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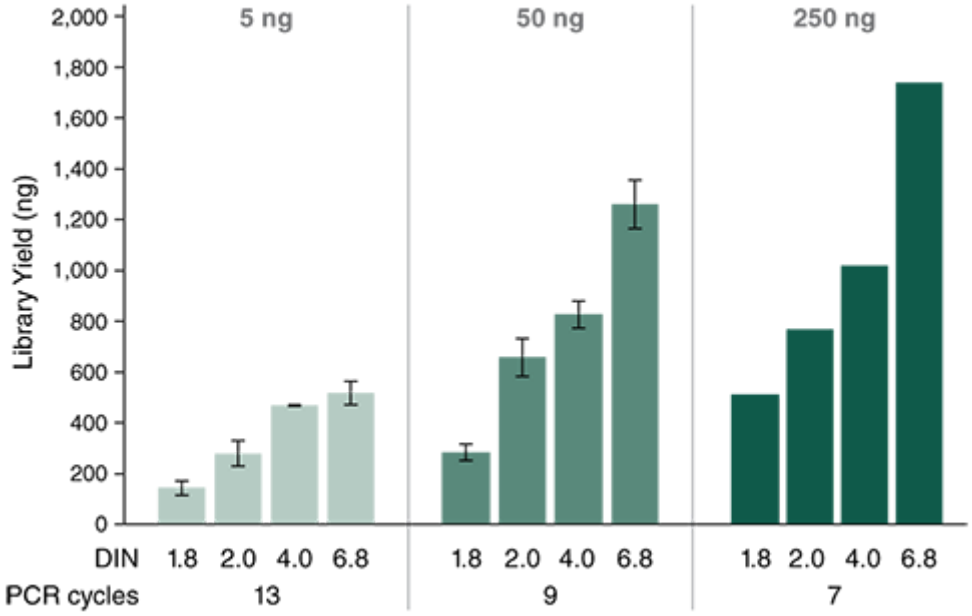
September 2023

Fixated on Improved FFPE DNA Library Quality?

Formalin fixation and paraffin embedding (FFPE) are essential steps towards the long-term cytoarchitectural preservation of some tissue samples, but these same steps can wreak havoc on the nucleic acids present in those samples. FFPE DNA is commonly plagued by deamination, nicking, oxidization, fragmentation and crosslinking, all of which make library prep more difficult. The NEBNext UltraShear™ FFPE DNA Library Prep Kit combines DNA repair with an enzymatic fragmentation step which are, together, shown to improve library quality and yield. View performance data on our latest solution for more meaningful library prep today!

The NEBNext UltraShear FFPE DNA Library Prep Kit enables robust library preparation from a range of sample inputs and quality



Libraries were prepared from 5, 50, or 250 ng of normal tissue FFPE DNA ranging in quality from DNA Integrity Number (DIN) 1.8 to 6.8, with the indicated PCR cycles. Libraries were prepared in triplicate for 5 ng and 50 ng input and 1 replicate for 250 ng. Each bar represents the average of triplicates with error bars indicating standard deviation for the 5 and 50 ng inputs. Robust library yields were obtained across sample qualities and input amounts. Most target enrichment workflows require a 200 ng library for hybrid capture input. Sufficient library yield can be obtained using a minimum of 50 ng FFPE DNA with the NEBNext UltraShear FFPE DNA Library Prep Kit.

Product Information

For FFPE DNA Library Prep without the enzymatic fragmentation step, we offer the NEBNext FFPE DNA Library Prep Kit, while NEBNext UltraShear is available as a standalone enzyme mix for fragmentation of challenging samples such as FFPE DNA.

Assemble With Confidence using NEBridge® Golden Gate Assembly

NEBridge Golden Gate Assembly reagents and NEBridge™ Ligase Fidelity Web Tools power high-complexity and high-fidelity Golden Gate Assemblies and are enabling advancements in synthetic biology research.

Learn More

- Clone seamlessly, with no scars remaining after assembly
- Perform single insert cloning in just 5 minutes using our fast protocols
- Generate libraries with high efficiencies
- Assemble multiple fragments (2–50+) in order, in a single reaction
- Experience high efficiency, even with regions of high GC content and areas of repeats
- Use with a broad range of fragment sizes (<100 bp to >15 kb)
- Simplify reaction setup with our suite of primer design and ligase fidelity tools

For convenience and value, NEB provides two optimized kits containing Type IIS restriction enzymes and a cloning vector:

NEBridge Golden Gate Assembly Kit (BsmBI-v2)

NEBridge Golden Gate Assembly Kit (BsaI-HF® v2)

For added flexibility, use NEBridge Ligase Master Mix with your choice of NEB Type IIS restriction enzymes:

NEBridge Ligase Master Mix

Try our suite of free online NEBridge™ tools

These tools enable the design of complex, high-fidelity Golden Gate Assemblies:

NEBridge Golden Gate Assembly Tool
Design assemblies and primers with appropriate Type IIS restriction sites and overhangs

NEBridge Ligase Fidelity Viewer™
Visualize overhang ligation preferences

NEBridge GetSet™ Tool
Predict high-fidelity overhang sets

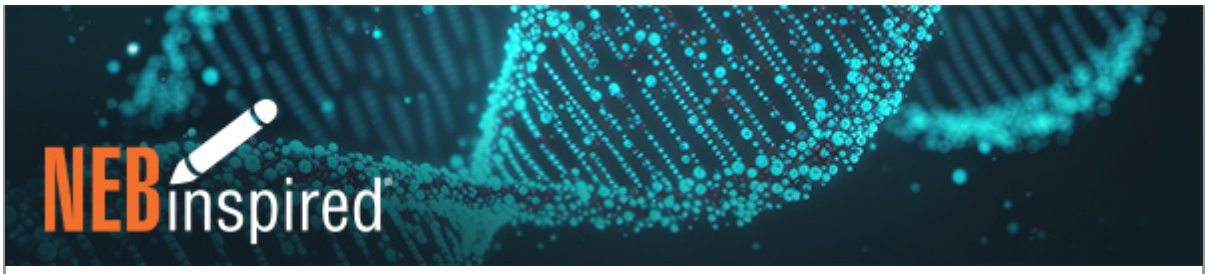
NEBridge SplitSet™ Tool
Split DNA sequence for scarless high-fidelity assembly

The NEB® Podcast Series

LESSONS from Lab & Life™

In NEB podcast episode #54 kicks off our molecular cloning series. Our Mutagenesis 101 podcast covers site-directed mutagenesis and multi-site mutagenesis techniques as well as frequently asked customer questions. Join us for a listen and learn the basics of mutagenesis from NEB Senior Technical Support Scientist Rachel Carver-Brown.

Listen on neb.com | Listen on Apple Podcasts | LISTEN ON Spotify



Bioinformatics is specifically involved in extracting, distilling, and understanding information contained in diverse scientific data, allowing research findings to be better understood, improving subsequent experiments, and furthering scientific goals. In this blog post, we explore bioinformatics applications to genetic sequencing and the ways proximity between molecular biologists and bioinformatic scientists accelerates progress, amplifying research and product development impacts.

Find out more in our latest blog post:

Sequencing Technologies and Bioinformatics: From data to workflow improvements

Read now

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