10x GENOMICS Authorized Distributor

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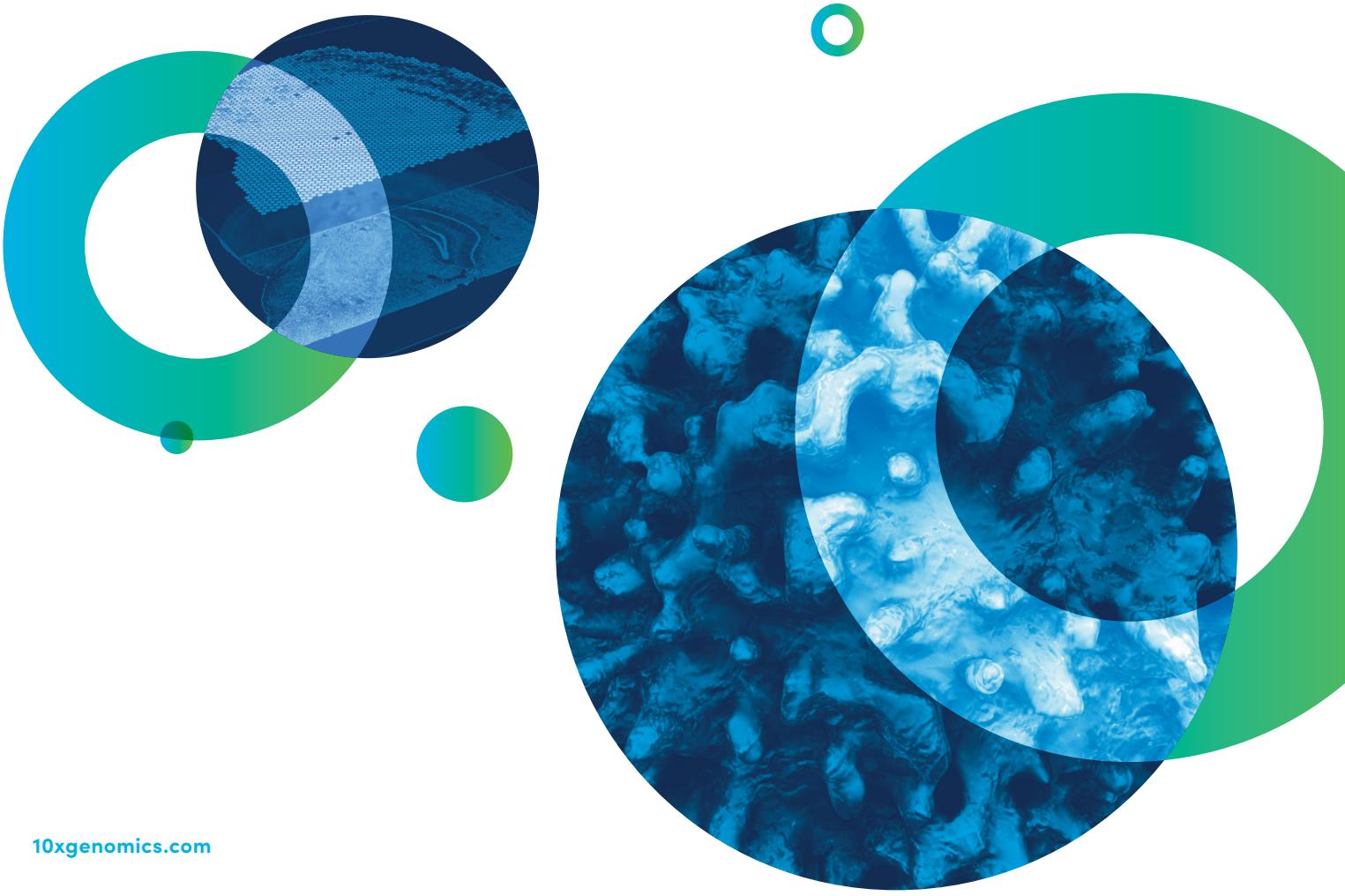
Resolve cancer

with single cell and spatial multiomics



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Our understanding of cancer is constantly evolving

Traditional approaches have enabled researchers to make great strides in understanding the complexities of cancer biology, and to translate groundbreaking discoveries into life-saving cancer treatments and therapies. However, many unanswered questions remain, requiring increased scale and resolution to be addressed. What mechanisms underlie differences in tumor development, progression, and metastasis in different individuals? How can varying responses to therapies be predicted across cancer types and patients?

Fundamentally alter your understanding of cancer and accelerate translational research with new single cell and spatial solutions that deliver the throughput, reproducibility, and multiomic capabilities you need.

Cutting-edge single cell and spatial analysis solutions from 10x Genomics unlock:

Multiomic characterization of the tumor, immune, and microenvironment contextures using solutions for transcriptomic, epigenomic, proteomic, and immunological analysis

Discovery and target validation from the same single cell or spatial gene expression library using whole transcriptome and targeted solutions

Decreased time to insight with cancer-specific or custom panels for targeted gene expression solutions and streamlined workflows

Large-scale and longitudinal studies using flexible, manual or automated single cell solutions to analyze hundreds to tens-of-thousands of cells in a single experiment

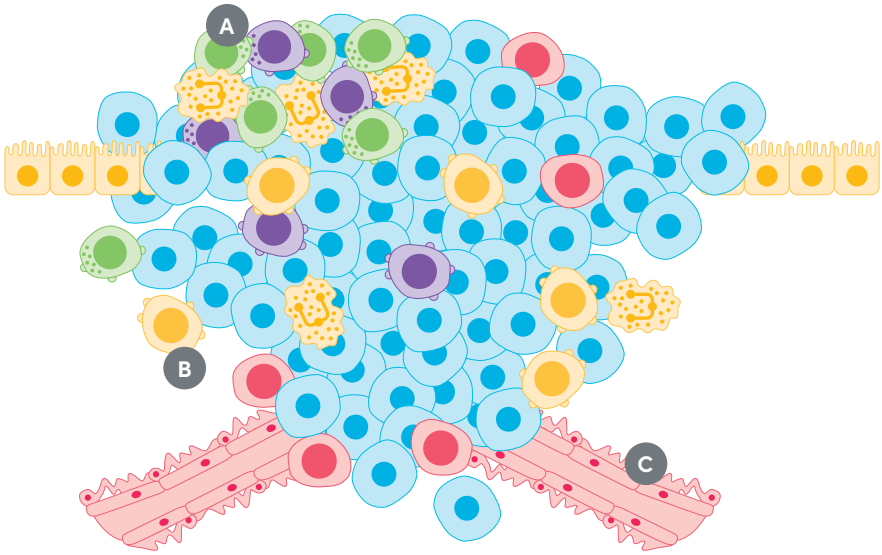
Reproducible results using validated products and protocols, and automated solutions

Explore the complex interactions of the immune and tumor microenvironment contexture

A How does cellular function and spatial organization affect immune cell accessibility and recruitment?

B What cell types and transcriptional programs shape the tumor microenvironment during cancer progression and metastasis?

C What are the growth factors and receptors induced by oncogenic, metabolic, and inflammatory pathways that contribute to tumor angiogenesis?



To address these questions and others, biological tools that can provide multiomic insights at single cell and spatial resolution are needed. 10x Genomics offers state-of-the-art solutions to help you precisely dissect the immune and tumor microenvironment contexture at scale.

Spatial Gene Expression

- Uncover the influence of tissue architecture on cancer progression, immune infiltration, and therapeutic response by combining histology with spatially resolved whole transcriptome analysis in tissue sections[1]

Single Cell Gene Expression

- Identify novel and rare cell types and states associated with tumor progression and metastasis that were previously masked by bulk analysis methods[2]

Single Cell Multiome ATAC + Gene Expression

- Investigate how alterations in epigenetic architecture lead to transcriptional heterogeneity, resulting in diversity of cell types, states, and dynamics in the tumor microenvironment

Single Cell Assay for Transposase Accessible Chromatin (ATAC)

- Uncover the epigenetic regulators driving diverse phenotypes and developmental trajectories in the tumor microenvironment[3]

Single Cell Immune Profiling

- Explore dynamic immune clone expansion and cellular phenotypes in the tumor microenvironment and periphery by measuring gene expression alongside full-length, paired B-cell and T-cell receptor sequences in single cells[4]

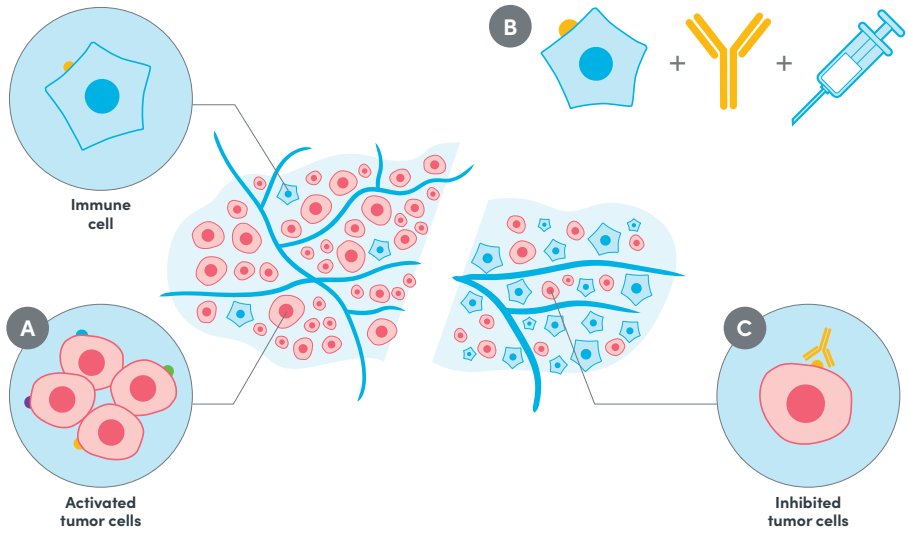
1. R Moncada et al., Integrating Microarray-Based Spatial Transcriptomics and Single-Cell RNA-seq Reveals Tissue Architecture in Pancreatic Ductal Adenocarcinomas. *Nat. Biotechnol.* 38, 333–342 (2020).
2. J Qian et al., A Pan-Cancer Blueprint of the Heterogeneous Tumour Microenvironment Revealed by Single-Cell Profiling. *bioRxiv.* (2020). doi.org/10.1101/2020.04.01.019646
3. AT Satpathy et al., Massively Parallel Single-Cell Chromatin Landscapes of Human Immune Cell Development and Intratumoral T Cell Exhaustion. *Nature.* 37, 925–936 (2019).
4. TD Wu et al., Peripheral T Cell Expansion Predicts Tumour Infiltration and Clinical Response. *Nature.* 579, 274–278 (2020).

Advance translational research of biomarkers and cancer therapy

A What are the relevant biomarkers needed to stratify responders and non-responders to a therapeutic intervention?

B How should therapies be deployed in combination within specific therapeutic windows to minimize resistance?

C What cells and molecular pathways have the highest therapeutic potential?



Identifying novel therapeutic targets and uncovering biomarkers associated with response and resistance will fundamentally revolutionize how cancer is treated. Single cell and spatial multiomic solutions from 10x Genomics provide researchers with the scale to perform longitudinal studies and the resolution to identify novel gene signatures associated with therapeutic outcomes.

Spatial Gene Expression

- Understand the spatial and phenotypic remodeling of immune, stromal, and tumor compartments within the tumor microenvironment in response to therapeutic interventions[5]

Single Cell Gene Expression

- Leverage large-scale CRISPR screening assays to discover new therapeutic targets and assess the effects of therapeutic agents on all the cells and molecular pathways in a tumor and its microenvironment[6]
- Validate hypotheses across large patient cohorts with targeted gene expression panels tailored to your genes of interest

Single Cell ATAC

- Understand the mechanisms of therapeutic response and resistance governed by epigenetic changes in distinct cellular populations[3]

Single Cell Immune Profiling

- Explore how therapeutic interventions shape immune cell clonality and phenotypes by interrogating gene expression alongside full-length, paired T-cell or B-cell receptor sequences[7]

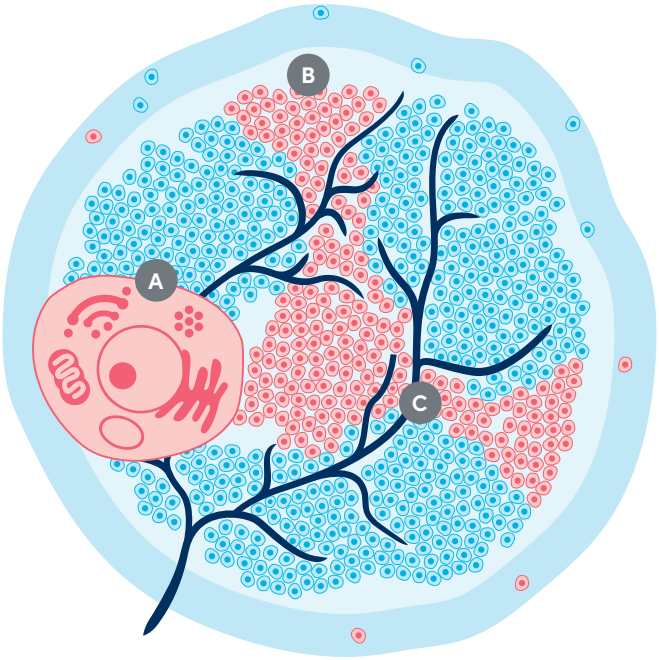
5. Y Wang, S Ma, WL Ruzzo, Spatial Modeling of Prostate Cancer Metabolic Gene Expression Reveals Extensive Heterogeneity and Selective Vulnerabilities. *Sci. Rep.* 10, 3490 (2020).
6. I Yofe, R Dahan, I Amit, Single-Cell Genomic Approaches for Developing the Next Generation of Immunotherapies. *Nat. Med.* 26, 171–177 (2020).
7. KE Yost et al., Clonal Replacement of Tumor-Specific T Cells Following PD-1 Blockade. *Nat. Med.* 25, 1251–1259 (2019).

Unmask the tumor contexture

A What are the genomic, transcriptomic, epigenetic, and proteomic mechanisms driving tumor heterogeneity, clonal evolution, and metastasis?

B How does intratumoral heterogeneity change in response to therapeutic intervention?

C How are tumor cell states influenced by spatial location within the tumor?



Single cell and spatial multiomic approaches are required to fully characterize the tumor contexture. Solutions from 10x Genomics provide the resolution and scale to build integrated single cell and spatial atlases, unmask intratumoral heterogeneity, and trace transcriptomic and epigenetic modulators of clonal evolution within tumors and across cancer types.

Spatial Gene Expression

- Refine pathological annotation by layering on spatially resolved whole transcriptome data to explore tumor heterogeneity evolution within the tumor[8]

Single Cell Gene Expression

- Reveal global transcriptional diversity within tumor clones to uncover mechanisms of therapeutic resistance and immune escape[9]
- Identify mechanisms underlying tumor development, progression, and metastasis by combining single cell gene expression with CRISPR perturbation screening or cell surface protein expression in the same single cells

Single Cell ATAC

- Unmask tumor cell diversity to reveal cell types, regulatory states, and biomarker signatures for different types of cancer[10]

Single Cell Multiome ATAC + Gene Expression

- Capture the complex interplay of transcriptional states and epigenetic regulators driving cancer evolution and intratumoral heterogeneity by simultaneously measuring gene expression and chromatin profiles, cell by cell

8. E Berglund et al., Spatial Maps of Prostate Cancer Transcriptomes Reveal an Unexplored Landscape of Heterogeneity. *Nat. Commun.* 9, 2419 (2018).
9. CA Stewart et al., Single-Cell Analyses Reveal Increased Intratumoral Heterogeneity After the Onset of Therapy Resistance in Small-Cell Lung Cancer. *Nat. Cancer.* (2020). doi.org/10.1038/s43018-019-0020-z
10. JM Granja et al., Single-Cell Multiomic Analysis Identifies Regulatory Programs in Mixed-Phenotype Acute Leukemia. *Nat. Biotechnol.* 37, 1458–11465 (2019).

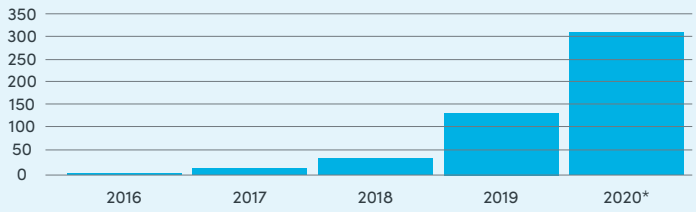
Technology comparison table

	Single cell resolution	Spatial context	Multiomic parameters	Breadth	Scale per sample
10x Genomics solutions					
Single Cell Gene Expression	Yes	No	Transcriptome plus Feature Barcode technology for cell-surface protein or CRISPR perturbation screening	Whole Transcriptome + Targeted	500–10,000 cells or nuclei Feature Barcode >1 billion parameters/cell
Single Cell ATAC	Yes	No	Epigenome via open chromatin	Whole Epigenome	500–10,000 nuclei
Single Cell Multiome ATAC + Gene Expression	Yes	No	Transcriptome and epigenome via open chromatin	Whole Epigenome + Whole Transcriptome	500–10,000 nuclei
Single Cell Immune Profiling	Yes	No	Transcriptome, full-length, paired B-cell and T-cell receptors plus Feature Barcode technology for cell-surface protein or antigen specificity	Whole Transcriptome + Targeted	500–10,000 cells Feature Barcode >1 billion parameters/cell
Spatial Gene Expression	1–10 cells	Yes	Transcriptome plus immunofluorescence for proteins	Whole Transcriptome + Targeted	Whole tissue section profiling
Traditional approaches					
Bulk RNA-seq	No	No	Transcriptome	Whole Transcriptome + Targeted	N/A
Flow Cytometry	Yes	No	Proteins	Targeted	15–20 parameters/cell
CyTOF (Mass Cytometry)	Yes	No	Proteins	Targeted	~100 parameters/cell
RNA In Situ Hybridization	Yes	Yes	No	Targeted	Whole tissue section profiling

Cancer publications using 10x Genomics

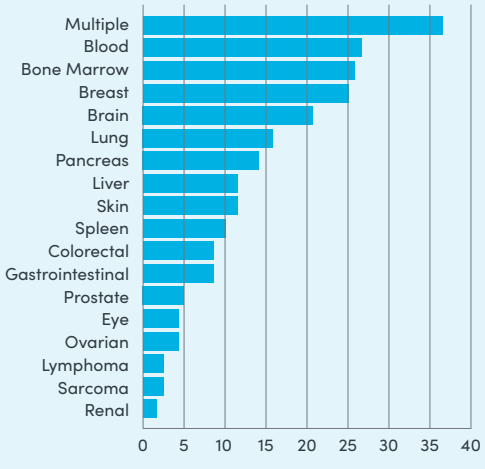
Papers published in top journals

Cumulative cancer publications by year



**Includes publications up to November 2020*

Broad array of sample types



Immune and tumor microenvironment contexture

Identify cell types, transcriptional phenotypes, and epigenetic regulators associated with the immune and stromal compartments

- *Single Cell Gene Expression with Feature Barcode technology*
- *Single Cell ATAC*
- *Spatial Gene Expression*
- *Single Cell Multiome ATAC + Gene Expression*

Determine mechanisms of immunotherapy response and resistance by profiling gene expression, identifying clonotypes, and interrogating TCR–antigen interactions in a single, multiomic assay

- *Single Cell Immune Profiling with Feature Barcode technology*

Discover drivers of tumor immunity with CRISPR screening assays

- *Single Cell Gene Expression with Feature Barcode technology*

Biomarkers and therapeutic development

Elucidate the differences between exceptional responders and non-responders before and after treatment

- *Single Cell Immune Profiling with Feature Barcode technology*
- *Single Cell ATAC*
- *Spatial Gene Expression*

Delineate synergistic, additive, neutral, or antagonistic effects on cellular and molecular targets of combination therapies

- *Single Cell Gene Expression with Feature Barcode technology*

Uncover the spatial and phenotypic changes in the tumor microenvironment in response to therapeutic interventions

- *Spatial Gene Expression*

Tumor contexture

Identify the transcriptional and epigenetic mechanisms underlying tumor development, progression, and metastasis

- *Single Cell Gene Expression with Feature Barcode technology*
- *Single Cell ATAC*
- *Single Cell Multiome ATAC + Gene Expression*

Unmask tumor cell diversity by identifying cell types, cell states, and cell-surface biomarkers unique to your cancer type

- *Single Cell Gene Expression with Feature Barcode technology*
- *Single Cell ATAC*
- *Single Cell Multiome ATAC + Gene Expression*

Explore clonal evolution and heterogeneity within the tumor

- *Spatial Gene Expression*

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