

# Comprehensive panel curated for disease and therapeutic target research

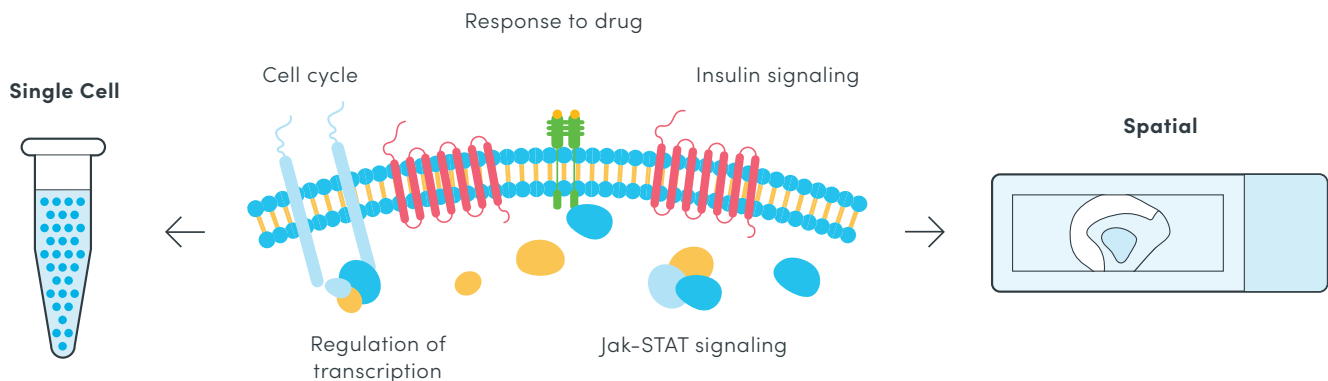
## Accelerate translational research with Targeted Gene Expression

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.

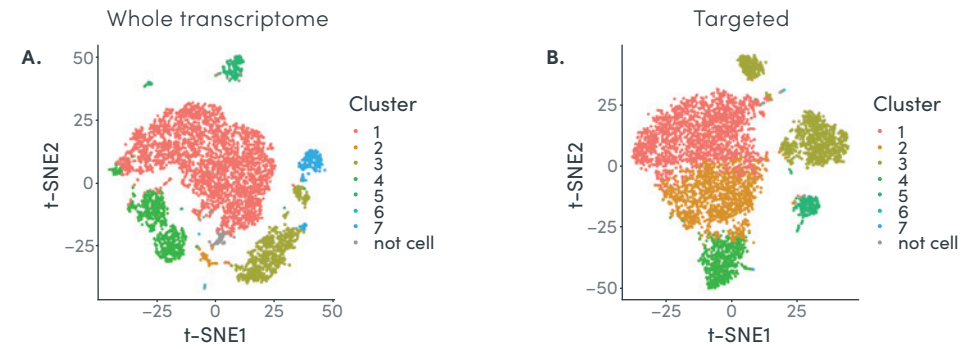
Compatible with Chromium Single Cell Gene Expression and Single Cell Immune Profiling, as well as Visium Spatial Gene Expression, the Human Gene Signature Panel enables comprehensive and efficient characterization of complex disease biology.

## Highlights

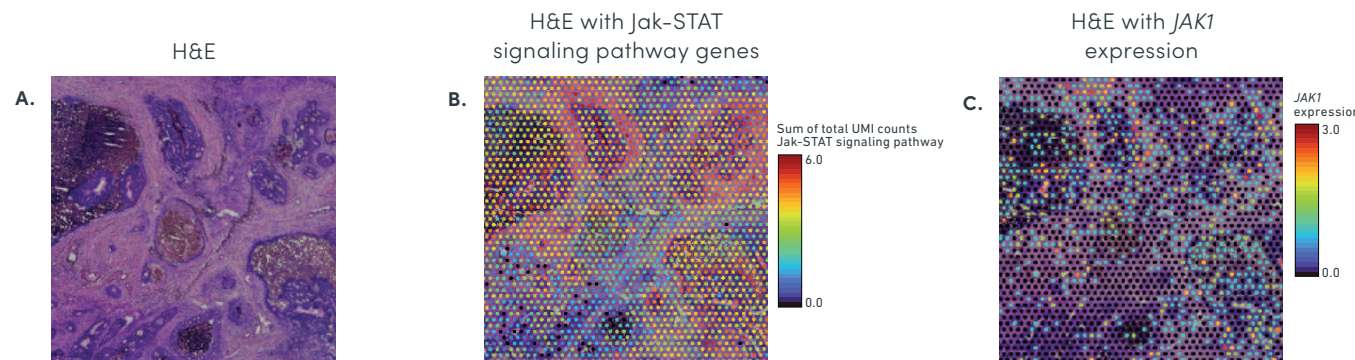
- Profile over 25 key signaling pathways with 1,142 target genes spanning 26 cell and tissue types curated from the Connectivity Map (CMap) and recent publications
- Analyze a wide variety of disease and drug targets in both single cells and intact tissue sections
- Customize panel content by adding up to 200 genes using our Custom Panel Designer
- Recover transcripts effectively with full tiling of probes across gene transcripts



**Figure 1. Accelerate your translational research with a comprehensive and curated gene panel.** The Human Gene Signature Panel is compatible with Single Cell Gene Expression, Single Cell Immune Profiling, and Spatial Gene Expression. Highlighted here are just a few of the pathways, tissue types, and cellular processes included in the panel content.



**Figure 2. Targeted Gene Expression with the Human Gene Signature panel preserves cell-type clustering and annotation of single cell data.** 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 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.



**Figure 3. Curated translational content refines spatial gene expression analysis.** A human colorectal cancer tissue section was H&E stained and processed using the Visium Spatial Gene Expression workflow, then enriched for genes of interest using Targeted Gene Expression with the Human Gene Signature Panel. Shown are the H&E image (A), H&E image overlaid with total UMI counts for 24 genes from the Jak-STAT signaling gene category of the Human Gene Signature Panel (B), and H&E image overlaid with *JAK1* expression level (C).

Pathway	Genes
AMPK signaling	28
cAMP signaling	32
Chemokine signaling	91
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.** Selection of 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
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.** Selection of 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
Host–virus interaction	62
Lipid biosynthesis	17
Liver regeneration	9
Mitosis	64
Neuron differentiation	12
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.**  
Selection of key functional annotation and process gene categories included in the Human Gene Signature Panel.

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 <a href="https://bit.ly/10xgenomics-custom-designer">bit.ly/10xgenomics-custom-designer</a>	<a href="#">Visit Designer</a>

### Compatible products

- Chromium Single Cell Gene Expression  
[10xgenomics.com/single-cell](https://10xgenomics.com/single-cell)
- Chromium Single Cell Immune Profiling  
[10xgenomics.com/vdj](https://10xgenomics.com/vdj)
- Visium Spatial Gene Expression  
[10xgenomics.com/spatial-gene-expression](https://10xgenomics.com/spatial-gene-expression)

## Applications

- Inform clinical trials by identifying key biomarkers
- Probe disease and drug targets
- Discover mechanism of action of small molecules
- Investigate signaling pathway inhibition and activation
- Dissect signaling 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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