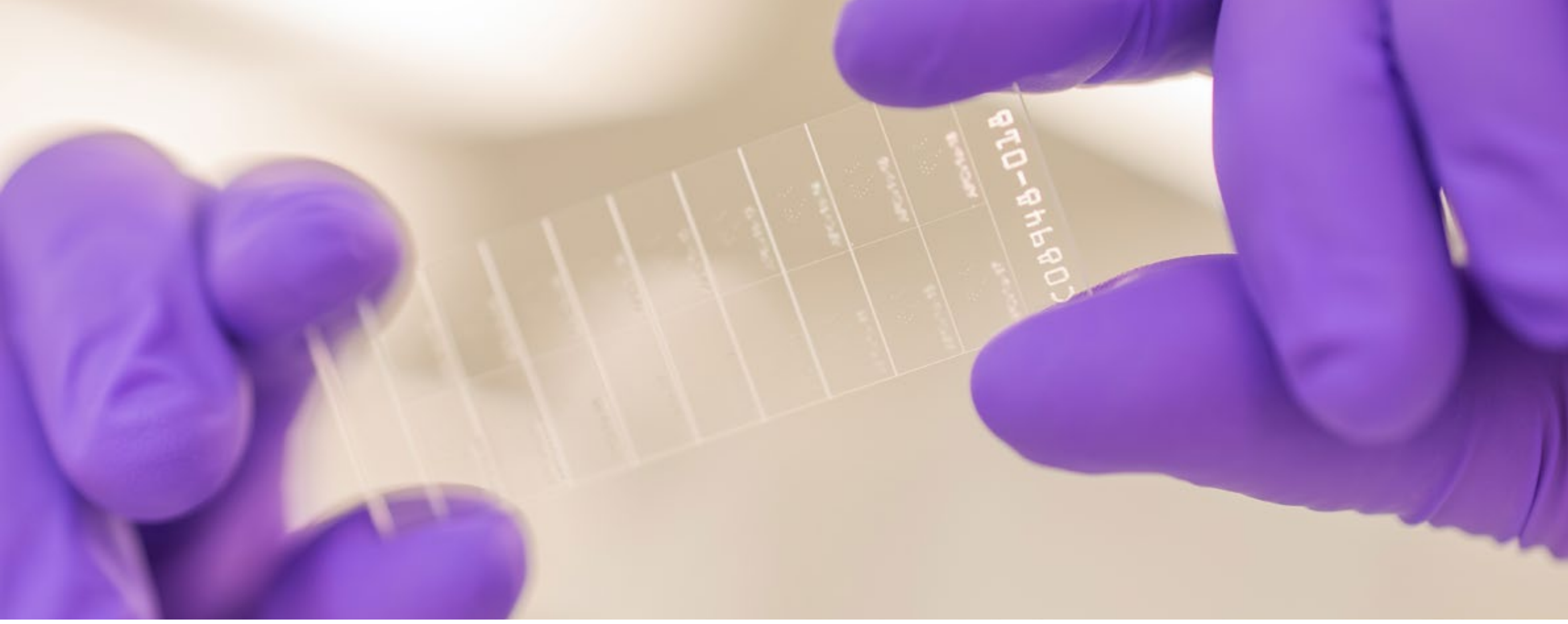


Advancing gene expression analysis through precision microarray development

Microarrays are powerful tools for multiplexed gene expression analysis, allowing researchers to measure the activity of thousands of genes simultaneously as well as differential RNA transcript expression. By hybridizing labeled RNA or cDNA samples to a grid of DNA probes, microarrays reveal which genes are turned on or off under specific conditions or variable levels of ongoing expression.

This high-throughput approach enables insights into cellular responses, disease mechanisms and therapeutic progress, and biomarker discovery.

1. Microarrays in the genomic era

Gene expression analysis has become foundational to understanding complex biological systems, enabling advancements in:

- Disease diagnostics and biomarker discovery
- Drug development and response profiling
- Personalized medicine and precision oncology

Microarray-based platforms remain a cornerstone in this field due to their ability to measure expression levels of thousands of genes simultaneously in a cost-effective, scalable format.

Delivering accurate and reproducible results across hundreds or thousands of samples depends on more than just good assay design – it requires precision engineering, rigorous quality control, and scalable manufacturing.

2. Why precision matters in gene expression microarrays

Spot uniformity = data integrity

Each feature on a microarray represents a unique gene probe or probe replicate.
Inconsistent spot size, morphology, or probe concentration across replicates can lead to:

- Increased replicate signal variation
- Reduced signal-to-noise ratio
- Variable sensitivity across the array

Advanced non-contact or piezoelectric microarray printing technologies ensure picoliter-level precision in deposition, promoting uniform hybridization kinetics and improving analytical performance.

Alignment and surface chemistry

Precision microfabrication ensures tight alignment tolerances between probes and sample flow paths. Combined with controlled surface functionalization, this supports:

- High probe binding efficiency
- Low background signal
- Reproducible assay conditions

Together, these enable more robust normalization and differential expression analyses – critical for clinical or regulatory use.

3. Quality: The foundation of clinical confidence

Batch-to-batch consistency

In diagnostics, especially clinical gene panels, reproducibility is non-negotiable. Every microarray must perform with precision, every time.

This is only achievable through:

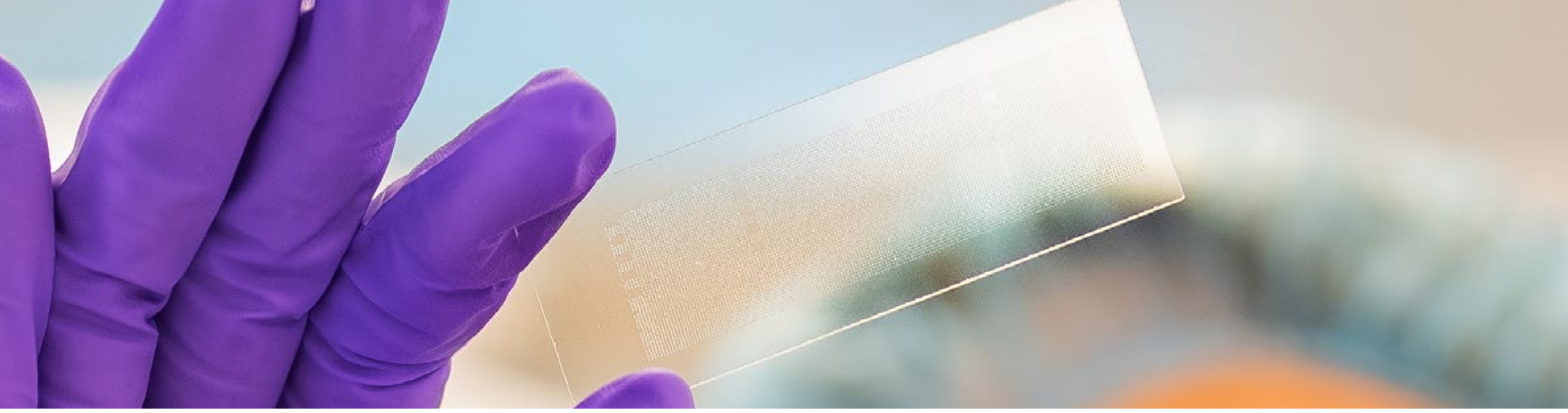
- ISO13485-compliant quality systems
- In-line and post-production QC analytics
- Robust supply chain traceability

Biological compatibility

Quality goes beyond mechanics. Non-reactive structural surfaces and materials must be biologically inert and compatible with:

- RNA/DNA integrity
- Fluorescent detection
- Hybridization stability

Thermoplastics, coated glass, and hybrid platforms optimized for nucleic acid binding significantly outperform traditional PDMS or non-coated slide-based solutions in these areas.



4. High-throughput development: Speed without compromise

As demand grows for population-scale genomic studies and rapid-response diagnostic tools (e.g., during pandemics), high-throughput microarray production is essential.

✓ Scalable printing

SCHOTT MINIFAB's precision microarray printing systems support:

- Thousands of arrays per production cycle
- Multiplexed gene panels with high spatial resolution
- Flexibility to accommodate customization at scale

✓ Rapid iteration & design-for-manufacture (DfM)

Early collaboration between scientists, engineers, and production experts ensures that:

- R&D designs are compatible with automated printing and QC
- Transition from prototype to scaled production is seamless
- Time to market is accelerated while controlling cost-of-goods (COGs)

5. Applications enabled by high-performance microarrays

Each application demands a highly sensitive, stable, and reproducible microarray platform, which is only achievable through precision product development.

- **Oncology**: Gene panels for tumor classification and therapy guidance
- **Infectious Disease**: Expression signatures for host-pathogen response
- **Neuroscience**: Transcriptomic profiling of brain tissue
- **Drug Discovery**: High-throughput screening for gene targets and pathways

6. Conclusion:

Bridging bioscience and engineering for impact

To fully realize the potential of gene expression analysis, diagnostics and life science innovators must partner with microarray manufacturers who bring:

✓ Biological understanding

✓ Engineering precision

✓ Quality-driven manufacturing

✓ Scalability at speed

At SCHOTT MINIFAB, we don't just build arrays – we engineer solutions that enable breakthroughs in health and science.

Discover more SCHOTT® Microarray applications

No matter your microarray application, we've likely encountered something similar and can assist you on your journey. With our experience and expertise, we will help guide you to success.

Visit **schott.com/minifab** to explore more applications.

Microarray vs RNA Seq

Discover the strengths and limitations of gene expression technologies to unlock scientific discovery

SCHOTT MINIFAB high precision and high-capacity non-contact Piezo dispense technology

There is a persistent narrative in the industry that *"sequencing has replaced microarrays."*

Microarrays and RNA sequencing (RNA-seq) serve **complementary roles** – each with distinct advantages depending on research goals, budget, scale, and downstream application.

From a CDMO perspective, it's critical to clarify that microarrays remain **a mature, reliable, and cost-effective solution** for many transcriptomic and diagnostic workflows.

Explore the following page and discover a clear and evidence-based comparison summary of these two technologies and their optimal applications.

Map your technology for your application →

Microarray vs RNA sequencing (RNA-seq):

Map your technology for your optimal application

Feature /Consideration	Microarrays	RNA-seq
Technology principle	Hybridization of labeled RNA to predefined probes representing known genes or cDNA transcripts. Measures **known genes and transcripts** with high precision.	Direct sequencing of cDNA to quantify all transcripts (known and novel). Detects **known and novel transcripts,** including isoforms and non-coding RNAs.
Throughput and data size	Compact datasets — thousands of genes in a single standardized file.	Extremely large datasets — millions of reads requiring complex pipelines.
Cost per sample	**Low** — typically **5–10× cheaper** than RNA-seq; ideal for large cohorts.	**High** — sequencing reagents, library prep, and storage add significant cost.
Turnaround time	**Fast** — from sample to data in **hours to a day**.	**Slower** — days to weeks depending on sequencing depth and analysis.
Data analysis requirements	Straightforward; well-established normalization and QC workflows.	Computationally intensive; requires bioinformatics pipelines and larger infrastructure.
Reproducibility	Highly reproducible across labs and platforms; ideal for standardized studies.	Excellent dynamic range, but more variable across instruments and analysis pipelines.
Quantitative precision	Strong for **relative expression differences**; linear within a known range. Quantitative with introduction of standard curve.	Superior for **absolute quantification** and detecting rare transcripts.
Dynamic range	Moderate (2–3 orders of magnitude). Extended (4-5) with signal-to-noise and assay optimization.	Very wide (5–6 orders of magnitude).
Sensitivity to noise and bias	Very low background achieved through controlled probe design, optimal substrate coating, and assay stringency.	Susceptible to library prep and alignment biases; normalization more complex.
Clinical and regulatory readiness	**Proven,validated technology —** FDA-cleared diagnostic microarrays exist (e.g., oncology, cytogenetics).	**Emerging clinical integration —** mostly research-grade with limited regulatory validation.
Scalability for population studies	Excellent — low cost per sample enables **hundreds or thousands of samples** per project.	Limited by sequencing cost and storage; often used on smaller cohorts.
Infrastructure needs	Compact instruments, minimal bioinformatics load.	Requires sequencers, servers, and specialized computational staff.
Best use cases	Differential gene expression, biomarker discovery, diagnostic panels, large-scale cohort studies, and regulatory assays.	Novel transcript discovery, splicing analysis, rare RNA detection, and deep transcriptome characterization.

Key takeaways

1. Microarrays excel in known, high-throughput, and cost-sensitive studies.

They're ideal when the target genes are known such as disease panels, biomarker validation, or clinical diagnostics, where **speed, reproducibility, and cost efficiency** matter most.

Best for: population studies, diagnostics, longitudinal monitoring, regulated assays.

2. RNA-seq excels in discovery and exploratory research.

When you need to find **new transcripts, isoforms, or non-coding RNAs**, RNA-seq offers unmatched depth but at higher cost and computational complexity.

Best for: early discovery, novel gene identification, mechanistic studies.

3. Microarrays remain the practical backbone of translational research.

Their **maturity, affordability, and regulatory acceptance** make them the preferred platform for bridging discovery to clinical use, particularly in diagnostics, pharmacogenomics, and global health.

Best for: scalable translational and applied research where standardization and reproducibility are essential.

In summary

Use microarrays when you want fast, reproducible, and affordable gene expression profiling across many samples or patients.

Use RNA-seq when you need to explore unknown transcriptomes, splice variants, or discover new RNA species.

Use both when you want discovery and validation — sequencing to find, microarrays to confirm and scale.

Microarray + RNA Seq = Discovery validation

To derive more information, these two platforms can be used in conjunction in one application enabling complex information gathering (i.e. Spatial transcriptomics).

Your innovation brought to life with a trusted, global CDMO partner

Bringing groundbreaking innovations to market for 25+ years

As your partner

Our role is to help you integrate required technologies strategically, offering custom microarray panels for targeted expression profiling that complement sequencing discoveries.

We ensure

- Optimized surface chemistries for sensitive hybridization
- Scalable, reproducible manufacturing for high-throughput studies
- Regulatory-grade quality for translational and diagnostic deployment

Your benefits

Experience faster, more cost-effective gene expression programs that move seamlessly from exploration to validation to clinical impact.

SCHOTT MINIFAB