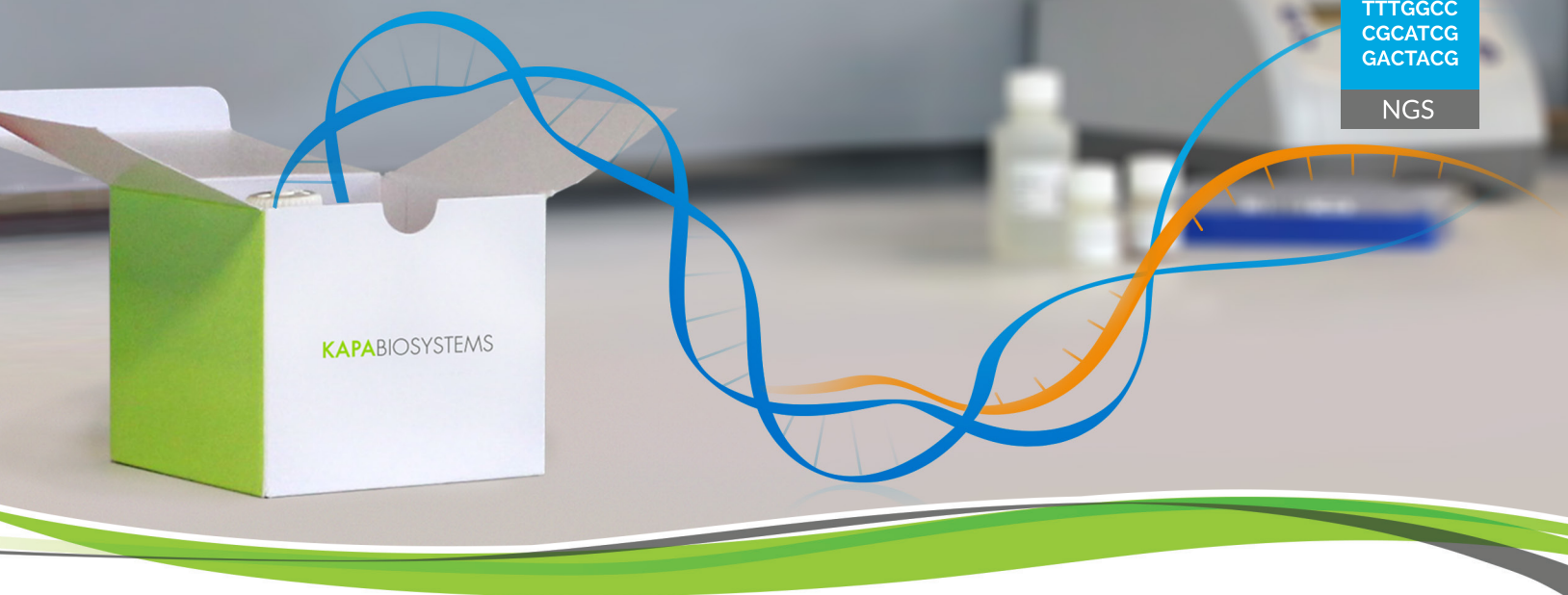


ATCGGCA
TTTGGCC
CGCATCG
GACTACG

NGS

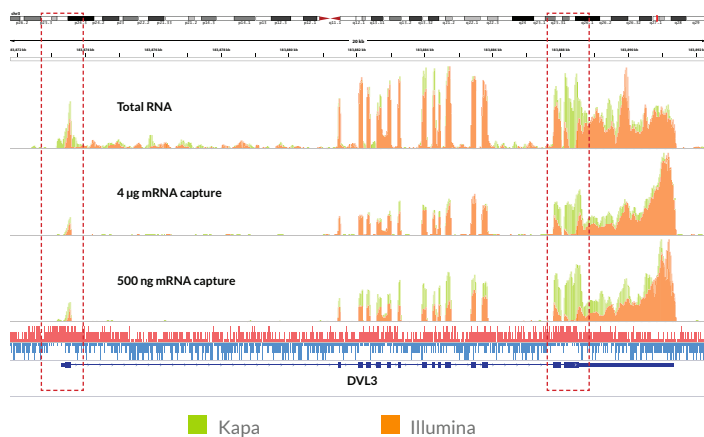


KAPA Stranded mRNA-Seq Kits *for Illumina*

Even difficult messages should be understood.

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

- 100 ng – 4 µg of total RNA
- Protocol allows for 99% strand specificity
- Kit includes KAPA mRNA Capture Beads
- Includes streamlined “with-bead” protocol



Uncover challenging transcripts

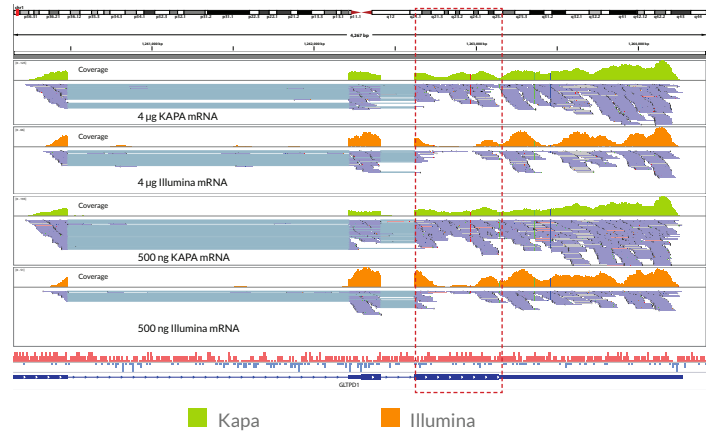
- Improved coverage of GC-rich transcripts
- Enhanced identification of exonic regions

Figure 1: 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 by the KAPA Stranded mRNA-Seq Kit in comparison to the Illumina® TruSeq™ Stranded mRNA Sample Prep Kit.

Detect low-abundance transcripts

- Enables identification of transcripts missed by competitor kits, even with high input
- High uniformity across varying amounts of sample input

Figure 2: Improved coverage of low abundance transcripts. GLTPD1, a lesser-expressed transcript, is covered more comprehensively with the KAPA Stranded mRNA-Seq Kit at 500 ng input total RNA (outlined in red). In comparison, Illumina® TruSeq™ Stranded mRNA Sample Prep Kit shows coverage gaps, even with higher inputs (4 µg).



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

Identify more genes

- Higher percentage of uniquely mapped reads compared to Illumina TruSeq Stranded mRNA Sample Prep Kits
- Lower duplication rates yield better coverage

Figure 3: Highly mapped reads and strand specificity enable sensitive detection of expressed genes. With similar numbers of filter-passed reads (>30M), KAPA Stranded mRNA-Seq libraries generate a greater percentage of mapped reads and lower duplication rates than analogous libraries prepared with the Illumina Stranded mRNA Sample Prep Kit while maintaining 99% strand specificity.

KAPA Stranded mRNA-Seq Kit



KAPA Stranded RNA-Seq Kit



Ordering Information

KAPA Stranded mRNA-Seq and RNA-Seq Kits contain all of the buffers and enzymes required for construction of stranded RNA-Seq libraries via the following steps: mRNA capture (KK8420 and KK8421 only), fragmentation, 1st and 2nd strand cDNA synthesis, and cDNA library construction, including A-tailing, adapter ligation, and library amplification.

Part No.	Description	Quantity
KK8420	KAPA Stranded mRNA-Seq Kit with mRNA Capture Beads	24 reactions
KK8421	KAPA Stranded mRNA-Seq Kit with mRNA Capture Beads	96 reactions
KK8400	KAPA Stranded RNA-Seq Kit without beads	24 reactions
KK8401	KAPA Stranded RNA-Seq Kit without beads	96 reactions

Kapa Biosystems

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