

Collect targets between
50 bp – 1.5 kb

Collect targets between
50 bp – 50 kb



Improving NGS Data Everywhere

Illumina

Sizing improves variant detection in paired-end sequencing. Use Pippin with Nextera tagmentation to improve assembly. Recommended in Nextera Mate Pair Sample Prep guide.

Ion Torrent

Tight size selection reduces emPCR bias which optimizes read length and improves throughput. Recommended in Exome Enrichment Guide and gDNA Fragment Library Prep guides.

Benefits of the Pippin platform:

- Eliminates variability and cross-contamination
- Improves genome assembly quality
- Minimal hands-on time
- High yield

PacBio

BluePippin's "High Pass" protocol can improve read-lengths by up to 95%. Recommended in ~20kb SMRTbell protocol.

454

Use Pippin to clean up unwanted fragments and primer-dimers for amplicon sequencing, increasing the efficiency of the run.

"If you have enough DNA, you can just skip the PCR — and you get much better coverage across the genome and a better assembly. That's easier to do on a Pippin."

— Dr. Matthew Clark
The Genome Analysis Centre

"You can tune up your sizing with the Pippin Prep, that's the beauty of it. It will adjust with these new sequencing technologies."

— Dr. Matthew Sullivan
Department of Ecology and Evolutionary Biology,
University of Arizona