Consistent single cell immune profiling results with an automated workflow

Automated Single Cell Immune Profiling

With Chromium Connect and the Single Cell Immune Profiling workflows, you can generate consistent and reproducible results across experiments and across users. Simultaneously examine cellular heterogeneity of the immune system and T- and B-cell repertoire diversity to discover new cell types, identify rare cell populations, and reveal clonal expansion in response to disease and therapeutic intervention. Along with turnkey software tools, Chromium Single Cell Immune Profiling for Chromium Connect allows you to optimize your lab productivity and accelerate time to results.

Figure 1. Increase consistency and productivity with Automated Single Cell Immune Profiling workflows. A. Simultaneously profile whole transcriptome 5' gene expression and immune repertoire (BCR/TCR) at the single cell level for hundreds to tens of thousands of cells. B. Streamline your lab operations, reduce human error, and improve laboratory efficiency. Run your single cell immune profiling experiments with confidence using integrated and validated workflows.

Highlights

• Minimize technical variation in gene expression and receptor sequence data to enable the consistency critical for reproducible multi-site studies
• Reveal clonal expansion associated with therapeutic response and resistance with minimal hands-on time to optimize laboratory productivity
• Characterize the immune response to disease and therapy with walk-away convenience
• Automate TCR and antibody discovery, and go from cells to sequencing-ready libraries with increased laboratory efficiency
• Choose from convenient, modular workflows to best fit your day-to-day operations

Benefits with automation

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<tbody>
<tr>
<td>Hands-on time</td>
<td>▼ 80%</td>
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<td>Pipetting steps</td>
<td>▼ 95%</td>
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<td>Interaction points</td>
<td>▼ 75%</td>
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10xgenomics.com/instruments/chromium-connect
Product features

- Simultaneously profile immune repertoire (BCR/TCR) and 5’ gene expression from the same cell with fully integrated automation for consistent and reproducible results across experiments, users, and sites
- Obtain paired, full-length receptor sequences from T cells and/or B cells with complete isotype resolution, from human or mouse samples
- Utilize pre- aliquoted, automation-specific reagents that are color-coded and 2D-barcoded for error-proof reagent tracking and loading to minimize waste and streamline lab operations
- Process from 1 to 8 samples as needed, accelerating time to results without wasting reagents or waiting on additional samples
- Run fully integrated and automated workflows, with < 1 hour of hands-on time and 8 hours of freedom to optimize laboratory productivity and scale projects
- Use a modular workflow with a safe stopping point to run and store cDNA, with the option to batch samples for library construction

Figure 2. Integrated and automated workflows enable walk-away convenience for Single Cell Immune Profiling. Start with a single cell suspension and leverage the pre-programmed steps in Chromium Connect for reagent loading, liquid handling, sample cleanup, incubation and cycling reactions, and library preparation. Multiple libraries can be prepared from a sample, including 5’ gene expression and full-length, paired T- or B-cell receptor sequences. Final libraries are compatible with short-read sequencers. Process data with Cell Ranger, and visualize sample heterogeneity and clonal expansion with Loupe Browser or Loupe V(D)J Browser, our easy-to-use analysis and visualization software.
**Figure 3. Reproducible Single Cell Immune Profiling data with Chromium Connect.** Comparison of single cell 5’ gene expression data reproducibility for manual vs. automated library preparation workflows. Median genes per cell and median UMI counts per cell (at 20,000 raw reads per cell) for multiple replicates, each targeting 5,000 cells from human peripheral blood mononuclear cell (PBMC) samples. Chromium Connect shows high data consistency across channels and runs.

**Figure 4. Consistent paired T-cell and B-cell receptor data with Chromium Connect.** Comparison of top 20 expanded clonotypes based on CDR3 nucleotide sequences with TCR sequencing (left) and BCR sequencing (right) from the same samples for manual versus automated library preparation workflows. The same clonotypes were recovered across experiments.

**Figure 5. Detection of all major blood cell types discerned with Automated Single Cell Immune Profiling.** Single cell barcode UMAP plots of 5’ gene expression, TCR clonotype, and BCR clonotype from 5,000 PMBCs prepared with the Automated Single Cell Immune Profiling workflow on Chromium Connect. As expected, TCR clonotypes and BCR clonotypes overlapped with T-cell and B-cell compartments, respectively. Data was analyzed by Cell Ranger and visualized using Loupe Browser. Major cell populations in each cluster were identified via marker gene expression. All major PBMC types were discerned comparably to the manual Single Cell Immune Profiling workflow.
## 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