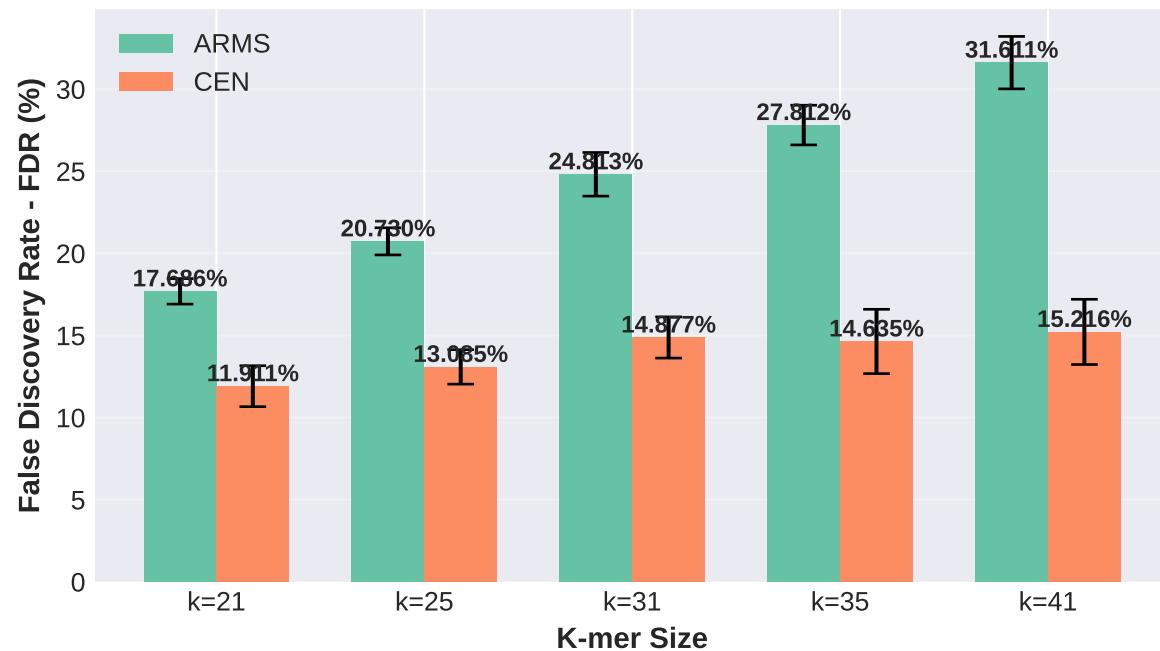


# Cross-Contamination Risk from Sequencing Errors

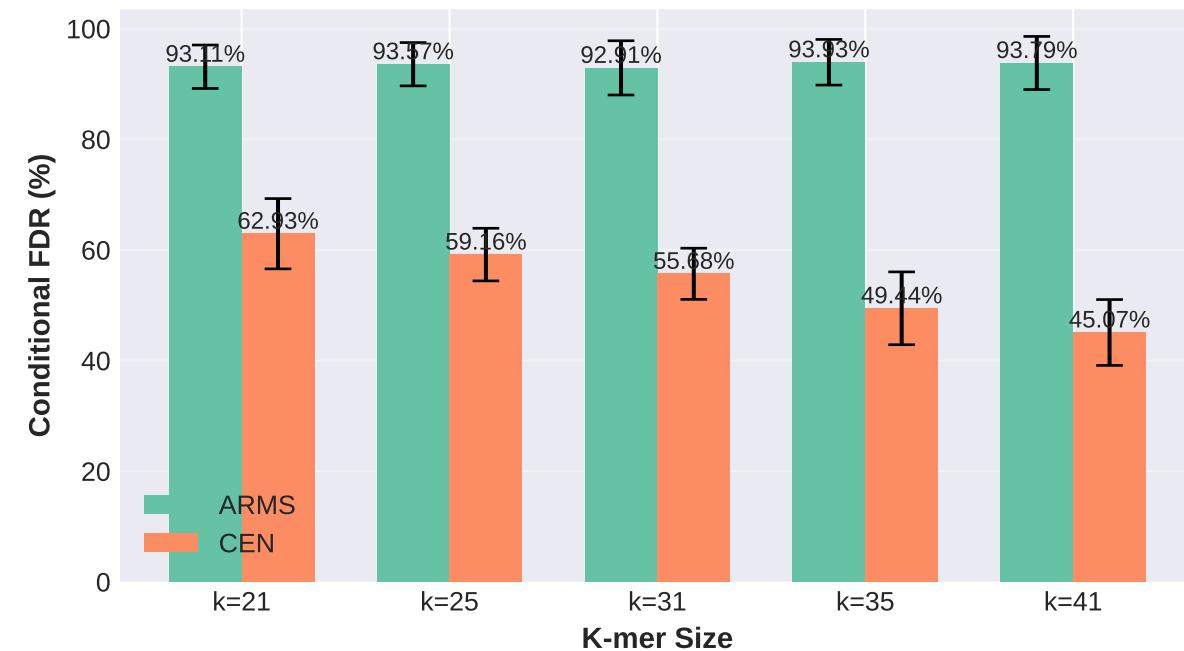
(1% per-base error rate, ONT-like)

Note: High conditional FDR expected

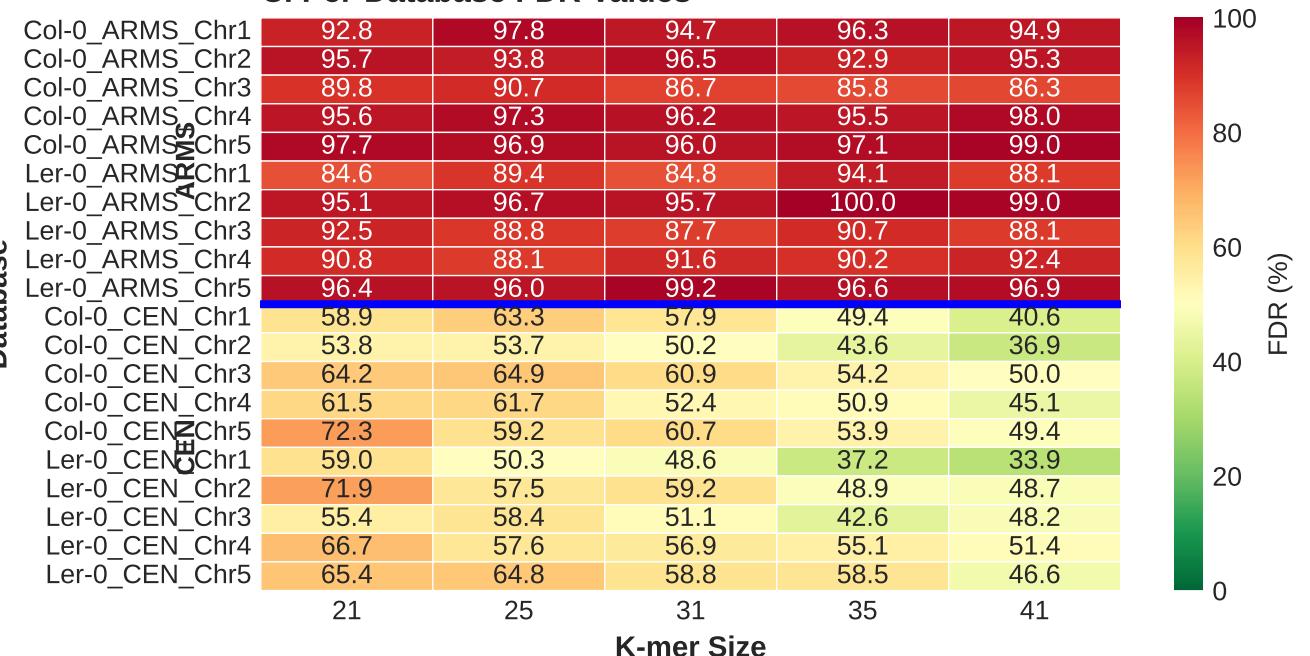
**A. False Discovery Rate (FDR = FP/(FP+TP))**



**B. FDR Among K-mers WITH Errors**



**C. Per-Database FDR Values**



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

