

Universal RNA-Seq with NuQuant[®]

PRODUCT SHEET



From sample to quantified libraries, a complete solution for whole transcriptome RNA-Seq

Universal RNA-Seq with NuQuant provides a single solution for the generation of stranded whole transcriptome RNA-Seq libraries, and is compatible with any sample type and RNA quality.

Why use Universal RNA-Seq with NuQuant?

1. **Reduced hands-on time**, with fewer bead purifications and a simplified workflow.
2. **DimerFree™** adaptor ligation technology, for fewer adaptor dimers and increased mapped reads.
3. **AnyDeplete®** integrated targeted depletion after library construction
 - Post library construction target depletion maximizes informative reads without manipulation of starting RNA

- No minimum input requirements for depletion.
 - Customizable target depletion for any transcript from any organism
4. **NuQuant** library quantification, providing fast and easy determination of library molarity in minutes.

Features

- Compatible with high quality fresh or FFPE total RNA
- Unique, preplated single or unique dual index (UDI) adaptors for every reaction to enable flexible multiplexing
- Integrated target depletion with AnyDeplete available for model organisms or customizable for your experiment
- Save time and cost of library QC with NuQuant
- Automation solutions available for multiple platforms

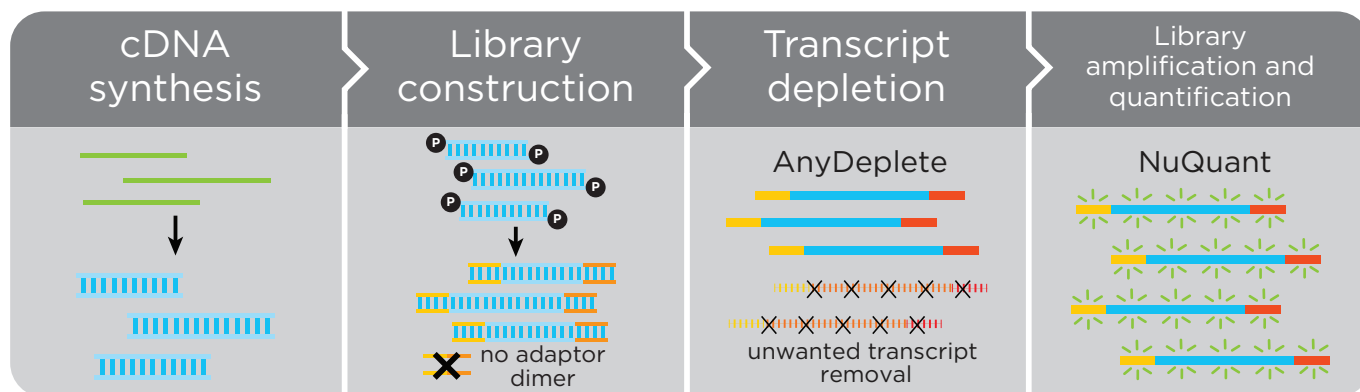


Figure 1: Universal RNA-Seq with NuQuant library preparation kits provide end-to-end solutions for strand-specific libraries.



Technical details

- 10–250 ng total RNA input range
- Stranded libraries
- High technical correlation across a wide input range

Applications

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

Available custom AnyDeplete probes

- Human rRNA + globin
- Rat rRNA + globin
- *Arabidopsis* cytoplasmic + chloroplast rRNA
- *S. cerevisiae* S288C (yeast) rRNA
- *C. elegans* (roundworm) rRNA
- *E. coli* (ATTC 25922) rRNA
- *E. coli* O157:H7 rRNA
- *L. monocytogenes* (SLCC2372) rRNA
- *B. pertussis* (Tohama I) rRNA
- *A. mellifera* (Honey bee) rRNA
- *B. taurus* (cow) rRNA
- *O. cuniculus* (rabbit) rRNA
- *S. scrofa* (pig) rRNA

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

Ordering information

Product Name	AnyDeplete probe pool included	Part no.	No. of reactions
Universal RNA-Seq with NuQuant, Human AnyDeplete	Human rRNA	0530	32, 96
Universal RNA-Seq with NuQuant, Mouse AnyDeplete	Mouse rRNA, globin	0531	32, 96
Universal RNA-Seq with NuQuant, <i>Drosophila</i> AnyDeplete	<i>Drosophila</i> rRNA	0532	32, 96
Universal RNA-Seq with NuQuant, Custom AnyDeplete	Custom AnyDeplete	*	
Universal RNA-Seq with NuQuant + UDI, Human AnyDeplete	Human rRNA	0537	96
Universal RNA-Seq with NuQuant + UDI, Mouse AnyDeplete	Mouse rRNA, globin	0538	96
Universal RNA-Seq with NuQuant + UDI, <i>Drosophila</i> AnyDeplete	<i>Drosophila</i> rRNA	0539	96
Universal RNA-Seq with NuQuant + UDI, Custom AnyDeplete	Custom AnyDeplete	*	

* Talk to your account executive or our Tecan NGS Technical Support team.

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Sample	RIN Score	Input (ng)	% Aligned	% rRNA	RefSeq genes FPKM >1
Brain (MAQC)	high	10	93	10.8	12848
FFPE1	2.3	100	91	11.5	9249
FFPE2	2.4	100	85	9.0	9935

Table 1: Universal RNA-Seq kits are compatible with degraded FFPE RNA. General library metrics for 3 samples. rRNA includes cytoplasmic and mitochondrial rRNAs.

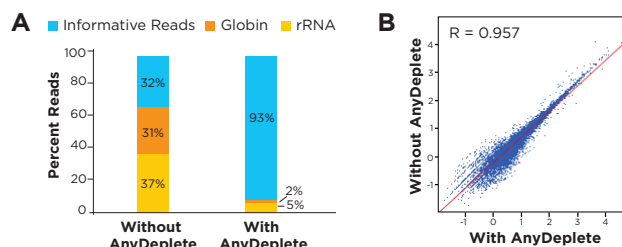


Figure 2: Expression profiling with AnyDeplete. **A)** rRNA and globin AnyDeplete probes were combined into one reaction to remove unwanted reads generated with 100 ng of whole blood RNA. **B)** Depletion of rRNA and globin with AnyDeplete did not perturb transcriptome profiles and increased sequencing efficiency and dynamic range.

Featured publications

1. Farris *et al.* Optimized Method for Robust Transcriptome Profiling of Minute Tissues Using Laser Capture Microdissection and Low-Input RNA-Seq. *Frontiers in Molecular Neuroscience*, 2017.
2. Schwalb *et al.* TT-seq maps the human transient transcriptome. *Science*, 2016.
3. Posczobutt *et al.* Expression Profiling of Macrophages Reveals Multiple Populations with Distinct Biological Roles in an Immunocompetent Orthotopic Model of Lung Cancer. *Journal of Immunology*, 2016.