Article | Published: 03 October 2018

Single-cell transcriptomics of 20 mouse organs creates a *Tabula Muris*

The Tabula Muris Consortium, Overall coordination, Logistical coordination, Organ collection and processing, Library preparation and sequencing, Computational data analysis, Cell type annotation, Writing group, Supplemental text writing group & Principal investigators

Nature **562**, 367–372 (2018) | Cite this article

A **collection** of **sc-RNA data** from **mouse** (>100k cells) from **20 organs and tissues**

“A mouse Atlas”

Intervention:

- Create a resource of single cell transcriptome data (mouse)
- Characterize various cell populations
- Comparisons across cell types
    - Same cell type in different tissues?

Data Description

3 female mice, 4 male mice
10-15 weeks (20 yrs in human)
20 organs

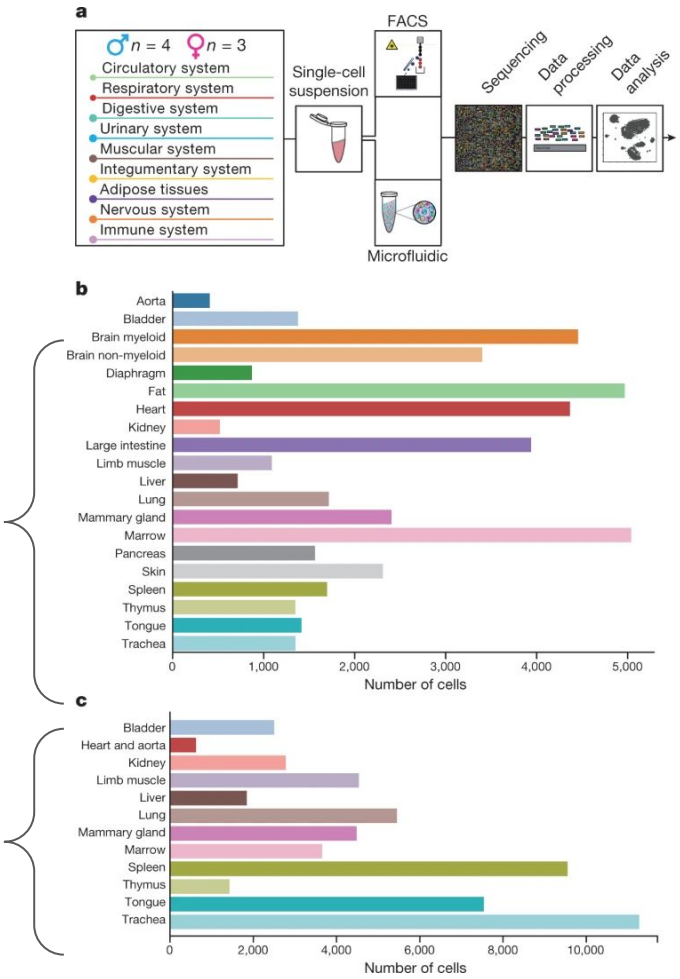
Two distinct technical approaches:

FACS-based full length transcript

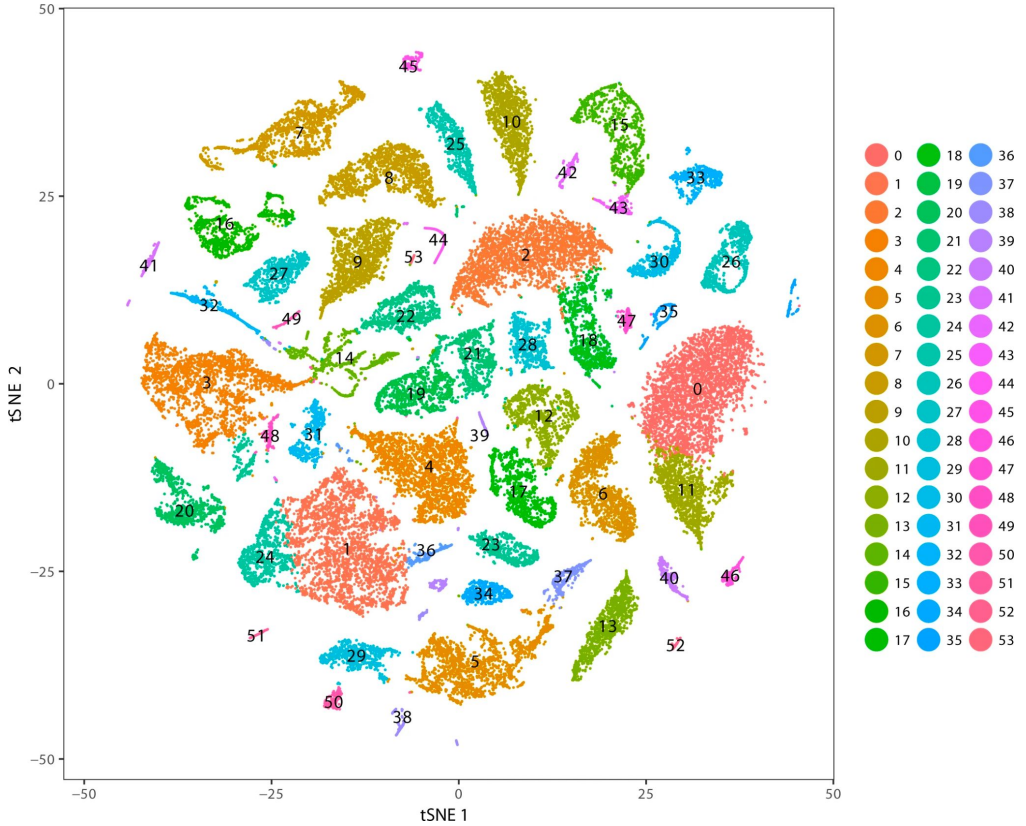
~ 45k cells
~800k reads

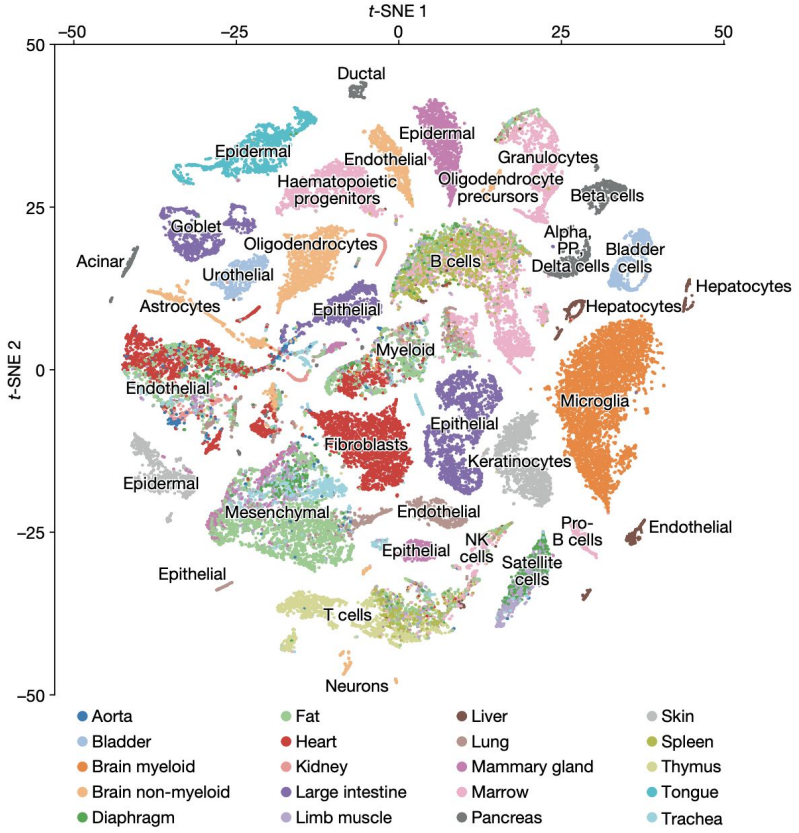
Microfluidic droplet-based 3’-end

~ 55k cells
~ 8k UMIs



How single-cell technology useful here?

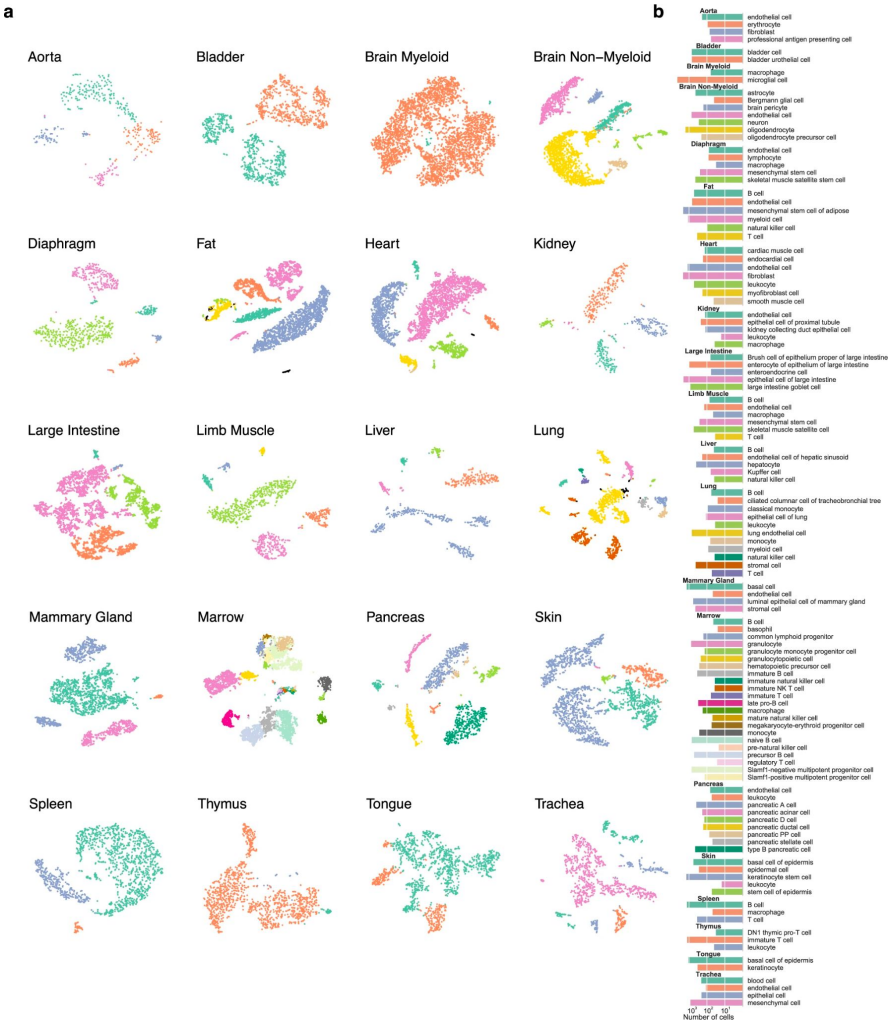




Organs/Tissue source is not sufficient to cluster cells

How single-cell technology useful here?

Many cell types in the different organs!

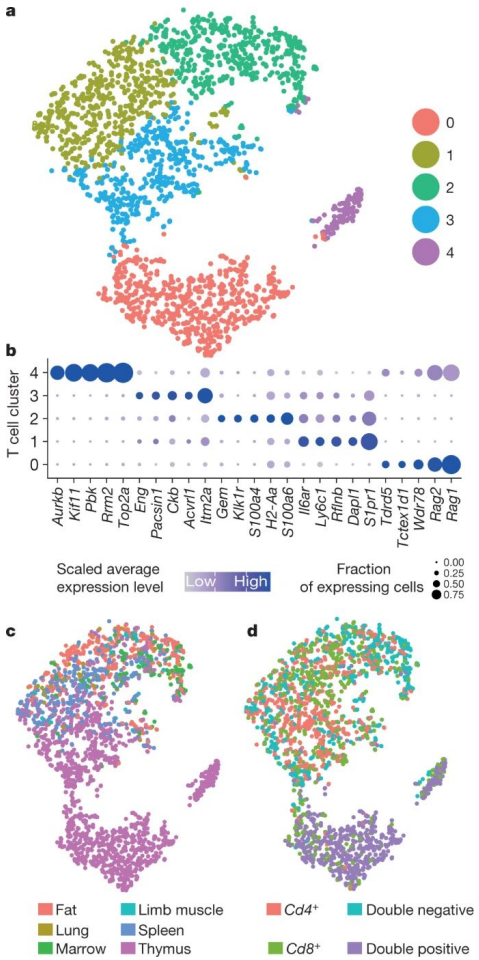


How single-cell technology useful here?

- Cell-types cluster together regardless of tissue.
  - Examples: T-cells, B-cells, Endothelial cells.

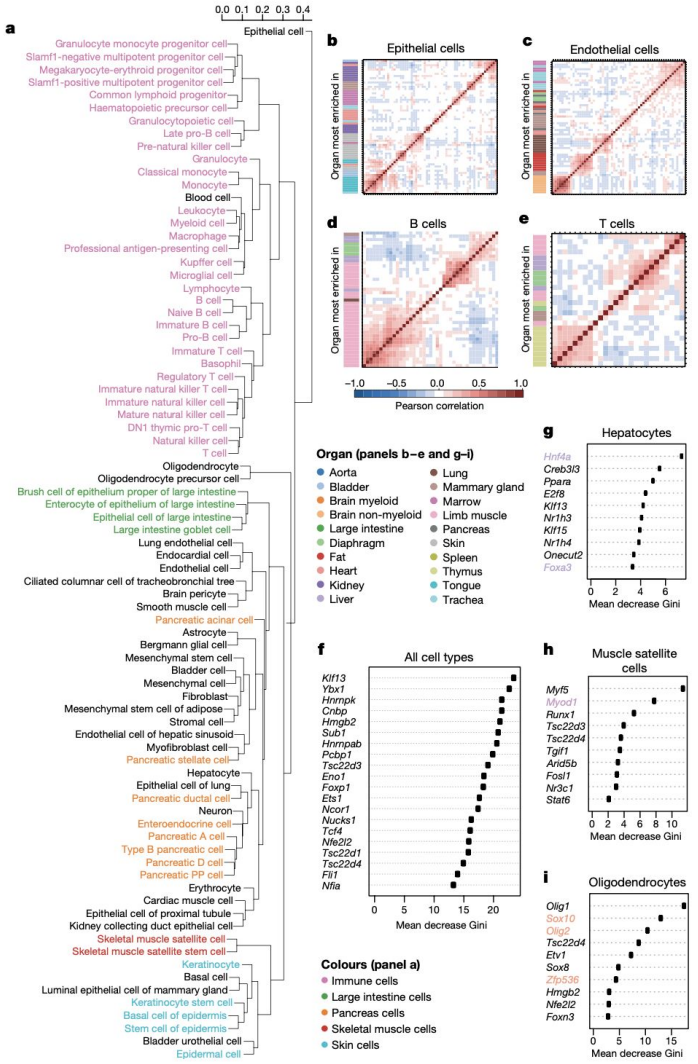
How single-cell technology useful here?

- Characterization of sub-populations
  - i.e., Cell states
    - Cluster 0: thymic cells undergoing VDJ recombination
    - Cluster 1: represents mature T cells
- Shared vs unique ‘signatures/markers’



How single-cell technology useful here?

- TFs recover cell-type relations
- Identify characteristic TFs
  - Cell type specific
  - tissue specific
- Identify TFs with notably dispersion
  - includes some already used in reprogramming.



In summary

- Single-cell recovers heterogeneity in tissues.
- Cell type information drives clustering in gene expression space.
- Cell-types include many subtypes
- Subtypes can be characterized by their gene expression and corresponding TFs
- Identification or rare cell types
- Atlas: Serve as a reference (baseline) for healthy cell populations