

# Single Cell Data Analysis Made Easy with Trailmaker™

## Turn single cell RNA sequencing data into meaningful insights

Single cell RNA-sequencing (scRNA-seq) is revolutionizing our understanding of cellular diversity and complexity, yet extracting biological insights can be arduous, time-consuming and confusing for non-experts. Trailmaker has been developed to make data analysis accessible and transparent, so that you can focus on scientific discoveries and publish your research faster.

Trailmaker enables users to process, integrate, explore, plot, and share Evercode data anytime and anywhere at the push of a button.

1

### Push-button Analytics

User-friendly modules accessible to anyone without the need for coding skills

2

### Interactive Insights

Assess quality, adjust filtering thresholds, annotate cell types and visualize a range of gene expression plots

3

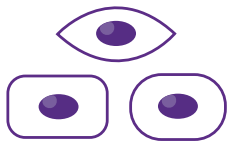
### From FASTQ to Figures

Import raw FASTQ files or data from different technologies, and export publication-ready figures

## FROM SAMPLES TO BIOLOGICAL INSIGHTS

Our end-to-end workflow guides you from samples to discoveries, offering flexible entry, stopping, and exit points throughout the entire process, from sample preparation to data analysis.

Evercode Cell/Nuclei  
Fixation



Evercode Combinatorial  
Barcoding Kits



Sequencing



Trailmaker Pipeline  
Module



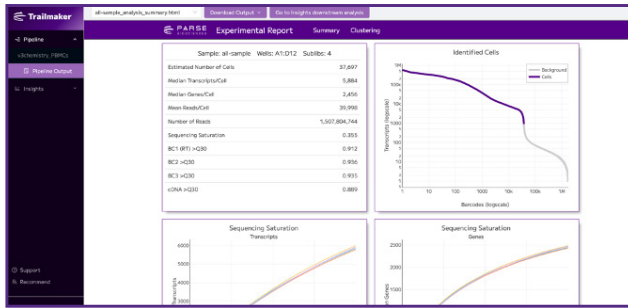
Trailmaker Insights  
Module



**Figure 1. Complete Solution for Single Cell RNA-seq Insights.** Evercode Fixation products ensure sample integrity, facilitating seamless handling and storage until batch processing. Evercode products enable scaling up sample and cell numbers per experiment with combinatorial barcoding, surpassing previous technology limitations. After sequencing, the Trailmaker Pipeline Module transforms raw data into count matrices, HTML reports, and log files. Finally, the Trailmaker Insights Module guides users from count matrices to customizable, interactive, and publication-ready figures.

# Interactive User-friendly Pipeline and Insights Modules

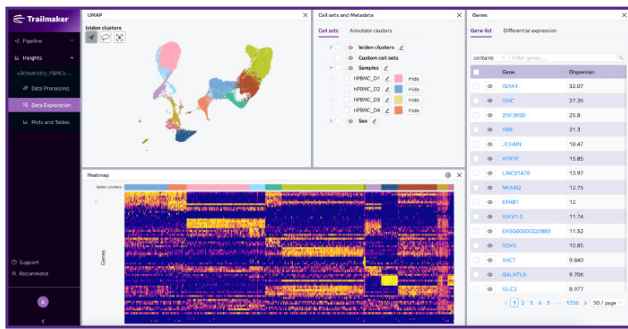
## Trailmaker Pipeline Module for FASTQ File Processing



## Trailmaker Insights Module for Downstream Analysis and Visualization



**Figure 2. Two Intuitive Modules Dedicated to Processing and Exploring Single Cell Data.** The Trailmaker Pipeline Module imports raw sequencing data (FASTQ files) together with the sample loading table and reference genome, outputting quality control reports, count matrices, and log files. The fully integrated Insights Module then leads users from count matrices through standard data QC and exploration to fully customized publication-ready figures. Flexible data entry and exit points across both modules enable seamless integration with existing workflows, whilst data sharing capabilities allow efficient and productive collaboration between bench scientists and bioinformaticians.



**Figure 3. Powerful data exploration generates insights into cell types and gene expression profiles.** UMAP plots can be colored by cluster, sample, and metadata of gene of interest; heatmap shows marker genes by default and can be customized to display gene profiles across groups; while differential expression comparisons and pathway analysis reveal the impact on biological function. All components are customizable and interconnected.

## GET STARTED WITH TRAILMAKER

Essential links for access and support

<https://app.trailmaker.parsebiosciences.com>

Create an account and start your analysis today!

FREE

<https://parsebiosciences.com/support-suite>

For more information and support  
[support@parsebiosciences.com](mailto:support@parsebiosciences.com)

## WATCH TRAILMAKER TUTORIAL VIDEO



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