

Targeted pathway interrogation (RUO)

Applications

Targeted Pathway Interrogation (RUO) using NanoString nCounter[®] technology enables highly sensitive, amplification-free digital quantification of gene and miRNA expression. These curated panels provide robust, reproducible insights into key biological pathways, immune states, cancer biology, and host responses across diverse sample types, even from limited or degraded RNA (e.g., FFPE).. The use of specific probes allow consistent profiling of low-abundance transcript/ genes, that would need deep sequencing

Input

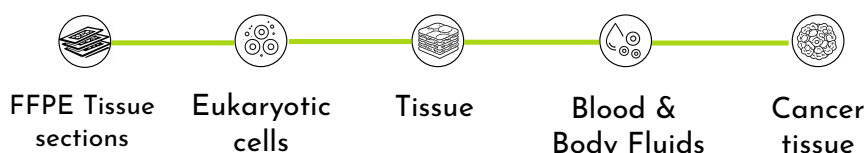


Total RNA

Conc: 100ng - 1 µg

DV 200 > 40%

Sample Types



Platform Bruker nCounter Sprint Profiler

Available NanoString Panels

Panel Name	Recommended Samples /Batch	Targets /Total genes	Organism	Panel Description
PanCancer Progression Panel	12	800	Human	Profiles genes driving tumor growth, invasion, metastasis, angiogenesis, and extracellular matrix remodeling across cancer types.
PanCancer Pathways Panel	12	810	Human	Covers 13 core cancer pathways including cell cycle, apoptosis, PI3K, MAPK, DNA damage, and transcriptional regulation.
PanCancer Immune Profiling Panel	12	810	Human	Comprehensive immune profiling covering adaptive, innate, checkpoint, cytokine, and inflammatory signaling in the tumor microenvironment.
CAR-T Panel	12	780	Human	Evaluates CAR-T cell function, persistence, exhaustion, activation, and tumor-immune interactions in cell therapy studies.
Neuroinflammation Panel	12	740	Human / Mouse	Profiles immune and inflammatory pathways involved in neurodegeneration, neuroimmune crosstalk, and CNS disorders.
Human miRNA Panel	12	827 human miRNAs and 577 mouse miRNAs	Human	Quantifies human microRNAs involved in cancer, development, immune regulation, and disease-associated post-transcriptional control.
PanCancer IO 360 [™] Panel	12	770	Human	End-to-end immuno-oncology profiling including tumor biology, immune infiltration, checkpoint pathways, and therapeutic response markers.
Breast Cancer 360 [™] Panel	12	799	Human	Breast cancer-specific panel integrating tumor signaling, intrinsic subtypes, immune response, and predictive biomarkers.

Tumor Signaling 360™ Panel	12	800	Human	Focuses on oncogenic signaling networks driving tumor growth, survival, metabolism, and therapeutic resistance.
PAM50 Signature (RUO)	12	50	Human	Gold-standard 50-gene expression signature for intrinsic breast cancer subtyping and risk stratification.
ADC Panel	12	790	Human	Designed for antibody-drug conjugate studies, profiling target expression, payload sensitivity, and resistance mechanisms.
Metabolic Pathways Panel	12	768 (Human), 768 (Mouse)	Human / Mouse	Covers core metabolic pathways including glycolysis, TCA cycle, lipid metabolism, amino acid metabolism, and mitochondrial function.
miRNA Human	12	827 human miRNAs and 577 mouse miRNAs	Human / Mouse	High-throughput digital profiling of disease-associated and regulatory human microRNAs.
Custom Respiratory Virus Panel	12	Custom	Human / Viral	Customizable panel to profile host response and viral gene expression in respiratory viral infections.
Autoimmune Profiling Panel	12	770 (Human), 770 (Mouse)	Human/ Mouse	Profiles immune dysregulation, cytokine signaling, and inflammatory pathways implicated in autoimmune diseases.
Host Response Panel	12	785 (Human), 785 (Mouse)	Human / Mouse	Captures innate and adaptive immune responses to infection, inflammation, and tissue injury.
Human Organ Transplant Panel	12	770	Human	Monitors immune activation, rejection, tolerance, and inflammation in solid organ transplantation.
Immune Exhaustion Panel	12	797	Human / Mouse	Focuses on T-cell exhaustion, checkpoint signaling, dysfunction markers, and chronic immune activation.
Myeloid Innate Immunity Panel	12	770 (Human), 754 (Mouse)	Human / Mouse	Profiles macrophage, dendritic cell, neutrophil biology, and innate immune signaling pathways.

Standard Deliverables

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- The project includes RNA QC,
- Probing for panel codeset. Hybridisation,
- Analyzing on the nanoString platform and providing the Gene Expression data/counts in .CSV file.
- Perform analysis on nSolver software to provide differentially expressed genes/transcript based on counts and normalized data with housekeeping reference genes.
- Graphical representation through heat map, histograms etc.

References

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- Sankaradoss A et al. Mol Ther. 2022; PMID:34999210.
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- Tiwari S et al. Noncoding RNA Res. 2024; PMID:39131689.
- Shankar M et al. Sci Rep. 2023; doi:10.1038/s41598-023-47751-z.