Short-read polishing of reference, overall errors
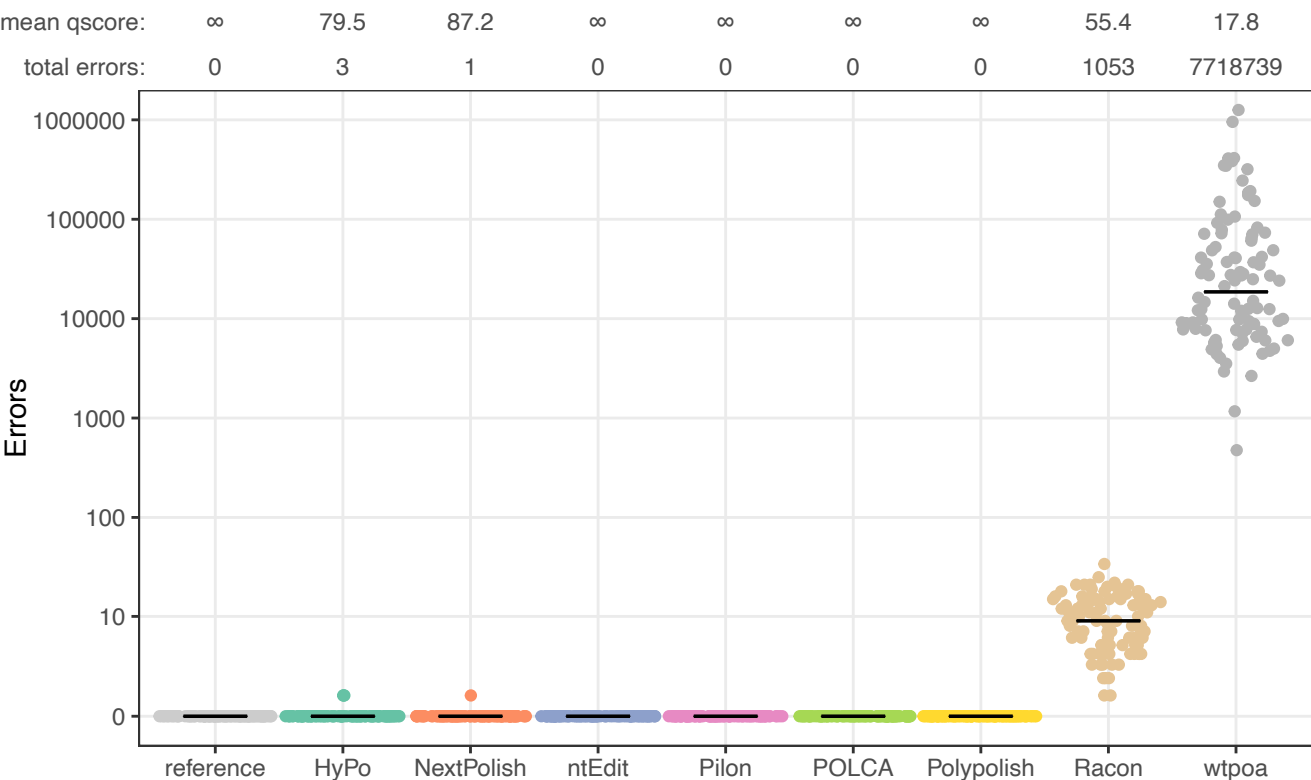

Figure S3: short-read polishing tool benchmarking results using 100 genomes with simulated Illumina reads, using the error-free reference sequence as input. Per-genome error rates are shown after one round of polishing with a single tool. Mean qscores and error totals are shown at the top of the plot, and the horizontal lines indicate median error rates for each polisher.