Single Cell Transcriptomics

Newsletter June 2022

Paper 1

Fulcher *et al.* Parallel measurement of transcriptomes and proteomes from same single cells using nanodroplet splitting., *Nature Methods*, 2022

To overcome the limitations of studying the proteome in parallel with other single-cell technologies, a group of researchers has developed a platform called nanoSPLITS (nanodroplet SPlitting for Linked-multimodal Investigations of Trace Samples). The platform offers unbiased measurement of the transcriptome from single cells and the mass spectrometry-based proteome from the same cells, while profiling more than 5000 genes and 2000 proteins per single cell. Using nanoSPLITS, the authors of this work have managed to identify marker genes and proteins for both modalities and quantify the amount of mRNA transcripts and proteins in a precise and unbiased manner. Moreover, nanoSPLITS is not restricted to two modalities only. The authors claim it is possible to combine it with other "omics" and, thus, get deeper insight into the interactions of different modalities between each other.

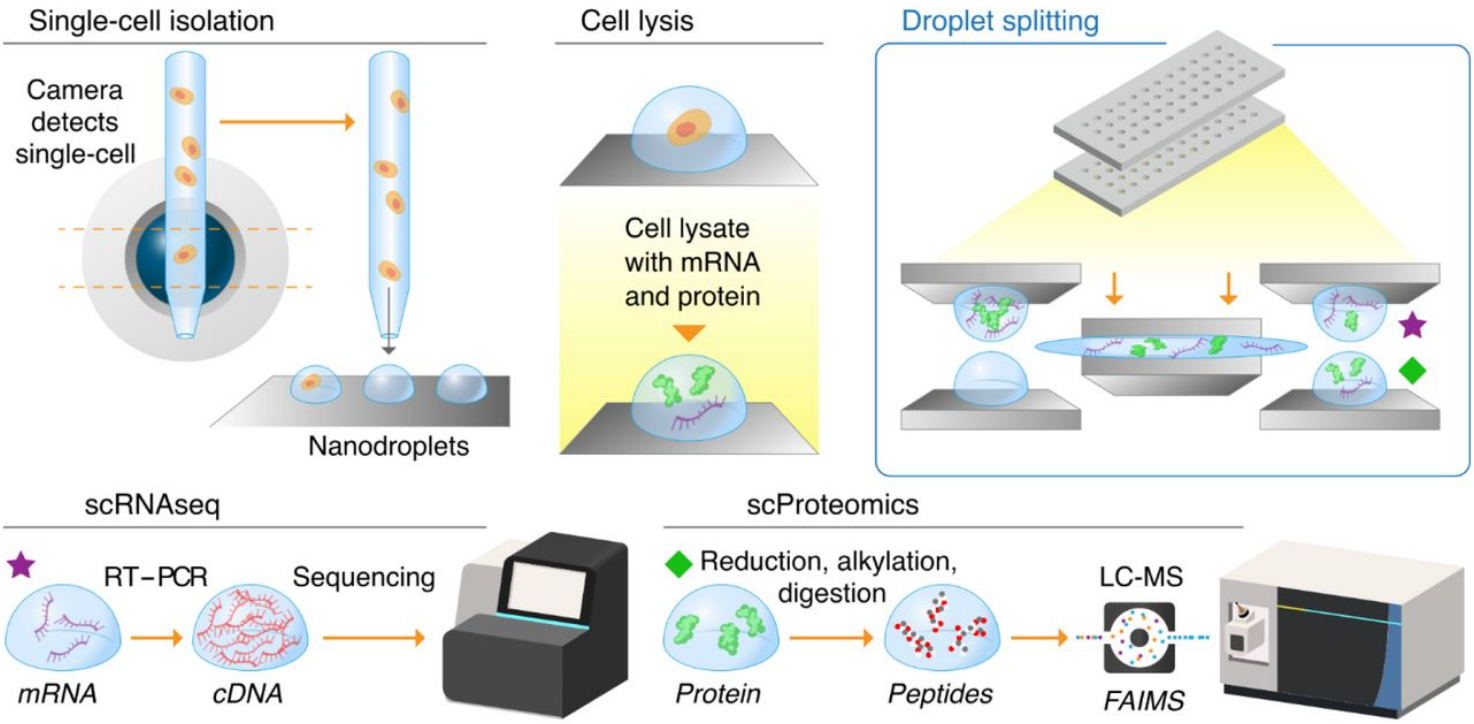

Figure 1. Overview of the nanoSPLITS-based single-cell multiomics platform.

Paper 2

Mund & Coscia, *et al.* Deep Visual Proteomics defines single-cell identity and heterogeneity., *Nature Biotechnology*, 2022

Researchers from the University of Copenhagen and the Max Planck Institute of Biochemistry in Germany introduced Deep Visual Proteomics (DVP) which connects the protein levels to cellular phenotypes while preserving the spatial context. Deep Visual Proteomics is a combination of artificial-intelligence-driven image analysis of cells, automated single-cell microdissection, and ultra-high sensitivity mass spectrometry. DVP offers the quantification of expressed proteins in a single cell, mapping of cell-type specific proteomes and identification of future drug targets. Using DVP, the authors of this paper managed to identify key pathways dysregulated in cancer progression. Furthermore, since a single slide contains hundreds of cells, this enables DVP to characterize rare cell types and interactions and, with further improvements, DVP could be able to study post-translational modifications on a single-cell level.

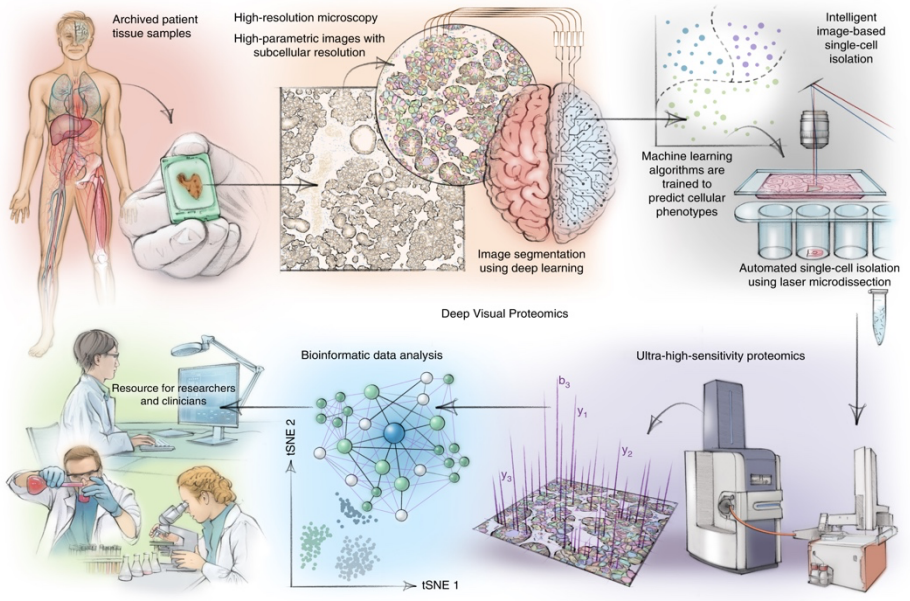

Figure 2. DVP concept and workflow.

Paper 3

Chen, *et al.* Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays., *Cell*, 2022

The authors of this article present a mouse organogenesis spatiotemporal transcriptomic atlas (MOSTA) generated by applying a combination of DNA nanoball (DNB)-patterned assays and in situ RNA capture called spatial enhanced resolution omics-sequencing (Stereo-seq). MOSTA shows detailed topographic information about the stepwise emergence of cell identities across several stages of mouse organogenesis. The authors have identified spatial domains of transcriptional regulators and their targets in specific tissues across different stages of the embryo. In addition, the ability of Stereo-seq to capture intronic transcripts allowed the researchers to study RNA velocity during embryogenesis, which resulted in the generation of transcriptomic maps of tangentially migratory interneurons in the developing cerebral cortex.

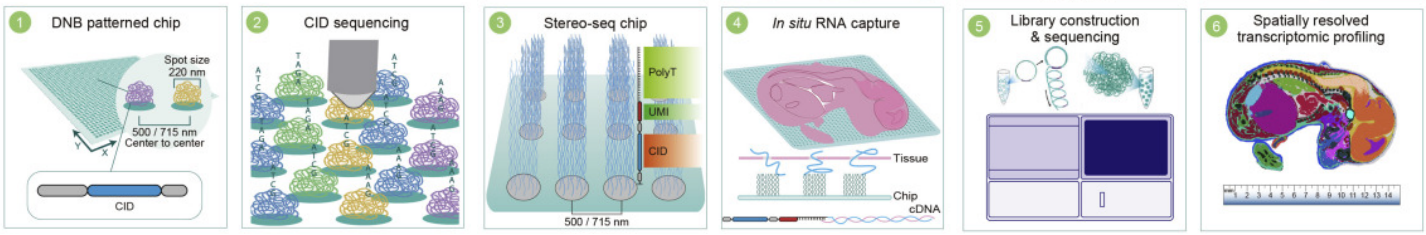

Figure 3. Stereo-seq concept and workflow.

New papers from Danish researchers

cyCombine allows for robust integration of single-cell cytometry datasets within and across technologies.
Pedersen, C.B., Dam, S.H., Barnkob, M.B. *et al.*, ***Nat Communications***, *2022*

Expression profile of synaptic vesicle glycoprotein 2A, B, and C paralogues in temporal neocortex tissue from patients with temporal lobe epilepsy (TLE).
Pazarlar, B.A., Aripaka, S.S., Petukhov, V. *et al..*, ***Molecular Brain***, *2022*

Next Single Cell Seminar

24th of June
TBA

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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