



# nCounter® GX Human Cancer Reference Kit



## Product Highlights

### Simple

- No need for cross-referencing databases

### Highly Curated

- Our expert bioinformaticists use a very rigorous process in selecting the most meaningful set of genes

### Efficient

- Multiplexed assay profiles 230 human cancer-related genes in one reaction

### Cost-effective

- Gold standard data at a fraction of the cost

### Quick Turnaround Time

- Complete kit with all consumables ready to ship next-day

## A Gene Set You Can Count On

The **nCounter GX Human Cancer Reference Kit** is a comprehensive set of 230 human cancer-related genes and six internal reference genes. These represent a broad range of relevant cancer-related processes, including:

- Cell cycle
- Cell differentiation
- Cell proliferation
- Apoptosis
- Angiogenesis
- Immune response

The methodology for selecting the genes included in the kit began with a broad list of candidate cancer-related genes compiled from multiple databases. The candidate gene list was then refined by using several criteria, primarily

verification that the expression levels of the genes included in the gene set changed in cancer samples.

Verification was performed using several public databases such as MSigDB, a repository of gene expression data developed by researchers at the Massachusetts Institute of Technology and the Broad Institute<sup>1</sup>. Other public databases were used to obtain functional gene expression information for each gene. The final nCounter Virtual Cancer Reference Gene Set consists of 230 cancer-related genes and 6 internal reference genes.

For the gene list and additional information about this gene set, visit the nCounter Pre-built Panels product page at [www.nanostring.com](http://www.nanostring.com).

1. Subramanian A, Tamayo P, et al. (2005) Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* 102(43):15545-15550.

## nCounter Analysis System Overview

The nCounter Analysis System from NanoString offers a cost-effective way to easily profile hundreds of gene transcripts simultaneously with high sensitivity and precision. The digital detection of target molecules and high levels of multiplexing eliminate the compromise between data quality and data quantity, bringing better sensitivity, reproducibility, and linearity to your results. It is ideal for studying defined gene sets across a large sample set, e.g., microarray validation, pathway analysis, biomarker validation, and splice variation analysis.

The system utilizes a novel digital technology that is based on direct multiplexed measurement of gene expression and offers high levels of precision and sensitivity (<1 copy per cell). The technology uses molecular “barcodes” and single molecule imaging to detect and count hundreds of unique transcripts in a single reaction.

## Included

| Genes List |        |         |          |        |          |           |        |
|------------|--------|---------|----------|--------|----------|-----------|--------|
| ABC1       | CDC25B | ERBB2   | HCK      | MCL1   | PCNA     | SPI1      | WNT1   |
| ABL1       | CDC25C | ERBB3   | HDAC1    | MET    | PCTK1    | SPP1      | WNT10B |
| AKT1       | CDH1   | ERBB4   | HIF1A    | MLH1   | PDGFA    | STAT1     | WT1    |
| AKT2       | CDH11  | ERCC2   | HMMR     | MLL    | PDGFRA   | STAT3     | XPC    |
| APC        | CDK4   | ERCC4   | HRAS     | MMP1   | PDGFRB   | SYK       | XRCC5  |
| AR         | CDK4   | ESR1    | HSP90AB1 | MMP14  | PIK3CA   | TAL1      | YES1   |
| AREG       | CDK6   | ETS1    | IFNGR1   | MMP2   | PIM1     | TEK       | YY1    |
| ATM        | CDKN1A | ETS2    | IGF1     | MMP3   | PLA2G2A  | TERT      |        |
| BCL2       | CDKN2A | ETV1    | IGFBP2   | MMP9   | PLAT     | TFDP1     |        |
| BCL2A1     | CDKN2B | ETV6    | IGFBP3   | MPL    | PLAUR    | TFE3      |        |
| BCL2L1     | CDKN2C | FANCG   | IGFBP6   | MSH2   | PLG      | TFRC      |        |
| BCL3       | CEBPA  | FAS     | IL1A     | MSH6   | PML      | TGFA      |        |
| BCL6       | CHEK1  | FAT1    | IL1B     | MST1R  | PPARG    | TGFB1     |        |
| BCR        | COL1A1 | FGF1    | IL4      | MTA1   | PRKAR1A  | TGFB1     |        |
| BIRC2      | CSF1R  | FGF2    | IL6      | MUC1   | PTEN     | TGFB2     |        |
| BIRC5      | CSF3   | FGFR1   | IL8      | MYB    | PTGS2    | TGFB3     |        |
| BLM        | CSF3R  | FGFR2   | IRF1     | MYBL2  | PTHLH    | THPO      |        |
| BMI1       | CSK    | FGFR3   | ITGB1    | MYC    | PTK7     | TIMP1     |        |
| BRAF       | CTGF   | FGFR4   | JUN      | MYCL1  | PTPN11   | TIMP2     |        |
| BRCA1      | CTNNB1 | FGR     | JUNB     | MYCN   | PTPRG    | TIMP3     |        |
| BRCA2      | CXCL9  | FLT1    | KDR      | NF1    | RAD54L   | TNF       |        |
| CASPI0     | CYP1A1 | FLT3    | KIT      | NGFR   | RAF1     | TNFRSF10B |        |
| CASP2      | DAP3   | FOLR1   | KRAS     | NOTCH1 | RARA     | TNFRSF1B  |        |
| CAV1       | DAPK1  | FOS     | LICAM    | NPM1   | RB1      | TNFSF10   |        |
| CCNA2      | DEK    | FOSL2   | LAMB1    | NQO1   | REL      | TOP1      |        |
| CCND1      | DLC1   | FRZB    | LCK      | NRAS   | RET      | TOP2A     |        |
| CCND2      | E2F1   | FYN     | LIF      | NTRK1  | RRM1     | TP53      | CLTC*  |
| CCND3      | E2F3   | GADD45A | LMO1     | NTRK2  | S100A4   | TPR       | GAPDH* |
| CCNE1      | EGF    | GAS1    | LMO2     | NTRK3  | SERPINE1 | TYMS      | GUSB*  |
| CD34       | EGFR   | GATA1   | LYN      | NUMA1  | SFPQ     | TYRO3     | HPRT1* |
| CD44       | EGR1   | GNAS    | MAP3K8   | OGG1   | SIAH1    | WEE1      | PGK1*  |
| CDC2       | EPS8   | GRB7    | MAPK10   | PCNA   | SOD1     | WFDC2     | TUBB*  |

\*Internal Reference Genes

## Assay Performance

| Description                             | Specifications   |
|---|--|
| Level of multiplexing                   | 230 genes known to be differentially expressed in human cancer                                       |
| Recommended amount of starting material | 100 ng or less of total RNA, or lysate from ~10,000 cells  |
| Sample types supported                  | Total RNA, cell lysates in GITC, FFPE-derived total RNA and PAXgene lysed whole blood, amplified RNA |
| Limit of detection                      | 15 zeptomole spike-in control (-1 copy per cell); 90% of the time                                    |
| Fold change sensitivity                 | > 1.5 fold (> 5 copies per cell)<br>> 2 fold change (> 1 copy per cell)                              |
| Spike correlation                       | R <sup>2</sup> ≥ 0.95  |
| Linear dynamic range                    | 7 x 10 <sup>5</sup> total counts   |
| Controls                                | 6 positive and 8 negative in each reaction   |

## Ordering Information

| Description                            | Quantity / Use | Part Number (P/N) |
|--|----------------|-------------------|
| nCounter GX Human Cancer Reference Kit | 12 assays      | XT-GXA-CR1-12     |
|  | 24 assays      | XT-GXA-CR1-24     |
|  | 48 assays      | XT-GXA-CR1-48     |
|  | 96 assays      | XT-GXA-CR1-96     |

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