

NGS Library Preparation Kits

Datasheet

Overview

Enzymes in ABclonal Technology's NGS library preparation kits undergo strict quality control procedures to ensure high purity, high protein mass concentration, high functional enzyme activity, and low contaminations. In particular, the team has perfected the process to purify T4 DNA ligase to achieve the best ligation efficiency in the industry. As a result, ABclonal is able to produce one of the best-yielding NGS library preparation kits in the industry while maintaining quality.

Non-Specific Nuclease Contamination QC

16-hour non-specific nuclease activity assay

Exonuclease Contamination QC

16-hour exonuclease activity assay (ssDNA, dsDNA)

Endonuclease (Nicking) Contamination QC

16-hour endonuclease (nicking) activity assay

RNase Contamination QC

4-hour RNase activity assay

Genomic DNA Contamination QC

E.coli genomic DNA contamination (qPCR)

Protein Purification Purity QC

Protein purity (SDS-PAGE)

Protein Mass Concentration QC

Protein concentration (Bradford, BCA)

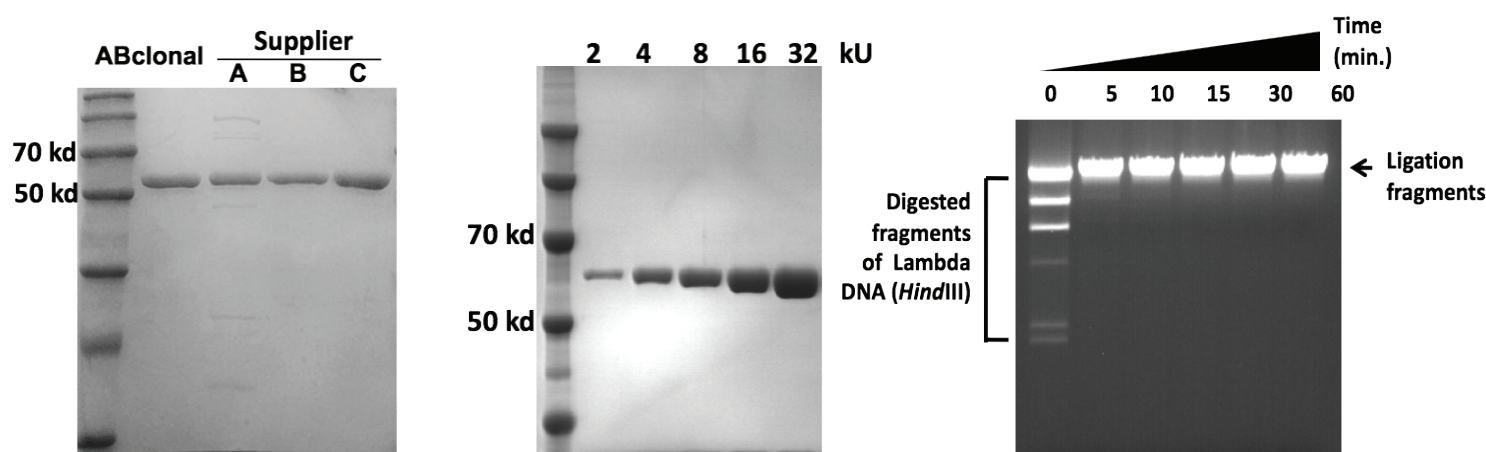
Functional Enzyme Activity QC

Functional activity and unit determination

Stability Test
Storage stability, freeze/thaw stability, shipping stability

T4 DNA Ligase

Purity and Functional Activity



DNA Library Preparation Kit

Rapid DNA Lib Prep Kit | StepWise DNA Lib Prep Kit



Overview

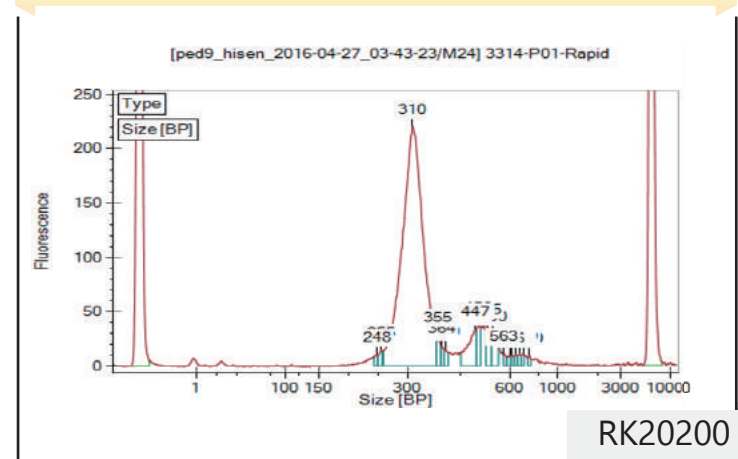
		Rapid DNA Lib Prep Kit	StepWise DNA Lib Prep Kit
Time		2 hr	2-3 hr
DNA Input		1ng-1µg	500pg-1µg
DNA Conversion Efficiency		~50%	~70%
Application	High-quality DNA	★★★★★	★★★★★
	CHIP DNA	★★★★★	★★★★☆
	cfDNA	★★★★★	★★★★★
	FFPE DNA	★★★★★	★★★★☆
	Single-cell cDNA	★★★★★	★★★★★

Test Results Using cfDNA and FFPE DNA Samples

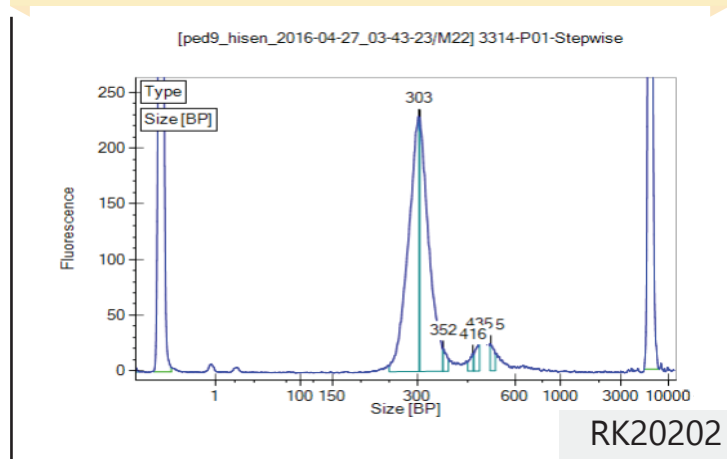
ID	DNA Type	Sample Name (Includes Repeated Trials)	DNA Input (ng)	Rapid DNA Lib Prep Kit Yield (ng)	StepWise DNA Lib Prep Kit Yield (ng)
1	cfDNA	7359P01-1	30.0	1359	1590
2	cfDNA	7359P01-2	45.0	1533	1710
3	FFPE DNA	7450W01-1	200.0	1671	1668
4	FFPE DNA	7450S01-1	200.0	1128	1320

32 cfDNA and FFPE DNA samples were used to construct DNA libraries for DNA target capture sequencing. PCR amplification: 7 cycles.

cfDNA Library Constructed by Rapid DNA Lib Prep Kit



cfDNA Library Constructed by StepWise DNA Lib Prep Kit

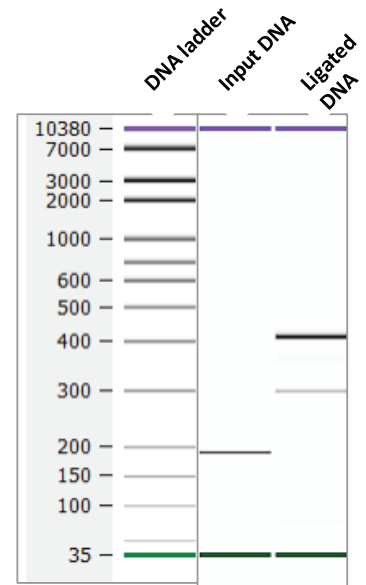
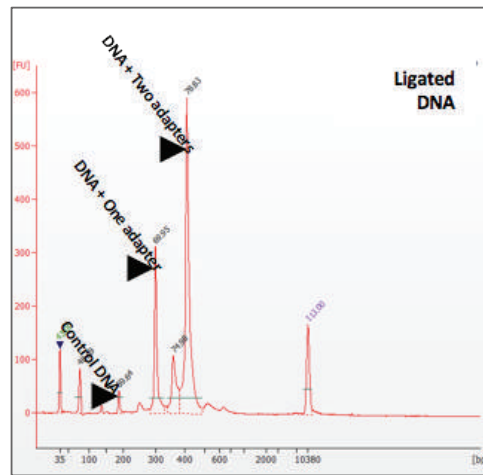
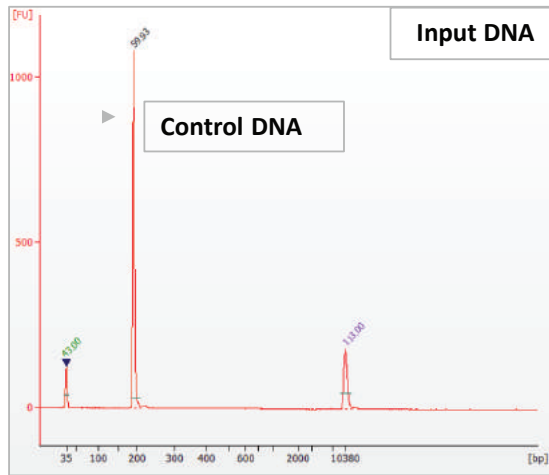


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For more information, visit abclonal.com/NGS-Lib-Prep-Kit

Rapid DNA Lib Prep Kit

Rapid DNA Lib Prep Kit DNA Conversion Test



RK20200

Lot-to-lot Variability

Test Design

~50 samples of
FFPE DNA

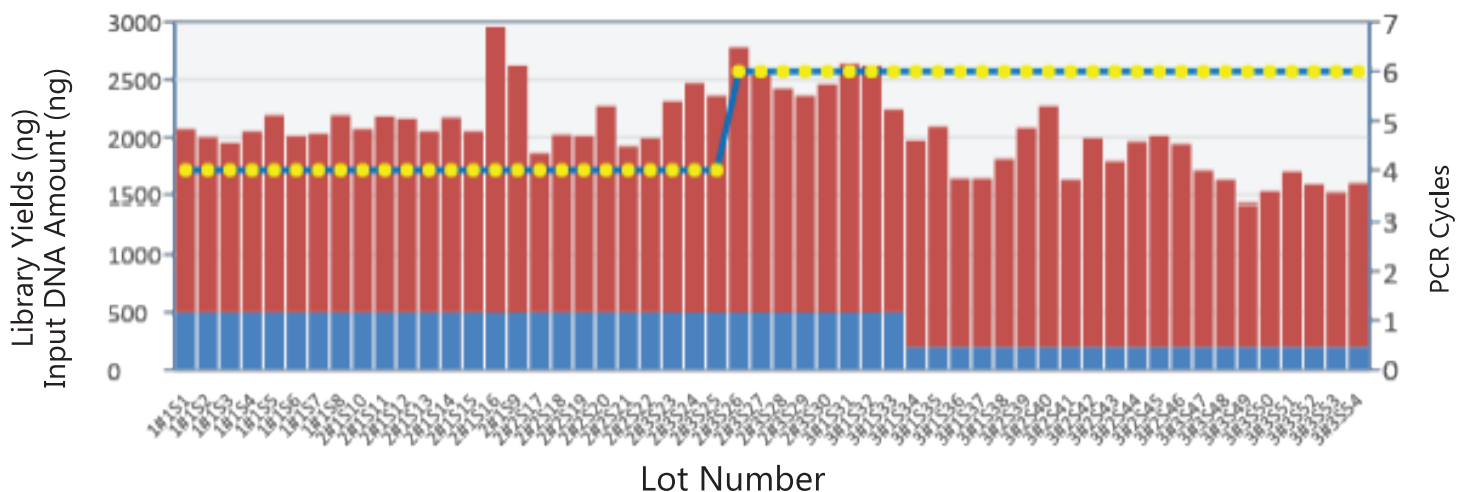
Several Lots
Rapid Reagents

DNA Libraries Construction
Input DNA amount:
200 or 500ng
PCR Cycles: 4 or 6 x cycles

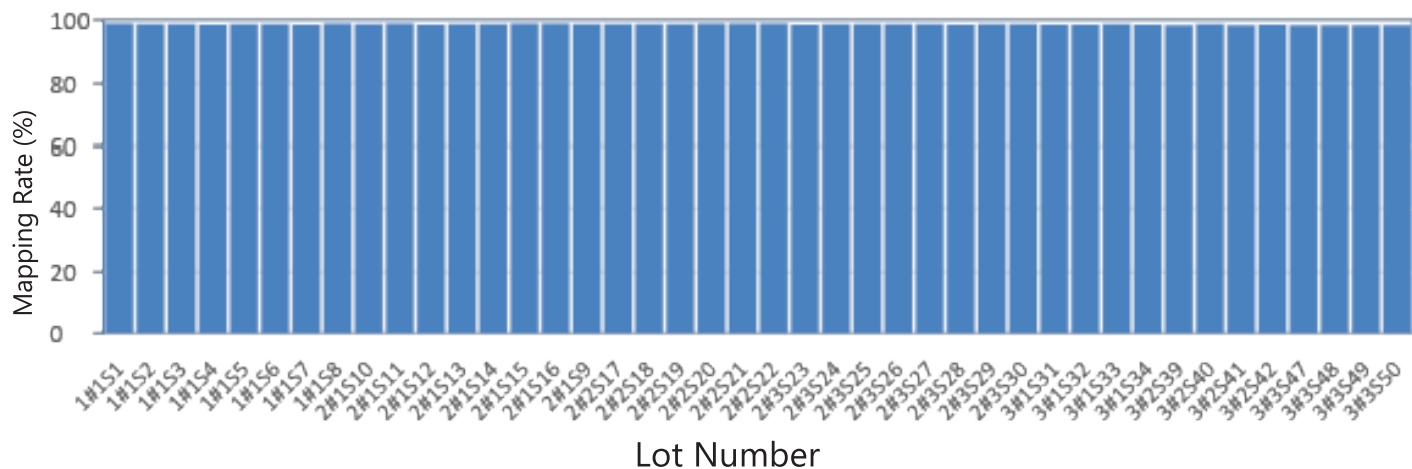
DNA Capture
by IDT Probes

DNA Sequencing
Mean_depth: <1000x;
>4000x

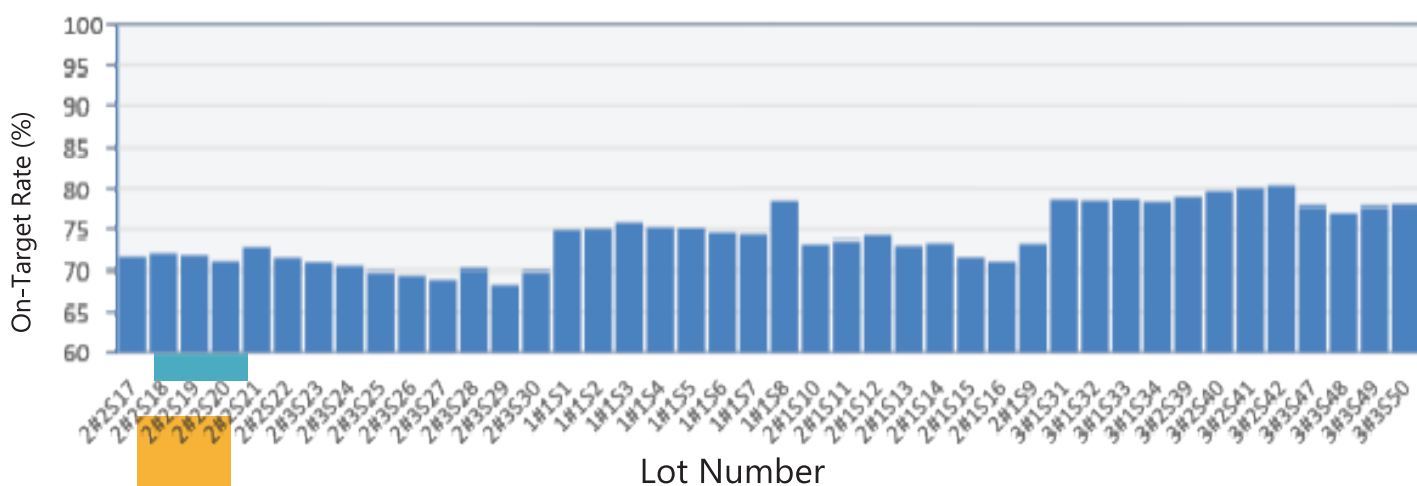
Rapid DNA Lib Prep Kit Library Yields



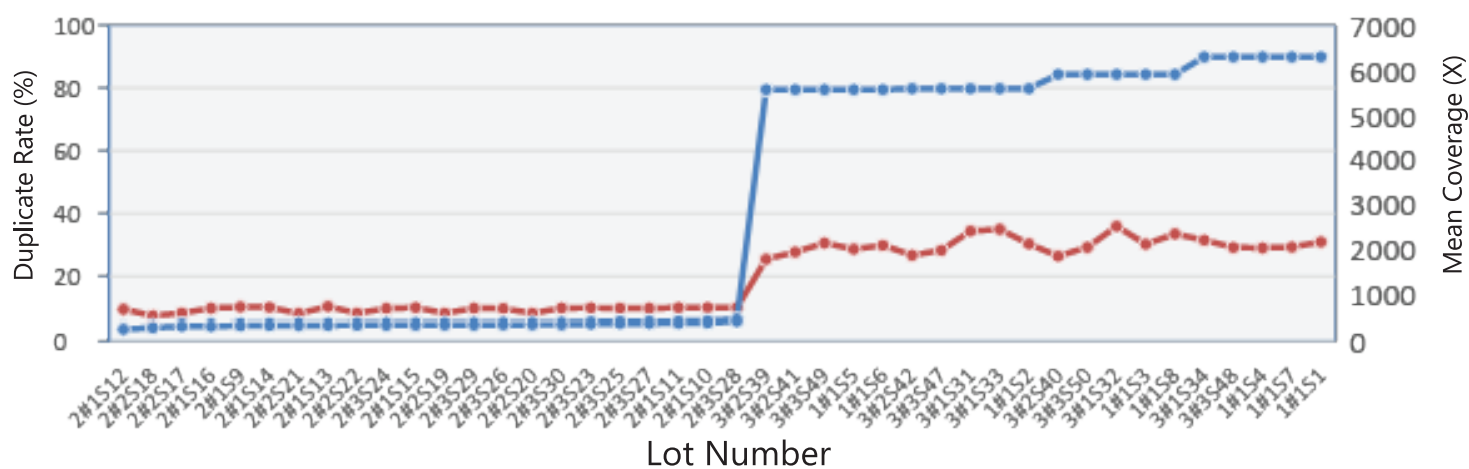
Rapid DNA Lib Prep Kit DNA Mapping Rate



Rapid DNA Lib Prep Kit On-Target DNA Capture



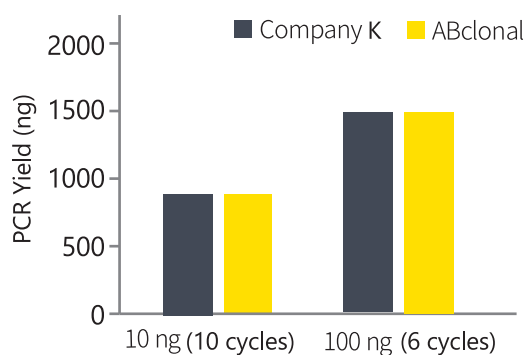
Rapid DNA Lib Prep Kit Mean Coverage and Duplicate Rate



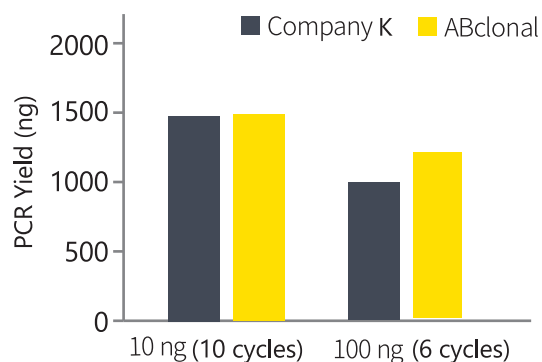
ABclonal vs. Industry

Rapid DNA Lib Prep Kit PCR Yields

Human FFPE DNA as Input DNA

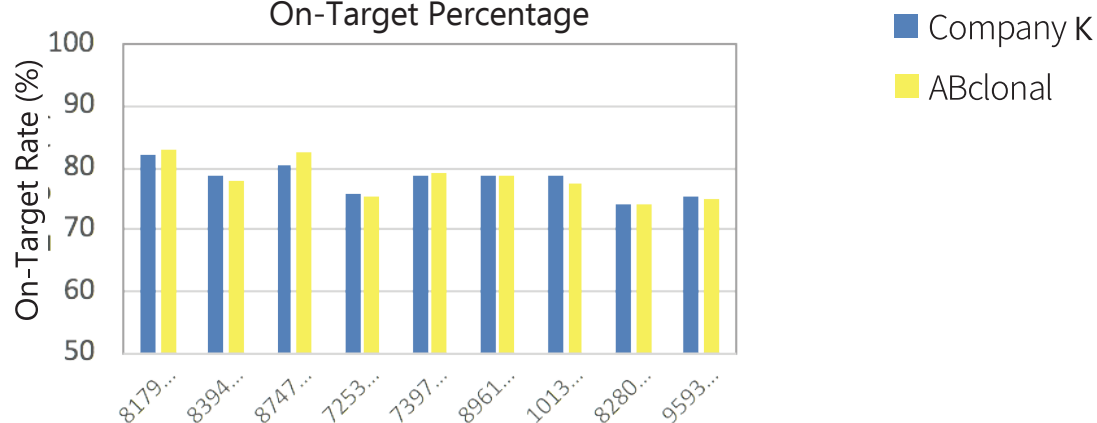


E. coli gDNA as Input DNA

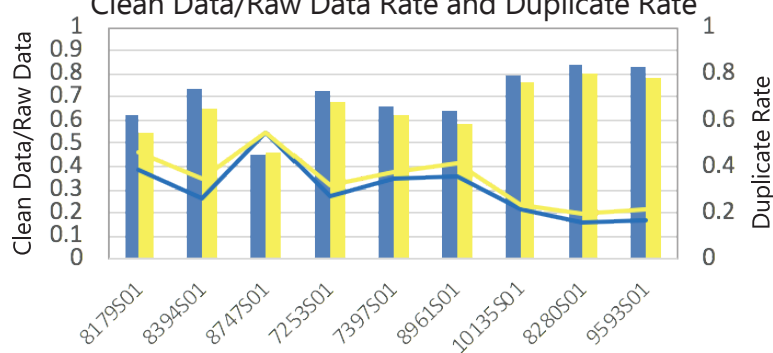


Rapid DNA Lib Prep Kit Data Using FFPE DNA Samples

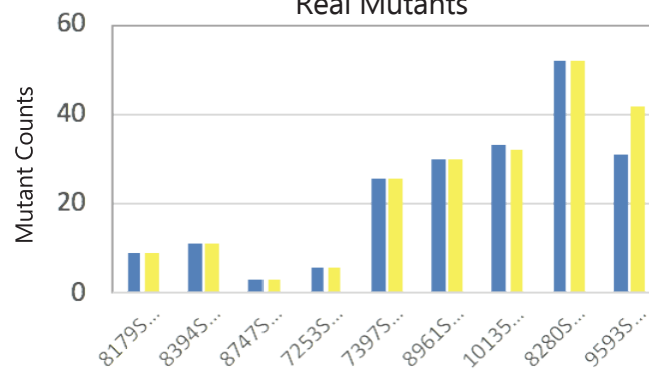
On-Target Percentage



Clean Data/Raw Data Rate and Duplicate Rate



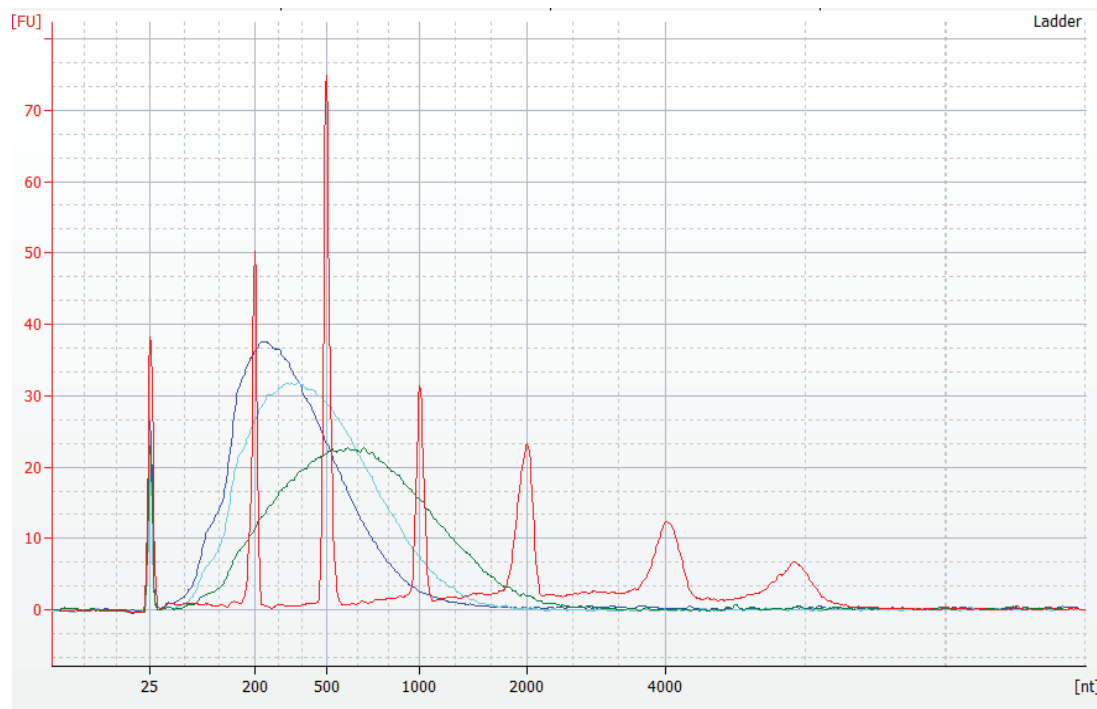
Real Mutants



mRNA Library Preparation Kit

Stranded mRNA-seq Lib Prep Kit | mRNA-seq Lib Prep Kit

mRNA Fragmentation Determination



Traces of fragmented mRNA as shown in an RNA 6000 Pico Chip using Bioanalyzer. mRNA isolated from mouse total RNA using Oligo dT beads and fragmented with Frag/Elute buffer at 94°C for 5, 10 or 15 minutes, and purified using 2.2× Agencourt RNAClean XP beads.

Quality Control

Mapping Rate

Sample	Total Reads	Reads Mapped	Mapping Rate	Unique Mappings	Unique Mapping Rate	rRNA (Contamination)
94°C/15 min	26,323,565	25,551,882	97.01%	23,465,151	89.14%	1.33%
94°C/10 min	23,319,935	22,648,738	97.12%	20,864,494	89.47%	1.43%
94°C/5 min	16,297,502	15,776,295	96.80%	14,506,861	89.01%	1.37%

RNA-Seq Libraries were constructed using ABclonal stranded mRNA-seq Lib Prep Kit. 1µg mouse total RNA input was used for RNA-seq library construction. mRNA isolated from mouse total RNA using Oligo dT beads and fragmented with Frag/Elute buffer at 94°C for 5, 10 or 15 minutes. PCR cycles: 8x.

Mapping Rate

Sample	Total Reads	Reads Mapped	Mapping Rate	Unique Mappings	Unique Mapping Rate	rRNA (Contamination)
1000 ng	32,513,725	32,007,016	98.66%	27,707,751	86.38%	0.141%
100 ng	36,132,343	35,000,706	96.87%	29,789,805	85.11%	0.17%
10 ng	32,886,917	28,634,935	87.07%	21,575,409	75.35%	0.19%

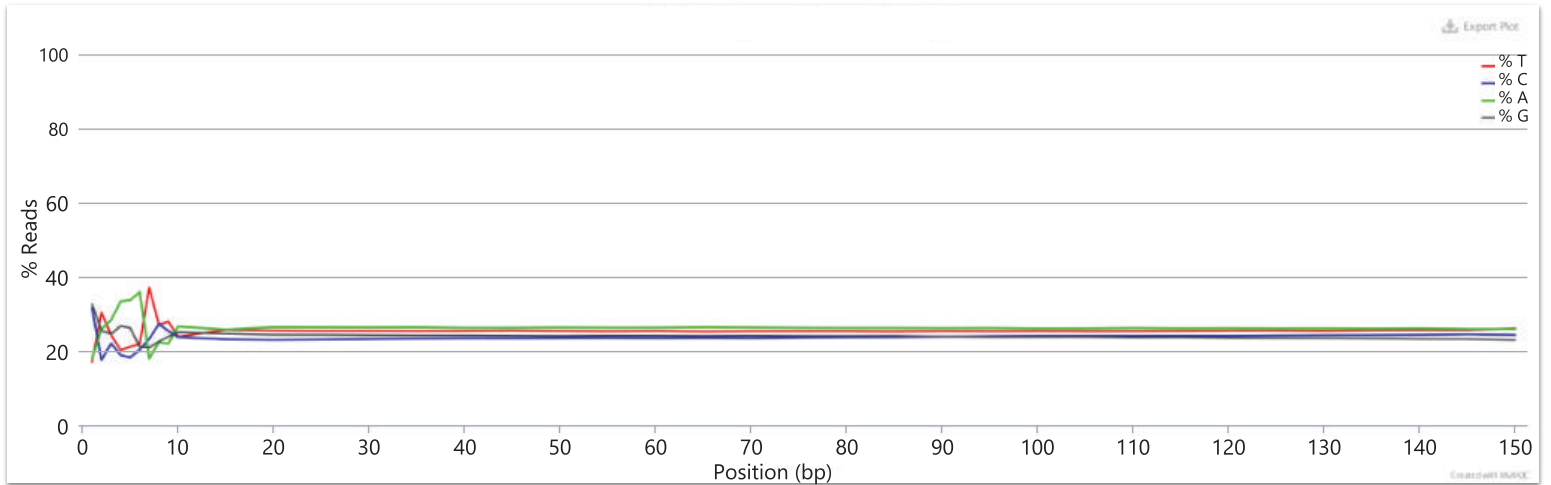
RNA-Seq Libraries were constructed using ABclonal stranded mRNA-seq lib prep kit. 10ng/100ng/1µg mouse total RNA input was used for RNA-seq library construction. mRNA isolated from mouse total RNA using Oligo dT beads and fragmented with Frag/Elute buffer at 94°C for 15 minutes. PCR cycles: 9x for 1µg, 13x for 100ng, 15x for 10ng.



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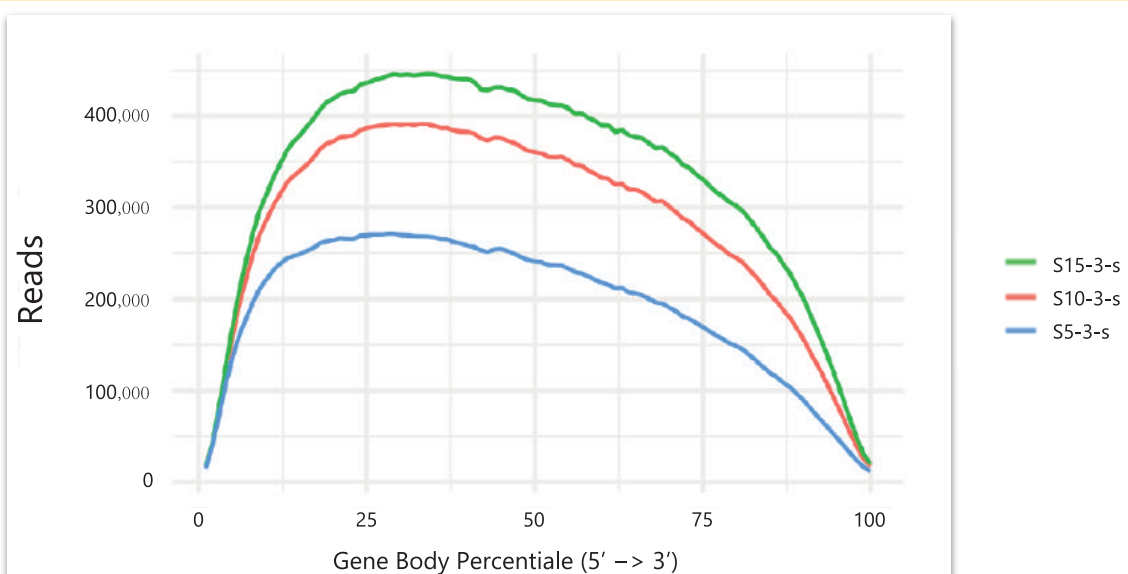
For more information, visit abclonal.com/NGS-Lib-Prep-Kit

Raw Data Per Base Sequence

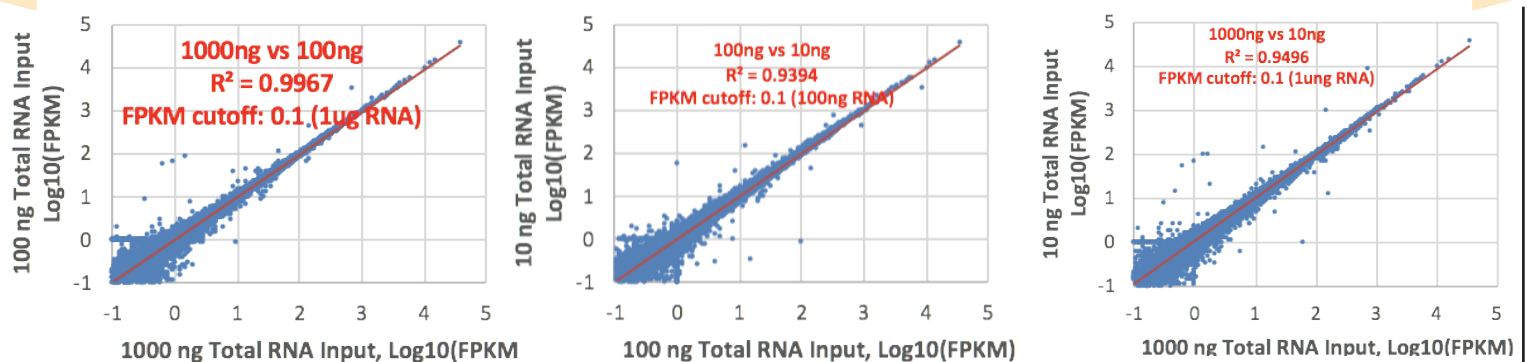


RNA-Seq Libraries were constructed using ABclonal stranded mRNA-seq lib prep kit. 1µg mouse total RNA input was used for RNA-seq library construction. mRNA isolated from mouse total RNA using Oligo dT beads and fragmented with Frag/Elute buffer at 94°C for 5 minutes. PCR cycles: 8x.

Gene Body Coverage



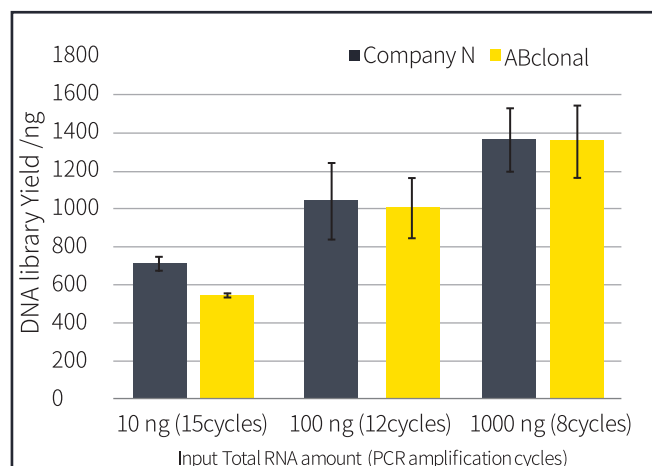
Rapid DNA Lib Prep Kit On-Target DNA Capture



RNA-Seq Libraries were constructed using ABclonal stranded mRNA-seq lib prep kit. 10ng/100ng/1µg mouse total RNA input was used for RNA-seq library construction. mRNA isolated from mouse total RNA using Oligo dT beads and fragmented with Frag/Elute buffer at 94°C for 15 minutes. PCR cycles: 9x for 1µg, 13x for 100ng, 15x for 10ng.

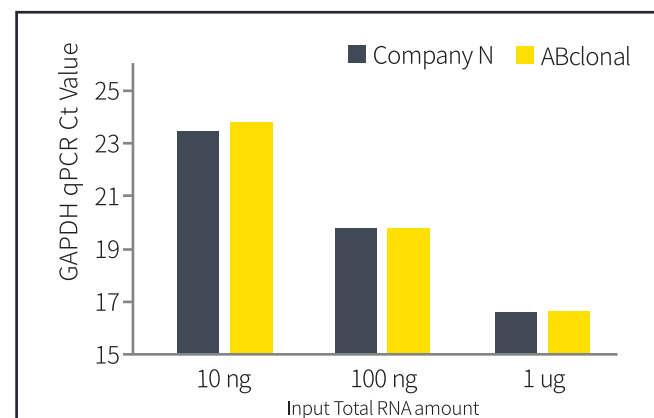
ABclonal vs. Industry

■ DNA Library Yield Test



10ng/100ng/1μg mouse total RNA input was used for RNA-seq library construction. mRNA was isolated from mouse total RNA using Oligo dT beads and fragmented with Frag/Elute buffer at 94°C for 15 minutes.

■ DNA Synthesis Efficiency Test



10ng/100ng/1μg mouse total RNA input was used for RNA-seq library construction. mRNA was isolated from mouse total RNA using Oligo dT beads and fragmented with Frag/Elute buffer at 94°C for 15 minutes. After second strand synthesis, double strand cDNA was diluted by 100-fold. Ct value of GAPDH gene was determined using qPCR.



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