Application

Whole Transcriptome Sequencing from degraded inputs

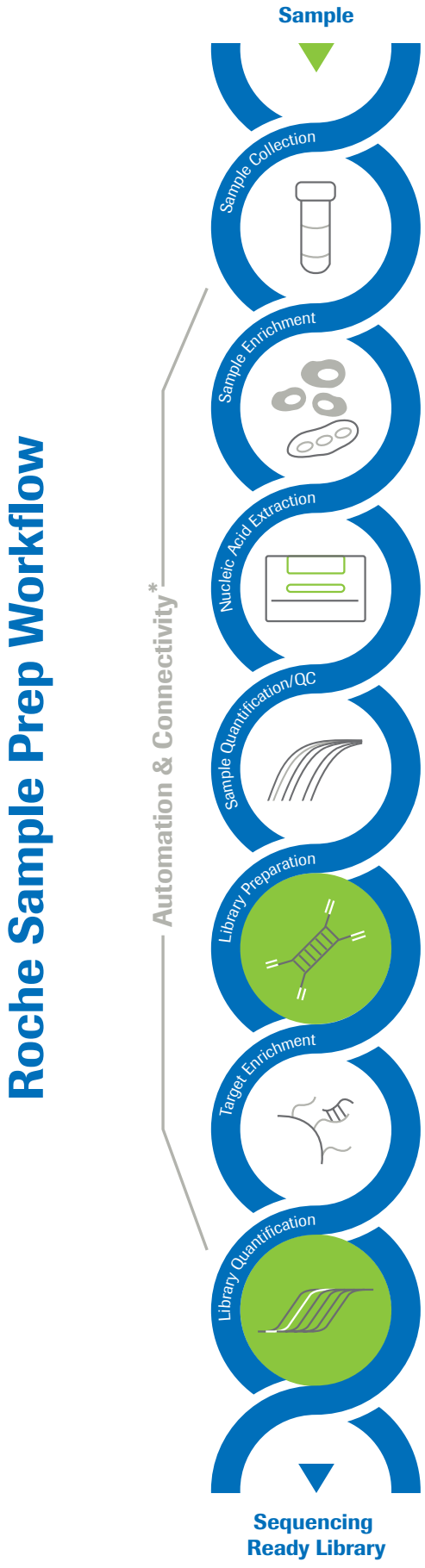
Unlock the Potential of Every Sample

Application:
Whole Transcriptome Sequencing from

Application Challenges

- **Unwanted content** (e.g., rRNA and highly abundant transcripts) and **low library quality** increases the amount of sequencing required to meet experimental objectives.
- Enrichment methods designed to capture poly-adenylated transcripts are not suitable for degraded samples and result in **3'-coverage bias**.
- RNA enrichment prior to cDNA library construction results in a **significant loss of input RNA**. High conversion rates are required to produce high-quality libraries for sequencing on Illumina® instruments.
- Degraded RNA inputs typically lead to **low library complexity** and **high duplication rates**.
- Library construction for whole transcriptome sequencing is a **long process** with **multiple handling steps**.
- Analysis and visualization of RNA-Seq data requires **advanced bioinformatics skills**.

Unlock the Potential of Every Sample



Data on file.
*Automation and Connectivity solutions are in development.
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degraded inputs

Solutions

KAPA RNA HyperPrep Kits with RiboErase (HMR) or **RiboErase (HMR) Globin** offer a complete library prep solution for whole transcriptome sequencing. Kits include **KAPA Pure Beads** for efficient, tunable reaction clean-ups and **KAPA HiFi HotStart ReadyMix** for high-efficiency, low-bias library amplification.

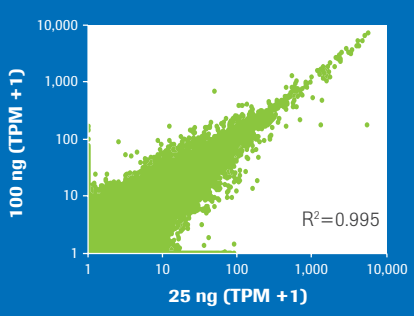
KAPA Adapters are QC-tested for NGS performance and barcode cross-contamination.

KAPA Library Quantification Kits enable accurate, qPCR-based library quantification. Compatible with Roche LightCycler® 96 and LightCycler® 480 real-time PCR systems.

Qualified, single-click **Genialis™** data analysis pipeline and visualization tools.

Benefits

- Improve sensitivity and sequencing economy through **highly efficient enzymatic depletion** of rRNA and/or globin transcripts,* irrespective of sample quality.
- **Achieve high conversion** of input RNA to sequencing-ready libraries, **low duplication rates** and **high library complexity** through carefully optimized protocols.
- Obtain **reliable and reproducible** results from degraded samples.
- **Reduce hands-on and overall time** through fewer enzymatic and reaction cleanup steps with our streamlined, **automation-friendly, single-day** workflow.
- **Take control of your data** with the intuitive, cloud-based Genialis software**, which offers pre-configured pipelines and real-time visualization tools for biologists with limited bioinformatics expertise.
- Enjoy greater peace of mind with **integrated support** for a complete whole transcriptome workflow solution.



KAPA RNA HyperPrep Kits with RiboErase (HMR) support reproducible and reliable whole transcriptome sequencing from FFPE-derived samples. 25 ng and 100 ng of RNA (RIN: 2.2; DV_{200}: 47%) extracted from thyroid FFPE material was used as input. The Pearson correlation plot shows extremely high agreement (R^2 = 0.995) in gene expression data (expressed as transcripts per kilobase million; TPM) for replicate libraries prepared from different input amounts of the same RNA extract.

* Depletion of custom content also supported.
**Not available in all countries.

Unlock the Potential of Every Sample

As the first step in the NGS workflow continuum, sample prep holds the key to unlocking the potential of every sample. Because NGS samples are precious, the best methods are needed to process more samples successfully, obtain more information from every sample, and optimize your sequencing resources. From sample collection to sequencing-ready libraries, Roche Sample Prep Solutions offer workflows for different sample types and sequencing applications that are **proven**, **simple** and **complete**.

Application Note

KAPA RNA HyperPrep Kits with RiboErase (HMR) offer a reliable, single-day library prep solution for whole transcriptome sequencing from FFPE-derived RNA. Roche Sequencing Solutions, 2018.

Webinar

Improved RNA-Seq with degraded inputs and tumor profiling using KAPA RNA HyperPrep Kits.
Presented by Dr. Nancy Nabilsi from Roche Sequencing Solutions (Kapa Biosystems), 25 January 2017.

Publications

Herbert, Z.T et al. Cross-Site Comparison of Ribosomal Depletion Kits for Illumina RNAseq Library Construction. *BMC Genomics*. 2018; 19:199. doi: 10.1186/s12864-018-4585-1

Li, J. et al. Accurate RNA sequencing from formalin-fixed cancer tissue to represent high-quality transcriptome from frozen tissue. *JCO Precis Oncol*. 2018. doi: 10.1200/PO.17.00091

Stebbing, J. et al. LMTK3 confers chemo-resistance in breast cancer. *Oncogene*. 2018; 37:3113 – 3130. doi: 10.1038/s41388-018-0197-0

Ordering information

Roche Cat. No.	KAPA Code	Description	Pack Size
08098131702	KK8560	KAPA RNA HyperPrep Kit with RiboErase (HMR)	24 reactions
08098140702	KK8561	KAPA RNA HyperPrep Kit with RiboErase (HMR)	96 reactions
08308314702	KK8562	KAPA RNA HyperPrep Kit with RiboErase (HMR) Globin	24 reactions
08308241702	KK8563	KAPA RNA HyperPrep Kit with RiboErase (HMR) Globin	96 reactions
08278555702	KK8722	KAPA Dual-Indexed Adapter Kit (15 µM)	96 x 20 µL
07960140001	KK4824	KAPA Library Quantification Kit (Illumina®/Universal)	500 reactions
07960298001	KK4854	KAPA Library Quantification Kit (Illumina/LC480)	500 reactions

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