NxSeq AmpFREE Low DNA Library Kit

Generate more unbiased data per library with this Illumina-compatible, high efficiency and cost-effective fragment DNA Library Kit

Higher efficiency libraries. Get more sequence data per library.

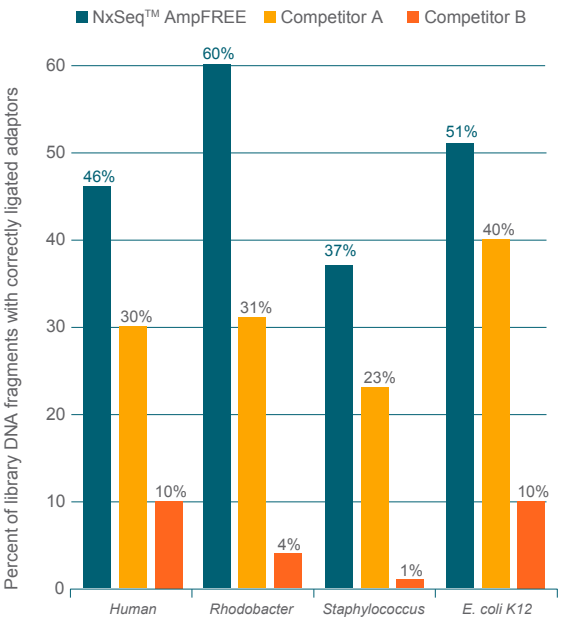

Figure 1. Percentage of library DNA with correctly ligated adaptors measured by qPCR. Duplicate libraries were prepped per kit/organism (*Human*, *Staphylococcus aureus*, *Rhodobacter sphaeroides* (1 library only), and *E. coli*) according to the manufacturer's recommended input amounts and protocols. Adaptor ligation efficiency was measured by qPCR using the Competitor A kit and matching amplified library as an internal standard.

Faster protocol. Streamline your workflow.

Faster and easier

LGC, Biosearch Technologies
2 hr 10 min
60 min hands-on
70 min hands-off

Competitor A
3 hours 5 min
105 min hands-on
80 min hands-off

Competitor B
3 hrs 25 min
120 min hands-on
85 min hands-off

- **Great performance:** High efficiency library construction produces more sequenceable fragments, better coverage and depth from single or multiplexed libraries.
- **Minimal bias:** PCR-free generation of libraries from ≥75 ng of sheared input DNA produces more uniform coverage.
- **Fast:** 2 hour, 10 minute protocol saves you time and gets your samples on the sequencer sooner.
- **Flexible:** Construct libraries from 75 ng to 1 µg of sheared input DNA.
- **Affordable:** Best priced and best performing PCR-free kit available.

Lucigen®

BIOSEARCH™ TECHNOLOGIES
GENOMIC ANALYSIS BY LGC

The proof: Better libraries increase the number of reads per library

Library kit	DNA input	Total number of sequencing reads per library	
		Staphylococcus aureus	*E. coli K12*
NxSeq AmpFREE Low DNA library Kit	75 ng	5,649,946	4,305,882
Competitor A	250 ng	4,838,726 (-15%)	1,647,452 (-62%)
Competitor B	1 µg	38,768 (-99%)	1,543,558 (-64%)

Table 1. Number of sequencing reads generated per library after multiplexing and running on a MiSeq Instrument. DNA fragment libraries were prepped in parallel for each kit/organism according to the manufacturer's recommended input amounts and protocols. Libraries were quantitated and normalised to 2 nM using the Bioanalyzer (size) and Qubit Fluorometer (amount). Equimolar amounts of each library were multiplexed and sequenced with a single MiSeq run using 2 x 150 bp chemistry. The number of sequencing reads obtained are shown as well as the percent reduction (%) in total reads compared to the appropriate NxSeq AmpFREE Kit results.

More proof with challenging FFPE samples: Significantly more reads from normal and FFPE sample libraries

Library kit	Sample type	Input amount	Total reads	Mapped reads (repeat masked)
NxSeq AmpFREE Low DNA Library Kit	Normal gDNA	75 ng	2,163,636	900,338
	FFPE gDNA	75 ng	1,767,818	688,074
	FFPE gDNA	150 ng	1,706,714	656,658
Competitor A	Normal gDNA	250 ng	1,567,276 (-28%)	650,296 (-28%)
	FFPE DNA	250 ng	1,270,870 (-28%)	487,872 (-29%)

Table 2. Number of sequencing reads generated from matching normal and FFPE gDNA sample libraries. DNA fragment libraries were prepped using the two indicated kits according to the manufacturer's recommended input amounts and protocols. Libraries were constructed from normal gDNA (Biochain, Cat. No. D1234142-S02) and DNA extracted from a matching FFPE human kidney tissue (Biochain Cat. No. T2234142-S02) using the Qiagen AllPrep DNA/RNA FFPE Kit. The gDNA samples were sheared to ~250 bp before starting library construction. Final libraries were quantitated and normalised to 2 nM using the Bioanalyzer (size) and Qubit Fluorometer (amount). Equimolar amounts of each library were multiplexed and sequenced with a single MiSeq run using 2 x 150 bp chemistry. The number of sequencing reads obtained are shown as well as the percent reduction (%) in total and mapped reads compared to the corresponding NxSeq AmpFREE Kit results using 75 ng of input DNA.

Ordering information

Cat no.	Size	Description
14000-1	**12 rxns**	NxSeq AmpFREE Low DNA Library Kit
14000-2	**48 rxns**	
14300-1	**12 × 4 rxns**	NxSeq Adaptors, Box 1
14400-1	**12 × 4 rxns**	NxSeq Adaptors, Box 2

The NxSeq Library Kit and Adaptors are only compatible with Illumina sequencers.

Components: Enzyme Mix, 2x Buffer, Ligase and Elution Buffer. NxSeq Adaptors must be purchased separately. Each box of NxSeq Adaptors contains (12) different indexed Illumina-compatible adaptors with enough of each one for 4 reactions.

Integrated tools. Accelerated science.

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