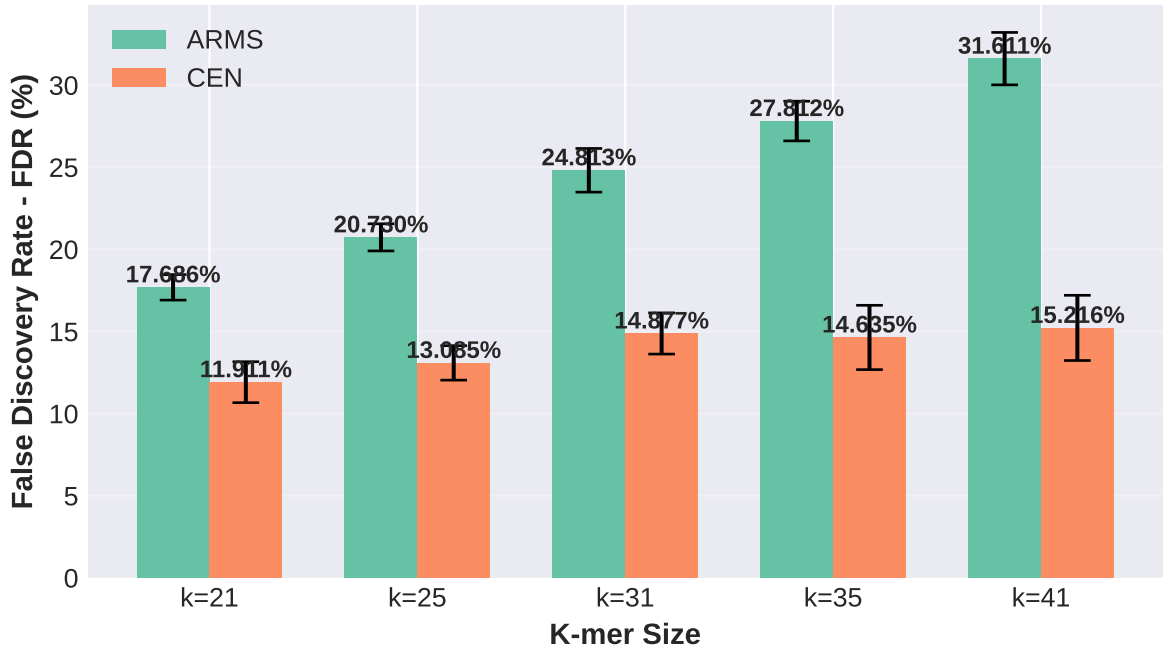


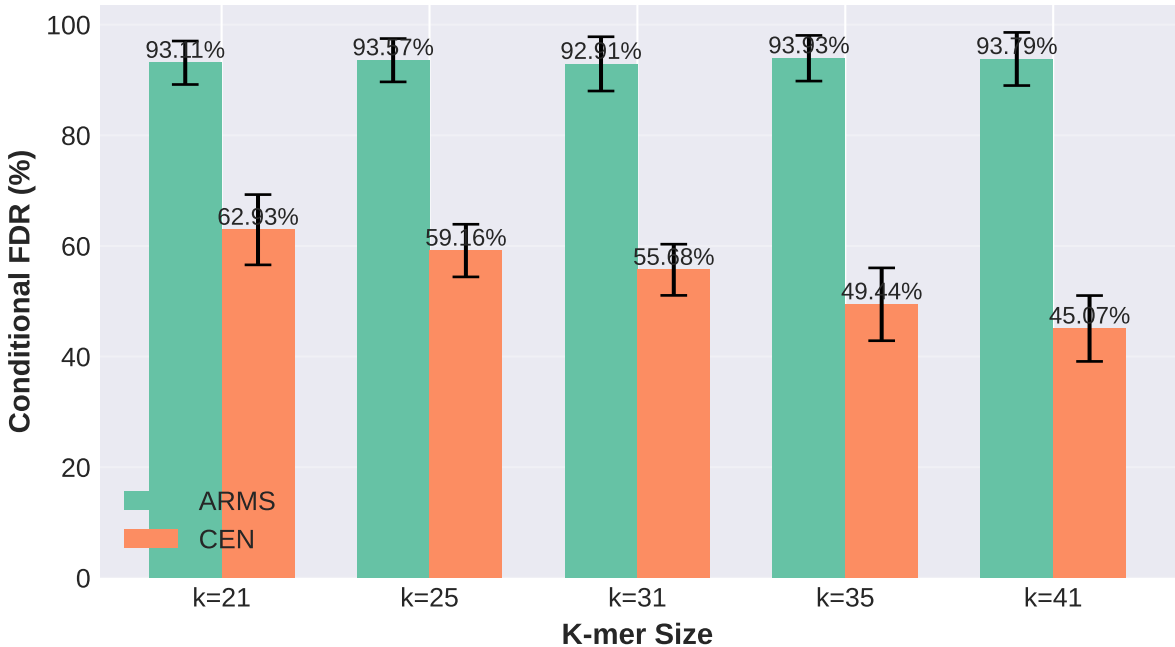
Cross-Contamination Risk from Sequencing Errors (1% per-base error rate, ONT-like)

Note: High conditional FDR expected

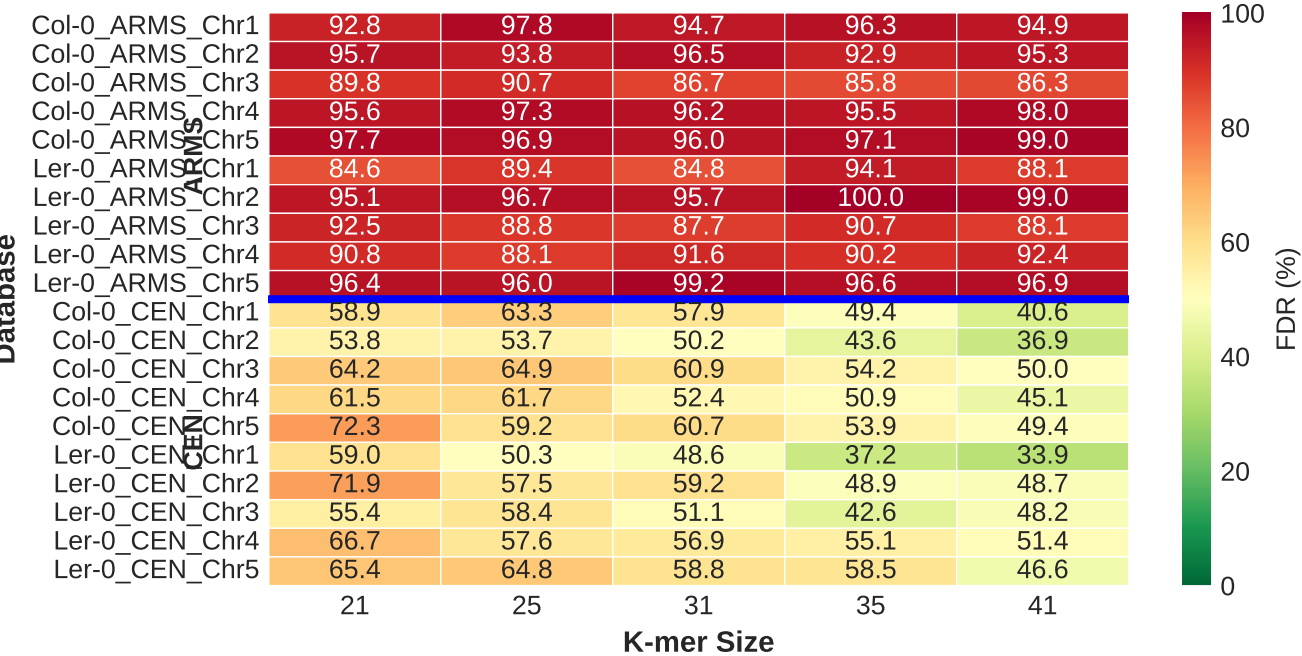
A. False Discovery Rate (FDR = FP/(FP+TP))



B. FDR Among K-mers WITH Errors



C. Per-Database FDR Values



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

