



Tumor Immune Microenvironment: A Holistic Approach Workshop

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#SITCworkshop



Society for Immunotherapy of Cancer



Decoding the Lung Cancer Immune Microenvironment Using Spatially-resolved Multiplexed Tissue Analysis

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Yale School of Medicine

Yale Cancer Center

Conflict of Interest disclosure (last 24 months)

Employee of: Yale University

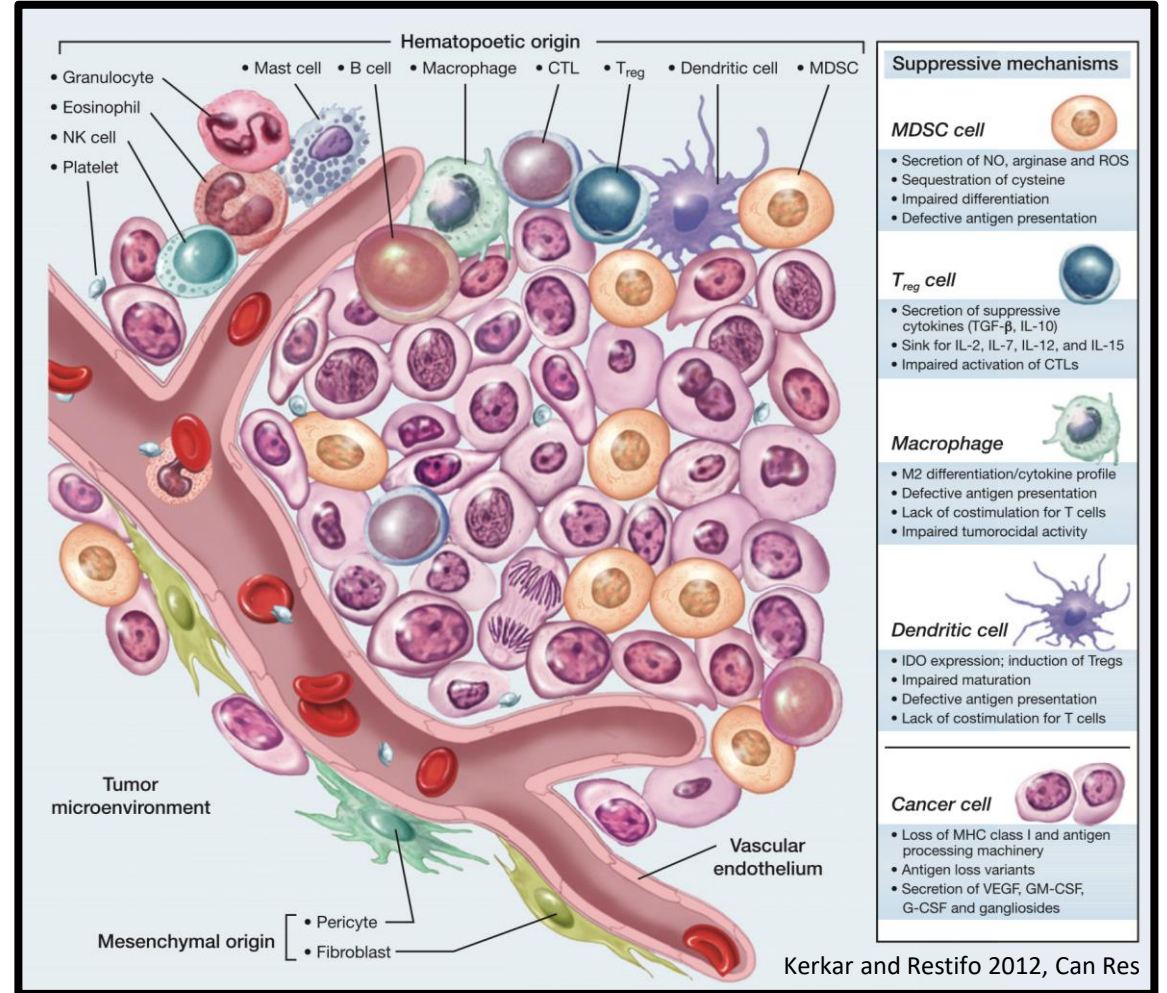
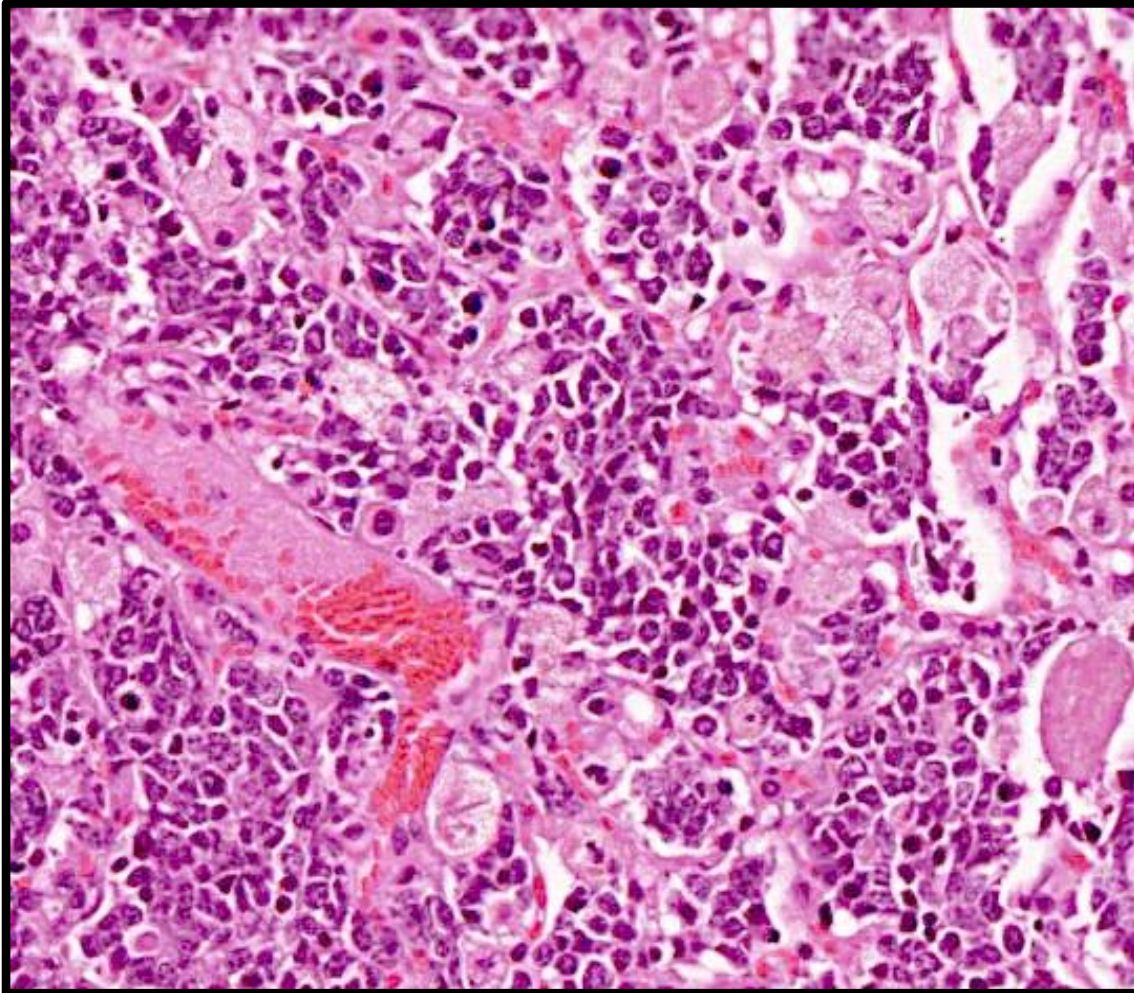
Consultant for: Clinica Alemana Santiago, Shattuck Labs, AstraZeneca, EMD Serono, Takeda, Torque/Repertoire Therapeutics, Takeda, Agenus, Genmab, OnCusp, Therapeutics, Bristol-Myers Squibb. Parthenon Therapeutics and Merck.

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Why studying the tumor microenvironment?

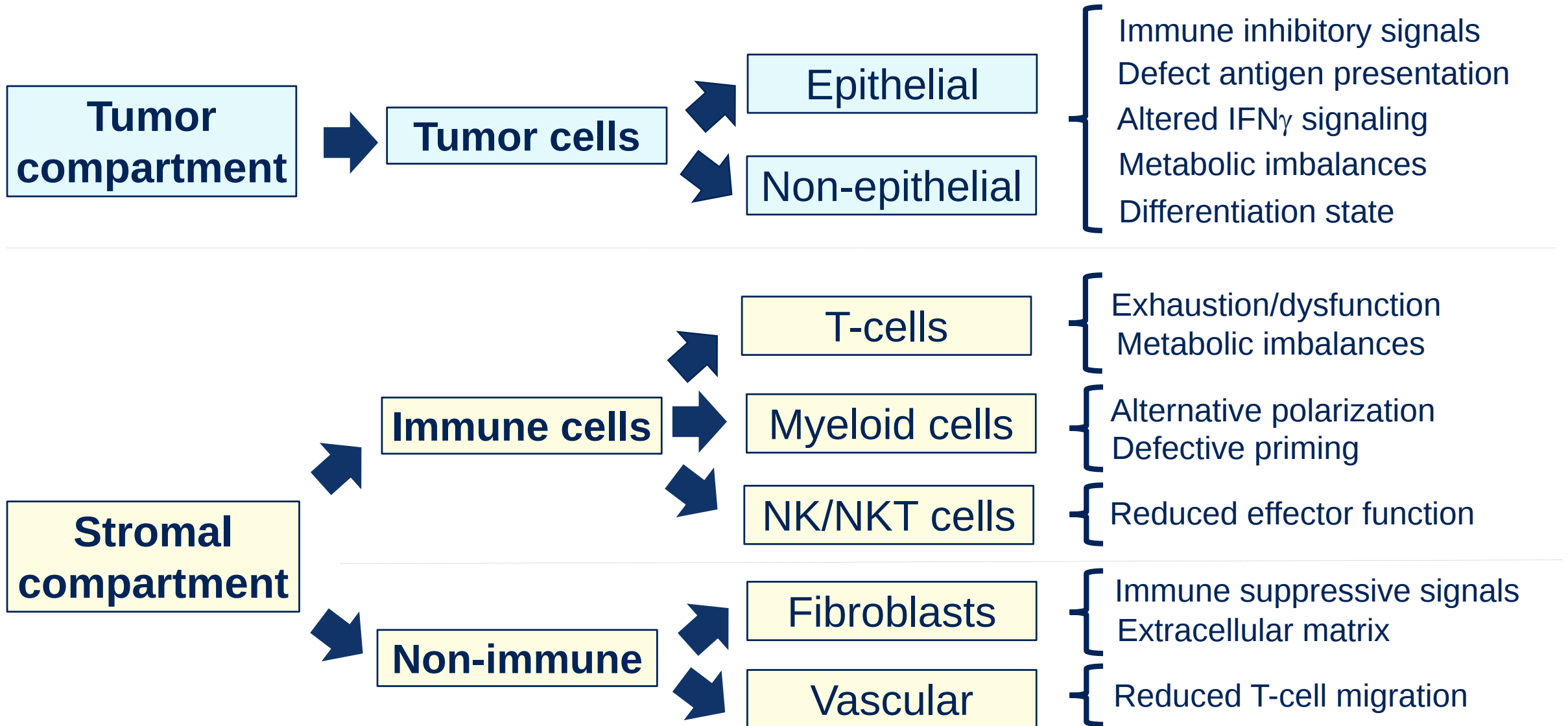
- Major role in immunotherapy sensitivity & resistance
 - *Local tolerogenic factors and suppression of effector responses.*
- Complex problem with unexplored determinants
 - *Multiple parameters, spatial features (heterogeneity) and dynamic nature*
- Tumors can display multiple immune evasion pathways
 - *Earlier tumors may be less complex*
- Identify “dominant” signals mediating tolerance and resistance
 - *Multiple altered pathways, few may be dominant*
- Therapies based on correcting a specific defect may have higher activity
 - *Non-corrective immune enhancers vs “corrective” immunotherapy*

Composition of the tumor microenvironment (TME)

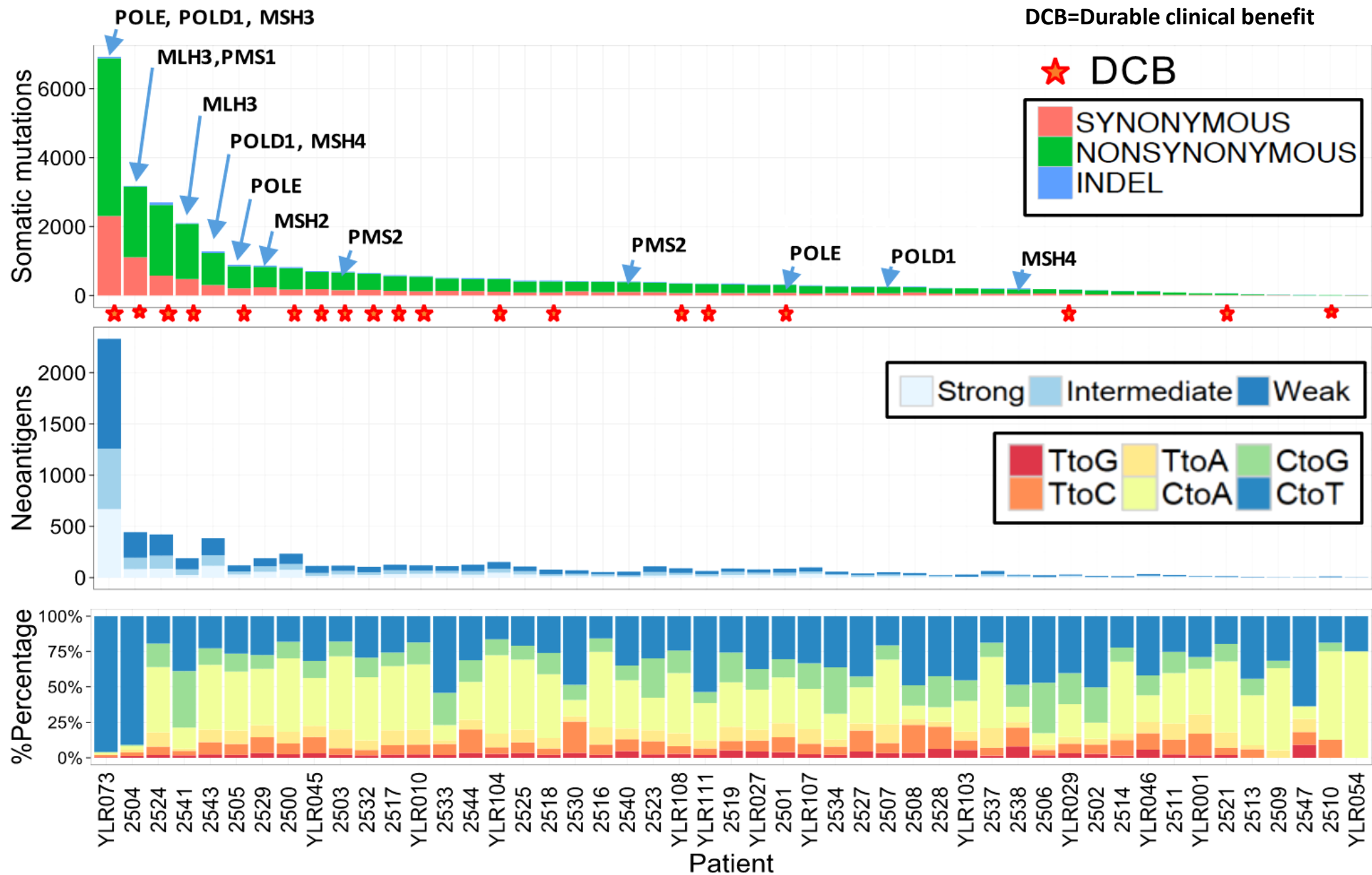


1. Tumor compartment= Epithelial tumor cells
2. Non-tumor compartment= Immune and non-immune cells

TME components and IO sensitivity & resistance

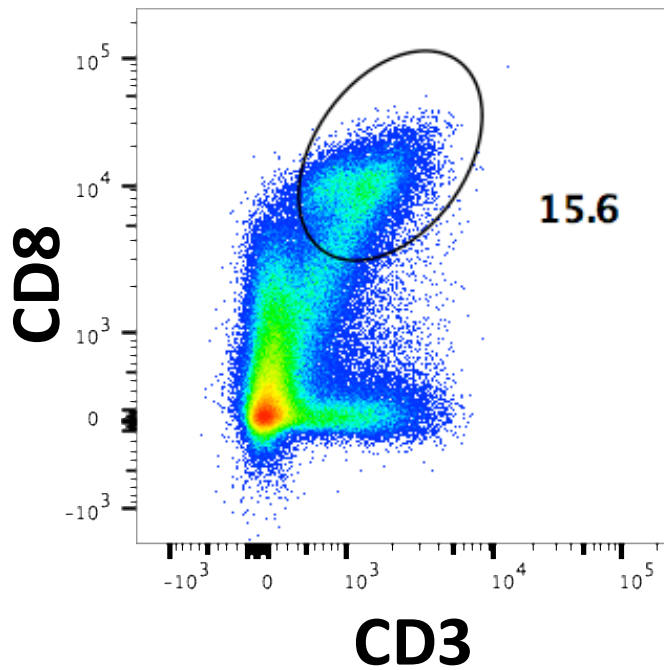


Tumor cells

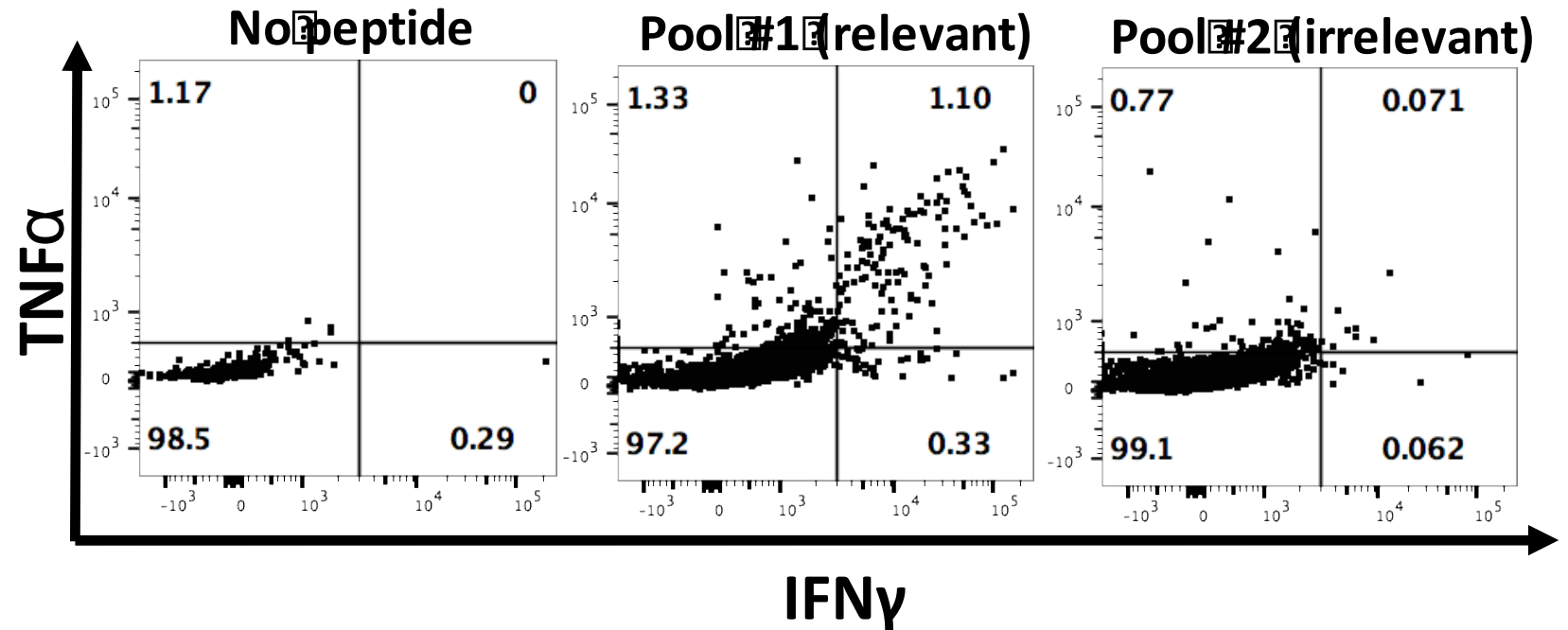


In vitro CD8 T-cell stimulation by mutant neopeptides

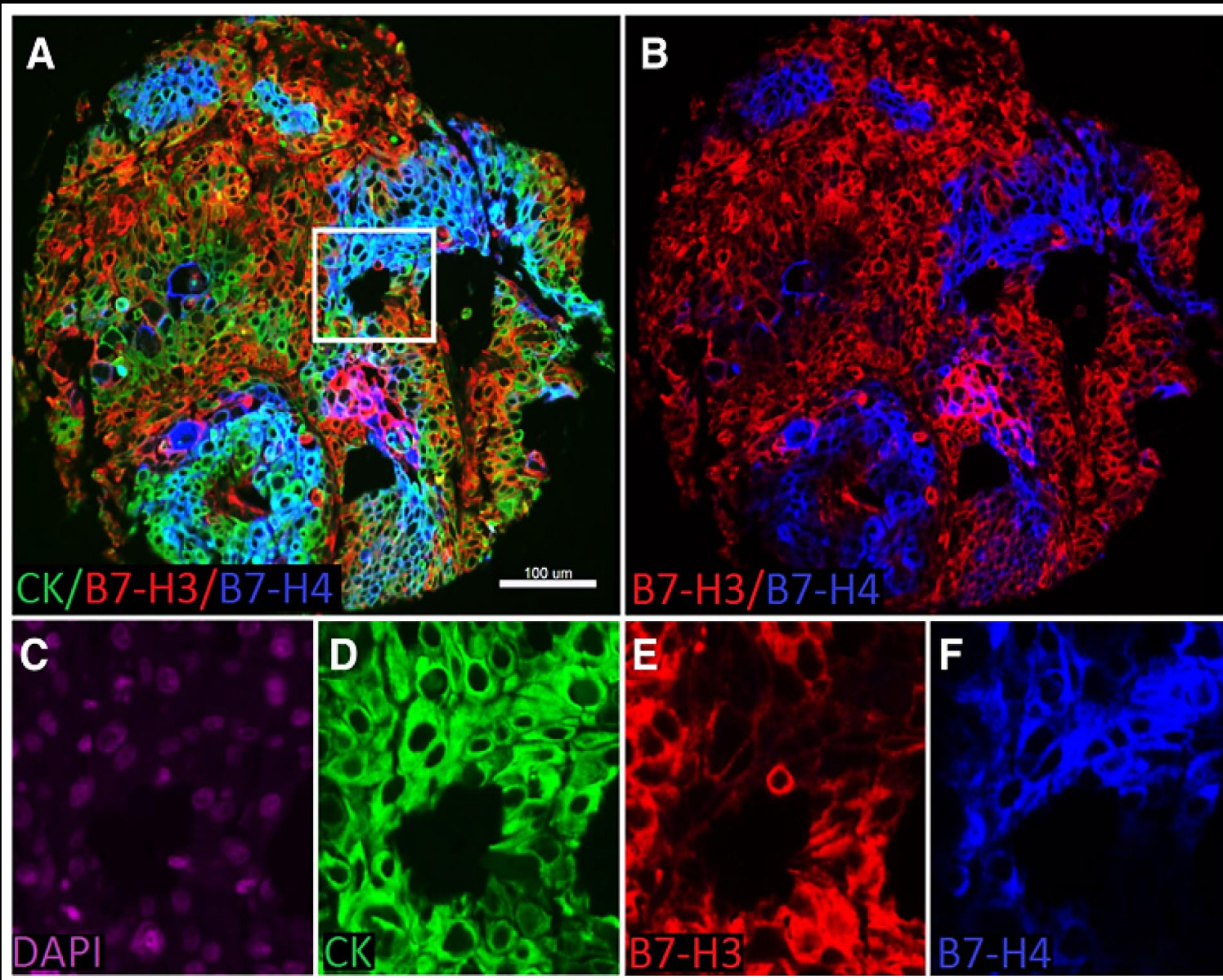
CD3⁺ CD8⁺ T cells



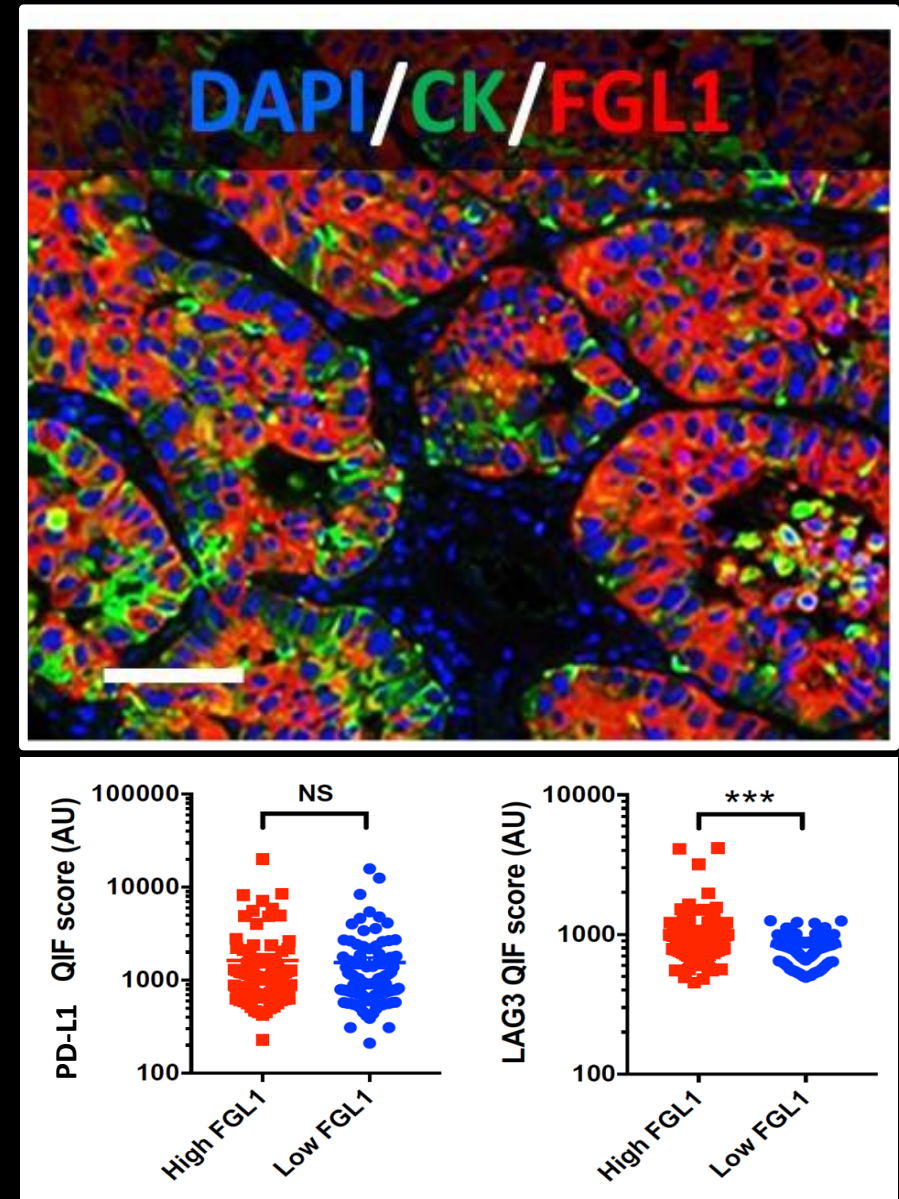
Artificial APC stimulation



Peptide pool #1: TMOD4, TENM2, MDM2, NXPE1, RHOT2(A), RHOT2(I), KIF5A, ARHGAP9

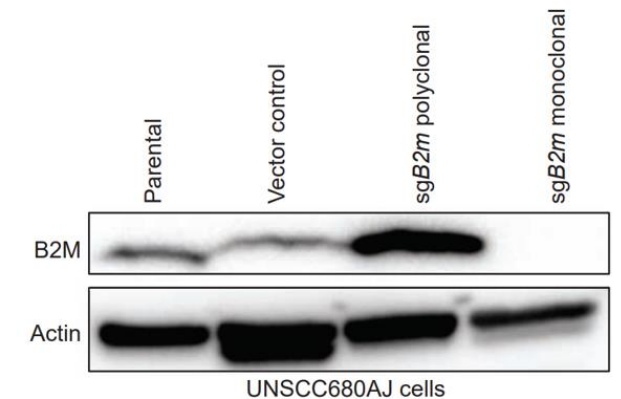
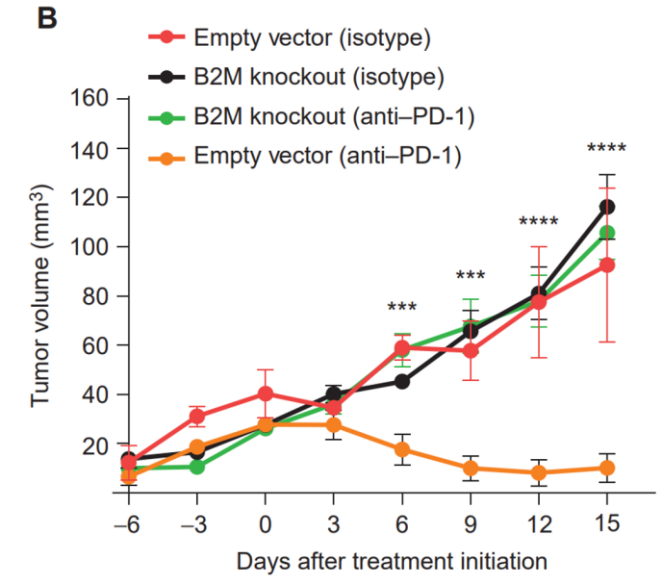
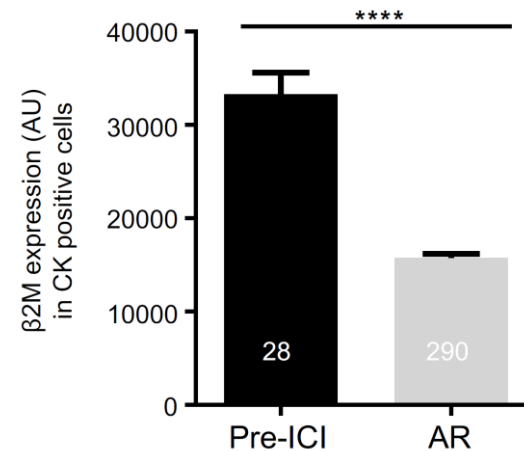
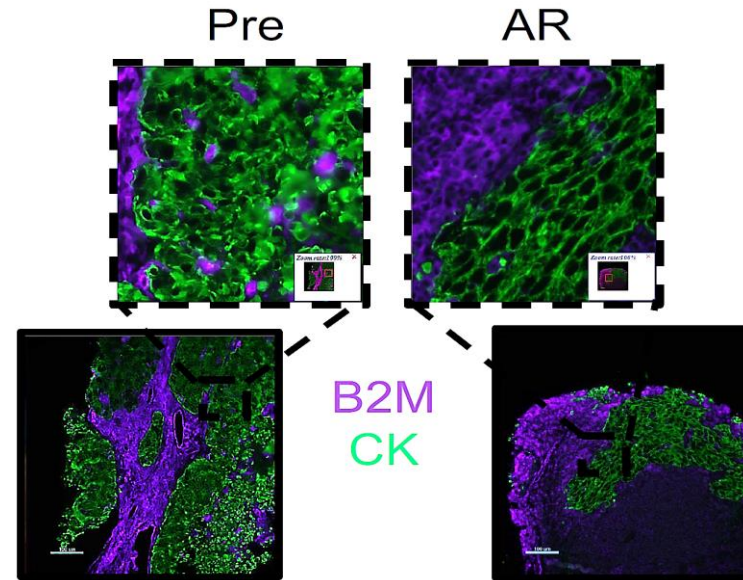
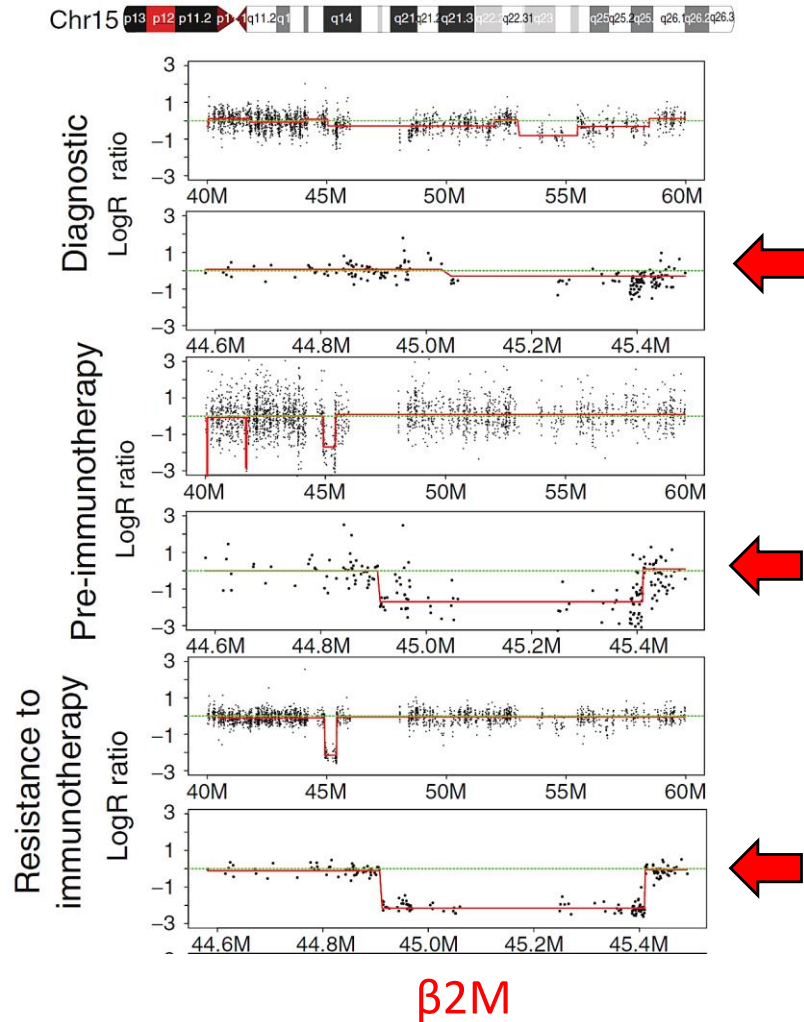


Altan et al., 2017 Clin Can Res

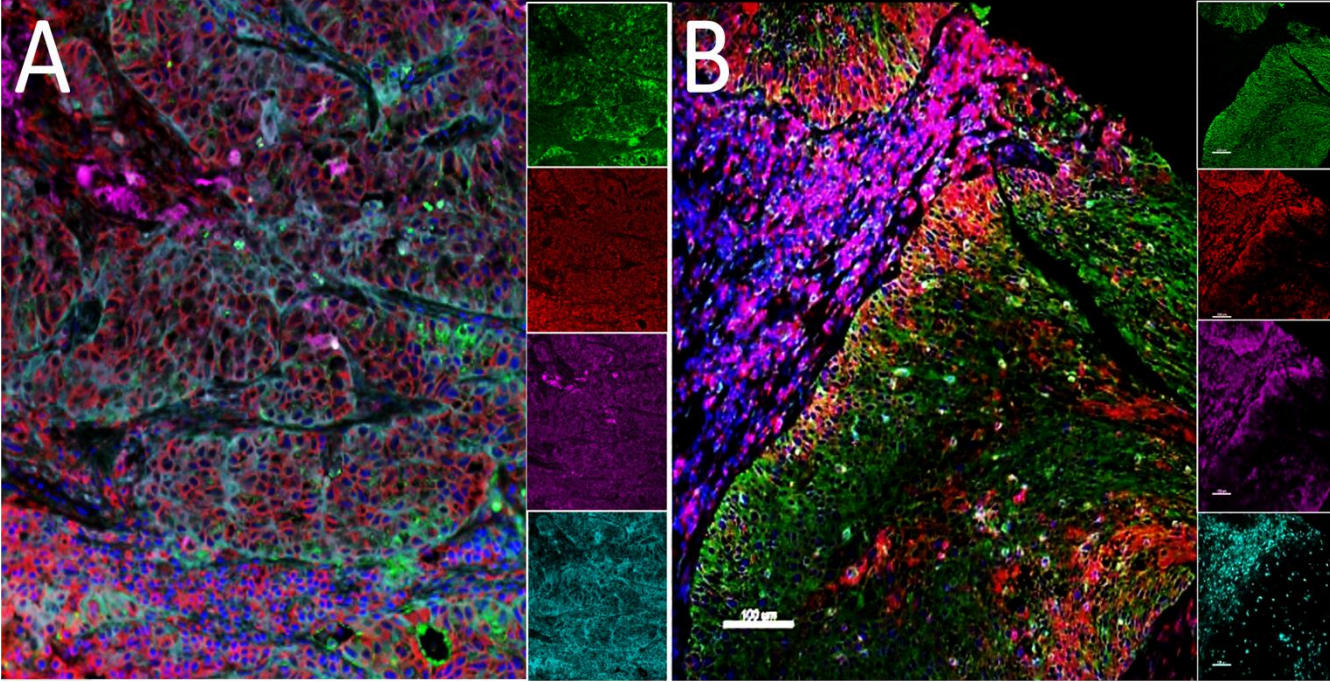


Wang et al. 2019, Cell

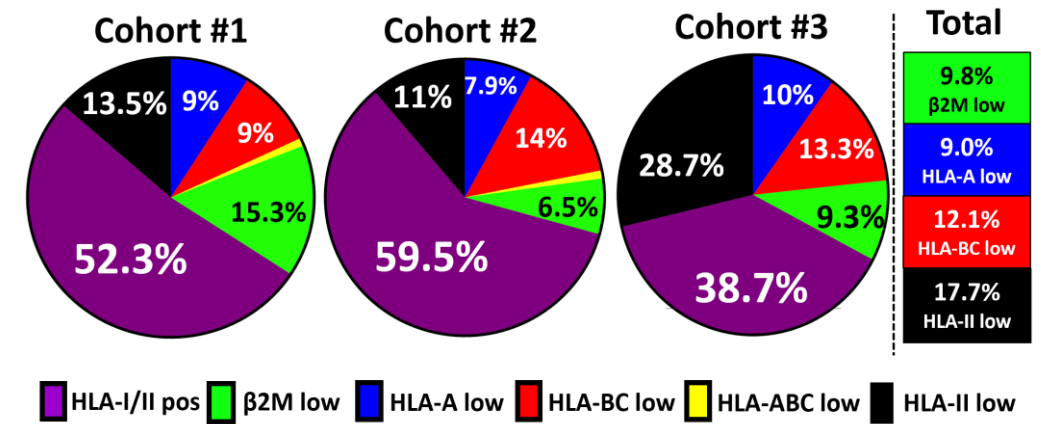
β 2M loss and acquired resistance to IO in NSCLC



DAPI/CK/B2M/HLA-BC/HLA-II

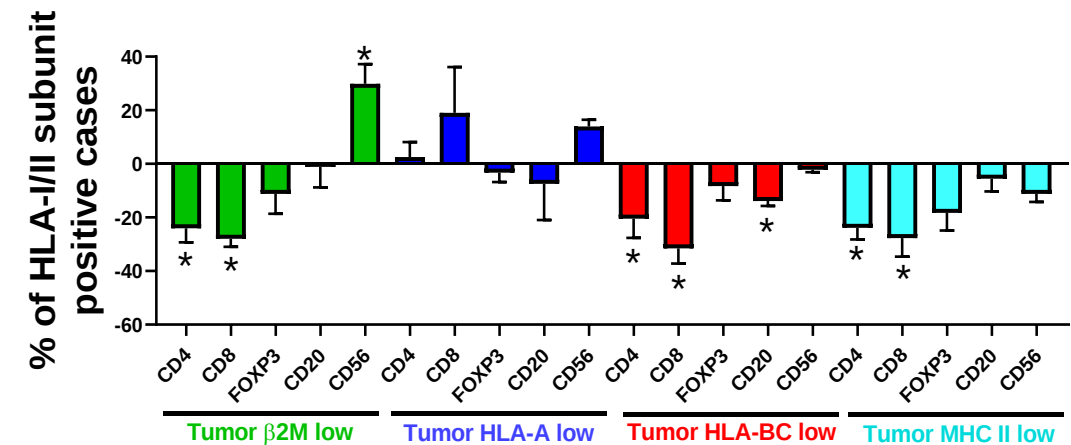


HLA class-I/II APM defects in IO naïve NSCLC

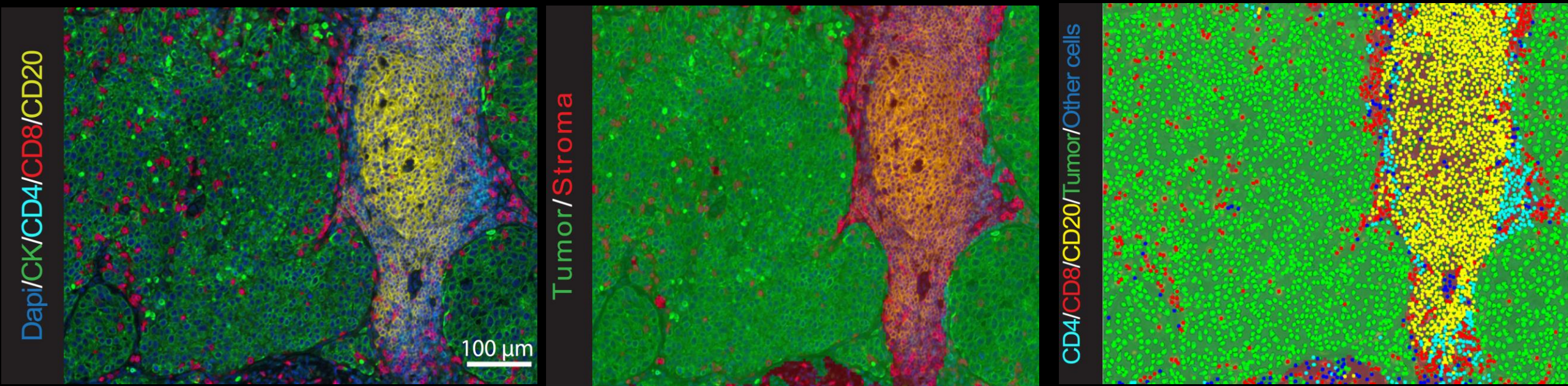


Deleterious mutations in <5% of NSCLCs

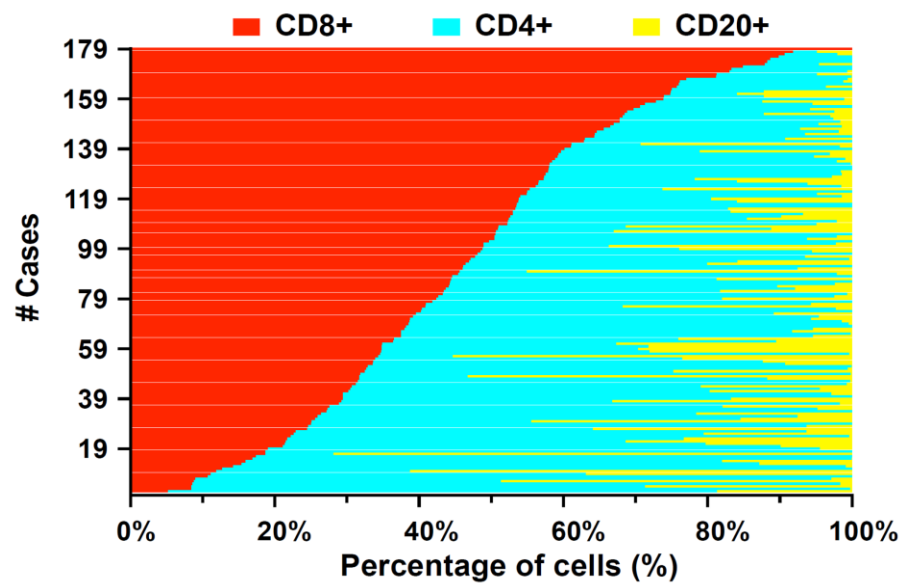
Immune contexture of HLA-I/II deficient NSCLS



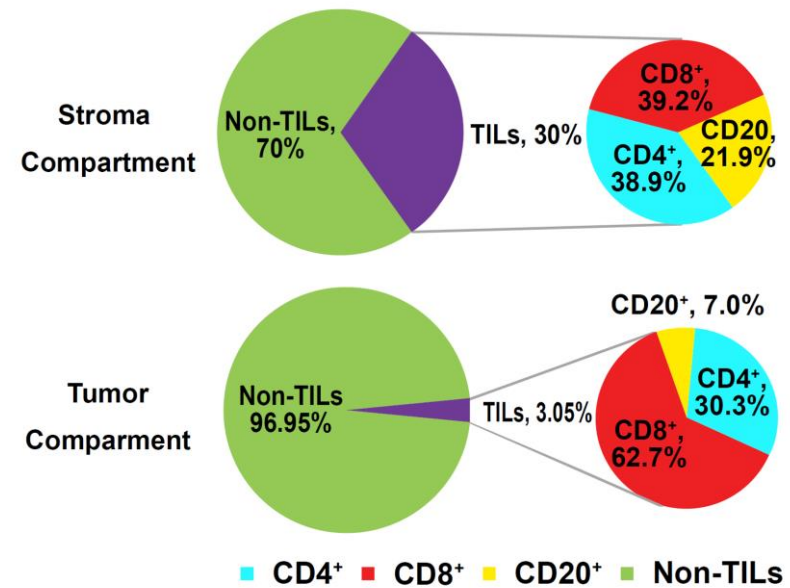
Non-tumor cells (T-cells)

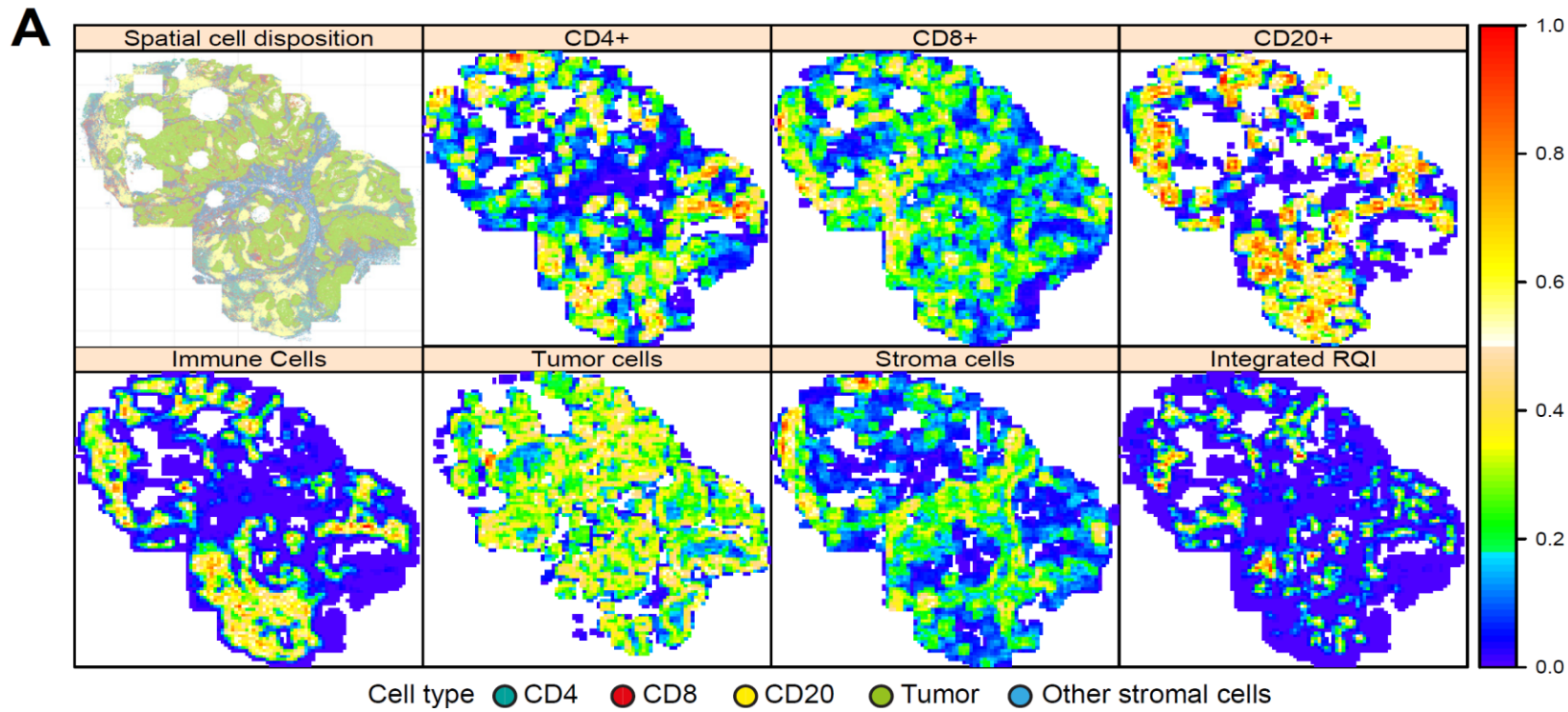


TILs in 179 NSCLCs

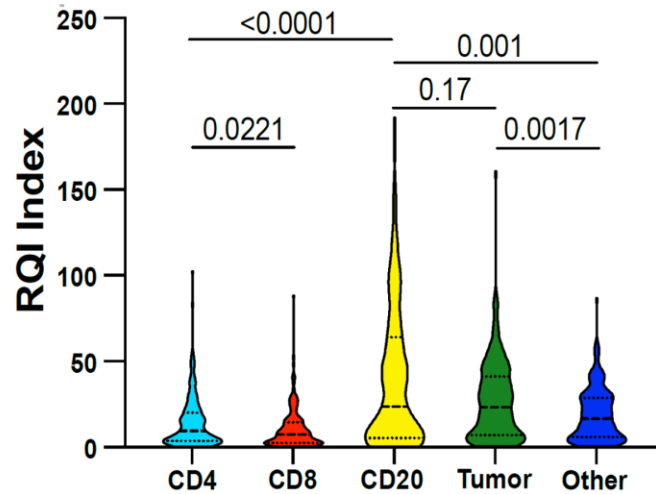


Spatial distribution

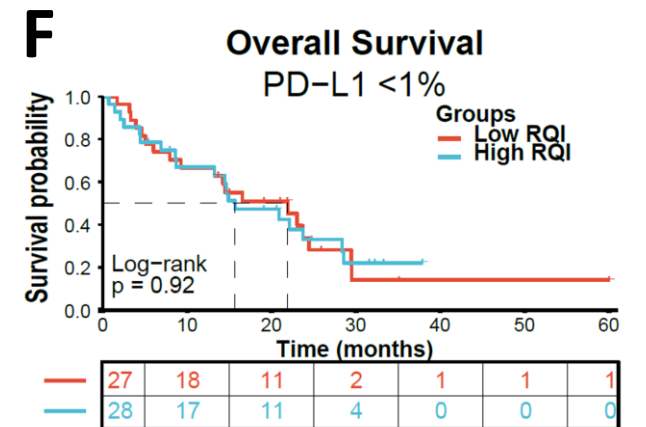
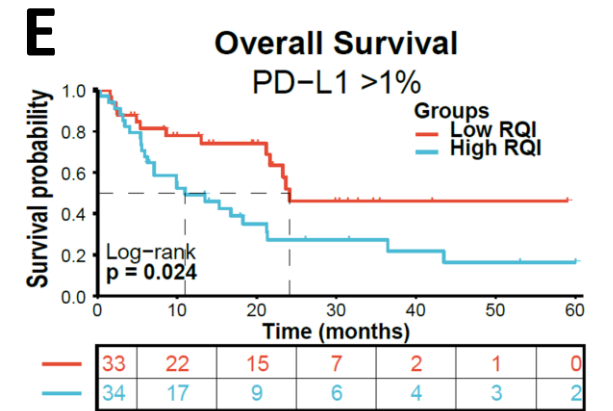
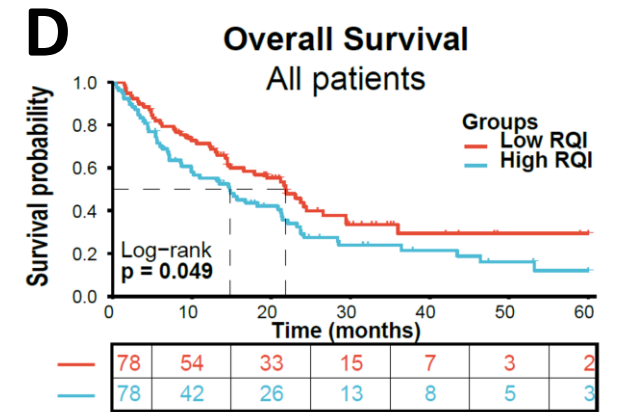
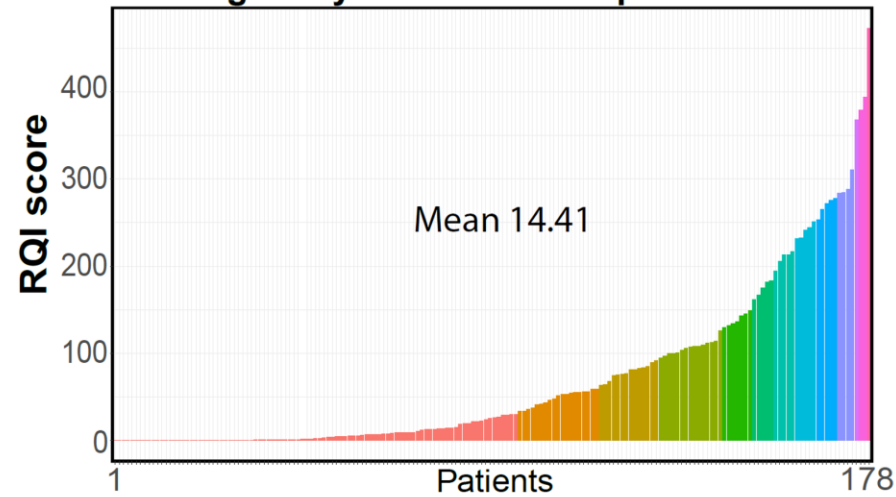


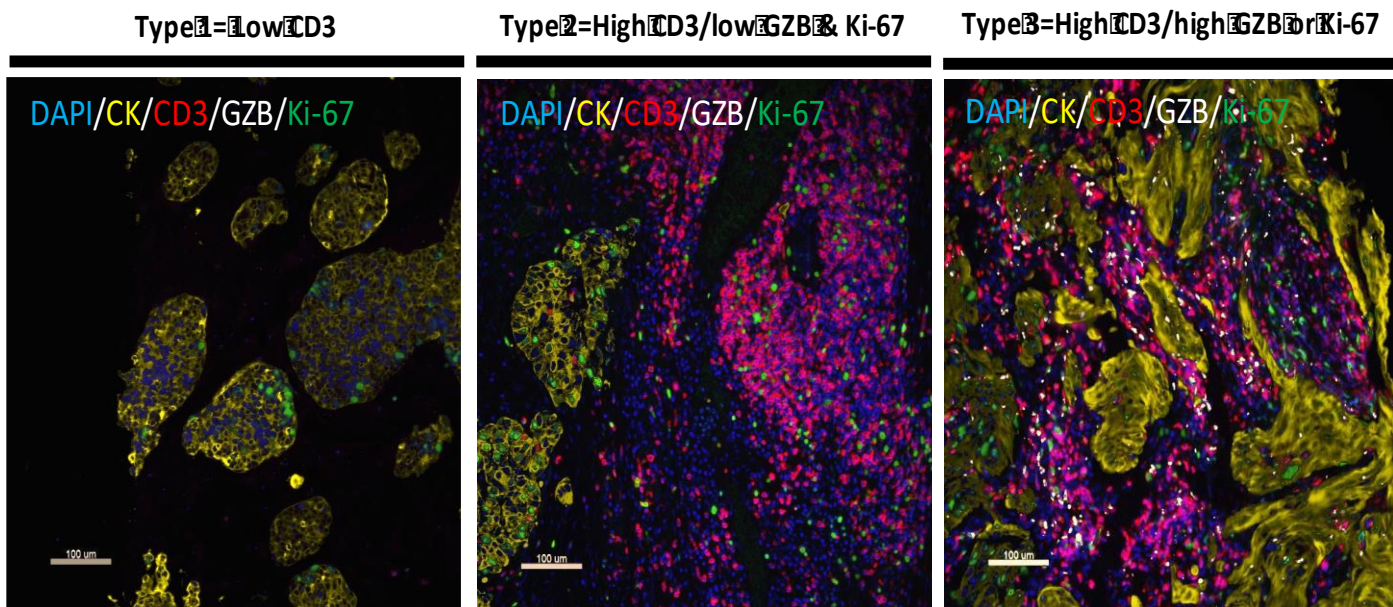


B Heterogeneity of individual cells

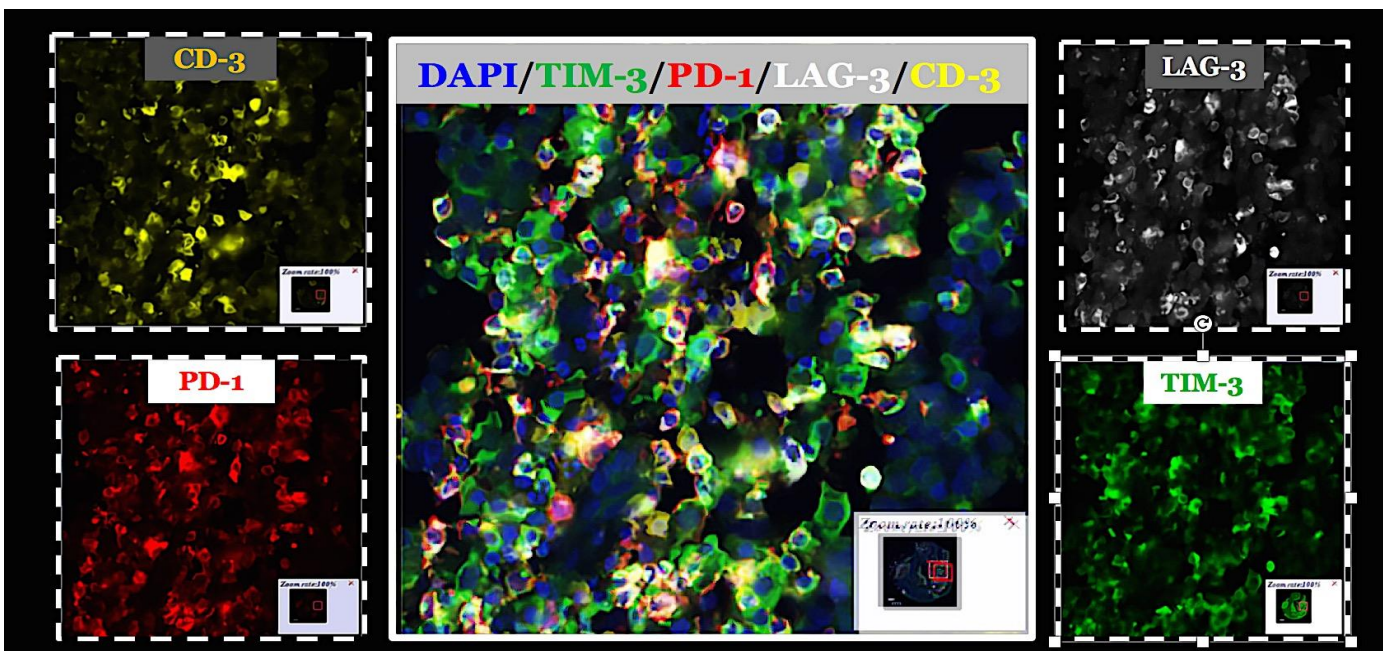


C Heterogeneity score for each patient

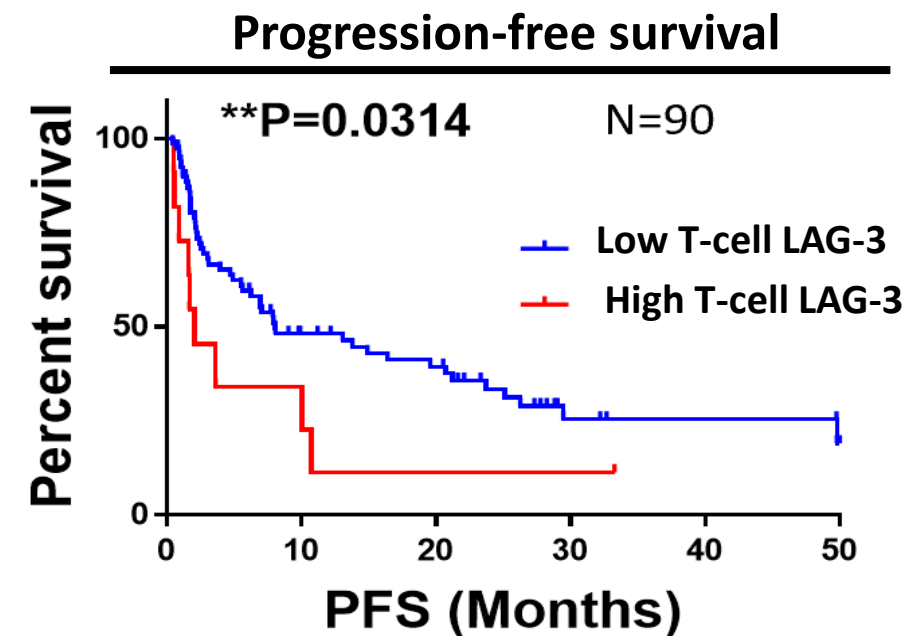
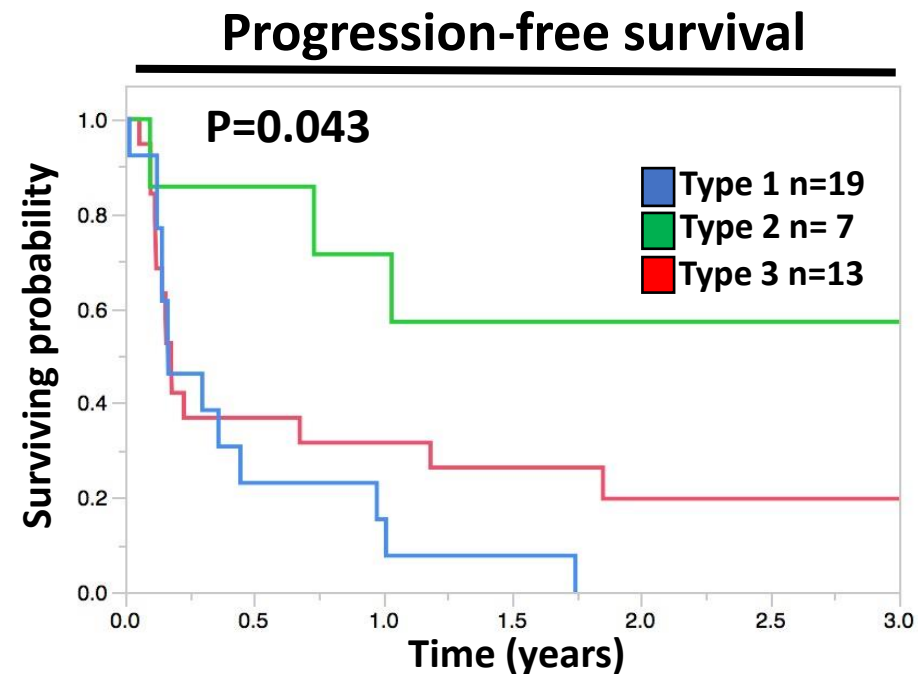




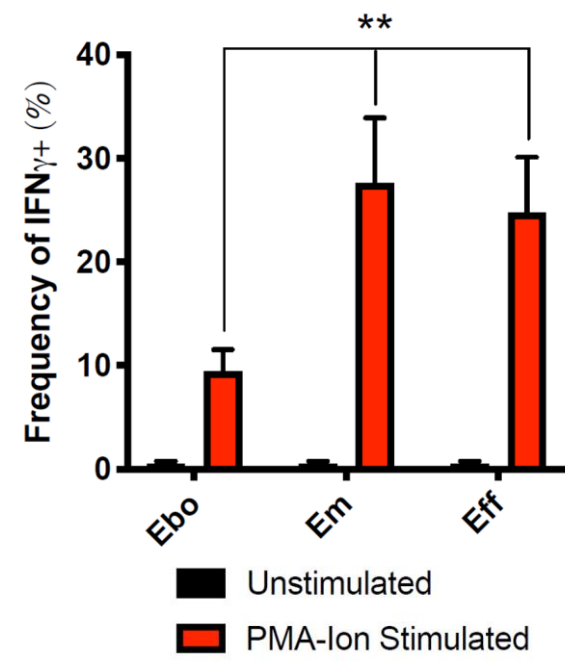
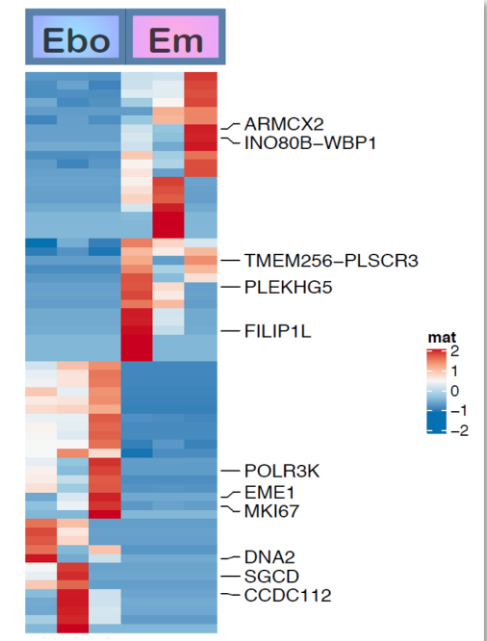
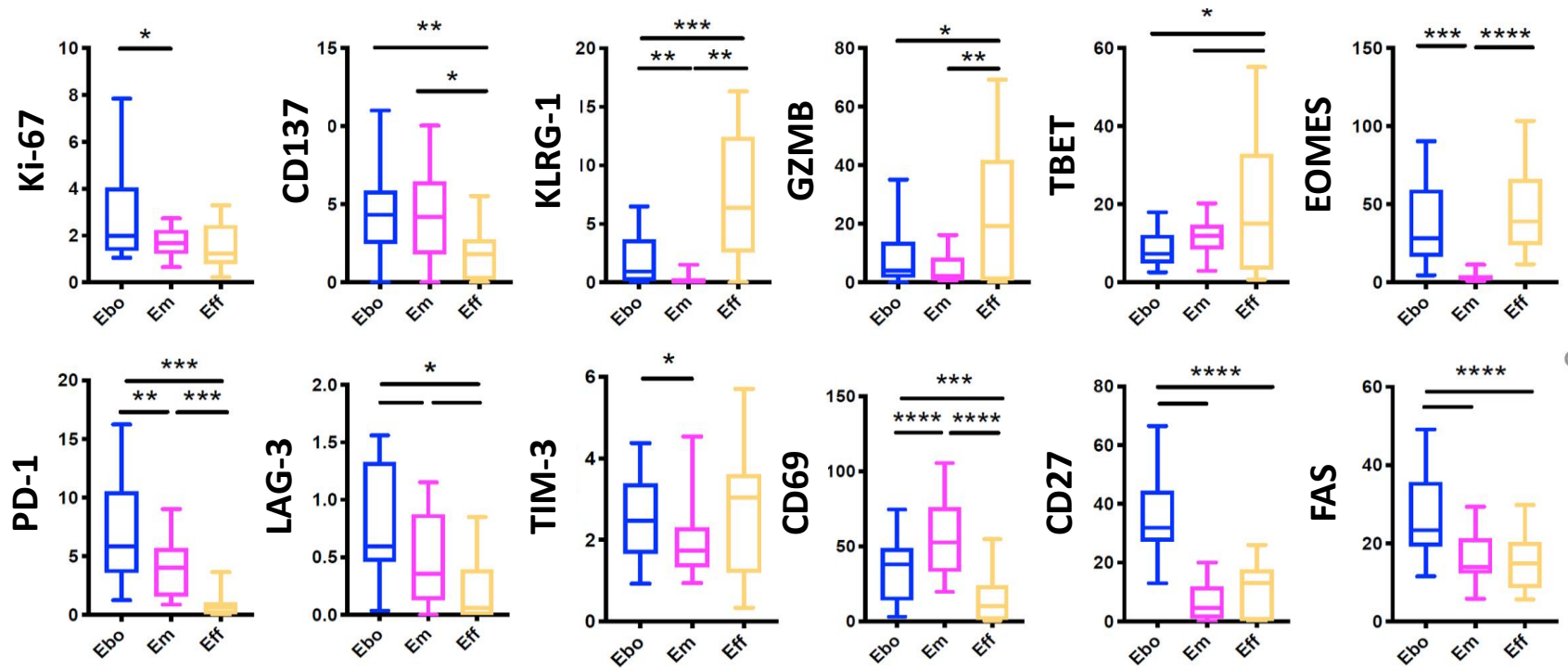
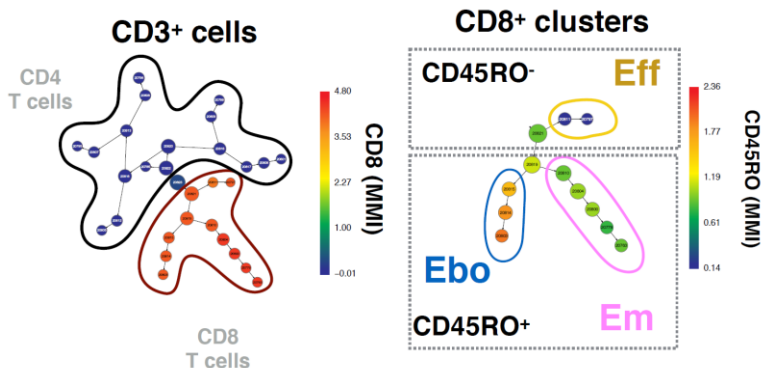
Gettinger et al., 2018 Nat Comm



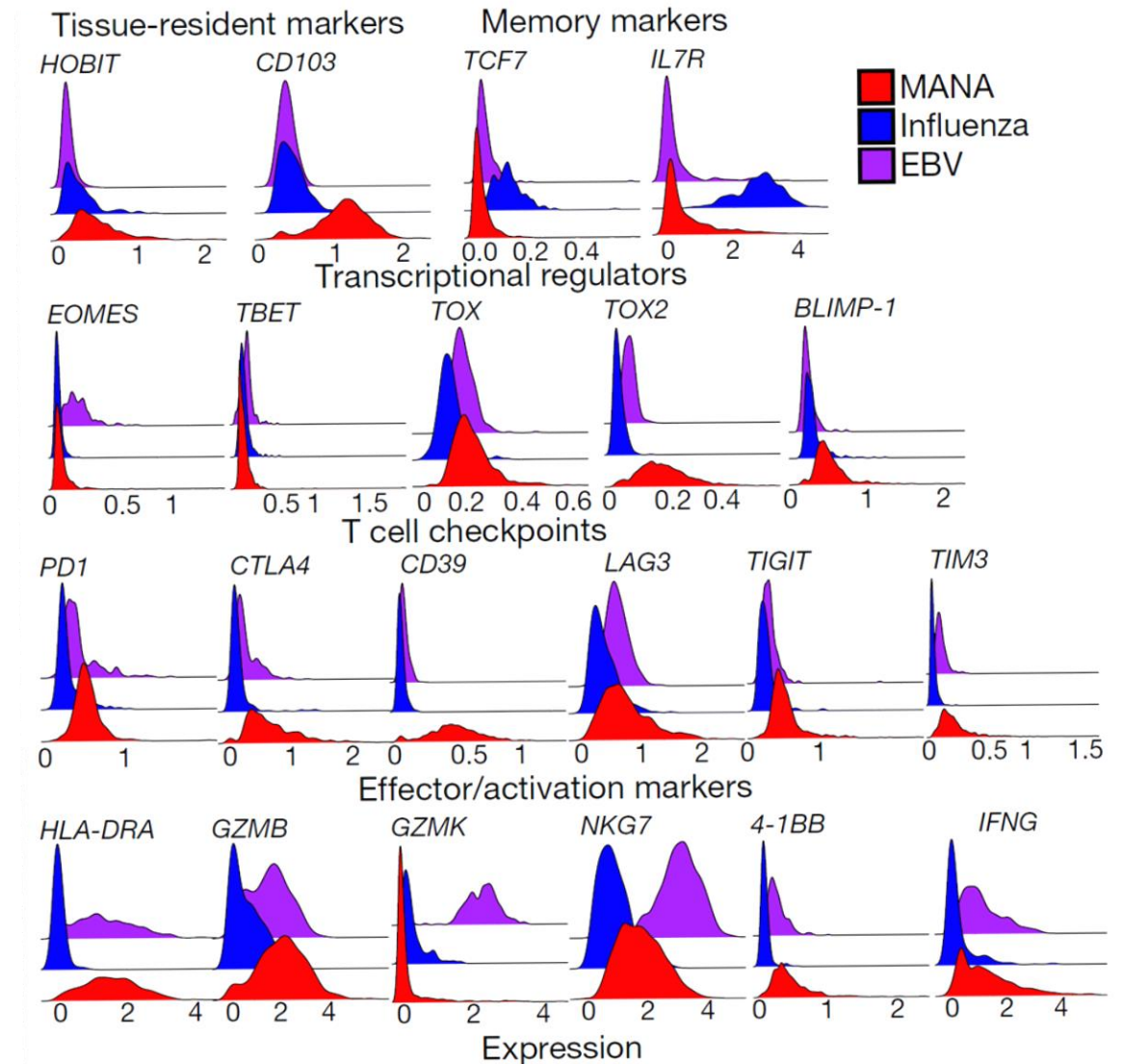
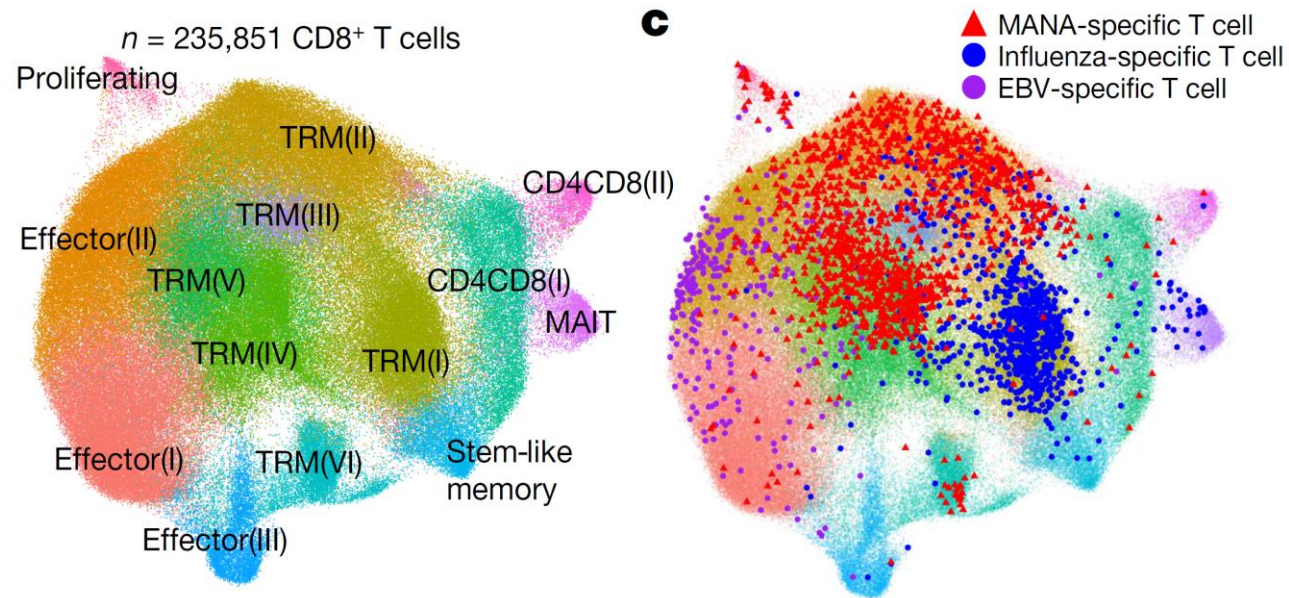
Datar et al., 2018 Clin Can Res

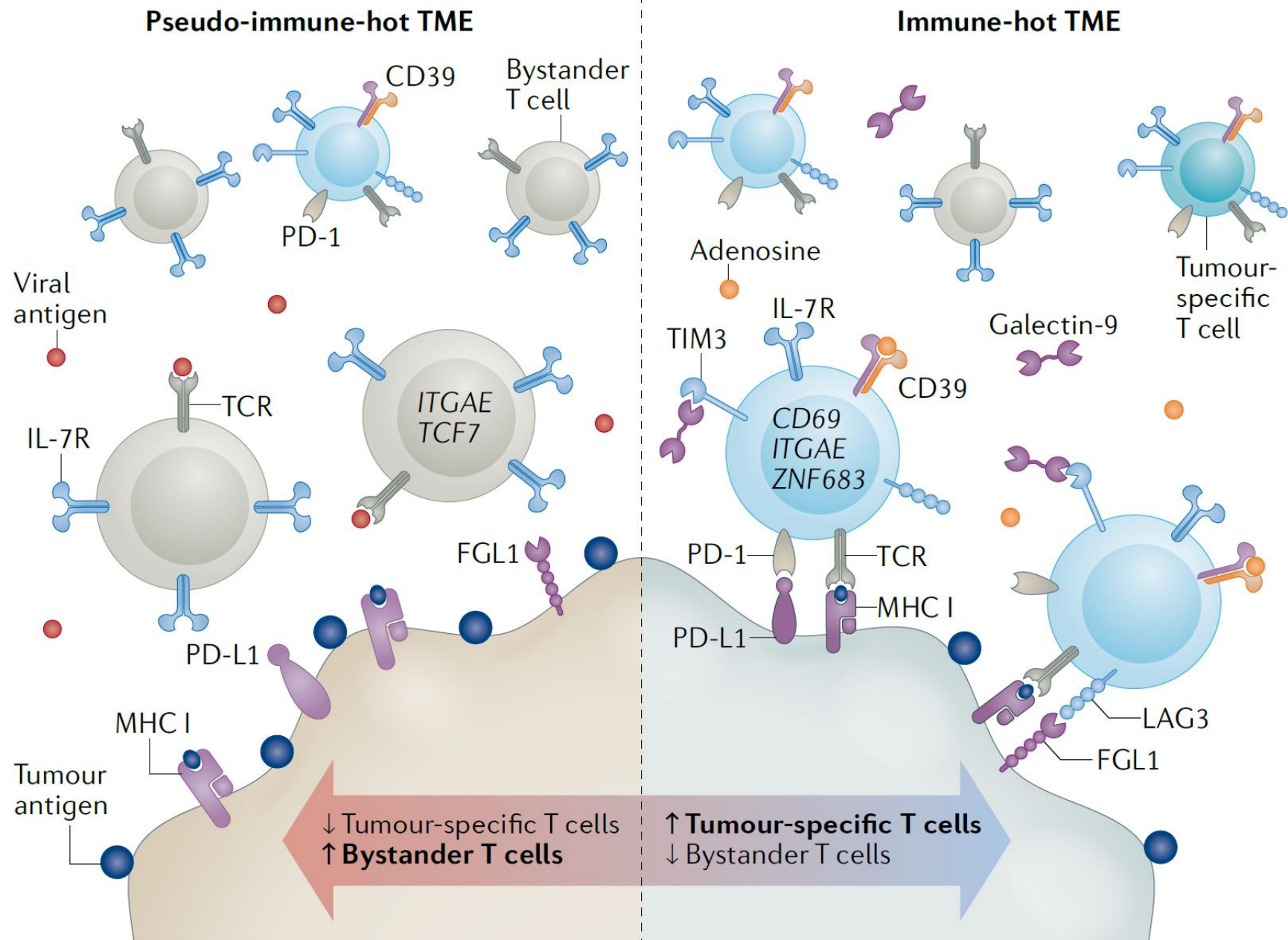


T-cell dysfunction in human NSCLC (Ebo)

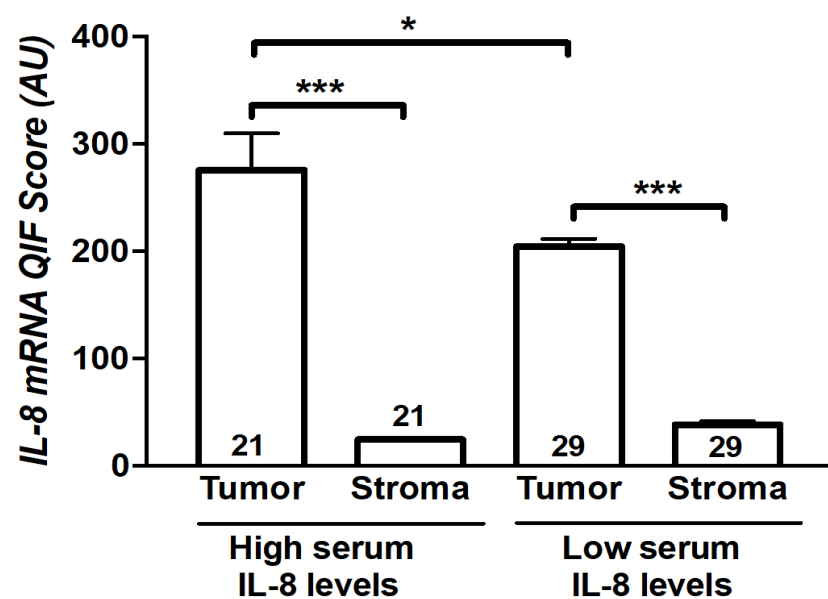
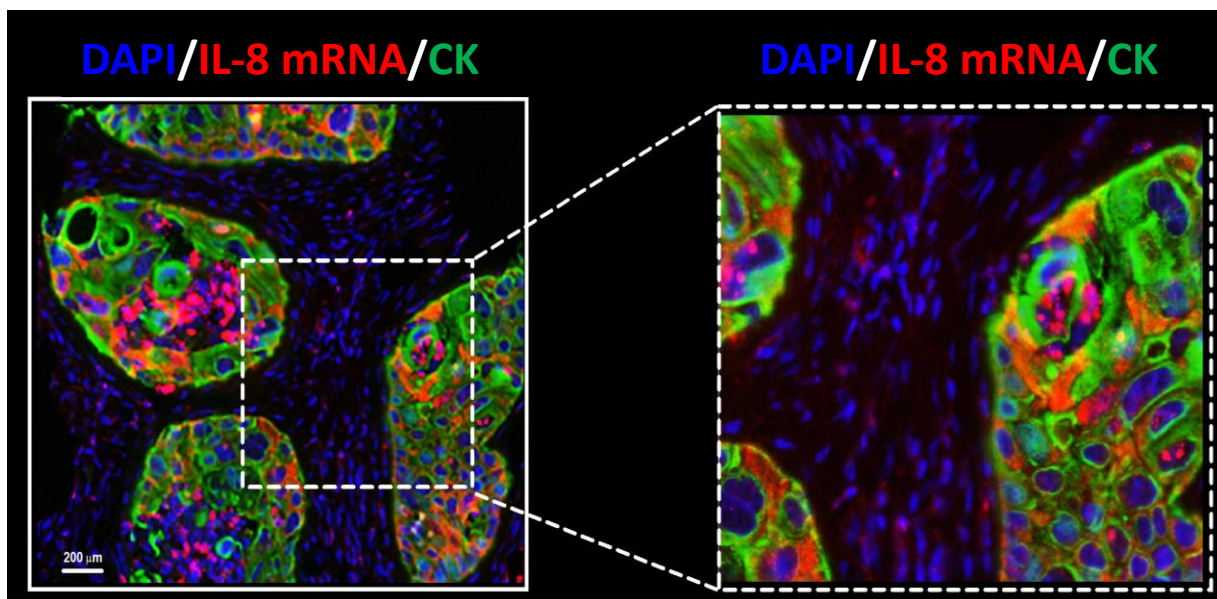


Tumor-antigen specific CD8+ T-cells in NSCLC by scRNASeq

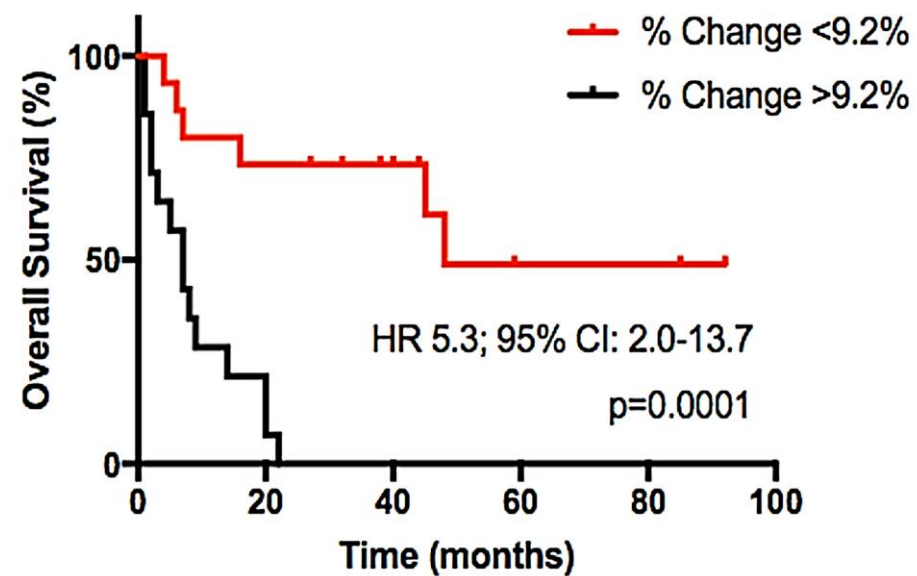




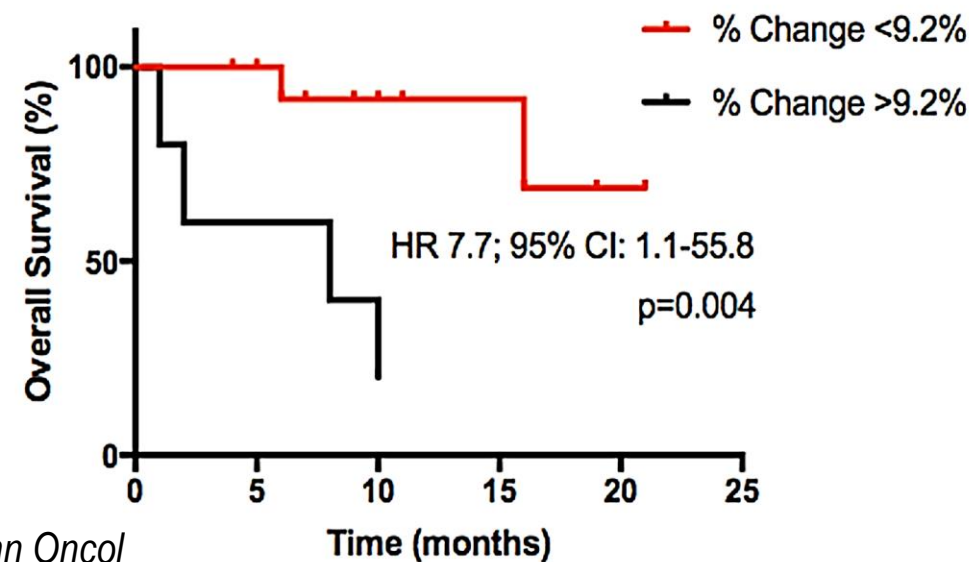
Non-tumor cells (Myeloid cells)

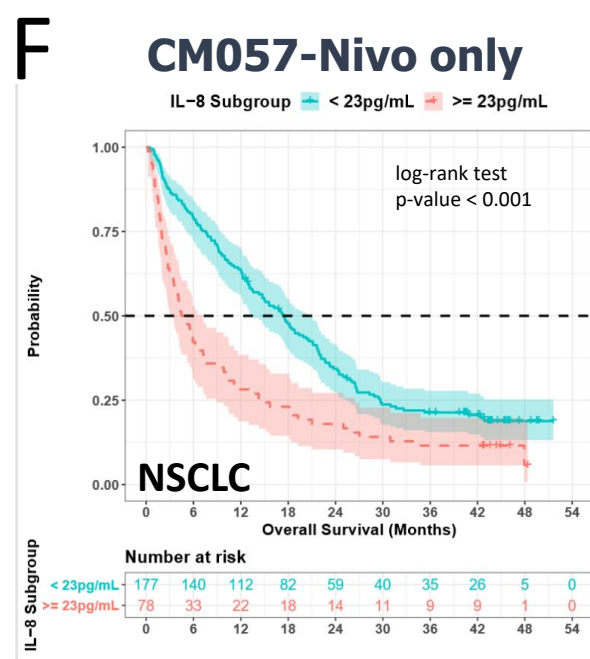
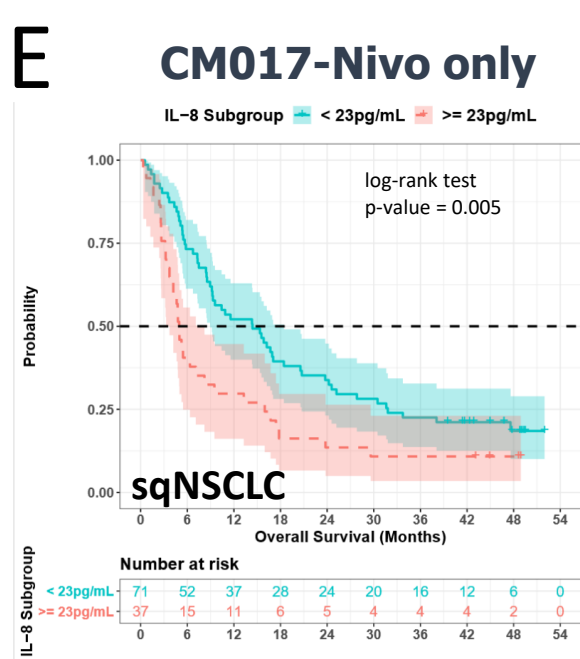
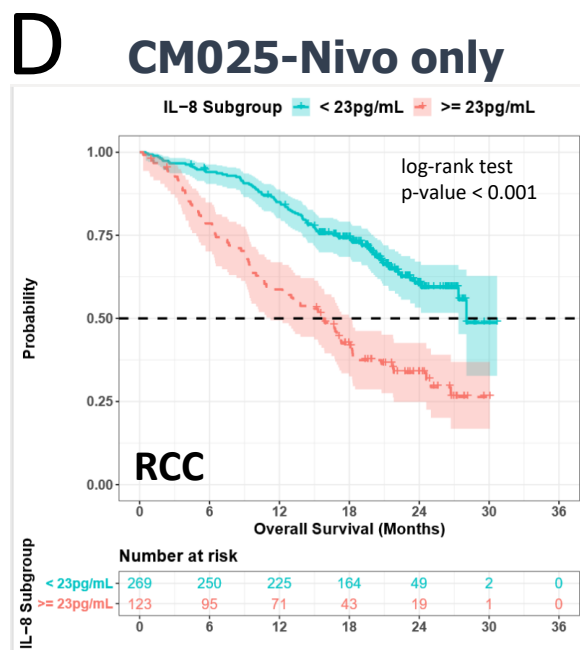
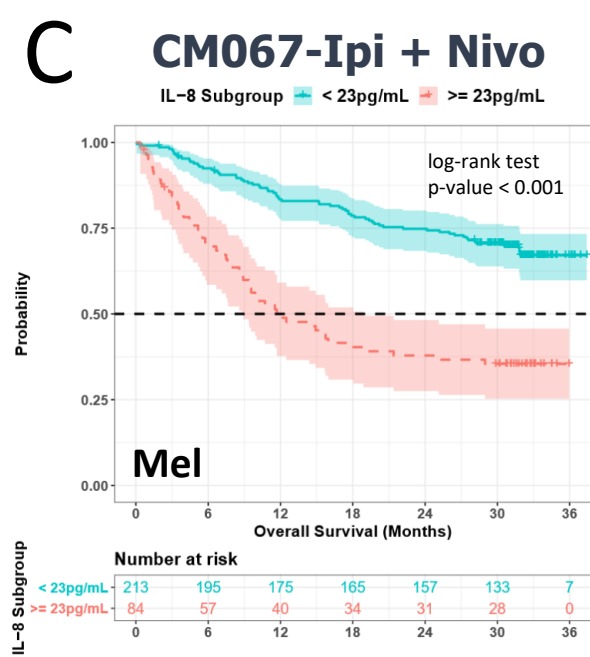
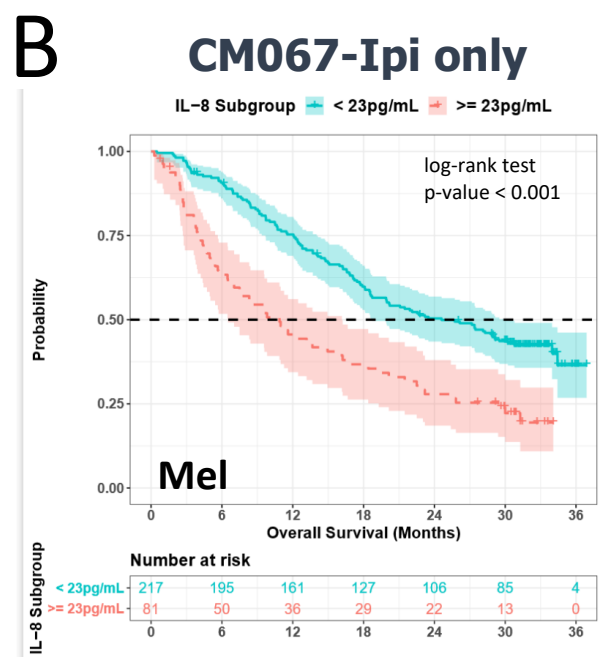
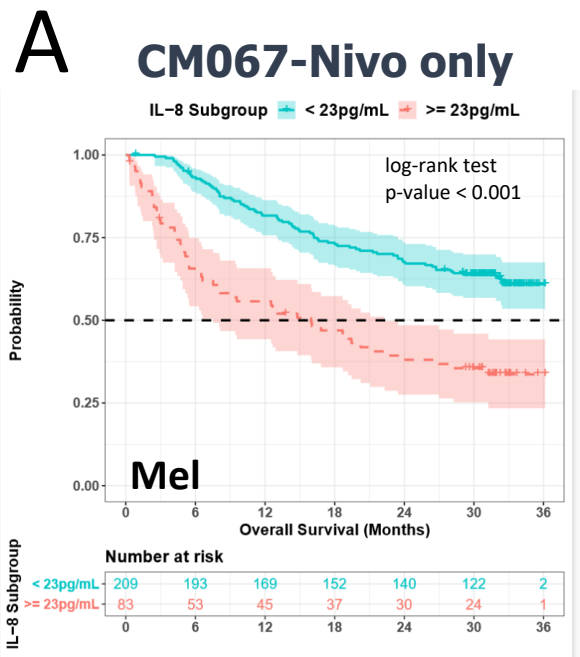


Melanoma

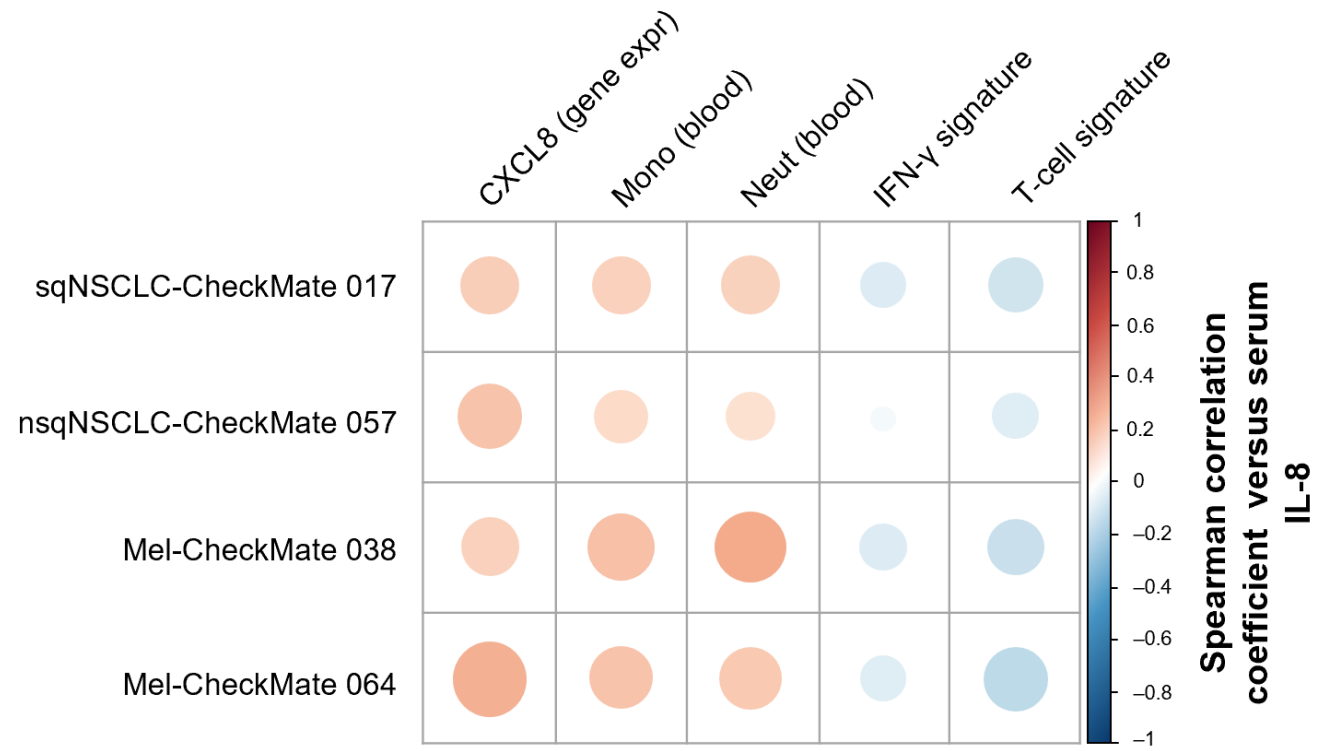
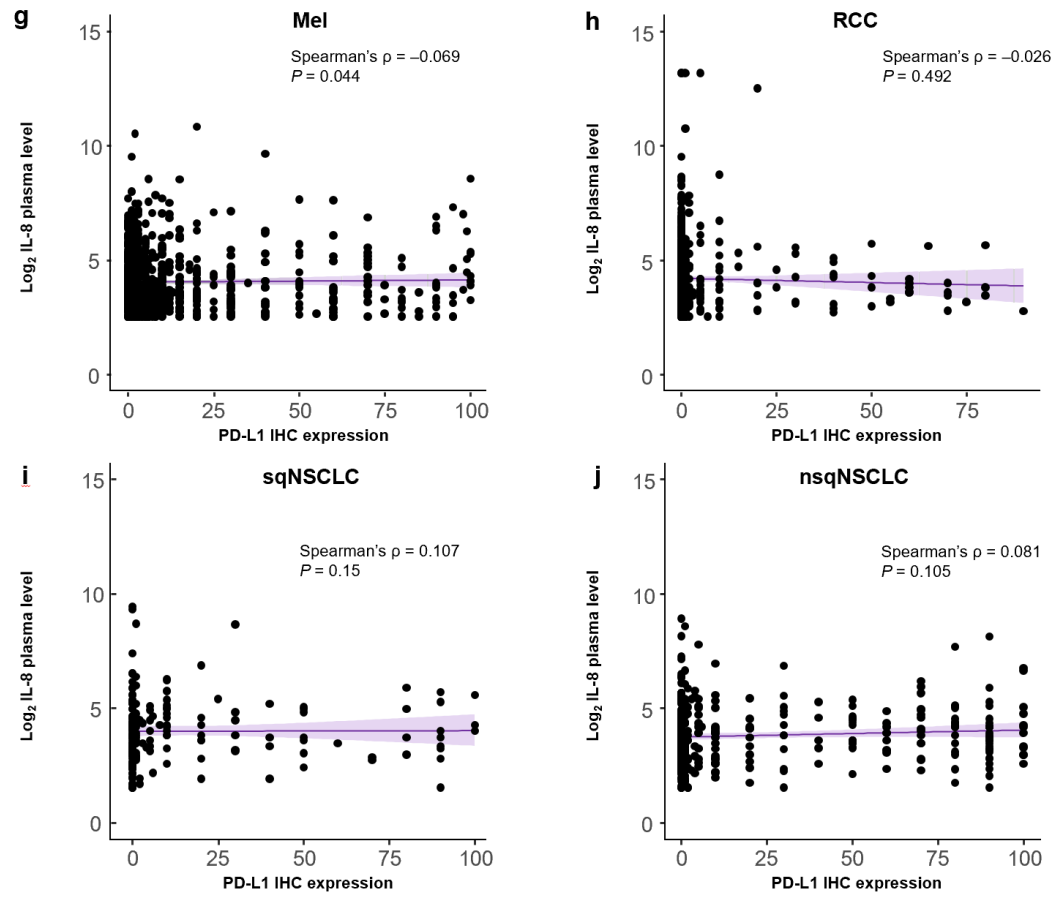


NSCLC



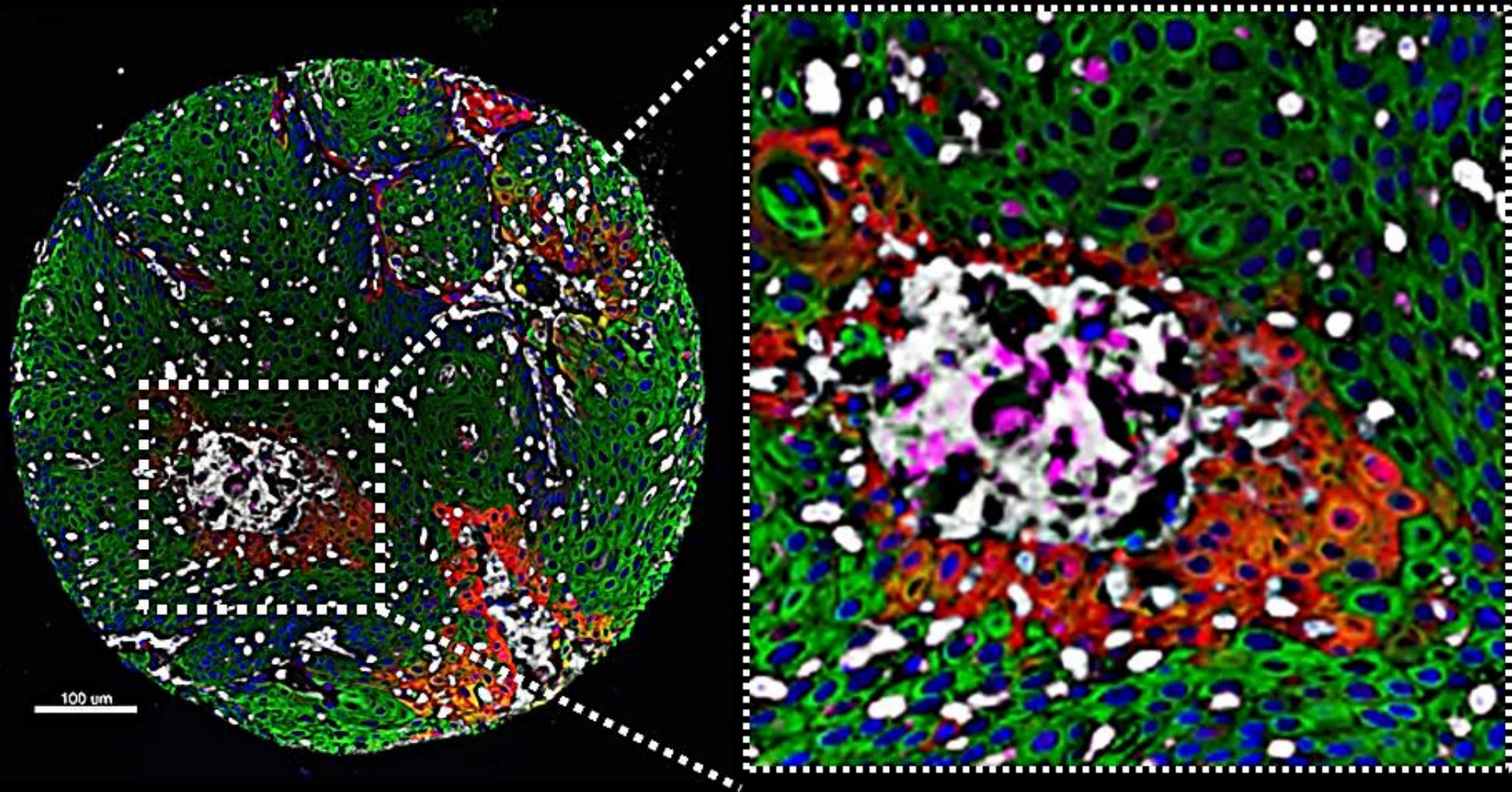


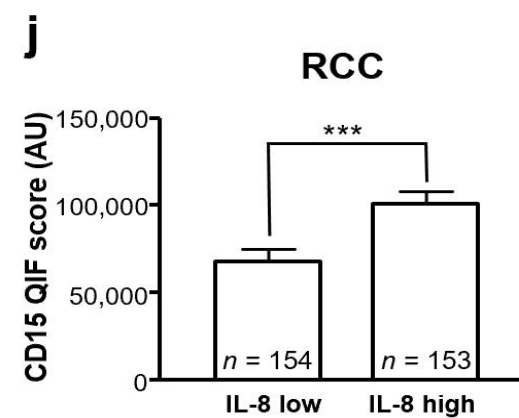
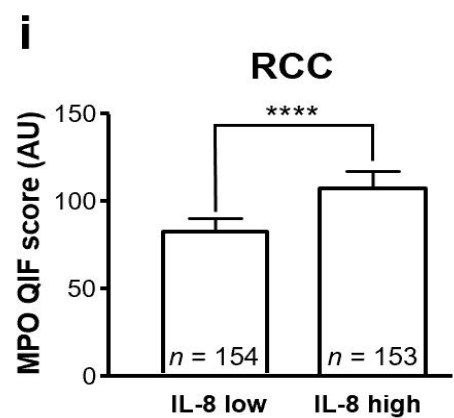
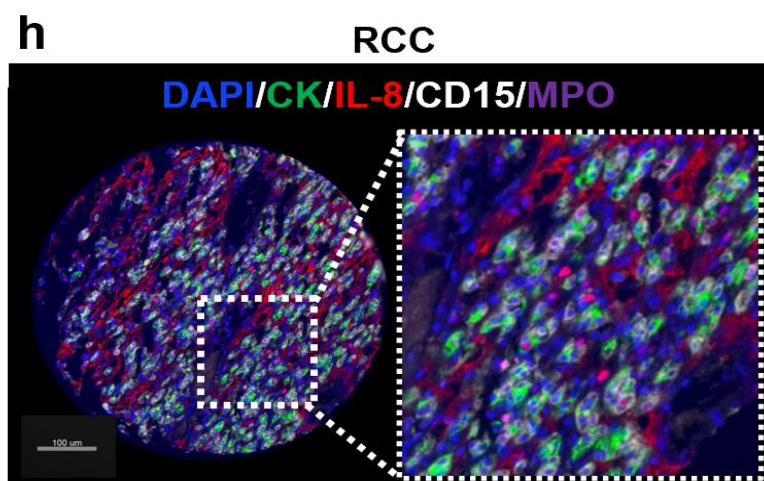
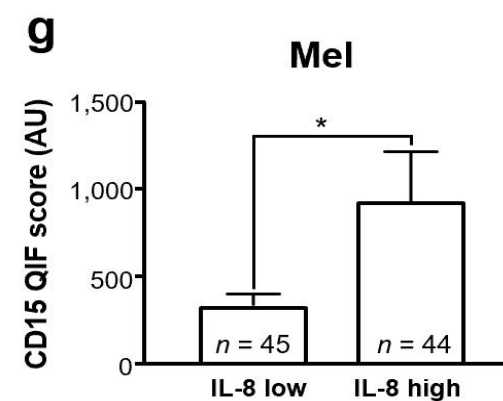
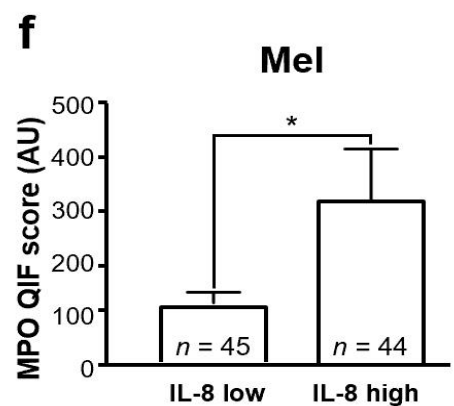
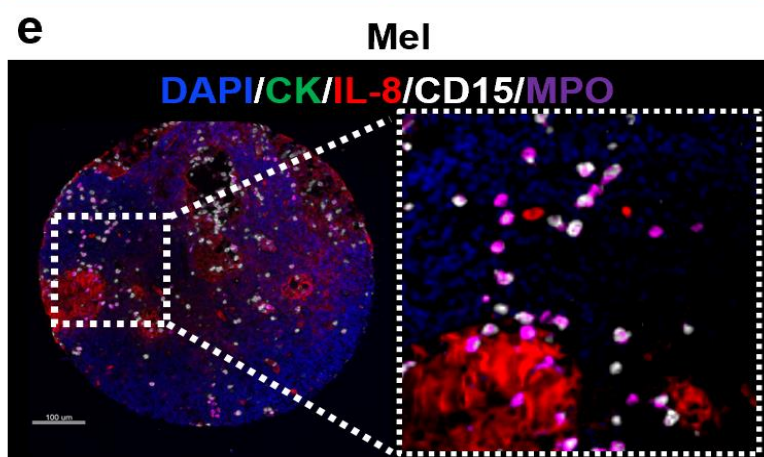
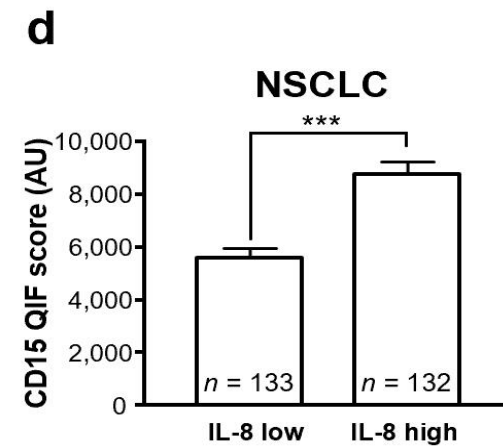
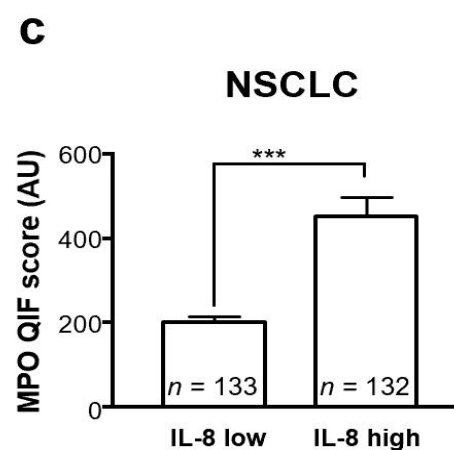
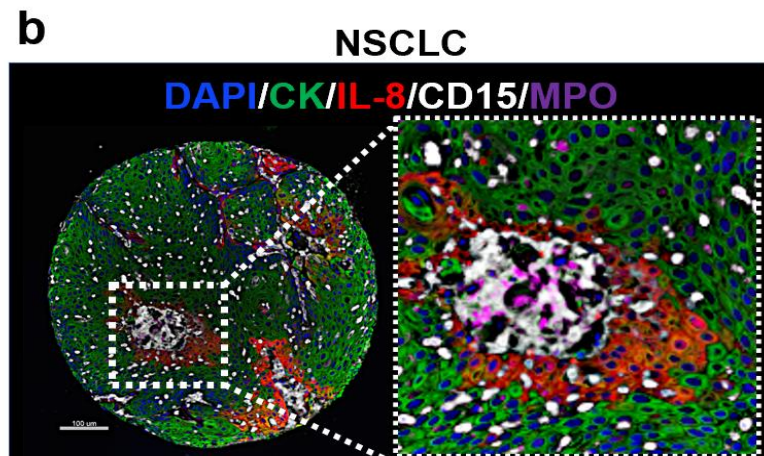
Effect of IL-8 is independent from PD-L1 expression and IFN γ responses



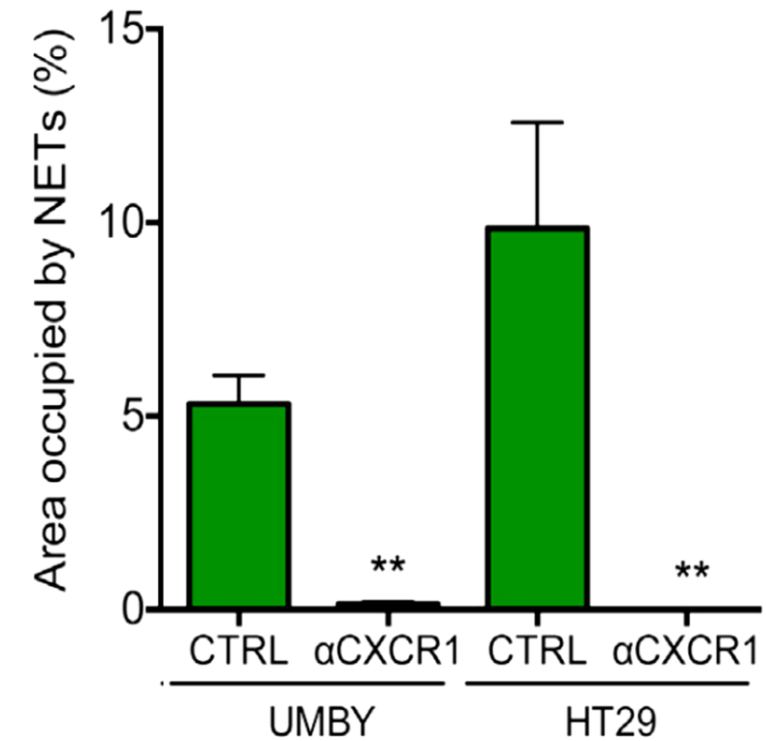
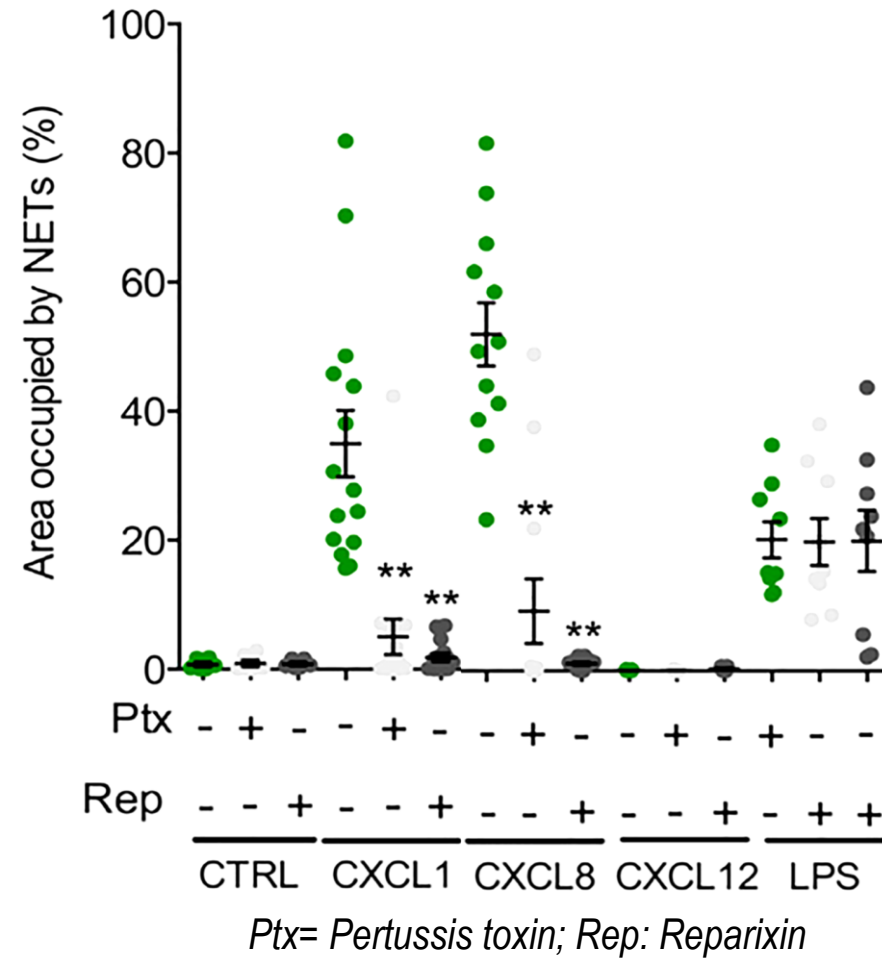
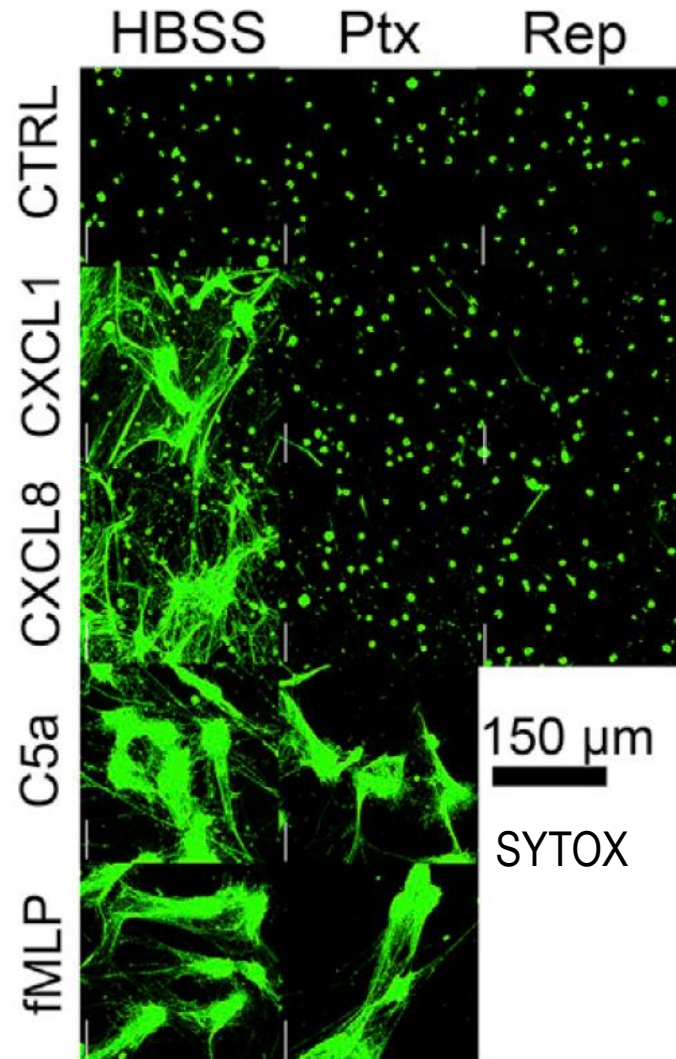
Measuring IL-8 and granulocytes in tumor tissue

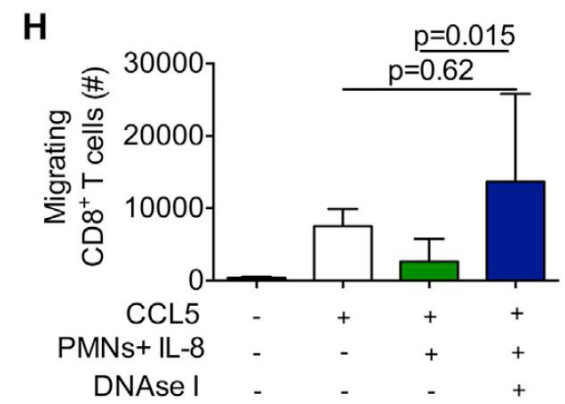
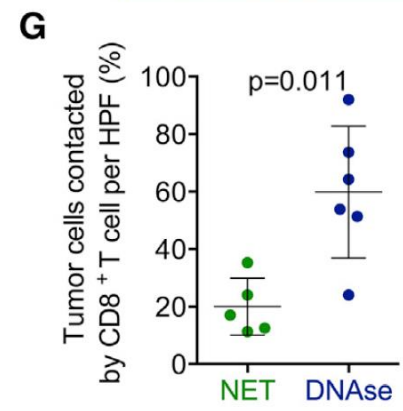
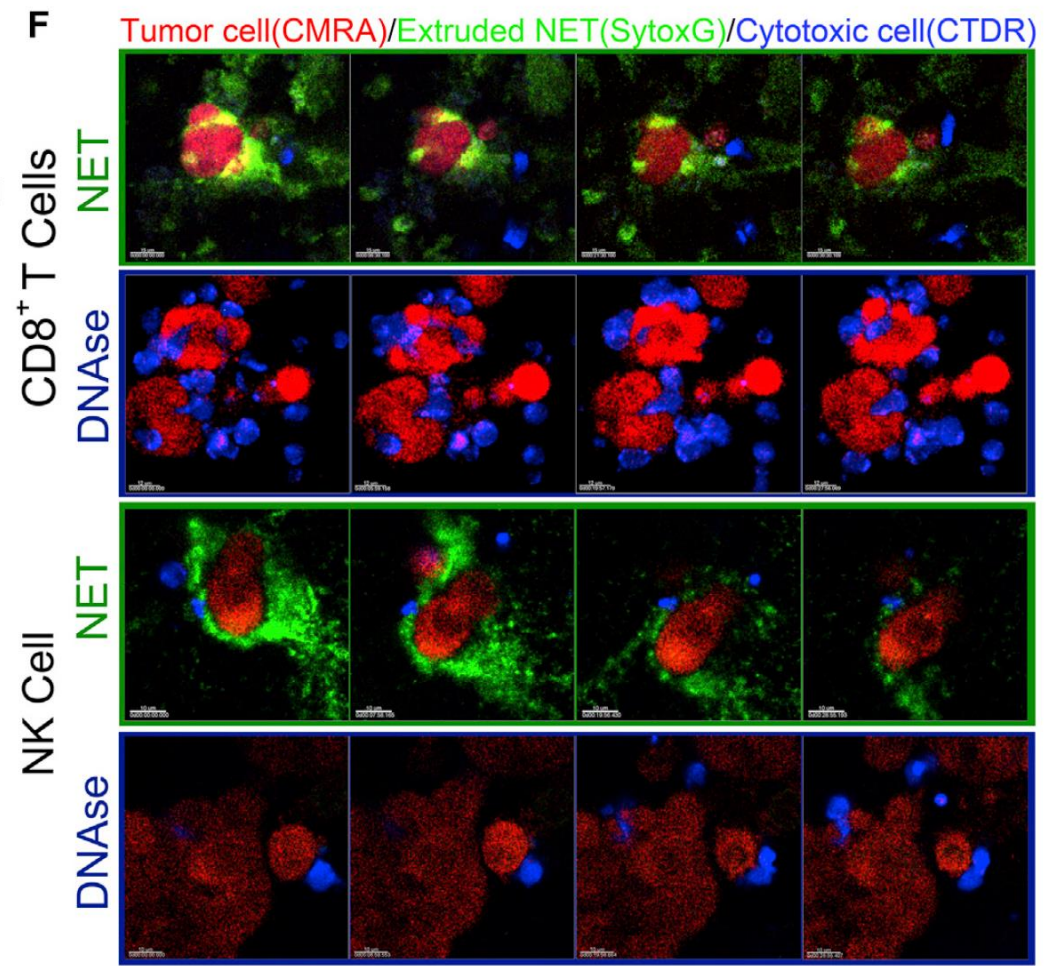
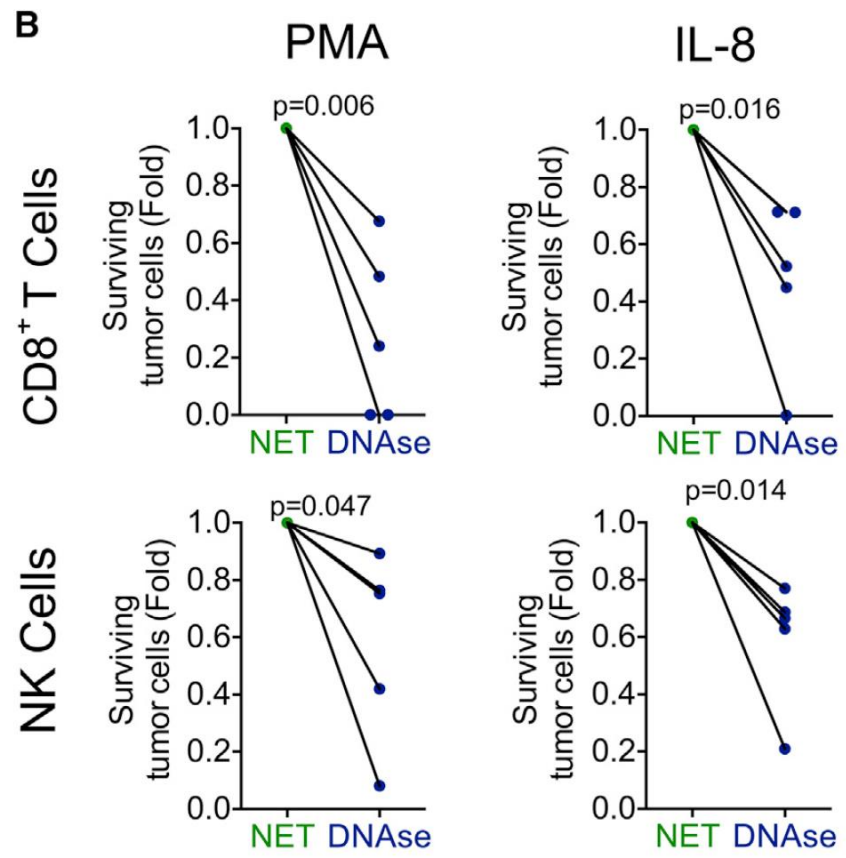
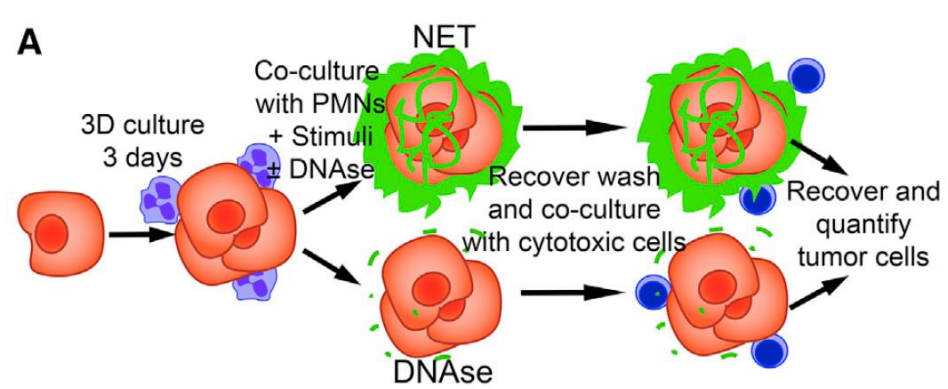
DAPI/CK/IL-8/CD15/MPO - High markers expression





Neutrophils and NETosis in human granulocytes

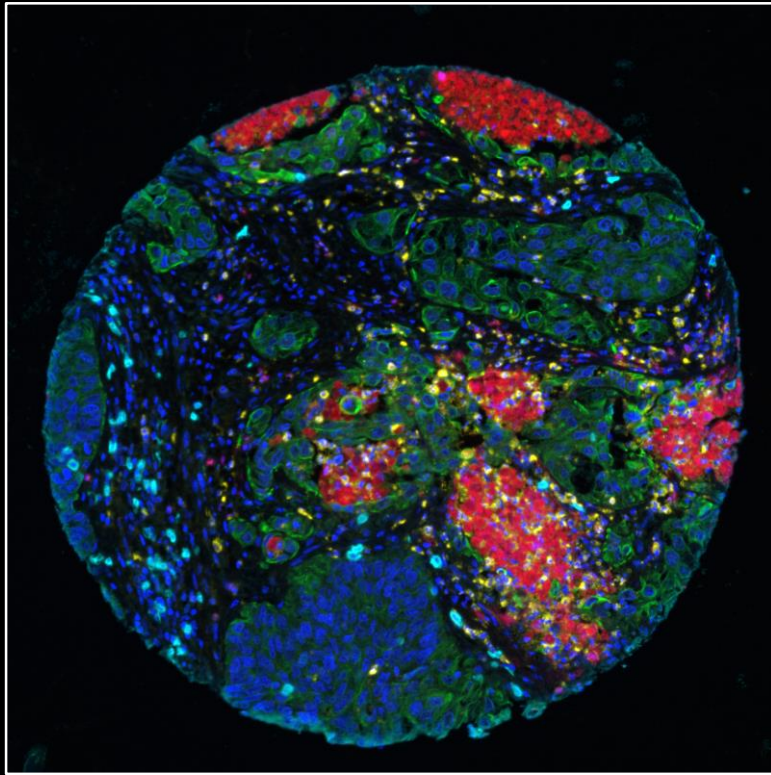




Automated NET measurement

Immunofluorescence

Dapi/**CK**/cit**H3**/**CD66b**/**CD8**



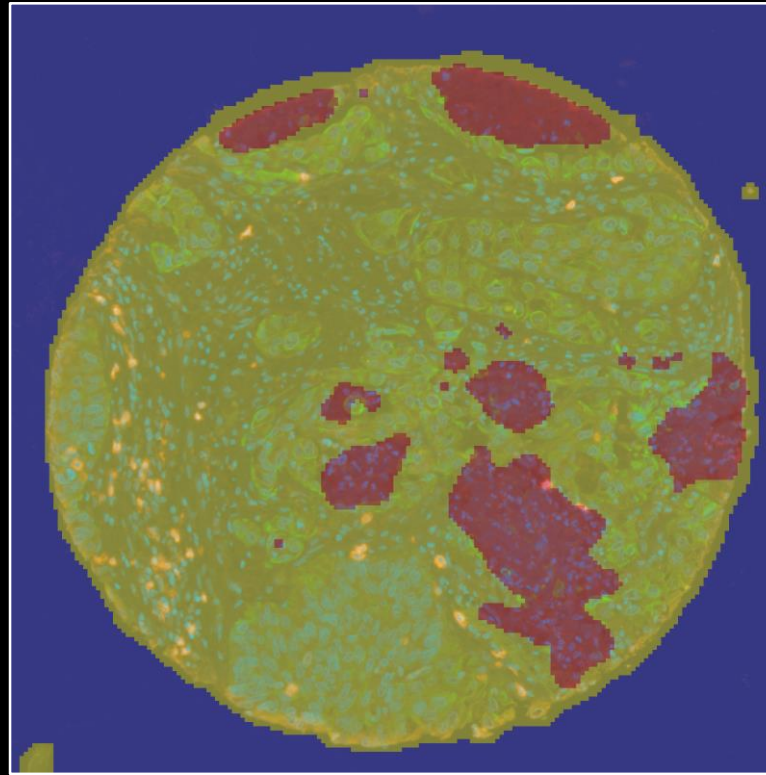
**MULTISPECTRAL
IMAGING**

Compartment segmentation

Background

NET

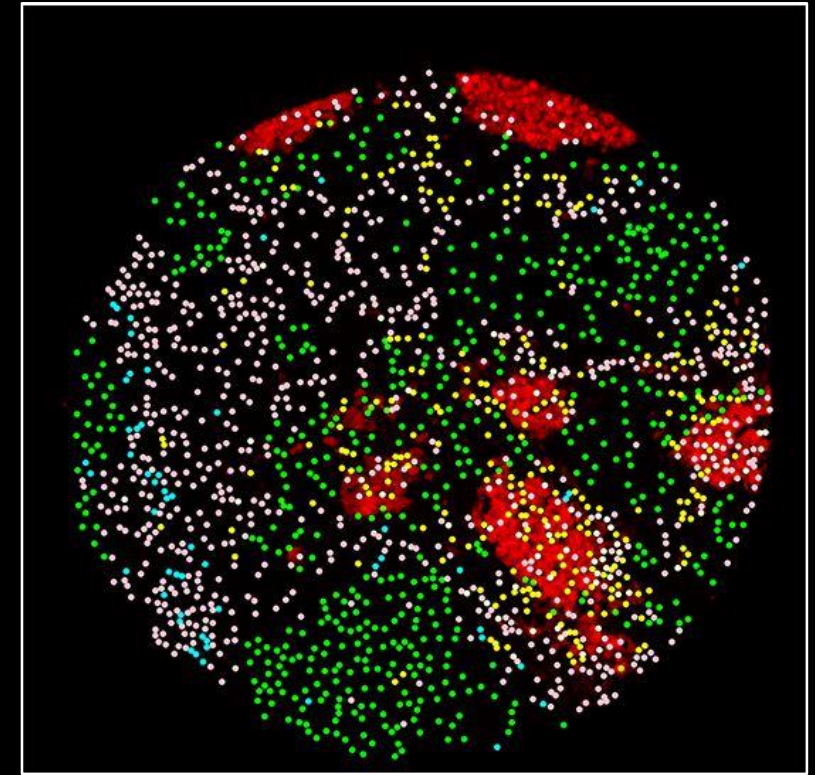
Tissue



**AREA
(mm²)**

Cells phenotype

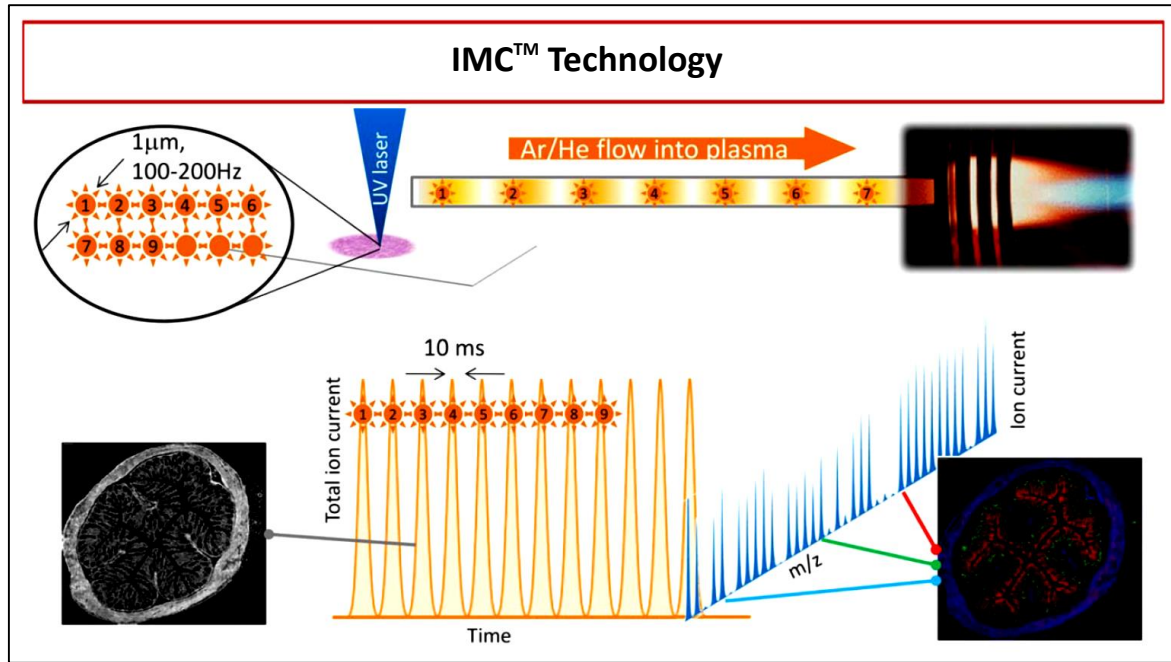
CK+/**Stromal+**/**CD66b+**/**CD8+**



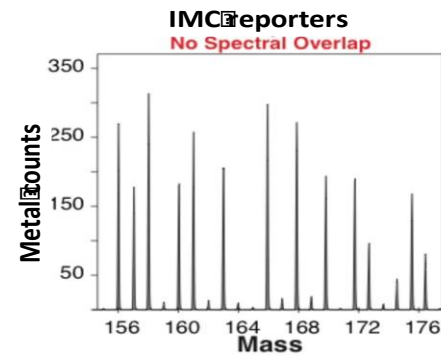
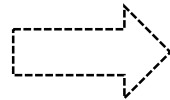
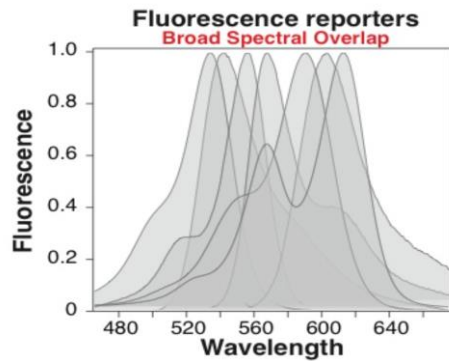
**Cell Density
(Cells/mm²)**

Integrated TME analysis

Yale IMC Immuno-oncology panel



Chang et al., 2017. Cytometry A. 91(2):160-169



Isotope	Target	Dilution	Category
Im115	LipoR	1:100	Membrane
Eu150	GAPDH	1:50	Structure
Yb176	Histone-3	1:500	Nuclei
Nd148	Pancytokeratin	1:50	Epithelial
Gd156	Vimentin	1:50	Stromal
Er170	CD3	1:50	T-lymphocytes
Gd156	CD4	1:50	T-helper
Dy162	CD8	1:50	T-cytotoxic
Gd155	FoxP3	1:25	T-regulatory
Dy161	CD20	1:50	B-lymphocytes
Tb159	CD68	1:50	Macrophages
Sm149	CD45RO	1:50	Memory T-cells
Yb173	Granzyme-B	1:25	Cytotoxicity
Er168	Ki-67	1:50	Proliferation
Nd145	T-bet	1:25	Effector function
Dy163	CD25	1:50	Activation
Tm169	B2-microglobulin	1:50	Antigen presentation
Nd150	PD-L1	1:50	B7-Immune regulation
Yb172	PD-L2	1:50	B7-Immune regulation
Sm152	B7-H3	1:50	B7-Immune regulation
Gd158	B7-H4	1:50	B7-Immune regulation
Yb171	IDO-1	1:50	Immune regulation
Gd160	PD-1	1:50	Immune regulation
Eu153	LAG-3	1:25	Immune regulation
Sm154	TIM-3	1:25	Immune regulation
Nd146	CD47	1:25	Immune regulation
Ho165	VISTA	1:50	Immune regulation

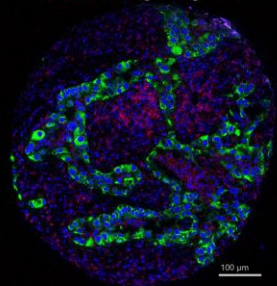
Structural components segmentation

Cell phenotype compartments

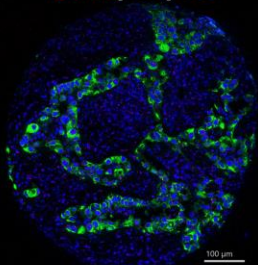
Functional markers immune

Immune regulation candidate targets

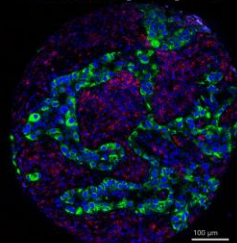
CD45RO/CK/H3



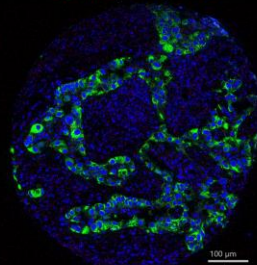
PDL1/CK/H3



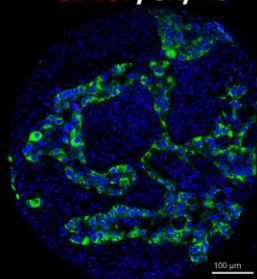
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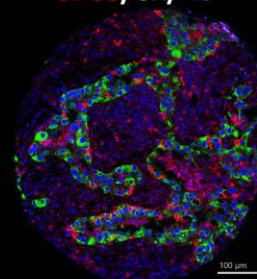
FGL1/CK/H3



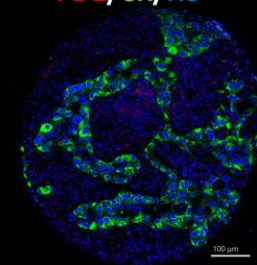
CD137/CK/H3



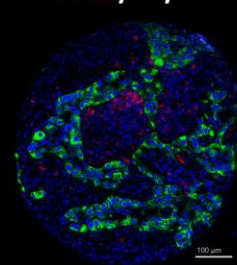
CD68/CK/H3



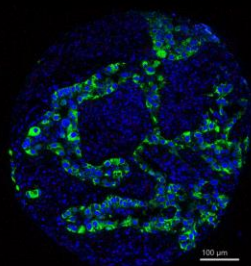
PD1/CK/H3



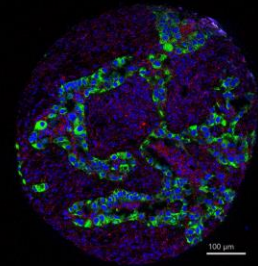
CD20/CK/H3



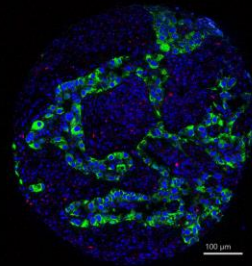
LAG3/CK/H3



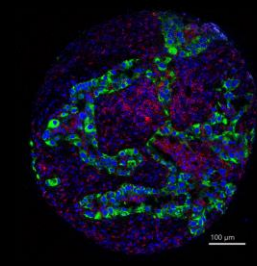
TIM3/CK/H3



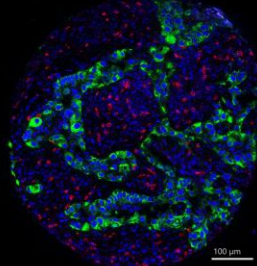
FOXP3/CK/H3



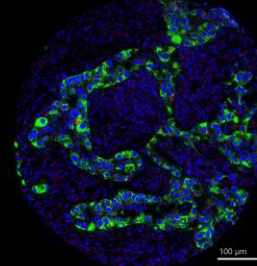
CD4/CK/H3



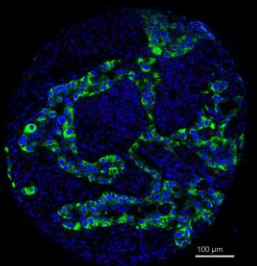
CD8/CK/H3



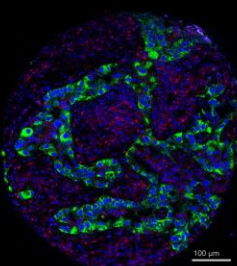
CD25/CK/H3



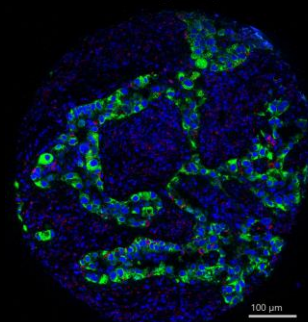
Arg1/CK/H3



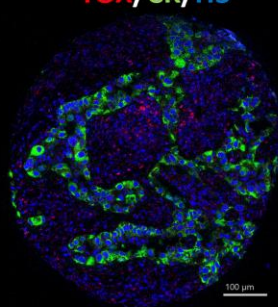
VISTA/CK/H3



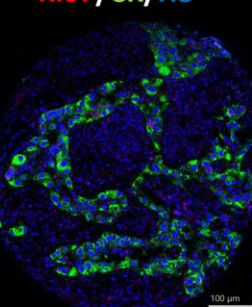
EOMES/CK/H3



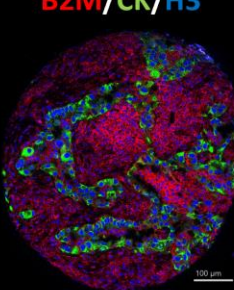
TOX/CK/H3



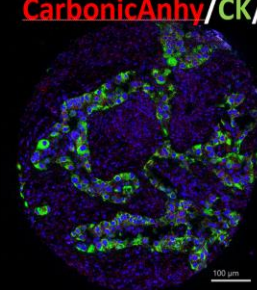
Ki67/CK/H3



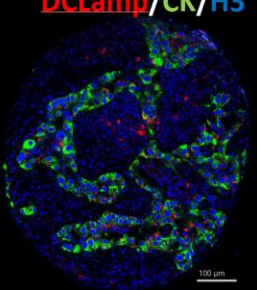
B2M/CK/H3



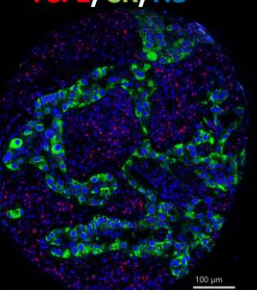
CarbonicAnhy/CK/H3



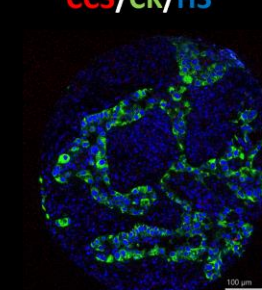
DCLamp/CK/H3



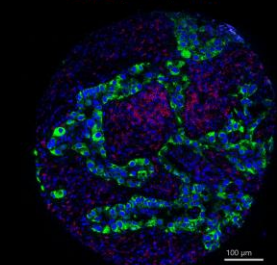
TCF1/CK/H3



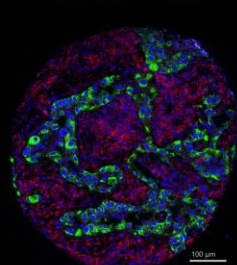
CC3/CK/H3



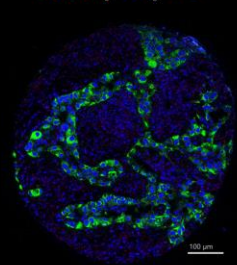
CD3/CK/H3



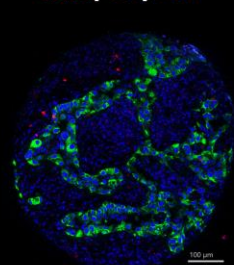
CD27/CK/H3



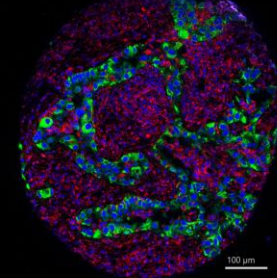
PDL2/CK/H3



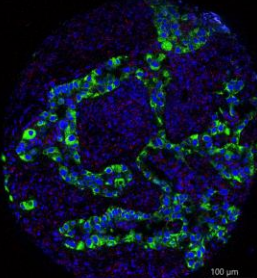
Gzb/CK/H3



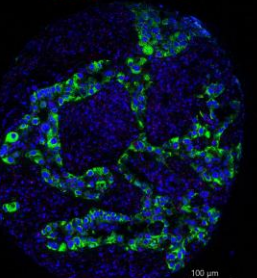
Vim/CK/H3



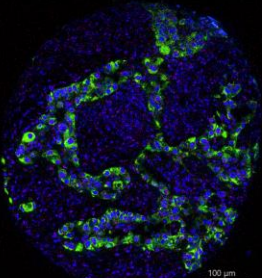
CD56/CK/H3



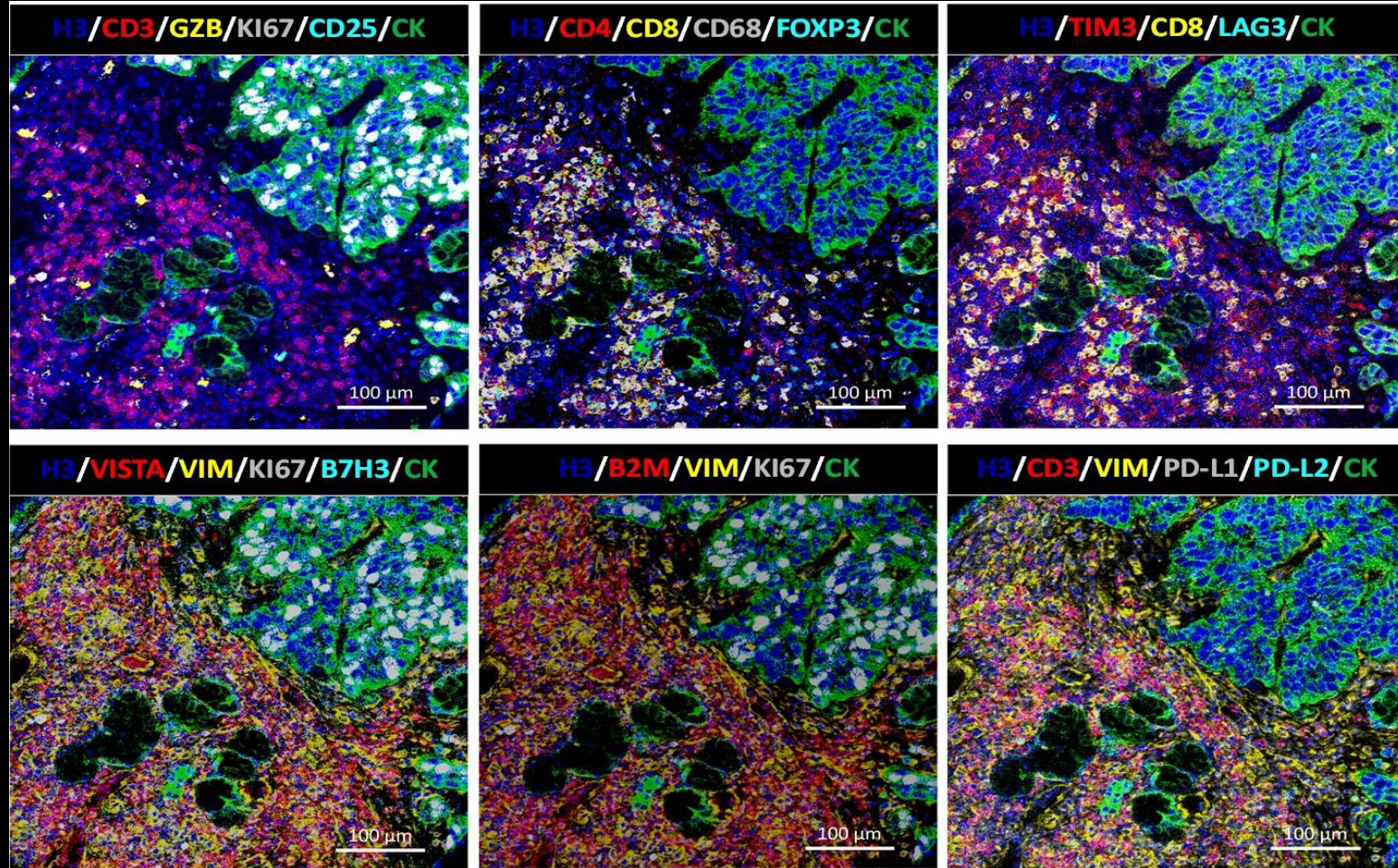
Tbet/CK/H3



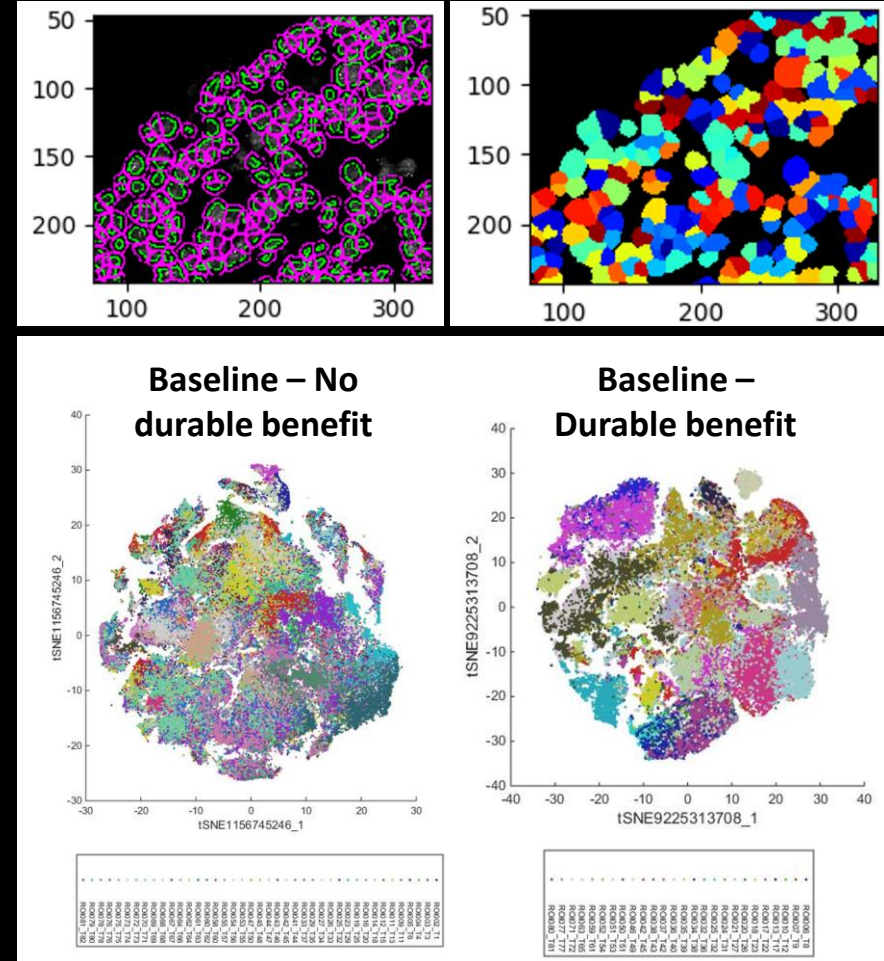
CD47/CK/H3



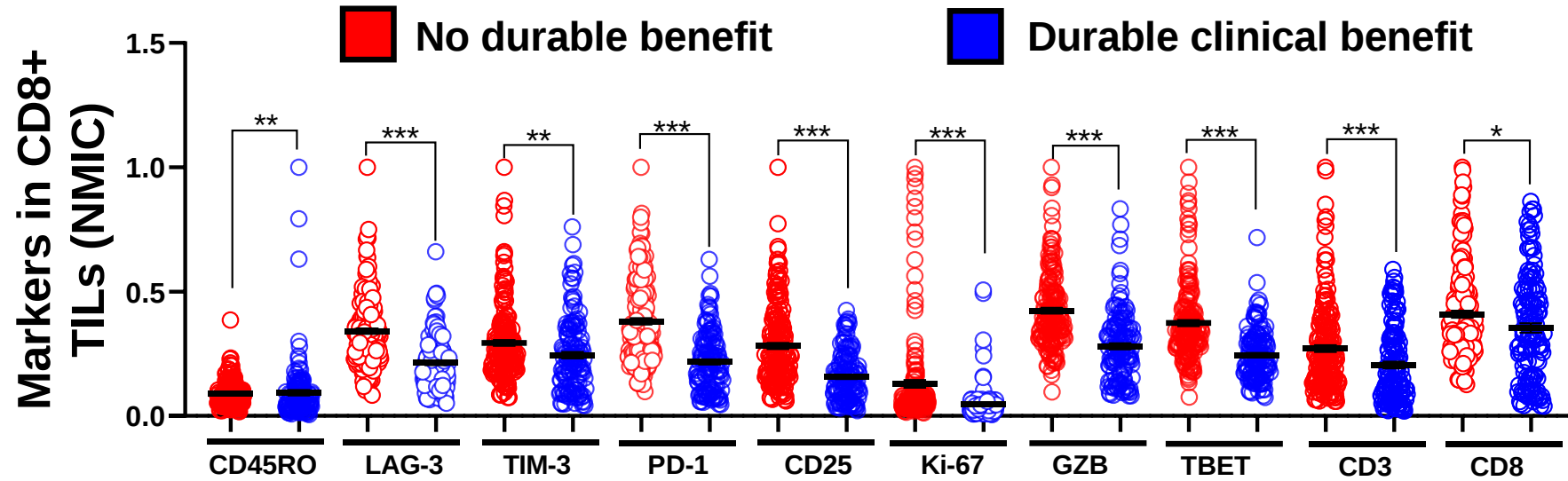
Integrated spatial visualization of selected markers



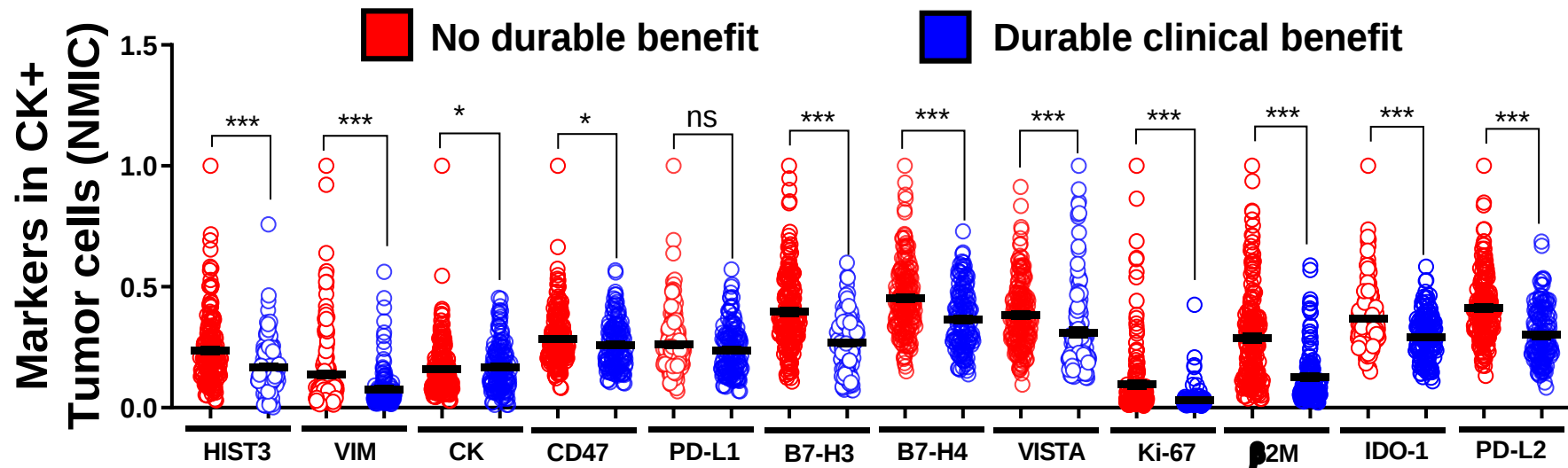
Segmentation and single-cell analysis



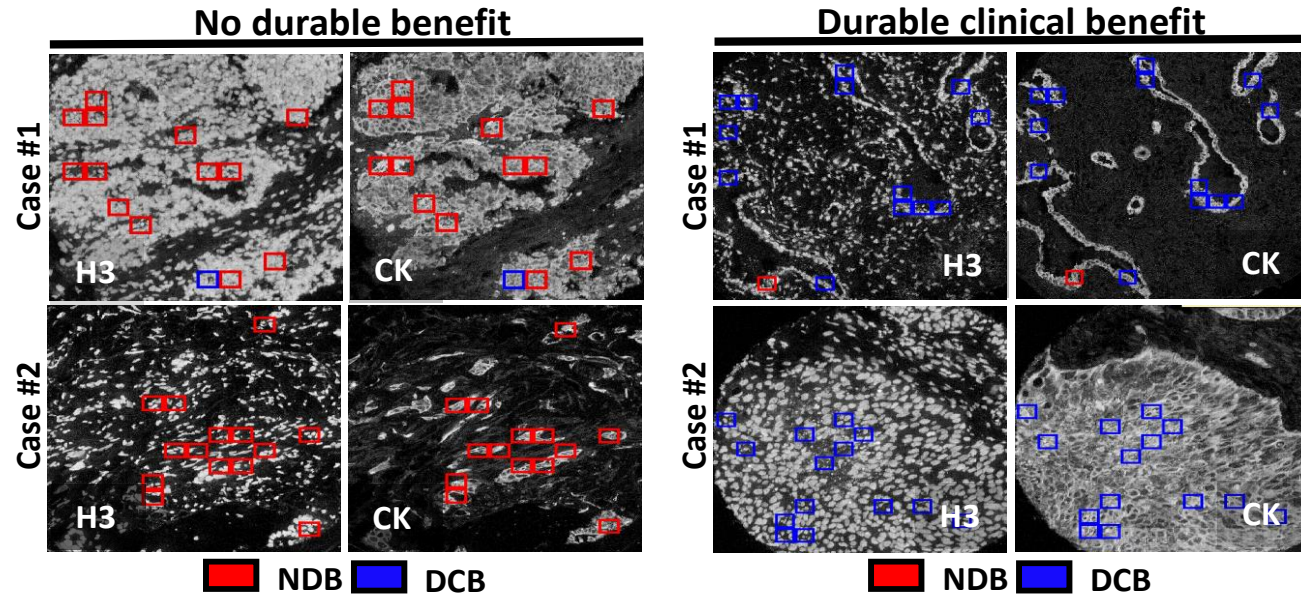
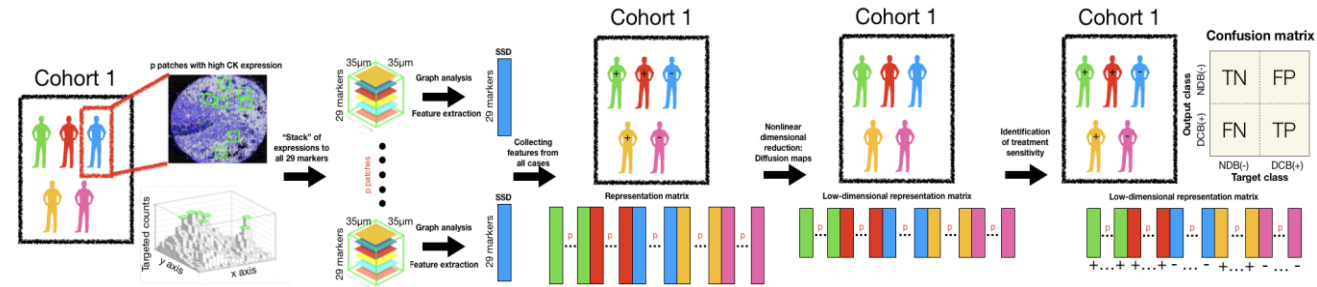
CD8+ TILs



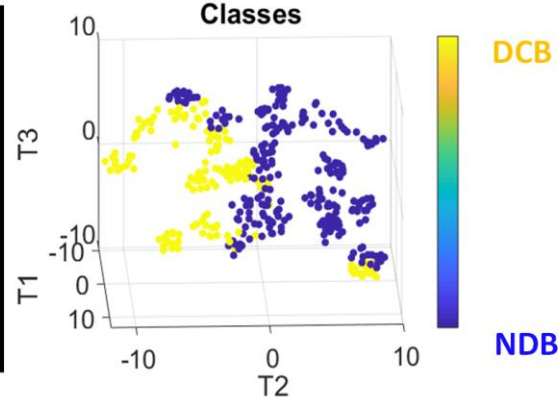
CK+ Tumor cells



Integration of TME components using manifold learning



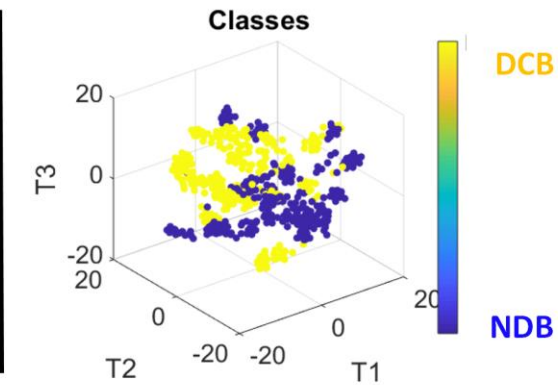
Cohort #1



Confusion Matrix

Output Class	Target Class		
	non	res	
non	17 58.6%	2 6.9%	89.5% 10.5%
res	1 3.4%	9 31.0%	10.0% 89.7%
	94.4% 5.6%	81.8% 18.2%	

Cohort #2



Confusion Matrix

Output Class	Target Class		
	non	res	
non	18 43.9%	3 7.3%	85.7% 14.3%
res	3 7.3%	17 41.5%	85.0% 15.0%
	85.7% 14.3%	85.0% 15.0%	85.4% 14.6%

Conclusions & take home message

- Resistance to immune checkpoint blockade can be tumor and immune-cell mediated.
- T-cell dysfunction in the TME is complex and associated with tumor antigenic exposure.
- Tumor-cells can express dominant immunoregulatory ligands in cancer subsets.
- Tumors can abrogate antigen presentation proteins associated with immune evasion and immunotherapy resistance in NSCLC.
- Developments allow deep and integrated spatial analysis of intact tumor specimens.
- Interaction of TME with patient features may provide additional context and value.

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