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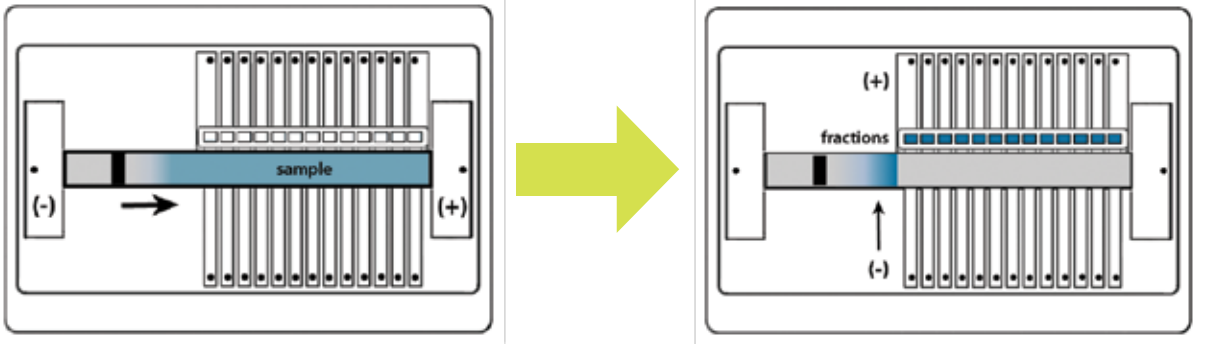
SageELF™

DNA Fractionation for Next Gen Sequencing

sage science

ELF: Electrophoretic Lateral Fractionation

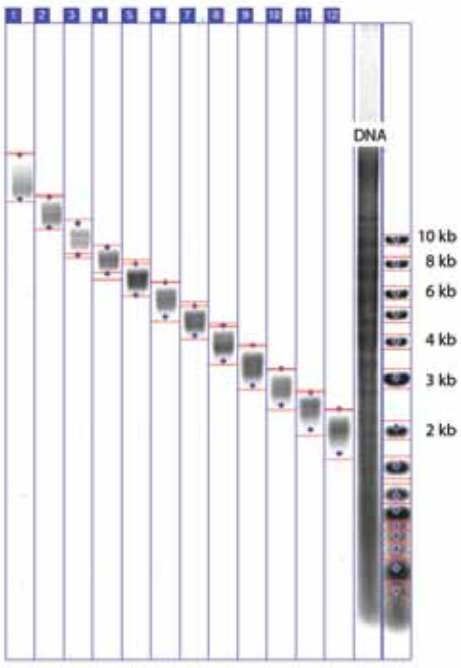
The SageELF is a novel tool for fractionating DNA samples for next-gen sequencing. Featuring a unique electrophoretic design, the platform slices DNA samples into 12 contiguous fractions, and collects them in separate buffer-filled sample wells. We've simplified the process to a few short steps: we provide the precast gel, software predicts the fractionation profile, and then you load your sample. After 2-3 hours, simply collect your fractions in buffer using a pipette.



The SageELF gel cassette separates DNA along an agarose gel column. At the end of a user-programmed run time, a second set of electrodes is activated. DNA fractions are then side-eluted into 12 membrane-bound wells. The cassette design includes a novel continuous buffering system which ensures DNA does not diffuse away from the gel during separation, and that fractions are evenly collected during electro-elution.

Whole Sample Fractionation for NGS:

- Construct libraries with multiple insert sizes
- Pool fractions to optimize library size and amount
- Reduce complexity of total RNA samples
- Recover and archive valuable samples



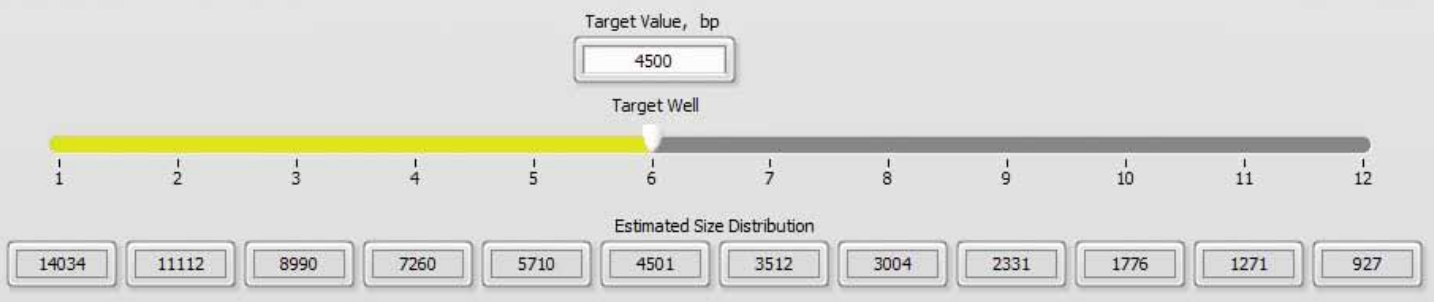
Fractions collected after 180 minutes. Analyzed by pulsed field electrophoresis (Pippin Pulse).

A New Frontier In DNA Size Selection

Multiple-size NGS libraries from a single sample provide more flexibility in addressing sequencing challenges such as structural rearrangements, splice variant discovery, closing gaps, and understanding complex genomes. The SageELF is a unique tool for serious genomic research, offering fuller utilization of DNA samples (and preservation of rare ones) and an avenue for obtaining deeper sequencing knowledge.

Finding Your Range

Using precast gel cassettes with different agarose resolutions, and electrophoresis voltage control (including pulsed-field), the SageELF offers a unique approach to DNA manipulation with minimal effort. To estimate the size of your fractions, select a target collection well and enter a size value. The software will predict the average size of DNA fragments that will be collected in the remaining wells:



Choose between two calibrated fractionation methods, and stay informed as Sage Science releases new ones:

- 100-2300bp (2% Agarose)
- 1-18kb (0.75% Agarose, with pulsed-field)

Specifications and FAQs

How accurate are the fraction size estimates?

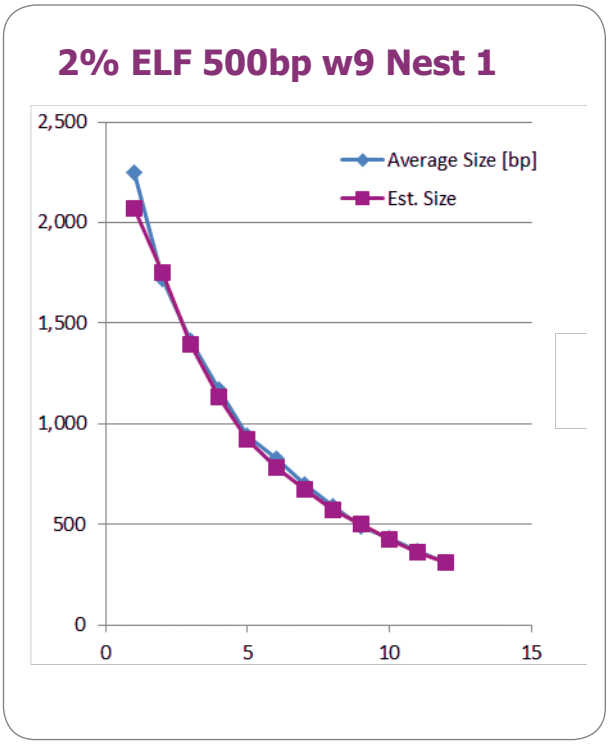
An internal standard is provided to normalize the run time. Fraction sizes are typically within 15% of the software input value (within the range provided) when the internal standard is used.

How much DNA is recovered?

Between 50-80% of a sample can be recovered if the whole sample is fractionated.

How narrow are the size distributions?

This depends on the electrophoresis protocol, the position of the collection well, and the relative size of the fragments collected. For smaller fragments (100-500 bp), minimum distributions have approximately 10% CV. Larger fragments (10kb and above) will have distributions with 20-30% CV.



A plot of the average fraction size (bp) recovered in each collection well (1-12). A 500 bp value was entered as a target in well 9.

In the Literature:

"Of the three sizing fractionation methods tested for target recovery efficiency, throughput, and risk of cross-sample contamination, Pippin Prep, an automated optical electrophoretic system that does not require gel extraction, was the most efficient and reproducible, with the tightest, most specific sizing."

— Extracted from Duhaime et al. "Towards quantitative metagenomics of wild viruses and other ultra-low concentration DNA samples: a rigorous assessment and optimization of the linker amplification method," Environmental Microbiology (2012) 14(9), 2526–2537.

"Bioanalyzer results suggested that [Pippin] automated size-selection libraries were substantially more consistent than gel extraction libraries. In contrast to automated size-selected samples, gel excision samples did not appear to saturate in the range of coverage observed. This is likely because size selection was imprecise or 'leaky,' with substantial representation of fragments of lengths relatively distant from the size-selection target mean. Careful practitioners can achieve roughly 50% of the precision and repeatability of automated DNA size selection."

— Extracted from Peterson et al. "Double Digest RADseq: An Inexpensive Method for De Novo SNP Discovery and Genotyping in Model and Non-Model Species," PLoS ONE 7(5): e37135. doi:10.1371/journal.pone.0037135