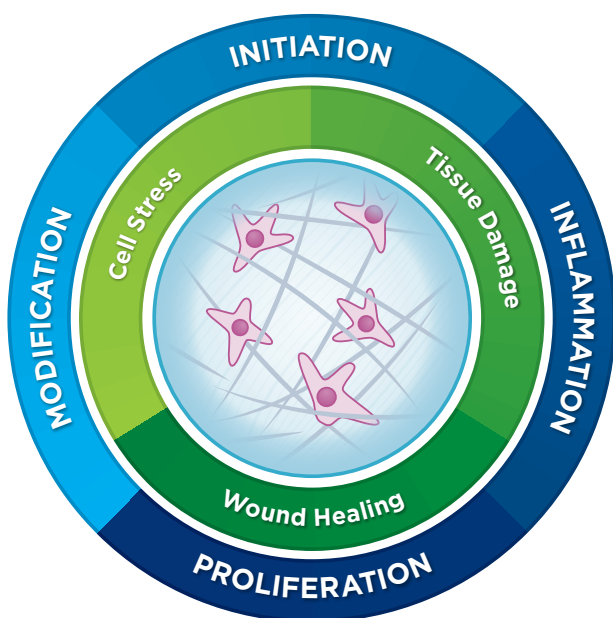


nCounter® Fibrosis Panel

Gene Expression Panel

Four Stages of Fibrosis • Disease Pathogenesis • Biomarkers of Progression

Uncover the mechanisms of disease pathogenesis, identify biomarkers of progression, and develop signatures for therapeutic response with the nCounter Fibrosis Panel. This gene expression panel combines hundreds of genes involved in the initial tissue damage response, chronic inflammation, proliferation of pro-fibrotic cells, and tissue modification that leads to fibrotic disease of the lungs, heart, liver, kidney, and skin.

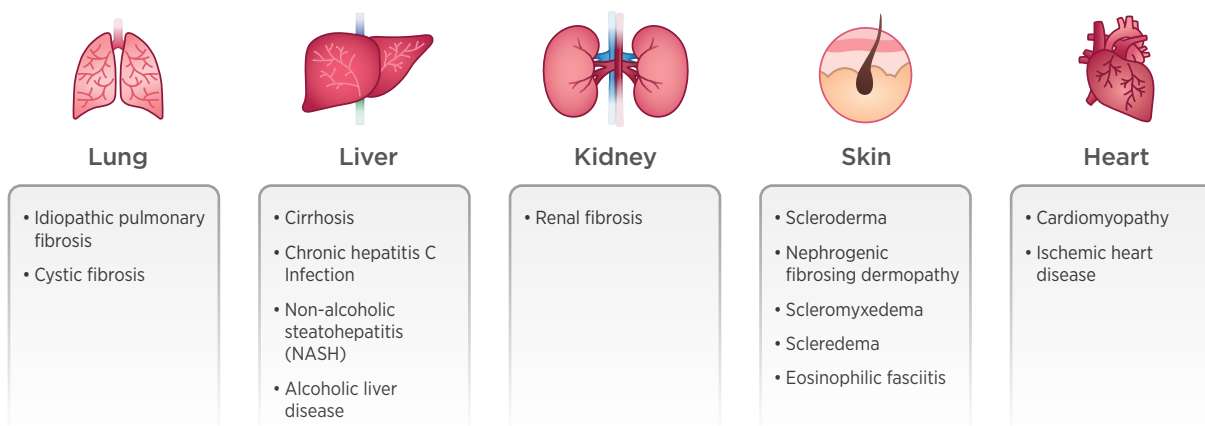


Product Highlights

- Profile 770 genes across 51 annotated pathways involved in the four stages of fibrosis
 - Initiation
 - Inflammation
 - Proliferation
 - Modification
- Study pathogenesis and identify biomarkers for fibrotic diseases of the lungs, heart, liver, kidney, and skin
- Understand the signaling cascade from cell stress to inflammation
- Quantify the relative abundance of 14 different immune cell types
- Identify biomarkers of therapeutic response

Feature	Specifications
Number of Targets	770 (Human), 770 (Mouse), including internal reference genes
Standard Input Material (No amplification required)	25-300 ng
Sample Input - Low Input	As little as 1 ng with nCounter Low Input Kit (sold separately)
Sample Type(s)	Cultured cells/cell lysates, sorted cells, FFPE-derived RNA, total RNA, fragmented RNA, PBMCs, and whole blood/plasma
Customizable	Add up to 55 unique genes with Panel-Plus and up to 10 custom protein targets
Time to Results	Approximately 24 hours
Data Analysis	nSolver™ Analysis Software (RUO)

Key Applications with the nCounter Fibrosis Panel



Gene Coverage Across the Four Stages of Fibrosis

Stage	Description	Pathways	Number of Human Genes	Number of Mouse Genes
Initiation	Cell and tissue damage, often specific to an organ or fibrotic disease, initiates a cascade of stress and immune responses.	Autophagy, Cholesterol Metabolism, Cytosolic DNA Sensing, De Novo Lipogenesis, Endotoxin Response, Fatty Acid Metabolism, Gluconeogenesis, Insulin Resistance/Signaling, MAPK Cell Stress, mTOR, Oxidative Stress, PPAR Signaling, Proteotoxic Stress, SASP	297	297
Inflammation	Inflammation is one of many responses to the initial damage, involving multiple immune cell types and signaling pathways. Chronic inflammation drives the proliferation of pro-fibrotic cells and tissue modification.	Adenosine Pathway, Chemokine Signaling, Complement Activation, Cytokine Signaling, Granulocyte Activity, Inflammasome, M1/M2 Activation, MHC Class II Antigen Presentation, Neutrophil Degranulation, NF-κB, Phagocytic Cell Function, Platelet Degranulation, Th1/Th2/Th17 Differentiation, TLR Signaling, Type I/Type II Interferon	369	369
Proliferation	Differentiation and proliferation of myofibroblasts are driven by upstream inflammation. These cells drive the wound-healing response that results in fibrotic damage.	Cell Cycle, ECM Synthesis, EMT, Focal Adhesion Kinase, Hedgehog Signaling, Hypoxia, Myofibroblast Regulation, Notch, PDGF Signaling, PI3K-Akt, Tgf-Beta, Wnt	287	287
Modification	Immune and myofibroblast cells contribute to extracellular matrix modification and tissue alterations that are characteristic of fibrotic disease.	Angiogenesis, Apoptosis, Collagen Biosynthesis & Modification, ECM Degradation, Epigenetic Modification, Hippo Pathway, Regulated Necrosis	159	161

Fibrosis Panel Functional Annotations

Functional annotations for different pathways and processes were assigned to the genes in the Fibrosis Panel. The pathways and processes that are included in this panel provide a comprehensive view of the pathogenesis of fibrotic disease.

Pathway	Number of Human Genes	Number of Mouse Genes	Pathway	Number of Human Genes	Number of Mouse Genes
Adenosine Pathway	51	53	Chemokine Signaling	23	22
Angiogenesis	37	37	Cholesterol Metabolism	26	24
Autophagy	39	39	Collagen Biosynthesis & Modification	27	27
Cell Cycle	49	49			

Pathway	Number of Human Genes	Number of Mouse Genes
Complement Activation	22	19
Cytokine Signaling	60	58
De Novo Lipogenesis	20	20
ECM Degradation	42	44
ECM Synthesis	38	38
EMT	88	88
Endotoxin Response	42	41
Epigenetic Modification	24	24
Fatty Acid Metabolism	55	57
Focal Adhesion Kinase	49	49
Gluconeogenesis	20	19
Granulocyte Activity	34	34
Hedgehog Signaling	24	24
Hippo Pathway	13	13
Hypoxia	16	16
Inflammasome	32	32
Insulin Resistance	38	38
Insulin Signaling	16	16
Internal Reference Gene	10	10
M1 Activation	12	12
M2 Activation	12	12
MAPK Cell Stress	67	67
MHC Class II Antigen Presentation	16	15

Pathway	Number of Human Genes	Number of Mouse Genes
mTOR	36	36
Myofibroblast Regulation	25	25
Neutrophil Degranulation	67	73
NF-kb	41	40
Notch	20	20
Oxidative Stress	18	18
PDGF Signaling	29	29
Phagocytic Cell Function	27	27
PI3K-Akt	89	89
Platelet Degranulation	33	34
PPAR Signaling	28	33
Programmed Cell Death	41	41
Proteotoxic Stress	43	43
SASP	15	15
TGF-beta	38	38
Th1 Differentiation	13	13
Th17 Differentiation	24	24
Th2 Differentiation	13	13
TLR Signaling	63	62
Type I Interferon	24	31
Type II Interferon	30	37
Wnt	38	38

Immune Cell Profiling Feature

Genes included in the Human Fibrosis Panel provide unique cell profiling data to measure the relative abundance of 14 different human immune cell types¹. The table below summarizes each cell type represented by gene content in the panel, as qualified through biostatistical approaches and selected literature in the field of immunology.

Relative Cell Type Abundance

Cell Type	Associated Human Genes
B cells	BLK, CD19, MS4A1, TNFRSF17, FCRL2, FAM30A, PNO, SPIB, TCL1A
CD45	PTPRC
CD8 T cells	CD8A, CD8B
Cytotoxic Cells	CTSW, GNLY, GZMA, GZMB, GZMH, KLRB1, KLRD1, KLRK1, PRF1, NKG7
Dendritic Cells	CCL13, CD209, HSD11B1
Exhausted CD8	CD244, EOMES, LAG3, PTGER4
Macrophages	CD163, CD68, CD84, MS4A4A

Cell Type	Associated Human Genes
Mast cells	MS4A2, TPSAB1/B2, CPA3, HDC
Neutrophils	CSF3R, S100A12, CEACAM3, FCAR, FCGR3A, FCGR3B, FPR1, SIGLEC5
NK CD56dim cells	IL21R, KIR2DL3, KIR3DL1, KIR3DL2
NK Cells	NCR1, XCL2, XCL1
T cells	CD3D, CD3E, CD3G, CD6, SH2D1A, TRAT1
Th1 Cells	TBX21
Treg	FOXP3

¹ Danaher P. et al. Gene expression markers of Tumor Infiltrating Leukocytes JIIC 2017

To view the annotated gene lists for the Fibrosis Panel, visit: <https://www.nanostring.com/fibrosis>

nSolver™ Analysis Software

NanoString offers advanced software tools that address the continuous demands of data analysis and the need to get simple answers to specific biological questions easy. Genes included in the Fibrosis panel are organized and linked to various advanced analysis modules to allow for efficient analysis of the pathways involved in fibrotic disease.

Advanced Analysis Modules available for Fibrosis:

- Normalization
- Quality Control
- Individual Pathway Analysis and Analysis of the Four Stages of Fibrosis
- Cell Profiling
- Differential Expression
- Gene Set Analysis
- Built-in compatibility for Panel-Plus and Protein analysis

Ordering Information

Gene Expression Panels arrive ready-to-use and generally ship within 24 hours following purchase

Product	Product Description	Quantity	Catalog Number
nCounter Human Fibrosis V2 Panel	Includes 760 genes; 10 internal reference genes for data normalization	12 Reactions	XT-CSO-HFIB2-12
nCounter Mouse Fibrosis V2 Panel	Includes 760 genes; 10 internal reference genes for data normalization	12 Reactions	XT-CSO-MFIB2-12
nCounter Master Kit (MAX or FLEX Systems) Reagents and Cartridges	Reagents, cartridges, and consumables necessary for sample processing on nCounter MAX and FLEX Systems	12 Reactions	NAA-AKIT-012
nCounter SPRINT Cartridge 1 Cartridge, 12 lanes	Sample Cartridge for nCounter SPRINT System	12 Reactions	SPRINT-CAR-1.0
nCounter SPRINT Reagent Pack	nCounter SPRINT Reagent Pack containing Reagents A, B, C, and Hybridization Buffer	192 Reactions	SPRINT-REAG-KIT

Selected Panel References

1. Danaher, P *et al.* Gene Expression Markers of Tumor Infiltrating Leukocytes. *J Immunother Cancer*. 2017;21(5):18.
2. Kazankov, K *et al.* The role of macrophages in nonalcoholic fatty liver disease and nonalcoholic steatohepatitis. *Nat Rev Gastroenterol Hepatol*. 2018;16(3):145-159.
3. Vukmirovic, M and Kaminski, N. Impact of Transcriptomics on Our Understanding of Pulmonary Fibrosis. *Front Med (Lausanne)*. 2018;5:87.
4. Mora, AL *et al.* Emerging therapies for idiopathic pulmonary fibrosis, a progressive age-related disease. *Nat Rev Drug Discov*. 2017;16(11):755-772.
5. Rosenbloom, J *et al.* Human Fibrotic Diseases: Current Challenges in Fibrosis Research. *Methods Mol Biol*. 2017;1627:1-23.
6. Musso, G *et al.* Non-alcoholic steatohepatitis: emerging molecular targets and therapeutic strategies. *Nat Rev Drug Discov*. 2016;15(4):249-274.
7. Sanders, FWB and Griffin, JL. De novo lipogenesis in the liver in health and disease: more than just a shunting yard for glucose. *Biol Rev*. 2016;91(2):452-468.
8. Meng, XM *et al.* TGF-β: the master regulator of fibrosis. *Nat Rev Nephrol*. 2016;12(6):325-338.
9. Szabo, G and Petrasek, J. Inflammasome activation and function in liver disease. *Nat Rev Gastroenterol Hepatol*. 2015;12(7):387-400.
10. Nanthakumar, CB *et al.* Dissecting fibrosis: therapeutic insights from the small-molecule toolbox. *Nat Rev Drug Discov*. 2015;14(10):693-720.
11. Selman, M and Pardo, A. Revealing the pathogenic and aging-related mechanisms of the enigmatic idiopathic pulmonary fibrosis. an integral model. *Am J Respir Crit Care Med*. 2014;189(10):1161-1172.
12. Wick, G *et al.* The Immunology of Fibrosis. *Annu Rev Immunol*. 2013;31:107-135.



For more information, please visit nanosttring.com

NanoString Technologies, Inc.

530 Fairview Avenue North
Seattle, Washington 98109
T (888) 358-6266
F (206) 378-6288
nanosttring.com
info@nanosttring.com

Sales Contacts

United States us.sales@nanosttring.com
EMEA: europe.sales@nanosttring.com
Asia Pacific & Japan apac.sales@nanosttring.com
Other Regions info@nanosttring.com

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

©2020 NanoString Technologies, Inc. All rights reserved. NanoString, NanoString Technologies, the NanoString logo, nCounter, IO 360 and nSolver are trademarks or registered trademarks of NanoString Technologies, Inc., in the United States and/or other countries.