The MERCURIUS™

FLASH-SEQ INFO GUIDE

ALITHEA
GENOMICS

Trusted by

BAYER Johnson & Johnson Roche syngenta AXXAM Stanford University

The MERCURIUS™

FLASH-SEQ TECHNOLOGY

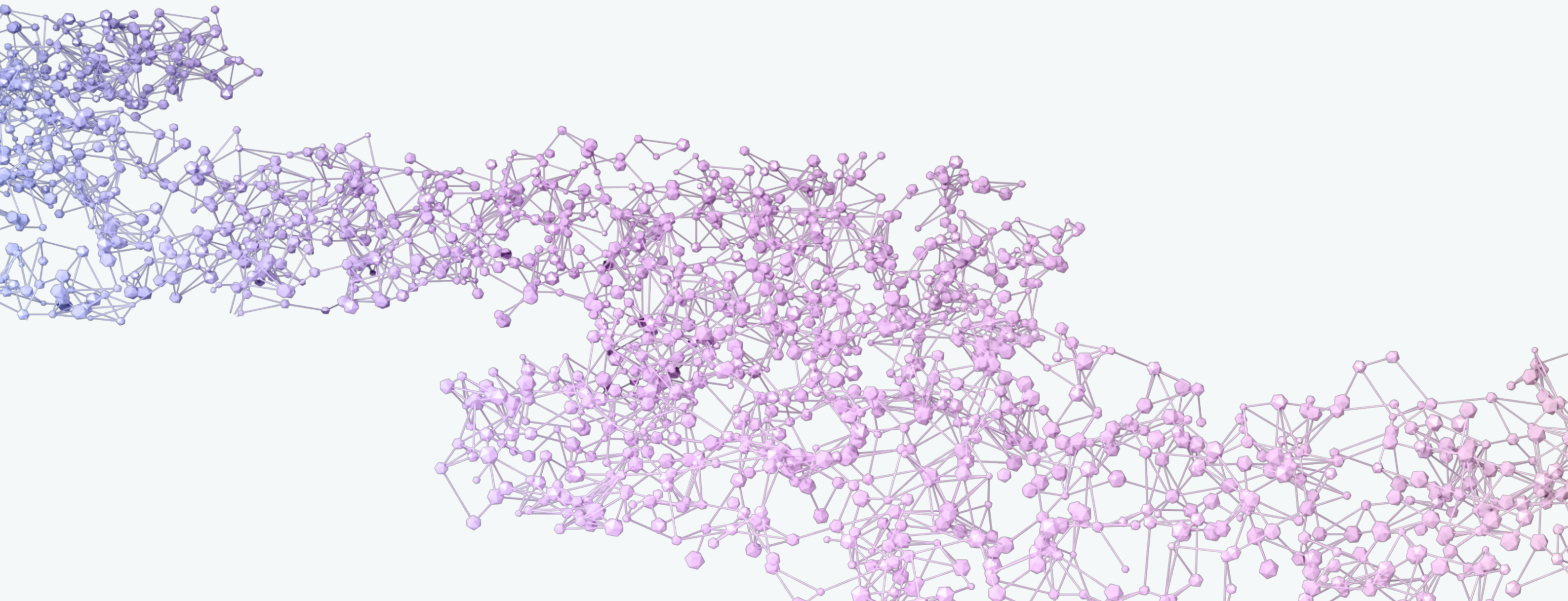
Ultra-sensitive, full-length, plate-based single-cell and low-input RNA-seq technology for FACS-sorted cells or low-input RNA samples

Ultra-sensitive, cost-effective and fast single-cell RNA-seq

MERCURIUS™ FLASH-seq provides full-length mRNA transcript coverage even for low-abundance genes, empowering researchers to explore differential gene expression, detect alternative splicing, and analyze isoform diversity—all critical for understanding complex biology, especially in rare cell populations.

The technology is based on the method first published in Nature Biotechnology, which offers unmatched sensitivity and reduces hands-on time compared to Smart-seq2 and Smart-seq3.

Our team has refined FLASH-seq to simplify the workflow, use a non-toxic tagmentation buffer and enhance sensitivity and data quality.



BENEFITS

Ultra-sensitive

Up to 2x more genes detected than other commercially available solutions. Ideal for rare cell profiling.

For ultra-low-input RNA

As low as 1 pg RNA input per well.

For isolated single-cells

Simply FACS-sort the cells into the buffer.

Full-length transcript coverage

From differential gene expression to splicing variants and isoform detection.

One-day lab workflow

Convenient and short protocol. From samples to sequencing-ready libraries in only 7H30.

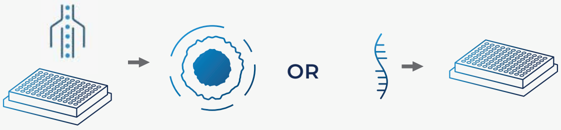
Suited to automation

Enables seamless integration into high-throughput workflow, further reducing hands-on time and increasing scalability, reproducibility and efficiency.

Experimental workflow at a glance

1. Cell sorting, lysis and RNA solubilization

10 minutes
10-30 minutes



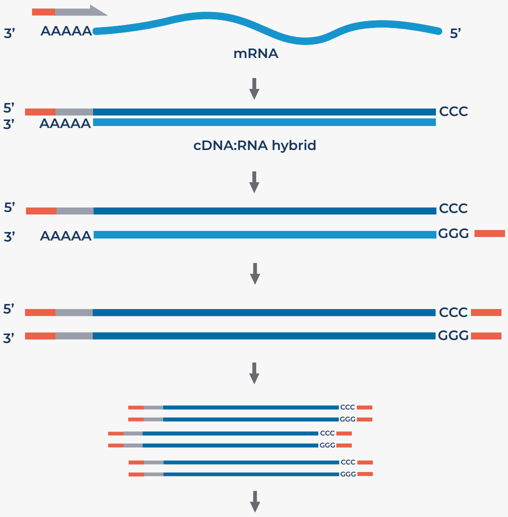
2. Reverse transcription and PCR

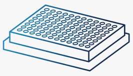
150 - 210 minutes
10 minutes

2A. Reverse transcription

2B. Strand-switching and TSO integration

2C. Second strand synthesis and cDNA amplification





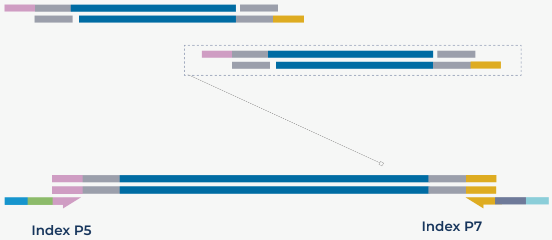
96 / 384 Plate

3. Tagmentation

15 minutes
10 minutes

4. Libraries indexing and amplification

25 minutes
15 minutes



5. Libraries QC and sequencing

5-80 minutes
10 minutes
19-48 hours

Tube

6. Sequencing data processing and analysis

1. Gene count matrices
2. QC report

Overall time

Incubation time: 3h20-4h20.

Hands-on time: 1h05-1h35.

QC time: 5min-1h20 (depending on the instrument used: Qubit or Fragment Analyzer).

Sequencing time: 19-48 hours (depending on instrument and sequencing run settings).

KITS

All our kits contain all the oligos and enzymes needed to go from FACS-sorted single-cells or low-input RNA samples to sequencing-ready libraries.

MERCURIUS™
Single-cell FLASH-seq

Library preparation kits for Illumina®, AVITI™, Ultima Genomics

- For FACS-sorted single-cells
- 96- and 384-well plate kit format
- Ultra-sensitive and rapid
- Plate-based
- Ideal for rare cell profiling and isoform detection

FIND OUT MORE

MERCURIUS™
Low-input FLASH-seq

Library preparation kits for Illumina®, AVITI™, Ultima Genomics

- For low-input RNA samples (from 1pg)
- 96-well plate kit format
- Ultra-sensitive and rapid
- Plate-based
- Ideal for rare cell profiling and isoform detection

FIND OUT MORE

SERVICES

You send us your samples, we do the rest. From FLASH-seq library prep to downstream analysis.

Single-cell FLASH-seq

Λ: Ships the plates containing our buffer.

Client: FACS-sorts cells in our dedicated 96- or 384-well plates. Snap-freeze the plate(s).

Low-input FLASH-seq

Client: Prepares the samples in 96-well plates.

Ship the samples to our service centers

Λ MERCURIUS™ **FLASH-seq library prep**

Λ **Library QC- Client checkpoint**

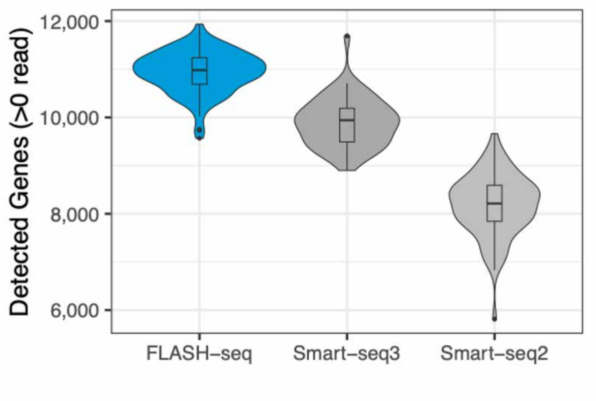
Λ **Sequencing**

Λ **Data analysis and reporting**

Λ Optional: downstream analysis

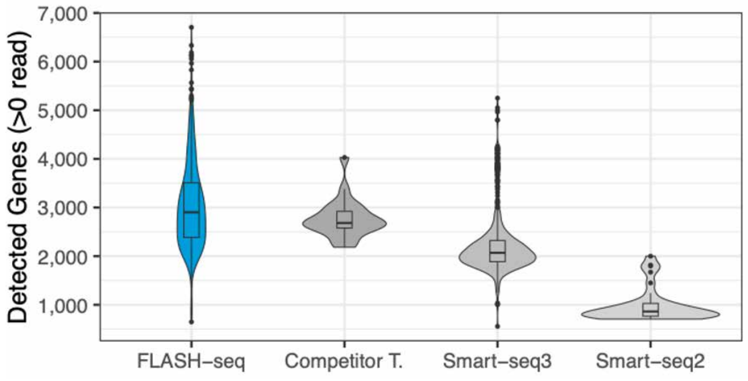
PERFORMANCE

Detecting 12’000+ genes per single cell is now possible … and affordable



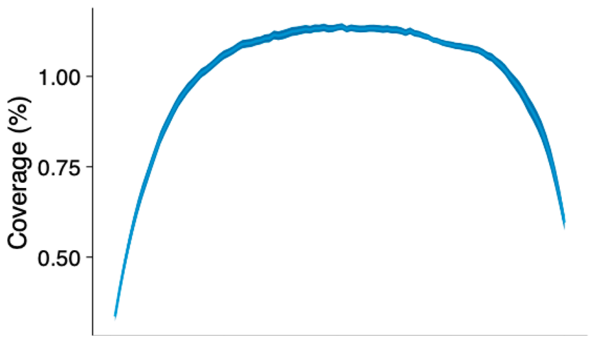
MERCURIUS™ FLASH-seq Shows The Highest Sensitivity In Gene Detection

The number of detected genes in HEK 293T cells processed with different protocols. Reads were downsampled to 500,000 raw reads.



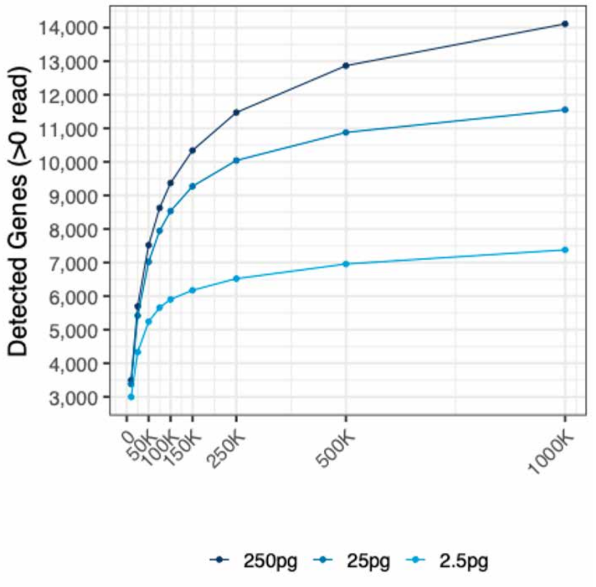
The Sensitivity Of MERCURIUS™ FLASH-eq Is Retained Even In Highly Heterogeneous Populations

Number of genes detected in human PBMCs, processed with different protocols, and the number of reads downsampled to 125,000 raw reads.



MERCURIUS™ FLASH-Seq Is A Full-Length ScRNA-Seq Protocol

Gene body coverage shows a uniform read distribution across the entire gene body for the FLASH-seq protocol.



MERCURIUS™ FLASH-Seq Shows High Sensitivity For Low Sample Inputs

The number of genes detected in HEK 293T cells using different RNA inputs (from 2.5 pg to 250 pg) at different sequencing depths.