Short-read vs hybrid polishing

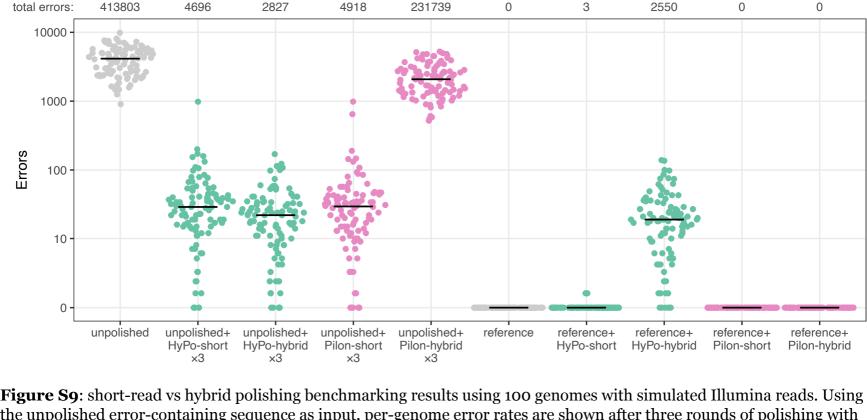
49.3

51.0

48.8

29.0

mean qscore:



31.1

79.5

51.4

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.