Multiomic profiling of the immune system at single cell resolution

Single Cell Immune Profiling v2 with Feature Barcode technology

Chromium Single Cell Immune Profiling provides a comprehensive approach to simultaneously examine cellular heterogeneity of the immune system, T- and B-cell repertoire diversity, and antigen specificity at single cell resolution. Discover new cell types and states using whole transcriptome analysis, or focus your search with targeted gene expression panels of interest. With our latest improvements, Single Cell Immune Profiling v2 vastly increases sensitivity, enabling detection of rare cell populations and phenotypes. Comprehensive immunophenotyping at this scale and resolution has never been more accessible.

Highlights

- Explore adaptive and innate immune cell diversity
- Identify and characterize rare cell types and biomarkers
- Analyze tissue microenvironment, disease progression, and drug immune response
- Perform large-scale antibody and TCR discovery for novel antigens
- Characterize immune response to infection by measuring clonal expansion and immune cell phenotypes
- Scale experiments economically by focusing on relevant genes and pathways with predesigned gene expression panels, or design a fully custom panel

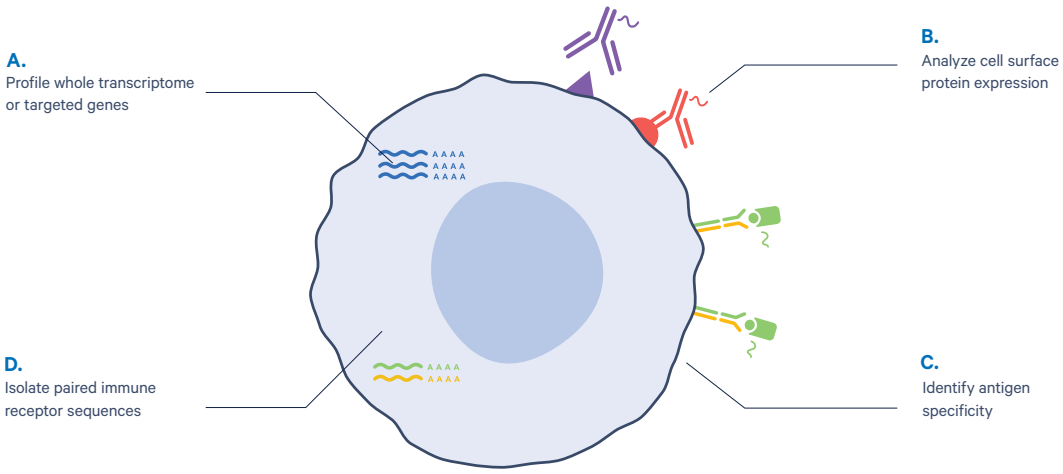


Figure 1. Fully characterize the adaptive immune response with multiomic profiling, including immune receptor mapping. Detect whole transcriptome or targeted gene expression, along with cell surface proteins; paired, full-length receptor sequences of T or B cells; and antigen specificity. **A.** Chromium Single Cell Immune Profiling provides sensitive whole transcriptome or targeted gene expression analysis at the single cell level, for hundreds to tens-of-thousands of cells per reaction. **B.** Measure up to hundreds of cell surface proteins at single cell resolution with Feature Barcode technology. **C.** Feature Barcode technology allows screening of the antigen specificity of T and B cells. **D.** Identify distinct clonotypes through corresponding paired, full-length immune receptor sequences.

Product features

- Profile thousands of genes at the single cell level by barcoding mRNA at the 5' end, for unbiased characterization of cell types and cell states
- Simultaneously profile immune repertoire (BCR/TCR) and gene expression from the same cell to enable correlation of clonotype with the corresponding cell subtype
- Obtain paired, full-length receptor sequences from T cells and/or B cells with complete isotype resolution, providing functional data for antibody/TCR discovery
- Combine gene expression analysis with detection of hundreds of cell surface proteins at high resolution for ultra-high parameter multiomic cytometry
- Combine with Targeted Gene Expression Panels to focus on the genes that matter most and accelerate your studies into actionable insights
- Utilize product partners for Feature Barcode technology (oligo-conjugated antibodies, oligo-conjugated MHCs) to easily perform multiomic profiling
- Leverage dual index libraries for superior sequencing data quality

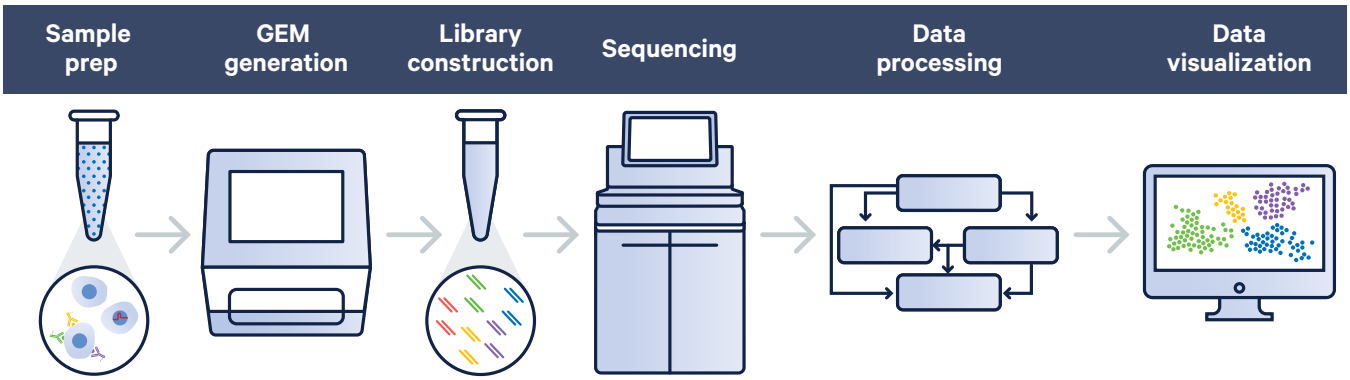
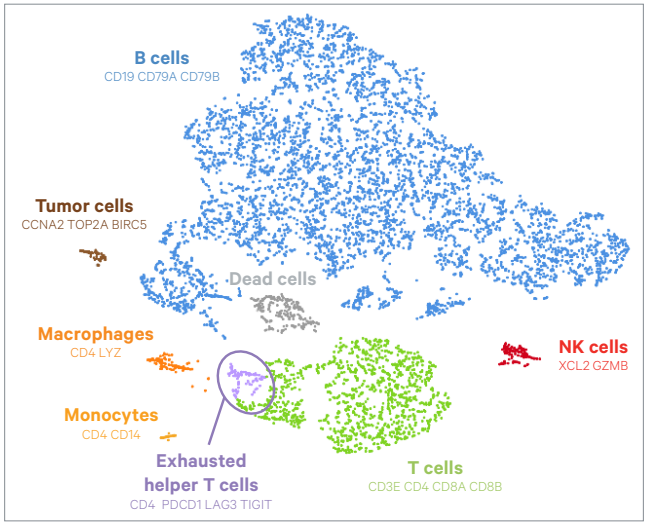


Figure 2. Efficient and streamlined workflow for multiomic profiling of the immune system. Start with a single cell suspension of unlabeled cells, oligo-conjugated antibody-labeled cells, or cells bound to oligo-conjugated MHCs. After GEM generation, up to three separate libraries can be constructed from a single sample, giving multiple readouts that can each be linked back to the same single cell. Process data with Cell Ranger and visualize sample heterogeneity and clonal expansion with Loupe Browser or Loupe V(D)J Browser, our fully integrated and easy-to-use analysis and visualization software tools.

A. Gene expression t-SNE



B. Protein expression t-SNE

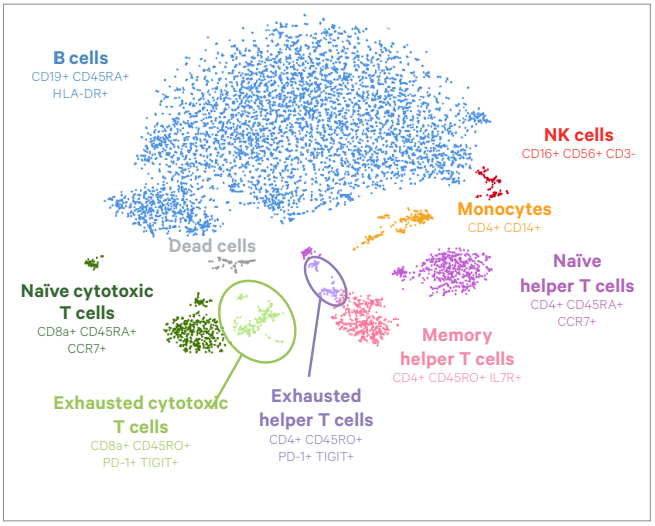
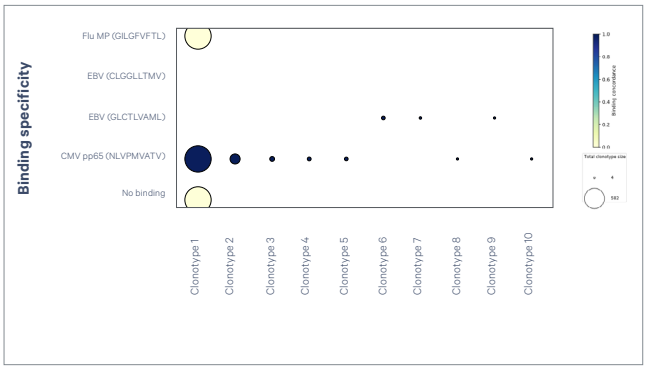
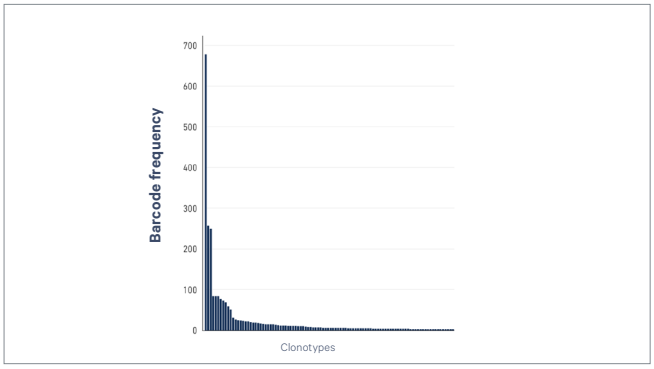


Figure 3. Multiomic data provides complementary insights into diverse immune cell populations in a complex cancer sample. A. t-SNE plot of 7,859 cells from a dissociated human melanoma sample. Each cell is represented by a single dot. Broad categories of immune cell populations were identified through gene expression signatures (as in Figure 1, A.), including cell populations that were not identified by protein markers such as macrophages (orange) and a small population of tumor cells (brown). **B.** t-SNE projection of the same sample clustered based on cell surface protein expression (as in Figure 1, B.) using a panel of 16 markers. Analysis of cell surface protein expression enabled further classification of T cells into naïve, memory, and exhausted subpopulations.

A. Antigen binding specificities



B. TCR clonotype frequency



C. Full-length sequences of clonotype 1: TCR alpha and beta chains

TCR alpha

TGGGGAGTCCACAGTTAGGCAGCGCACTTCTGAAAGGGTGTCAATTCTCGTTGTGTTCCACACTCATGGGGGATTTCCTCAAAGTTTATGAAGTTGGCCTGAAGAA
AGCAGTTACTTCGACCCCTCTTTGTGAACCACAGGAAACTGAACATAGGGCAGAGCGTTTCTAGGACATTTATGGGAGCTGGTCTCTGATTGGCTAGGCAACCAG
ATGCAGAATCCTGTTTTCTGAAGCAGAATATTCCACAGATTTTGGCTGCAAAACGTTTTTCTGCTGTGGGTACGTGAGCAGGAAACATGGAGAAGAATCCTTTGG
CAGCCCCATTACTAATCCTCTGGTTTCATCTTGACTGCGTGAGCAGCATACTGAACGTGGAACAAAGTCCTCAGTCACTGCATGTTCAGGAGGGAGACAGCACCAA
TTTCACCTGCAGCTTCCCTTCCAGCAATTTTTATGCCTTACACTGGTACAGATGGGAAACTGCAAAAAGCCCCGAGGCCTTGTTTGTAATGACTTTAAATGGGGATG
AAAAGAAGAAAGGACGAATAAGTGCCACTCTTAATACCAAGGAGGGTTACAGCTATTTGTACATCAAAGGATCCCAGCCTGAAGACTCAGCCACATACCTCTGTGC
CTTCATCACCGGTAACCAGTTCTATTTTGGGACAGGGACAAGTTTGACGGTCATTCCAAATATCCAGAACCCTGACCCTGCCGTGTACCAGCTGAGAGAC

TCR beta

GAGAGTCCTGCTCCCCTTTCATCAATGCACAGATACAGAAGACCCCTCCGTCATGCAGCATCTGCATGAGCATCGGCCTCCTGTGCTGTGCAGCCTTGTCTCTC
CTGTGGGCAGGTCCAGTGAATGCTGGTGTCACTCAGACCCCAAAATTCCAGGTCCTGAAGACAGGACAGACATGACACTGCAGTGTGCCCAGGATATGAACCAT
GAATACATGTCCTGGTATCGACAAGACCCAGGCATGGGGCTGAGGCTGATTCATTACTCAGTTGGTGCTGGTATCACTGACCAAGGAGAAGTCCCCAATGGCTAC
AATGTCTCCAGATCAACCACAGAGGATTTCCCGCTCAGGCTGCTGTCGGCTGCTCCCTCCCAGACATCTGTGTACTTCTGTGCCAGCAGCCTGGTTACCGGGAC
AGGGGCATACGGCTACACCTTCGGTTCGGGGACCAGGTTAACCGTTGTAGGAGGACCTGAACAAGGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGA

Figure 3. Accelerate actionable insights with immune receptor mapping at single cell resolution across thousands of cells. Characterization of anti-CMV T cells from a CMV⁺ donor by antigen binding specificity, clonotype frequency, and paired, full-length T-cell receptor sequences. **A.** The ten largest antigen-binding clonotypes are plotted along with their binding specificities and binding concordances, as defined by dCODE Dextramer® Reagent binding (as in Figure 1, C.). "No binding" is defined as a clonotype showing no binding to peptide–MHC (pMHC) on the y-axis. The presence of a circle indicates that at least one member of the clonotype was specific for a particular pMHC. Circle size indicates the total number of cells for the given clonotype. Circle color indicates the proportion of cells within the clonotype that bind the specific pMHC, with darker colors having higher binding concordance. **B.** TCR clonotypes are ranked by frequency. The top CMV-specific clonotype has 678 cells. **C.** Shown are paired, full-length TCRα and β chain V(D)J sequences (see Figure 1, D.) for the top expanded clonotype in Figure 4, B. V(D)J nucleotides are color coded as follows: 5'UTR (gray), V (red), D (purple), J (green), C (blue), and CDR3 (bold).

Gene expression and / or immune repertoire profiling	Product code
Chromium Next GEM Single Cell 5' Kit v2, 16 rxns	1000263
Chromium Next GEM Single Cell 5' Kit v2, 4 rxns	1000265
Chromium Next GEM Chip K Single Cell Kit, 48 rxns	1000286
Chromium Next GEM Chip K Single Cell Kit, 16 rxns	1000287
Library Construction Kit, 16 rxns	1000190
Dual Index Kit TT Set A, 96-rxns	1000215

V(D)J amplification kits		Product code
Human T cell	Chromium Single Cell Human TCR Amplification Kit, 16 rxns	1000252
Human B cell	Chromium Single Cell Human BCR Amplification Kit, 16 rxns	1000253
Mouse T cell	Chromium Single Cell Mouse TCR Amplification Kit, 16 rxns	1000254
Mouse B cell	Chromium Single Cell Mouse BCR Amplification Kit, 16 rxns	1000255

Feature barcode technology products	Product code
5' Feature Barcode Kit, 16 rxns	1000256
Dual Index Kit TN Set A, 96-rxns	1000250

Instrument compatibility	Product code
Chromium iX & Accessory Kit, 12 Mo. Warranty	1000328
Chromium iX & Accessory Kit, 24 Mo. Warranty	1000329
Chromium X & Accessory Kit, 12 Mo. Warranty	1000331
Chromium X & Accessory Kit, 24 Mo. Warranty	1000332
Chromium X Upgrade Package	1000330
Chromium Controller & Next GEM Accessory Kit, 12 Mo. Warranty	1000202
Chromium Controller & Next GEM Accessory Kit, 24 Mo. Warranty	1000204

Software	
Cell Ranger go.10xgenomics.com/vdj/cell-ranger	Download
Loupe Browser go.10xgenomics.com/vdj/loupe-cell	Download
Loupe V(D)J Browse go.10xgenomics.com/vdj/loupe-vdj	Download

Compatible partner products	
Compatible Partner Product: Biolegend TotalSeq™-C go.10xgenomics.com/totalseq-C	Learn More
Compatible Partner Product: Immudex dCODE Dextramers® go.10xgenomics.com/dCODE-Dextramers	Learn More

Product specifications

- Efficiently partition 500–10,000 cells per channel, for up to 80,000 cells per run
- Scalable; run up to 8 samples in parallel
- Cell size flexibility, no lower limits
- High cell capture rates of up to 65%
- Low doublet rates of under 0.8% per 1,000 cells

Other throughput options

- For high-throughput (HT) single cell immune profiling experiments (2,000–320,000 cells), see the Product Sheet for Chromium Single Cell Immune Profiling HT

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LIT000089 - Rev C - Product Sheet - Multiomic profiling of the immune system at single cell resolution

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