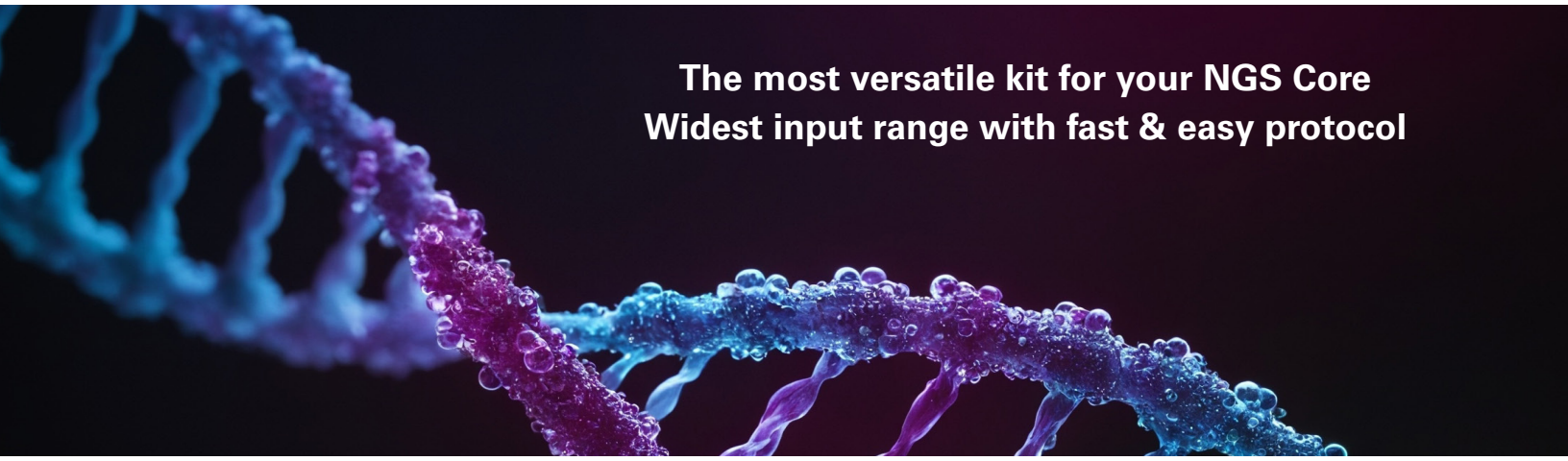
SMART-Seq® Total RNA Pico Input (ZapR® Mammalian) with/without UMIs



Widest input range

- Expanded RNA input: 250 pg–1 µg total RNA
- Any quality RNA: RIN 2–10, DV200 >25% including highly degraded FFPE samples
- Compatible with human, mouse, and related species

Expanded flexibility

- Incorporate unique molecular identifiers (UMIs) for improved data accuracy
- Automation-friendly workflow
- Globin removal (coming soon!)

Complete workflow

- Improved ZapR rRNA depletion included
- Easy single-day library prep with depletion (~6.5 hr)
- Free Cogent™ NGS bioinformatics pipeline for intuitive data analysis

Most comprehensive data insights

- Coding and non-coding RNAs: mRNA, lncRNA, lincRNA, circRNA, etc.
- Full 5′-to-3′ transcript coverage
- Stranded libraries

PRODUCTS

Choose your RNA-seq library prep kit & accessories

	Products	Cat. #
Library prep kits (with/without UMIs)	SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian)	634354, 634355, 634356
	SMART-Seq Total RNA Pico Input (ZapR Mammalian)	634357, 634358, 634359
Indexing with up to 384 UDIs	Unique Dual Index Kit (1-96)	634752
	Unique Dual Index Kit (97-192)	634753
	Unique Dual Index Kit (193-288)	634754
	Unique Dual Index Kit (189-384)	634755
Library clean-up beads	NucleoMag NGS Clean-up and Size Select	744970.5, 744970.50, 44970.500
RNA purification kits	NucleoSpin RNA	740955.50, 740955.250
	NucleoSpin RNA XS	740902.10, 740902.50, 740902.250
	NucleoSpin totalRNA FFPE	740782.50, 740782.250
	NucleoSpin totalRNA FFPE XS	740969.50, 740969.250
	NucleoMag RNA	744350.1, 744350.4

that's GOOD science!™

Key performance data

Enhanced rRNA depletion and higher recovery of biologically relevant reads with as little as 250 pg RNA

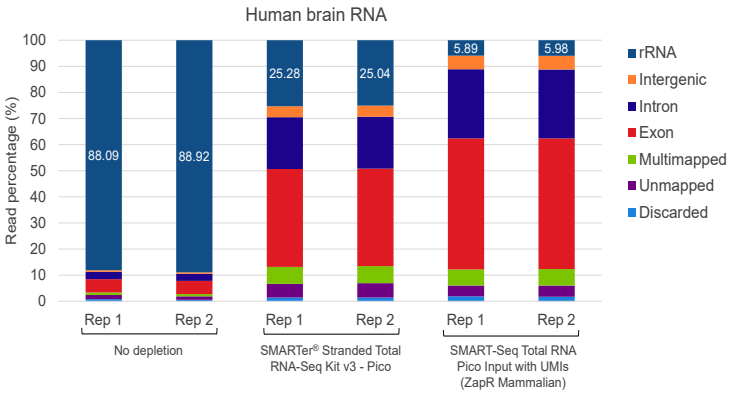


Figure 1. Enhanced rRNA depletion with as little as 250 pg RNA. The improved rRNA depletion technology in SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian) significantly reduces unwanted rRNA reads and enhances the yield of biologically relevant reads compared to the original SMARTer Stranded Total RNA-Seq Kit v3 - Pico. Libraries were prepared from 250 pg of human brain RNA using the respective kits or left untreated. Data analysis was performed with Cogent NGS Analysis Pipeline (CogentAP) using 3 x 10^6 paired-end reads.

Expanded input range up to 1 µg with consistent, reliable performance

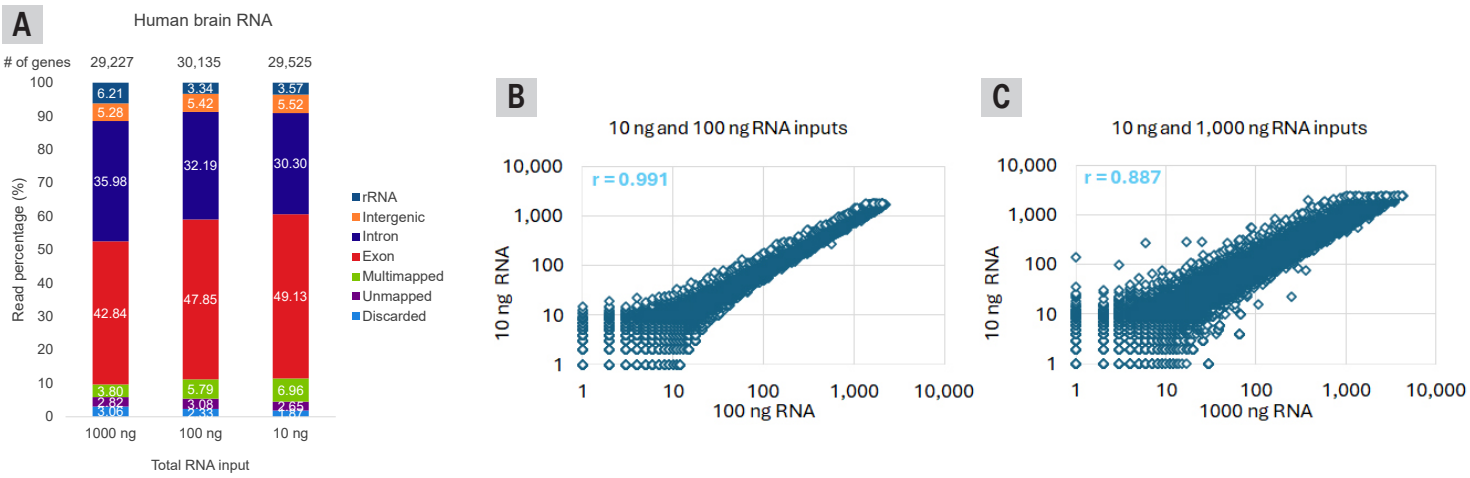
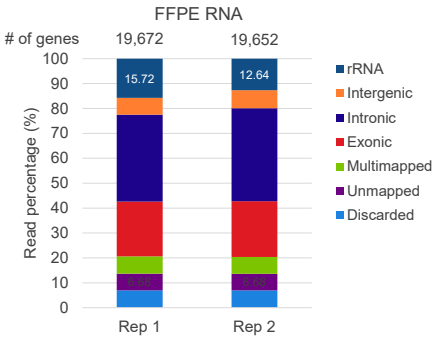


Figure 2. Consistent performance even with higher inputs. Libraries of human brain RNA were prepared using SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian). Data analysis was performed with CogentAP using 22 x 10^6 paired-end reads and represents an average of duplicates. **Panel A.** Sequencing data shows highly consistent read distribution profiles with less than 10% unwanted rRNA reads across all input amounts. **Panels B & C.** Scatterplots illustrate the high correlation between libraries across the input range. Pearson correlation coefficients are indicated.

Protocol modification for library prep from high inputs: To prepare libraries using >10 ng total RNA, adjust PCR 1 and PCR 2 cycles as indicated. >10 ng–100 ng: PCR 1 = 5 cycles, PCR 2 = 14 cycles | >100 ng–200 ng: PCR 1 = 5 cycles, PCR 2 =12 cycles | >200 ng–1000 ng: PCR 1 = 3 cycles, PCR 2 = 12 cycles PCR 2 cycles may be increased if library yields are low. It is essential to use RNA free of gDNA contamination. For all other steps, follow the user manual for the respective kit.



High-quality data from degraded FFPE samples

Figure 3. SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian) efficiently depletes rRNA and mt rRNA and enriches for RNAs of interest from total RNA isolated from FFPE tissue samples. Libraries were prepared from 10 ng of ZapR-depleted FFPE RNA (RIN = 3, DV200 = 77%). Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads.

Learn more at takarabio.com/SMART-SeqTotalRNA

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