

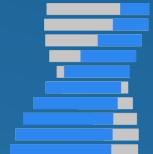
# Single Cell Genomics @ NGI

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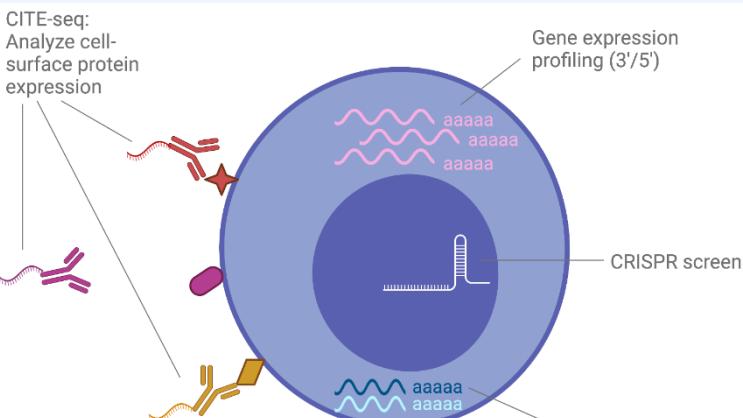
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 SciLifeLab

# Our Services

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**Gene Expression**



CITE-seq:  
Analyze cell-surface protein expression

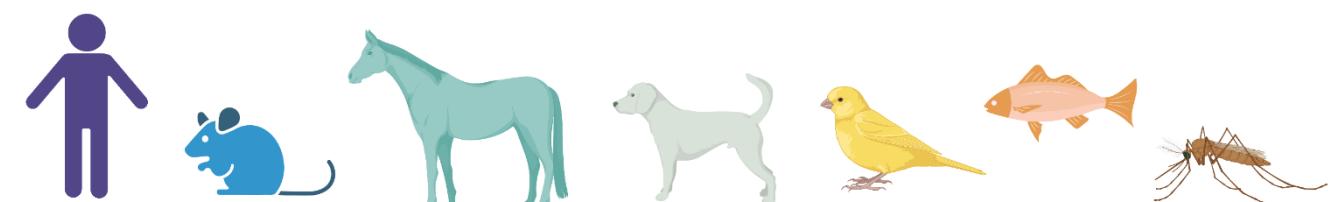
Gene expression profiling (3'/5')

CRISPR screen

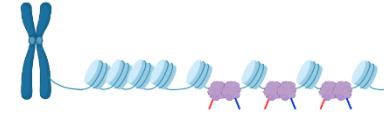
VDJ, B/T cell receptors

10x Genomics

- 3'/5' GEX
- CITE-seq
- Cell hashing
- VDJ
- FLEX



**Epigenetics**

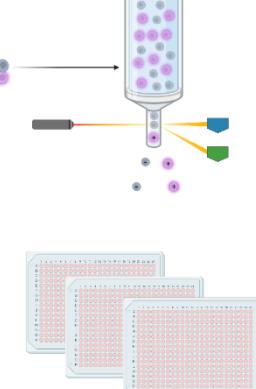


10x Genomics

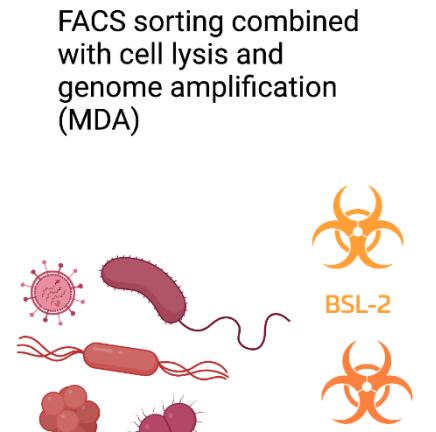
- scATAC-seq
- scATAC + GEX

scWBGS (SPLAT)

- Raine et al, 2022



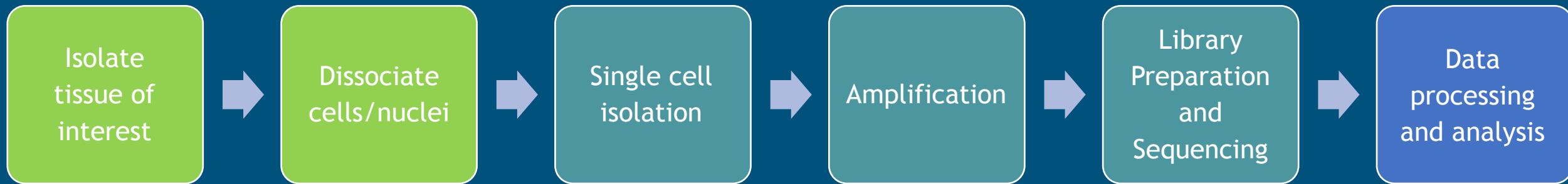
FACS sorting combined  
with cell lysis and  
genome amplification  
(MDA)



 BSL-2

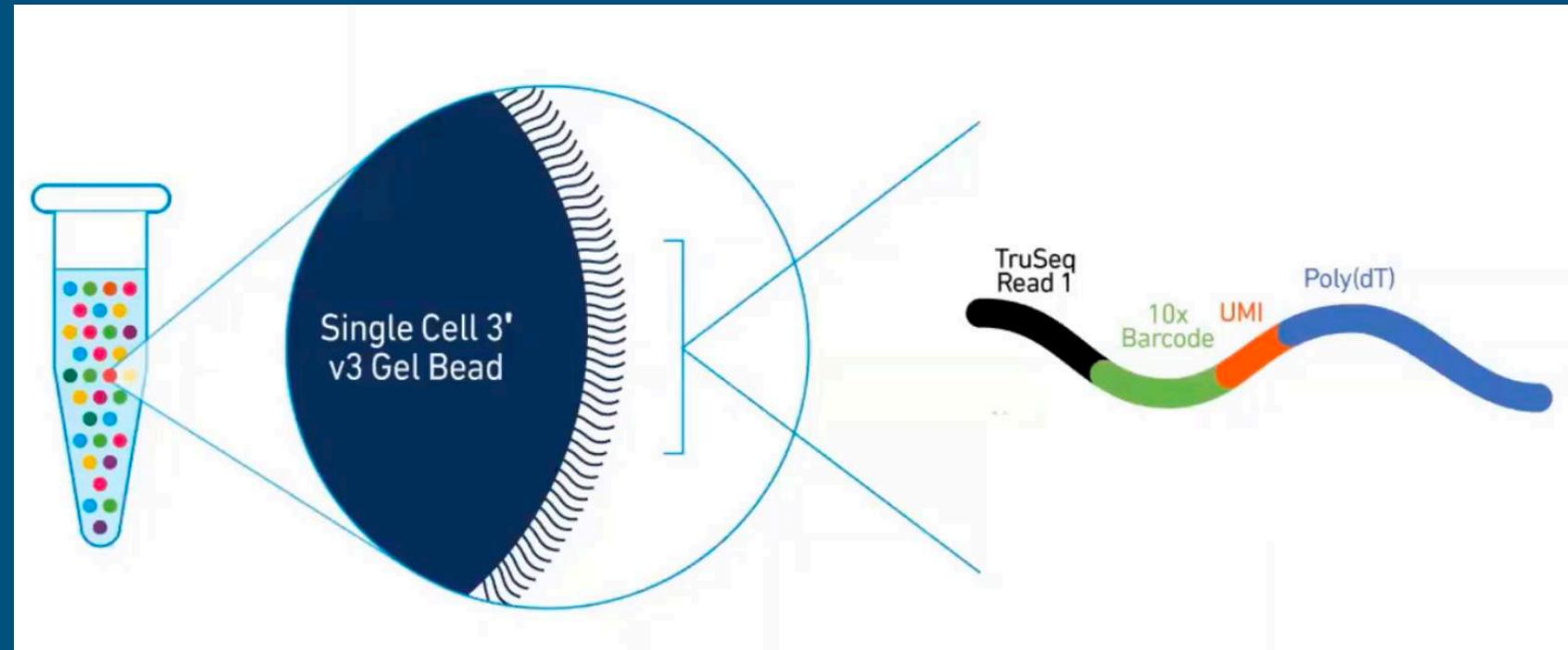
 BSL-3

# Single cell sequencing workflow

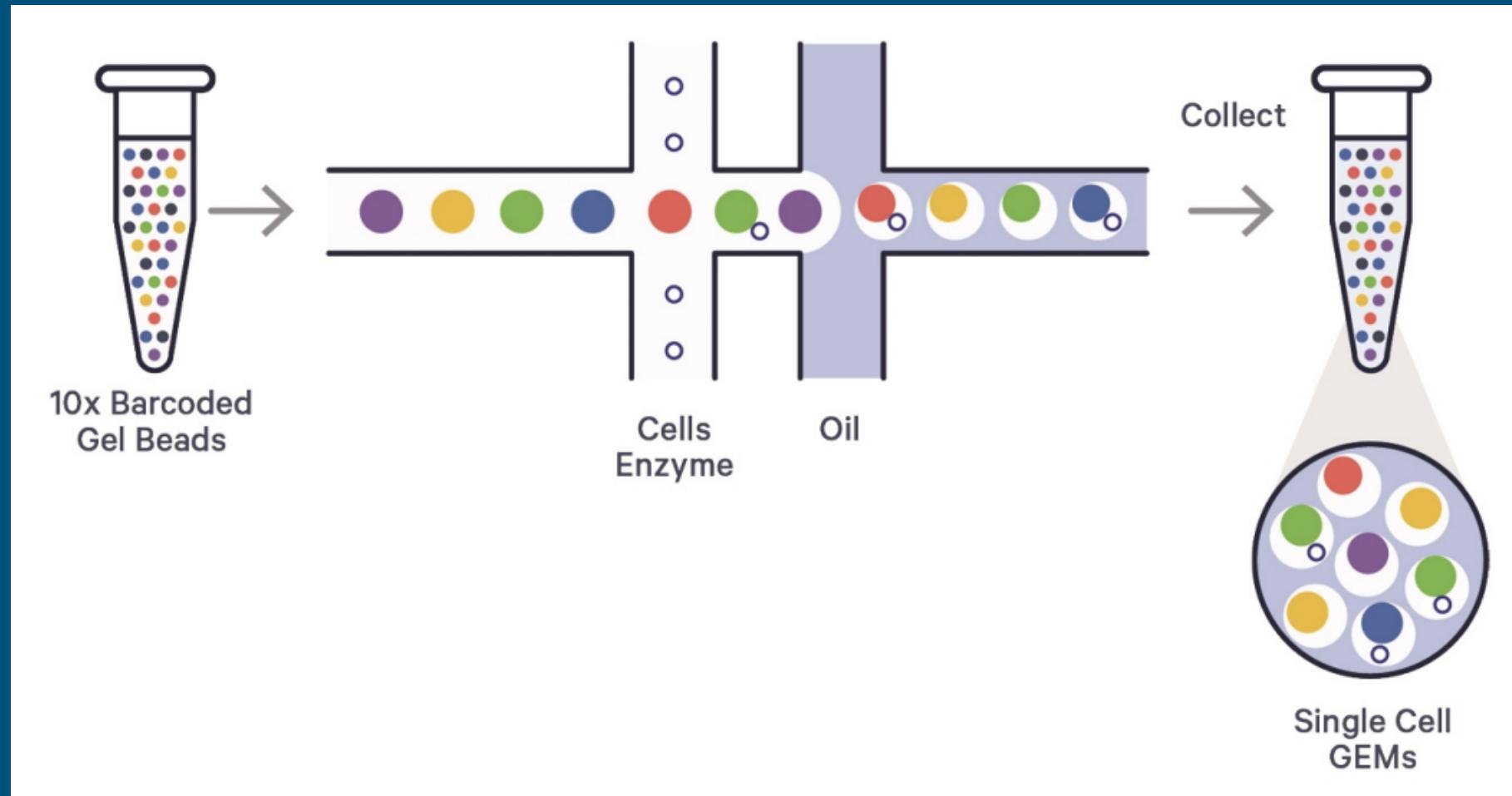


- User Consultations
  - Experimental design
- Quality control of single-cell preparations prior to the experiment
  - Sample submission guidelines for samples/cells/nuclei for different applications
- Initial bioinformatics

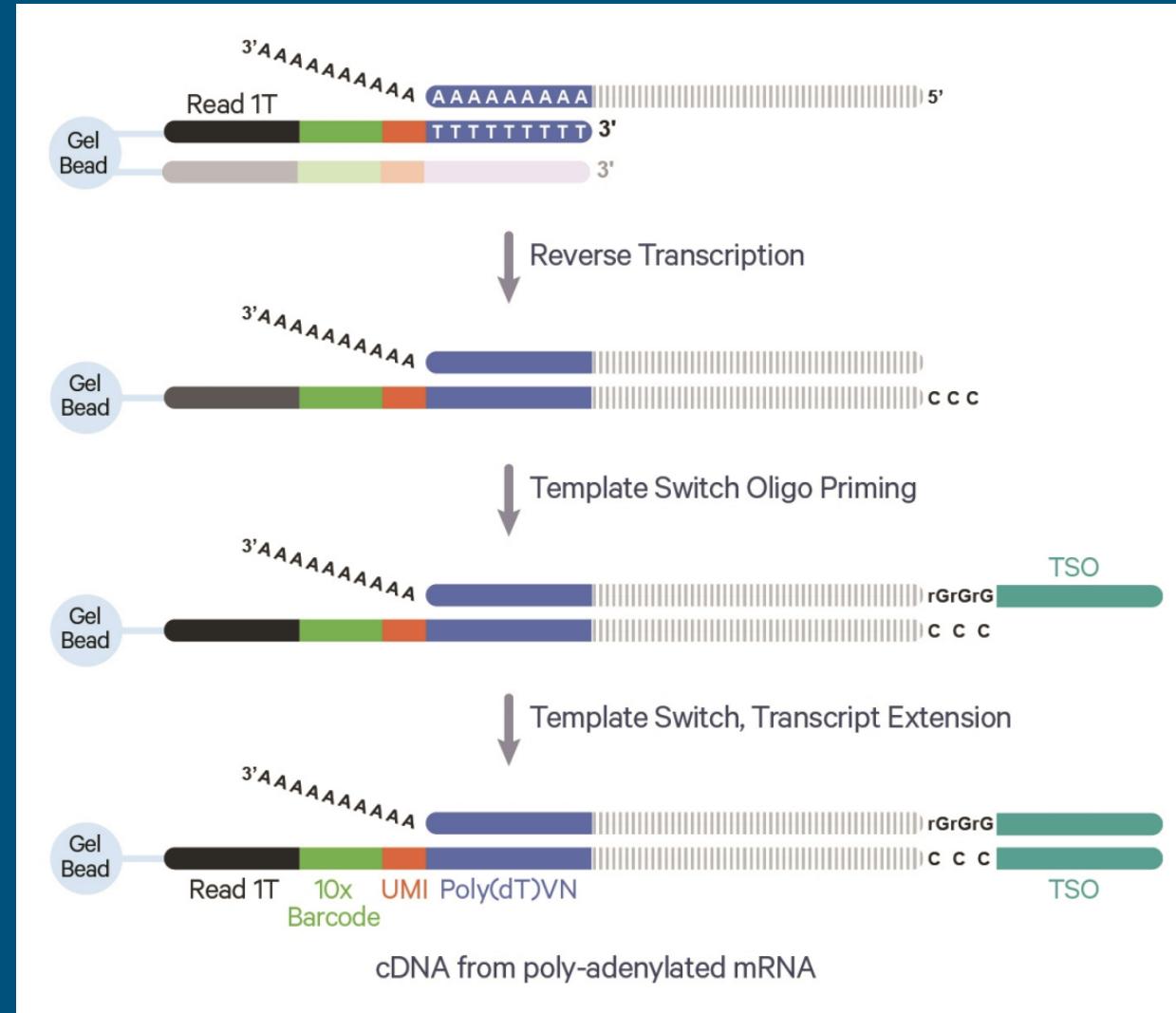
# 10X Chromium single cell sequencing



# 10X Genomics 3' GE



# 10X Chromium single cell sequencing



# Long-read sequencing for full-length information

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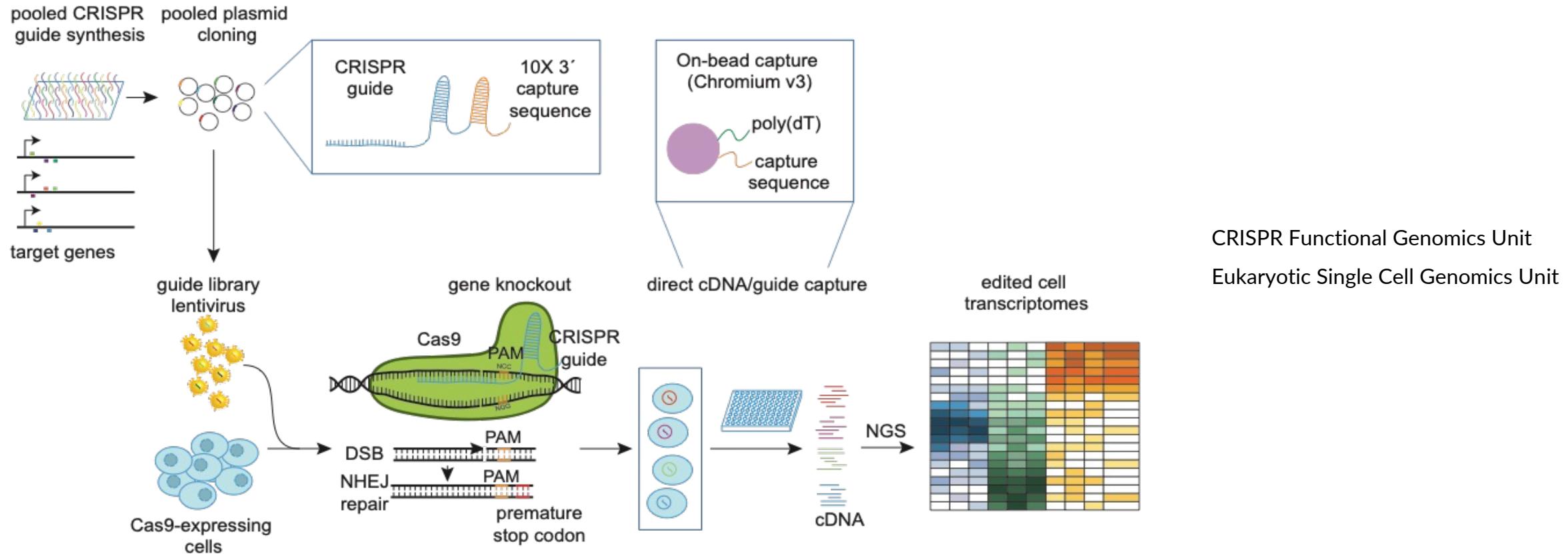


OR

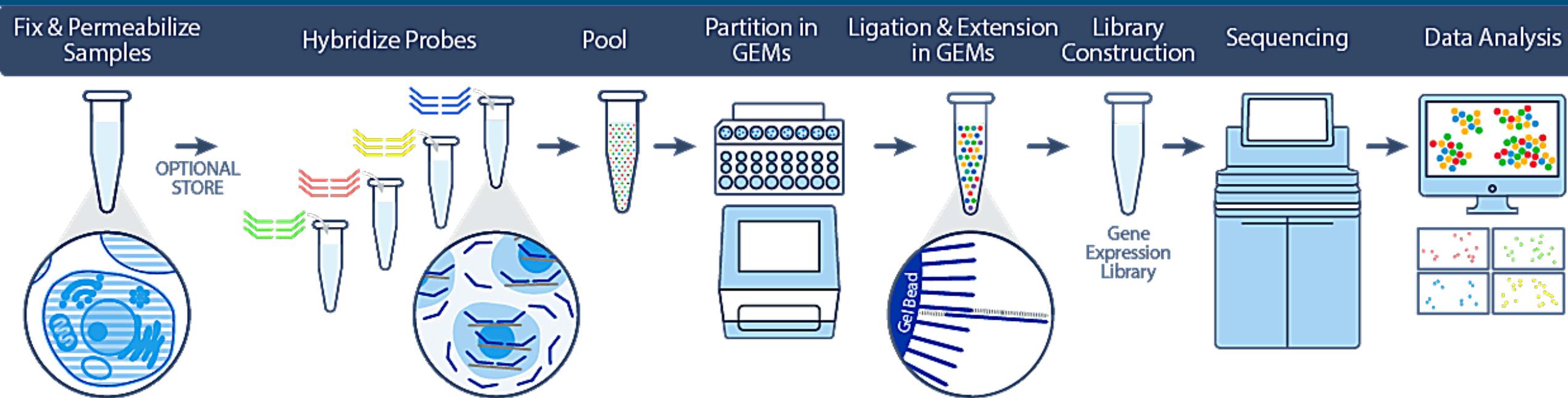


# Pooled CRISPR screens with single-cell readout

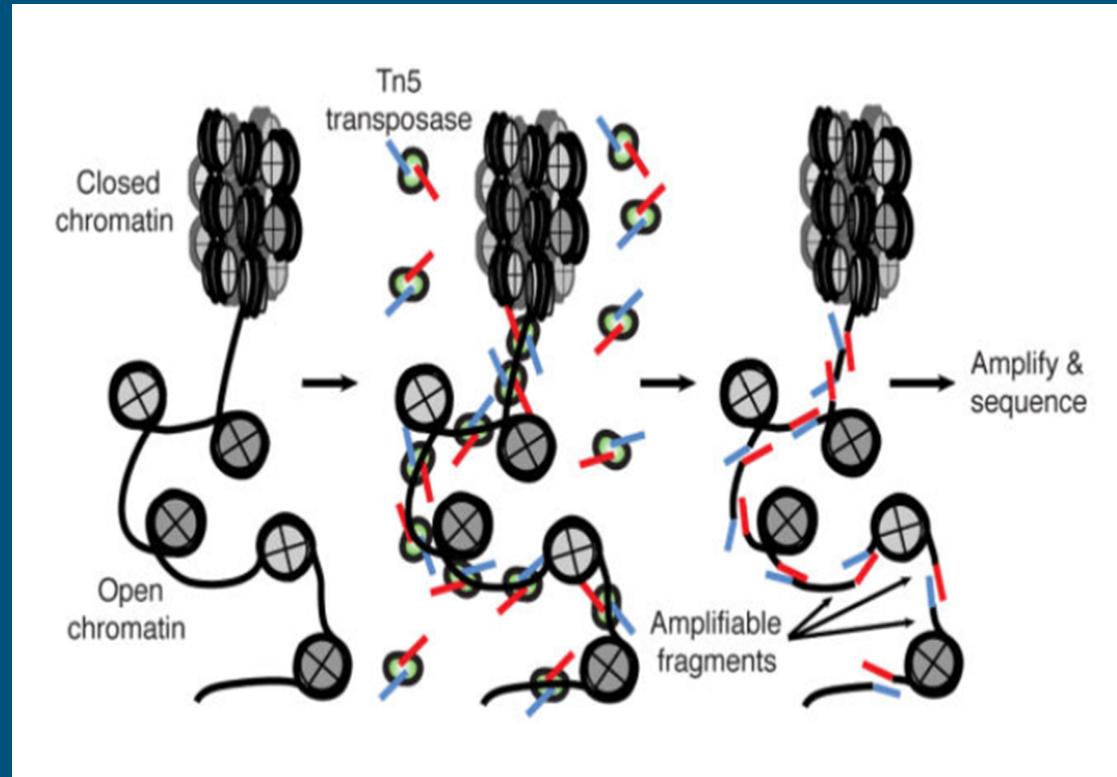
- Small, custom libraries (currently 100's of guides, number is limited by scRNA-Seq cost)
- Guide libraries include a capture sequence compatible with 10xGenomics kits
- Enables, simultaneous capture of mRNA and guide RNA from single cells
- Compatible with CRISPR-KO, CRISPR-activation, CRISPR-inhibition



# Fixed Single Cell Analysis - 10X Chromium



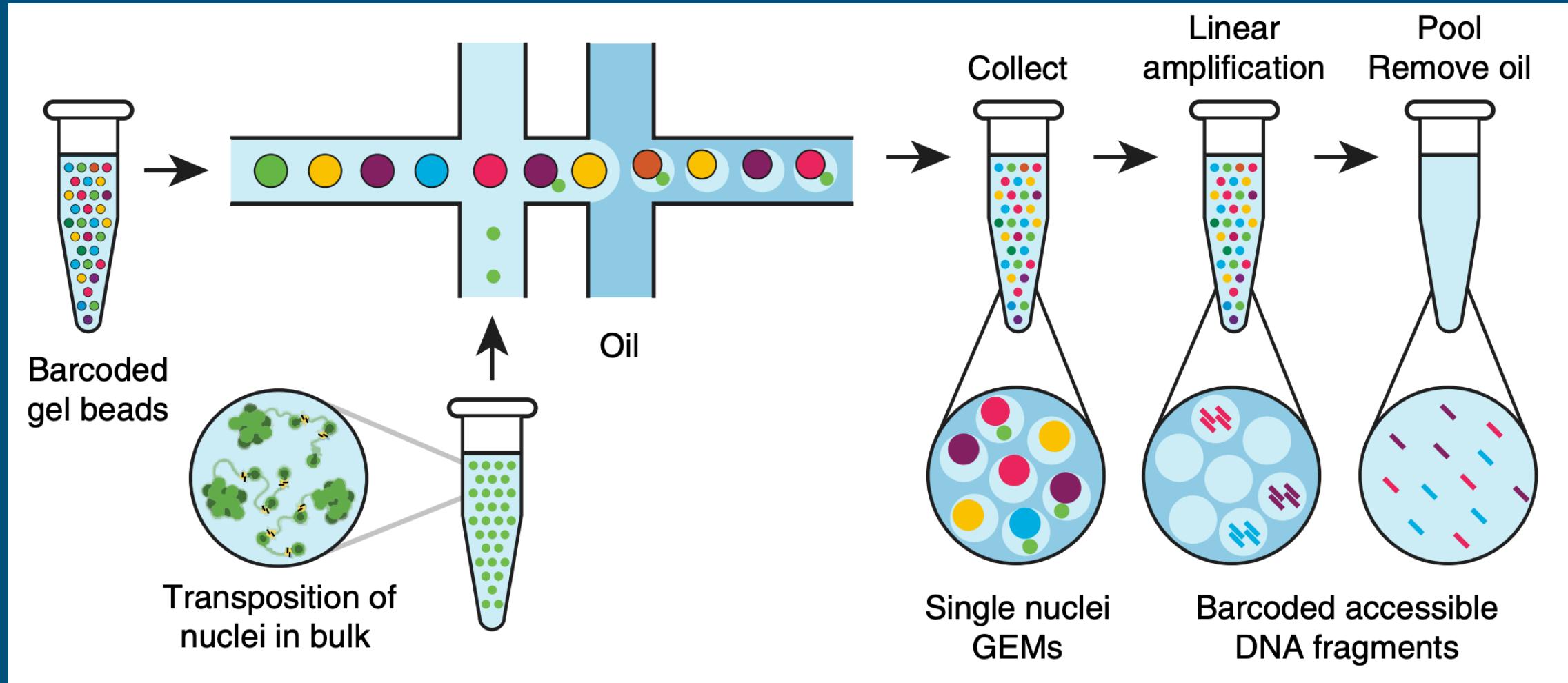
# Single-cell ATAC-sequencing



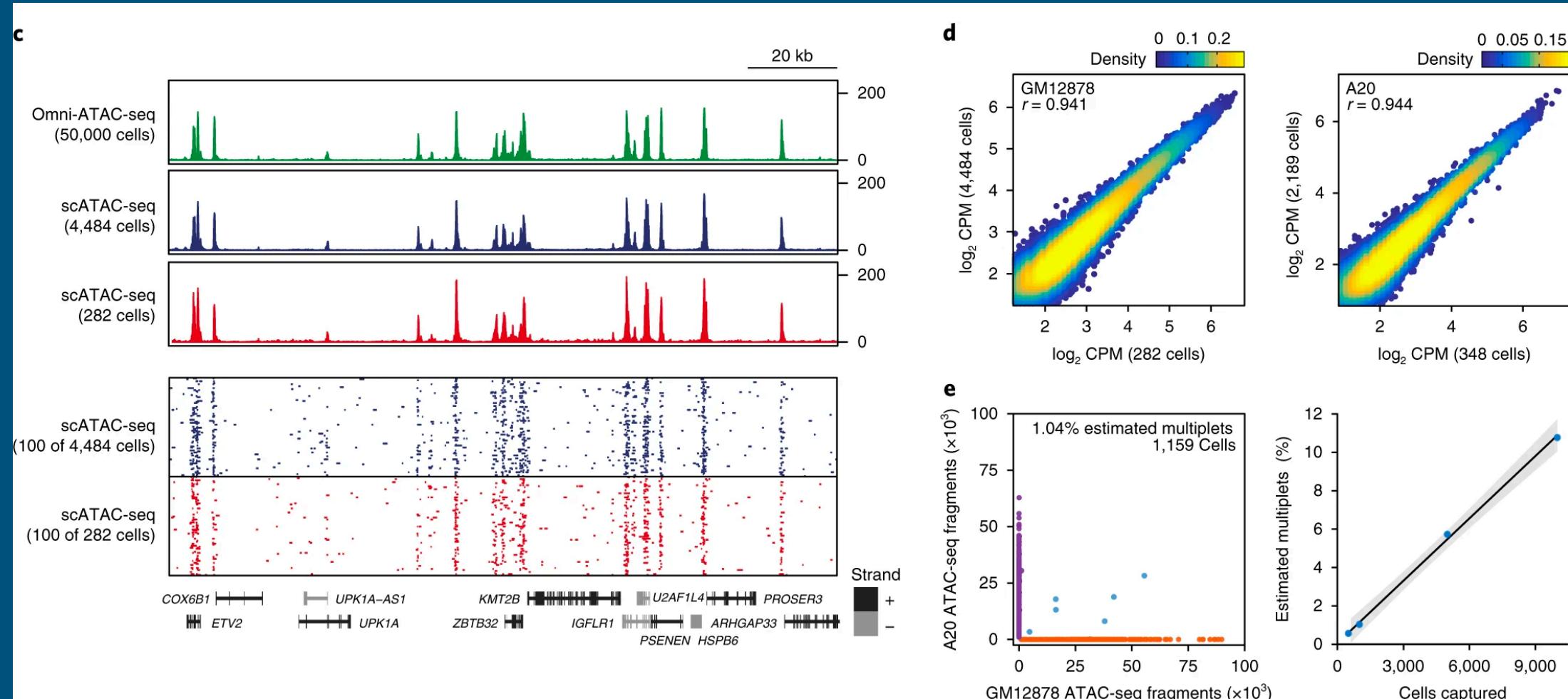
- Subpopulations with different chromatin accessibility profiles
- Increased understanding of gene regulatory networks upstream on gene expression

Multiome available: 3' GE + ATAC from the same cell

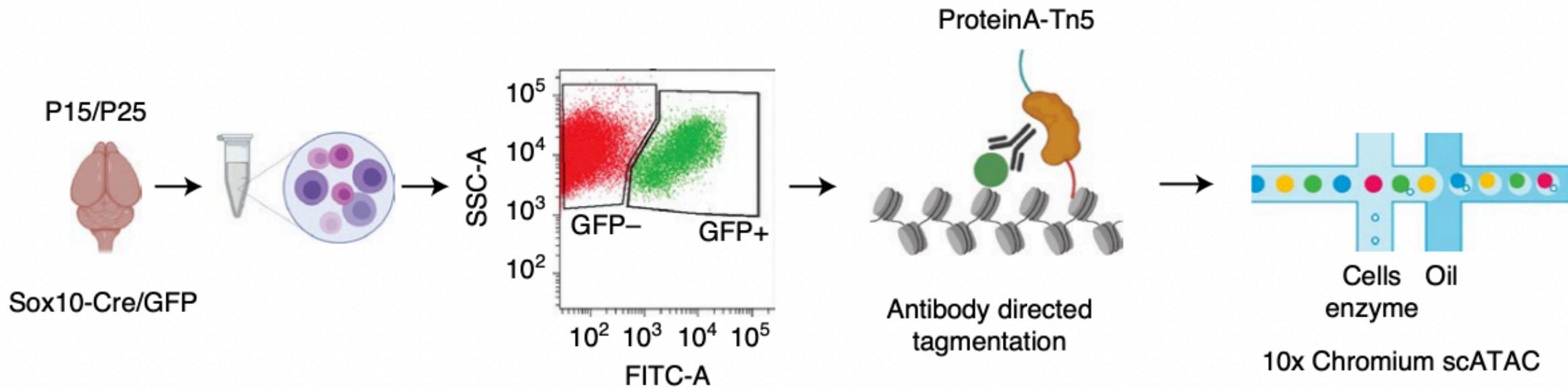
# Single-cell ATAC-sequencing



# Single-cell ATAC-seq sequencing



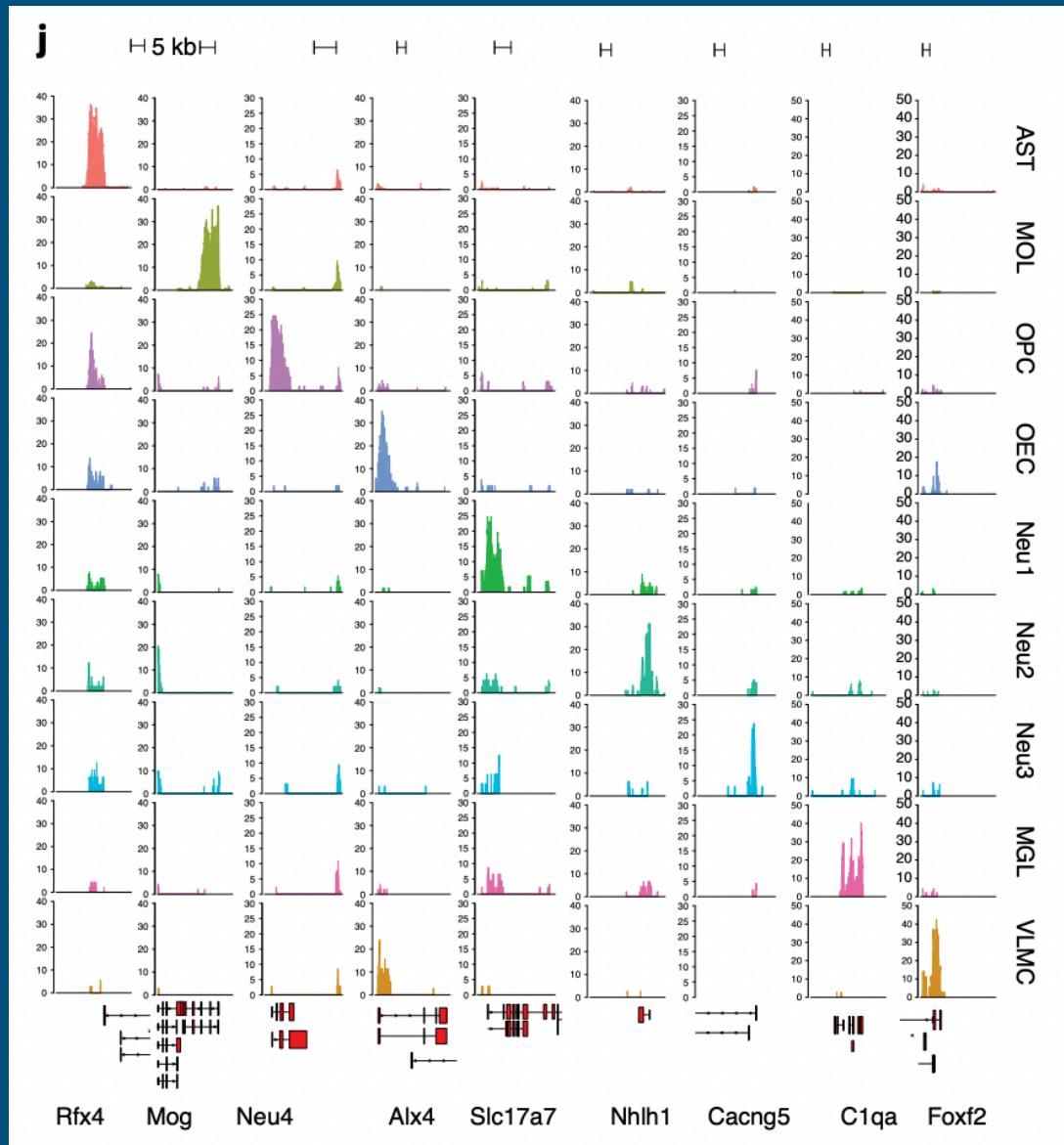
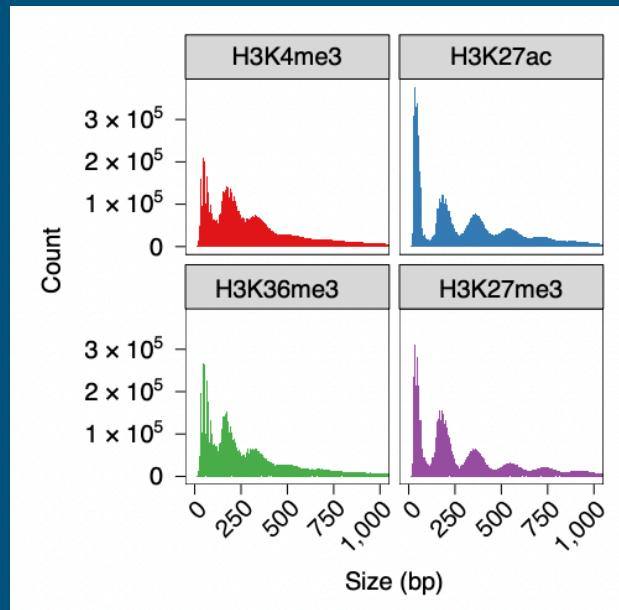
# scCUT&Tag



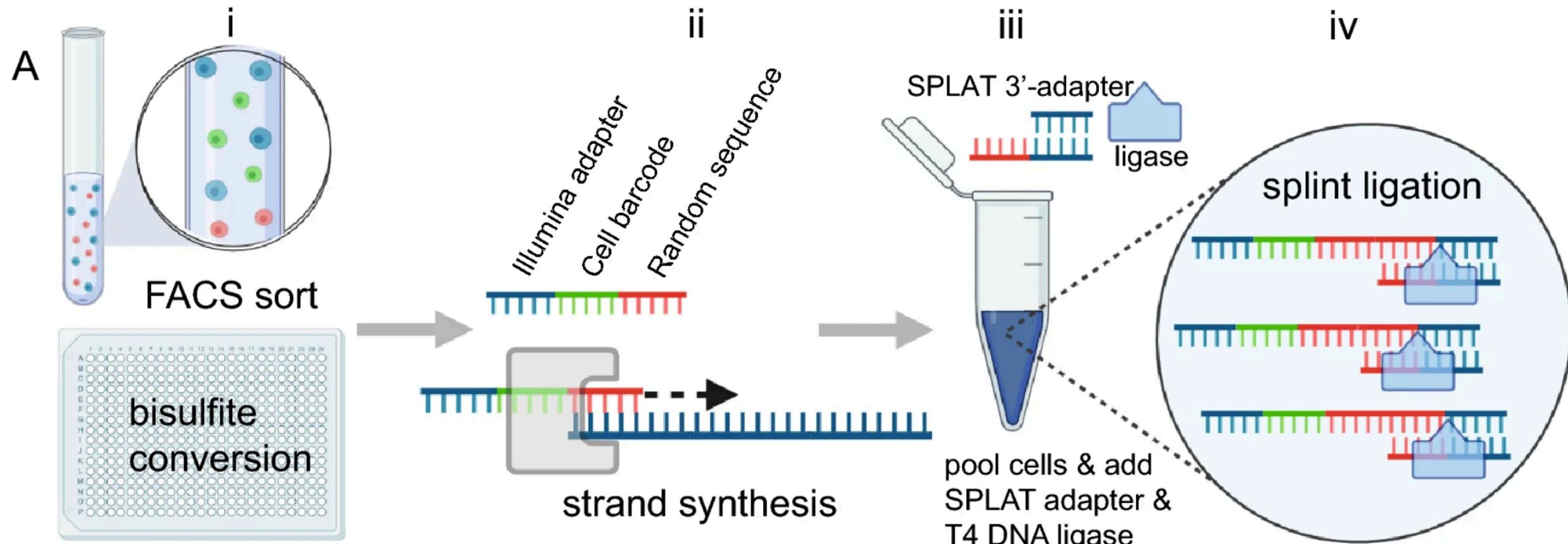
# scCUT&Tag

Tn5-H3K4me3

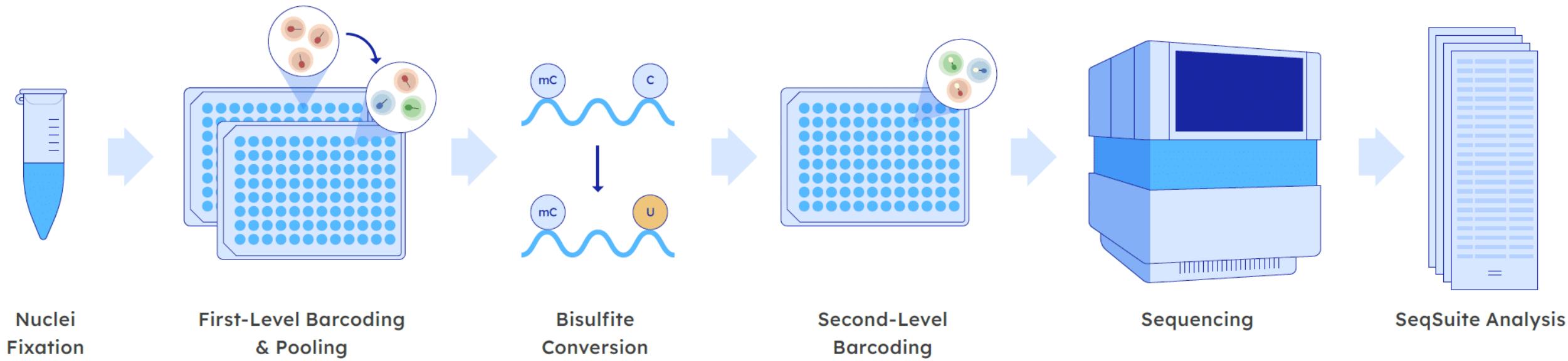
→ Mapping active promoters



# sc Splinted Ligation Adapter Tagging for WGBS



# Scale Biosciences - Single cell methylation



# 10X Genomics workflow at NGI

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## Provided by the user:

- Single cell suspension
  - High viability (preferably above 90%)/intact nuclei
  - Free of debris
  - Counted
  - Ab staining (if desired)

## Done at NGI:

- QC of provided samples
- GEM generation & Library generation
- Sequencing & upstream data analysis

# How to get in touch?

- Contact us at [support@ngisweden.se](mailto:support@ngisweden.se)
- Visit [ngisweden.scilifelab.se](http://ngisweden.scilifelab.se)
- Place an order



NGI Sweden Order Portal

This portal is for submitting orders for services provided by the National Genomics Infrastructure Sweden (NGI). To place an order, log in with your user credentials, choose the application most suitable for your project, and fill in the required details.

If you are uncertain about the choice of technology, please select the "Request a meeting" option. Information on what we offer can be found on our [homepage](#).

While we do accept projects from other countries, we prioritise projects from Sweden-based researchers, and this is largely dependent on our current queues. **NGI reserves the right to decline external i.e. non-Sweden based projects.**

New system for data delivery coming soon!

We will have a new data delivery system soon. Please check our website for more details.

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Questions?

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or [support@ngisweden.se](mailto:support@ngisweden.se)

Thanks!

