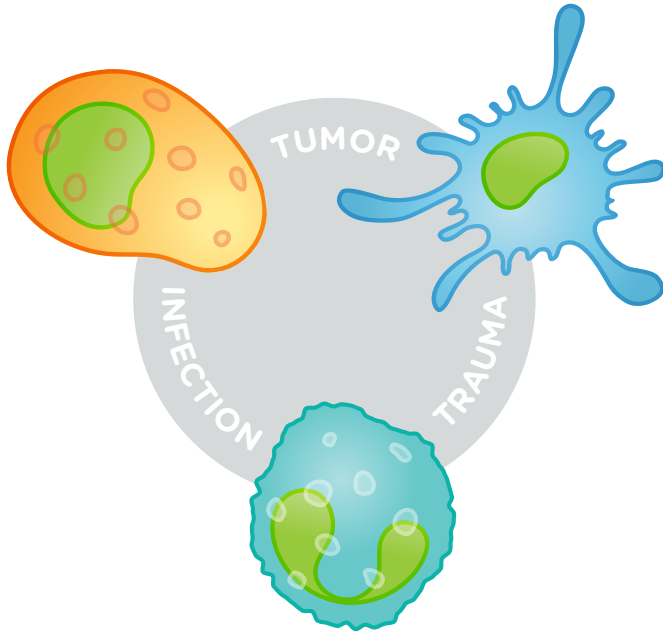




nCounter® Myeloid Innate Immunity Gene Expression Panel

Immuno-Oncology • Autoimmune Disease • Infectious Disease



The nCounter Myeloid Innate Immunity panels are designed to encompass all aspects of the myeloid innate immune response for use in basic and translational research studies. Each human or mouse panel provides an effective means to comprehensively measure, quantitatively and qualitatively, the attributes of the innate immune response by evaluating relative enrichment of genes that mark recruitment, activation, and effector function of selected myeloid subtypes.

Applications

- Mechanisms of Immune Evasion
- Damage Response, Wound Healing & Tissue Repair
- Immune Regulation
- Disease Pathogenesis
- Treatment Responders & Non-Responders


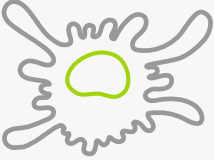

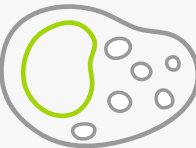
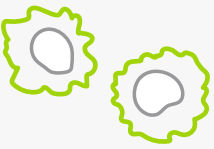
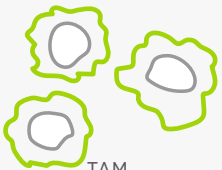
Product Highlights

- Comprehensive panels for either human or mouse experiments.
- Genes representing all major myeloid cell types and their various functions including: neutrophils, eosinophils, mast cells, dendritic cells, monocytes, and macrophages with 19 functional and pathway annotations.
- Customize with Panel-Plus, a custom spike-in product of 55 genes or less that allows for the creation of a panel and experiment uniquely your own.

Feature	Specifications
Number of Targets	770 (Human), 754 (Mouse) including internal reference genes
Standard Input Material (No amplification required)	25 ng–300 ng
Sample Material - Low Input	As little as 1 ng with nCounter RNA Low Input Kit and Panel specific primer pools (sold separately)
Sample Type(s)	FFPE-derived RNA, total RNA, fragmented RNA, cell lysates and PBMC sorted cells
Customizable	Add up to 55 unique genes with Panel Plus
Time to Results	Approximately 24 hours
Data Analysis	nSolver™ Analysis Software (RUO) and the ROSALIND® Platform

Innate Immunity Myeloid Cells

Genes included in the Myeloid Innate Immunity Panel were chosen based on their abundance/presence in the target cell and their ability to discern activation, polarization and effector phenotypes related to malignancy or infection. The table below gives a description of different myeloid cell types and the number of genes in the human or mouse panel that are reported to be associated with these cells based on the current literature.

Cell Type	Cell Description	Immune Regulatory Function	Associated Human Genes	Associated Mouse Genes
 <p>Macrophage</p>	Scavengers of dead or dying cells and cellular debris. Regulates important homeostatic and developmental functions, e.g., terminal end bud migration, angiogenesis, tissue repair, dendritic cell maturation, etc. by secreting a diversity of pro- and anti-inflammatory cytokines, chemokines, proteases and factors.	Adaptive Immune System Activation and Suppression	333 genes	332 genes
 <p>Dendritic Cell</p>	Cells that process antigens and present them to prime T cells for activation, thereby acting as messengers between the innate and adaptive immune systems.	Adaptive Immune System Activation	262 genes	264 genes
 <p>Eosinophil</p>	Leukocytes responsible for combating parasites and some types of infections. Effector production of growth factors such as TGF- β , VEGF, and PDGF, as well as cytotoxic factors.	Pro-inflammatory	99 genes	103 genes
 <p>Neutrophil</p>	Phagocytic granulocytes that act as first-responders and migrate towards sites of inflammation. Typically, a hallmark of acute inflammation which express markers of classical activation.	Acute inflammation	138 genes	137 genes
 <p>Mast Cell</p>	Early instigator of inflammation, and regulator of tissue homeostasis by secreting cytokines, chemokines, proteases, and heparin mediators that regulate vascular permeability, fibroblast responses and recruitment of peripheral blood cells into tissues.	Immune modulation	152 genes	147 genes
 <p>IMCs</p>	Immature myeloid cells (IMCs), also known as Myeloid Derived Suppressor Cells (MDSCs), are a heterogeneous group of cells that are transitory in differentiation towards granulocytic or macrophage subtypes. These can significantly suppress lymphocyte activation by paracrine mechanisms.	Strong immune suppression of both innate and adaptive immune system activity	173 genes	169 genes
 <p>TAM</p>	Recruited macrophages in tumor tissue are known as tumor associated macrophages (TAMs) - these are distinct from resident macrophages. Akin to macrophages, these are key regulators of tumor angiogenesis and proficient in orchestrating adaptive immune response.	Pro-tumor (Angiogenesis) and Anti-tumor. Variable dependent on tumor type	177 genes	178 genes

Smart Content in every Panel

nCounter Gene Expression panels are developed in collaboration with leading experts in the field. Each panel is curated to include the most current and relevant genes along with the following features:

- Functionally annotated gene lists with sortable gene to function pathway mapping
- Individual probe accession numbers, aliases and target sequence information
- Gene expression analysis for optimal performance on nCounter Analysis System for research use



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



ROSALIND is a cloud-based platform that enables scientists to analyze and interpret differential gene expression data without the need for bioinformatics or programming skills. ROSALIND makes analysis of nCounter data easy, with guided modules for:

- Normalization
- Quality Control
- Individual Pathway Analysis
- Differential Expression
- Gene Set Analysis

nCounter customers can access ROSALIND at www.rosalind.bio/nanostring

Myeloid Innate Immunity Panel Functional Annotations

Functional annotations for 19 different pathways and processes were assigned across all genes in the Myeloid Innate Immunity Panels allowing for a practical view of important aspects of the innate immune response.

Annotation	Human Genes	Mouse Genes
Angiogenesis	61	62
Antigen Presentation	64	57
Cell Cycle and Apoptosis	21	19
Cell Migration and Adhesion	101	97
Chemokine signaling	75	65
Complement Activation	18	17
Cytokine Signaling	157	153
Differentiation and Maintenance of Myeloid Cells	54	51
ECM remodeling	73	70
Fc Receptor Signaling	67	68
Growth Factor Signaling	186	184
Interferon Signaling	34	29
Lymphocyte activation	131	134
Metabolism	92	87
Pathogen Response	91	80
T-cell Activation and Checkpoint Signaling	33	30
TH1 Activation	19	19
TH2 Activation	20	20
TLR signaling	68	64
Internal Reference Genes	40	20

To view the complete gene lists for either the Human or Mouse Myeloid Innate Immunity Panels, visit: <http://www.nanostring.com/myeloid-innate-immunity/>

Ordering Information

Gene Expression Panel CodeSets arrive ready-to-use and generally ship within 24-hours following purchase.

Product	Product Description	Quantity	Catalog Number
nCounter Human Myeloid Innate Immunity Panel V2	Includes 770 genes, including 40 internal reference genes for data normalization.	12 Reactions	XT-CSO-HMII2-12
nCounter Mouse Myeloid Innate Immunity Panel V2	Includes 754 genes, including 20 internal reference genes for data normalization.	12 Reactions	XT-CSO-MMII2-12
nCounter Analysis System Master Kit Reagents and Cartridges	Reagents, cartridges, and consumables necessary for sample processing on the nCounter Analysis System.	12 Reactions	NAA-AKT1-012
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 & Hybridization Buffer	192 Reactions	SPRINT-REAG-KIT
Low Input RNA Reagent Kit	48rxn kit for profiling from low sample input amounts	48 Reactions	LOW-RNA-48
Human Myeloid Innate Immunity Primer Pools	MTE primer pools for Low Input RNA profiling (770 genes) 730 immune related human genes + 40 internal reference controls. Master Kit, RNA Low Input Kit & Panel CodeSet Required	12 Reactions	PP-HMII2-12
Mouse Myeloid Innate Immunity Primer Pools	MTE primer pools for Low Input RNA profiling (754 genes) 734 immune-related human genes + 20 internal reference controls. Master Kit, RNA Low Input Kit & Panel CodeSet Required	12 Reactions	PP-MMII2-12

Selected Panel References

- Murray PJ et al. Macrophage Activation and Polarization: Nomenclature and Experimental Guidelines. *Immunity*, Volume 41, Issue 1, 17 July 2014
- Xue, J. et al. Transcriptome-based network analysis reveals a spectrum model of human macrophage activation. *Immunity* 40, 274–288 (2014).
- Davis BP and Rothenberg ME. Eosinophils and cancer. *Cancer Immunol Res.* 2014;2(1):1-8.
- Lakschevitz FS, Visser MB, Sun C and Glogauer M. Neutrophil transcriptional profile changes during transit from bone marrow to sites of inflammation. *Cell Mol Immunol.* 2015;12(1):53-65.
- Fridlender ZG, Sun J, Mishalian I, Singhal S, Cheng G, Kapoor V, Horng W, Fridlender G, Bayuh R, Worthen GS and Albelda SM. Transcriptomic analysis comparing tumor-associated neutrophils with granulocytic myeloid-derived suppressor cells and normal neutrophils. *PLoS One.* 2012;7(2):e31524.
- Gregory AD and Houghton AM. Tumor-associated neutrophils: new targets for cancer therapy. *Cancer Res.* 2011;71(7):2411-6.
- Chaussabel D, et al. Unique gene expression profiles of human macrophages and dendritic cells to phylogenetically distinct parasites. *Blood.* 2003 Jul 15;102(2):672-81.
- Ruffell B, et al. Macrophage IL-10 Blocks CD8+ T Cell-Dependent Responses to Chemotherapy by Suppressing IL-12 Expression in Intratumoral Dendritic Cells. *Cancer Cell*, Volume 26, Issue 5, 10 November 2014
- Broz ML, Binnewies M, Boldajipour B, Nelson AE, Pollack JL, Erle DJ, Barczak A, Rosenblum MD, Daud A, Barber DL, Amigorena S, Van't Veer LJ, Sperling AI, Wolf DM, Krummel MF. Dissecting the tumor myeloid compartment reveals rare activating antigen-presenting cells critical for T cell immunity. *Cancer Cell.* 2014 Nov 10;26(5):638-52.
- Kuramasu A, Kubota Y, Matsumoto K, Nakajima T, Sun XM, Watanabe T, Saito H, Ohtsu H. Identification of novel mast cell genes by serial analysis of gene expression in cord blood-derived mast cells. *FEBS Lett.* 2001 Jun 1;498(1):37-41.
- Jayapal M, Tay HK, Reghunathan R, Zhi L, Chow KK, Rauff M, Melendez AJ. Genomewide gene expression profiling of human mast cells stimulated by IgE or FcεpsilonR1 aggregation reveals a complex network of genes involved in inflammatory responses. *BMC Genomics.* 2006 Aug 16;7:210.

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.

©2019-2022 NanoString Technologies, Inc. All rights reserved. NanoString, NanoString Technologies, nCounter, nSolver, and the NanoString logo are trademarks or registered trademarks of NanoString Technologies, Inc., in the United States and/or other countries.