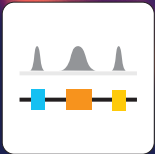


Universal Plus mRNA-Seq.

PRODUCT SHEET



Expand your ability to do mRNA-Seq

Universal Plus mRNA-Seq is a comprehensive solution for mRNA-Seq studies that features a vastly simplified workflow. Universal Plus mRNA-Seq integrates Tecan's AnyDeplete™ technology - to enable elimination of unwanted transcripts - and our novel NuQuant® assay, to simplify library quantification and pooling. These unique features reduce cost and workflow time, allowing you to collect data faster.

Why use Universal Plus mRNA-Seq?

- 1. Broad sample range:** enables previously inaccessible samples as low as 10 ng
- 2. DimerFree library prep:** more efficient and robust library preparation
- 3. Customizable transcript depletion:** AnyDeplete maximizes informative data from mRNA sequencing
- 4. Integrated NuQuant technology:** easy library quantification for multiplexing

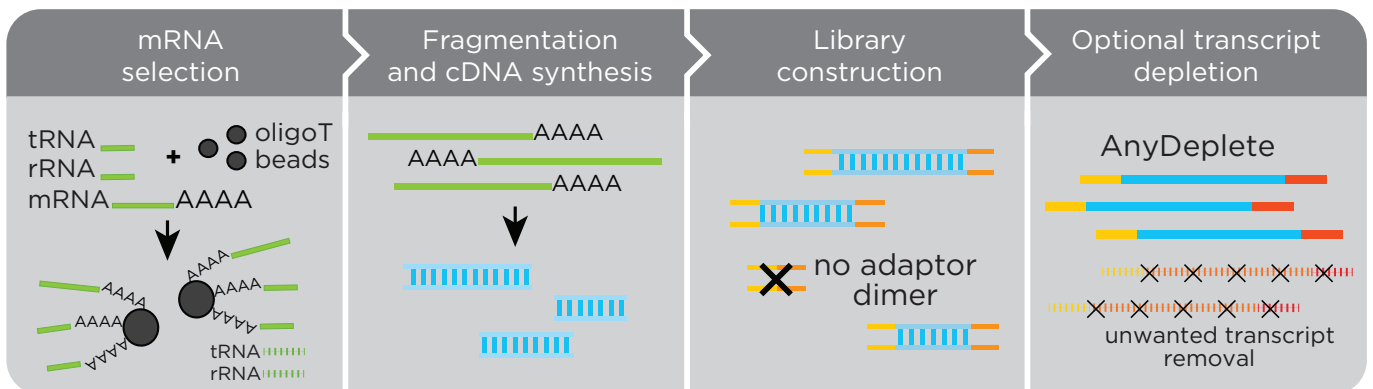


Figure 1: Universal Plus mRNA-Seq is a complete end-to-end solution for mRNA sequencing, with a simple easy-to-follow workflow.



Features

- Broad sample range (10 ng to 1 µg)
- Integrated NuQuant for simple library quantification and pooling
- Efficient library preparation without adaptor titration
- Pre-plated, uniquely barcoded adaptors included for every sample
- Available with Unique Dual Indexes (UDI) to mitigate index hopping
- Customizable transcript depletion after library preparation
- Fully automatable

Technical details

- Input range: 10 ng - 1 µg total RNA
- Even 5'-3' transcript coverage
- High correlation across a wide input range
- Simple fluorescence-based library molarity determination with NuQuant

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 or experiment specific

Ordering information

Product name	Part no.	No. of reactions
Universal Plus mRNA-Seq	0508	8, 32, 96, automation
Universal Plus mRNA-Seq with NuQuant	0520	24, automation
Universal Plus mRNA-Seq with NuQuant, Hu Globin AnyDeplete	0521	24, automation
Universal Plus mRNA-Seq with NuQuant, Custom AnyDeplete	0522	24, automation

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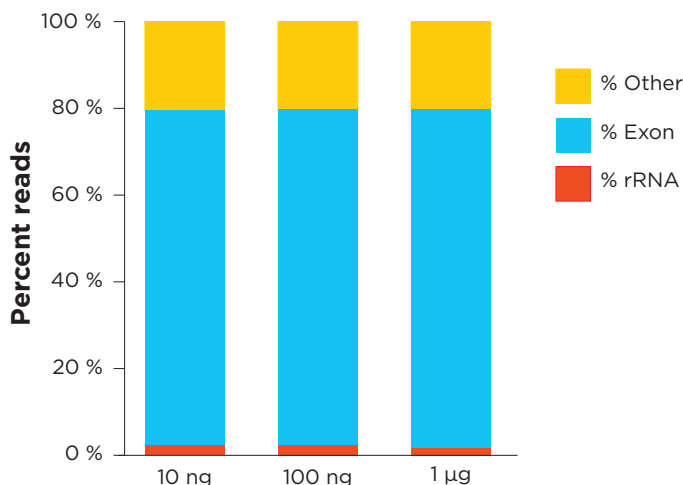
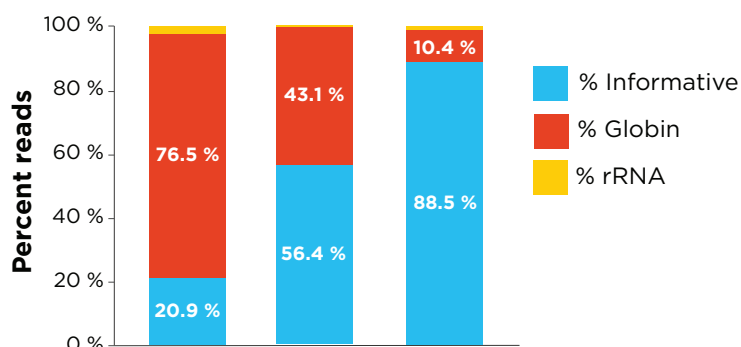


Figure 2: Read alignment metrics are consistent from 10 ng to 1 µg total K562 RNA inputs, allowing access to data from low input samples. Other includes intron, intergenic and multialigned reads.



Adult globin AnyDeplete	—	+	+
Fetal globin AnyDeplete	—	—	+
Number of RefSeq genes with FPKM >1	8326	8975	9388

Figure 3: Sequencing read metrics from 500 ng cord blood total RNA without AnyDeplete, with Adult Globin AnyDeplete and with custom Fetal and Adult Globin AnyDeplete. Informative reads include all reads not mapped to globin or rRNA transcripts.

