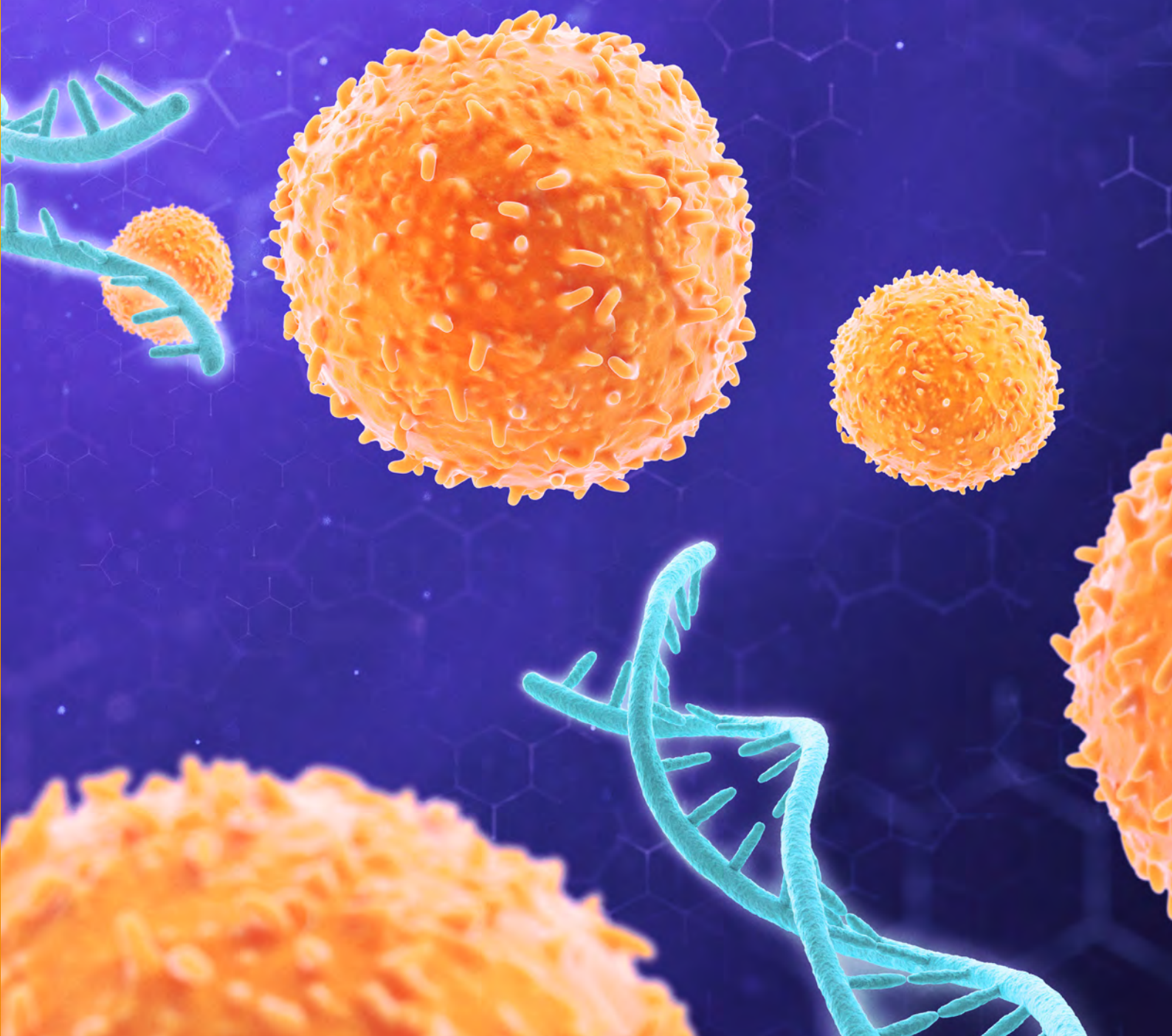
Miltenyi Biotec

Cell and nuclei preparation for genomics

Start smart and achieve new heights in genomic analysis



Improved sample quality makes the difference

Enhance your genomic outcomes

Reliable genomic data begin with high-quality samples. Standardized workflows, supported by gentle dissociation tools like our gentleMACS® Technology, help to maintain sample integrity and reduce the risk of costly experimental repetitions.

Ensure data fidelity

Tissue samples undergo molecular alterations from the moment of collection. Using optimized reagents and streamlined workflows minimizes cellular stress and preserves native molecular profiles for accurate analysis.

Adapt with ease

From fresh to formalin-fixed paraffin-embedded (FFPE) tissues, consistent preparation is key.
We have a solution for every step in the preparation of cells and nuclei for excellent genomic analysis results. From tissue storage to quality control, our technologies will help your research achieve new heights.

EXPLORE

Take a look at our full MACS® Sample Preparation portfolio:

▸ **miltenyibiotec.com/sample-preparation**

LEARN MORE

Get to know our gentleMACS Octo Dissociator with Heaters:

▸ **miltenyibiotec.com/gentlemacs-octo**

Content

Short-term storage and sequencing

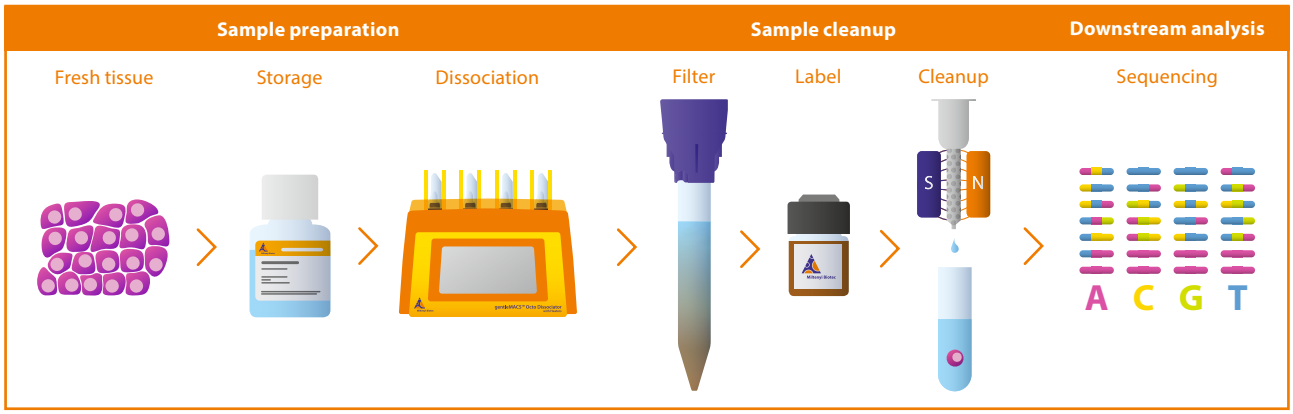


Figure 1: Schematic representation of the sample processing workflow following storage in MACS® Tissue Storage Solution. Samples can be stored or transported in the solution before undergoing tissue dissociation. The resulting single-cell suspension is then subjected to a cleanup step to remove debris and dead cells, ensuring high-quality input for downstream applications such as bulk or single-cell RNA sequencing (scRNA-seq).

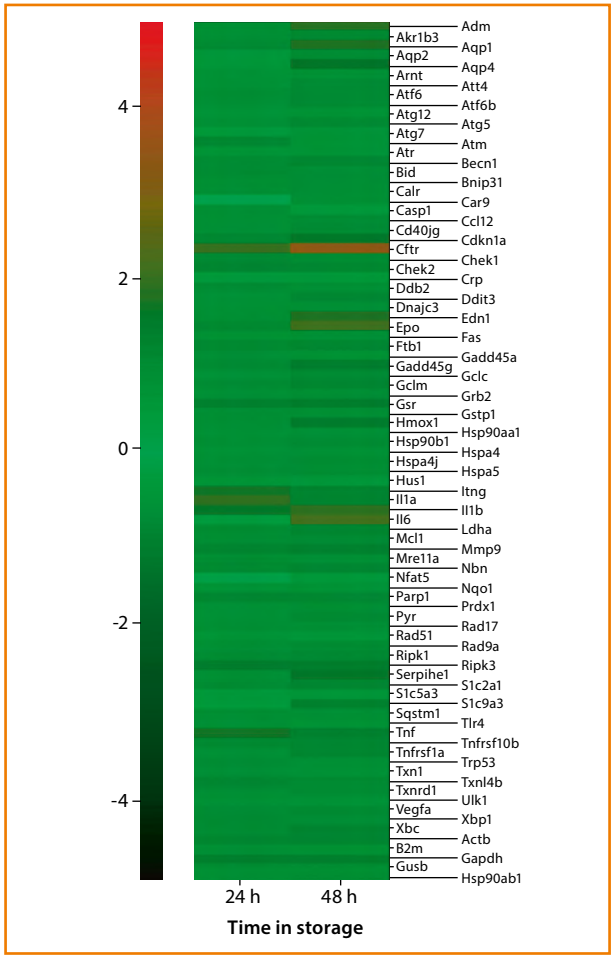


Figure 2: Differential expression of cellular stress-related genes in fresh and stored tumor cells. RNA was extracted from CT26 tumor cells, either freshly isolated or stored in MACS Tissue Storage Solution, and analyzed for stress-related gene expression. The heat map displays fold changes in expression levels relative to fresh tissue.

Preservation of the transcriptomic landscape

Maintaining stable transcriptomic landscapes during storage and transport is crucial in order to prevent alterations to gene expression. To achieve this, it is essential to maintain cell viability and cellular composition. The MACS Tissue Storage Solution creates an optimized environment that mitigates stress responses and preserves transcriptomic fidelity for up to 48 hours at 2–8 °C. Comparative analyses confirm that gene expression profiles remain stable. This ensures the production of accurate and reproducible genomic data, particularly for rare or sensitive samples.

ACCESS MORE

Get instant access to application notes in the field of cell and tissue storage:

▸ **miltenyibiotec.com/data2download**

Long-term storage and sequencing

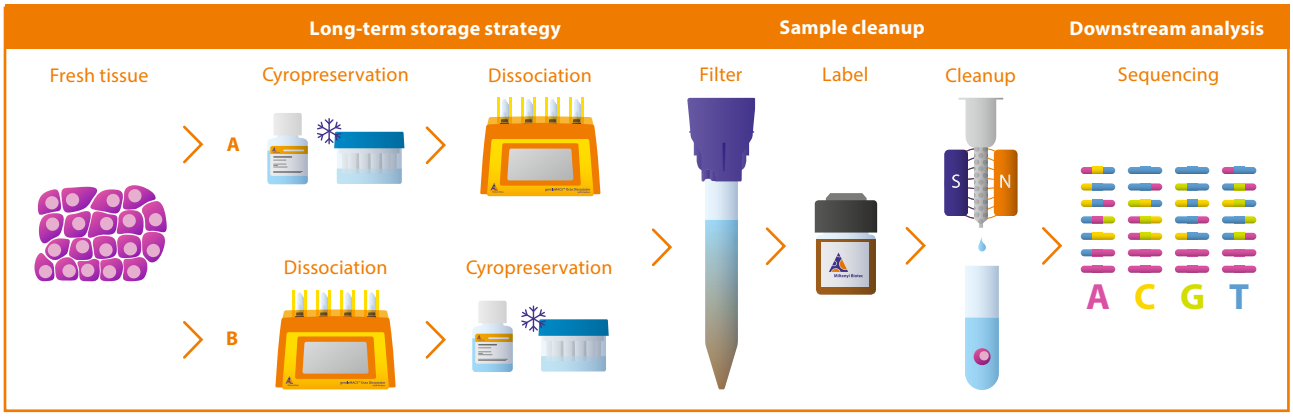


Figure 3: Schematic overview of two long-term storage (cryopreservation) strategies for tissue samples. Tissues are either preserved as intact tissue pieces (A) or dissociated and cryopreserved as a single-cell suspension (B). If the tissue is preserved as intact pieces, the samples undergo dissociation upon thawing. Both sample types then proceed through cleanup and quality control steps. The final single-cell suspensions are then used for downstream applications such as scRNA-seq.

High-quality scRNA-seq from cryopreserved samples

Conventional cryopreservation methods often compromise cell viability and introduce transcriptional artifacts. The MACS Freezing Solution, an animal-component-free cryoprotectant, ensures optimal preservation of intact tissue pieces and cells in suspension. Validated by scRNA-seq, the MACS Freezing Solution preserves sample viability and maintains cellular composition, ensuring high data integrity. It also provides flexibility for customized workflows, whether you choose to preserve your samples as intact tissue or cells in suspension, without compromising sequencing accuracy.

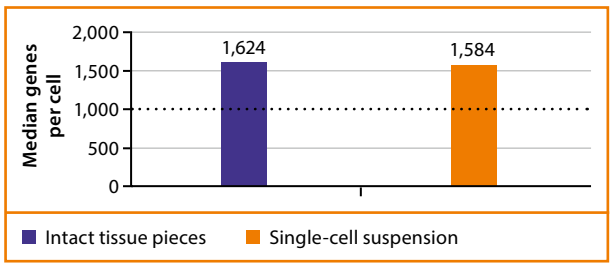


Figure 4: Quality control metrics for scRNA-seq of non-small cell lung cancer (NSCLC) samples from human, cryopreserved with MACS Freezing Solution, either as single-cell suspensions or intact tissue pieces. Median genes per cell were compared. One sample was frozen as intact tissue and later dissociated using gentleMACS Octo Dissociator with Heaters and Tumor Dissociation Kit, human. Another sample was dissociated before freezing. Samples with median genes per cell above 1,000 are considered high-quality samples.

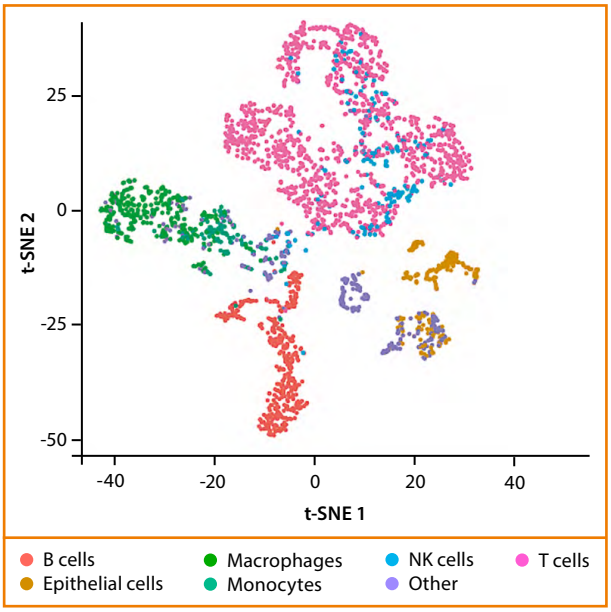


Figure 5: t-SNE plot of scRNA-data from a combined NSCLC sample derived from two human donors (intact tissue pieces and single-cell suspension). Each dot represents an individual cell, colored according to its annotated cell type. Distinct clusters reveal the cellular heterogeneity of the tumor microenvironment, including immune, stromal, and malignant cell populations.

LEARN MORE

Choose the right solution for your experiment. Get to know our MACS Storage Solutions:

▸ **miltenyibiotec.com/storage-solutions**

Sample cleanup for optimized sequencing results

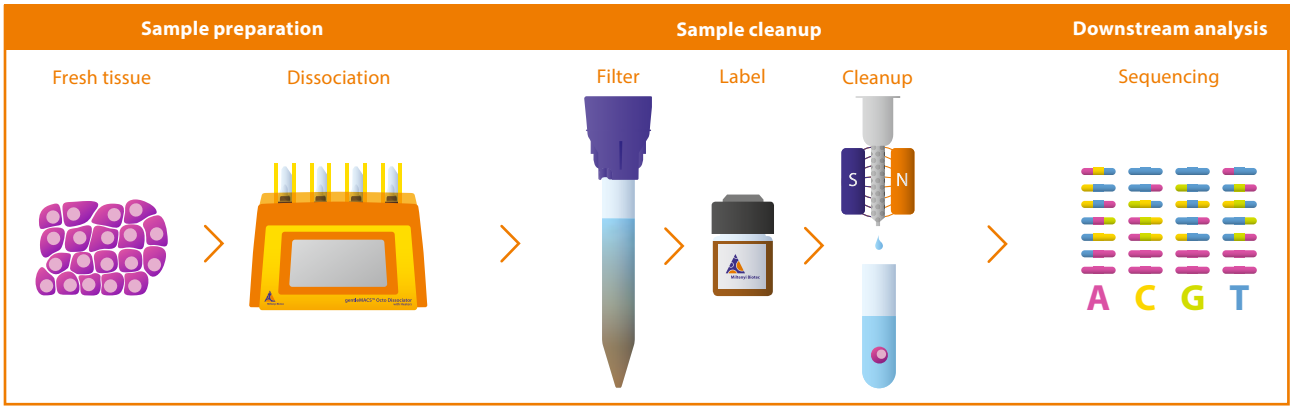


Figure 6: Schematic workflow of sample processing for scRNA-seq. Tissue dissociation is performed using the gentleMACS Octo Dissociator with Heaters, followed by cleanup of the single-cell suspension with the Cell Suspension Cleanup Kit, human (CSCK). The purified suspension is evaluated for quality using the MACSQuant® Analyzer Flow Cytometer before proceeding to downstream applications requiring high-purity single-cell samples.

Improve sample purity for sequencing human samples[1]

The accuracy of scRNA-seq is highly dependent on sample purity. Dead cells, erythrocytes, and cellular debris introduce background noise that can obscure meaningful signals, as well as increase sequencing costs.

The Cell Suspension Cleanup Kit (CSCK) enables an efficient, one-step cleanup process using MACS Cell Separation Technology, which reduces the time between sample preparation and sequencing. Fewer steps also mean less operator dependency, minimizing cell loss, and reducing the likelihood of errors during manual handling. The depletion of contaminants without the need for erythrocyte lysis is highly effective in reducing cellular stress, preserving transcriptomic integrity, and increasing sequencing accuracy.

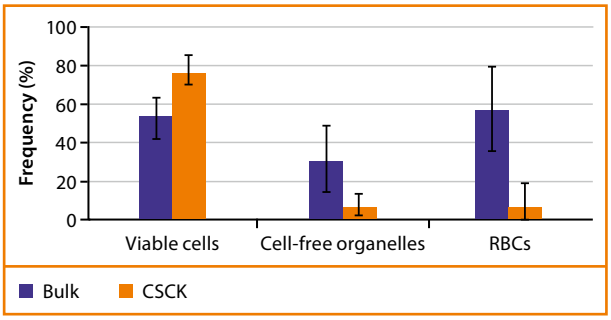


Figure 7: Effective one-step sample cleanup. Human ovarian cancer tissue was processed using the gentleMACS Octo Dissociator with Heaters and the Tumor Dissociation Kit, human. Cell viability before and after cleanup with the CSCK, was evaluated by flow cytometry using propidium iodide (PI) staining and doublet exclusion. CSCK improved viability rate to ~80% while reducing cell-free organelles and red blood cells (RBCs) to <8% (n = 3 to 5).

1 Please note, the Cell Suspension Cleanup Kit, human, is not compatible with digestion enzymes degrading glycophorin A, including the following Miltenyi Biotec Kits: Brain Tumor Dissociation Kit (P), human (# 130-095-942); Umbilical Cord Dissociation Kit, human (# 130-105-737); Embryoid Body Dissociation Kit, human and mouse (# 130-096-348); Whole Skin Dissociation Kit, human (# 130-101-540); Multi Tissue Dissociation Kit 2 (# 130-110-203). As a workaround for these samples, you can deplete RBCs using the Red Blood Cell Lysis Solution (# 130-094-183) and subsequently use either the Cell Suspension Cleanup Kit, human, to deplete dead cells and organelles, or, if only dead cells shall be removed, the Dead Cell Removal Kit (# 130-090-101).

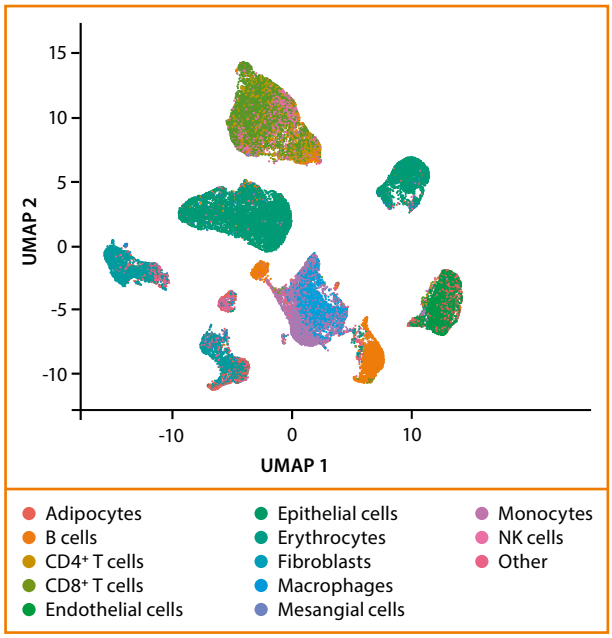


Figure 8: UMAP visualization of a human ovarian tumor sample processed with the Cell Suspension Cleanup Kit, human. scRNA-seq sequencing was performed using the 10× Genomics® platform. The high purity achieved through sample cleanup enables detailed annotation and clear clustering of distinct cell types, facilitating a comprehensive analysis of the tumor microenvironment.

Enhancing signal clarity for confident analysis

Efficient removal of unwanted material, such as dead cells, cell-free organelles, and erythrocytes minimizes background noise, and improves sequencing quality. By reducing mitochondria- and erythrocyte-specific reads, this workflow enhances sensitivity and specificity, allowing deeper insights into transcriptional heterogeneity and increasing confidence in downstream biological interpretations.

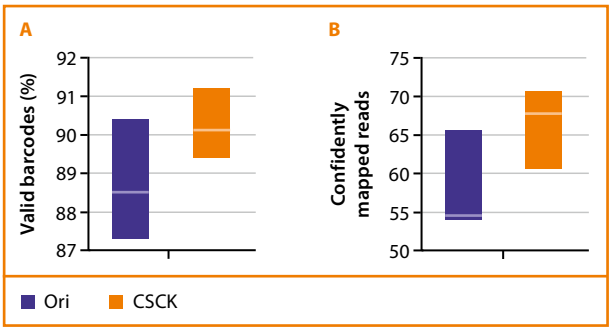


Figure 9: scRNA-seq quality metrics comparing unprocessed (Ori) and tumor samples cleaned up with CSCK. (A) Distribution of valid barcodes. (B) Proportion of reads mapped confidently to the transcriptome, demonstrating improved data quality following cleanup (n = 3).

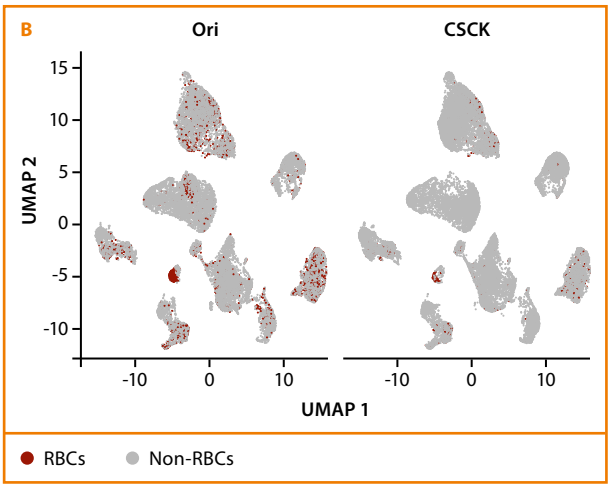


Figure 10: UMAP plots comparing scRNA-seq data from unprocessed (Ori) samples and samples cleaned up with CSCK. Highlighted HBB gene expression (in red) reveals contamination from erythrocytes (RBCs). CSCK reduces contaminants significantly, leading to improved sample quality.

LEARN MORE

Need guidance to cleanup your mouse tissue samples for sequencing?

▸ **miltenyibiotec.com/data2download**

Optimize nuclei preparation for snRNA-seq

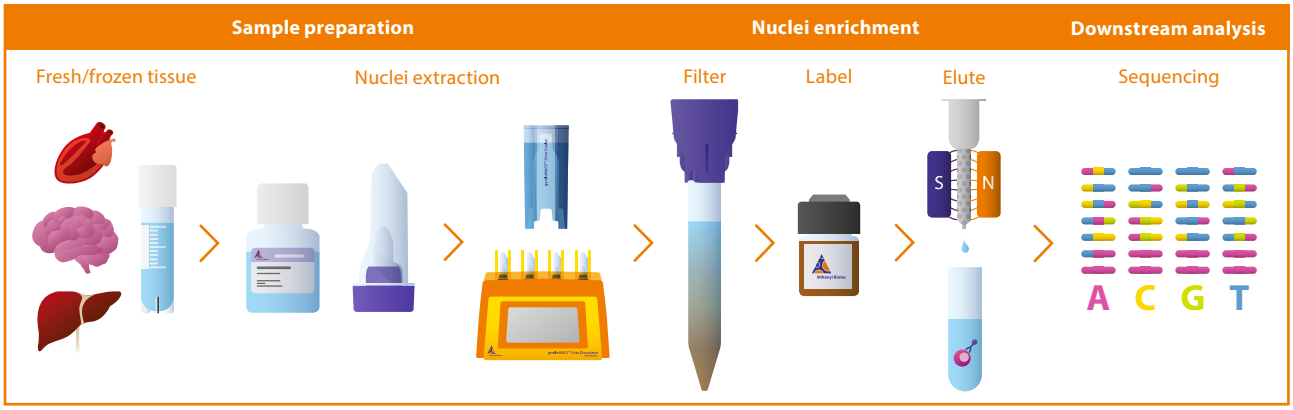


Figure 11: Schematic workflow for automated nuclei extraction and enrichment. Fresh or frozen samples are processed using the Nuclei Extraction Buffer and the gentleMACS Octo Dissociator with Heaters for automated nuclei extraction. Extracted nuclei are then magnetically enriched using Anti-Nucleus MicroBeads to optimize sample purity and quality for downstream applications such as snRNA-seq.

Single-nucleus RNA sequencing (snRNA-seq) is indispensable for analyzing complex tissues, particularly when the dissociation of a specific sample into viable single cells is unpromising, for example snap-frozen tissue. The gentleMACS Octo Dissociator with Heaters automates nuclei extraction, ensuring reproducibility.

Combined with the Nuclei Extraction Buffer and gentleMACS Octo Coolers, this workflow prevents transcriptional artifacts, while Anti-Nucleus MicroBeads selectively enrich intact nuclei from challenging samples such as brain and liver tissue.

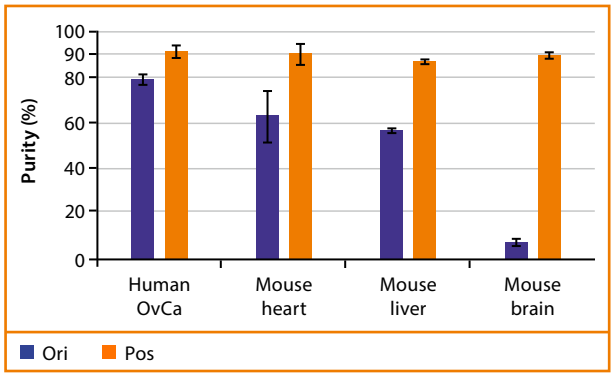


Figure 12: Purity assessment of enriched nuclei after Anti-Nucleus MicroBeads-based isolation using MACS Technology for different tissue types and species, such as human ovarian cancer (OvCa). Purity levels of original (Ori) and enriched (Pos) nuclei were measured with the MACSQuant Analyzer 10 and visualized by DAPI staining. Notably, the purity of intact nuclei extracted from mouse brain tissue increased dramatically, from 8% to 92% (a 12-fold increase, n = 3).

Identification of cell type populations with enriched nuclei

snRNA-seq enables high-resolution transcriptomic profiling, revealing cellular heterogeneity with exceptional clarity. Enriched nuclei facilitate distinct clustering in t-SNE plots, ensuring robust and reproducible subcluster identification across independent experiments. The precision of nuclei extraction and enrichment enhances biological interpretations and supports reliable transcriptomic studies across a wide range of tissue types and species.

DIVE DEEPER

Optimize your nuclei preparation workflow for genomic application:

▸ **miltenyibiotec.com/data2download**

LEARN MORE

See how enriched nuclei generate high-quality snRNA-seq results with the Chromium™ Single Cell 5′ v1.1 Reagent Kit (10× Genomics) and an Illumina® System.

▸ **miltenyibiotec.com/nuclei-preparation**

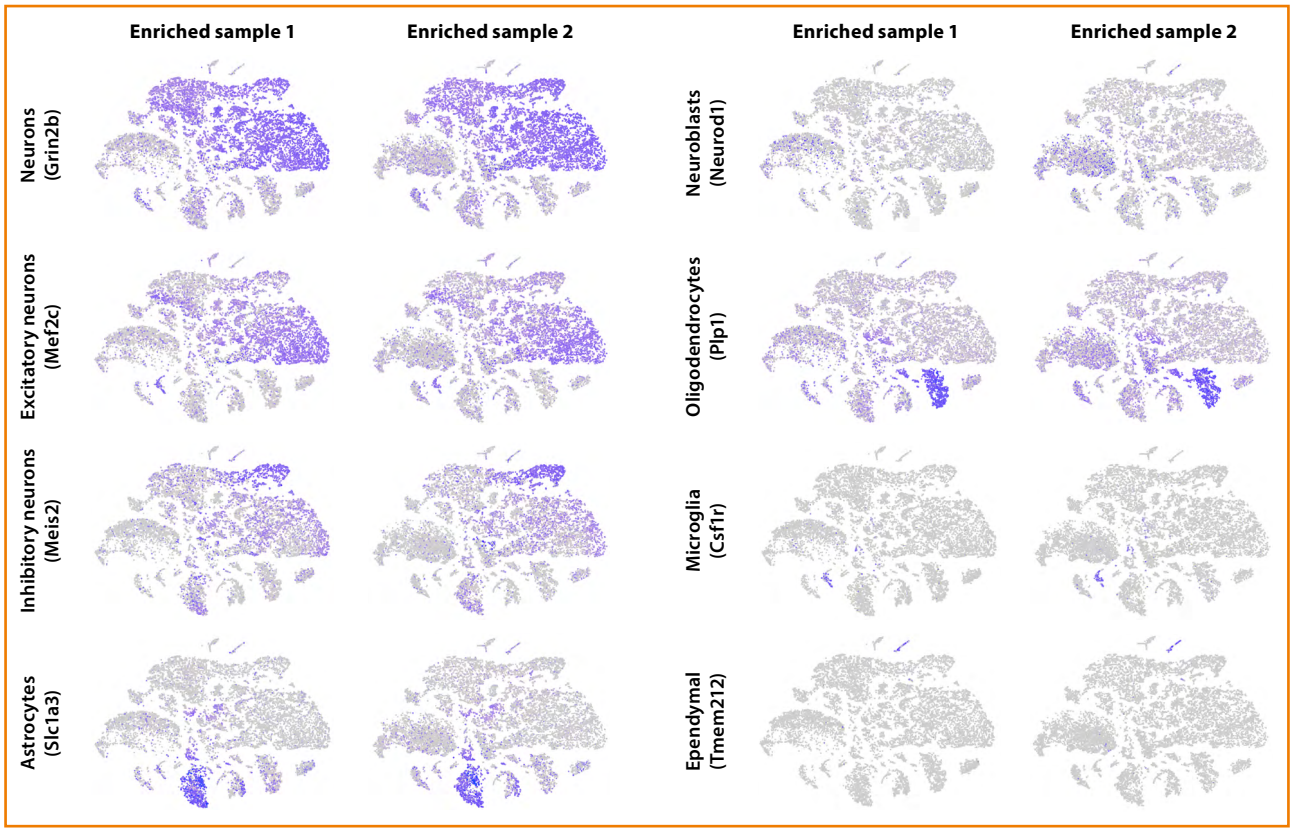


Figure 13: Reproducible and robust snRNA analysis with enriched nuclei using Anti-Nucleus MicroBeads. t-SNE plots illustrating distinct gene markers and their corresponding cell types. Barcoded cDNA libraries were generated using the Chromium Single Cell 5′ v1.1 Reagent Kit (10× Genomics) and sequenced on an Illumina® platform. Purple dots indicate cells expressing marker genes for the specified cell types, while gray dots represent all other cells.

FFPE tissue preparation for RNA sequencing

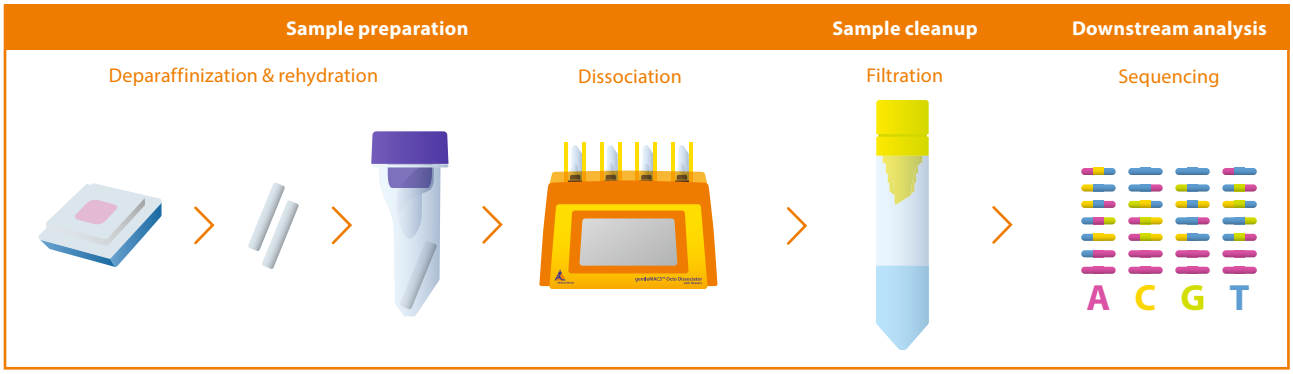


Figure 14: Schematic workflow for nuclei extraction from FFPE tissue samples. FFPE samples are processed using the gentleMACS Octo Dissociator with Heaters and the FFPE Tissue Dissociation Kit for RNA Profiling. The extracted nuclei are then prepared for downstream applications such as snRNA-seq.

Dissociation of FFPE tissue for RNA sequencing

FFPE tissues are an easily accessible but challenging resource for transcriptomic analysis. The FFPE Tissue Dissociation Kit for RNA Profiling enables the extraction of high-quality single-nucleus suspensions from FFPE tissue samples while preserving RNA integrity. Validated across various tissue types, this workflow enables reproducible sequencing results, unlocking new potential for molecular and translational research.

LEARN MORE

Want to increase the sequencing sensitivity of your FFPE sample for tumor profiling?

▸ **miltenyibiotec.com/data2download**

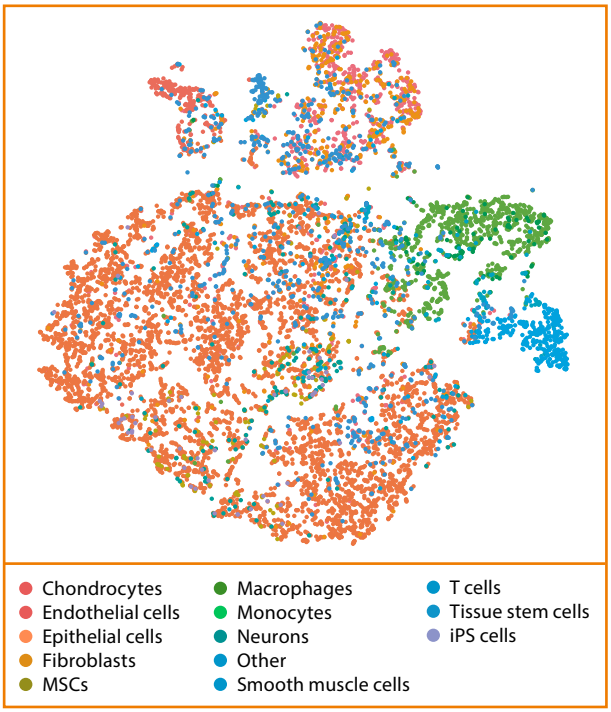


Figure 15: Exemplary t-SNE plot displaying cell type annotations of a breast cancer tumor sample. The tissue was dissociated on the gentleMACS Octo Dissociator with Heaters using the FFPE Tissue Dissociation Kit for RNA Profiling, and libraries were prepared with the Chromium Fixed RNA Profiling Assay (10× Genomics) before sequencing on an Illumina NextSeq® 2000.

Optimized RNA profiling of FFPE tissue

Accurate snRNA-seq from FFPE tissue requires stringent quality control. Internal and external validations across different tissue types revealed that the FFPE Tissue Dissociation Kit for RNA Profiling improves key QC parameters – including median reads, median genes, and UMI counts per cell – by an average factor of more than 1.5 over the use of Liberase™ TH Research Grade (Roche®).[2]

In addition, the kit significantly reduces the amount of mitochondrial mRNA contamination. This reduces background noise and ensures a higher proportion of informative, confidently mapped nuclear transcripts, providing robust, reproducible sequencing results.

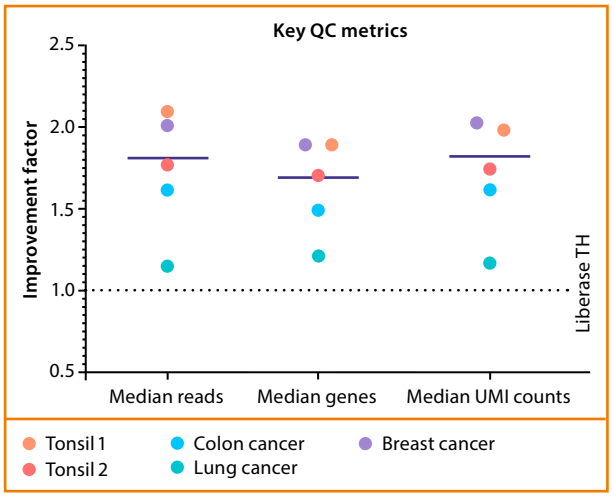


Figure 16: Sequencing QC metrics comparison. Factor of improvement in QC metrics for snRNA-seq using the FFPE Tissue Dissociation Kit for RNA Profiling (circles) normalized to Liberase TH (dotted line) on median reads, median genes, and median UMI counts per cell across three FFPE tumor samples (breast, colon, and lung cancer) and two healthy FFPE tonsil tissues.

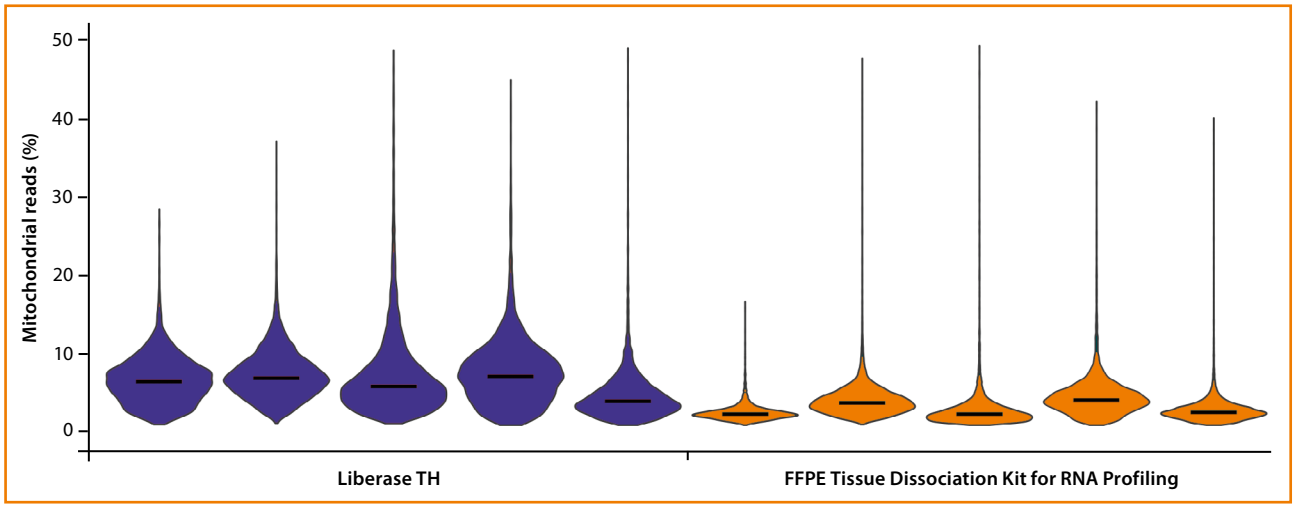


Figure 17: Comparison of mitochondrial read percentages across five different tissue samples of different donors processed with either FFPE Tissue Dissociation Kit for RNA Profiling or Liberase TH. Reduction in mitochondrial read content when using the FFPE Tissue Dissociation Kit for RNA Profiling highlights the impact of dissociation methods on data quality.

2 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 October 2025)

Preparation of large and sensitive cell types for scRNA-seq

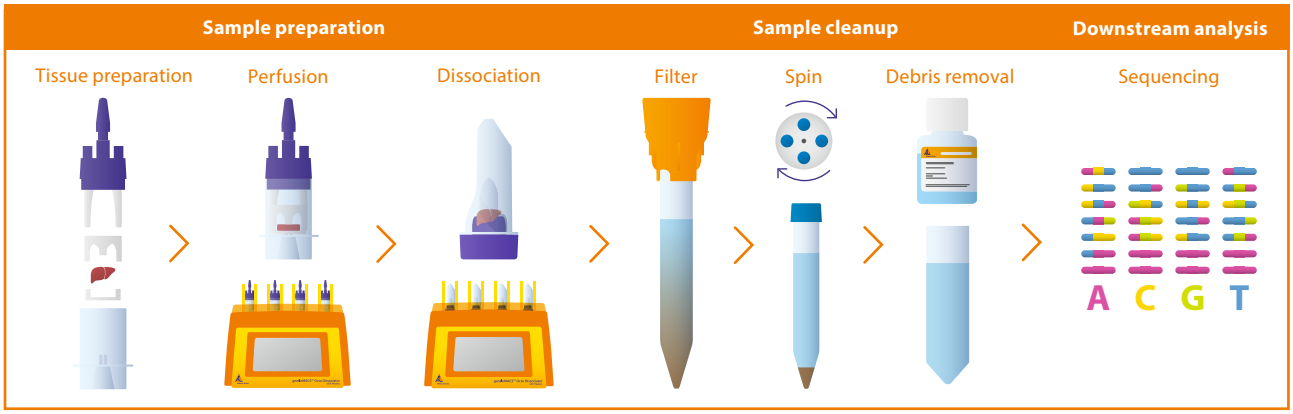


Figure 18: Experimental workflow for the preparation of single-cell suspensions from mouse liver. Hepatocytes and non-parenchymal cells (NPCs) are isolated using gentleMACS Perfusion Technology. Single-cell suspensions are then cleaned with either Debris Removal Solution alone (hepatocyte fraction) or with a combination of RBC lysis buffer and Debris Removal Solution (NPC fraction) to optimally prepare the single-cell suspensions for subsequent downstream analysis, such as scRNA-seq.

Automated perfusion for the isolation of delicate cell types

For sensitive cell types, such as hepatocytes or cardiomyocytes, *ex vivo* perfusion is essential to maintain viability and integrity after tissue dissociation.

The gentleMACS Perfusion Technology automates the perfusion of up to eight rodent livers or mouse hearts in parallel, leading to standardized and reproducible single-cell suspensions suitable for culture, flow cytometry, and scRNA-seq.

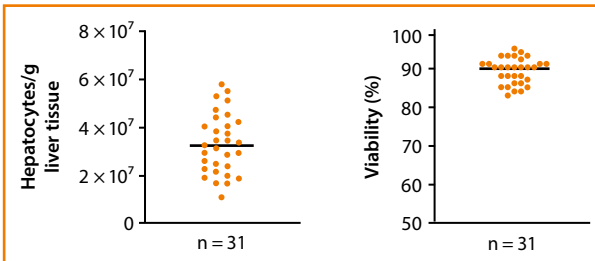


Figure 19: Overview of average yield and viability that can be reached for hepatocytes isolated from the mouse left lateral liver lobe using gentleMACS Perfusion Technology. Cell count was determined using forward and side scatter based on the size and granularity of the hepatocytes and the viability was determined using PI and analyzed directly by MACSQuant Analyzer (n = 31, Balb/c and C57BL/6, 6–12 weeks).

Isolation and single-cell sequencing of viable hepatocytes

The average of hepatocyte yield per gram of mouse liver is around 3.4×10^7 with a viability of around 90% enabling the isolation of enough cells and highest quality input for following scRNA-seq experiments.

GET TO KNOW

Want to learn more about *ex vivo* tissue perfusion or isolation of other delicate cell types, such as cardiomyocytes?

▸ **miltenyibiotec.com/perfusion-technology**

scRNA-seq of delicate cell types

Hepatocytes isolated using gentleMACS Perfusion Technology are ideal for scRNA-seq. This workflow combines automated perfusion and cleanup of samples for high-quality single-cell sequencing results, providing a reliable, high-throughput solution for liver cell research. It supports optimal data quality and reproducibility.

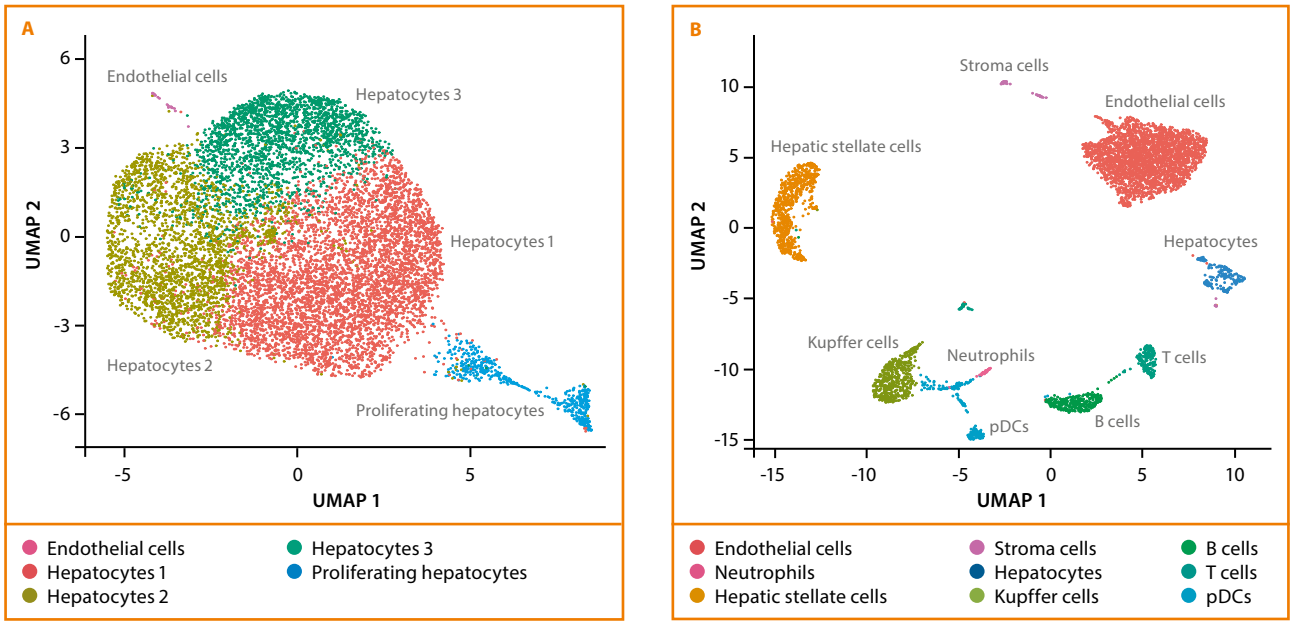
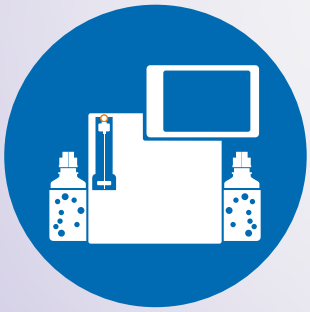


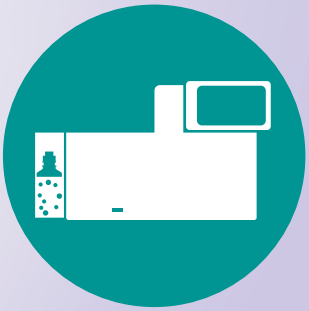
Figure 20: UMAP plots showing hepatocyte subtypes (A) and non-parenchymal cell-types (B) using Evercode™ Whole-Transcriptome technology (Parse® Biosciences). Barcoded cDNA libraries were sequenced on an Illumina platform.

Discover automated solutions for streamlined downstream processing and analysis



autoMACS® Neo Separator

MACSQuant® Tyto® Family



MACSima® Platform

Automated PBMC isolation directly from whole blood for improved single-cell data

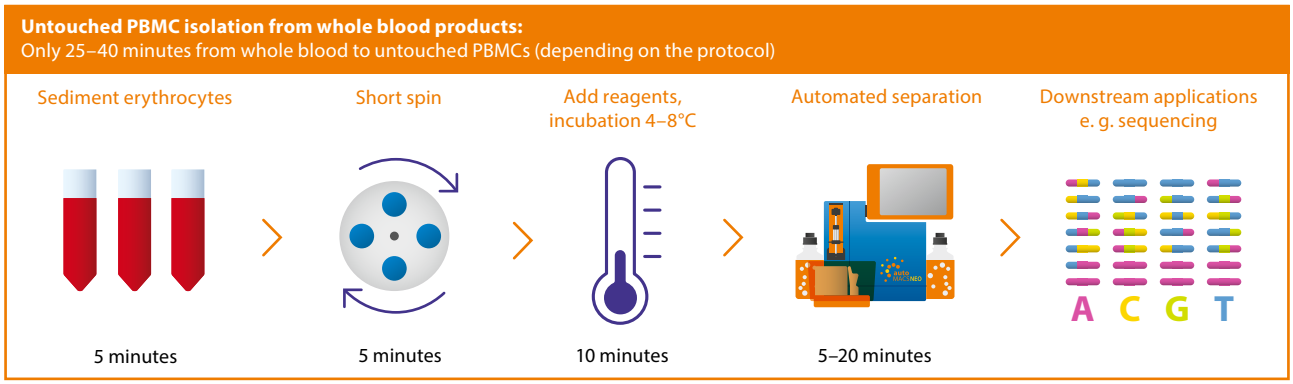


Figure 21: Automated workflow for peripheral blood mononuclear cell (PBMC) isolation on autoMACS® Instruments. Starting from a whole blood sample and following the protocol of the StraightFrom® Whole Blood PBMC Isolation Kit, human, including a sedimentation, spin, and incubation step prior to automated isolation of PBMCs using either autoMACS Instrument or MultiMACS™ Separator. PBMCs can be immediately used for downstream applications such as single-cell RNA sequencing.

The StraightFrom Whole Blood PBMC Isolation Kit, human, in combination with the autoMACS NEO Separator enables direct, hands-free isolation of PBMCs from whole blood. This streamlined approach eliminates manual processing steps, which significantly reduces processing time and minimizes cellular stress.

As demonstrated in scRNA-seq experiments, cells isolated with our automated solution show reduced signs of stress-induced gene expression in comparison to PBMCs isolated with the conventional density gradient centrifugation workflow utilizing Ficoll® (GE Healthcare™), ensuring unbiased, high-quality data for downstream applications.

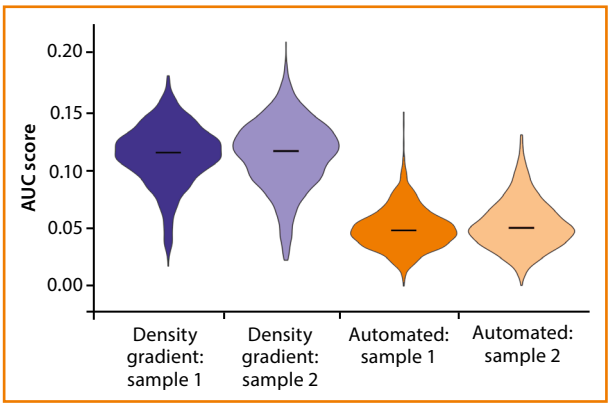


Figure 22: Violin plot showing the area under the curve (AUC) scores for inflammatory response and autoimmune signature genes in scRNA-seq data. Samples processed with density gradient centrifugation (Density gradient: sample 1 and 2) exhibit elevated scores, indicating stress-induced gene expression. In contrast, samples processed with our automated workflow using the StraightFrom Whole Blood PBMC Isolation Kit, human (Automated: sample 1 and 2) show minimal activation of these pathways, highlighting the reduced cellular stress and improved sample integrity.

LEARN MORE

Want to learn how to isolate untouched PBMCs in just 25 minutes:

▸ **miltenyibiotec.com/pbmc-isolation**

LEARN MORE

Get to know our autoMACS NEO Separator in detail:

▸ **miltenyibiotec.com/automacs-NEO-instrument**

Optimize your sequencing outcome with gentle and efficient cell sorting

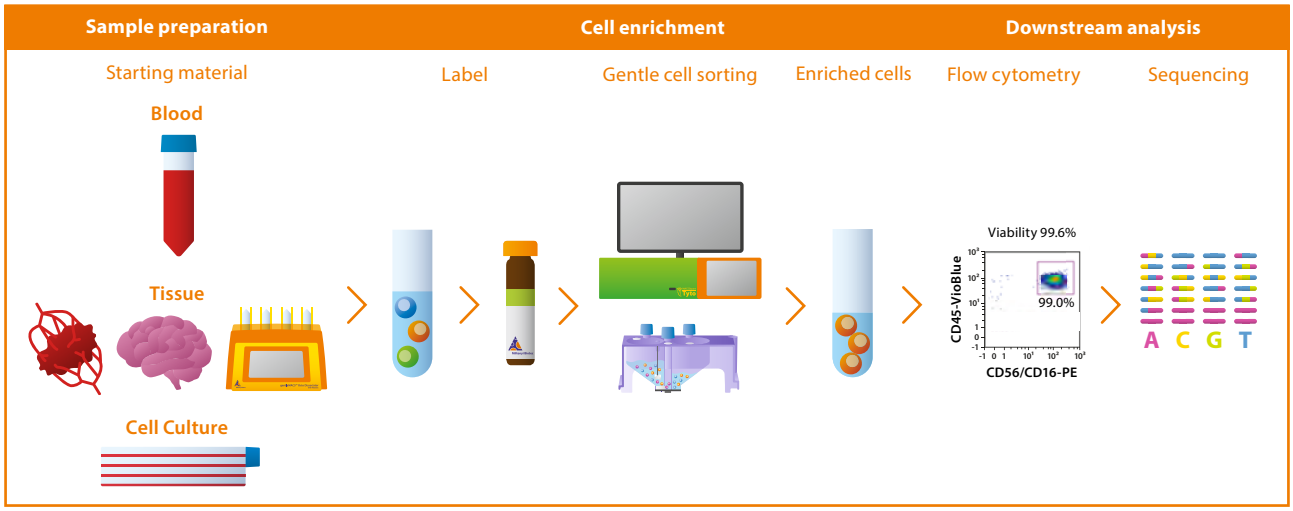


Figure 23: Automated workflow for isolation of fragile cells. Cells are extracted from up to eight samples using the gentleMACS Octo Dissociator with Heaters, debris is removed, and cells of interest sorted with the MACSQuant Tyto Cell Sorter. Enriched cells are concentrated in convenient volumes, bypassing the need for an additional centrifugation step, and are immediately ready for downstream analyses, such as flow cytometry and sequencing.

The MACSQuant Tyto Family of cell sorters innovates cell sorting with its unique microchip-based system that ensures gentle, contamination-free sorting in a closed and sterile cartridge.

Multiparameter cell sorting enables the isolation of target cells with highest purities based on the combination of different parameters, including simultaneous depletion of dead cells and debris. However, conventional droplet-based sorters with excessive pressure, high shear forces, and electrical charges can cause high stress to cells and lead to transcriptional changes, thereby introducing bias in downstream gene expression analysis. Additionally, the sorted cells remain undiluted in the buffer, eliminating the need for an extra centrifugation step that could cause stress and cell loss. As a result, cells sorted on the MACSQuant Tyto can be directly utilized for subsequent downstream genomic analysis.

Head-to-head comparison of MACSQuant Tyto to a conventional droplet sorter highlights not only the increase in standard QC metrics such as number of genes and number of UMI counts per cell, but also the reduction in stress-related genes compared to conventional droplet sorters.

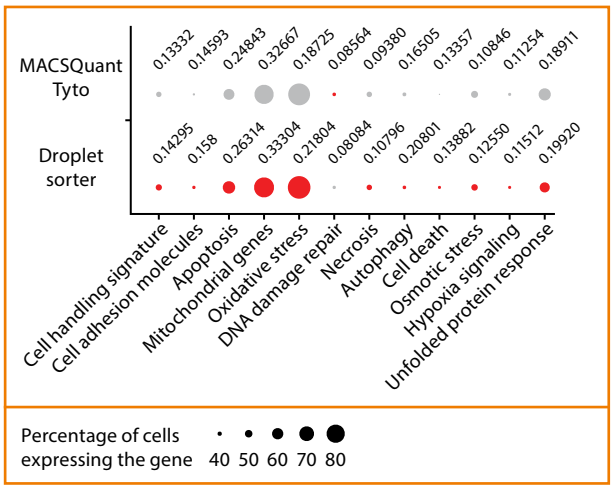


Figure 24: Side-by-side comparison of gene expression of murine epithelial cells sorted on the MACSQuant Tyto and on a conventional droplet-based cell sorter as demonstrated in figure 23. Dots colored in red indicate which dataset shows higher gene activation. The dot size indicates a relative gene expression level.

LEARN MORE

Realize better genomics results through gentle cell sorting:

▸ **miltenyibiotec.com/genomics-Tyto**

Unlock the spatial dimension of your sequencing results

Figure 25: Multiomics workflow using the MACSima Imaging Cyclic Staining (MICS) technology on the MACSima Platform. MICS technology enables repeated cycles of staining, imaging, and signal erasure to analyze hundreds of proteins without harming the sample. Integrating RNAsky® Detection Probes seamlessly adds spatial RNA probe labeling, detection, and analysis within the same sample.

Accelerate your multiomics research with the power of spatial biology

The MACSima Platform offers everything you need for seamless, rapid assay development from a single source:

- Pretested antibodies: 600+ off-the-shelf antibodies and plug-and-play antibody panels
- RNAsky Reagents: easy sample preparation workflow with predefined and custom probe panels
- MACSima System: walk-away solution for automated spatial biology experiments
- MACS iQ View Software: visualization and analysis of spatial multiomics data in record time

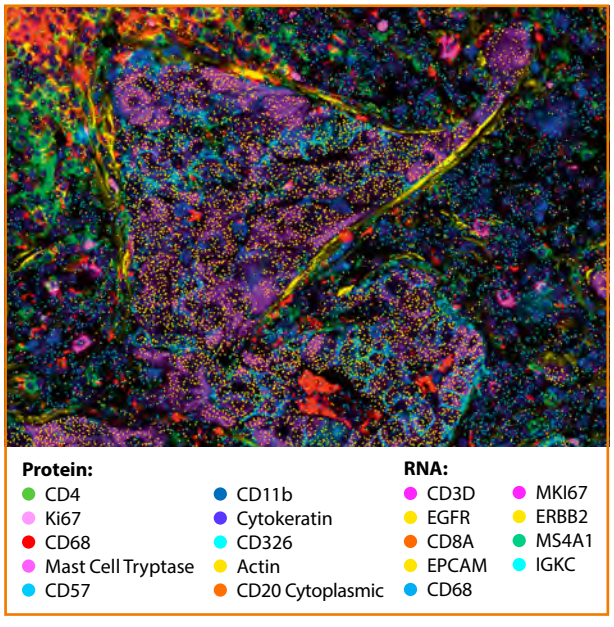


Figure 26: Simultaneous detection and analysis of 40 protein markers and 27 RNAs in non-small cell lung cancer (NSCLC) FFPE tissue.

Customized RNA detection panels for spatial multiomics

Target any gene with RNAsky Design and ensure reproducible results with the MACSima Platform. The RNAsky Workflow enables consecutive protein detection on the same section while preserving epitope integrity and tissue morphology. RNAsky Technology complements the MACSima Platform's spatial biology workflow, ideal for applications such as:

- Cross-validation of upstream screening methods
- Detecting secreted factors (e.g. chemokines or cytokines)
- Protein-RNA co-expression analysis
- Replacing unavailable or poorly performing antibodies

Analyze enormous data stacks with ease

The MACS iQ View – Spatial Biology Analysis Software is specifically developed to process the massive data stacks generated by the MACSima Platform, enabling scientists to fully harness the power of spatial biology. This intuitive software can easily handle even the most complex multiomics datasets, delivering clear results fast and helping you to publish with confidence.

EXPLORE MORE

Your tissue sample is full of secrets, just waiting to be unlocked. Start your journey of discovery at:

▸ **miltenyibiotec.com/MACSima-platform**

Best practice tips

1. Use next-generation sequencing–validated MACS Storage Solutions for short- and long-term storage if you are planning to process your samples for sequencing experiments.
2. Boost the reliability of your experiments by using automated procedures, such as dissociating your sample using the gentleMACS Technology in combination with the Tissue Dissociation Kits and the respective specialized programs.
3. For downstream cell separation and sorting, streamline your workflow with the autoMACS NEO Separator for magnetic cell isolation and the MACSQuant Tyto for gentle, high-purity cell sorting in a fully enclosed, sterile system.
4. For human cell suspensions, use the Cell Suspension Cleanup Kit, human, to increase the viability and purity of your cell suspension, optimizing it for sequencing experiments. As well as depleting dead cells and cell-free organelles, it also removes RBCs, eliminating the need for potentially harmful RBC lysis solution.
5. When viability is below 90%, use the Dead Cell Removal Kit to remove dead cells from non-human and human cell suspensions that have been previously processed with enzymes degrading Glycophorin A, e.g., Enzyme P. Use the RBC Lysis Solution if erythrocytes exceed 30%.
6. Remove accumulated debris and cell clumps from your sample with MACS SmartStrainers before analysis. This allows for more accurate cell counts and avoids clogging during cell sorting as well as on the single-cell genomics platform.

7. Some cells tend to aggregate after tissue dissociation due to free floating DNA. An additional DNase wash after dissociation might help reduce cell aggregates.

8. Extraction of nuclei should be done under cooling conditions, for example, using the gentleMACS Octo Cooler. After that, nuclei should be enriched with Anti-Nucleus MicroBeads to ensure that the input for your sequencing analysis meets the highest quality standard to get reproducible data.

9. When preparing FFPE tissue for RNA sequencing, we recommend using scrolls measuring between 10 and 50 µm in thickness. The optimal size was found to be 20 µm, as this is the thickness at which the enzymes can most successfully extract the nuclei.

Product information

Product	Order no.
Instruments and accessories	
gentleMACS Octo Dissociator with Heaters	130-134-029
gentleMACS Octo Coolers (4 pieces)	130-130-533
gentleMACS Perfusion Sleeves	130-128-752
autoMACS NEO Separator	130-120-327
MACSQuant Tyto Cell Sorter	130-103-931
MACS MultiStand	130-042-303
QuadroMACS™ Separator	130-090-976
MACSima System	130-121-164
For more information about the MACSima Platform visit **miltenyibiotec.com/MACSima-platform**	
For more information about the MACSQuant Analyzers visit **miltenyibiotec.com/macsquant4genomics**	
Reagents	
MACS Tissue Storage Solution	130-100-008
MACS Cell Storage Solution	130-130-263
MACS Freezing Solution	130-129-552
Cell Suspension Cleanup Kit, human	130-135-177
Tumor Dissociation Kit, mouse	130-096-730
Tumor Dissociation Kit, human	130-095-929
Anti-Nucleus MicroBeads	130-132-997
Nuclei Extraction Buffer	130-128-024
FFPE Tissue Dissociation Kit for RNA Profiling	130-134-089
Liver Perfusion Kit, mouse and rat	130-128-030
StraightFrom Whole Blood PBMC Isolation Kit, human	130-126-359
For a complete list of Tissue Dissociation Kits, visit **miltenyibiotec.com/TDK4genomics**	
For a complete list of MicroBeads and Isolation kits, visit **miltenyibiotec.com/kits4genomics**	
For a complete list of StraightFrom products visit **miltenyibiotec.com/SF4genomics**	
Consumables	
gentleMACS C Tubes	130-093-237
gentleMACS Perfusers	130-128-151
MACS SmartStrainers (e.g. 100 µm)	130-098-463
Pre-Separation Filters (e.g. 20 µm)	130-101-812
LS Columns	130-042-401

EXPLORE MORE

Find more downloadable application data here:

▸ **miltenyibiotec.com/data2download**

▸ miltenyibiotec.com/cellprep_genomics

Miltenyi Biotec

Germany/Austria
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

USA/Canada
Miltenyi Biotec, Inc.
1201 Clopper Road
Gaithersburg, MD 20878,
USA
Phone 800 FOR MACS
Phone +1 866 811 4466
Fax +1 877 591 1060
macsus@miltenyi.com

Australia
Miltenyi Biotec
Australia Pty. Ltd.
Unit 11, 2 Eden Park Drive
Macquarie Park, NSW 2113
Australia
Phone +61 2 8877 7400
Fax +61 2 9889 5044
macsau@miltenyi.com

Benelux
Miltenyi Biotec B.V.
Dellaertweg 9C
2316 WZ Leiden
The Netherlands
macsnl@miltenyi.com
Customer service for:
The Netherlands
Phone 0800 4020120
Fax 0800 4020100
Belgium
Phone 0800 94016
Fax 0800 99626
Luxembourg
Phone 800 24971
Fax 800 24984

China
Miltenyi Biotec Technology &
Trading (Shanghai) Co., Ltd.
Room A401, 4/F
No. 1077, Zhangheng Road
Pudong New Area
201203 Shanghai, P.R. China
Phone +86 21 6084 0210
Fax +86 21 6235 0953
macscn@miltenyi.com.cn

France
Miltenyi Biotec SAS
10 rue Mercoeur
75011 Paris, France
Phone +33 1 56 98 16 16
macsfr@miltenyi.com

Hong Kong
Miltenyi Biotec Hong Kong Ltd.
Unit 301, Lakeside 1
No. 8 Science Park West Avenue
Hong Kong Science Park
Pak Shek Kok, New Territories
Hong Kong
Phone +852 3751 6698
Fax +852 3619 5772
macshk@miltenyi.com.hk

India
Miltenyi Biotec India Pvt. Ltd.
Vatika Business Centre,
Floor No. 6
Divya Sree Omega
Kondapur, Serilingampally
K.V. Rangareddy
Telangana 500084, India
Phone +91 040 45175910
macsin@miltenyi.com

Italy
Miltenyi Biotec S.r.l.
Via Paolo Nanni Costa, 30
40133 Bologna, Italy
Phone +39 051 6 460 411
Fax +39 051 6 460 499
macsit@miltenyi.com

Japan
Miltenyi Biotec K.K.
NEX-Eitai Building 5F
16-10 Fuyuki, Koto-ku
Tokyo 135-0041, Japan
Phone +81 3 5646 8910
Fax +81 3 5646 8911
macsjp@miltenyi.com

Nordics and Baltics
Miltenyi Biotec Norden AB
Medicon Village
Scheeletorget 1
223 81 Lund, Sweden
macsse@miltenyi.com
Customer service for:
Sweden
Phone 0200 111 800
Fax +46 280 72 99
Denmark
Phone 80 20 30 10
Fax +46 46 280 72 99
Norway, Finland, Iceland,
and Baltic countries
Phone +46 46 280 72 80
Fax +46 46 280 72 99

Singapore
Miltenyi Biotec Asia Pacific Pte Ltd.
438B Alexandra Road, Block B
Alexandra Technopark
#06-01
Singapore 119968
Phone +65 6238 8183
Fax +65 6238 0302
macssg@miltenyi.com

South Korea
Miltenyi Biotec Korea Co., Ltd.
Donggeuk 7F,
562 Nonhyeon-ro
Gangnam-gu
Seoul 06136, South Korea
Phone +82 2 555 1988
Fax +82 2 555 8890
macskr@miltenyi.com

Spain
Miltenyi Biotec S.L.
C/Virgilio 2,
Edificio II, Planta –1
28223 Pozuelo de Alarcón
Madrid, Spain
Phone +34 91 512 12 90
Fax +34 91 512 12 91
macses@miltenyi.com

Switzerland
Miltenyi Biotec Swiss AG
Soodstrasse 52
8134 Adliswil
Switzerland
Phone +41 32 623 08 47
Fax +49 2204 85197
macsch@miltenyi.com

United Kingdom
Miltenyi Biotec Ltd.
Almac House, Church Lane
Bisley, Surrey GU24 9DR, UK
Phone +44 1483 799 800
Fax +44 1483 799 811
macsuk@miltenyi.com

www.miltenyibiotec.com

Miltenyi Biotec provides products and services worldwide. Visit **www.miltenyibiotec.com/local** to find your nearest Miltenyi Biotec contact.

130-130-159.02