## Start smart

The success of your experiment relies on the preparation of the sample. Therefore, we offer solutions for storing, preparing, and processing any type of sample, including fresh, frozen, cryopreserved, and fixed tissue, to maximize the quality of your sample input.

Get cleaner, more accurate sequencing results:
Our FFPE Dissociation Kits presented here enable you to enrich your target cells or nuclei and significantly reduce background noise for high-quality data across diverse tissues.

**GET IN TOUCH**

Automate your sample preparation by requesting a quote or demo today:
▸ **miltenyibiotec.com/gentleMACS-consult**

**LEARN MORE**

Explore the workflows we support for genomic analysis:
▸ **miltenyibiotec.com/genomics-brochure**

**GET TO KNOW**

Investigate our workflow to extract and enrich intact nuclei:
▸ **miltenyibiotec.com/intact-nuclei**

## Product table

| Product | Order no. |
|---|---|
| **Instruments and accessories** | |
| gentleMACS® Octo Dissociator with Heaters | 130-134-029 |
| autoMACS® NEO Separator | 130-120-327 |
| **Reagents** | |
| FFPE Tissue Dissociation Kit for RNA Profiling | 130-134-089 |
| FFPE Tissue Dissociation Kit | 130-118-052 |
| Anti-Cytokeratin MicroBeads, human | 130-123-094 |
| Cytokeratin LMW Antibody, anti-human, REAfinity® (e.g., APC) | 130-112-745 |
| Vimentin Antibody, anti-human, REAfinity (e.g., FITC) | 130-116-508 |
| **Consumables** | |
| gentleMACS C Tubes | 130-093-237 |
| Pre-Separation Filters (20 µm) | 130-101-812 |
| Pre-Separation Filters (30 µm) | 130-041-407 |
| Pre-Separation Filters (70 µm) | 130-095-823 |

### Reference


1. Wölwer, C. *et al.* (2019) Enrichment of tumor cells from FFPE lung adenocarcinoma resection specimens increases sensitivity of mutation analysis. Application note. miltenyibiotec.com/macrodissection



Miltenyi Biotec

**Miltenyi Biotec B.V. & Co. KG**
Friedrich-Ebert-Straße 68 | 51429 Bergisch Gladbach | Germany
Phone +49 2204 8306-0 | Fax +49 2204 85197
macsde@miltenyi.com | **www.miltenyibiotec.com**

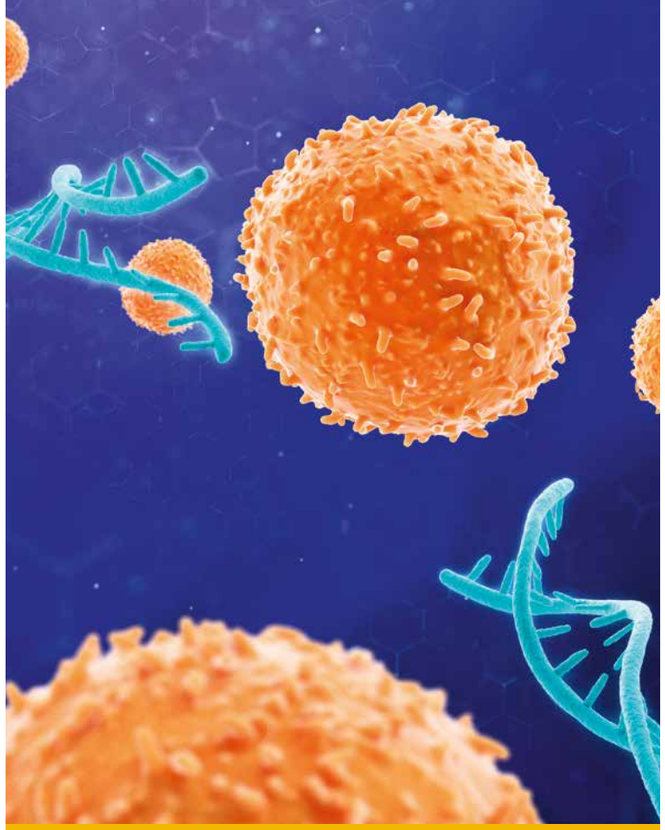
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130-140-094

# FFPE tissue preparation for genomics and transcriptomics

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## Intro

Formalin-fixed, paraffin-embedded (FFPE) tissue samples are a readily available resource for large-scale studies. However, these samples present challenges for highly sensitive sequencing applications.

Learn about our solutions for processing FFPE samples for DNA and RNA sequencing. These solutions allow you to perform molecular profiling and single-nucleus RNA sequencing (snRNA-seq). Find the ideal kit for your application and use it with our gentleMACS® Technology, which offers:

- Automation for streamlined and time-saving sample processing
- Reproducibility to ensure consistent results
- Operator-independent workflows that minimize manual variation
- High-throughput sample processing with eight independent positions



## Efficient FFPE preparation for DNA sequencing

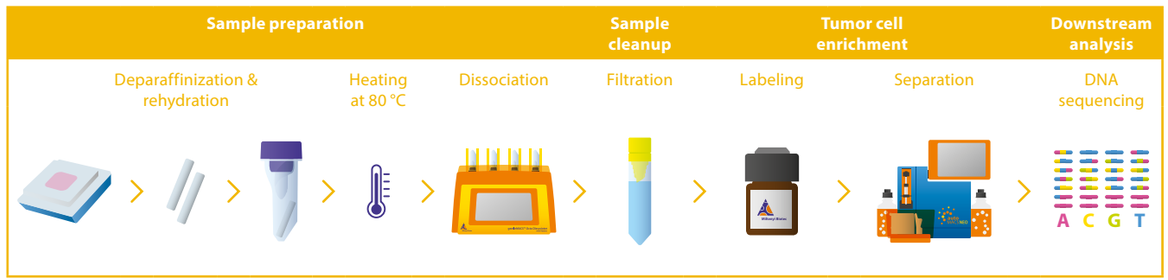



**Figure 1: Schematic workflow for the dissociation of FFPE tissue for cell separation and DNA sequencing.** FFPE tissue sections (25–50 µm thick) are cut from an FFPE tissue block and transferred to a gentleMACS C Tube. The protocol includes deparaffinization and rehydration of the samples, as well as heat-induced antigen retrieval to reverse the effects of formalin. Next, enzymatic and mechanical dissociation are processed on the gentleMACS Octo Dissociator with Heaters. Once the automated dissociation process is complete, larger debris particles are removed using a 20 µm Pre-Separation Filter. Cancer cells or healthy cells can then be separated using MACS® Cell Separation Technology before processing the sample further for DNA sequencing.

| Specimen ID | Preprocessing prior DNA extraction | Concentration of extracted DNA (ng/µL) | DNA input for NGS | Driver mutation identified | Coverage | Allele frequency |
|---|---|---|---|---|---|---|
| Specimen 1 (70% tumor cells) | Macrodissection | 48.80 | 40 | EGFR: c.2236_2250del; p.E746_A750de | 1,471 | 52.3% |
| | Enriched tumor cells | 38.00 | 40 | EGFR: c.2236_2250del; p.E746_A750del | 2,522 | 59.9% |
| Specimen 2 (10% tumor cells) | Macrodissection | 4.78 | 20 | KRAS: c.34G>T; p.G12C | 388 | 11.0% |
| | Enriched tumor cells | 0.46 | 20 | KRAS: c.34G>T; p.G12C | 623 | 28.0% |
| Specimen 3 (< 5% tumor cells) | Macrodissection | 5.64 | 40 | KRAS: c.34G>T; p.G12C | 405 | 1.0% |
| | Enriched tumor cells | 2.12 | 40 | KRAS: c.34G>T; p.G12C | 951 | 7.0% |

**Table 1:** Sequencing results from DNA extracted after macrodissection or from enriched tumor cells.[1]

The FFPE Tissue Dissociation Kit reliably dissociates FFPE tissue into single-cell suspensions and restores cell surface epitopes, which enables the subsequent separation of tumor cells from healthy cells. With the help of Anti-Cytokeratin MicroBeads, human, MACS Technology enables the specific enrichment of tumor cells. This surpasses the capabilities of macrodissection or even laser microdissection and allows direct and reliable sequencing of the isolated tumor cells. Even diffuse or low-tumor-content tissues can be prepared for high-quality DNA sequencing in any standard laboratory. This process yields cleaner, more well-defined cell populations. Flow cytometric analysis and sorting can be easily performed using anti-cytokeratin antibodies for epithelial cells, such as tumor cells, or anti-vimentin antibodies for healthy cells, such as stromal cells or tumor-infiltrating lymphocytes (TILs), after dissociation.

**Key advantages:**

- Optimized workflow analysis of DNA from FFPE tissue
- High tumor cell purity for accurate variant detection
- Clear separation of germline and somatic mutations
- Higher sensitivity without deeper sequencing

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Investigate our application note on sensitive genetic analysis of FFPE carcinoma samples by NGS:

▸ **miltenyibiotec.com/FFPE-appnote**

## Optimized nuclei isolation for FFPE snRNA-seq

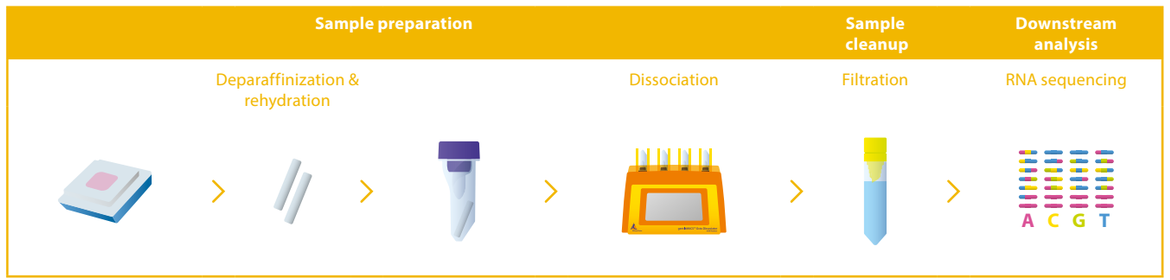



**Figure 2: Schematic workflow for nuclei extraction for RNA sequencing from FFPE tissue samples.** FFPE tissue sections are prepared by cutting 25–50 µm thick slices from an FFPE tissue block and placed in a gentleMACS C Tube. The protocol includes deparaffinization and rehydration of the samples. Next, enzymatic and mechanical dissociation are performed using the gentleMACS Octo Dissociator with Heaters. After dissociation, larger debris particles are removed using a 20 µm Pre-Separation Filter. The isolated nuclei are then ready for the RNA-sequencing process, e.g. snRNA-seq.

The FFPE Tissue Dissociation Kit for RNA Profiling enables the analysis of transcriptomes from FFPE samples at single-cell level. More precisely, it gently and efficiently extracts nuclei from FFPE tissue samples for subsequent snRNA-seq, preserving transcriptomic integrity, which results in high-quality data. Thus, this kit helps you to achieve excellent cell annotation in your UMAP and t-SNE plots. This kit has been validated with the GEM-X Flex Gene Expression Kit from 10× Genomics®.

**Key advantages:**

- Optimized workflow for FFPE snRNA-seq
- Preserves RNA quality and nuclei integrity
- Improved reads, genes, and UMI counts per cell
- Low fraction of mitochondrial reads
- Clear identification of rare cell populations

A direct comparison revealed that the FFPE Tissue Dissociation Kit for RNA Profiling produced higher quality control metrics for different cancer (breast, colon, lung) and healthy tissue (tonsil) samples than Liberase™ TH (Roche®), an alternative enzyme mixture that can be used for manual dissociation of FFPE tissue. Using the FFPE Tissue Dissociation Kit for RNA Profiling increased the number of reads and genes per cell, as well as the UMI counts per cell, while reducing the fraction of mitochondrial reads (fig. 3). These improvements ultimately lead to clearer separation of cell types in UMAP and t-SNE clustering.*

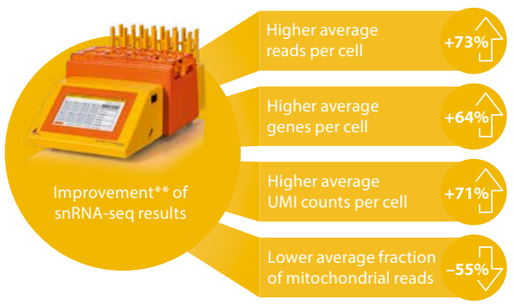



**Figure 3: QC improvement of snRNA-seq.** Average percent improvement in QC metrics for snRNA-seq using the FFPE Tissue Dissociation Kit for RNA Profiling, normalized to the results obtained using Liberase TH, across five different FFPE tissue samples.

ACCESS MORE

** For the underlying data, please refer to:

▸ **miltenyibiotec.com/comparison-data**

* Comparison was performed against Liberase TH Research Grade, which is used in an established tissue dissociation workflow for FFPE samples, as described in the demonstrated protocol CG000784 | Rev B, 10× Genomics: https://cdn.10xgenomics.com/image/upload/v1744998411/support-documents/CG000784_DemonstratedProtocol_SamplePrep_from__FFPETissueSections_GEM-X_Flex_GeneExpression_Rev_B.pdf (accessed May 2026)