WEBINAR SUMMARY

Optimizing Single-Cell Multi-Modal Analysis of Challenging Samples with LeviCell

Webinar Presented by Dr. Agne Antanaviciute

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Navigating the Challenges of Multi-Modal Single-Cell Analysis

Single-cell analysis techniques, including RNA sequencing (scRNA-seq), can be valuable yet costly. Fortunately, techniques like cell hashing enable the processing of multiple samples simultaneously, optimizing resource use. However, challenges persist to obtain high-quality data:

- High-interest, precious samples often contain low live cell counts, fragile subtypes, extensive debris, and dead cells;
- Further processing for cell hashing can degrade sample quality even more due to longer handling.

These challenges result in near-unusable scRNA-seq data with high number of mitochondrial-mapping reads per cell, high ambient RNA signal, low number of genes detected, and low signal-to-noise antibody data. Tools such as Fluorescence-Activated Cell Sorting (FACS) and bead-based methods often worsen these problems by causing cell stress, low cell recovery, and antibody signal loss due to non-specific binding. The LeviCell® system is the game-changer by quickly and gently removing dead cells and debris without biasing the proportions of cell populations while ensuring high live cell recovery and robust compatibility with cell hashing for multi-modal single-cell analysis.

KEY HIGHLIGHTS

LeviCell enhanced the quality of challenging samples for scRNA-seq

- 5x increase in cell recovery compared to using FACS
- Preservation of cell populations and subtypes
- Superior signal-to-noise ratio for cell hashing results

Enhanced Multi-Modal Analysis With LeviCell

To fully evaluate the performance of LeviCell for single-cell multi-modal analysis of challenging samples, four human gut tissue samples were processed for sequencing using cell hashing to obtain a single pooled sample. The pool was divided into two workflows, one without viability enrichment and one using LeviCell. The two obtained samples were processed for scRNA-seq, and, at data analysis, the cells were traced back to each of the four originating samples. LeviCell-processed sample data exhibited a better signal-to-noise ratio, yielding cleaner data (Figure 1A).

Representation Matters: Preserving Cell Types

One concern with any cell viability or subtype enrichment process is the risk of preferential enrichment or depletion due to specific cell fragility and subsequent death. Upon applying quality control metrics to the same human gut tissue sample datasets, the LeviCell data recapitulated cell subtype representation of the heterogeneous populations present in the human gut as accurately as the non-LeviCell data (Figure 1B).

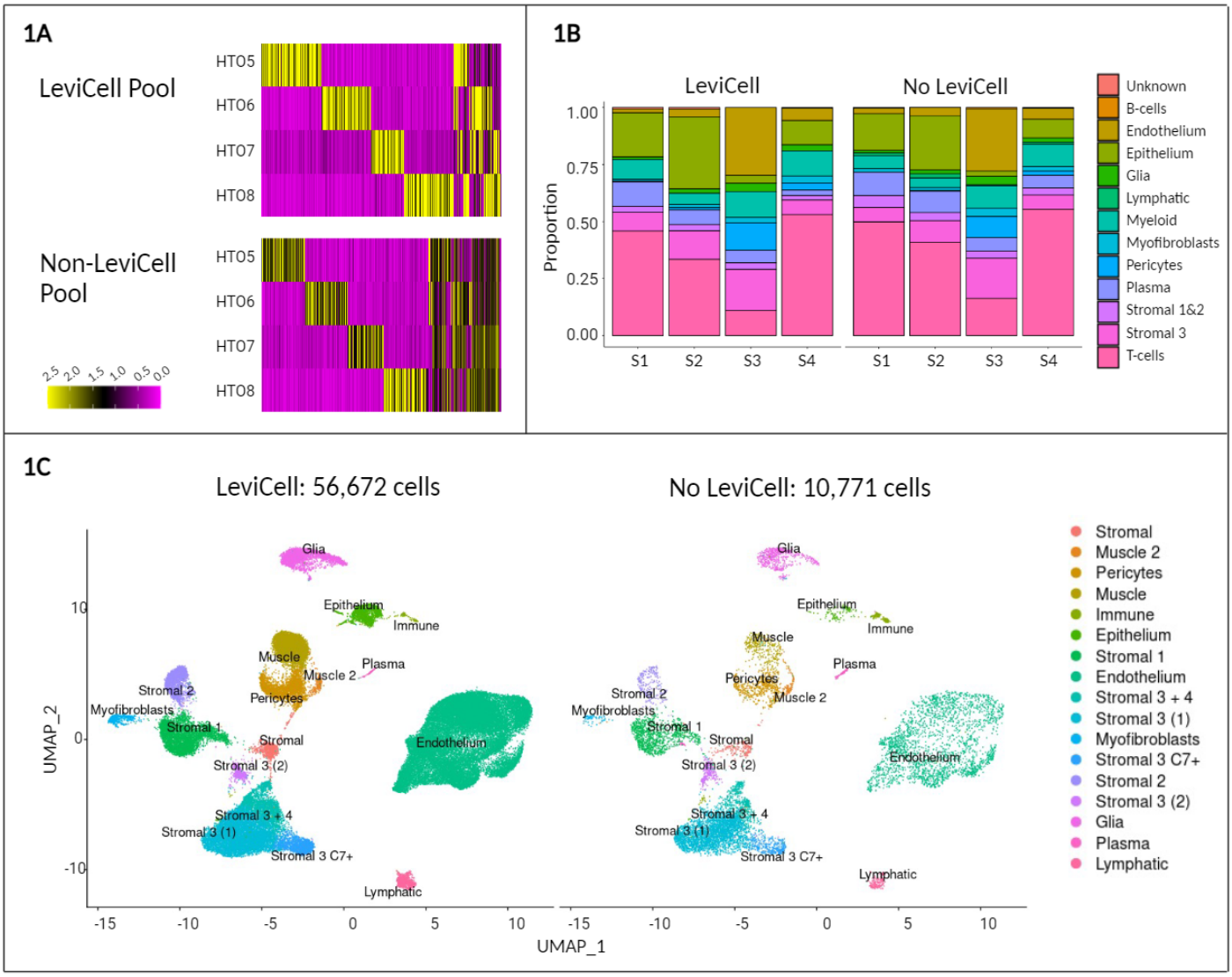

Figure 1. A. Heatmaps of hashtag oligo (HTO) demultiplexing results shows that the sample pool processed using LeviCell exhibited higher signal-to-noise ratio than the pool that omitted LeviCell processing. B. LeviCell data effectively replicated the diversity and representation of all cell subtypes observed in the non-LeviCell data. C. LeviCell data generated around 5x more high-quality single-cells as compared to FACS ("No LeviCell") when using challenging and sensitive human gut biopsy samples.

Rescuing Challenging Samples to Yield High-Quality Data

LeviCell's robustness was further tested using samples that had previously suffered from low cell yields when using FACS, generating poor-quality data (Figure 1C). The results were stark: LeviCell samples generated 5x more high-quality single-cell data than FACS, demonstrating LeviCell's benefits when working with challenging samples.

Conclusions

The transformative potential of LeviCell for multi-modal single-cell analysis is clear. It significantly boosted cell yield and quality of scRNA-seq data, from these challenging samples, without biasing cell subtype representation. LeviCell outperformed alternative methods, translating into cost savings and improved data quality.