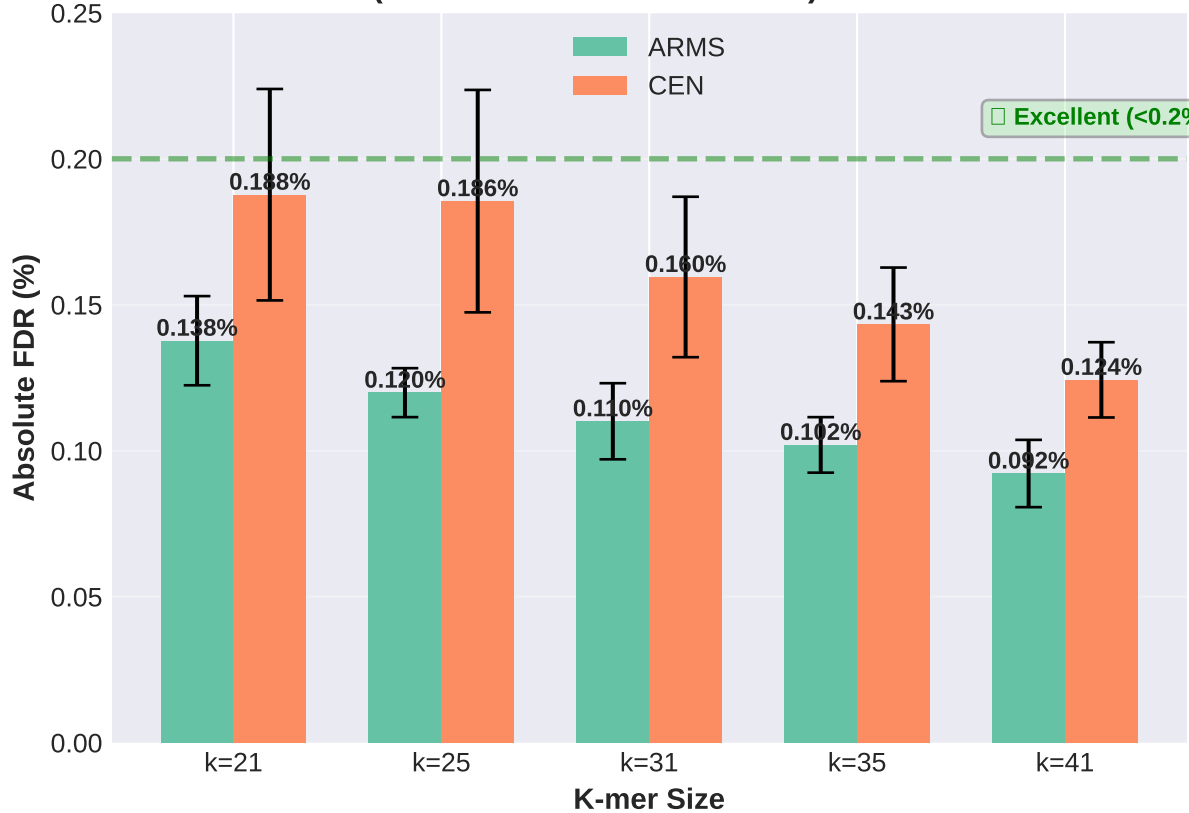
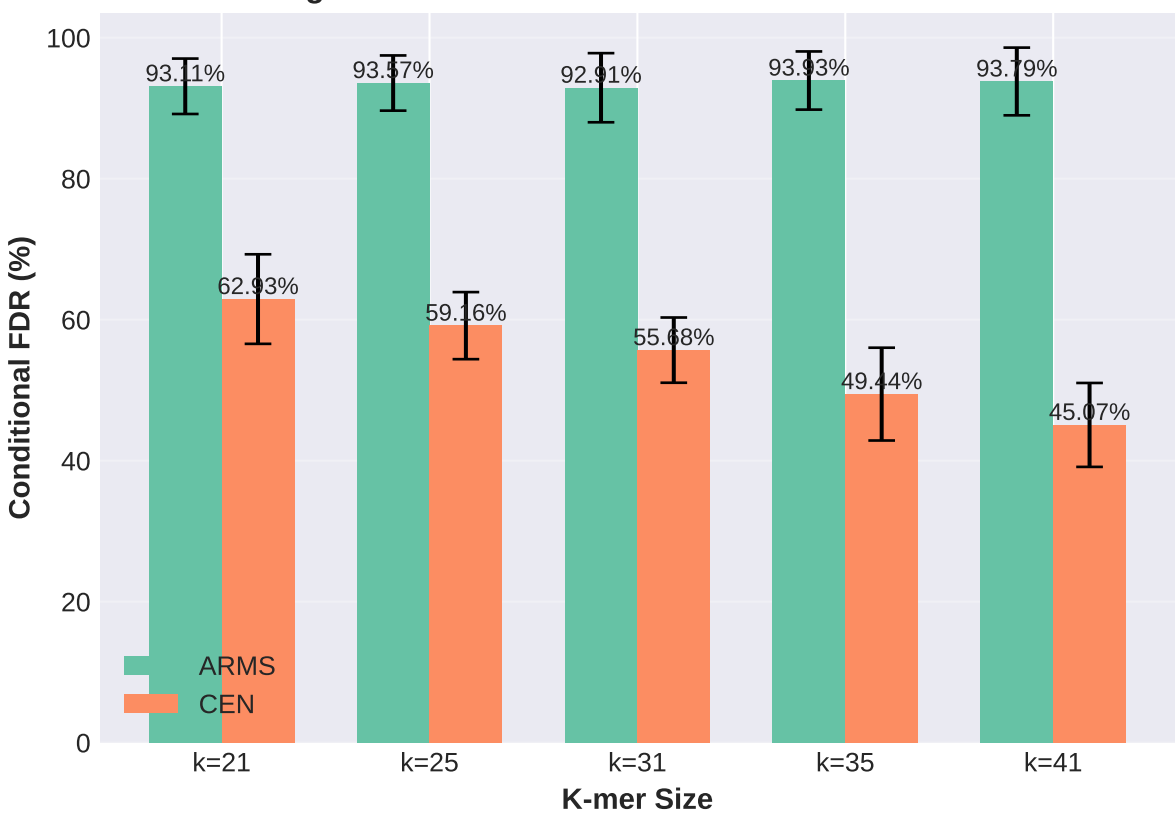


Cross-Contamination Risk from Sequencing Errors
(1% per-base error rate, ONT-like)

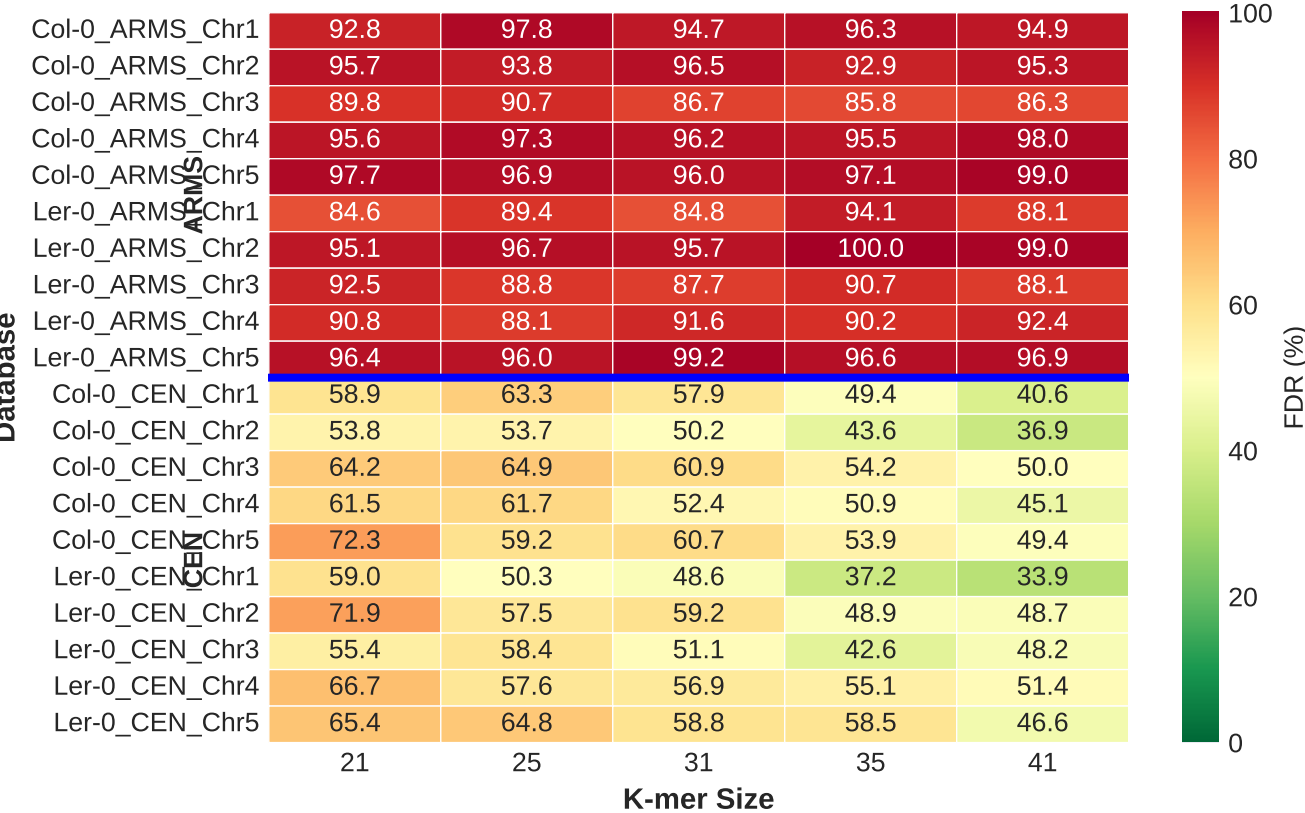
A. Absolute FDR (% of ALL k-mers that are FP)



B. FDR Among K-mers WITH Errors



C. Per-Database FDR Values



D. Database Conditional FDR Ranking (averaged across k-sizes)

