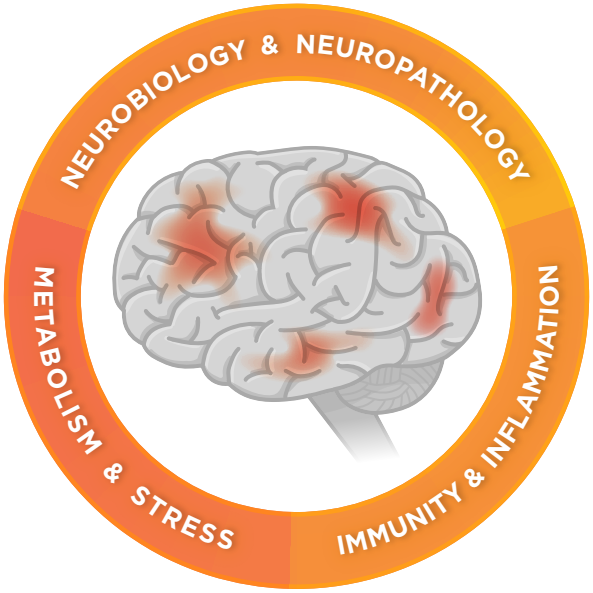
nCounter® Neuroinflammation Panel

Gene Expression Panel

Neuroimmune interactions • CNS and peripheral immune cell profiling

The nCounter Neuroinflammation panels are designed to rapidly analyze important aspects of neuroimmune interactions for a complete view of the complex interplay between the immune and nervous systems. Each human and mouse panel provides comprehensive evaluation of the pathways, processes, and cell types that are involved in neuroinflammation.



Applications

- For research of neurodegenerative disease, traumatic brain injury, psychiatric disorders, neuropathic pain, CNS infection, and others
- Gene expression profiling of neuroimmune interactions
- Response to drug treatment and signature generation
- Biomarker characterization

Product Highlights

- Comprehensive assessment of 23 neuroinflammation pathways and processes
- Unique cell typing analysis feature measures the relative abundance of 5 CNS and 14 peripheral immune cells
- Customizable with Panel Plus option – add up to 55 genes of your choosing
- nCounter workflow is streamlined, user-friendly, and efficient with just 15 minutes total hands-on time

Feature	Specifications
Number of Targets	770 (Human), 770 (Mouse) including internal reference genes
Sample Material - Standard (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 seperately)
Sample Type(s)	FFPE-derived RNA, total RNA, fragmented RNA, PBMCs, whole blood/plasma, iPSCs, cerebrospinal fluid
Customizable	Add up to 55 unique genes with Panel Plus
Time to Results	Approximately 24 hours
Data Analysis	nSolver™ Analysis software and the ROSALIND® Platform

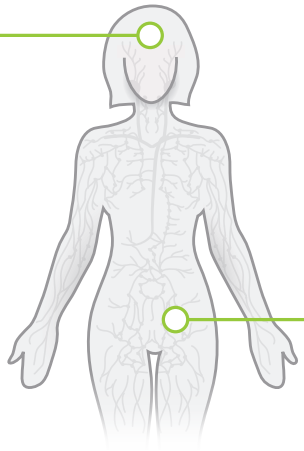
CNS and Peripheral Immune Cell Profiling

Genes included in the Neuroinflammation Panels provide unique cell profiling data for measuring the relative abundance of 5 central nervous sytem and 14 peripheral immune cell types in a single sample[1]. The table below summarizes each cell type represented by gene content in the panel qualified through biostatistical approaches and selected literature in the field of neuroinflammation research.

Cell Function

CNS Cells

- Neurons
- Microglia
- Astrocytes
- Oligodendrocytes
- Endothelial cells



Peripheral Immune Cells

- B cells
- Dendritic cells
- Exhausted CD8
- Macrophages
- T cells
- CD8 T cells
- Neutrophils
- Mast Cells
- Cytotoxic cells
- Tregs
- NK CD56dim cells
- NK cells
- CD45+ cells
- Th1 cells

Core Themes and Annotations

Classification	Cell Type	Associated Human Genes	Associated Mouse Genes
CNS cells	Neurons	6	6
	Microglia	6	6
	Astrocytes	8	8
	Oligodendrocytes	15	15
	Endothelial cells	9	9
Peripheral Immune Cells	B cells	7	7
	Dendritic cells	2	2
	Exhausted CD8	4	4
	Macrophages	4	4
	T cells	6	6
	CD8 T cells	2	2
	Neutrophils	5	3
	Mast cells	4	4
	Cytotoxic cells	9	8
	Treg	1	1
	NK CD56dim cells	2	3
	NK cells	2	2
	CD45+ cells	1	1
	Th1 cells	1	1

[1] Danaher P. et al. Gene expression markers of Tumor Infiltrating Leukocytes JITC 2017

Neuroinflammation Panel Functional Annotations

Functional annotations for 23 pathways and processes were assigned across the genes in the Neuroinflammation Panels. The 23 pathways and processes represent three core themes of neuroinflammation: immunity and inflammation, neurobiology and neuropathology, and metabolism and stress.

Immunity and Inflammation

The role of innate immunity in many neurological disorders is now widely accepted in the research world although the relative contributions of these processes to the progression and/or amelioration of these diseases is incompletely understood. Several key processes and pathways are assessed in this panel to provide a comprehensive view of the immune and inflammatory response in the nervous system.

NF-kB	Microglia function	Innate immune response
Adaptive immune response	Cytokine signaling	Inflammatory signaling

Neurobiology and Neuropathology

Neuropathology research today requires a broad view of all the underlying aspects of neurological disorders and injury, including assessment of neurotransmission, neuron-glia interactions, neuroplasticity, cell integrity, neuroinflammation, and metabolism. There are 13 pathways and processes included in this panel to evaluate the impact of neuroinflammation and immune actions in the nervous system on neuropathology.

Angiogenesis	Apoptosis	Neurons and neurotransmission	Cell cycle	Astrocyte function
Insulin signaling	Notch	DNA damage	Epigenetic regulation	Wnt
Oligodendrocyte function	Matrix remodeling	Growth factor signaling		

Metabolism and Stress

Metabolic dysfunction and stress have been shown to influence brain activity and disrupt CNS homeostasis and cognitive function by adopting neurotoxic functions. The genes selected for this panel are designed to assess important aspects of metabolism and stress that are known to impact neuroinflammation.

Autophagy	Carbohydrate metabolism	Lipid metabolism	Cellular stress

To view the annotated gene lists for the Neuroinflammation panels, visit: **www.nanostring.com/neuroinflammation**

Ordering Information

Product	Product Description	Quantity	Catalog Number
nCounter Human Neuroinflammation Panel	Includes 770 genes, including 13 internal reference genes for data normalization	12 Reactions	XT-CSO-HNROI1-12
nCounter Mouse Neuroinflammation Panel	Includes 770 genes, including 13 internal reference genes for data normalization	12 Reactions	XT-CSO-MNROI1-12
nCounter Analysis System Master Kit Reagents and Cartridges	Reagents, cartridges, and consumables necessary for sample processing on the nCounter Analysis System	12 Reactions	NAA-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
Low Input RNA Reagent Kit	48rxn kit for profiling from low sample input amounts	48 Reactions	LOW-RNA-48
nCounter Human Neuroinflammation Primer Pools	MTE primer pools for Low Input RNA profiling (770 genes) 757 neuroinflammation related human genes + 13 internal reference controls. Master Kit, RNA Low Input Kit, and Panel CodeSet Required	12 Reactions	PP-HNROI1-12
nCounter Mouse Neuroinflammation Primer Pools	MTE primer pools for Low Input RNA profiling (770 genes) 757 neuroinflammation related mouse genes + 13 internal reference controls. Master Kit, RNA Low Input Kit, and Panel CodeSet Required	12 Reactions	PP-MNROI1-12

Selected Panel References

1. Butovsky O, Jedrychowski MP, Cialic R, Krasemann S, Murugaiyan G, et al. Targeting miR-155 restores abnormal microglia and attenuates disease in SOD1 mice. Ann Neurol. 2015 Jan;77(1):75-99. PubMed PMID: 25381879; NIHMSID: NIHMS679333; PubMed Central PMCID: PMC4432483.
2. Chiu IM, Morimoto ET, Goodarzi H, Liao JT, O'Keeffe S, et al. A neurodegeneration-specific gene-expression signature of acutely isolated microglia from an amyotrophic lateral sclerosis mouse model. Cell Rep. 2013 Jul 25;4(2):385-401. PubMed PMID: 23850290; NIHMSID: NIHMS499259; PubMed Central PMCID: PMC4272581.
3. Holtman IR, Raj DD, Miller JA, Schaafsma W, Yin Z, et al. Induction of a common microglia gene expression signature by aging and neurodegenerative conditions: a co-expression meta-analysis. Acta Neuropathol Commun. 2015 May 23;3:31. PubMed PMID: 26001565; PubMed Central PMCID: PMC4489356.
4. Orre M, Kamphuis W, Osborn LM, Jansen AHP, Kooijman L, et al. Isolation of glia from Alzheimer's mice reveals inflammation and dysfunction. Neurobiol Aging. 2014 Dec;35(12):2746-2760. PubMed PMID: 25002035.
5. Raj DD, Jaarsma D, Holtman IR, Olah M, Ferreira FM, et al. Priming of microglia in a DNA-repair deficient model of accelerated aging. Neurobiol Aging. 2014 Sep;35(9):2147-60. PubMed PMID: 24799273.
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7. Wang Y, Cella M, Mallinson K, Ulrich JD, Young KL, et al. TREM2 lipid sensing sustains the microglial response in an Alzheimer's disease model. Cell. 2015 Mar 12;160(6):1061-71. PubMed PMID: 25728668; NIHMSID: NIHMS661638; PubMed Central PMCID: PMC4477963.
8. Zhang Y, Chen K, Sloan SA, Bennett ML, Scholze AR, et al. An RNA-sequencing transcriptome and splicing database of glia, neurons, and vascular cells of the cerebral cortex. J Neurosci. 2014 Sep 3;34(36):11929-47. PubMed PMID: 25186741; PubMed Central PMCID: PMC4152602.

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