

Short-read vs hybrid polishing

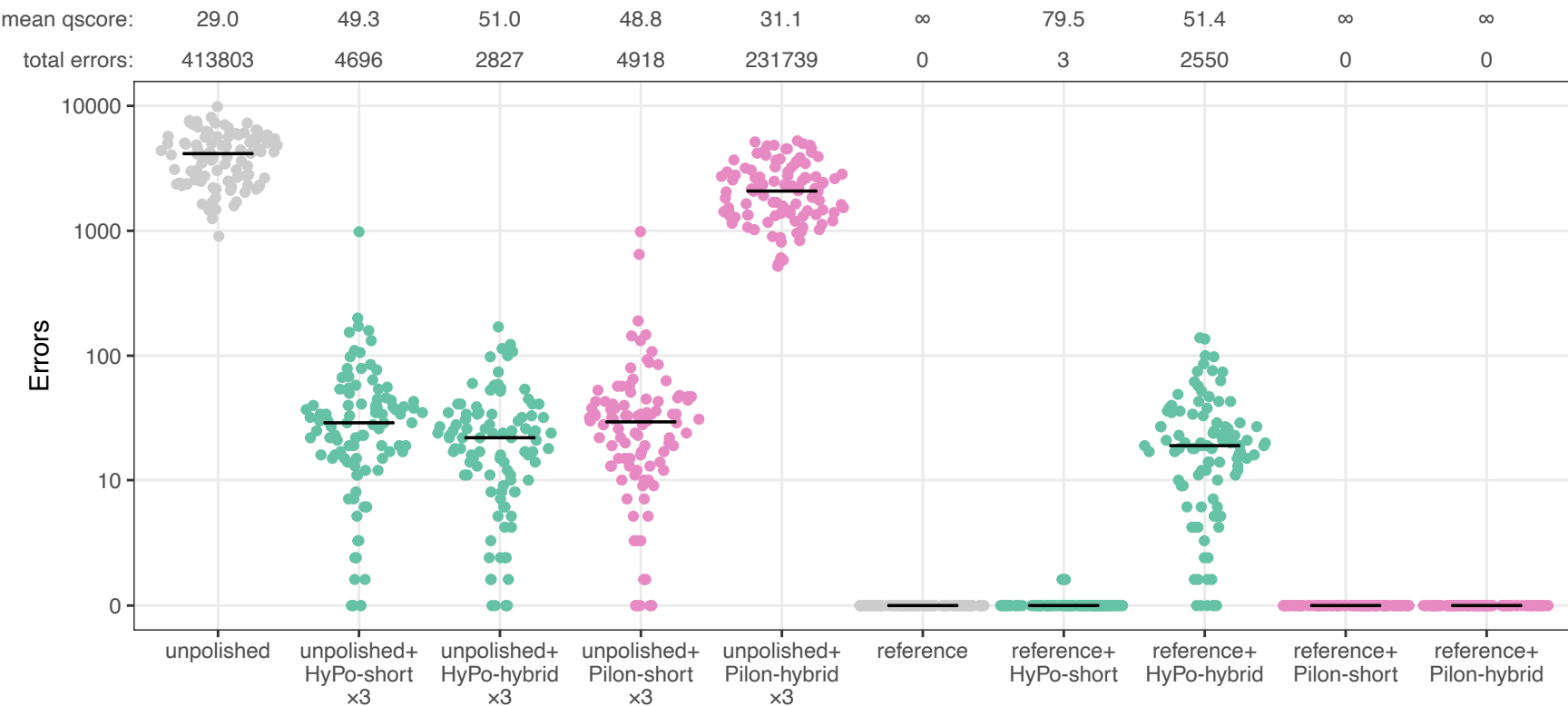


Figure S5: short-read vs hybrid polishing benchmarking results using 100 genomes with simulated Illumina reads. Using the unpolished error-containing sequence as input, per-genome error rates are shown after three rounds of polishing with a single tool. Using the error-free reference sequence as input, per-genome error rates are shown after one round of polishing with a single tool. Mean qscores and error totals are shown at the top of the plot, and the horizontal lines indicate median error rates for each polisher.