

# KAPA Stranded mRNA-Seq

Even difficult messages should be understood

IDENTIFY  
MORE GENES

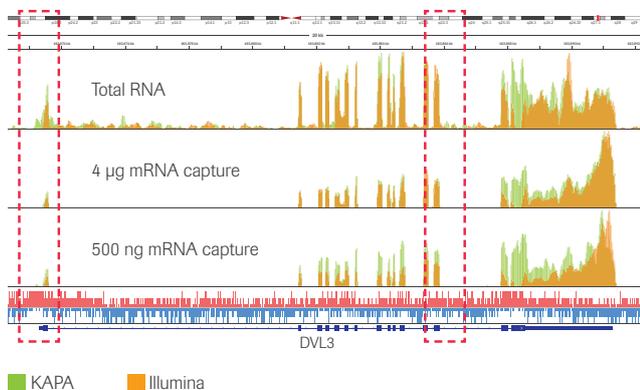
KAPA Stranded mRNA-Seq Kits generate libraries with greater than 99% strand specificity and superior quality. Kits are optimized for improved coverage of GC-rich and low-abundance transcripts, resulting in the identification of more genes. KAPA Stranded mRNA-Seq Kits contain KAPA HiFi for high-efficiency, low bias library amplification.

## Benefits

- Generate libraries from 100 ng - 4 µg total RNA input
- 99% strand specificity
- KAPA mRNA Capture Beads included
- Streamlined “with-bead” protocol improves library construction efficiency
- Qualified automation methods

## Uncover challenging transcripts

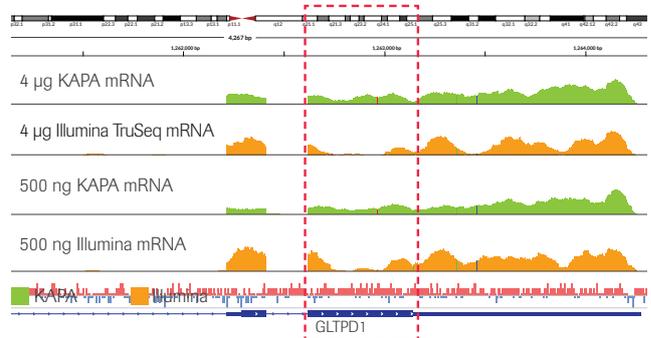
- Improved coverage of GC-rich transcripts
- Enhanced identification of exonic regions



**Improved coverage of GC-rich transcripts.** The 5'- and 3'- exons (outlined in red) of the DVL3 transcript contain regions of very high GC content. These regions are covered to a significantly greater depth in libraries constructed with the KAPA Stranded mRNA-Seq Kit (green), as compared to libraries prepared with the Illumina TruSeq Stranded mRNA Sample Prep Kit (orange).

## Detect low-abundance transcripts

- Identify transcripts missed in libraries constructed with competitor kits from higher inputs
- Improved transcript detection across a range of RNA inputs



**Better characterization of low-abundance transcripts.** GLTPD1, a low-abundance transcript, is covered more comprehensively with the KAPA Stranded mRNA-Seq Kit than with the Illumina® TruSeq® Stranded mRNA Sample Prep Kit. Even with higher input amounts (4 µg), the Illumina data has coverage gaps.

KAPABIOSYSTEMS

## Identify more genes

- Lower duplication rates and more uniquely mapped reads yield more useful data from the same amount of sequencing

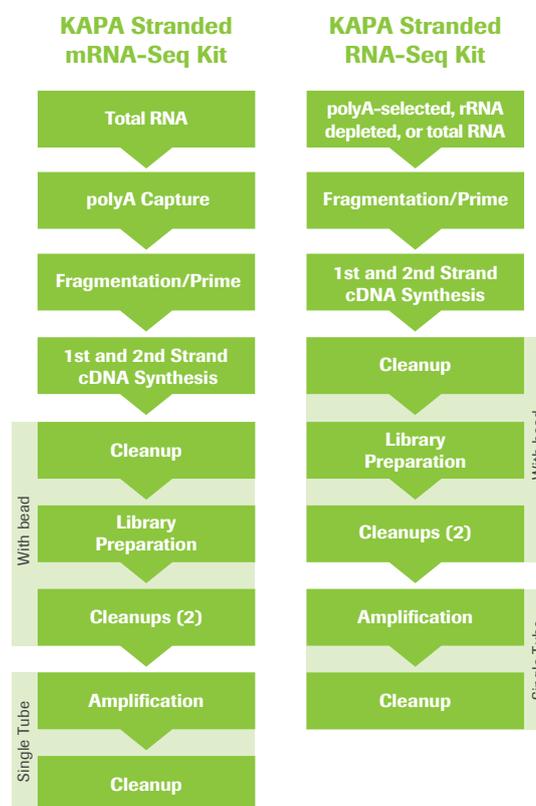
Sample Input	Library Prep	Uniquely Mapped	Duplication Rate	Transcripts Detected	Genes Detected
4 µg	KAPA	76%	24%	112,136	21,016
	Illumina	69%	31%	111,370	20,547
500 ng	KAPA	71%	29%	110,690	20,644
	Illumina	64%	36%	109,810	20,134

### High mapping rates and low duplication rates enable efficient detection of expressed genes.

With a similar number of passed-filter reads (~30 M), KAPA Stranded mRNA-Seq libraries yielded a higher percentage of mapped reads and lower duplication rates than libraries prepared with the Illumina® TruSeq® Stranded mRNA Sample Prep Kit from the same sample and inputs.

## Complete and convenient RNA library prep solutions

- KAPA Stranded mRNA-Seq Kits contain all necessary buffers and enzymes required for the construction of stranded mRNA-Seq libraries (See workflow on right). KAPA HiFi HotStart ReadyMix, the gold standard for NGS library amplification, is also included. Adapters and beads for library prep cleanups are not included, but can be ordered separately.
- Kits without the mRNA Capture module are available for workflows where the input is total RNA, or mRNA generated with a different mRNA enrichment method or kit. KAPA Stranded RNA-Seq Kits are compatible with the SeqCap RNA workflow.



### Ordering information

Roche Cat. No.	KAPA Code	Description	Kit Size
07962193001	KK8420	KAPA Stranded mRNA-Seq Kit, with mRNA Capture module	24 rxn
07962207001	KK8421	KAPA Stranded mRNA-Seq Kit, with mRNA Capture module	96 rxn
07962142001	KK8400	KAPA Stranded mRNA-Seq Kit (no enrichment module)	24 rxn
07962169001	KK8401	KAPA Stranded mRNA-Seq Kit (no enrichment module)	96 rxn

Published by:

#### Roche Sequencing Solutions, Inc.

4300 Hacienda Drive  
Pleasanton, CA 94588

[sequencing.roche.com](http://sequencing.roche.com)

Data on file.

For Research Use Only. Not for use in diagnostic procedures.

KAPA and SeqCap are trademarks of Roche. All other product names and trademarks are the property of their respective owners.

©2017 Roche Sequencing Solutions, Inc. All rights reserved.