



# Seminar

## Application of single-cell RNA Sequencing analysis in science research

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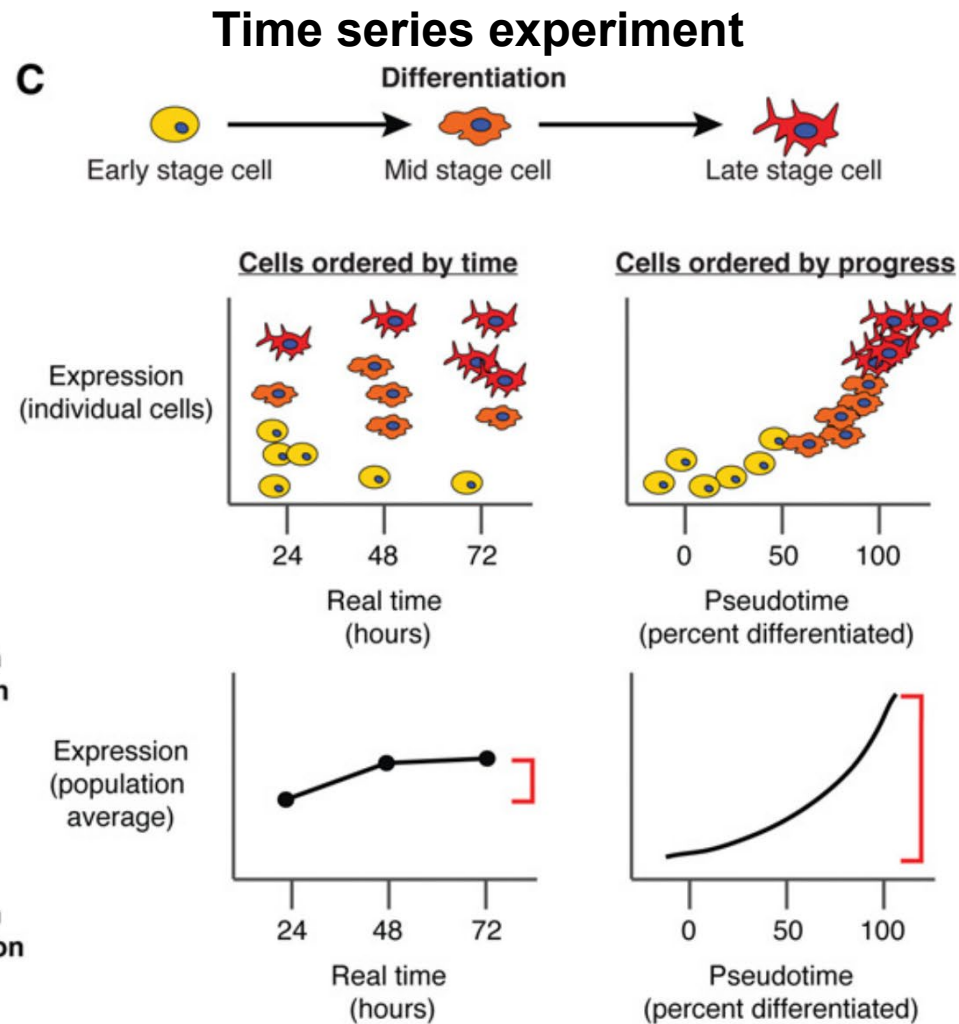
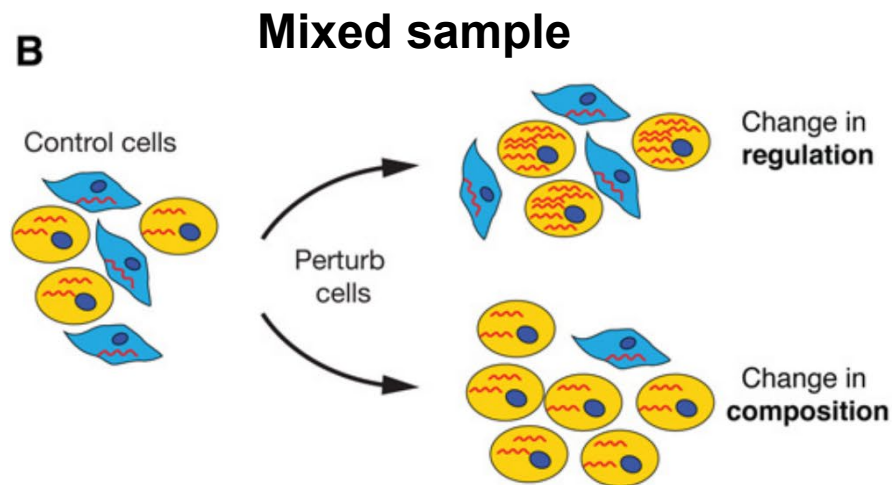
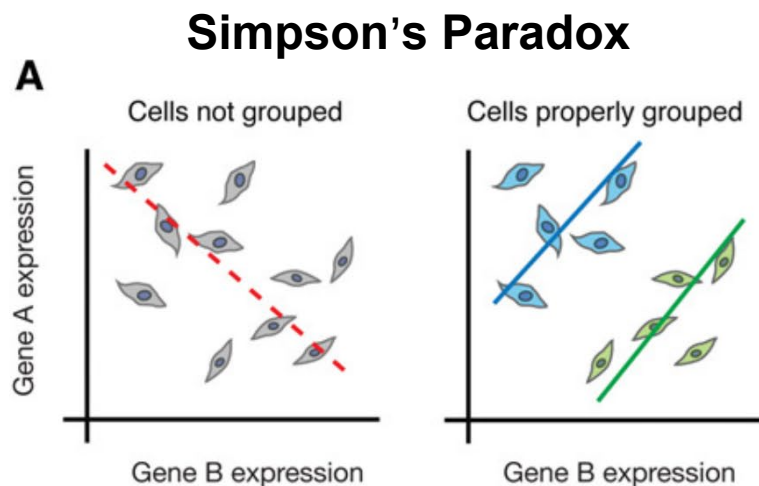


# PART 1

## Background



# Background – Why we need single-cell RNA sequencing analysis



Trapnell C et al. *Genome Res* (2015) 25:1491–1498.

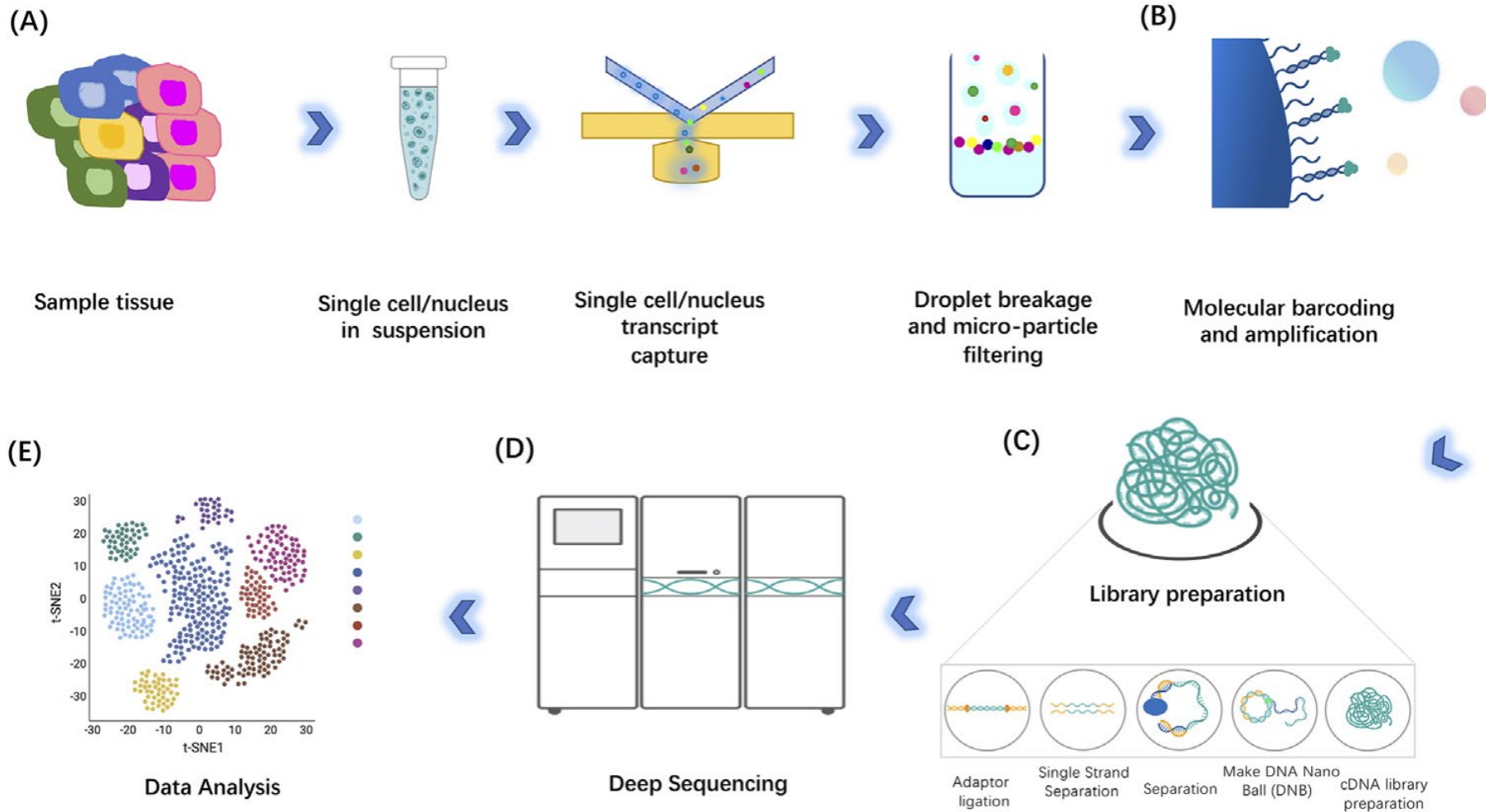


# PART 2

## Introduction



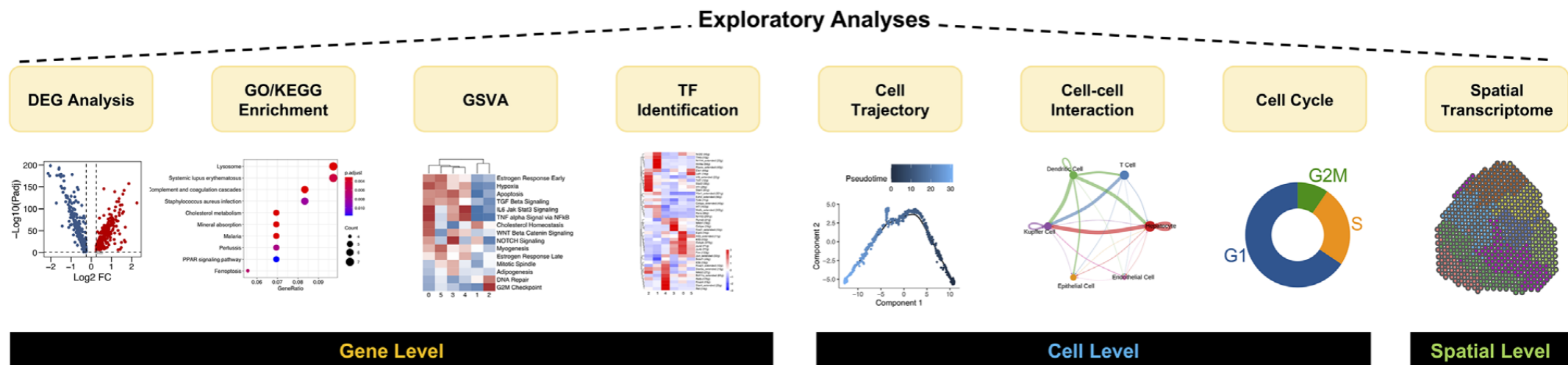
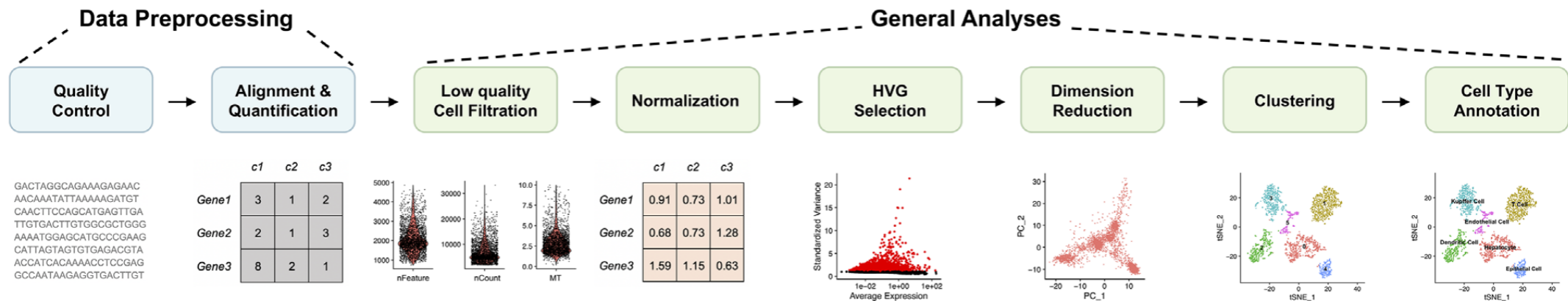
# Introduction – The steps of single-cell RNA sequencing analysis



Jovic Dragomirka, et al. Clin Transl Med, (2022) 12: e694.



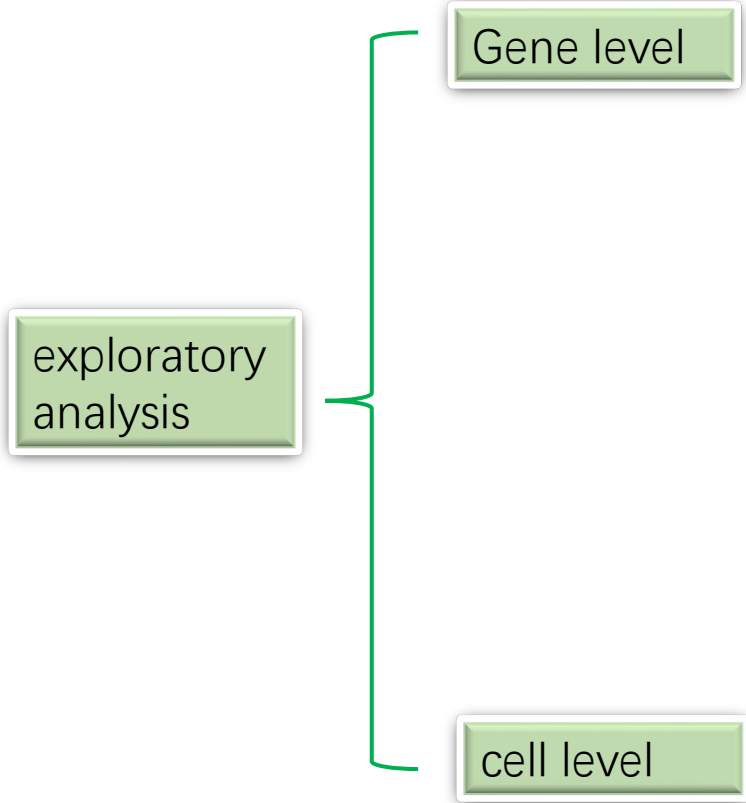
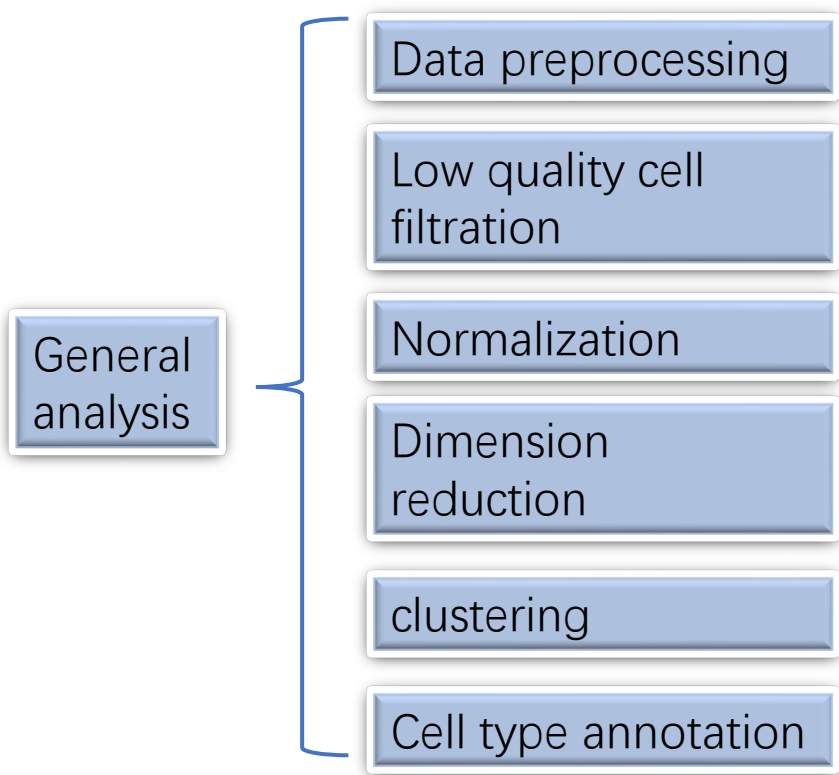
# Introduction – Data Analysis



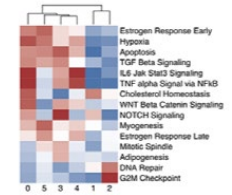
Jovic Dragomirka, et al. Clin Transl Med, (2022) 12: e694.



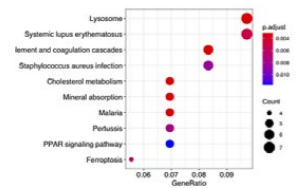
# Introduction – Data Analysis



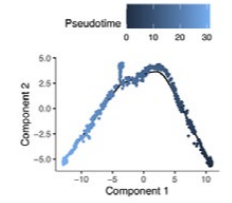
**GSEA**



**GO/KEGG Enrichment**



**Cell Trajectory**



**Cell Cycle**





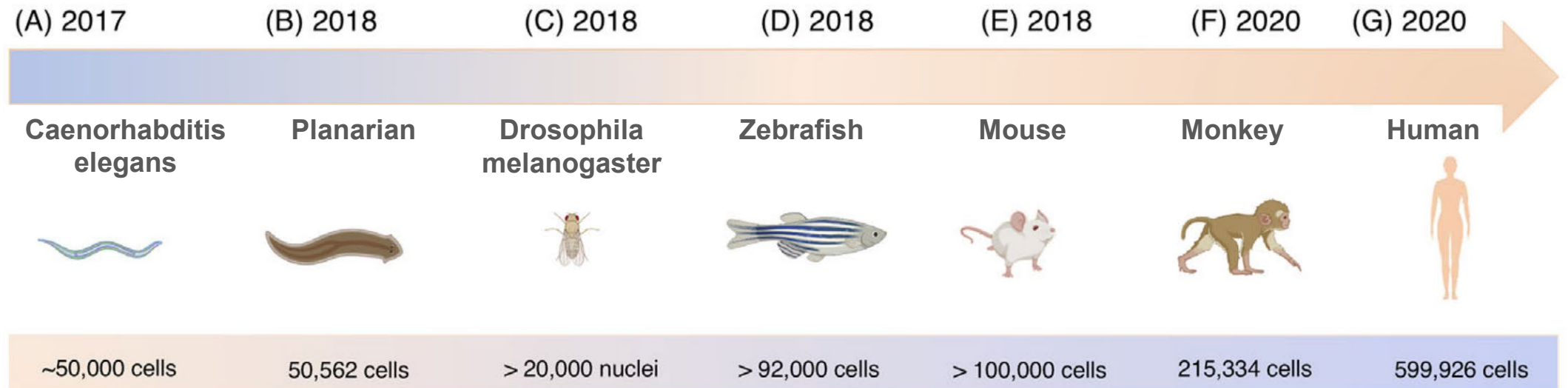


# PART 3

# Application



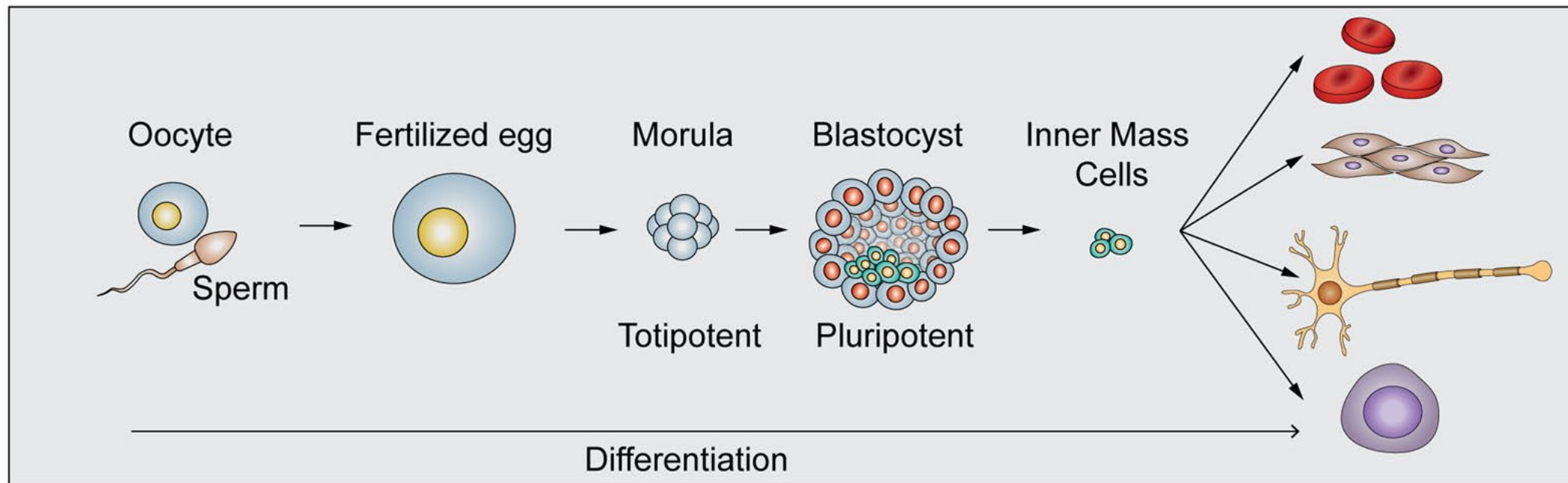
# Application 1 – Single-cell RNA sequencing analysis Atlas



Jovic Dragomirka, et al. Clin Transl Med, (2022) 12: e694.



# Application 2 – Lineage tracing



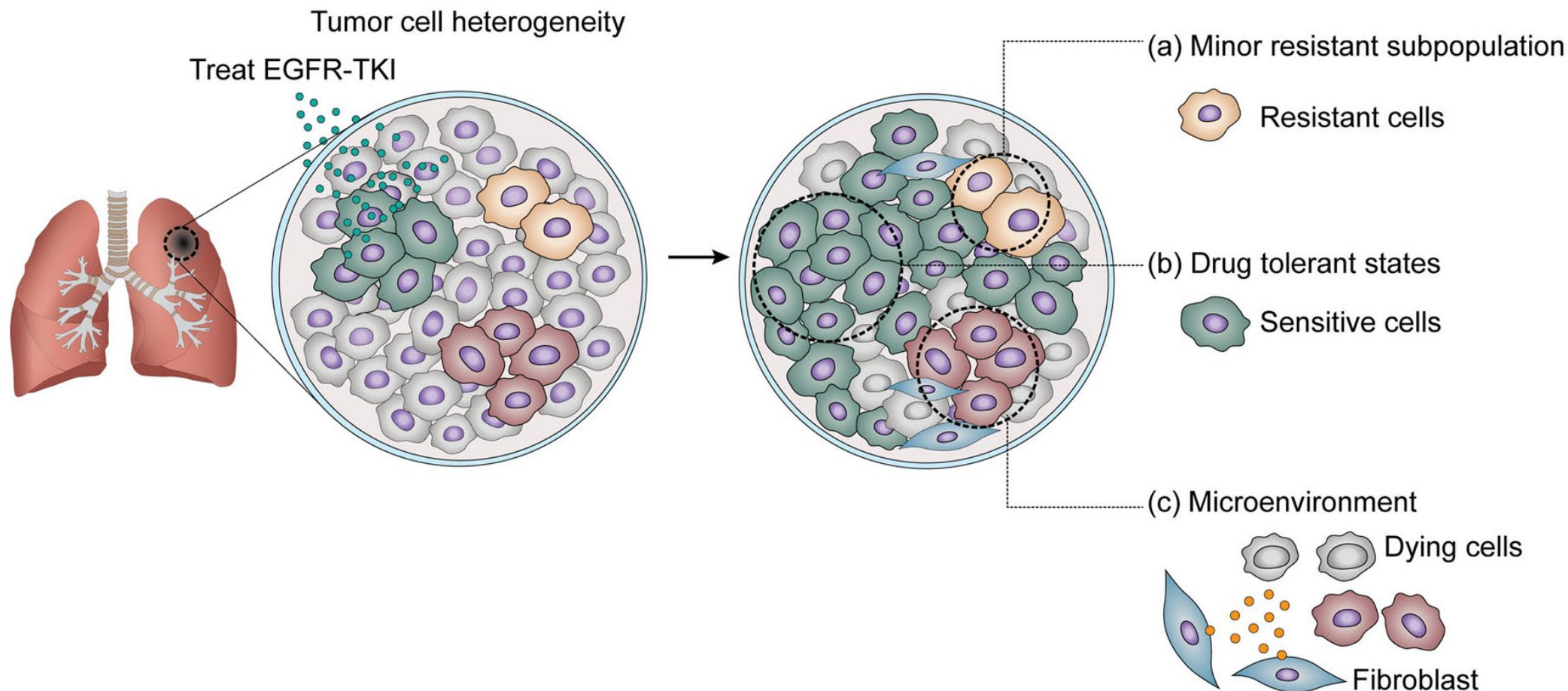
**Lineage tracing:** sequential readout of mRNA levels in a single cell to reconstruct lineage phylogeny over many generations

**Stem cells:** identifying genes involved in stem cell regulatory networks

Hwang Byungjin , et al. Exp Mol Med, (2018) 50: 1-14.



# Application 3 – Development of antitumor drugs

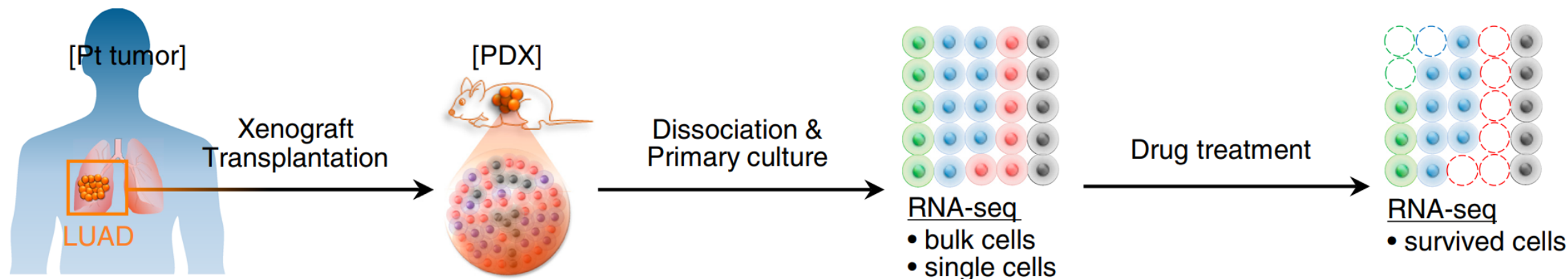


Hwang Byungjin , et al. *Exp Mol Med*, (2018) 50: 1-14.



# Application 3 – Development of anticancer drugs

Patient-derived xenograft cells (PDX) were isolated and cultured from xenograft tumors, and subjected to drug screening



Pt tumor : patient tumor  
LUAD: Lung adenocarcinoma

Kim Kyu-Tae, et al. *Genome Biol.*(2015) 16: 127.



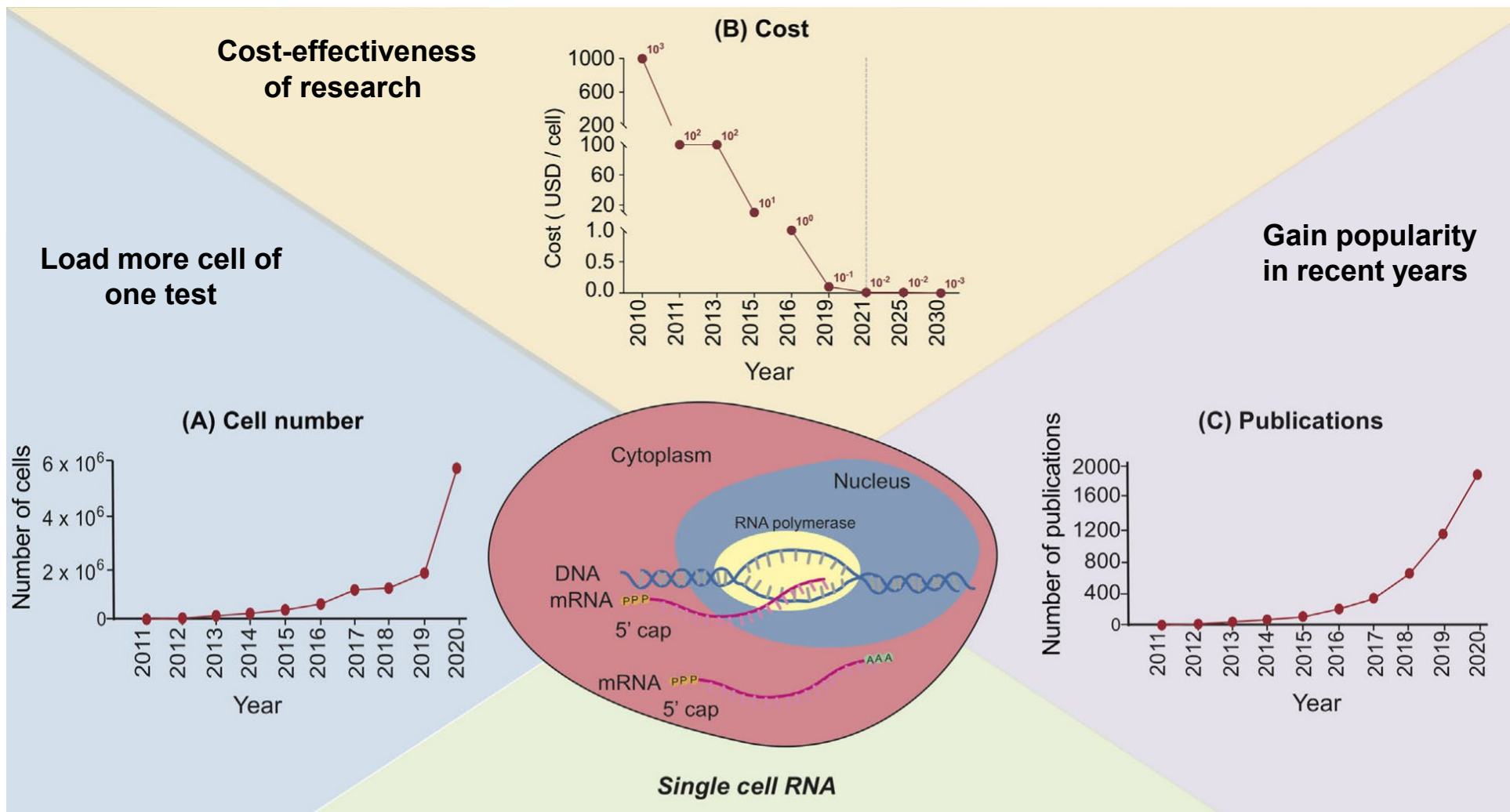
# PART 4

## In science research





# Technological Development – We can use it for scientific research






Jovic Dragomirka, et al. Clin Transl Med, (2022) 12: e694.



## nature communications

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# Single cell transcriptomic analysis of HPV16-infected epithelium identifies a keratinocyte subpopulation implicated in cancer

[Mary C. Bedard](#), [Tafadzwa Chihanga](#), [Adrean Carlile](#), [Robert Jackson](#), [Marion G. Brusadelli](#), [Denis Lee](#), [Andrew VonHandorf](#), [Mark Rochman](#), [Phillip J. Dexheimer](#), [Jeffrey Chalmers](#), [Gerard Nuovo](#), [Maria Lehn](#), [David E. J. Williams](#), [Aditi Kulkarni](#), [Molly Carey](#), [Amanda Jackson](#), [Caroline Billingsley](#), [Alice Tang](#), [Chad Zender](#), [Yash Patil](#), [Trisha M. Wise-Draper](#), [Thomas J. Herzog](#), [Robert L. Ferris](#), [Ady Kendler](#), [Bruce J. Aronow](#), [Matthew Kofron](#), [Marc E. Rothenberg](#), [Matthew T. Weirauch](#), [Koenraad Van Doorslaer](#), [Kathryn A. Wikenheiser-Brokamp](#), [Paul F. Lambert](#), [Mike Adam](#) , [S. Steven Potter](#)  & [Susanne I. Wells](#) 

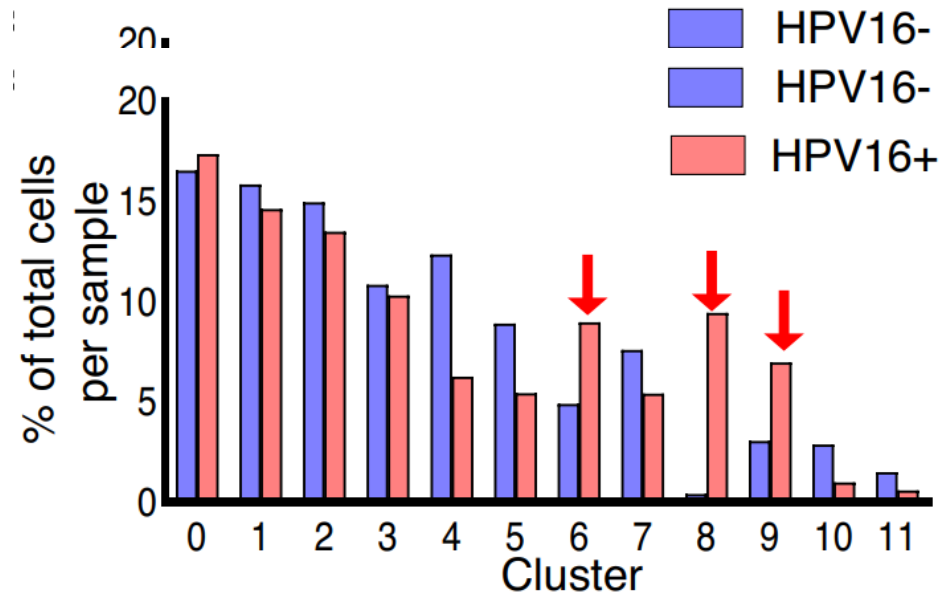
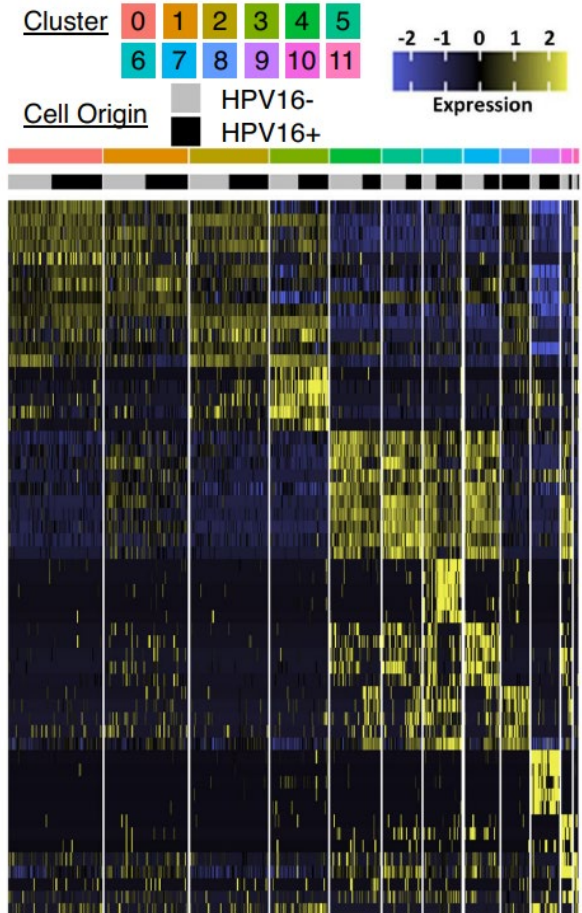
Bedard, M.C. et al. Nat Commun. (2023) 14, 1975.





# Single-Cell analysis related article

ScRNAseq help them found a subset keratinocyte associated with HPV16 infected and cancer formation.



Distribution of cells in HPV16+ and HPV16- epithelium reveals enrichment of HPV16+ cells in C6, C8, and C9 (arrows).

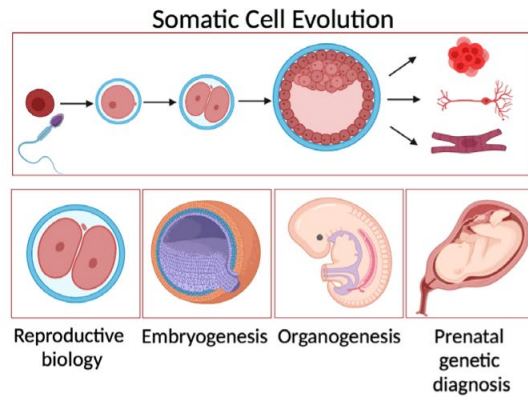
Unbiased clustering reveals 12 transcriptomically distinct cell populations displayed as a heatmap.

Bedard, M.C. et al. Nat Commun. (2023) 14, 1975.

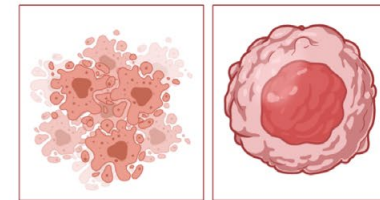


# Single-cell analysis is very helpful to us

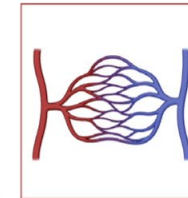
(A) Development



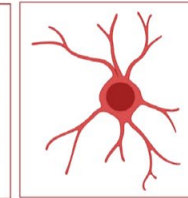
(F) Cancer Biology



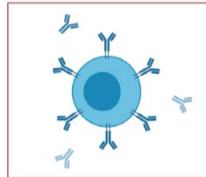
(G) Vascular Biology



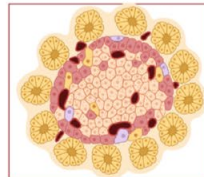
(H) Neurobiology



(B) Immunology



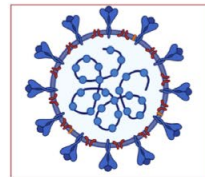
(C) Diabetes



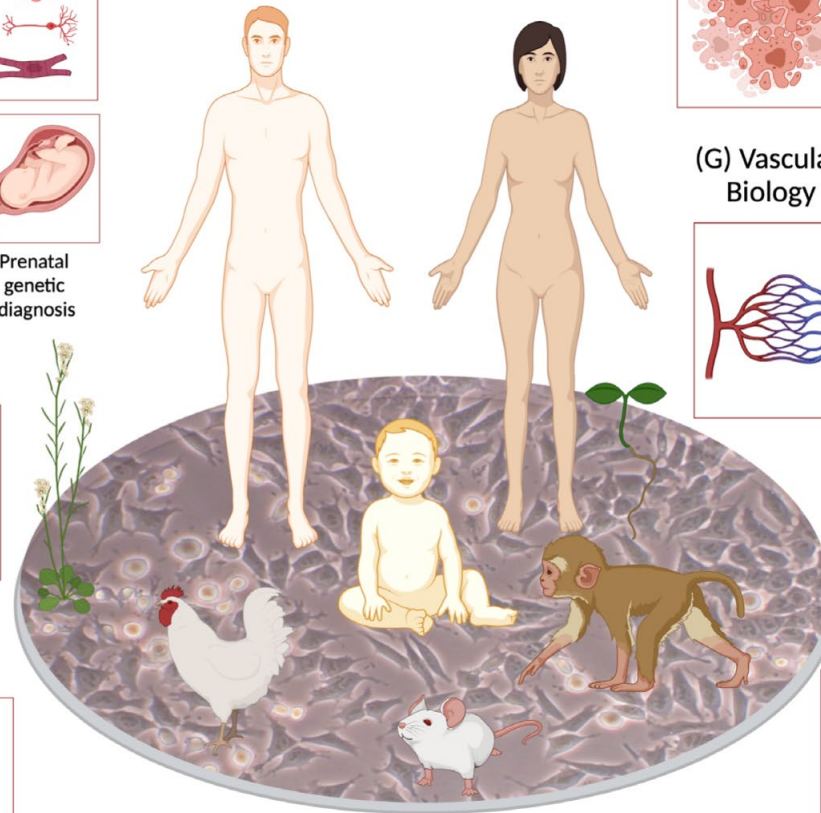
(D) Microbiology



(E) COVID-19



(I) Clinical Diagnostic



Jovic Dragomirka, et al. Clin Transl Med, (2022) 12: e694.



# Reference

- [1] Trapnell C .Genome Res. Defining cell types and states with single-cell genomics. [J]. (2015) 25:1491–1498
- [2] Tang, F., Barbacioru, C., Wang, Y. *et al.* mRNA-Seq whole-transcriptome analysis of a single cell. *Nat Methods* . [J]. 2009, 6, 377–382
- [3] Shalek, A., Satija, R., Adiconis, X. *et al.* Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. *Nature* . [J]. 2013, 498, 236–240
- [4] Islam, S., Zeisel, A., Joost, S. *et al.* Quantitative single-cell RNA-seq with unique molecular identifiers. *Nat Methods* . [J]. 2014, 11, 163–166
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- [6] Jovic Dragomirka, et al. Clin Transl Med, Single-cell RNA sequencing technologies and applications: A brief overview.[J]. 2022, 12: e694.
- [7] Hwang Byungjin , et al. Exp Mol Med, Single-cell RNA sequencing technologies and bioinformatics pipelines.[J]. 2018, 50: 1-14.
- [8] Kim Kyu-Tae, et al. Genome Biol, Single-cell mRNA sequencing identifies subclonal heterogeneity in anti-cancer drug responses of lung adenocarcinoma cells.[J]. 2015, 16: 127.
- [8] Bedard, M.C., Chihanga, T., Carlile, A. et al. Single cell transcriptomic analysis of HPV16-infected epithelium identifies a keratinocyte subpopulation implicated in cancer. *Nat Commun*. [J]. 2023, 14, 1975

