Fast and highly sensitive full-length scRNA-seq using FLASH-seq

V. Hahaut[*1], *M. D. Rumper*[2,3], *Q. Zhou*[2,3]
[1]*Alithea Genomics, Epalinges, Switzerland*
[2] *Laboratory of Systems Biology and Genetics, Institute of Bioengineering, School of Life Sciences, Ecole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland*
[3] *Swiss Institute of Bioinformatics, Lausanne, Switzerland*

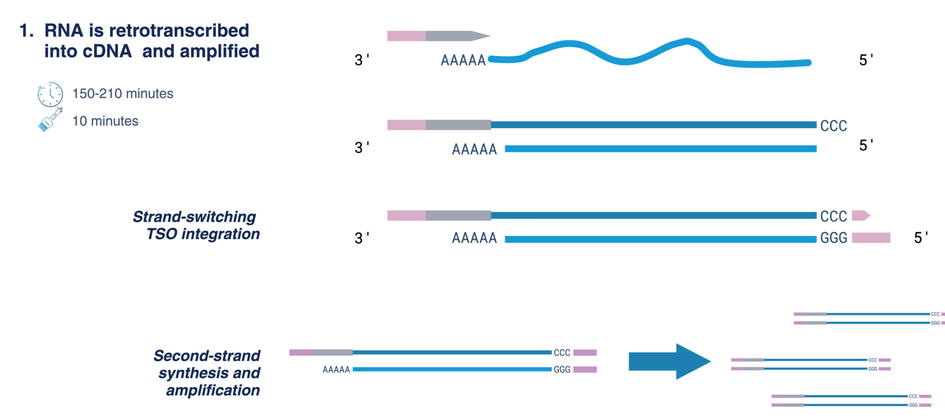
1 Introduction

Single-cell RNA sequencing (scRNA-seq) has experienced rapid advancements, with methods like emulsion droplets (i.e. 10x Genomics), which have enabled researchers to analyze thousands of cells simultaneously. However, compared to SMART full-length sequencing protocols, these methods capture only the 3' ends of mRNAs and still lack the sensitivity needed for comprehensive transcriptome analysis of individual cells, which is crucial for studying rare cell populations.

FLASH-seq was designed to address these limitations (Hahaut *et al*, 2022, Nat. Biotech.), and presents several advantages for your research:

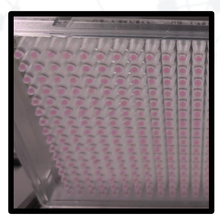
- **Full-length** coverage
- **High sensitivity** - 50-100% more genes than 10x Genomics
- **Ultra-low inputs** (single-cells or 1 to 100 pg input)
- **Isoform** detection
- **Fast protocol** (4h30-7h30)
- **Rare cells** capture
- Captures **TCR/BCR** and **SNPs** information

Since its release, FLASH-seq has been widely adopted by both academic and pharmaceutical groups. At **Alithea Genomics**, we improved the protocol and, for the first time, can offer it to a wider audience in the form of a **service or kit.**

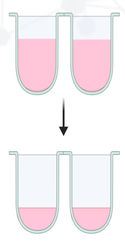


2 FLASH-seq by Alithea Genomics

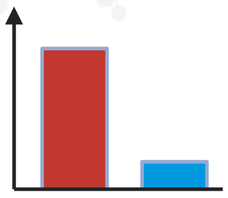
Transferring a protocol from academia to a commercial product required several modifications to ensure reproducible results.



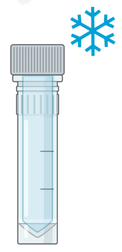
Dyes to ensure proper reagent dispensing



Volumes adapted for manual and automated pipettings



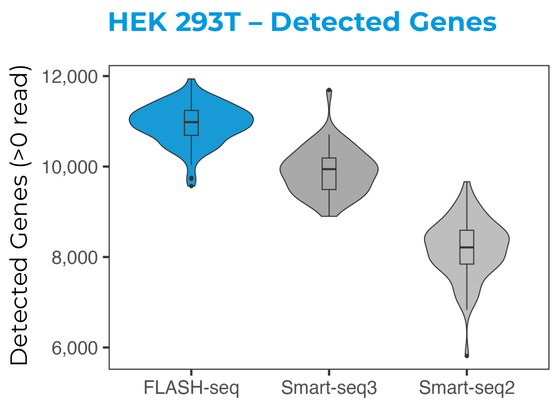
Optimised assay (e.x. MT rRNA)

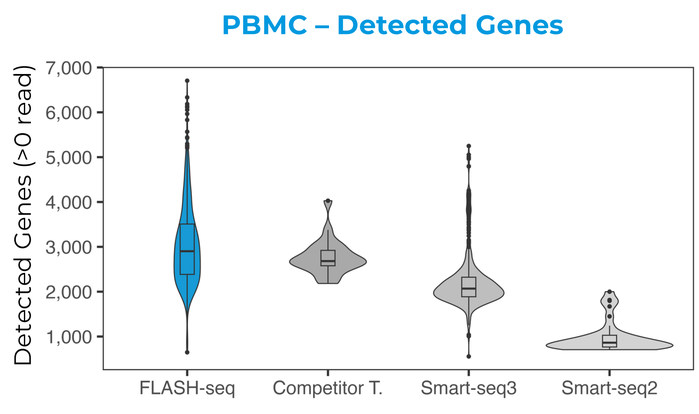


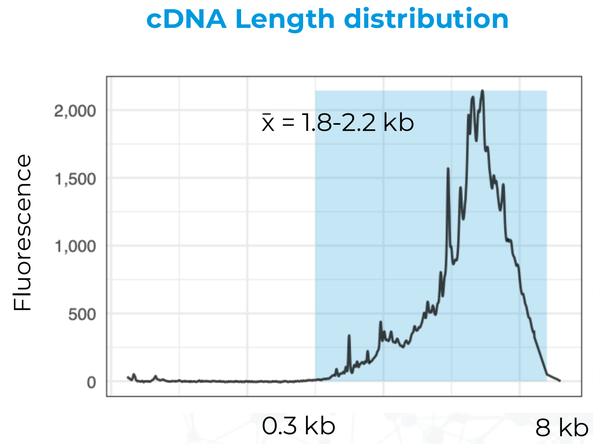
Pre-mixing reagents and freezing study

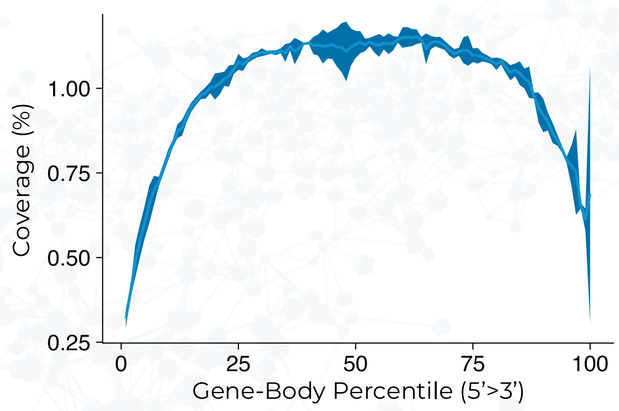
Novel non-toxic Tn5 buffer!

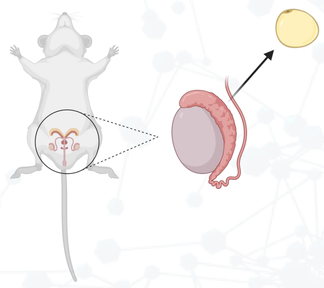
3 Performances





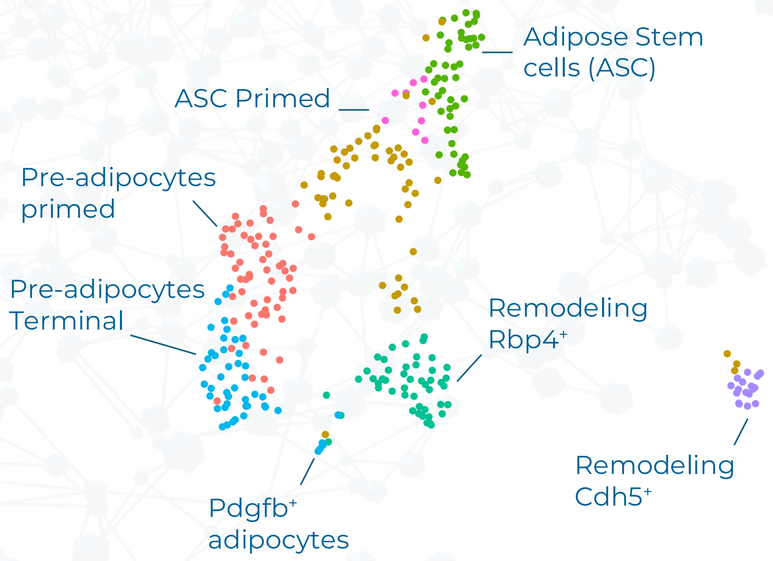






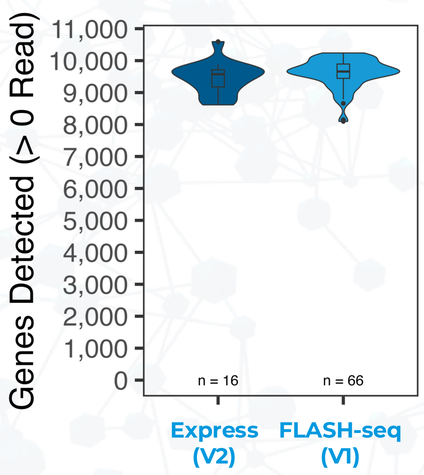
Heterogenous population

FLASH-seq provides high-quality fine-grained results for heterogeneous cell population and can help discriminate new cell populations (e.g. Remodelling APCs) that were not detectable in 10x Genomics.



4 Future Improvements

The two main bottlenecks for full-length scRNA-seq protocols are the enzymes (= sensitivity) and the protocol durations. We have been working on the latter and demonstrated that the FLASH-seq protocol could be reduced to a total duration of <2h30 without loss in data quality by modifying the lengthy initial RT-PCR procedure.



5 Conclusions

FLASH-seq is an **ultra-sensitive scRNA-seq protocol** that is now accessible to all laboratories, regardless of whether they have an automation system. Thanks to **Alithea Genomics**, this technology is now available as both **kit and service**.

Reach out to us:
info@alitheagenomics.com
www.alitheagenomics.com

Europe: Epalinges, Switzerland
USA: Frederick, MD