



Bruker Cellular Analysis

nCounter[®] Multiomics Expression Analysis

University of Wisconsin
Sponsored by Translational Research Initiatives in Pathology Laboratory (TRIP)
February 24, 2026



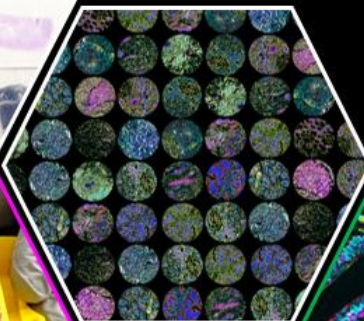
HISTOLOGY



- Process/embed and sectioning
 - Formalin-fixed
 - Frozen

- Tissue decalcify
- RNase-free technique
- H&E, other routine stains
- Special stains

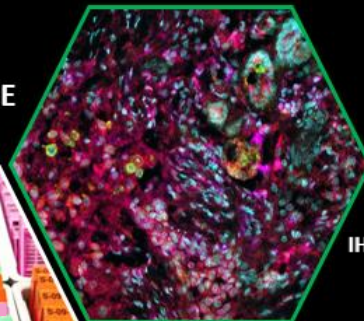
TMA CREATION



CONTROL TISSUE REPOSITORY



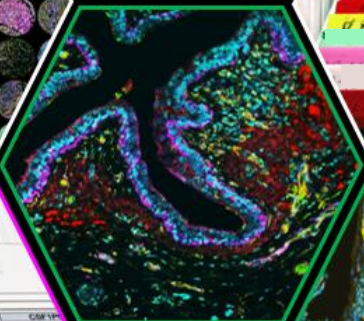
IHC/ISH



IHC & ISH:

- Chromogenic (BF)
- Immunofluorescent (IF)
- Automated or manual
- Single or multiplex
- Validation & optimization of antibodies

IMAGING



- Imaging Systems:
- Vectra
 - Nuance
 - APERIO

MOLECULAR SERVICES



DNA/RNA extraction:

- FFPE
- Fresh tissue

Tissue collection:

- FFPE sections/curls
- Tissue block punch
- Macrodissections

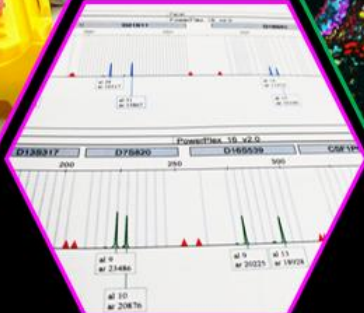
Molecular Profiling

- nCounter MAX

Short tandem repeat (STR) analysis:

- Cultured human cells
- Extracted DNA

HUMAN CELL LINE AUTHENTICATION

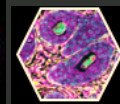
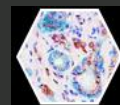
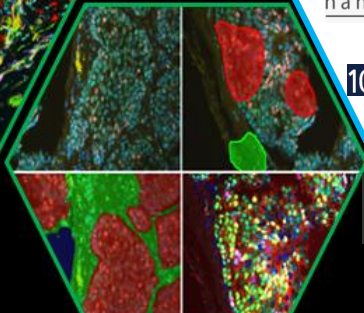


SPATIAL -OMICS

- GeoMx: RNA and protein
- Visium w/ CytAssist
- Visium HD for higher resolution
- Xenium and MERSCOPE support



MORPHOMETRIC ANALYSIS



- Board-certified pathologist
- Certified histotechnologist
- Experienced staff



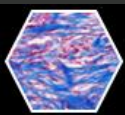
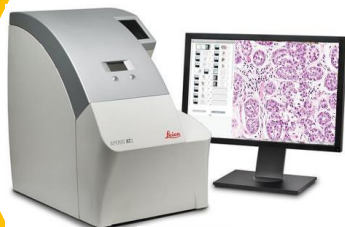
Spatial Biology Resources

Brightfield

Whole slide scanner

- High throughput (400 slides)
- 20x and 40x magnification
- Z-stacking capability
- ImageScope software

Aperio AT2



Multispectral

Vectra



Automated scanner

- Integrated machine learning software
- Brightfield and fluorescent
- 4x to 40x magnification
- Fields of view and TMA
- InForm software for analysis

Microscope

- Brightfield and fluorescent
- 4x to 40x magnification
- Nuance/ InForm software

Nuance

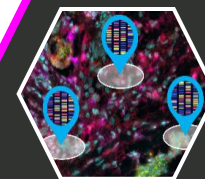
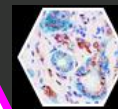


Spatial -Omics

GeoMx DSP

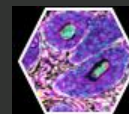


Visium with CytAssist



High-plex transcriptomics and proteomics

- Whole transcriptome analysis
- 1400+ proteome mapping
- 20x magnification
- Visium HD for higher resolution
- Xenium and MERSCOPE support
- Partnership with UW Biotech Center for NGS workflows



Workflow for project submission

Molecular Profiling: nCounter



Request consultation (Karla and nCounter rep)

- Amount and type of samples*
- Type of panel
- Need RNA/DNA extractions
- nCounter QC: DV200/ Nanodrop
- IRB documents (if applicable)

- nCounter reagents:
Request quote from NanoString

Request
budget
estimates
from TRIP

Submit
project
request(s);
create
accounts

- TRIP: iLab
- NanoString University: to start learning nSolver software for data analysis

- nCounter kits
- Research samples*
- E-mail sample list and QC results

Coordinate
drop off of
materials

TRIP staff will
follow up with
questions/
project status

Data analysis
with free
nSolver
software

- Investigator installs on personal computer
- Video tutorials available

*Clinical blocks/slides are requested through Surgical Pathology and will come directly to TRIP

Agenda

- nCounter overview of technology: Seth Meyers
- Wheeler lab case study presentation: Dr. Bridget Crossman
MerTK Modulates the TNBC Tumor Microenvironment
- Bruker nCounter Office hours
 - HSLC 1229
 - 2pm-4pm Cole Sweeney Regional Account Manager

Thank you to the TRIP Lab!

- Rebecca Baus
- Maggie Baus
- Toshi Kinoshita
- Anu Singh
- Karla Esbona, PhD – Director

trip@pathology.wisc.edu

Lab: 2214 WIMR

1111 Highland Avenue, Madison, WI

<https://research.pathology.wisc.edu/trip-home/>

nCounter[®] Analysis System

Seth Meyers

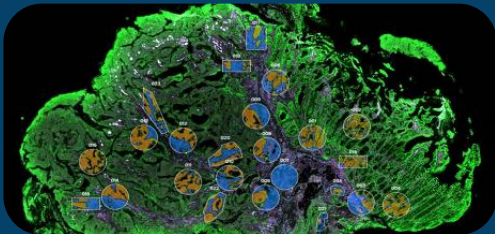
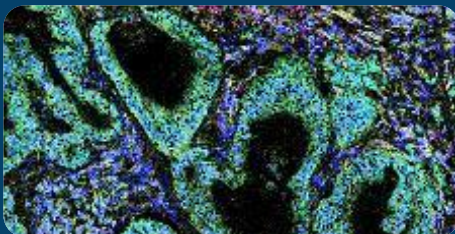
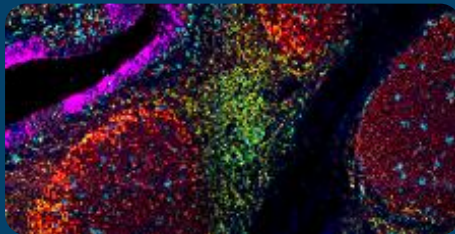
District Sales Manager NA East – Bruker Cellular Analysis

February 24, 2026



Platforms optimized to deliver industry-leading performance for your application objective

Platforms excel with FFPE tissues and diverse sample or disease types

Spatial biology			
Bulk	Regional	Single Cell and Sub-Cellular	
 nCounter®  • Robust, direct molecule detection • Rapid turnaround, minimal hands-on time • Flexible multiomic assays • Simplified data analytics	 GeoMx® DSP  • High Plex, whole transcriptome RNA, 1,200+ protein multiomics • Fast and flexible platform • High sensitivity	 CosMx™ SMI  • High Plex detection 6K→19K RNA, 70+ proteins • Accurate cell segmentation • Comprehensive data analysis with AtoMx™ SIP	 CellScape™  • Best in class resolution • Highest dynamic range • Robust, straightforward assay • Flexible assays, high-plex ~100 proteins

The nCounter® Platform is the Most Innovative Targeted Gene Expression and Multiomics Technology on the Market Today

1994



Microarrays
Pre-defined hybridization

1996



Quantitative PCR

2006



RNA Sequencing
Sequence reads

2008
2013
2022



nCounter®
Direct Digital Detection

nCounter® Gene Expression Analysis
Leverages amassed sequencing knowledge
Generates high-impact data: Biological answers vs. just data
Direct Detection: Robust & Reproducible

**>8,000
peer reviewed
publications utilize
nCounter**

nCounter® Analysis System

Accelerate your biomarker discovery
with confidence & peace of mind



ROBUST PERFORMANCE

- Direct hybridization provides rapid sample to answer
- compatible with most bulk sample types of any kind

THEMATIC PANELS & CUSTOM OPTIONS

- Choose from a menu of 25+ pre-built panels
- Options to create your own custom product or add-on to any pre-built panel

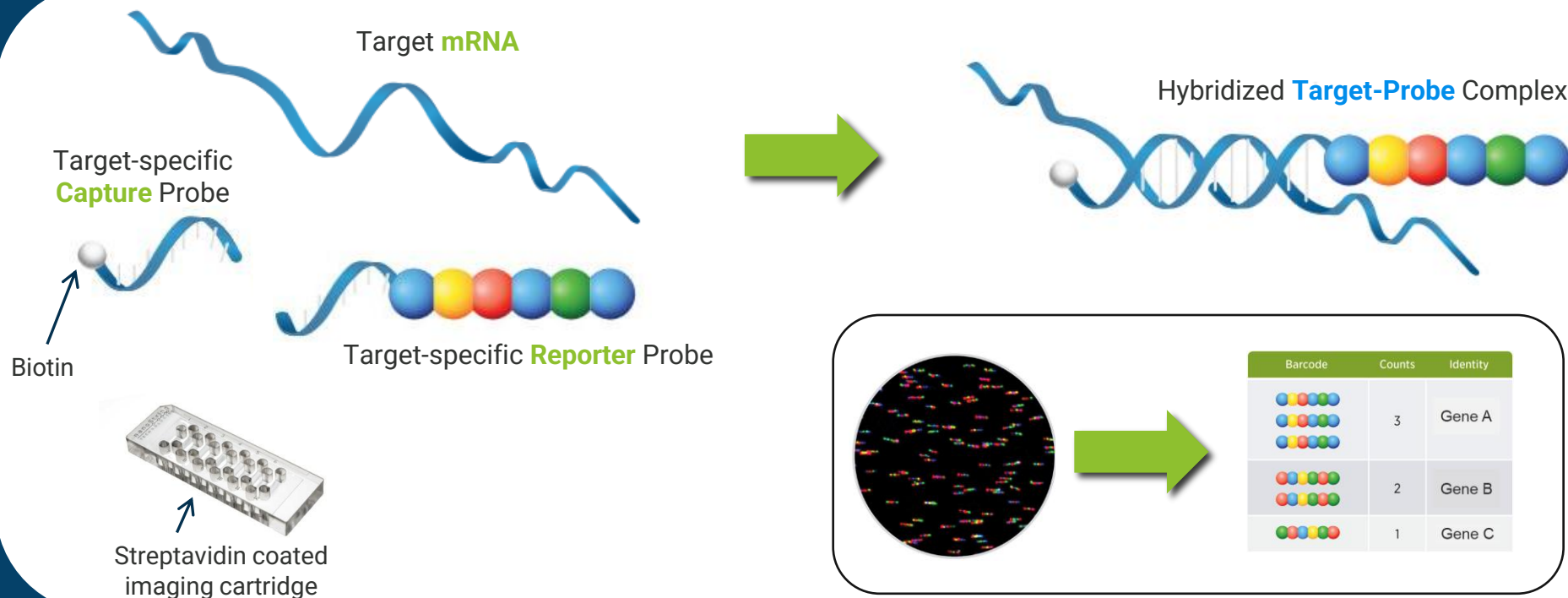
MULTIOMICS CAPABILITIES

- Profile RNA + Protein from the same sample in the same run with a user-friendly protocol

SIMPLIFIED DATA ANALYSIS

- Multiple easy-to-use options to get you from sample to insight faster and easier than ever before.

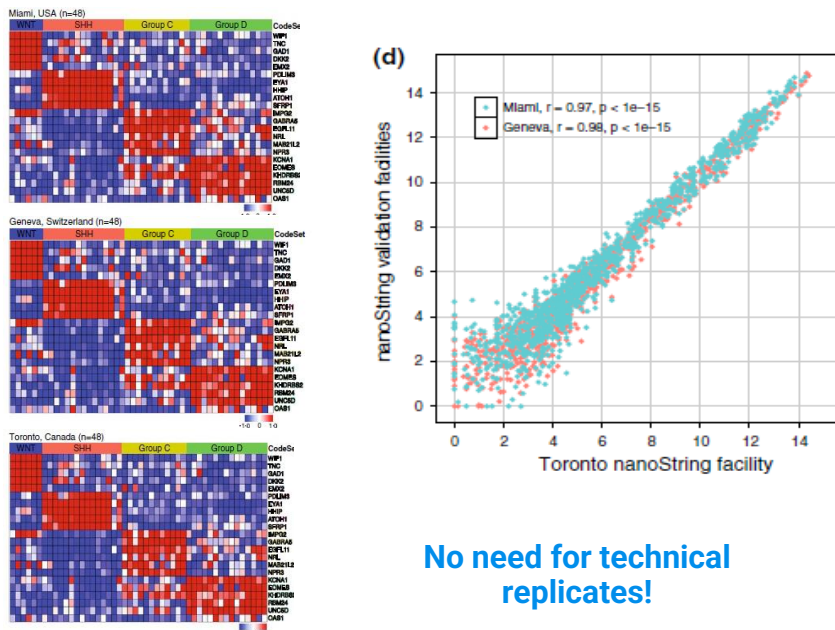
Direct digital detection removes the need for enzymes and prevents amplification bias



Enzyme-free, hybridization-based technology delivers best-in-class detection on biobanked (FFPE) samples

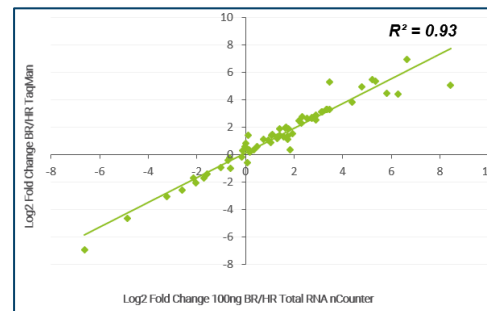
nCounter chemistry and instrumentation is incredibly reproducible, reliable, and correlative

3 labs, 3 countries, *same result*



Rapid, Reliable, & Reproducible Molecular Sub-grouping of Clinical Medulloblastoma Samples
Northcott P.E. et al., *Acta Neuropathologica*

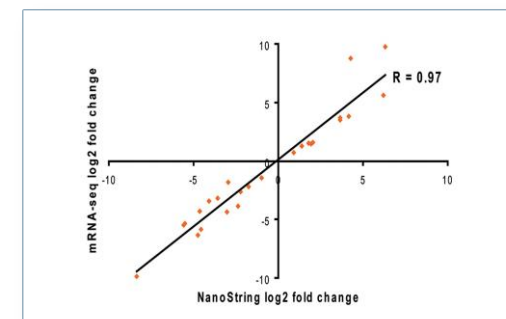
nCounter – qPCR / RNAseq



PCR MAQC data from: Canales et al. *Nature Biotechnology* 24, 1115 - 1122 (2006)

High correlation of nCounter vs TaqMan (qPCR).
Note that higher plex of nCounter allows for deeper pathway-biology analysis than qPCR

Excellent agreement of
Illumina RNA-Seq data
demonstrates clear digital-
path for translation



Sun et al., PLoS ONE, February 2011

The gold standard for FFPE – nCounter is ready for your challenging sample types

Broad Sample Compatibility

PURIFIED RNA

FFPE

FRESH FROZEN



BLOOD

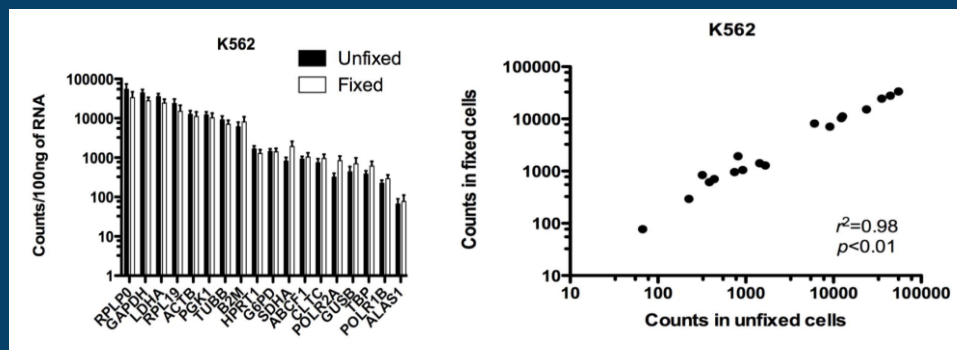
PLASMA

SERUM

CELL LYSATES



Even Low-Quality Samples Succeed

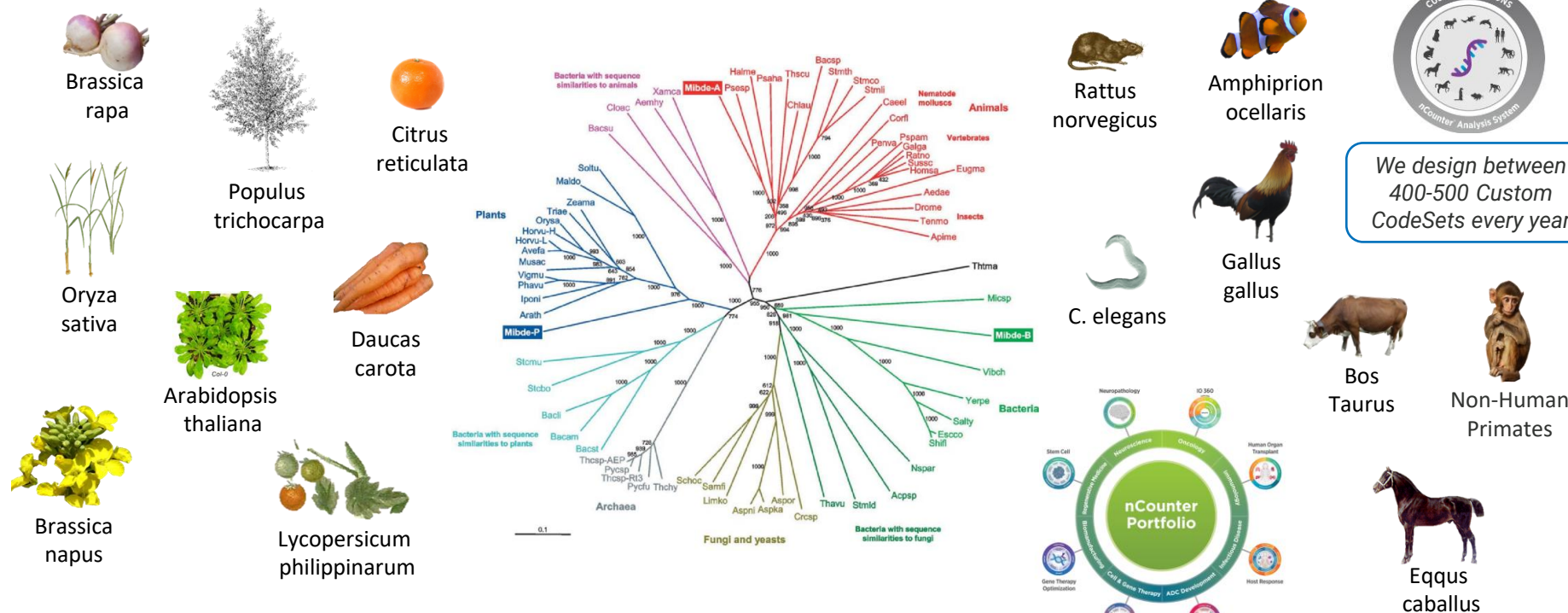


Decades Old FFPE Directly Correlates with Fresh Frozen

“quantitation of mRNA transcripts by [nCounter], but not by RT-qPCR, is equally efficient in fixed and unfixed cells.”

Russell JN, Clements JE, Gama L (2013)
Quantitation of gene expression in formaldehyde-fixed and fluorescence-activated sorted cells.
PLoS ONE 8(9):e73849.

Your experts with probe design. Any Target. Any Species.



Background

Biomarker discovery requires a robust and sensitive method for multiplexing and analyzing gene expression in diverse tissue types with varying sample quality

Research Question

What is the performance of the nCounter platform on key clinical concerns including: technical and biological replicates, sample quality, sample quantity, stability for cartridges and CodeSets, freeze-thaw, and lot-to-lot variability?

Results

nCounter system meets all performance criteria to qualify as a reliable platform for clinical trial samples as determined through extensive testing by a major biopharmaceutical company

"This study demonstrates nCounter offers several key advantages:

- Sensitivity,
- Reproducibility,
- Technical robustness, and
- Utility for clinical application."

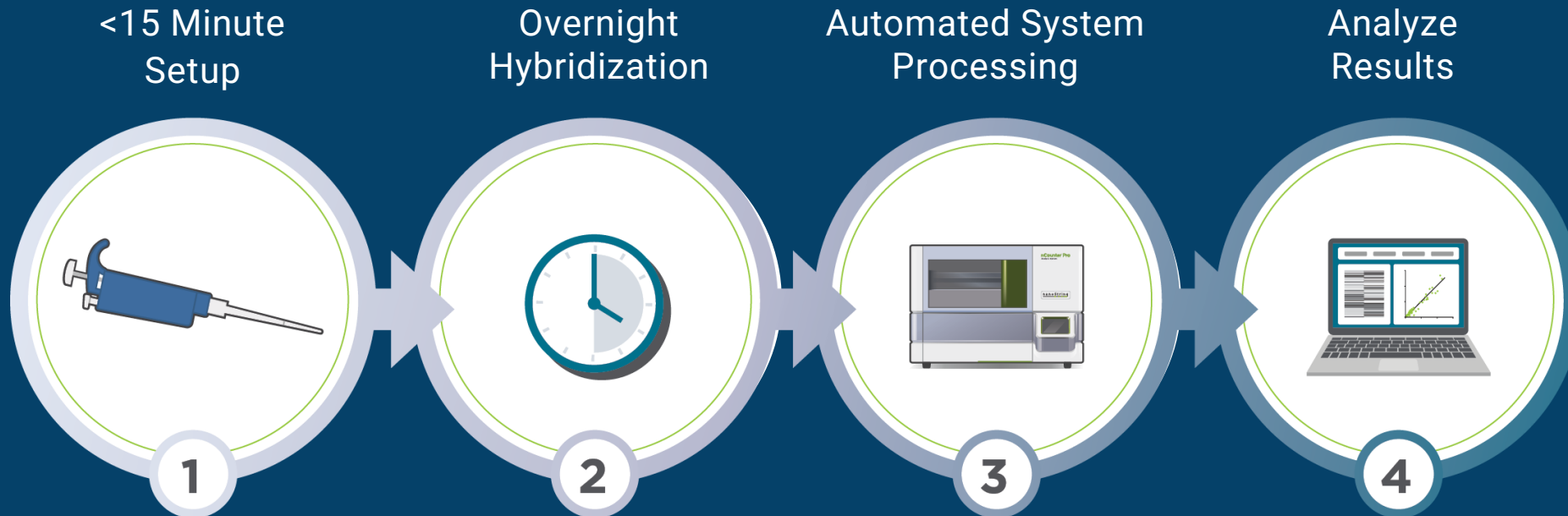


Margaret H. Veldman-Jones
AstraZeneca Oncology &
Discovery Sciences Innovative Medicine
Macclesfield, UK and Waltham, MA
Senior Cell Scientist

Evaluating Robustness and Sensitivity of the NanoString Technologies nCounter Platform to Enable Multiplexed Gene Expression Analysis of Clinical Samples (*Cancer Research*, 2015)



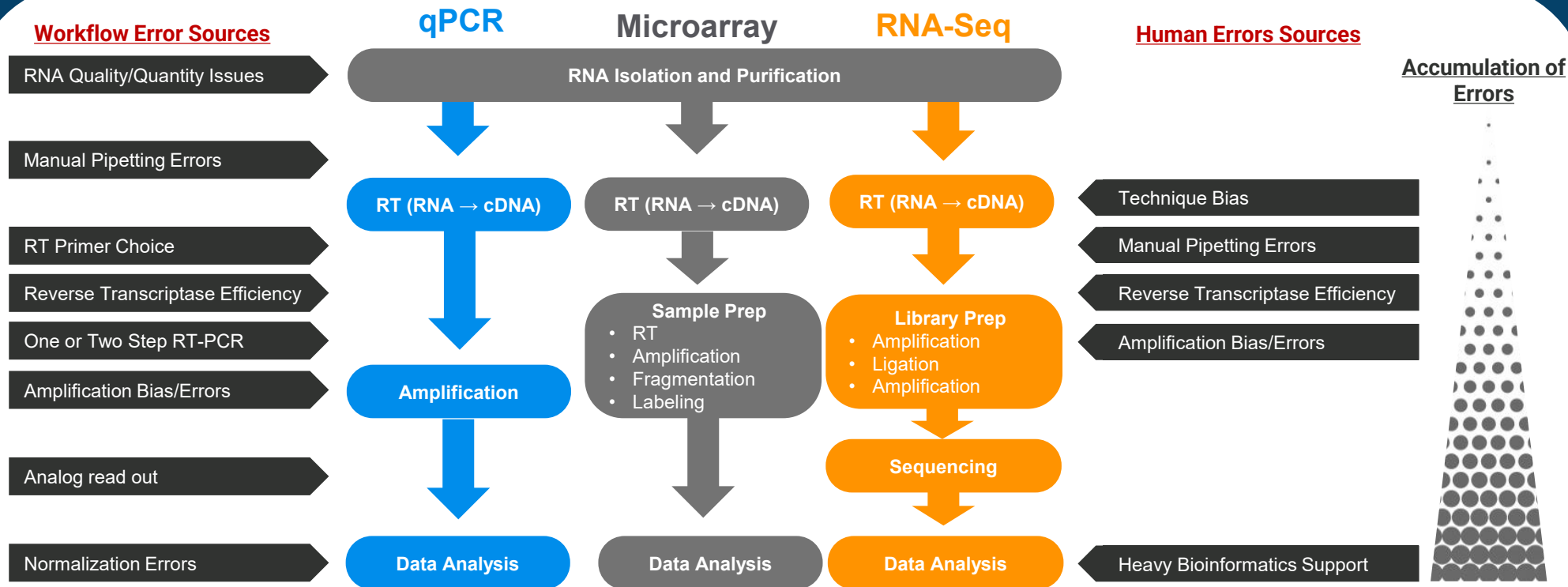
Sample to Analyzed result in less than 24 hours (~22hrs) for Gene Expression Panels



Accelerate Project Timelines with nCounter Gene Expression Automated Workflow

More plex than qPCR, more specific than microarrays, and more sensitive RNA-Seq. Easier workflow than all three.

Complex workflows contain numerous steps where biases & errors can be introduced into the data



nCounter does not require Amplification or Library Prep and has minimal hands-on steps - creating a more robust and error-free workflow.

Biomarker Development PanCancer IO360 Panel



Journal of Translational Medicine



THE UNIVERSITY OF
SYDNEY

Cross-platform comparison of immune signatures in immunotherapy-treated patients with advanced melanoma using a rank-based scoring approach

Yizhe Mao^{1,2,3†}, Tuba N. Gide^{1,2,3†}, Nurudeen A. Adegoke^{1,2,3}, Camelia Quek^{1,2,3}, Nigel Maher^{1,2,3,4}, Alison Potter^{1,2,3,4}, Ellis Patrick^{5,6}, Robyn P. M. Saw^{1,2,7,8}, John F. Thompson^{1,2,7,8}, Andrew J. Spillane^{1,2,8,9}, Kerwin F. Shannon^{1,7,8,10}, Matteo S. Carlino^{1,2,11}, Serigne N. Lo^{1,2}, Alexander M. Menzies^{1,2,8,9}, Inês Pires da Silva^{1,2,3,10}, Georgina V. Long^{1,2,3,8,9†}, Richard A. Scolyer^{1,2,3,4†} and James S. Wilmott^{1,2,3*†} 

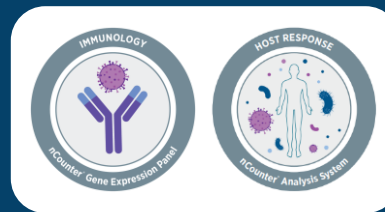
“...nCounter® PanCancer IO360™ can generate a similar immune profile to that generated by the WTS platform in advanced melanoma Patients...it is also a reliable and practical approach to analyze the variations of immune signatures between response status and conduct cross-platform analysis.”

*“The median ranks of **770 genes in the [nCounter] platform** and **22,297 genes in the WTS platform** followed a relatively uniform distribution...”*

*“The cross-platform comparisons confirmed that singscores derived via **[nCounter] and WTS were comparable**. When singscore of WTS generated by the overlapping genes to the [nCounter] gene set, the **signatures generated highly correlated cross-platform scores**”*

Immune Response

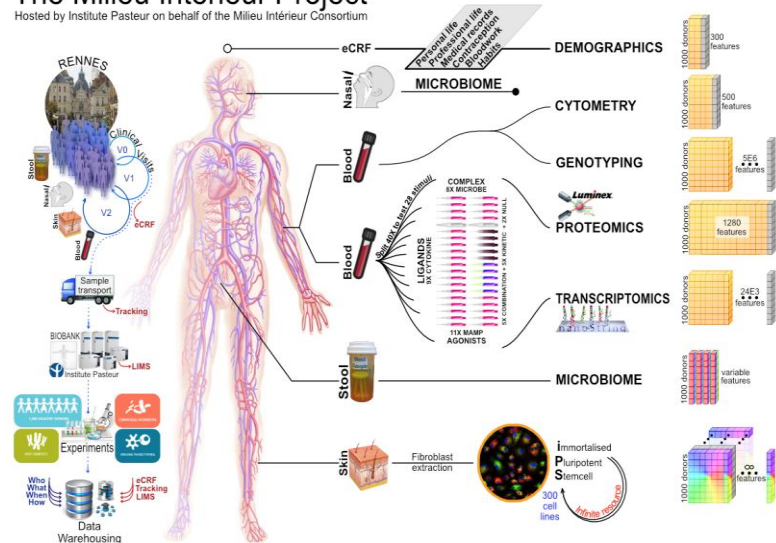
Human Immunology V2 & Host Response Panels



Centre for
Immunology & Infection
免疫与感染研究中心

The Milieu Intérieur Project

Hosted by Institut Pasteur on behalf of the Milieu Intérieur Consortium



"We tested several different techniques and compared how well they worked for our samples... **samples include Heparin which tends to interfere with reverse transcriptase in conventional PCR-based approaches.** We also have a lot of red blood cells & globin RNA, which can also interfere with and overwhelm sequencing approaches."

"Given these technical challenges, we were very pleased to find that the **[iCounter] technology let us have high throughput, reproducible results regardless of our sample preparation protocol.**"

"[iCounter's] gene expression panels feature key immune response genes important to our study. **We don't waste time focusing on genes that won't be induced, and it lends confidence to our statistical analysis.**"

Immune Response

Immune Exhaustion Panel & Lung Organoids



A comparative analysis of RNA-Seq and NanoString technologies in deciphering viral infection response in upper airway lung organoids

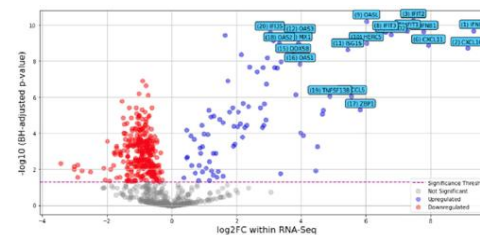
Mostafa Rezapour^{1*}, Stephen J. Walker², David A. Ornelles³,
Muhammad Khalid Khan Niazi¹, Patrick M. McNutt²,
Anthony Atala² and Metin Nafi Gurcan¹

¹Center for Artificial Intelligence Research, Wake Forest University School of Medicine, Winston-Salem, NC, United States, ²Wake Forest Institute for Regenerative Medicine, Wake Forest University School of Medicine, Winston-Salem, NC, United States, ³Department of Microbiology and Immunology, Wake Forest University School of Medicine, Winston-Salem, NC, United States

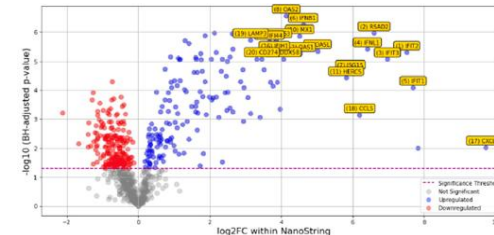
*"The case of MPV (virus used in study) illustrates the **potential superiority of [nCounter] over RNA-Seq** for certain viral infections where early and accurate detection of a small number of genes is critical. **[nCounter's] methodology allows for a more direct and quantifiable approach**, making it exceptionally useful...This technology enhances the ability to detect subtle yet significant changes in gene expression that are pivotal in the early stages of viral infection."*

*"In this study, we delved into the **comparative analysis of gene expression data across RNA-Seq and [the nCounter] platform.**"*

RNA Seq



[nCounter]



*"The concordance observed here supports the **complementary use of RNA-Seq and [nCounter] in comprehensive genomic studies**, ensuring a deeper and more accurate exploration of gene expression dynamics in health and disease."*

Bruker Spatial Biology is your partner in research.

>30 Field Application Scientists
>25 Field Service Engineers



>8,000
Publications

Over 1,000 Instruments Worldwide



Free Online University

Large Global Commercial Organization

- >300-person commercial team
- >100 global support professionals
- Network of ~40 Distributors

nCounter Products & Applications

Large portfolio of panels ready to ship – with custom options available (and popular!)

Platform Capabilities

- RNA, Protein, miRNA, CNV
- Multiomics: RNA + Protein
- Immune Cell Profiling
- Validated & Research Signature Assays
- Laboratory Developed Tests



Prep Station

Digital Analyzer

25 Customizable Gene Expression Panels



Thematically designed with up to 800 Genes

Custom Solutions

- Any species/Any gene
- 20-800 plex

Data Analysis

- Multiomics Analysis
- Pathway Analysis
- Signature Reports
- Cloud solutions

Targeted panels to fit your research needs

Oncology

- Hallmarks of Cancer (Hu/Mm)
 - Immune Profiling, Pathways, & Progression
- IO360 (Hu/Mm)
- Breast Cancer 360 (Hu)
- Tumor Signaling (Hu)
- Canine IO
- ADC Development

Immunology

- Immunology (Hu/Mm)
- Inflammation (Hu/Mm)
- Autoimmune Profiling (Hu/Mm)
- Myeloid (Hu/Mm)
- Organ Transplant (Hu)
- Host Response (Hu/Mm)
- Immune Exhaustion (Hu/Mm)

Neuroscience

- Neuropathology (Hu/Mm)
- Neuroinflammation (Hu/Mm)
- Glial Panel (Hu/Mm)

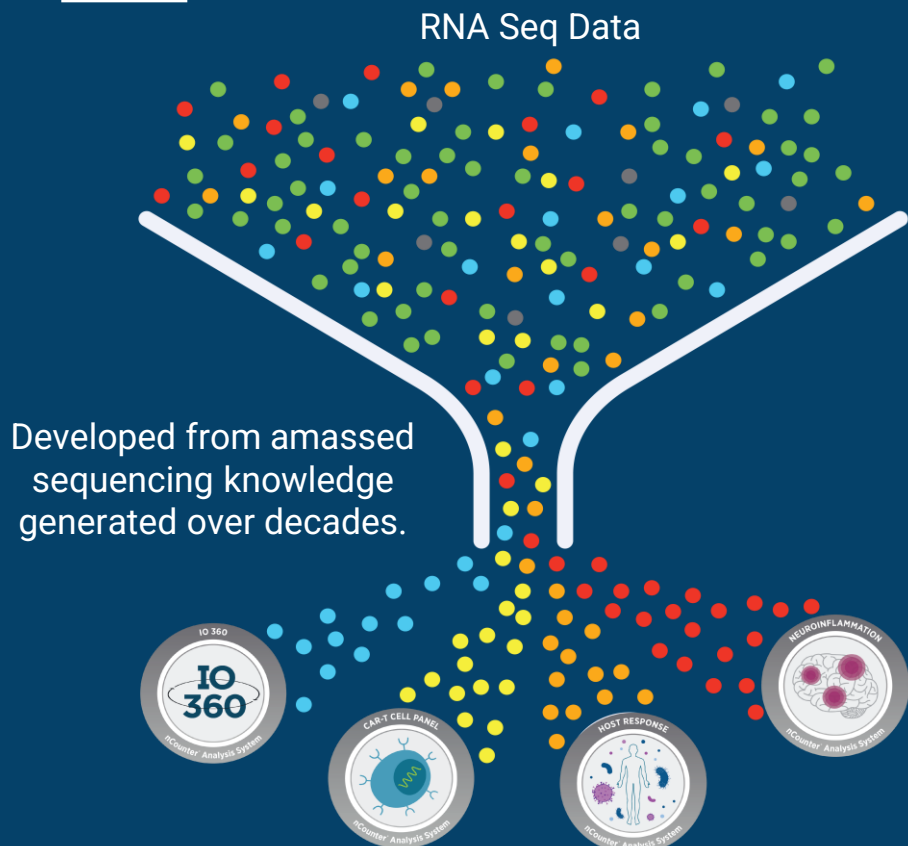
Cell & Gene Therapy

- Stem Cell (Hu/Mm)
- CAR-T Characterization (Hu)
- Gene Therapy Optimization (Hu)

Multi-Market

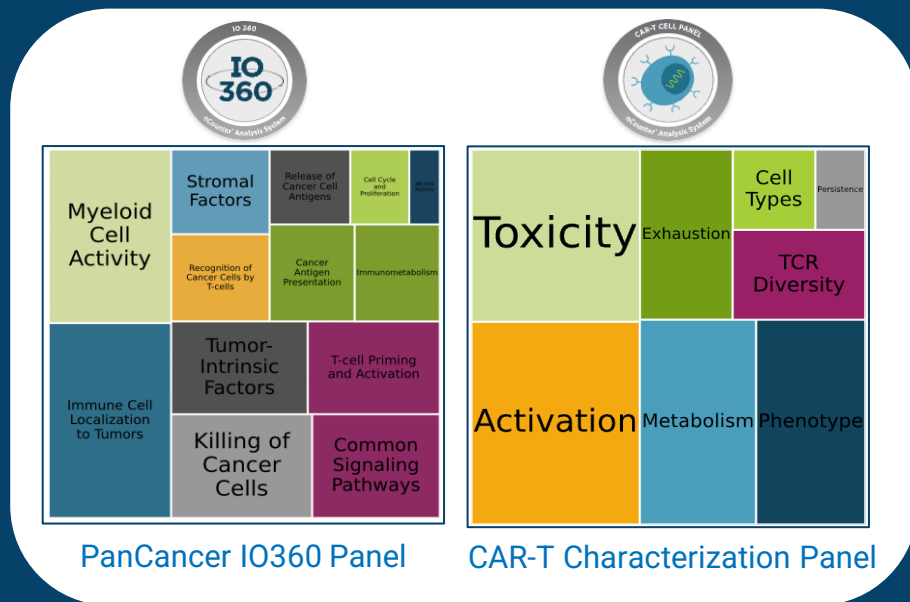
- CVD Pathophysiology (Hu/Mm)
- Fibrosis (Hu/Mm)
- Metabolic Pathways (Hu/Mm)
- miRNA

nCounter Thematic Gene Expression Panels



nCounter Gene Expression Panels

Panels assemble the relevant pathways and processes known to play a role in the specific disease or research area.



Built to address important biological questions & deliver actionable biology versus just more data!

nCounter Multiomics Products & Workflow

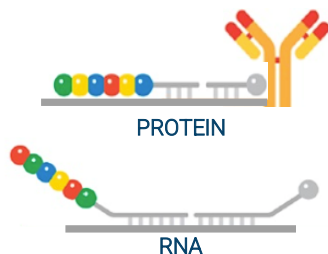
Evolving the nCounter Advancing Multiomics Research

Unique Multiomics capabilities no other commercial platform can offer!



RNA and Protein analysis
from the same platform
FFPE Tissue-Whole Slide

Direct digital counting used
for both analytes.



Multiomics Protocols
based on *simple*
nCounter workflow

RNA + Protein
Whole Slide FFPE

3-simple steps
3-days from Sample to Data



Curated Content
Designed with purpose to
sync with GX panels

PAST

Focus on GX & miRNA



CURRENT

Multiomics Solution
GX Panel + Protein Panel



Speed to biological
answers

Multianalyte harmonized
biological annotations for
simplified Multiomics
analysis:

- ✓ Pathway Scoring
- ✓ Differential Analysis
- ✓ RNA-Protein Correlation
- ✓ Protein Only Analysis
- ✓ And more...

nCounter Multiomics Portfolio

Bringing RNA + Protein to Immunology and Oncology

Choice of RNA Panels
(Current)

+

Choice of Protein Panels
(NEW)

=

Powerful Multiomics Solution
RNA + Protein
(NEW)

- Menu of 25+ Panels



- Protein content to complement GX panels for functional read out.
- Address biology gaps
- "Smaller" stackable Protein panels 200-300 plex utilizing validated antibodies

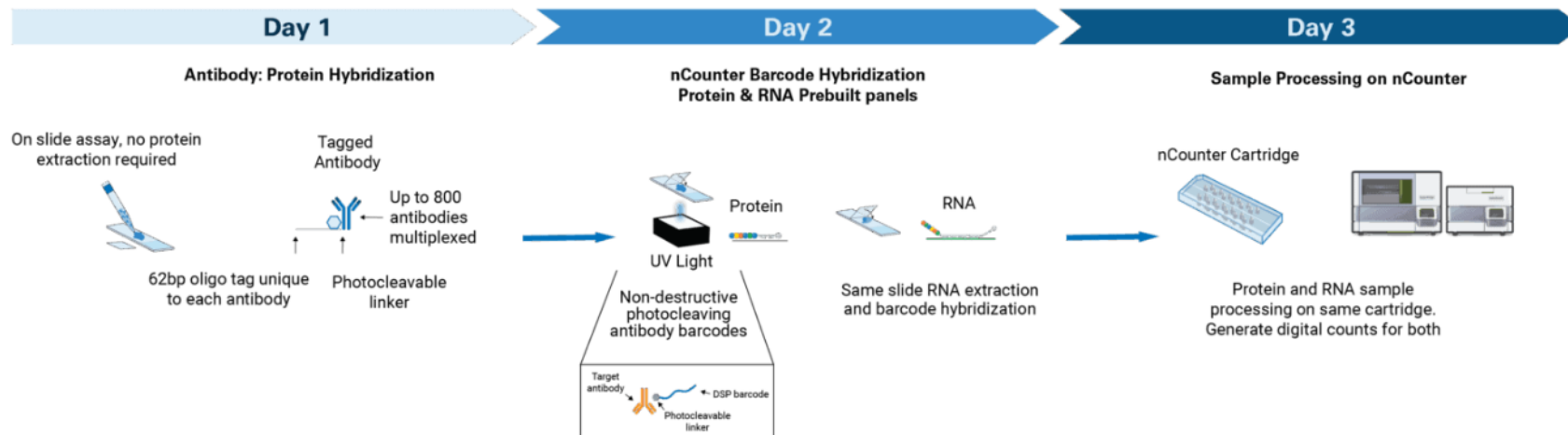


- Same sample
- Same slide
- Same digital output
- Combined data analysis



nCounter Multiomics Workflow Snapshot

Whole slide FFPE



Borrowing Lessons from GeoMx

- On slide assay
- Validated antibodies
- Photocleavable barcodes

Utilizing the same Gene Expression Assay

- Extracted RNA (100ng-300ng)
- Pre-built panels or custom
- Direct detection barcodes

Simultaneous Measurement & Combined Analysis

- nCounter Data Analysis Pipeline

nCounter Protein Panels

Content Summary



nCounter Immune Pathways Protein Panel

204 Targets

Adaptive Immunity, Innate Immunity, Immune Signaling & Trafficking, Metabolism, Cellular Processes, Signaling Pathways

~90% content overlap with GeoMx IPA panel
All use same clone content

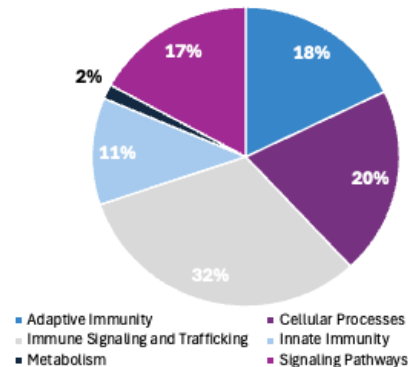
nCounter Tumor Signaling Protein Panel

325 Targets

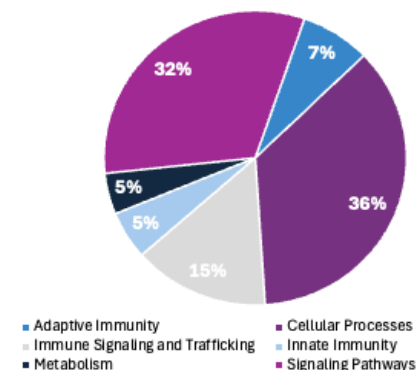
nCounter Immune Protein Core

21 Targets: Housekeeping genes, IgG controls and essential immune targets for use across panels

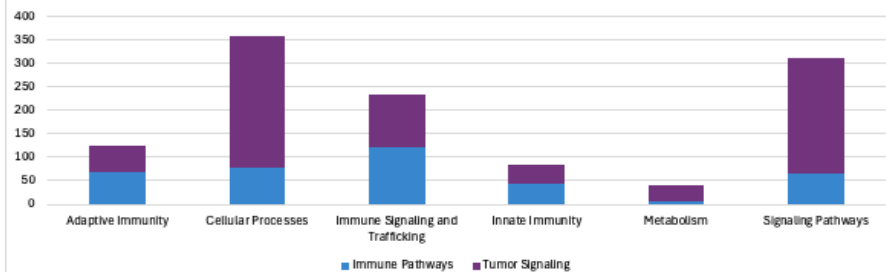
Immune Pathways Protein Panel



Tumor Signaling Protein Panel



Theme Coverage for Immune Pathways and Tumor Signaling



Upcoming Webinar



BRUKER

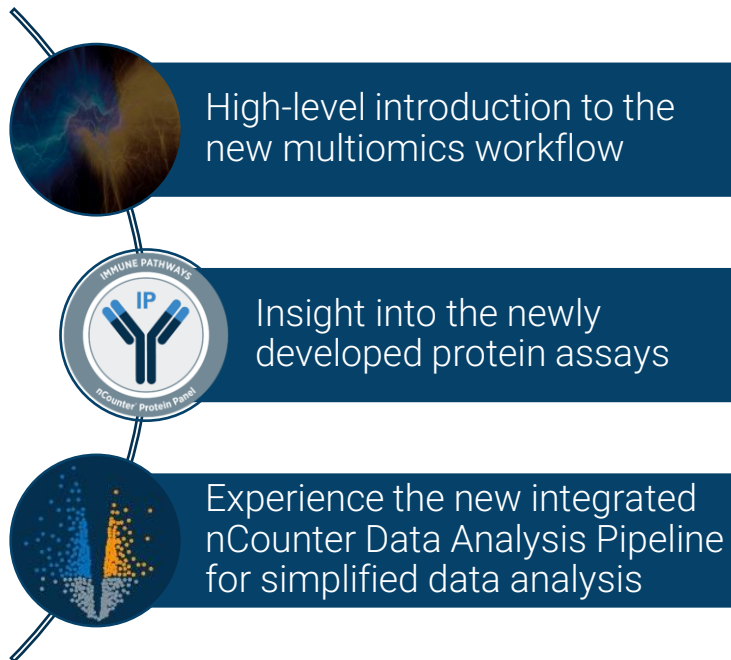
nCounter

ANALYSIS SYSTEM

WEBINAR

**A NEW ERA FOR NCOUNTER:
INTRODUCING SIMPLE, SCALABLE,
BULK MULTIOMICS**

WEDNESDAY, MARCH 4TH
8:00 AM PST / 11:00 AM EST / 5:00 PM CET



nCounter Data Analysis

nCounter Data Analysis Solutions

Desktop



nCounter Data Analysis Pipeline *BETA*

- Free open-access analysis platform for download
- Ideal for researchers looking for a simple on-premises option with advanced analysis capabilities

Cloud



EuropaXp OMICS CLOUD

- 3rd party fee-based cloud-based option
- Ideal for researchers who would prefer additional guidance in their analysis and/or are working through multi-site collaborations.

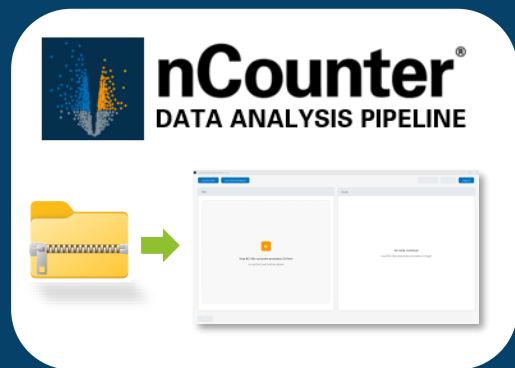
Other Options

Data Analysis Services

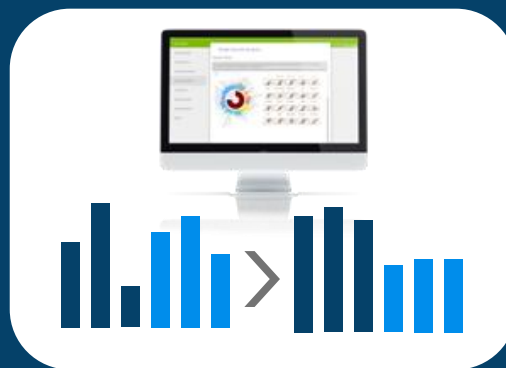


- Fee-for-service by Bruker Spatial Biology scientists.
- Ideal for researchers who prefer more extensive data analysis support

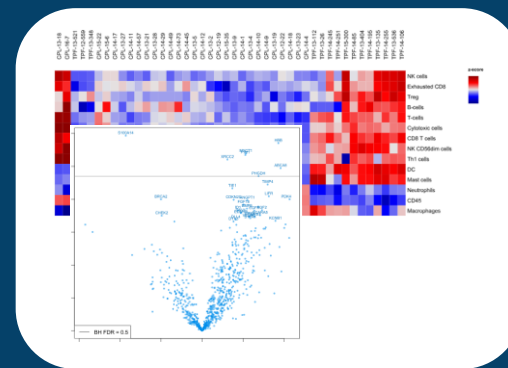
nCounter Data Analysis Pipeline



Import data



QC and Normalization

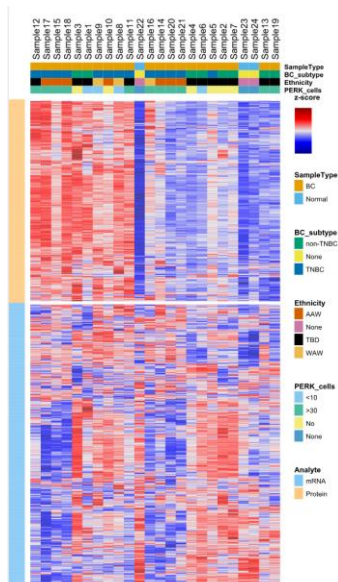


Biological Analysis

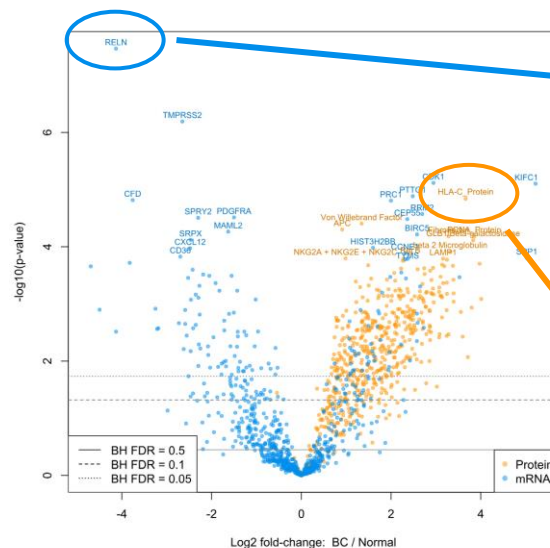
Fast, Simple Data Analysis

Delivering differential multiomics insights in under 5 minutes

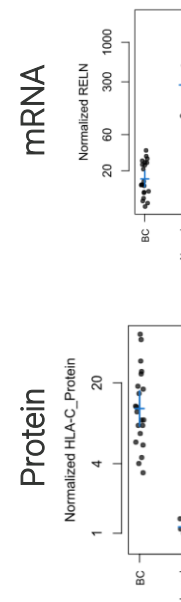
Whole-panel multiomics heatmap



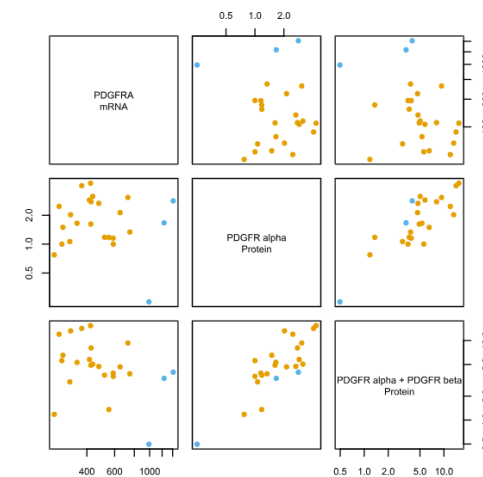
Differential expression: volcano plots



Single probes



Related probes



Upcoming Webinar



BRUKER

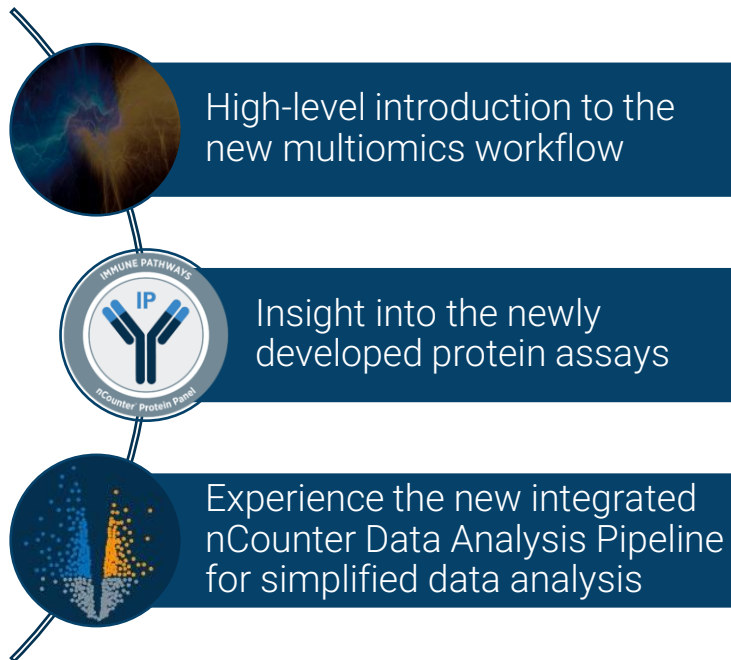
nCounter

ANALYSIS SYSTEM

WEBINAR

**A NEW ERA FOR NCOUNTER:
INTRODUCING SIMPLE, SCALABLE,
BULK MULTIOMICS**

WEDNESDAY, MARCH 4TH
8:00 AM PST / 11:00 AM EST / 5:00 PM CET



MerTK Modulates the TNBC Tumor Microenvironment

BRIDGET CROSSMAN

February 24, 2026

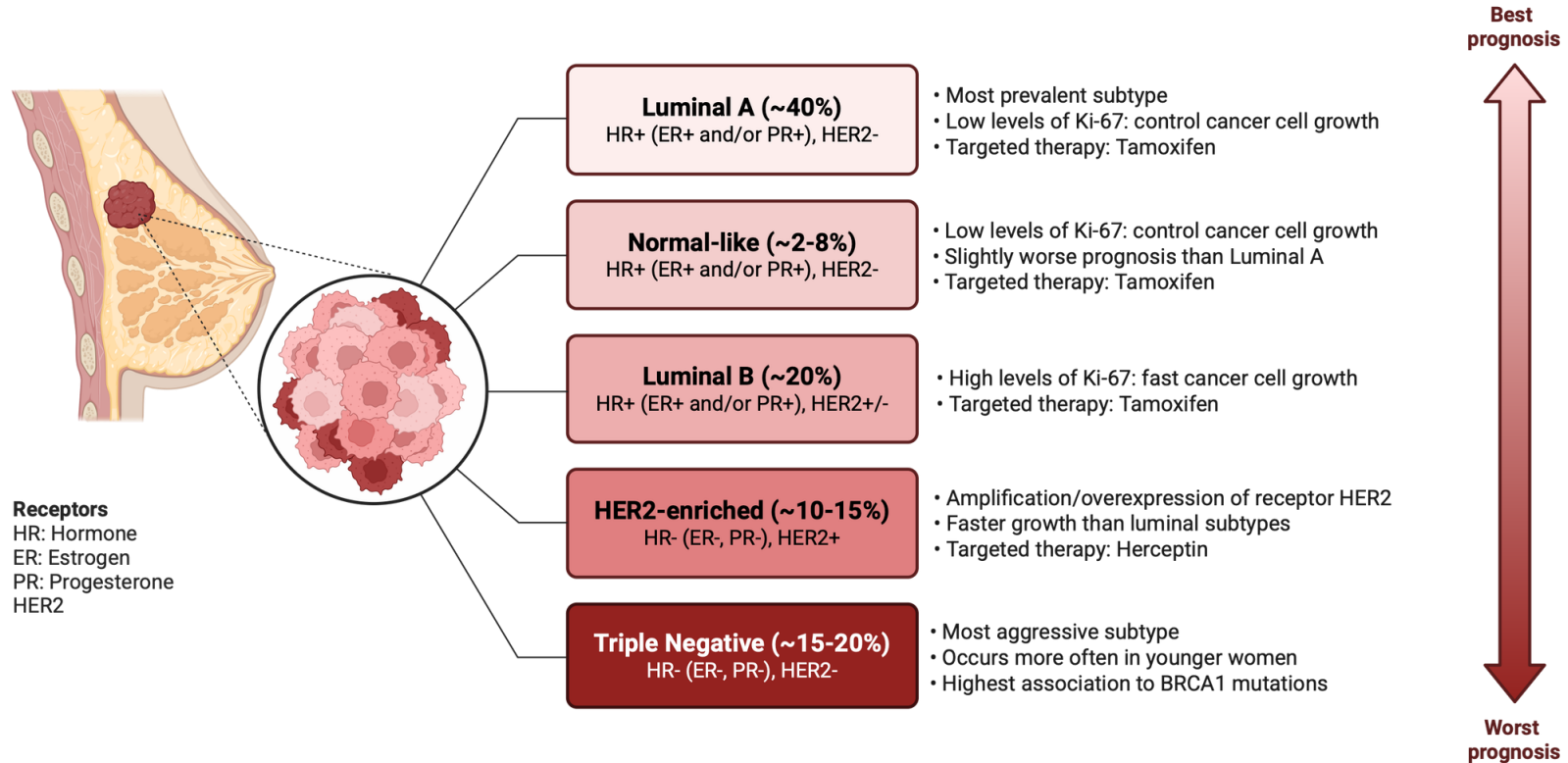
PhD Candidate, Cellular and Molecular Biology Program

Wheeler Lab, Department of Human Oncology, SMPH



TRIPLE NEGATIVE BREAST CANCER

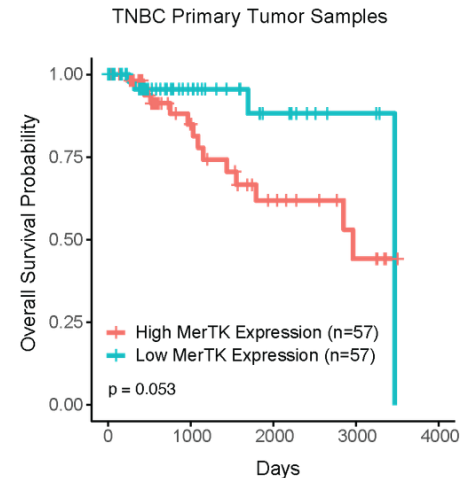
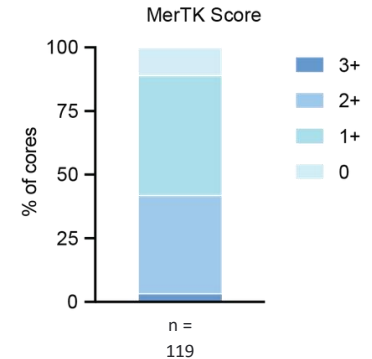
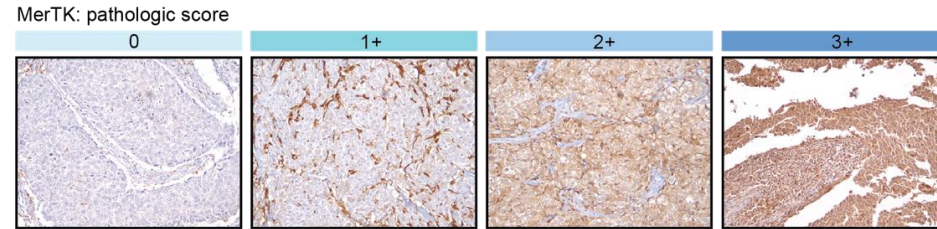
5 Main Intrinsic or Molecular Subtypes of Breast Cancer



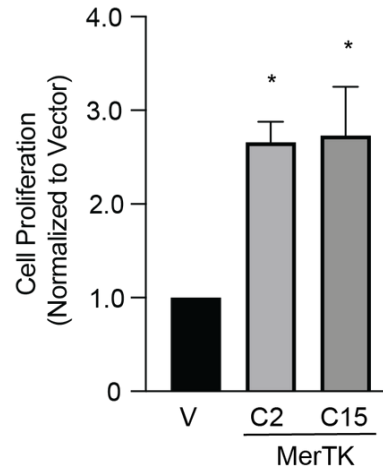
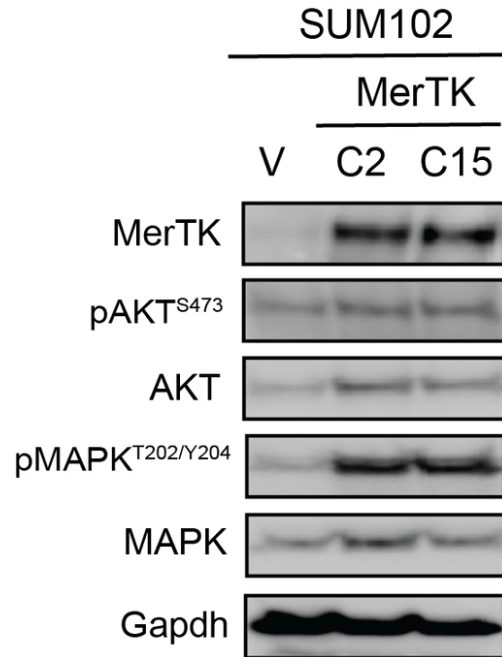
MERTK EXPRESSED IN TNBC, ASSOCIATED WITH SURVIVAL DISADVANTAGE

MerTK

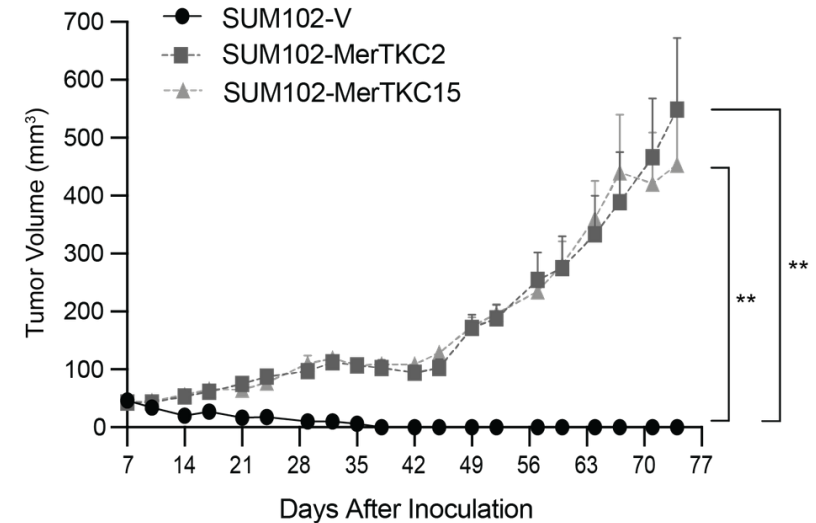
- TAM family of RTKs
- Associated with solid tumor progression
- Proliferation
- Migration
- Cell cycle
- Metabolism



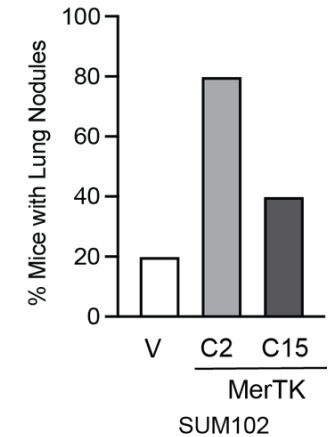
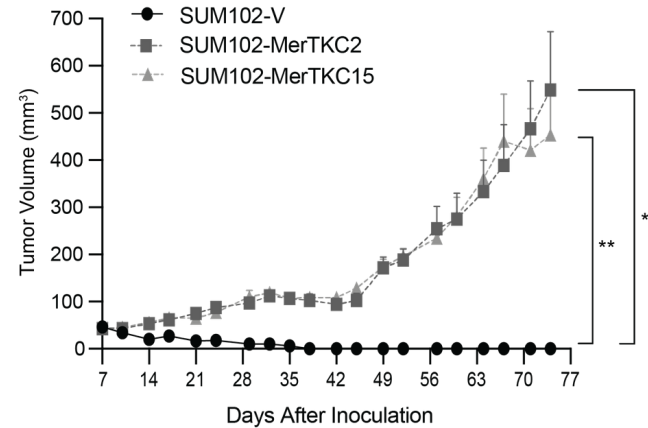
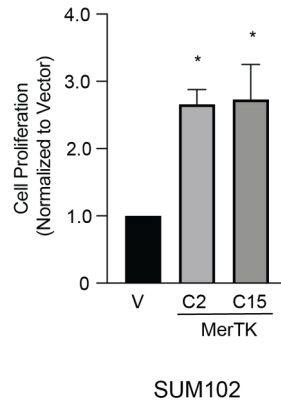
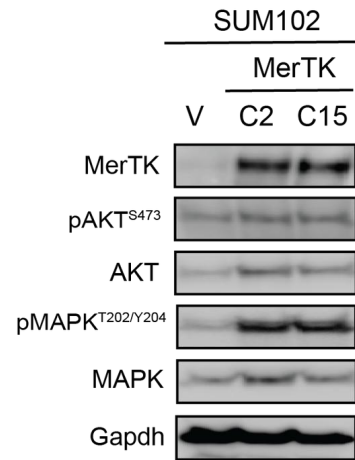
MERTK-EXPRESSING HUMAN TNBC CELL LINES ARE ONCOGENIC



SUM102



MERTK-EXPRESSING HUMAN TNBC CELL LINES ARE ONCOGENIC

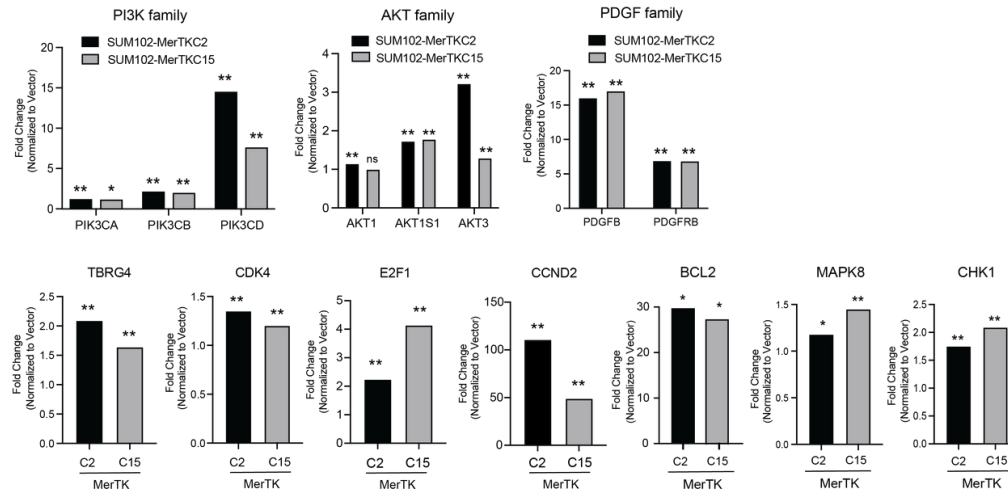
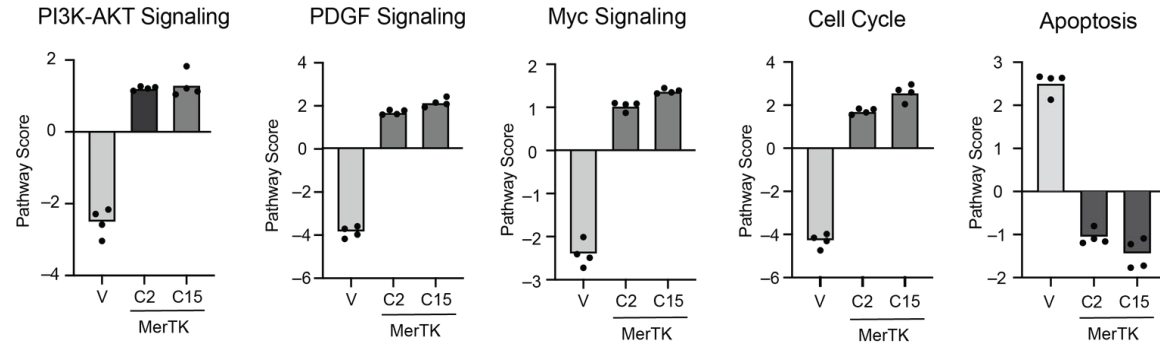
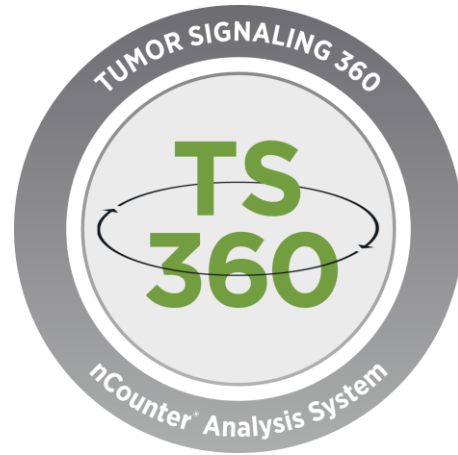


ONCOGENIC SIGNALING PATHWAYS UPREGULATED WITH MERTK OVEREXPRESSION

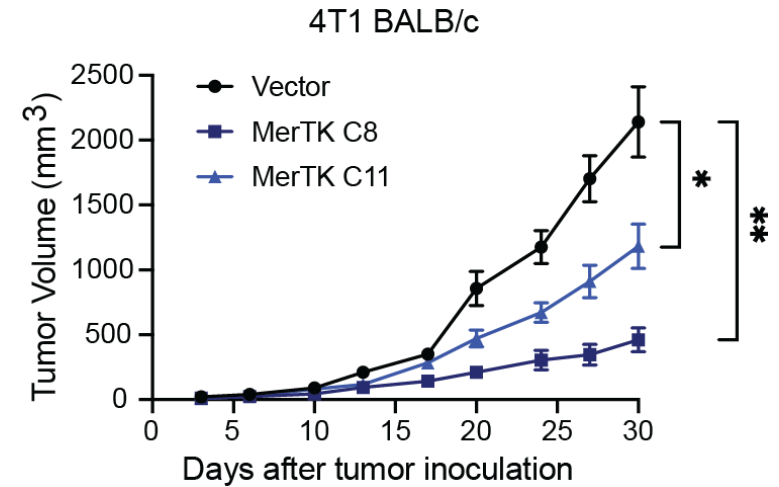
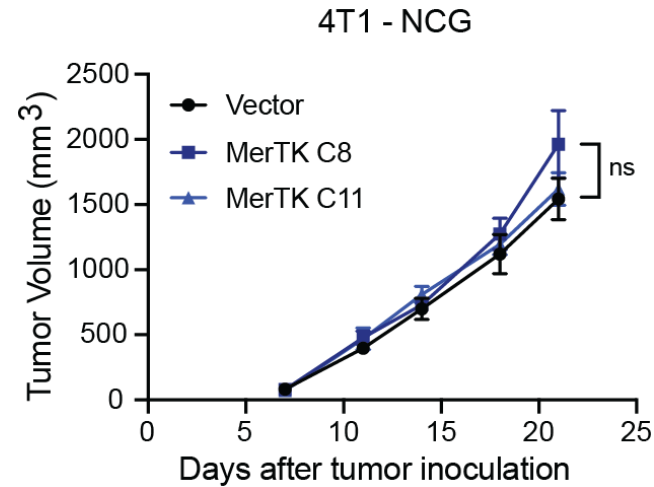
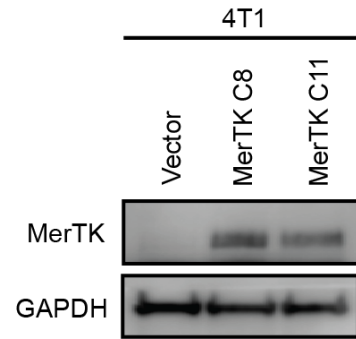
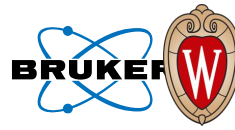


nCounter Tumor Signaling 360

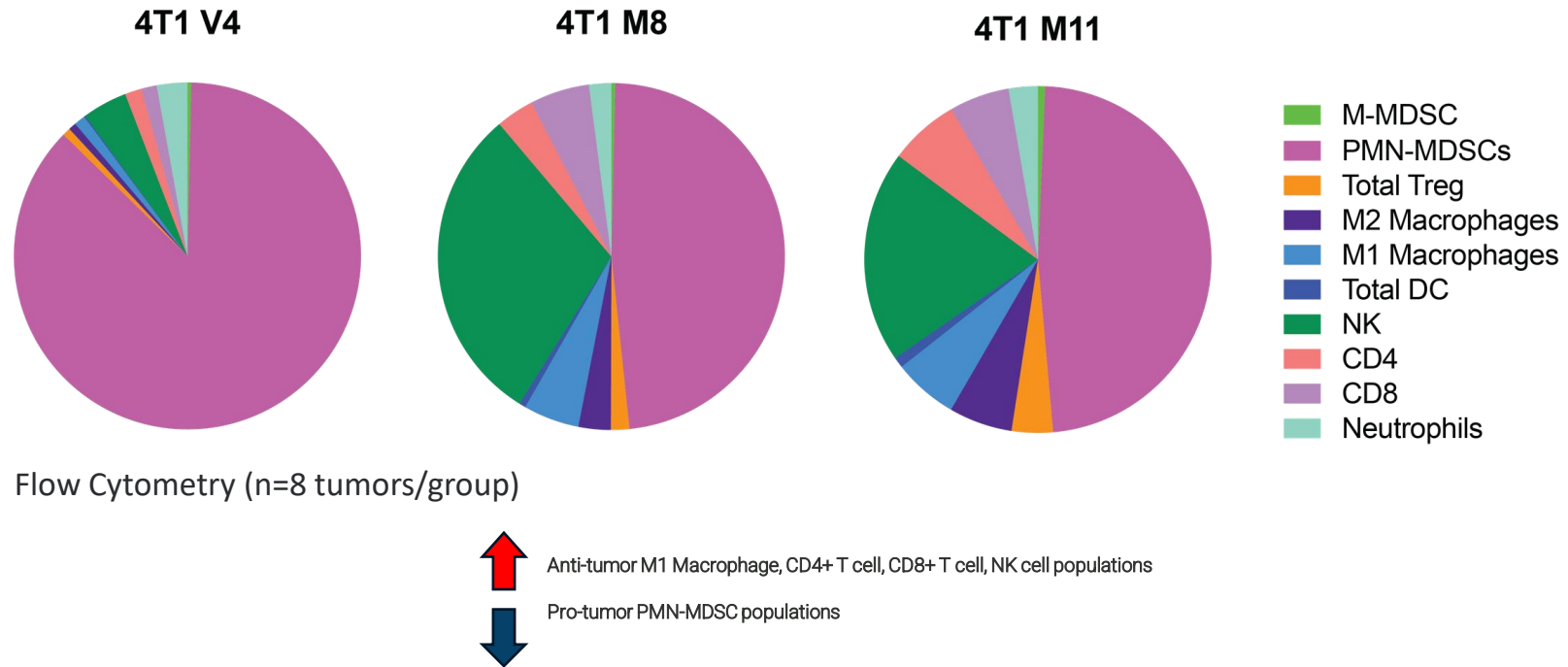
- RNA isolated from cultured cell lines

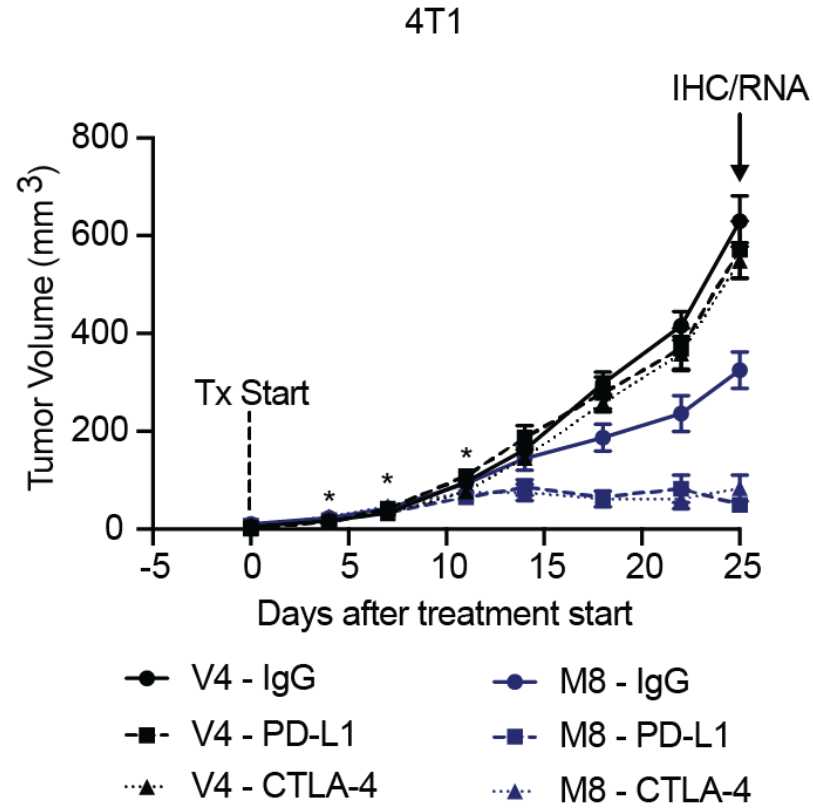


MERTK OVEREXPRESSION SUPPRESSES MOUSE TUMOR GROWTH IN SYNGENEIC MICE



MERTK OVEREXPRESSION PROMOTES ANTITUMOR IMMUNE INFILTRATION

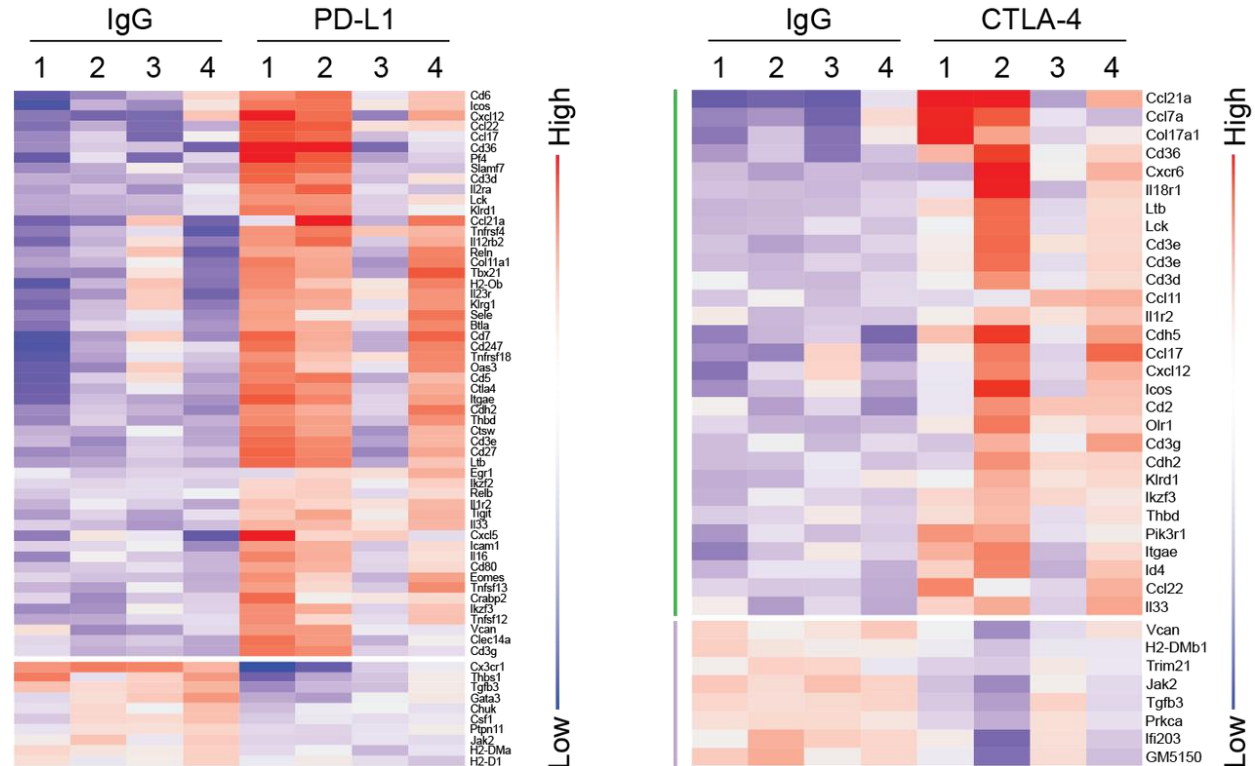
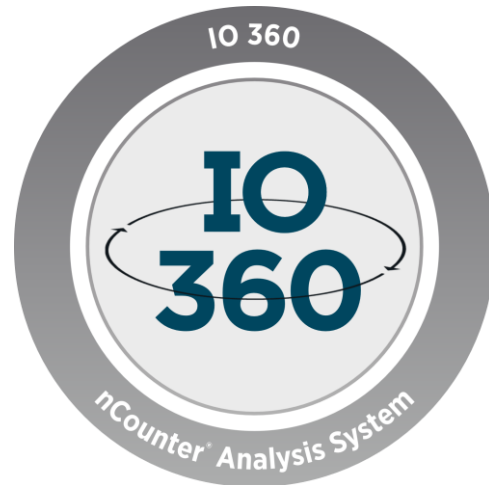




DIFFERENTIAL GENE EXPRESSION IN MERTK-OVEREXPRESSING TUMORS FOLLOWING ICI

nCounter PanCancer IO 360

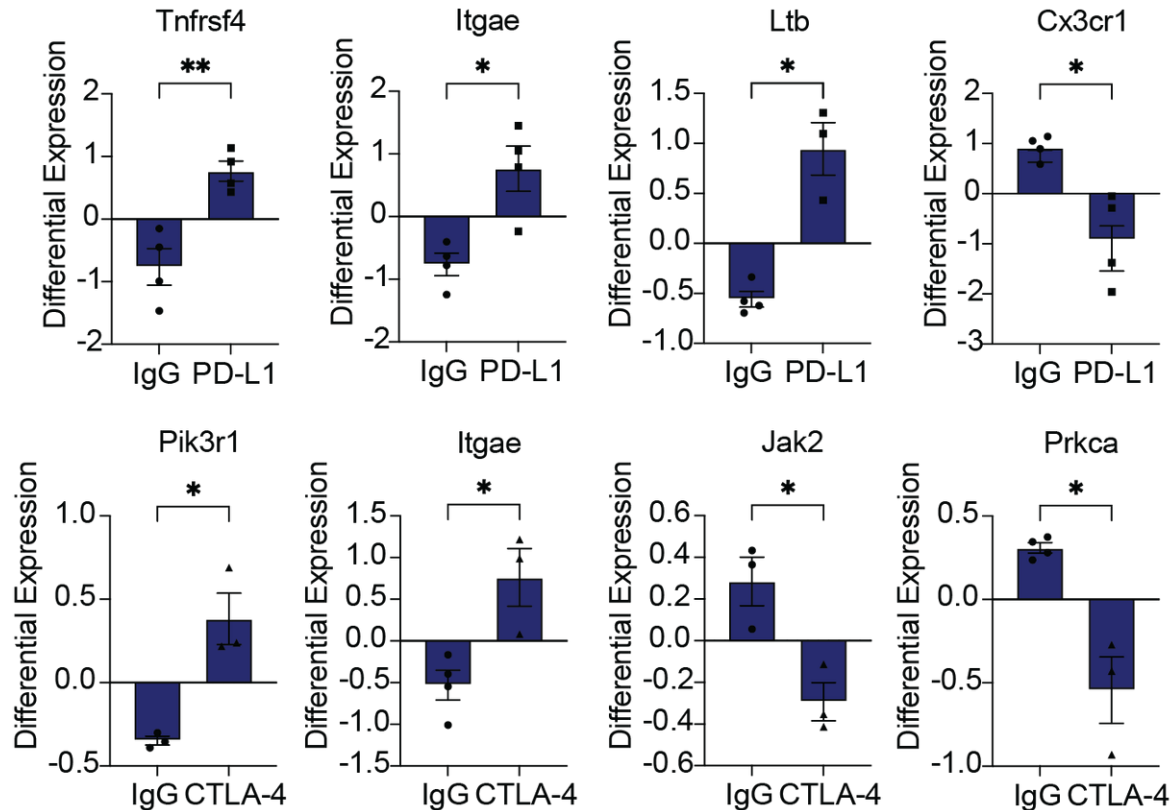
- RNA isolated from flash frozen tumor chunks



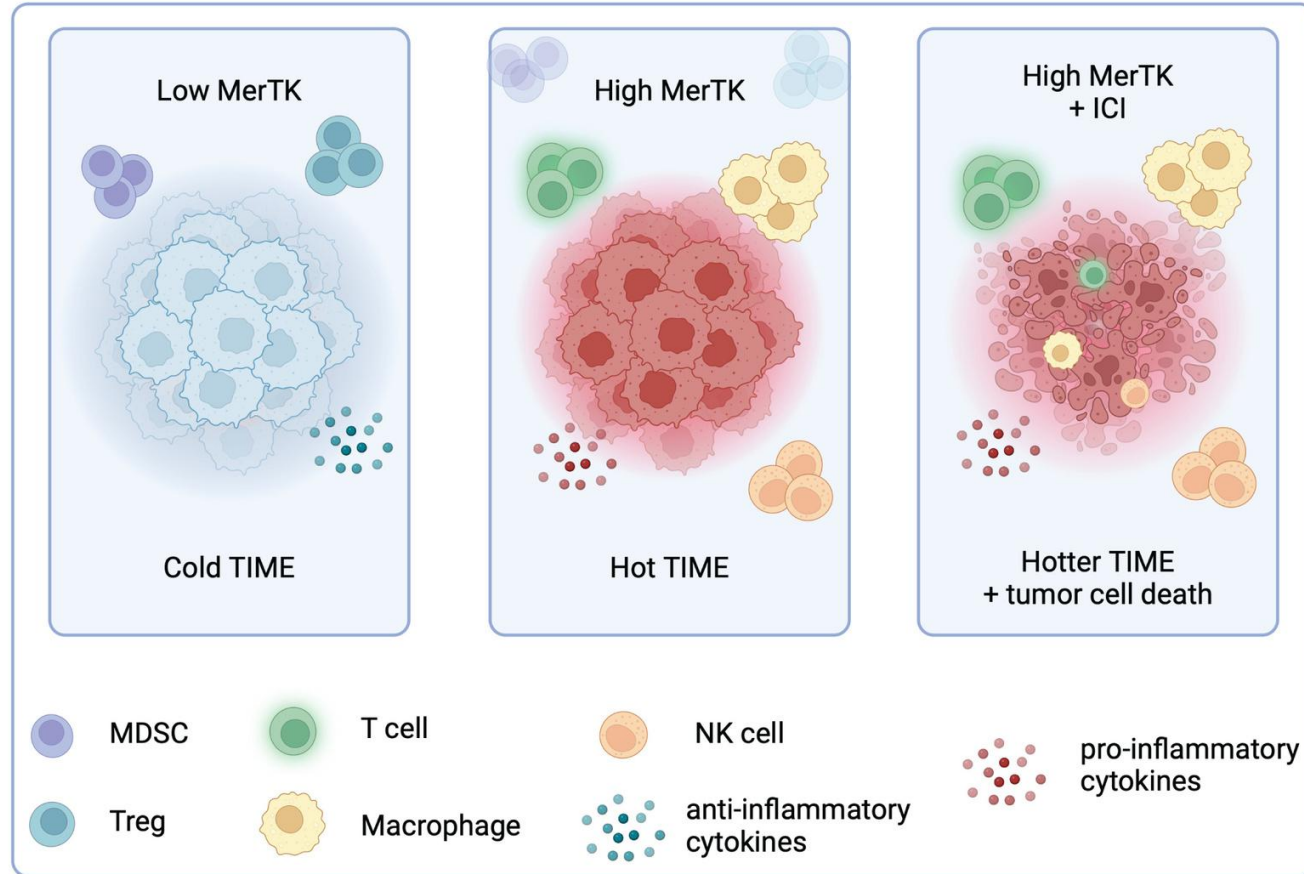
DIFFERENTIAL GENE EXPRESSION IN MERTK-OVEREXPRESSING TUMORS FOLLOWING ICI

nCounter PanCancer IO 360

- RNA isolated from flash frozen tumor chunks



MERTK PROMOTES AN ANTI-TUMOR IMMUNE MICROENVIRONMENT



THANK YOU

Wheeler Lab

- Deric Wheeler, PhD
- Mari Iida, PhD
- Regan Harmon
- Madeline Wolfe
- Candie Lin
- Jennifer Yoon
- Addison Sloan
- Addison Schnarr

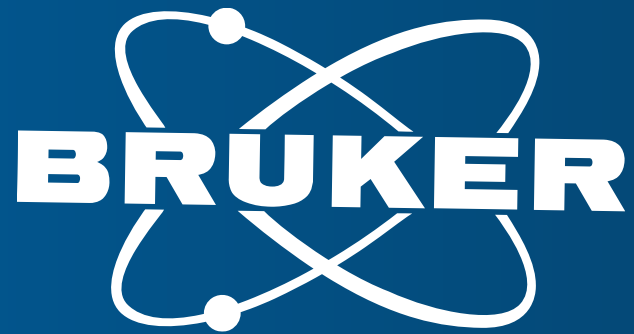
TRIP Lab

- Rebecca Baus
- Maggie Baus
- Karla Esbona, PhD
- Toshi Kinoshita
- Anu Singh

UWCCC Flow Cytometry Core

UWCCC Experimental Animal Pathology Lab

BRMS animal facilities, technicians and vets



Innovation with Integrity