PIPseq™ 3' Single Cell RNA Kits v4.0 for Gene Expression Analysis

Fluent BioSciences

Single-cell RNA sequencing (scRNA-Seq) has enabled unprecedented insight into the biology and pathology of individual cells across a broad range of discovery and disease applications. However, specialized capital equipment, high reagent costs, lack of accessibility, and scalability are key factors limiting the wide-scale adoption and use of single-cell technologies.

Fluent BioSciences has updated the PIPseq 3' Single Cell RNA product line to version 4 chemistry. This novel technology, published in Nature Biotechnology ("Microfluidics-free single-cell genomics with templated emulsification"), uses a simple vortexer and standard lab equipment to enable researchers to conduct single-cell RNA sequencing studies affordably and at a wide range of scales.

Key features of v4 kits:

- Highest cell capture rate in the market (up to 80%)
- Improved lysis chemistry, enabling 60% more genes per cell than v3 kits (in PBMC samples)
- Higher sequencing efficiency, more reads in your cells of interest
- New workflow yielding higher quality nuclei data

Scalable kits

- T2 Kit*: Profile up to 2,000 single cells per reaction (8 reactions per kit)
- T20 Kit*: Profile up to 20,000 single cells per reaction (4 reactions per kit)
- T100 Kit*: Profile up to 100,000 single cells per reaction (2 reactions per kit)
- Unique Dual Index (UDI-96) Kit for multiplex sample preparation of PIPseq libraries

Multi-omics capability

- Cell surface epitope profiling
- Sample multiplexing

Benefits:

- Easy to implement (no complex instrumentation or consumables)
- Flexibility to process any number of reactions per kit as needed
- Cost-effectively scale from pilot and low cell diversity projects to complex tissue analysis all with the same technology
- Conveniently and quickly process cells and capture RNA at point of collection with < 10 min of hands-on time
- User-friendly PIPseeker™ software for downstream analysis

**Kits include all reagents necessary for cell capture and library preparation to produce sequencing-ready libraries*

Visit us at fluentbio.com to learn more about our products and obtain a quote.

Streamlined Workflow

01 Sample Prep

02 Library Prep

03 Sequencing

04 Data Analysis

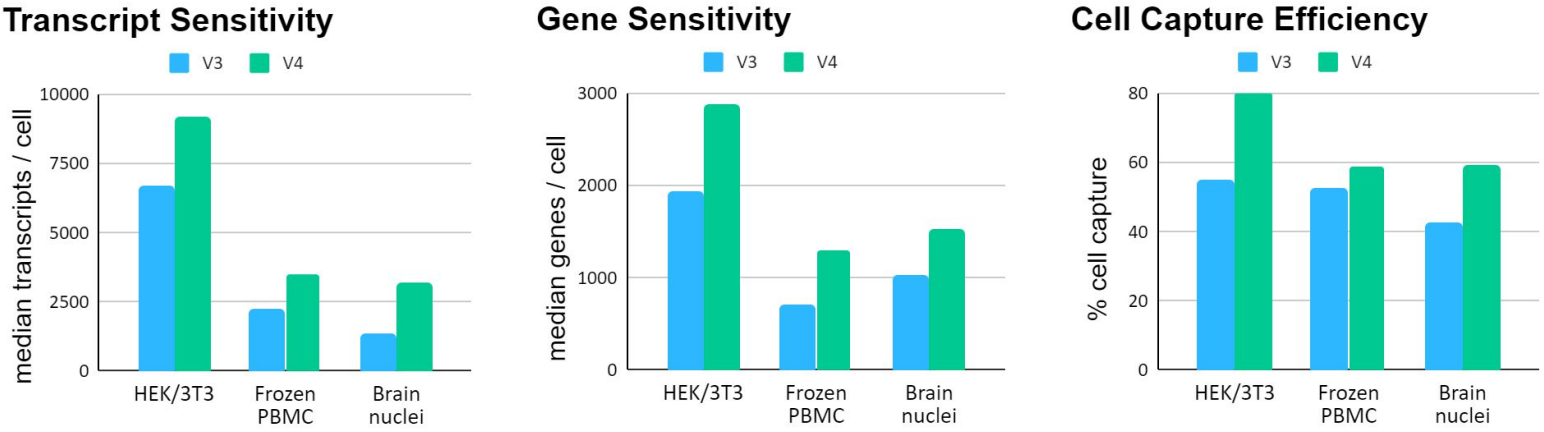
During sample preparation, the cell suspension of interest is mixed with template particles and segregated into Particle-templated Instant Partitions (PIPs) by simple vortexing. The cells in PIPs are then lysed on a thermal device and the mRNA is captured by barcoded oligonucleotides incorporated with the template particles. cDNA is generated from the captured mRNA via reverse transcription and amplified to create a cDNA library for each individual cell. These are then processed into sequencing libraries using standard library preparation methods followed by next generation sequencing and then analyzed via Fluent PIPseeker software for data analysis.

"The ease with which we have been able to generate large numbers of single-cells for challenging neuronal samples is amazing. Sequencing quality, including genes detected, and doublet errors are on par with other methods. PIPseq will be an impactful addition to the laboratory repertoire for any researcher."

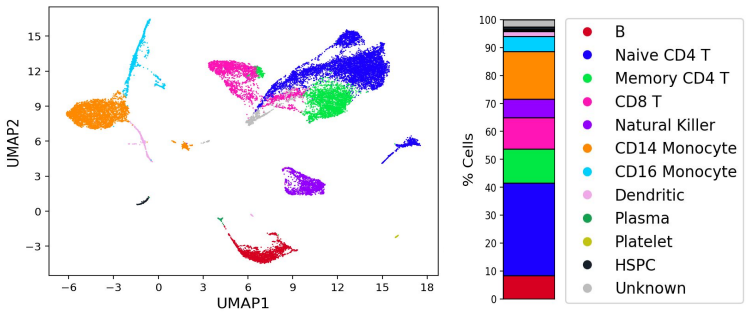
Asst. Professor, Department of Neuroscience, NYU Langone, New York City

Dr. Shane Liddelow

V4 chemistry performance improvements



PIPseq T20 3' Single Cell RNA v3.0 and v4.0 reagent kits were used with 40,000 cells or nuclei as input to both kits. Sequencing depth for HEK/3T3 and PBMCs was 20,000 reads per cell while sequencing depth for brain nuclei was 15,000 reads per cell.



PIPseq T20 3' Single Cell RNA v4.0. 40,000 cryopreserved PBMCs were used as input.

Visit us at fluentbio.com to learn more about our products and obtain a quote.