

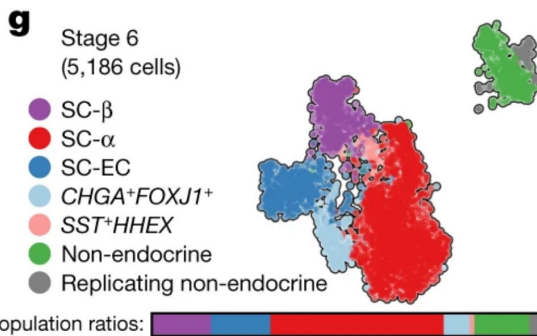


# Single Cell Transcriptomics

## Newsletter June 2019

### Paper 1

Veres, A. et al. [Charting cellular identity during human in vitro  \$\beta\$ -cell differentiation](#) *Nature*, 2019.

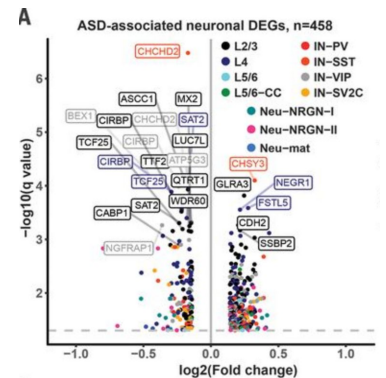


Recently invented protocols for in vitro generation of  $\beta$ -cells are the most promising candidates for development of cell-based therapies for diabetes. However, one of the challenges of these techniques is heterogeneity of produced populations. To address this issue, the authors performed comprehensive study of in vitro differentiation of more than 100,000 human cells undergoing in vitro  $\beta$ -cell differentiation. They described differentiation fates of different cell types, characterized gene-expression dynamics and developed a lineage model of in vitro  $\beta$ -cell differentiation.

### Paper 2

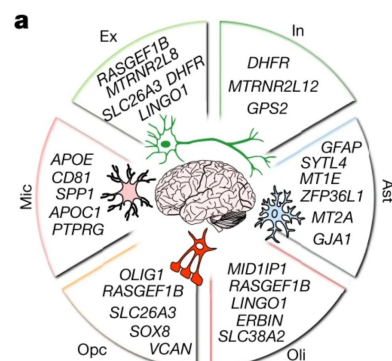
Velmeshev, D. et al. [Single-cell genomics identifies cell type-specific molecular changes in autism](#) *Science*, 2019.

Researches from UCSF used scRNA-seq to sequence 104k cells from cortical tissue from 15 patients with autism and 16 healthy ones. Using linear mixed model they identified autism-associated transcriptomic changes in specific cell types and brain layers. They also compared changes in ASD to those in patients with sporadic epilepsy only by sequencing 22k cells from 8 epilepsy and 7 healthy patients. The authors found that synaptic signaling of upper-layer excitatory neurons and the molecular state of microglia are preferentially affected in autism. Moreover, they showed that dysregulation of specific groups of genes in cortico-cortical projection neurons correlates with clinical severity of autism.



### Paper 3

Mathys, H. et al. [Single-cell transcriptomic analysis of Alzheimer's disease](#) *Nature*. 2019.

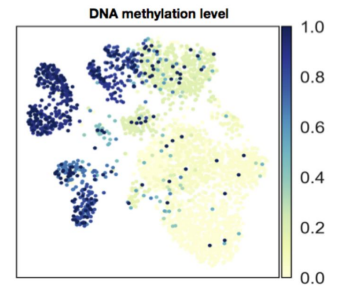


In this work, Mathys et al. aim on characterizing the complex cellular changes in patients with Alzheimer's disease. The authors sequenced 80,660 single nucleus from the prefrontal cortex of 48 individuals and applied Self-organizing map approach to identify genesets, associated with different pathological traits. Particularly, it showed that the strongest disease-associated changes appeared early in pathological progression and were highly cell-type specific, whereas genes upregulated at late stages were common across cell types and primarily involved in the global stress response. Furthermore, transcriptional responses were substantially different between sexes in several cell types.

## Paper 4

Danese, A. et al. [EpiScanpy: integrated single-cell epigenomic analysis](#) *bioRxiv*, 2019.

Popular scRNA-seq python package [scanpy](#) now works with epigenetics! New package allows to analyse single-cell DNA methylation and single-cell ATAC-seq data in the way compatible with the main package. More specifically, it provides clustering, visualization, pseudotime and differential methylation / open chromatin calling routines.



## Next Single Cell Seminar

Date: 28<sup>th</sup> June 2019, Location: Mærsk Tower, Top Floor

**9:00 – 9:40**

Andrea Asenjo Martinez, BRIC - Maturation of mouse inhibitory interneurons during postnatal neurogenesis

**10:00 – 10:40**

Gaurav Singh Rathore, Danstem - Mapping human neurogenesis in an in vitro model of human brain development using single-cell RNA-seq

**10:40 – 11:00** Coffee and Discussion

Contact: [viktor.petukhov@bric.ku.dk](mailto:viktor.petukhov@bric.ku.dk) & [mykhailo.batiuk@bric.ku.dk](mailto:mykhailo.batiuk@bric.ku.dk)