

RetroSCOPE[®] FFPE Single Nucleus Whole Transcriptome Library Kit

Unlock whole transcriptome information from FFPE samples.



Formalin-Fixed Paraffin-Embedded (FFPE) tissue preservation is the gold standard for long-term archiving in clinical pathology. Singleron's RetroSCOPE FFPE Single Nucleus Transcriptome Library Kit uses random primers to measure gene expression from FFPE samples. This technology



demonstrates high sensitivity even from degraded samples, detects both coding and non-coding RNAs, and enables comprehensive transcriptome coverage. These capabilities make it

particularly valuable for investigating tumor heterogeneity, biomarker discovery, and retrospective studies using archived clinical samples.

RetroSCOPE at a glance

Unbiased discovery

Capture poly(A) and non-poly(A) RNAs such as ncRNA and microRNA.

Whole transcriptome profiling

Whole gene coverage, expressed mutations /SNPs and splicing isoforms.

Applicable to all species

Supporting research in humans, mice, and more.

RetroSCOPE FFPE Technical Workflow

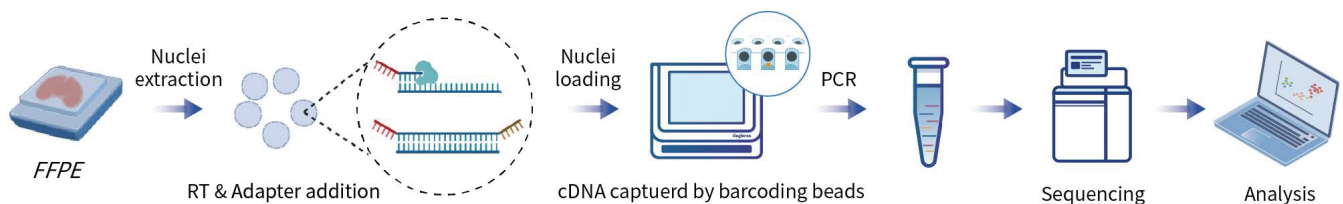


Figure 1. Singleron RetroSCOPE FFPE single nucleus transcriptome sequencing workflow.

Sensitive Gene Detection Across Diverse Tissue Types

The RetroSCOPE kit enables robust gene detection across various tissue types, delivering high-quality single nuclei RNA sequencing data, including a high fraction of reads in cells across tissue types. Using our optimized workflow, nuclei were successfully extracted with intact morphology. Subsequent sequencing and data analysis shows high number of genes detected per nucleus and low background noise.

Tissue Type	Est. Number of Cells	Fraction Reads in Cells	Median UMI per Cell	Total Genes	Median Genes per Cell
Kidney	6,361	85.75%	7,539	41,328	1,762
Lung	4,107	89.66%	13,916	43,372	3,314
Muscle	7,183	80.29%	9,744	42,746	2,213
Stomach	6,873	86.53%	10,582	42,135	2,342

Figure 2. QC metrics from FFPE single-nuclei transcriptome sequencing is conducted using diverse tissue samples from mouse.

Whole Transcriptome Profiling for FFPE Samples

Low-quality samples were recoverable using RetroSCOPE FFPE Single Nucleus Transcriptome Library Kit, providing high-quality data from compromised samples.

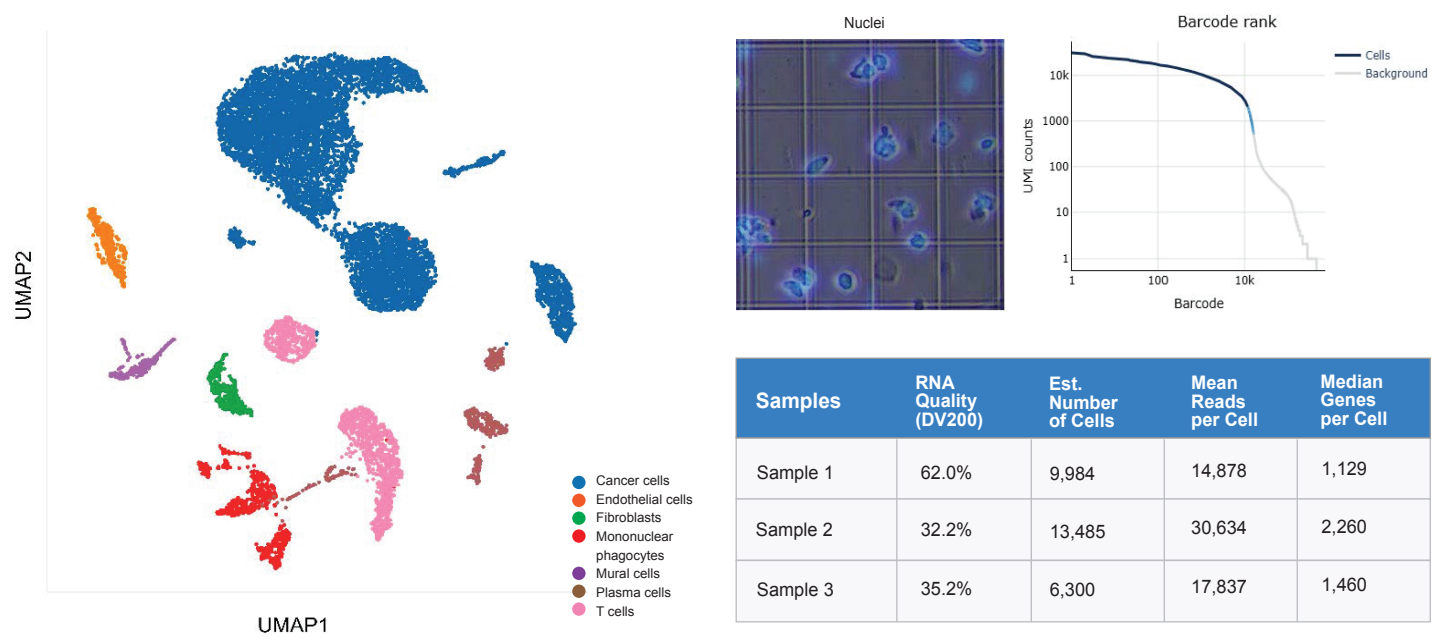


Figure 3. Human bladder cancer FFPE samples stored at room temperature for two years maintained high gene detection rates and consistent gene expression levels. Left: UMAP plot showing cell clusters by gene expression. Right: Key quality control metrics.

Discover the Full Story – Includes Coding and Non-Coding RNAs

Analysis of mouse bladder cancer FFPE samples reveals differential expression of both coding and non-coding RNAs across distinct cell types.

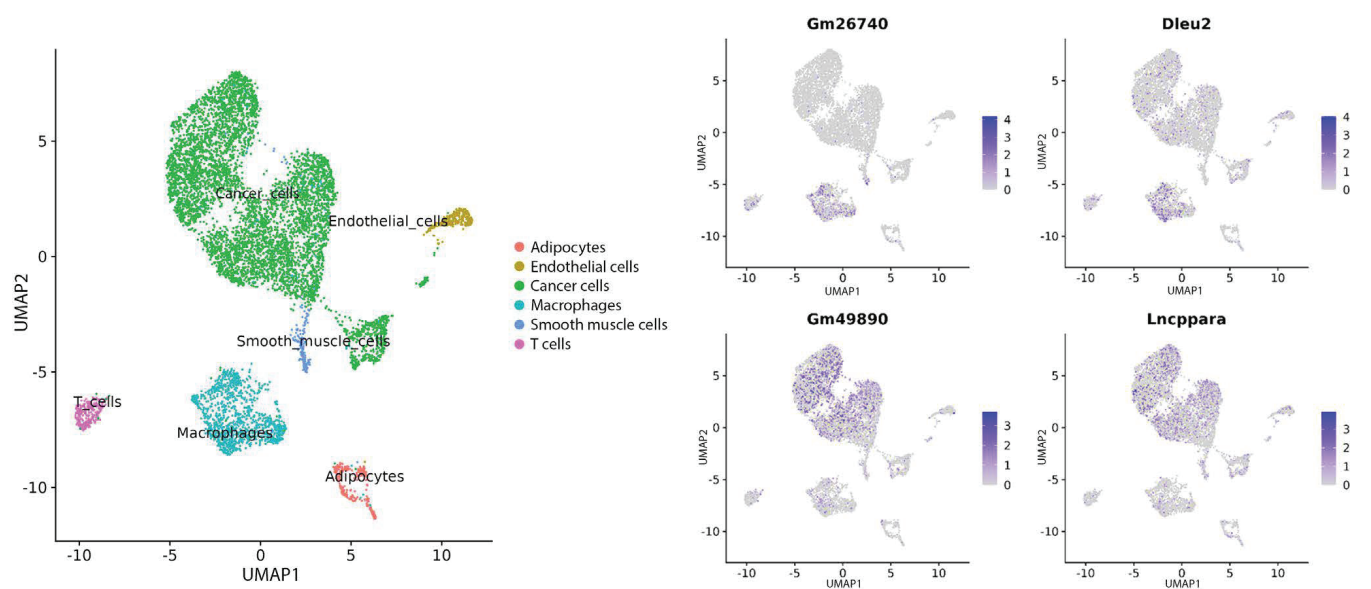


Figure 4. Mouse bladder cancer FFPE single-nucleus sequencing data clustered by gene expression profile. Data shows the distribution of four non-coding RNAs, which are known to be upregulated in specific cell types. Gm26749 and Dieu2 are enriched in macrophages, while Gm49890 and long non-coding RNA near Ppara (Lncppara) are mostly found in cancer cells.