

Distributed by:



Pippin™

Automated
DNA Size
Selection

NGS Library
Construction



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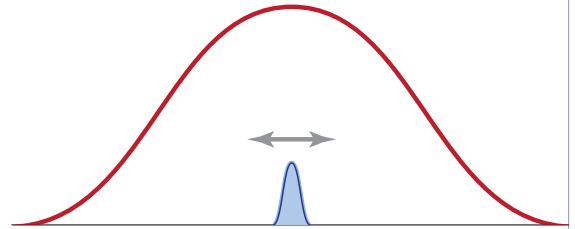
Flexible and Versatile

Size Selection modes

Tight:

Narrowest fragment range based on a target size

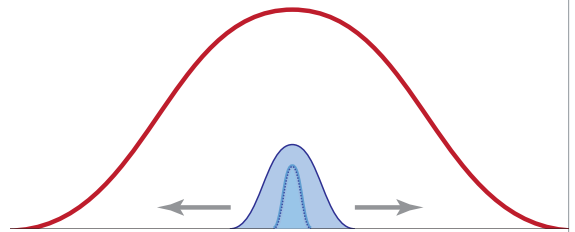
- Paired-end sequencing
- Emulsion prep



Range:

Set with start and end base pair values

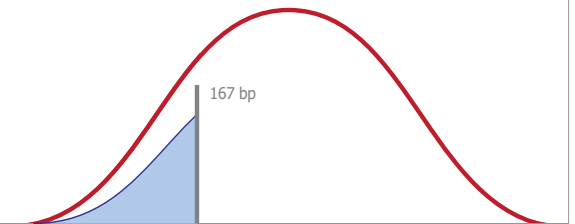
- RNA-seq
- Genotyping by sequencing
- ChIP-seq
- MicroRNA



Low-Pass:

Collects pre-library nucleic acids below a threshold

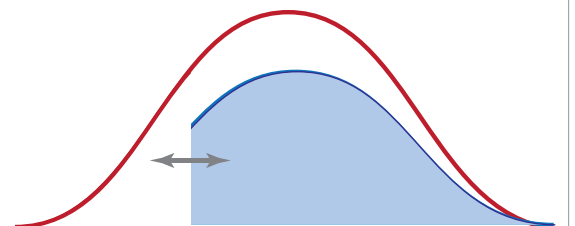
- Cell free DNA analysis



High-Pass:

Collects sizes above a base pair threshold

- Long-range genomics
- Long-read sequencing



Fragment Length (bp)

DNA Amount

Pippin Prep™

BluePippin™

PippinHT

Unlike any other method, automated DNA size selection allows users to select the optimal median fragment size, or adjust the base-pair range of selection. For any NGS platform, and particularly for multi-platform labs, the Pippin system's flexibility streamlines workflows and improves data quality.

A High Value Step

For Short-Read Sequencing...

Key Applications and Benefits

ddRAD-seq

Precisely collects fragments generated between restriction sites

RNA-seq

Removes unincorporated adapters from libraries

ATAC-seq

Purifies amplicon libraries

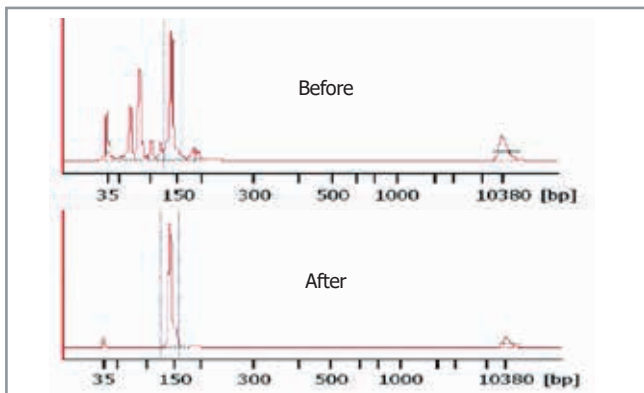
ChIP-seq

Improves identification of binding sites

cfDNA-seq

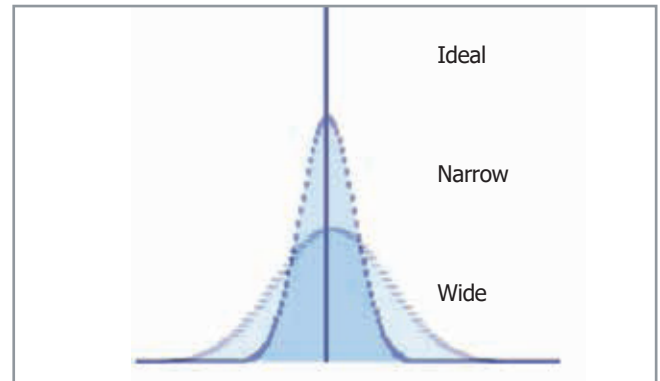
Size-selects nucleosome-associated DNA peaks from plasma

Remove Dimers and Unwanted Artifacts



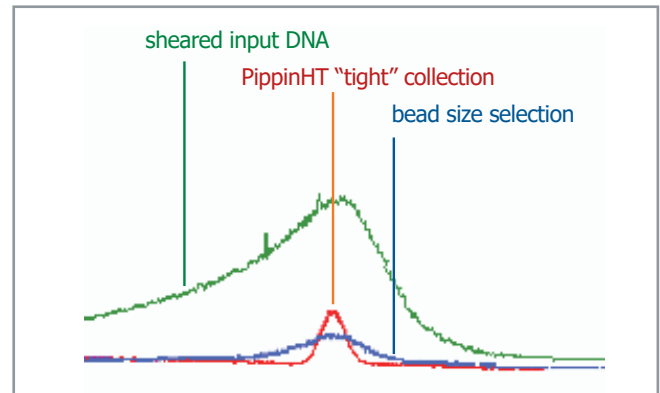
Using a PippinHT, unwanted artifacts can be removed from microRNA libraries using a range setting. 24 samples can be processed with a 30 minute run time.

Optimize Size Selection for NGS Platforms



Smaller DNA fragments will preferentially copy when amplified. This can create bias during clustering or emulsion preps. The presence of larger fragments can also lead to sequencing inefficiencies.

Improve Library Quality



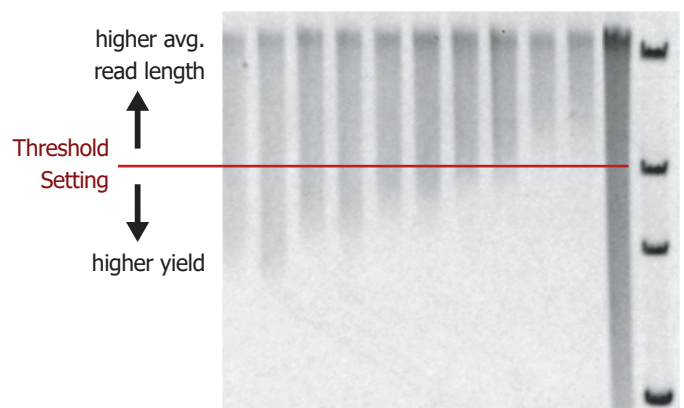
Bead-based size selection produces a significantly wider size distribution than Pippin. The product yield with beads is lower than Pippin, and the fragment range is not easily optimized.

...And Long-Read Sequencing

Pulsed-field enabled BluePippin and PippinHT systems are standard equipment for working with high molecular weight DNA.

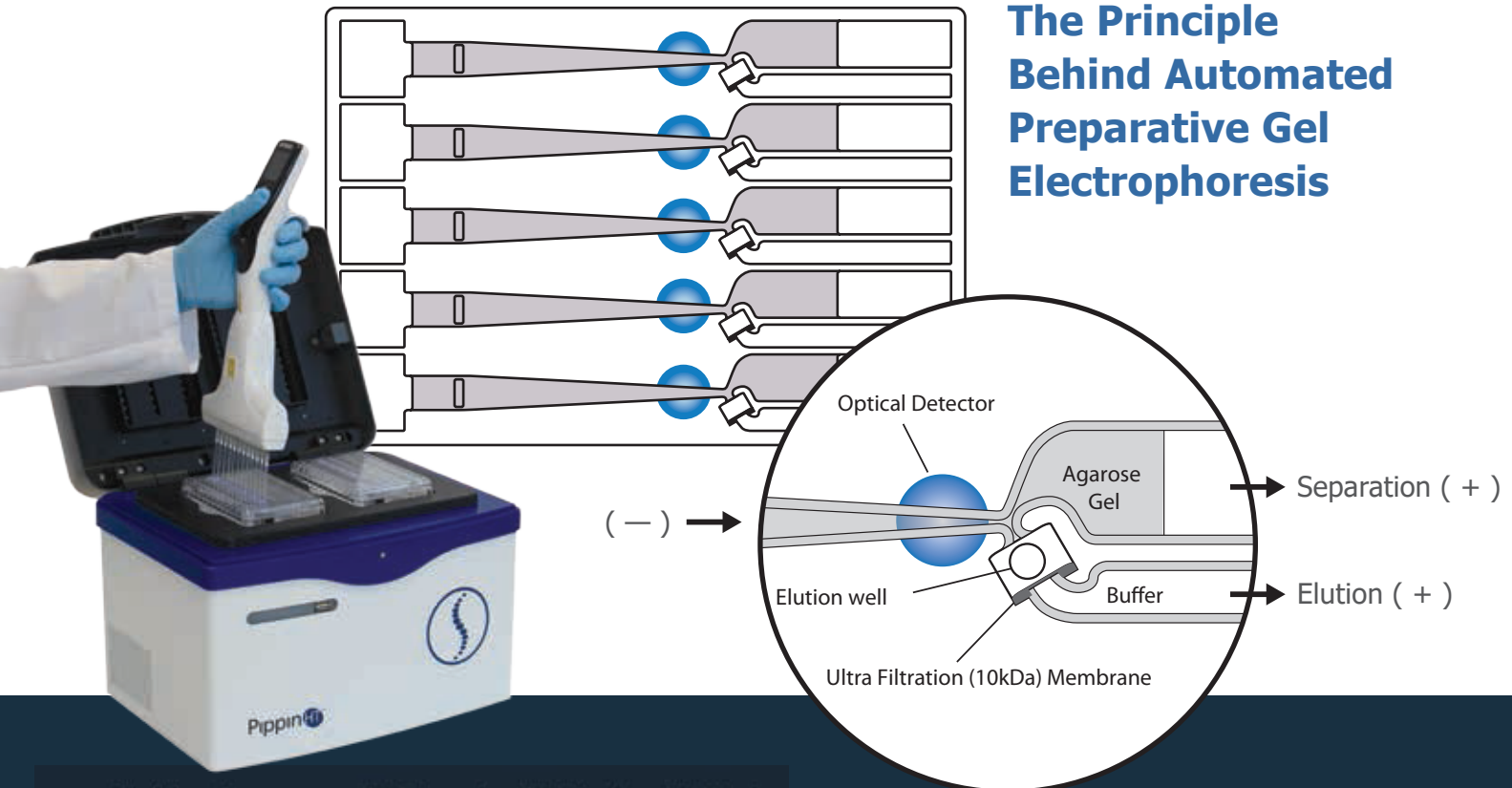
- **Single-Molecule Sequencing**
- **PacBio® HiFi™ CCS and CLR**
- **Oxford Nanopore™**

High-Pass Size Selections



High-pass removal of smaller DNA lets 3rd-gen sequencers focus on the longest fragments.

Pre-cast agarose gel cassette



The Principle Behind Automated Preparative Gel Electrophoresis



Set Your Collection Range with Easy-to-Use Software

Selection Chart	Pippin Prep	BluePippin	PippinHT
Max. DNA input	5 µg	5 µg	1.5 µg
Max. Sample Capacity	5	5	24
Pulsed-Field	No	Yes	Yes
Run Times (100 bp - 1.5 kb)	50-90 min	50-90 min*	25-45 min*
Size Selection Range	100 bp - 1.5 kb	100 bp - 50 kb	100 bp - 1.5 kb
High-Pass Size Filtering	No	Yes	Yes
Low-Pass Size Filtering	Yes	Yes	Yes

Specifications*

Accuracy	> 93%
Reproducibility	> 92%
Min. Size Distribution as CV	8%
Recovery	50-80%

* Pulsed-field protocols for HMW size selection may require up to several hours. Inquire at info@sagescience.com for run times and performance specifications.



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