

Comprehensive panel curated for cancer research

Accelerate cancer research with targeted gene expression

As cancer 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 Cancer Genome Atlas Program (TCGA) and recent publications, the 10x Genomics Human Pan-Cancer Panel for targeted gene expression enables you to profile key pathways and biomarkers critical to tumor biology, the tumor microenvironment, and immune response in both single cells and intact tissue sections*.

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 Solutions, as well as Visium Spatial Gene Expression Solution*, the Human Pan-Cancer Panel enables comprehensive and efficient characterization of your cancer samples.

Highlights

- Contains 1,253 target genes for profiling a wide variety of tumors, the tumor microenvironment, and tumor immune status
- Curated content from The Cancer Genome Atlas Program (TCGA), recent publications, and cancer experts, spanning 33 cancer types, key biomarkers, pathways, and cell-type signatures
- 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, frozen, or fixed cell lines and tissues

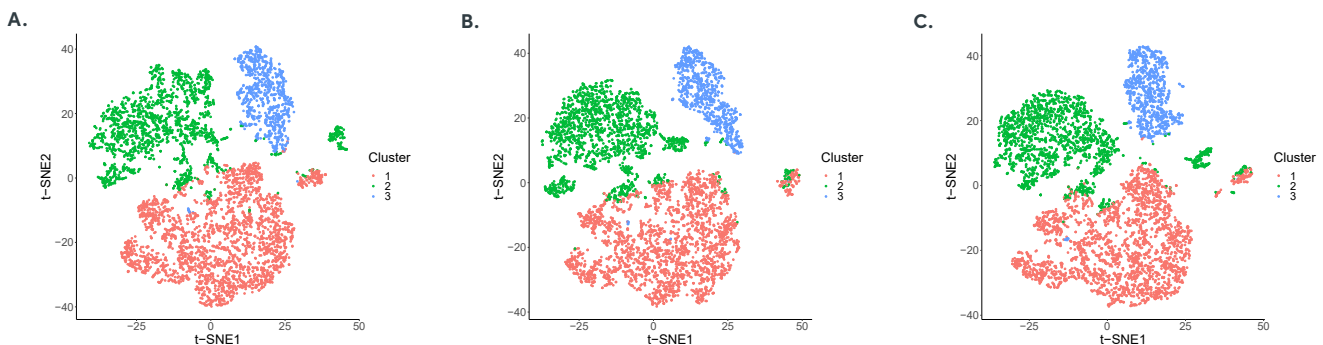


Figure 1. Cell-type clustering and annotation is preserved in targeted samples Representative data from approximately 6,000 glioblastoma cells run with the Chromium Single Cell Gene Expression 3' v3 Workflow. A. Whole transcriptome analysis identified three major cell type clusters, when sequenced at 70,000 reads per cell (about 60% sequencing saturation). B. Cell clustering based on an in silico subset of genes found in the Human Pan-Cancer Panel. C. Cell clustering based on target enrichment for genes found in the 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.

Pathway	Genes
B-cell receptor signaling	50
cAMP signaling	60
Chemokine signaling	48
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 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
Colon cancer	8
Colorectal cancer	143
Endometrial cancer	25
Epithelial ovarian cancer	90
Esophageal adenocarcinoma	139
Esophageal cancer	20
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
Urinary bladder cancer	3

Table 2. Panel Design Highlights: Cancer Tissue Types Key cancer tissue-type categories included in the Pan Cancer Panel

Cellular Process	Genes
Acetylation	306
Apoptosis	93
ATP-binding	195
Cell cycle	106
Central carbon metabolism in cancer	65
Chromosomal rearrangement	98
Differentiation	95
DNA repair	74
DNA replication	62
Focal adhesion	119
Natural killer cell-mediated cytotoxicity	76
Nucleotide excision repair	56
Nucleotide-binding	222
Proteoglycans in cancer	65
Transcription regulation	283
Transcriptional misregulation in cancer	115
Ubiquitin-mediated proteolysis	57

Table 3. Panel Design Highlights: Cellular Processes Key cellular-process gene categories included in the Pan-Cancer Panel

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	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

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

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

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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