

Evercode™ Whole Transcriptome

Scalable Single Cell Sequencing, No Instrument Required

Evercode™ split-pool combinatorial barcoding delivers unmatched scalability, flexibility, and data quality—without the need for complex instrumentation. Cells are fixed and permeabilized up front, turning them into their own reaction vessels and preserving the transcriptome at the moment of collection. This powerful approach allows researchers to batch and process samples on their own schedule and break free from the limitations of traditional single cell workflows.

The Cell
is the
Reaction
Compartment

- Flexible Scalability
- Unmatched Data Quality
- No Instrument Required
- Fix the Moment - Run it Later

INSIDE THE EVERCODE BARCODING WORKFLOW

The scale you want, the freedom to run on your terms—no instrument required.

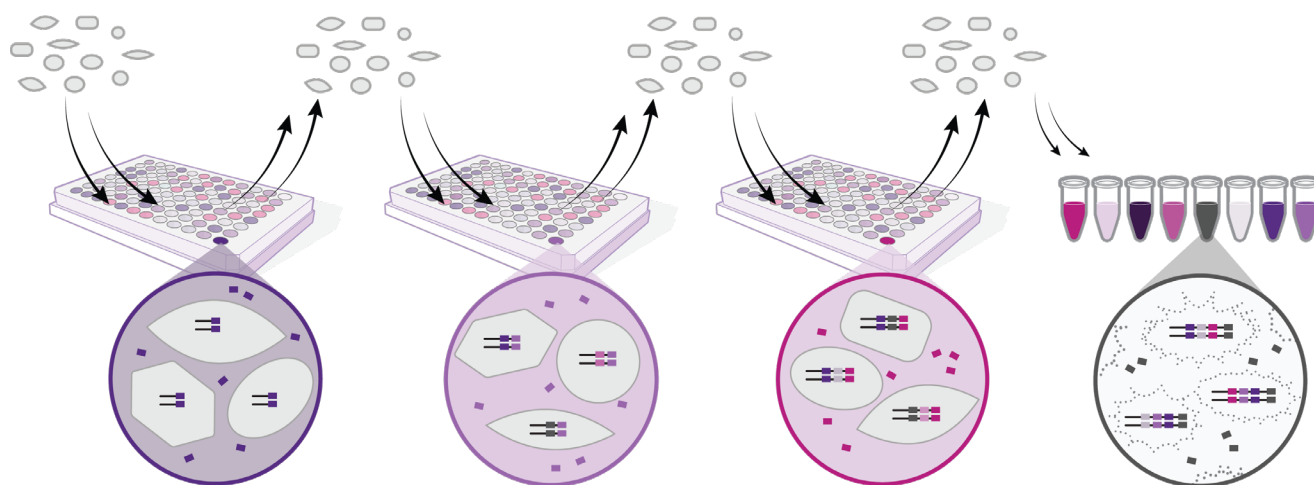


Figure 1. Combinatorial Barcoding Overview. Cells are first fixed and permeabilized, turning them into individual reaction vessels. Transcripts are labeled through multiple rounds of split-pool indexing, with barcodes added at each step. This process generates a unique barcode combination for every cell, enabling millions of single cell transcriptomes to be captured in a single experiment. After sequencing, the Parse analysis pipeline reconstructs individual cell profiles based on their barcode combinations.

A Better Way to Do Single Cell Sequencing

The Evercode workflow combines fixation-based prep, flexible scaling, and intuitive analysis built to work the way researchers do.



"The ability to store fixed frozen cells greatly simplified our time course experiment."

- Merrick Pierson Smela, Church Lab, Harvard University

"We detected rare cell types with Evercode's higher sensitivity."

- Yi Xie, Jacques Behmoaras & Enrico Petretto, Duke-NUS Medical School



"One assay works with all our samples, no matter the size."

- Zhenhe Zhang, University of Washington Medicine, Cardiology

"Parse has been a true partner, from data generation and technology to empowering the scientific community."

- Johnny Yu, CTO, Tahoe Therapeutics

Figure 2. UMAP of 5 Million Mouse Nuclei. Using Parse's Evercode Nuclei Fixation v3 and WT Penta kits, we profiled 5,011,382 nuclei from seven flash-frozen mouse tissues to generate a cross-tissue single cell transcriptomic atlas, revealing diverse cell types and states across organ systems.

A PRODUCT CONFIGURATION FOR EVERY SIZE OF EXPERIMENT

Easy to Use Whole Transcriptome (WT) Kits

Easy to Use Whole Transcriptome (WT) Kits				High Throughput Services
WT Mini	WT	WT Mega	WT Penta	GigaLab
10k cells up to 12 samples	100k cells up to 48 samples	1M cells up to 384 samples	5M cells up to 384 samples	10M-1B+ cells 1 - 1,000+ samples
Whole Transcriptome		TCR/BCR Profiling	CRISPR Screens	Gene Panels



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