Core Labs Deploy Pippin Automated DNA Sizing Platform

Whether they're using sequencers from Illumina, Ion Torrent, PacBio, or 454, core labs around the world have found that Pippin Prep and BluePippin automated DNA size selection tools from Sage Science have tremendous benefit. Accurate and reproducible sizing is a critical step for studies involving microRNA, DNA or RNA sequencing, splice variant analysis, ChIP-seq, and more.Below, we offer snapshots of Sage Science core lab customers to show how they are using our sizing tools.

CORE LAB:: DNA Facility

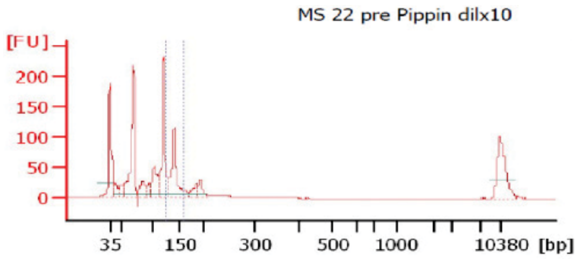
INSTITUTION:: University of Iowa

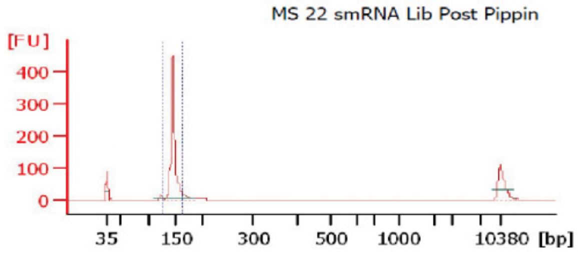
DIRECTOR:: Kevin Knudtson

HOW PIPPIN HELPS:: Knudtson's team uses Pippin Prep for next-gen sequencing, ChIP-seq, and particularly for isolating microRNAs. They use Pippin to improve accuracy and reliability for any protocol that involves running a manual gel.

KEY BENEFITS:: More efficient loading of flow cells, accurate selection of microRNAs and removal of low molecular weight content, speeds up sample turnaround time.

CUSTOMER QUOTE:: *"Cutting a slice out of a gel is a very subjective thing to do, and it can be technically challenging to repeat that same cut," Knudtson says. "But when we run these out on the Pippin Prep, we're getting exactly what we hope to receive. I can have different technicians do the same procedure and essentially get the same band or answer back when they're processing samples."*





CORE LAB:: BioMicro Center

INSTITUTION:: Massachusetts Institute of Technology

DIRECTOR:: Stuart Levine

HOW PIPPIN HELPS:: Levine brought in Pippin Prep because its very precise sizing was necessary for splice variant analysis with RNA-seq and microRNA analysis.

KEY BENEFITS:: Tighter sizing than other automated methods, and far more cost-efficient than loading and running manual gels.

CUSTOMER QUOTE:: *"What Pippin let us do was get into areas that we hadn't been able to before," Levine says. Plus, because the platform can handle very large DNA fragments as well as short ones, "it's extremely useful both for the ability to do sample preparation now and for the ability to work with these future technologies."*

CORE LAB:: DNA Technologies Laboratory

INSTITUTION:: National Research Council of Canada

GROUP LEADER:: Andrew Sharpe

HOW PIPPIN HELPS:: Sharpe and his colleagues use Pippin Prep and BluePippin for paired-end libraries (200bp – 400 bp) as well as longer mate-pair libraries (3 Kb – 10 Kb) for Illumina and 454 sequencing, often for large plant and fungal genomes.

KEY BENEFITS:: The team creates multiple libraries with different insert sizes to boost the accuracy of the final genome assembly.

CUSTOMER QUOTE:: *"Having the Pippin makes things quite a lot more efficient on the labor side," Sharpe says. "The nice thing with the Pippin Prep is being able to easily get those discrete size ranges.*

CORE LAB:: Molecular Biology Core Facilities

INSTITUTION:: Dana-Farber Cancer Institute

ASSOCIATE DIRECTOR:: Zach Herbert

HOW PIPPIN HELPS:: Herbert uses Pippin Prep with Illumina's Nextera sample prep for small genome studies and for some larger amplicon projects.

KEY BENEFITS:: Tighter sizing optimizes reproducibility, flow cell clustering on the MiSeq, and downstream analysis in the Nextera workflow. It also improves efficiency for pooled samples.

CUSTOMER QUOTE:: *"For low- to medium-throughput size selection where you want to minimize sample loss and maximize reproducibility, I think the Pippin is a great instrument," Herbert says.*

CORE LAB:: Norwegian High-Throughput Sequencing Centre

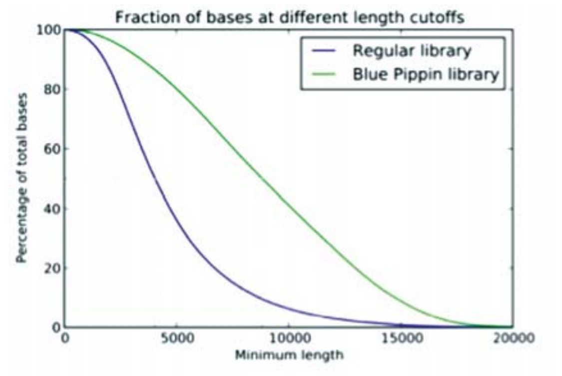
INSTITUTION:: University of Oslo

DAILY LEADER:: Lex Nederbragt

HOW PIPPIN HELPS:: The core facility brought in a BluePippin to help generate even longer average reads from its PacBio RS II sequencer.

KEY BENEFITS:: Because BluePippin removes smaller fragments during library production, the PacBio sequencer can focus on longer DNA fragments. Early tests showed a doubling of average read length by adding a size selection step with BluePippin.

CUSTOMER QUOTE:: *"The length distribution shifts significantly to longer reads after BluePippin cleanup," Nederbragt writes in a blog post describing his team's use of the sizing tool. "We have now started sequencing bacterial genomes with BluePippin treated libraries, and those show even longer average raw readlengths."*



CORE LAB:: GenCore

INSTITUTION:: New York University's Center for Genomics and Systems Biology

MANAGER:: Paul Scheid

HOW PIPPIN HELPS:: The GenCore team uses Pippin Prep for automated size selection with its Illumina (HiSeq 2500 and MiSeq) and Ion Torrent (PGM) pipelines for infectious disease and model organism sequencing projects. Two of the most common applications are de novo sequencing and double digest RAD-seq.

KEY BENEFITS:: Pippin improves accuracy for tracking specific structural variants, targets the exact fragment size range needed for emulsion PCR, and helps control the number of loci targeted in ddRAD-seq projects.

CUSTOMER QUOTE:: *"I just don't think that there are any other platforms out there that allow the level of granularity that Pippin does in terms of size selection,"* Scheid says.

CORE LAB:: Genomics Resource Core

INSTITUTION:: Institute for Genome Sciences at the University of Maryland

LABORATORY MANAGER:: Naomi Sengamalay

HOW PIPPIN HELPS:: The GRC team evaluated BluePippin for extending PacBio read lengths and wrote about the results on their blog.

KEY BENEFITS:: Automated size selection with BluePippin nearly doubled the mean subread length, as well as subread lengths measured at the 90th and 95th percentiles, for test organisms sequenced at GRC. Also, BluePippin allowed the team to more data per zero-mode waveguide on the sequencer, improving instrument throughput.

CUSTOMER QUOTE:: *"As the fragment length increases, the percentage of SMRTbell adapter sequence decreases and the percentage of library insert increases," the blog post reports. "Using BluePippin size selection, we have achieved yields of >500 M passed filter bases from individual SMRTcells."*

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