Short-read vs hybrid polishing 29.0 49.3 51.0

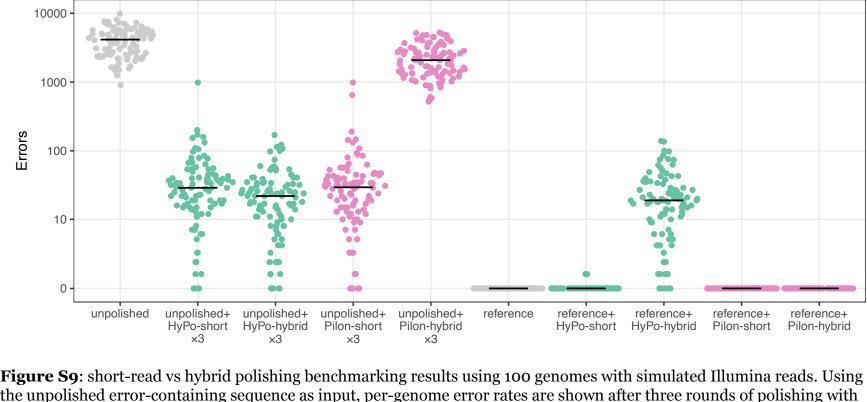
4696

2827

413803

mean qscore:

total errors:



31.1

231739

0

48.8

4918

79.5

3

51.4

2550

0

0

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 ascores and error totals are shown at the top of the plot, and the horizontal lines indicate median error rates for each polisher.