Next-Generation Sequencing

Breaking perfomance barriers in NGS library preparation

that's GOOD science!®

SMARTer® NGS

TaKaRa

Clontech TaKaRa cellartis

SMARTer NGS

Speed your journey to the most elusive answers.

We understand that cutting-edge research requires high-performance products that provide the sensitivity necessary to detect meaningful biological phenomena. For translational research and clinical studies, we recognize the need for user-friendly solutions that are amenable to high-throughput applications and automation, and that enable analysis of clinically relevant samples with high reproducibility. That is why we focus on developing best-in-class tools—backed with expert support—to help you achieve the results you need regardless of your research application.

Our broad NGS portfolio provides unmatched sensitivity for all of your demanding sequencing applications—regardless of sample type or input amount. While our NGS roots began with the adaptation of our SMART® cDNA synthesis technology for RNA-seq applications, our SMARTer NGS solutions now also leverage the innovations of ThruPLEX® and PicoPLEX® technologies for DNA-seq.

Sensitivity. Reproducibility. Reliability. Ease of use. Scalability.

Breaking performance barriers

Whole transcriptome analysis

Targeted sequencing

DNA sequencing

that's GOOD science!®

Whole transcriptome analysis (from mammalian samples)

Single-cell or ultra-low-input RNA-seq

1–1,000 cells; 10 pg–10 ng RNA
Oligo(dT) priming

Full-length cDNA

SMART-Seq® HT Kit

cDNA synthesis from 1–100 cells or 10 pg–1 ng total RNA, for high-throughput applications (RIN 8–10)**

SMART-Seq v4 Ultra® Low Input RNA Kit for Sequencing

cDNA synthesis* from 1–1,000 cells or 10 pg–10 ng total RNA (RIN 8–10)**

SMART-Seq v4 Ultra Low Input RNA Kit for the Fluidigm® C1™ System

cDNA synthesis* from single cells

3′ end only

SMART-Seq v4 3′ DE Kit

cDNA synthesis (compatible with Illumina library prep only) from 1–100 cells or 10 pg–1 ng total RNA

Low-input total RNA-seq

250 pg–100 ng RNA
Random priming

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

Illumina® library construction from 250 pg–10 ng total RNA† (RIN 2–10)** DV200 ≥25

SMARTer Stranded Total RNA Sample Prep Kit - Low Input Mammalian

Illumina library construction from 10–100 ng total RNA† (RIN 3–10)*

SMARTer Universal Low Input RNA Library Prep Kit

Illumina library construction from ≥200 pg rRNA-depleted RNA‡ (RIN 2–3)**

High-input total RNA-seq

100 ng–1 µg RNA
Random priming

SMARTer Stranded Total RNA Sample Prep Kit - HI Mammalian

Illumina library construction from 100 ng–1 µg total RNA† (RIN 3–10)**

Targeted sequencing

Small RNA-seq

SMARTer smRNA-Seq Kit for Illumina

Illumina library construction from 1 ng–2 µg total RNA or enriched smRNA (RIN >8)**

Immune repertoire profiling

Human

Single-cell TCR

SMARTer Human scTCR a/b Profiling Kit

Illumina library construction from single T cells

Bulk TCR

SMARTer Human TCR a/b Profiling Kit

Illumina library construction from 10 ng–3 µg total RNA or 50–10,000 purified T cells

Mouse

Bulk TCR

SMARTer Mouse TCR a/b Profiling Kit

Illumina library construction from 10 ng–500 ng total RNA or 1,000–10,000 purified T cells

Bulk BCR

SMARTer Mouse BCR IgG H/K/L Profiling Kit

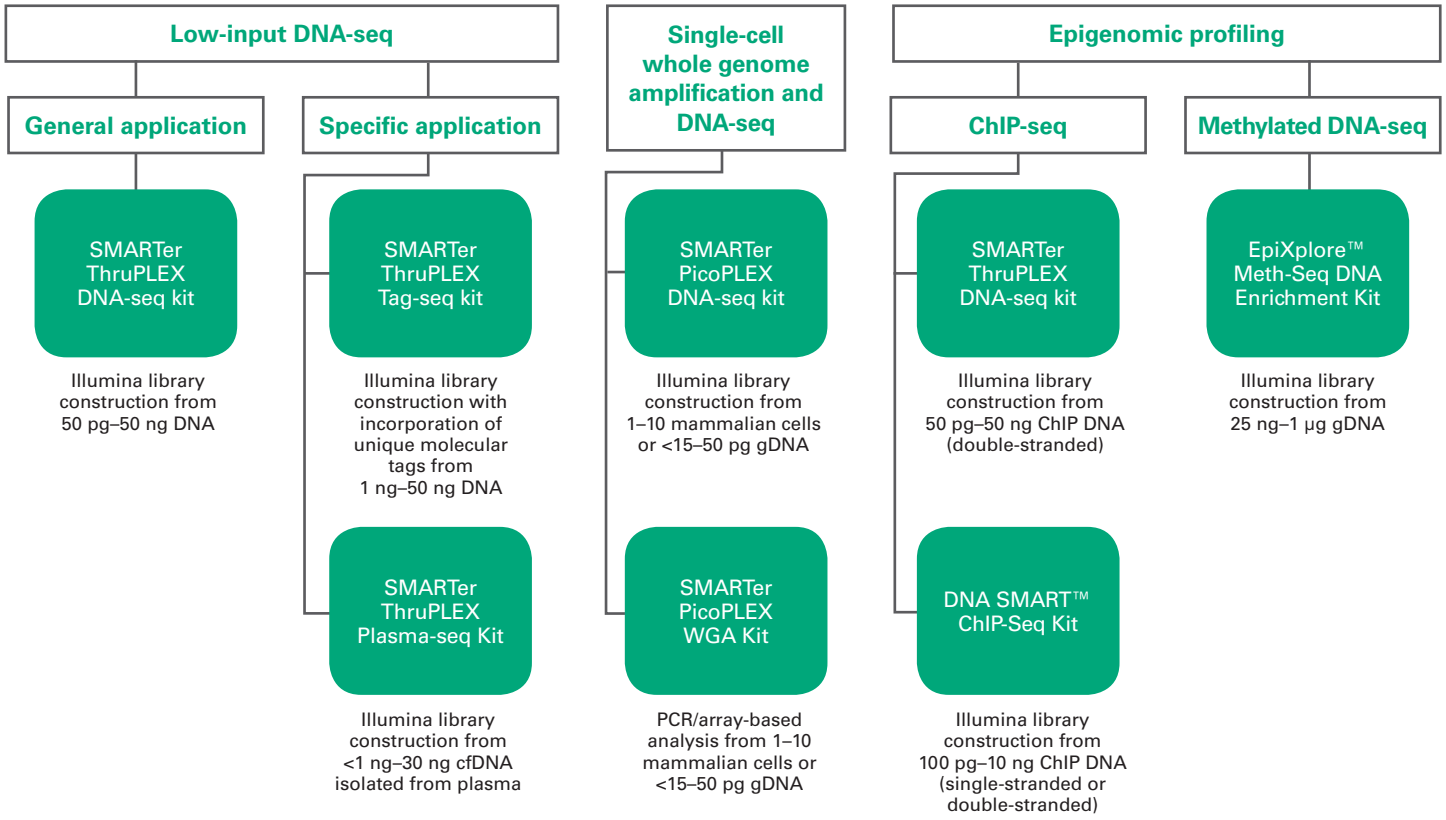
Illumina library construction from 10 ng–3 µg total RNA or 50–10,000 purified B cells

Targeted RNA-seq

SMARTer Target RNA Capture for Illumina

cDNA synthesis from ≥10 ng total RNA (downstream Illumina library prep kit required)

DNA sequencing



For non-mammalian or rRNA-depleted samples, use

SMARTer Stranded RNA-Seq Kit for Illumina library construction from 100 pg–100 ng rRNA-depleted or polyA⁺-enriched RNA

SMARTer Universal Low Input RNA Kit for Sequencing* for cDNA synthesis from ≥200 pg rRNA-depleted RNA derived from 2–100 ng of total RNA

SMARTer Universal Low Input RNA Library Prep Kit for Illumina library construction from ≥200 pg rRNA-depleted RNA (RIN 2–3)**

* Compatible with Illumina or Ion Torrent library preparation

† rRNA removal included

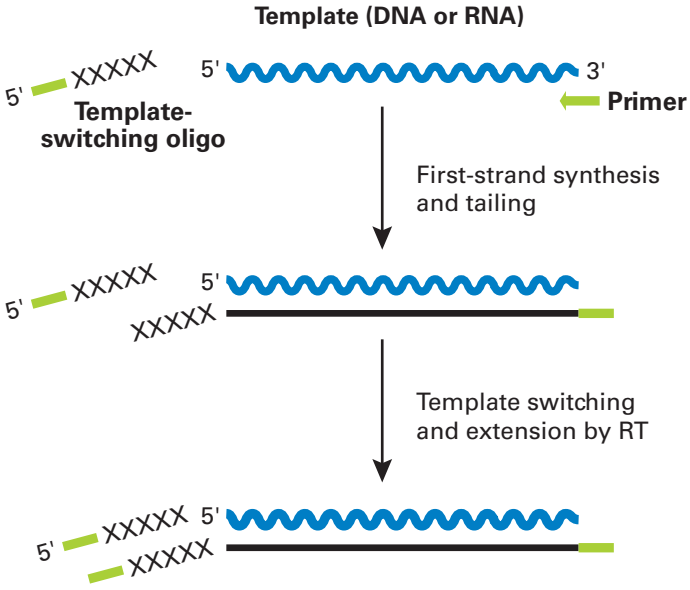
‡ For mammalian rRNA removal, we recommend **RiboGone™ - Mammalian**, specifically designed to remove rRNA from low-input samples (10–100 ng of total RNA)

** Recommended RNA quality

SMART technology overview

What is SMART technology?

SMART (**S**witching **M**echanism **a**t the 5′ end of **R**NA **T**emplate) technology leverages the ability of certain reverse transcriptases (RTs) to add non-templated nucleotides (depicted by Xs in the diagram) upon reaching the 5′ end of a template. A carefully designed template-switching oligo can pair with these additional nucleotides, providing a new template for the RT to continue cDNA synthesis. This process allows for the incorporation of adapter sequences for subsequent PCR amplification (depicted in green) at both ends of a template, ensuring full-length template coverage.



Workflow for SMART technology

Why adopt SMART technology?

- Exquisite sensitivity and reproducibility
- Full-length template coverage
- Ligation-free adapter incorporation
- High-quality sequencing libraries
- Simplified workflows, single-tube protocols

SMARTer NGS applications

	DNA SEQUENCING	TARGETED SEQUENCING	WHOLE TRANSCRIPTOME ANALYSIS
SMART technology	• ChIP-seq • Meth-seq	• Targeted RNA-seq • Small RNA-seq • Immune profiling	• Single-cell/ultra-low-input RNA-seq • Total RNA-seq
SMARTer ThruPLEX technology	• Illumina library construction • Targeted sequencing • ChIP-seq	• Targeted DNA-seq with major enrichment platforms	
SMARTer PicoPLEX technology	• Whole genome amplification • Aneuploidy/CNV detection		

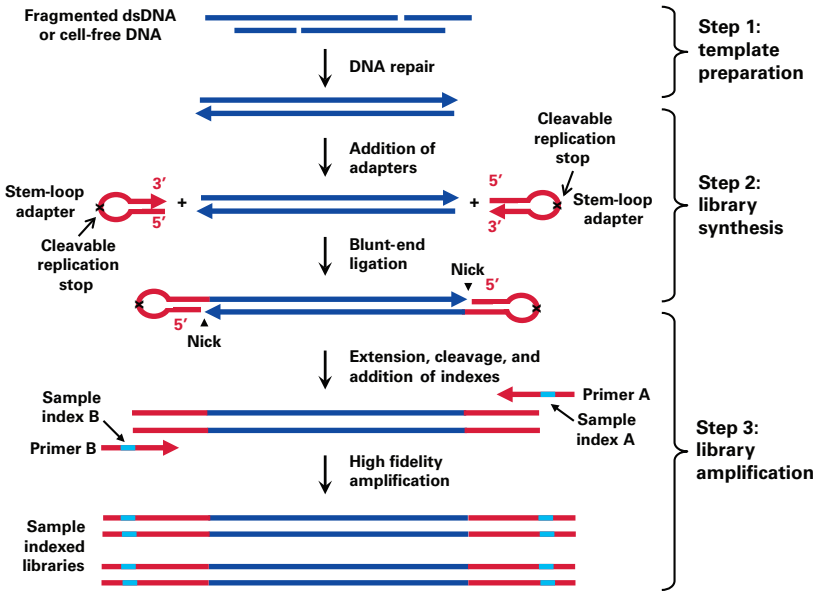
SMARTer ThruPLEX technology overview

What is SMARTer ThruPLEX technology?

ThruPLEX technology starts with fragmented, double-stranded DNA (blue), which is repaired in a highly efficient process. Stem-loop adapters (red) with blocked 5′ ends are ligated to the 5′ ends of the DNA, leaving nicks at the 3′ ends. The adapters cannot ligate to each other and do not have single-strand tails, reducing non-specific background in sequencing data. The 3′ ends of the DNA are then extended to complete library synthesis, and Illumina indexes are added through a high-fidelity amplification.

Why adopt SMARTer ThruPLEX technology?

- High sensitivity with low background
- Simplified workflows, single-tube protocols
- Accurate representation of GC-rich sequences and high library diversity
- Analysis of diverse inputs, including FFPE DNA, gDNA, ChIP DNA, cfDNA, cDNA, amplicons, etc.
- Compatible with major target-enrichment platforms



Workflow for SMARTer ThruPLEX technology

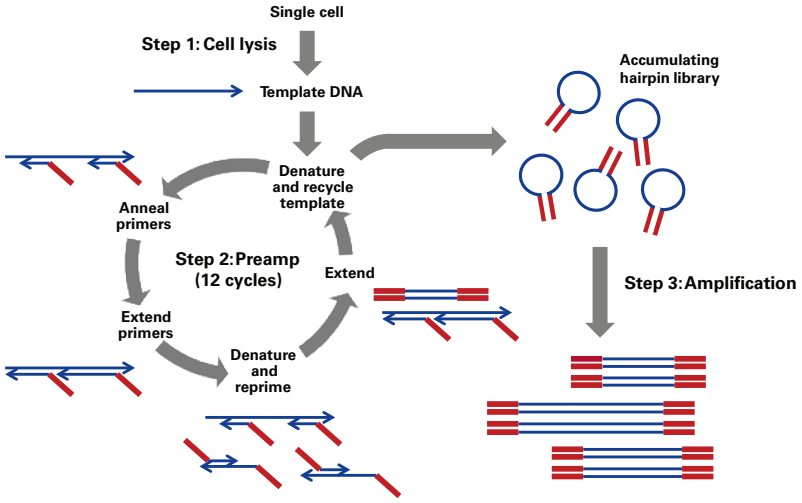
SMARTer PicoPLEX technology overview

What is SMARTer PicoPLEX technology?

PicoPLEX technology uses single-cell or picogram inputs of genomic DNA as a template for multiple cycles of quasi-random priming and linear whole genome amplification, followed by exponential library amplification.

Why adopt SMARTer PicoPLEX technology?

- Robust, highly reproducible whole genome amplification from single-cell or ultra-low inputs
- Gold standard for detection chromosomal aneuploidies and copy number variations
- Simplified workflows, single-tube protocols



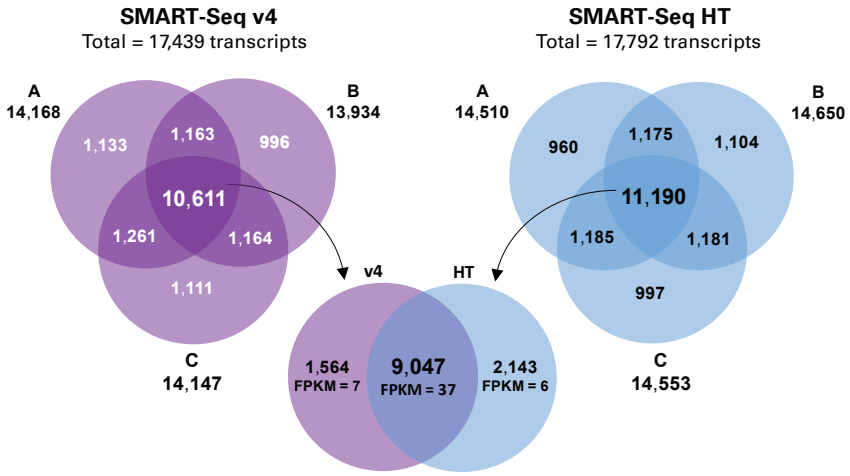
Workflow for SMARTer PicoPLEX technology

Single-cell RNA-seq

Single-cell RNA-seq using oligo(dT) priming is a powerful approach for resolving biologically relevant differences between individual cells, and allows for analysis of rare or precious samples, including stem cells, circulating tumor cells, and tissue biopsies. In order to obtain meaningful data from single cells, NGS library preparation methods must be robust and sensitive enough to reproducibly capture RNA molecules present in minute quantities.

SMART-Seq v4 kits

- Solutions for single-cell and ultra-low inputs
- Ligation-free protocols
- Improved chemistry relative to previous versions and locked nucleic acid (LNA)-enhanced oligos
- Accurate representation of GC-rich transcripts
- Compatible with all Illumina sequencing platforms



High overlap of transcripts identified for data generated with the SMART-Seq v4 and SMART-Seq HT kits. Libraries prepared from 10 pg of Mouse Brain Total RNA were evaluated for the overlap in the number of transcripts identified (FPKM >0.1) between technical replicates within each kit, and found to be very similar (61–63% overlap). Transcripts identified by all three replicates for each kit were then compared against each other, indicating an overlap of 71%. The overlapping transcripts have an average expression level of 37 FPKM, while the transcripts uniquely identified with individual kits are less abundant, averaging between 6–7 FPKM, indicating that the transcripts more likely to not be identified are the ones expressed at low levels.

SMART-Seq HT Kit

- Inputs of 1–1,000 cells or 10 pg–1 ng of total RNA
- One-step RT-PCR
- Single-tube protocol
- Even gene-body coverage
- Optimized for high-throughput applications

SMART-Seq v4 3′ DE Kit

- Inputs of 1–100 cells or 10 pg–1 ng of total RNA
- Designed specifically for differential expression analysis
- 3′ focusing of sequencing reads reduces costs and saves time

SMART-Seq v4 Ultra Low Input RNA Kit for Sequencing

- Inputs of 1–1,000 cells or 10 pg–10 ng of total RNA
- Single-tube protocol
- Even gene-body coverage

SMART-Seq v4 Ultra Low Input RNA Kit for the Fluidigm C1 System

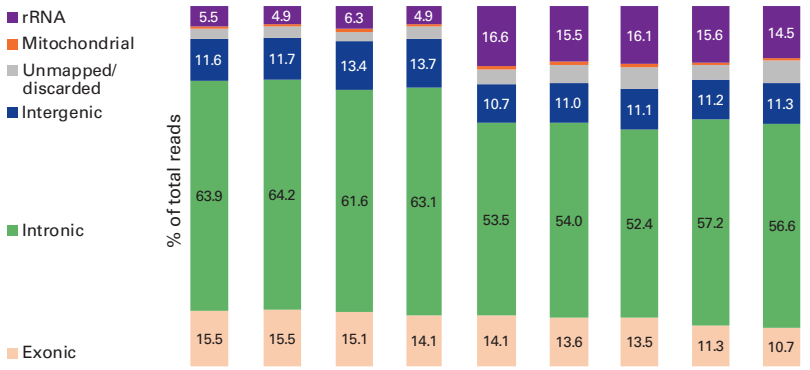
- Analysis of single cells isolated on the Fluidigm C1 platform
- Library preparation can be completed in two working days

Total RNA-seq

Total RNA-seq using random priming is the preferred method for analyzing both coding and non-coding RNA and for generating libraries from FFPE or degraded samples. However, the typical abundance of ribosomal RNA (rRNA) in total RNA inputs and the identification of non-coding and antisense RNA without strand-of-origin information pose significant challenges for this approach.

SMARTer total RNA-seq kits

- Solutions for inputs of varying quantity and quality, including degraded RNA (e.g., FFPE & cell-free samples)
- Ligation-free protocols
- Generation of Illumina-ready sequencing libraries
- Multiplexing of up to 96 samples



FFPE tissue	Breast (normal)				Lung (cancer)				
Sample (DV_{200})	A (66%)		B (68%)		C (30%)			D (28%)	
Input amount	10 ng	40 ng	10 ng	72 ng	10 ng	50 ng	90 ng	10 ng	50 ng
% duplicates	36	28	46	27	56	41	28	59	36
Transcripts ≥1 FPKM	10,023	9,916	9,348	8,716	10,592	10,346	10,495	9,305	9,251
Transcripts ≥0.1 FPKM	21,831	21,855	20,662	20,491	22,119	22,370	22,546	21,416	21,961
Pearson/Spearman	0.99/0.9		0.98/0.88		0.99/0.88		0.99/0.88	0.99/0.95	

Sequencing metrics for FFPE samples. The distribution of reads shows that the majority of reads map to intronic regions for all samples, with 10–15% of reads mapping to exonic regions, and 5–15% of reads mapping to ribosomal sequences depending on the tissue of interest (observed consistently for all experiments). We find that there are comparable numbers of transcripts identified with fragments per kilobase per million reads mapped (FPKM) >1, and a high degree of correlation across input amounts. In addition, we find that highly degraded lung (cancer) samples have a high degree of correlation in the number of transcripts identified (FPKM >1) across the multiple input types.

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

- Inputs of 250 pg–10 ng of mammalian total RNA
- Strand-of-origin information
- Compatible with degraded inputs
- Generates libraries in ~6 hours

SMARTer Stranded Total RNA Sample Prep Kit - Low Input Mammalian

- Inputs of 10–100 ng of mammalian total RNA
- Strand-of-origin information
- Compatible with degraded inputs
- Includes RiboGone - Mammalian rRNA-depletion technology
- Generates libraries in ~5 hours

SMARTer Stranded Total RNA Sample Prep Kit - HI Mammalian

- Inputs of 100 ng–1 µg of mammalian total RNA
- Strand-of-origin information
- Includes RiboGone - Mammalian rRNA-depletion technology
- Generates libraries in ~5 hours

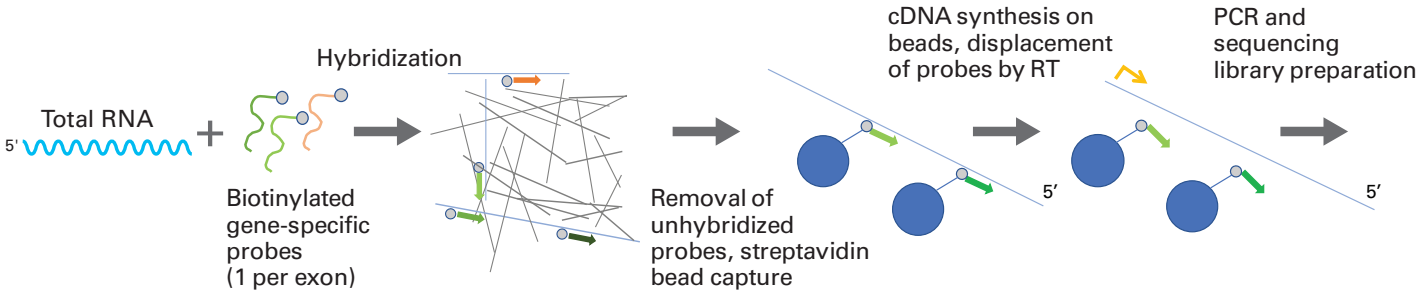
SMARTer Universal Low Input RNA Library Prep Kit

- Inputs of ≥200 pg of rRNA-depleted RNA of any species
- Compatible with degraded inputs

Targeted RNA-seq

The ability to analyze the entire transcriptome in a single RNA-seq experiment has revolutionized biomedical research, but for some applications a targeted approach is more practical. For studies involving a predetermined set of genes, targeted RNA-seq allows for the analysis of rare transcripts—including those resulting from alternative splicing or gene fusion events—using fewer sequencing reads than would be required in the context of a global analysis.

SMARTer Target RNA Capture for Illumina employs biotinylated DNA probes that are designed by the user to hybridize with transcripts of interest and are bound by streptavidin-coated capture beads (indicated below by blue circles). cDNA synthesis is performed on hybridized transcripts using SMART-Seq v4 chemistry with oligo(dT) priming. The Nextera® XT DNA Library Preparation Kit can then be used to generate Illumina-ready sequencing libraries.



Workflow for SMARTer Target RNA Capture for Illumina

About SMARTer Target RNA Capture for Illumina

- Inputs of 10 ng–1 µg of total RNA
- User-designed DNA probes enrich for transcripts of interest
- Ligation-free protocol
- Requires ~3 hours of active time
- Recommended for analysis of up to 100 genes per reaction

Targeted transcript enrichment from various cell types/tissues					
	Fold-Enrichment				
	K562	KBM-7	HURR	HBR	
GAPDH	0.52	0.33	0.23	0.47	Not targeted
ERCC-002	0.45	0.07	0.02	0.13	
ABL1	324	325	656	329	Targeted
ALK	20	1	563	302	
CDKN2A	0.20	205	135	16	
FGFR1	27	603	644	437	
HPRT1	270	314	294	282	
KRAS	227	158	203	144	
RB1	323	585	604	108	
RET	6	29	459	369	
TP53	24	1455	943	119	
Percentage of reads on target					
With capture	16%	37%	28%	14%	
No capture	0.07%	0.10%	0.07%	0.05%	

Demonstrated enrichment of targeted transcripts with SMARTer Target RNA Capture for Illumina. Sequencing reads for transcripts targeted with the kit (ABL1, ALK, etc.) are highly enriched relative to data for untargeted transcripts (GAPDH and ERCC-002).

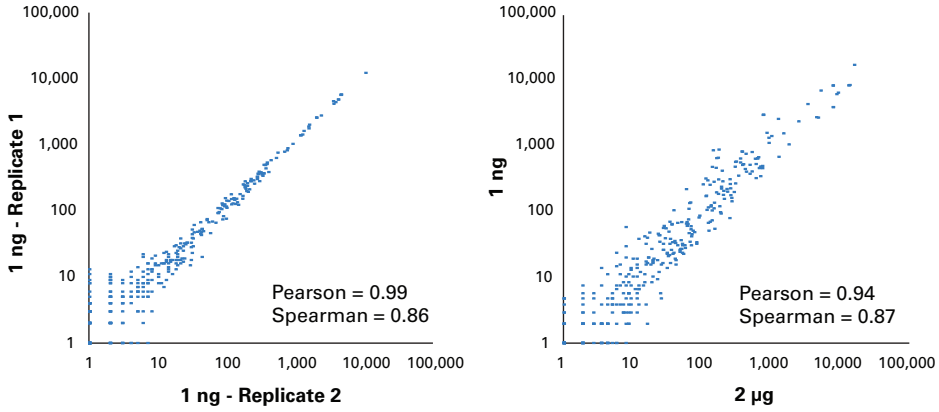
Small RNA-seq

The ability to identify and analyze diverse small RNA species—including miRNAs, siRNAs, piRNAs, and snoRNAs—has benefited greatly from the development of NGS technology. However, small RNA-seq library preparation is not without its challenges, which can include time-consuming enrichment steps prior to cDNA synthesis, and sample misrepresentation due to biases in small RNA end modification, reverse transcription, and PCR amplification.

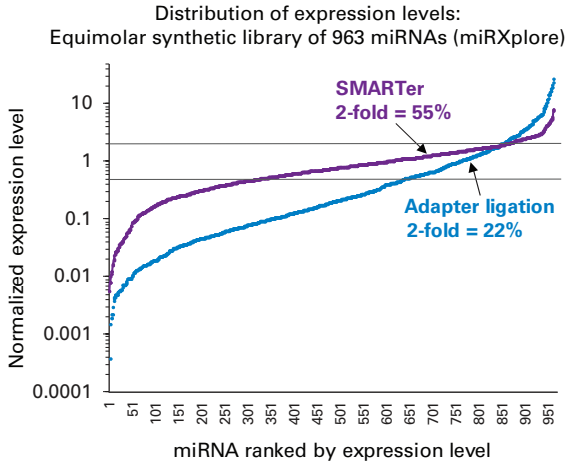
The SMARTer smRNA-Seq Kit for Illumina leverages SMART technology coupled with 3′ polyadenylation to generate Illumina-ready small RNA-sequencing libraries. In contrast with library construction methods that isolate small RNAs via adapter ligation, this approach uses 3′ polyadenylation and SMART technology to minimize the likelihood of sample representation bias.

About the SMARTer smRNA-Seq Kit for Illumina

- Inputs of 1 ng–2 µg of total RNA or enriched small RNA
- Suitable for analysis of diverse smRNAs 15–150 nt in size, including miRNAs, siRNAs, piRNAs, and snoRNAs
- Ligation-free, single-tube protocol
- Multiplexing of up to 96 samples



High reproducibility across technical replicates and varying input amounts for data generated with the SMARTer smRNA-Seq Kit for Illumina. Strong correlations are observed for sequencing data generated from human brain total RNA, both in replicates (1 ng inputs, left panel) and across varying input amounts (1 ng vs. 2 µg inputs, right panel).



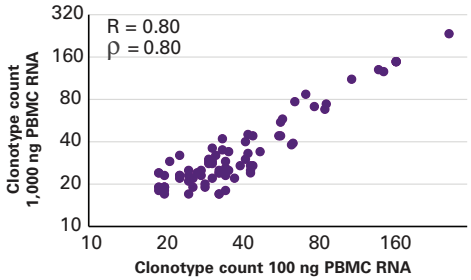
Improved accuracy of SMARTer small RNA-seq vs. an adapter ligation-based approach. Sequencing data generated for an equimolar pool of 963 synthetic miRNAs using the SMARTer smRNA-Seq Kit for Illumina (purple line) more closely approaches known normalized expression values (expression = 1) relative to data produced using an adapter-ligation approach (blue line).

Immune profiling

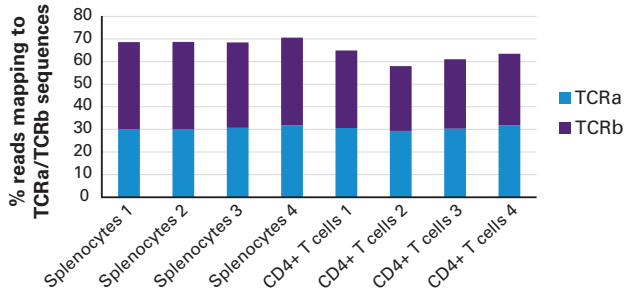
SMARTer immune profiling kits leverage SMART technology and a 5′-RACE-based approach to capture full-length information from V(D)J variable regions, starting with RNA samples. These kits streamline the process of sample preparation and give reproducible results from a wide range of input amounts (10–1,000 ng) from mouse or human samples (purified cells, spleen, PBMCs, Jurkat cells, and hybridomas), and are highly sensitive in detecting low-abundance transcripts.

SMARTer bulk TCR a/b profiling kits

- Inputs of 10 ng–3 µg of human blood total RNA or 50–10,000 T cells (human kit), and 10 ng–500 ng mouse blood total RNA or 1,000–10,000 T cells (mouse kit)
- Full-length sequence information for TCRa and/or TCRb
- Ligation-free generation of Illumina-ready libraries
- Multiplexing of up to 96 samples



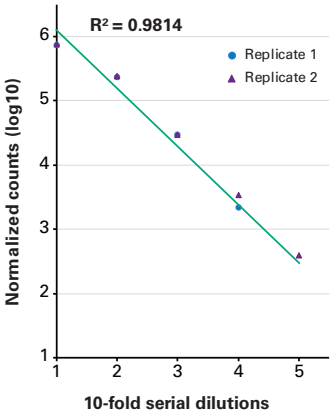
Consistent transcript representation across varying input amounts for data generated with the SMARTer Human TCR a/b Profiling Kit. Measured frequencies of various TCR clonotypes correlate strongly for libraries generated from 1,000-ng or 100-ng inputs of PBMC total RNA.



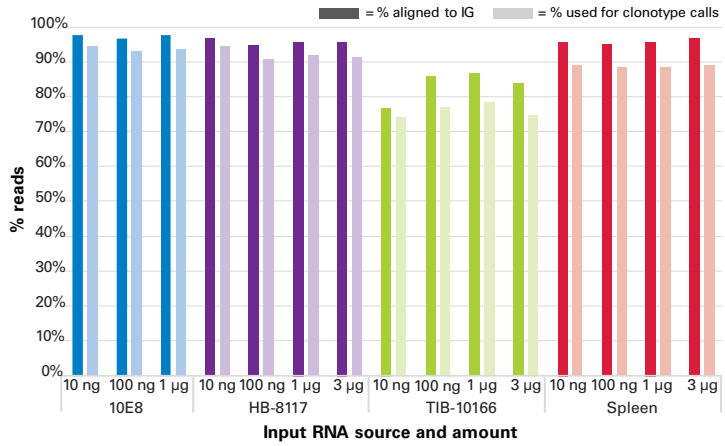
High proportions of on-target reads mapping to mouse TCRa and TCRb CDR3 sequences for data generated with the SMARTer Mouse TCR a/b Profiling Kit. Sequencing libraries were generated from total RNA extracted from total splenocytes or enriched CD4+ T cells. High proportions of on-target reads mapping to TCRa or TCRb CDR3 were observed for each input.

SMARTer Mouse BCR IgG H/K/L Profiling Kit

- Input: 10 ng–3 µg of total RNA or 1,000–10,000 purified B cells from spleen, lymph node, PBMCs, or hybridoma
- Full-length V(D)J CDR3 variable region sequence from heavy, kappa, and lambda chains
- Optimized PCR pooling strategy for highly sensitive detection of different chains from the same sample
- Extremely sensitive and specific clonotype detection



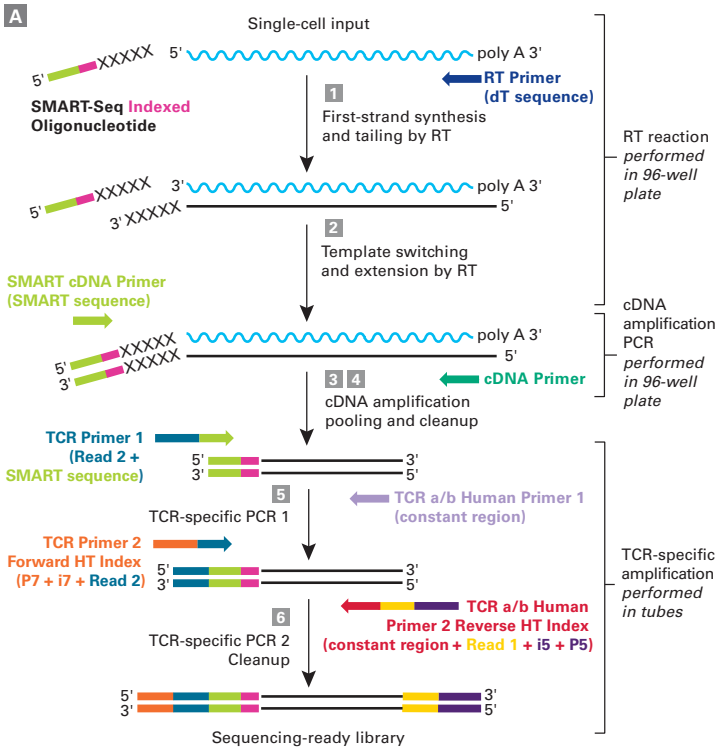
Clonotype counts with the SMARTer Mouse BCR IgG H/K/L Profiling Kit. Counts were Log10 transformed and plotted on the y-axis. The x-axis represents the 10-fold serial dilutions of TB127 RNA in spleen RNA; 1 = 10% (1 ng TB127 RNA in 10 ng spleen RNA); 2 = 1% (100 pg TB127 RNA in 10 ng spleen RNA); 3 = 0.1% (10 pg TB127 RNA in 10 ng Spleen RNA); 4 = 0.01% (1 pg TB127 RNA in 10 ng spleen RNA) and 5 = 0.001% (100 fg TB127 RNA in 10 ng spleen RNA).

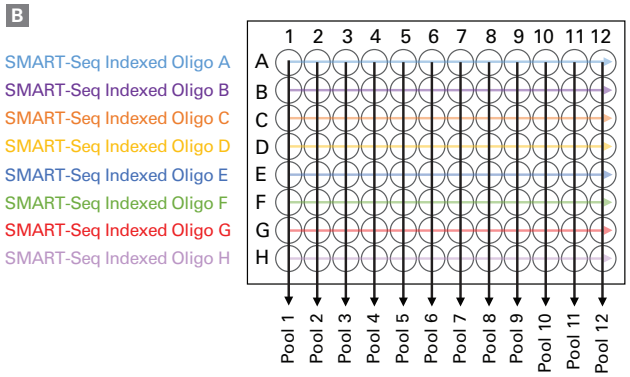


Mapping statistics using SMARTer Mouse BCR IgG H/K/L Profiling Kit. With samples from spleen and 3 different hybridomas, this kit produces a high percentage of reads aligned to IG, and the majority of them being used for clonotype calls for all ranges of input. Dark colors = % aligned to IG, light colors = % used in clonotype calls.

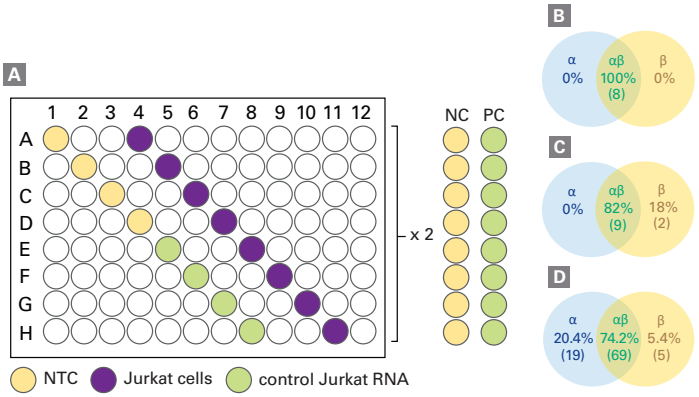
SMARTer Human scTCR a/b Profiling Kit

- **Flexible workflow**—Illumina-ready libraries from FACS or manually sorted single cells
- **Ease of use**—optimized indexing allows for pooling 96 cells into 12 libraries which can be further multiplexed for running in a single flow-cell lane
- **Sensitivity**—RACE-based approach allows for the detection of low-abundance TCR variants
- **Specificity**—full-length reads, with a majority of reads on target, and with accurate pairing information





SMARTer Human scTCR a/b Profiling Kit workflow and pooling strategy. Panel A. Step 1: dT-primed first-strand cDNA synthesis, with the addition of nontemplated nucleotides to the 5′ end of each mRNA template. Step 2: Template switching and addition of the SMART-Seq Indexed Oligos. Each of the eight different SMART-Seq Indexed Oligos contains a unique six-base in-line index that serves as a cell barcode to allow downstream cell identification after pooling. Step 3: Amplification of double-stranded cDNA. Step 4: Pooling and cleanup. **Panel B.** Samples are pooled by column, such that each pool contains eight cells, each with a differently indexed SMART-Seq Indexed Oligo. Step 5: TCR-specific PCR-1 to amplify variable regions of TCRa and/or TCRb transcripts. Double-stranded cDNA is used as template to incorporate the Illumina Read 2 sequence (TCR Primer 1). Reverse primers are complementary to the constant region of TCRa and TCRb (TCR a/b Human Primer 1). Step 6: TCR-specific PCR-2 to add in Illumina adaptor and index sequences, and amplify the entire V(D)J sequence and a portion of the constant region. These indexes also allow for multiplexing of up to 96 samples in a single flow-cell lane.



Analysis of TCR α/β pairing in PBMCs in a 96-well format. Panel A. Shows a schematic of the plate setup with no template for negative controls (NEG) and RNA from Jurkat cells for the positive controls (POS). **Panels B–D.** The α, β, and α/β pairs are shown for Jurkat total RNA (**Panel B**), Jurkat cells (**Panel C**), and PBMCs treated with OKT3 (which activates the T-cell response; **Panel D**). α/β pairing information was obtained for 100% of the Jurkat RNA samples, 82% of the Jurkat cells, and 72% of the PBMCs.

	1	2	3	4	5	6	7	8	9	10	11	12
A	NEG		βα	αβ	β	α	βα		αβα	β		αβ
B	α	NEG	αβ	αβ	αβ	αβ	βα	α	αβ	β	ααβ	βα
C	βα	αβ	NEG	β	αβ	ααβ		αβ	αβ	βα	βα	αβ
D	αβ	αβ	αβ	NEG	βα	αβ	αβ	αβα	αβ	αβ	αβ	αβ
E	αβ	αβ	αβ	ααβ	POS	αβ	αβ	αβα	αα	αβ	β	αβ
F	αβ	β		αβ	α	POS	β	αβ	αβα		αβ	αβ
G	αβ	αβ	β	α	αβ		POS	βα	βα	αβ	αβ	α
H	αβ	α	α	αβ	βα	αβ	αβ	POS	αβ	αβ	αβ	αβ

α only	8
αα	1
β only	8
ββ	0
αβ	57
ααβ	7
αββ	0
NEG	4
POS	4
No call	7

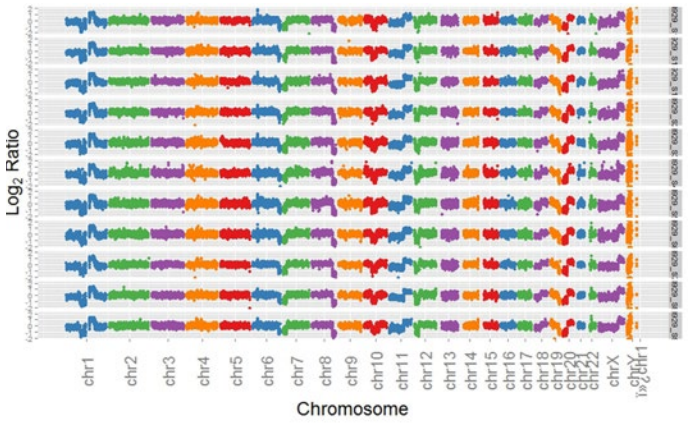
TCR α/β clonotype and pairing in CD4+ T cells. Summary of clonotype and pairing information: four wells were negative controls (NEG) and four wells were positive controls (POS). Cell information was obtained for 88 wells. At least one TCR chain sequence was identified in 81/88 wells (92%). α and β chains were identified in 64/88 wells (73%), and 7 of these wells contained two functional alpha sequences (α/ α/β). A single α- and a single β-sequence pairing (α/β) was identified in 57/88 wells (65%).

Single-cell WGA and DNA-seq

By enabling highly accurate detection of aneuploidy and copy-number variation (CNV) from single cells, advances in whole genome amplification combined with NGS and array-based technologies have revolutionized clinical applications such as preimplantation genetic screening and diagnosis (PGS/PGD). Widespread adoption of this approach has been driven by the development of user-friendly workflows that are cost-effective and yield reproducible results.

About SMARTer PicoPLEX kits

- Compatible with single-cell or ultra-low inputs
- Gold standard for detection of chromosomal aneuploidies and copy number variations
- Accurate and reproducible results
- Solutions for both NGS and PCR/array-based approaches
- Three-step, single-tube protocol that can be completed in less than 3 hours
- Works with embryo biopsies, circulating fetal cells, circulating tumor cells (CTCs), microbial cells, and cell/DNA from laser capture microdissection (LCM) and needle biopsies



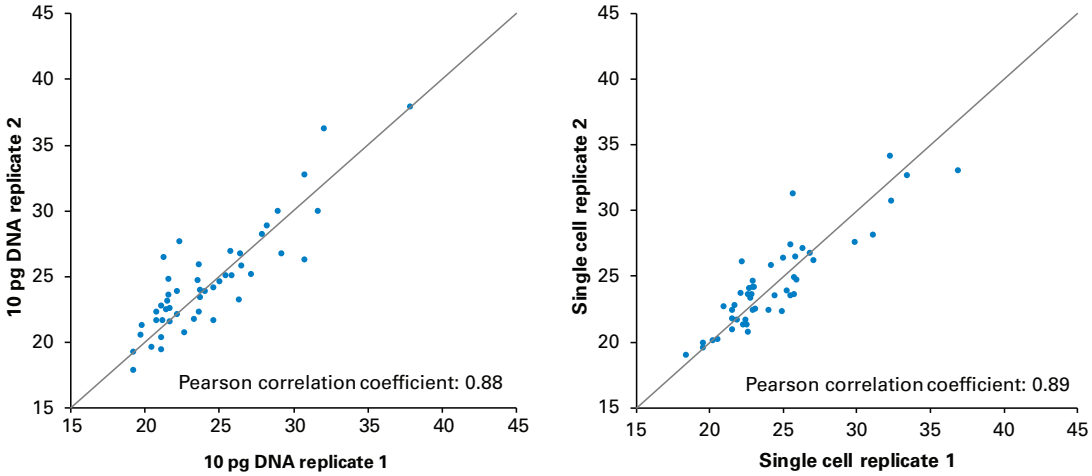
Highly reproducible CNV detection over the entire genome with the SMARTer PicoPLEX DNA-seq kit. Amplified libraries from 11 individual flow-sorted H929 cells were sequenced and downsampled to 250,000 total reads. 35-base single-end reads were mapped to the entire genome.

SMARTer PicoPLEX DNA-seq kit

- Inputs of 1–10 cells or <15 pg–50 pg of DNA
- Illumina-ready sequencing libraries

SMARTer PicoPLEX WGA Kit

- Inputs of 1–10 cells or <15 pg–50 pg of DNA
- Amplified DNA for array or PCR-based analysis
- Compatible with downstream library prep workflows on Illumina or IonTorrent instruments



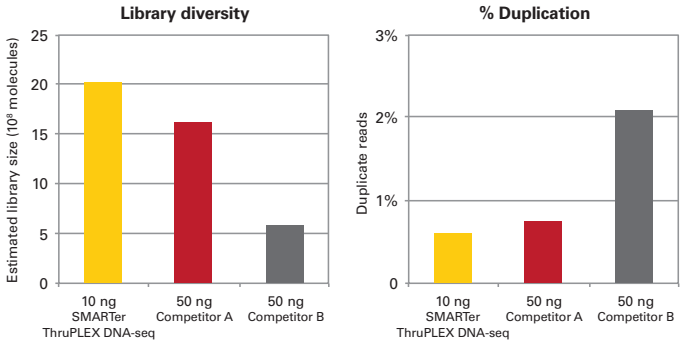
Highly reproducible results from the SMARTer PicoPLEX WGA Kit. WGA products were generated in parallel from single cells or 10 pg of DNA using the SMARTer PicoPLEX WGA Kit. 50 ng of each WGA product was tested with 48 human qPCR assays representing a range of GC-content to quantify the systematic and stochastic bias. Ct values were measured and plotted on correlation diagrams. The high correlation coefficients illustrate the reproducible nature of SMARTer PicoPLEX technology.

Low-input DNA-seq

In a typical DNA-seq workflow, input DNA is first purified and mechanically sheared to yield short, double-stranded DNA molecules. For analysis on Illumina platforms, sequencing libraries containing proper adapters and indexes must then be generated from this input material. To ensure that sequencing libraries are of the highest quality, especially when working with limiting DNA inputs, the library preparation method must be highly efficient and accurate, and it must avoid purification or transfer steps where DNA can be lost or contaminated.

About SMARTer ThruPLEX kits

- Precious samples go further: high-performance Illumina-ready sequencing libraries from low-input amounts
- Fast and simple workflow reduces user error and contamination: 3 steps in a single tube or well in ~2 hours, no intermediate purification step
- Solutions for diverse inputs, including FFPE DNA, gDNA, ChIP DNA, cfDNA, cDNA, amplicons, etc.
- Compatible with major target-enrichment platforms such as Agilent SureSelect, Roche Nimblegen SeqCap EZ, and IDT xGen Lockdown probes



The SMARTer ThruPLEX DNA-seq kit outperforms other NGS library prep kits. The SMARTer ThruPLEX DNA-seq kit yielded more diverse libraries (left panel) with less input gDNA and generated fewer duplicates (right panel) at 25M read pairs than other kits.

SMARTer ThruPLEX DNA-seq kit

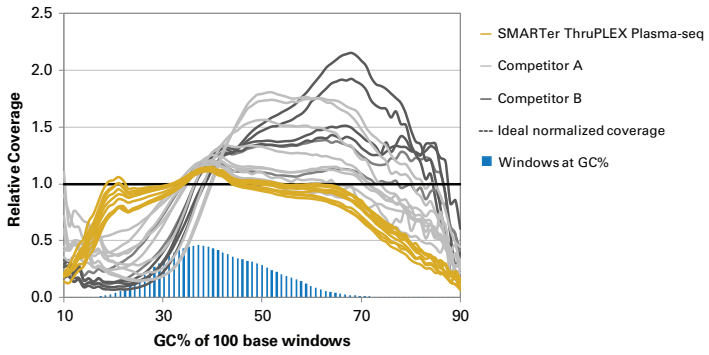
- Inputs of 50 pg–50 ng fragmented dsDNA
- Suitable for all DNA-seq applications and input types
- Widely used to prepare ChIP-seq libraries

SMARTer ThruPLEX Plasma-seq kit

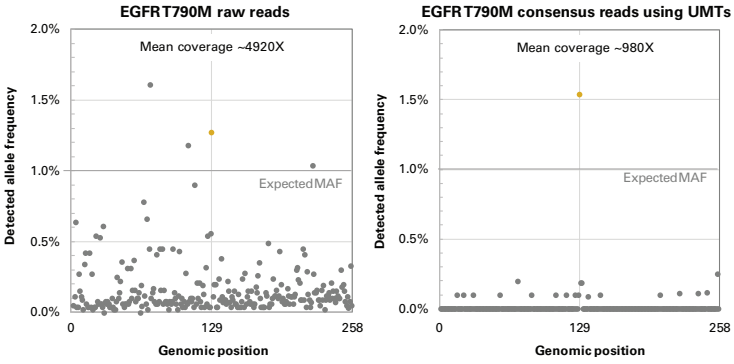
- Inputs of <1–30 ng fragmented dsDNA
- Optimized for cell-free DNA isolated from plasma

SMARTer ThruPLEX Tag-seq kit

- Inputs of 1 ng–50 ng fragmented dsDNA
- Incorporation of ~16 million unique molecular tags (UMTs or UMIs)
- UMT-based deduplication and error correction to improve sensitivity and specificity of variant detection



The SMARTer ThruPLEX Plasma-seq kit provides the most reproducible and unbiased GC coverage across the human genome. SMARTer ThruPLEX Plasma-seq libraries showed minimal variability across the individual plasma samples tested. Libraries were prepared from cell-free DNA isolated from 1 ml of plasma samples and sequenced on an Illumina NextSeq® 500.



The SMARTer ThruPLEX Tag-seq kit allows confident variant detection. SMARTER ThruPLEX Tag-seq libraries were prepared with Horizon cfDNA reference standards using 30 ng of input DNA. Libraries were enriched with a custom capture panel and sequenced to a mean raw coverage of ~5,000X. Data was processed using the Curio bioinformatics platform. Background errors or false positive calls (left panel) were dramatically reduced when UMT information was utilized (right panel), providing greater separation between signal and noise for more confident variant detection. True mutations are depicted by yellow dots.

Sequencing accessories

Ribosomal RNA removal

RiboGone - Mammalian enables removal of mammalian rRNA from 10–100 ng inputs, including degraded RNA samples. The kit eliminates ≥95% of riboso mal RNA sequences from NGS data, including sequences from *5S, 5.8S, 18S,* and *28S* nuclear rRNA, and *12S* mtRNA.

Library quantification

The **Library Quantification Kit** provides a highly sensitive, qPCR-based method specifically for quantification of Illumina libraries.

Magnetic bead separation

The **SMARTer-Seq® Magnetic Separator - PCR Strip** holds up to 24 0.2-ml PCR tubes in two rows, and is designed for capture of magnetic beads in 10–20 minutes. It is ideally suited for DNA purification and size-selection techniques used with most NGS library preparation kits.

NGS Learning Center

Visit the Takara Bio NGS Learning Center to find more information about our NGS kits.

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

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