WT1 Detection by RNAscope™ in Human Cancers



Wilms' tumor gene (WT1) is expressed in various human malignancies, including both hematological and solid cancers. While expression is found in normal tissues, overexpression of *WT1* is a common feature in various cancers as its protein product is a potent transcriptional regulator acting as a tumor suppressor. Antibody-based detection of transcription factors has been historically difficult due to the rigid structure of protein-protein interactions, which may mask unidentified structural configurations. The RNAscope RNA *In Situ* Hybridization Platform, including chromogenic and fluorescent detection reagents and target-specific probes, allows for the detection of *WT1* at the single mRNA molecule level in individual cells, all while providing spatial and morphological context. The double Z probe design allows for simultaneous signal amplification and suppression of non-specific background staining, ensuring target-specific detection.

Figure 1: RNAscope detection of WT1 in normal and malignant tissues



Image Footnote:

- A Papillary serous adenocarcinoma of uterus (uterine cancer) high expression
- B Papillary serous adenocarcinoma of uterus (uterine cancer) low expression
- C Infiltrating ductal carcinoma (breast cancer)
- D Normal fallopian tube

Expression of WT1 was interrogated in both tumor and normal archival Tissue Microarrays (TMA) as well as cell lines on a Cell Pellet Array (CPA) using RNAscope 2.5 Brown Detection on an automated instrument using standard pretreatment conditions. The types of tumor and normal tissues included on the TMAs are listed in Table 1 and Table 2, respectively. The cell lines included in the CPA are listed in Table 3.

Materials and Methods

Study Samples

- Tumor TMA (120 cores, 1 slide)
- Normal TMAs (75 cores , 2 slides)
- Cell Pellet Array (60 cores, 2 slides)

Instrument, Assay, and Protocol

Instrument: Leica BOND RX

RNAscope Assay

• BOND RNAscope Detection Reagents - Brown (Cat. No. 201000)

Target Probe: HS-WT1 (Cat. No. 415588)

Standard RNAscope LS Brown assay pretreatment conditions were used as follows:

- Staining Protocol: RNAscope DAB ISH
- Preparation: Bake and Dewax
- Protease: 15 mins @ 40°C
- HIER: RNAscope Target Retrieval 15 mins @ 95°C

Expression of WT1 in CPA

Figure 2: RNAscope detection of WT1 in various cell lines



Table 1: Cell lines included on CPA			
PANEL 1		PANEL 2	
Tissue Type	Cell Line Name	Tissue Type	Cell Line Name
Breast Cancer	HS-578T BT-549 MCF7 T-47D MDA-MB-231 MDA-MB-468	Breast Cancer	SF-295 PFSK-1 A172 SW1088 DAOY U251-MG
Lung Cancer	H23 H226 H322 H460 H522 A549 EKVX HOP-62	Skin Cancer	UACC-62 A431 MALME-3M M14 SK-MEL-2 SK-MEL-5 SK-MEL-28 SNU-16
Prostate Cancer	HOP-92 PC-3 DU-145 LNCAP 22RV1	Cancer Pancreatic Cancer	SNU-1 KATOIII MIAPACA2 PANC1 BXPC3
Colon Cancer	SNU-C1 COLO205 HT29 SW-620 HCT-15 HCT-116	Leukemia	RPMI-8226 HL-60 MOLT-4 CCRF-CEM K-562 A498
Ovarian Cancer	SK-OV-3 IGR-OV1 PA-1 CAOV-3 SW626 OVCAR-3 OVCAR-8	Renal Cancer	CAKI-1 ACHN 786-0

Green Shaded Lines: RT-PCR analysis was performed

Image Footnote:

- A PFSK-1 (glial tumor)
- B COLO 205 (colon cancer)
- C UACC-62 (skin cancer)
- D H23 (lung cancer)

Expression of WT1 in Tumor TMA

Figure 3: RNAscope detection of WT1 in human cancers



Image Footnote:

A - Colorectal adenocarcinoma

B - Papillary serous adenocarcinoma of uterus (uterine cancer)

Table 2: Cancer types included in our tumor TMA			
Breast Bladder Colorectal Head and Neck Ovary Lung			
Prostate Melanoma Kidney Pancreas			
Figure 6: Tumor TMA layout			
4 2 3 4 5 6 7 8 9 10 11 12 13 14 45 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 48 50 51 52 53 54 55 57 58 59 60			
61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 85 87 88 89 90			
91 92 93 94 95 96 97 98 99 100 301 107 103 104 105 106 407 108 109 110			
111 112 113 114 115 116 117 118 119 120			

Expression of WT1 in Normal TMA

Figure 4: RNAscope detection of WT1 in normal human tissues



Image Footnote: A - Kidney (glomeruli) B - Uterus (myometrium)

Table 3: Tissues included in normal TMAs			
Adrenal Gland Breast Bladder Cerebellum			
Cerebrum Colon Cervix Fallopian Tube			
Gallbladder Kidney Liver Lung Pancreas Prostate			
Seminal Vesicle Skin Spleen Stomach			
Testis Thyroid Uterus			
Figure 9: Normal TMA scematic			
13 14 15 16 17 18 6 7 8 9 10 19 20 21 22 23 24 11 12 13 14 25 26 27 28 29 30			
31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60			

Cell Pellet Expression Analysis: RNAscope Validation with qPCR

Orthogonal validation of RNAscope vs. RT-PCR for WT1 expression was performed, demonstrating the specificity and quantitative nature of the RNAscope methodology (Figure 11). Expression by RNAscope RNA ISH was compared with qPCR across multiple cell pellet samples. RNAscope dot number was found to correlate with RT-PCR quantitation for WT1.

Figure 11: RNAscope In Situ Hybridization detects WT1 mRNA expression levels that correlate with RT-PCR for WT1 while providing tissue context and morphology



Identify Therapeutic Biomarkers with RNAscope with Pharma Assay Services

The RNAscope In Situ Hybridization Platform, including detection reagents and target-specific probes, is a robust technology that allows for the identification of RNA expression patterns and localization at the single cell level with spatial and morphologic context. RNAscope is highly sensitive and specific due to its double Z probe design, resulting in an extremely high signal-to-noise ratio of staining in FFPE tissues relative to traditional RNA ISH, allowing researchers to visualize, localize, and quantify biomarker expression simultaneously. The technology is readily available on automated staining platforms, including the Leica Bond and Ventana Ultra platforms, for ease of use, high reproducibility, and seamless fit into the research laboratory workflow. Furthermore, RNAscope provides labs with the opportunity to add new biomarkers to their experiments and provide better options for problematic IHC antibodies. See for yourself with the WT1 Dataset, which includes *WT1* expression in various tumors (120 TMA cores), normal tissues (75 TMA cores), and cell lines (60 CPA cores).



To request a quote, contact: acd_sales@bio-techne.com

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