

**Supplemental table S3.** Closing gaps in a human genome draft assembly using Sealer with different  $k$  value ranges.

	Run 1 ( $k=250 - 120$ , step 10)	Run 2 ( $k=125 - 40$ , step 5)	Run 1 + Run 2 combined
Number of gaps closed	58,432	62,244	120,676
% closed	24.6	26.2	50.8
Average gap size ( $\pm$ S.D. bp)	$5.55 \pm 72.73$	$55.72 \pm 73.77$	$31.58 \pm 77.40$
Longest gap closed (bp)	195	403	403
Longest overlap closed (bp)	149	125	149