

Evercode™ TCR

Single Cell Immune Profiling

T Cell Receptor + Whole Transcriptome
Up to 1 Million Cells

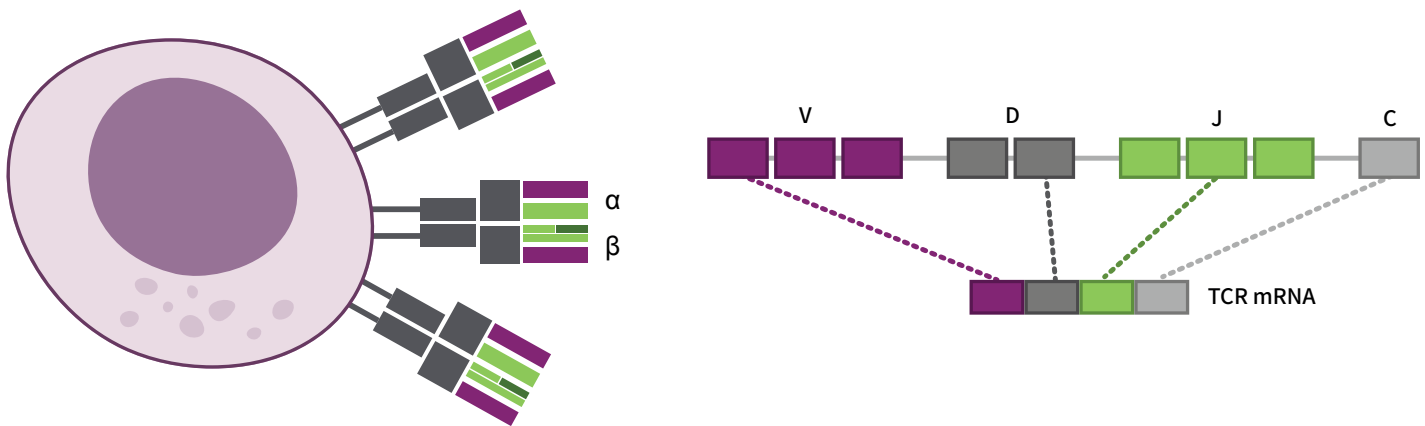
| UNMATCHED SCALE

| UNCOVER TCR DIVERSITY

| SENSITIVE DETECTION

T Cell Receptor (TCR) Profiling

T cells play a central role in the adaptive immune system. The T Cell Receptor (TCR) is a protein complex that enables recognition and response to an enormous breadth of antigens. Each TCR is composed of two chains that combine and add to the diversity of a possible receptor: the alpha chain (TCR alpha) and the beta chain (TCR beta). The enormous diversity of the TCR results from recombination of the variable (V), the diversity (D), and the joining (J) gene segments and the insertion of random nucleotides at junctions.



APPLICATIONS OF EVERCODE TCR

Explore a wide variety of adaptive immunity applications through Evercode TCR, which is capable of mapping paired TCR sequences in up to 1 million T cells together with their whole transcriptome profiles.

UNDERSTAND IMMUNE RESPONSE

Examine how different T cell subtypes respond to specific antigens

QUANTIFY IMMUNE REPERTOIRES

Detect paired alpha-beta chains to characterize the immune repertoire complexity

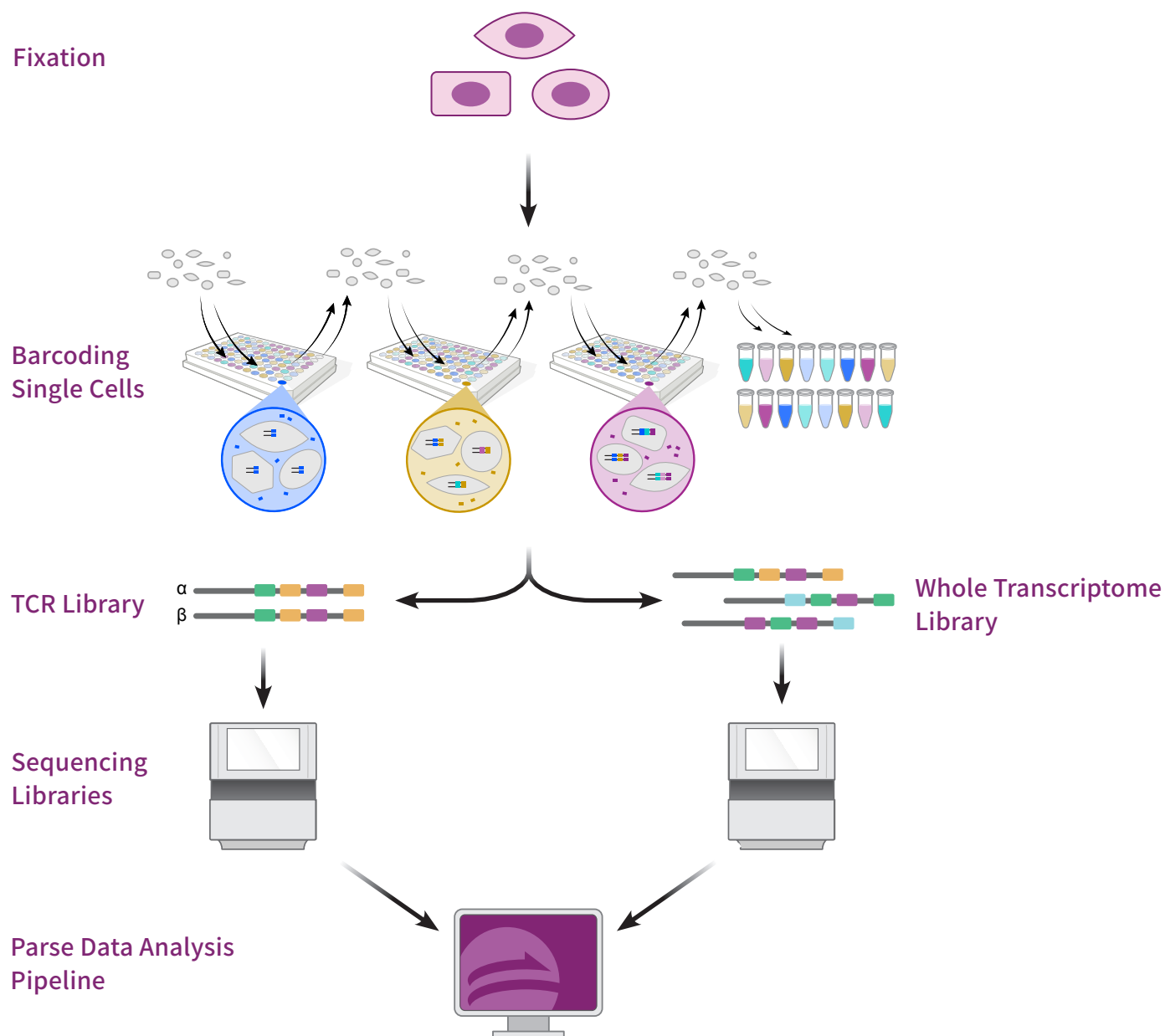
TRACK CLONOTYPES

Track clonotypes across time, tissue, and disease states

ADVANCE CELL THERAPIES

Understand impacts of T cell diversity for cell therapy

The Evercode Solution



HIGH TCR DETECTION IN ACTIVATED AND PRIMARY T CELLS

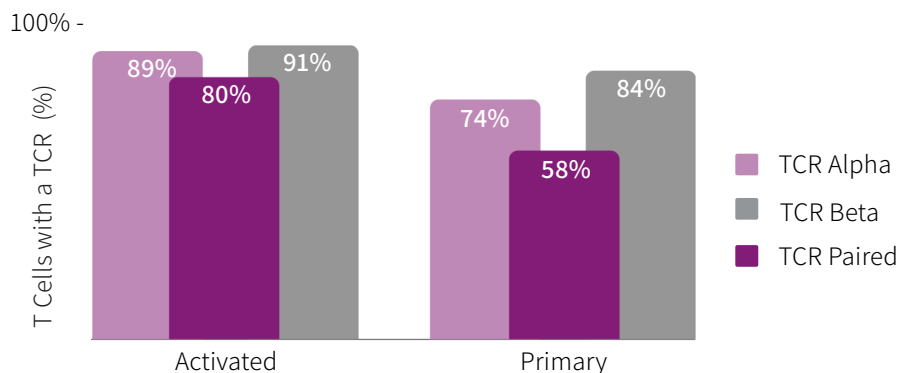


Figure 1: High TCR Chain Identification Rate.

Isolated T cells from healthy donor PBMCs were either directly profiled (Primary) or placed in culture for 3 days and activated with CD3/CD28 beads and IL-2 (Activated). Among T cells with a detected TCR, the cells profiled with the TCR alpha (light pink), TCR beta (grey), or both for the same cell (purple) are represented in percentages.

1 Million Cells in a Single Experiment

Scale matters: Capture the diverse immune repertoire with the power of 1 million T cells. The Evercode TCR Mega kit enables the study of TCR clonotype diversity and T cell states at an unprecedented resolution.

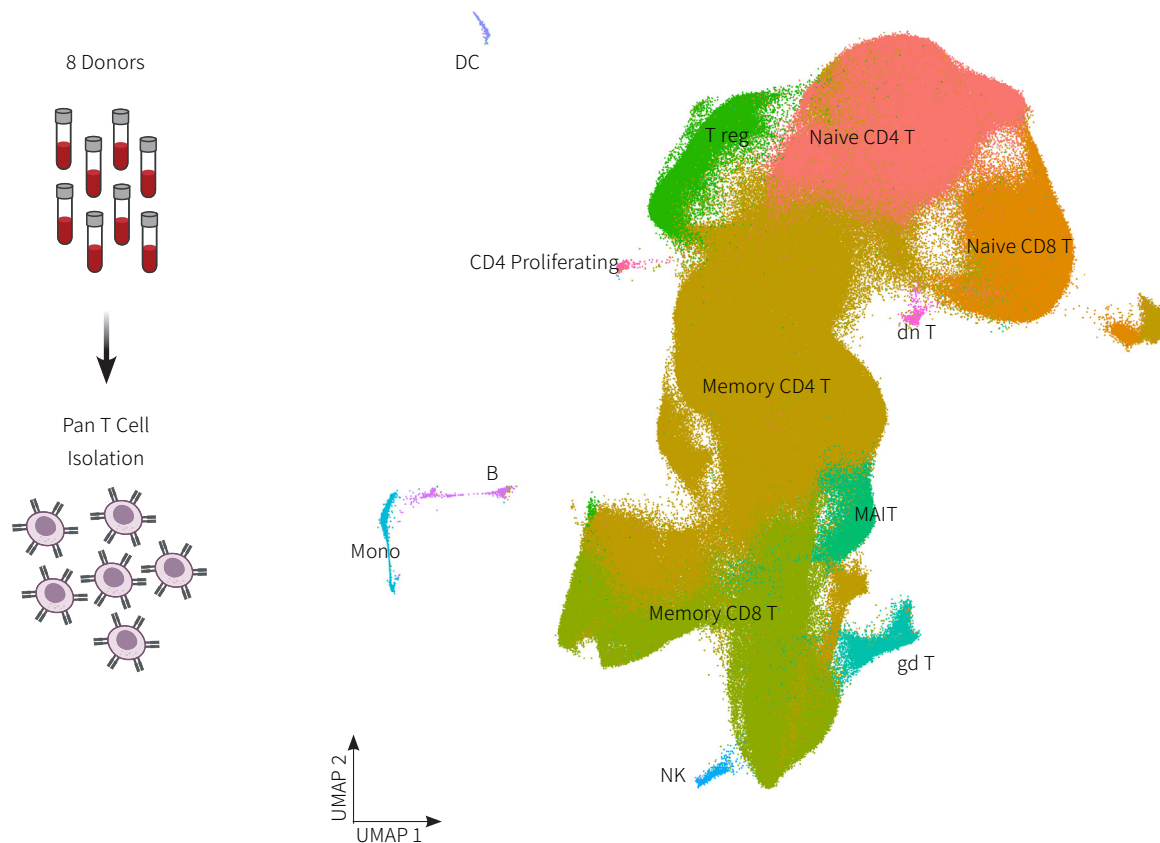


Figure 2: RNA clustering of T cells. Pan T cells were isolated from the PBMCs of 8 donors, fixed, and prepared together with an Evercode TCR Mega kit. All major T cell subtypes and a small percentage of infiltrating non-T cells were resolved in a single experiment.

SENSITIVE CLONOTYPE DETECTION AT SCALE

Revealing the complexity of the immune repertoire requires sensitive detection of TCRs along with whole transcriptome profiles. Across nearly 1M cells, Evercode TCR recovered at least one TCR chain in 88% of all T cells.

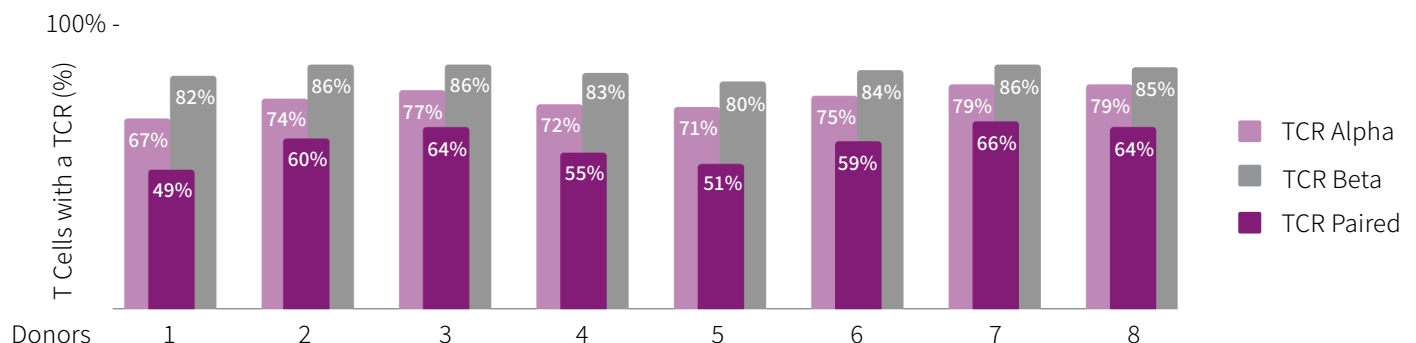


Figure 3: TCR chain assignments across 8 donors. High rate of chain assignments to both TCR alpha and beta. Among T cells with a detected TCR, paired alpha-beta chain assignments ranged between 49% - 66%.

Accurate Detection of TCRs

Ensuring accurate TCR assignments in single T cell analysis is critical. Whole transcriptome analysis identified a MAIT (Mucosal Associated Invariant T) cell cluster in previous RNA clustering (Figure 2). MAIT cells are a distinct subset that expresses semi-invariant TCR alpha chains formed by rearrangement of highest frequency between TRAV1-2 and TRAJ33, with TRAJ12 and TRAJ20 also present in lower frequency clones ([Suliman et al, 2022](#)). The vast majority of semi-invariant MAIT alpha chain clonotypes mapped to the WT derived MAIT cluster. Furthermore, other MAIT clonotypes overlapped with a MAIT cell marker, SLC4A10 ([Park et al, 2019](#)), confirming the correct matching of TCR to cell type (Figure 4).

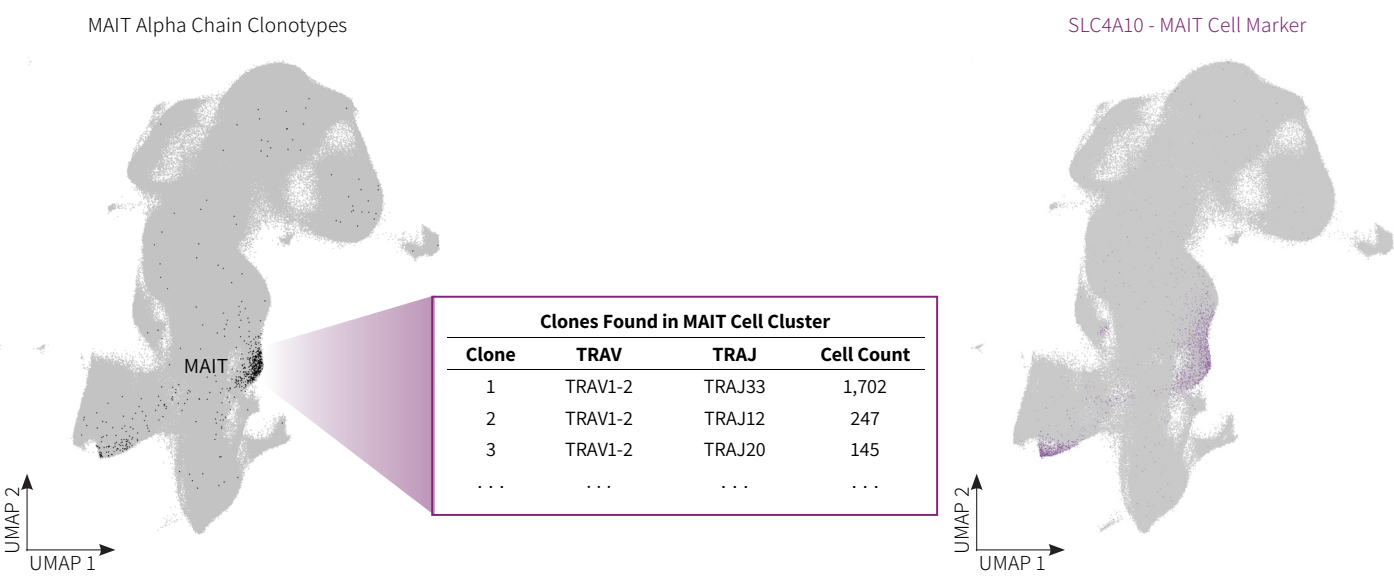


Figure 4: TCR Chain Detection on MAIT Cells.

UMAP generated with the Whole Transcriptome dataset identified a cluster of MAIT cells. Expression of well documented MAIT semi-invariant TCR alpha chains (black) overlaps with MAIT cell clusters and MAIT cell marker SLC4A10 (purple).

COMPREHENSIVE IMMUNE REPERTOIRE DETECTION

The Evercode TCR kit generates the most comprehensive immune repertoire detection from a single experiment to date. Nearly five hundred thousand unique beta chain clonotypes were identified across the 8 donors with vast majority being classified as rare clonotypes.

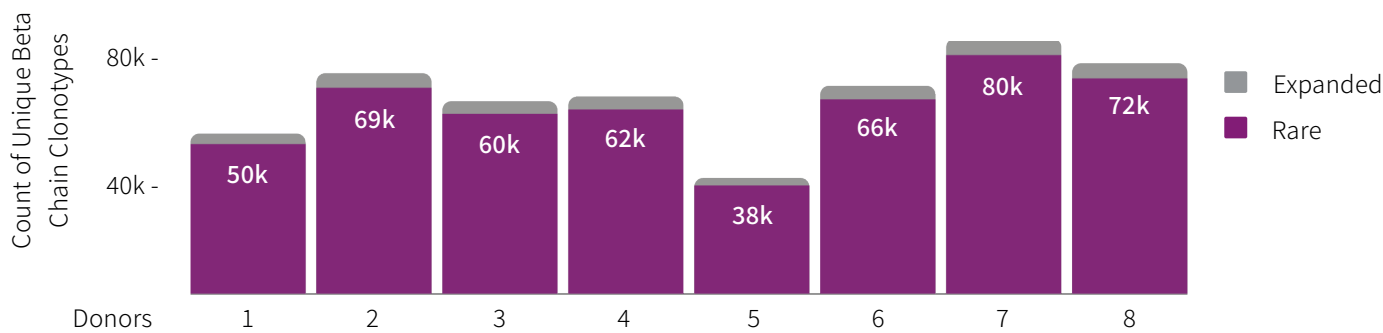


Figure 5: Number of unique beta chain clonotypes across donors. The rare clonotypes (purple) are defined as only being detected in 1 or 2 cells and the majority of detected clonotypes are rare.

Scale from Pilot to Millions of Cells

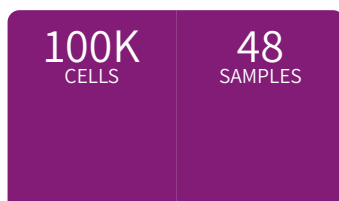
Experiments are rapidly accelerating in both the number of samples and cells, to provide a fuller picture of biological processes and the context of disease. Other single-cell technologies require samples to be analyzed immediately and are limited by the number of samples that can be analyzed together, which can introduce batch effects. Regardless of scale, Evercode TCR technology has a kit to fit every study.

TCR Mini



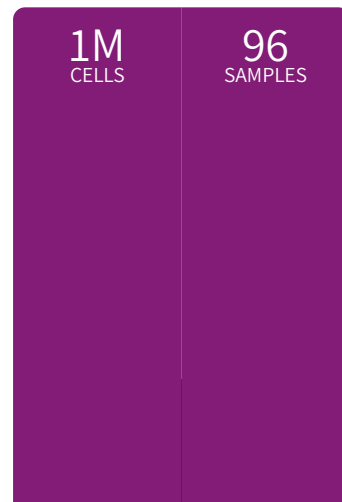
Explore single cell TCR sequencing benefits in repertoire diversity

TCR



Comprehensive TCR sequencing across samples, replicates, or timepoints

TCR Mega



Scale matters: Capture the diversity of immune repertoire at scale

PRODUCT ORDERING INFORMATION

PRODUCT	PART NUMBER
Evercode TCR Mini Up to 10,000 cells and up to 12 samples with Human TCR + WT	ECT01010
Evercode TCR Up to 100,000 cells and up to 48 samples with Human TCR + WT	ECT01030
Evercode TCR Mega Up to 1,000,000 cells and up to 96 samples with Human TCR + WT	ECT01050
Evercode Cell Fixation v2 Up to 4 samples	ECF2001

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