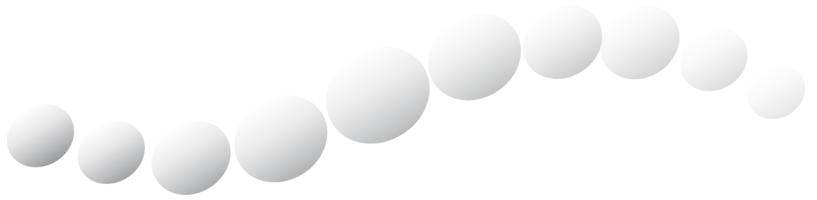


NEW

PippinHT™

DNA Size Selection for NGS



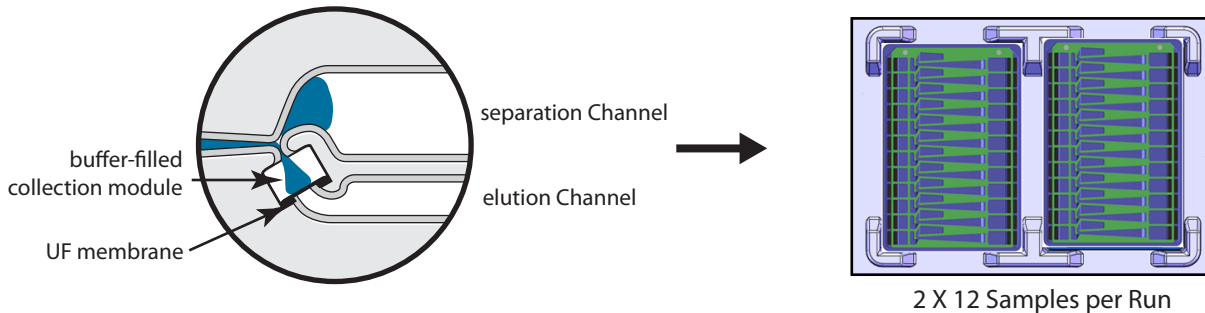
Size-Select up to 24 DNA Samples in 30 Minutes

Benefits:

- Generates higher quality libraries for improved sequence informatics
- Fragment sizes and ranges are reproducibly collected, providing consistent results, run-to-run
- Flexible programming allows collection of multiple size ranges, or up to 24 collections of the same fragment range



Automated Preparative Electrophoresis



Sage's proprietary technology, featuring electro-elution from agarose, has been configured to run 12 samples on an SBS-footprint gel cassette— **for higher throughput workflows and with a lower cost per sample.**

Specifications:

Sample Capacity	Maximum Sample Load	Run Times	Target Range	Min. Size Distribution as Expressed by (CV)	Accuracy*	Reproducibility**
12 samples/cassette	1.5 µg	20-90 minutes	90 - 2000 bp	≤8%	≥ 90%	≥ 90%
2 cassettes (24 samples)/run		30 min for 500 bp				

* 100% minus the deviation of actual target value (Agilent Bioanalyzer) from software input value divided by the actual value.

** 100% minus 2X standard deviation of replicate samples.

Take Good Care of Your Library.



Automated Size Selection: An indispensable tool for NGS library construction.

Selected References Citing Pippin DNA Size Selection

Paired-End Sequencing

Sheaffer, K.L. *et al.* DNA methylation is required for the control of stem cell differentiation in the small intestine. *Genes Dev.* 28: 652-664 (2014)

Mate-Pair Sequencing

Srivastava, A. *et al.* Discovery of transgene insertion sites by high throughput sequencing of mate pair libraries. *BMC Genomics*, 15:367 (2014)

Long Read Sequencing

Benson, M.A. *et al.* Evolution of hypervirulence by a MRSA clone through acquisition of a transposable element. *Molecular Microbiology*, 93(4), 664-681 (2014)

miRNA isolation

Singhal, R. *et al.* FOXO1 regulates expression of a microRNA cluster on X chromosome. *AGING*, 5:5 (2013)

ChIP-seq

Lane, A. A., *et al.* Triplication of a 21q22 region contributes to B cell transformation through HMGN1 overexpression and loss of histone H3 Lys27 trimethylation. *Nature Genetics*, 46:618-623 (2014)

Wharton, K., *et al.* Methylation and Next-Generation Sequencing of free circulating DNA from human plasma. *BMC Genomics*, 15:476 (2014)

Lin, C.Y. *et al.* Transcriptional Amplification in Tumor Cells with Elevated c-Myc. *Cell*, 151, 56-67 (2012)