



Optimize RESOURCES

Roche Sample Prep Solutions for RNA-Seq: Sequence what matters.

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 sequencing resources. Roche Sample Prep Solutions offer workflows for different sample types and RNA-Seq applications that are proven, simple, and complete.

Benefits

Single-day library construction

inclusive of RNA enrichment

Streamlined

automation-friendly RNA enrichment and library prep protocols

Robust and reliable

performance across different sample types and input amounts

Higher success rates

with lower input and degraded samples

Integrated service and support

for the entire workflow from RNA to sequencing-ready library



Flexible workflow options for a variety of applications

- Stranded library construction solutions for the sequencing of both coding and non-coding transcripts
- Compatible with a variety of sample types and input amounts, of both high-quality and degraded RNA

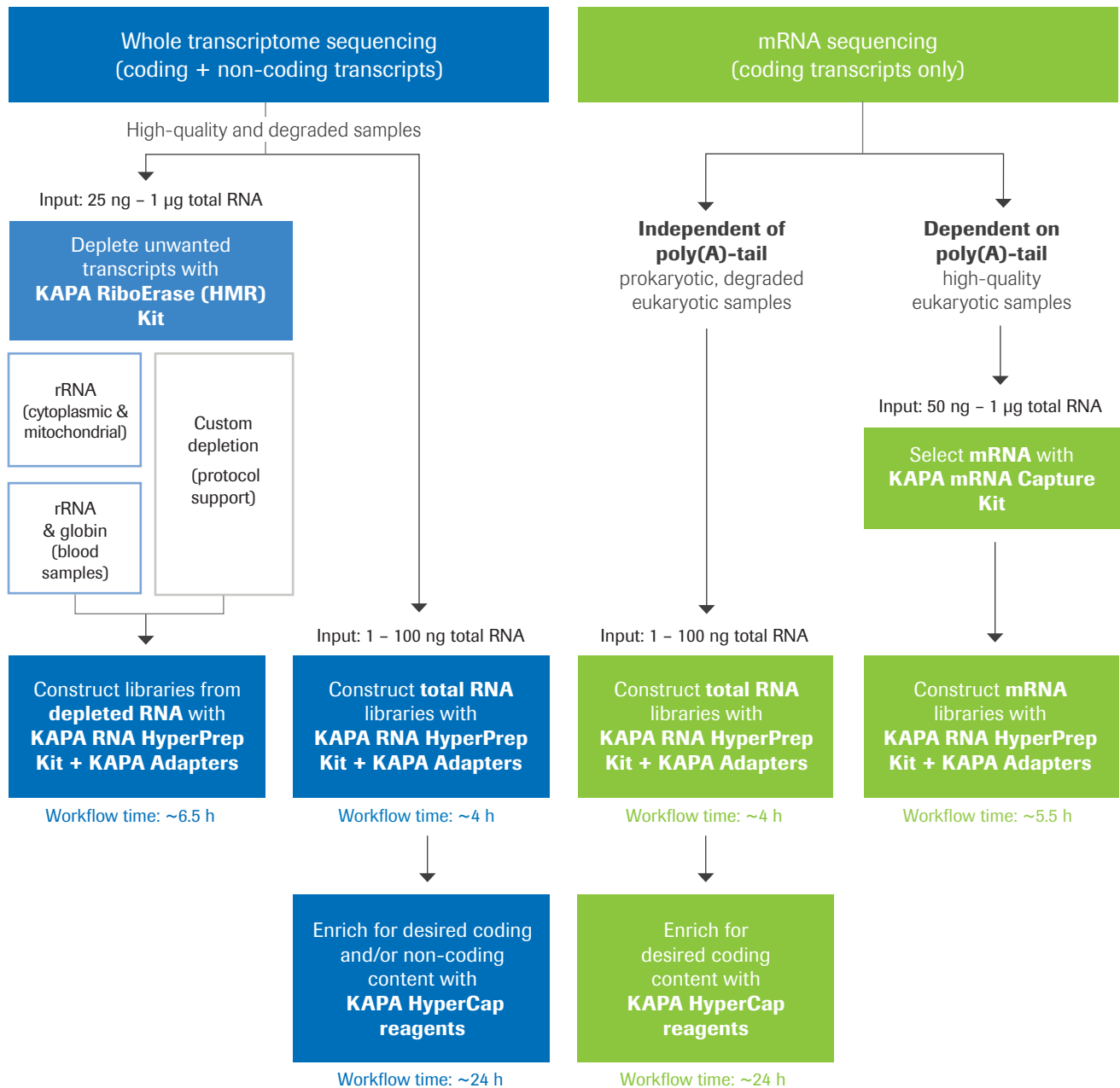


Figure 1. Roche Sample Prep Solutions for RNA-Seq. KAPA RNA HyperPrep Kits provide a streamlined, versatile core library construction solution, that may be combined with various enrichment options, either before or after library preparation. Depending on the sample type and experimental design, unwanted rRNA and/or other transcripts (e.g., globin in blood samples) may be enzymatically depleted using KAPA RiboErase (HMR) Kits; or poly(A)-tailed mRNA may be selected with KAPA mRNA Capture Kits prior to library construction. Alternatively, total RNA libraries may be prepared and coding or non-coding content selected by hybridization capture, using KAPA HyperCap reagents.

HMR: human, mouse, and rat. User-supplied probe sets may be used to deplete additional transcripts from these species, or transcripts from other species. All KAPA HyperPrep Kits contain KAPA Pure Beads for reaction cleanups.

Single-day, single-tube library prep

- Reduce hands-on and overall turnaround time with fewer enzymatic and cleanup steps
- Produce strand-specific libraries from input RNA in approximately 4 hours
- Complete the entire workflow, inclusive of upfront RNA enrichment, in a standard work day
- Achieve high throughput and consistency with automation-friendly workflows

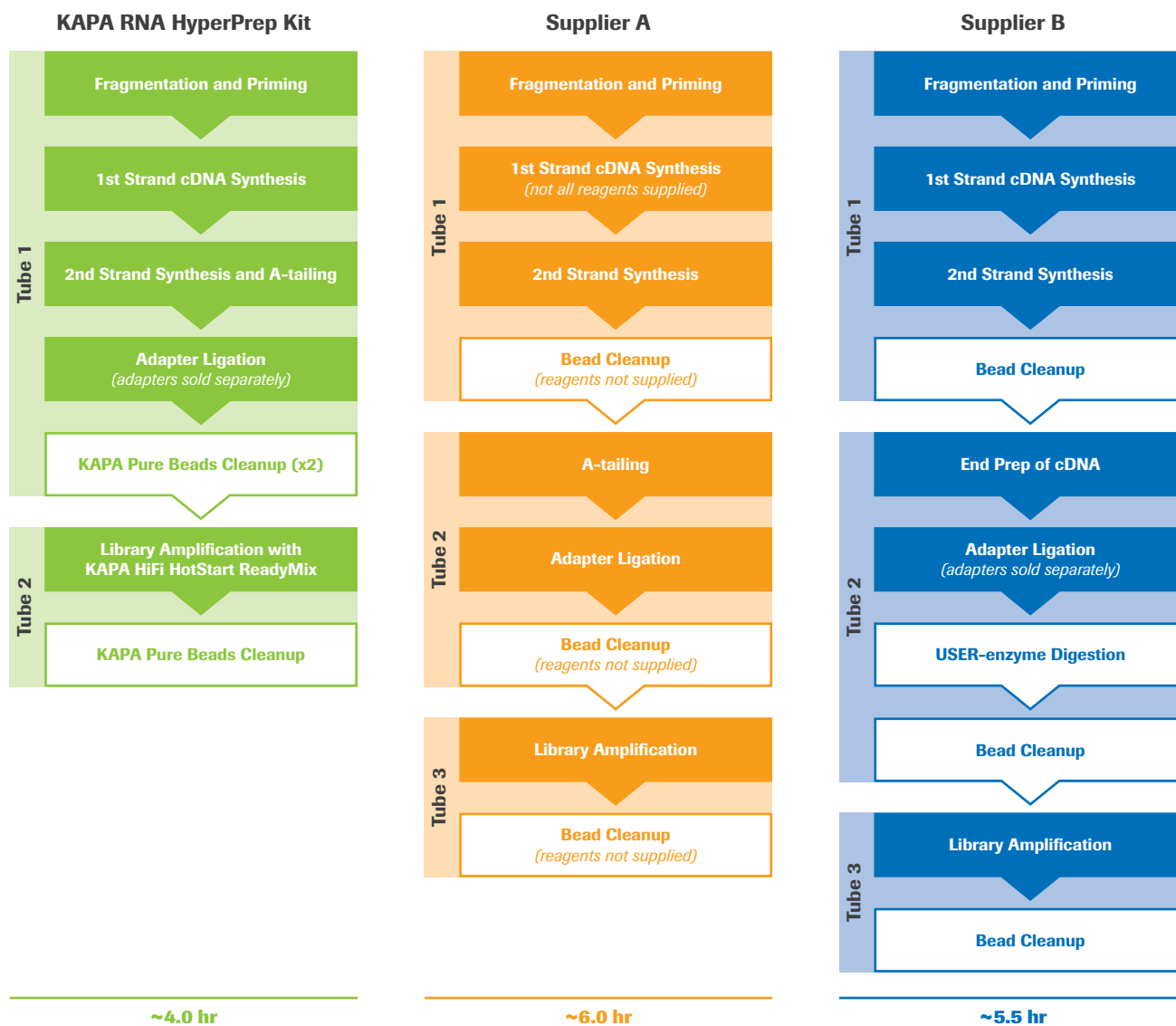
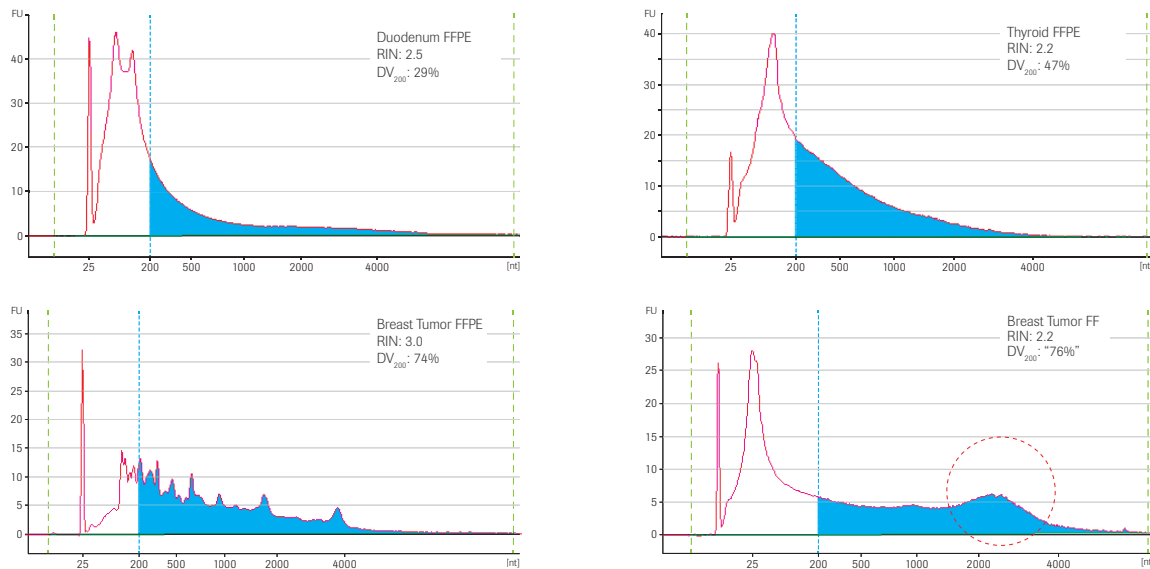


Figure 2. Single-day, single-tube library prep. Streamlined, strand-specific library construction. The novel chemistry employed in KAPA RNA HyperPrep Kits allows for fewer enzymatic and cleanup steps, which reduces hands-on and overall library prep time. RNA depletion with KAPA RiboErase (HMR) or KAPA RiboErase (HMR) Globin Kits adds approximately 2.5 hours to the overall workflow time, whereas mRNA capture adds approximately 1.5 hours. The entire workflow, from input RNA to sequencing-ready library, can easily be completed in a standard workday. All KAPA RNA HyperPrep library construction workflows are automation-friendly.

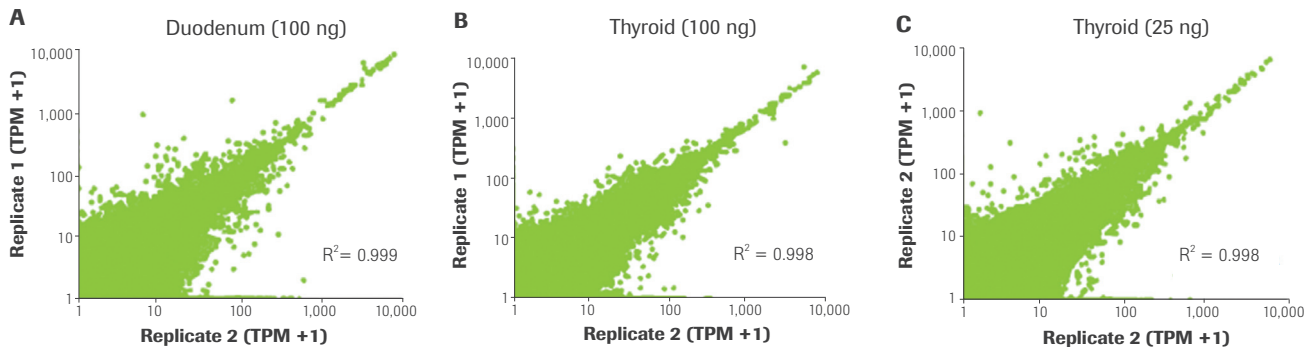
Robust results from FFPE samples

- Construct high-quality libraries from FFPE-derived RNA of variable quality
- High reproducibility between replicates and different input amounts; and high transcript expression correlation between paired fresh-frozen and FFPE samples confer confidence in sequencing results

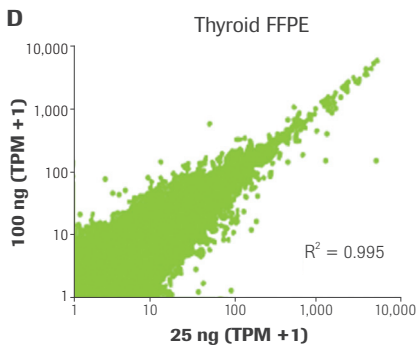
Electropherograms for RNA extracts derived from FFPE and fresh-frozen (FF) samples



Reproducibility between replicates



Reproducibility between quantities



Agreement between fresh frozen and FFPE

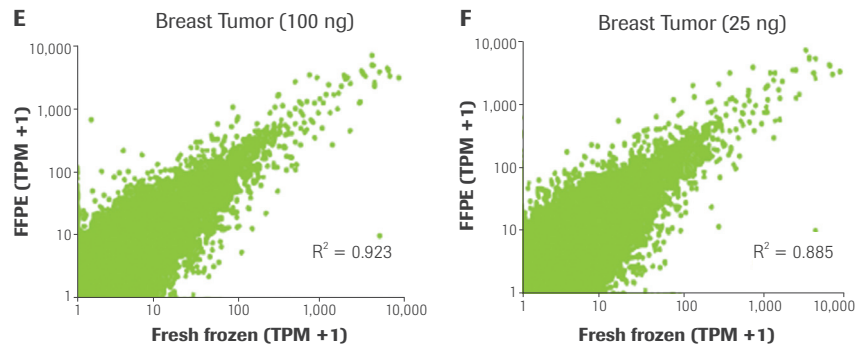


Figure 6. Robust and reproducible results from FFPE samples. Top: Libraries were constructed with the KAPA RNA HyperPrep Kit with RiboErase (HMR), from three different FFPE-derived RNA samples, and a fresh-frozen (FF) sample originating from the same biological specimen as the breast tumor FFPE sample. RIN and DV_{200} values are different quality scores, determined with the Agilent 2100 Bioanalyzer, RNA 6000 Pico Kit and Agilent Expert software. The breast tumor FFPE sample likely contains a significant amount of cross-linked material (circled), which artificially inflated the DV_{200} value.

Bottom: Libraries were prepared from 25 ng or 100 ng inputs of the respective samples. Paired-end (2 x 100 bp) sequencing was performed on an Illumina® HiSeq® 2500 instrument. After removal of residual rRNA and duplicate reads, data were sub-sampled to 14 million reads per sample. Pearson correlation plots are shown for replicates of the same sample and input (**A, B and C**), different inputs of the same sample (**D**), and between the fresh-frozen and FFPE breast tumor samples, for both the 25 and 100 ng inputs (**E and F**).

Process more samples successfully, get more information from every sample, and optimize your sequencing resources with solutions that are **proven, simple, and complete.**

Ordering Information for KAPA RNA HyperPrep Kits

Roche cat. no.	KAPA code	Description*	Kit size
08098093702	KK8540	KAPA RNA HyperPrep Kit	24 rxn
08098107702	KK8541	KAPA RNA HyperPrep Kit	96 rxn
08098131702	KK8560	KAPA RNA HyperPrep Kit with RiboErase (HMR)	24 rxn
08098140702	KK8561	KAPA RNA HyperPrep Kit with RiboErase (HMR)	96 rxn
08308314702	KK8562	KAPA RNA HyperPrep Kit with RiboErase (HMR) Globin	24 rxn
08308241702	KK8563	KAPA RNA HyperPrep Kit with RiboErase (HMR) Globin	96 rxn
08098115702	KK8580	KAPA mRNA HyperPrep Kit	24 rxn
08098123702	KK8581	KAPA mRNA HyperPrep Kit	96 rxn

*All KAPA RNA HyperPrep Kits contain KAPA Pure Beads for reaction cleanups

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4300 Hacienda Drive
Pleasanton, CA 94588

sequencing.roche.com

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