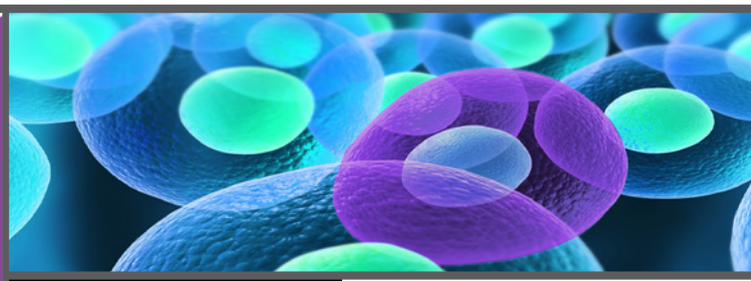
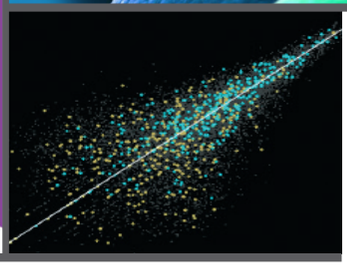
Next-Generation Sequencing

Innovative solutions with SMART® technology





that's GOOD science!®

TaKaRa Clontech

SMARTer® tools for NGS

Our mission is to support scientists who push frontiers to make impactful discoveries, by supplying innovative technologies. We believe in providing both best-in-class tools and expert scientific support to meet the needs of cutting-edge research.

Takara Clontech kits for next-generation sequencing (NGS) have exceptional sensitivity and reproducibility, giving scientists greater confidence in their data, leaving more time to answer interesting questions. The core technology of our kits for NGS is the inherently sensitive SMART template switching mechanism, which has made our SMARTer kits the leader in ultra-low input RNA-seq experiments. SMART technology is not limited to single-cell mRNA-seq: it is ideal for many other NGS applications, including total RNA-seq and low-input ChIP DNA sequencing.

What is SMART technology?

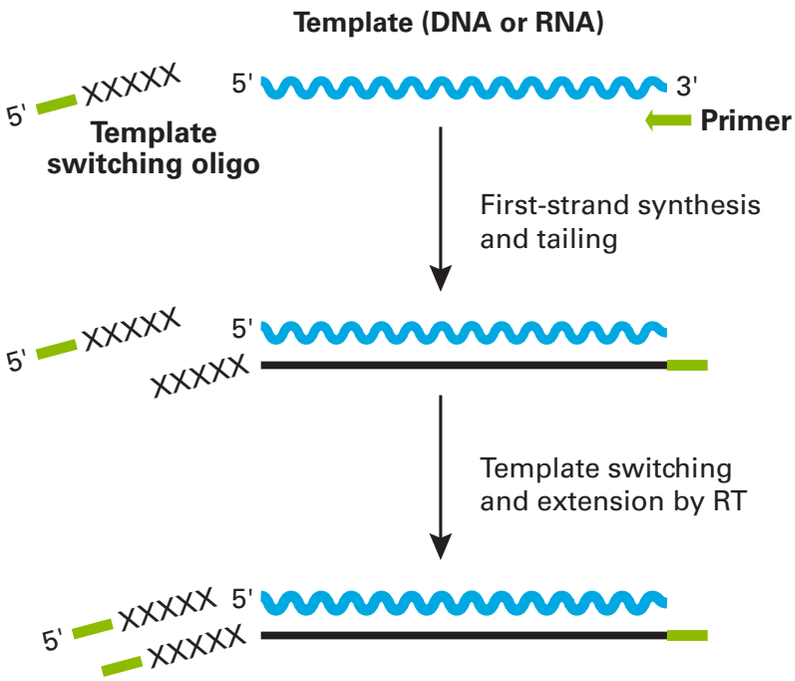
Template switching SMART technology is at the heart of our sequencing library preparation and cDNA synthesis kits.

This reaction produces full-length cDNA coverage, in a cap-independent manner, from RNA in a single-tube reaction.

Why adopt SMART technology?

- **A simplified workflow**
- **Full-length gene body coverage**
- **Exquisite sensitivity and reproducibility**
- **High-quality sequencing libraries**

The industry standard for sensitive, single-cell and ultra-low input analysis



SMART technology is based on the ability of certain reverse transcriptases (RTs) to add additional non-template nucleotides when they reach the 5′ end of the template. A carefully-designed template switching oligo can pair with these additional nucleotides, providing a new template for the RT to continue replication.

Total RNA-seq

Low-input (100 pg—100 ng), high-input (100 ng—1 µg), and total RNA of any quality

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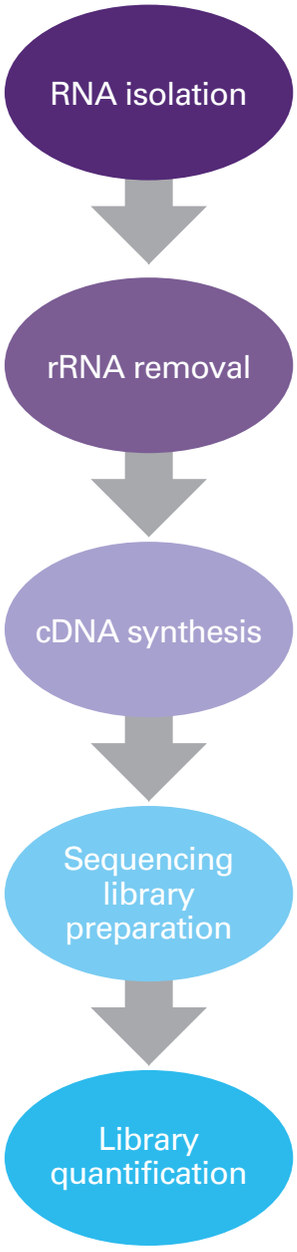
What are the challenges of total RNA-seq?

Total RNA-seq using random priming is the preferred method for generating data from both coding and non-coding RNA. However, abundant transcripts, like **ribosomal RNA**, and identification of **non-coding and antisense RNA** without strand of origin information are major challenges for total RNA-seq. Additionally, **degraded RNA** (e.g., RNA from FFPE samples) requires different strategies than high-quality RNA.



Low-input mammalian samples

RiboGone™ - Mammalian kits reduce rRNA in human, mouse, or rat total RNA to a small percentage of all reads. SMARTer Stranded kits work seamlessly with these kits to generate Illumina-specific, stranded RNA-seq libraries:

- **Low-input:** 10–100 ng of total RNA, or 100 pg–100 ng of rRNA-depleted or poly(A)-purified RNA
- **Rapid workflow:** From total RNA to sequencing libraries in ~5 hours

High-input mammalian samples

The SMARTer Stranded - HI kits incorporate RiboGone rRNA removal technology and Illumina library preparation into one seamless workflow:

- **Any quality RNA:** Full-length or degraded total RNA (100 ng–1 µg)
- **Streamlined protocol:** A single, 5 hour protocol for rRNA removal and stranded library preparation for Illumina platforms

Low-input degraded mammalian samples

SMARTer Universal kits work with RiboGone technology to apply template switching to the most difficult RNA samples:

- **Degraded RNA:** Highly degraded total RNA (10–100 ng)
- **Broad platform compatibility:** Use with Ion Torrent library prep kits or the Low Input Library Prep Kit for Illumina sequencing

SMARTer Universal kits maintain representation of fragments <200 bp, to ensure accurate RNA-seq data from FFPE samples.

After preparing your Illumina libraries, quantify them with the Library Quantification Kit.

NGS Resource Portal

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Visit the Clontech® NGS Resource Portal to find more information about our NGS kits.

www.clontech.com/NGS

- FAQs
- Selection Guide
- Technical Notes
- Citations
- Webinars
- ...and more

Did you know?

The majority of our kits for NGS are available in 12–96 reactions (larger reaction sizes are available for some kits) with up to 96 Illumina sequencing indexes.

Our products for NGS are compatible with leading sequencing platforms, including those from Illumina or Ion Torrent.

Single-cell RNA-seq

Single cells, few cells, or ultra-low inputs of total RNA (1–1,000 cells; 10 pg–10 ng)

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Why study single cells?

Populations of seemingly identical cells can hide biologically-relevant transcriptome differences.

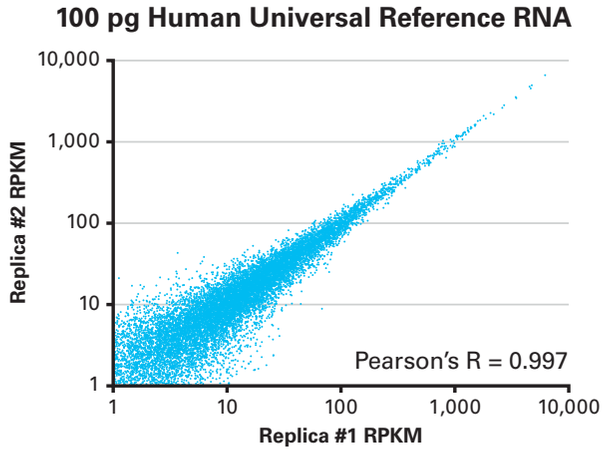
The ability to **study rare or precious samples**—including stem cells, circulating tumor cells, and tissue biopsies—requires extraordinary sensitivity and reproducibility.

Single-cell and ultra-low input mRNA-seq

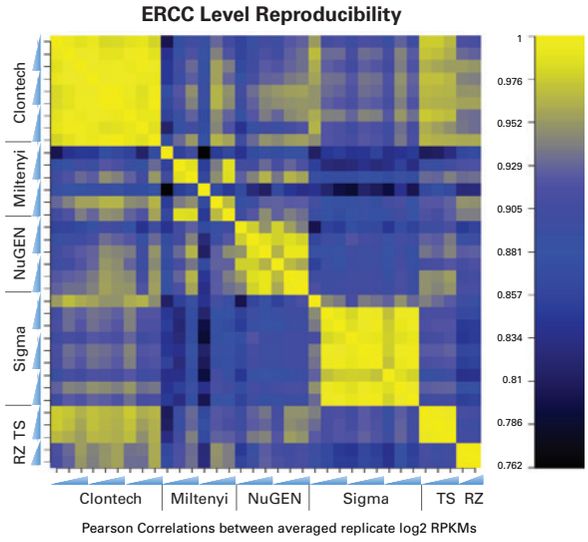
The **SMARTer Ultra™ Low** family of mRNA-seq kits provides the perfect solution for ultra-low input transcriptomics. We continue to develop industry-standard kits that you can count on to provide:

- **High-quality RNA-seq data:** A large number of genes identified, full-length gene information, great representation of GC-rich genes, and extremely low rRNA reads
- **A single-tube protocol:** Minimizes sample loss and decreases the chance of contamination
- **Superior performance with multiple platforms:** cDNA libraries are compatible with Illumina® and Ion Torrent library prep and sequencing platforms

For high-throughput single-cell experiments, we offer kits compatible with **Fluidigm C_1** systems.



The high reproducibility of RNA-seq data generated with SMARTer Ultra Low kits is shown in this comparison of two library replicates produced from 100 pg of input RNA.



SMARTer Ultra Low kits have been evaluated by the Association of Biomolecular Resource Facilities. For more data from ABRF visit:
www.clontech.com/ABRF

ChIP-seq

Single-stranded or double-stranded, low-input (100 pg–10 ng) ChIP DNA

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Why is library prep from low-input ChIP experiments difficult?

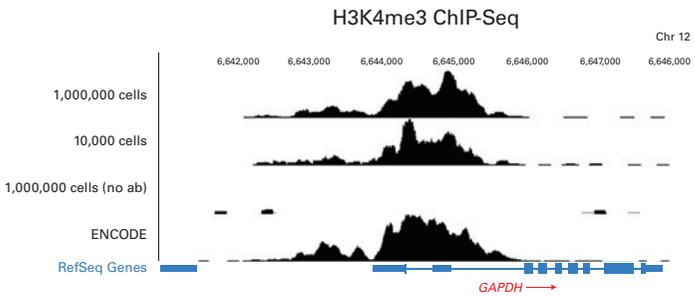
ChIP experiments using low numbers of cells typically produce **small quantities of DNA,** particularly when antibodies against transcription factors are used. Ligation-based sequencing library preparation protocols are **inefficient** for these small sample inputs, resulting in **low complexity and reproducibility**.

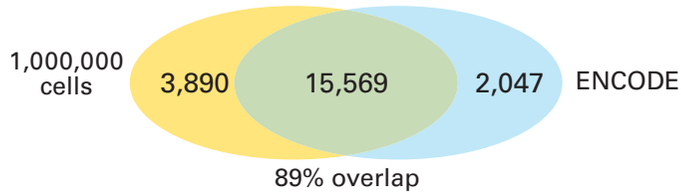
The DNA SMART™ ChIP-Seq kits use a novel application of SMART technology to generate ChIP-seq libraries in a ligation-free manner.

ChIP-seq library prep from low-input DNA

Library prep with DNA template switching allows:

- **Flexible inputs:** Single-stranded or double-stranded DNA; 100 pg–10 ng
- **Excellent reproducibility:** High non-redundant rate even from very low input amounts
- **A single-tube protocol:** Illumina-ready ChIP-seq libraries in as little as 4 hours; precious samples are preserved retaining good complexity





The robustness of the DNA SMART ChIP-Seq Kit is highlighted by the high overlap between peaks identified in ChIP-seq libraries prepared from 1 million or 10,000 HEK 293T cells and peaks identified by the ENCODE project (293 cells, U. Washington).

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