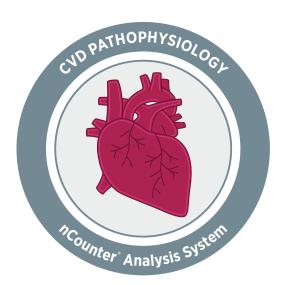


# nCounter® CVD Pathophysiology Panel

## Gene Expression Panel - Cardiovascular Disease (CVD)

Heart Disease • Arteriosclerosis • Hypertension • Cardiotoxicity • Regenerative Medicine

Rapidly advance your cardiovascular research with molecular insights that provide quick, actionable results. Explore how cardiovascular disfunction contributes to heart disease, hypertension and arteriosclerosis. Study the cardiotoxic effects of immune therapies or assess the role of aging and cell renewal in cardiac regenerative medicine.



## **Product Highlights**

- Directly profile 800 genes across 50 pathways involved in CVD pathophysiology
  - Cardiovascular Pathology
  - Cardiovascular Physiology
  - Vascular Inflammation
  - Cellular Aging & Renewal
  - Metabolism
  - Mechano Signaling
  - Regulatory Signaling
  - Epigenetic Remodeling
- Measure cardiotoxicities resulting from therapeutic treatment
- Study the MOA of approved CVD drugs
- Explore cardiomyocyte recovery and regeneration
- Quantify the presence and relative abundance of 16 cell types present in cardiac tissue
- Compatible with a variety of sample types including blood, cardiac tissue, organoids, stem cells, engineered cell lines, explants, and organs on a chip
- Generate data in 24 hours with less than 30 minutes hands on time and simple data analysis

Feature	Specifications		
Number of Targets	800 (Human and Mouse), including 10 internal reference genes for data normalization.		
Sample Input - Standard (No amplification required)	25-300 ng		
Sample Input - Low Input	As little as 1 ng with nCounter Low Input Kit; low input protocol and primer designs available.		
Sample Type(s)	Blood, cardiac biopsies, xenografts, cultured cells/cell lysates, FFPE-derived RNA, total RNA, fragmented RNA		
Customizable	Add up to 55 unique genes with Panel-Plus		
Time to Results	Approximately 24 hours		
Data Analysis	nSolver™ Analysis Software (RUO), Advanced Analysis for cell profiling, ROSALIND® platform		

## Key Applications with the nCounter CVD Pathophysiology Panel

## **Heart Disease/Hypertension** /Arteriosclerosis

#### What molecular characteristics contribute to cardiovascular disease?

Study key pathways involved in cardiovascular pathology, physiology and pathway signaling.

Understand the impacts of lipid metabolism and metabolic disorders on CVD.

Explore the role of epigenetic remodeling enzymes in the initiation and progression of CVD.

## **Cardiotoxicity**



#### How can cardiotoxicity be avoided?

Characterize the effects of immune response, inflammation, and immunomodulatory pathways on cardiac function.

Explore the cardiotoxic effects of immune therapies.

Assess novel drug targets for efficacy in the context of approved drug MOAs.

## **Regenerative Medicine**



### How can regenerative medicine help treat cardiovascular disease?

Uncover the roles of cellular aging, senescence and renewal on CVD.

Understand the relative abundance of cardiac specific cell types and their impact on gene expression pathways in regenerative tissue cultures.

#### **Panel Themes**

The CVD Pathophysiology Panel includes annotations across 8 functional themes related to cardiovascular disfunction and disease. Pathway coverage is outlined in the table below.

- Atherosclerosis
- Cardiac Hypertrophy
- Cardiomyopathy
- Foam Cell Formation
- Ischemia
- Myocarditis

- **Cardiovascular Physiology**
- Cardiac Muscle Contraction
- Pericarditis
- Hypertension

Thrombosis

• Hemostasis

- Cardiac
- Electrophysiology GABAergic Signaling
- Muscle Contraction • Vasopressin System
- Cardiac Morphogenesis

**Cardiovascular Inflammation** 

- eNOS Activation
- IL-1 Signaling • IL-6 Signaling
- Other Cytokine Signaling TLR Signaling
- JAK-STAT Signaling • mTOR Signaling
- NF-kappaB Signaling
- PI3K-AKT Signaling
- PPAR Signaling
- Immune Cell Infiltration TNF Signaling
  - Checkpoint Signaling

## Cellular Aging & Renewal

- Apoptosis
- Autophagy
- Cell Cycle
- Senescence & Quiescence • Telomere Maintenance

## Metabolism

- Fatty Acid Metabolism Cholesterol
- Glucose Metabolism Hypoxia Response
- Lipid Metabolism
- Metabolism
- Lipoprotein Clearance
- Oxidative Stress

#### **Mechano Signaling**

- ECM Remodeling
- Hippo Signaling Integrin Signaling
- Rho ROCK Signaling

#### **Regulatory Signaling**

- Calcium Signaling
- EGFR Signaling
- MAPK Signaling Notch Signaling
- TGF-beta Signaling VEGF Signaling
  - Wnt Signaling
- **Epigenetic Remodeling**
- Histone Modifications Acetyl Transferases
- Deacetylases
- Methyl Transferases

## **Cardiac Cell Profiling Feature**

Genes included in the CVD Pathophysiology Panel provide unique cell profiling data to measure the relative abundance of 16 different cardiac cell types. The table below summarizes the genes included in each cell type signature, as qualified through biostatistical approaches and selected literature in the field of cardiovascular disease.

CellType	Associated Human Genes	
Cardiomyocytes (Atrial, Ventricular)	FHL2, MYL4, MYL7	
Fibroblasts	DCN, PDGFRA	
Endothelial Cells	CDH5, PECAM1, VWF	
Mesothelial Cells	BNC1, MSLN	
Vascular Smooth Muscle Cells	MYH11	
Pericytes	ABCC9, KCNJ8	
Neuronal Cells	NRXN1, PLP1	
Adipocytes	FASN, GPAM, LEP	
T Cells (Th1, CD45, CD8, Tregs)	PTPRC, CD8A, CD8B, CD3D, CD3E, CD3G, CD6, TBX21, FOXP3	
Cytotoxic Cells	CTSW, GNLY, GZMA, GZMB, GZMH, KLRB1, KLRK1, NKG7, PRF1	
NK Cells	KIR3DL1, NCR1, XCL1/2	
Macrophages	CD163, CD68, CD84, MS4A4A	
Dendritic Cells	CCL13, CD209	
Neutrophils	CSF3R, FCGR3A/B, FPR1	
Mast Cells	CPA3, HDC, MS4A2	
B Cells	CD19, MS4A1, SPIB, TNFRSF17	

### **Customization with Panel Plus**

Customize your research project by adding up to 55 user-defined genes of interest with nCounter Panel Plus. Panel Plus capacity enables researchers to address content specific to their cardiovascular research areas of interest. Expand on pathways and core themes of the panel or include infectious disease content (i.e. COVID).

## **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 easily. Genes included in the CVD Pathophysiology Panel are annotated to allow for efficient analysis of relevant pathways.

## Analysis Modules available for CVD Pathophysiology:

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

 Built-in compatibility for Panel Plus and Protein analysis



### **ROSALIND® Platform**

- 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 free of charge at <a href="https://www.rosalind.bio/nanostring">https://www.rosalind.bio/nanostring</a>

## **Ordering Information**

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

Product Description	Quantity	Catalog Number
800 genes, including 10 internal reference genes for data normalization. Codeset Only.	12 Reactions	XT-HSCVD-12
800 genes, including 10 internal reference genes for data normalization. Codeset only.	12 Reactions	XT-MSCVD-12
Standard containing a pool of synthetic DNA oligonucleotides that correspond to the target sequence of each of the unique probe targets in the panel.	12 Reactions	PSTD-H-CVD-12
Standard containing a pool of synthetic DNA oligonucleotides that correspond to the target sequence of each of the unique probe targets in the panel.	12 Reactions	PSTD-M-CVD-12
Kit for use with low input protocol; primer designs available.	48 Reactions	LOW-RNA-48
Reagents, cartridges, and consumables necessary for sample processing on the nCounter Analysis System	12 Reactions	NAA-AKIT-012
Sample Cartridge for nCounter SPRINT System	12 Reactions	SPRINT-CAR-1.0
nCounter SPRINT Reagent Pack containing Reagents A, B, C, and Hybridization Buffer	192 Reactions	SPRINT-REAG-KIT
	800 genes, including 10 internal reference genes for data normalization. Codeset Only.  800 genes, including 10 internal reference genes for data normalization. Codeset only.  Standard containing a pool of synthetic DNA oligonucleotides that correspond to the target sequence of each of the unique probe targets in the panel.  Standard containing a pool of synthetic DNA oligonucleotides that correspond to the target sequence of each of the unique probe targets in the panel.  Kit for use with low input protocol; primer designs available.  Reagents, cartridges, and consumables necessary for sample processing on the nCounter Analysis System  Sample Cartridge for nCounter SPRINT System  nCounter SPRINT Reagent Pack containing Reagents A, B, C, and	800 genes, including 10 internal reference genes for data normalization. Codeset Only.  800 genes, including 10 internal reference genes for data normalization. Codeset only.  12 Reactions  Standard containing a pool of synthetic DNA oligonucleotides that correspond to the target sequence of each of the unique probe targets in the panel.  Standard containing a pool of synthetic DNA oligonucleotides that correspond to the target sequence of each of the unique probe targets in the panel.  Kit for use with low input protocol; primer designs available.  Kit for use with low input protocol; primer designs available.  Reagents, cartridges, and consumables necessary for sample processing on the nCounter Analysis System  12 Reactions  12 Reactions  12 Reactions  12 Reactions  12 Reactions

### **Selected Panel References**

- 1. Litvinuková, M. et al. Cells of the adult human heart. Nature 588, 466-472 (2020).
- 2. Ferrucci, L. & Fabbri, E. Inflammageing: chronic inflammation in ageing, cardiovascular disease, and frailty. Nat Rev Cardiol 15, 505–522 (2018)
- 3. Fung, G., Luo, H., Qiu, Y., Yang, D. & McManus, B. Myocarditis. Circulation Research 118, 496-514 (2016).
- 4. Liu, Y. et al. RNA-Seq identifies novel myocardial gene expression signatures of heart failure. Genomics 105, 83–89 (2015).
- 5. Sweet, M. E. et al. Transcriptome analysis of human heart failure reveals dysregulated cell adhesion in dilated cardiomyopathy and activated immune pathways in ischemic heart failure. BMC Genomics 19, 812 (2018).

## For more information visit nanostring.com/CVD

## **Bruker Spatial Biology**