Short-read polishing of reference, overall errors 55.4 17.8 mean gscore: 79.5 87.2 3 total errors: 0 0 0 1053 7718739 0 1000000 100000 10000 1000 100 10 0

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.

Pilon

POLCA

Polypolish

Racon

wtpoa

ntÉdit

HvPo

reference

NextPolish