Universal Plus mRNA-Seq

www.nugen.com

Expand your ability to do mRNA-Seq

Universal Plus mRNA-Seq is a comprehensive solution for standard mRNA-seq studies with a vastly simplified workflow. As a novel feature, Universal Plus mRNA-Seq incorporates the ability to eliminate unwanted transcripts from mRNA-seq libraries using the proprietary AnyDeplete technology. This strategy, typically employed for whole transcriptomics studies, expands the data that can be obtained from an mRNA-seq experiment.

Why use Universal Plus mRNA-Seq?

Universal Plus mRNA-Seq has several unique features:

1. Broad dynamic input range, from 1 µg to as low as 10 ng, enables access to previously inaccessible low input samples.
2. Library construction, that includes the proprietary **DimerFree** technology, allows for more efficient and robust library preparation.
3. Customizable transcript depletion with **AnyDeplete** maximizes informative data from mRNA sequencing.

Features

- Broad dynamic input range (10 ng to 1 µg)
- Random and oligo(dT) priming
- Stranded libraries
- Efficient library preparation without adaptor titration
- Pre-plated adapters
- Unique barcodes included for every sample
- Customizable transcript depletion after library preparation
- Fully automatable

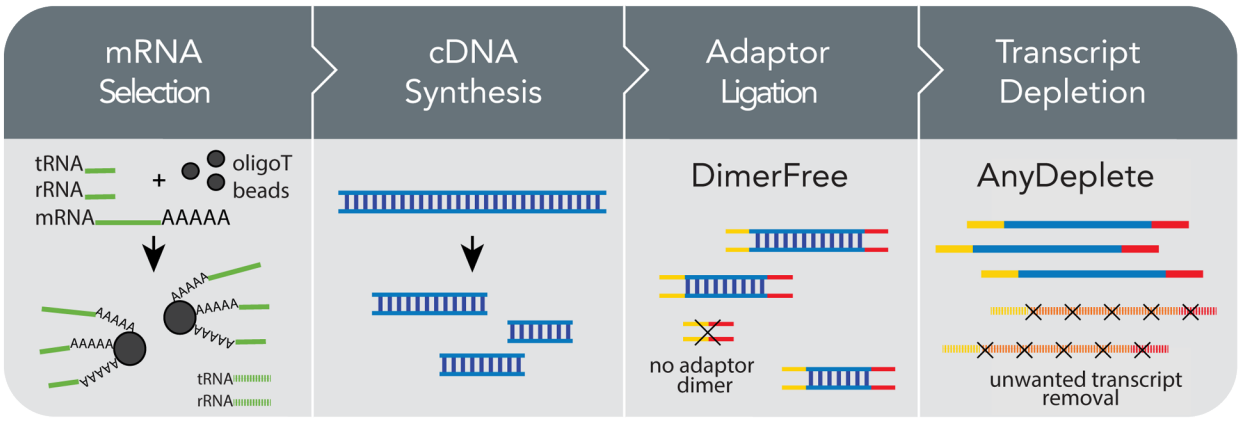

Figure 1 Universal Plus mRNA-Seq is a complete end-to-end solution for mRNA sequencing, with a simple easy to follow workflow.

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NuGEN®

Available in Canada from...

MJS BioLynx INC.

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

Technical details

- Input range: 10 ng - 1 µg total RNA
- Even 5′-3′ transcript coverage
- High correlation across wide input range
- Simplified workflow

Applications

- mRNA sequencing
- Gene expression analysis
- Transcript discovery
- Splice variant and isoform analysis
- Gene fusion detection

Why use AnyDeplete?

- Removes unwanted transcripts after library preparation
- Add new probes to existing probe sets without re-optimization
- Customizable to make the kit species-specific or experiment specific

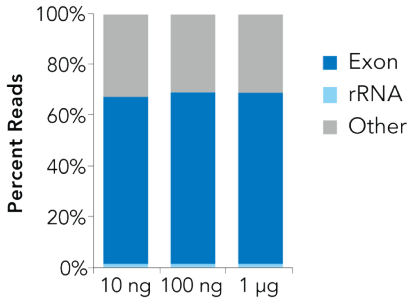
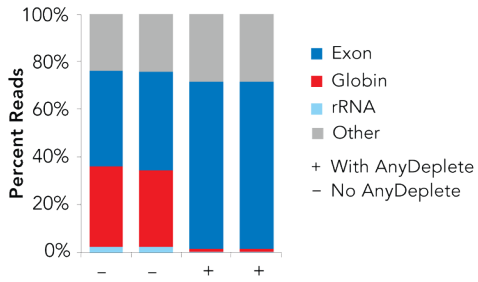


Figure 2 Read alignment metrics are consistent from 1 µg to 10 ng total K562 RNA inputs, allowing access to data from low input samples. Other includes intron, intergenic, unaligned and multialigned reads.



Sample	rRNA	globin	Exon	Genes over FPKM > 1
Without AnyDeplete	2.5%	32.8%	40.9%	9771
With AnyDeplete	0.1%	1.3%	70.3%	9985

Figure 3 Read alignment metrics from 100ng whole blood mRNA-seq. Targeted globin transcript depletion increases the number of reads mapping to exons, resulting in over 200 more genes detected. FPKM based on **RefSeq** transcripts. Other includes intron, intergenic, unaligned and multialigned reads.

Ordering Information	Part No.	Reaction Size
Universal Plus mRNA-Seq	0508	8, 32, 96, Automation
Universal Plus mRNA-Seq w/ Human globin AnyDepete	Contact your Account Executive	
Universal Plus mRNA-Seq w/ Human mitochondria AnyDepete	Contact your Account Executive	

AnyDeplete probe sets can be customized to any transcript from any organism. For kits with custom probe sets, contact your Account Executive or request a quote on our website.

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