Trio RNA-Seq

www.nugen.com

High sensitivity whole transcriptome analyses

Trio RNA-Seq offers a complete, best in class, whole transcriptomics solution for FFPE, challenging samples and detection of rare transcripts. Designed for robust and reliable transcript analysis, Trio RNA-Seq can help you consistently capture more information from virtually any sample. Trio RNA-Seq integrates the proven technology from the highly published Ovation® RNA-Seq System V2 to provide a complete workflow from total RNA to library.

Why use Trio RNA-Seq?

Trio combines three powerful technologies:

1. **Single Primer Isothermal Amplification (SPIA)** enables better access to limited and degraded samples.
2. Enzymatic fragmentation and **DimerFree** library construction allows for more efficient and robust library preparation.
3. Customizable transcript depletion with **AnyDeplete** maximizes informative sequencing reads from whole transcriptome data.

This powerful combination helps increase sensitivity while maintaining unbiased libraries with no adaptor dimers, improving detection of rare transcripts and decreasing sequencing costs via higher multiplexing.

Features

- Integrated DNase treatment
- Unbiased, highly reproducible RNA amplification
- Enzymatic fragmentation
- Efficient library preparation with unique barcodes for every sample
- Customizable transcript depletion after library preparation
- Automation friendly

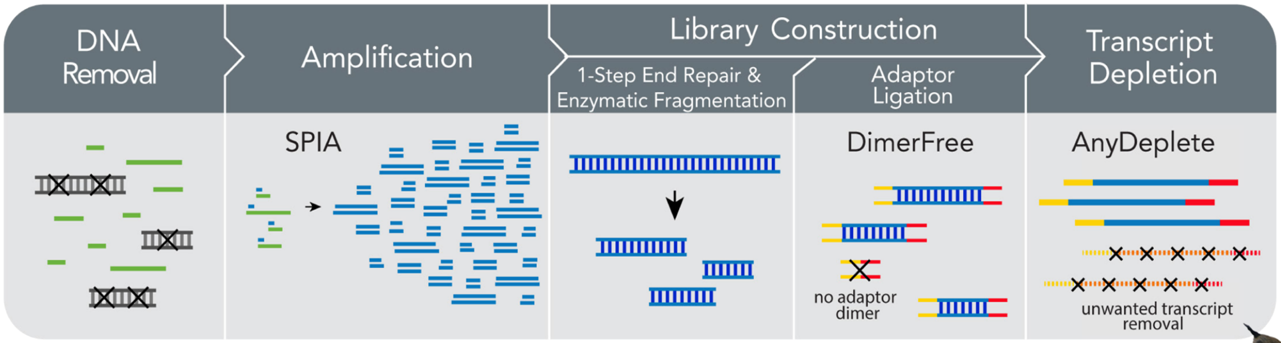

Figure 1 Trio RNA-Seq is a complete workflow, incorporating three proprietary technologies.

NuGEN®

M01441v1

Available in Canada from…

MJS BioLynx INC.

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

Technical details

- Input range: 500 pg - 50 ng total RNA
- Even 5′-3′ transcript coverage
- High correlation across wide input range
- Simplified workflow

Applications

- Whole transcriptomics
- Viral discovery and detection
- Analysis of rare and precious materials
- A wide variety of sample sources:

  Liquid biopsy, FFPE, LCM, degraded samples, cell lines and tissue

Why use SPIA?

- Unbiased transcriptome amplification preserves biological information from samples
- Tolerant to inhibitors from difficult sample sources

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

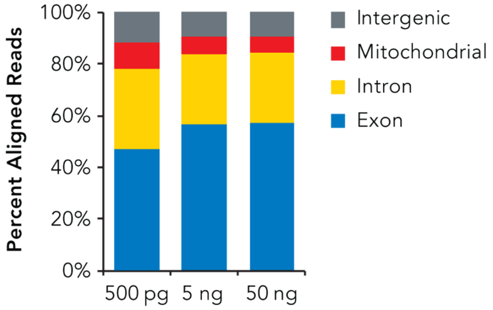

Figure 2 Consistent high quality data from a wide input range allows access to any sample.

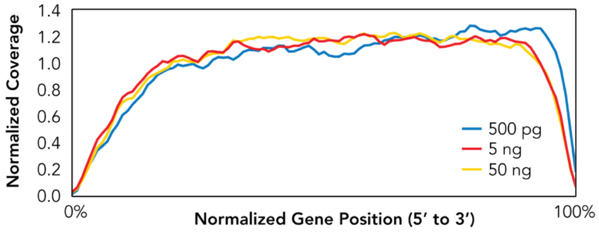

Figure 3 Complete transcript coverage enables splice isoforms, novel splice sites, and fusion analysis.

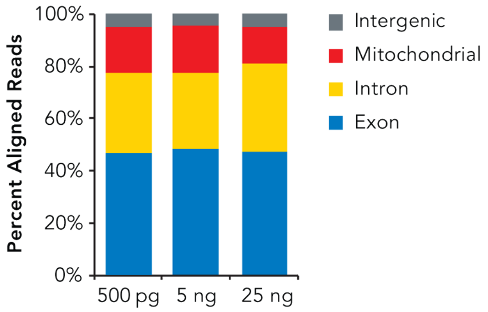

Figure 4 Distribution of reads in libraries using inputs of 500 pg, 5 ng and 25 ng of Human Liver FFPE RNA (RIN 3.6).

Ordering Information	Part No.	Reaction Size
Trio RNA-Seq, with Human rRNA AnyDeplete	0506	8, 32, 96, Automation
Trio RNA-Seq, with custom AnyDeplete probe set	Contact your Account Executive	

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

NuGEN Technologies, Inc.

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