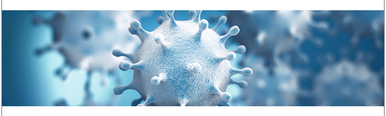
NEW ENGLAND BioLabs® be INSPIRED drive DISCOVERY stay GENUINE

February 2021



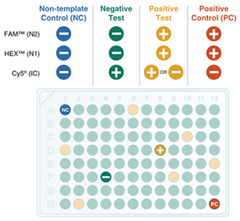
New product:

Luna® SARS-CoV-2 RT-qPCR Multiplex Assay Kit

the Luna SARS-CoV-2 RT-qPCR Multiplex Assay Kit is a research use only (RUO) kit optimized for real-time qualitative detection of SARS-CoV-2 nucleic acid using hydrolysis probes.

- Multiplex detection of 2019-nCoV_N1 and 2019-nCoV_N2 targets and human RNase P gene enables high throughput workflows
- Reduce background amplification from genomic DNA by use of a modified RNase P Internal Control reverse primer to target an exon-exon boundary
- Increase sensitivity with Luna Probe One-Step RT-qPCR 4X Mix with UDG allowing for more sample input
- Compatible with low reaction volumes including 384-well plate formats

The kit features a primer/probe mix specific to two regions of the SARS-CoV-2 virus N gene [based on sequences provided by the Centers for Disease Control and Prevention (CDC)]. The probes have been modified to contain different fluorophores (N1: HEX; N2: FAM) to enable multiplexing. An internal control primer and probe set, designed to amplify the human RNase P gene, is also included in the primer mix. The reverse primer of this target has been modified from the CDC design to target an exon/exon boundary to reduce background amplification from possible contaminating genomic DNA.



Using the Luna SARS-CoV-2 RT-qPCR Multiplex Assay Kit, up to 94 different samples can be assessed in a single 96-well plate. Anticipated results for each sample type are shown (in each fluorophore channel).

Learn More

Golden Gate Assembly

New England Biolabs® is pleased to announce the launch of PaqCI™, an isoschizomer of AarI. Unlike AarI, PaqCI cuts to completion and does not exhibit star activity under optimal conditions.

5′...CACCTGC(N)$_4$▼...3′
3′...GTGGACG(N)$_4$▲...5′

PaqCI is a Type IIS restriction enzyme that has a 7-basepair recognition sequence, useful for avoiding domestication issues in Golden Gate Assembly. This enzyme requires more than one site to efficiently cleave. To achieve optimal cleavage, PaqCI Activator is provided with the enzyme.

We have provided a protocol for Golden Gate Assembly using PaqCI, along with guidelines for PaqCI Activator amounts.

Learn how you can push the limits of your Golden Gate Assembly, and find out how NEB® has achieved high efficiency assembly with 35+ fragments.

Product Details

Extracting Genomic DNA? Why not Migrate to Monarch®!

NEB offers two convenient solutions for the extraction of genomic DNA from biological samples.

Monarch HMW DNA Extraction Kits

Our novel, glass bead-based approach for the rapid isolation of ultra-high molecular weight DNA.

- Quickly and easily isolate High Molecular Weight (HMW) DNA from several sample types
- Tune the size of isolated DNA by adjusting the agitation speed during lysis
- Obtain best-in-class yields of highly pure and intact DNA for excellent performance in long read sequencing

Missed our webinar? Watch it now.
The Product Developer of our Monarch HMW DNA Extraction kits introduces the technology, walks you through the workflow, and shares some long read sequencing data produced with purified HMW DNA.

Learn More

Request a Sample from your Local Distributor

Monarch Genomic DNA Purification Kit

Our more traditional, spin-column-based workflow for gDNA extraction.

- Isolate large, intact gDNA fragments with a peak size >50 kb
- Purified DNA has outstanding quality metrics
- Perfect choice upstream of applications like cloning, qPCR and NGS

> *This kit yielded the highest purity DNA I have ever seen from a commercial spin column kit.*
>
> – Researcher, Lake Superior State University

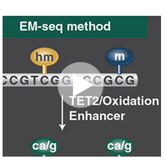
Learn More

Request a Sample from your Local Distributor

NEBinspired™

Our new science blog, NEBinspired, was designed to share inspirational stories about trends in the life sciences, lab tips to help you save time, and life lessons to reflect on.

In our latest post, Harvesting improved methylome sequencing accuracy, read how a team from the University of California Los Angeles published an in-depth comparison of the Enzymatic Methyl-seq method to Whole Genome Bisulfite Sequencing (WGBS) with *Arabidopsis thaliana* samples. After discovering how researchers can improve methylome data outcomes for any eukaryotic sample, you might become an EM-seq convert.



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