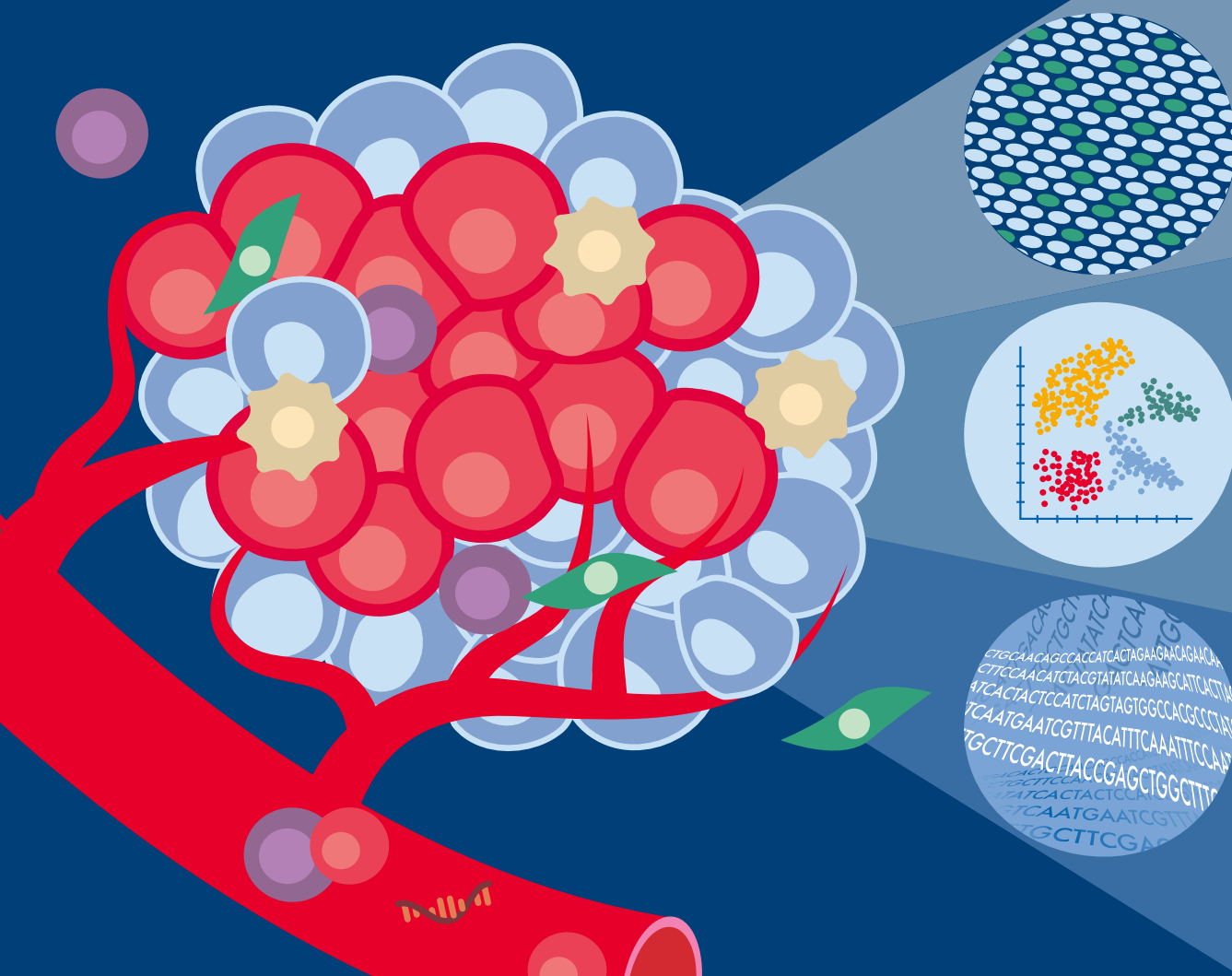


See the tumor microenvironment in all its complexity

Resolve heterogeneity, reveal tumor-immune interactions and move from discovery to validation with integrated molecular solutions.



To resolve tumor-immune complexity, take a multiscale view

Cancer develops within a complex, dynamic cellular ecosystem where tumor and immune cells form heterogeneous, co-evolving populations. Their interactions influence immune surveillance, immune escape and clonal evolution, shaping tumor progression and response to therapy.

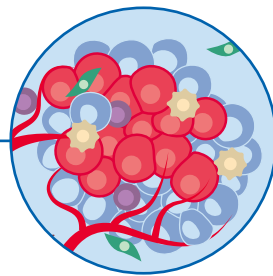
Understanding this system requires technologies that can illuminate biology across scales: From broad signals within the tumor microenvironment (TME) to single-cell molecular detail, and from exploratory approaches to targeted analysis.

We offer a dedicated portfolio of cancer research tools to support this work. From nucleic acid extraction to NGS, digital PCR (dPCR) and bioinformatic analysis, we have what you need to generate consistent data and move your research forward.

Profile the whole
tumor population

Tumor tissue

Recover single-cell
detail



Bulk analysis

captures the dominant biological signals across the TME when you want to:

- Characterize dominant, tissue-wide molecular signals
- Track changes across cohorts and over time
- Strengthen and extend biological insights from single-cell discoveries

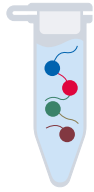


Single-cell analysis

resolves the molecular states and diversity of individual cells in the TME when you want to:

- Resolve cellular complexity in heterogeneous samples
- Connect individual cell identity to function
- Uncover mechanisms of resistance and response, identifying rare therapy-resistant tumor clones

Everything you need for your molecular cancer research



Bulk tumor analysis

We support bulk tumor analysis from nucleic acid extraction to data analysis, so you can spend less time troubleshooting and more time interpreting data.



Single-cell sequencing

Using Parse Biosciences' Evercode™ protocol, profile the full transcriptome or immune repertoire across millions of individual cells – from fresh or FFPE samples, with no instrument required.

Nucleic acid isolation

Ensure success for downstream analysis

Isolate high-quality nucleic acids from any sample type, including challenging FFPE tissue, using gold-standard QIAGEN sample prep technology.

Discovery by NGS

Explore the molecular landscape of the tumor

Use QIAseq® DNA-seq, RNA-seq or multimodal sequencing to profile tumor tissue and analyze contributions from the microbiome and non-tumor cells.

Targeted analysis by dPCR

Detect and quantify targets with absolute precision

Precisely quantify molecular signals, detect rare variants and confirm findings using QIAcuity® dPCR – all without the need for a standard curve.

Data analysis

Turn raw data into meaningful insights

Analyze genomic, transcriptomic and microbial data with intuitive bioinformatics tools from GeneGlobe® and QIAGEN Digital Insights.

Create a single cell suspension

Lock in gene expression for up to six months

For fresh samples, dissociate into single cell suspensions and fix. Samples can be stored for up to six months or processed immediately.

Alternatively, work with archived and newly prepared FFPE samples.

Barcoding, library prep & sequencing

Exponentially scale up your experiments

Barcode transcripts in individual cells or nuclei using a streamlined, split-pool combinatorial process. Then, generate libraries ready for NGS.

Data analysis

Simplify your single-cell data analysis with Trailmaker

Trailmaker software streamlines your analysis pipeline from FASTQ files to publication-ready figures, with flexible data entry and exit points.

Scalable single-cell RNA sequencing

Characterize cellular diversity and uncover mechanisms within the TME with Parse Biosciences' Evercode single-cell sequencing technology. Evercode supports applications ranging from whole-transcriptome and immune repertoire profiling to targeted sequencing and ultra-large-scale studies, across sample inputs ranging from cell suspensions to archived FFPE tissue. Dedicated analysis tools help you move efficiently from pilot studies to atlas-scale projects.

- Combinatorial barcoding allows you to dramatically scale up the number of cells and samples per experiment, profiling millions of cells at once
- Fix and store samples as they come in for up to six months, ideal for time-course studies
- Detect weakly expressed genes and avoid ambient RNA contamination common in droplet-based single-cell sequencing

Table 1. Selection guide for single-cell RNA-seq assays

Application	What do you want to understand?	What we recommend
Tumor microenvironment profiling	Resolve tumor, immune and stromal cell populations and their transcriptional states within the tumor microenvironment	Evercode WT
Archival tumor sample analysis	Recover cell type composition and gene expression from archived tumor samples	Evercode WT FFPE
T cell repertoire profiling	Track T cell clonality, expansion and functional states of tumor-infiltrating lymphocytes	Evercode TCR
B cell repertoire profiling	Analyze B cell diversity, clonotypes and antibody-related responses within the tumor microenvironment	Evercode BCR
Functional genomics / perturbation screening	Interrogate how perturbations influence tumor progression, immune response and therapy resistance	Evercode WT + CRISPR Detect



See how single-cell approaches can uncover tumor heterogeneity and microenvironment dynamics at <https://parse.bio/4u0bu7l>



"Evercode TCR's simple protocols and impressive throughput allowed us to make new discoveries about T cell responses to metastatic cancers."

Nathan Reticker-Flynn, PhD, Assistant Professor, Stanford University

Characterize immune repertoire complexity with single-cell TCR and BCR profiling

Explore adaptive immune responses with Evercode TCR and BCR profiling, which combines single-cell, whole-transcriptome gene expression with paired-receptor sequencing in the same workflow.

- Capture full-length, natively paired TCR or BCR chains for deeper insights into cellular context and functional relevance
- Achieve sensitive clonotype detection and measure clonotype diversity over time (**Figure 1**)

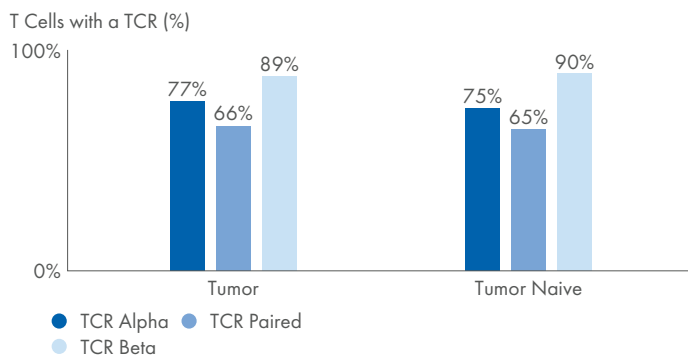


Figure 1. Achieve sensitive, single-cell clonotype detection. Paired TCR chain sequencing is critical to accurately identifying clones, defining their antigen specificity and tracking their expansion across tissue compartments. Three controls and six tumor samples from a mouse transplant model of lymph node (LN) metastasis were analyzed with Evercode TCR. Evercode TCR provided sensitive detection of clonotypes, capturing paired alpha and beta chains in a large subset of cells.



Watch how single-cell sequencing reveals immune dynamics, clonality and tumor-immune interactions in cancer: <https://parse.bio/3PvAB4d>



Transcriptome-wide TME profiling across cancer subtypes

The Evercode Whole Transcriptome single-cell kit enables unbiased profiling of cellular composition and gene expression. This approach reveals differences in cell type abundance and transcriptional programs that can distinguish cancer subtypes and help explain differences in disease biology (**Figure 2**).

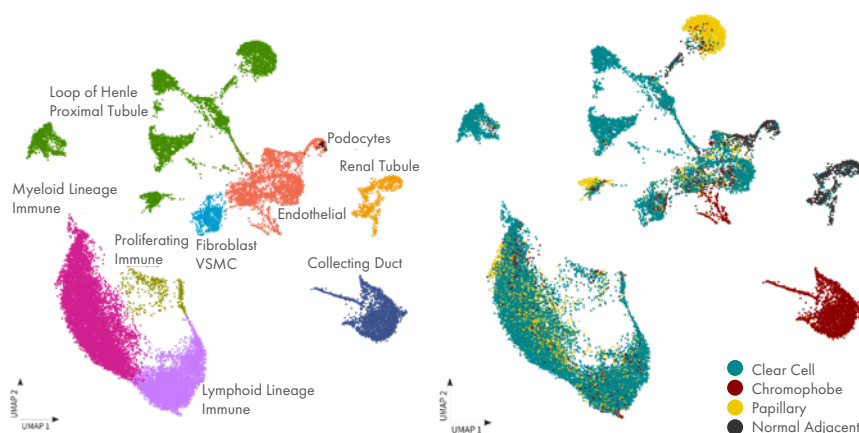


Figure 2. Identify differences in TME composition across tumor subtypes.

Single-cell analysis resolves tumor, immune and stromal populations across renal cancer subtypes.

Whole-transcriptome single-cell analysis for FFPE tissues

Study archived tumor samples at single-cell resolution with Evercode WT FFPE. Using reverse transcription chemistry optimized for fragmented RNA, the kit provides reliable gene expression analysis from archived samples, enabling cohort-scale discovery.

- Capture full transcriptomic complexity, including isoforms, SNPs and lncRNAs (**Figure 3**)
- Measure gene expression accurately from FFPE samples to reliably identify distinct cell states

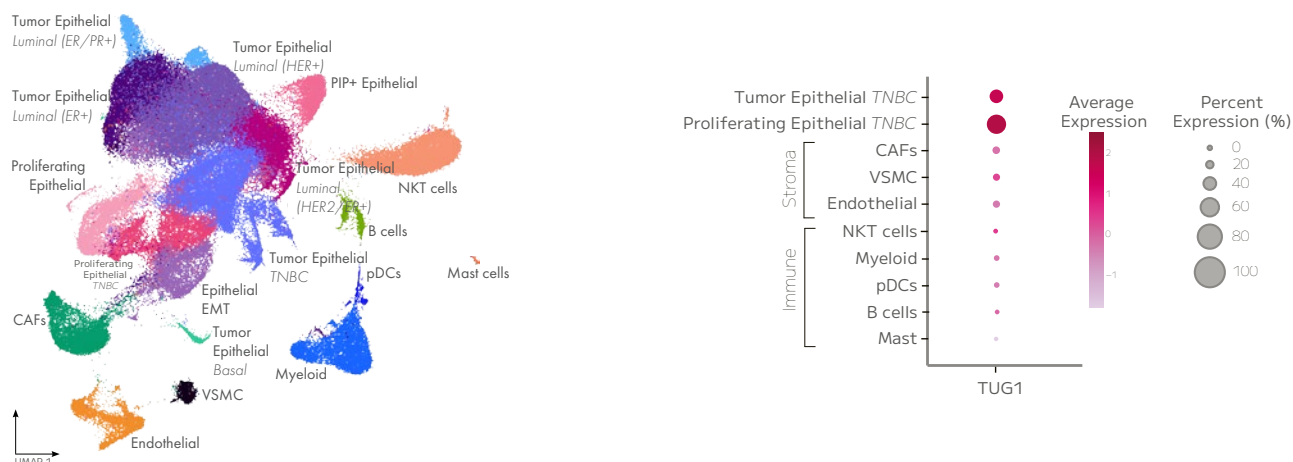


Figure 3. Nuclei from human breast cancer FFPE samples were profiled, capturing diverse tumor epithelial states alongside stromal and immune populations. Robust detection of coding and noncoding transcripts reveals that the oncogenic lncRNA TUG1 is enriched in proliferating and TNBC epithelial cells, highlighting the power of unbiased profiling to resolve gene expression and the regulatory landscape.



Examine single-cell datasets capturing subtype-specific transcriptional programs and proliferative tumor-cell states at <https://parse.bio/4nSabWV>



Single-cell data analysis made easy with Trailmaker

Simplify single-cell RNA-seq data analysis with Trailmaker. Quickly process, integrate and explore Evercode Whole Transcriptome data, generate publication-ready figures, and easily share your findings with colleagues.



Watch this on-demand webinar to get a practical, step-by-step introduction to single-cell RNA-seq data analysis with Trailmaker: <https://parse.bio/4v8nViD>



High-quality nucleic acid isolation from any sample type

Always start your experiments with high-quality DNA and RNA. Our trusted sample prep is guaranteed to deliver, even from the toughest samples.

- Fast, reliable spin column or magnetic bead chemistry yields high-quality DNA and RNA
- Works across a wide range of sample types, including FFPE tissue, stool and low-input samples
- Scalable, standardized protocols with automation support and extensive validation behind them

Table 2. Selection guide for nucleic acid isolation kits

	FFPE tissue	Fresh/frozen tissue & blood	Microbiome from tissue & stool
Common challenges	• Cross-linking • Cytosine deamination • Fragmentation • Lengthy procedures	• Low sample input • Variable tissue matrix, cellular debris and protein contamination • RNA instability • Labor-intensive phenol-based methods	Tissue • Low bacterial biomass in tissue matrix • High host DNA background • Uneven distribution of bacterial cells in tissue matrix Stool • Degradation of bacterial cells • High inhibitor concentration
Solutions	• Remove paraffin without xylene or similar solvents • Use kits that integrate uracil-N-glycosylase (UNG) treatment • Use fully-automatable kits	• Use kits that remove contaminants and inhibitors efficiently • Use micro kits and MinElute® columns for small sample inputs • Isolate DNA & RNA from the same sample • Use phenol-free kits • Use kits that ensure isolation of RNA smaller than 200 nt • Use stabilization reagents	Tissue • Perform mechanical lysis to thoroughly homogenize tissue, thereby reducing bias • Use kits that remove host DNA effectively Stool • Use kits that remove inhibitors in stool samples
Recommended DNA kits	• QIAamp® DNA FFPE Advanced UNG Kit • EZ1&2® DNA FFPE UNG Kit*	• QIAamp Fast DNA Tissue Kit • EZ1&2 DNA Tissue Kit* • DNeasy® Blood & Tissue Kits (for animal samples) • QIAamp DNA Blood Mini Kit • EZ1&2 DNA Blood Kits* • QIA sprint® DNA Tissue/Cells PrepSet† • QIA sprint DNA Blood PrepSet†	Tissue • QIAamp DNA Host-Free Microbiome Kit Stool • QIAamp PowerFecal® Pro DNA Kit
Recommended RNA kits	• RNeasy® and miRNeasy FFPE Kits • EZ2® RNA FFPE Kits*	• RNeasy and miRNeasy Advanced Kits • QIAamp RNA Blood Mini Kit • EZ2 RNA/miRNA Tissue/Cells Kit* • QIA sprint RNA Tissue/Cells PrepSet†	• RNeasy PowerFecal Pro Kit
Recommended DNA & RNA kits	• AllPrep® DNA/RNA FFPE Kit • EZ2 DNA/RNA AllPrep FFPE Kit*	• AllPrep DNA/RNA Kits	• AllPrep PowerFecal Pro DNA/RNA Kit • EZ2 PowerFecal Pro DNA/RNA Kit*

*For automated, magnetic bead-based nucleic acid purifications on EZ2 Connect or †QIA sprint Connect

Pass the pipetting to the robots

Automate your nucleic acid isolations with our range of extraction instruments. With most steps handled for you, you can spend less time pipetting and more time on the science. Learn more at www.qiagen.com/sample-prep-systems

Table 3. Selection guide for nucleic acid isolation instruments

				
	QIASprint Connect	EZ2 Connect	QIAcube® Connect	QIAmini®
Recommended applications	High-throughput isolations	High-volume liquid biopsy and FFPE tissue processing	Automating manual kits	Low-throughput isolations with minimal set-up
Sample throughput	Up to 192 (2 x 96)	Up to 24	Up to 12	Up to 8
Sample types supported	Fresh/frozen tissue, cells, whole blood, stool (more coming soon)	FFPE and fresh/frozen tissue, plasma, urine, cells, whole blood, stool	Virtually any sample type	Fresh/frozen tissue, cells, stool, whole blood
Dimensions	49 x 74 x 64 cm	72 x 57.5 x 56 cm	65 x 58 x 62 cm	21 x 26 x 32 cm
Extraction technology	Magnetic particle	Magnetic particle	Silica membrane spin column	Magnetic particle
Prefilled reagents	No	Yes	No	Yes

An easy start for FFPE tissue with EZ2 Connect

Take the complexity out of working with FFPE samples by automating your extractions on EZ2 Connect. Find practical tips to get the most out of your FFPE samples in our technical guidelines at www.qiagen.com/clp/ffpe-tech-guide

- Specialized kit chemistry and a standardized automated workflow reduce hands-on variability and support reliable isolation of high-quality DNA, RNA or both from the same sample (**Figure 4**)
- Automation with EZ2 Connect requires just one manual step for deparaffinization upfront
- Optional artifact removal with Uracil-N-Glycosylase treatment for some kits

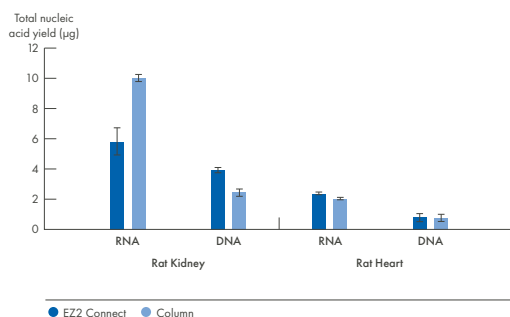
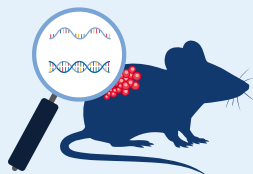


Figure 4. Higher yields of DNA and RNA with EZ2 Connect. DNA and RNA were extracted from FFPE rat kidney and FFPE rat heart tissues, either separately using the standard column procedure, or simultaneously with the EZ2 AllPrep DNA/RNA FFPE Kit on an EZ2 Connect instrument. RNA yields were measured via fluorometer. EZ2 Connect delivered higher yields compared to the column procedure for all nucleic acids, except RNA from rat kidney, demonstrating efficient extraction of RNA and DNA from the same cell population.



Working with another challenging sample type, patient-derived xenograft (PDX) tumors? This application note outlines a protocol for WES and WTS from PDX tissue to support tumor neoantigen discovery: www.qiagen.com/neoantigen-discovery



"We use QIAGEN kits to extract RNA from dorsal root ganglia from mice, which is about the size of a pin head, to analyze the expression of inflammatory genes and get reliably good yields."

Hannah Wardill, PhD, Associate Professor, Supportive Oncology Research Group, University of Adelaide

Improve tissue microbiome profiling with host DNA removal and unbiased lysis

Studying the role of the tissue microbiome in cancer can be challenging, as high levels of host DNA and uneven bacterial distribution make it difficult to isolate the microbial genome. The QIAamp DNA Host-Free Microbiome Kit addresses this challenge with integrated host DNA depletion and optimized tissue dissociation, ensuring efficient access to microbial signals.

Learn more in our interactive booklet at www.qiagen.com/microbiome-solutions

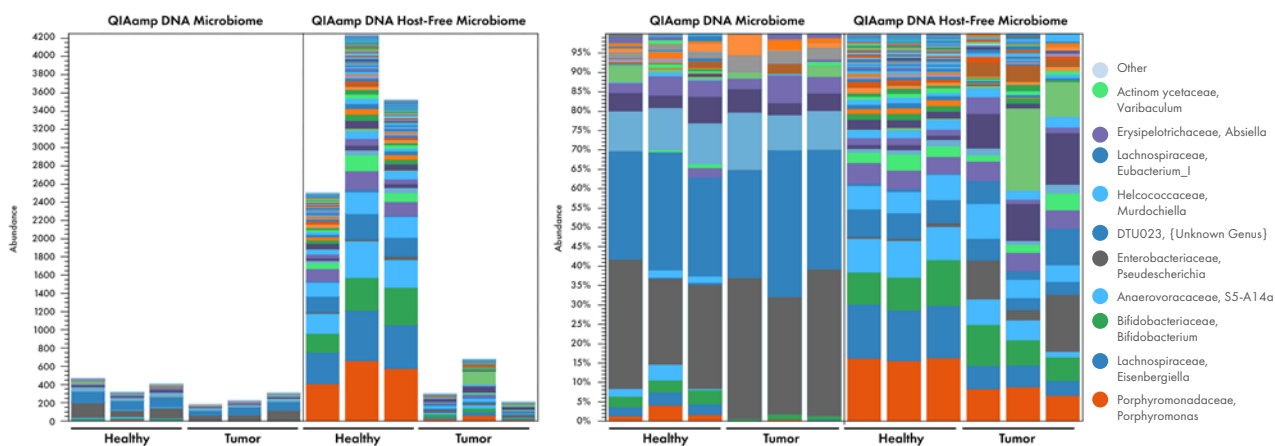


Figure 5. Identify microbiome changes in colon tumors vs. healthy tissue. Microbial DNA was extracted from human adenocarcinoma and adjacent healthy tissue using the QIAamp DNA Host-Free Microbiome Kit. Libraries were prepared with the QIAseq FX DNA Library UDI-A Kit and sequenced. Taxonomic profiles were generated using the UHGG database with QIAGEN CLC Genomics Workbench and the CLC Microbial Genomics Module. The results indicate a clear differentiation between the tumor and adjacent healthy tissue, with dysbiosis evident in the tumor microbiome.

High-performance NGS for bulk tumor profiling and T cell receptor analysis

Maximize the discovery power of NGS with QIAseq technology. Our QIAseq chemistry can handle even the most challenging samples, so you can confidently explore gene expression, immune signals, rare variants and more.

- Error-corrected sequencing using Unique Molecular Indices (UMIs)
- Optimized chemistry for low-input, degraded, GC-rich or otherwise tough samples
- Integrated analysis tools through GeneGlobe and QIAGEN CLC Genomics Workbench

Table 4. Selection guide for NGS kits and panels

Analyte	What kind of experiment are you running?	What we recommend
DNA	Whole genome and metagenome sequencing	QIAseq FX DNA Library Kit
	Whole exome and targeted exome sequencing	QIAseq Human Exome Kits
	Targeted DNA sequencing	QIAseq Targeted DNA Pro Panels
	Long-read sequencing	QIAseq xHYB Long Read Panels (Hereditary cancer and custom)
	DNA methylation status	QIAseq Targeted Methyl Panels
RNA	Whole transcriptome sequencing	QIAseq FastSelect® RNA Library Kits
	T cell receptor sequencing	QIAseq Targeted RNA-seq Panel for T cell Receptor
	miRNA sequencing	QIAseq miRNA Library Kit
	Fusion and exon-skipping detection	QIAseq RNA Fusion XP Panels
	rRNA and globin RNA removal	QIAseq FastSelect rRNA and Globin mRNA Removal Kits
	Targeted gene expression	QIAseq Targeted RNA Custom Panels
DNA & RNA	Amplicon-based multimodal sequencing	QIAseq Multimodal Panels (Pan-cancer, sarcoma, leukemia, lung and custom)
	Hybrid capture-based multimodal sequencing	QIAseq Multimodal DNA/RNA Library Kit QIAseq xHYB Human Panels



Benefit from unprecedented ease-of-use and biological insights with our catalog of targeted DNA panels for your cancer research. Custom panel design is also available.

Learn more: www.qiagen.com/qiaseq-targeted-pro



Increase your unique RNA-seq reads, discover more biology

If you're not studying rRNA, why waste sequencing reads on it? QIAseq FastSelect technology makes it easy to deplete >95% rRNA transcripts in as little as 14 minutes, even from low-input or degraded samples like FFPE (**Figure 6**).

- Works with most RNA library kits, including QIAGEN kits
- Efficient rRNA and/or globin mRNA removal with just one pipetting step
- Get complimentary access to the RNA-seq Analysis Portal on GeneGlobe

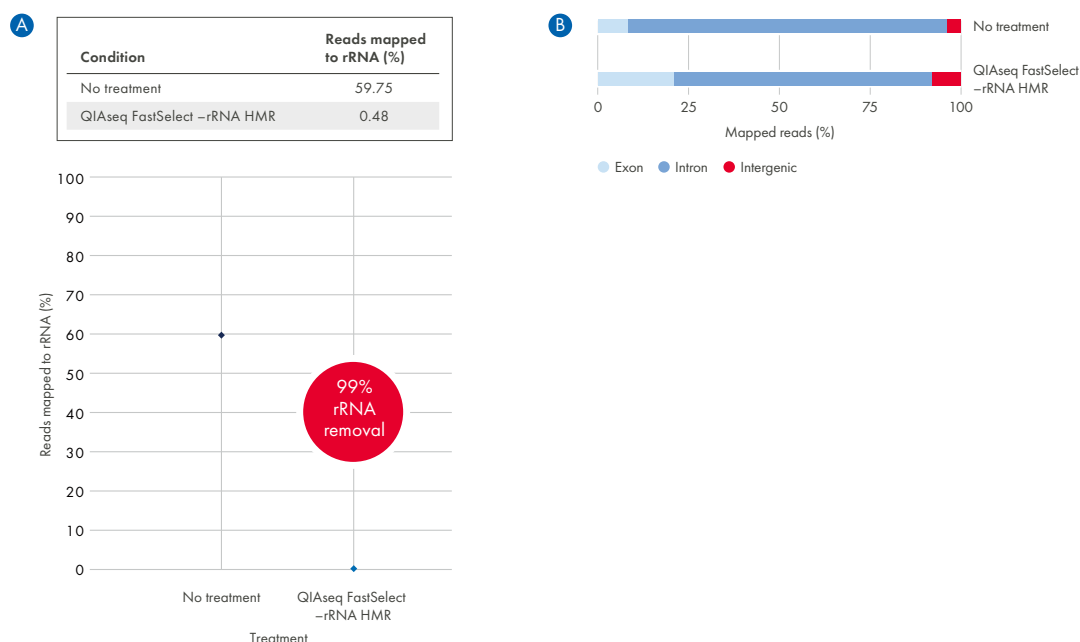
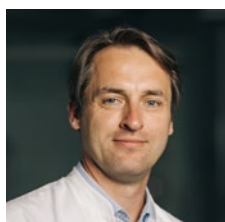


Figure 6. QIAseq FastSelect –rRNA HMR removes rRNA from FFPE RNA samples. A) QIAseq FastSelect results in highly efficient removal of rRNA from fragmented samples. The percentage of reads mapped to rRNA is shown. B) Exon/intron/intergenic read mapping is shown. QIAseq FastSelect results in a substantial increase in the percentage of reads mapped to exonic regions.



Working with low-quality FFPE RNA? Read this application note to see how FastSelect technology can help you rescue low RIN RNA for reliable RNA-seq:
<http://www.qiagen.com/QIAseq-FastSelect-FFPE-AN>



“We teamed up with NGS team from QIAGEN and we co-developed a FastSelect reagent customized to our purposes.”

Rastislav Horos, DVM, PhD, Chief Technology Officer, Hummingbird Diagnostics

Overcome challenges in miRNA profiling

miRNAs play an important role in cancer biology but profiling them can be difficult. QIAseq miRNA Library Kits can help you generate reliable, reproducible miRNA data across a wide range of sample types.

- Gel-free miRNA protocol significantly speeds up library construction
- Elimination of adapter dimers and hY4 RNA results in reproducible data from low-input biofluid samples
- Integrated UMIs for accurate quantification of individual miRNA molecules (**Figure 7**)
- Easily analyze your miRNA-seq data with complimentary access to the RNA-seq Analysis Portal

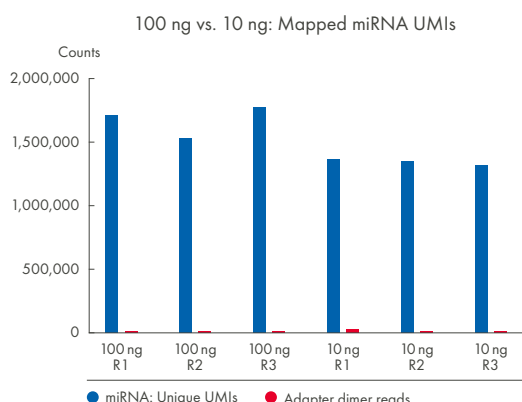


Figure 7. UMIs improve miRNA quantification. UMIs are attached early in the workflow, ensuring that bias from library amplification and sequencing is minimized. In addition, adapter dimers account for only a small percentage of reads in comparison to mapped reads, even with the gel-free, bead-based purification.

Comprehensive T cell receptor (TCR) profiling

Capture the full complexity of the immune response in cancer with the QIAseq Targeted RNA-seq Panel for T cell Receptor, delivering accurate, bias-reduced profiling of TCR alpha, beta, gamma and delta genes (**Figure 8**).

- Profile single TCRs or perform a combined analysis in a single tube
- UMI technology removes amplification, duplication and sequencing artifacts to increase accuracy
- Get complimentary access to GeneGlobe Analyze for data analysis, including read alignment and clonotype reports

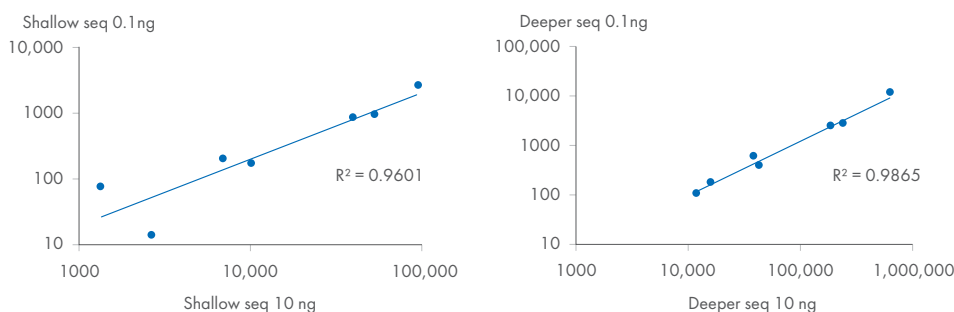


Figure 8. Consistent TCR expression across different input levels. Correlation of TCR clonotype detection between different input amounts (10 ng vs. 0.1 ng) with known clonotypes and relative expression levels. Both shallow sequencing (reads per UMI = 1.5–1.9) and deeper sequencing (reads per UMI = 2.8–4.7) results show highly correlated relative TCR clonotype levels, despite a 100-fold difference in input.

Focused analysis of target genes with dPCR

Detecting extremely rare variants or measuring subtle molecular changes with a high degree of precision is crucial in cancer research. That can be especially challenging in samples like FFPE tissue and liquid biopsy where nucleic acids may be degraded or present at low levels. QIAcuity dPCR helps address these challenges with sensitive, precise assays for mutation detection, CNV analysis, gene expression and miRNA profiling.

Table 5. Selection guide for dPCR and qPCR kits and assays

Application	dPCR	qPCR
Mutation analysis	dPCR LNA® Mutation Assays dPCR PanCancer Kits	
CNV analysis	dPCR CNV Probe Assays*	
miRNA biomarker profiling	miRCURY® LNA miRNA PCR Assays for Digital PCR*	miRCURY LNA miRNA PCR Assays* and Panels
Gene expression analysis	QuantiNova® LNA PCR Assays for Digital PCR*	QuantiNova LNA PCR Assays* and Panels
Microbial analysis	dPCR Microbial DNA Detection Assays*	Microbial DNA qPCR Assays and Arrays*

* Custom design tool for dPCR and qPCR assays available on GeneGlobe.

Detect rare variants and CNV mutations with high sensitivity

Our dedicated oncology assays for QIAcuity dPCR use locked nucleic acid (LNA)-enhanced chemistry to deliver the extreme sensitivity needed for detecting low-frequency cancer mutations and subtle copy number variations.

dPCR CNV probe assays

- Quantify up to 12 CNVs in a multiplex reaction to capture genome instability and complex alterations
- Measure copy number changes below 1.2-fold in about two hours (**Figure 9**)

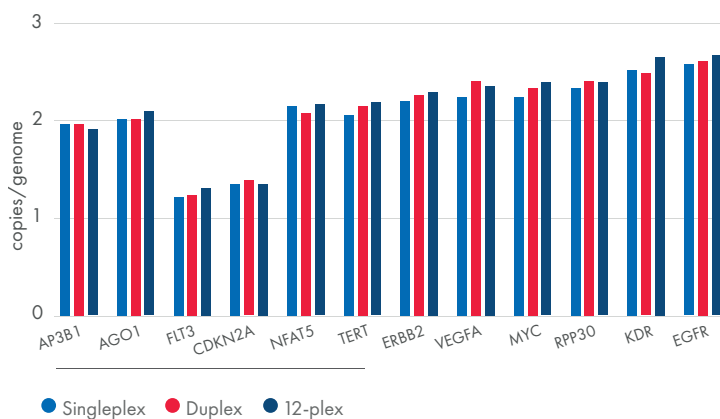


Figure 9. dPCR quantifications using single, duplex or 12-plex reactions are highly concordant. The copy number of ten genes of interest in U-2 OS sarcoma cell line were analyzed by 12-plex dPCR reactions. The average copy number of the reference genes AGO1 and AP3B1 was used for normalization. All ten gene targets were also quantified in singleplex and duplex for comparison. The results from both the singleplex, duplex and 12-plex reactions revealed genome instability in the sarcoma cell line, with the gene of interest copy numbers varying from 1.25 to 2.7.

dPCR LNA Mutation Assays

- Wet-lab tested assays available for more than 200 targets, including common oncogenes
- Detect rare variants down to 0.1% mutation frequency with high reproducibility

Quantify the faintest gene and miRNA expression changes with high precision

If you need to measure low-abundance RNA targets, QIAcuity dPCR can help. Our QuantiNova LNA assays for gene expression and miRCURY LNA miRNA assays for miRNA expression provide absolute quantification across a wide range of sample types, no standard curve required.

QuantiNova LNA assays for gene expression studies

- Detect weakly expressed genes, starting from just a single RNA copy
- Quantify expression changes over a wide dynamic range (log5)



Learn more about our dPCR assays for gene expression analysis at www.qiagen.com/dpcr-gene-expression



miRCURY LNA miRNA assays

- Quantify miRNAs with high resolution, even from as little as 1 pg starting material (**Figure 10**)
- Easily distinguish closely related miRNAs and mature miRNA from precursors

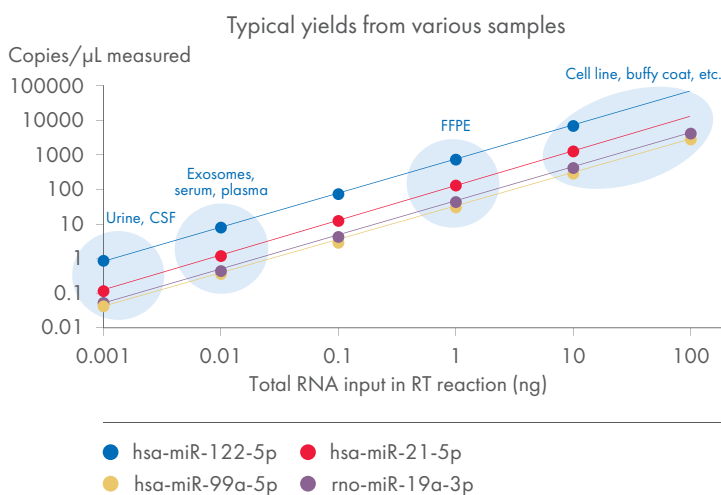


Figure 10. Accurate and precise detection of miRNAs across a broad RNA input range and sample types. miRNAs were quantified from serial dilutions of AM6000 total RNA, using 0.001 – 100 ng of input RNA and miRCURY LNA miRNA PCR Assays for Digital PCR. All miRNA assays demonstrated linear readout ($R^2 > 0.99$), enabling robust quantification, including low-expressed and AT-rich miRNAs.

What's next in cancer research



Johnny Yu

PhD, Tahoe, Co-Founder
and Chief Scientific
Officer

Generating a 100M cell atlas for AI-powered drug discovery

Current drug discovery models are limited by the scale and quality of available data. Johnny Yu and his team at Tahoe are addressing this limitation by generating large-scale single-cell datasets to train AI models that can uncover new therapeutic targets. Parse Biosciences' single-cell sequencing tech is helping Tahoe build these high-quality datasets.

"I want to highlight Parse both for being a tremendous partner on the experimental data generation side, the technology side, but also for being really good partners for enabling the community."



Asha Palat

Department of Biology
and Biochemistry,
University of Houston*

Targeting tumor metabolism to reshape the TME

Tumor cells depend on altered metabolic pathways to fuel growth and suppress immune responses. By targeting cancer cell metabolism, Asha Palat aims to weaken tumors and enhance immune activity within the TME. Because this work often involves low-input, challenging samples, generating high-quality RNA is critical – so she uses QIAGEN RNA isolation kits.

"Nothing else matches the consistency, quality and concentration of RNA that I get from these kits."



* Current affiliation:
Program Alliance Manager,
BostonGene



**Nathalie
Labarrière**

PhD, Team Leader, French
Institute of Health
and Medical Research,
University of Nantes

Harnessing the immune system as medicine

How do T cells recognize and respond to tumors and why does that response often fall short? By studying tumor-immune interactions, Nathalie Labarrière and her team seek to improve strategies like adoptive cell therapy to better harness the immune system to target cancer. QIAGEN has been an important partner for labs like hers.

"It's really rare that a private company is interested in real scientific collaboration because it is an efficient approach to advancements in research."



Expert-curated genomic knowledge with bioinformatics tools and services

Complete workflow design

- **GeneGlobe Design & Analysis Hub**

Create tailored qPCR and NGS assays for specific instruments and targets, and analyze data with web-based tools for gene and miRNA expression, mutation detection and copy number variation.

- **RNA-seq Analysis Portal**

Align reads, explore differential expression and uncover pathway insights from your RNA-seq data – all in a few hours. This fast, accessible and comprehensive web-based platform integrates seamlessly with dPCR and qPCR validation tools.

Bioinformatic solutions

- **QIAGEN CLC Genomics Workbench Premium**

Analyze NGS and 'omics data using user-friendly, ultra-fast pipelines that are accessible to biologists. The workbench helps you annotate variants, detect low-frequency mutations and handle UMIs with custom tools designed for targeted panels, WGS and other 'omics data.

- **QIAGEN Ingenuity® Pathway Analysis (IPA®)**

Discover activation and inhibition relationships, master regulators and molecular pathways in minutes. With the largest curated knowledge base available, IPA provides context for your data that supports your publications.



Explore solutions for cancer research:
www.qiagen.com/applications/cancer-research



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