Short-read vs hybrid polishing
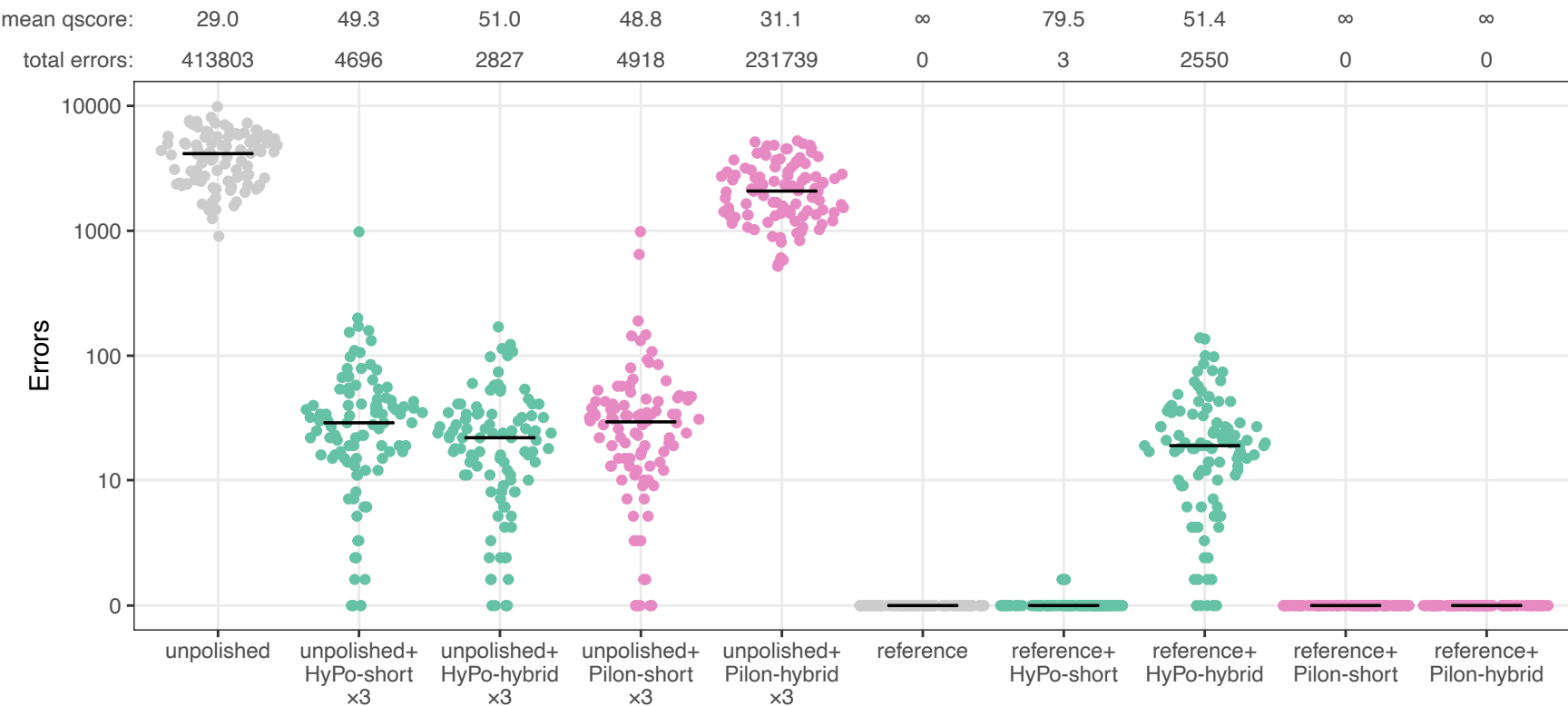
mean qscore:	29.0	49.3	51.0	48.8	31.1	∞	79.5	51.4	∞	∞
total errors:	413803	4696	2827	4918	231739	0	3	2550	0	0

Figure S6: 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.