

DNA Size Selection for PacBio® Hi-Fi™ CCS Reads: New SageELF™ Waveforms

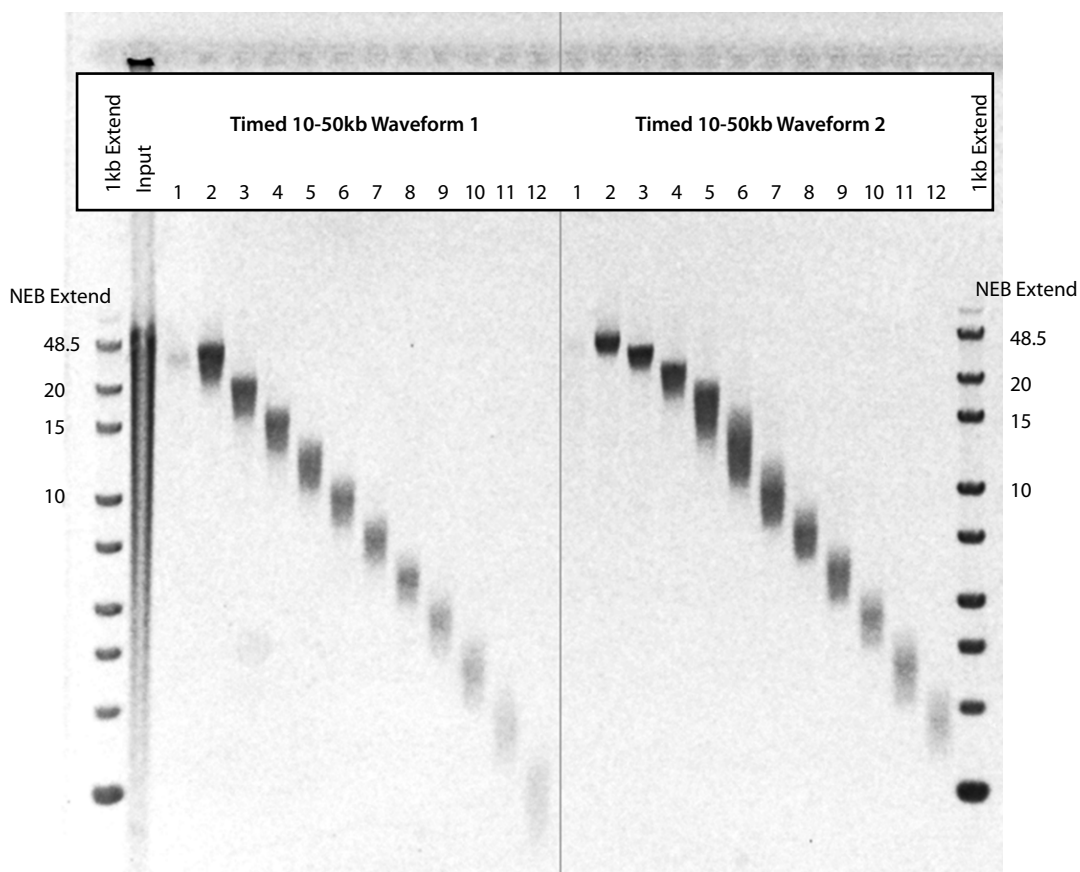


PacBio Hi-Fi sequencing has become the gold standard for genomic assembly. By repeatedly sequencing around a SMRT Bells, high consensus sequencing accuracy can be achieved on 10 - 20kb (and ultimately beyond) templates. Advances in assembly programs such as HiCanu¹ have been used to accurately assemble centromeres, segmental duplications and allelic variants with Hi-Fi sequencing data.



Hi-Fi sequencing is most efficient when SMRT-Bell templates are similarly sized within a library optimized to a PacBio Sequel's movie length. In order to size these libraries, many researchers prefer Sage Science's SageELF system for whole sample DNA fractionation. The SageELF offers the best way to achieve narrow fragment distributions with high molecular weight DNA.

Recently, Sage has developed two new SageELF waveforms that users have found particularly useful for selecting narrow size ranges between 10-50kb. Shown in the gel image below, the waveform result is slight variations in size range (and hence DNA amount) for users to select from elution wells of a SageELF cassette. Run times are 3 hours 45 minutes.



Gel Images of SageELF DNA fractions using new timed waveforms for PacBio Hi-Fi libraries

¹Nurk, S. et al., 2019, *HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads.* *BioRxiv preprint*, <https://doi.org/10.1101/2020.03.14.992248>