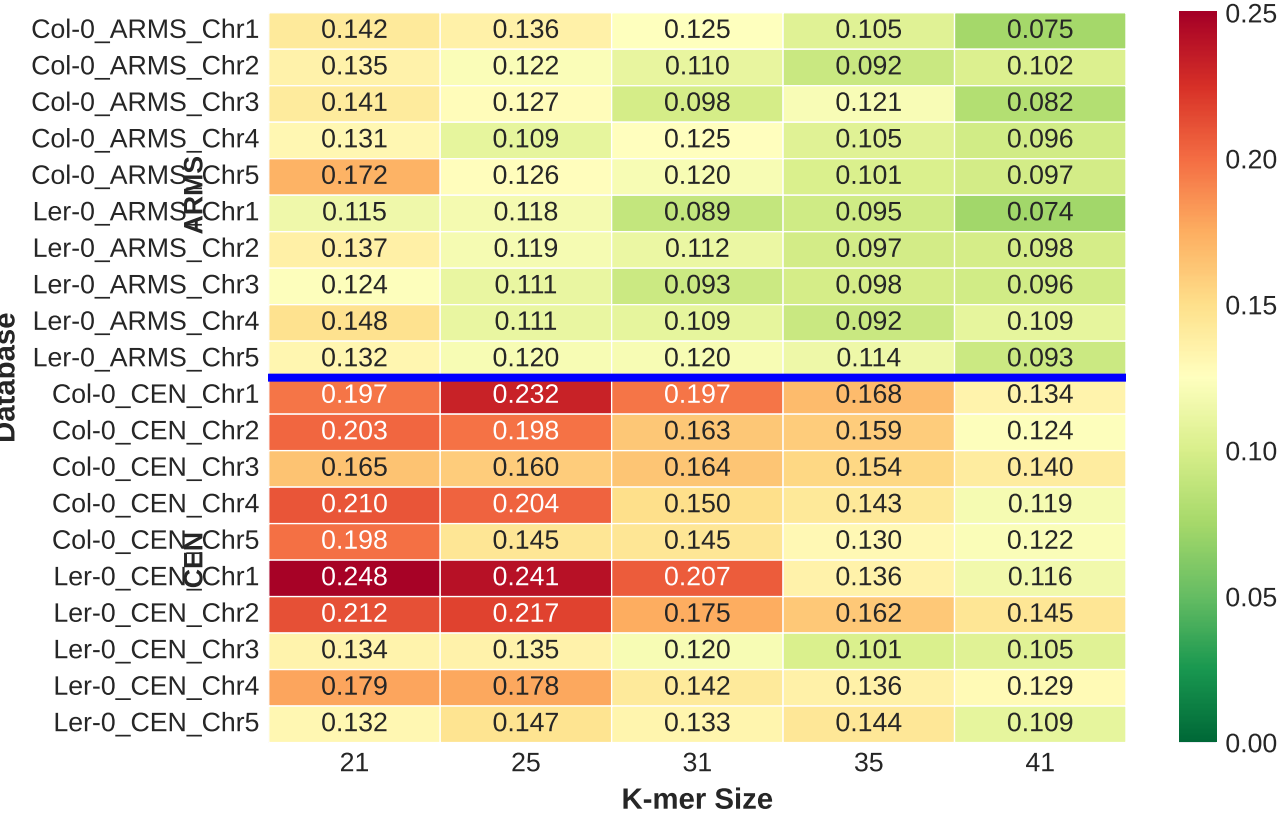
A. False Positive Risk (ALL K-mers)



B. False Positives (of K-mers WITH Errors)



C. Per-Database False Positive Rates



D. Database Vulnerability Ranking
(averaged across k-sizes)

