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 Whole Transcriptome 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.
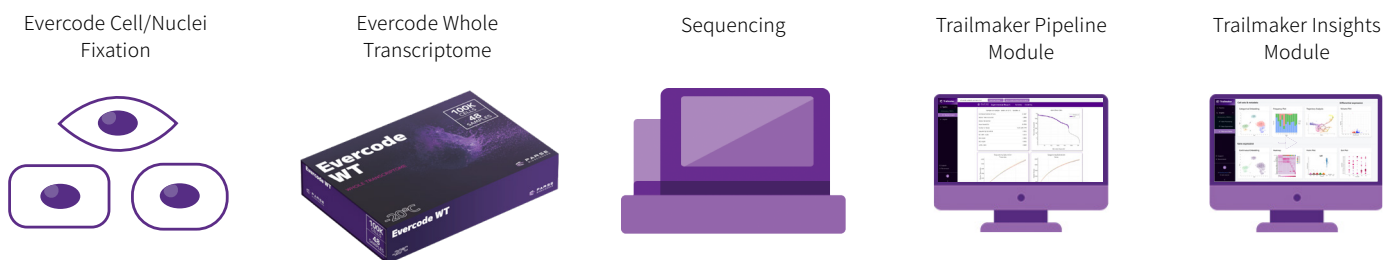
Evercode Cell/Nuclei Fixation

Evercode Whole Transcriptome

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 Whole Transcriptome 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.

PARSE BIOSCIENCES

Interactive User-friendly Pipeline and Insights Modules
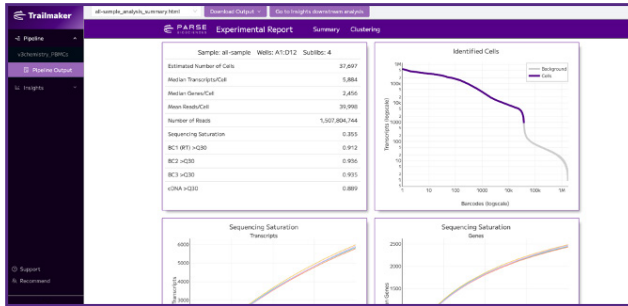
Figure 2. Two Intuitive Modules Dedicated to Processing and Exploring Single Cell Data. The Trailmaker Pipeline Module imports raw sequencing data (FASTQ files) together with the sample loading table and reference genome, outputting quality control reports, count matrices, and log files. The fully integrated 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.
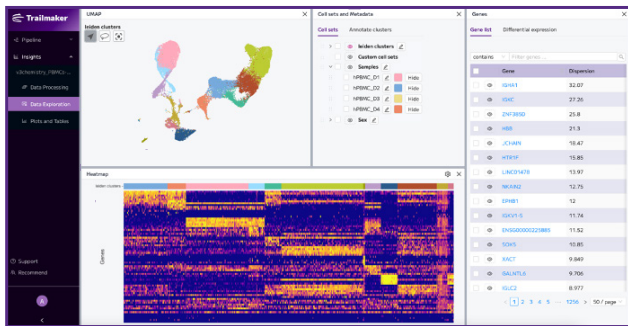

Figure 3. Powerful data exploration generates insights into cell types and gene expression profiles. UMAP embedding plot can be colored by cluster, sample, and metadata or gene of interest; heatmap shows marker genes by default and can be customized to display gene profiles across groups; while differential 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

WATCH TRAILMAKER TUTORIAL VIDEO

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