

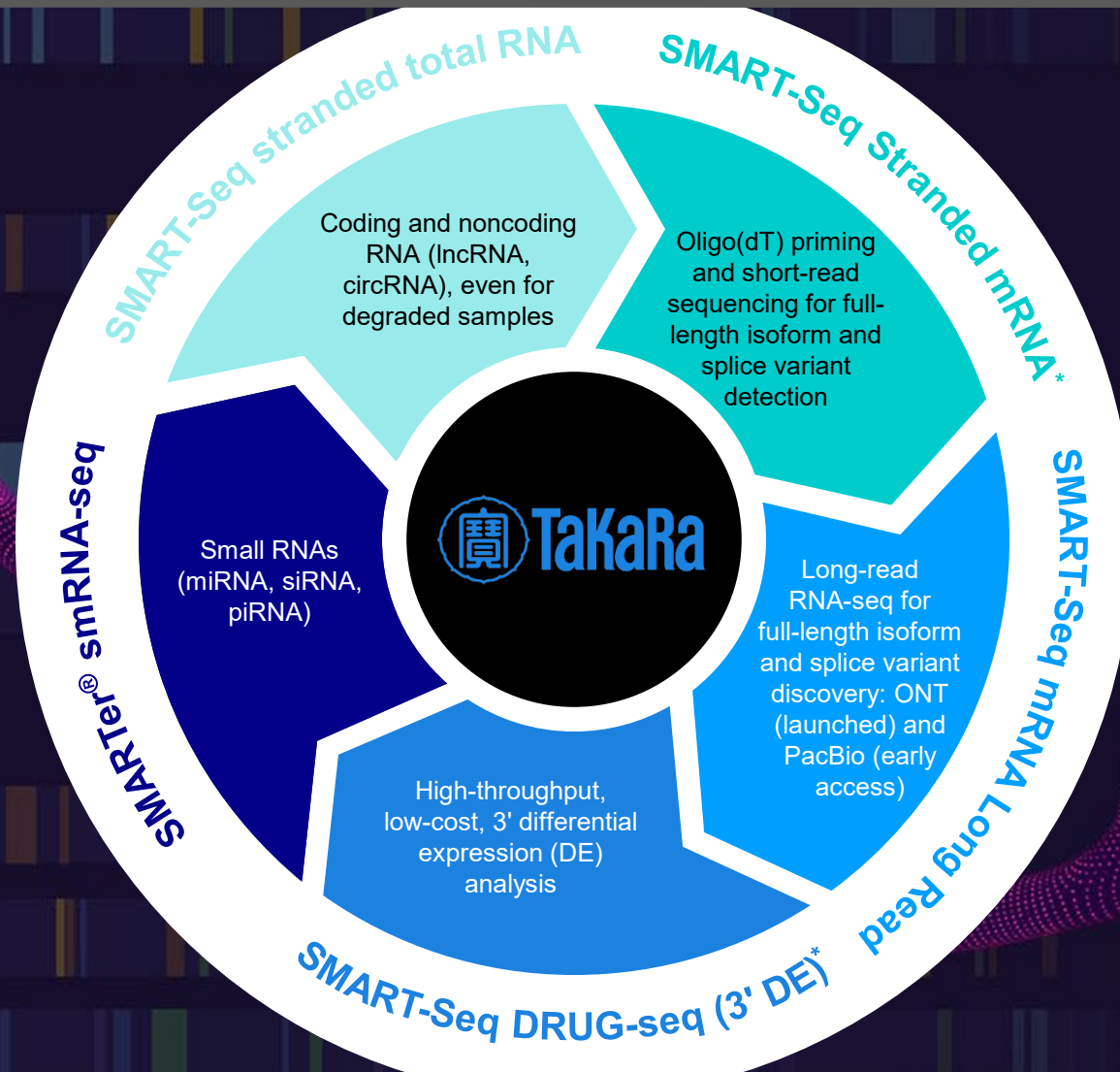
# Advancing RNA-seq to the next level with SMART-Seq<sup>®</sup> innovations

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that's  
**GOOD**  
science!<sup>®</sup>

# Takara Bio: Versatile RNA-seq solutions



**View our poster (#27)**  
Tuesday 3/31, 12:30–1:30 pm

**Visit us at booth 717**  
throughout the event!

\*Launching in 2026

# From complexity to clarity: Key advantages of Takara Bio RNA-seq



Decode the transcriptome  
with precision and  
simplicity



**Universal  
sample  
compatibility**

Wide input range (pg to  $\mu$ g)

Direct cell input and RNA input

Validated for challenging sample types  
(FFPE, cfRNA, etc.)

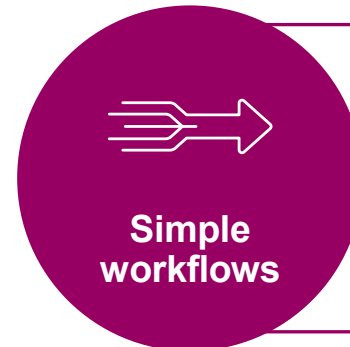


**Sensitivity  
& accuracy**

Industry-leading cDNA length

Ultra-high sensitivity and lowest LOD

Robust reproducibility



**Simple  
workflows**

Fewer steps and faster workflow

High-throughput library prep

Compatible with automation

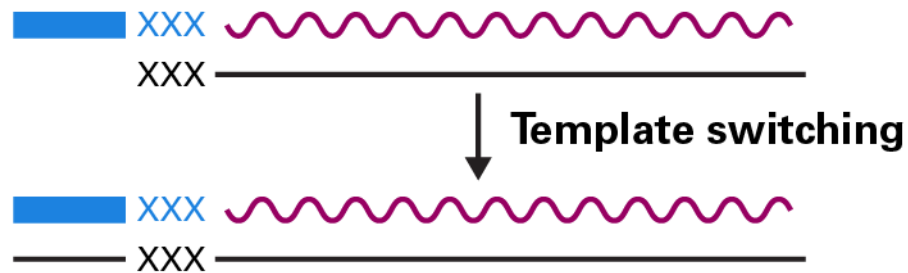
**Superior  
performance,  
streamlined  
workflow**

# Unique technologies for the highest resolution and sensitivity

## SMART® technology

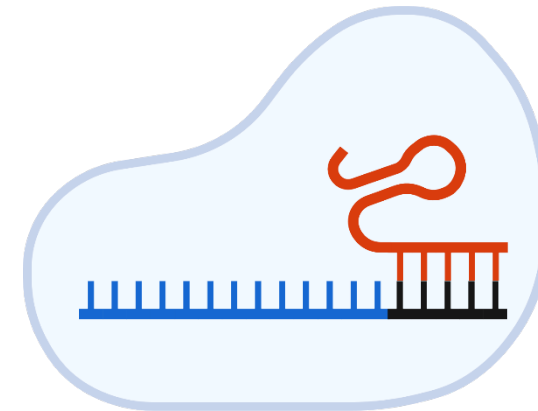
- Template-switching chemistry enables full-length cDNA synthesis
- Ideal for accurate isoform and gene fusion detection

Template switch oligo



## ZapR® technology

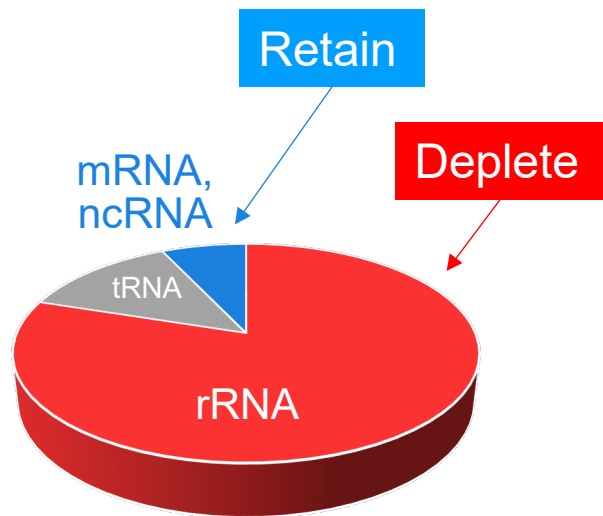
- Cas9-guided post-RT depletion of unwanted targets
- Maximize library complexity with retention of low-abundance targets



Created with [BioRender.com](https://BioRender.com).

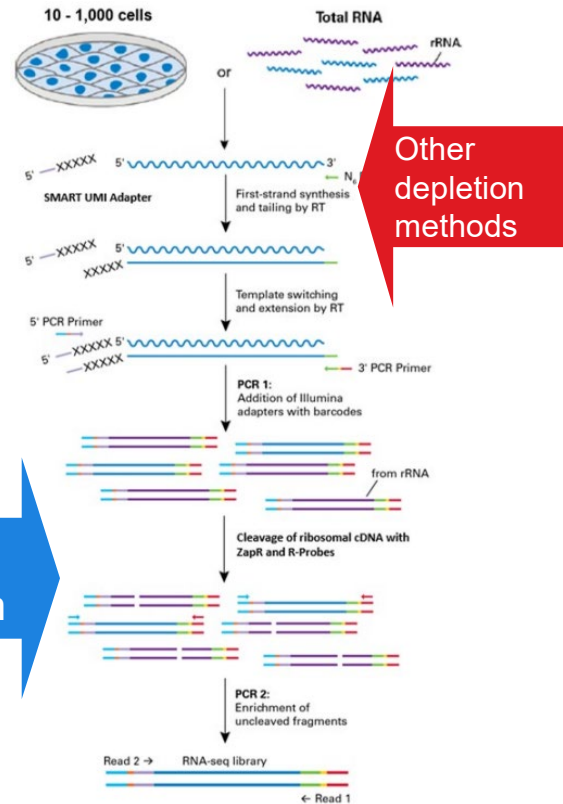
# Maximize informative reads with SMART-Seq

Cellular RNA content is dominated by rRNA

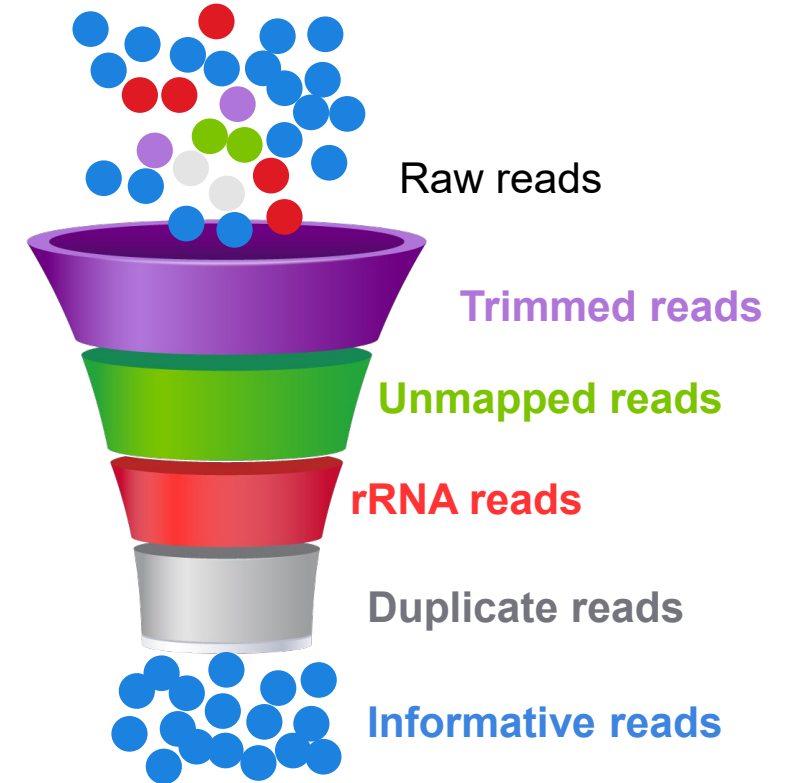


ZapR approach preserves library complexity

Reverse transcription  
cDNA amplification  
ZapR ribodepletion  
Library amplification



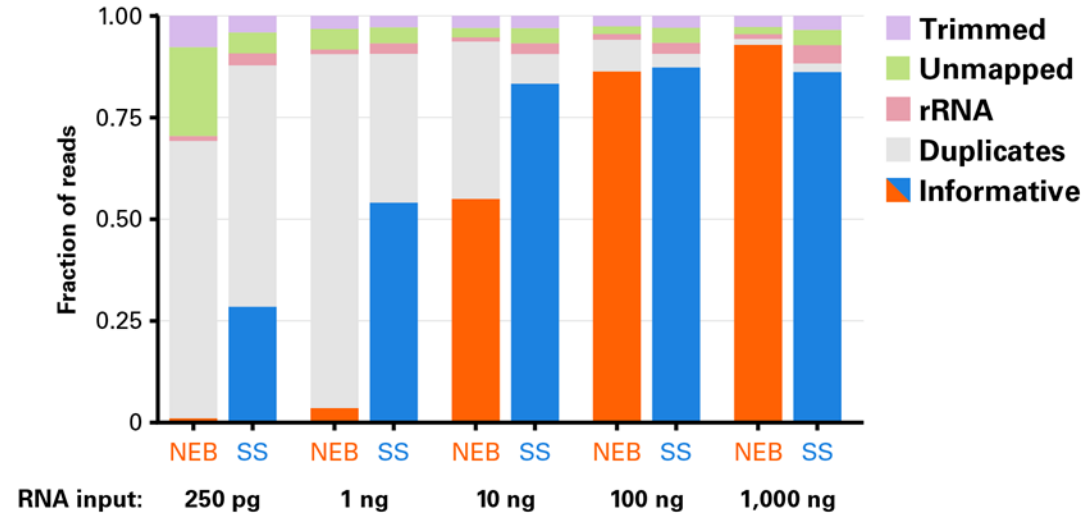
SMART-Seq + ZapR enriches for informative reads



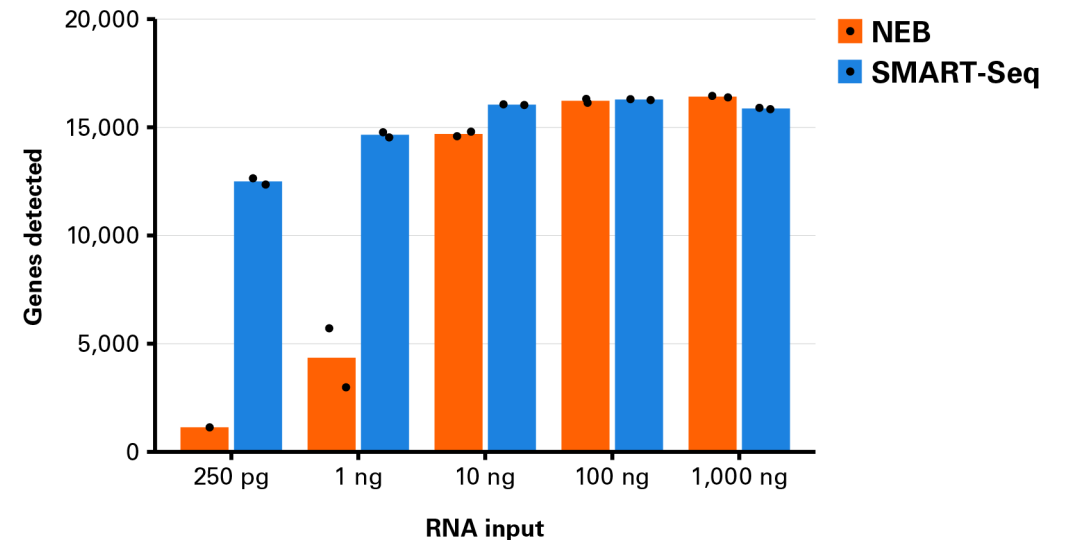
\*Proportions by mass in a mammalian cell; figure adapted from: "Non-coding RNA: what is functional and what is junk?" (Palazzo, A.F. et al. 2022, *Front. Genet.*) under a [CC BY 4.0](https://creativecommons.org/licenses/by/4.0/) license.

# More informative reads enable superior gene detection

Read fates for SMART-Seq vs. NEB\*



Gene counts† for SMART-Seq vs. NEB\*



\*NEBNext Ultra II Directional RNA Library Prep kit with NEBNext rRNA Depletion Kit v2 (Human/Mouse/Rat), and SMART-Seq Total RNA Library Prep with ZapR Depletion (with UMIs) kit were used; SS = SMART-Seq.

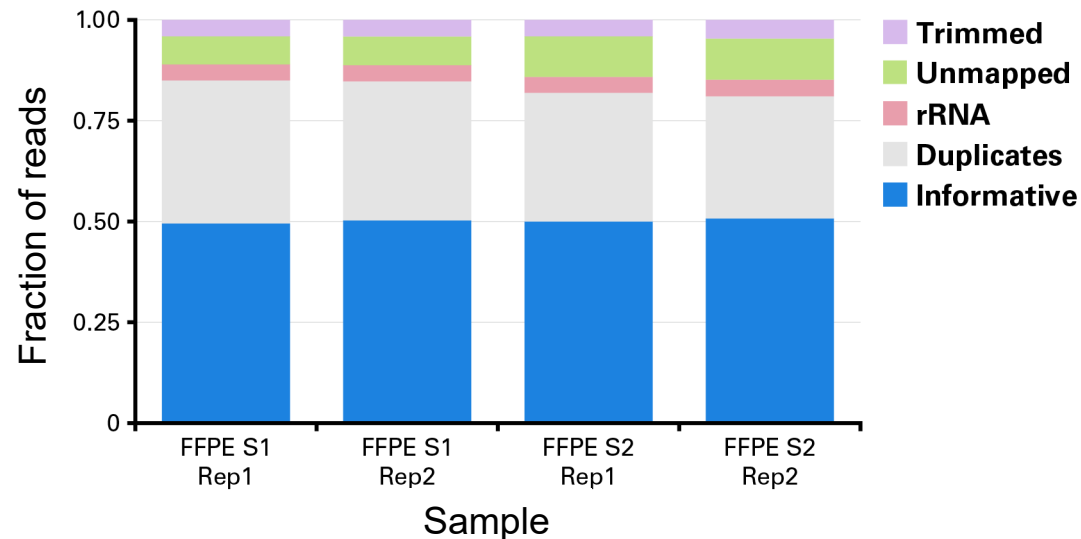
†Number of genes with 10 or more counts; the mean of two replicates is shown for each sample.

# SMART-Seq chemistry accommodates low-input and low-quality samples

Generate high-quality data from degraded FFPE samples

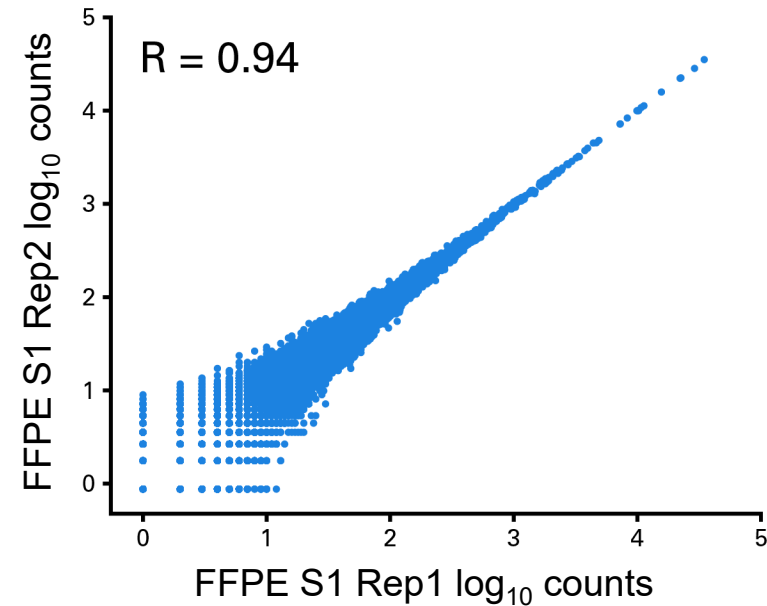
## FFPE samples

- Input: 10 ng
- Sample quality: RIN = 3, DV200 = 77%
- Sequencing depth: 6 M paired-end reads



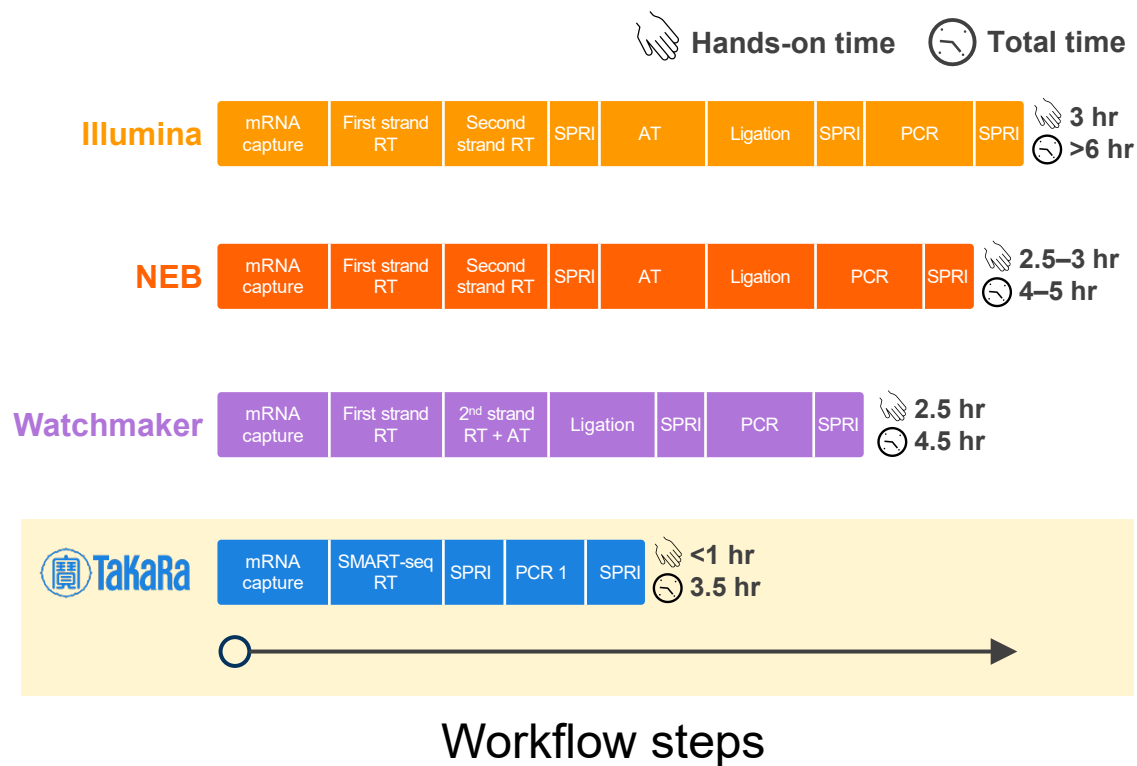
Achieve high reproducibility with low-quality samples

## Reproducibility across replicates



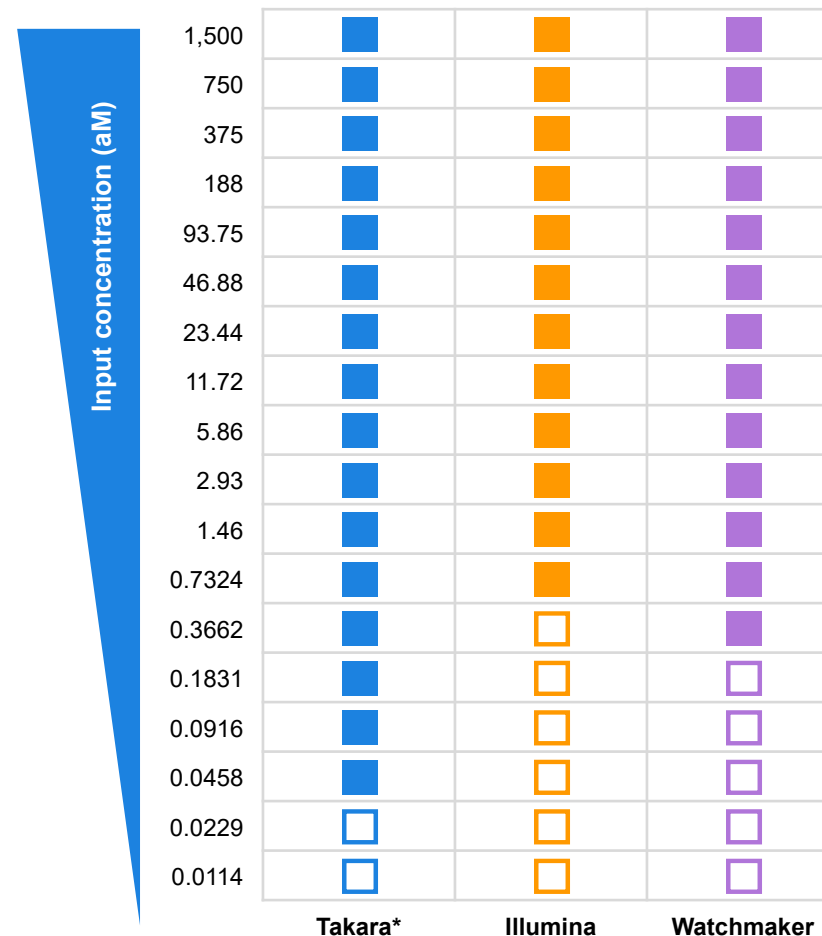
# Fastest sample-to-library workflow for stranded mRNA

## Streamline your workflow with SMART-Seq Stranded mRNA



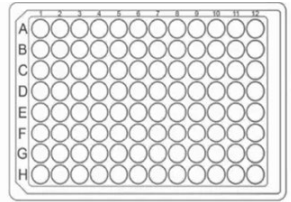
\*The SMART-Seq Stranded mRNA Kit was paired with ZapR technology for enhanced limit of detection.  
 SPRI = solid phase reversible immobilization; AT = A-tailing

## Enable low limit of detection (LOD)

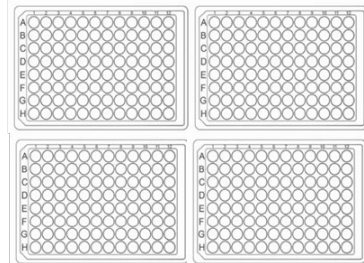


# Enable high-throughput 3' mRNA-seq with DRUG-seq

96 in-line barcodes



384 UDIs



High-throughput

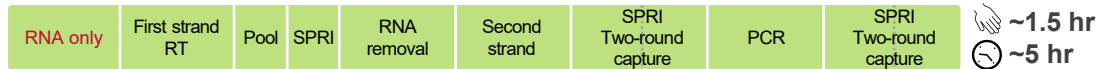
36,864 samples

Hands-on time ⌚ Total time

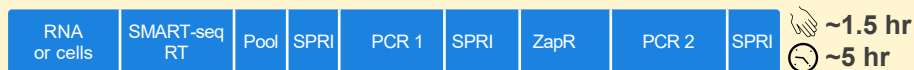
**Alithea Genomics**



**Lexogen**



**Takara**

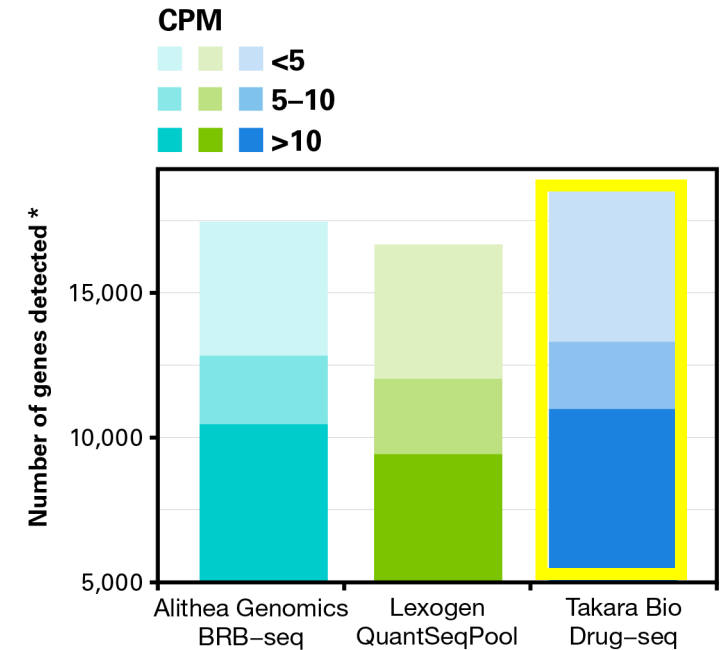


Flexible sample input range and sample type

RNA: 10–200 ng  
Direct cells: 1,000–20,000

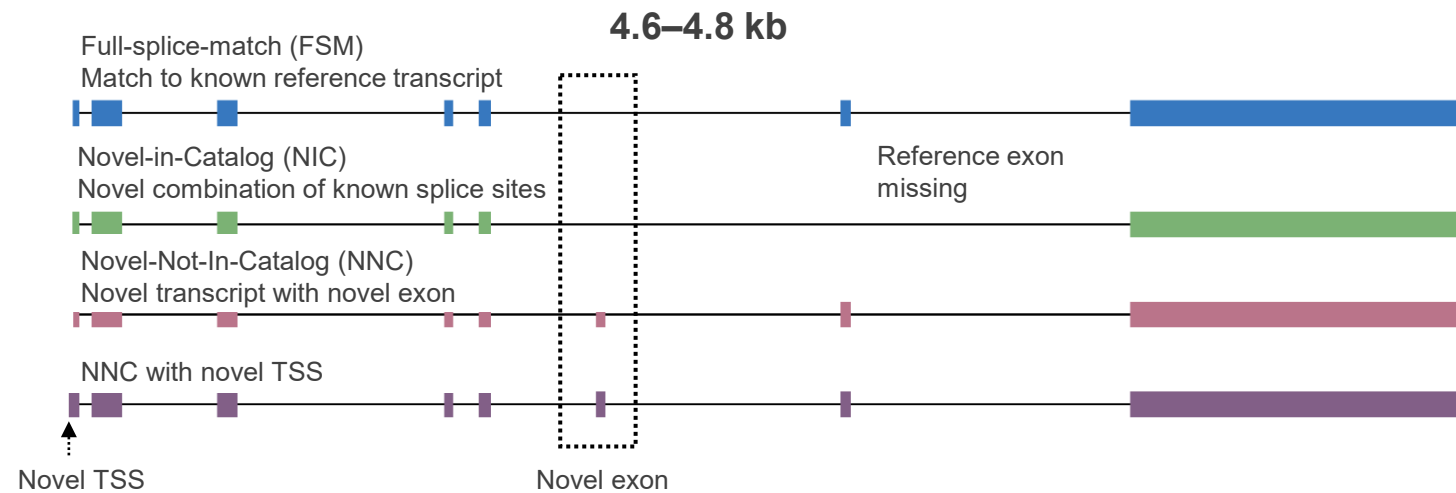
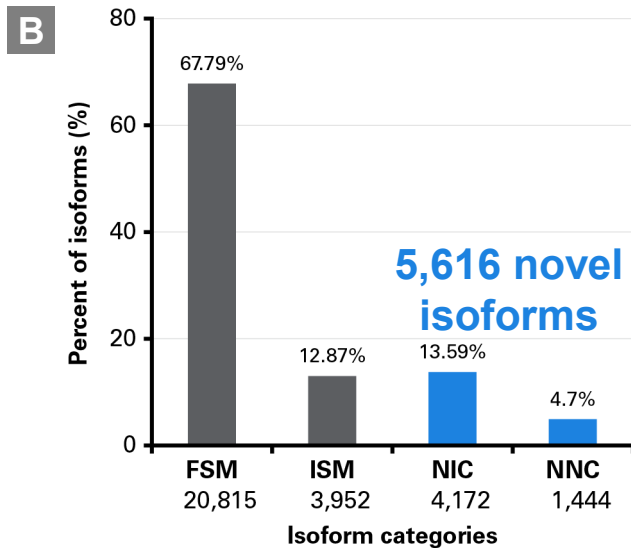
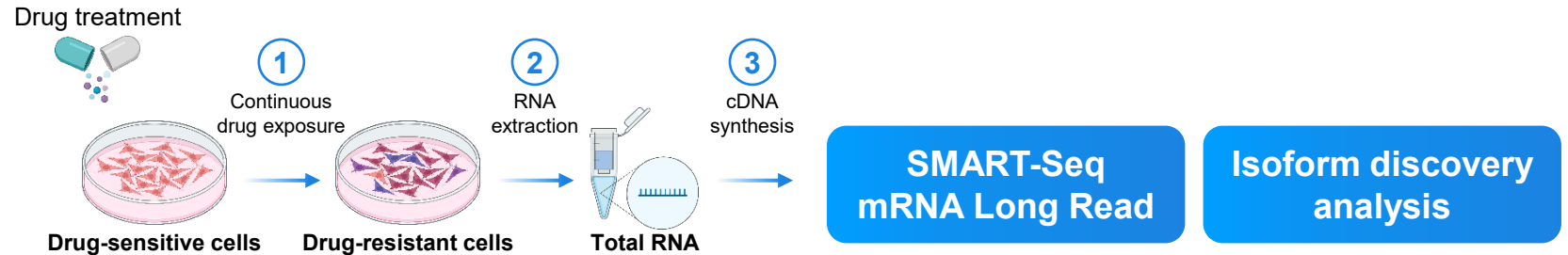
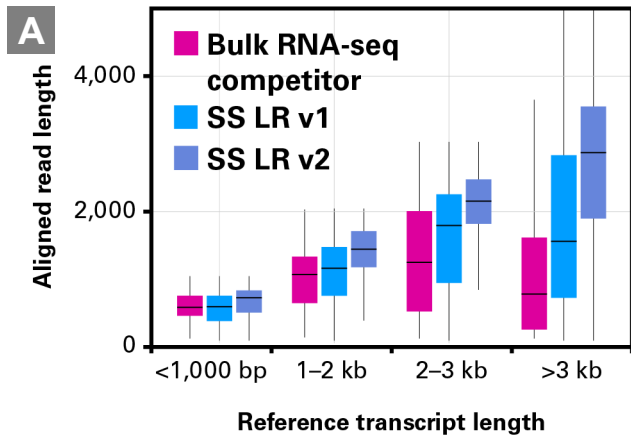
Easy workflow

Highest sensitivity



\*1 million reads/sample, human brain RNA

# Capture full-length reads with SMART-Seq mRNA Long Read



The sensitivity of SMART-Seq technology coupled with leading read-length performance empowers isoform discovery

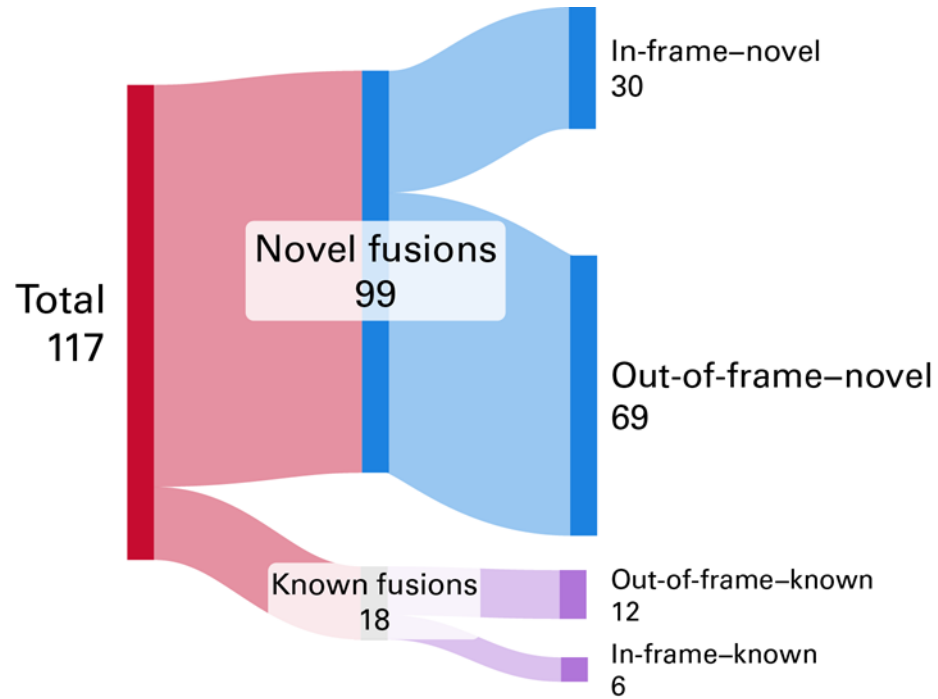
Data in panel B were generated from SQANTI3 analysis. Isoform view (right) was generated using FLAIR.

# Discover gene fusion isoforms with SMART-Seq mRNA Long Read

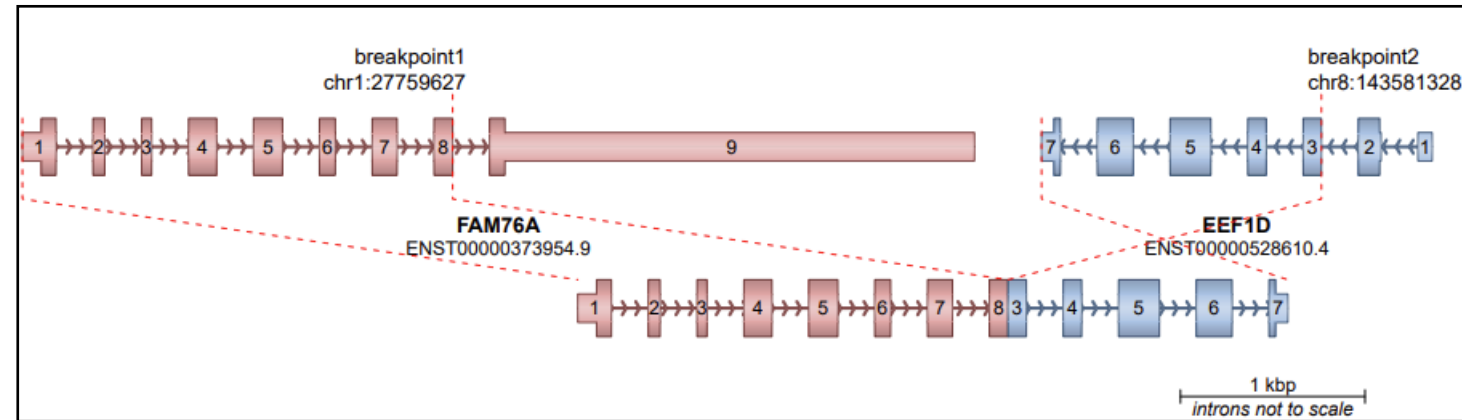
Fusion isoform identification [JAFFAL]

Fusion isoform filtering

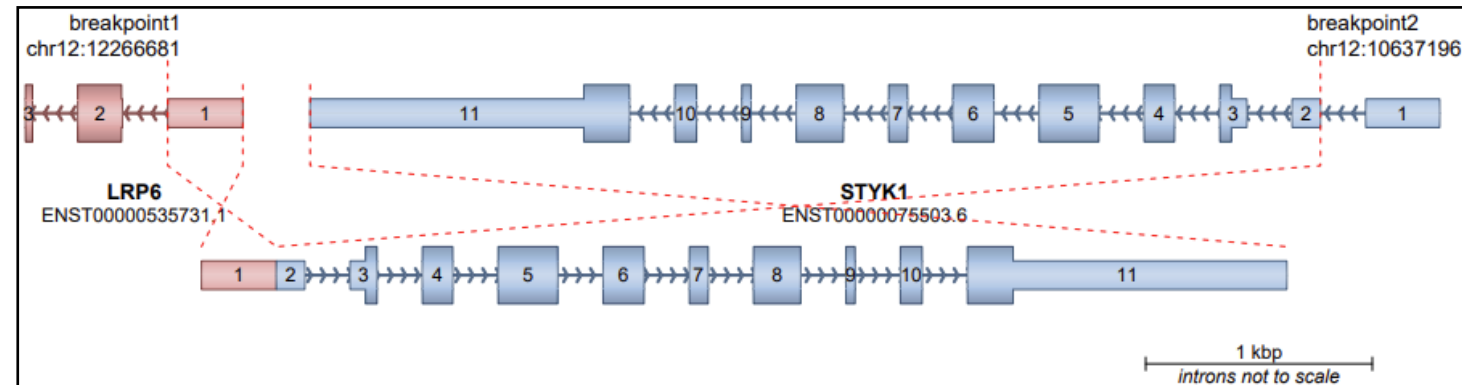
- High confidence
- Read support  $\geq 2$



In-frame—novel



Out-of-frame—novel



Sankey plot (left) generated at SankeyMATIC.com. Gene fusion images (right) were generated using Arriba.

# Takara Bio's end-to-end RNA-seq solutions

## Reagents



### SMART-Seq portfolio

- Maximize sensitivity and full-length transcript coverage
- Preserve library complexity with ZapR target depletion
- Boost accuracy and minimize bias with UMIs



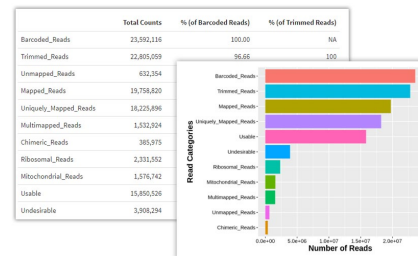
*Our reagents streamline your workflow, save you time, and reduce costs*

## Bioinformatics



### Cogent™ bioinformatics tools

- Free software for data analysis and visualization
- User-friendly, cloud-ready, and scalable



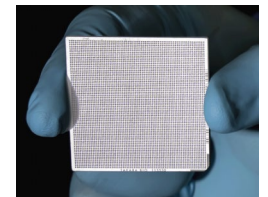
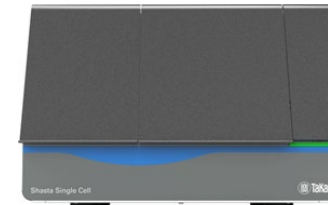
*Create publication-ready visuals with our free analysis tools*

## Automation



### Shasta® Single Cell System

- Bulk RNA-seq dispensing
- Miniaturized nanoliter-scale dispensing (as low as 25 nl)
- 5,184 nanowell reactions



*Takara Bio also supports NGS automation protocols for other liquid handlers*



that's  
**GOOD**  
science!®