

Collect targets between
90 bp – 1.5 kb



BluePippin™

Collect targets between
90 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.

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