

Single Cell Genomics @ NGI

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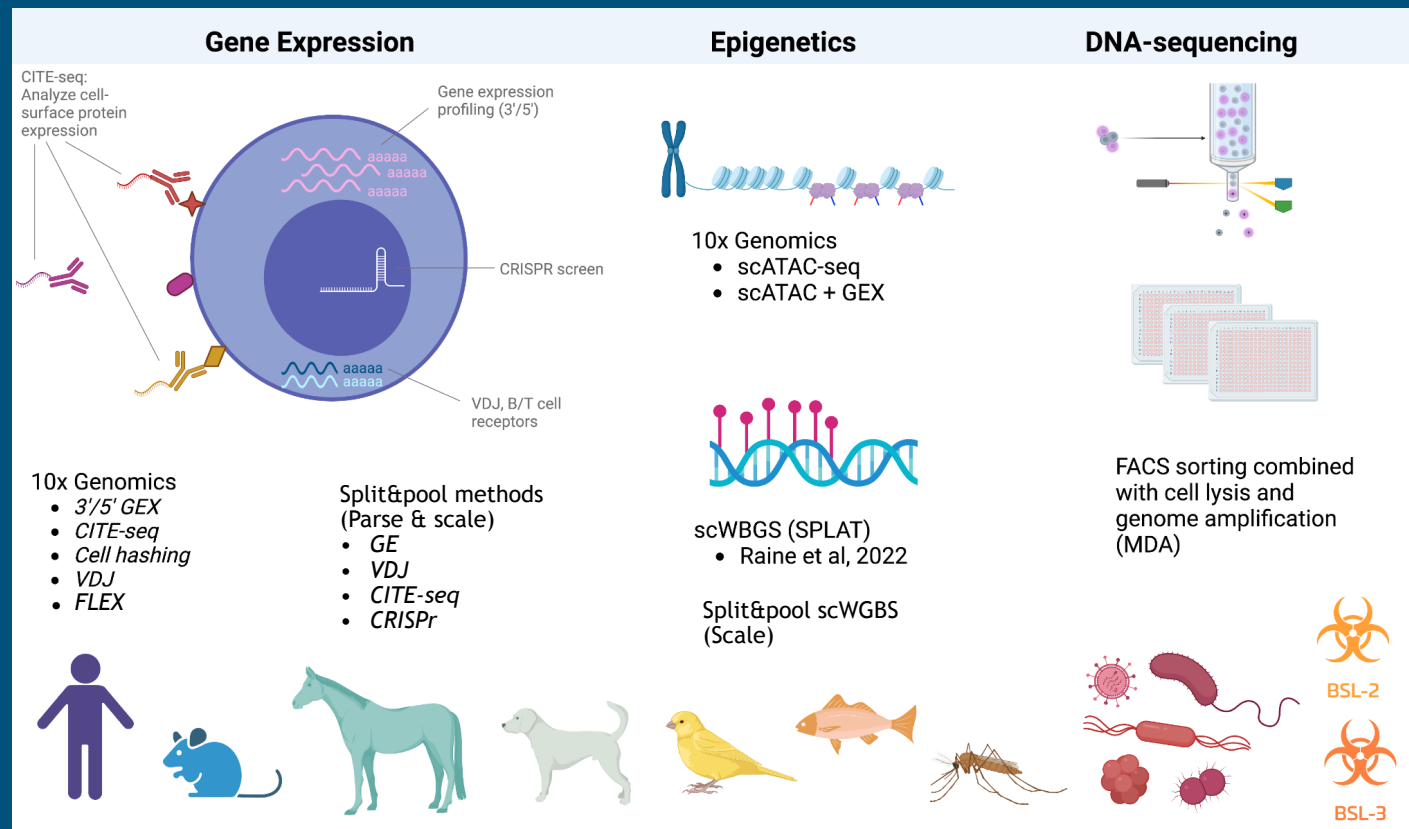
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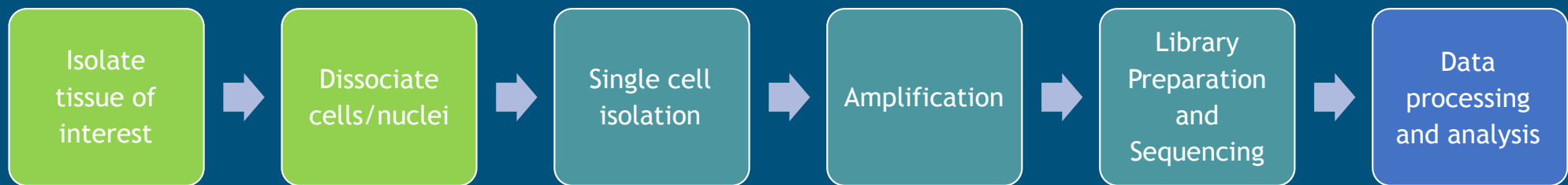
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Our Services

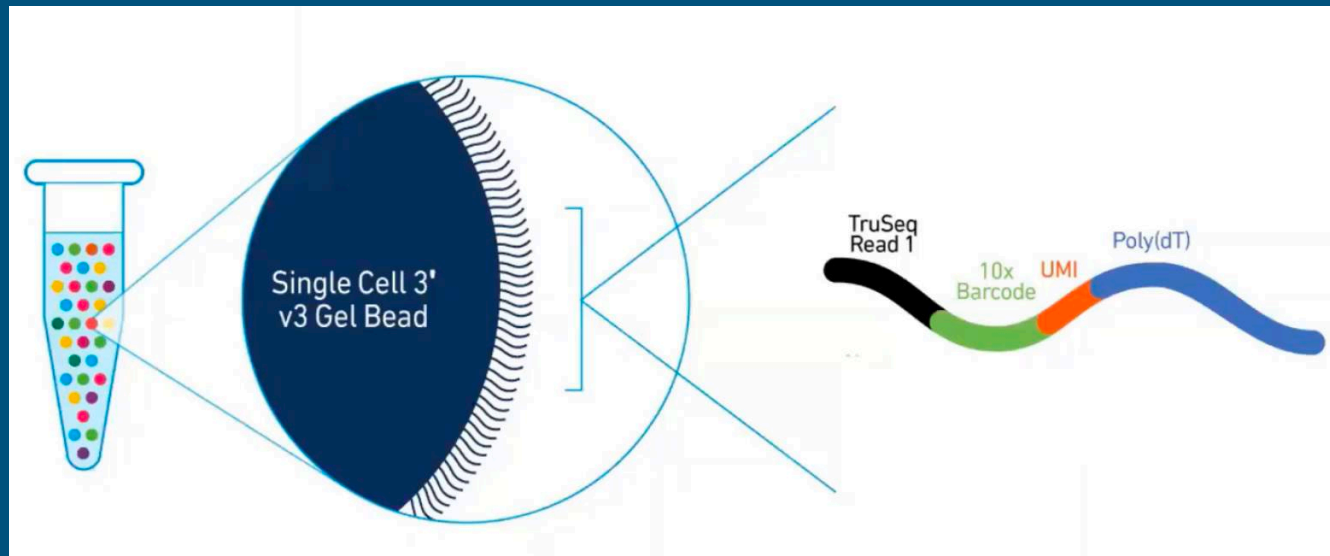


Single cell sequencing workflow

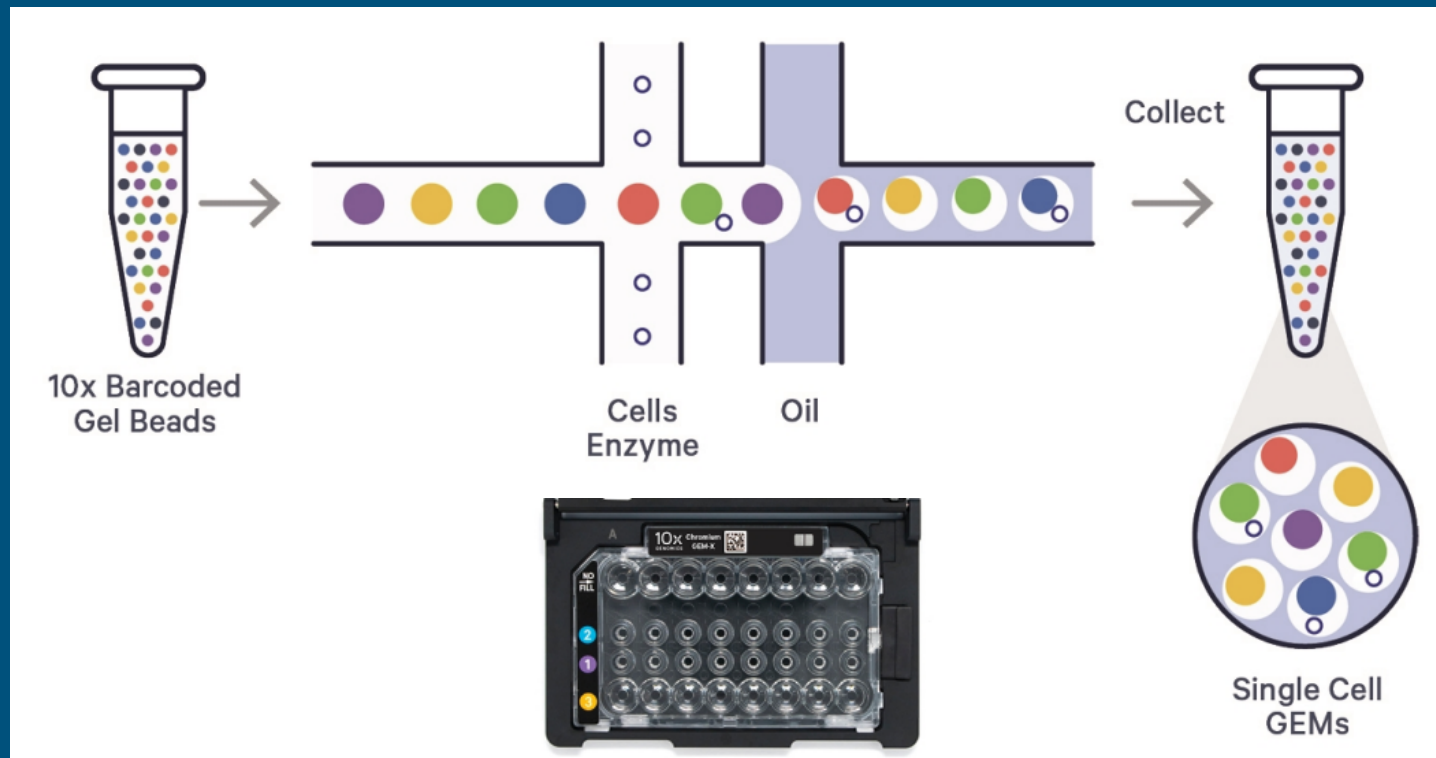


- User Consultations
 - Experimental design
- Quality control of single-cell preparations prior to the experiment
 - Sample submission guidelines for samples/cells/nuclei for different applications
- Initial bioinformatics

10X Chromium single cell sequencing



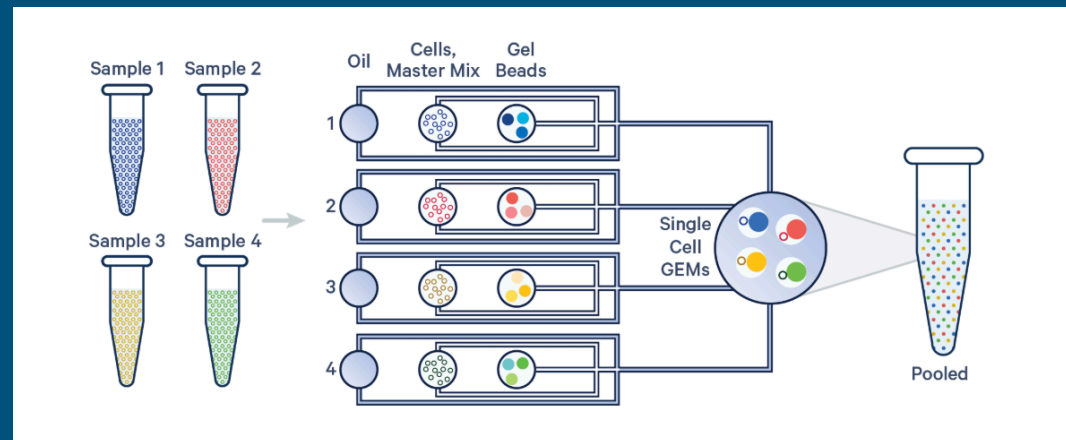
10X Genomics 3' GE



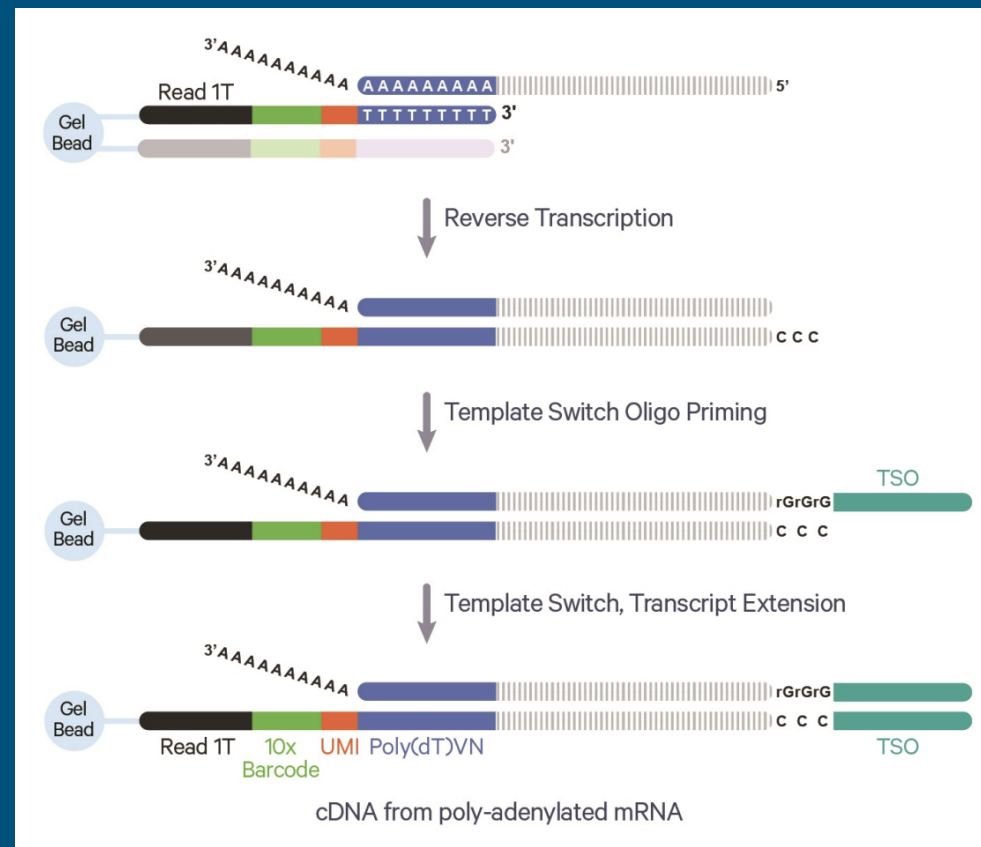
Easy multiplexing with OCM for 3' and 5' workflows

OCM: On Chip Multiplexing

- Combine up to 4 samples per reaction
- Up to 5000 cells per sample
- Cost efficient



10X Chromium single cell sequencing



Adapted from <https://cdn.10xgenomics.com>

Long-read sequencing for full-length information

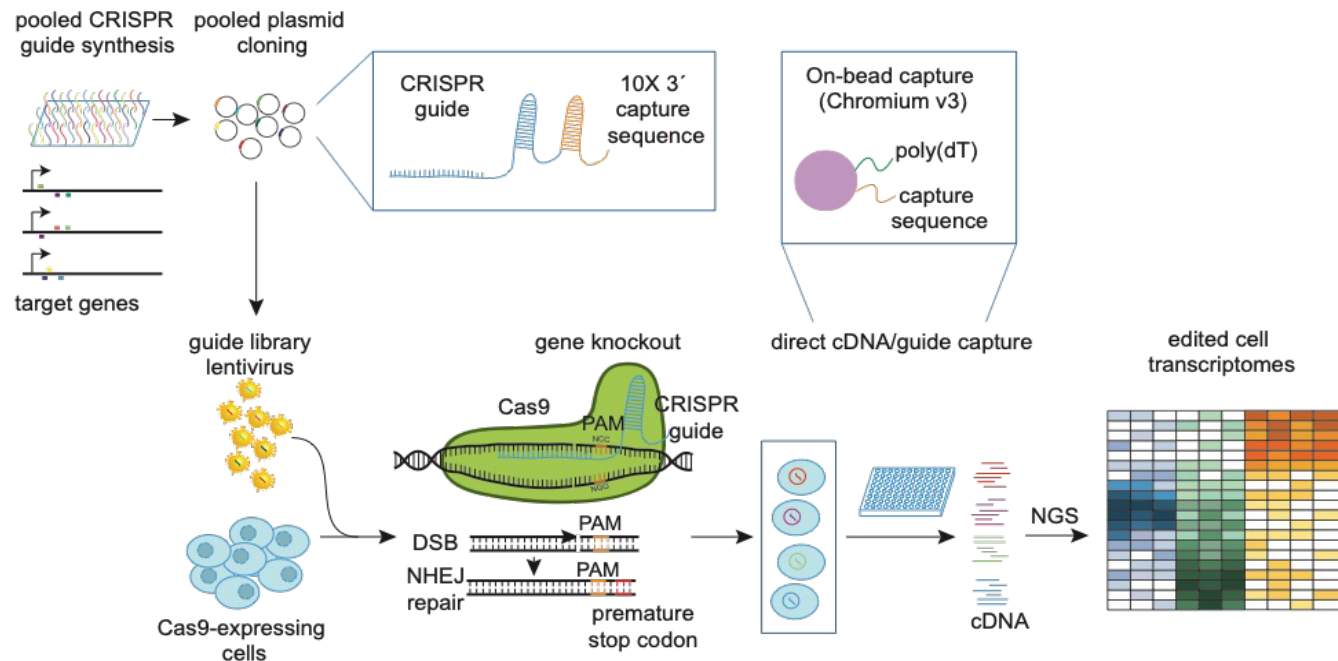


OR



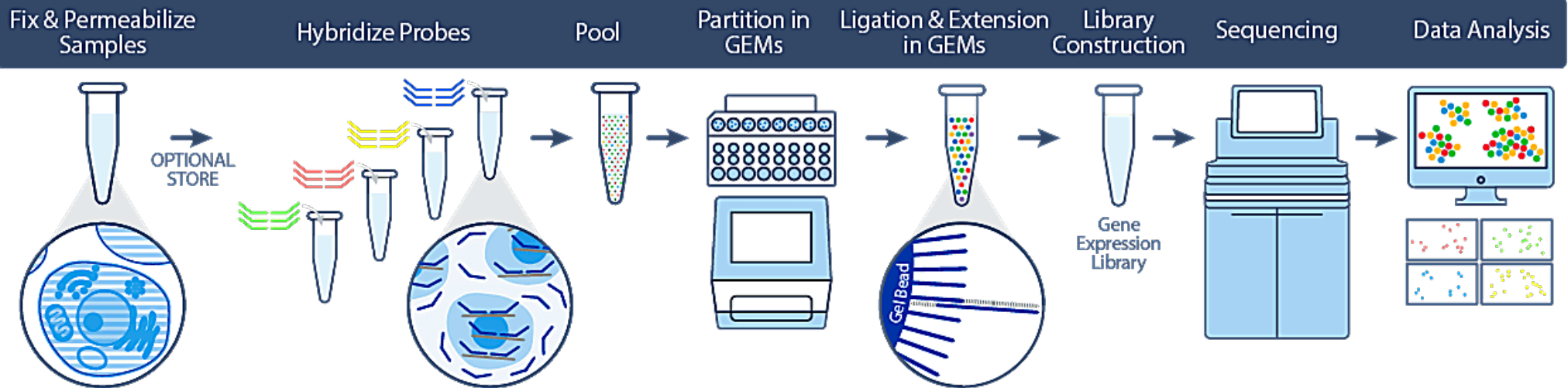
Pooled CRISPR screens with single-cell readout

- 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

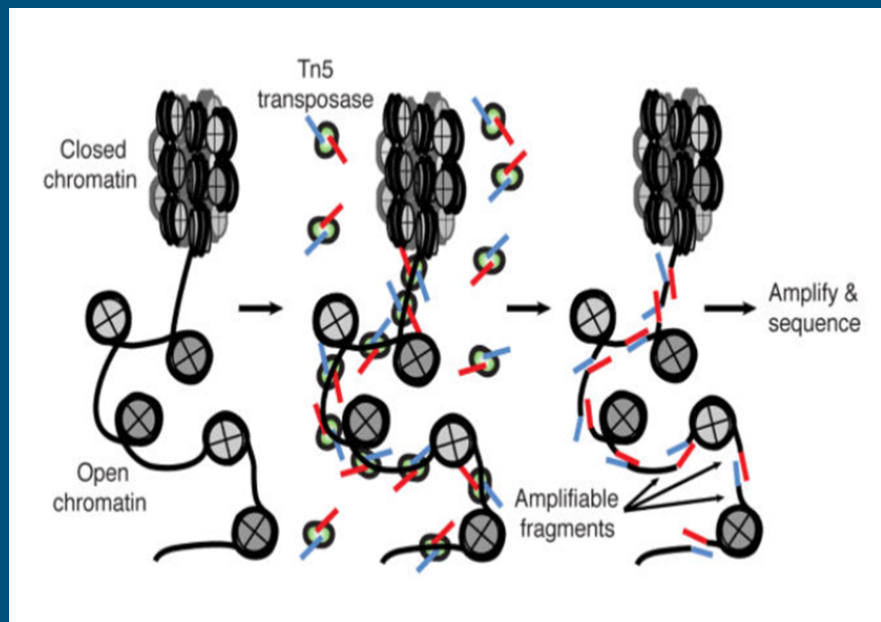


CRISPR Functional Genomics Unit
Eukaryotic Single Cell Genomics Unit

Fixed Single Cell Analysis - 10X Chromium



Single-cell ATAC-seq

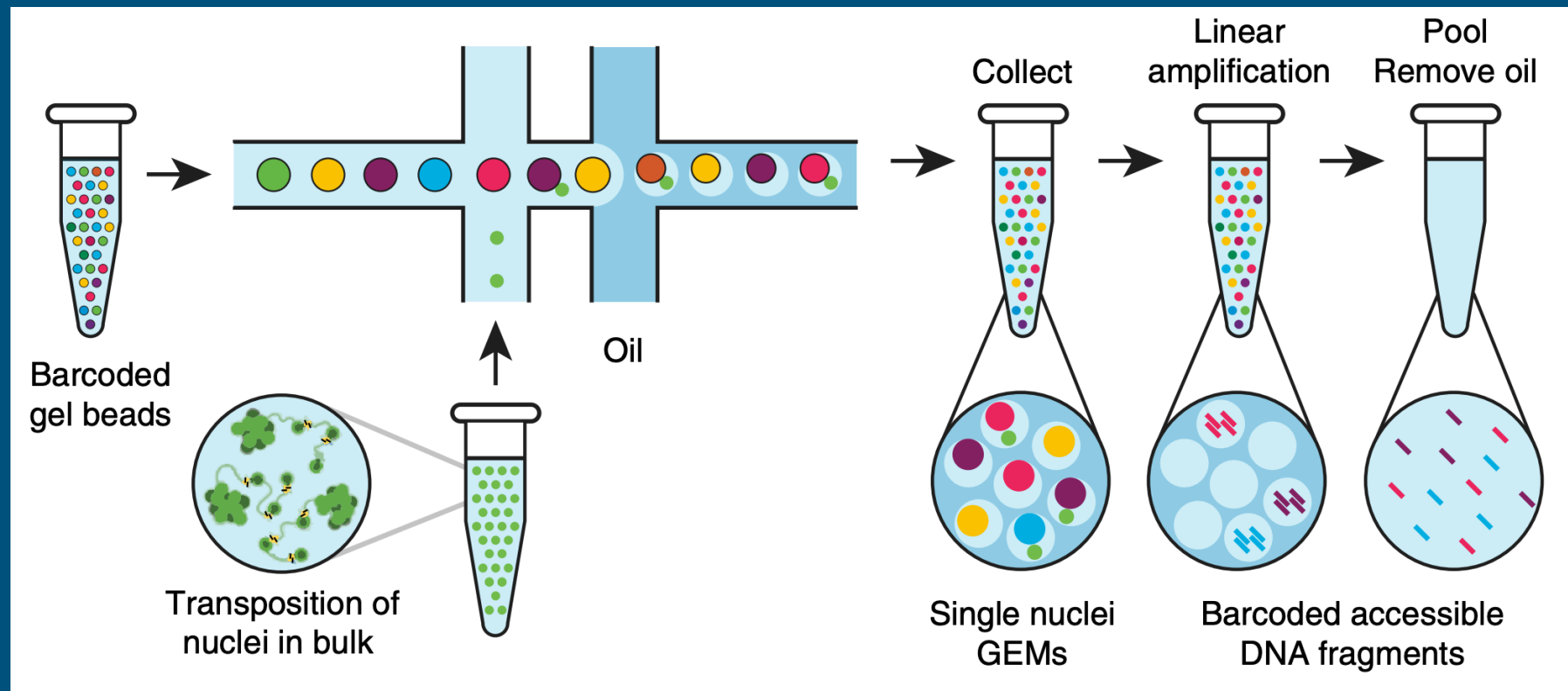


- Subpopulations with different chromatin accessibility profiles

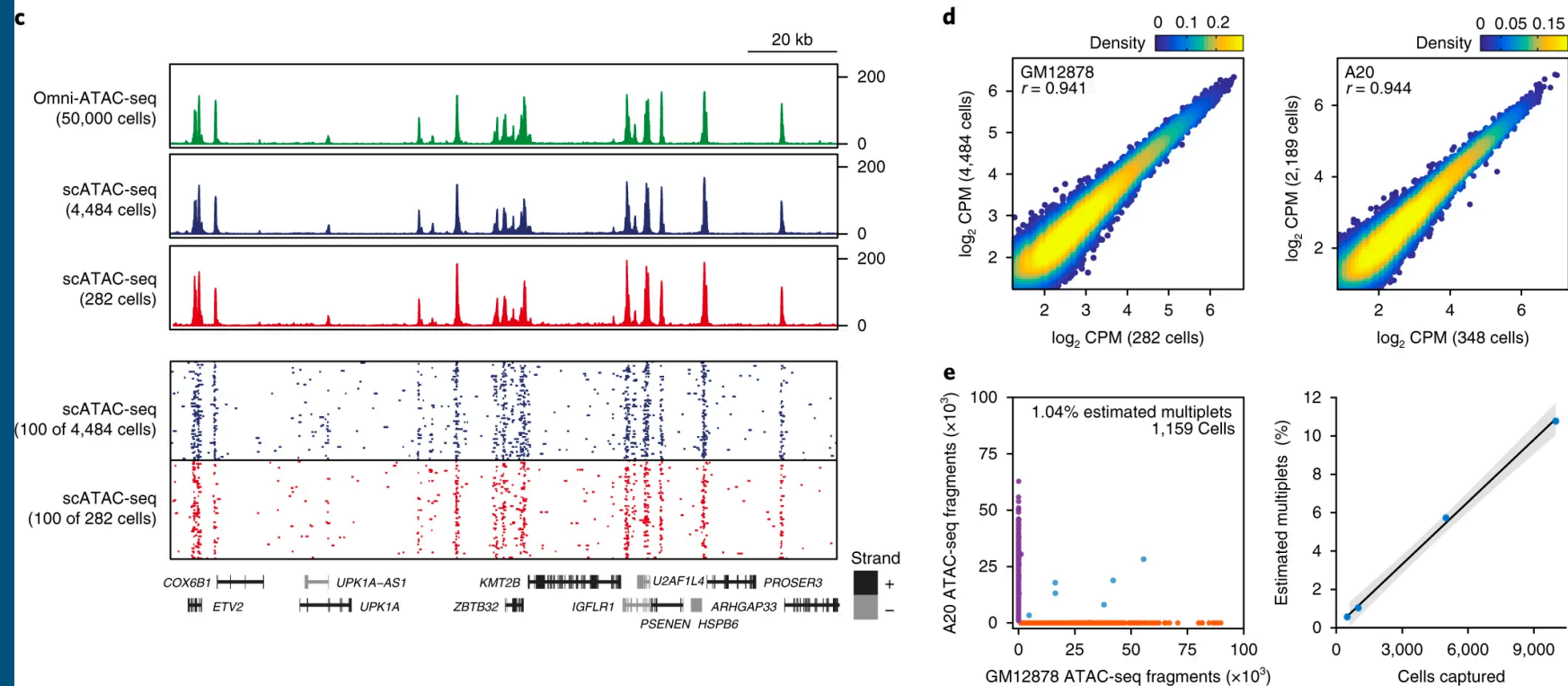
→ Increased understanding of gene regulatory networks upstream on gene expression

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

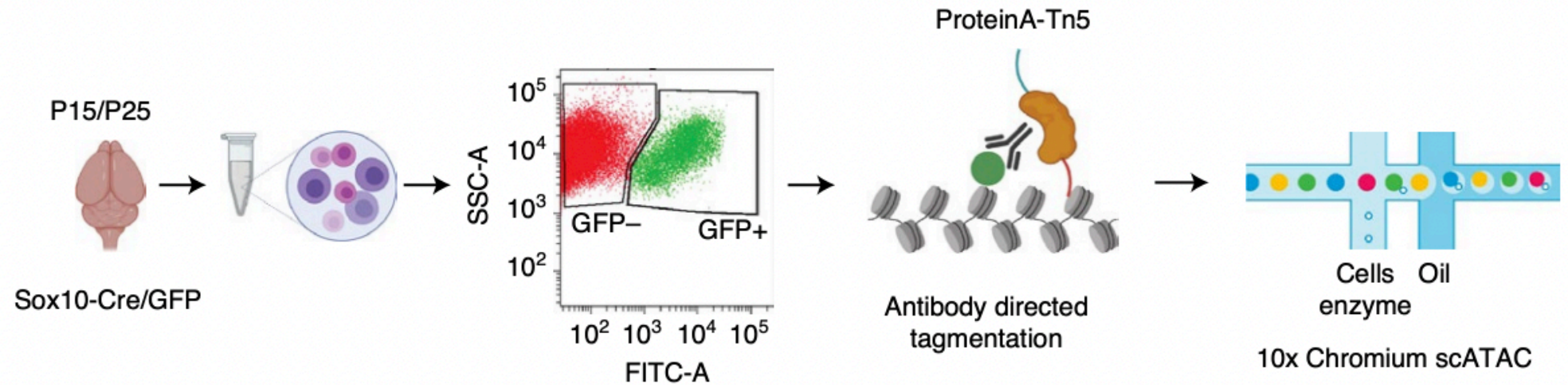
Single-cell ATAC-seq



Single-cell ATAC-seq



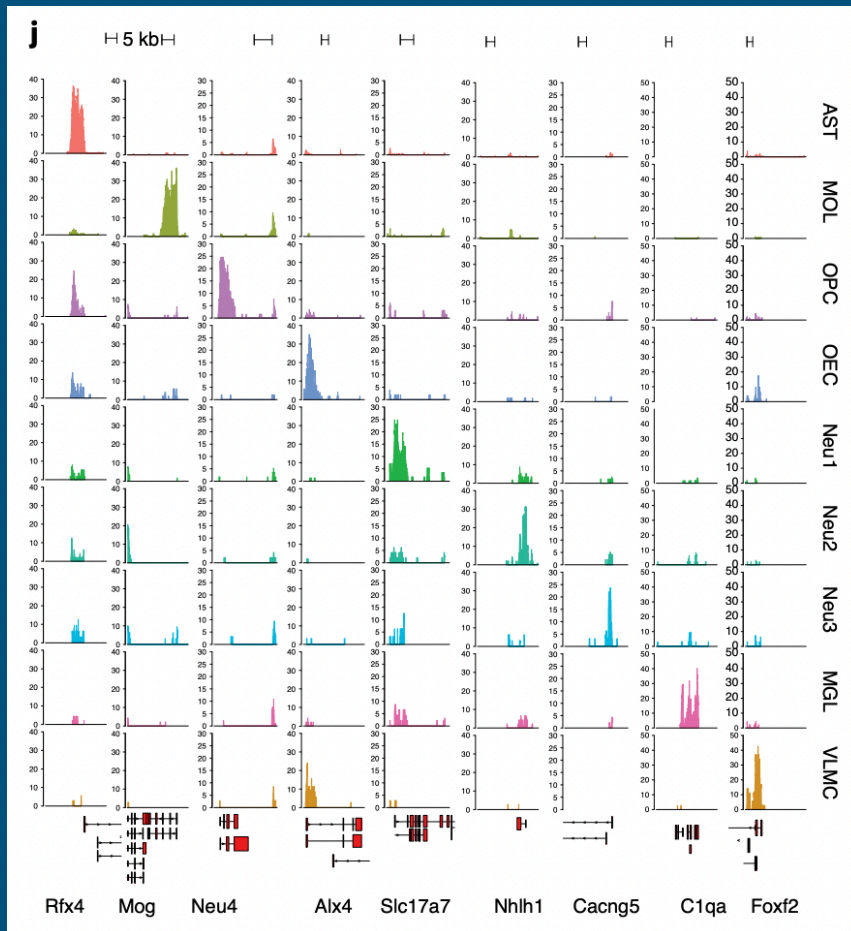
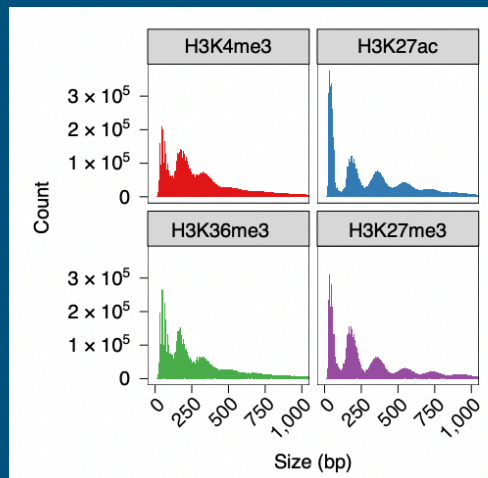
scCUT&Tag



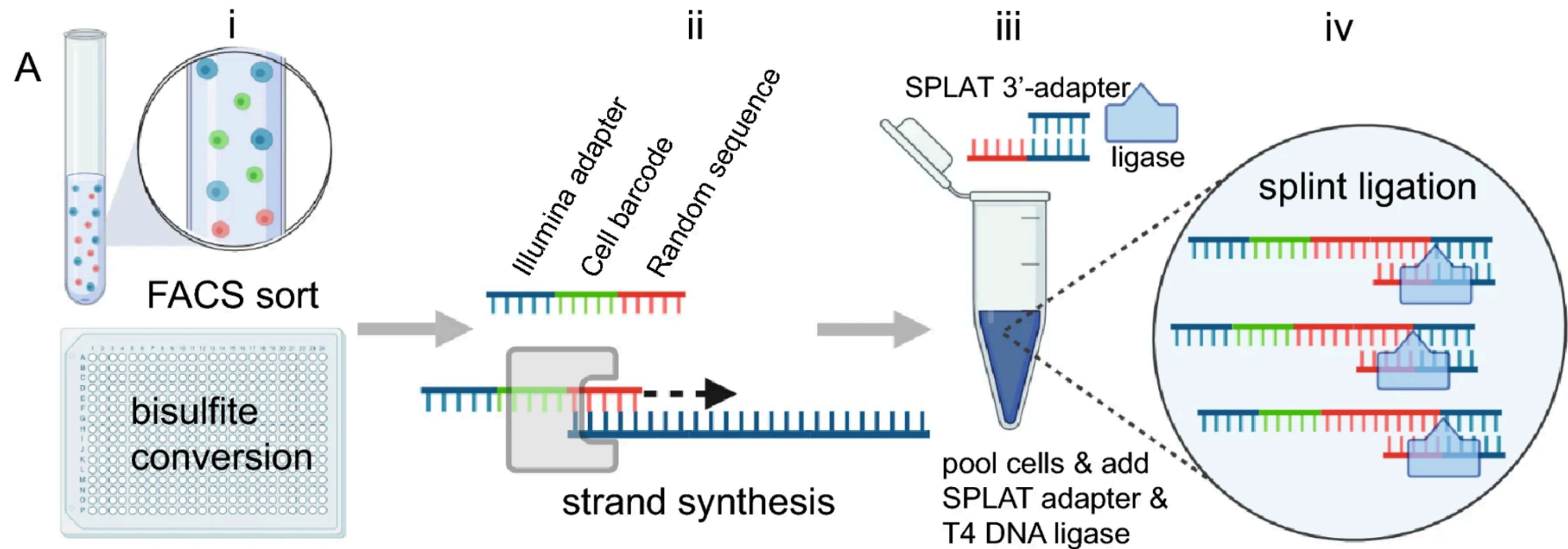
scCUT&Tag

Tn5-H3K4me3

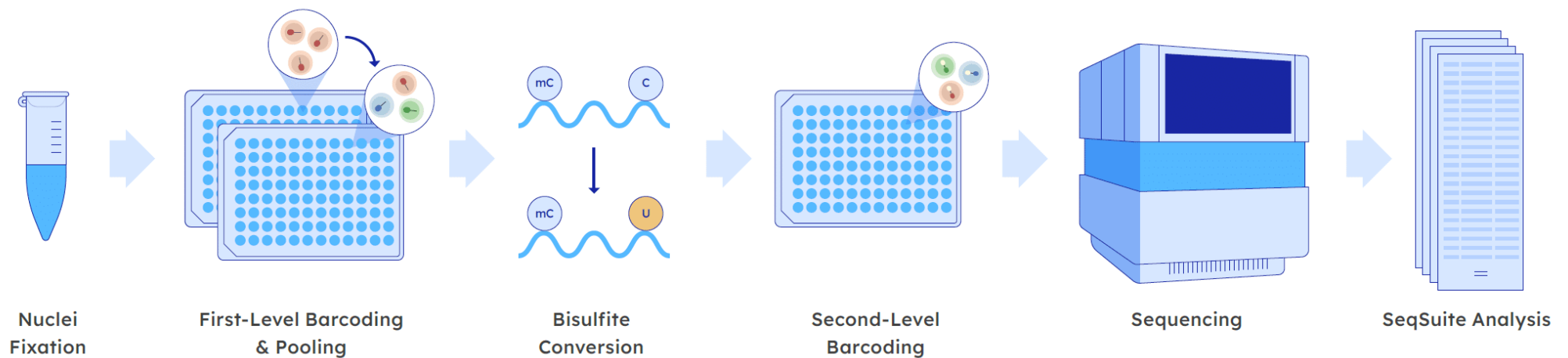
→ Mapping active promoters



sc Splinted Ligation Adapter Tagging for WGBS



Scale Biosciences - Single cell methylation



10X Genomics workflow at NGI

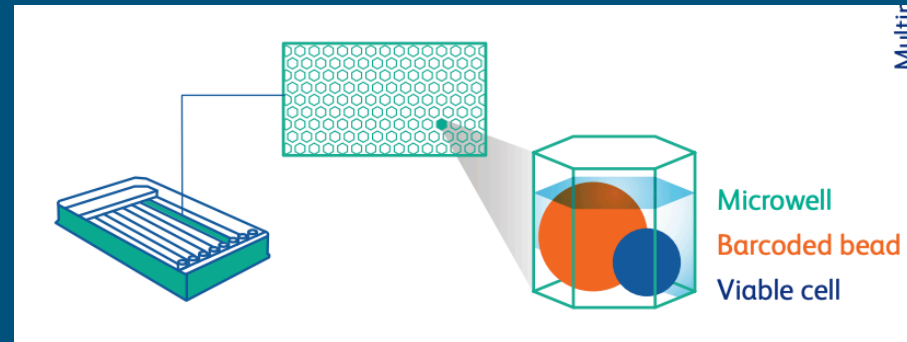
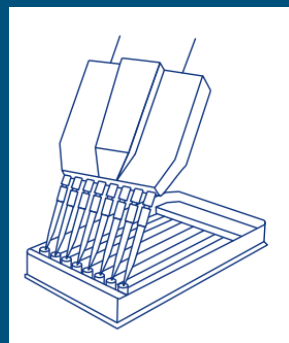
Provided by the user:

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

Done at NGI:

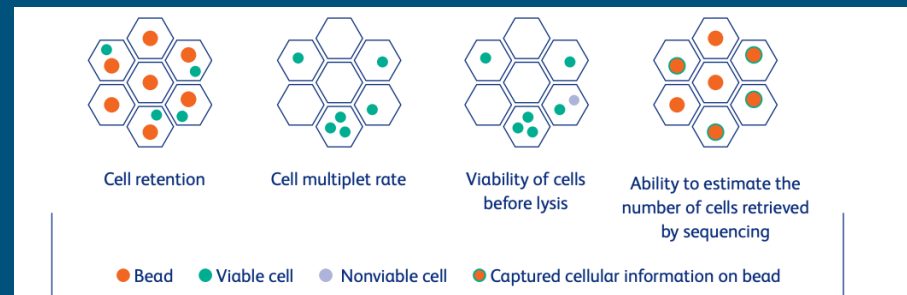
- QC of provided samples
- GEM generation & Library generation
- Sequencing & upstream data analysis

BD Rhapsody HT Express - coming soon....



Multiplexed

GE (WT or targeted)
ATAC
Multiome (GE+ATAC)
Ab-staining
BCR/TCR



How to get in touch?

- Contact us at support@ngisweden.se
- Visit ngisweden.scilifelab.se
- Place an order



Next-Generation Sequencing and Genotyping for Swedish Research

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!



HOME APPLICATIONS TECHNOLOGIES BIOINFORMATICS RESOURCES NEWS ABOUT US CONTACT **NEW ORDER**

Method of the Year 2022!

NGI offers long-read sequencing methods, a technology recently nominated as Method of the Year by Nature Methods.

[Read more](#)

Getting started at NGI

always ask on that we

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Thanks!

Questions?

Contact: support@ngisweden.se

