Universal Plus Total RNA-Seq with NuQuant®

PRODUCT SHEET

From total RNA to quantified libraries – a complete solution for whole transcriptome RNA-Seq

Universal Plus Total RNA-Seq with NuQuant provides a simple solution for the generation of stranded whole transcriptome RNA-Seq libraries ready for Illumina sequencing, and is compatible with varying quality input material from a range of sample types.

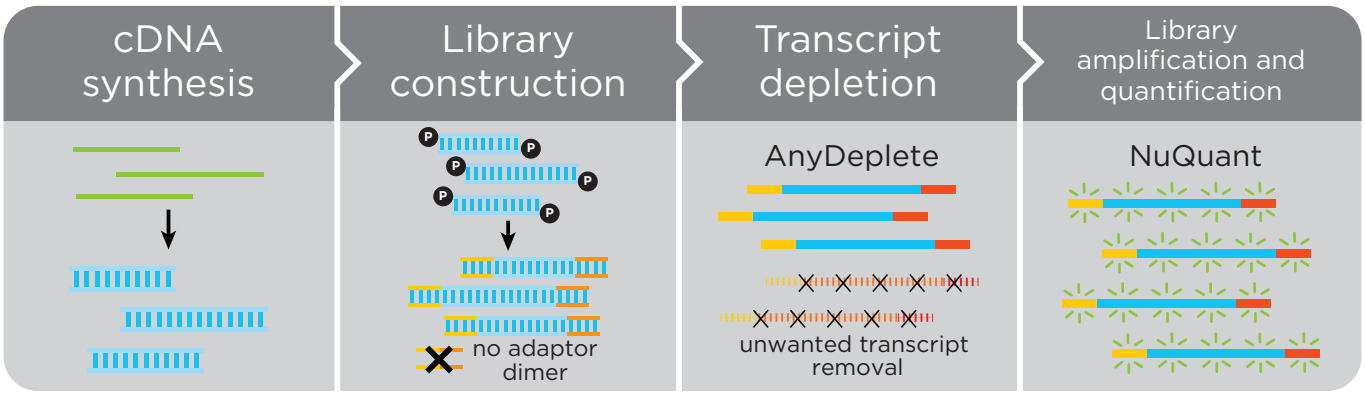
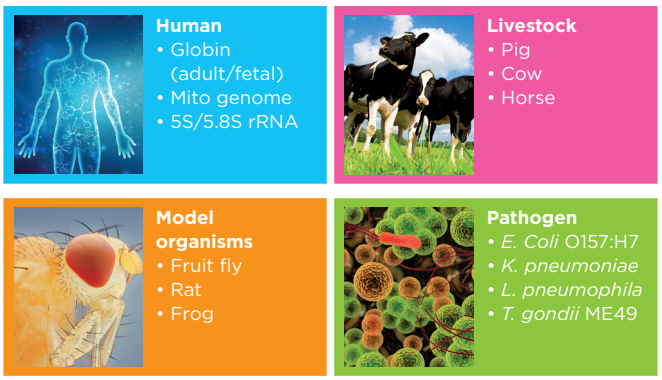


Figure 1: Universal Plus Total RNA-Seq library preparation kits provide end-to-end solutions for strand-specific libraries.

Why use Universal Plus Total RNA-Seq

1. **Reduced hands-on time** – with fewer bead purifications and a simple workflow
2. **384 Unique Dual Index (UDI) adaptors** – for flexible multiplexing and sequencing
3. **AnyDeplete**® integrated targeted rRNA depletion after library construction:
   - Highly specific depletion maximizes informative reads
   - Lower input requirements than other depletion methods
   - Customizable for any transcript from any organism
4. **NuQuant**® library quantification – providing fast and easy determination of library molarity in minutes

Available custom AnyDeplete probes



Contact Tecan NGS Technical Support for detailed target information for each design.

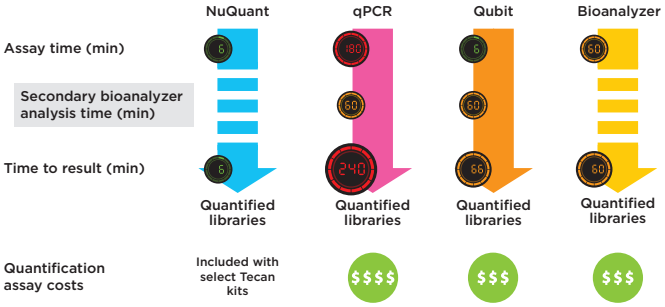


Figure 2: **Comparison of library quantification methods.** NuQuant is integrated into the kit and provides simple fluorescence-based determination of molar library concentration in minutes, without additional cost.

Features

- Compatible with high quality fresh or FFPE/degraded total RNA samples
- Up to 384 unique, preplated UDI adaptors with DimerFree® technology included with the kit for every reaction
- Efficient target depletion of rRNA with AnyDeplete available for model organisms, or customizable to your desired targets
- Saves time and costs for library QC with NuQuant
- Automation-friendly

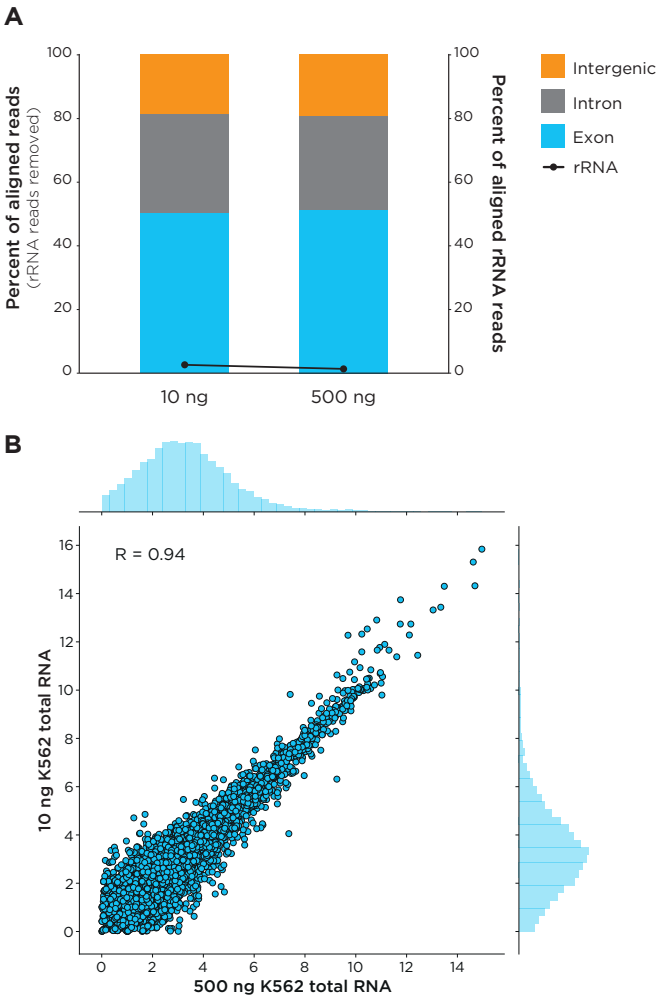


Figure 3: **Consistent data across a broad input range.** A) Total RNA-Seq libraries were generated with 10 ng and 500 ng of K562 total RNA (N=3). Metrics from the different libraries show similar results, demonstrating effective performance across the entire recommended input range. B) FPKM correlation between 10 ng and 500 ng input libraries shows an R value of 0.94, indicating similar data regardless of the 50-fold difference in input amounts.

Sample	DV200 (%)	Input (ng)	% aligned	% rRNA	% exon
Liver FFPE	64	100	95.3	13.8	31.8
Kidney FFPE	41	150	78.6	32.5	32.3

Table 1: **The Universal Plus Total RNA-Seq with NuQuant kit is compatible with FFPE and degraded RNA.** FFPE samples with a DV200 value (percentage of RNA fragments greater than 200 bases) of 64 % and 41 % were used to generate libraries (N=3). Even highly degraded FFPE samples generated high quality libraries with good alignment and a high percentage of exons, providing a single solution for whole transcriptome RNA-Seq for any sample type.

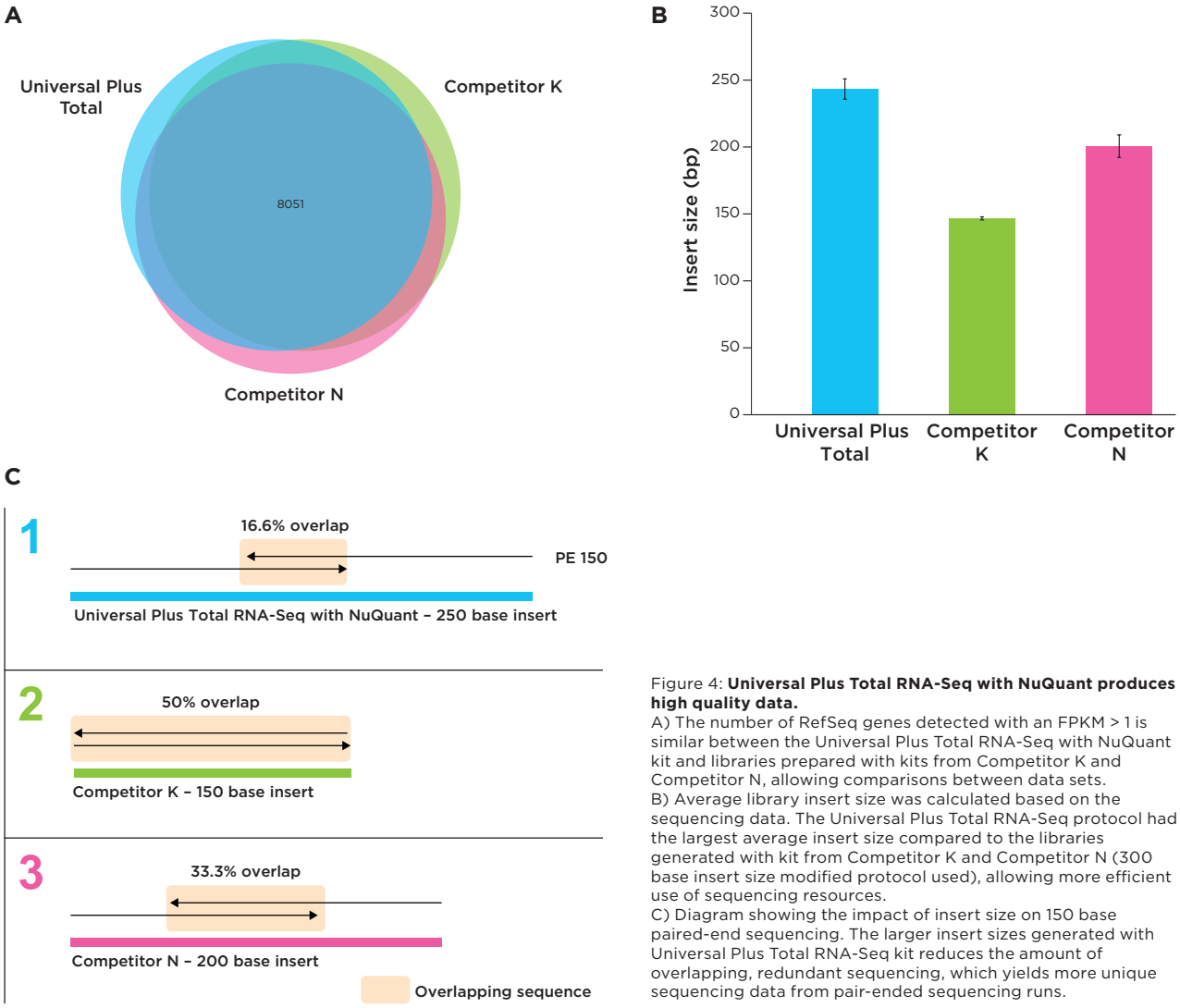


Figure 4: **Universal Plus Total RNA-Seq with NuQuant produces high quality data.**
A) The number of RefSeq genes detected with an FPKM > 1 is similar between the Universal Plus Total RNA-Seq with NuQuant kit and libraries prepared with kits from Competitor K and Competitor N, allowing comparisons between data sets.
B) Average library insert size was calculated based on the sequencing data. The Universal Plus Total RNA-Seq protocol had the largest average insert size compared to the libraries generated with kit from Competitor K and Competitor N (300 base insert size modified protocol used), allowing more efficient use of sequencing resources.
C) Diagram showing the impact of insert size on 150 base paired-end sequencing. The larger insert sizes generated with Universal Plus Total RNA-Seq kit reduces the amount of overlapping, redundant sequencing, which yields more unique sequencing data from pair-ended sequencing runs.

Technical details

- 10-500 ng total RNA input range
- Robust chemical fragmentation
- Stranded libraries
- Consistent data across a wide input range
- Compatible with FFPE and degraded RNA samples
- Optimized protocol for larger insert size libraries

Applications

- Whole transcriptome profiling
- Gene expression analysis
- Transcript discovery
- Splice variant detection

Ordering information

Product name	AnyDeplete probe pool included	Part no.	Barcodes	No. of reactions
Universal Plus Total RNA-Seq with NuQuant, Human AnyDeplete	Human rRNA	9156-24	1-24	24
		9156-A01	1-96	96
		9156B-A01	97-192	96
		9156C-A01	193-288	96
		9156D-A01	289-384	96
Universal Plus Total RNA-Seq with NuQuant, Mouse AnyDeplete	Mouse rRNA, globin	9157-24	1-24	24
		9157-A01	1-96	96
		9157B-A0	97-19	96
		9157C-A01	193-28	96
		9157D-A01	289-384	96
Universal Plus Total RNA-Seq with NuQuant, Custom AnyDeplete*	Custom rRNA	9158-24	1-24	24
		9158-A01	1-96	96
		9158B-A01	97-192	96

*Contact your local Tecan sales representative for more information

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