CROWN BIOSCIENCE

Single Cell Gene Expression Analysis Service

A JSR Life Sciences Company

FACTSHEET

Overview

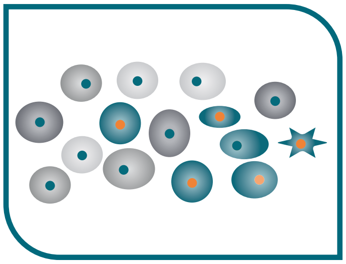
Single cell transcriptome analysis enables gene expression profiling of individual cells and opens the opportunity to characterize heterogenous cell populations.

Crown Bioscience has implemented the 10x Genomics "Chromium Single Cell Gene Expression" solution, which is suitable for investigating different biological samples on a single cell level and offers a comprehensive workflow starting from sample preparation to the provision of the whole transcriptome sequencing data of single cells.

End-to-end solution: Single Cell Gene Expression Analysis Service Workflow

1. Sample Preparation

Preparation of single cell suspensions, e.g., viable PBMCs, primary and secondary cell culture; dissociated tumor cells from fresh patient-derived tissue samples or cell nuclei (currently under development)



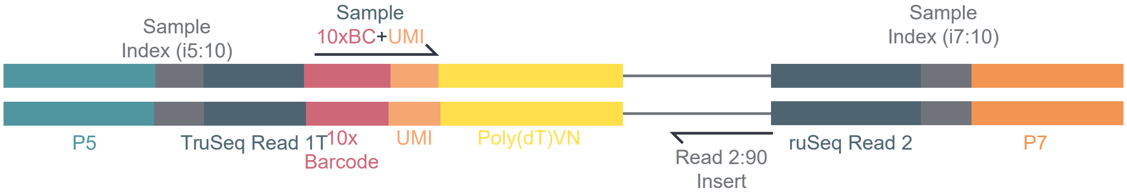
2. Single Cell Partitioning

10x Genomics Chromium Controller for partitioning of hundreds to tens of thousands of cells (500-10,000 cells)

3. Single Cell Library Construction

Single cell gene expression (3′ gene expression profiling) and Single Cell Immune Profiling (5′ gene expression alongside V(D)J repertoire profiling and antigen specificity of T and B cells)

Chromium Single Cell 3′ Gene Expression Dual Index Library

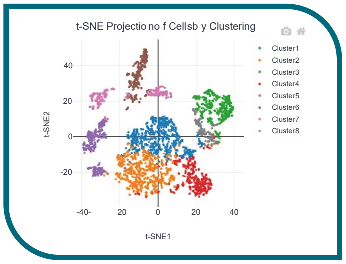


4. Sequencing

Sequencing on NovaSeq™6000 (Illumina)

5. Single Cell Analysis

Raw as well as processed data from 10x Genomics Cell Ranger Pipeline, including files for interactive single cell data visualization and evaluation via 10x Genomics Loupe Browser software

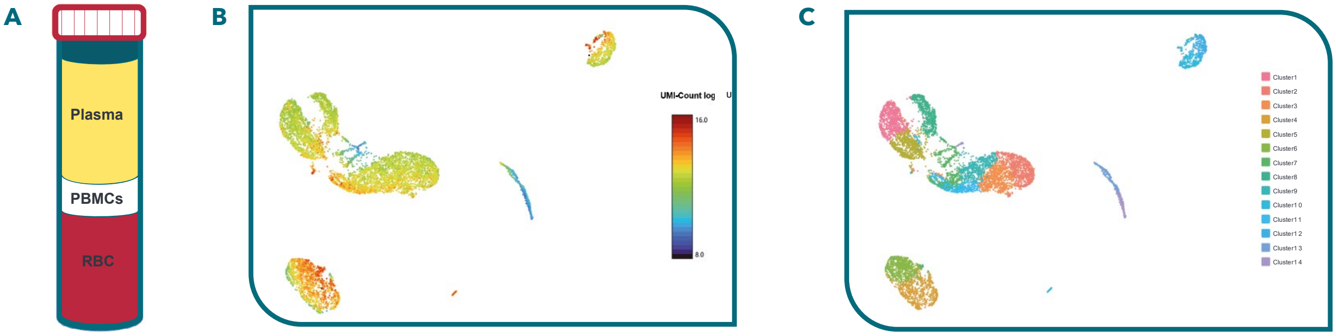


Your Benefits

- 10x Genomics Certified Service Provider for single cell gene expression
- Covering the entire workflow from sample to data
- Scientific support throughout the entire workflow
- All data files provided for individual processing
- Easy to interpret results
- Combining single cell gene expression analysis with other in-house multi-omics tools, e.g., Flow Cytometry, Spatial Transcriptomics, fluorescent multiplex Immunohistochemistry (dependent on starting material)

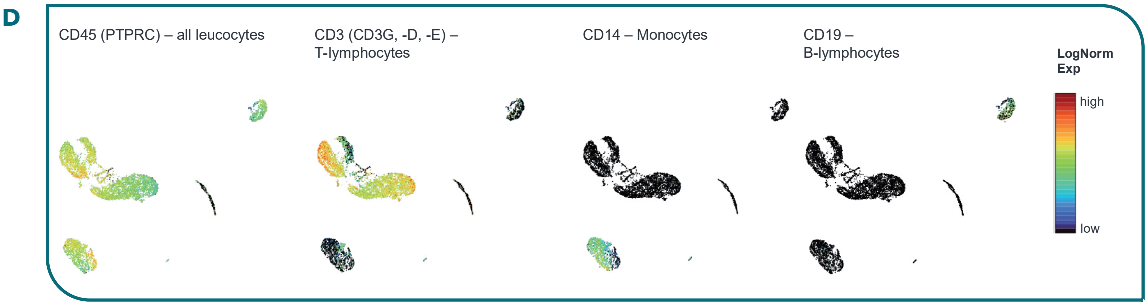
10x GENOMICS | Certified Service Provider

Characterization of cell populations using an example of Peripheral Blood Mononuclear Cells (PBMCs)



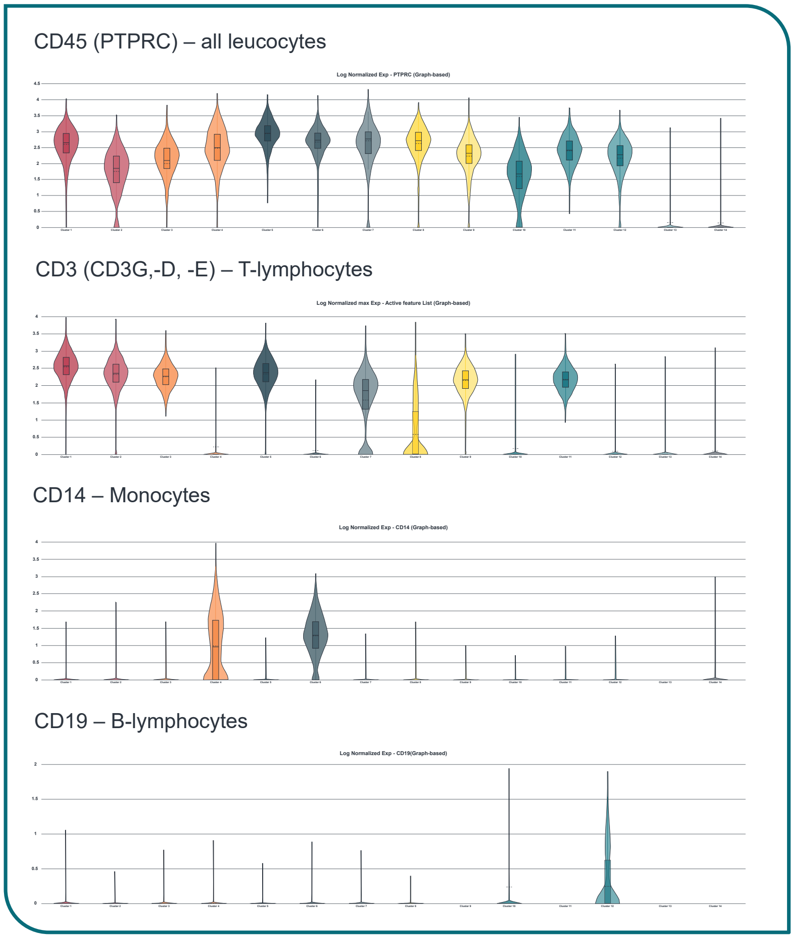
A) Isolation of PBMCs; single cell analysis of PBMCs showing B) UMAP-plot of total UMI counts for each cell-barcode as well as C) UMAP-plot of cells by graph-based cluster analysis using Loupe-Browser software

UMAP-plot of marker positive cells



D) Example: gene expression analysis of different markers for cell characterization, e.g. differentiation of leucocytes CD45 with monocyte (CD14), T-lymphocyte (CD3) and B-lymphocyte (CD19) markers

Violin plot of gene expression of selected markers within different clusters, violin plot showing LogNorm fold changes, reflecting gene expression normalized by UMI counts



Get in touch

US: +1 (301) 228 9739
Germany: +49 40 69 63 572 0

busdev@biospecimenservices.com
www.biospecimenservices.com