

# Certificate of Analysis

## SMARTer® Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian Components

Catalog Nos.	Amount	Lot Number
634415 (Not sold separately; sold as a part of 634411)	12 rxns	Specified on product label.
634417 (Sold separately; also sold as a part of 634412)	48 rxns	Specified on product label.
634418 (Sold separately; also sold as a part of 634413)	96 rxns	Specified on product label.
634419 (Sold separately; also sold as a part of 634414)	192 rxns	Specified on product label.

### Description

The SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian Components are used with indexing primers to generate strand-specific RNA-seq libraries for Illumina® sequencing from 250 pg–10 ng inputs of purified total RNA. This kit incorporates Takara Bio’s proprietary SMART® (Switching Mechanism at the 5' end of RNA Template) technology and includes refinements to the SMARTer method for stranded RNA-seq that simplify the library preparation workflow and improve sequencing performance. This method was developed to work with either high- or low-quality total RNA, does not require additional rRNA removal methods or kits, and produces sequencing libraries that retain strand-of-origin information. The integrated removal of cDNAs derived from rRNA—typically present in high abundance following cDNA synthesis from total RNA inputs—makes the workflow extremely sensitive, yielding data that is highly reproducible with low mapping to rRNA. The new library design featured in the SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian improves sequencing performance compared to the original SMARTer Stranded Total RNA-Seq Kit - Pico Input Mammalian, particularly for NextSeq® and MiniSeq™ instruments carrying the two-channel SBS technology.

### Package Contents

#### Package 1:

634415 (12 rxns)	634417 (48 rxns)	634418 (96 rxns)	634419 (192 rxns)	
55 µl	225 µl	450 µl	900 µl	SMART TSO Mix v2*
20 µl	80 µl	160 µl	320 µl	R-Probes v2*
5 µl	5 µl	5 µl	5 µl	Control Total RNA (1 µg/µl)

#### Package 2:

634415 (12 rxns)	634417 (48 rxns)	634418 (96 rxns)	634419 (192 rxns)	
20 µl	80 µl	160 µl	320 µl	ZapR™ v2
15 µl	55 µl	110 µl	220 µl	SMART Pico Oligos Mix v2*
50 µl	200 µl	400 µl	800 µl	5X First-Strand Buffer
25 µl	100 µl	200 µl	400 µl	SMARTScribe™ RT (100 U/µl)
8 µl	25 µl	50 µl	100 µl	RNase Inhibitor (40 U/µl)
50 µl	200 µl	400 µl	800 µl	ZapR Buffer (10X)
50 µl	200 µl	2 x 200 µl	4 x 200 µl	SeqAmp™ DNA Polymerase
1.25 ml	4 x 1.25 ml	10 ml	2 x 10 ml	SeqAmp CB PCR Buffer (2X)
1.25 ml	1.25 ml	2 x 1.25 ml	5 ml	Tris Buffer (5 mM)
50 µl	200 µl	400 µl	800 µl	PCR2 Primers v2
1.25 ml	4 x 1.25 ml	10 ml	2 x 10 ml	Nuclease-Free Water

\* Takara Bio proprietary sequences

#### Takara Bio USA, Inc.

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## Storage Conditions

- Store Package 1 at  $-70^{\circ}\text{C}$
- Store all other components at  $-20^{\circ}\text{C}$
- Do not freeze R-Probes more than 3 times. We recommend aliquoting R-Probes into multiple vials to avoid repeated freeze/thaw cycles

## Expiration Date

- Specified on product label.

## Shipping Conditions

- Dry ice

## Product Documents

Documents for our products are available for download at [takarabio.com/manuals](http://takarabio.com/manuals)

The following documents apply to this product:

- SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian User Manual

## Quality Control Data

A sample kit from each lot was tested as follows: 250 pg of Control Total RNA (Human Brain) was converted to an Illumina-ready cDNA sequencing library with the SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian as described in the User Manual, using 5 cycles in PCR1 and 16 cycles in PCR2 steps, and an elution volume of 20  $\mu\text{l}$ . Purified libraries were quantified using the Qubit 2.0 Fluorometer (Life Technologies) with a dsDNA HS Assay Kit, resulting in an output of at least 2 ng/ $\mu\text{l}$ . Libraries were diluted to 1.5 ng/ $\mu\text{l}$ , and 1  $\mu\text{l}$  of the dilution was analyzed with an Agilent Bioanalyzer and High Sensitivity DNA Kit (Agilent, Cat. No. 5067-4626). The Bioanalyzer electropherogram showed a broad distribution from 200 bp to 1,000 bp with an average size in the 350–450 bp range. The libraries were sequenced on an Illumina platform and confirmed to contain less than 20% of the reads mapping to rRNA (5S, 5.8S, 18S and 28S) and less than 2% of the reads mapping to mitochondrial ribosomal RNA (m12S and m16S).

It is certified that this product meets the above specifications, as reviewed and approved by the Quality Department.

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