Comprehensive panel curated for disease and therapeutic target research

Accelerate drug discovery and translational research with targeted gene expression

As clinical translational research moves from discovery to validation, targeted workflows help you efficiently validate hypotheses and explore the cell types and biomarkers most important to you. With curated content from the Connectivity Map (CMap) and recent publications, the 10x Genomics Human Gene Signature Panel for targeted gene expression enables you to comprehensively profile key cellular processes and signaling pathways associated with disease in both single cells and intact tissue sections*.

Containing over 1,000 genes and spanning more than 25 pathways, the Human Gene Signature Panel is designed to accelerate your translational studies. Explore the effects of activating and inhibiting important signaling pathways, test putative drug targets, and investigate therapeutic mechanisms of action. Focus your research on key genes and the specific cellular and molecular activity they elicit, while increasing sample throughput and conserving sequencing costs. Leverage the pre-designed panel or add up to 200 additional genes to customize your study. Compatible with Chromium Single Cell Gene Expression and Single Cell Immune Profiling Solutions, as well as Visium Spatial Gene Expression Solution*, the Human Gene Signature Panel enables comprehensive and efficient characterization of complex disease biology.

Highlights

- 1,142 genes to profile a wide variety of important signaling pathways and disease and drug targets
- Curated content from the Connectivity Map database and recent oncology and immunology publications, spanning over 25 pathways and 26 cell and tissue types
- Compatibility across 10x Genomics solutions, including single cell and spatial* gene expression assays
- Customizable panel content with the ability to add up to 200 additional genes using our Custom Panel Designer
- Full-tiling across gene transcripts, with an average of 40 probes per gene
- Validated gene content across different sample types, including fresh and frozen cell lines and tissues

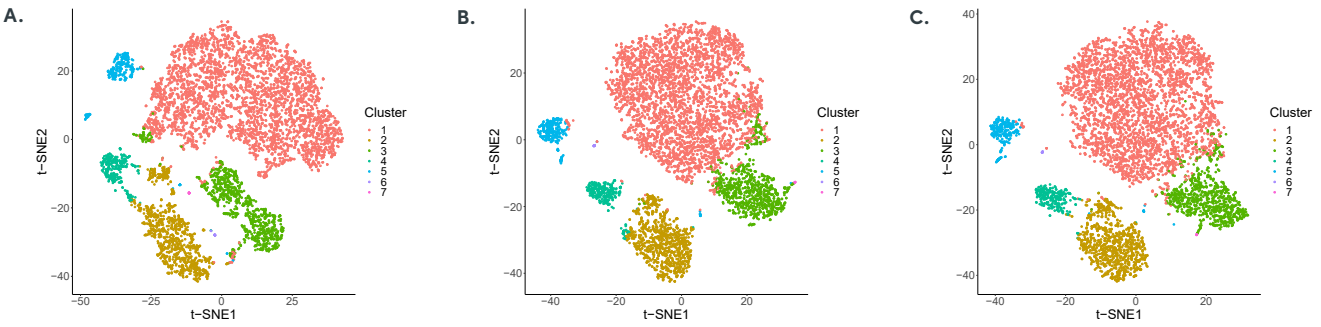

Figure 1. Cell-type clustering and annotation is preserved in targeted samples Representative data from approximately 6,500 cells from bone marrow mononuclear cells of a multiple myeloma patient, transcriptionally profiled with the Chromium Single Cell Gene Expression 3' v3 Workflow. The final libraries underwent target enrichment with the Human Gene Signature panel, and cell clustering is compared on the union of cells called in the two sequencing libraries. A. Whole transcriptome analysis identified seven cell clusters, when sequenced at 66,000 reads per cell (about 75% sequencing saturation). B. Cell clustering based on an in silico subset of genes found in the Human Gene Signature Panel. C. Cell clustering based on target enrichment for genes found in the Human Gene Signature Panel, sequenced and subsampled to 3,000 reads per cell. All major cell subpopulations were preserved compared to the whole transcriptome parent sample and the in silico subset.

Pathway	Genes
AMPK signaling	28
cAMP signaling	32
Chemokine signaling	43
ErbB signaling	40
Estrogen signaling	29
FoxO signaling	43
Glucagon signaling	17
HIF-1 signaling	31
Hippo signaling	20
Insulin signaling	36
Jak-STAT signaling	24
MAPK signaling	59
MicroRNAs in cancer	47
mTOR signaling	18
NF-kappa B signaling	19
p53 signaling	29
Pathways in cancer	108
PI3K-Akt signaling	69
Rap1 signaling	46
Ras signaling	49
Signaling pathways regulating pluripotency of stem cells	40
T cell receptor signaling	35
TGF-beta signaling	17
Thyroid hormone signaling	29
TNF signaling	28
VEGF signaling	23
Wnt signaling	26

Table 1. Panel Design Highlights: Pathway Genes Key pathway gene categories included in the Human Gene Signature Panel.

Tissue or Cell Type	Genes
B cell	34
Bone marrow	92
Colon	91
Coronary artery	8
Embryonic kidney	11
Endothelial cell	8
Epithelium	299
Eye	86
Fetal brain	62
Fetal brain cortex	23
Fibroblast	22
Hippocampus	37
Kidney	125
Liver	192
Lung	246
Lymph	60
Mammary gland	44
Muscle	86
Ovary	71
Pancreas	79
Placenta	301
Platelet	66
Skeletal muscle	43
Skin	171
T cell	39
Uterus	155

Table 2. Panel Design Highlights: Tissue Types Key tissue-type categories included in the Human Gene Signature Panel.

Functional Annotation and Process	Genes
Acetylation	415
Aging	25
Alzheimer disease	6
Angiogenesis	16
Apoptosis	84
Brain development	25
Cell aging	11
Cell cycle	140
Cell division	86
Cell proliferation	67
Cell–cell adhesion	45
Cellular response to hypoxia	25
Chromatin regulator	33
Differentiation	50
DNA damage	48
DNA repair	80
DNA replication	75
DNA-binding	183
Forebrain development	7
Host–virus interaction	62
Lipid biosynthesis	17
Liver regeneration	9
Mitosis	64
Neuron differentiation	12
Oncogene	4
Osteoblast differentiation	12
Placenta development	10
Regulation of cell proliferation	41
Response to drug	56
Somatic stem cell population maintenance	21
Telomere maintenance via recombination	15
Transcription regulation	206
Tumor suppressor	20
Wound healing	18

Table 3. Panel Design Highlights: Functional Annotation and Processes
Key functional annotation and process gene categories included in the Human Gene Signature Panel.

*Optimized protocol, support, and software for targeted panels with spatial gene expression coming September 2020

Products	Product Code
Target Hybridization Kit, 16 rxns	1000248
Library Amplification Kit, 16 rxns	1000249
Human Gene Signature Panel, 4 rxns	1000258
Human Gene Signature Panel, 16 rxns	1000245
Custom Panel Designer	Coming soon

Compatible Products
Chromium Single Cell Gene Expression Solution 10xgenomics.com/single-cell
Chromium Single Cell Immune Profiling Solution 10xgenomics.com/vdj
Visium Spatial Gene Expression Solution* 10xgenomics.com/spatial-gene-expression

Applications

- Identify biomarkers of therapeutic response to inform clinical trials
- Capture unique gene expression signatures
- Probe disease and drug targets
- Discover mechanism of action of small molecules
- Measure effects of activation or inhibition of signaling pathways
- Dissect signalling pathways with targeted CRISPR screens

Curated content sources

1. F Behan et al., Prioritization of cancer therapeutic targets using CRISPR-Cas9 screens. *Nature*. 568, 511–6 (2019).
2. F Sanchez-Vega et al., Oncogenic Signaling Pathways in the Cancer Genome Atlas. *Cell*. 173, 321–37 (2018).
3. H Fang et al., A genetics-led approach defines the drug target landscape of 30 immune-related traits. *Nat. Genet*. 51, 1082–91 (2019).
4. A Subramanian et al., A Next Generation Connectivity Map: L1000 platform and the first 1,000,000 profiles. *Cell*. 171, 1437–52 (2017).

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LIT000084 Rev B Human Gene Signature Panel Product Sheet