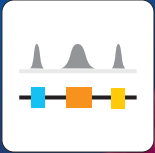


Trio RNA-Seq.

PRODUCT SHEET



High sensitivity whole transcriptome analyses

Trio RNA-Seq offers a complete, best in class, whole transcriptomics solution for challenging formalin-fixed, paraffin-embedded (FFPE) 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 uses the proven technology from the highly cited Ovation® RNA-Seq System V2 to provide a complete workflow, from total RNA to finished libraries.

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 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.

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

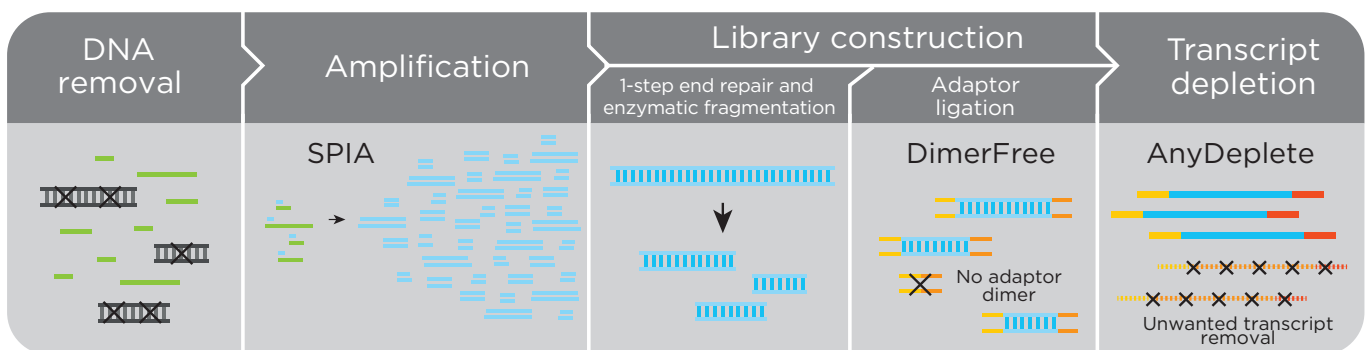


Figure 1: Trio RNA-Seq is a complete workflow, incorporating three proprietary technologies.



Technical details

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

Applications

- Whole transcriptomics
- Viral discovery and detection
- RNA-Seq from a wide variety of sample sources: liquid biopsy, FFPE, laser capture microdissection (LCM), degraded samples, cell lines and tissues

Why use SPIA?

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

Why use AnyDeplete?

- Remove unwanted transcripts after library preparation
- Add new probes to existing probe sets without re-optimization
- Customizable depletion of species- or experiment-specific transcripts

Ordering information

Product Name	Part no.	No. of reactions
Trio RNA-Seq, Human rRNA	0506	8, 32, 96, automation
Trio RNA-Seq + UDI, Human rRNA	9143	96, automation
Trio RNA-Seq, Mouse rRNA	0507	8, 32, 96, automation
Trio RNA-Seq, Custom AnyDeplete	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 via our website.

For Research Use Only. Not for use in diagnostic procedures.

www.tecan.com

Australia +61 3 9647 4100 **Austria** +43 62 46 89 330 **Belgium** +32 15 42 13 19 **China** +86 21 220 63 206 **France** +33 4 72 76 04 80 **Germany** +49 79 51 94 170 **Italy** +39 02 92 44 790 **Japan** +81 44 556 73 11 **Netherlands** +31 18 34 48 17 4 **Nordic** +46 8 750 39 40 **Singapore** +65 644 41 886 **Spain** +34 93 595 25 31 **Switzerland** +41 44 922 89 22 **UK** +44 118 9300 300 **USA** +1 919 361 5200 **Other countries** +41 44 922 81 11

Tecan, Ovation, SPIA, DimerFree and AnyDeplete are registered trademarks and trademarks of Tecan Group Ltd., Männedorf, Switzerland or of Tecan Genomics, Inc., Redwood City, USA.

© 2019 Tecan Genomics, Inc., all rights reserved. For disclaimer and trademarks please visit www.tecan.com

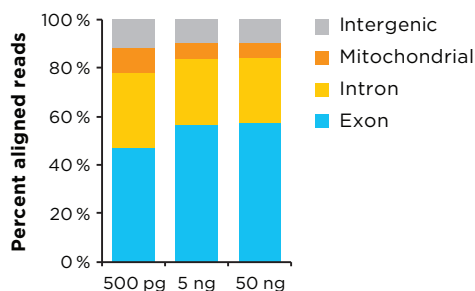


Figure 2: Consistent high quality data from a wide input range allows access to any sample.

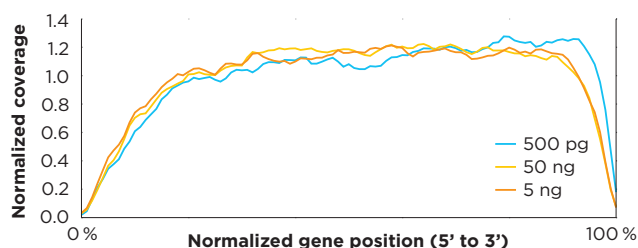


Figure 3: Complete transcript coverage enables splice isoforms, novel splice sites, and fusion analysis.

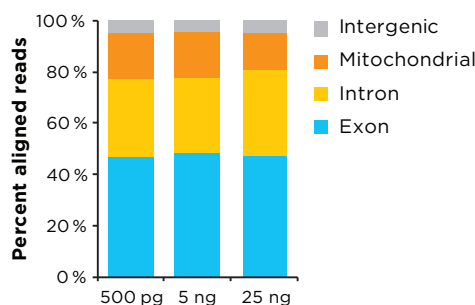


Figure 4: Distribution of reads in libraries from inputs of 500 pg, 5 ng and 25 ng of human liver FFPE RNA (RIN 3.6).

