PIPseq™ V 3' Single Cell RNA Kits for Gene Expression Analysis

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 enhanced the PIPseq 3' Single Cell RNA product line to improve user experience and make it even easier for researchers to conduct single cell studies at their benchtop. The PIPseq V kits improve user experience by lowering ambient RNA background, improving 50% in genes and transcripts in certain cell types and reducing sequencing artifact for more usable NGS data. . Fluent anticipates that these customer-focused changes will continue to lower the barrier to entry for researchers adopting single cell technologies.

Key Features in PIPseq V Kits:

- Up to 50% Improvement in Genes and Transcripts in certain cell types
- Lower Ambient RNA Background
- Sequencing Artifact Reduction that provides more usable NGS data

Benefits:

- Compatible with DSP/methanol fixation protocols
- 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

Scalable Kits

- **T2 Kit*:** Profile up to 2,000 single cells per reaction (8 reactions per kit)
- **T10 Kit*:** Profile up to 10,000 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

**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

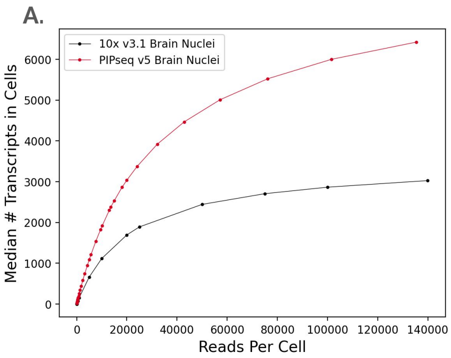
03 Sequencing

04 Data Analysis

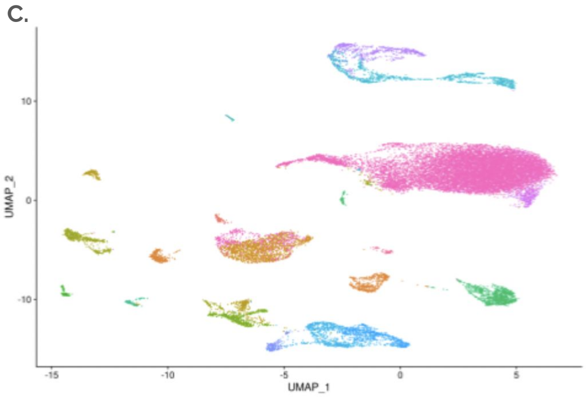
During sample preparation, the cell suspension of interest is mixed with template particles and segregated into Particle-templated Instant Partitions (PIPs) by simple vortexing. The cells in PIPs are then lysed on a thermal device and the mRNA is captured by barcoded oligonucleotides incorporated with 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**

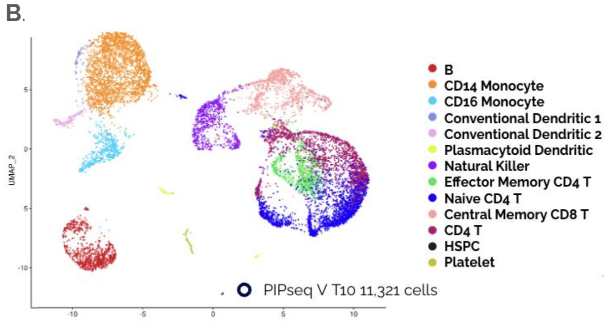
PIPseq V Chemistry Across Multiple Sample Types



A. PIPseq V reveals substantially more gene sensitivity than 10X Chromium v3.1 in a deeply sequenced matched sample of mouse brain nuclei.



C. 12,000 captured cells from mouse brain were processed through PIPseq V and resolved by UMAP analysis.



B. Over 11,000 captured cells from PBMCs processed through PIPseq V and resolved by UMAP analysis.

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