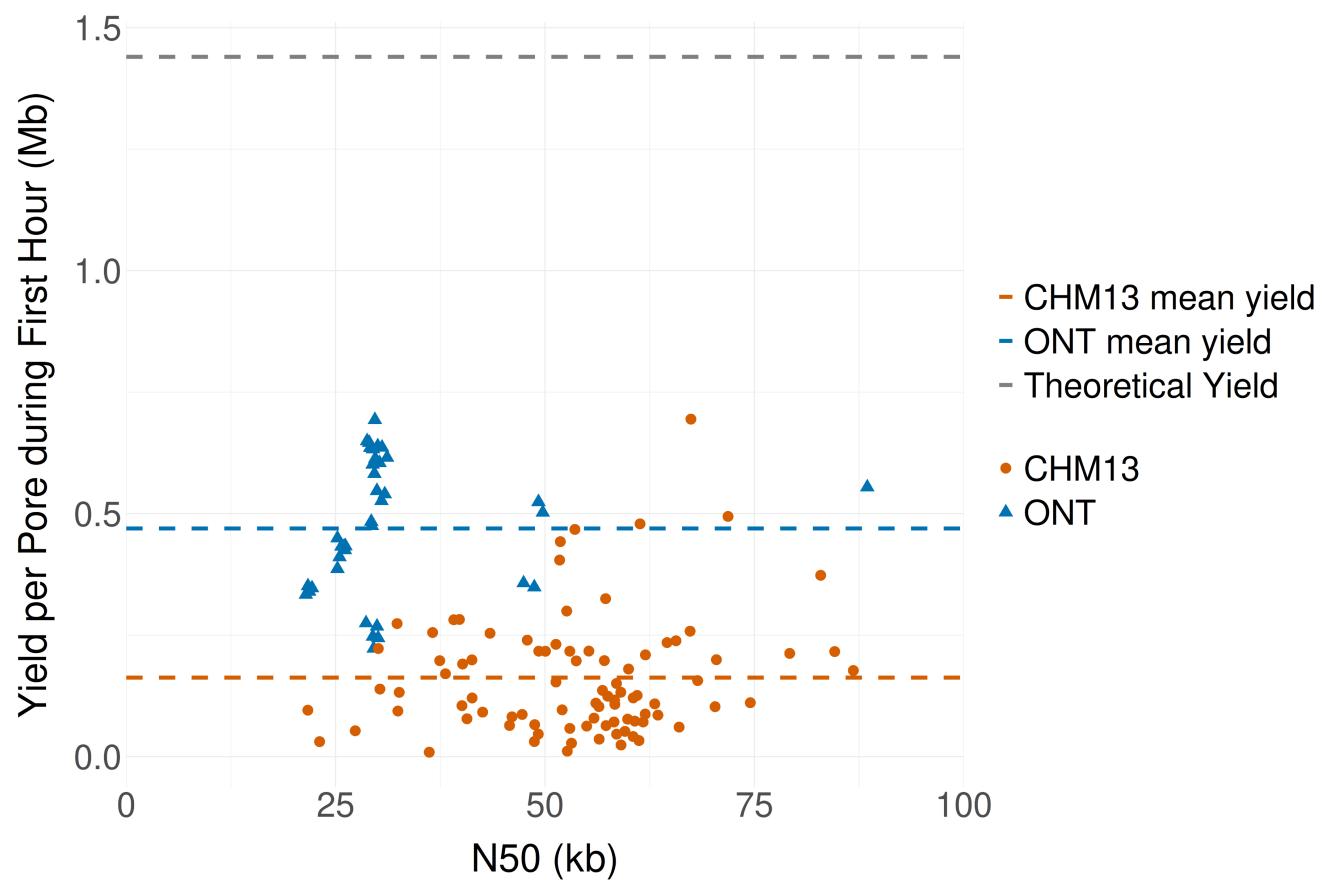
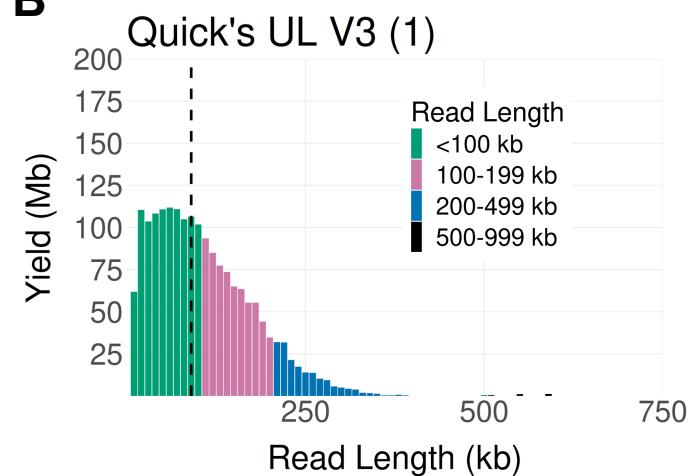
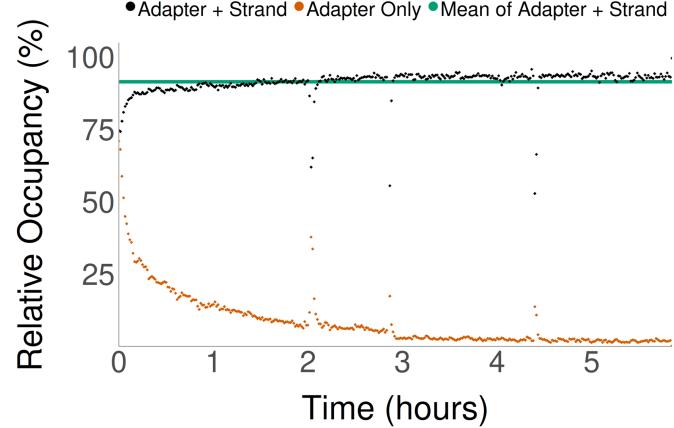
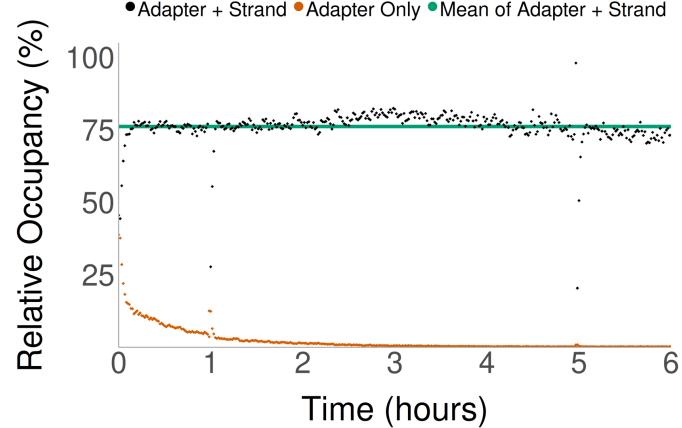
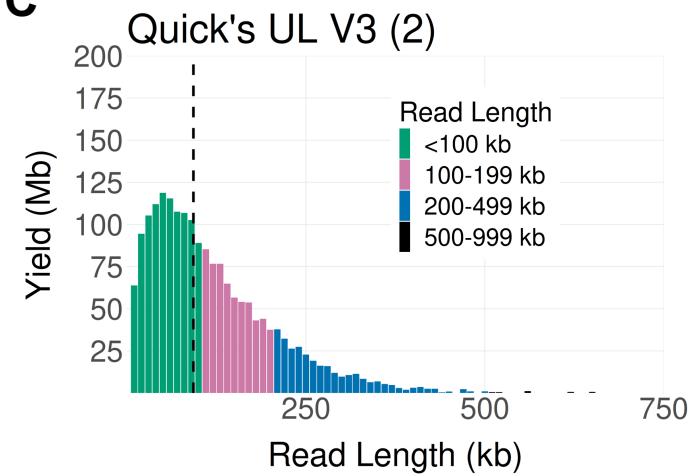
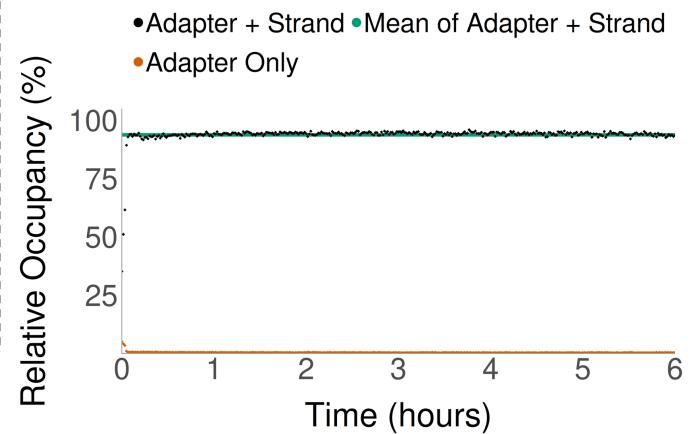
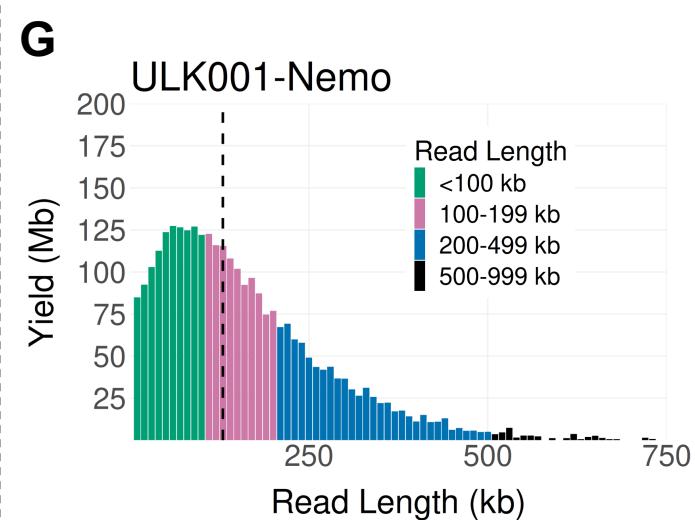
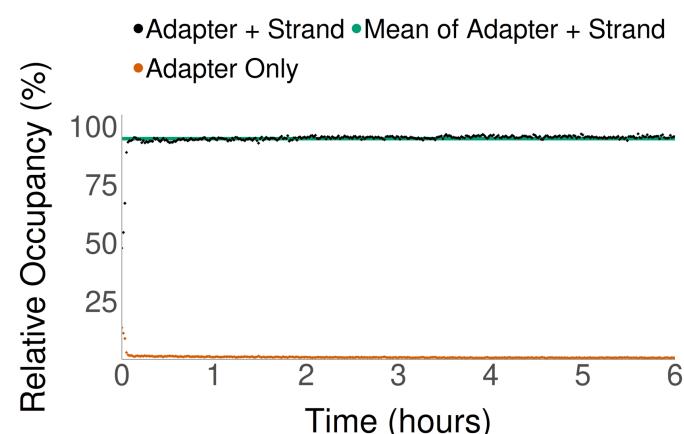
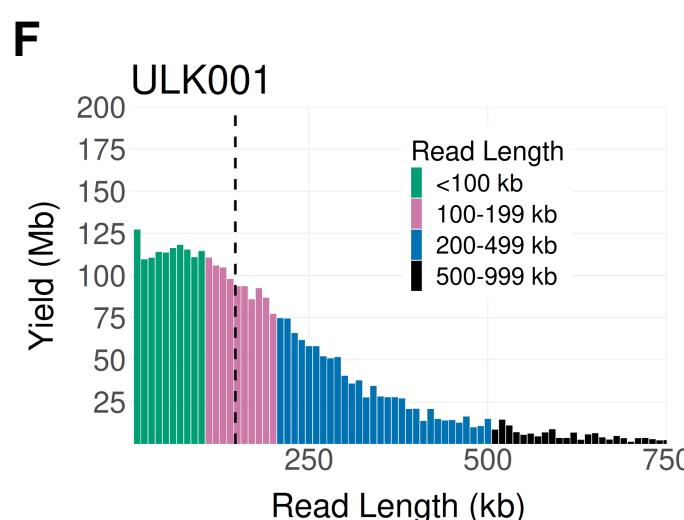
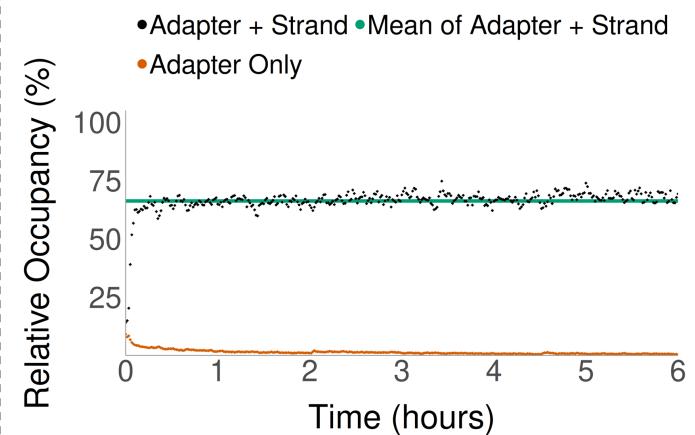
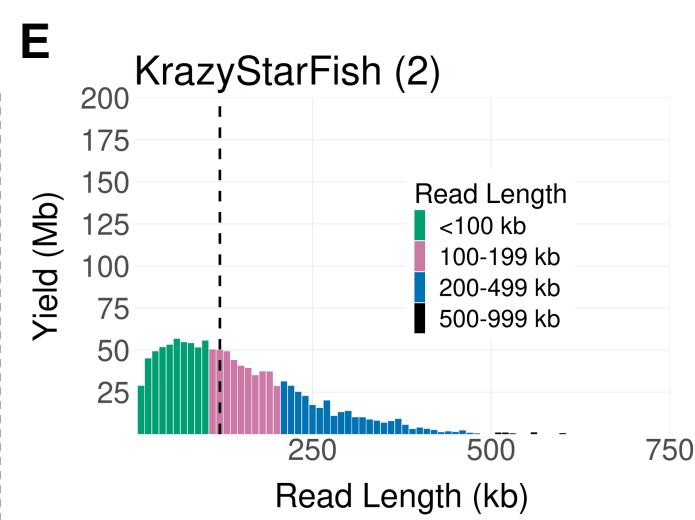
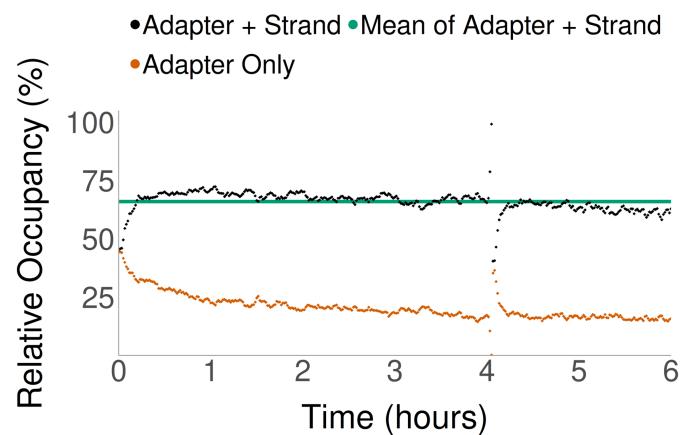
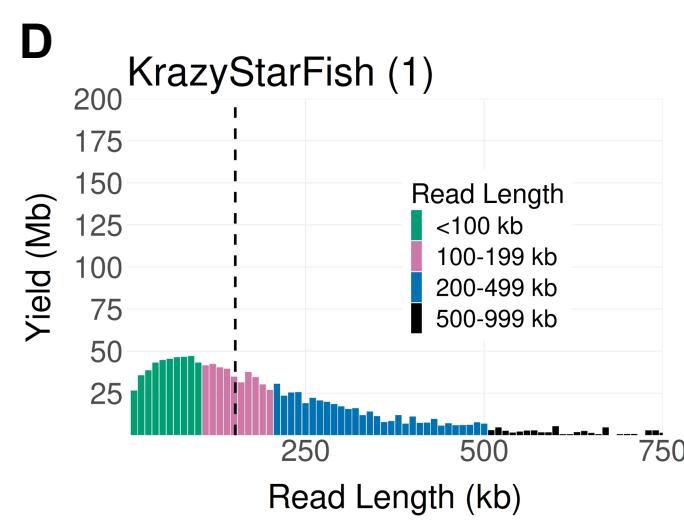


A**B****C**



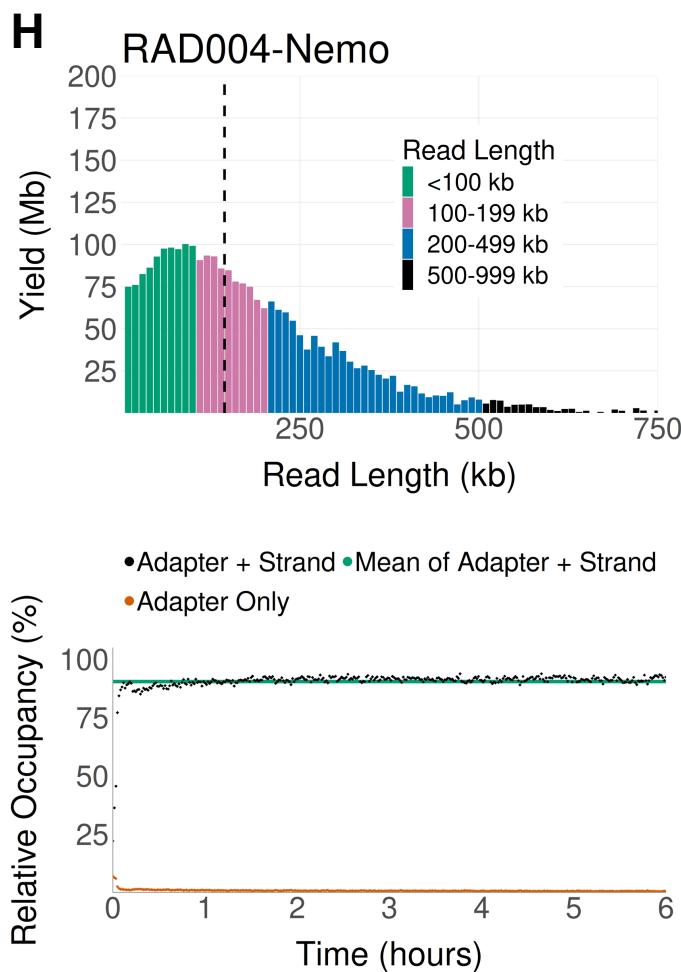


Figure S1. Comparison of sequencing outputs of early ultra-long (UL) library preparation protocols. Sequencing yields of the CHM13 ultra-long data (Logsdon et al. 2021) were lower on average compared to publicly available ONT data (GM24385 and GM24631) obtained from ligation-based libraries (A). We previously developed two protocols based on the RAD004 kit: Original Quick's UL v3 (B-C) and KrazyStarFish (KSF) (D-E). New protocols based on Nemo clean-up were developed afterward, with comparable outputs to the control ULK001 protocol (F-H).

(B-H) Upper panels = read length distribution with N50 value shown as a black dashed line; lower panels = timelapse of relative pore occupancy. All data show 6 hours of run time. All libraries were prepared from GM12878 cells, loaded on MinION flow cells, and sequenced on the GridION platform.