Pippin™

Automated DNA Size Selection

NGS Library Construction



sage science

Flexible and Versatile

Pippin Prep™

BluePippin™

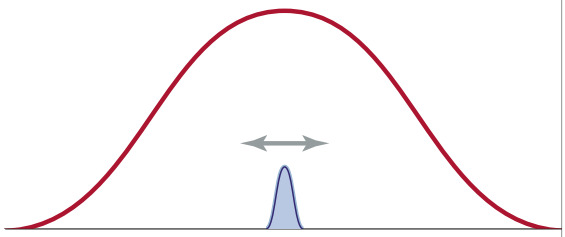
PippinHT

Size Selection modes

Tight:

Narrowest fragment range based on a target size

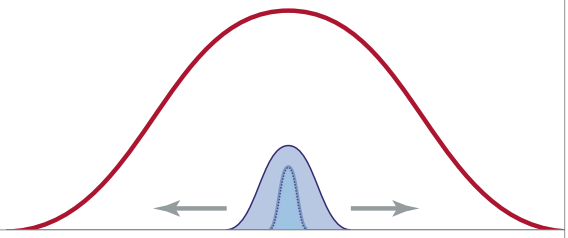
- Paired-end sequencing
- Emulsion prep



Range:

Set with start and end base pair values

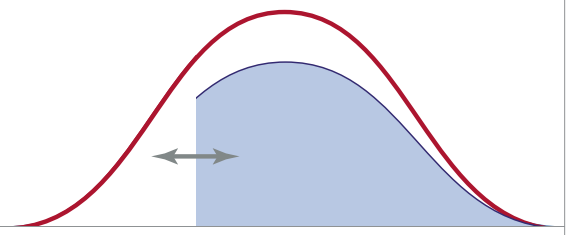
- RNA-seq
- Gentoyping by sequencing
- ChIP-seq
- MicroRNA



High-Pass:

Collects sizes above a base pair threshold

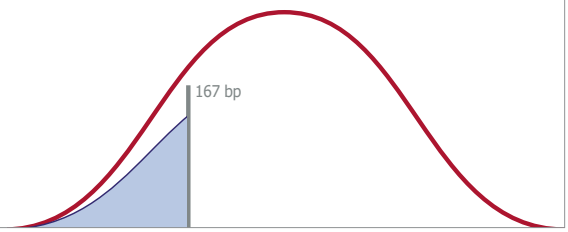
- Long-range genomics
- Long-read sequencing



Low-Pass:

Collects pre-library nucleic acids below a threshold

- Cell free DNA analysis



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.

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A High Value Step

For Short-Read Sequencing...

Key Applications and Benefits

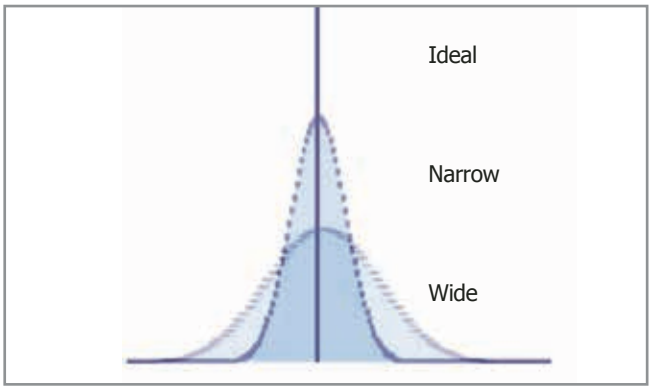
Paired-end Sequencing
Narrow size distributions improve assembly

RNA-seq
Removes adapter dimers from libraries

ddRAD-seq
Precisely collects fragments generated between restriction sites

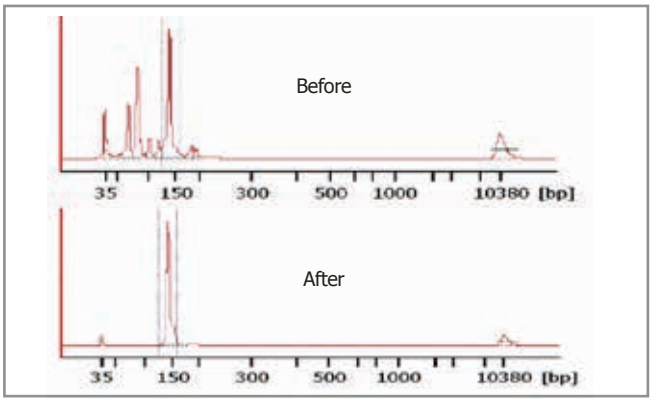
ChIP-seq
Improves identification of binding sites

Optimize Size Selection for NGS Platforms



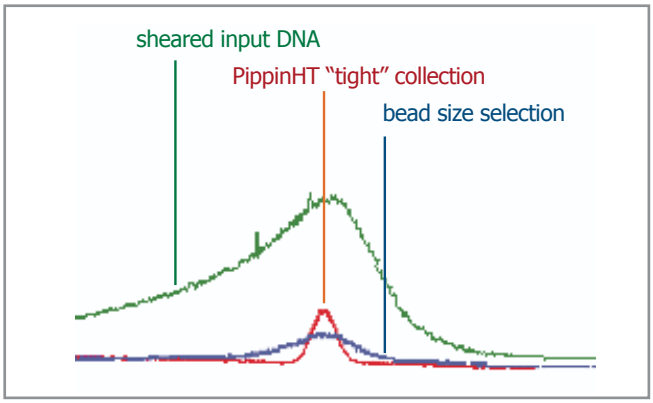
Smaller DNA fragments will preferentially copy when amplified. This can create bias during clustering or emulsion preps. The presence of larger fragments can also lead to sequencing inefficiencies.

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.

Improve Library Quality



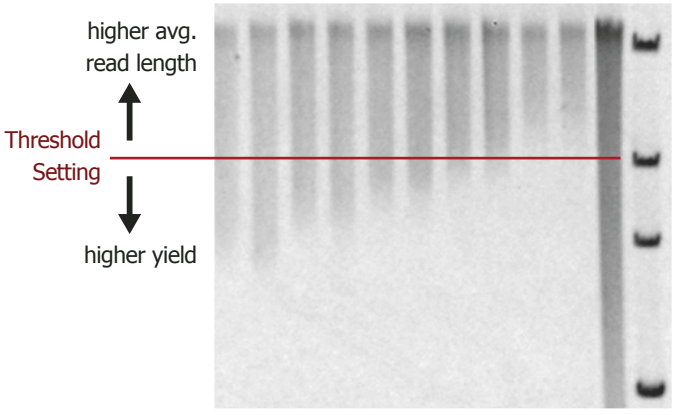
Bead-based size selection produces a signicantly wider size distribution than Pippin. The product yield with beads is lower than Pippin, and the fragment range is not easily optimized.

...And Long-Range Genomics

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

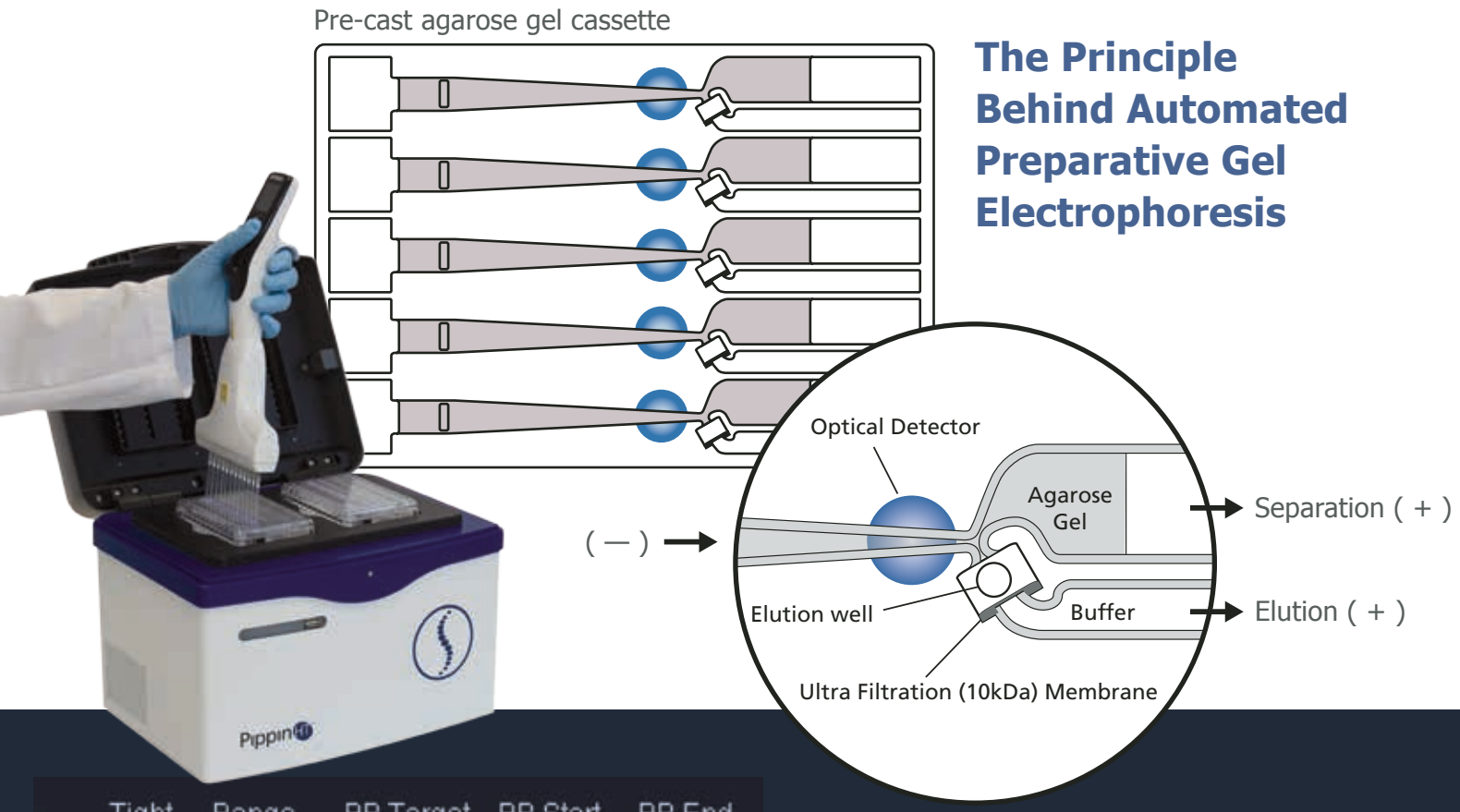
- **Single Molecule Sequencing**
- **Nanopore Sequencing**
- **Droplet Barcode Sequencing**

High-Pass Size Selections



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

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	No	No	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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