

Transcriptional Signatures of Immune Surveillance and a Favorable Tumor Immune Micro- environment

SITC Cancer Immune Responsiveness Workshop

September 4, 2019

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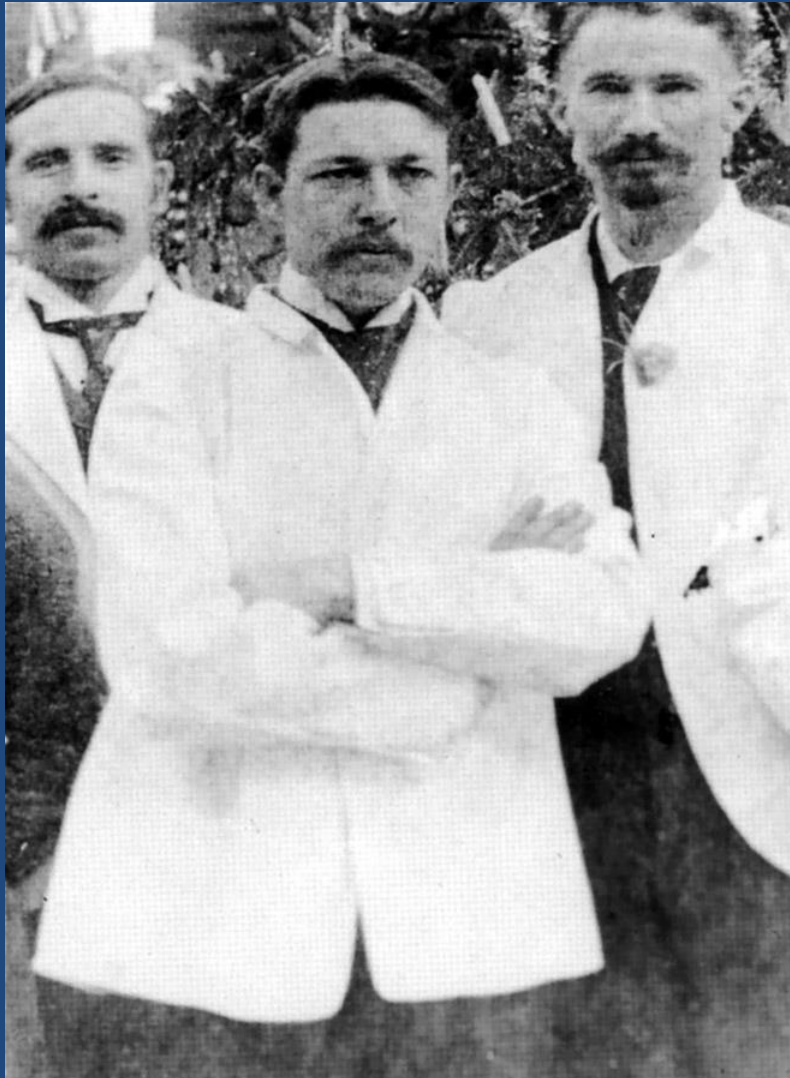
Disclosures

- Research Funding from Amgen
- Research materials provided by NanoString and Perkin Elmer (now Akoya)

Talk Outline

1. Introduction
2. Transcriptional Signature of Immune Surveillance
3. Cellular Composition of the tumor immune micro-environment (TiME) in melanoma
4. Methods to study the TME in formalin fixed archival tissues

The long history of cancer immunotherapy



New York Times - July 29, 1908

ERYSIPELAS GERMS AS CURE FOR CANCER

**Dr. Coley's Remedy of Mixed
Toxins Makes One Disease
Cast Out the Other.**

MANY CASES CURED HERE

**Physician Has Used the Cure for 15
Years and Treated 430 Cases—
Probably 150 Sure Cures.**

Following news from St. Louis that two men have been cured of cancer in the City Hospital there by the use of a fluid discovered by Dr. William B. Coley of New York, it came out yester-

Chemotherapy- still “20th century medicine”

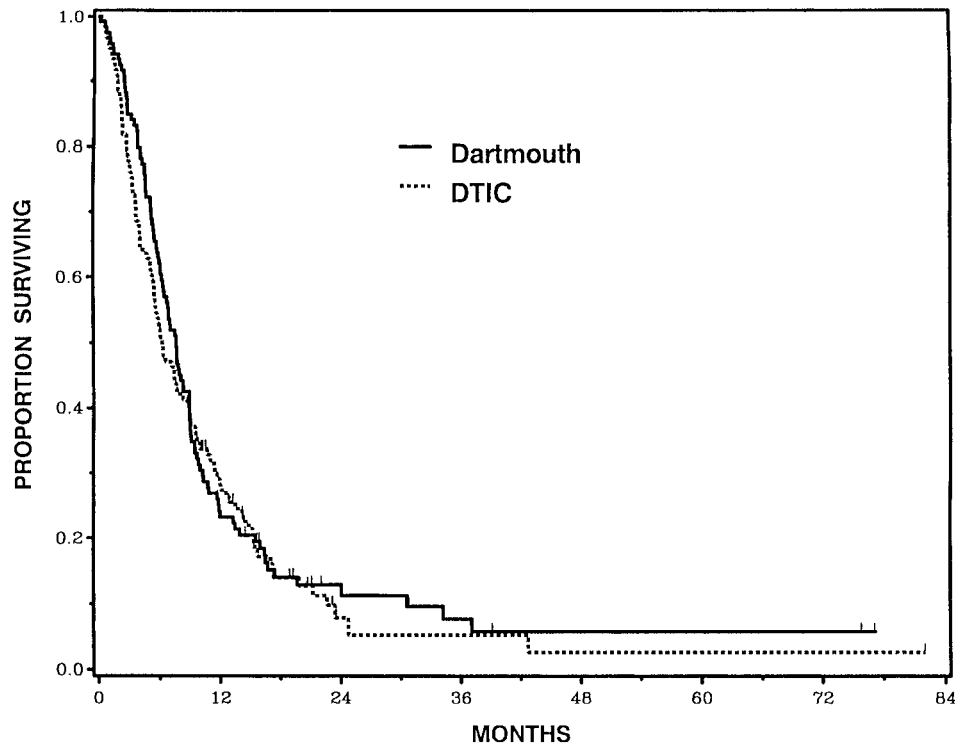
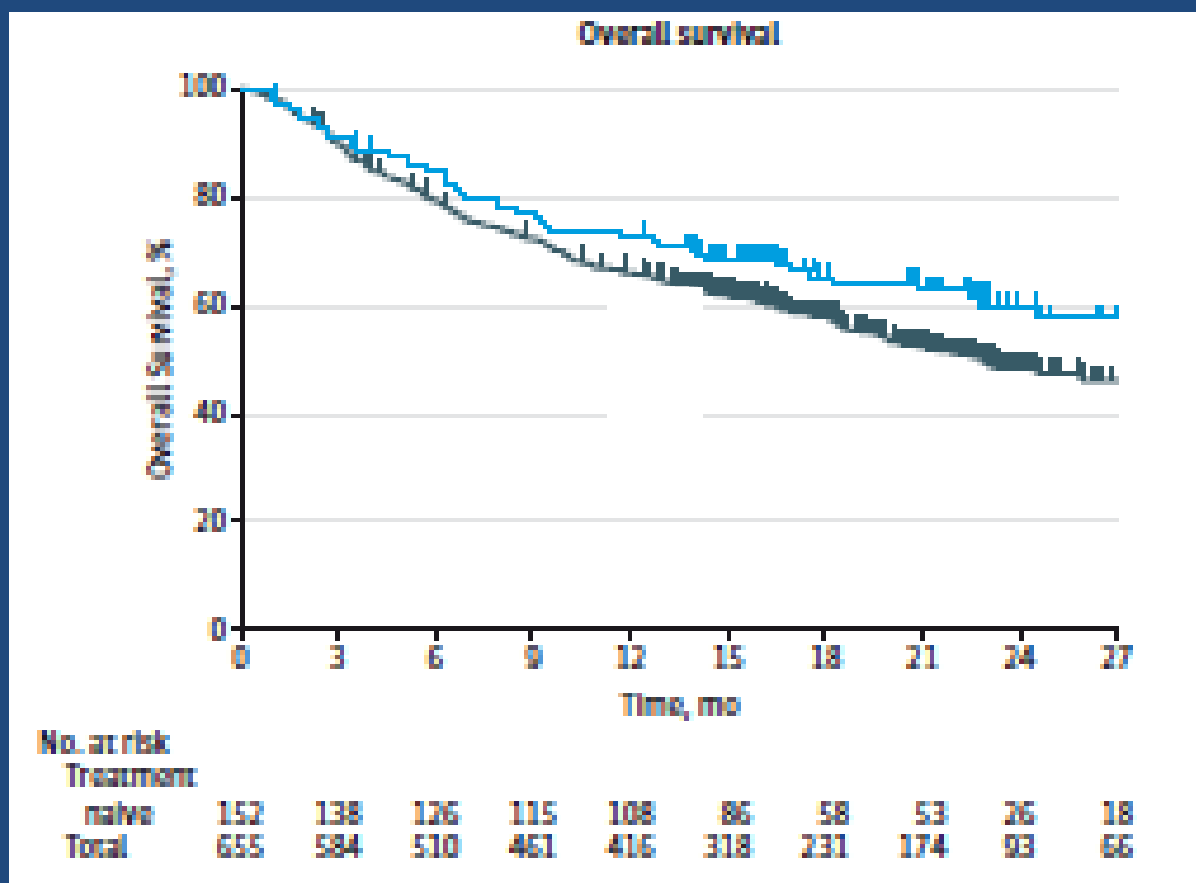


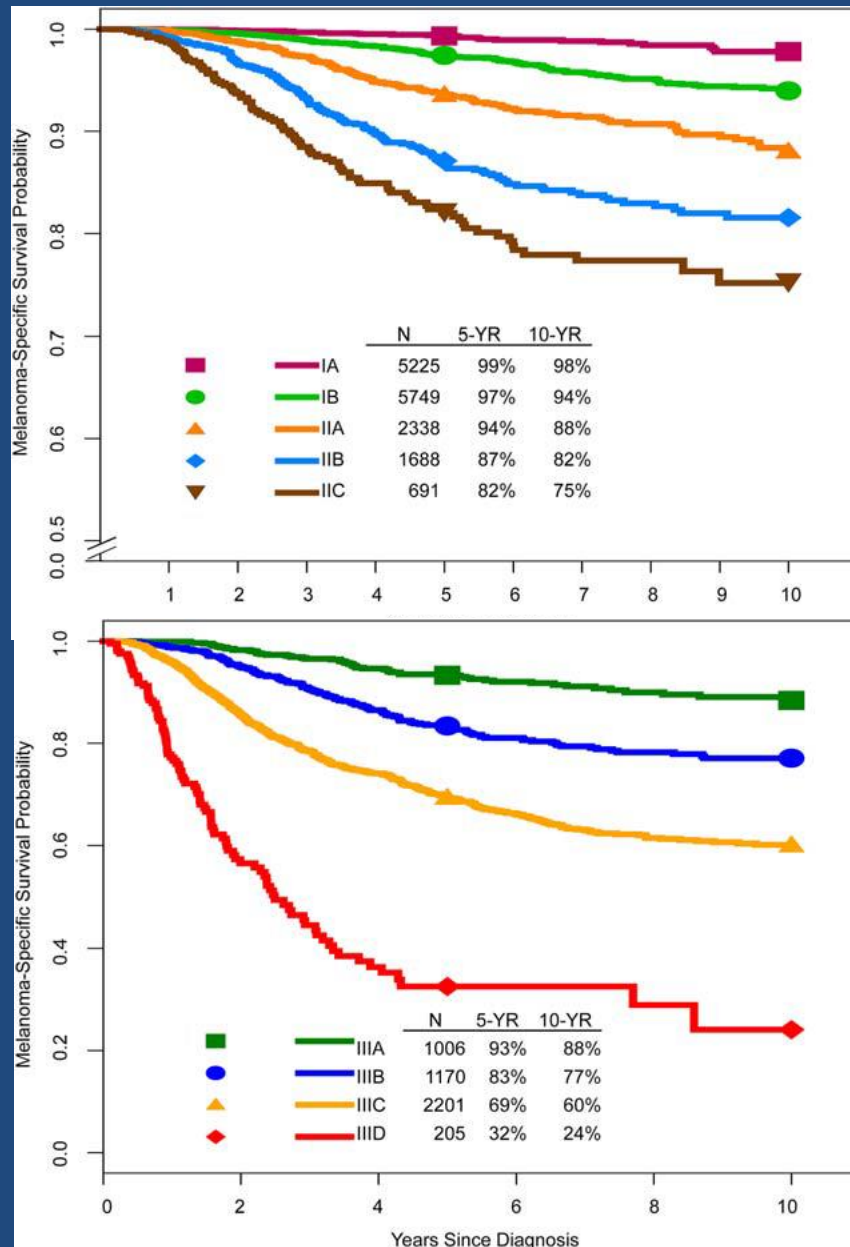
Fig 1. Kaplan-Meier survival plot of all 240 patients randomized based on intent to treat. Median survival time on Dartmouth regimen was 7.7 months (95% CI, 6.3 to 8.9 months) versus 6.3 months (95% CI, 5.4 to 8.7 months) on dacarbazine ($P = .52$). Tick marks represent censored patients.

Chapman et al, “Phase III multicenter randomized trial of the Dartmouth regimen versus dacarbazine in metastatic melanoma,” *Journal of Clinical Oncology*, 1999.

Pembrolizumab: Survival from Multiple Trials in Treatment Naïve (Light Blue) and Pre-Treated (Dark Blue) Patients



The clinical problem of stage II-III resectable melanoma



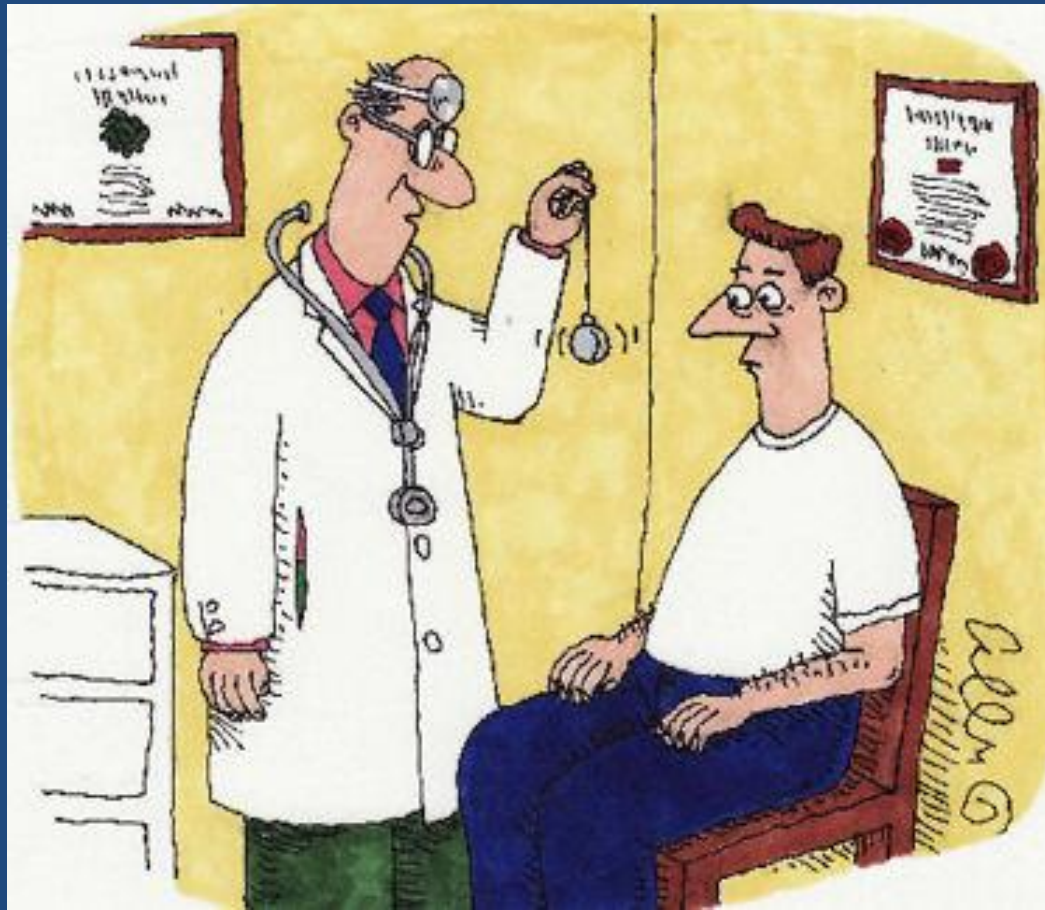
What do we tell the patient?

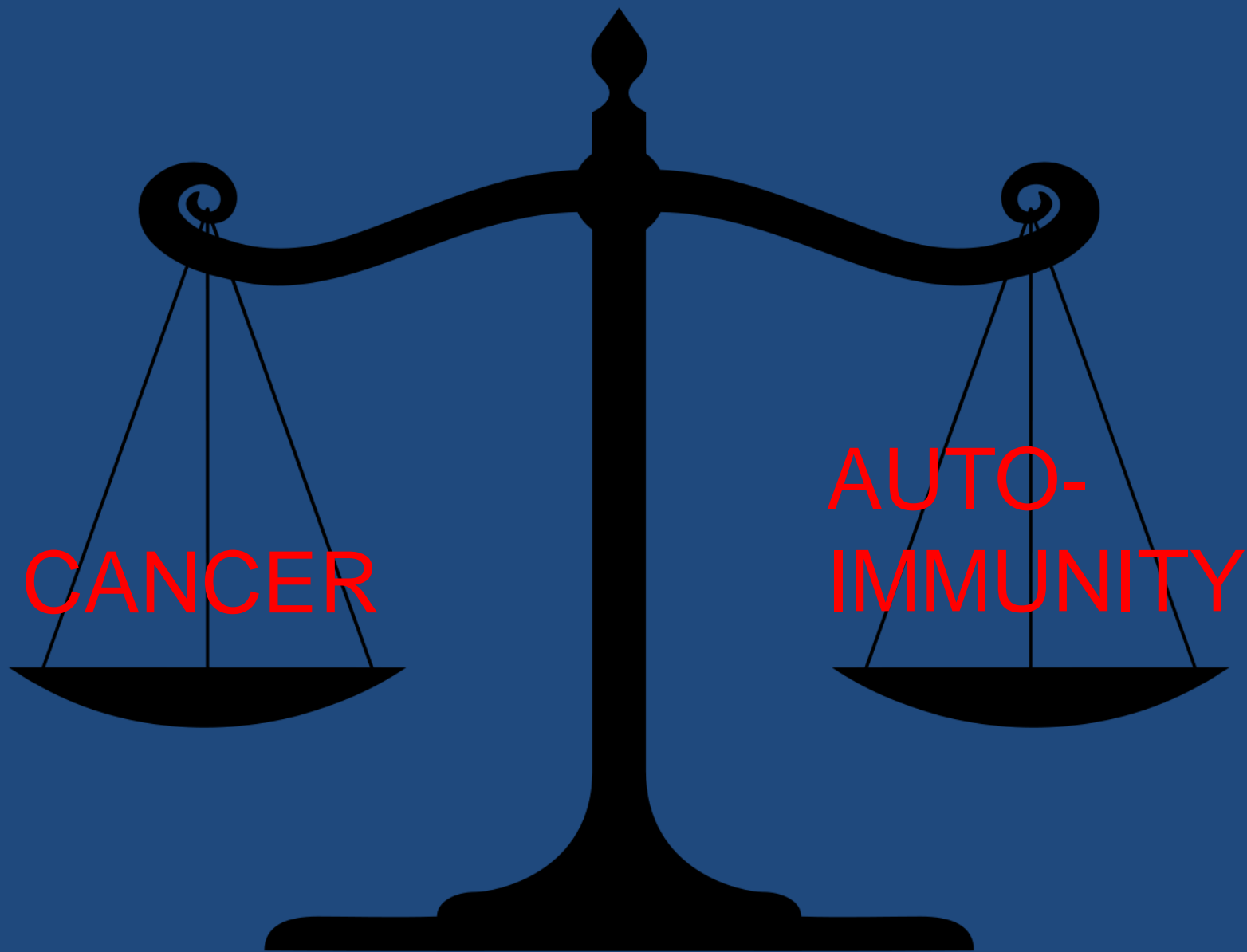
Should she take interferon or an experimental treatment?

Should she get scans? How often?

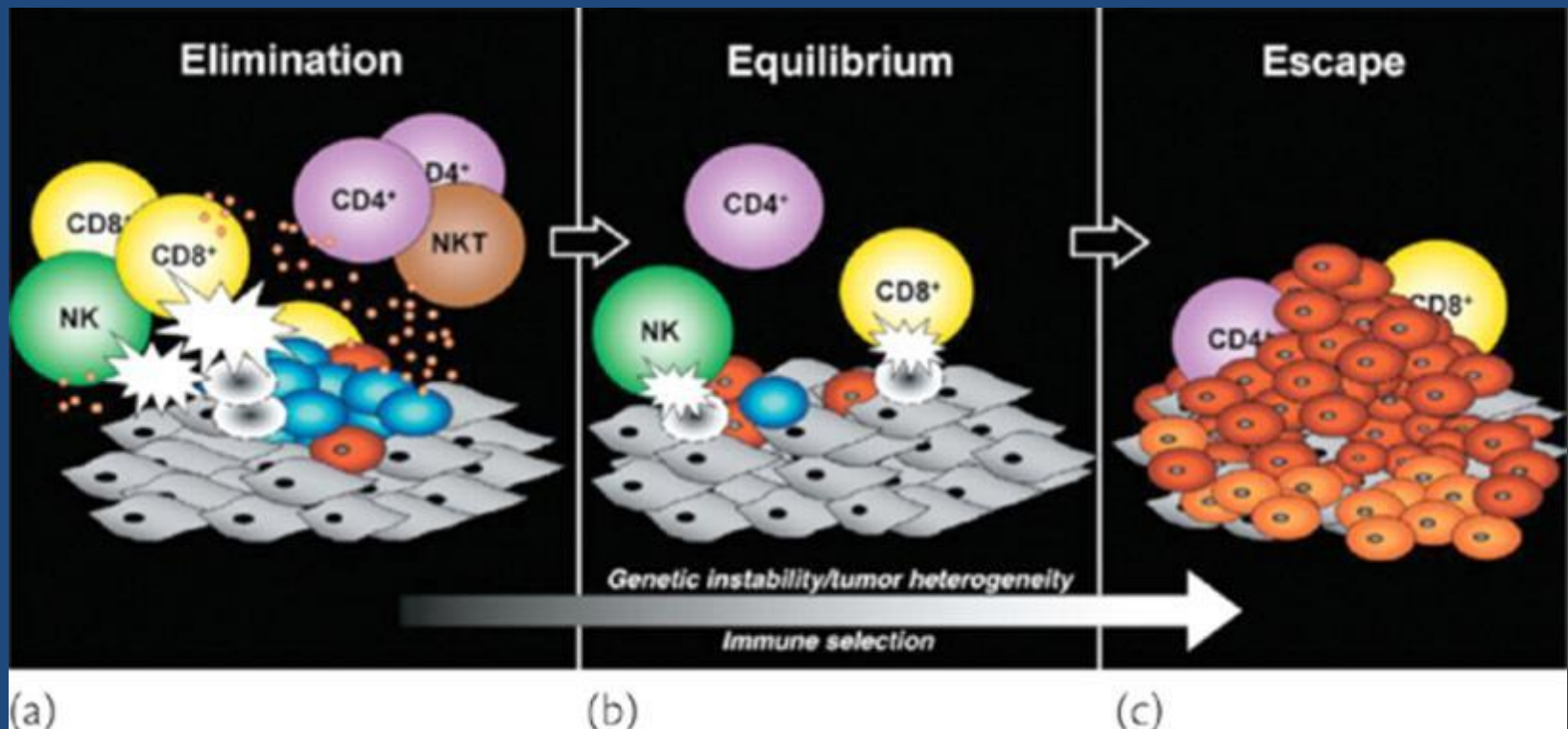
Gershenwald et al, "Melanoma Staging: Evidence-Based Changes in the AJCC 8th Edition Cancer Staging Manual," 2017

“Is your immune system working?”



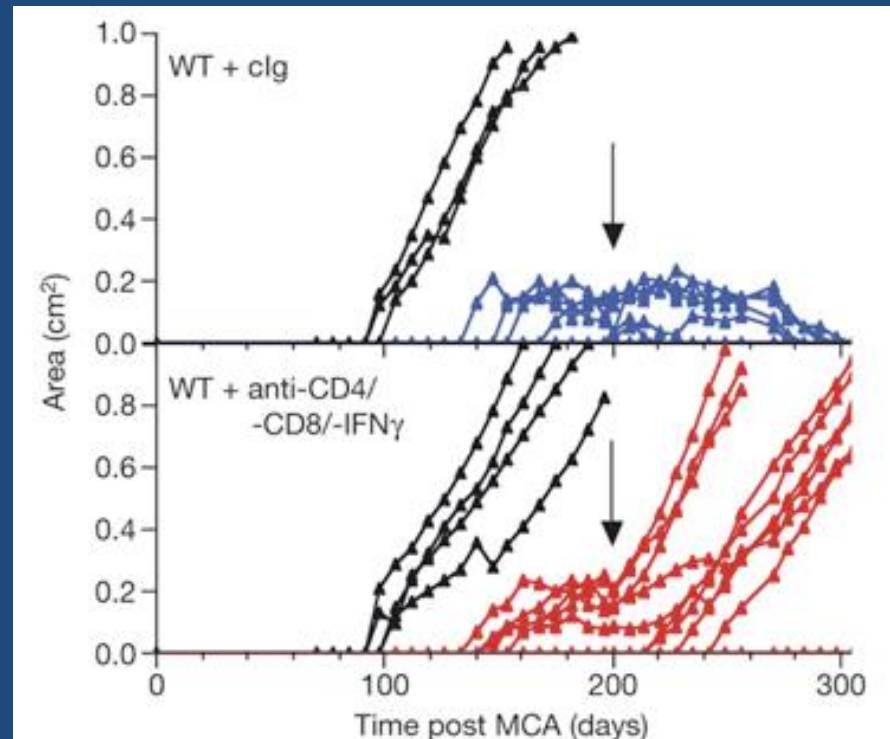
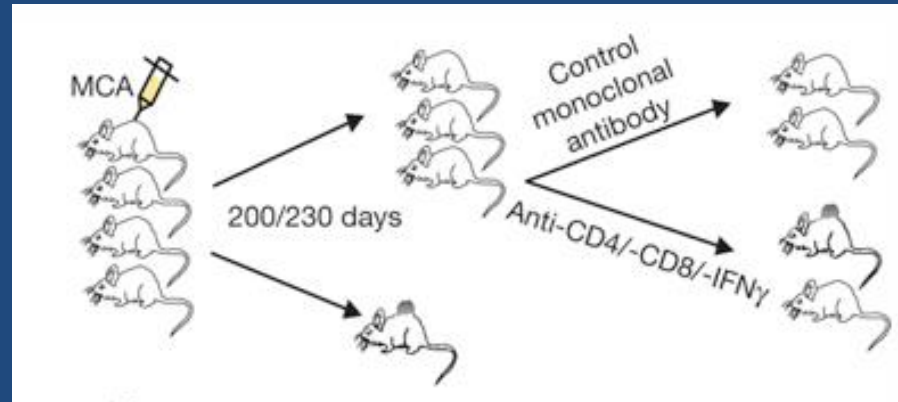


Hypothesis- One of the factors increasing risk of micrometastasis is Weakened Immunosurveillance



Can we identify patients who have weaker immune surveillance and require additional immunotherapy after surgery?

Immune surveillance controls dormant tumors



Transcriptional Signature of Immune Surveillance- Melanoma Immune Panel (MIP)

mRNA copy number for 446 genes in a training set of primary tumors from patients with resectable stage II-III melanoma

Characteristics of the Training Set

Characteristics Training Set (N=40)

Clinical characteristics

Gender

Male--no.(%) 28 (70)

Female--no.(%) 12 (30)

Age median (range) -- no. 67 (29-87)

Location of tumor

Trunk--no.(%) 24 (60)

Extremity--no.(%) 16 (40)

Stage

II--no. (%) 18 (45)

III--no. (%) 22 (55)

Pathological characteristics

Depth (mm) -- median (range)* 2.7 (1.2 -13)

Ulceration

Absent--no.(%) 21 (52)

Present--no.(%) 19 (48)

Tumor-infiltrating lymphocytes

Absent--no.(%) 7 (17)

Non-brisk--no. (%) 28 (70)

Brisk--no.(%) 5 (13)

Mitoses --median (range) 6.5 (0-26)

Patient outcome

Disease progression-- no. (%) 21 (52)

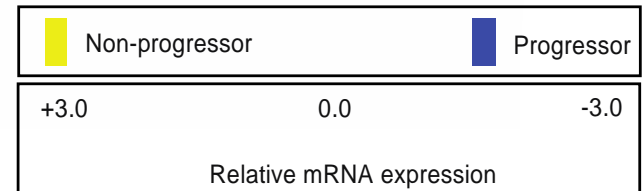
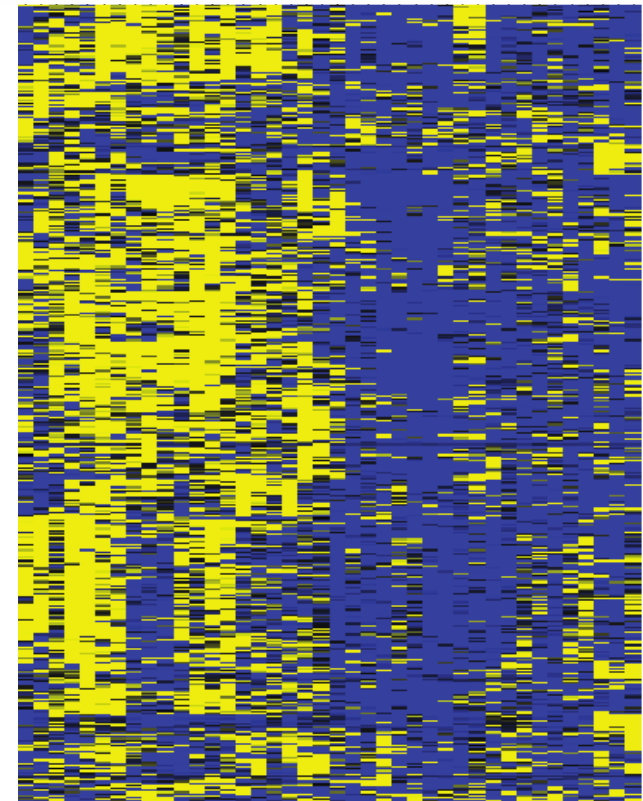
Died from melanoma--no.(%) 17 (43)

Patient Follow-up (months)

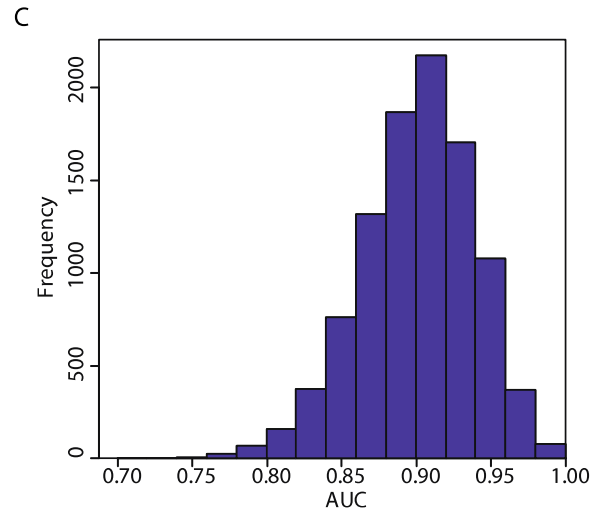
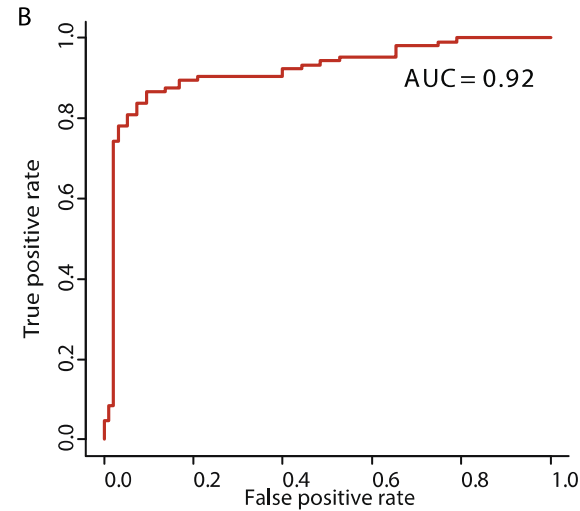
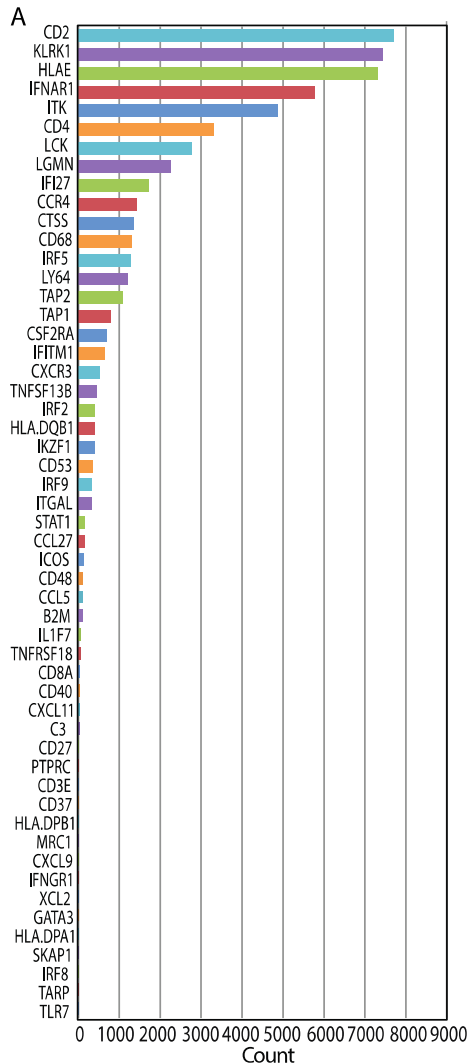
Time to death--median (range) 19 (6-81)

Time to censoring-- median(range) 61 (25-130)

* Depth is available for 39 patients.



Defining Melanoma Immune Profile- a 53 immune gene panel predictive of non-progression



Screen of publicly available primary melanoma expression data (GEO) identifies subnetwork of 758 gene module with immune function containing 42 out of the 53-gene immune panel

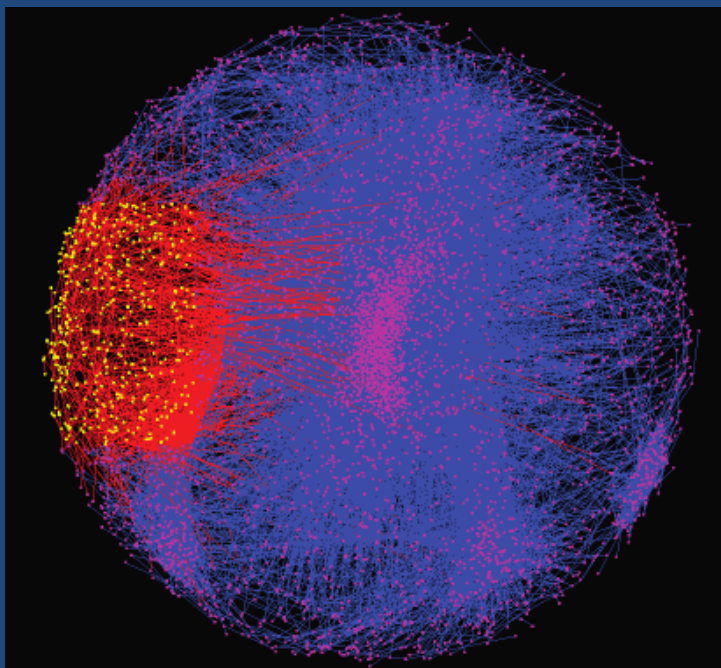
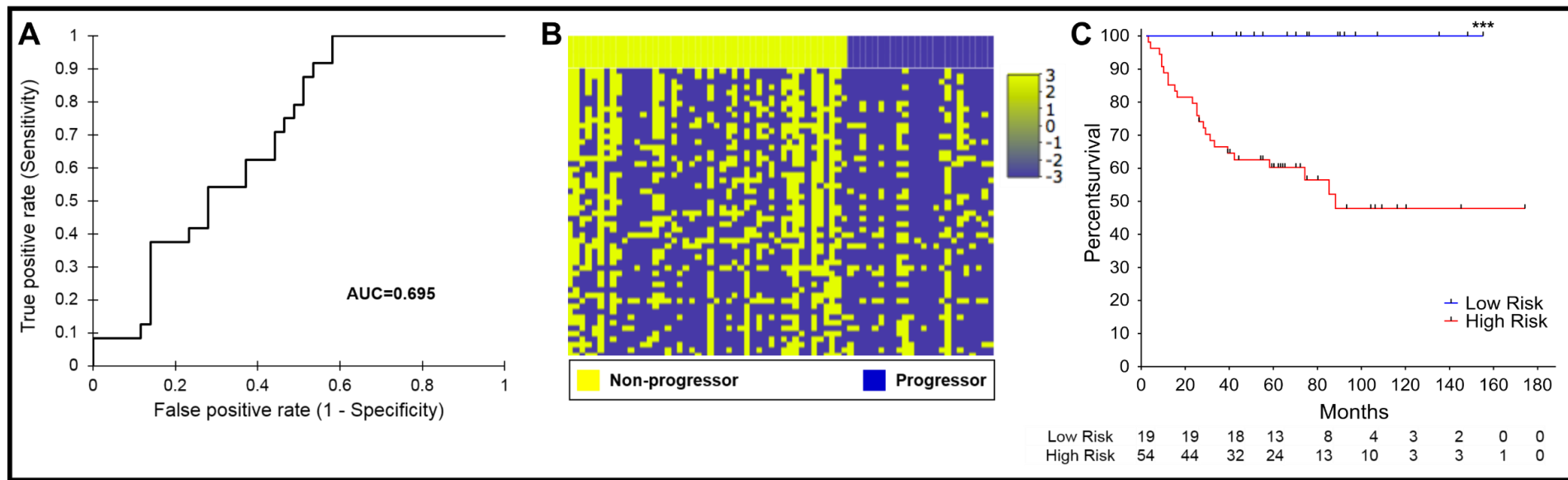


Table S6. Relative mRNA counts for top 25 hub genes comparing progressors and non-progressors in the training set.

Gene Symbol	Out-Degree	Log2 Fold Change	T-Statistic	P Value	FDR
CCR5	12	-0.5754	1.9699	0.0593	0.1598
CD8A	12	-0.9392	2.5076	0.0182	0.1021
CD3D	11	NT*	NT	NT	NT
CD8B	11	NT	NT	NT	NT
IKZF1	11	-0.5553	2.3094	0.0265	0.1044
BTK	10	-0.4292	2.3713	0.0234	0.1044
LCK	10	-0.9079	2.9279	0.0063	0.1021
CD3E	9	-0.6031	2.192	0.0357	0.1205
CD53	9	-0.5731	2.425	0.0222	0.1044
COPS2	9	NT	NT	NT	NT
CXCL9	9	-0.7667	1.9471	0.0592	0.1589
EGFR	9	NT	NT	NT	NT
EPS8L1	9	NT	NT	NT	NT
FGFR3	9	NT	NT	NT	NT
GPS1	9	NT	NT	NT	NT
MS4A1	9	NT	NT	NT	NT
PPP3CB	9	NT	NT	NT	NT
CD1A	8	-0.1511	0.5498	0.5857	0.6981
CD2	8	-0.9678	3.4058	0.0020	0.0852
CD58	8	-0.0554	0.3335	0.7406	0.8211
CD81	8	NT	NT	NT	NT
IL2RB	8	NT	NT	NT	NT
NCOR2	8	NT	NT	NT	NT
PRKD2	8	NT	NT	NT	NT
TNFRSF1B	8	NT	NT	NT	NT

* Not tested. Data is only available for those hub genes selected as part of the 446 gene panel.

Confirming MIP in a third independent patient population

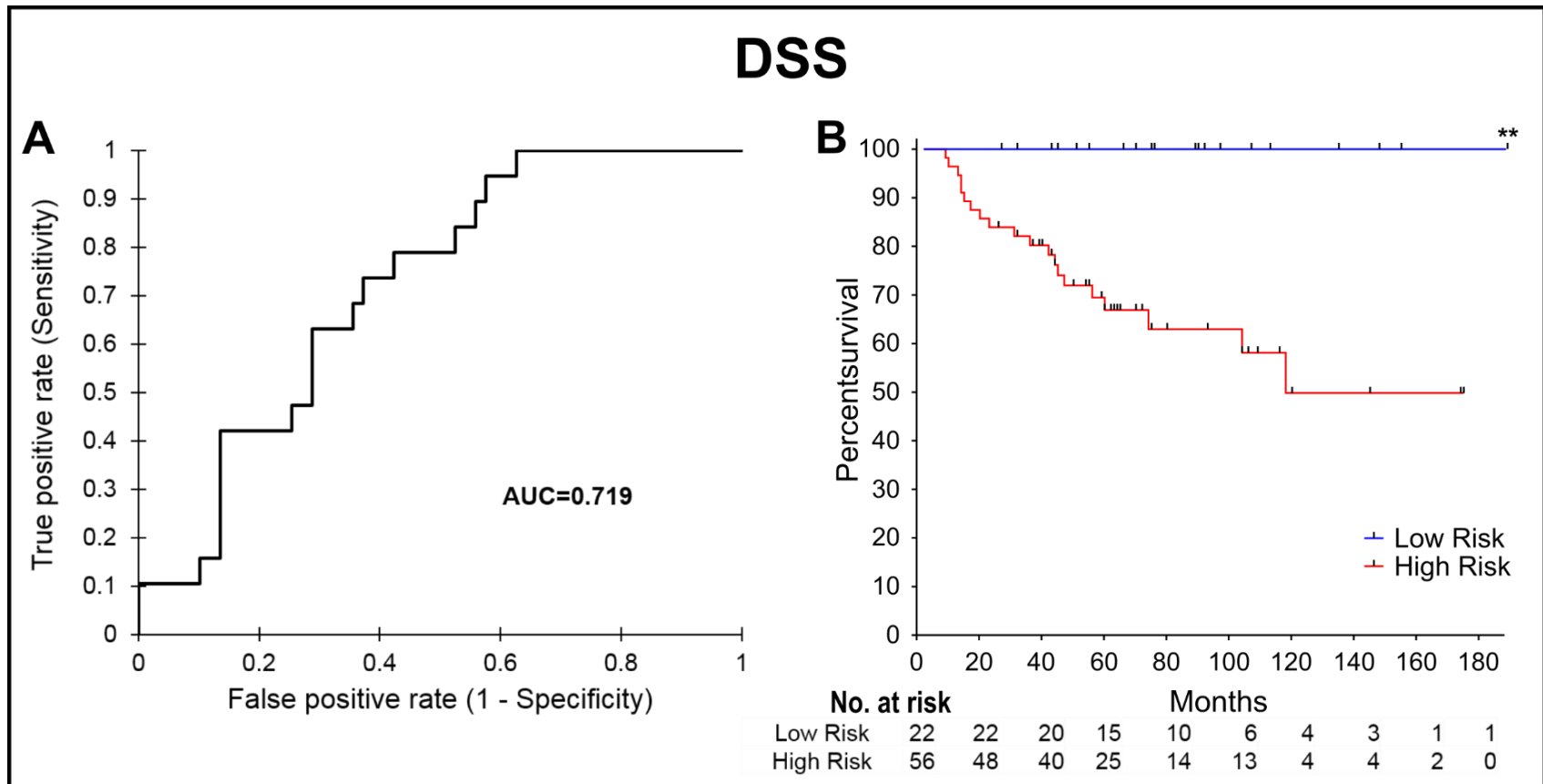


Receiver Operating Characteristic (ROC) curve analysis (AUC)=0.695, $p=0.008$).

Heat map Yellow indicates higher expression and blue indicates lower expression of each gene in the color scale.

Kaplan-Meier (KM) curve for Distant Metastasis-Free Interval (DMFI) ($p=0.0009$)

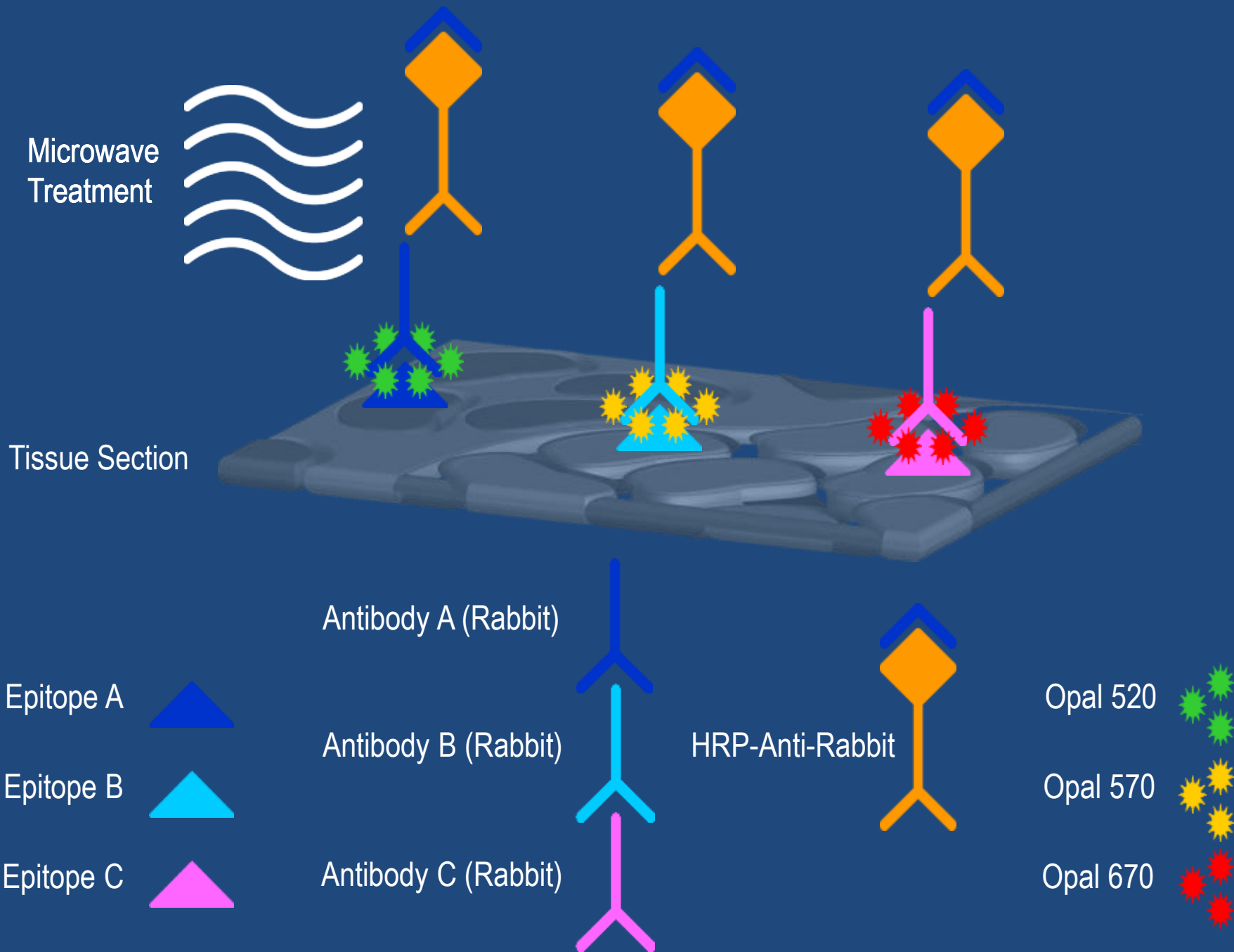
Confirming MIP in a third independent patient population



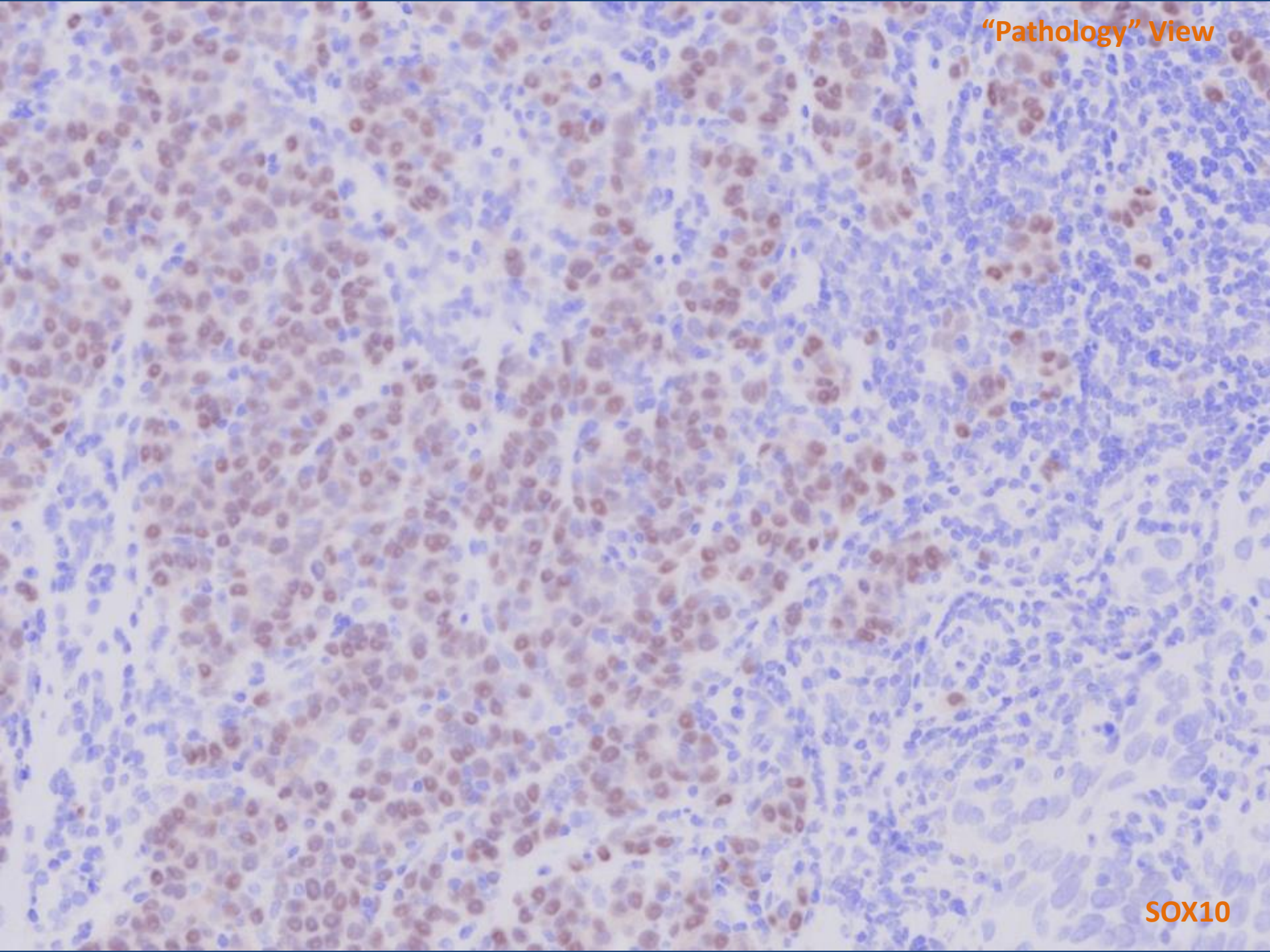
AUC curve for DSS, (n=78, AUC=0.719, p=0.004).

KM curve for DSS (p=0.003).

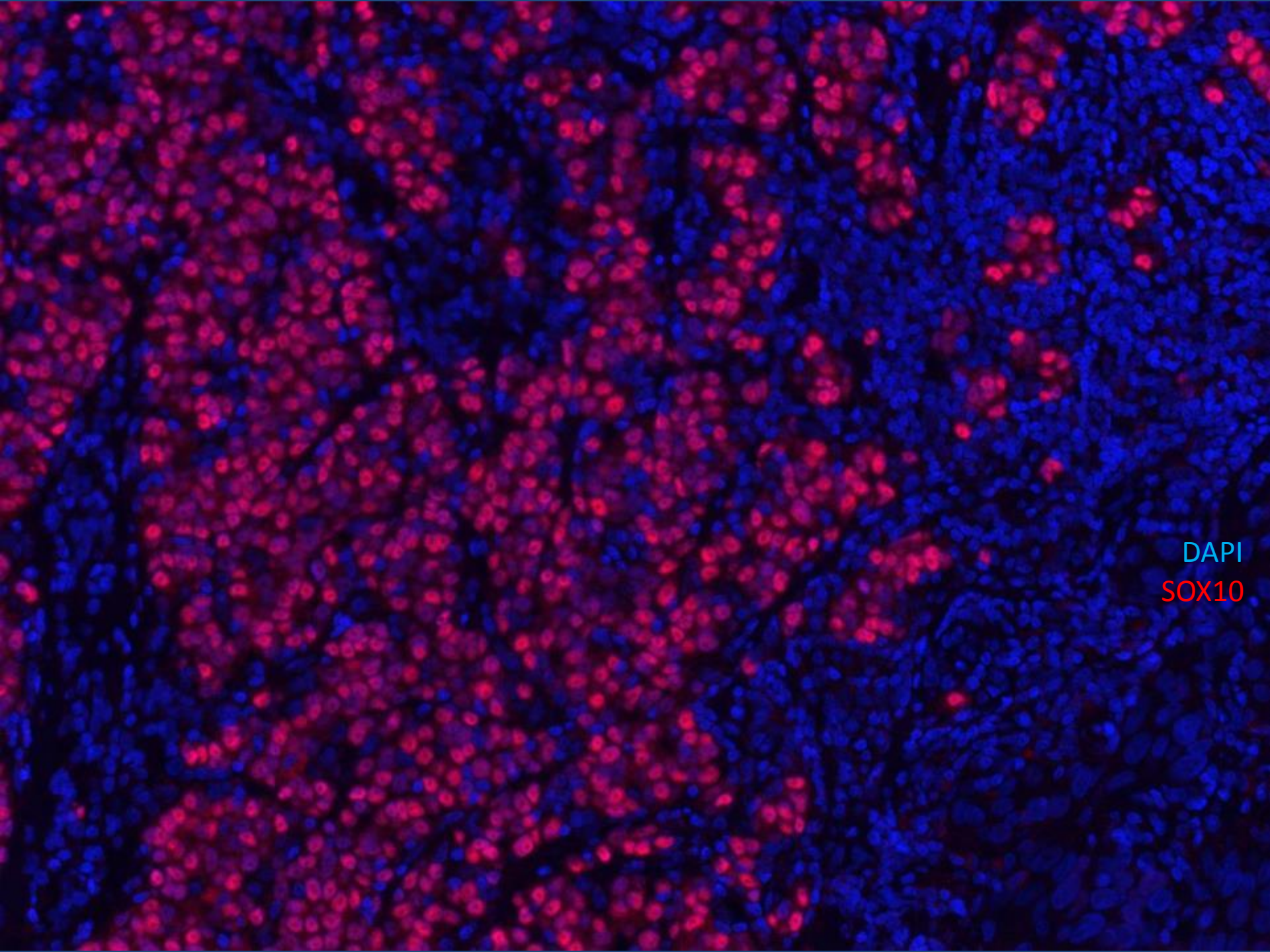
Cellular Composition of the TIME in melanoma



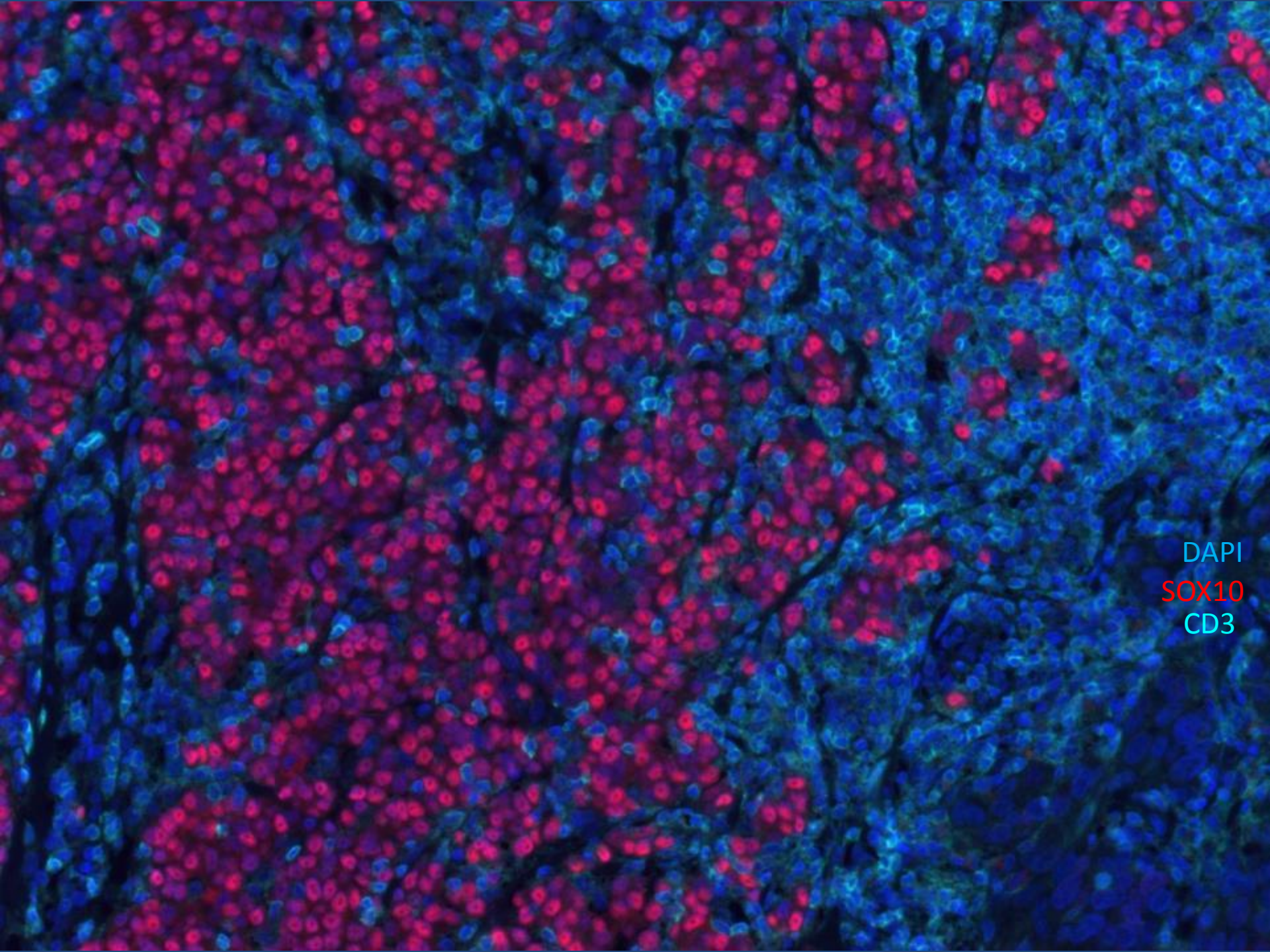
“Pathology” View



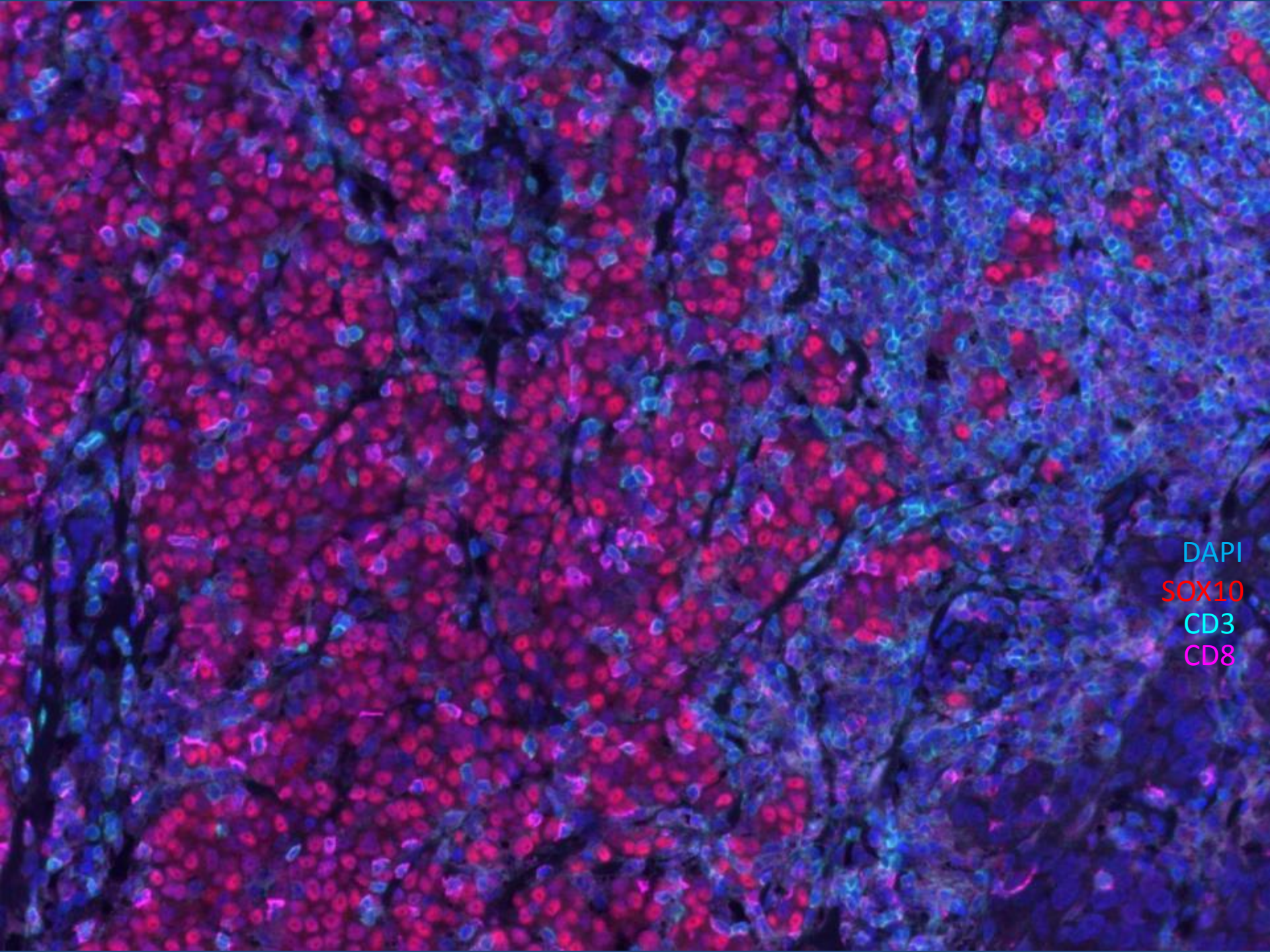
SOX10



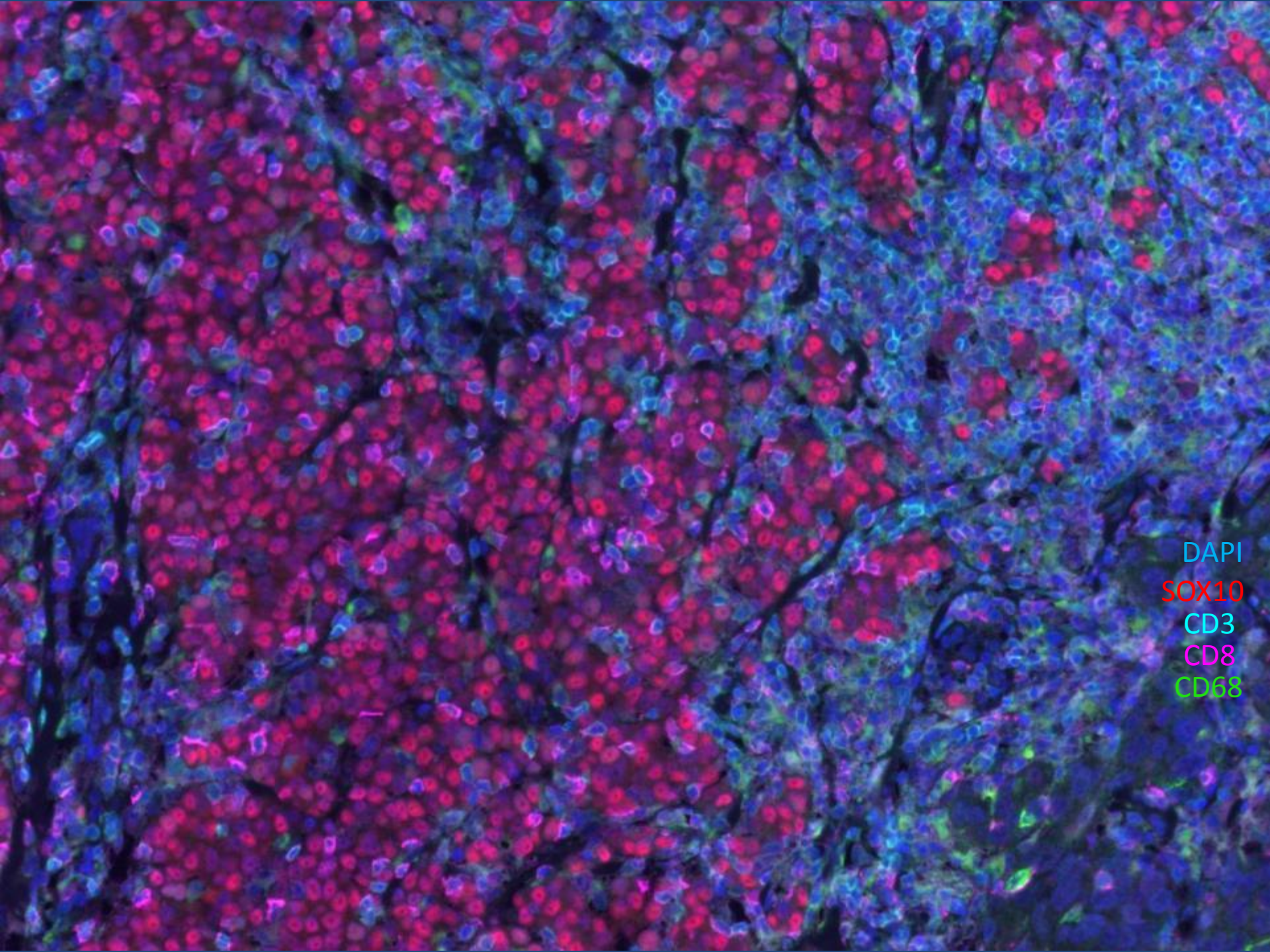
DAPI
SOX10



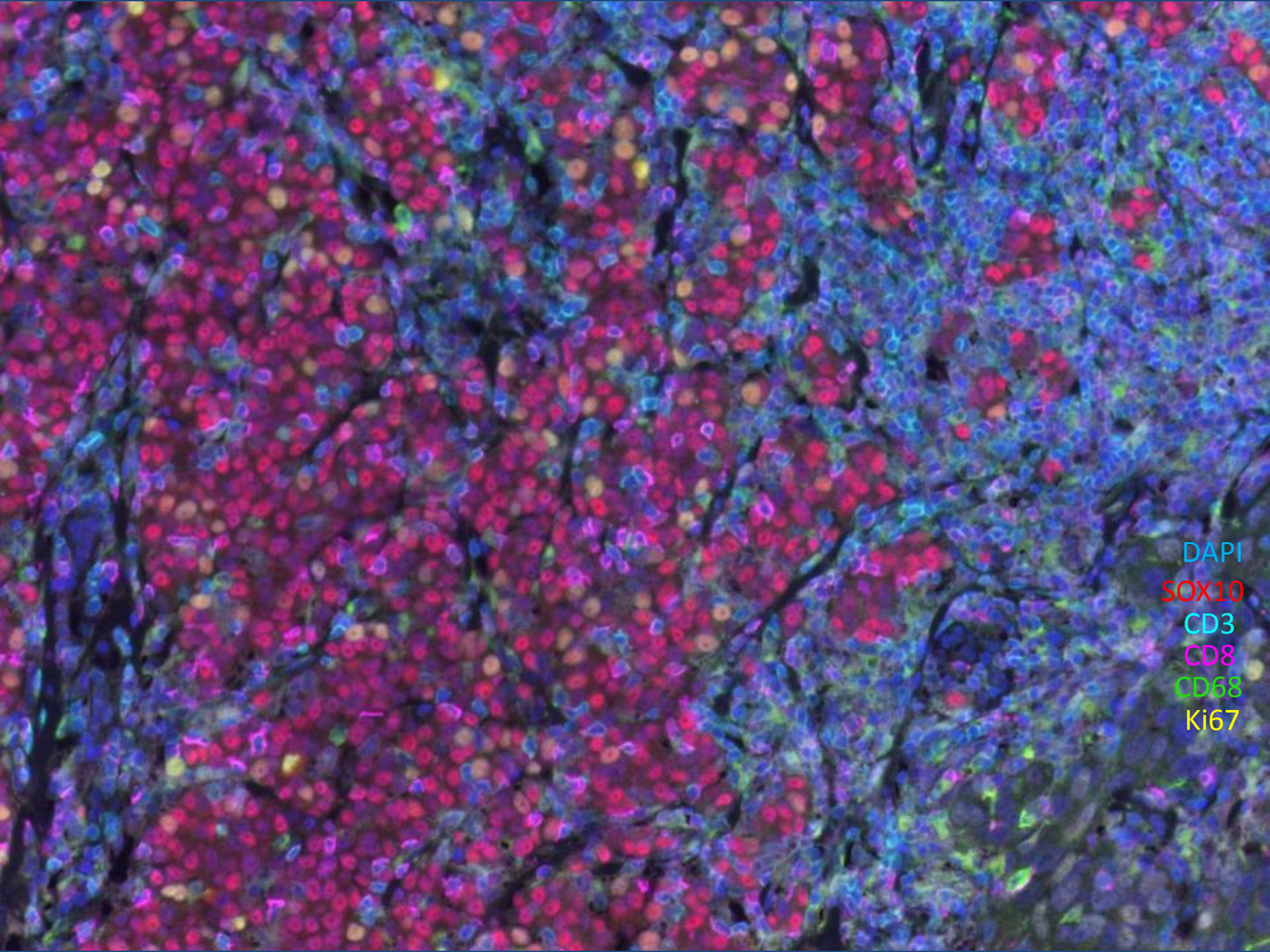
DAPI
SOX10
CD3



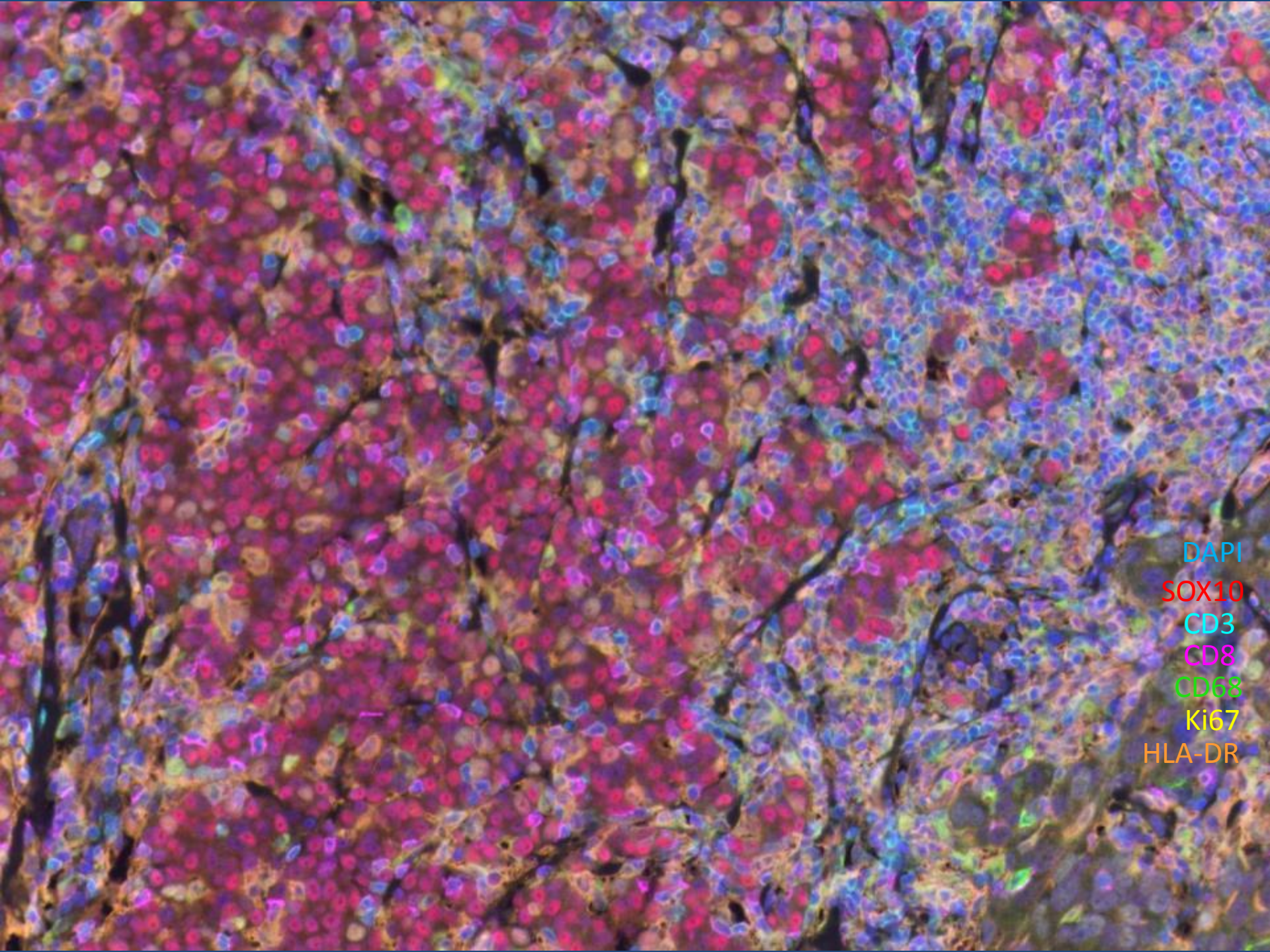
DAPI
SOX10
CD3
CD8



DAPI
SOX10
CD3
CD8
CD68



DAPI
SOX10
CD3
CD8
CD68
Ki67



DAPI

SOX10

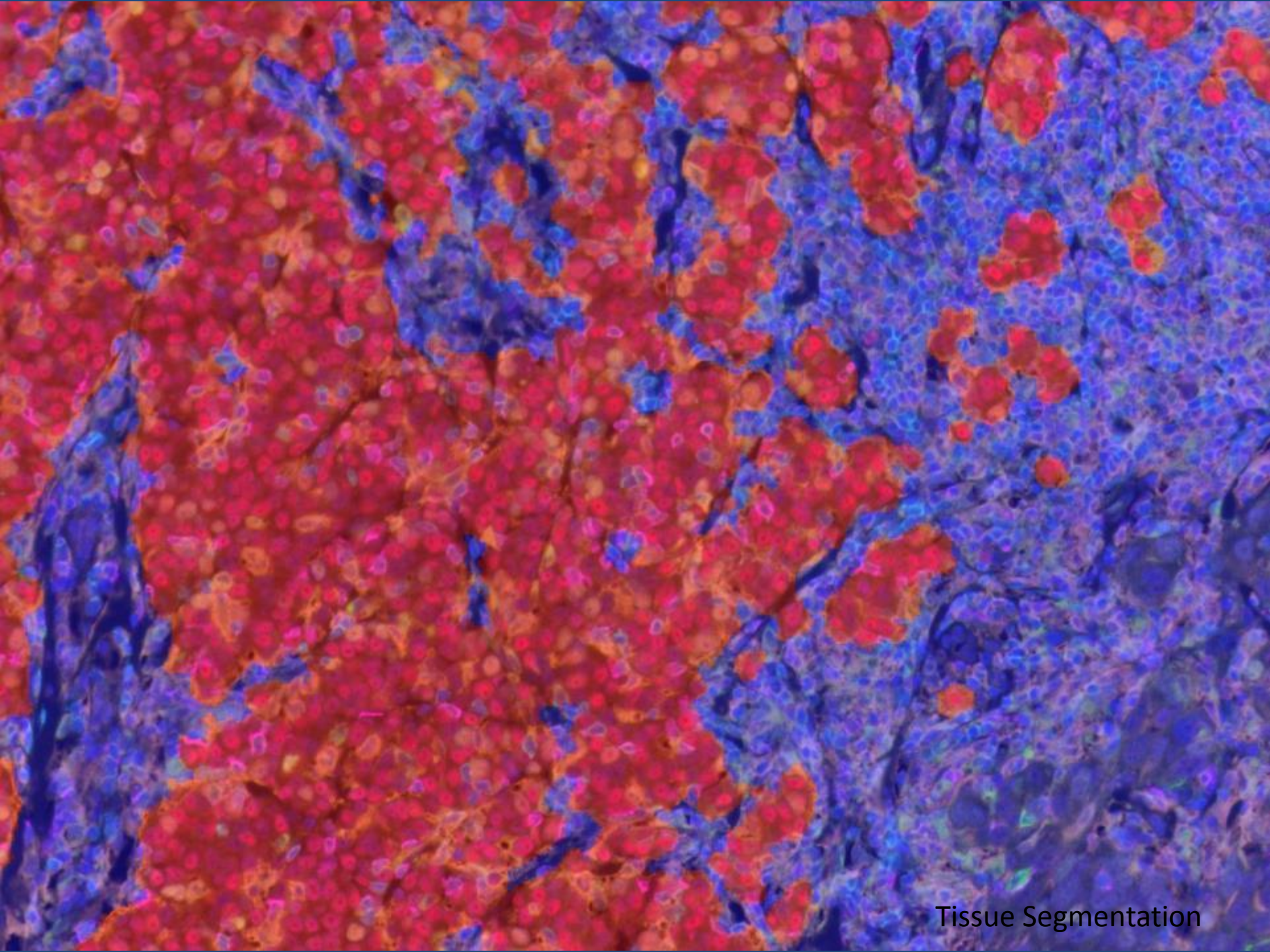
CD3

CD8

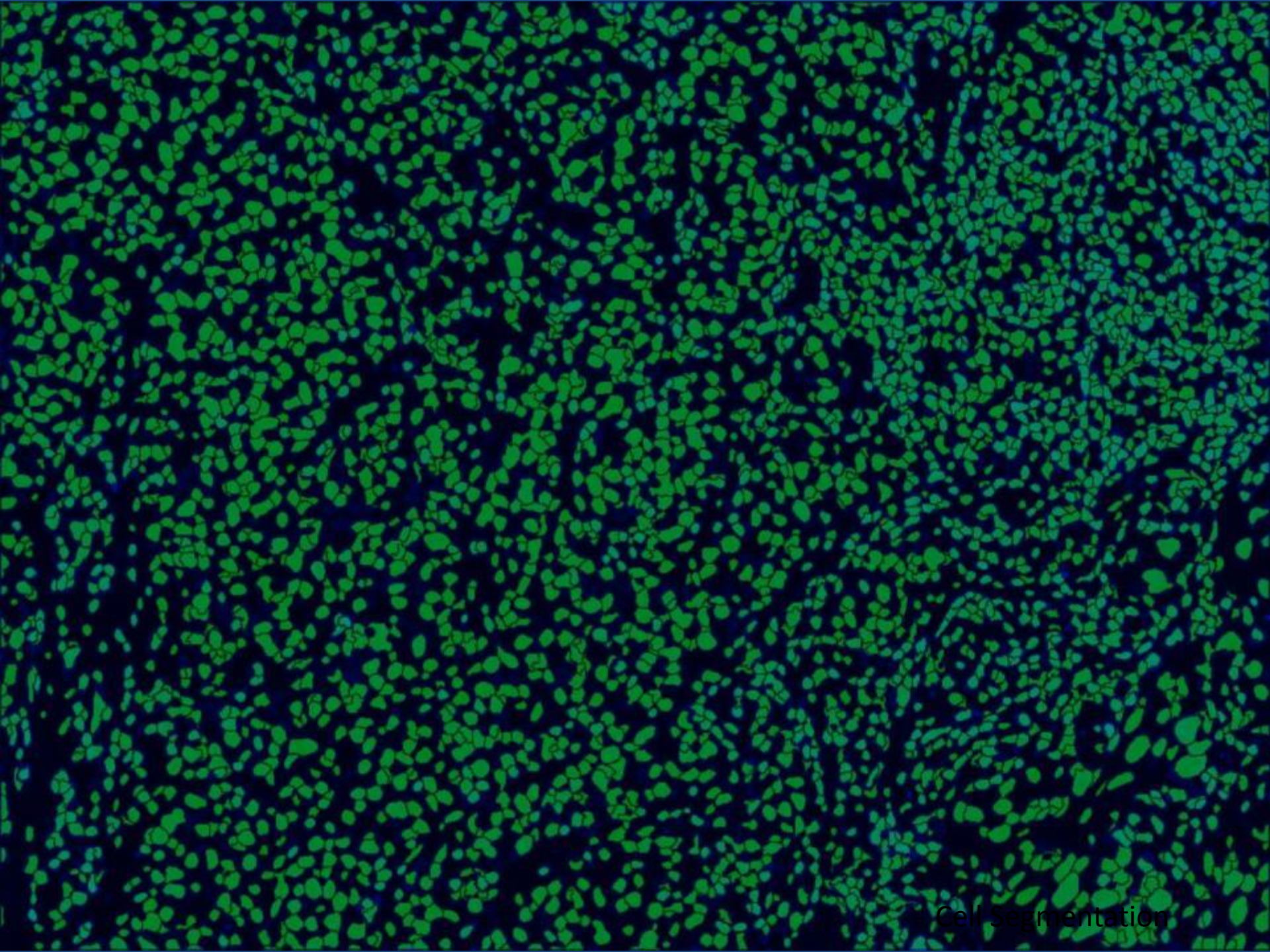
CD68

Ki67

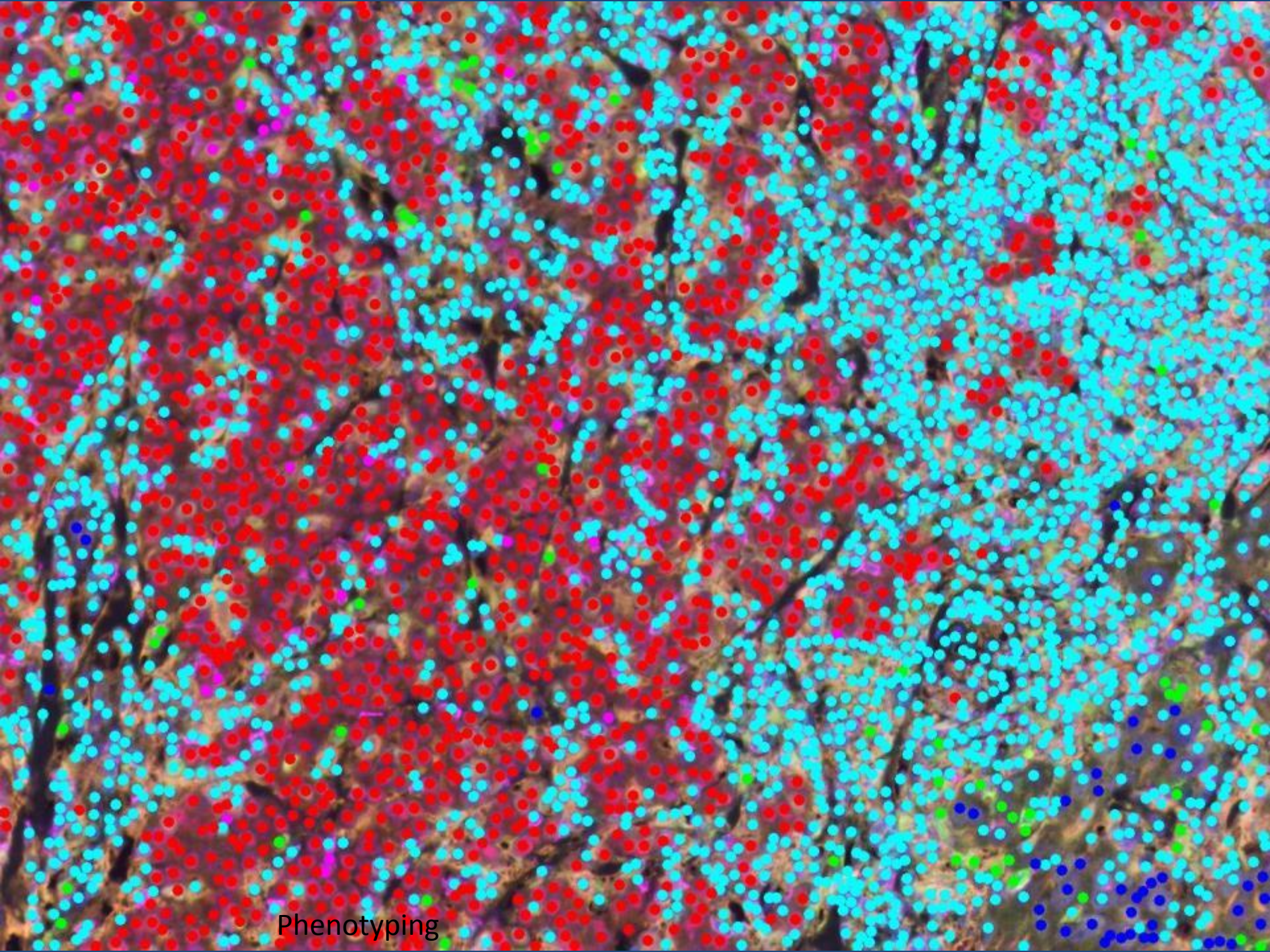
HLA-DR



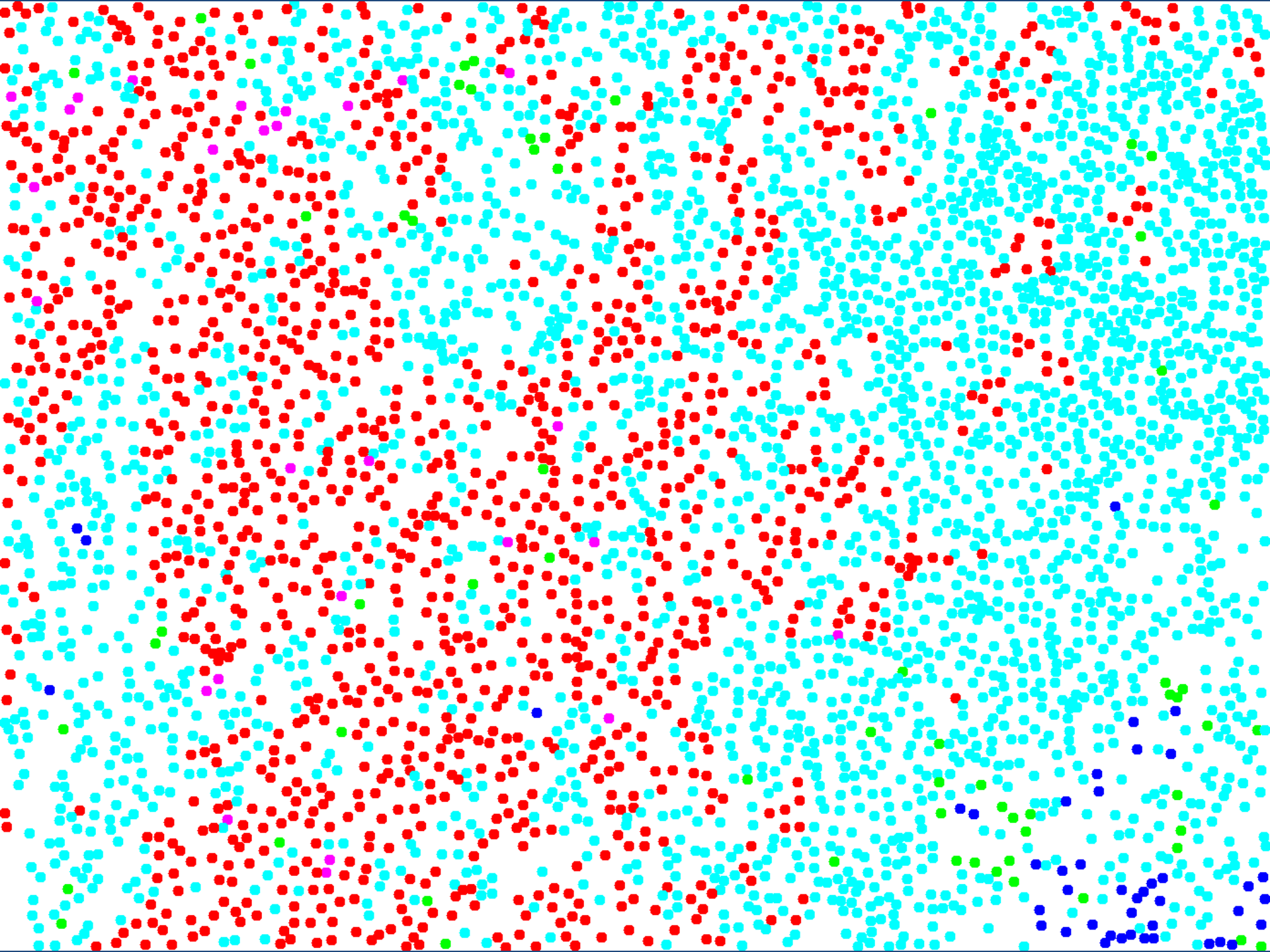
Tissue Segmentation



Cell Segmentation



Phenotyping

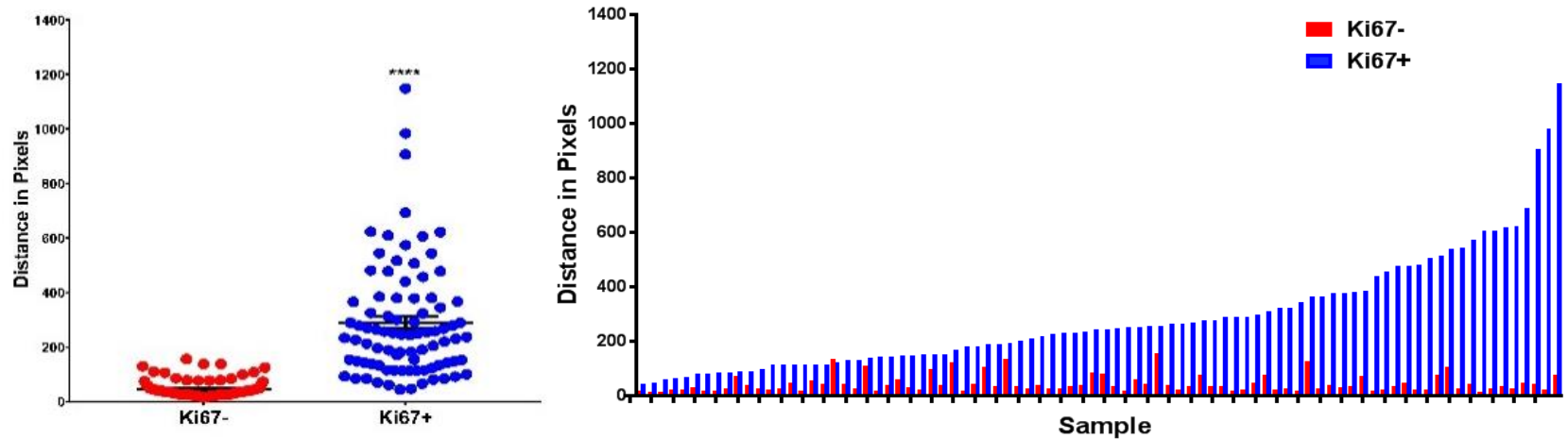


**Table 1: Melanoma Patient Characteristics
(n=104)**

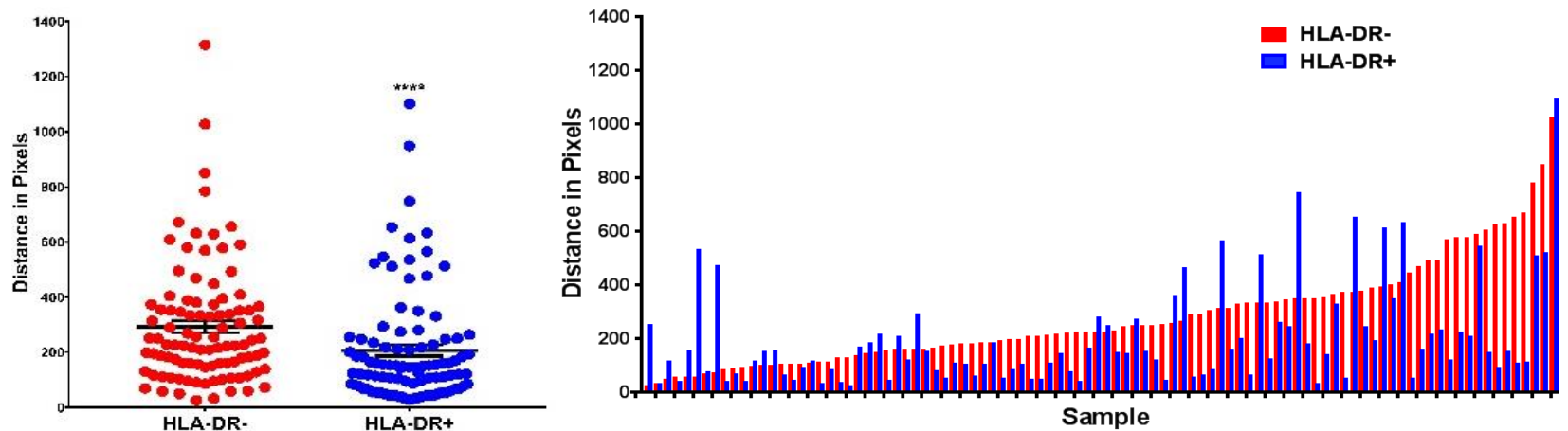
<u>Clinical Characteristics</u>		
<u>Gender</u>		
Male, no. (%)	75	(72.1)
Female, no. (%)	29	(27.9)
<u>Age</u>		
Median, no., (range)	74.5	(22-96)
<u>Location of Tumor</u>		
Trunk, no. (%)	61	(58.7)
Extremity, no. (%)	41	(39.4)
Unknown, no. (%)	2	(1.9)
<u>Stage</u>		
II, no. (%)	91	(87.5)
III, no. (%)	13	(12.5)
<u>Pathological Characteristics</u>		
<u>Depth (mm)</u>		
Median, no. (range)	2.5	(0.6-26)
<u>Ulceration</u>		
Absent, no. (%)	36	(34.6)
Present, no. (%)	65	(62.5)
Unknown, no. (%)	3	(2.9)
<u>TILs</u>		
Absent, no. (%)	2	(1.9)
Non-Brisk, no. (%)	59	(56.8)
Brisk, no. (%)	33	(31.7)
Unknown, no. (%)	10	(9.6)
<u>Outcome Characteristics</u>		
<u>Patient Follow Up (months)</u>		
Median, no. (range)	45	(4-173)
<u>Overall Survival (months)</u>		
Alive (at least 2 years), no. (%)	31	(29.8)
Dead, no. (%)	73	(70.2)
<u>Disease Specific Survival (DSS) (months)</u>		
Alive without melanoma, no. (%)	42	(40.4)
Dead with melanoma, no. (%)	22	(21.2)
Unknown, no. (%)	40	(38.4)

Representing Biology with Distance

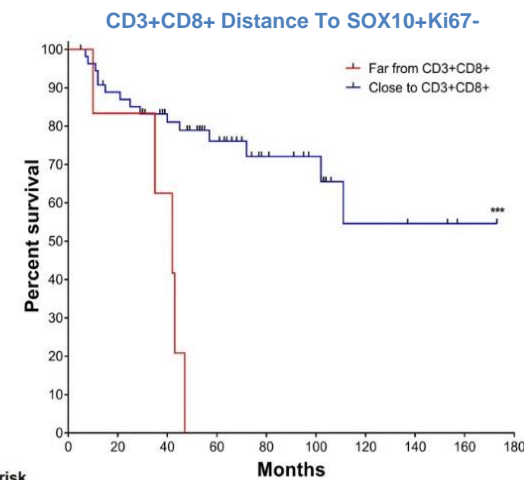
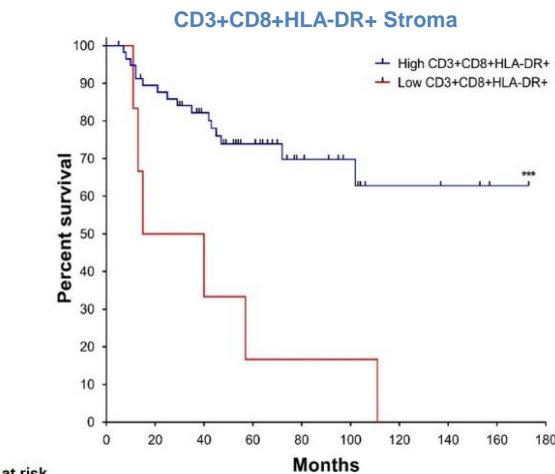
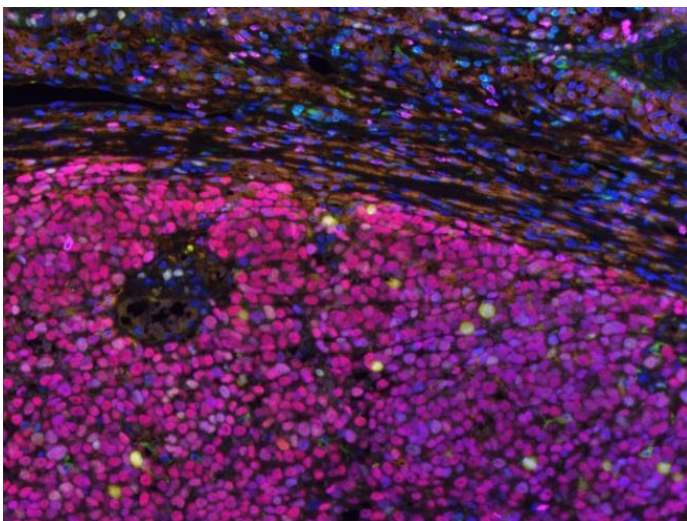
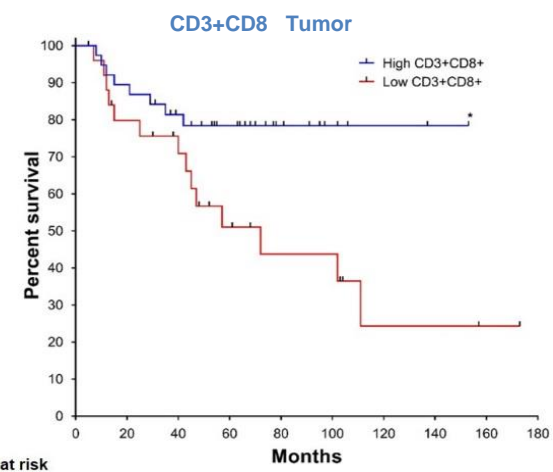
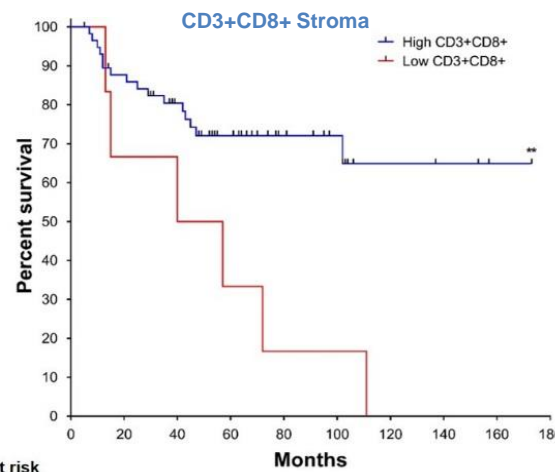
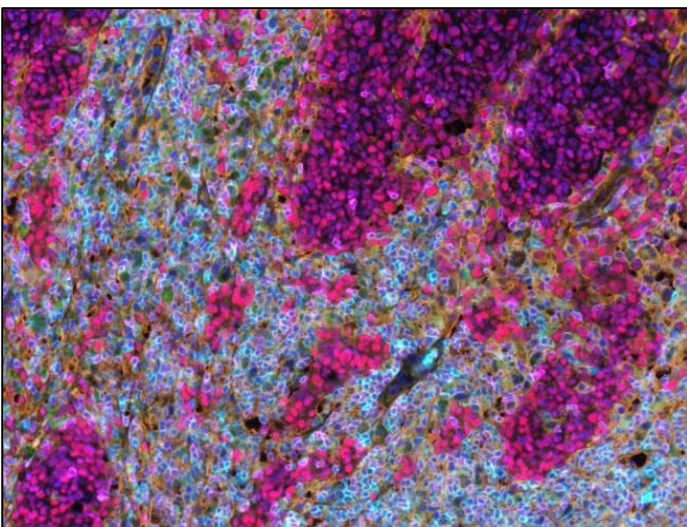
Distance of CD3+CD8+ to SOX10+ Tumor



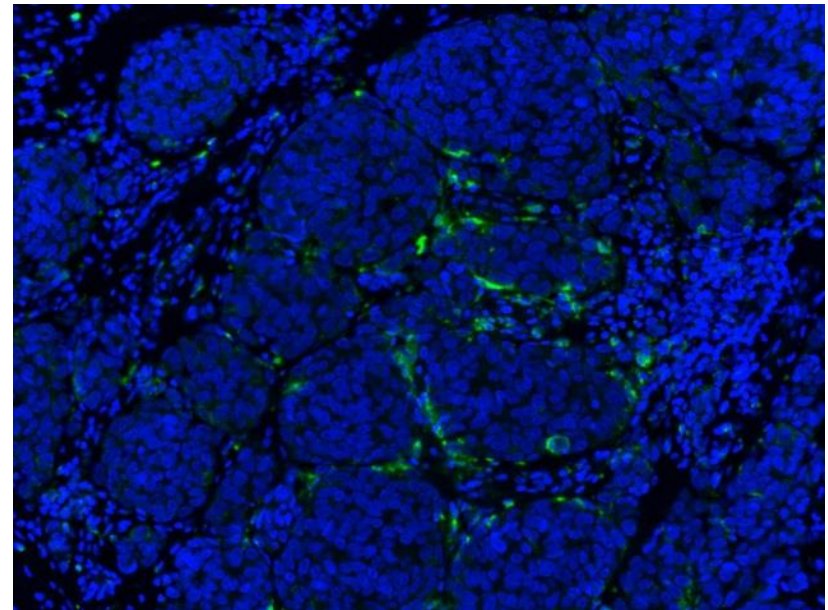
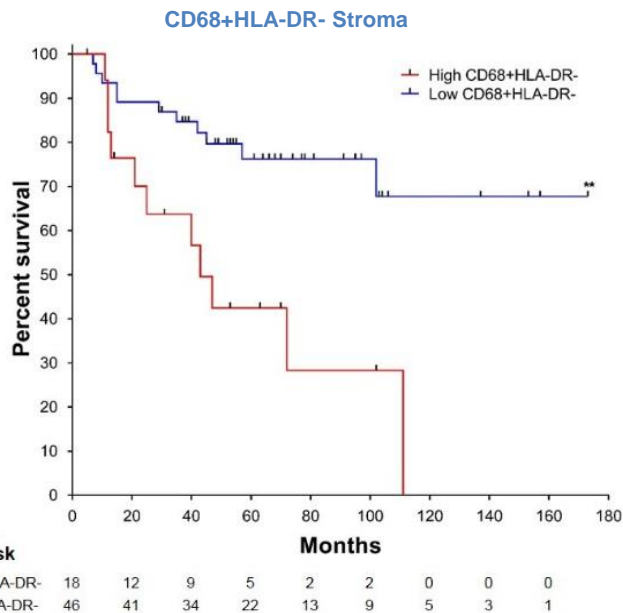
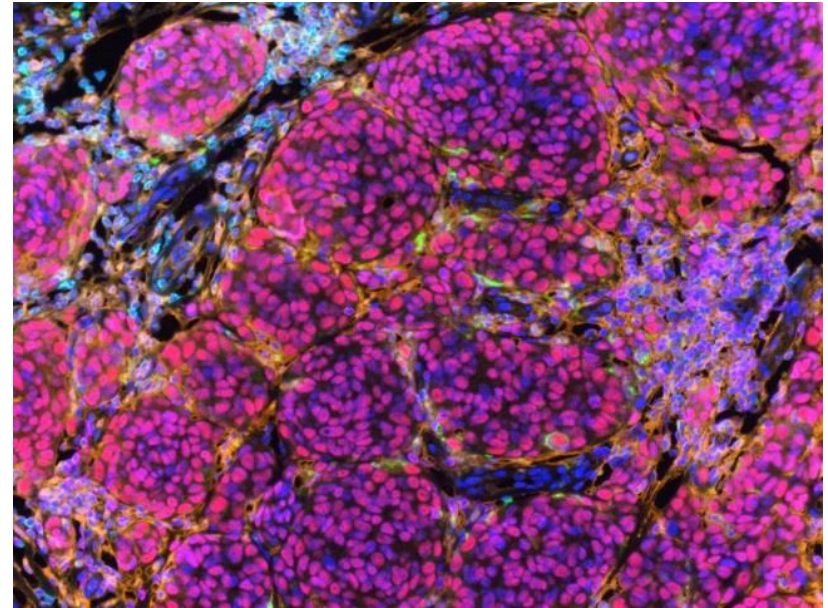
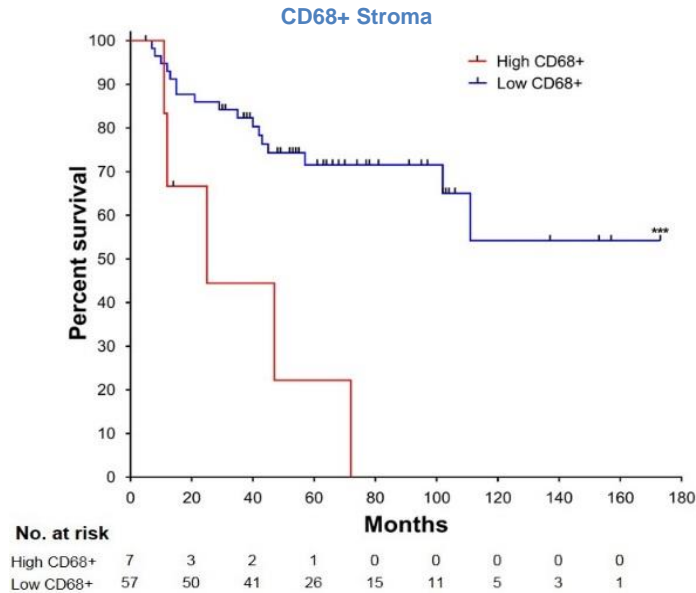
Distance of CD3+CD8+ to CD68+ Macrophages



CD3+CD8+ CTLs Correlate with DSS

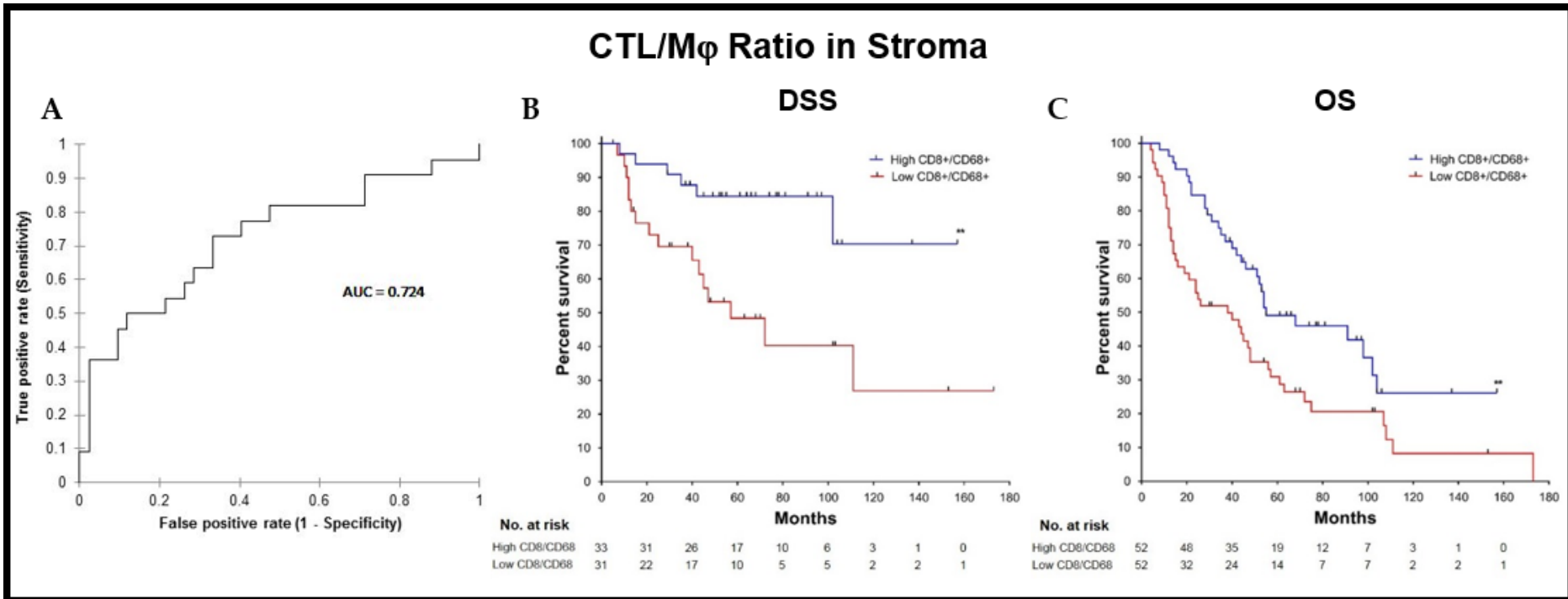


Density of CD68+ Macrophages Correlate with DSS



Gartrell RD, Marks DK, Hart T, et al: Characterizing the tumor microenvironment (TME) in primary melanomas using multiplex immunohistochemistry (mIHC). Journal of Clinical Oncology 35:9580-9580, 2017

Ratio of CD8+/CD68+ as Biomarker

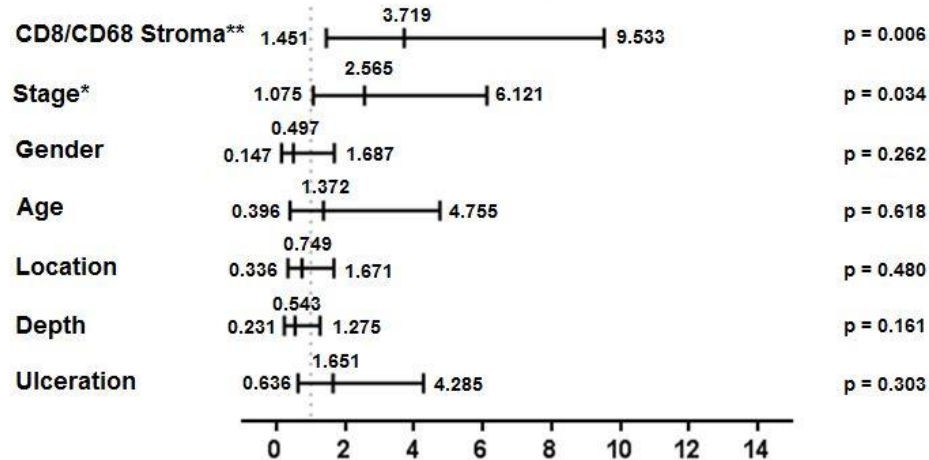


Ratio of CD8+/CD68+ as Biomarker

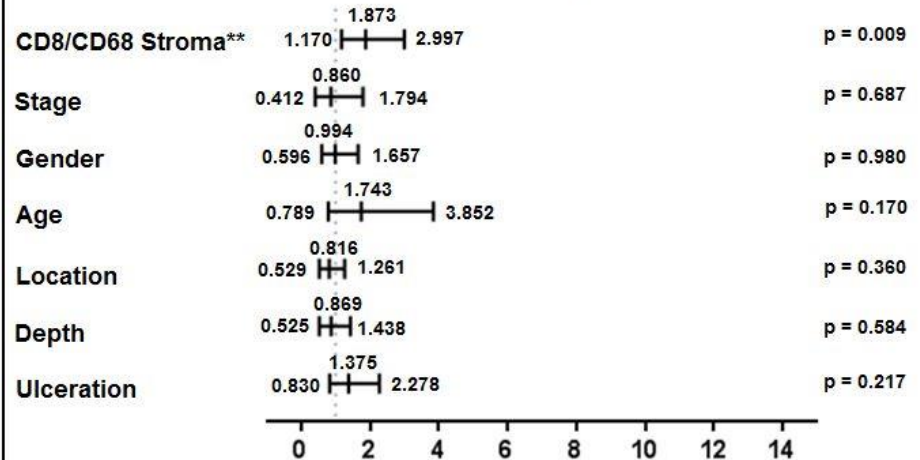
DSS

OS

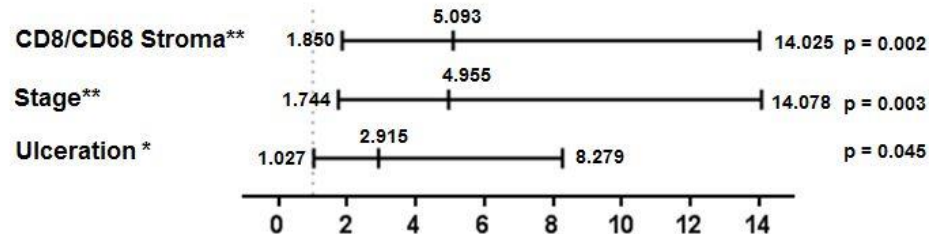
Univariable Analysis



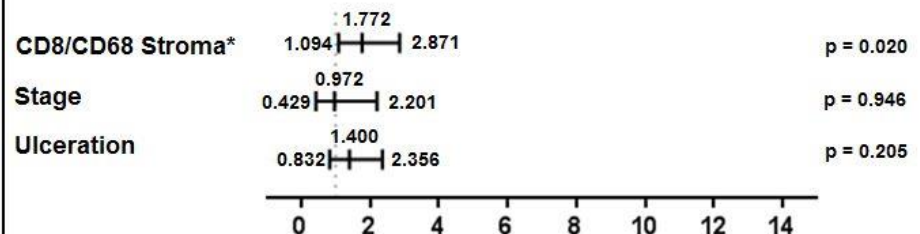
Univariable Analysis



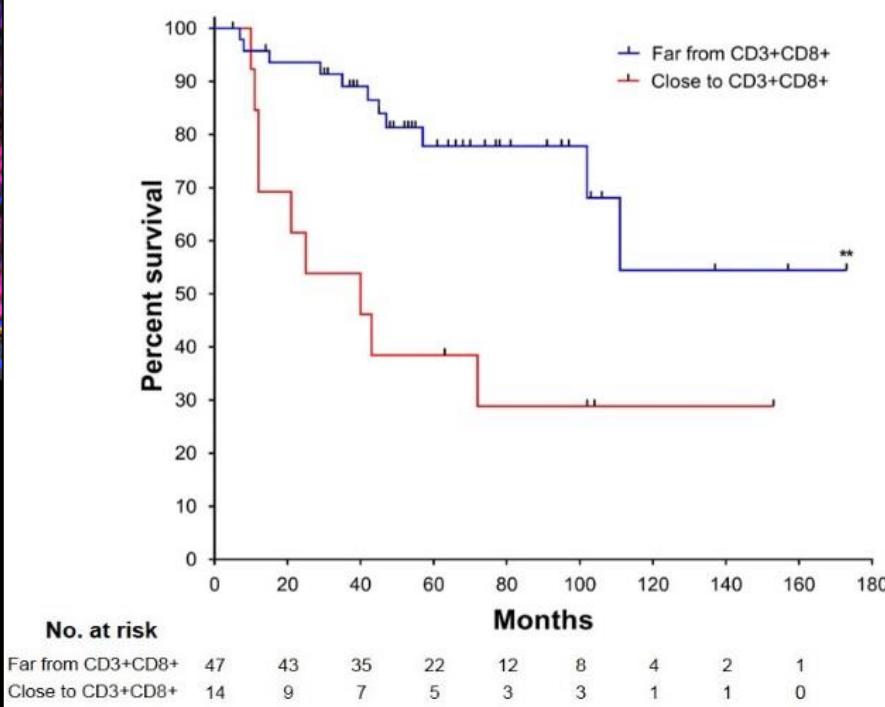
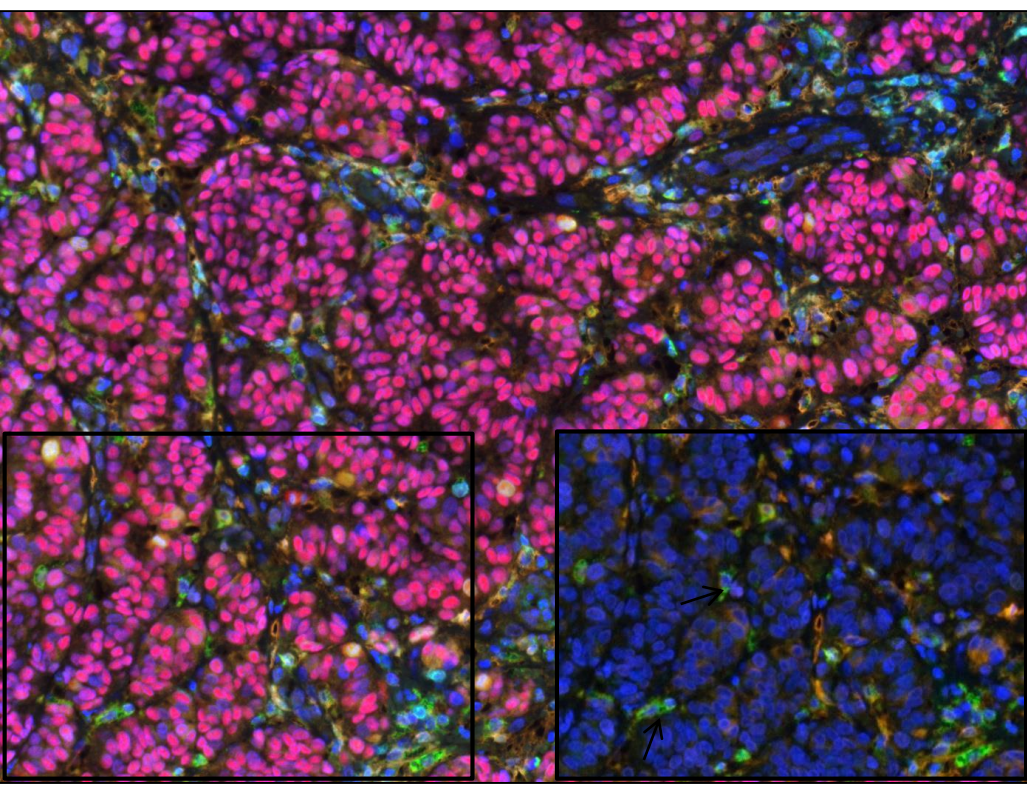
Multivariable Analysis (p=0.002)



Multivariable Analysis (p=0.066)

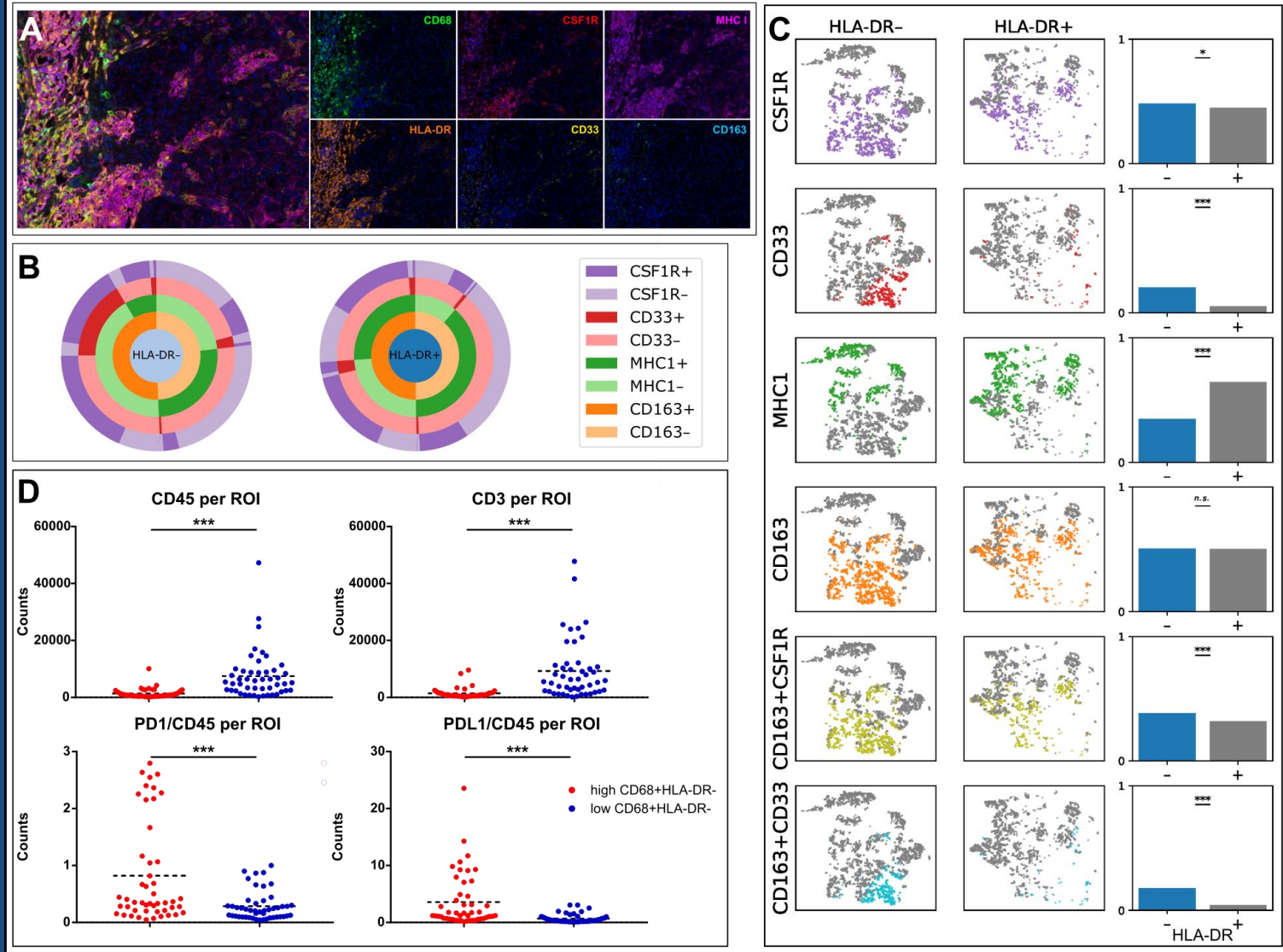


CD3+CD8+ Distance to CD68+HLA-DR- Macrophages Correlates with DSS



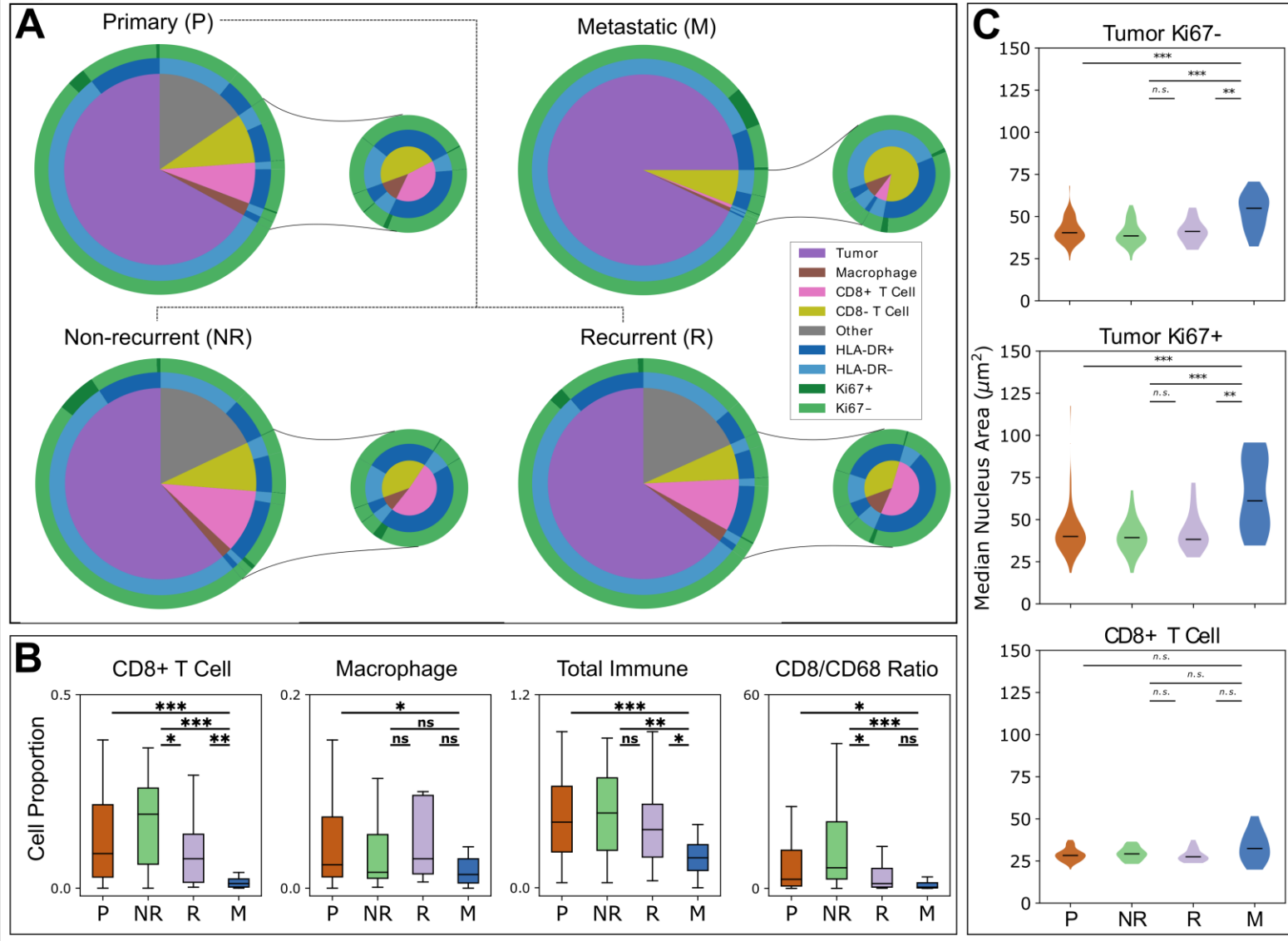
Characterization of HLA-DR- Macrophages

Figure 5



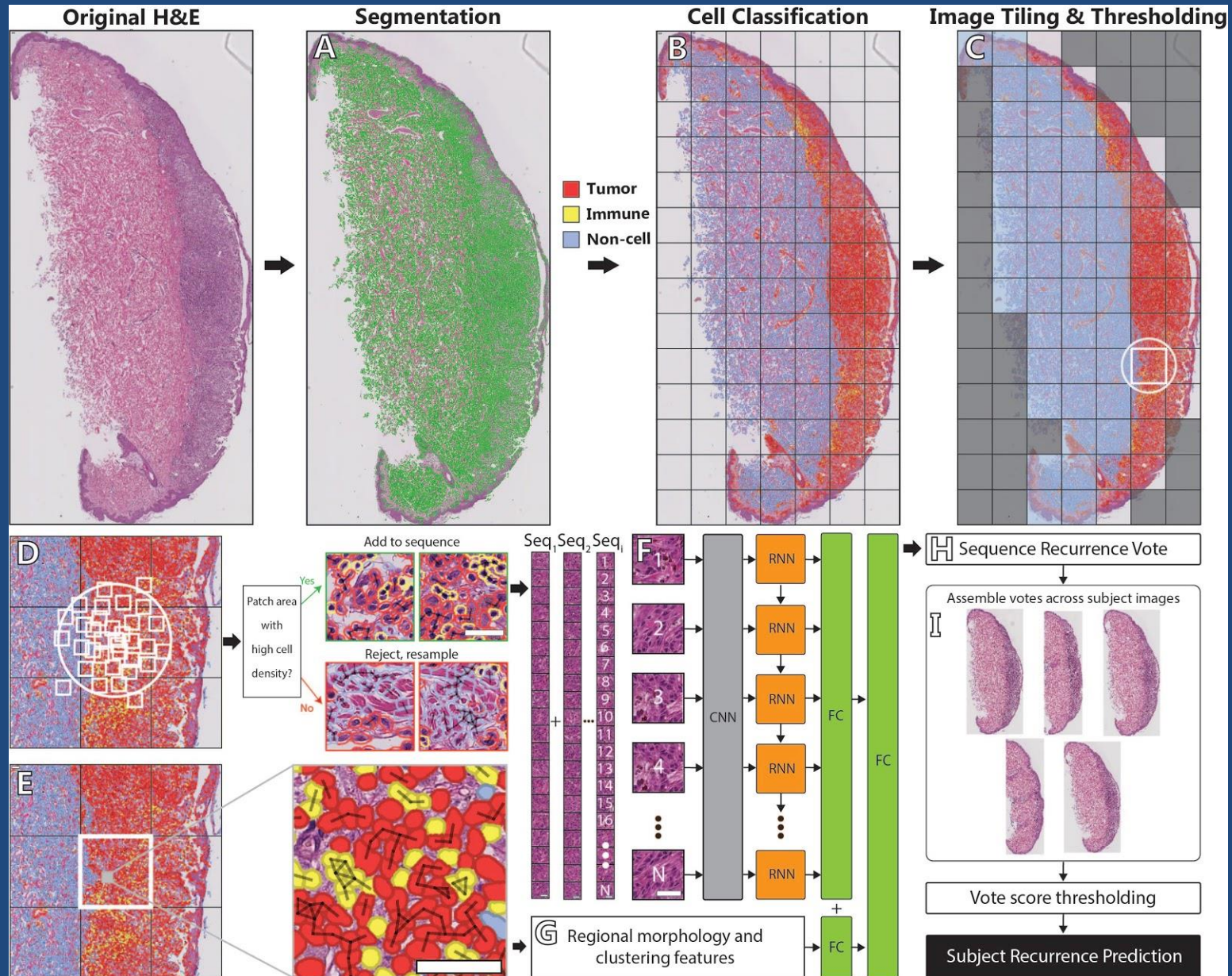
Comparison of Primary to Metastatic Tumors

Figure 1



Novel Methods to Study the TiME- Image Analysis

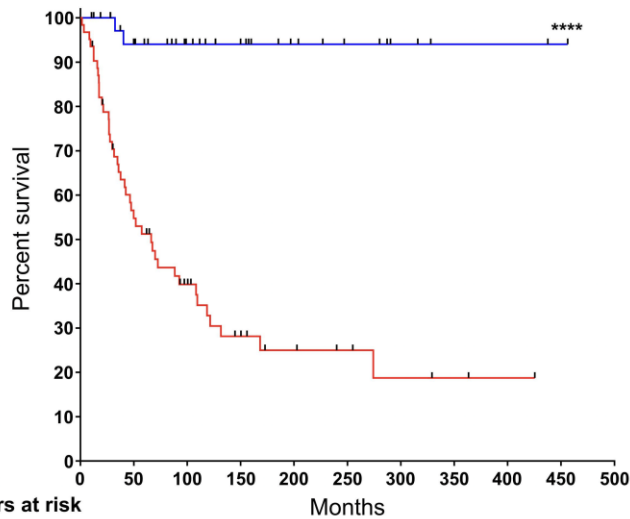
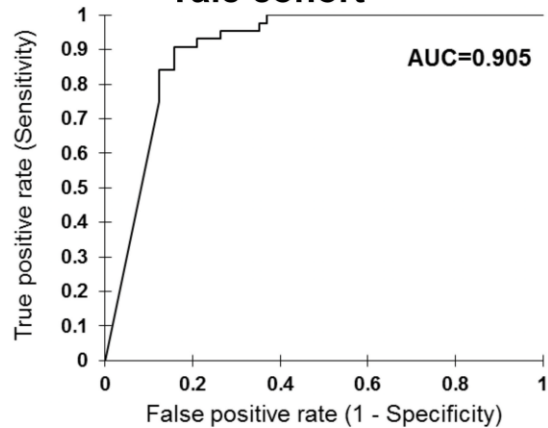
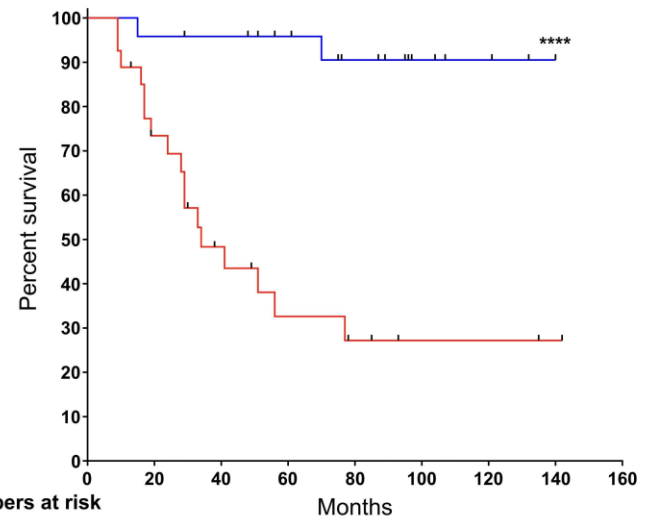
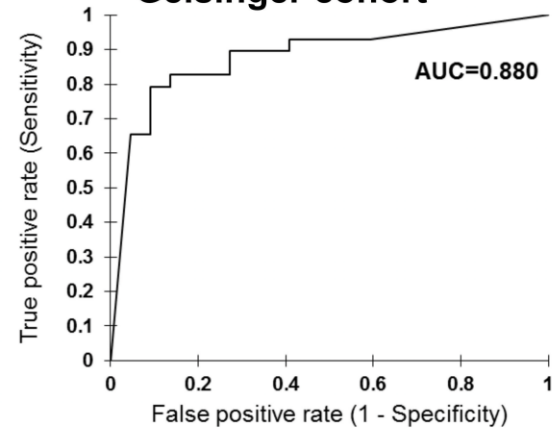
And onto image analysis applying AI to tiles selected using QuPath



Univariable Cox Training, Yale, and GHS

<i>Training set</i>				<i>YUMC</i>				<i>GHS</i>			
Hazard ratio	95% CI	<i>P</i>		Hazard ratio	95% CI	<i>P</i>		Hazard ratio	95% CI	<i>P</i>	
Score	N/A	N/A	N/A	Score****	55.023	9.486 to 319.157	< 0.0001	Score***	20.135	3.865 to 104.882	<0.001
Stage***	3.374	1.826 to 6.234	<0.001	Stage	N/A	N/A	N/A	Stage	1.472	0.579 to 3.743	0.417
Gender	0.665	0.285 to 1.554	0.347	Gender	0.597	0.331 to 1.078	0.087	Gender	1.695	0.681 to 4.222	0.257
Age	1.009	0.983 to 1.036	0.449	Age	1.016	0.994 to 1.038	0.165	Age	1.024	0.990 to 1.059	0.163
Depth***	1.087	1.039 to 1.138	<0.001	Depth**	1.203	1.048 to 1.381	0.009	Depth	1.153	0.998 to 1.331	0.053
Ulceration*	2.605	1.209 to 5.611	0.014	Ulceration	1.412	0.777 to 2.568	0.258	Ulceration	2.696	0.969 to 7.498	0.057

Supplementary table 3. Univariable Cox regression analysis in training cohort. Univariable Cox analysis of disease-specific survival.

A**Yale cohort****B****Geisinger cohort**

Conclusions

- GOAL is to provide better guidance to patients with early stage melanoma and clinicians taking care of them
- The tumor immune micro-environment has a large impact on patient outcomes
- Using FFPE specimens, quantification of RNA transcripts of immune genes (Nanostring) and precise measurement of densities and spatial localization of cells (qmIF) provide biomarkers of clinical utility
- More accurate immune biomarkers allow for streamlined clinical trial design and a more personalized approach to each patient based on their immune parameters.
- Multiple methods are under development (RNA, protein, digital image analysis based) and testing is ongoing on E1697

Acknowledgements!

Saenger Laboratory

Multiplex IF- Robyn Gartrell MD, Emanuelle Rizk, Zoe Blake, Yan Lu, Camden Esancy, Thomas Hart, Douglas Marks MD, ThomasENZler MD

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Yale Collaborators

David Rimm and laboratory (Pok Fai Wong, Balazs Acs)

Harriet Kluger

Computational Collaborators

Raul Rabadan PhD, Andrew Chen (CUMC), Rui Chang PhD (U of Arizona)

Jing Wang MD PhD, Prathamesh Kulkarni PhD, Eric Robinson (NYU)

Pathology Collaborators

Basil Horst MD PhD (UBC) , Kevin Gardner MD PhD (CUMC)

Biostatistics

Sandra Lee PhD

RPCI Collaborators

John Krolewski MD PhD, Mark Ernstoff MD

Human Immune Monitoring Core

Chuck Drake MD PhD. Xiang Wang MD, Yan Lu MD

Melanoma Clinical Team-

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QmIF Collaborator

Edward Stack PhD (Jounce)