

Comprehensive panel curated for cancer research

Accelerate cancer research with Targeted Gene Expression

Containing over 1,000 genes and spanning 33 cancer types, the Human Pan-Cancer Panel is designed to accelerate your understanding of the complexity of cancer biology. Gain deeper insights into pathways that play crucial roles in oncogenesis, proliferation, and metastasis using this pre-designed panel or customize it to include your genes of interest.

Compatible with Chromium Single Cell Gene Expression and Single Cell Immune Profiling, as well as Visium Spatial Gene Expression, the Human Pan-Cancer Panel enables comprehensive and efficient characterization of your cancer samples.

Highlights

- Profile key pathways and biomarkers with 1,253 target genes spanning 33 cancer types, curated from The Cancer Genome Atlas (TCGA) and recent publications
- Analyze tumor biology, the tumor microenvironment, and immune response 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

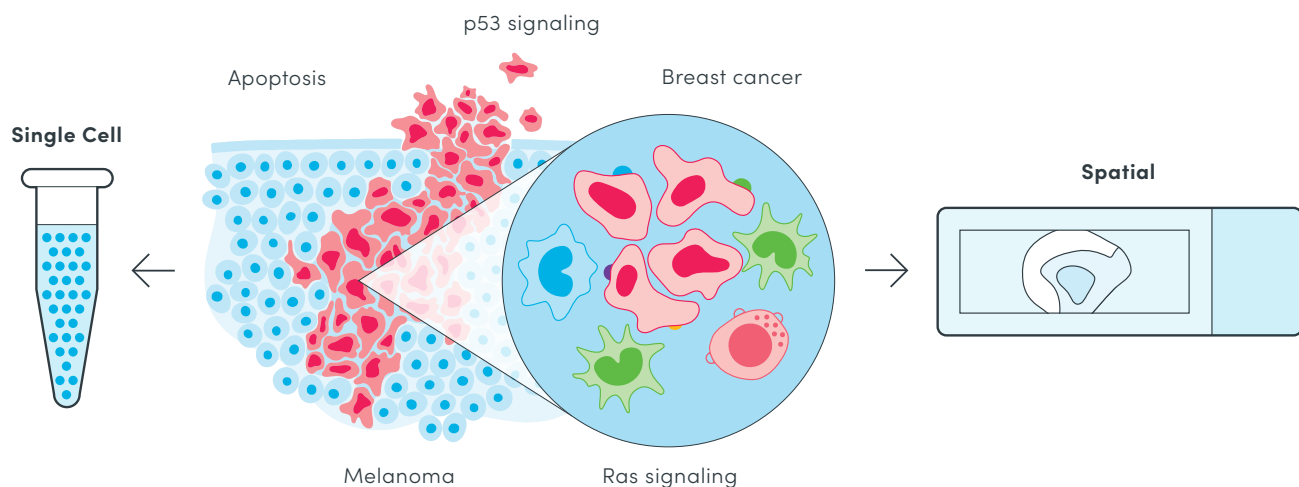


Figure 1. Accelerate your cancer research with a comprehensive and curated gene panel. The Human Pan-Cancer Panel is compatible with Single Cell Gene Expression, Single Cell Immune Profiling, and Spatial Gene Expression. Highlighted here are just a few of the pathways, cancer types, and cellular processes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

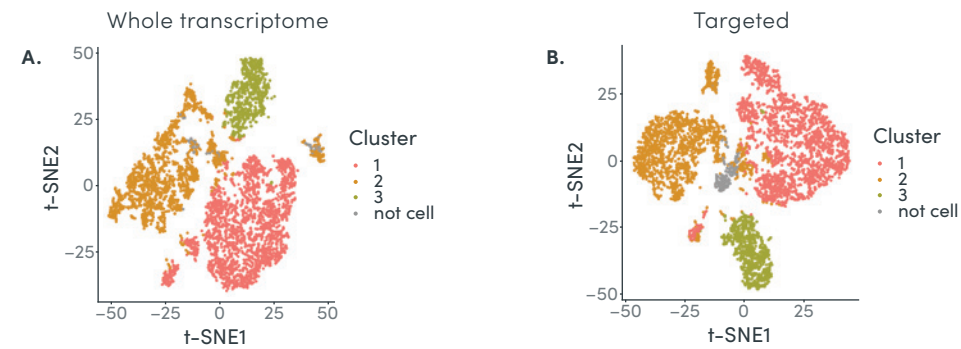


Figure 2. Targeted Gene Expression with the Human Pan-Cancer Panel preserves cell-type clustering and annotation of single cell data. Representative data from approximately 6,000 glioblastoma cells run with the Chromium Single Cell Gene Expression 3' v3 workflow. A. Whole transcriptome analysis identified three major cell type clusters when sequenced at 70,000 reads per cell (about 60% sequencing saturation). B. Cell clustering based on target enrichment for genes found in the 10x Genomics Human Pan-Cancer Panel, sequenced and subsampled to just 2,000 reads per cell. All major cell subpopulations were preserved compared to the whole transcriptome parent sample. Cells identified in the parent sample but not in the targeted sample, or vice versa, are colored gray in each sample.

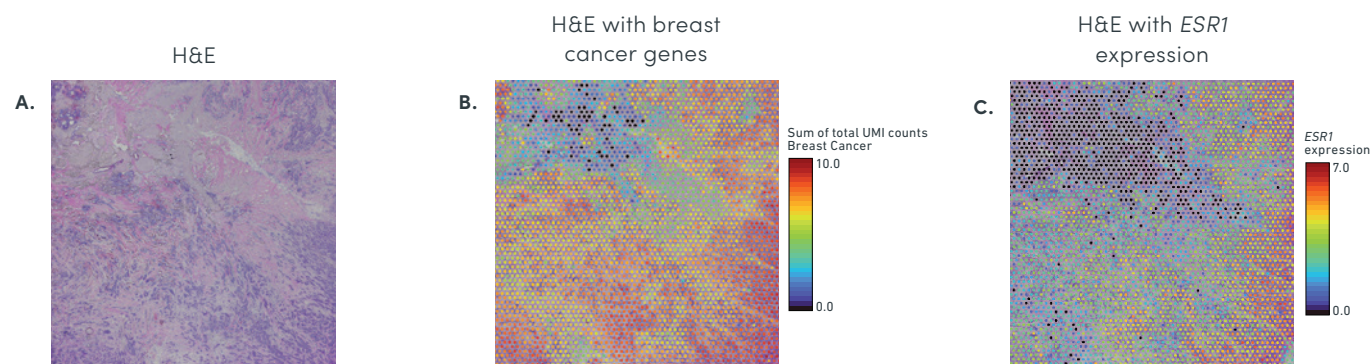


Figure 3. Curated cancer content refines spatial gene expression analysis. A human breast cancer tissue section was H&E stained and processed using the Visium Spatial Gene Expression workflow, then enriched for genes of interest using Targeted Gene Expression with the Human Pan-Cancer Panel. Shown are the H&E image (A), H&E image overlaid with total UMI counts for 196 genes from the breast cancer gene category of the Human Pan-Cancer Panel (B), and H&E image overlaid with *ESR1* expression level (C).

Pathway	Genes
B-cell receptor signaling	50
FoxO signaling	57
Glucagon signaling	56
Hedgehog signaling	65
Hippo signaling	56
Insulin signaling	45
Jak-STAT signaling	124
MAPK signaling	165
mTOR signaling	51
NF-kappa B signaling	46
Notch signaling	87
p53 signaling	49
PI3K-Akt signaling	211
Ras signaling	150
T-cell receptor signaling	84
TGF-beta signaling	79
TNF signaling	70
Toll-like receptor signaling	56
Wnt signaling	84

Table 1. Panel design highlights: pathway genes. Selection of key pathway gene categories included in the Pan-Cancer Panel.

Cancer tissue type	Genes
Acute myeloid leukemia	110
Adenocarcinoma	6
Bladder cancer	180
Brain cancer	20
Breast cancer	196
Cervical cancer	34
Colorectal cancer	143
Endometrial cancer	25
Epithelial ovarian cancer	90
Esophageal adenocarcinoma	139
Gastric cancer	24
Head and neck cancer	41
Kidney cancer	15
Liver cancer	16
Lung cancer	177
Melanoma	70
Non-small cell lung cancer	55
Oral cancer	19
Ovarian cancer	140
Pancreatic cancer	94
Prostate cancer	128
Rectal cancer	6
Stomach cancer	43
Testicular cancer	9
Thyroid cancer	53

Table 2. Panel design highlights: cancer tissue types. Selection of key cancer tissue-type categories included in the Pan Cancer Panel.

Cellular process	Genes
Acetylation	306
Apoptosis	93
Cell cycle	106
Chromosomal rearrangement	98
Differentiation	95
DNA repair	74
DNA replication	62
Focal adhesion	119
Natural killer cell-mediated cytotoxicity	76
Transcription regulation	283
Ubiquitin-mediated proteolysis	57

Table 3. Panel design highlights: cellular processes. Selection of key cellular-process gene categories included in the Pan-Cancer Panel.

Applications

- Profile response to targeted and combination therapies
- Inform clinical trials with functional biomarker analysis
- Tumor-immune cell interactions
- Tumor heterogeneity and microenvironment
- Mechanisms of tumorigenesis and metastasis

Products	Product code
Target Hybridization Kit, 16 rxns	1000248
Library Amplification Kit, 16 rxns	1000249
Human Pan-Cancer Panel, 4 rxns	1000260
Human Pan-Cancer Panel, 16 rxns	1000247
Custom Panel Designer bit.ly/10xgenomics-custom-designer	Visit Designer

Compatible products

Chromium Single Cell Gene Expression
10xgenomics.com/single-cell

Chromium Single Cell Immune Profiling
10xgenomics.com/vdj

Visium Spatial Gene Expression
10xgenomics.com/spatial-gene-expression

Curated content sources

1. C Kandoth et al., Mutational Landscape and Significance Across 12 Major Cancer Types. *Nature*. 502, 333–339 (2013).
2. KA Hoadley et al., Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*. 173, 291–304e6 (2018).
3. MH Bailey et al., Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*. 173, 371–385e18 (2018).
4. The Cancer Genome Atlas Research Network (TCGA).

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