



Unique Dual Indexes for Next Gen Sequencing



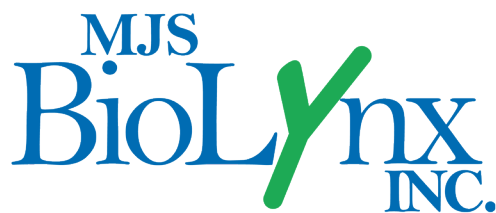
Get more accurate data and eliminate mis-assigned reads due to index hopping!

NuGEN's Unique Dual Indexes enable the detection of index hopping, a sequencing phenomenon that can lead to mis-assignment of reads to the incorrect sample. Use of an additional index can enable detection and eliminate mis-assigned reads from a dataset.

- Up to 384 Unique Dual Indexes are available
- Conveniently configured in a pre-plated format as 96 unique barcode pairs, so manual preparation of barcode pairs is completely eliminated
- Each sample will have index1 and index2 barcodes that are completely unique from all other samples on the plate.

Index hopping has been shown to occur at a higher frequency in patterned flow cell sequencing platforms, such as the HiSeq 3000, HiSeq 4000, NovaSeq.

Visit www.biolynx.ca/nugen-udi or contact us for more information.



1-888-593-5969 • www.biolynx.ca • tech@biolynx.ca





Ovation® Ultralow Library System V2

A simple, fast and scalable solution for producing DimerFree libraries that can be used for a broad range of next generation sequencing applications at input levels ranging as low as 10 pg to 100 ng.

Product Number	Description	Pkg Size
NU9149A01	Ovation® Ultralow System V2 + Unique Dual Index + Molecular Tag	96 reactions

Celero™ DNA-Seq Library System

One kit that produces both PCR and PCR-free DimerFree libraries in three simple steps. It features an addition-only workflow that eliminates the post-ligation bead purification. The NuQuant™ quantitation method saves both time and cost in measuring library concentration for pooling.

NU0360AUDI	Celero™ DNA-Seq Barcode Set A + Unique Dual Index	96 reactions
NU0360BUDI	Celero™ DNA-Seq Barcode Set B + Unique Dual Index	96 reactions

Universal Plus mRNA-Seq

A unique solution for mRNA-Seq featuring a broad input range from 10 ng to 1 µg of total RNA and optional integrated depletion of unwanted transcripts.

NU914496	Universal Plus mRNA-Seq + Unique Dual Index	96 reactions
NU9144A01	Universal Plus mRNA-Seq + Unique Dual Index, Automation Enabled	96 reactions
NU914796	Universal Plus mRNA-Seq with Human Globin AnyDeplete + Unique Dual Index	96 reactions
NU9147A01	Universal Plus mRNA-Seq with Human Globin AnyDeplete + Unique Dual Index, Automation Enabled	96 reactions

Trio RNA-Seq

Combines three powerful technologies to provide a streamlined solution for whole transcriptome analysis, uniquely suited for rare transcript detection and unbiased pathogen discovery. Single Primer Isothermal Amplification (SPIA) enables access to limited and degraded samples. Enzymatic fragmentation and DimerFree library construction allows efficient and robust library preparation. AnyDeplete transcript depletion after library construction maximizes informative sequencing reads from whole transcriptome data.

NU914396	Trio RNA-Seq + Unique Dual Index, Human rRNA AnyDeplete	96 reactions
NU9143A01	Trio RNA-Seq + Unique Dual Index, Human rRNA AnyDeplete, Automation Enabled	96 reactions

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