PippinHT™ DNA Size Selection for NGS

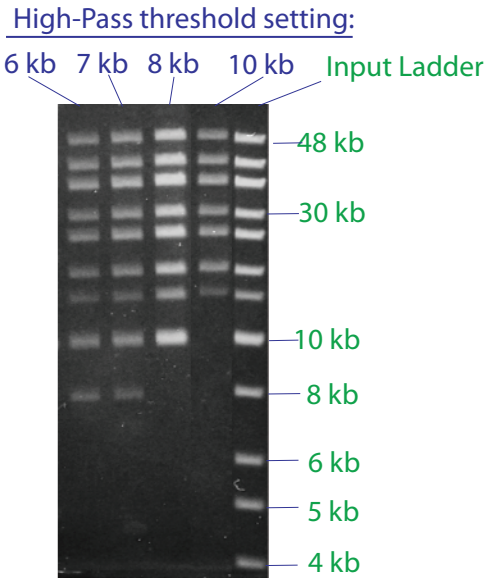
PippinHT vs. BluePippin High-Pass: A Performance Comparison

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:

The high pass protocol is a method by which lower molecular weight fragments from a DNA are filtered from a sheared sample. Users set a size threshold in software, and all fragments above that threshold are automatically collected.

For this test, a ladder is (shown below) is loaded on the PippinHT and collected at four threshold settings (6, 7, 8 and 10kb). The amount of ladder collected was compared to the input amount. Each sample was run in duplicate. Collected DNA was measured with a Qubit fluorometer, and compared an equivalent test run on the BluePippin.



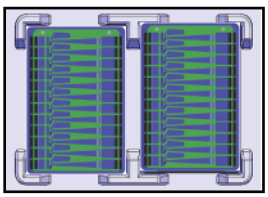
Results:

Amount of DNA Recovered (average)

High Pass Threshold	BluePippin (1.25 μg input)	PippinHT (0.75 μg input)
6 kb	406 ng (32%)	385 ng (51%)
7 kb	300 ng (24%)	395 ng (53%)
8 kb	290 ng (23%)	369 ng (49%)
10 kb	244 ng (20%)	282 ng (38%)
Max. input amount.:	5 μg	1.5 μg

Conclusions:

Sample recovery for high pass protocols run on the PippinHT have 2X higher recovery, and a more consistent recovery, than comparable protocols run on the Blue Pippin.



2 X 12 Samples per Run

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Take Good Care of Your Library.

Automated Size Selection: An Indispensable Tool for NGS

Third-gen sequencing such as PacBio® captures long-range genomic information using unprecedented read lengths. These analyses unravel complex genomes and enable studies of structural rearrangements that cannot be achieved using short read sequencing alone.

Automated DNA size selection is the most effective method to filter out short library fragments, or to bin large fragment ranges, and maximize these long read capabilities.

Selected References Citing PacBio Sequencing with Pippin DNA Size Selection

Wang, M., *et al.*, **PacBio-LITS: a large-insert targeted sequencing method for characterization of human disease-associated chromosomal structural variations.** BMC Genomics (2015) 16:214

Huddleston, J., *et al.*, **Reconstructing complex regions of genomes using long-read sequencing technology.** Genome Research (2015) 24:688-696

Kim, K.E., *et al.*, **Long-read, whole-genome shotgun sequence data for five model organisms.** Scientific Data 1, Article number: 140045 (2014)

Conlan, S, *et al.*, **Single-molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing Enterobacteriaceae.** Sci Transl Med 17 September 2014: Vol. 6, Issue 254

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