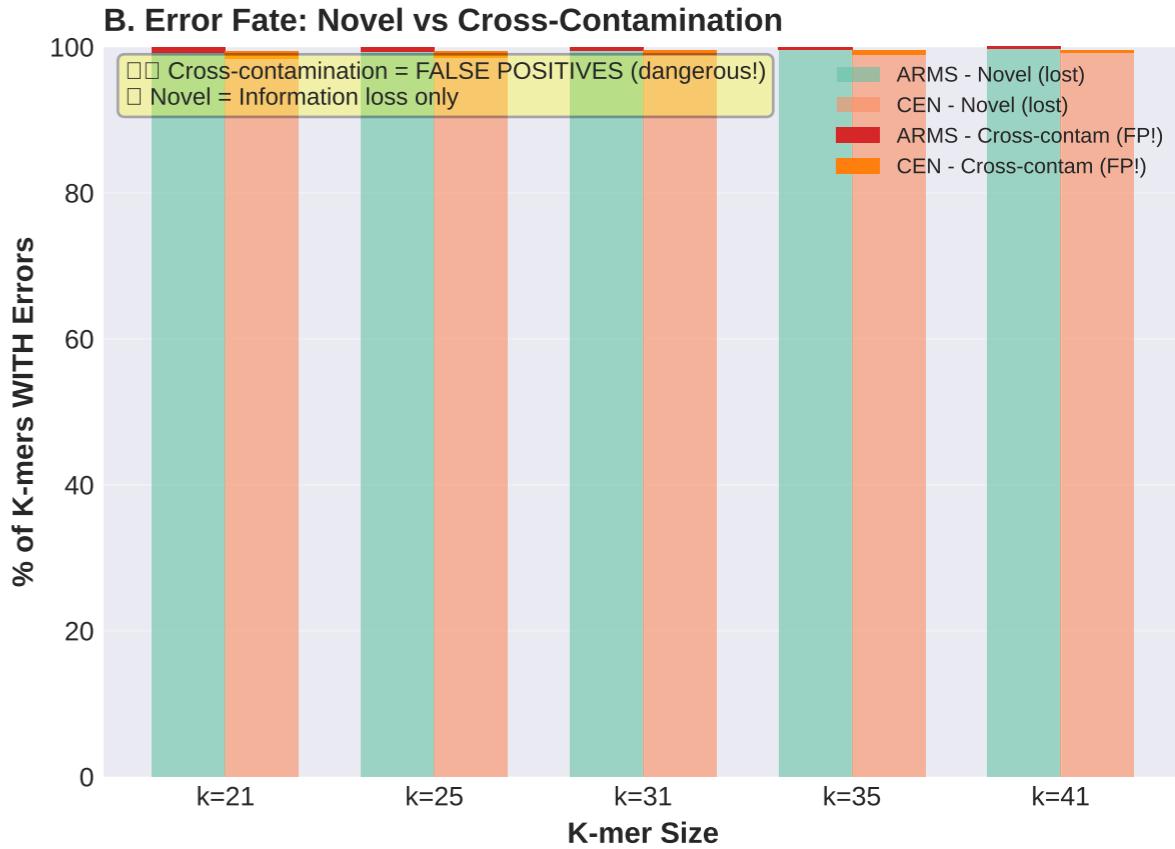
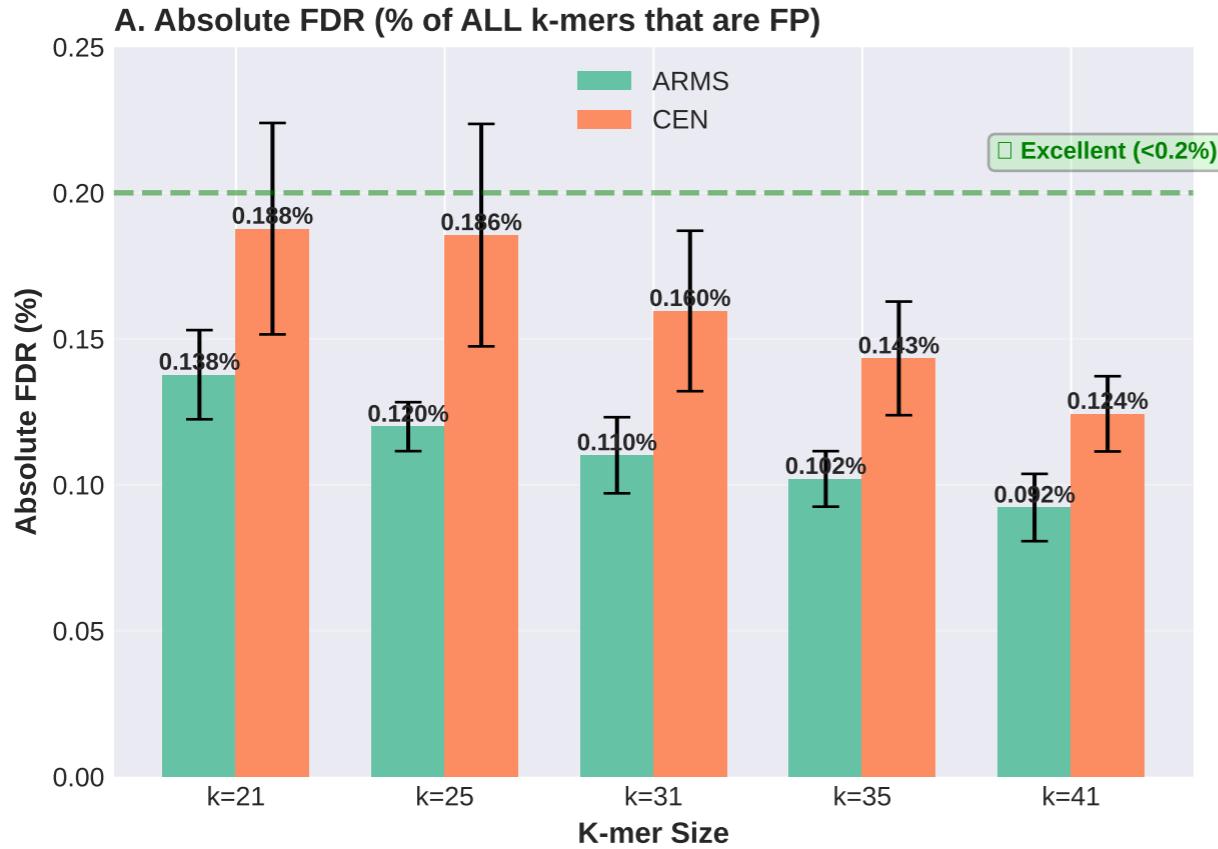
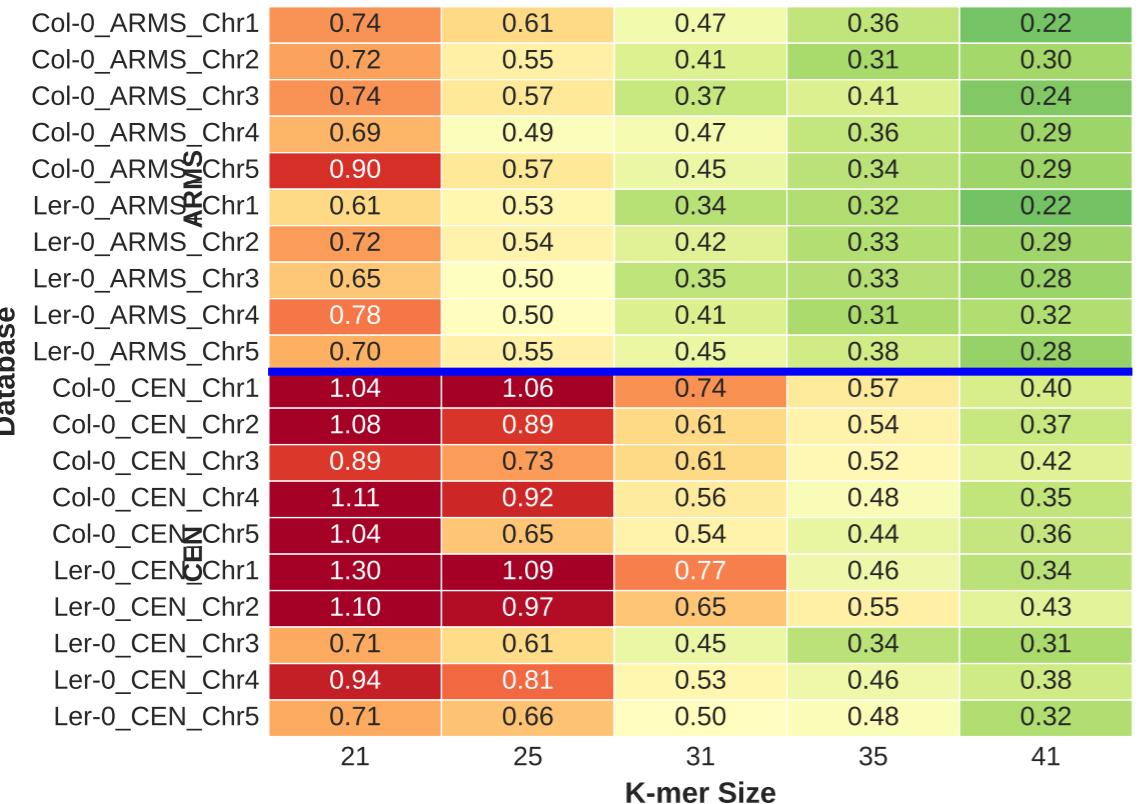


Cross-Contamination Risk from Sequencing Errors (1% per-base error rate, ONT-like)



C. Cross-Contamination Rate (False Positives!)



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

