TECHNICAL NOTE

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Unlocking the Power of Single Cell Analysis

Introduction

Single-cell RNA sequencing (scRNA-seq) is a transformative technology empowering scientists to delve into the transcriptomes of individual cells, and unravel the information of cellular identities, functions, and interactions. With the advent of scRNA-seq, scientists can now peer into the rich landscape of gene expression variations, revealing rare cell types, transitional states, and dynamic responses to stimuli with single-cell resolution.

Overall, scRNA-seq has paved the way for significant advancements across diverse disciplines such as developmental biology, cancer research, neuroscience, immunology, drug discovery and development, and more. Its potential applications extend to driving the progress in personalized medicine and disease treatment.

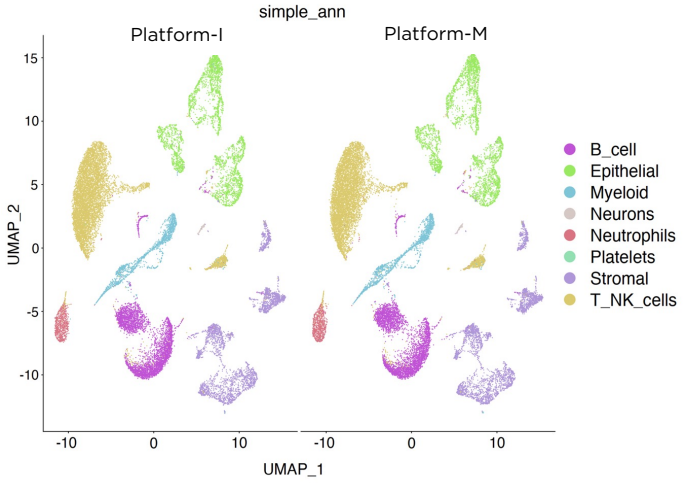
Mirxes offers a comprehensive sequencing solution for scRNA-seq libraries. In this Technical Note, we present a comparison of sequencing data generated by distinctive sequencing platforms from Company-M and Company-I respectively. Chromium Next GEM Single Cell 5' v2 libraries (10x Genomics) were obtained from a client and sequenced on Platform-I at the client's designated facility and Platform-M at Mirxes Genomics Lab.

Data analysis of datasets from both sequencers was conducted independently by the client

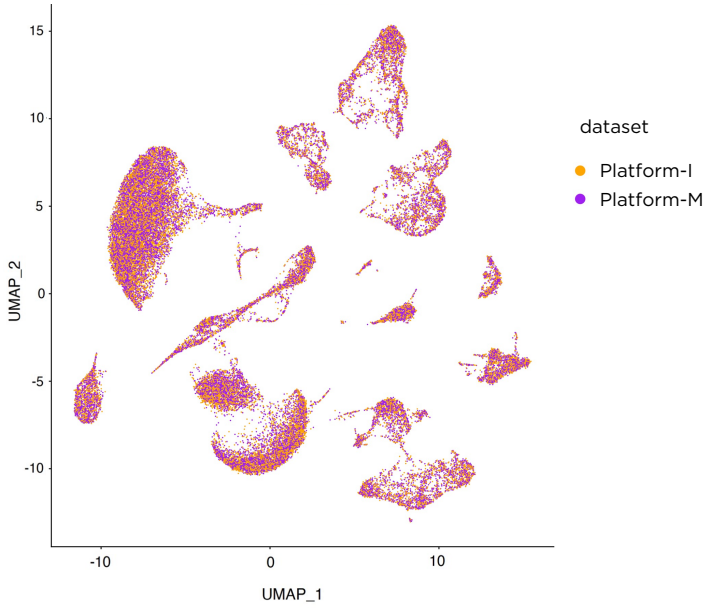
Parallel downstream analysis conducted on both datasets (Figure 1) unveiled a striking resemblance in performance of both platforms

QC metrics of datasets for both sequencers (Figure 2 and 3) demonstrated highly comparable sequencing quality across platforms

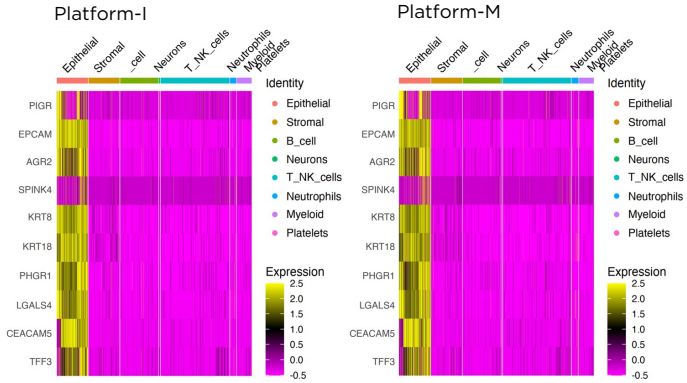
Figure 1: In the downstream analysis, the two datasets exhibited nearly perfect overlap in UMAP plots and shared highly identical gene expression profiles. Analysis is shown for one of the 5' GEM libraries.



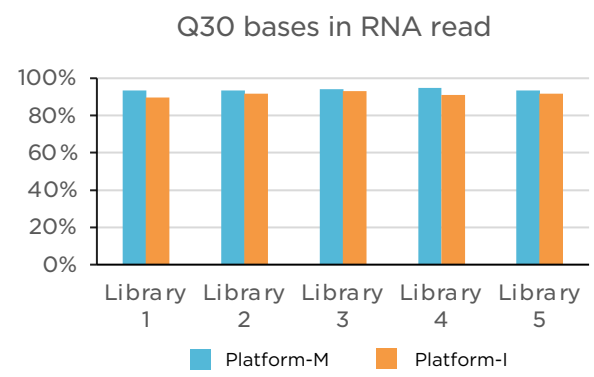
A) UMAP plot projecting cell types detected using SingleR

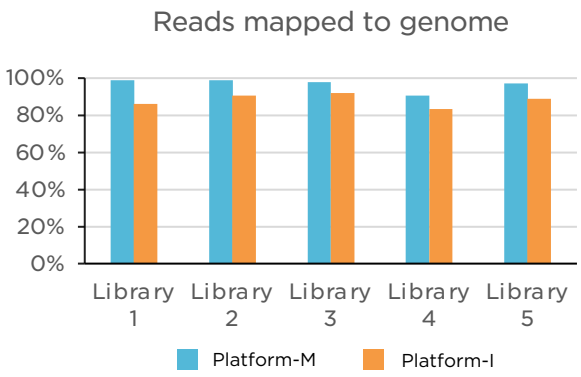


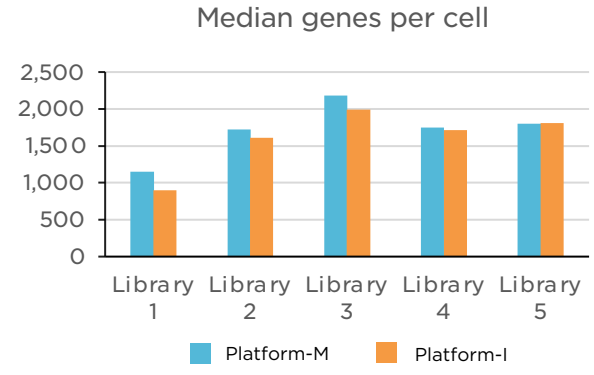
B) Merged UMAP plot for both datasets

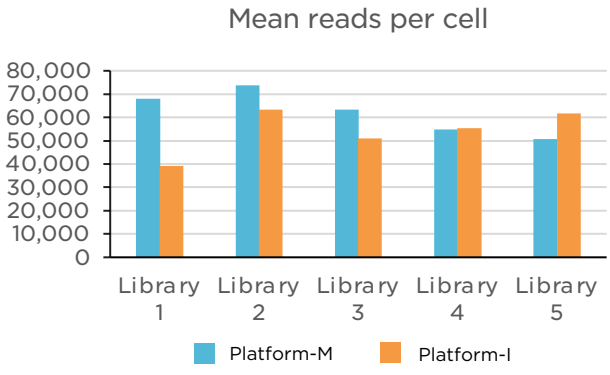


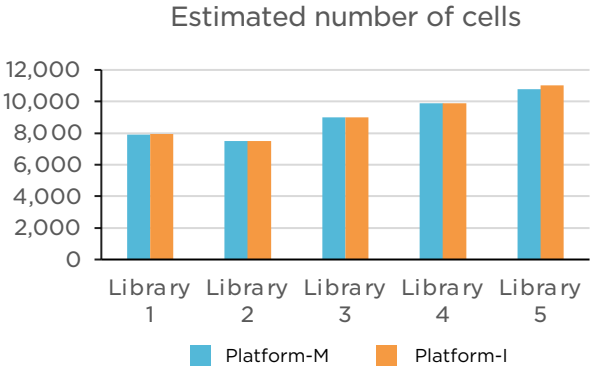
C) Heatmap showing expression profiles of epithelial marker genes











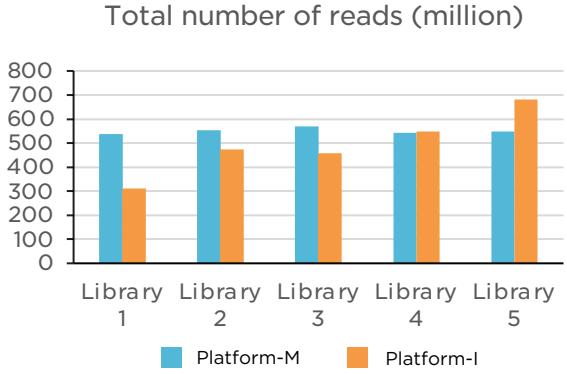
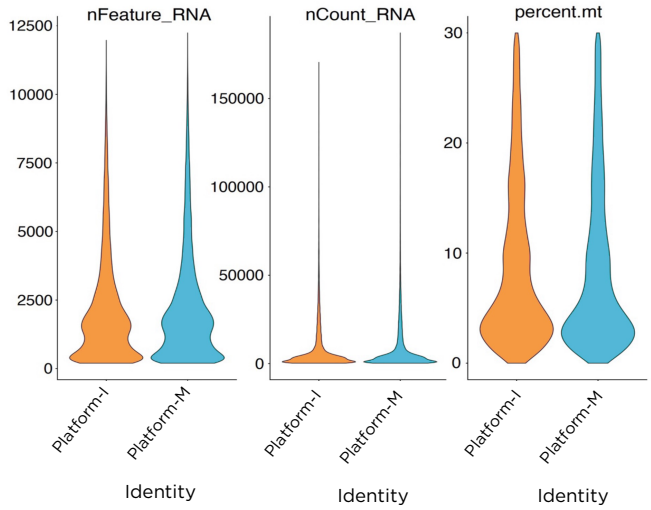
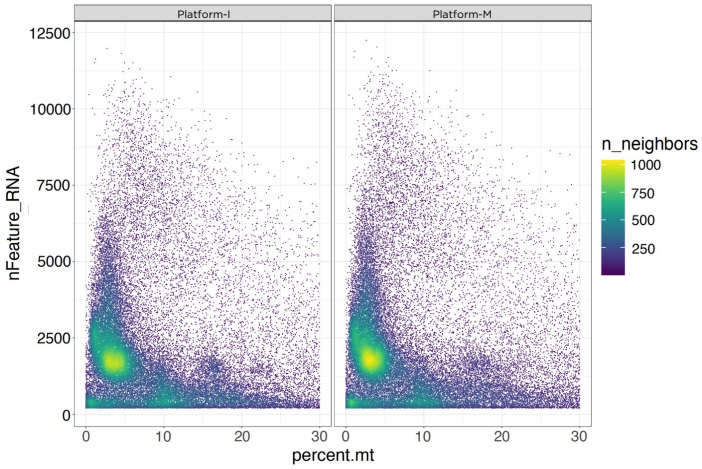


Figure 2: The two datasets showed similar sequencing quality Q30 scores in RNA read. Platform-M consistently achieved a high percentage of reads mapped to the genome. Overall, there was no significant difference observed between the two datasets, suggesting that the performance of the two sequencing platforms is comparable.

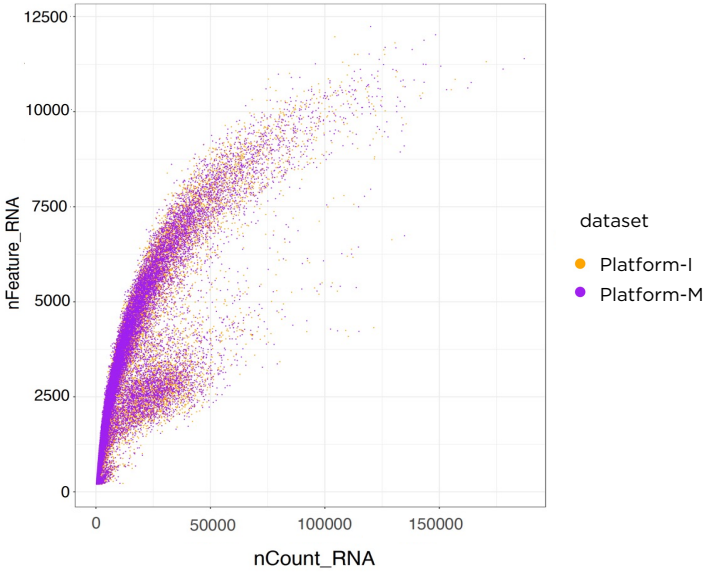
Figure 3: There was high similarity in sequencing quality metrics of the datasets from both sequencers. Data is shown for one of the 5' GEM libraries.



A) Distribution of unique genes, total UMI counts, and percentage of mitochondrial genes



B) Scatter plot depicting the relationship between the unique genes and total UMI counts



C) Scatter plot depicting the relationship between the unique genes and percentage of mitochondrial genes

Conclusion

The analysis revealed no significant difference between both sequencers in terms of the base quality scores, the number of detected genes per cell, and the percentage of reads mapped to the genome. This observation highlights the comparable performance of both platforms in terms of data quality and alignment accuracy.

The downstream analysis further strengthens these findings, as evidenced by the nearly perfect overlap of cells in the UMAP plot and the highly similar gene expression profiles. These compelling results provide additional support for the striking resemblance between the two datasets, further substantiating the notion of equivalent performance.

In summary, the comprehensive evaluation of sequencing outcomes obtained from the two datasets suggest a lack of discernible distinctions. These findings emphasize the remarkable similarity in performance between the two platforms, demonstrating their potential for achieving comparable results in single-cell RNA sequencing experiments.

Mirxes Service

Service	Sample Type	Optimum Input Amount	Volume	Library Concentration	Library Size
scRNA-seq sequencing	scRNA-seq libraries	≥ 200 ng	≥ 20 µl	≥ 2 ng/µl	200 - 700 bp

Please note that these requirements serve only as a guide. Please contact us for further assessment if your samples do not meet the requested amounts.

Bioinformatics Analysis and Support

Secondary Analysis Package:

- Sequence alignment file (BAM)
- Gene count matrix
- QC statistics (cell barcode, UMI, and alignment statistics)

Additional Tertiary Analysis:

- Data curation
- Clustering
- Annotation
- DEG
- Pathway analysis
- CNV (for tumor)
- Pseudo-temporal analysis
- **Many other options!**

Contact Us

Email: us-sales@mirxes.com **Website:** mirxes.us

This Technical Note includes client's unpublished data. Data analysis and comparison are conducted and provided by the client and are printed with client's permission.