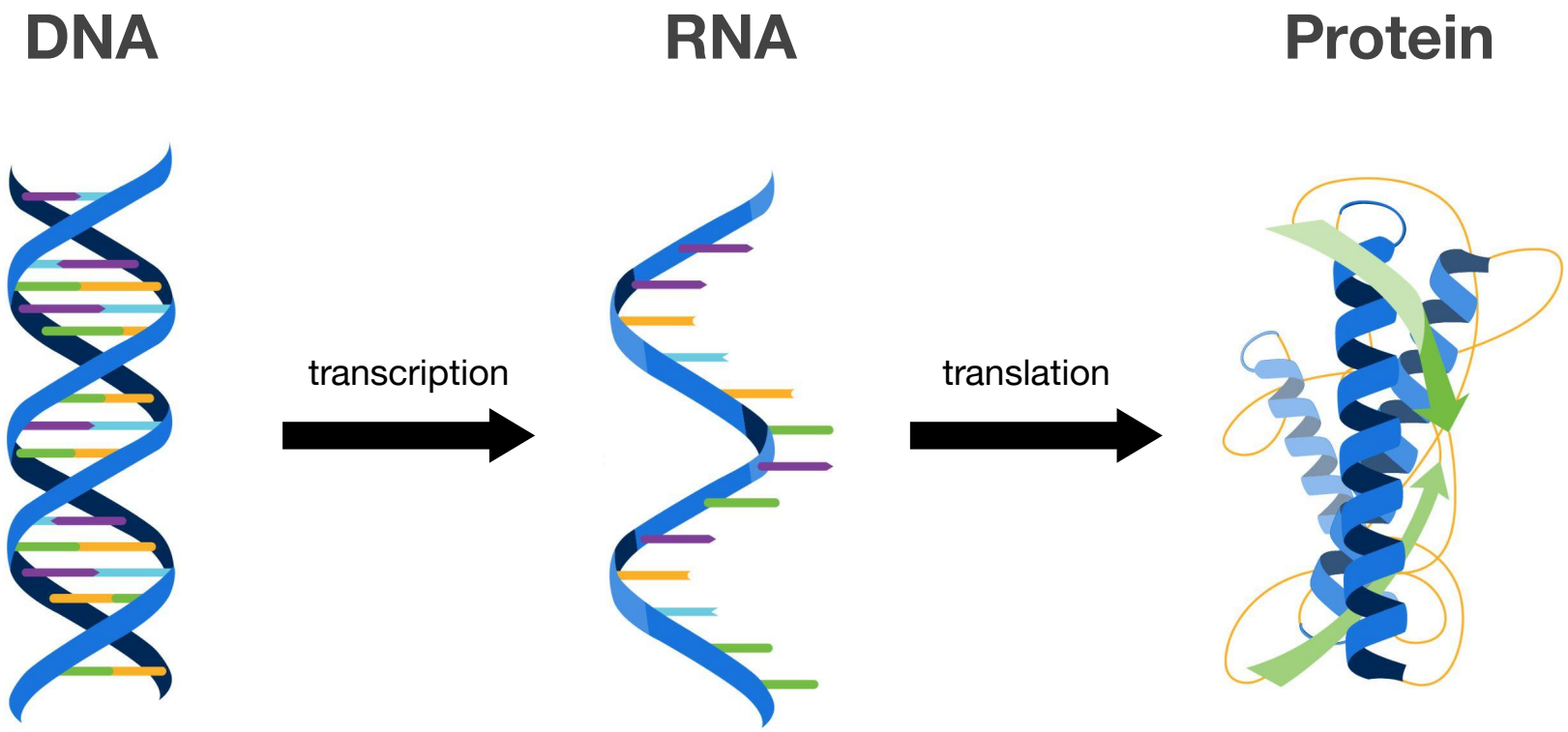
LA's BeST @USC

Single-Cell RNA Sequencing Project

Kelly Street
Assistant Professor
Division of Biostatistics
Keck School of Medicine
June 17, 2024

USC University of Southern California

The Central Dogma



Cell Types

44.5M Cells

ALL CELLS

- Blood
- Kidney
- Bone
- Liver
- Brain
- Lung
- Pancreas
- Heart
- Immune System
- Skin

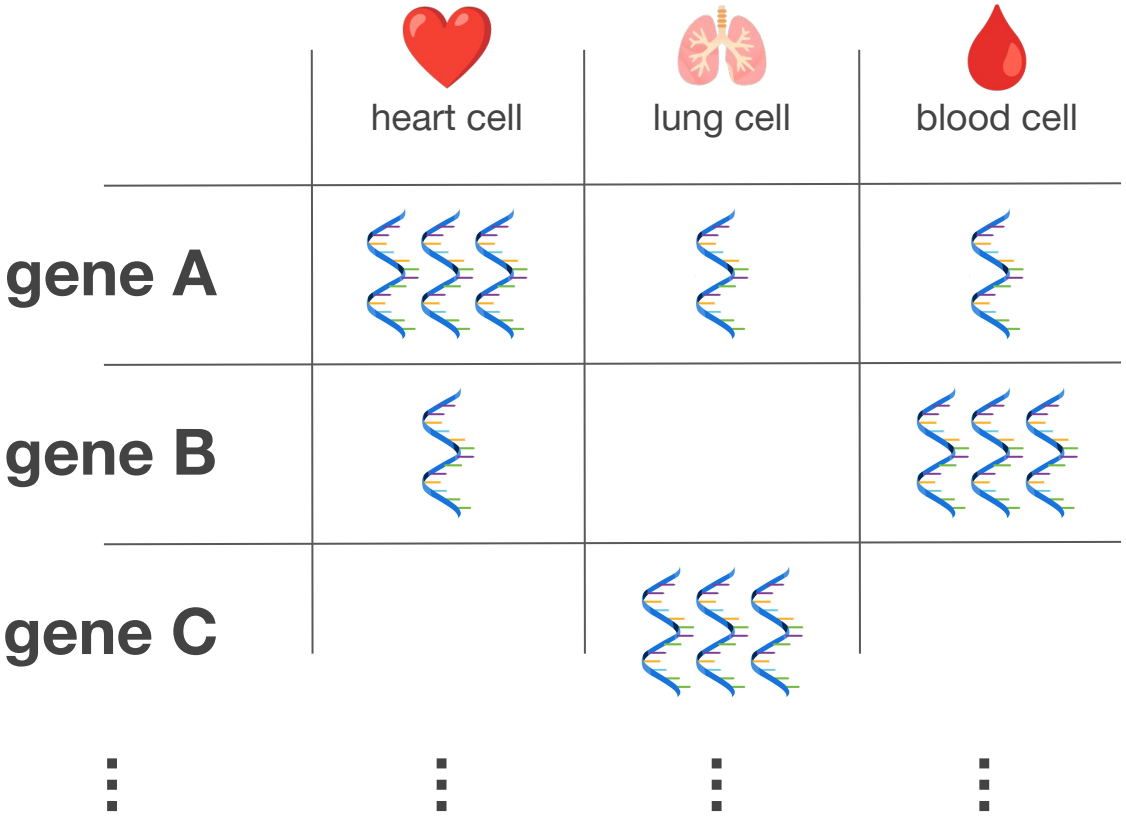
HUMAN CELL ATLAS

Why Single Cell?

Bulk

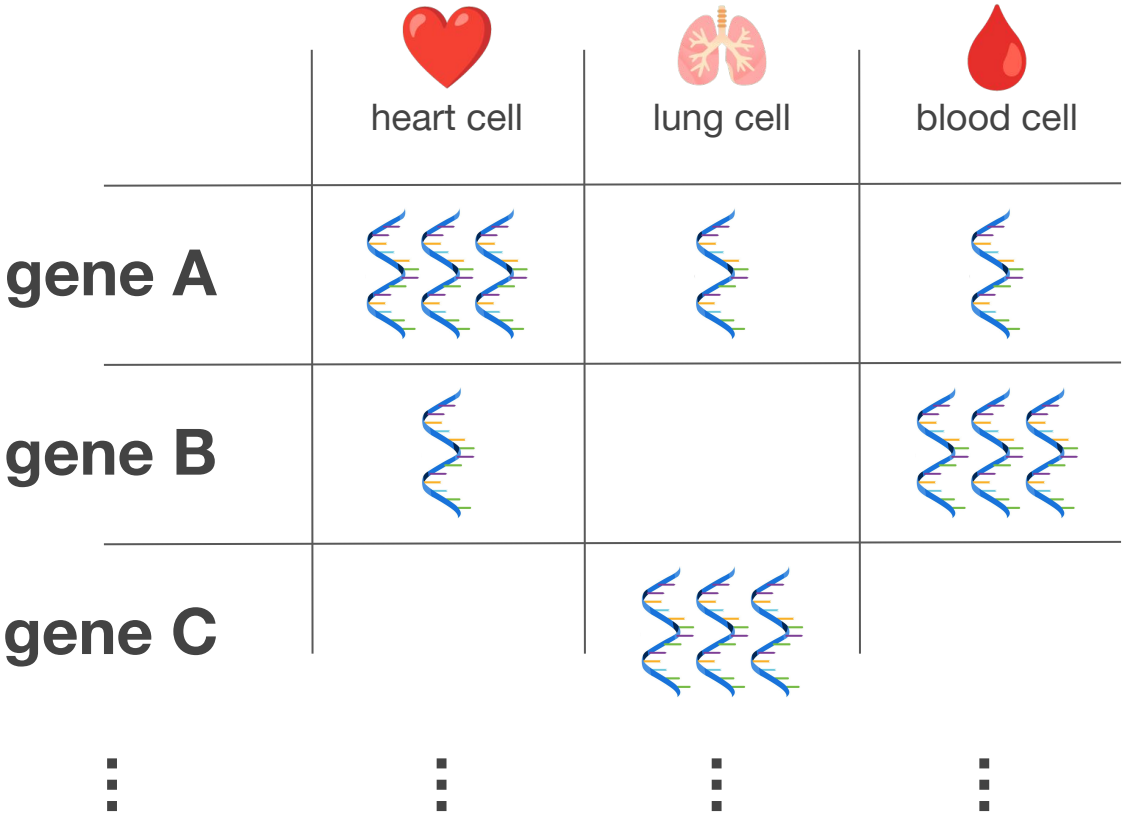
Single Cell

Gene Expression



The Human Genome Project estimated that we have **20,000 - 25,000** genes

Gene Expression



Single-Cell RNA Sequencing

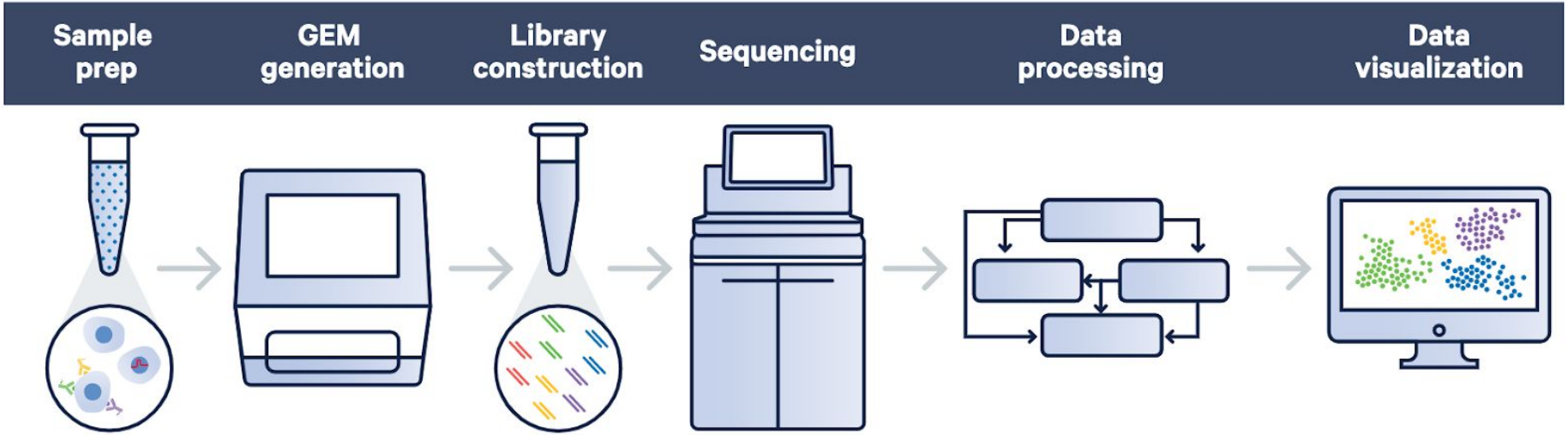
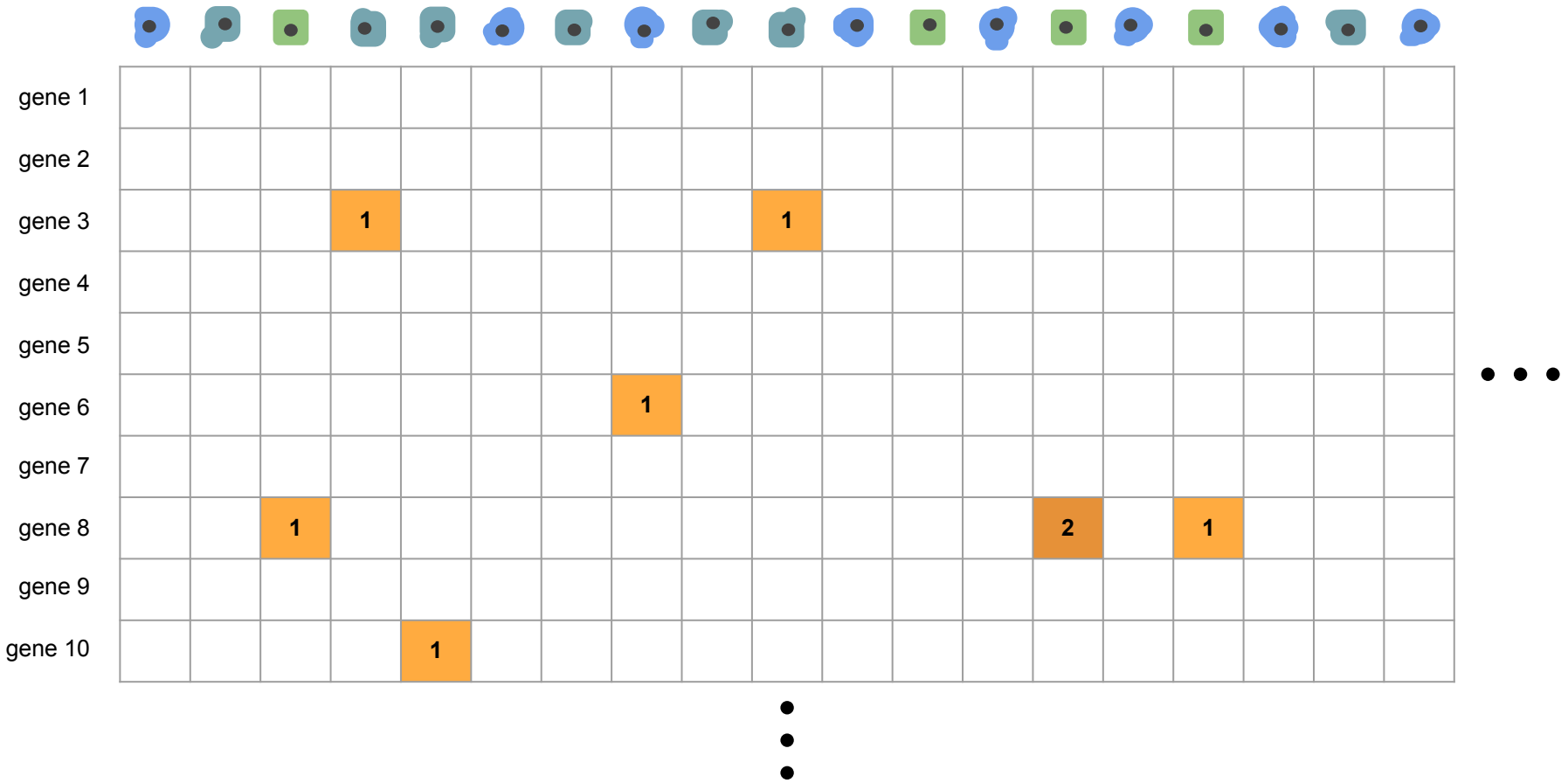


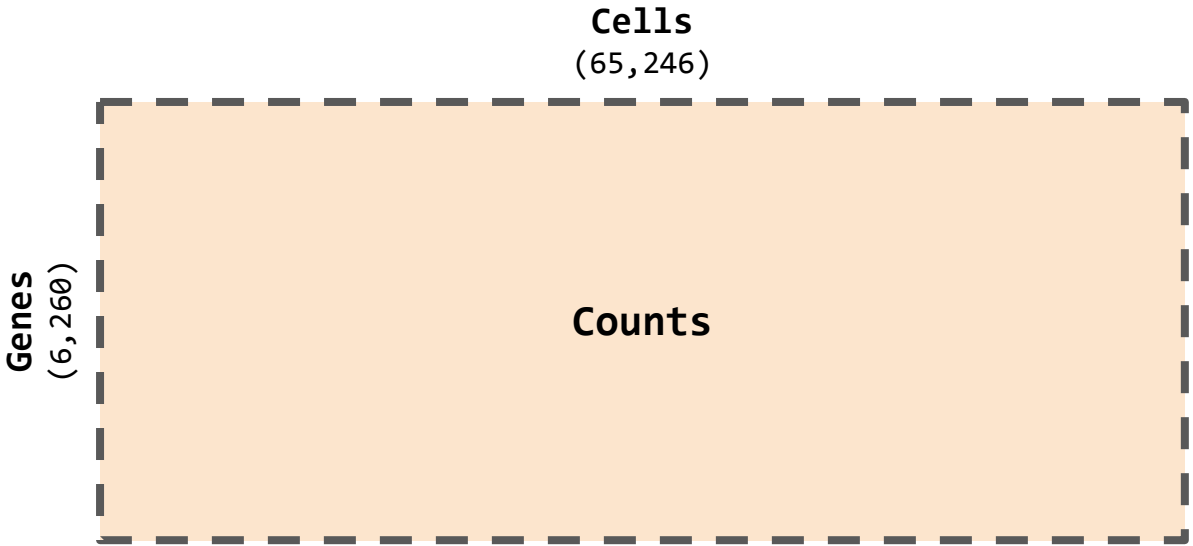
Figure 2. Efficient and streamlined workflow for multiomic profiling of biological systems. Start with a single cell suspension of unlabeled cells, oligo-conjugated antibody-labeled cells, or cells expressing compatible CRISPR guides. After GEM generation, separate libraries can be constructed from a single sample, including gene expression and cell surface protein or CRISPR guide libraries, generating multiple readouts that can be linked back to the same single cell. Process data with Cell Ranger, and visualize sample heterogeneity with Loupe Browser, our fully integrated and easy-to-use analysis and visualization software.

10x GENOMICS

scRNAseq Data



scRNAseq Data



Renal Cell Carcinoma

CellPress

Cancer Cell

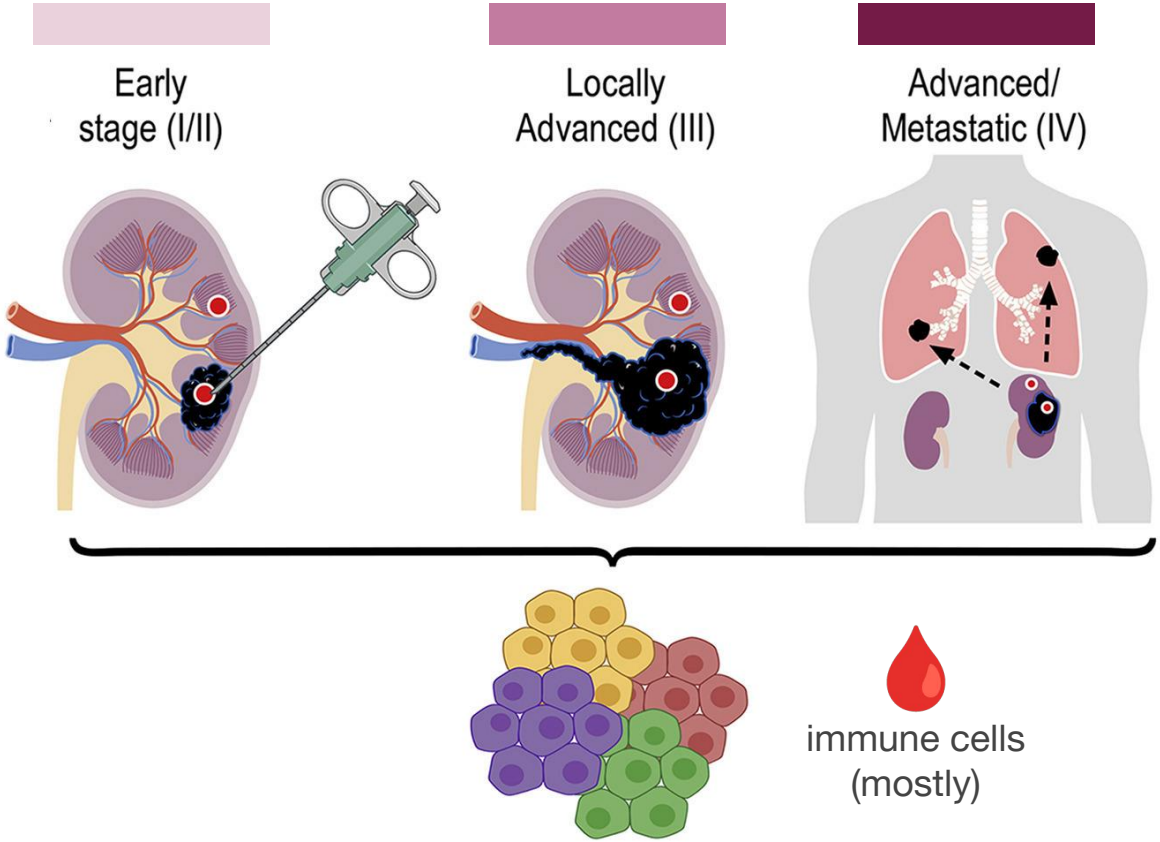
Article

Progressive immune dysfunction with advancing disease stage in renal cell carcinoma

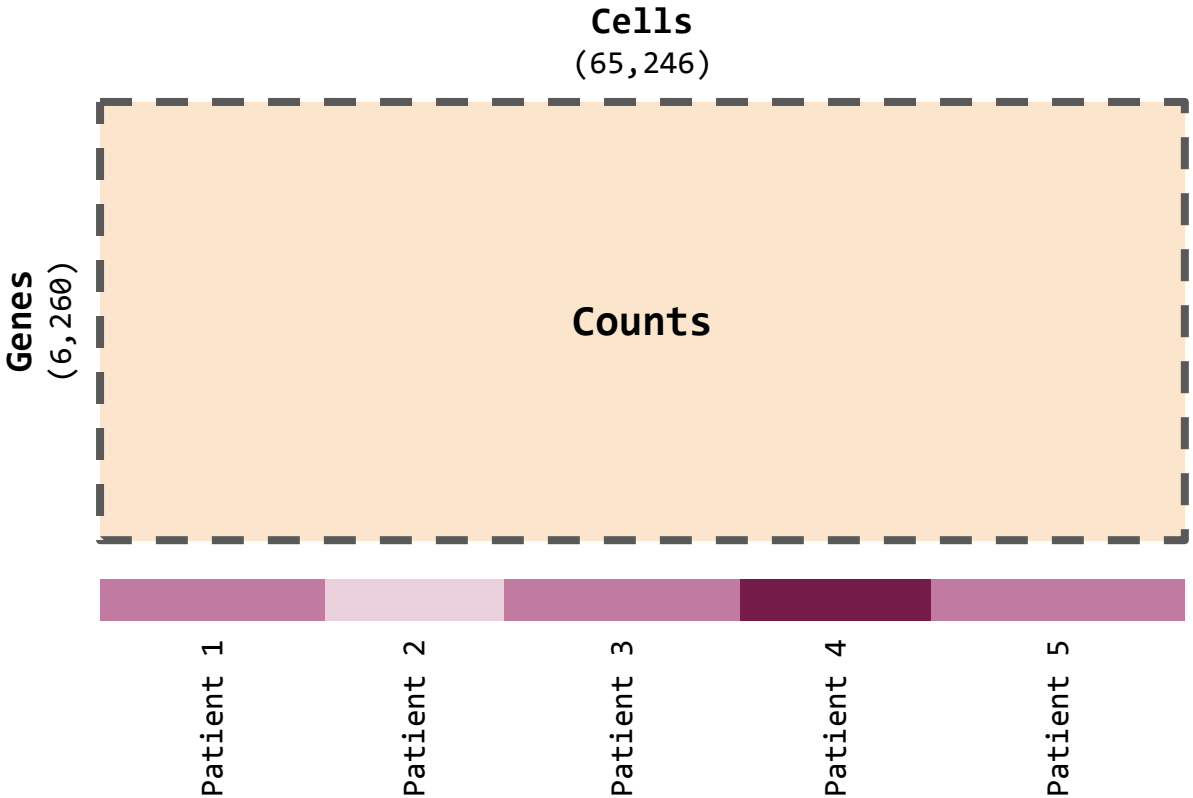
David A. Braun,[1,2,3,17] Kelly Street,[4,5,17] Kelly P. Burke,[1,2,6] David L. Cookmeyer,[2,6] Thomas Denize,[2,7] Christina B. Pedersen,[8,9] Satyen H. Gohil,[1,2,3,10] Nicholas Schindler,[1] Lucas Pomerance,[1,2] Laure Hirsch,[1,2] Ziad Bakouny,[1] Yue Hou,[1,11] Juliet Forman,[1,3,11] Teddy Huang,[1,11] Shuqiang Li,[1,3,11] Ang Cui,[3,12] Derin B. Keskin,[1,3,11] John Steinharter,[1] Gabrielle Bouchard,[1] Maxine Sun,[1] Erica M. Pimenta,[1,2] Wenxin Xu,[1,2] Kathleen M. Mahoney,[1,2,13] Bradley A. McGregor,[1,2] Michelle S. Hirsch,[2,7] Steven L. Chang,[2,14] Kenneth J. Livak,[1,11] David F. McDermott,[2,13] Sachet A. Shukla,[3,11] Lars R. Olsen,[8,9] Sabina Signoretti,[2,7,15] Arlene H. Sharpe,[2,6,7,16] Rafael A. Irizarry,[4,5] Toni K. Choueiri,[1,2,18] and Catherine J. Wu[1,2,3,18,19,*]

[1]Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA 02215, USA
[2]Harvard Medical School, Boston, MA 02215, USA
[3]Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA
[4]Department of Data Science, Dana-Farber Cancer Institute, Boston, MA 02215, USA
[5]Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston, MA 02215, USA
[6]Department of Immunology, Blavatnik Institute, Harvard Medical School, Boston, MA 02215, USA
[7]Department of Pathology, Brigham and Women's Hospital, Boston, MA 02115, USA
[8]Section for Bioinformatics, Department of Health Technology, Technical University of Denmark, Kongens Lyngby, Denmark

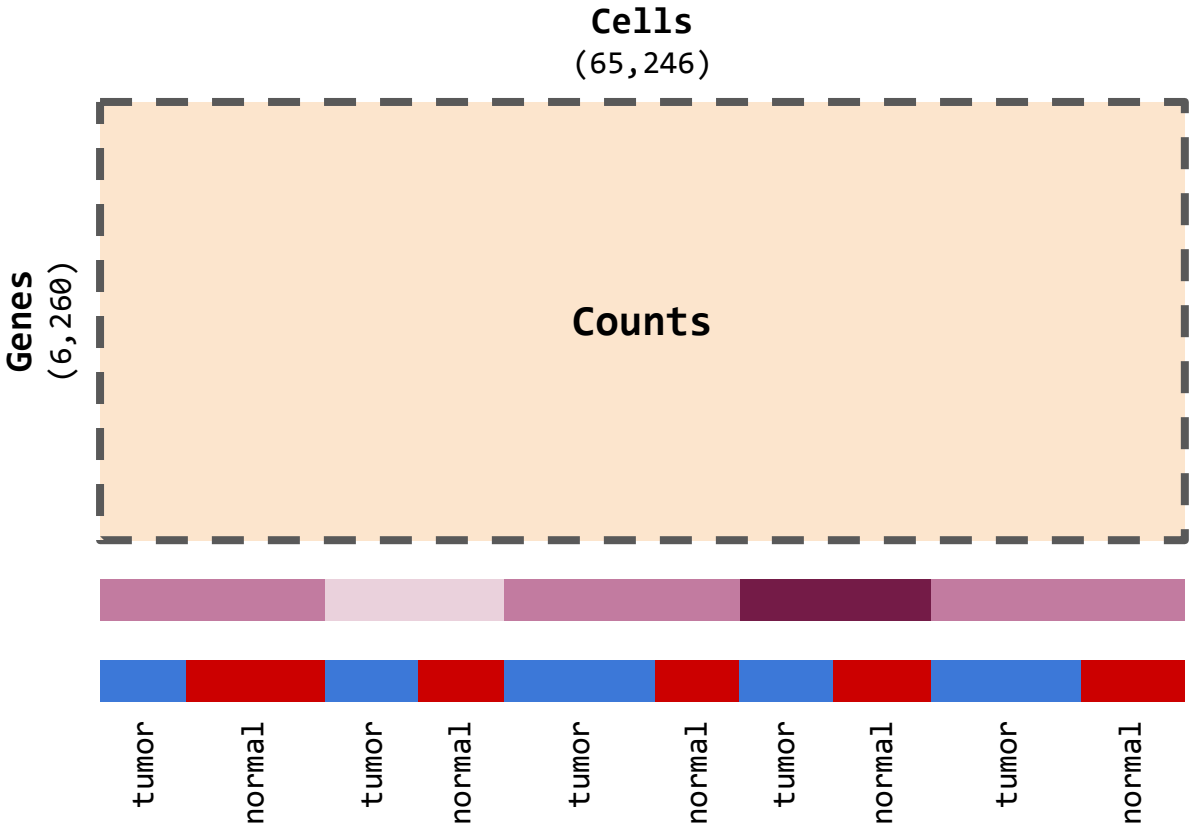
Renal Cell Carcinoma



Gene Expression



Gene Expression

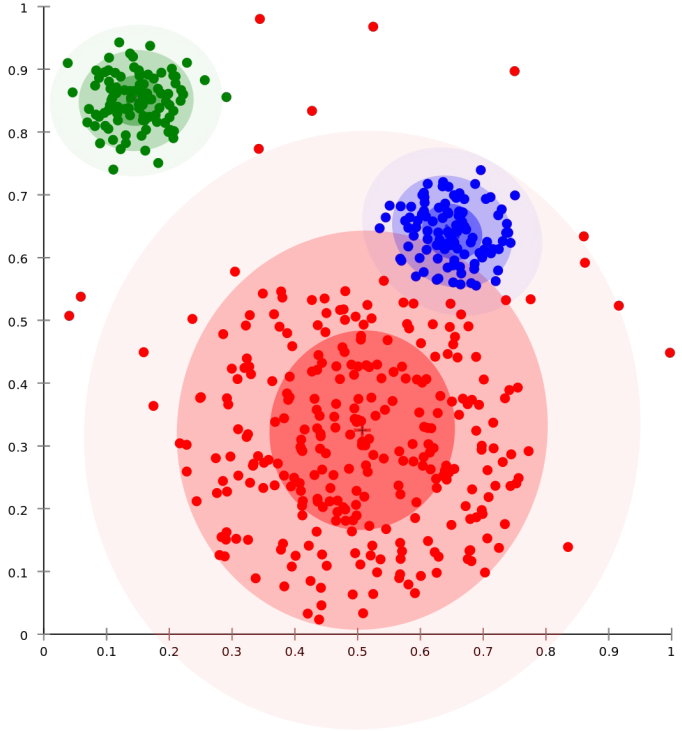


Question 1:

What **cell types** are present?

Clustering

Identify groups of cells with **similar** expression profiles

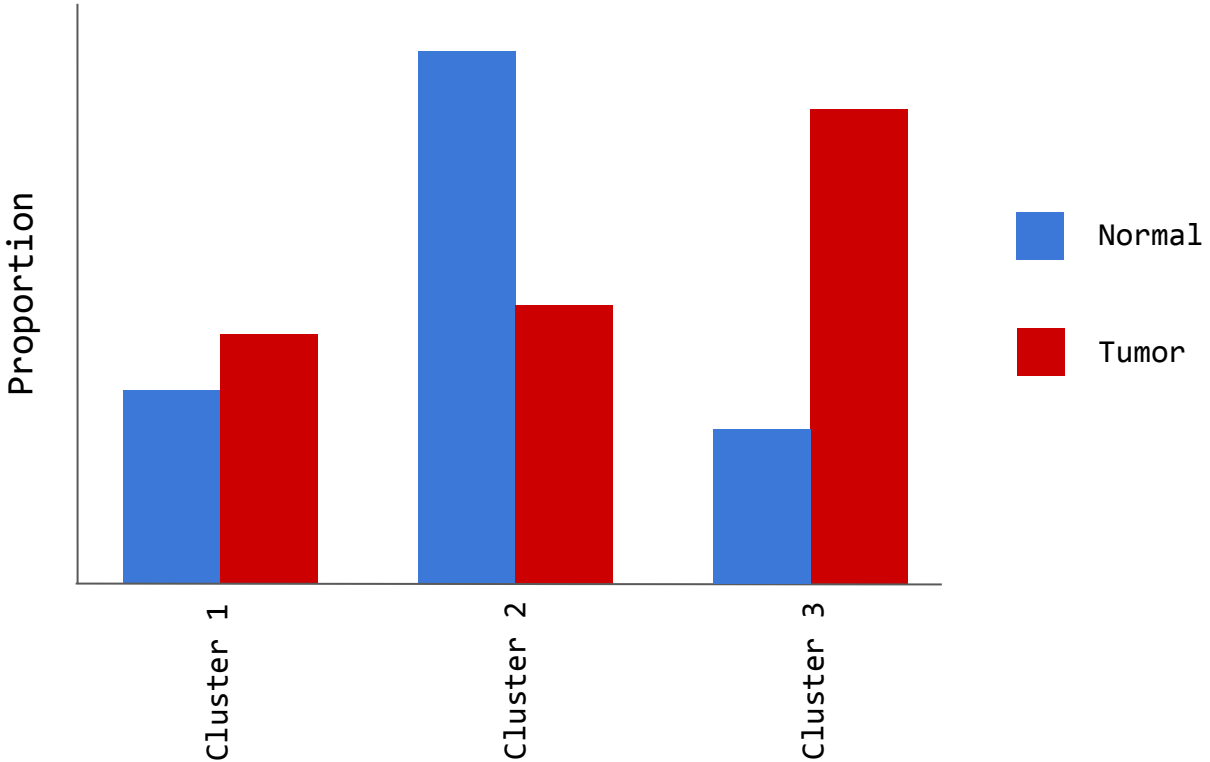
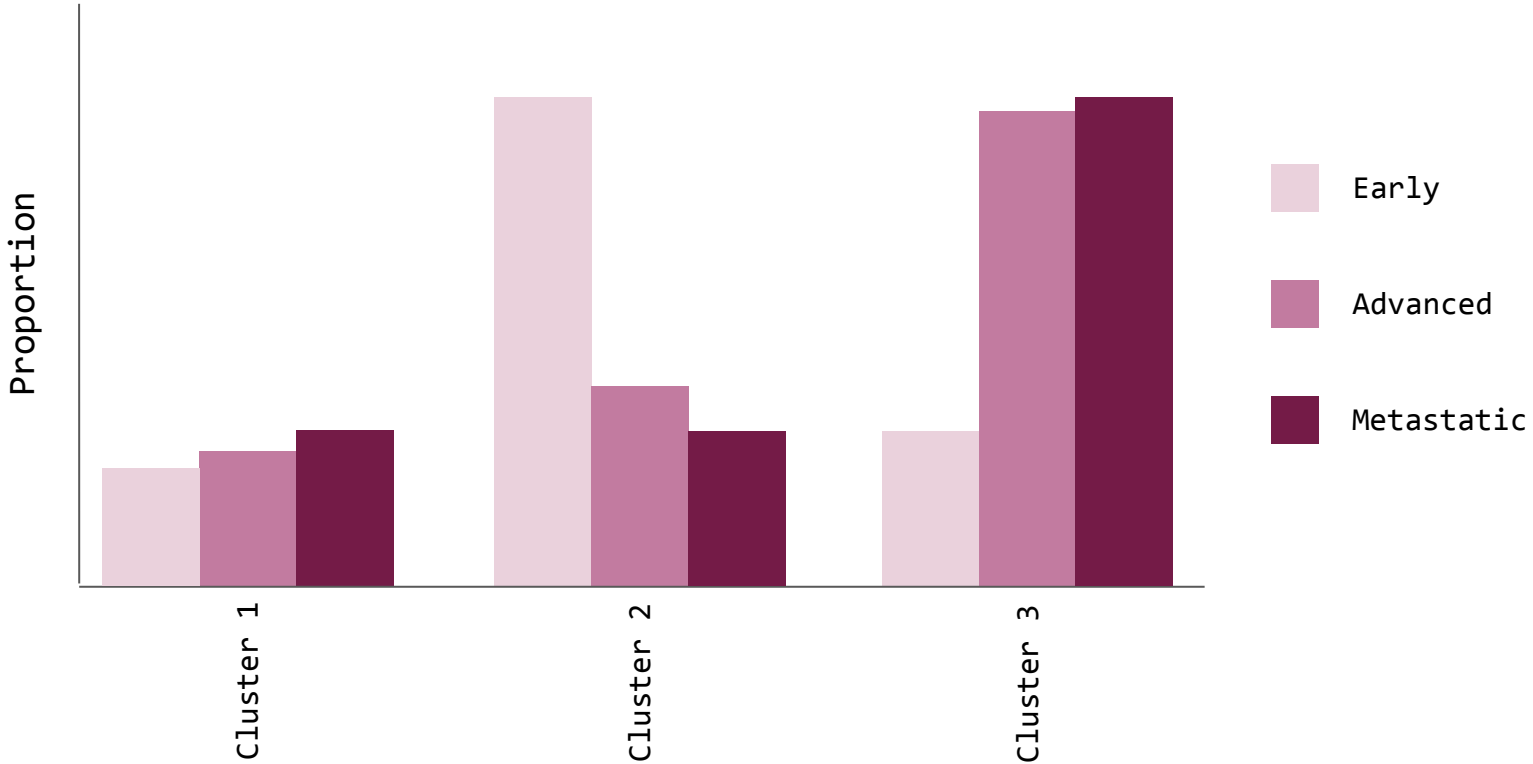


WIKIMEDIA COMMONS

Question 2:

Which cell types are **associated with disease**?

Differential Abundance



Differential Abundance