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

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

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).

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.

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.
Identify more genes

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

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

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

<table>
<thead>
<tr>
<th>Roche Cat. No.</th>
<th>KAPA Code</th>
<th>Description</th>
<th>Kit Size</th>
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<tbody>
<tr>
<td>07962193001</td>
<td>KK8420</td>
<td>KAPA Stranded mRNA-Seq Kit, with mRNA Capture module</td>
<td>24 rxn</td>
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<td>07962207001</td>
<td>KK8421</td>
<td>KAPA Stranded mRNA-Seq Kit, with mRNA Capture module</td>
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<td>07962142001</td>
<td>KK8400</td>
<td>KAPA Stranded mRNA-Seq Kit (no enrichment module)</td>
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<tr>
<td>07962169001</td>
<td>KK8401</td>
<td>KAPA Stranded mRNA-Seq Kit (no enrichment module)</td>
<td>96 rxn</td>
</tr>
</tbody>
</table>

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Data on file.

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