# 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 predesigned 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 $10 x$ 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 |
| Ubanscriptional misregulation in cancer | 115 |
| Cbin-mediated proteolysis | 57 |

Table 3. Panel Design Highlights: Cellular Processes Key cellularprocess 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 | 1000247 |
| 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

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## 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, 371385e18 (2018).
4. The Cancer Genome Atlas Research Network (TCGA)

## Resources from 10x Genomics

We are dedicated to helping you get the most out of your 10x Genomics system by offering multiple helpful resources:

## 10x University

Immerse yourself in 10x University, a comprehensive step-by-step learning and training environment containing video tutorials and trainings.
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[^0]:    Visium Spatial Gene Expression Solution*
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