

Overcome the barriers of single cell RNAseq for frozen samples

- GEXSCOPE® Single Nucleus RNAseq Library Kit

The GEXSCOPE® Single Nucleus RNAseq kit is a high throughput scRNAseq library preparation solution for frozen cells and frozen tissues. After robust single nucleus separation step, single nuclei are partitioned into SCOPE™ microwell chip, mRNA captured and labeled by the Barcoding Beads, and amplified into cDNA and sequencing libraries. The kit enables gene expression profiling and cell type analysis from up to 10,000 single nuclei simultaneously on one chip and allows traditionally difficult sample types to be analyzed.

Features

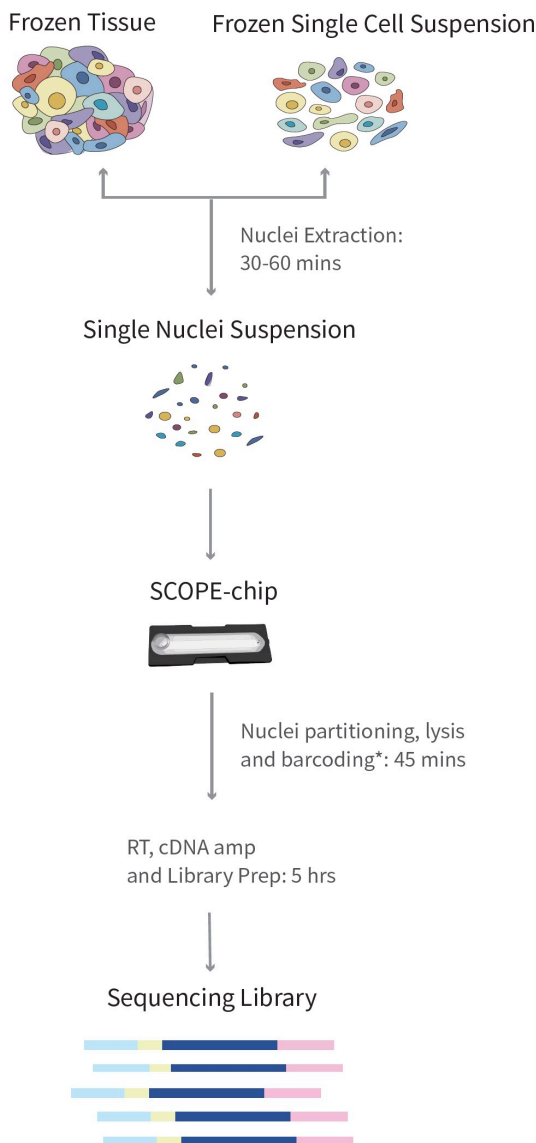


Figure 1: Streamlined workflow: sample to library within one workday

- 1. Comprehensive:** complete gene expression profiling from single nucleus of frozen sample
- 2. High throughput:** simultaneous analysis of 3' end mRNA from up to 10,000 single nuclei per chip
- 3. Robust and fast workflow:** from frozen tissue to sequencing library within one workday
- 4. Compatibility:** suitable for irregular-shaped and large morphology cells, such as neurons
- 5. Broad applications:** from any frozen clinical samples, such as biopsies and surgical resections.

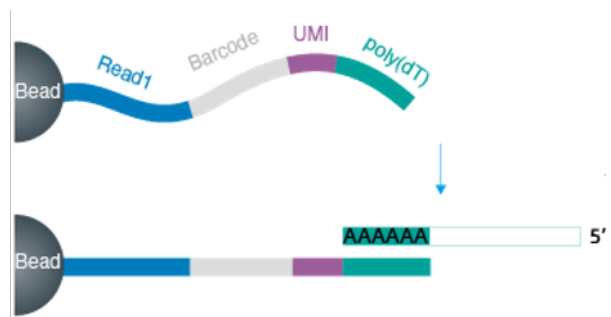


Figure 2: The illustration of Barcoding Beads. The Beads attached to an oligo containing the nucleus barcode, UMI and Poly(dT) to capture mRNA Poly(dA) tails

Robust Solutions for single cell sequencing under clinical setting

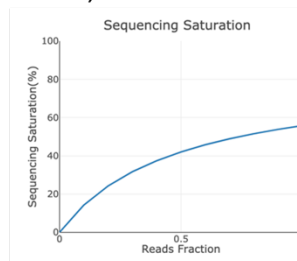
Single cell RNA sequencing normally requires highly viable cells from fresh samples. However, the collection, storage, and transportation of surgical and clinical samples remain as the major bottleneck during the single cell sequencing process. With our solution to analyze mRNA from single nuclei of frozen tissues, clinical samples can be frozen, and analyzed in longitudinal and cross-center clinical studies.

Demo Dataset

A)

Estimated Number of Cells	17,773
Fraction Reads in Cells	56,20%
Mean Reads in Cell	31,733
Median UMI per Cell	3,360
Total Genes	21,130
Median Genes per Cell	1,800
Saturation	55.79%

B)



C)

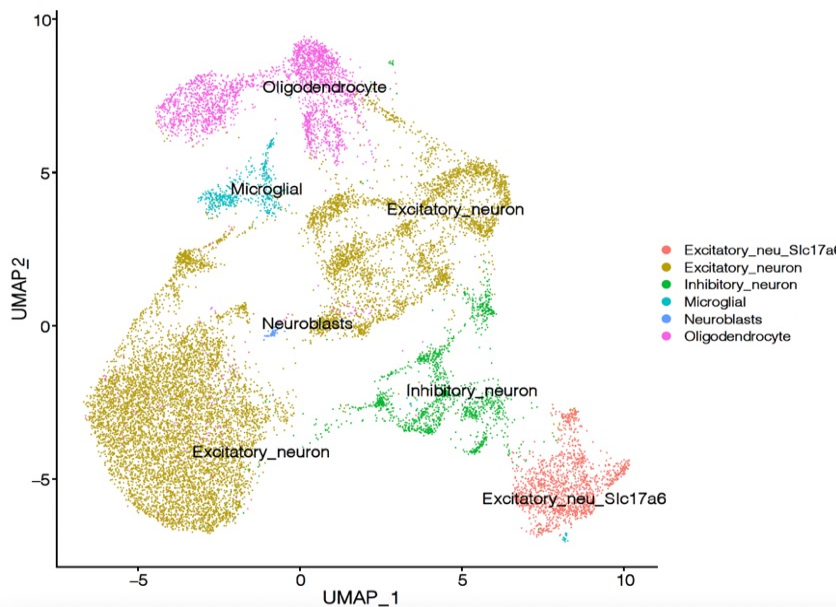
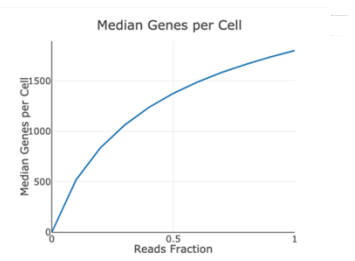


Figure 3. Frozen mouse hippocampus (a brain region) were analyzed using GEXSCOPE Single Nucleus RNAseq library Kit. A) Table of QC metrics for single nuclei sequencing. B) Graph showing the sequencing saturation curve and C) median genes per cell. The x-axes show the reads fraction; y axes shows the percentage of saturation and median genes per cell, respectively. D) mRNA from single nuclei were extracted sequenced from frozen mouse hippocampus. Seven different cell types were successfully identified based on expression profiles of marker genes.

Overcome the limitation of cell morphology

The GEXSCOPE single nucleus RNAseq kit provides a solution to process frozen cell or tissue samples and extract mRNA from nucleus to be analyzed for scRNAseq, allowing traditionally difficult tissue types to be analyzed, such as brain tissue or muscle tissue.

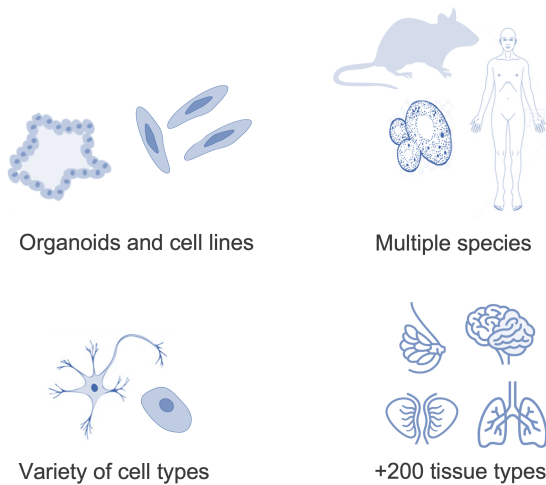


Figure 4. Illustration of species, tissue, cell and sample types can be used for GEXSCOPE Single Nucleus RNAseq Library Kit.

1. Frozen tissues of various tissue types
2. Cells or tissues from various species (human, mouse, etc)
3. Cells with large diameter or irregular shape (e.g. heart muscle cells, neurons)
4. Frozen cells isolated from cell flowcytometry

Ordering Information:

Product		Application
GEXSCOPE® Single Nucleus RNA Library Kit	2 / 16	1005011 / 1005012

More Products:

Product	Application
GEXSCOPE® Single Cell RNA Library Kit	Single cell mRNA library construction from fresh tissue or cell samples
GEXSCOPE® Single Cell V(D)J Library Kits	Simultaneous analysis of TCR/BCR sequences and mRNA expression profiles in single cells
DynaSCOPE™ Single Cell RNA Dynamics Library Kit (Tissue)	Analysis of Nascent RNA at single cell level

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