

PippinHT vs. Pippin Prep: A Performance Comparison

We've conducted a side-by-side analysis to determine how well the new PippinHT stacks up as the newest member of the Pippin family.

Experimental Design:

Replicate sheared DNA samples were size selected at four target sizes, ten times each, on both the Pippin Prep and PippinHT. The collections were analyzed on an Agilent Bioanalyzer. For both platforms, we used 2% agarose cassettes using internal standards.

Results:

Programmed Target

Pippin Prep™

PippinHT™

| Programmed Target | | Pippin Prep™ | PippinHT™ |
|-------------------|------------------|--------------|-----------|
| 150 bp | Average Size | 155 bp | 143 bp |
| | Average Run Time | 52 min | 27 min |
| | Accuracy | 97% | 96% |
| | Reproducibility | 92% | 86% |
| 275 bp | Average Size | 295 bp | 271 bp |
| | Average Run Time | 61 min | 32 min |
| | Accuracy | 93% | 99% |
| | Reproducibility | 94% | 99% |
| 400 bp | Average Size | 428 bp | 388 bp |
| | Average Run Time | 71 min | 37 min |
| | Accuracy | 97% | 97% |
| | Reproducibility | 92% | 92% |
| 500 bp | Average Size | 534 bp | 492 bp |
| | Average Run Time | 79 min | 41 min |
| | Accuracy | 93% | 98% |
| | Reproducibility | 96% | 96% |

Accuracy:

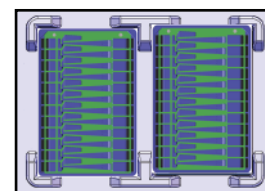
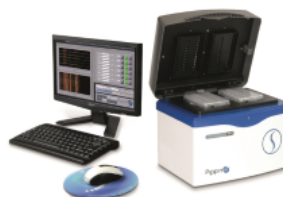
For a set of given (programmed) targets, $100 - ([\text{mean of averagesize (Agilent Bioanalyzer)} - \text{programmed size}] * 100)$

Reproducibility:

For a set of given (programmed) targets, $100 - 2 * CV (\%)$ or $100 - (2 * [\text{Stdev of averagesize (Bioanalyzer)} / \text{mean of averagesize (Bioanalyzer)}] * 100)$

Conclusions:

The PippinHT matches the performance of the Pippin Prep with five times the sample capacity, and in about half the run time.



2 X 12 Samples per Run



Take Good Care of Your Library.

Automated Size Selection: An Indispensable Tool for NGS

A properly sized library improves the performance of next-gen sequencers such as Illumina and Ion Torrent. Optimal results (more useful reads per flow cell, higher-quality assemblies) are achieved when uniformly sized fragments are used for cluster generation or amplification templates. Key methods that are improved with size selection include:

Paired-end sequencing - Narrow and uniform fragment distributions allow for more accurate alignment and facilitate identification of structural variants. Pippin size selection provides narrower distributions, reproducibly, and with no sample contamination.

miRNA isolation - Automated size selection is routinely used to isolate miRNA libraries away from unligated adapters and larger artifacts, providing a savings in time and effort and eliminating unwanted reads.

ChIP-seq - Studies benefit from the flexibility provided by automated size selection. Users can accurately select narrow or broad ranges of fragments, depending on the factor that is analyzed.

Selected References Citing Pippin DNA Size Selection

Paired-End Sequencing

Kagale, S. *et al.*, The emerging biofuel crop *Camelina sativa* retains a highly undifferentiated hexaploid genome structure. *Nature Communications* 5:3706 (2014)

miRNA isolation

Weedon-Fekjaer, M.S., *et al.*, Placental miR-1301 is dysregulated in early-onset preeclampsia and inversely correlated with maternal circulating leptin. *Placenta* 35:9, 707-719 (2014)

ChIP-seq

Kurachi, M., *et al.*, The transcription factor BATF operates as an essential differentiation checkpoint in early effector CD8+ T cells. *Nature Immunology* 15:4 (2014)



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