PippinHT™

DNA Size Selection for NGS

ДИА•М современная лаборатория

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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.

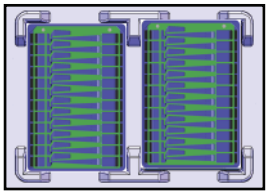
Results:

Programmed Target		Pippin Prep™	PippinHT™
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 - ([mean of averagesize (Agilent Bioanlyzer) - programmed size]*100)
Reproducibility:
For a set of given (programmed) targets, 100 - 2*CV (%) or 100 - (2*[Stdev of averagesize (Bioanalyzer) / 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

sage science

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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 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 more accurate alignment and facilitate identification 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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