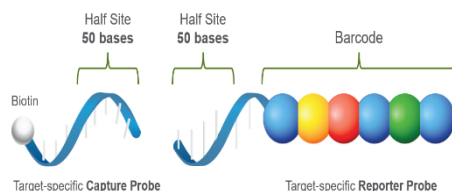




Genomic Profiling Services: nCounter vs RNA-Seq

CHOOSING THE RIGHT TOOL FOR TRANSCRIPTOMIC INSIGHTS

Gene-expression profiling is a cornerstone of discovery and translational research, enabling quantitative analysis of molecular pathways across disease models and therapeutic interventions. Among the most widely adopted platforms are NanoString nCounter and RNA sequencing (RNA-seq). Although both technologies quantify RNA abundance, they differ fundamentally in methodology, sensitivity, data complexity, and ideal use cases.

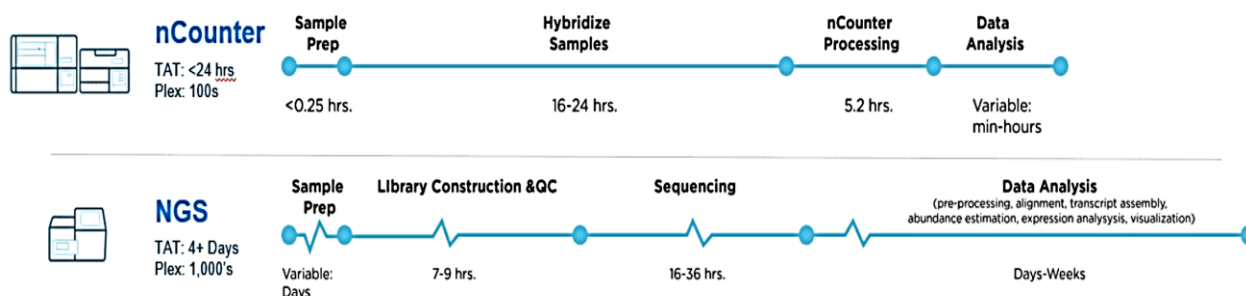


NanoString nCounter Gene Profiling



NGS Sequencer

TECHNICAL COMPARISON OF nCOUNTER VS RNAseq



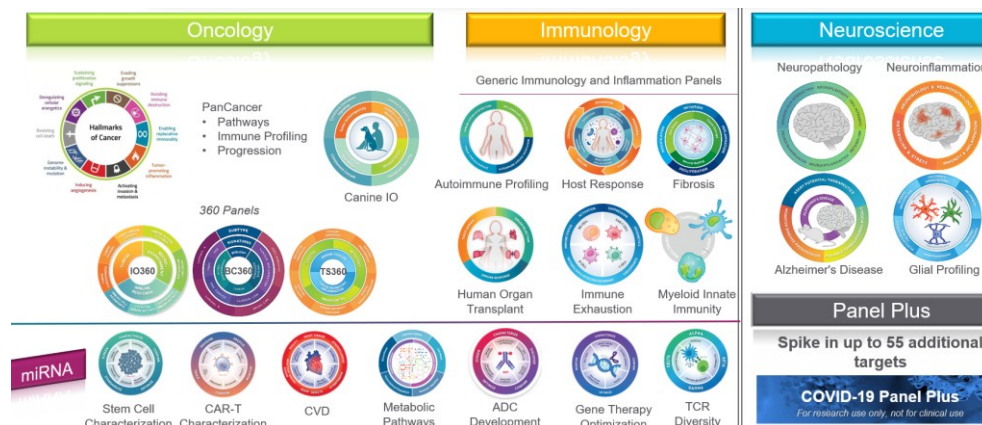
FEATURES	NanoString nCounter	RNA-seq
Principle	Direct digital detection of mRNA using color-coded probe pairs (no amplification)	Sequencing of cDNA fragments after reverse transcription and amplification
Detection method	Fluorescent barcode hybridization (optical counting)	Next-generation sequencing (Illumina, etc.)
Workflow complexity	Simple — hybridize → wash → count	Complex — RNA extraction → library prep → sequencing → bioinformatics
Quantification	Absolute (molecule counting)	Relative (read counts normalized to depth)
Dynamic range	~3–4 logs	~5–6 logs
Sample input	~25–300 ng RNA (works with FFPE)	~100 ng–1 µg RNA (RNA quality critical)
STRENGTHS & USE CASES		
Targeted analysis	Excellent for focused panels (e.g., 50–800 genes)	Genome-wide (20,000+ genes)
Low-quality or FFPE samples	Works very well	Often problematic (RNA degradation affects library prep)
Quantitative reproducibility	High — no enzymatic bias	Can vary due to amplification and GC bias
Throughput & cost	Lower cost per sample for targeted panels	High upfront cost, but more comprehensive
Data analysis	Simple (NanoString nSolver or ROSALIND)	Complex (alignment, normalization, differential expression, pathway analysis)
Turnaround time	1–2 days	1–2 weeks
Regulatory/CLIA use	Used in diagnostics (e.g., Prosigna breast cancer assay)	Less common in clinical diagnostics



DATA CONTENT AND INTERPRETATION

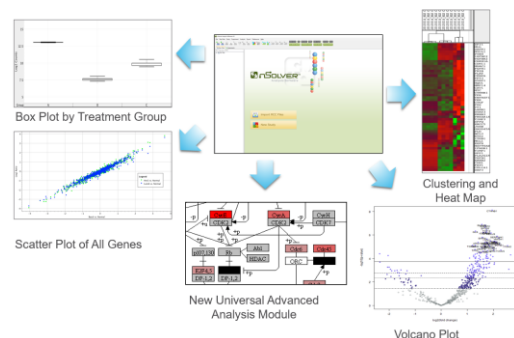
- **NanoString nCounter** provides **targeted profiling** (Each panel contains 800+ plex data cover relevant biology for targeted applications + 55 genes with Panel Plus)—ideal when gene signatures are known (e.g., immune response panels, oncology pathways). The data is straightforward and requires minimal bioinformatics support.

Currently Available Panels

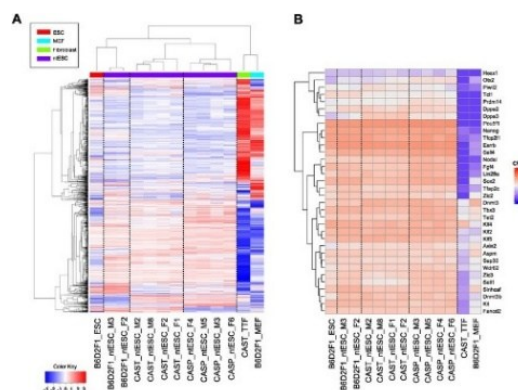


- **RNA-seq** delivers **unbiased transcriptome-wide coverage**, identifying novel transcripts, splice variants, and non-coding RNAs. However, it demands advanced computational analysis and larger data storage capacity.

RESULT FORMATS



nCounter Digital Data Output:
Simple Visualizations via nSolver™ 4.0



RNA-seq Analysis:
Hierarchical Clustering Heatmap

SUMMARY AND RECOMMENDATIONS

RESEARCH GOAL	RECOMMENDED TECHNOLOGY
Focused validation of known gene sets (e.g., immune response, fibrosis, signaling pathways)	☒ NanoString nCounter
Biomarker development in FFPE tissues	☒ NanoString nCounter
Quantitative comparison across many samples	☒ NanoString (more reproducible)
Clinical or translational research with limited sample quality	☒ NanoString
Discovery of novel transcripts, splice variants, or non-coding RNAs	☒ RNA-seq
Exploratory transcriptomics in new systems	☒ RNA-seq