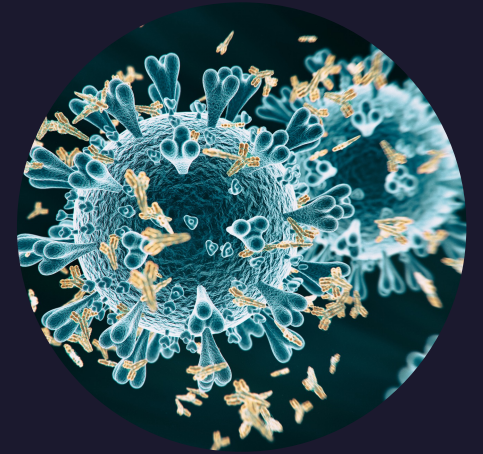
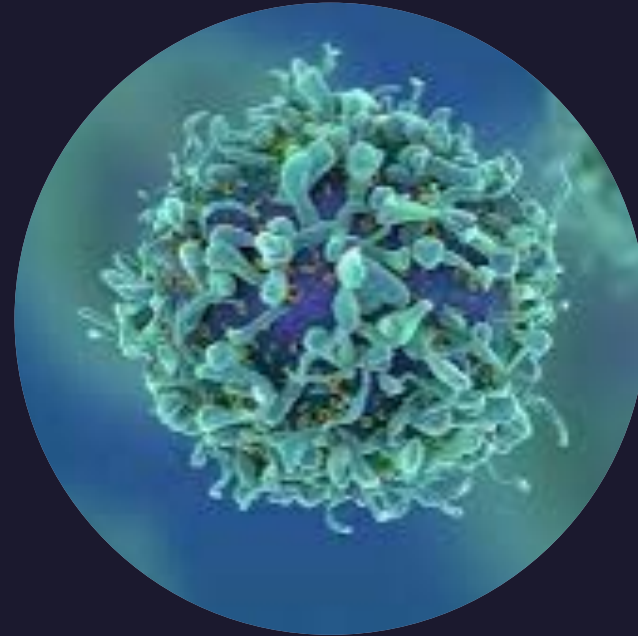


Outline

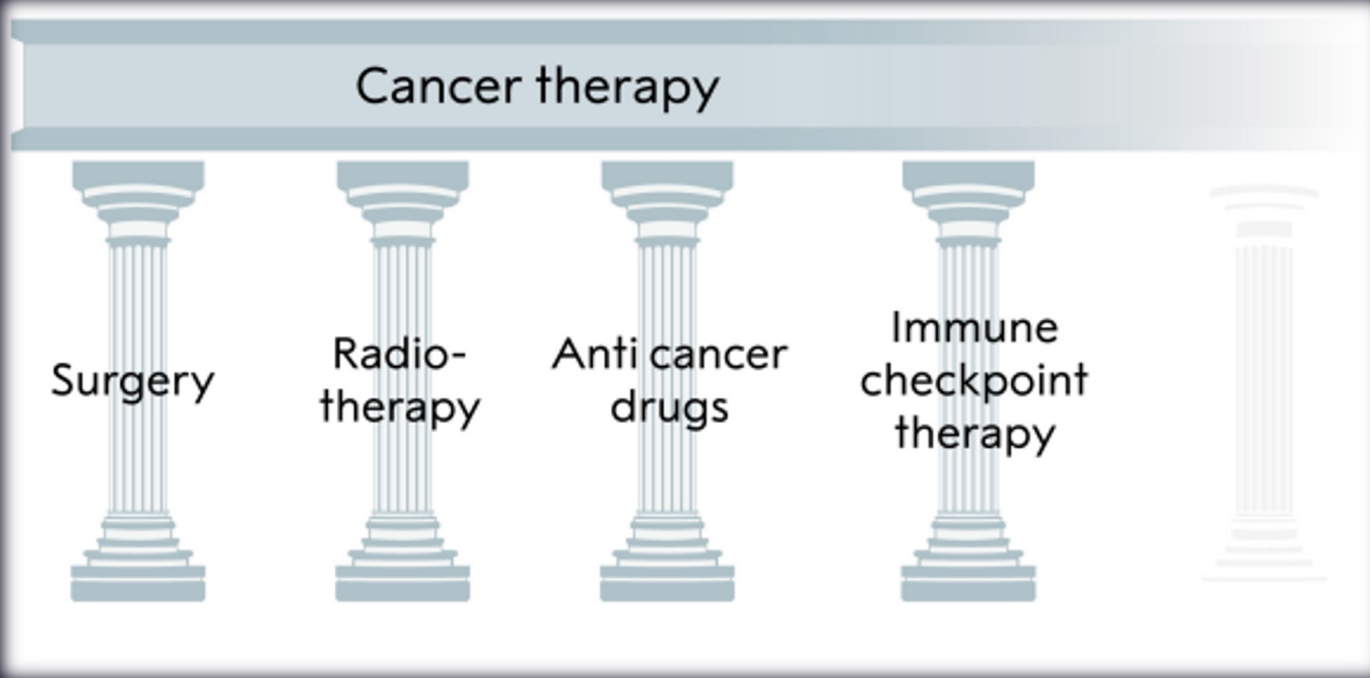
- Introduction of myself
- Introduction of the pathway
- Overall Goal
- Key Questions
- Current Findings
- Future



Introduction

- Immunotherapy has revolutionized cancer treatment and rejuvenated the field of tumor immunology. Several types of immunotherapy, including adoptive cell transfer (ACT) and immune checkpoint inhibitors (ICIs), have obtained durable clinical responses, but their efficacies vary, and only subsets of cancer patients can benefit from them.
- Immune infiltrates in the tumor microenvironment (TME) have been shown to play a key role in tumor development and will affect the clinical outcomes of cancer patients.
- Comprehensive profiling of tumor-infiltrating immune cells would shed light on the mechanisms of cancer–immune evasion, thus providing opportunities for the development of novel therapeutic strategies.

Immune Oncology

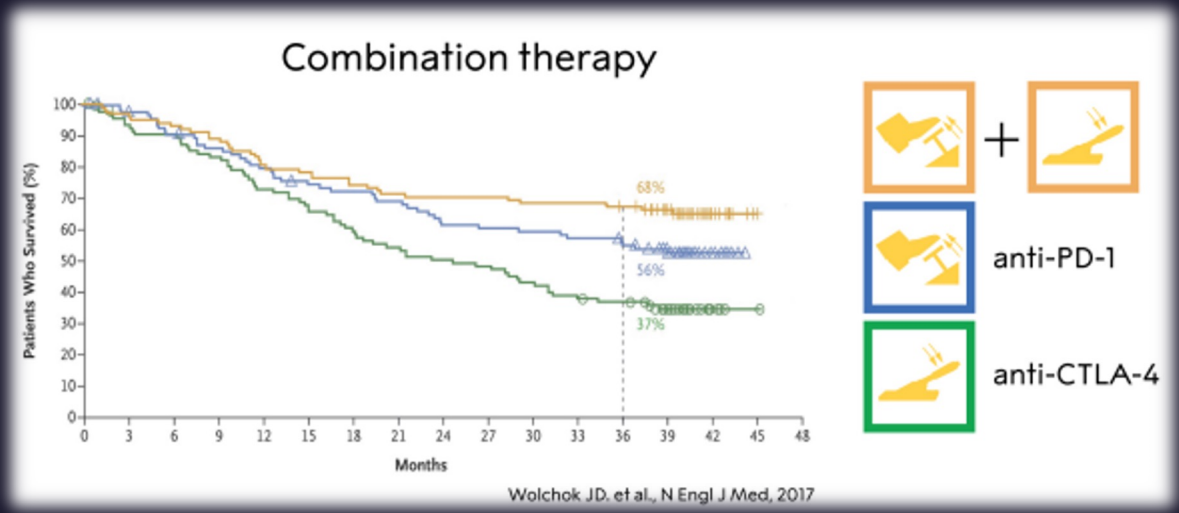
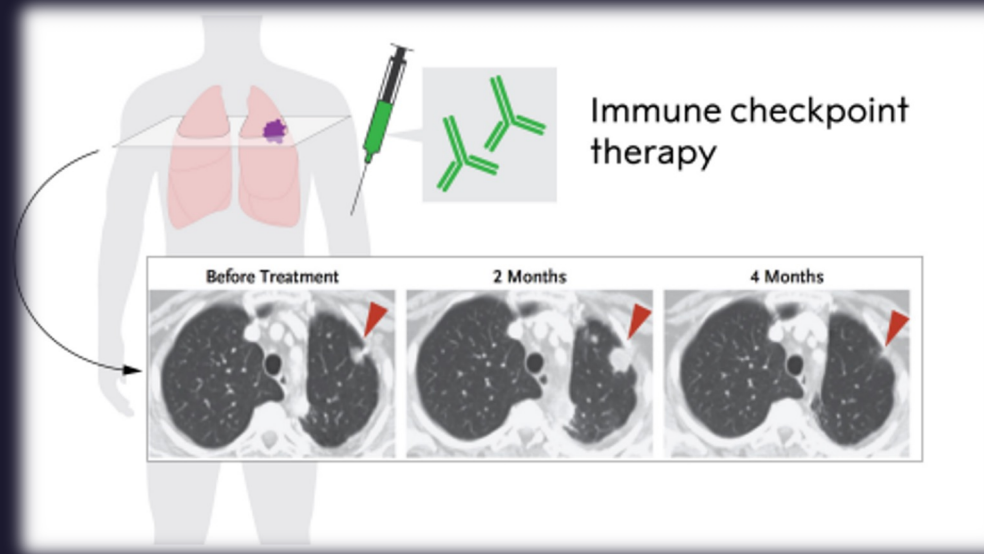
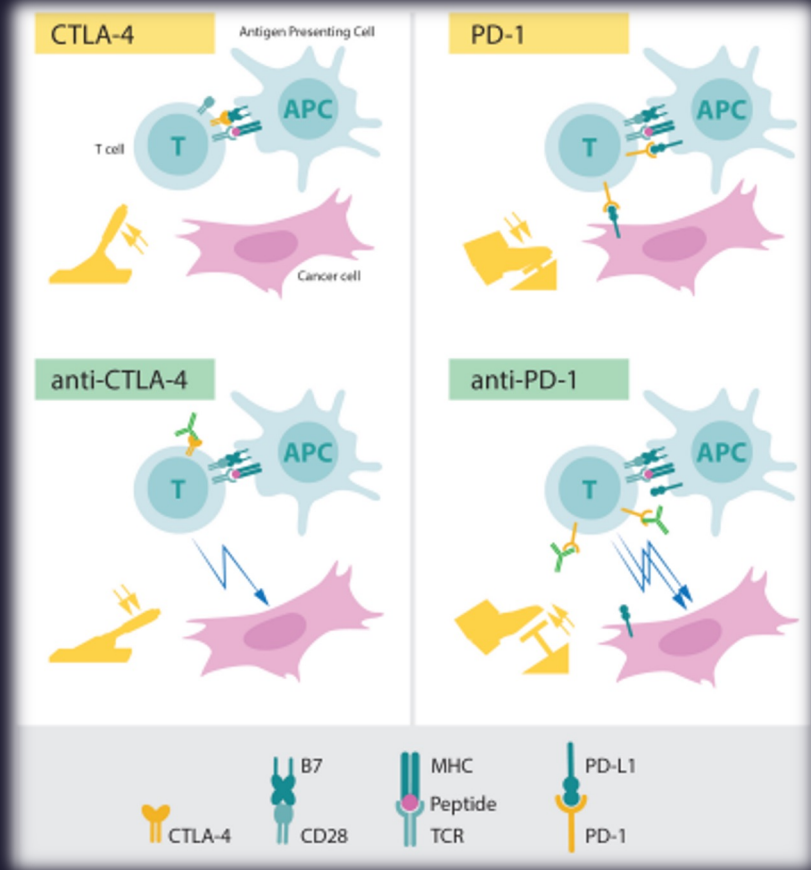


The Nobel Prize in Physiology or Medicine 2018 was awarded jointly to James P. Allison and Tasuku Honjo "for their discovery of cancer therapy by inhibition of negative immune regulation"

<https://www.nobelprize.org/uploads/2018/10/advanced-medicineprize2018>

Drs James P. Allison, PhD (UT MDACC, USA) and Tasuku Honjo, MD (Kyoto University, Japan) were the first to identify an immune checkpoint pathway, the CTLA-4 receptor. Their discovery then led to the development of ipilimumab, an anti-CTLA-4 checkpoint immunotherapy, which was first approved by the FDA in 2011 for melanoma. Currently, there are six FDA-approved checkpoint immunotherapies. Two of them, ipilimumab and nivolumab (an anti-PD-1 checkpoint immunotherapy) are approved in combination for the treatment of melanoma, while pembrolizumab (anti-PD-1) is approved as a first-line option for patients with advanced lung cancer and atezolizumab (anti-PD-L1) is approved as a first-line option for patients with advanced bladder cancer who are ineligible for chemotherapy.

Immune Oncology



Overall Goal

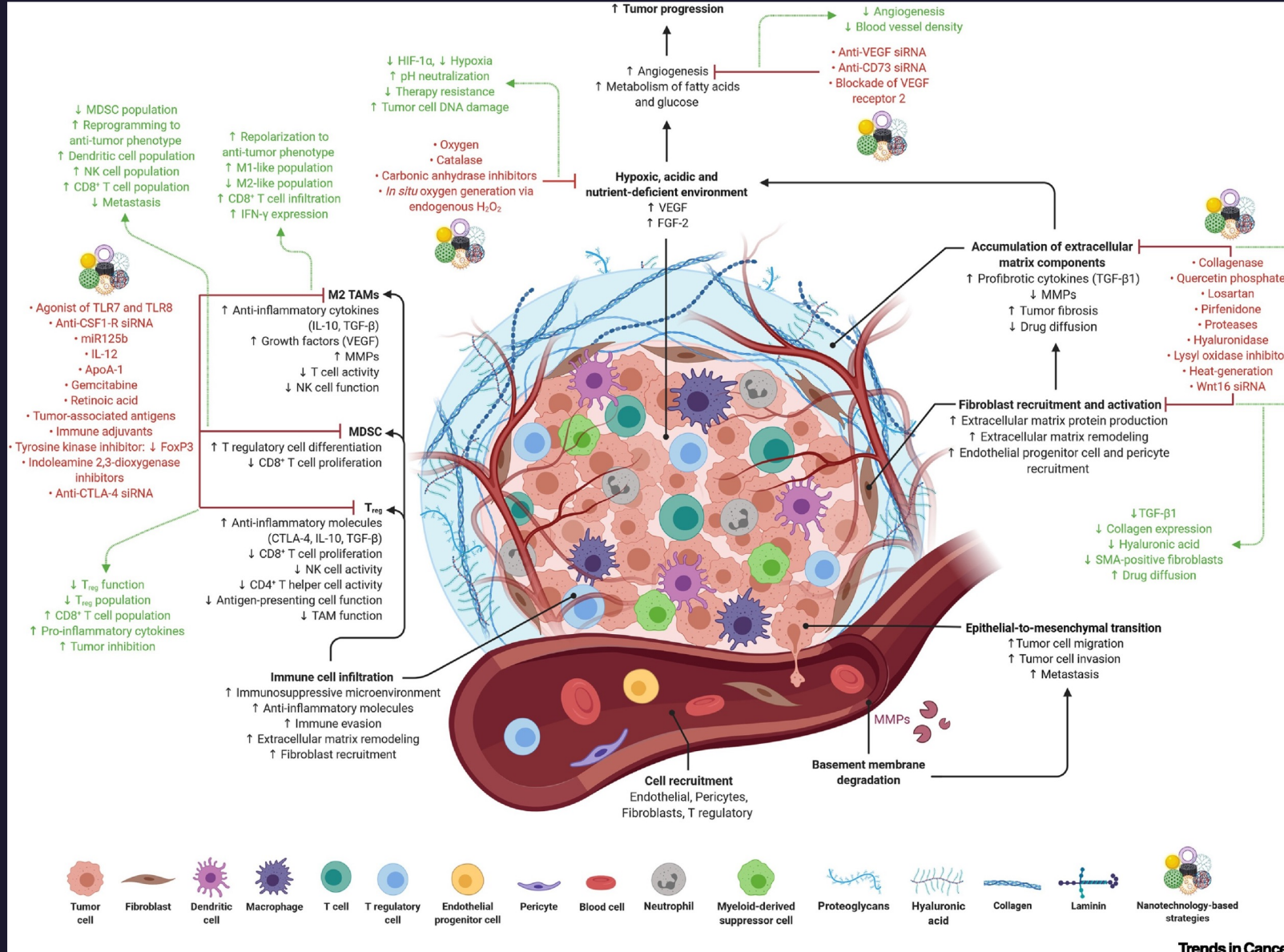
Specifically, we aim to clarify the predictive role and validate an initial set of immune-related markers. We target stably expressed innate inflammatory enzymes and their mediators (iNOS, COX-2/mPGES1, and CD74/CD44/MIF) along with their associated downstream post-translational modifications (PTM) as Nitrotyrosine (NT).

Each of these markers, individually as well as in “signatures” are being tested currently for predictive value.

Key Questions

- Why do some patients respond while others don't?
- Can we identify biomarkers that predict response?
- Can we identify markers for immune-related toxicities?
- Can we identify markers to enable patient selections to increase the number of responders?
 - Monotherapy?
 - Combination therapies –if so, what combo?
- Ultimately, can we identify other pathways that can be targeted!

THE TUMOR MICROENVIRONMENT



Schematic representation of the tumor microenvironment (TME), which comprises stromal and immune cells and extracellular matrix components, among others, involved in metabolic, cellular, and tissue remodeling.

THE TUMOR MICROENVIRONMENT – Melanoma

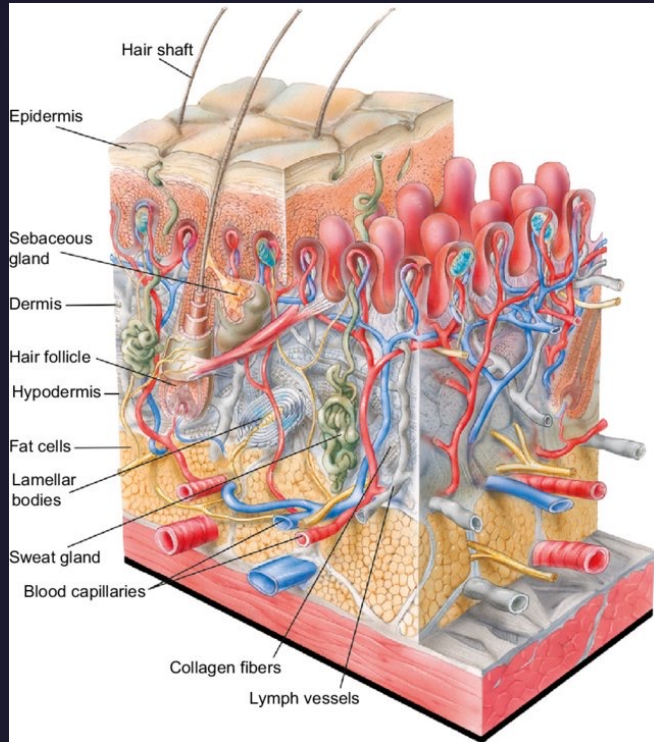
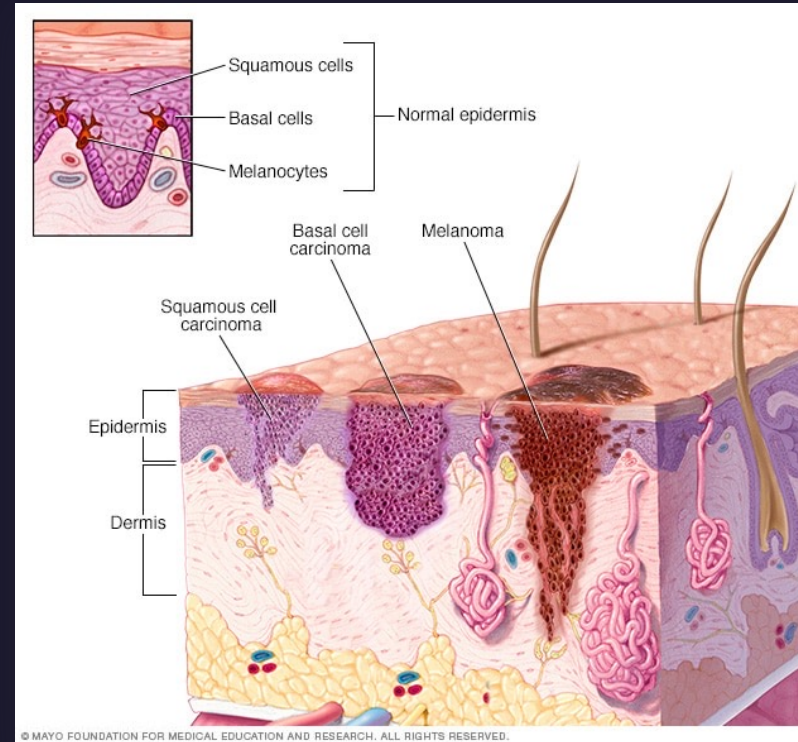


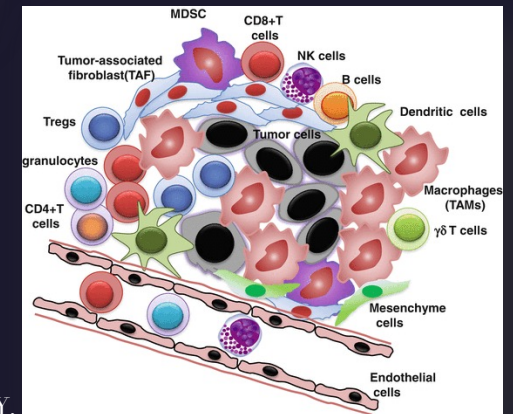
Illustration: © www.julius-ecke.de



© MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH. ALL RIGHTS RESERVED.

<https://www.mayoclinic.org/-/media/kcms/gbs/>

Structure drives the normal function?



In: Torres-Cabala C., Curry J. (eds) Genetics of Melanoma. Cancer Genetics. Springer, New York, NY.

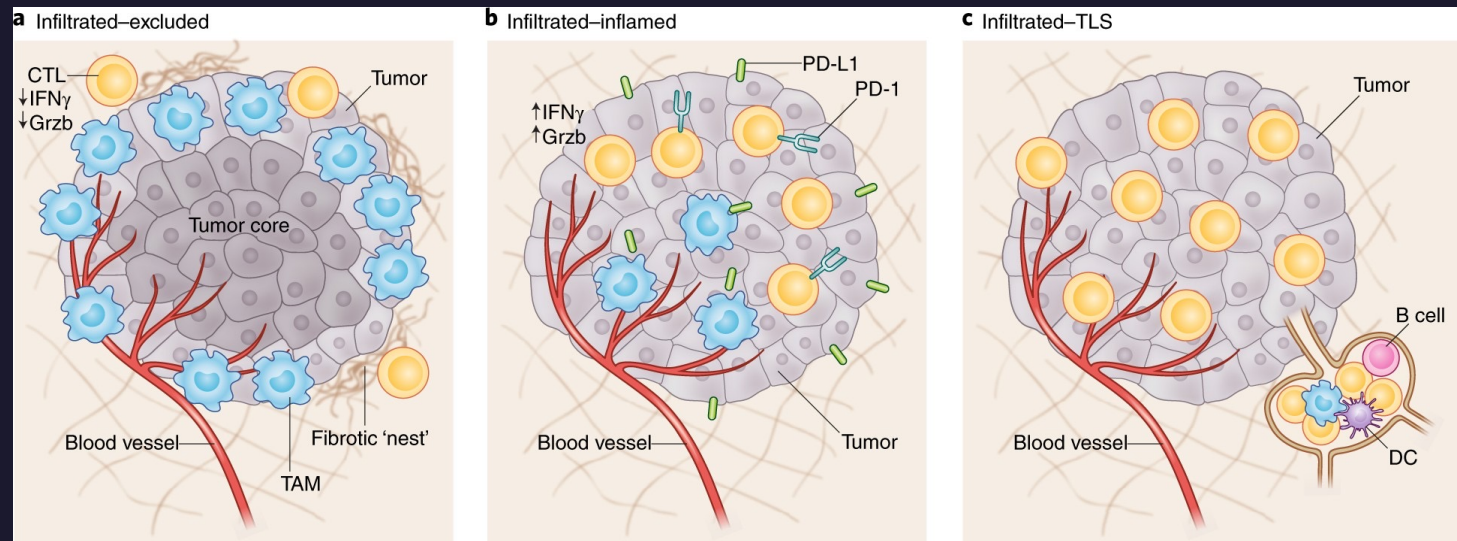
THE TUMOR IMMUNE MICROENVIRONMENT (TIME)

The past decade has seen a revolution in cancer treatments by moving away from drugs that target tumors broadly and toward the use of immunotherapies that modulate immune responses against tumors.

Retrospective analyses of patient populations treated with Immune Checkpoint Blockade (ICB) have revealed that there are classes of TIME that are associated with those tumors more inclined to ICB responsiveness.

Infiltrated-Excluded (I-E) TIMEs -- “cold” tumors.

TIMEs that are broadly populated with immune cells but are relatively void of CTLs in the tumor core. CTLs localized along the border of the tumor mass in the invasive margin or ‘caught’ in fibrotic nests. I-E TIMEs, compared with more inflamed TIMEs, contain CTLs with low expression of the activation markers *GZMB* (*GRZB*) and *IFNG* and poor infiltration of CTLs into the tumor core. -melanoma



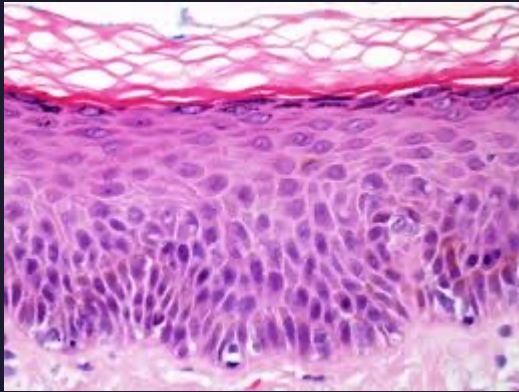
Infiltrated-inflamed (I-I) TIMEs -- “hot” tumors

High infiltration of CTLs expressing PD-1 and leukocytes and tumor cells expressing the immune-dampening PD-1 ligand PD-L1.

A subclass of I-I TIMEs, TLS-TIMEs, display histological evidence of tertiary lymphoid structures (TLSs), cellular composition is similar to that in lymph nodes. TLSs are often correlated with a positive prognosis. Similarly to lymph nodes, TLSs can contain a substantial diversity of lymphocytes, including naive and activated conventional T cells, Treg cells, B cells and DCs. TLSs are generally present at the invasive tumor margin and in the stroma, and are thought to act as sites of lymphoid recruitment and immune activation.

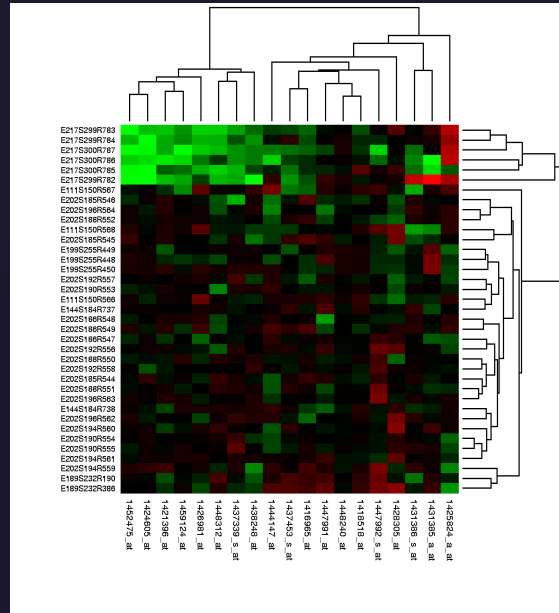
HOW DO WE STUDY TUMOR MICROENVIRONMENT

Imaging



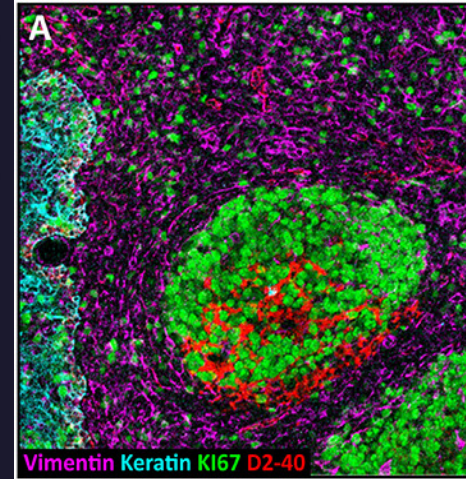
*Tissue Intact
Few Proteins
Lots of Tissue Use*

Omics



*Many Genes
Minimal Tissue Use
No Tissue Architecture*

Multiplexed Imaging



*Tissue Intact
Many Proteins
Minimal Tissue Use*

<https://doi.org/10.5389/fimmu.2019.02555G>

<https://commons.wikimedia.org/wiki/File:Heatmap.jpg>

THE PANELS



Hyperion Metal

CD3	HLA-A,B,C	PTEN
CD4	HLA-DR	p-Tyrosine
CD8a	EOMES	T-bet
CD11b	CXCR2	HIF-1a
CD11c	CXCR-4	PD-1
CD19	SOX-10	PD-L1
SOX-10	SI00A9	PD-L2
CD20	Vimentin	pERK
CD31	FoxP3	GzmB
CD44	VEGF	Ki67
CD45	Arginase-1	
CD56		
CD68		
CD134		



Vectra Opal

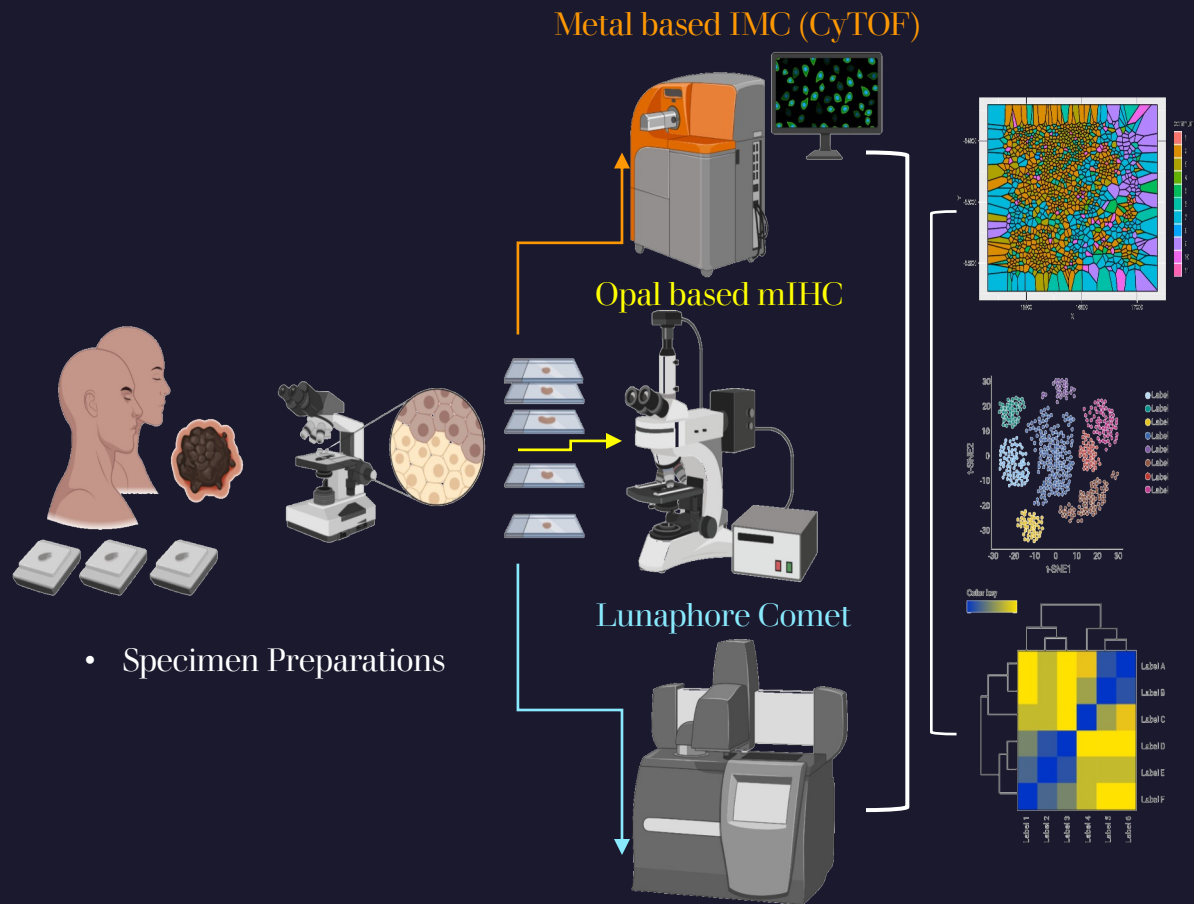
iNOS
 NT
 mPGES1
 CD74
 MIF
 CD44
 DAPI



Lunaphore Comet

SOX10	CD45
Ki67	CD3
iNOS	CD4
NT	CD8
mPGES1	CD20
CD74	CD56
CD44	CD68
MIF	CD163
Arginase-1	GrzB
	HLA-DR

COMPUTATIONAL ANALYSIS PIPELINE



- Immune composition variability could be measured
- Spatial enrichment analysis may reveal subtypes of immune-tumor organization
- Immune composition and tissue architecture could reveal more information on the same marker's functional outcome
 - CD74+ cells could be in both tumor and immune cells area but MIF+ cells proximity may change the outcome.
- Tissue organization (mixed versus compartmentalized) may correlate with immune response to the given treatment.
 - Compartmentalized phenotype correlates with better overall survival.

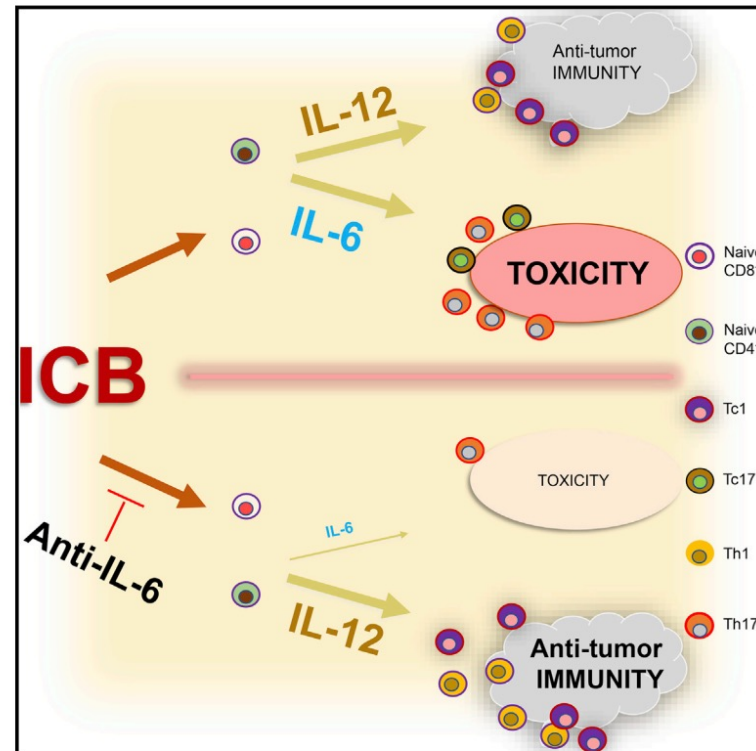
Current Findings

A network diagram consisting of numerous white circular nodes connected by thin white lines, set against a dark blue background. The nodes are arranged in a complex, interconnected pattern, resembling a molecular structure or a data network. The lines vary in thickness, with some appearing as simple thin lines and others as thicker, glowing blue bands. The overall effect is a sense of depth and connectivity.

Cancer Cell

Interleukin-6 blockade abrogates immunotherapy toxicity and promotes tumor immunity

Graphical abstract



Authors

Yared Hailemichael, Daniel H. Johnson, Noha Abdel-Wahab, ..., Patrick Hwu, Suhendan Ekmekcioglu, Adi Diab

Correspondence

adiab@mdanderson.org

In brief

Hailemichael et al. find that expression of interleukin-6, a Th17-cell differentiation cytokine, and neutrophil and chemotactic markers increase in inflamed tissue of patients and mice receiving immunotherapy. Blockade of IL-6 reduces Th17 and increases Th1 and CD8⁺ T effector cell density in tumor, mitigates ICB-induced autoimmunity, and potentiates antitumor immunity.

Article

Interleukin-6 blockade abrogates immunotherapy toxicity and promotes tumor immunity

Yared Hailemichael,^{1,18} Daniel H. Johnson,^{1,14,18} Noha Abdel-Wahab,^{1,2,15,18} Wai Chin Foo,³ Salah-Eddine Bentebibel,¹ May Daher,⁴ Cara Haymaker,⁵ Khalida Wani,⁵ Chantal Saberian,¹ Dai Ogata,¹ Sang T. Kim,² Roza Nurieva,^{6,17} Alexander J. Lazar,^{3,5,16} Hamzah Abu-Sbeih,⁷ Faisal Fa'ak,¹ Antony Mathew,⁷ Yinghong Wang,⁷ Adewunmi Falohun,² Van Trinh,⁸ Chrystia Zobniw,⁸ Christine Spillson,¹ Jared K. Burks,⁹ Muhammad Awiwi,¹⁰ Khaled Elsayes,¹⁰ Luisa Solis Soto,⁵ Brenda D. Melendez,¹ Michael A. Davies,¹ Jennifer Wargo,^{11,16} Jonathan Curry,³ Cassian Yee,^{1,6} Gregory Lizee,^{1,6} Shalini Singh,⁶ Padmanee Sharma,^{6,12,13} James P. Allison,^{9,13} Patrick Hwu,¹ Suhendan Ekmekecioglu,¹ and Adi Diab^{1,19,*}

¹Department of Melanoma Medical Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

²Section of Rheumatology & Clinical Immunology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

³Department of Pathology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

⁴Department of Stem Cell Transplantation, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

⁵Department of Translational Molecular Pathology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

⁶Department of Immunology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

⁷Department of Gastroenterology, Hepatology, and Nutrition, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

⁸Pharmacy Clinical Programs, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

⁹Department of Leukemia, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

¹⁰Department of Abdominal Imaging, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

¹¹Department of Surgical Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

¹²Department of Genitourinary Medical Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

¹³The Immunotherapy Platform, The University of Texas MD Anderson Cancer Center, Houston, TX, USA

¹⁴Precision Cancer Therapies Program, Department of Hematology and Medical Oncology, Ochsner Health, New Orleans, LA, USA

¹⁵Department of Rheumatology and Rehabilitation, Assiut University Hospitals, Faculty of Medicine, Assiut University, Egypt

¹⁶Department of Genomic Medicine, The University of Texas MD Anderson Cancer Center, Houston, TX

¹⁷The University of Texas MD Anderson Cancer Center UTHHealth Graduate School of Biomedical Sciences (GSBS), Houston, TX, USA

¹⁸These authors contributed equally

¹⁹Lead contact

*Correspondence: adiab@mdanderson.org

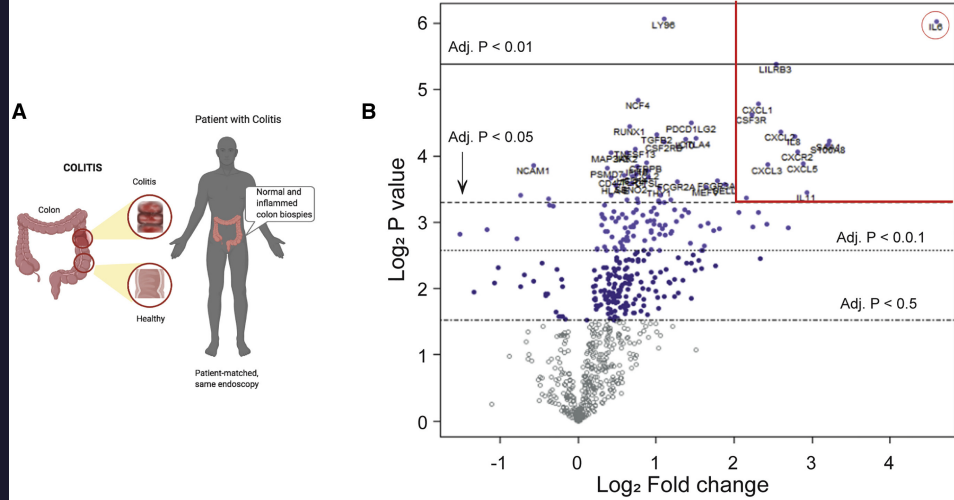
<https://doi.org/10.1016/j.ccell.2022.04.004>

SUMMARY

Immune checkpoint blockade (ICB) therapy frequently induces immune-related adverse events. To elucidate the underlying immunobiology, we performed a deep immune analysis of intestinal, colitis, and tumor tissue from ICB-treated patients with parallel studies in preclinical models. Expression of interleukin-6 (IL-6), neutrophil, and chemotactic markers was higher in colitis than in normal intestinal tissue; T helper 17 (Th17) cells were more prevalent in immune-related enterocolitis (irEC) than T helper 1 (Th1). Anti-cytotoxic T-lymphocyte-associated antigen 4 (anti-CTLA-4) induced stronger Th17 memory in colitis than anti-program death 1 (anti-PD-1). In murine models, IL-6 blockade associated with improved tumor control and a higher density of CD4⁺/CD8⁺ effector T cells, with reduced Th17, macrophages, and myeloid cells. In an experimental autoimmune encephalomyelitis (EAE) model with tumors, combined IL-6 blockade and ICB enhanced tumor rejection while simultaneously mitigating EAE symptoms versus ICB alone. IL-6 blockade with ICB could de-couple autoimmunity from antitumor immunity.

Highlights

- Immunotherapy increases expression of Th17 and Tc17 cell differentiation cytokine IL-6
- Th17 cells are more prevalent in enterocolitis than Th1
- IL-6 blockade reduces Th17, increases Th1 and Tc1 cell density in ICB-treated tumors
- Blockade of IL-6 decouples ICB antitumor immunity and toxicity



IL-6-mediated inflammation was observed in immune checkpoint blockade induced immune-related enterocolitis (irEC) samples from patients with cancer

(A) Schematic diagram for sample collection for gene expression profiling and multiplex IHC analyses.

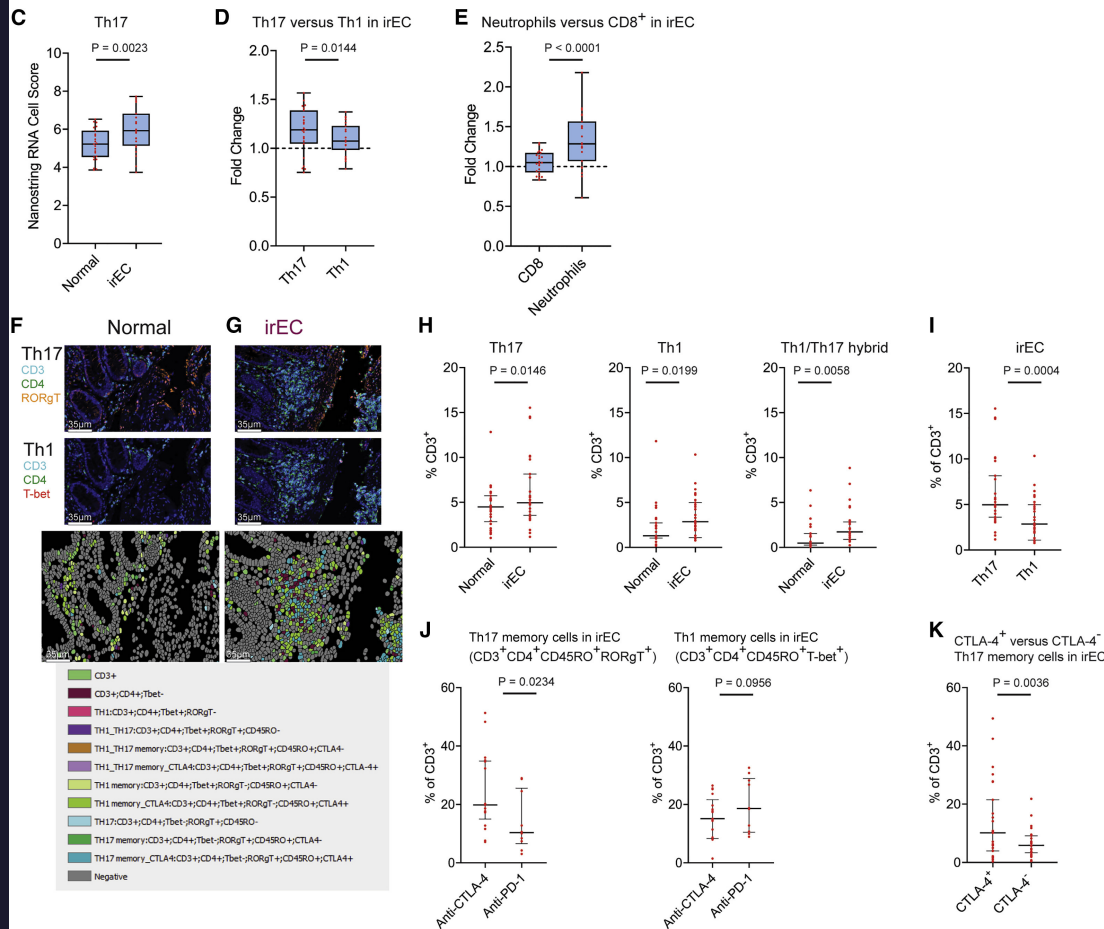
(B) Volcano plot of irEC compared with normal intestinal tissue. Significantly upregulated genes with log₂ fold change >2 are shown inside the red lines. IL-6 log₂ fold change (red circle).

(C–E) Box plots visualize estimate of abundance of immune cell subset populations using expression of characteristic genes.

(C) Th17 cells within irEC compared with normal colon tissue.

(D) Th17 cells compared with Th1 cells in irEC.

(E) Neutrophils compared with CD8⁺ cells in irEC.



(F and G) Example of multiplex IHC with cell type annotation and visualizations.

(F) Normal intestinal tissue

(G) irEC tissue samples.

(H) Percentage of total T cells from multiplex IHC in normal intestinal tissue compared with irEC tissue samples.

(I) Percentage of Th17 cells compared with Th1 cells in irEC.

(J) Percentage of Th17 or Th1 memory cells in irEC induced by anti-CTLA-4 compared with anti-PD-1 monotherapy.

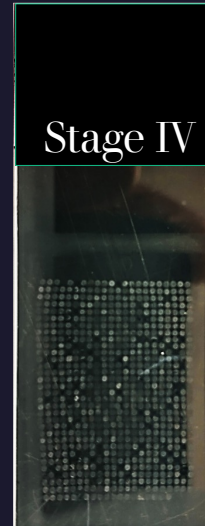
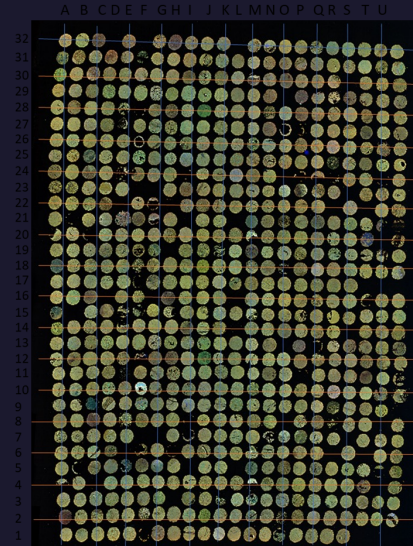
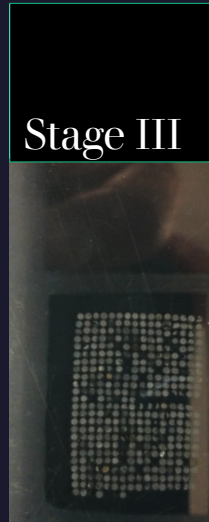
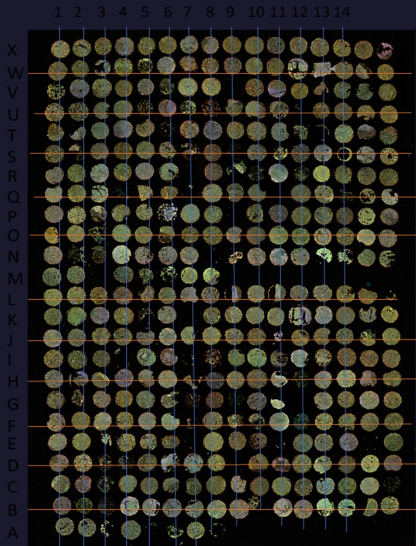
(K) CTLA-4 expression among Th17 memory cells in irEC. Data are presented as median and IQR (n = 27, unpaired t test).

Current Cohorts to Establish Signatures

Slide	Stage III		Stage IV	
	Fluorescent	Metal	Fluorescent	Metal
Antibody Conjugation	Fluorescent	Metal	Fluorescent	Metal
# of Core (ROI)	384	301	704	640
# of Plex	7	36	7	37
Type of file	.qptiff	.mcd & .txt	.qptiff	.mcd & .txt

IO TMA	
Fluorescent	Metal
77	77
7	36
.qptiff	.mcd & .txt

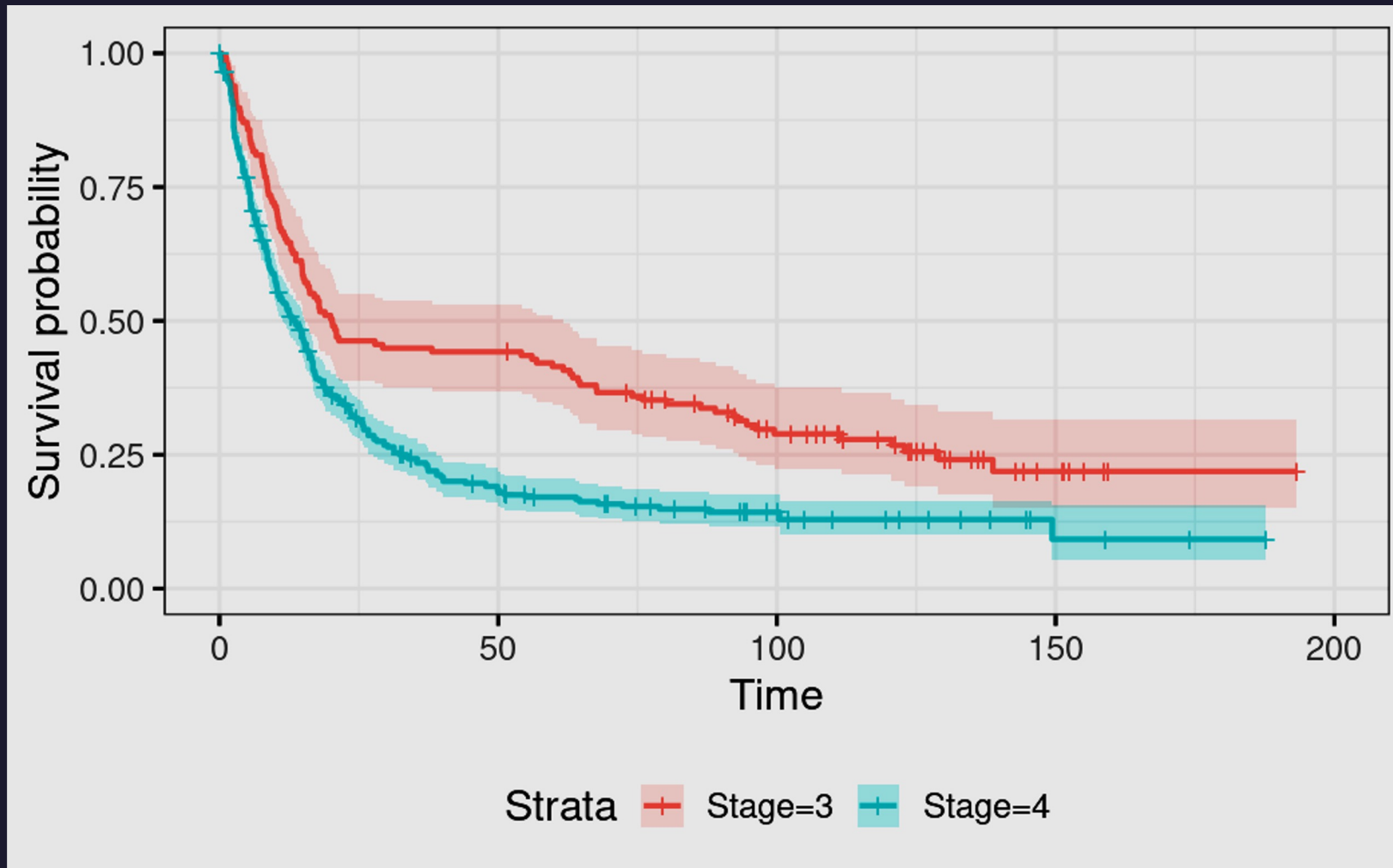
TIL Samples	
Fluorescent	Metal
130	45
7	36
.qptiff	.mcd & .txt



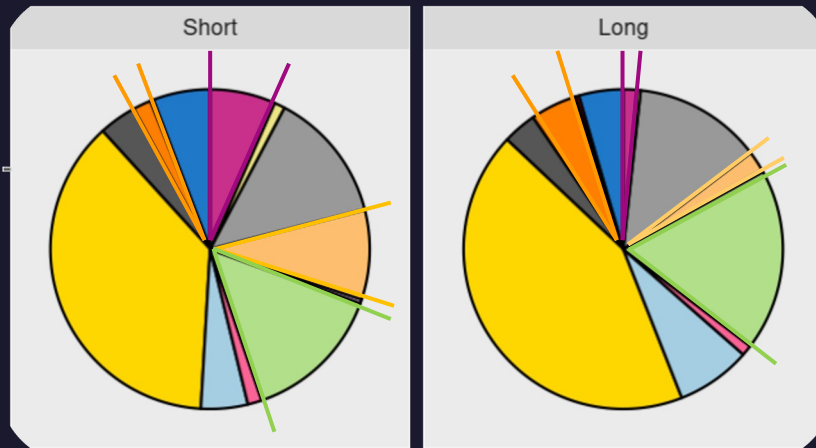
IO TMA 77

TIL Grow Treated 45	TIL Grow Un Treated 37	TIL No Grow Un Treated 48
------------------------	---------------------------	------------------------------

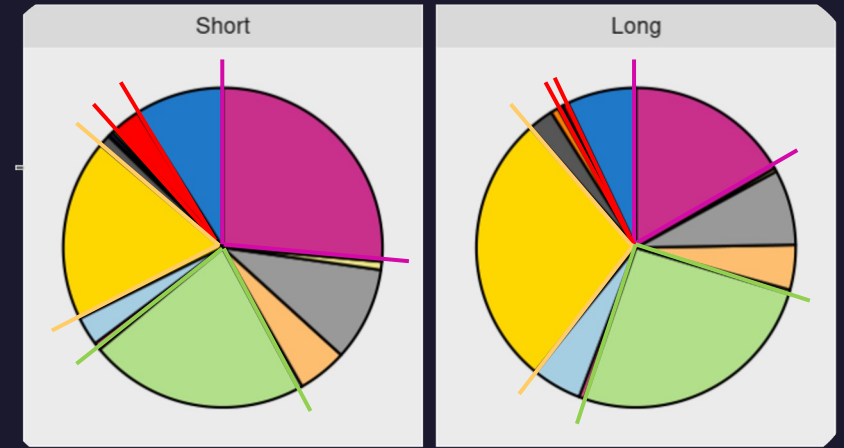
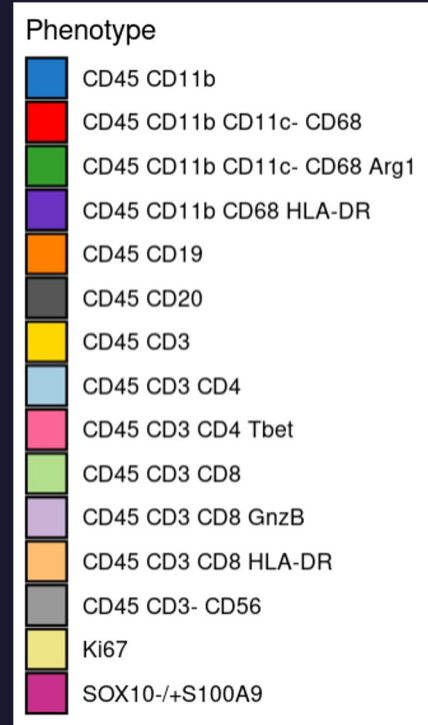
KM Survival Plots - Stage III and IV Melanoma TMA



Phenotype Frequencies Across Survival Groups

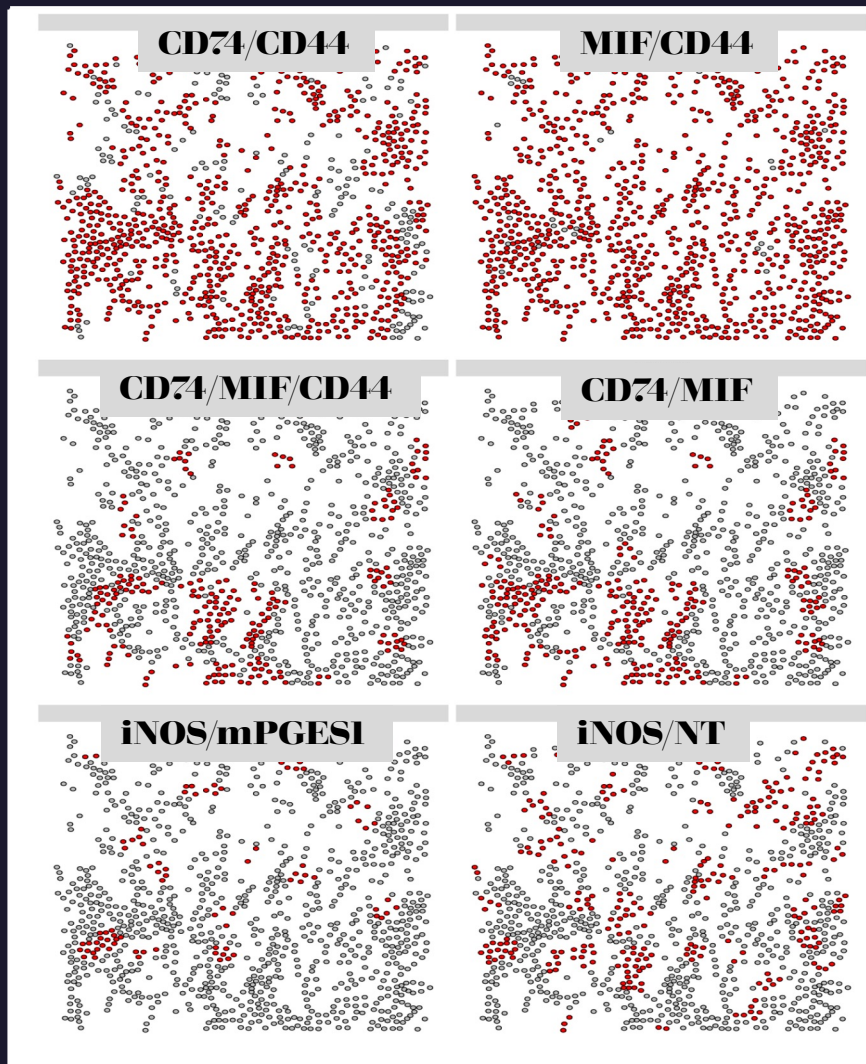


Stage III

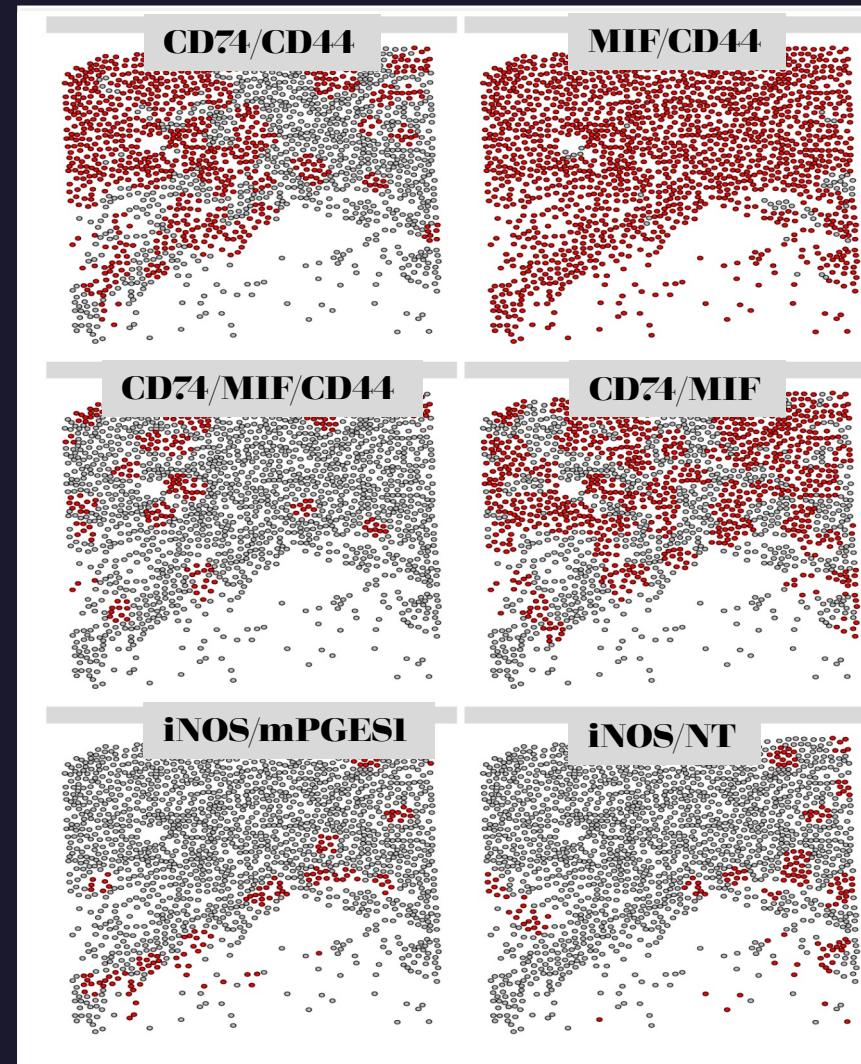


Stage IV

Spatial Analyses on Neighborhoods



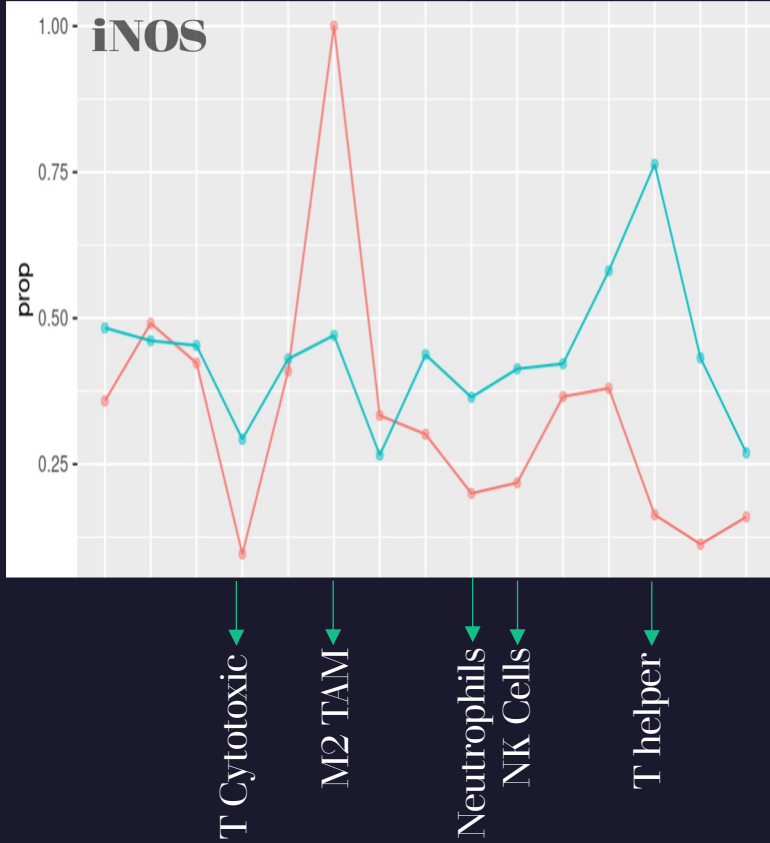
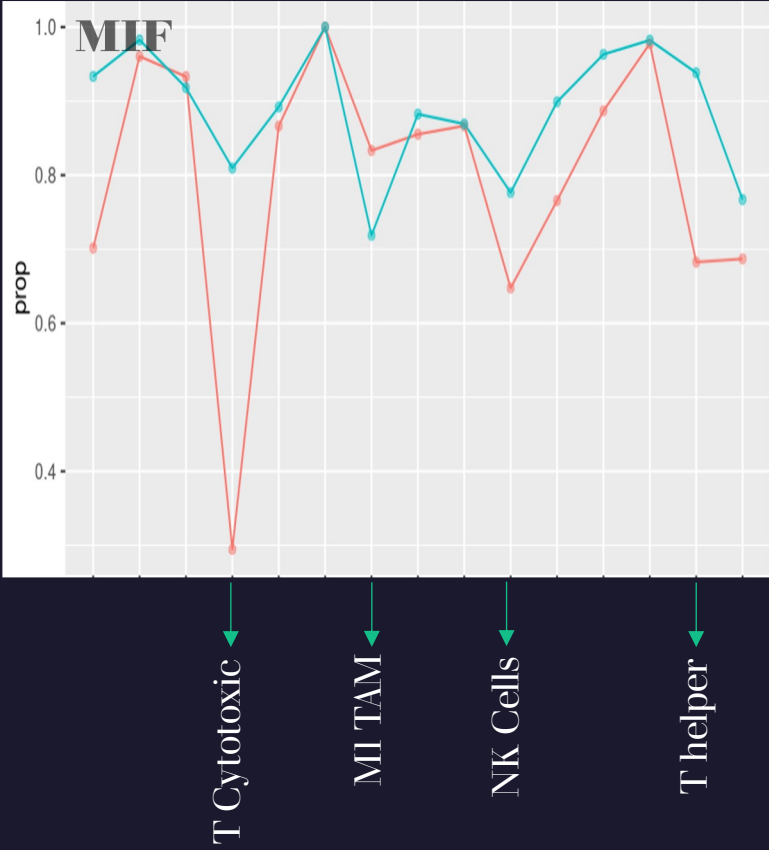
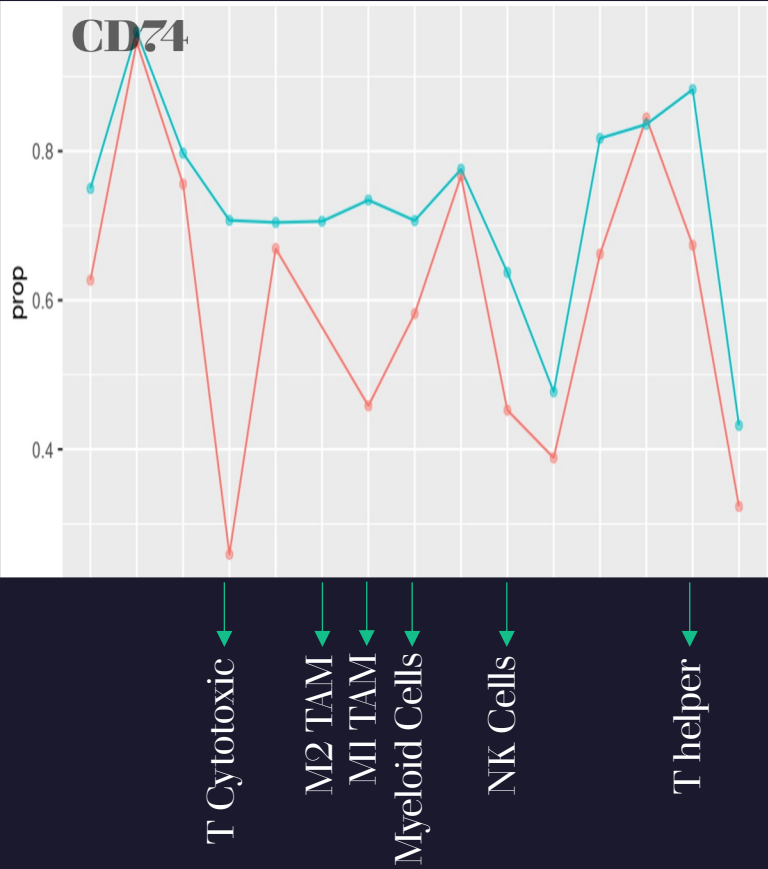
Stage III



Stage IV

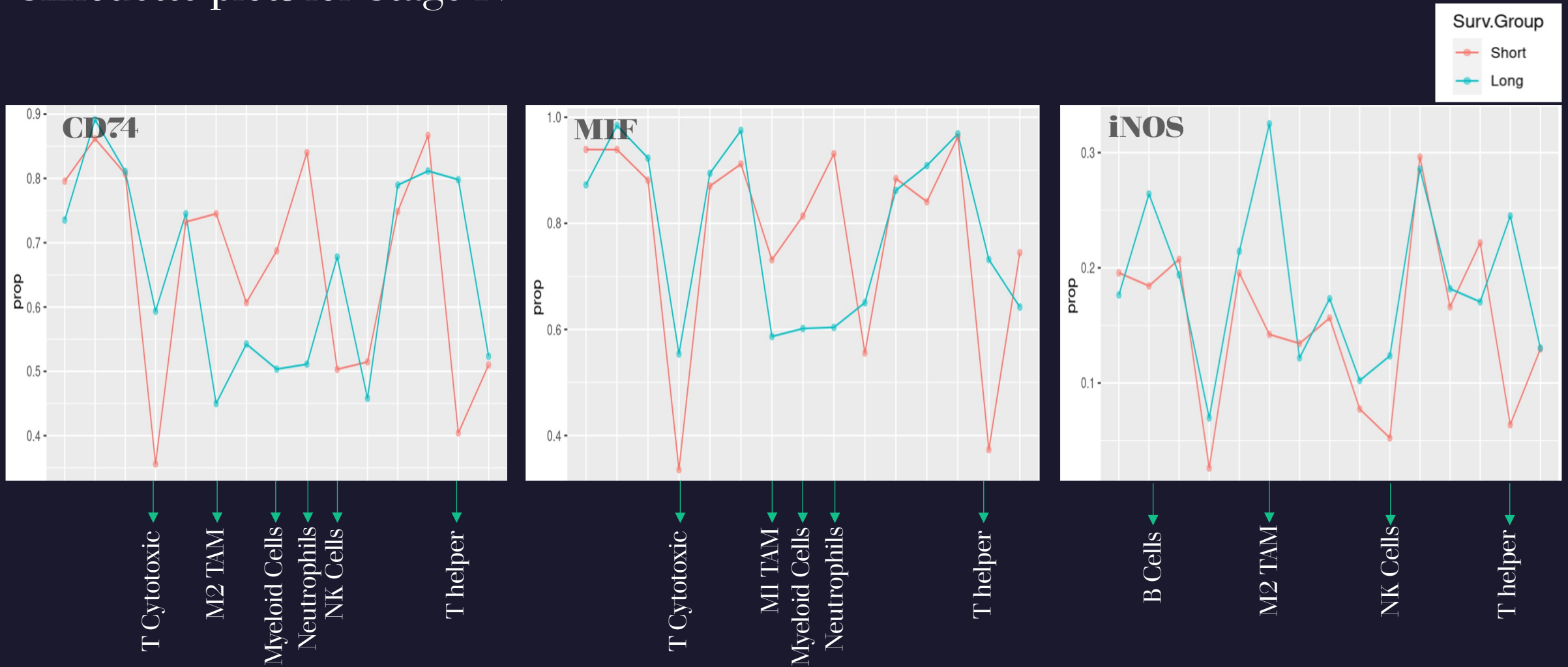
Cell Type Proportions in Neighborhoods

Silhouette plots for Stage III



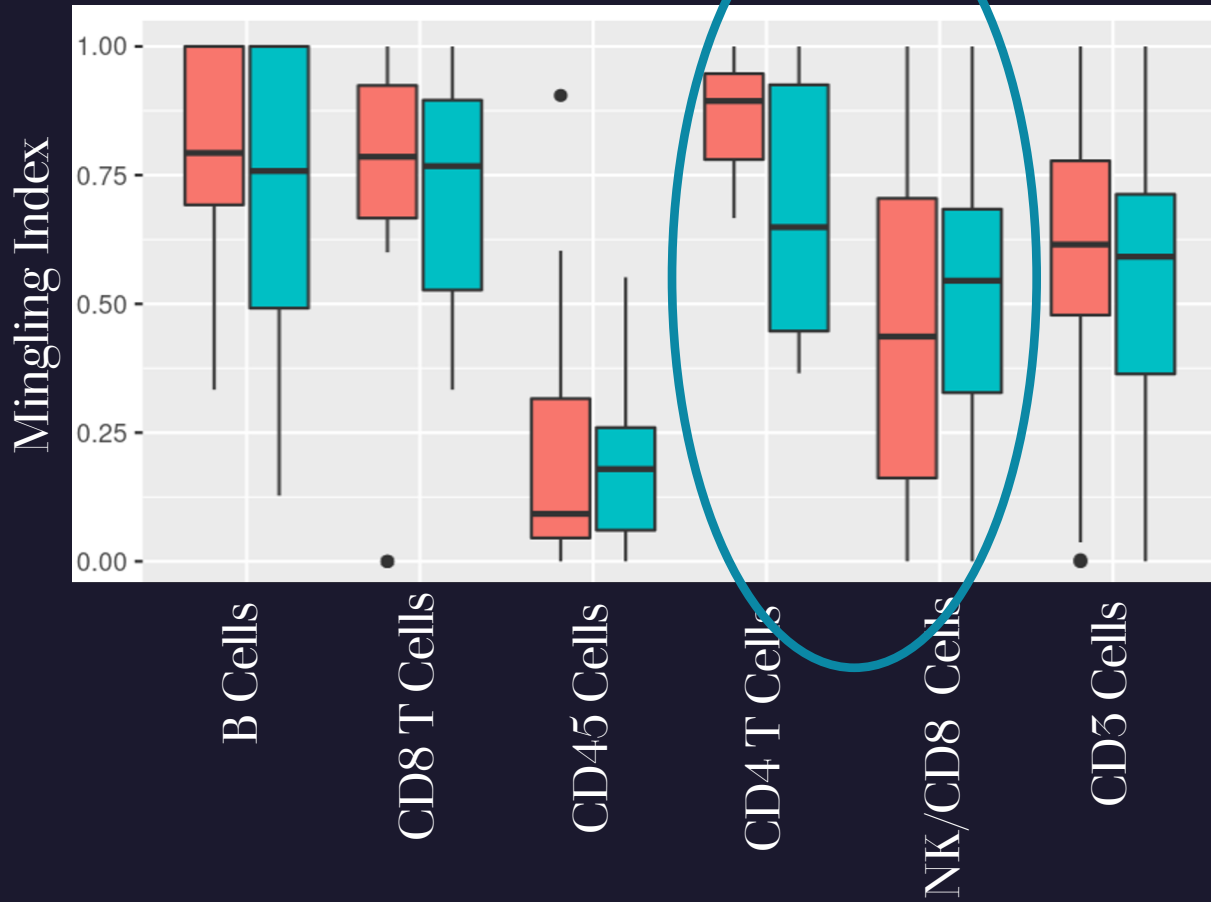
Cell Type Proportions in Neighborhoods

Silhouette plots for Stage IV

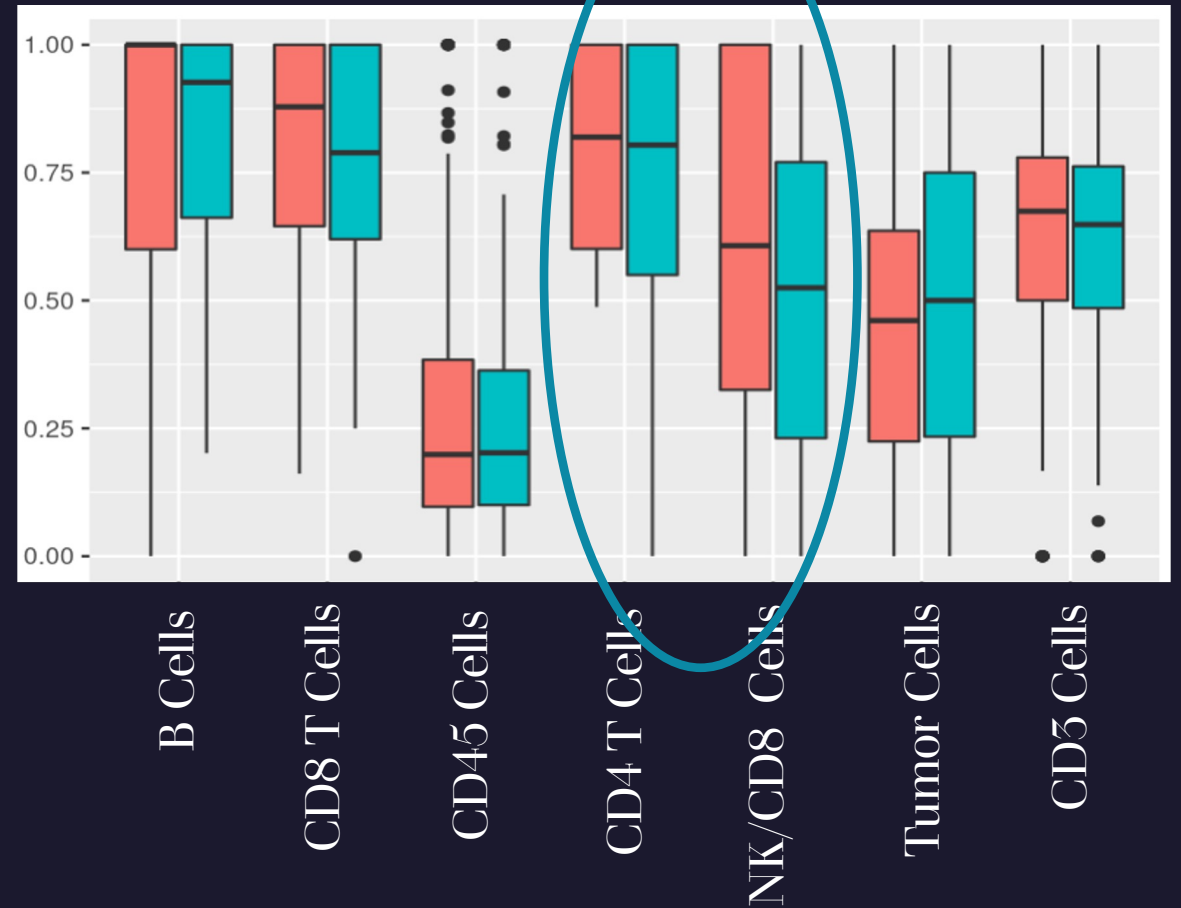


Mingling of Communities

Stage III

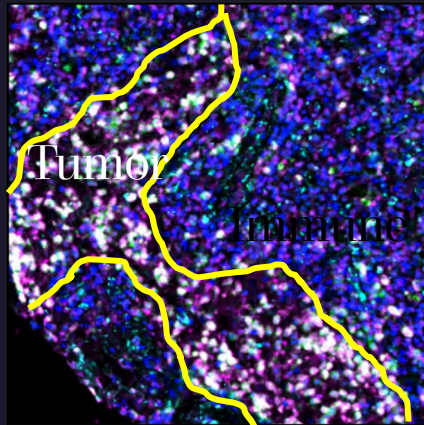


Stage IV

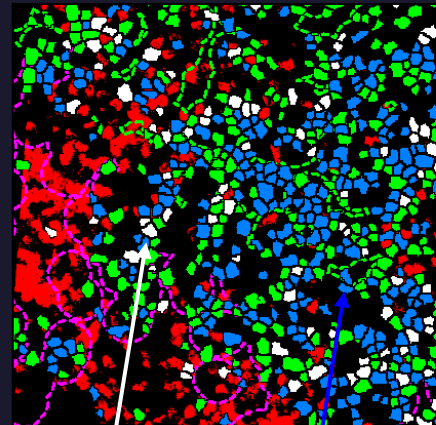


Structured Immune Composition and Organization in Melanoma

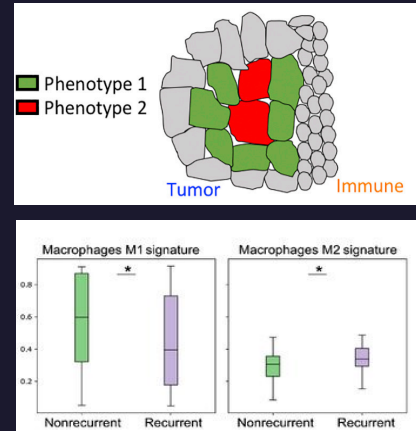
Tissue Segmentation



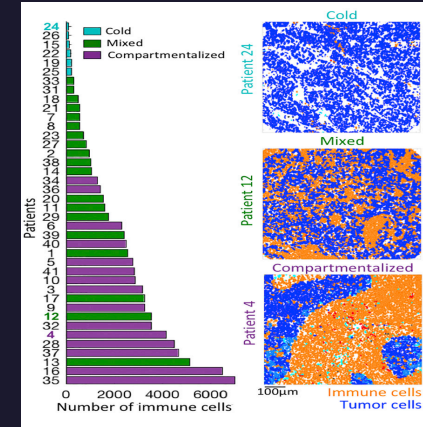
Pseudo Coloring



Assessment of Proximity/
Immune Cell Signature



Spatial Architecture



Survival Information

