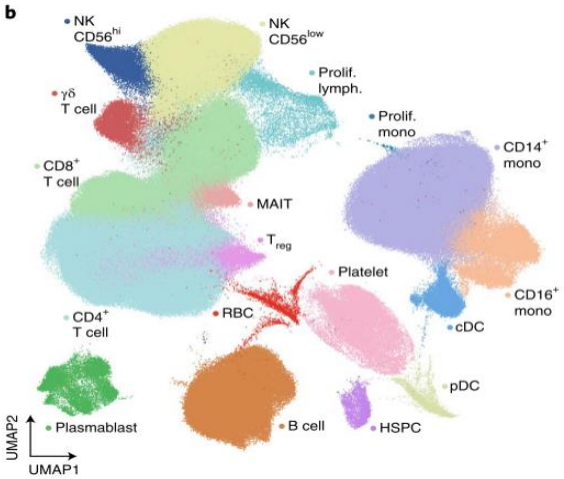
Single Cell Transcriptomics

Newsletter May 2021

Paper 1

Stephenson *et al.* **Single-cell multi-omics analysis of the immune response in COVID19,** *Nature Medicine, 2021.*



In the first paper authors combined transcriptome and surface proteome from peripheral blood mononuclear cells (PBMCs) from individuals with asymptomatic, mild, moderate, sever and critical COVID19 symptoms. Analysis was conducted on 1,141,860 cells from 146 samples and lead to 18 cell subsets with an additional 27 cell states identified following subclustering. They discovered the expression of type I/III interferon response genes in monocytes, hematopoietic stem and progenitor cells (HSPCs) and plasmacytoid dendritic cells (DCs) in regards to symptom severity.

Investigators confirmed increase in proliferative CD4+ and CD8+ T cells and decrease in γδ T cells related to disease severity. Moreover, they identified enrichment of IFNγ and IL-2 antigen-specific T cells in asymptomatic group, whilst the enrichment of CD8+ effector T cells in severe COVID19 cases. Such changes in T cells affect antigen-specific short-lived effector cells leading to uncontrolled inflammation and immunopathology. Scientists observed a significant decrease in IgA2 in symptomatic patients in comparison to asymptomatic donors which indicated that maintenance of a robust mucosal humoral immune response could dictate severity of symptoms in COVID19 patience.

Paper 2

Bocchi *et al.* **The coding and long noncoding single-cell atlas of the developing human fetal striatum**, *Science, 2021*

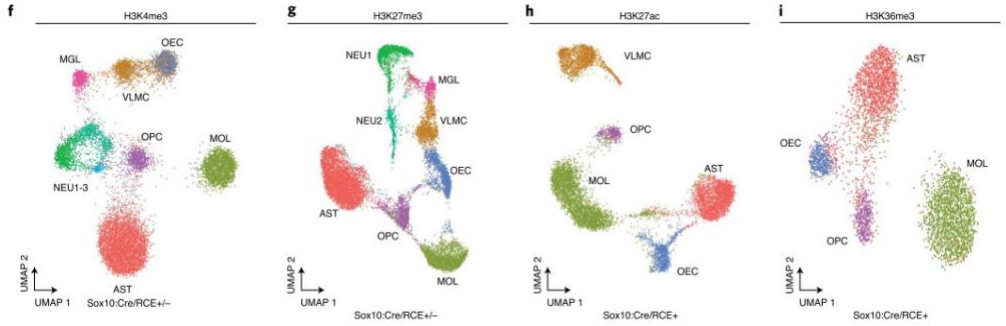
Striatum is a brain region playing important roles in motor control,learning, behavior, cognition and emotional responses. There is a lack of in-depth cell type characterization of striatum during its embryonic development. Thus, investigators aimed to create a comprehensive single-cell atlas of this region during the early human fetal development with the focus on protein-coding and long intergenic noncoding RNAs (lincRNAs).

Scientist analyzed lateral ganglionic eminence (LGE), embryonic area giving rise to medium spiny neurons (MSNs) of striatum. Transcriptomic data of 96,789 single cells revealed 15 distinct transcriptomic profiles. Notable, investigators observed that both types of MSNs cells (D1- and D2-MSNs) originate from a common progenitor. Also they confirmed distinct cell lineages of MSNs and interneurons in striatum. Investigators identified gene networks controlling development of MSNs. And with the help of in silico knockout of transcription factors controlling these networks they predicted potential arrest and blockage of a specific MSN subtype development, or even potential change of MSN fates. This paper further increases the knowledge about critical stages of striatum development in the human brain.

Paper 3 and 4

Bartosovic *et al.* [Single-cell CUT&Tag profiles histone modifications and transcription factors in complex tissues], *Nature Biotechnology, 2021*

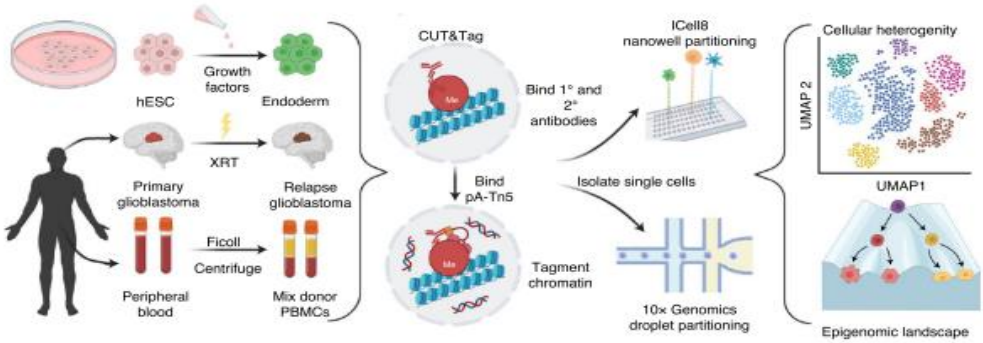
Scientists from Karolinska Institut in Sweden used CUT&Tag Technology, a method to measure bulk histone modifications in combination with droplet-based single-cell library preparation to generate high-throughput data on chromatin modifications of single cells. The CUT&Tag Technology generated tens of thousands of cells in the mouse central nervous system to discover acetylated and methylated histones. Obtained data was sufficient to resolve cells into distinct populations based on histone modifications and helped to better understand promoter mark spreading, bivalency and enhancer-promotor interactions.



scCUT&Tag dataset is available at https://ki.se/en/mbb/oligointernode and https://mouse-brain-cutandtag.cells.ucsc.edu.

Wu *et al.* [Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression], *Nature Biotechnology, 2021*

To prove the ability of CUT&Tag Technology to distinguish distinct cell types, the team used H1 human embryonic stem cells (hESCs) to dig deeper into polycomp group (PcG) silenced regions marked by histone H3 Lys27 trimethylation (H3K27me3). Investigators observed that CUT&Tag Technology has the ability to distinguish human blood cell types and allows generation of the cell-type specific PcG landscapes from heterogeneous tissues. The power of technology was also demonstrated using profiling of H3K27me3 in the tumor microenvironment detecting heterogeneity in PcG activity before (n=1,311 single cells) and after (n=1,168 single cells) tumor treatment.



Next Single Cell Seminar

Date: 28th May 2021, online

15:00 – 16:00

Seth Blackshaw, Johns Hopkins University School of Medicine

Building and Rebuilding the Hypothalamus

If you would like to announce anything single cell related, being it job announcement, event, your published paper, technology development etc, please contact us.

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