Evercode™ Whole Transcriptome

Scalable Single Cell Sequencing, No Instrument Required

Easy to Get Started
Flexible Workflow
Unmatched Sensitivity

PARSE
BIOSCIENCES

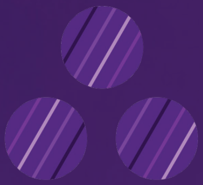
Single Cell RNA-Seq in Any Lab

Simple Workflow

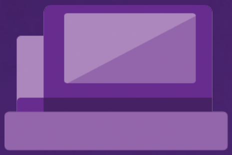
An instrument-free workflow takes isolated cells or nuclei to biological insights

1. **Fixation of Cells or Nuclei**

2. **Barcoding and Library Prep**



3. **Sequencing**



4. **Data Analysis**

No Instrument Required

Step away from the limitations of hardware-based offerings for a more elegant solution to single cell RNA sequencing (scRNA-seq) and single nuclei RNA sequencing (snRNA-seq).

Exponentially Scalable

Evercode's combinatorial barcoding enables you to dramatically scale up the cells and samples per experiment.

Unmatched Data Quality

Better detect lowly expressed genes and avoid ambient RNA common in droplet-based single cell sequencing.

No Instrument Required

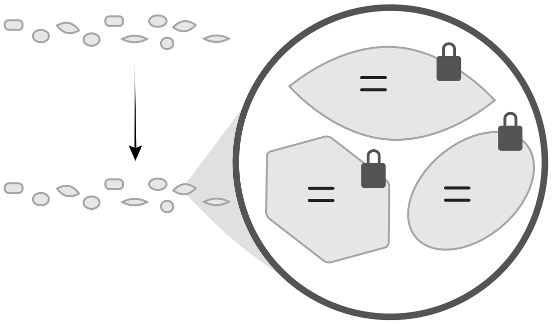
If you have a centrifuge, thermal cycler, and some pipettes, you’re ready to go.

Cell and Nuclei Fixation

Fix and store samples as they come in for up to 6 months and then run together later on your schedule. Ideal for time-courses and cross-site collaborations.

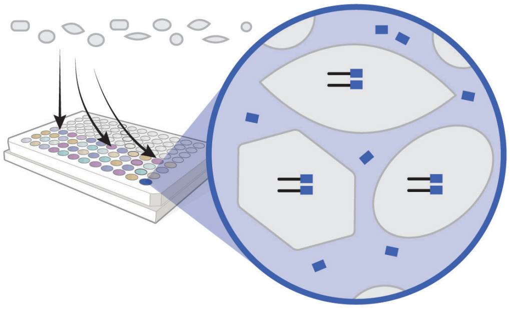
Fixation

Cells/nuclei samples are fixed and permeabilized.



Barcoding Round 1

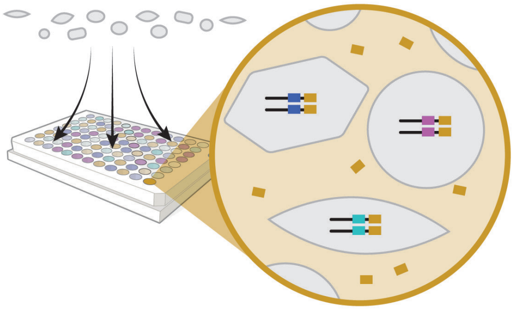
Split | Fixed cells/nuclei are distributed into wells, and the first sample-specific barcodes are added by in-cell reverse transcription.



Pool | All the cells are pooled together.

Barcoding Round 2

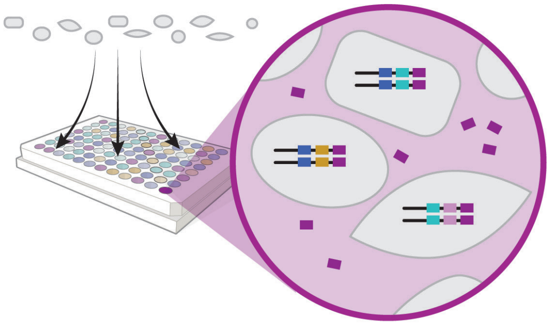
Split | The pooled cells are distributed across a plate, and an in-cell ligation adds the second barcode.



Pool | All the cells are pooled together.

Barcoding Round 3

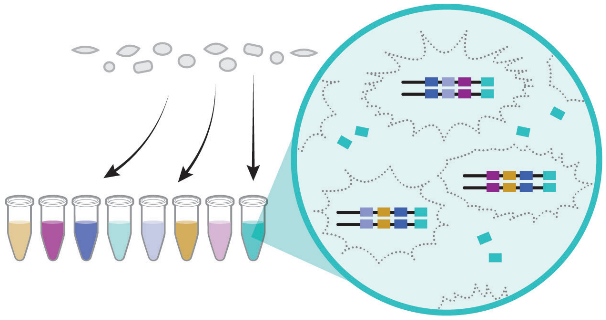
Split | The pooled cells are again distributed across a plate, and a third barcode is added via in-cell ligation reaction.



Pool | All the cells are pooled together.

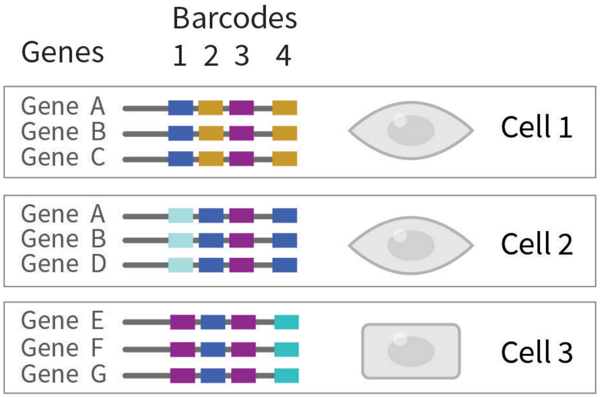
Lysis and Library Prep

Split | The pooled cells are distributed across several sublibraries then lysed. The fourth barcode is added via PCR.



Sequencing and Analysis

Each transcript is assigned to a single cell based on a unique combination of barcodes.



No Instrument Required with Combinatorial Barcoding

The Cell Is the Reaction Compartment

Cells are first fixed and permeabilized, turning them into their own reaction vessels, removing the need to capture individual cells in droplets or microwells. The split-pool barcoding process then labels cells with an exponentially large number of barcode combinations making it possible to easily scale beyond other technologies.

Single Cell Data Analysis Made Easy with Trailmaker

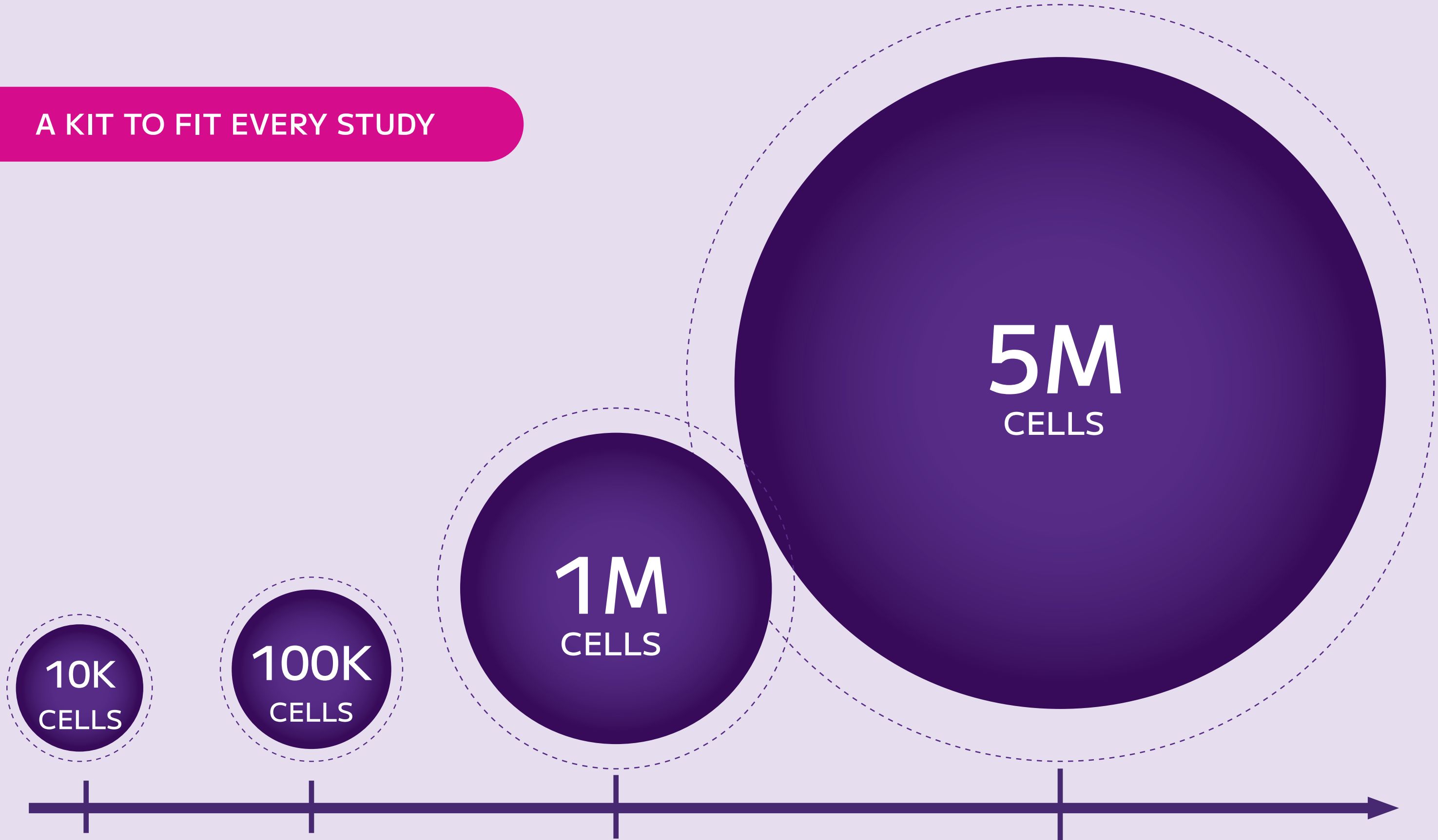
Every kit comes with our data analysis platform, Trailmaker™, which transforms sequencing output (FASTQ) into understandable results and publication-ready figures. Trailmaker enables users to process, integrate, explore, plot, and share Evercode Whole Transcriptome data anytime and anywhere with push-button analytics.

Seamlessly Scale Your Single Cell Projects

From Pilot to Millions of Cells & Hundreds of Samples

Regardless of scale, Evercode technology has a kit to fit every study. Whether you want to generate proof of concept results or perform cell atlassing studies, our technology labels cells with thousands to millions of barcode combinations making it possible to easily scale beyond other technologies.

A KIT TO FIT EVERY STUDY



Evercode WT
UP TO 12 SAMPLES
Generate proof of concept data

Evercode WT
UP TO 48 SAMPLES
Comprehensive gene profiling across samples, replicates, or timepoints for most studies

Evercode WT Mega
UP TO 384 SAMPLES
Expand your science by profiling up to 1 million cells per run across 100s of conditions or samples

Evercode WT Penta
UP TO 384 SAMPLES
Discover previously unknown cell types and subtypes with the power of characterizing up to 5 million cells

Fix Now. Run Later.

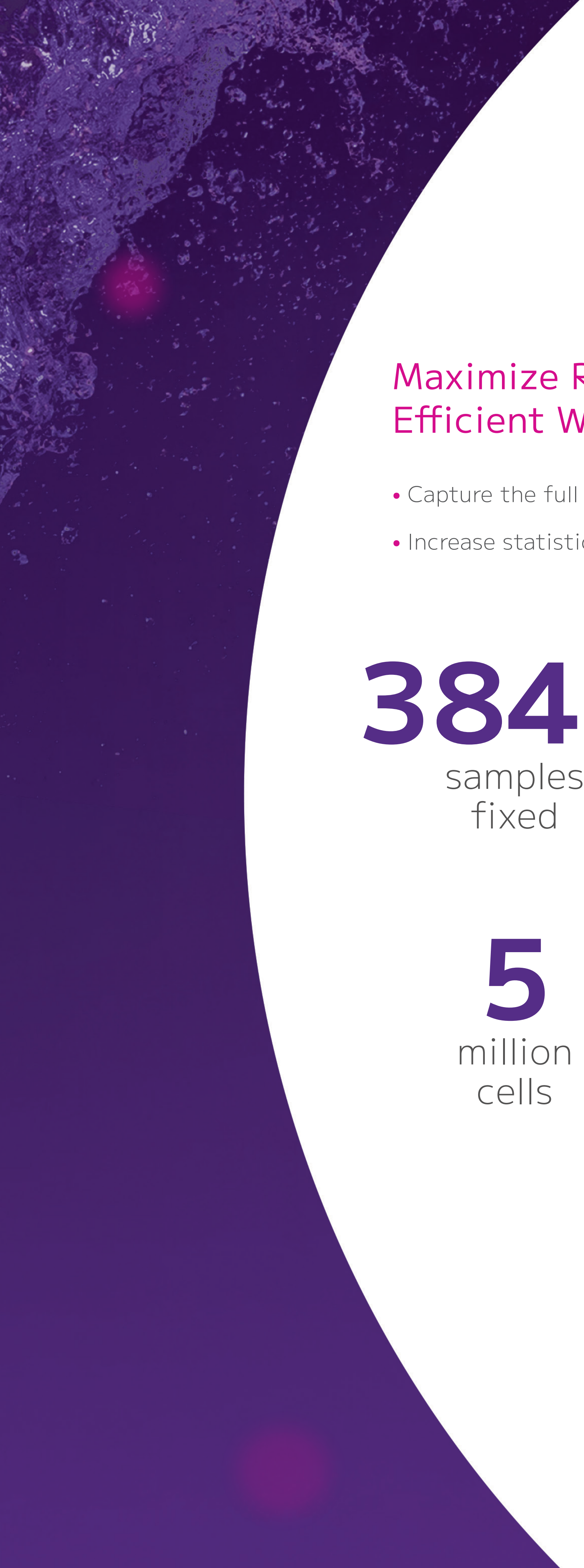
Many studies require collection of samples over time, and increasingly require larger sample and cell numbers. Evercode Fixation gives you the flexibility to stabilize a wide range of sample types at the point of collection, preserving transcriptional profiles and enabling storage for up to 6 months until they can be processed all together.

Fixation of Nuclei and Cells

Easily work with collaborators and service providers

Minimize bias from batch effects

Conduct time-course studies conveniently



Maximize Research Impact Through Efficient Workflow

- Capture the full heterogeneity of complex samples
- Increase statistical power by including more replicates

384 samples fixed » **1** hour

5 million cells » **2** days

Effortlessly Scale to Millions of Cells

5,011,382 NUCLEI IN 1 EXPERIMENT

Evercode™ Whole Transcriptome paired with our fixation enables the collection, preservation, and profiling of millions of cells across tissues and conditions in a single experiment.

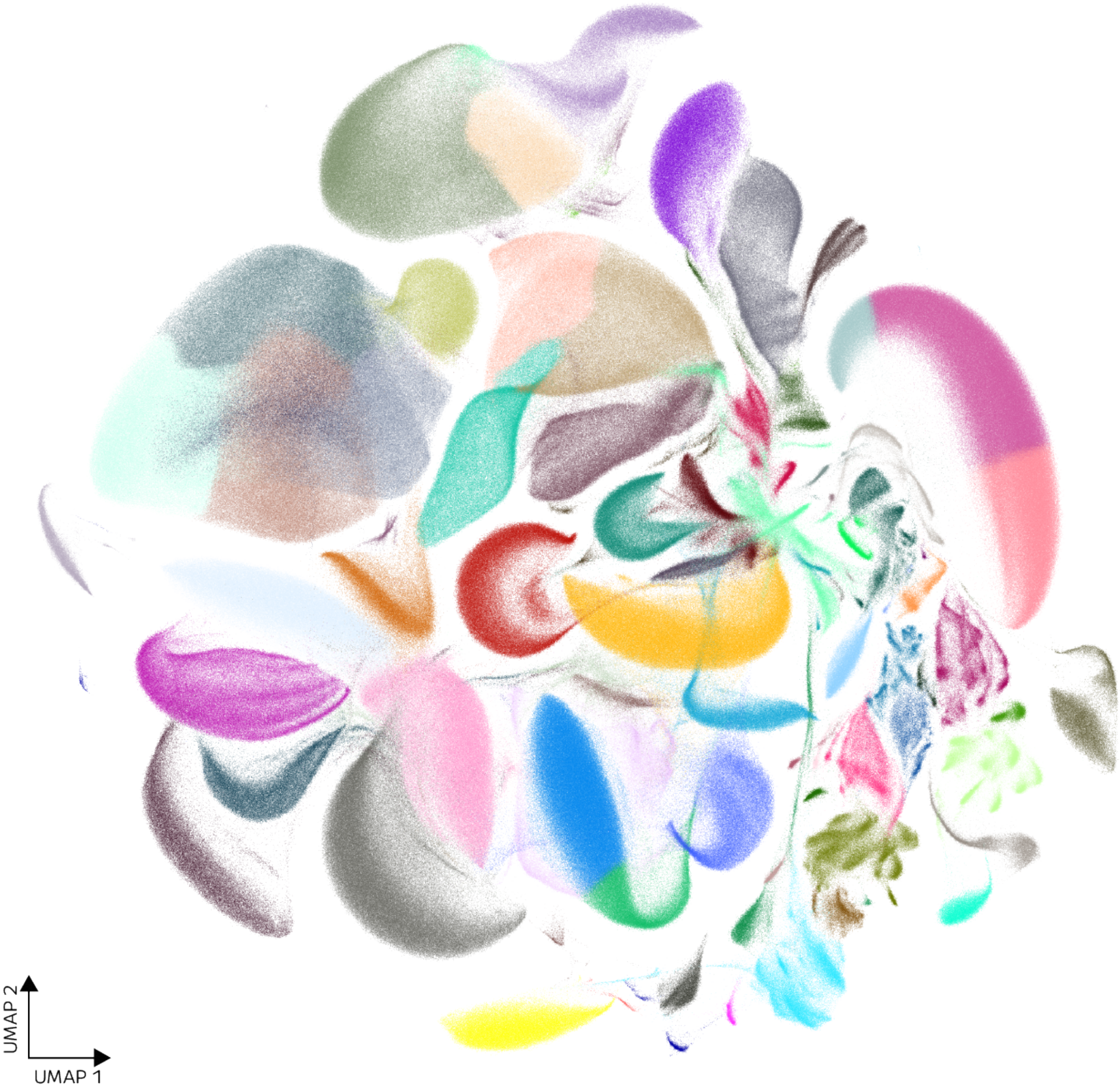


Figure 1. UMAP of 5 Million Mouse Nuclei. Nuclei isolated from seven flash-frozen mouse tissues were processed using Parse Biosciences' Evercode Nuclei Fixation v3 and WT Penta kits, enabling the construction of a cross-tissue single cell transcriptomic atlas. Clustering and annotation of the 5,011,382 cells revealed a rich landscape of cell types and states across major organ systems.

The Most Scalable Technology

More Cells, More Samples, One Kit

Parse Biosciences Evercode combinatorial barcoding technology scales exponentially without increasing effort or risking batch effects. Droplet-based assays are limited by scaling linearly.

Pilot Project
40,000 cells

Evercode WT

1 Chip
Chromium GEM-X
v4 3' Kit

Average Published Study in 2024
~1,000,000 cells

Evercode WT
Mega

7 Chips
Chromium GEM-X
v4 3' Kit

Cell Atlas
5,000,000 cells

Evercode WT
Penta

32 Chips
Chromium GEM-X
v4 3' Kit

More Genes, Less Sequencing

Evercode™ Whole Transcriptome v4 enables comprehensive, unbiased transcript detection across the full transcriptome. By capturing more usable biological signal per read, v4 delivers higher transcript detection at matched sequencing depths.

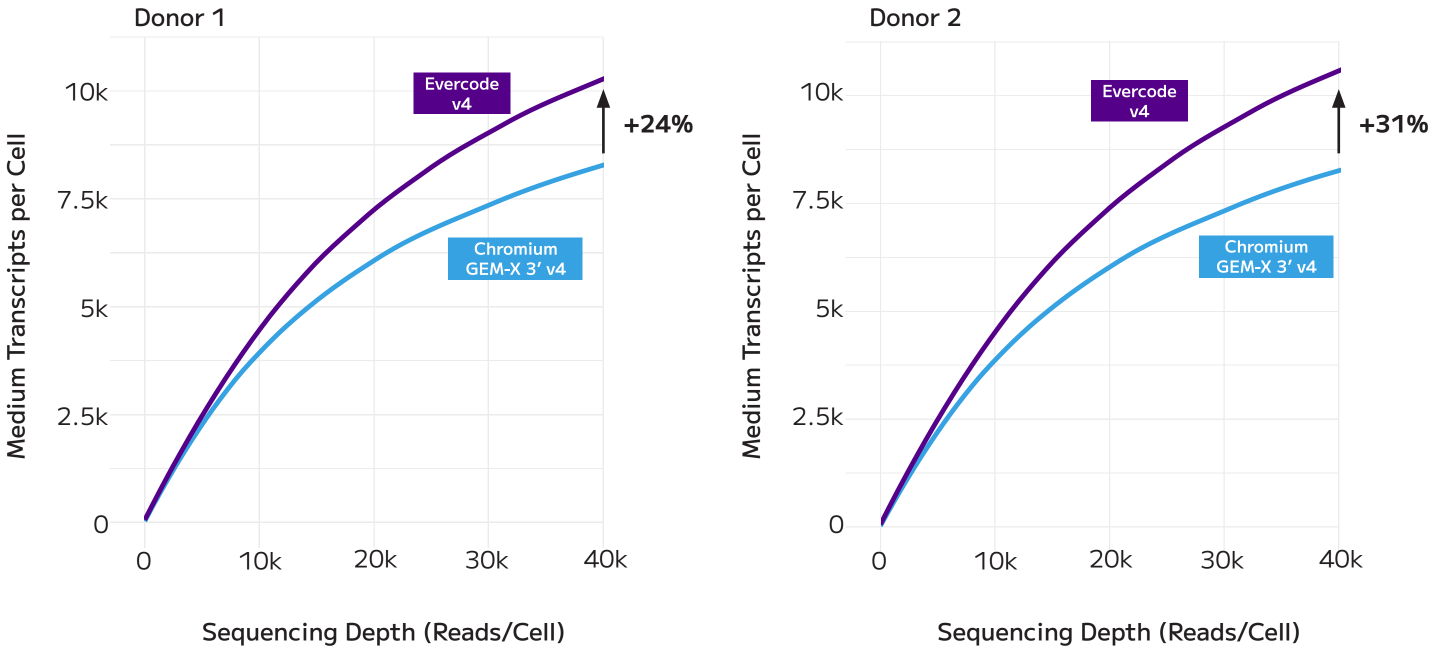


Figure 2. Transcript Detection. Median transcripts detected per cell in PBMCs across different sequencing depths for two donors; donor 1 (left) and donor 2 (right). Aliquots for each donor were split and sent to different laboratories for processing with either Evercode WT v4 or Chromium GEM-X 3′ v4 technologies and analyzed by their respective data analysis pipelines.

Transition Seamlessly to Evercode

Integrates with Existing Data

Integration of the data from Evercode WT v4 and GEM-X 3′ v4 resulted in highly concordant clustering and cell proportions, indicating both technologies result in unbiased capture of cell types.

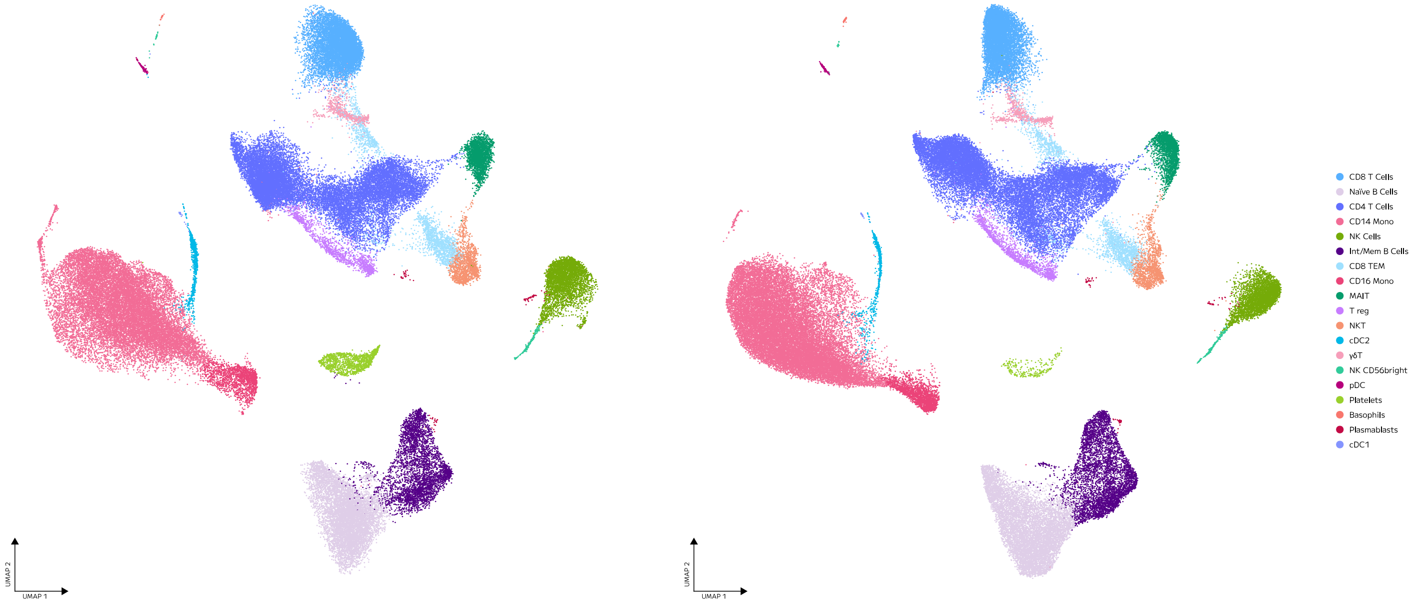


Figure 3. Integrated Evercode WT v4 and Chromium GEM-X 3′ v4 Clustering. Roughly 75,000 cells from Evercode WT v4 and and Chromium GEM-X 3′ v4 were integrated, clustered, annotated, and visualized separately in annotated UMAPs. Integration resulted in highly concordant clustering, with major annotated cell populations aligning across both UMAPs.

Preserved Cellular Integrity, Cleaner Data

Global stress-associated gene expression

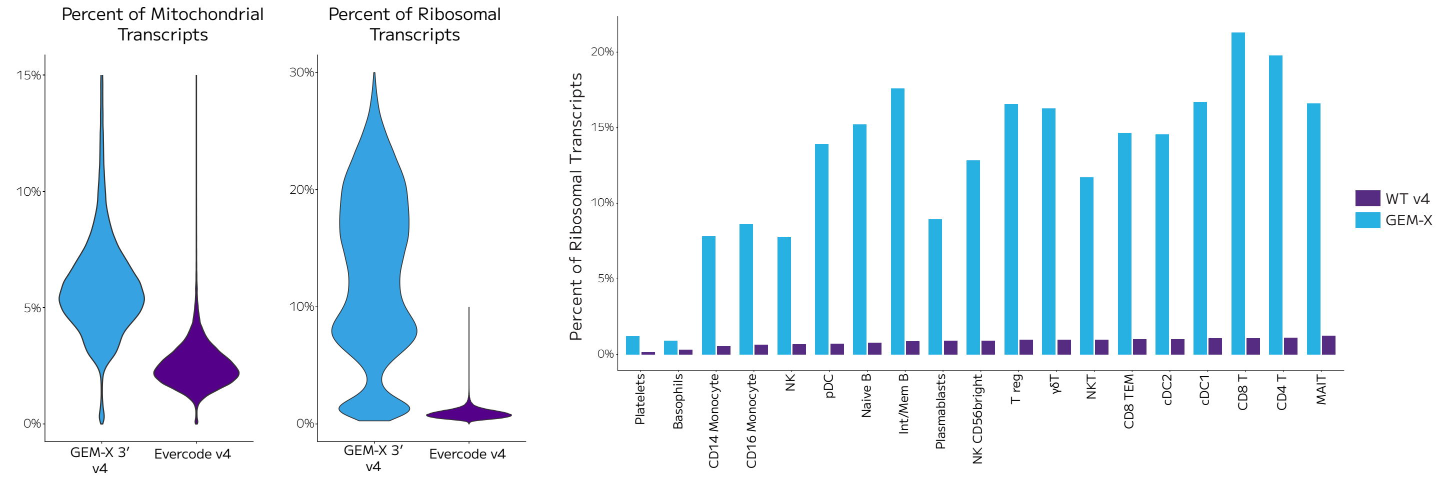


Figure 4. Increased Mitochondrial and Ribosomal Signal in Chromium GEM-X 3′ v4. Initial standard QC filtering has been applied for both technologies, including removing multiplets and filtering out cells with 10% or more mitochondrial transcripts to show what would still remain in both technologies. (A) Violin plots showing the distribution of mitochondrial and ribosomal reads across cells processed with Chromium GEM-X 3′ v4 and Evercode WT v4. (B) Ribosomal transcript percentages across cell-type clusters, showing consistently elevated ribosomal signal in Chromium GEM-X 3′ v4 across clusters, potentially reflecting increased cellular stress associated with sample processing constraints.

Comparison of ambient RNA across technologies

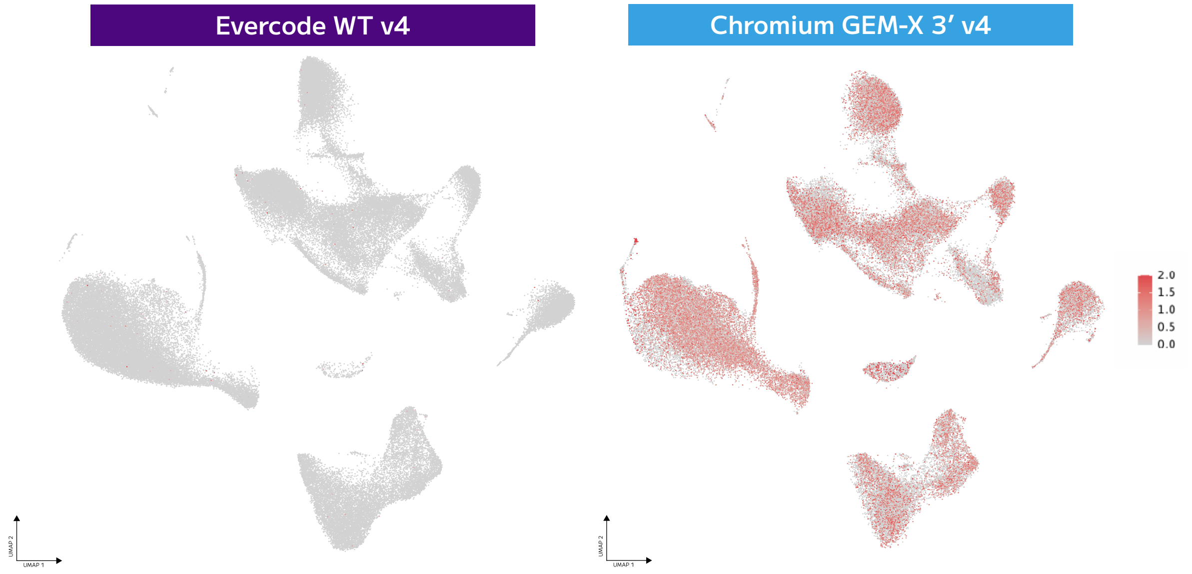


Figure 5. Reduced Ambient RNA Expression in Evercode. PBMCs processed with Evercode WT v4 and Chromium GEM-X 3′ v4 were independently clustered, annotated, and visualized using UMAP. Expression of hemoglobin beta (HBB) is shown for both technologies as a qualitative assessment of ambient RNA.

Analyze the Full Transcriptome

Detect More Genes

A complete understanding of gene regulation and disease biology requires looking beyond protein-coding transcripts. Chromium Flex v2 is designed to capture primarily protein-coding genes, limiting detection of other RNA biotypes. In contrast, analysis of median transcripts detected showed that Evercode WT v4 consistently detected more genes across all RNA biotypes, including protein-coding genes, providing a more comprehensive view of the transcriptome.

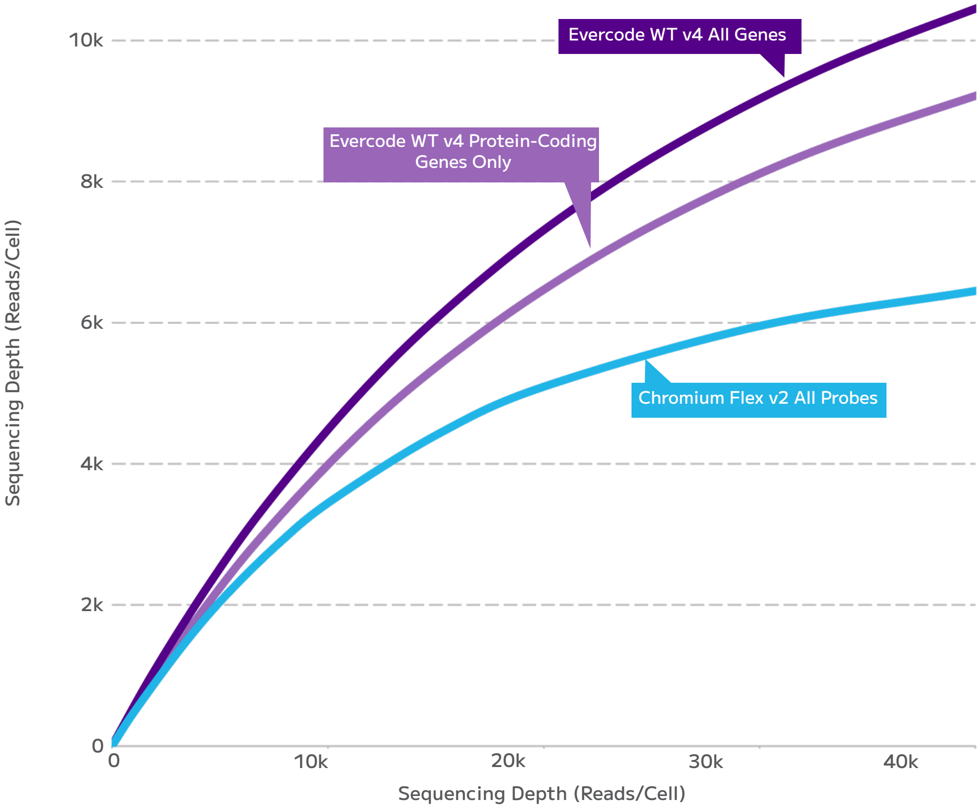
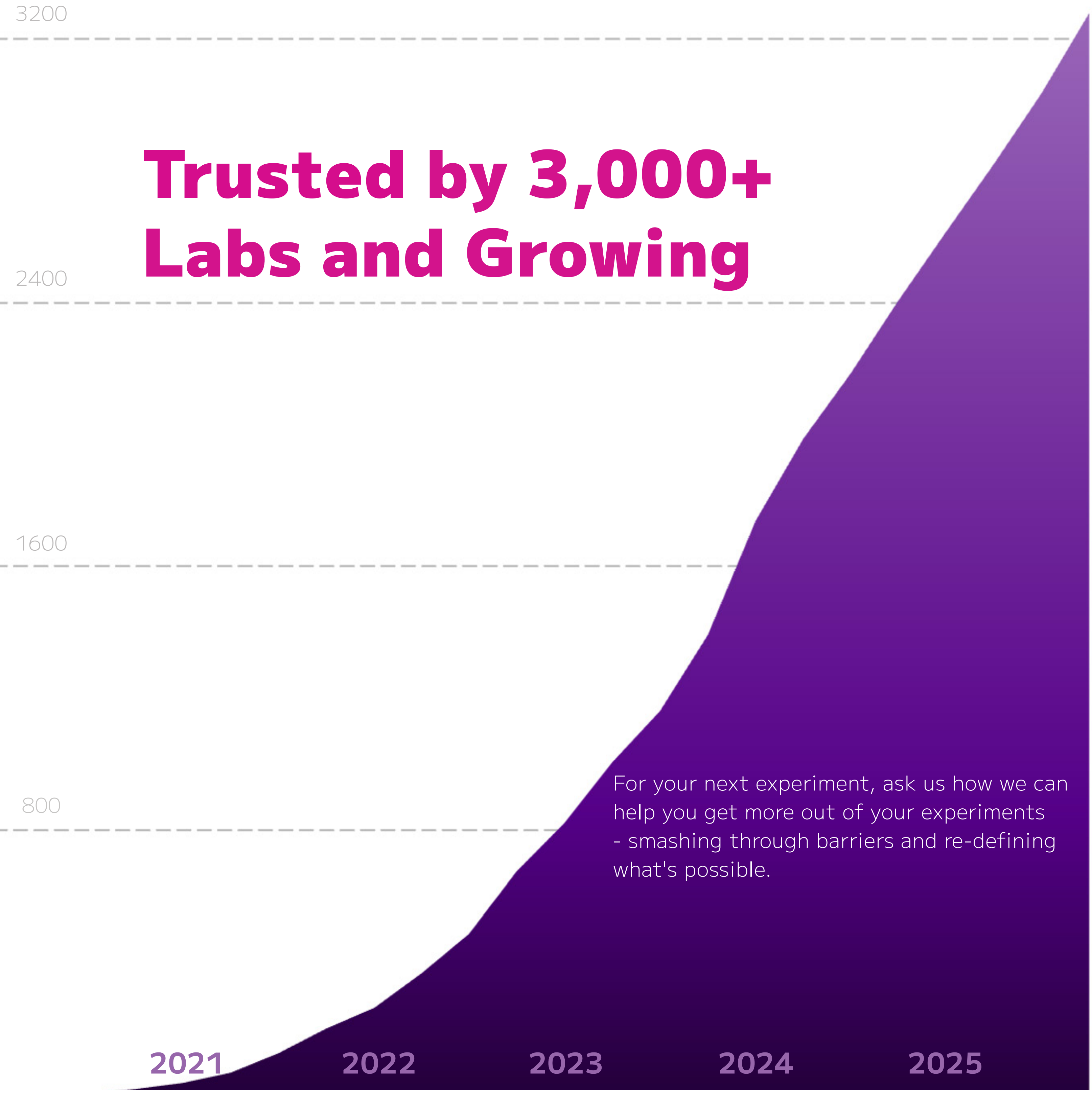


Figure 4. Detected Transcripts and RNA Biotypes Comparison. Total transcripts detected in human PBMCs across sequencing depths, including protein-coding genes and other RNA biotypes. Other biotypes comprise lncRNA, miRNA, snRNA, snoRNA, miscRNA, pseudogenes, and Ig/TCR genes.

Trusted by 3,000+ Labs and Growing



For your next experiment, ask us how we can help you get more out of your experiments - smashing through barriers and re-defining what's possible.

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PRODUCT	PART NUMBER
Evercode WT Mini v4 Up to 10,000 cells or nuclei and up to 12 samples	ECWT4100
Evercode WT v4 Up to 100,000 cells or nuclei and up to 48 samples	ECWT4300
Evercode WT Mega v4 Up to 1,000,000 cells or nuclei	
Up to 96 samples	ECWT4500
Up to 384 samples	ECWT4530
Evercode WT Penta v4 Up to 5,000,000 cells or nuclei	
Up to 96 samples	ECWT4700
Up to 384 samples	ECWT4730
Evercode Cell or Nuclei Fixation v4 Up to 1,000,000 cells or nuclei	
Up to 12 samples	ECFC4300
High throughput fixation for 96 samples	ECFC4501
Evercode Cell or Nuclei Low Input Fixation v4 Input as low as 10,000 cells or nuclei	
Up to 12 samples	ECLC4301
High throughput fixation for 96 samples	ECLC4501

More Cells, More Samples, More Clarity

parsebiosciences.com | **info@parsebiosciences.com**

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