nanoString™

nCounter® PanCancer Panels Collection
Pathway Deregulation • Immune Profiling • Cancer Progression
A collection of gene expression panels developed around the hallmarks of cancer

REFERENCE The Hallmarks of Cancer. Originally published in Cell, 144, Hanahan D & Weinberg RA, Hallmarks of Cancer: The Next Generation, 646–674, Copyright Elsevier 2011.

Highlights of the PanCancer Panel Collection

- Comprehensive coverage of all ten Hallmark of Cancer included in three distinct panels.

- >1,850 unique genes included across all panels.

- Customize with up to 30 additional user-defined genes.

- Compatible with protein panels for multi-omic assays.

The PanCancer Panels Collection

| Panel	Description
nCounter PanCancer Immune Profiling Panel	Explore the immune response to cancer.
nCounter PanCancer Pathways Panel	Understand basic cancer biology and pathway deregulation.
nCounter PanCancer Progression Panel	Investigate cancer progression and metastasis.

The Hallmarks of Cancer are one of the most widely recognized organizing principles for the holistic study of cancer today. Its profoundly simple framework was first introduced in 2000 by authors Douglas Hanahan and Robert Weinberg and defines a distinct set of acquired capabilities that distinguish cancer from normal tissue. The Hallmarks help explain the complexities of cancer by describing a common set of capabilities present in cancer cells. These processes that, if unstopped, will allow cancer cells to thrive and proliferate in the unique tumor environment they create. This framework, represented in the now famous Hallmarks of Cancer wheel, is often the first roadmap researchers use to study all types of cancer.

NanoString has embraced the Hallmarks of Cancer philosophy and shares the vision to bring simplicity to an otherwise extremely complex disease and to enable productive research. Our collection of three nCounter PanCancer Panels delivers a family of multiplex gene expression assays to enable basic and translational research into pathway deregulation studies, the emerging area of immune profiling, and cancer progression.

nCounter® PanCancer Panels Collection

The NanoString PanCancer panels provide researchers with our most highly-multiplexed gene expression panels and represent over 1,850 unique genes. Designed for universal research of any cancer type.

Overlapping & Unique Content in the PanCancer Panels:
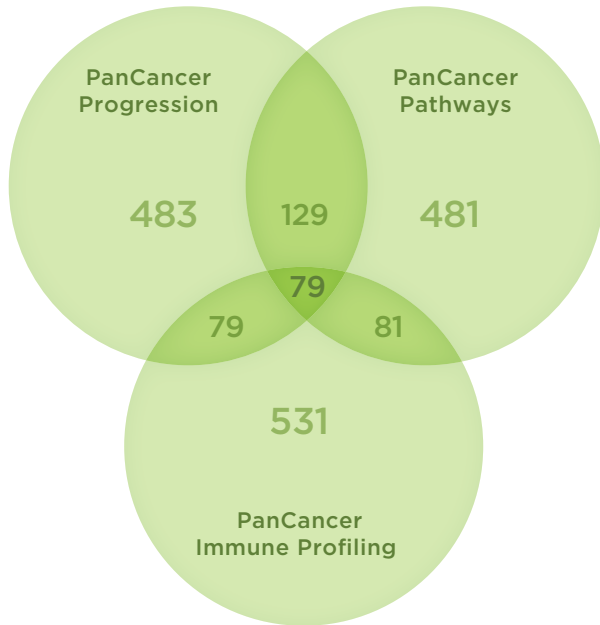
ABOVE Human PanCancer Panels Venn diagram with >1,850 unique genes. The genes shared between these panels are members of the PI3K, JAK-STAT, and TGF- pathways, as well as normalization genes.

PanCancer Progression Panel (Human)

770 Cancer Progression Genes

- 277 angiogenesis genes
- 269 epithelial-mesenchymal transition genes
- 254 extracellular matrix genes
- 173 metastasis genes
- 30 references genes

PanCancer Pathways Panel (Human & Mouse)

770 Cancer Pathway Genes

- 606 pathway genes for 13 canonical pathways
- 124 cancer driver genes
- 40 reference genes

PanCancer Immune Profiling Panel (Human & Mouse)

770 Cancer Pathway Genes

- 24 different immune cell types
- 30 CT antigens
- > 500 genes covering innate and adaptive immune response
- 40 reference genes

RNA:Protein Analysis

Simultaneous analysis of RNA and protein targets enable you to see more from a single sample. Measure both gene expression and cell response from as few as 150,000 cells (up to 500,000 cells for PBMCs and primary cells). The nCounter Protein Plus PanCancer Immune Profiling Panel includes 30 immunology-related protein targets that can be used with any PanCancer Gene Expression Panel.

Protein Panels	Protein Targets
nCounter Protein Plus PanCancer Immune Profiling Panel	30

nCounter Panel-Plus

Customize PanCancer panels with the optional Panel-Plus feature, and add up to 30 of your preferred genes to create a panel that is uniquely your own.

Single Cell Analysis

All PanCancer panels are also available in a single cell format. These kits include validated primer pools for multi-target enrichment. Primer pools are provided at no additional charge for the study of single cells or for studies using low input samples

nSolver™ Data Analysis Software

NanoString offers advanced software tools that address the continuous demands of data analysis and helps answer the specific biological questions encompassed in our most popular PanCancer Panels.

PanCancer Pathways Advanced Analysis Module

- Score pathway deregulation with end-to-end analysis.

- Generate follow-on research hypotheses using pathway visualizations.

- Measure gene expression with 730 essential genes representing all major cancer pathways including: Wnt, Hedgehog, Apoptosis, Cell Cycle, RAS, P13K, STAT, MAPK, Notch, TGF-, Chromatin Modification, Transcriptional Regulation and DNA Damage Control

## PanCancer Immune Profiling Advanced Analysis Module

- Set up wide-ranging exploratory analyses, including estimation of immune cell abundance, detection of CT antigens and differential expression testing in minutes with a simple wizard

- Measure gene expression with 730 essential genes representing 16 different cancer immune cell types and populations, major immune response categories, and 30 common cancer testis antigens

- Intuitive step-by-step wizard allows gene sets and cell abundance analysis to be customized

## Advanced Analysis Capabilities:

- Normalization

- QC

- Pathway Scoring (Pathways)

- Differential Expression

- Gene Set Analysis

- Pathview Plot Analysis

- Cell Type Profiling (Immune Profiling)

- Single Gene Select gene descriptions (Immune Profiling)

- CT Antigen Expression (Immune Profiling)

- Built-in compatibility for Panel Plus analysis

Advanced analysis modules provide an interactive html report with multiple layers of information along with pathway visualization mapsfor generating follow-on hypotheses.

To access annotated demo data sets and details on how to use the advanced analysis software please visit:
www.nanostring.com/products/nSolver
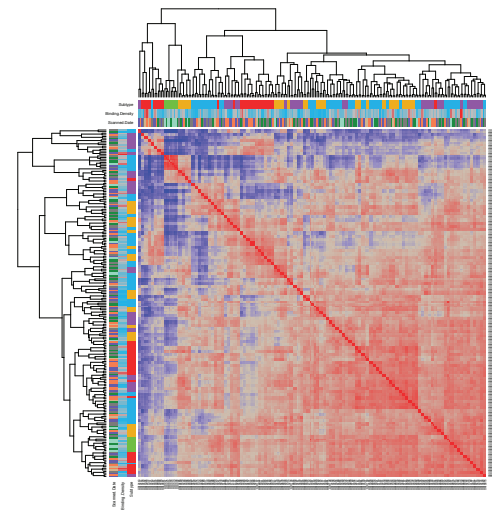
Example 1: Heatmap of the samples' correlation matrix. Blue indicates low correlation and red indicates high correlation.
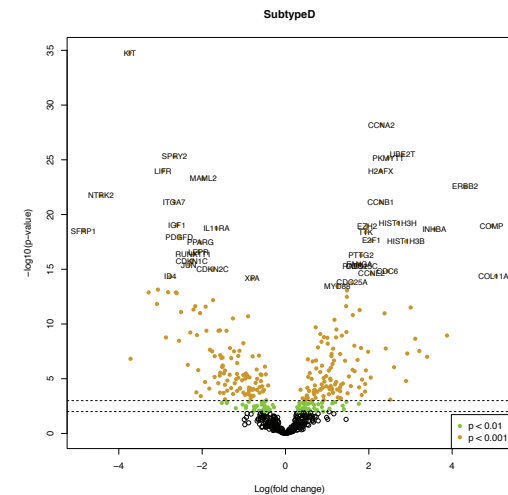
Example 2: Volcano plot of the comparison between two sets of samples (shows fold change vs. log 10 p-value).
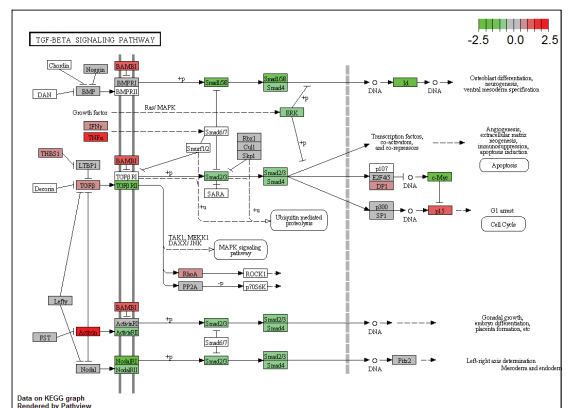
Example 3: Pathview plot of differential expression between two sets of samples in the TGF-Beta Pathway. Green indicates down-regulated genes, red indicates up-regulated genes, and grey indicate genes that do not meet the p-value threshold.

Selecting Your Panel

Fully-annotated gene lists in Excel format are available online for each of the PanCancer panels. All gene lists include the official gene name, accession number, alias, target sequence, and sortable annotations. The table lists some of the major gene categories or pathways along with the panel in which they are best represented.

Panel Name	Category/Pathway	Number of Genes	Representative Hallmarks
PanCancer Immune Profiling	Adaptive immunity	104	Avoiding immune destruction
	Humoral immunity	41	Avoiding immune destruction
	Inflammation	66	Tumor-promoting inflammation
	Innate immunity	200	Tumor-promoting inflammation
PanCancer Pathways	Cancer driver genes	124	—
	Cell cycle and apoptosis	137	Resisting cell death
	Chromatin modification	22	Genome instability and mutation
	DNA repair	50	Genome instability and mutation
	Hedgehog pathway	28	Resisting cell death
	JAK-STAT pathway	86	Sustaining proliferative signaling
	MAPK pathway	157	Sustaining proliferative signaling
	Notch pathway	24	Enabling replicative immortality
	PI3K pathway	201	Deregulating cellular energetics
	RAS pathway	142	Sustaining proliferative signaling
	TGF-pathway	51	Evading growth suppressors
	Transcriptional misregulation	101	Genome instability and mutation
	Wnt pathway	78	Enabling replicative immortality
PanCancer Progression	Angiogenesis	277	Inducing angiogenesis
	Epithelial-mes enchymal transition	269	Activating invasion and metastasis
	Extracellular matrix	254	Activating invasion and metastasis
	Metastasis	173	Activating invasion and metastasis

For more information, please visit nanostring.com/products