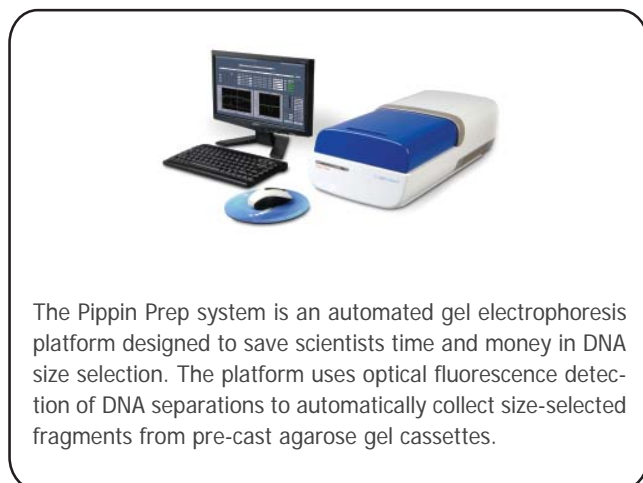


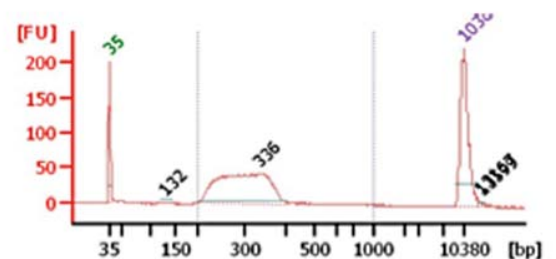
ChIP-Seq: High Recoveries of Valuable Samples

ChIP-seq often requires enrichment of nanogram amounts of starting material, and size selection of a wide range of DNA fragments. The Pippin system provides more flexibility and higher recovery than competing methods. New lower volume (25 µl) collection modules improve the ChIP workflow better than ever.

1. Enter a base pair range in software
2. Load samples onto a pre-cast agarose gel cassette
3. At the end of the run, collect the DNA with a pipettor



Pippin Prep Size Selection, 1:10 dilution



Manual Size Selection 1:3 dilution

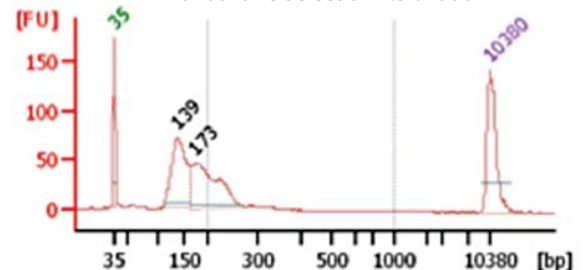


Figure. A comparison of size selection of duplicate ChIP seq libraries. The manual method shows presence of primer-dimer peaks and absence of fragments above 300 bp. Sample recovery with the Pippin Prep is significantly higher. Data courtesy of the Center for Functional Epigenetics, DFCI.

“BioAnalyzer Tracings confirm that the Pippin Prep size selection selected more accurate broad size ranges with good yield across the full size range ...”

— Dr. Thomas Westerling,
Center for Functional Cancer Epigenetics, Dana Farber Cancer Institute



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