Pippin

DNA Size Selection

Automated Preparative
Gel Electrophoresis

sage science

BluePippin™

Collect targets between
90 bp – 50 kb

FEATURING PULSED-FIELD POWER

Pippin Prep™

Collect targets between
90 bp – 8 kb

Pippin

DNA Size Selection

An Automated Alternative to Manual Prep Gels

Pippin instruments are the best alternative to excising DNA from agarose slab gels and purifying with kits. In addition to significant savings in labor and effort, users see a better yield of higher-quality DNA than is possible with manual gels. Independent studies show that automated size selection with Pippin is more precise, reproducible, and higher throughput than is possible with manual gels.

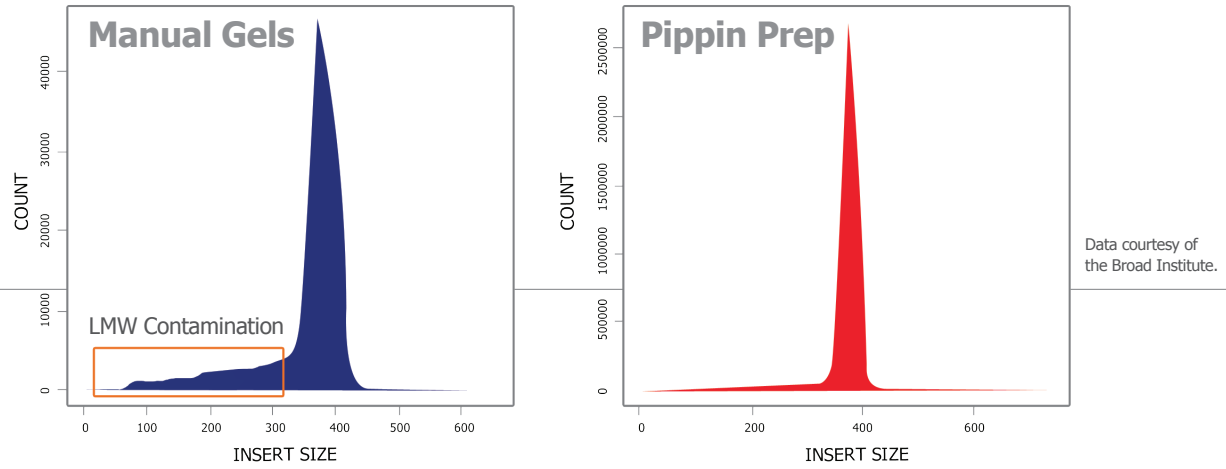
We offer the Pippin Prep for reproducible collections of smaller fragments, up to 8 kb. Our BluePippin facilitates the collection of larger fractions, up to 50 kb.

Key application areas:

- Library construction for paired-end sequencing
- Library construction for mate-pair sequencing
- Template preparation for clonal amplification of DNA on beads
- Library construction for Chromatin Immunoprecipitation (ChIP) techniques
- Isolation of miRNA libraries from adapter dimer and larger cDNAs
- RNA-seq
- Automated collection of PCR bands or restriction fragments

Benefits of the Pippin DNA size selection system:

- Minutes of labor saves time compared to manual gel purification
- Provides narrow fragment size distributions
- Minimal low molecular weight contamination reduces wasted reads and ambiguous indel calling
- Individual sample channels allow for multiplexing without sample cross-contamination
- Reproducible extractions provide more consistent results



Data courtesy of the Broad Institute.

The Advantages of Narrow Size Distributions for DNA Sequencing

Pippin size selection provides a narrow and uniform DNA fragment size distribution, with minimal LMW contamination. This provides key advantages to single-end and paired-end sequencing. For bead-based systems, a tightly sized library reduces amplification bias toward smaller fragments, providing a more efficient sequencing run. For paired-end sequencing, narrow size distributions provide optimal libraries for identifying indels and other structural variants.

Select and Collect

Size select DNA by entering a base pair target value, and the Pippin will collect the narrowest (Tight) distribution of fragments possible, centered on the target size. DNA may also be collected by entering a base pair range up to the allowable range of the gel cassette.

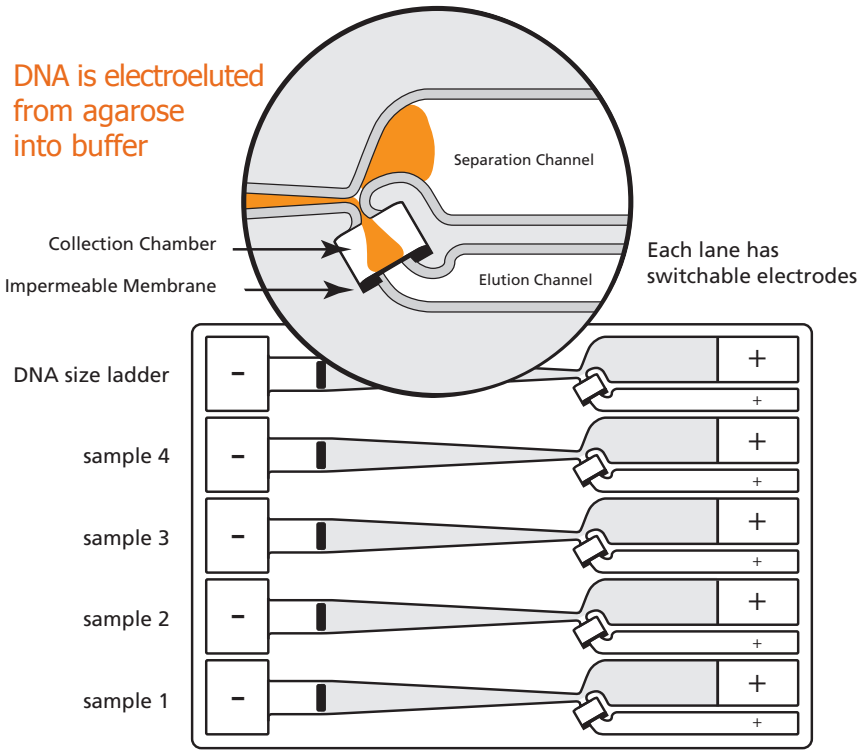
Specifications

Gel Cassettes:	**Target Range**
3.0% Agarose	90 bp – 250 bp
2.0% Agarose	100 bp – 600 bp
1.5% Agarose	250 bp – 1500 bp
0.75% Agarose (Pippin Prep)	2 kb – 8 kb
0.75% Agarose (BluePippin)	1 kb – 50 kb
Instruments:	
Optical Detection	Pippin Prep: 535 nm excitation, 640 nm emission BluePippin: 470 nm excitation, 525 nm emission
Power	100-240 VAC, 2.5 A, 50-60 Hz
Weight	15 lbs / 7 kg
Dimensions	7h x 11w x 21d (in), 18h x 28w x 53d (cm)

How the System Works

Pippin gel cassettes are pre-cast with agarose and are disposable. Sizing is determined by the detection of DNA markers run in one dedicated lane, or in some cases, by running internal standards within the sample lanes. Sample capacity is 4 or 5 lanes, depending on cassette type and electrophoresis protocol.

Each sample lane is physically separate, and features a branched configuration to which 3 electrodes are applied. DNA is separated along a gel column until the programmed fragment range reaches the branch point. By switching the active electrode, DNA is diverted into a membrane-bound buffer chamber. When the size range has been collected, the active electrode is switched back to the separation channel, and the sample can be removed with a standard pipette.



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

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