Parallel measurement of transcriptomes and proteomes from same single cells using nanodroplet splitting

CELLENION
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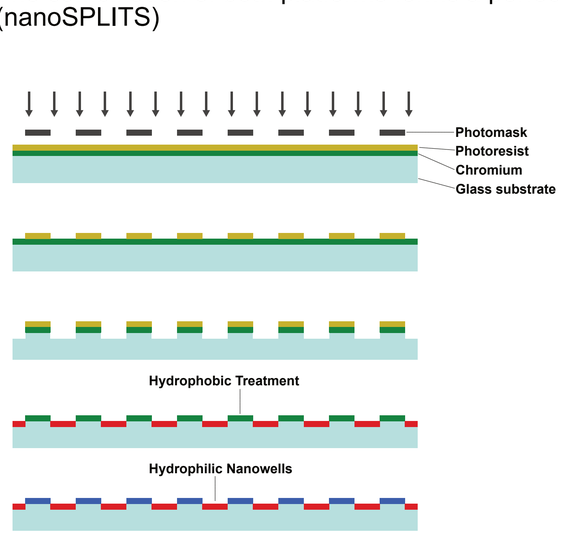
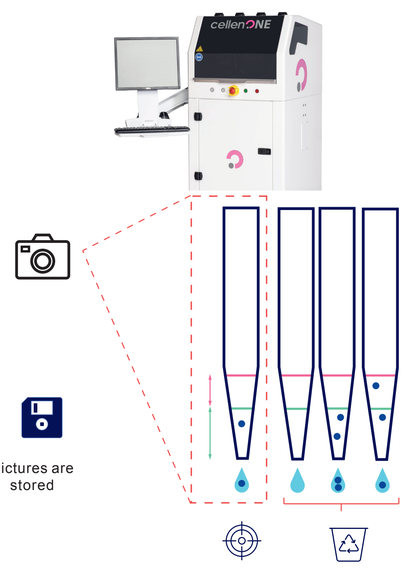
Combination of cellenONE and NanoPOTS for Nanovolume multiomics of the same single cell

- The cellenONE platform enables highly accurate single cell and nano volume dispensing
- The nanoPOTS platform provides a robust and efficient nanonvolume substrate for omics solutions
- The combination of both platforms forms a perfect basis for a multiomics approach (nanoSPLITS)



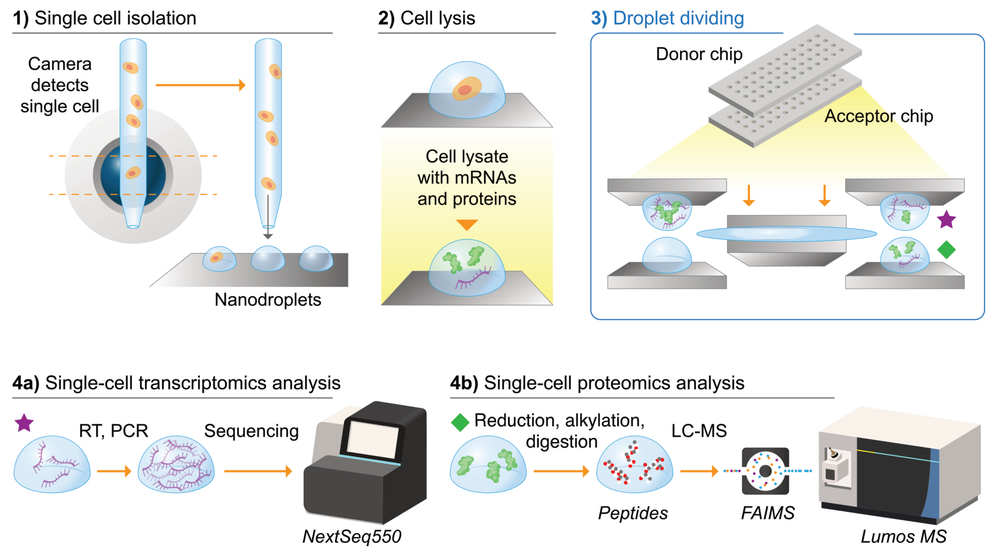


Take Home Message:

nanoSPLITS provides multimodial expression data from the same single cell

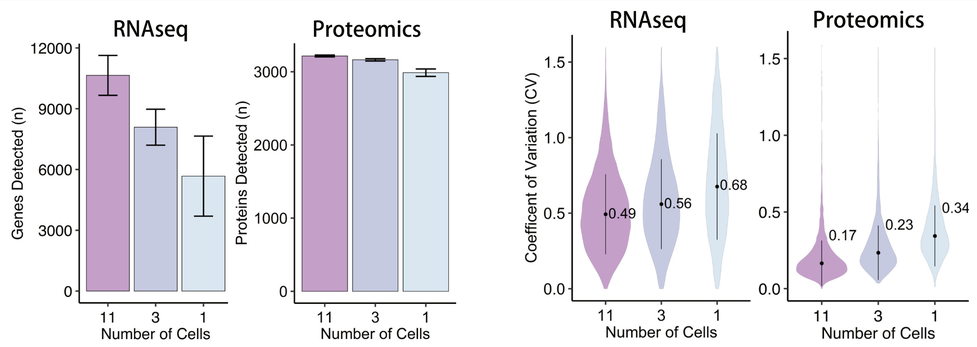
- nanoSPLITS precisely quantifies the abundances of both mRNA transcripts and proteins
- Unbiased protein detection via mass spectrometry
- Very high sensitivity in both modalities
- nanoSPLITS will enable greater insights into how the different modalities interact with each other

Overview of the nanoSPLITS-based single cell multiomics platform.

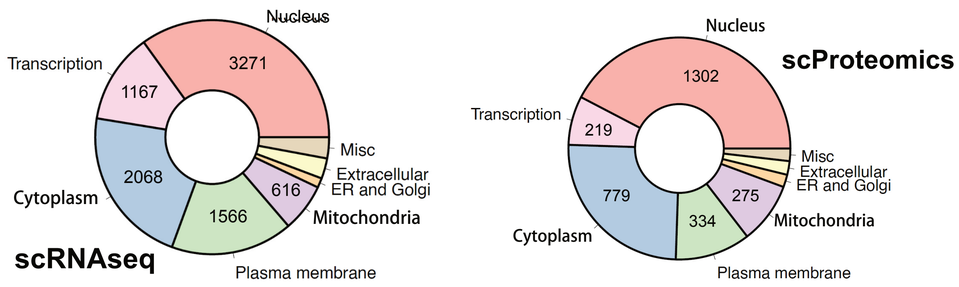


- Lysis and single-cell disepesning using the cellenONE
- Molecule splitting by drop seperation between 2 chips
- Parallel Proteomics and transcriptomics preperation from the same cell

NanoSPLITS shows high sensitivity for proteomics and transcriptomics

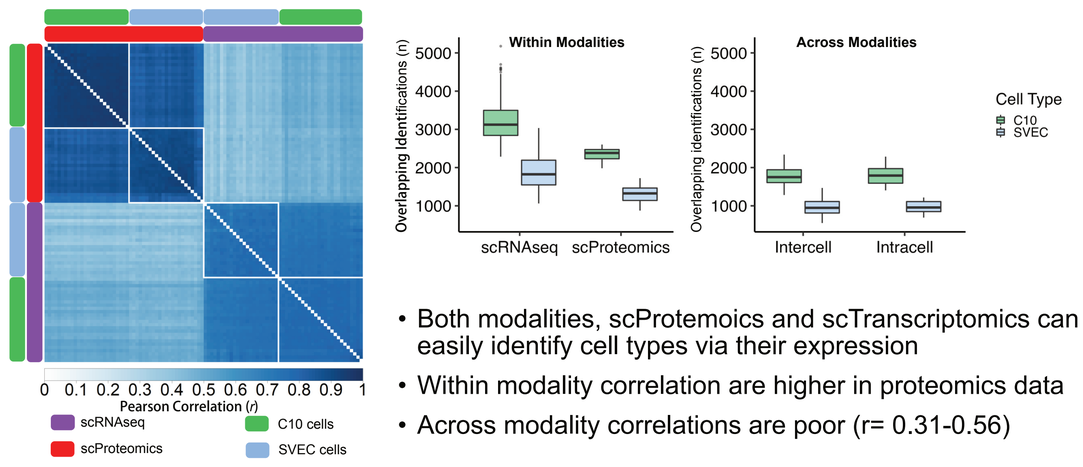


- In single C10 cells, the nanoSPLITS workflow detected
  - 5848 genes (>5 reads) in the transcriptomic data
  - 2934 proteins(1% FDR) in the proteomics data
- CVs of transcriptomic data are significantly higher than for proteomics data



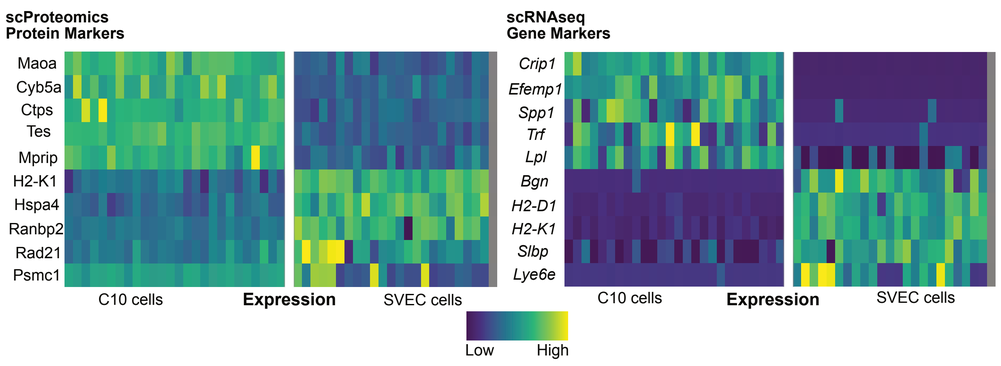
- Proteomics and transcriptomics data show similar distributions of gene ontologies within the respective datasets, e.g. for cellular components

Protein and RNA expression show poor correlation within the same single cell

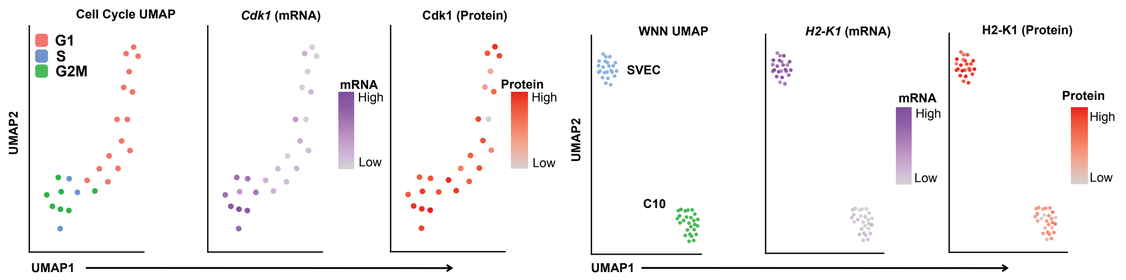


- Both modalities, scProtemoics and scTranscriptomics can easily identify cell types via their expression
- Within modality correlation are higher in proteomics data
- Across modality correlations are poor (r= 0.31-0.56)

NanoSPLITS based multiomics aproach increases specificity of analysis



- Modalities show different top 5 markers to distuingish celltypes (C10, SVEC)
- H2-K1 can be found in both modalities as a cell type marker



- Combined data shows superior performance in clustering
- Identification of cell cycle derived subpopulations in C10 cells validates the high sensitivity of nanoSPLITS despite droplet splitting.

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Zhu, Y., Piehowski, P.D., Zhao, R., Chen, J., Shen, Y., Moore, R.J., Shukla, A.K., Petyuk, V.A., Campbell-Thompson, M., Mathews, C.E., et al. (2018). Nanodroplet processing platform for deep and quantitative proteome profiling of 10-100 mammalian cells. Nat. Commun. 9, 882. .