

One RNA-seq library prep kit.
Any input or quality.

Versatile



Use for samples of varying quality (RIN 2–10, DV200 >25%) and input amounts (250 pg–1 µg)

Affordable



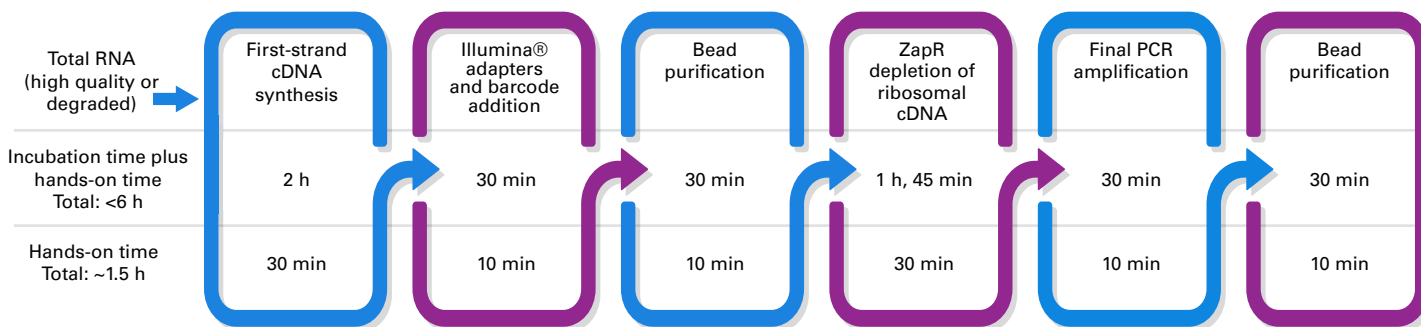
Save >40% in reagent cost/sample with **built-in ribodepletion** and free Cogent™ data analysis

Sensitive



Discover **MORE** insights with a technology that preserves library complexity and detects more genes and transcripts

Get sequencing-ready libraries with only ~1.5 hr hands-on time!



PRODUCTS

Only one choice to make—with or without UMIs

	Products	Cat. #
Library prep kits	SMART-Seq Total RNA Library Prep with ZapR Depletion (with UMIs)	634354, 634355, 634356
	SMART-Seq Total RNA Library Prep with ZapR Depletion	634357, 634358, 634359

Key performance data

Obtain reliable performance across input amounts—up to 1 µg

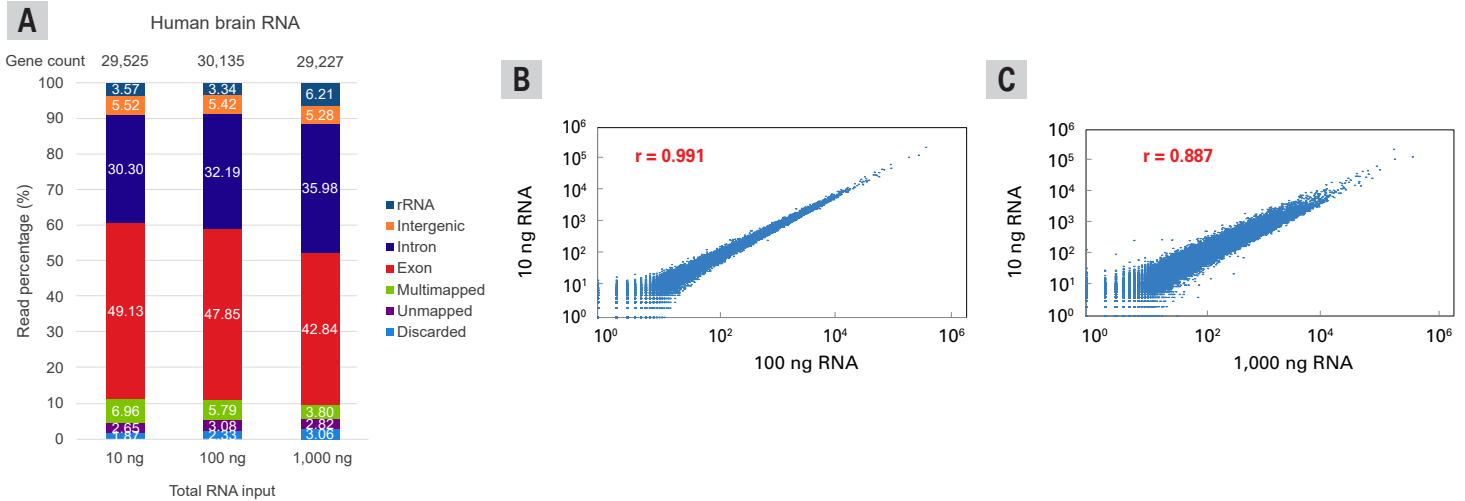


Figure 1. Consistent performance. Libraries of human brain RNA were prepared using SMART-Seq Total RNA Library Prep with ZapR Depletion (with UMIs). Data analysis was performed with CogentAP using 22×10^6 paired-end reads and represents an average of duplicates.

Panel A. Sequencing data shows highly consistent read distribution profiles across all input amounts. **Panels B & C.** Scatterplots illustrate the high correlation between libraries across the input range. Pearson correlation coefficients are indicated.

Attain ultrasensitive gene detection from degraded formalin-fixed paraffin-embedded (FFPE) samples

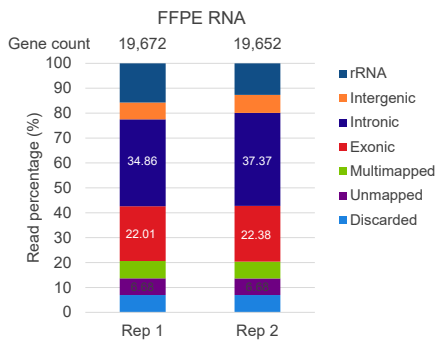


Figure 2. SMART-Seq Total RNA Library Prep with ZapR Depletion (with UMIs) efficiently enriches for RNAs of interest from total RNA isolated from FFPE tissue samples.

Libraries were prepared from 10 ng of RNA (RIN = 3, DV200 = 77%) from an FFPE sample. Data analysis was performed with Cogent™ NGS Analysis Pipeline (CogentAP) using 3×10^6 paired-end reads.

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

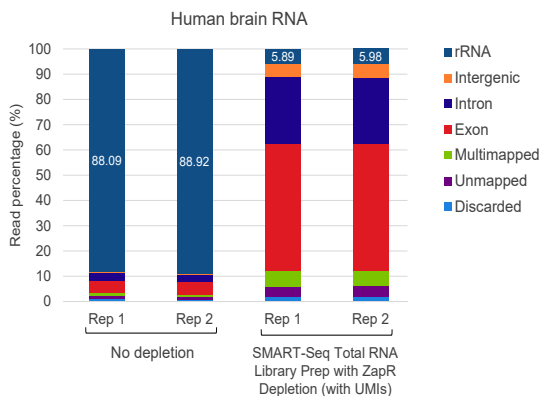


Figure 3. Enhanced rRNA depletion. The improved rRNA depletion technology in SMART-Seq Total RNA Library Prep with ZapR Depletion (with UMIs) significantly reduces unwanted rRNA reads and enhances the yield of biologically relevant reads. Libraries were prepared from 250 pg of human brain RNA using SMART-Seq Total RNA Library Prep with ZapR Depletion (with UMIs) kit or left untreated. Data analysis was performed with CogentAP using 3×10^6 paired-end reads.



Learn more at
takarabio.com/one-kit-for-cores

that's
GOOD
 science!