



# SITC 2017

November 8-12  
NATIONAL HARBOR  
MARYLAND  
Gaylord National Hotel  
& Convention Center



Society for Immunotherapy of Cancer

# Concurrent Session 105: Building Personalized Vaccines and Technologies for Hematologic Malignancies and Solid Tumors

Co-Chairs:

Matthew M. Gubin, PhD – *Washington University of Medicine*  
Catherine J. Wu, MD – *Dana-Farber Cancer Institute*

2:05 – 2:25 p.m.            **Cancer Neoantigens as Targets for Therapeutic Anti-Tumor Responses**

Matthew M. Gubin, PhD – *Washington University School of Medicine*

2:25 – 2:45 p.m.            **Tumor Vaccines in AML**

David E. Avigan, MD – *Beth Israel Deaconess Medical Center*

2:45 – 3:05 p.m.            **Improvement in Epitope Discovery**

Catherine J. Wu, MD – *Dana-Farber Cancer Institute*

3:05 – 3:20 p.m.            **Predictive Biomarkers for Response to Anti-CTLA-4 and Anti-PD-1 Immunotherapy in Melanoma Patients**

Priyanka Subrahmanyam, PhD – *Stanford University*

SITC  
2017

# CANCER NEOANTIGENS AS TARGETS FOR THERAPEUTIC ANTI-TUMOR RESPONSES

*Session 105: Building Personalized Vaccines and Technologies  
for Hematologic Malignancies and Solid Tumors*

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Department of Pathology and Immunology  
Washington University School of Medicine

CHiPs

The Andrew M. and Jane M. Bursky Center for  
Human Immunology & Immunotherapy Programs

#SITC2017

# Presenter Disclosure Information

*Matthew M. Gubin*

The following relationships exist related to this presentation:

*No Relationships to Disclose*

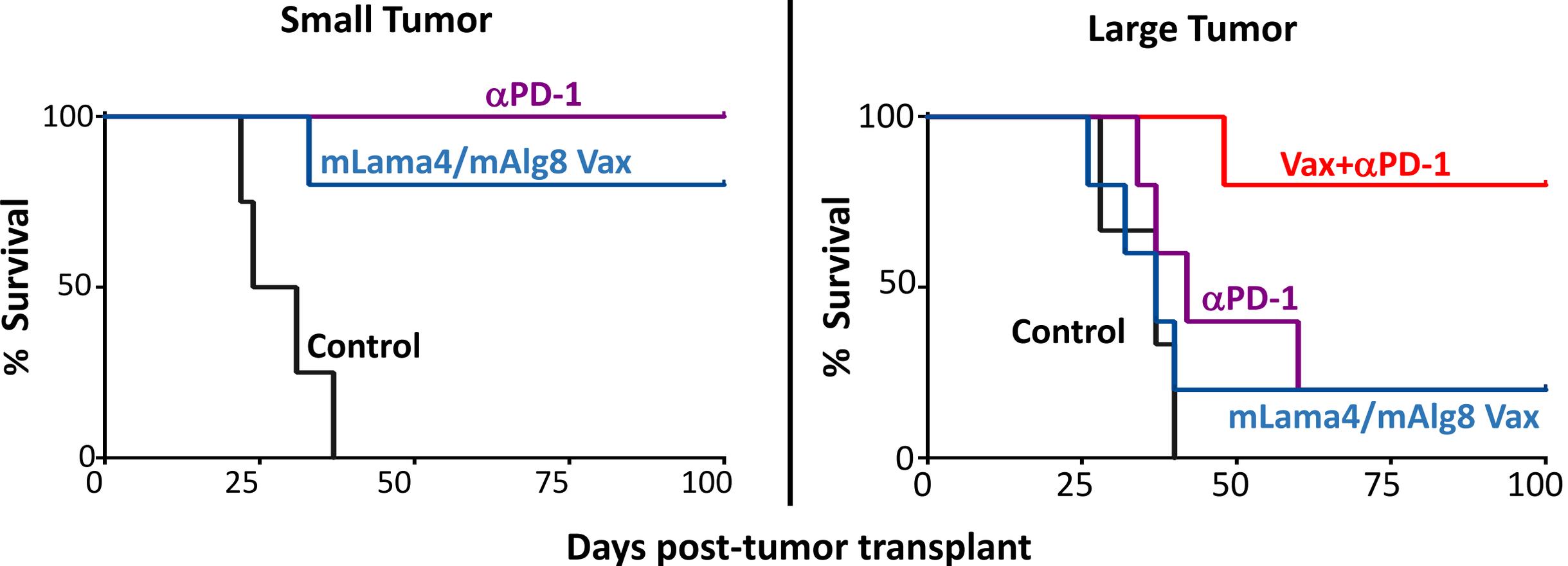
## Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens

*Nature* **515**:577-581 (2014)

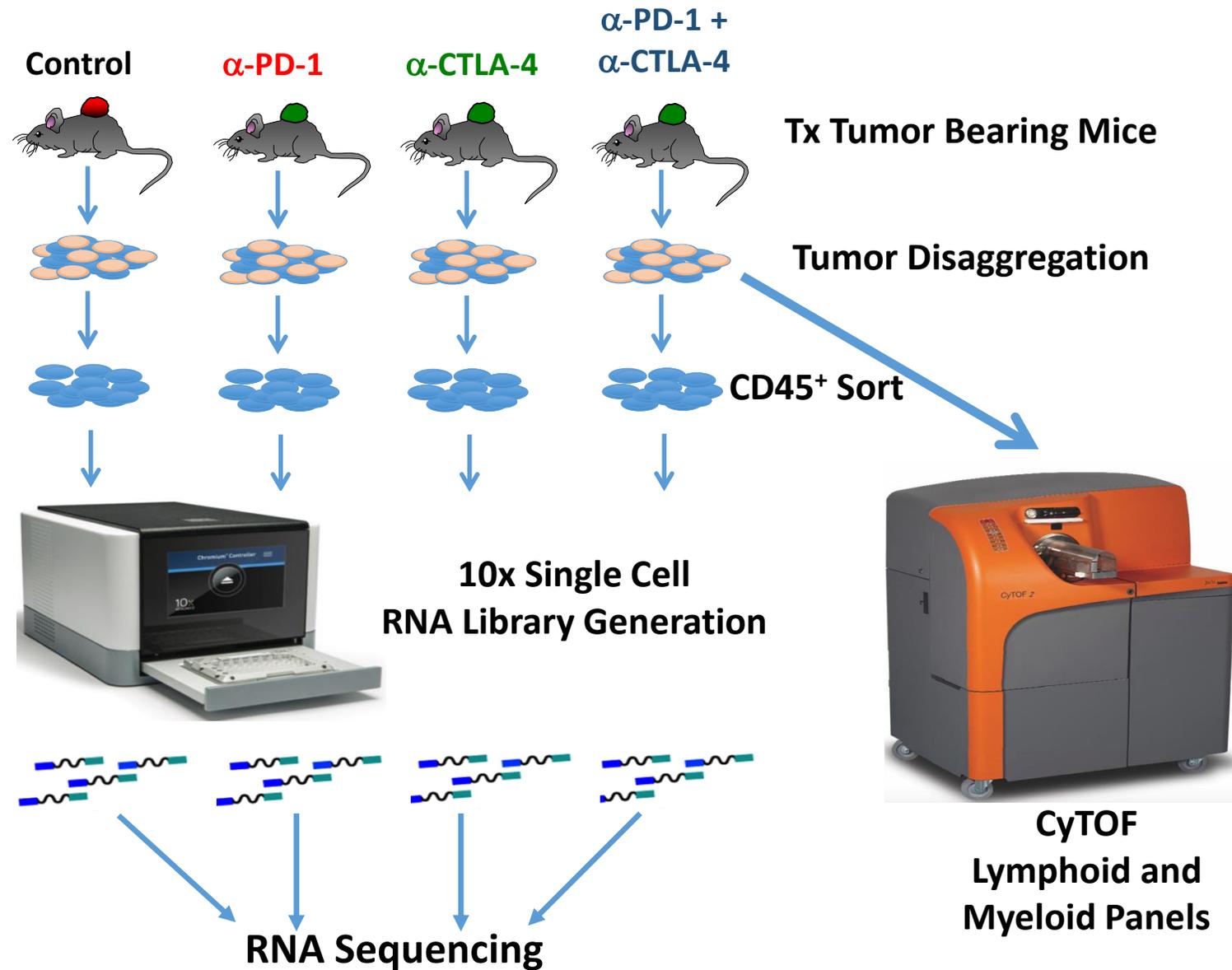
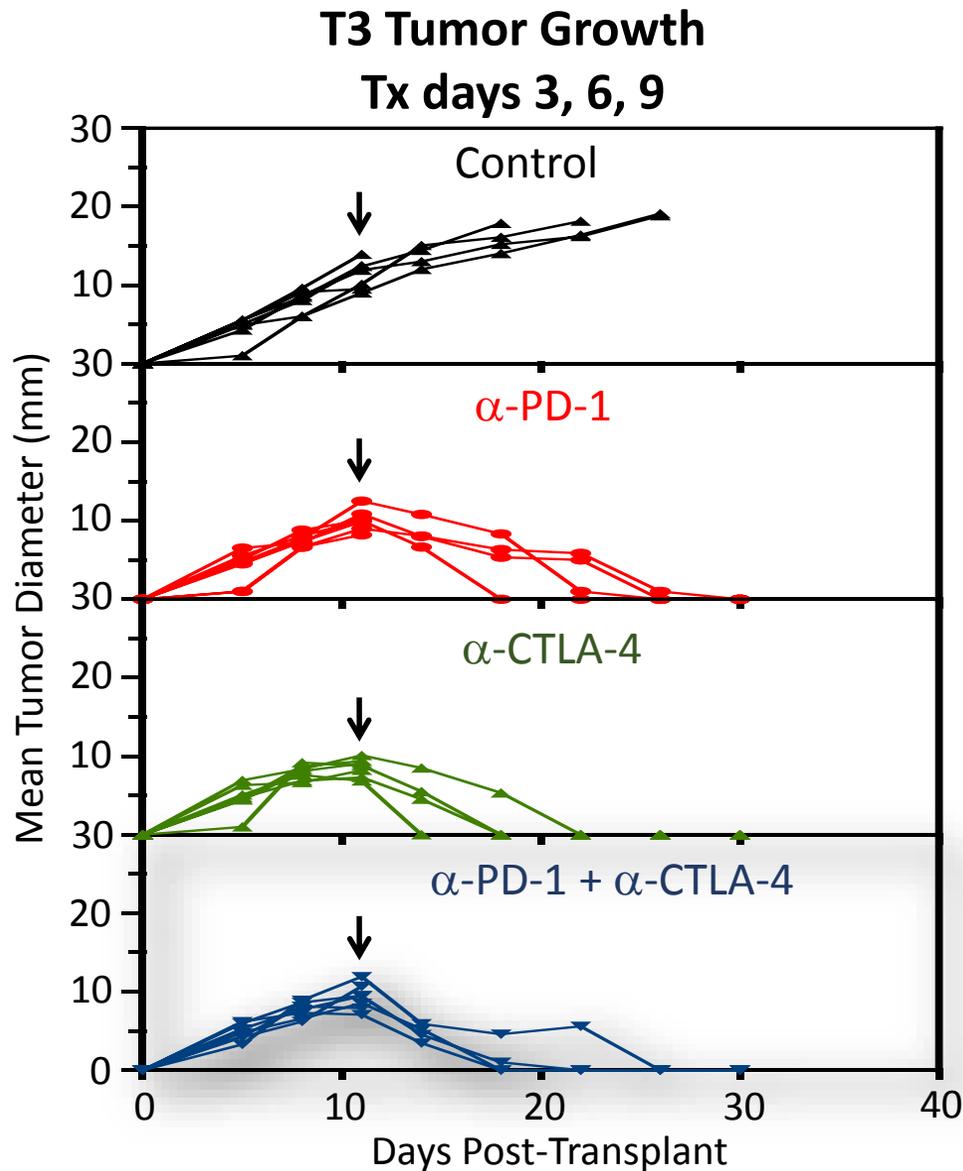
Matthew M. Gubin<sup>1</sup>, Xiuli Zhang<sup>2</sup>, Heiko Schuster<sup>3</sup>, Etienne Caron<sup>4</sup>, Jeffrey P. Ward<sup>1,5</sup>, Takuro Noguchi<sup>1</sup>, Yulia Ivanova<sup>1</sup>, Jasreet Hundal<sup>6</sup>, Cora D. Arthur<sup>1</sup>, Willem-Jan Krebber<sup>7</sup>, Gwenn E. Mulder<sup>7</sup>, Mireille Toebes<sup>8</sup>, Matthew D. Vesely<sup>1</sup>, Samuel S. K. Lam<sup>1</sup>, Alan J. Korman<sup>9</sup>, James P. Allison<sup>10</sup>, Gordon J. Freeman<sup>11</sup>, Arlene H. Sharpe<sup>12</sup>, Erika L. Pearce<sup>1</sup>, Ton N. Schumacher<sup>8</sup>, Ruedi Aebersold<sup>4,13</sup>, Hans-Georg Rammensee<sup>3</sup>, Cornelis J. M. Melief<sup>7,14</sup>, Elaine R. Mardis<sup>6,15</sup>, William E. Gillanders<sup>2</sup>, Maxim N. Artyomov<sup>1</sup> & Robert D. Schreiber<sup>1</sup>

- Whole exome sequencing/RNA-Seq plus epitope prediction revealed that the T3 sarcoma cells express ~700 nonsynonymous mutations; 2 function as dominant neoantigens
- Tumor-specific mutant neoantigens are favored targets for T cells reinvigorated by immune checkpoint blockade
- Neoantigen-specific CD8<sup>+</sup> T cells display both overlapping and distinct changes upon either anti-CTLA-4 or anti-PD-1 immune checkpoint blockade therapy
- Tumor-specific mutant neoantigen personalized vaccines display therapeutic efficacy

# Personalized Cancer Neoantigen Vaccine Extends the Immune Checkpoint Blockade Therapeutic Window for T3 Tumors



# High Dimensional Analysis of Immune Checkpoint Blockade-Mediated T3 Sarcoma Rejection



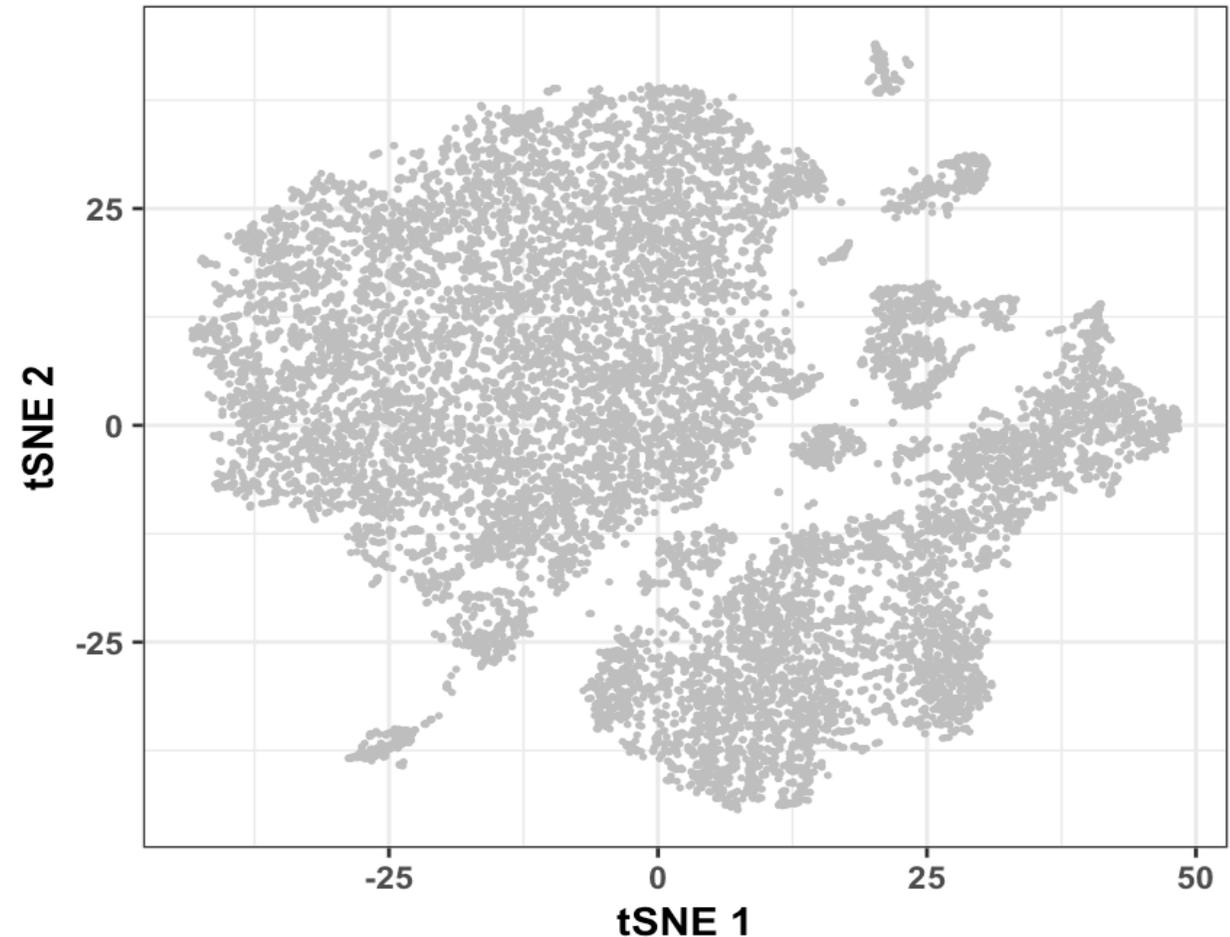
# Visualization by tSNE: Fitting Data into 2 Dimensions

tSNE (t-distributed stochastic neighbor embedding):  
Non-linear dimensionality reduction technique that aims to put data into 2 or 3 dimensional space and save the “distance” between each two dots.

Transcriptionally similar cells will be close to each other.

<http://www.jmlr.org/papers/volume9/vandermaaten08a/vandermaaten08a.pdf>

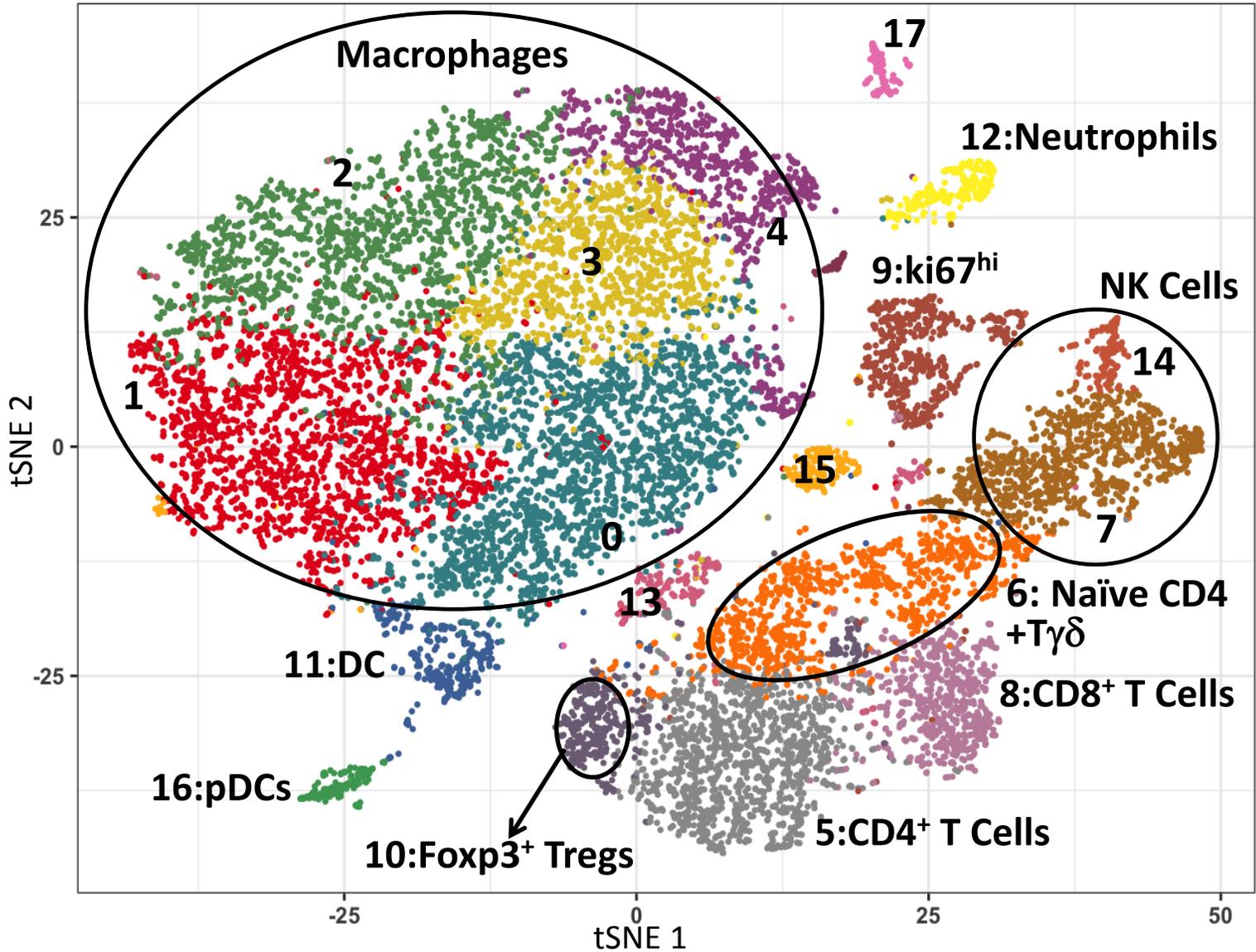
14493 cells



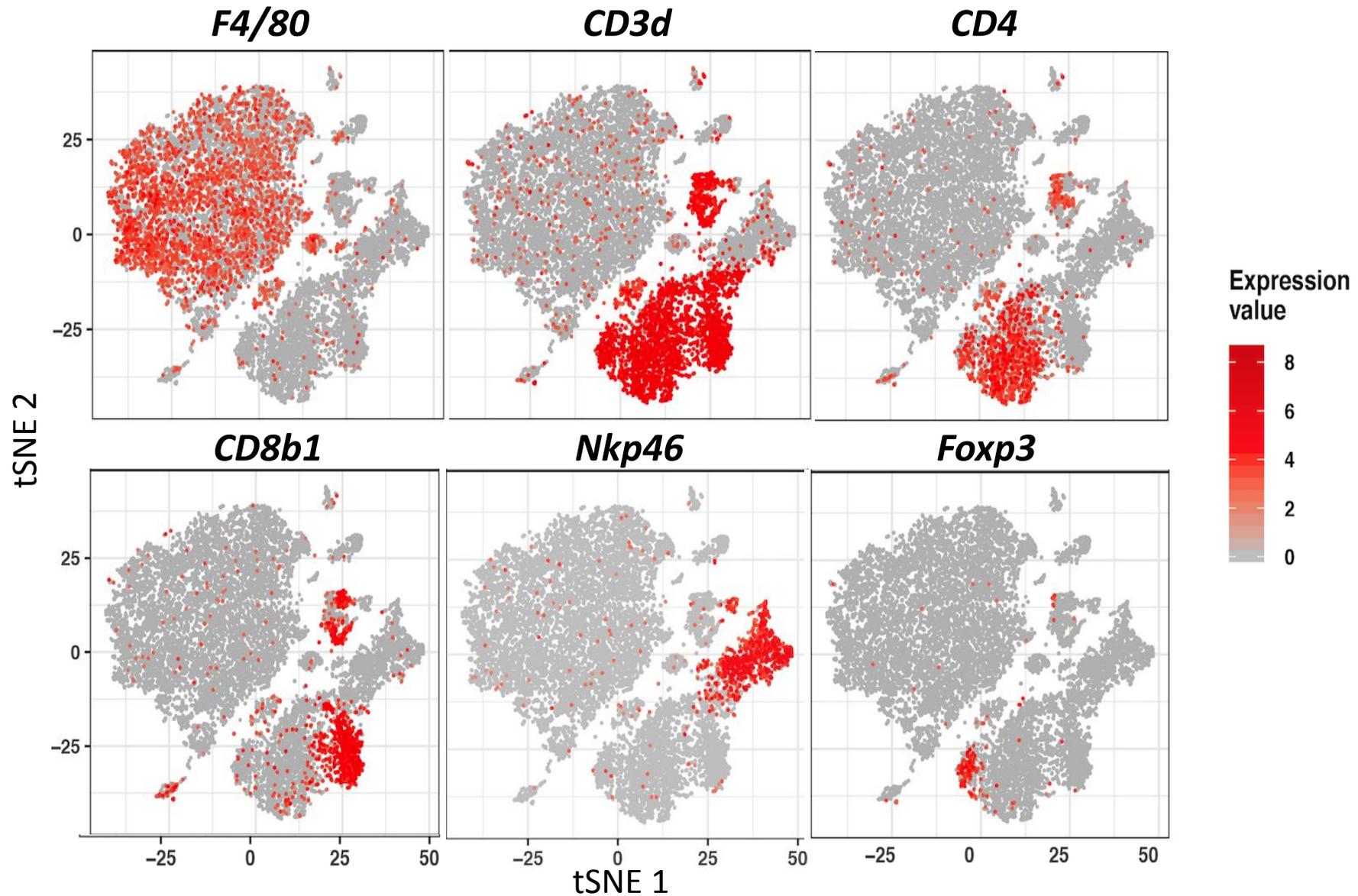
# Annotation of Immune Cell Clusters Infiltrating Into T3 Sarcomas +/- Immune Checkpoint Blockade (scRNASeq)

14493 cells

Graph Based Clustering



# Using Known Markers to Test Whether Clustering Makes Sense

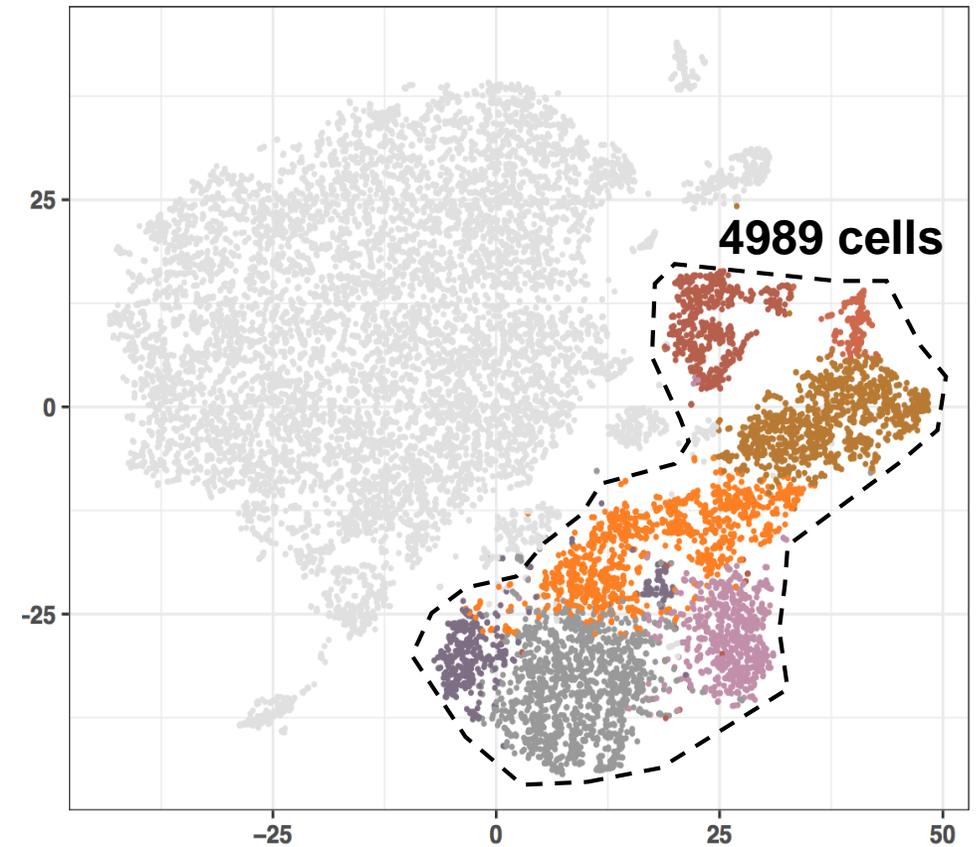
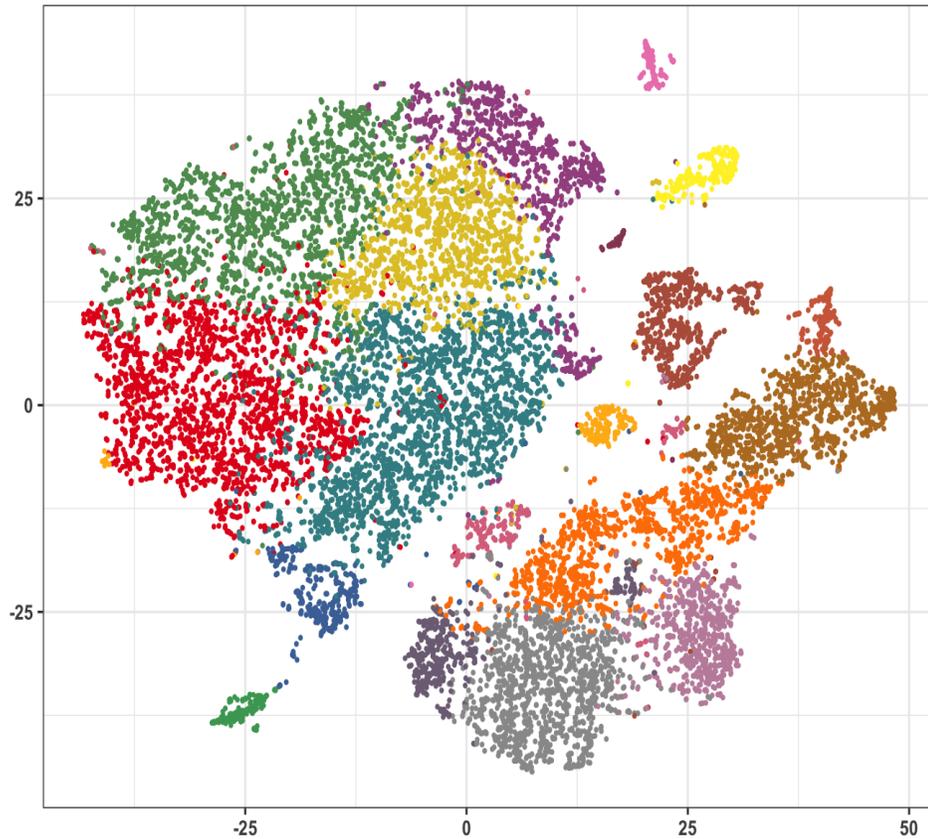




*A glimpse into the complexity of the  
tumor infiltrating lymphoid compartment*

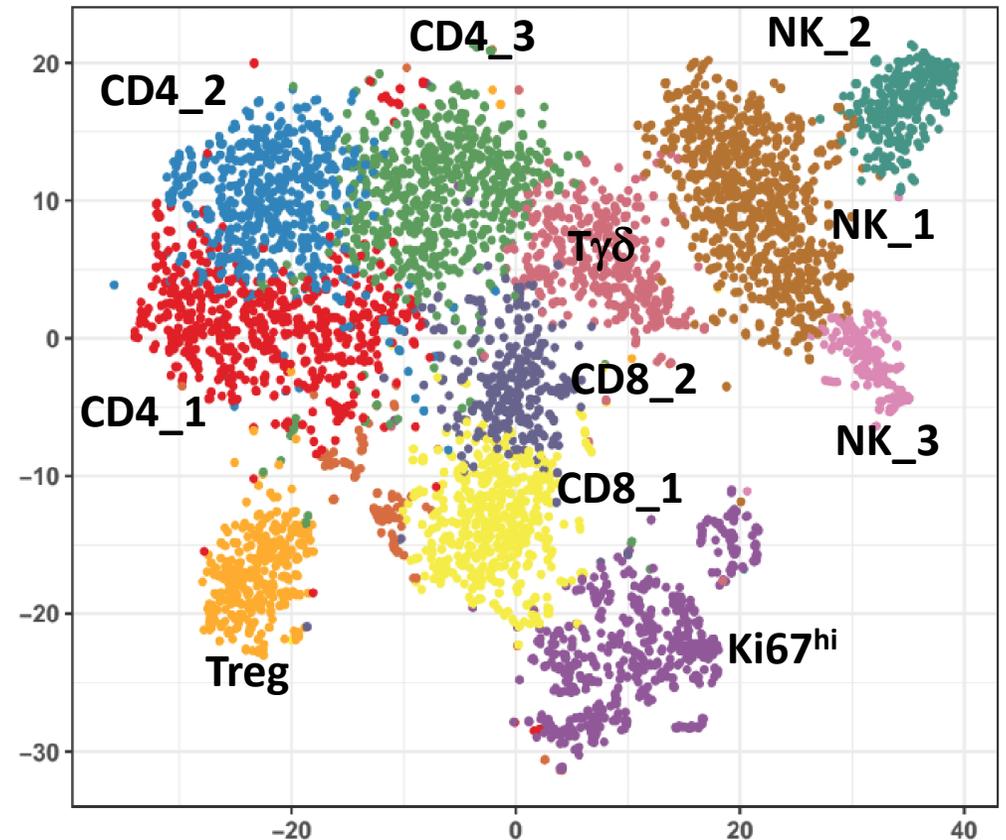
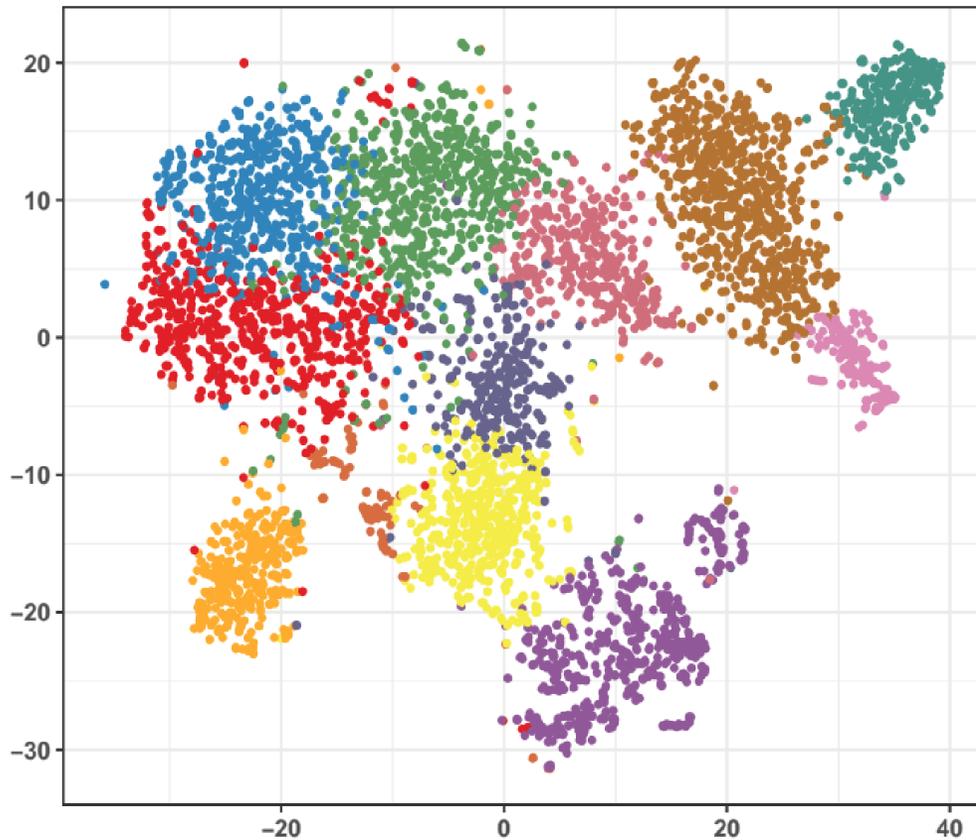
# Focus on Lymphoid Compartment (**scRNASeq**)

14493 cells



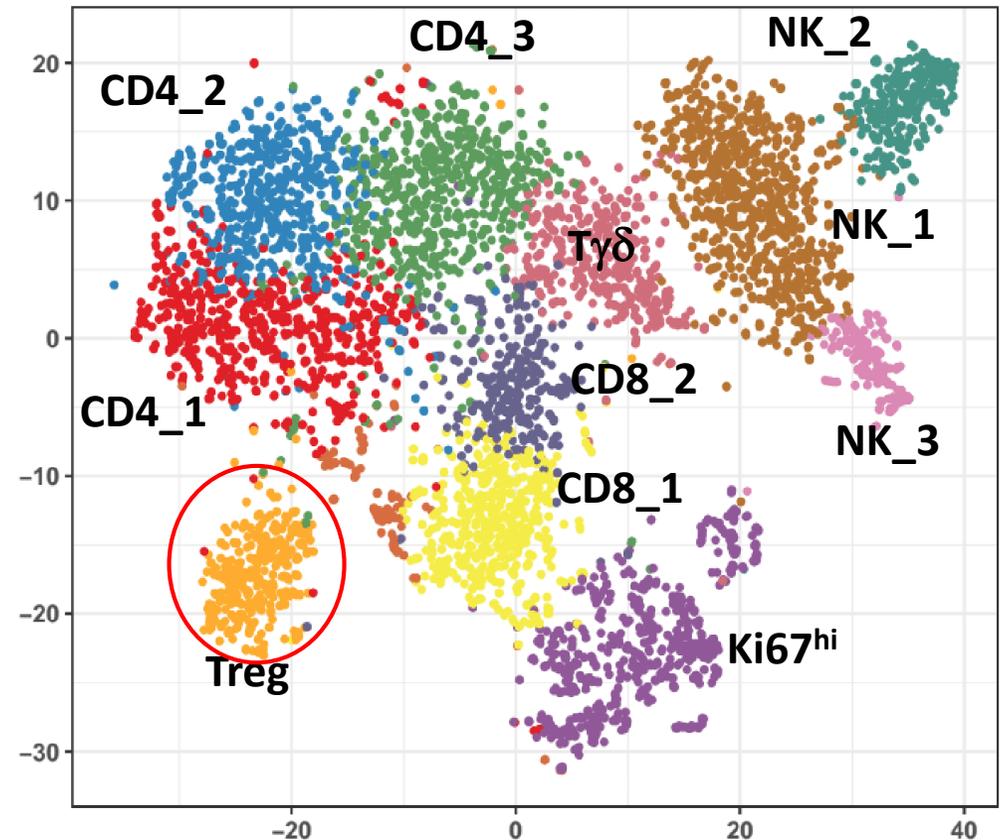
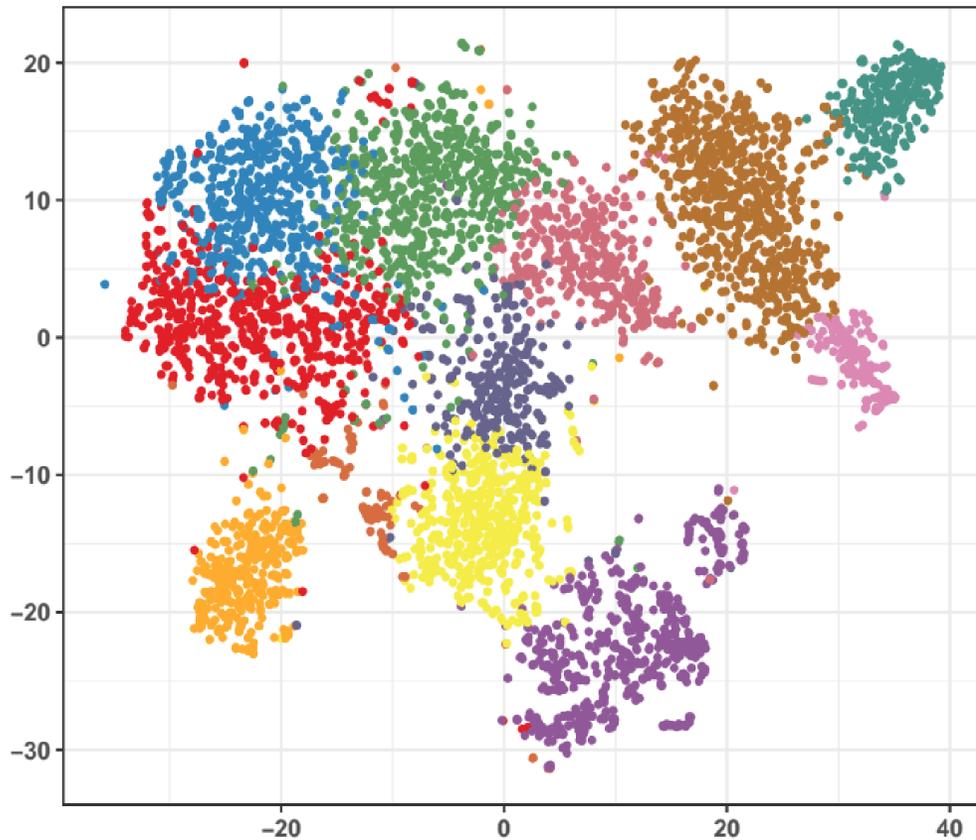
# Lymphoid Compartment Annotation (scRNASeq)

Lymphoid: 4989 cells

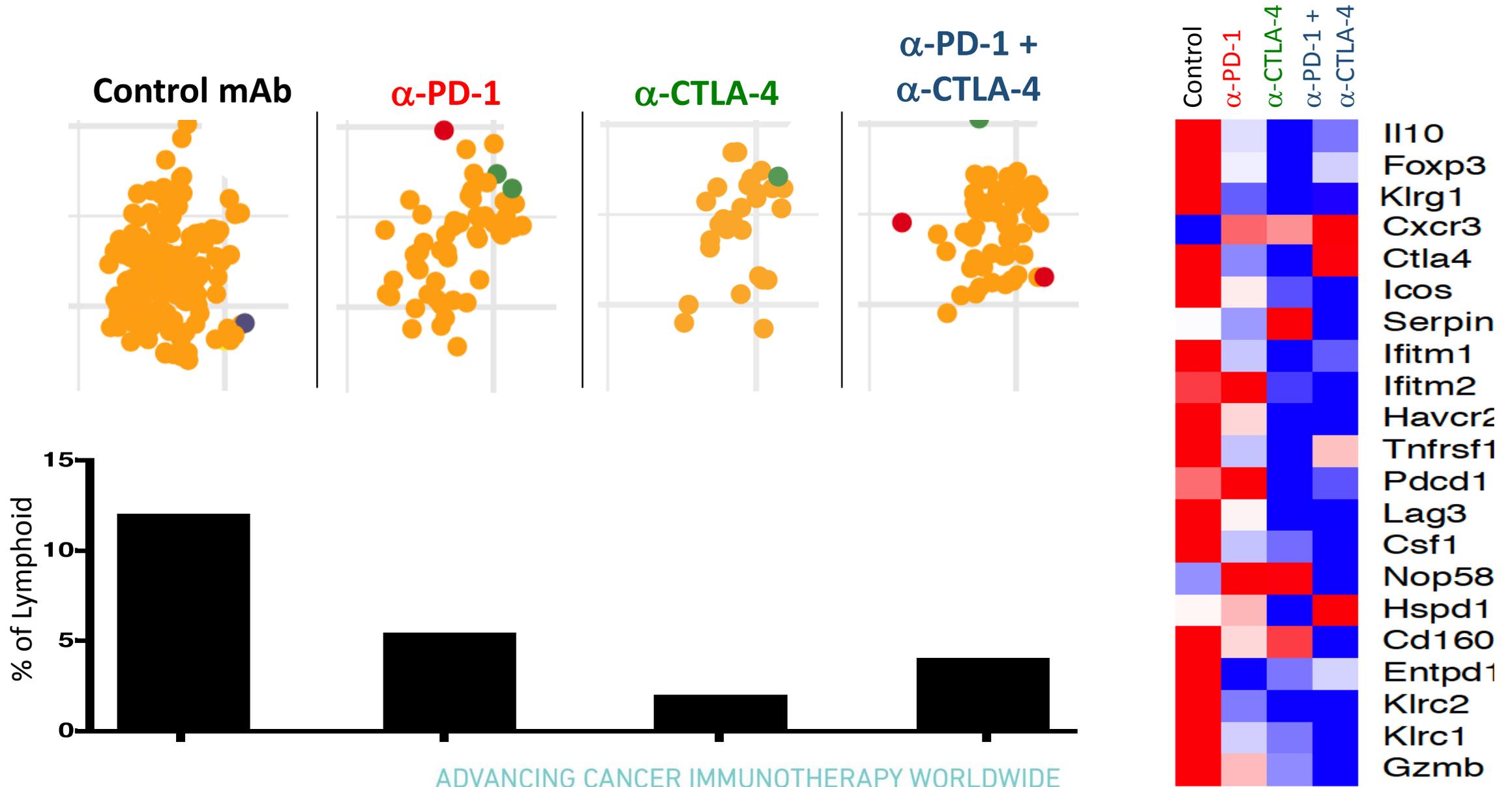


# Lymphoid Compartment Annotation (scRNASeq)

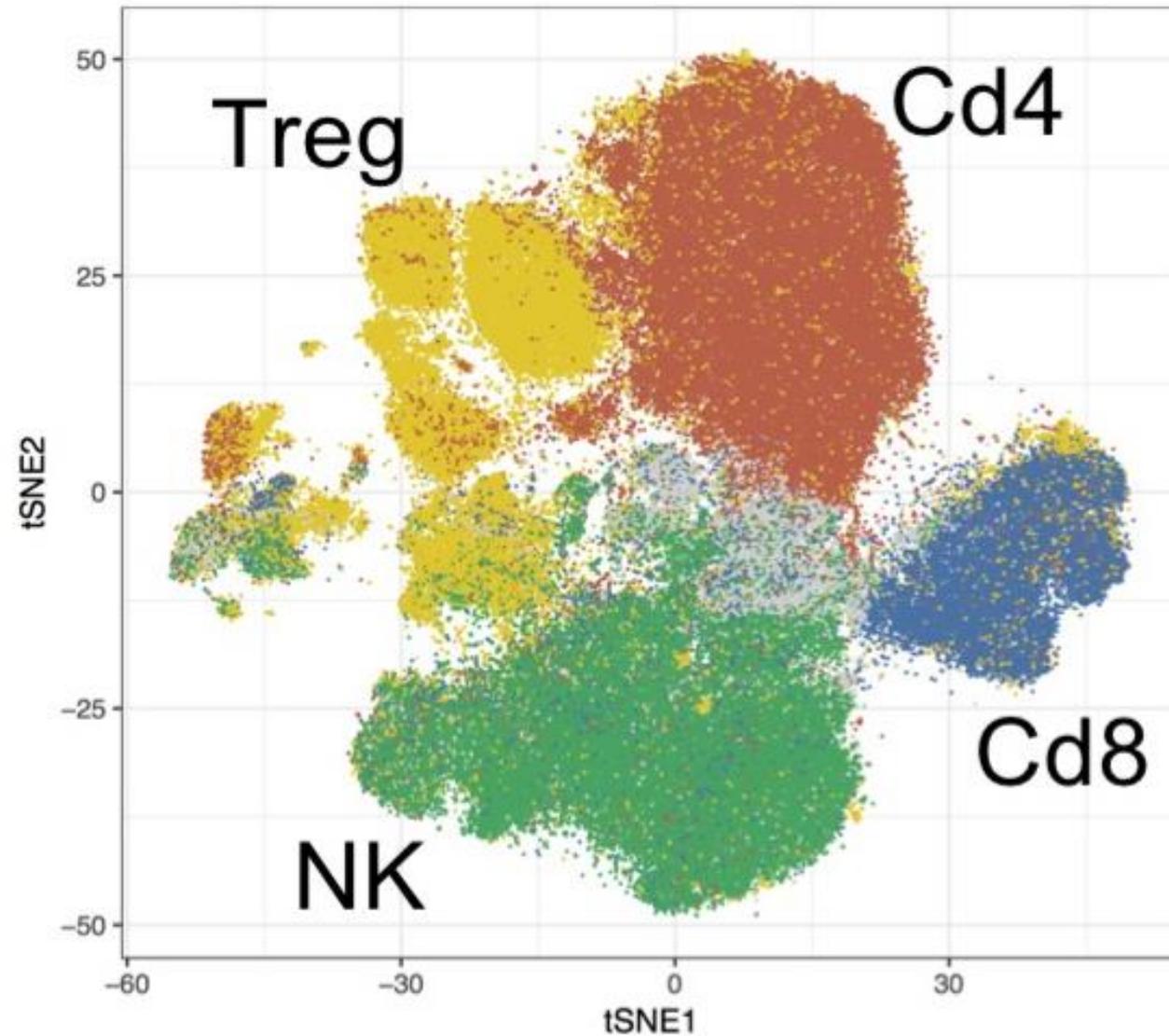
Lymphoid: 4989 cells



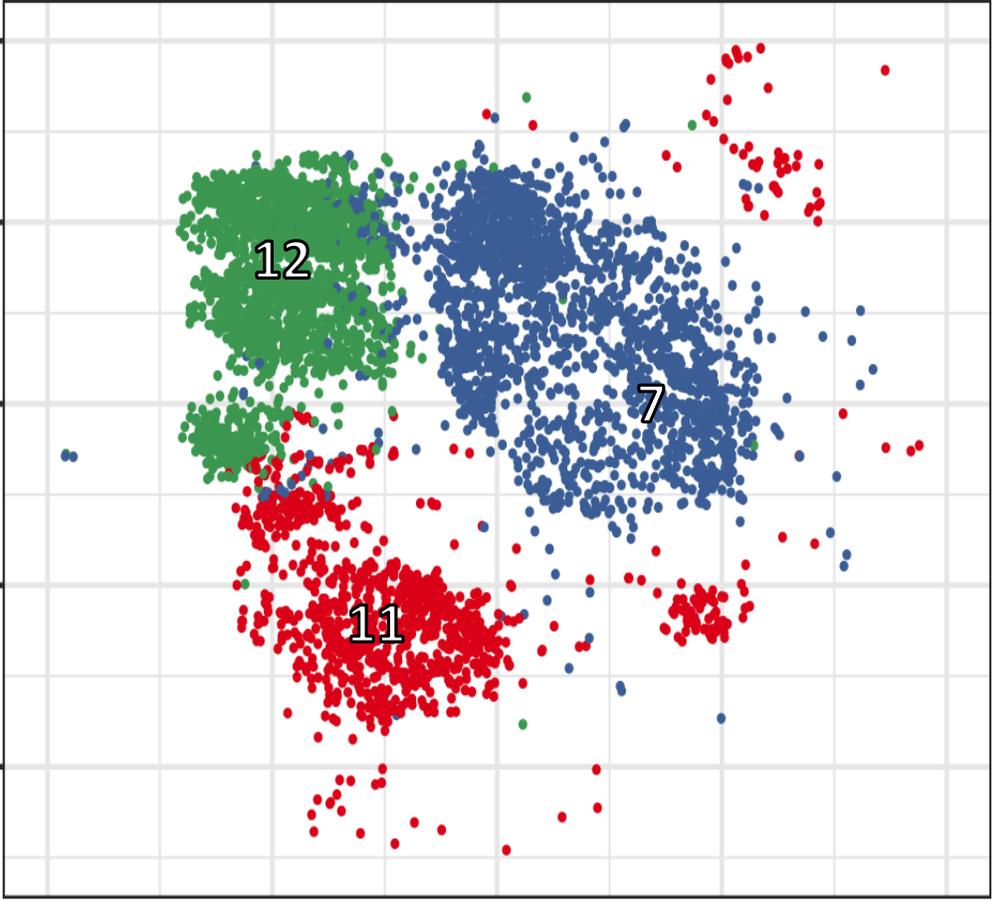
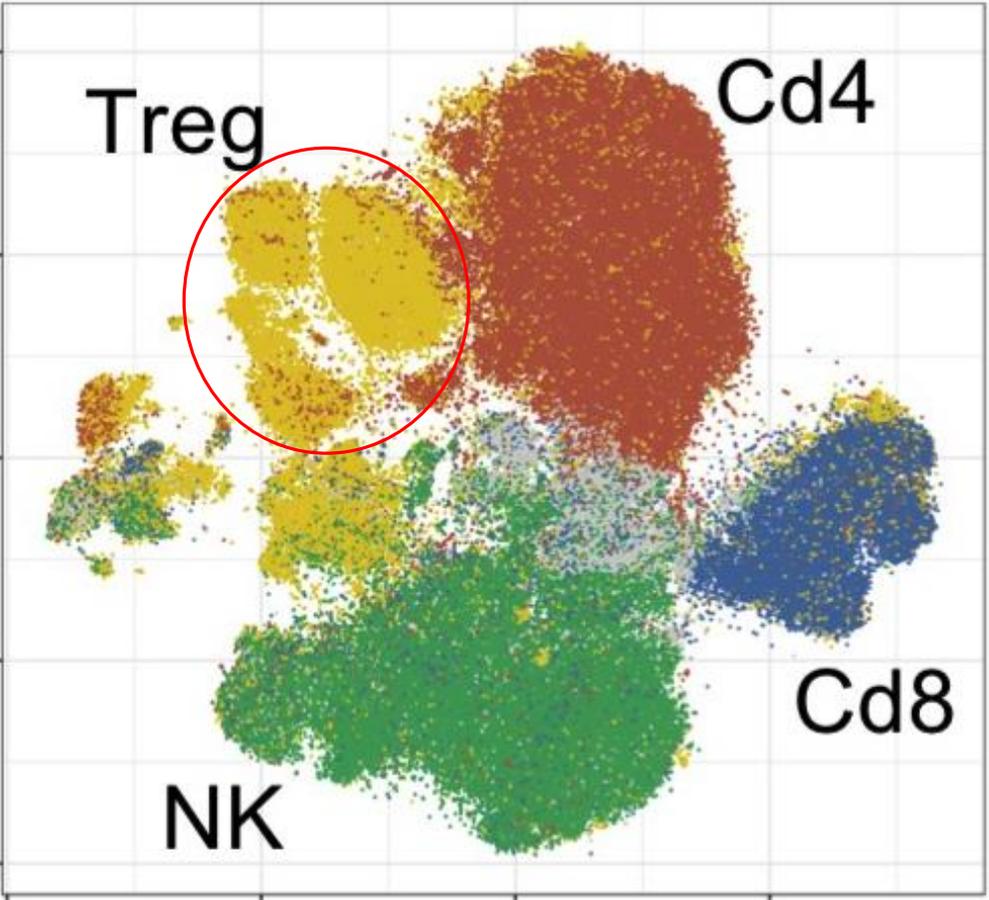
# Immune Checkpoint Blockade Alters Intratumoral Tregs (scRNASeq)



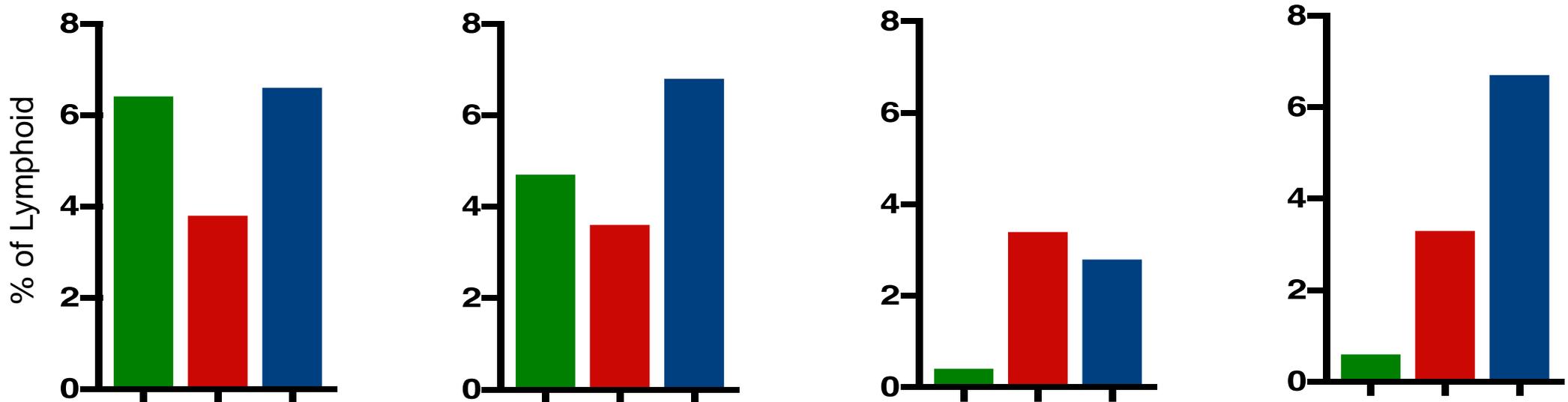
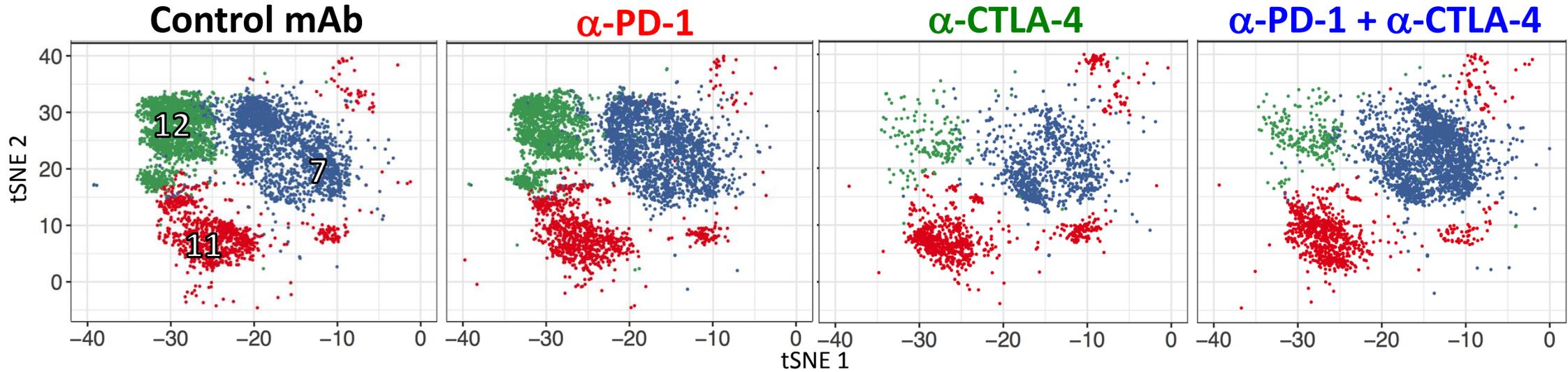
# CyTOF Analysis Identifies Defined Populations of Lymphoid Cells Infiltrating T3 Tumors (37 mAb markers)



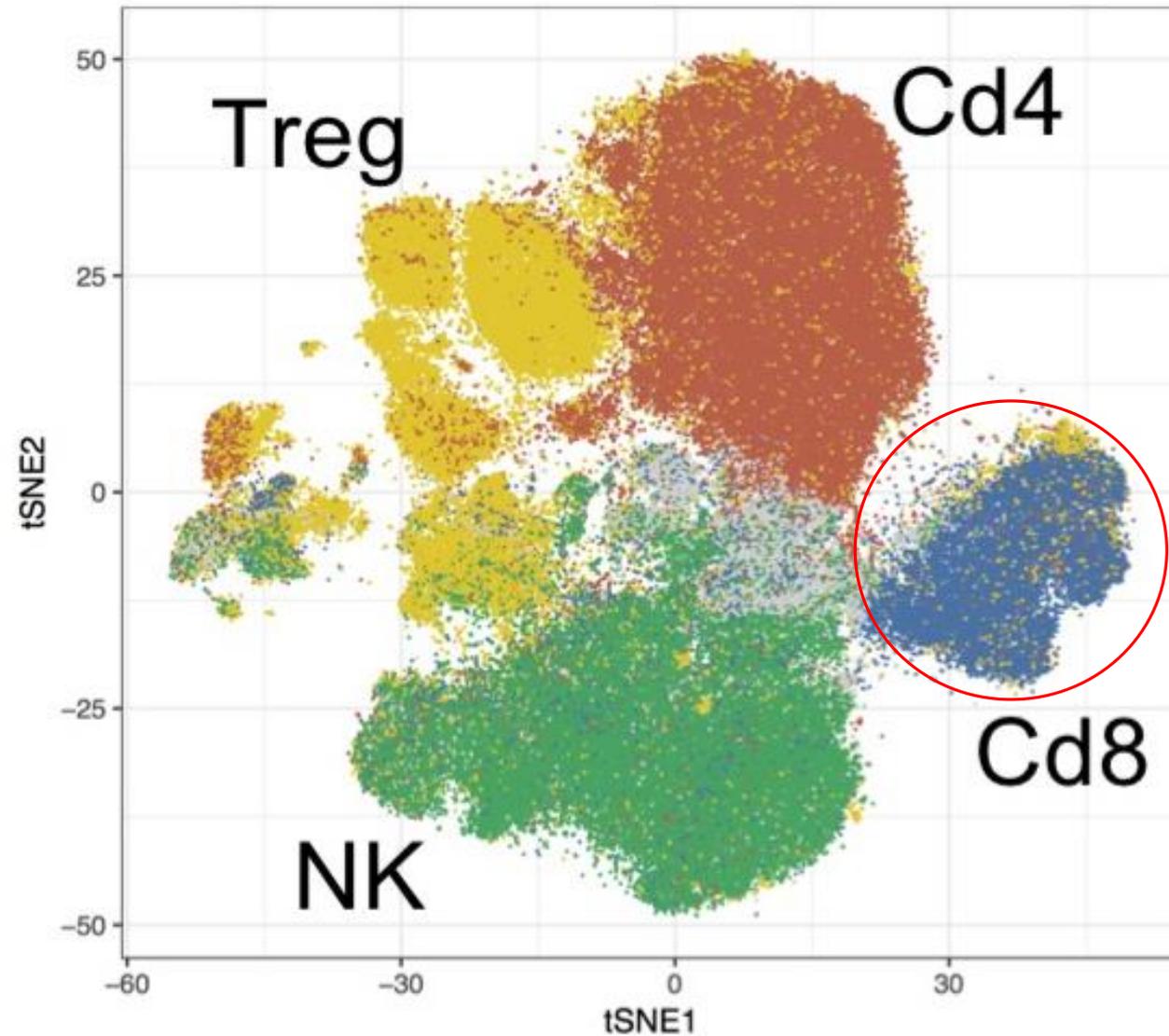
# CyTOF Analysis Identifies Defined Populations of Lymphoid Cells Infiltrating T3 Tumors



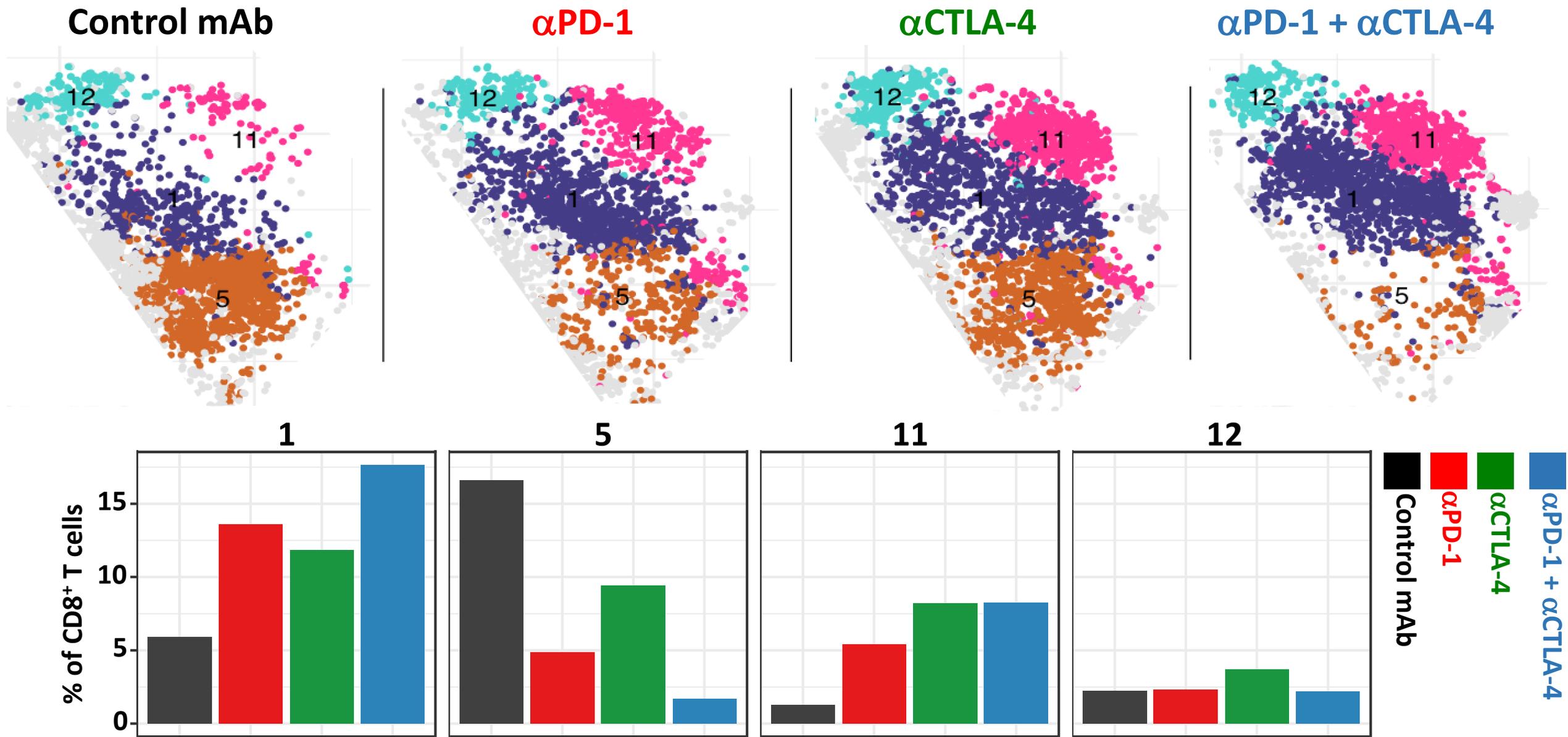
# Specific Treg Subpopulations Are Depleted by Immune Checkpoint Blockade Immunotherapy (CyTOF)



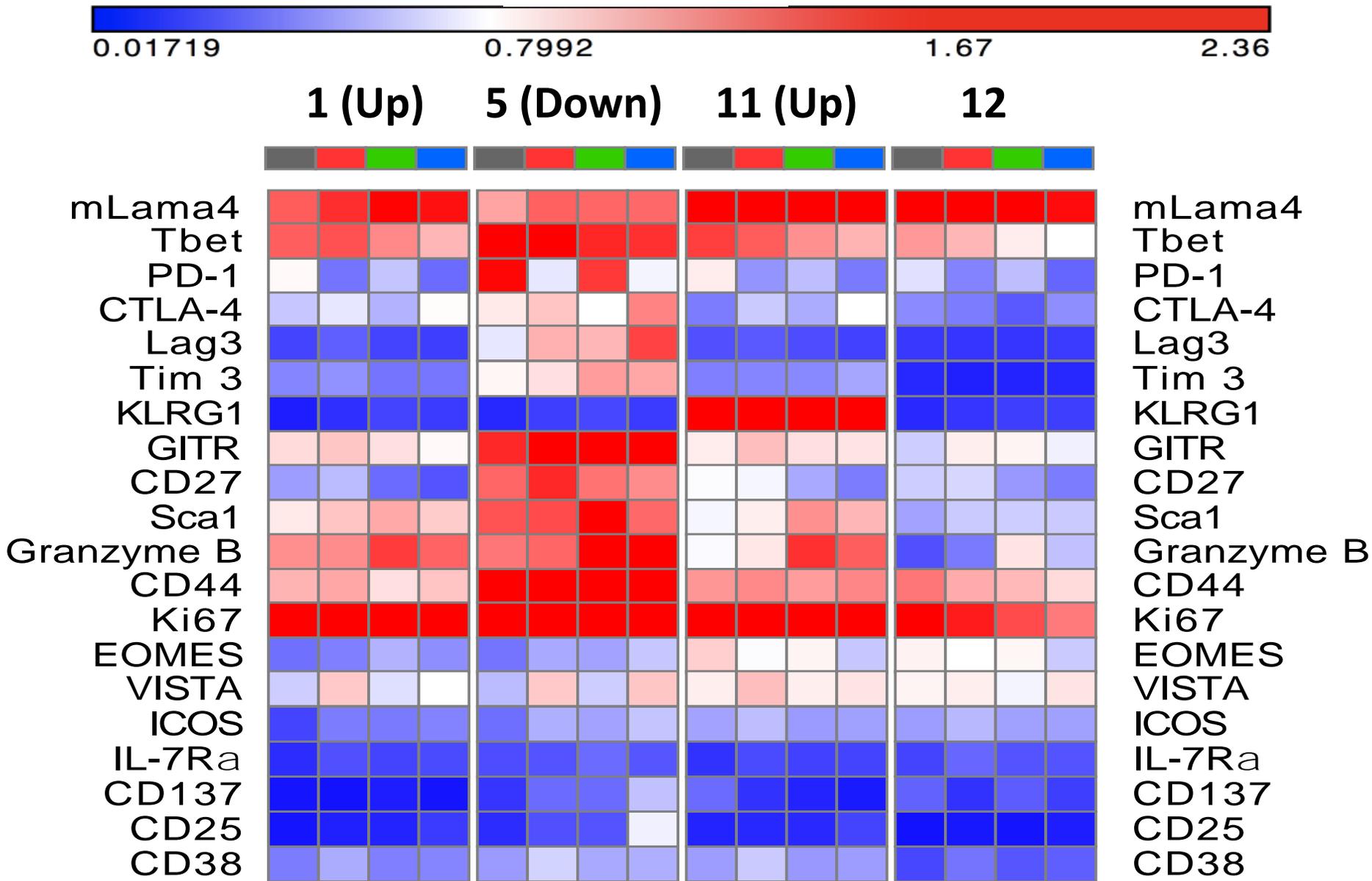
# CyTOF Analysis Identifies Defined Populations of Lymphoid Cells Infiltrating T3 Tumors



# Immune Checkpoint Blockade Therapy Remodels the Tumor Infiltrating CD8<sup>+</sup> T Cell Compartment (CyTOF)



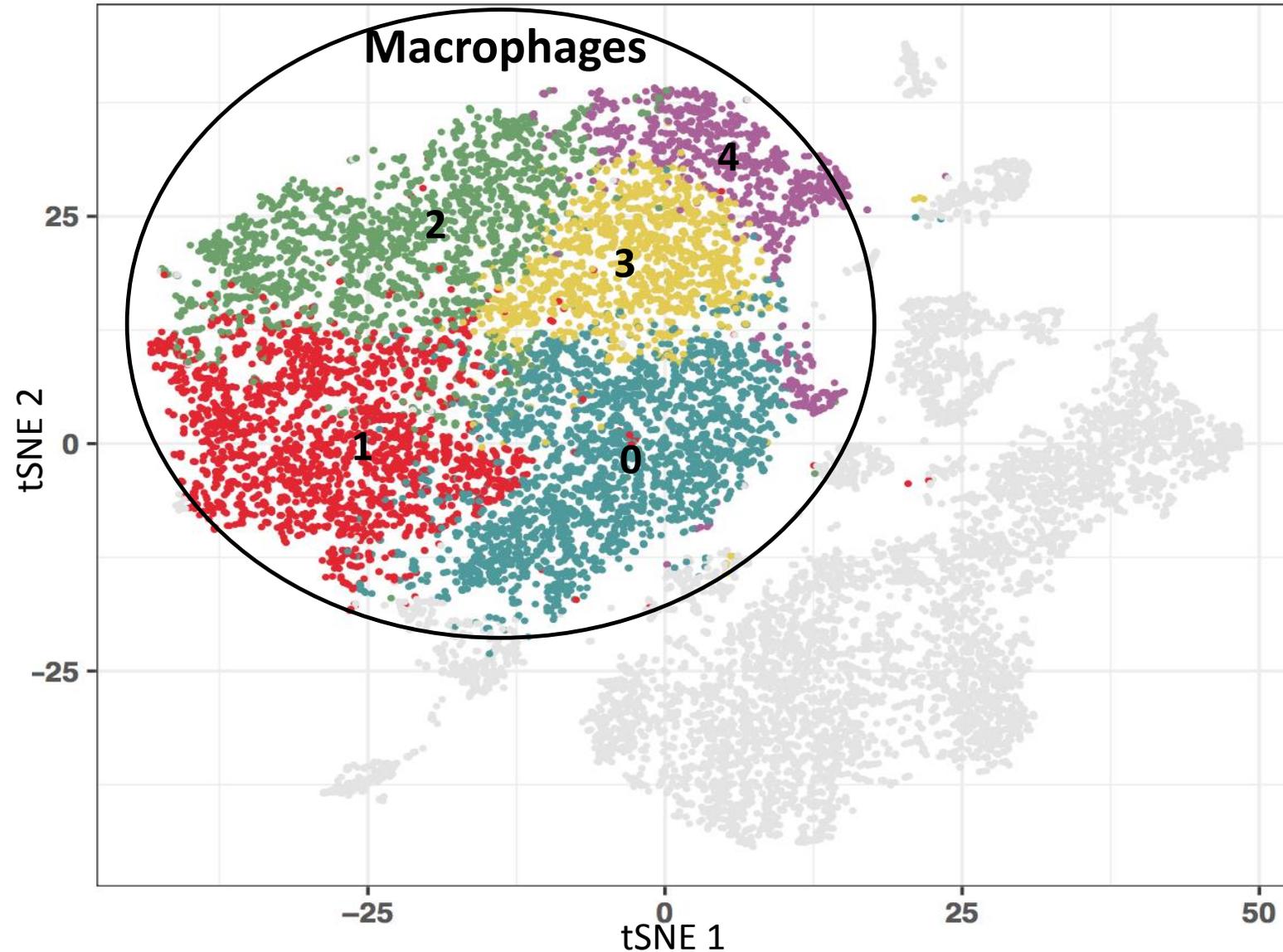
# Immune Checkpoint Blockade Therapy Remodels the Tumor Infiltrating CD8<sup>+</sup> T Cell Compartment (CyTOF)





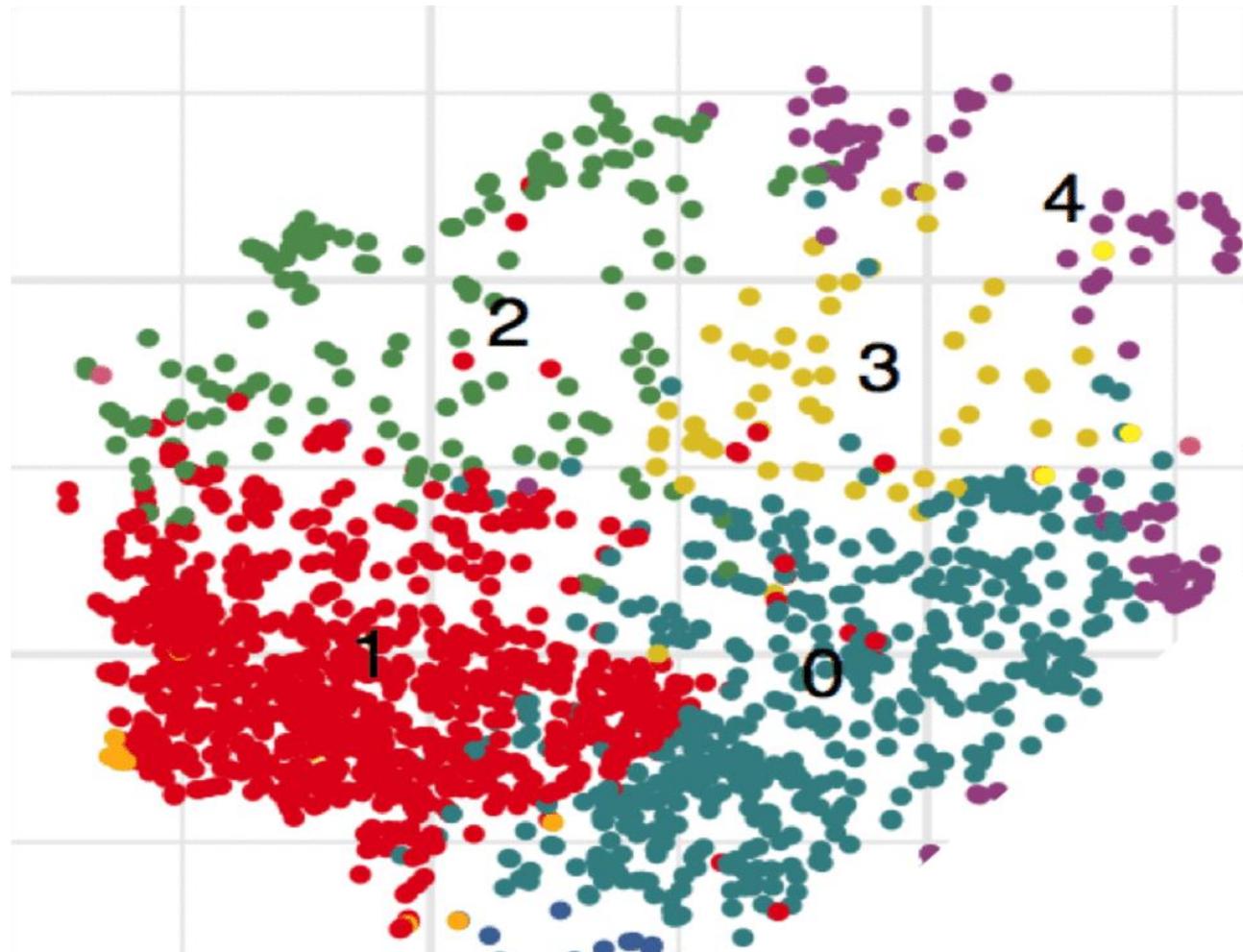
*A glimpse into the complexity of the  
tumor infiltrating macrophage compartment*

# Five Macrophage Sub-Populations in T3 Tumors Tx With Immune Checkpoint Blockade Therapy (scRNAseq)



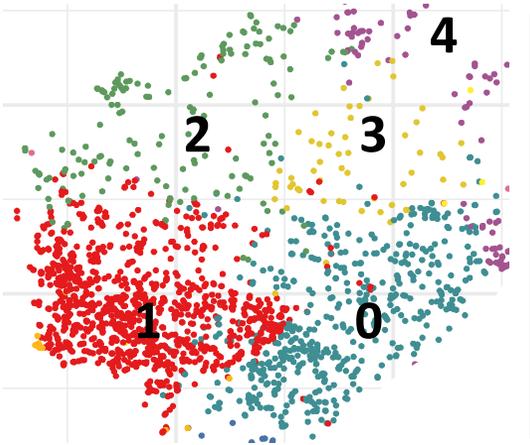
# Shifts in Macrophage Subpopulations Upon Immune Checkpoint Blockade Treatment (scRNAseq)

Control mAb

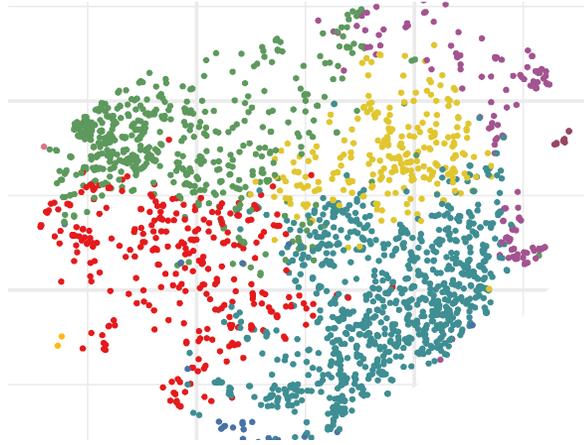


# Distinct Remodeling Patterns of the Macrophage Compartment Post-Immune Checkpoint Blockade (**scRNAseq**)

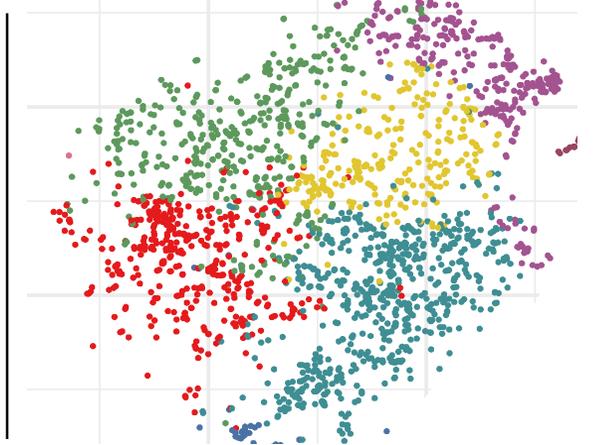
Control mAb



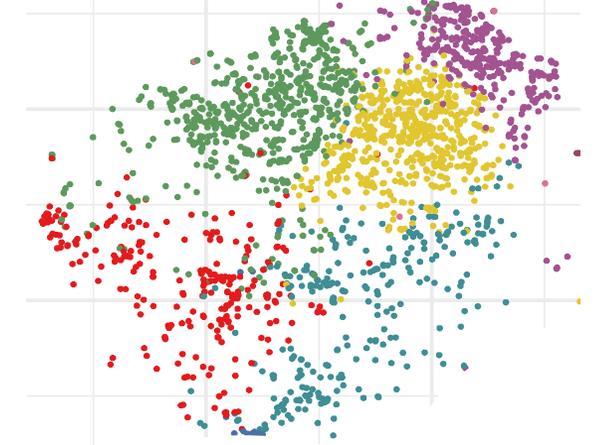
**$\alpha$ PD-1**



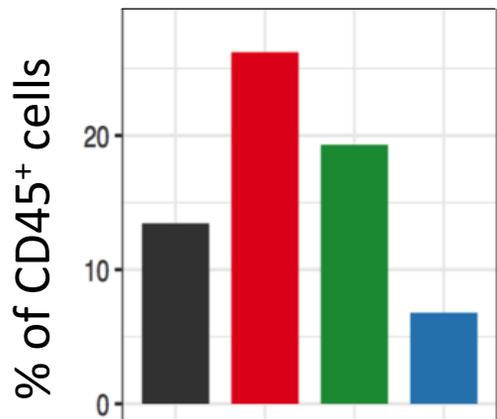
**$\alpha$ CTLA-4**



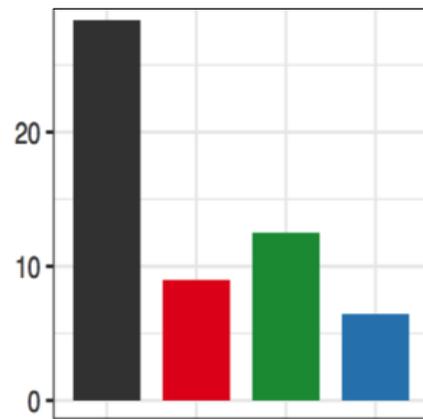
**$\alpha$ PD-1 +  $\alpha$ CTLA-4**



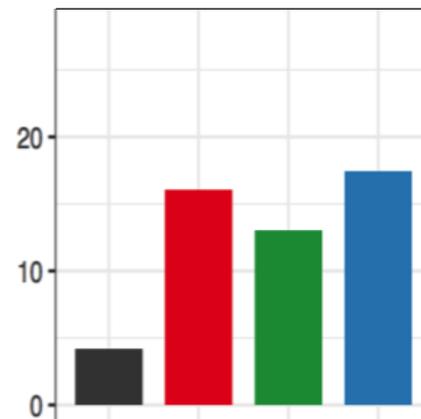
Cluster 0



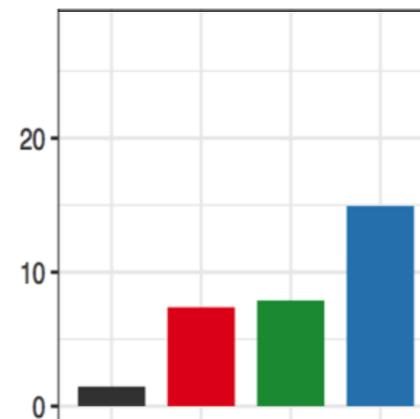
Cluster 1



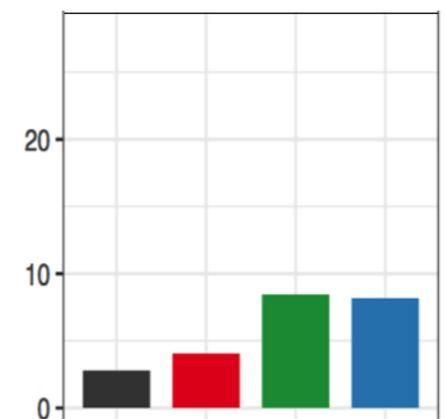
Cluster 2



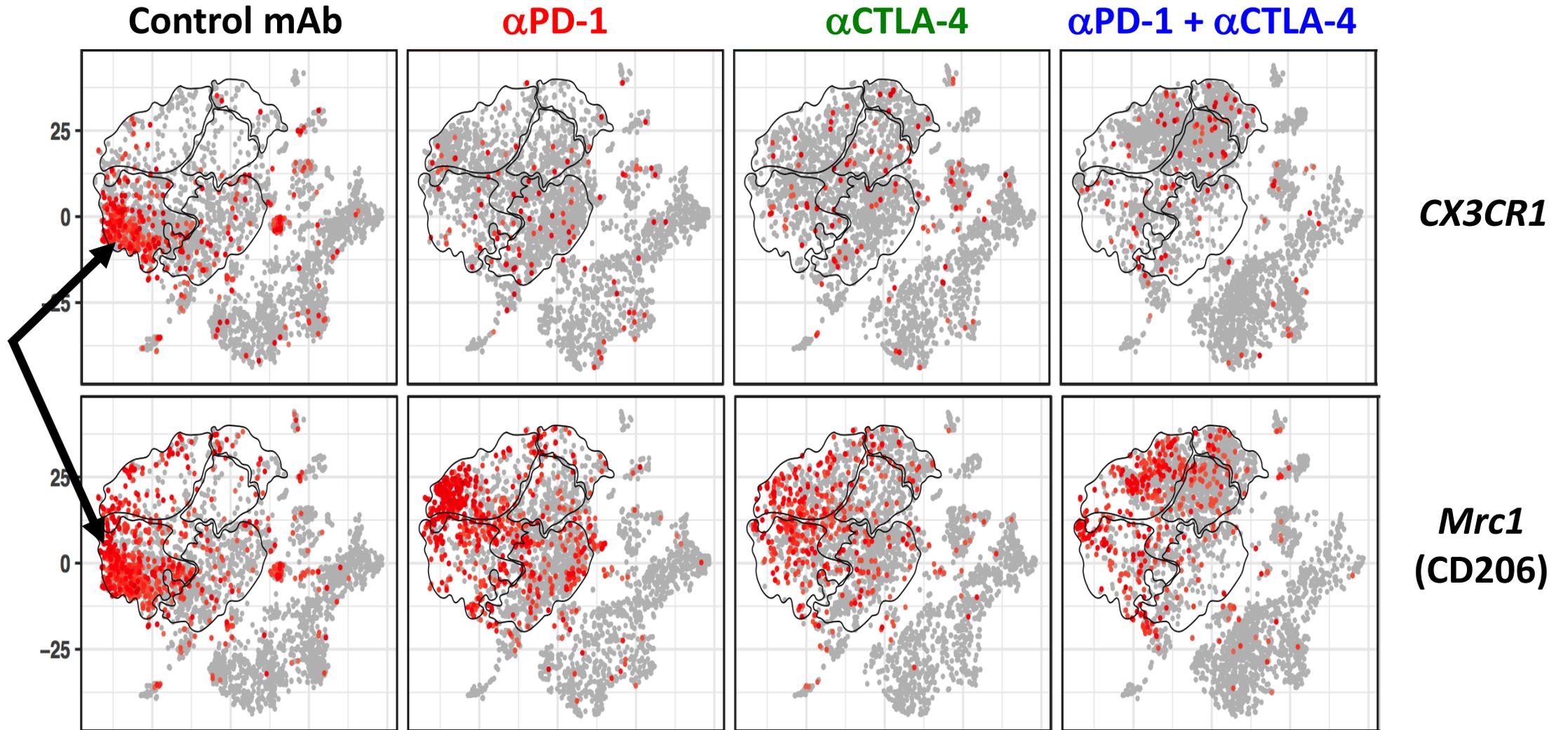
Cluster 3



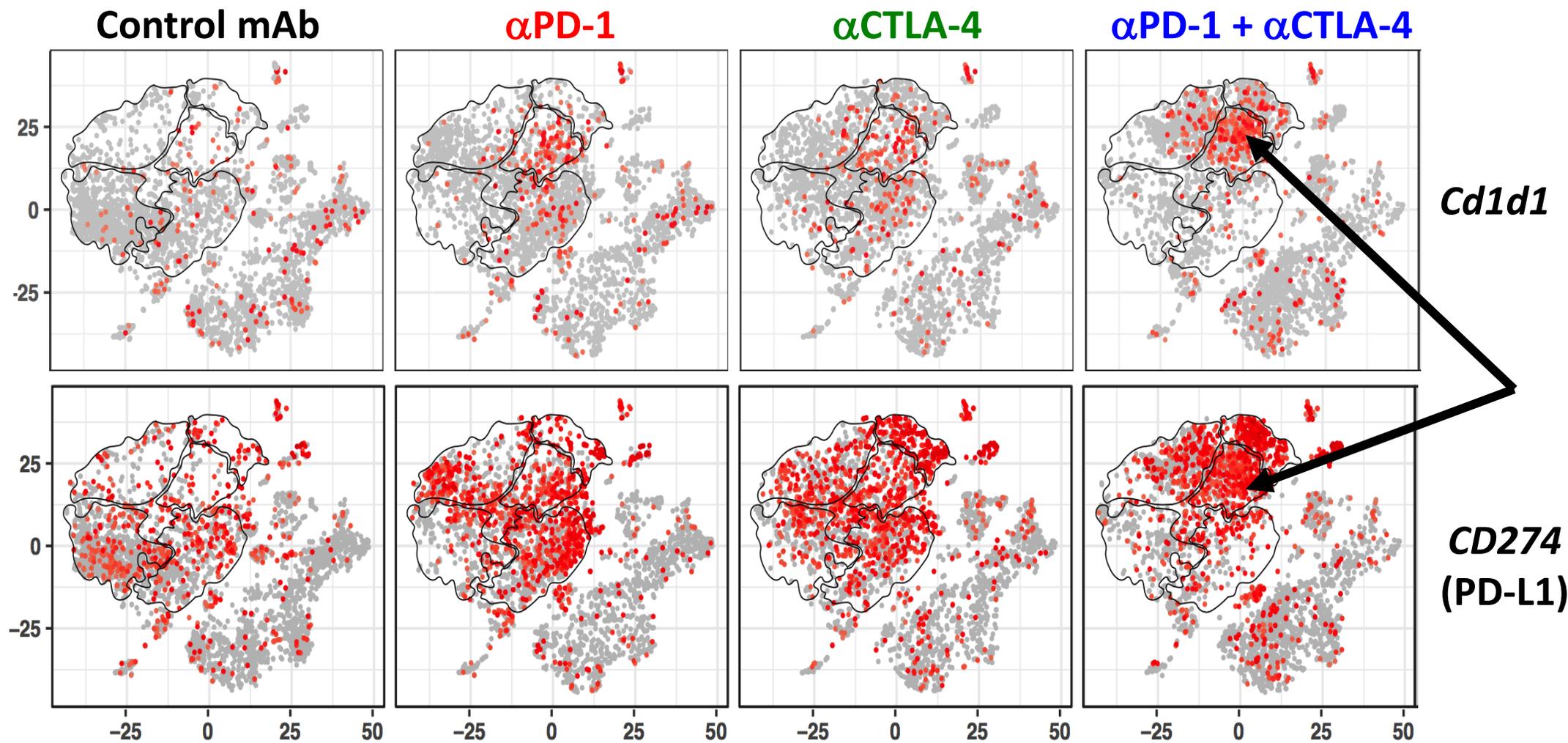
Cluster 4



# Cluster 1: Expression of *Mrc1* (CD206) and Exclusive Expression of *CX3CR1* (*scRNAseq*)



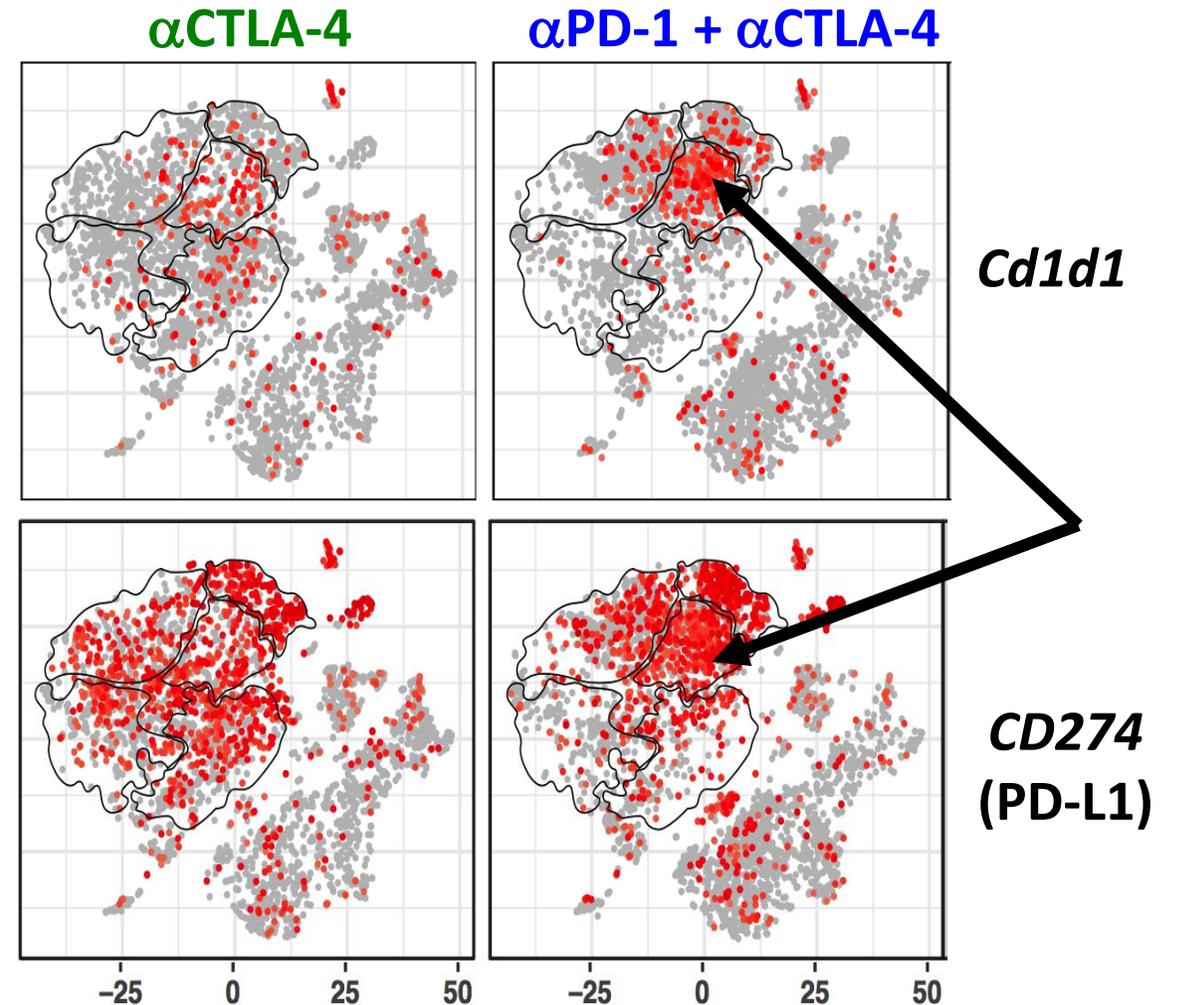
# Cluster 3: Elevated Expression of *Nos2*, *PD-L1 (CD274)* and *CD1d1 (scRNAseq)*



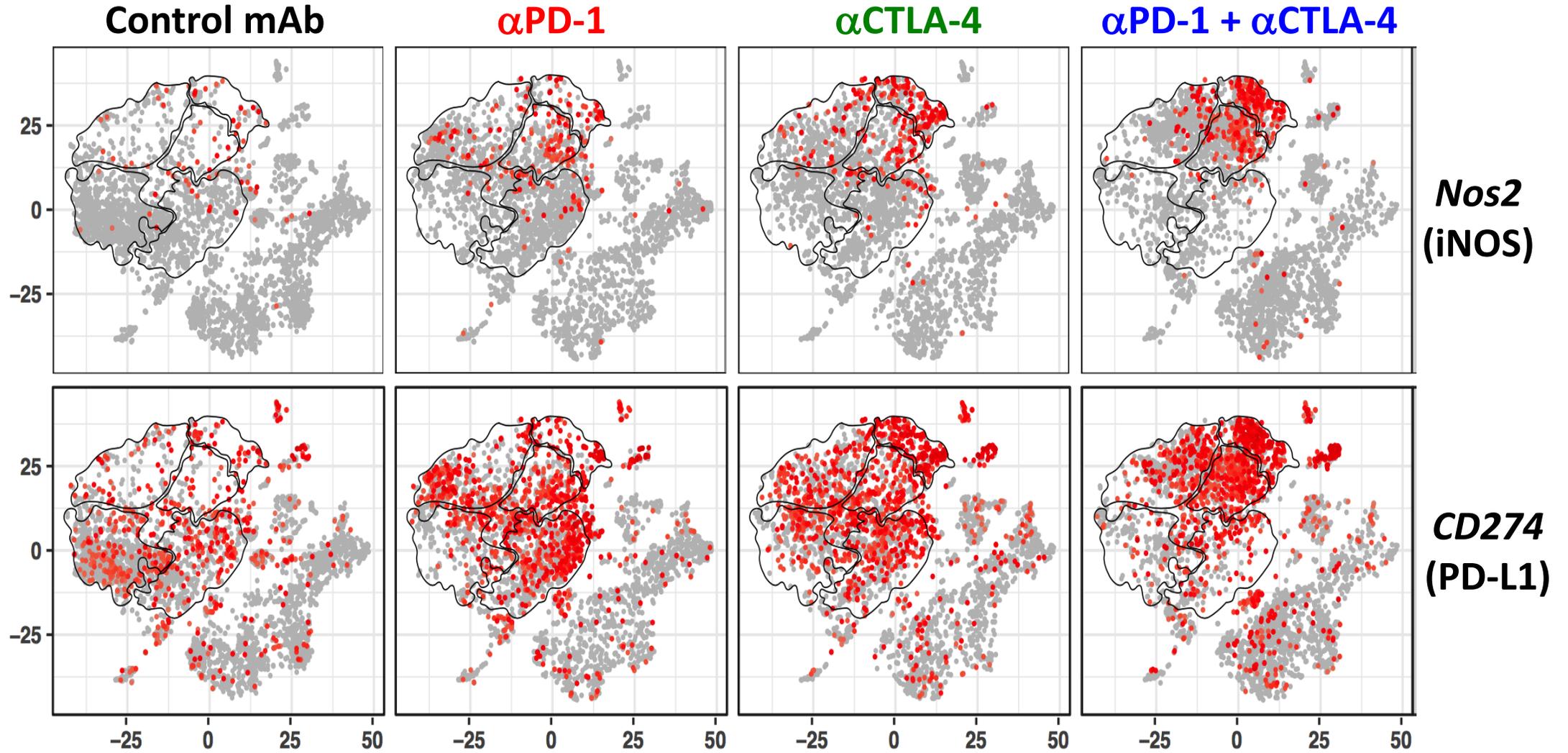
# Cluster 3: Elevated Expression of *Nos2*, *PD-L1 (CD274)* and *CD1d1 (scRNAseq)*

Cluster 3 has enrichment in pathways such as:

- Hypoxia
- TNF $\alpha$  signaling of NF- $\kappa$ B
- Glycolysis



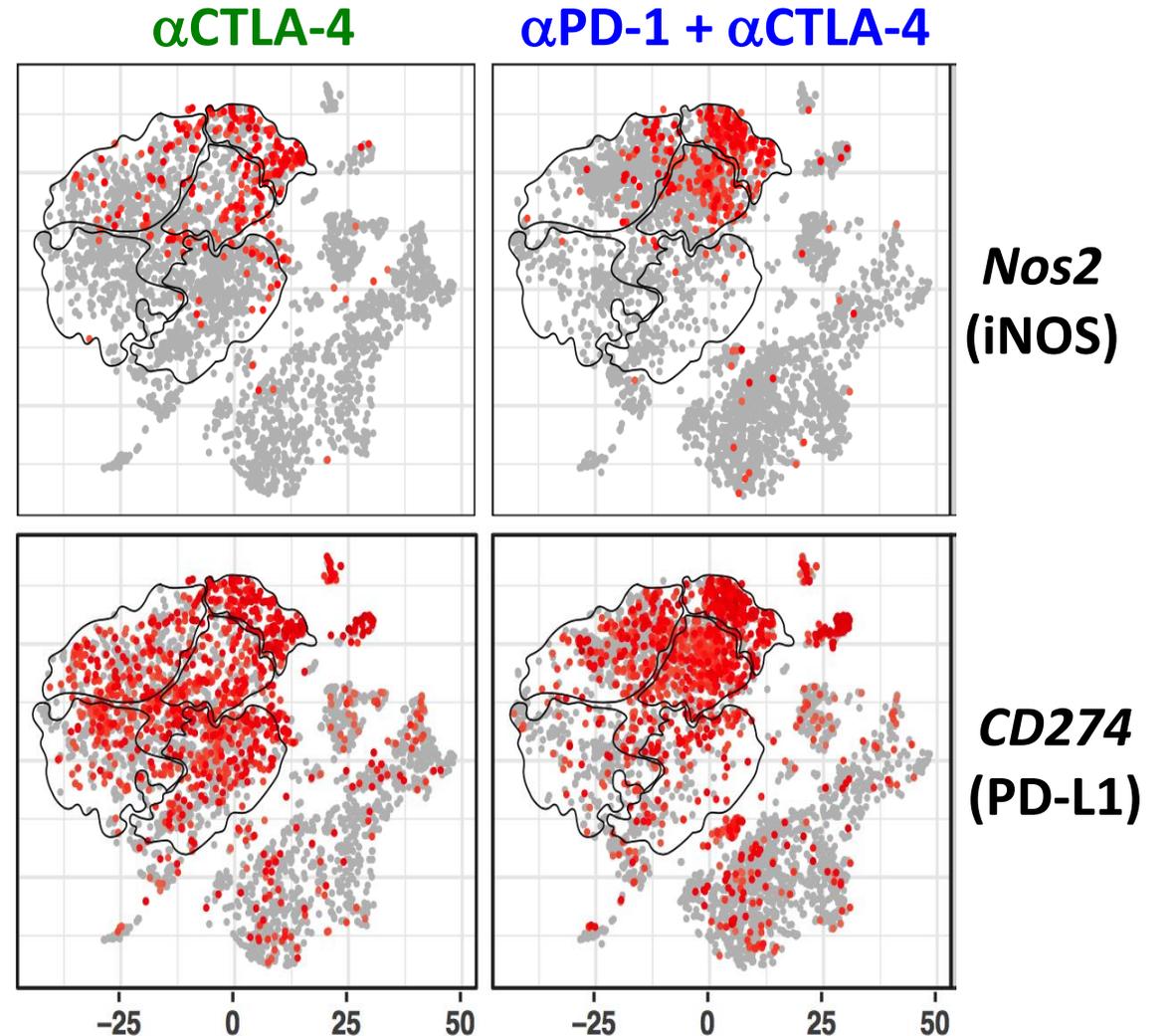
# Cluster 4: Elevated Expression of Inflammation-Related Genes: *Nos2* (iNOS), *CD274* (PD-L1) (**scRNAseq**)



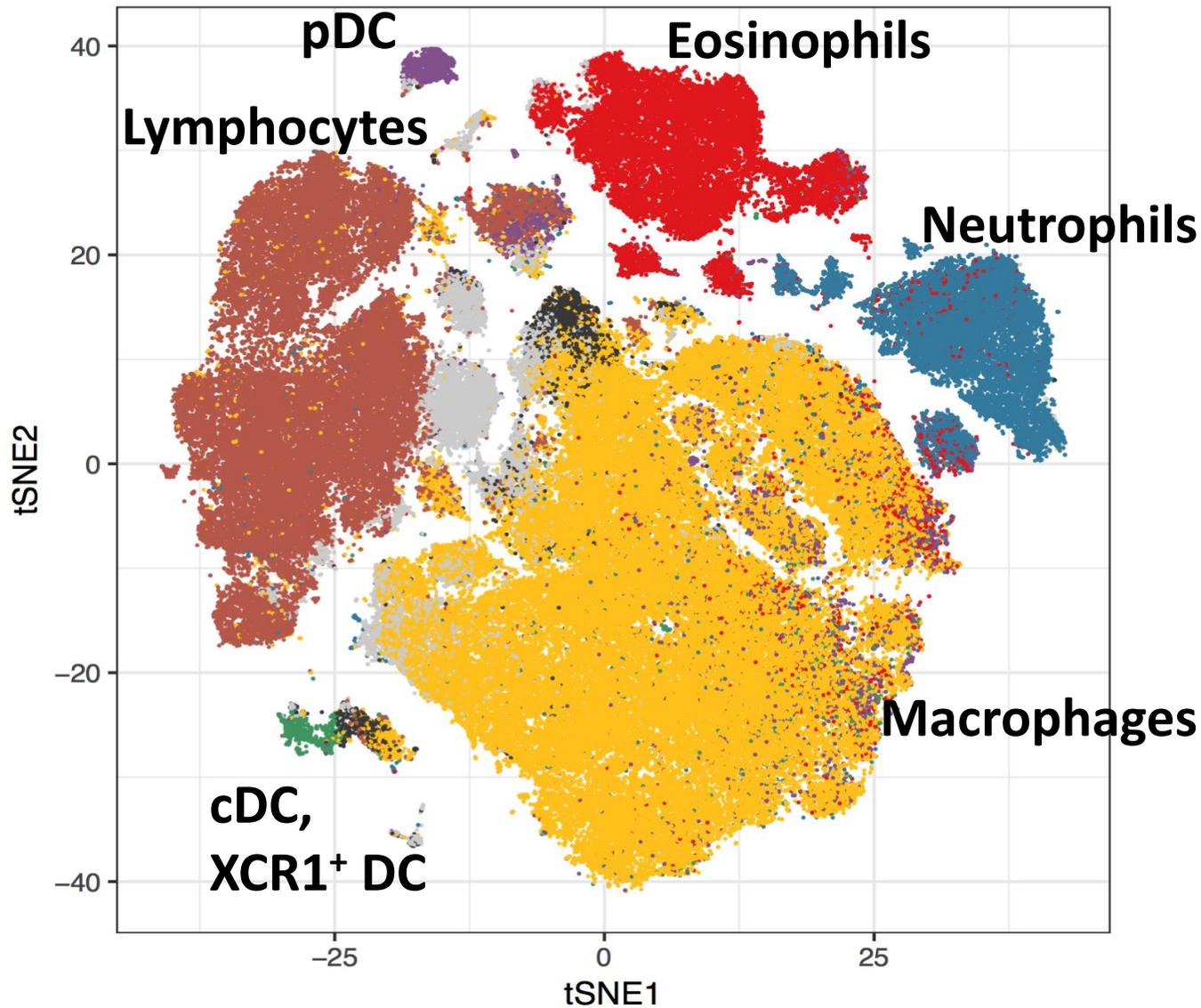
# Cluster 4: Elevated Expression of Inflammation-Related Genes: *Nos2* (iNOS), *CD274* (PD-L1) (**scRNAseq**)

Cluster 4 has enrichment in pathways such as:

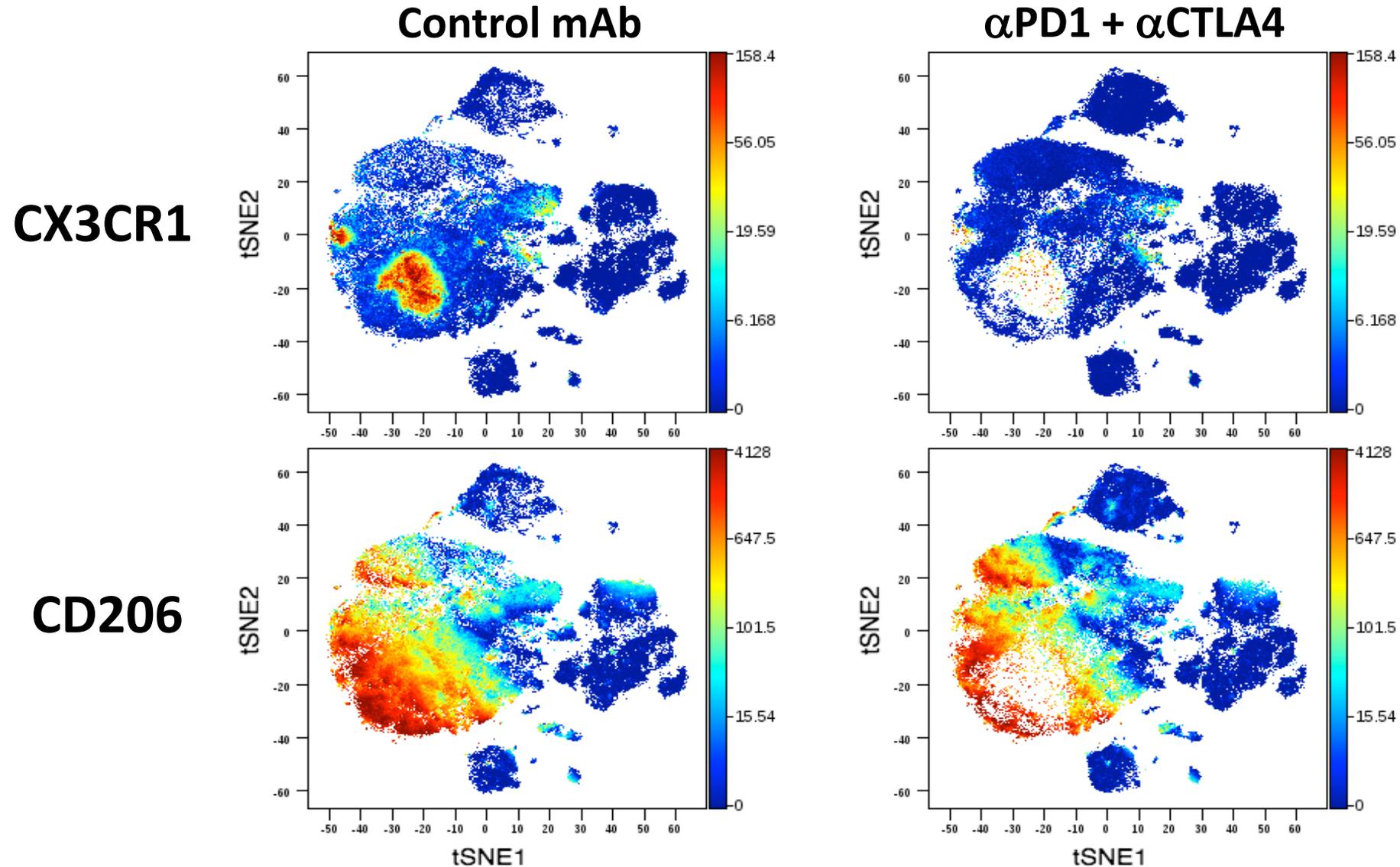
- Hypoxia.
- TNF $\alpha$  signaling via NF $\kappa$ B
- Interferon- $\gamma$  Response
- Inflammatory response



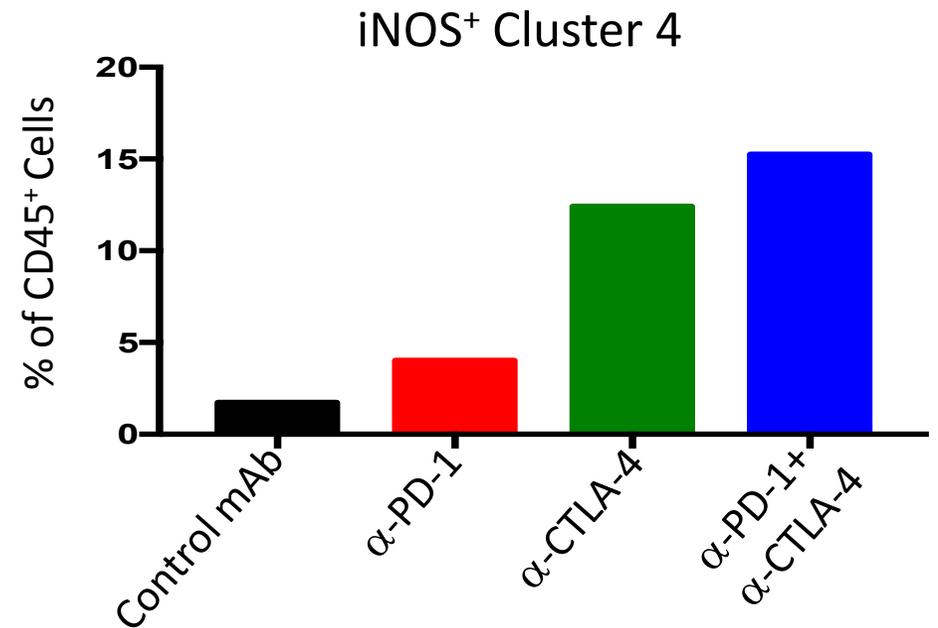
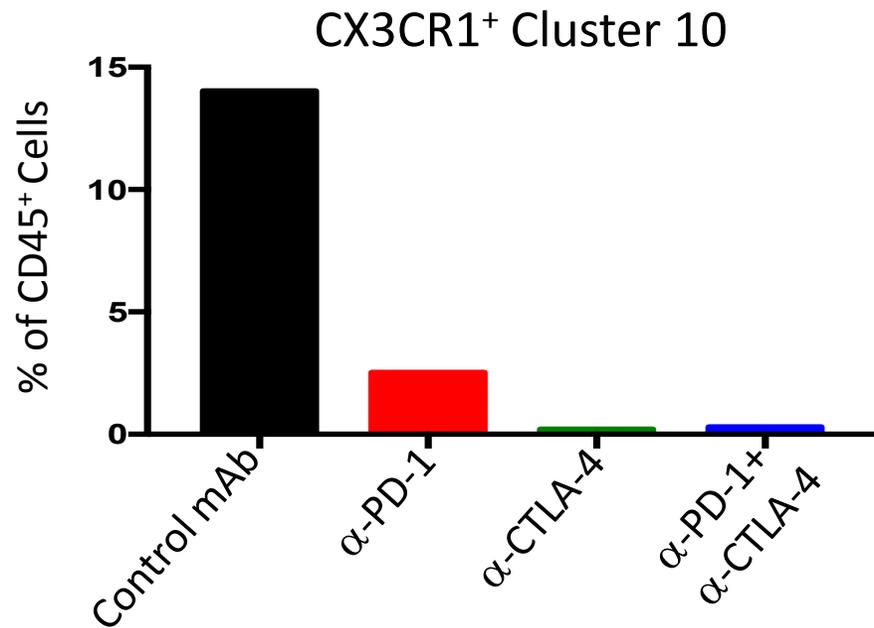
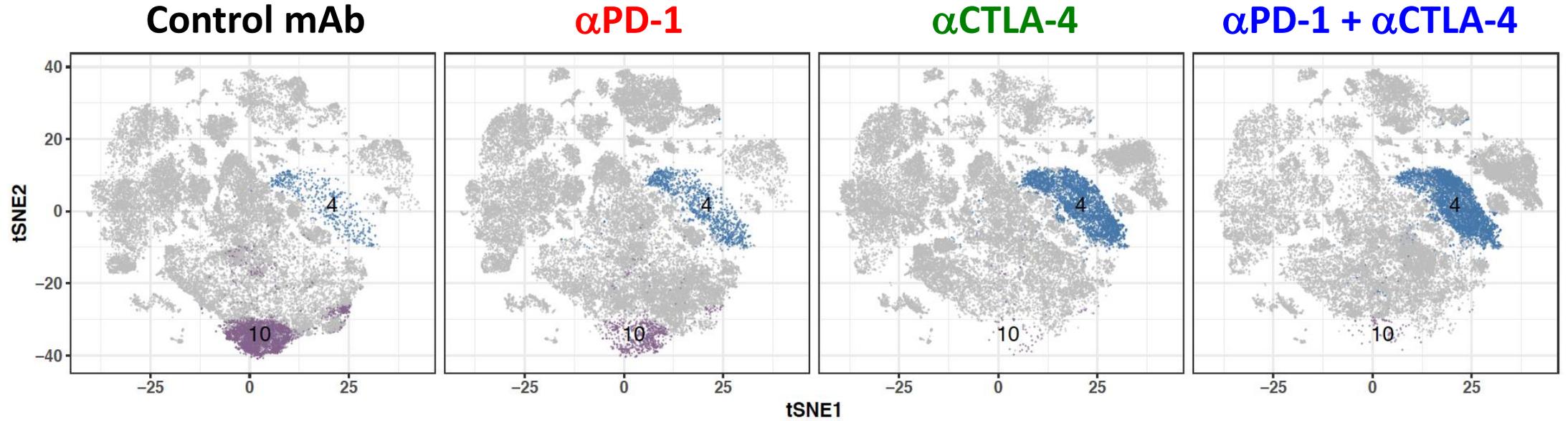
# CyTOF Clustering of T3 Tumor-Infiltrating Lymphoid and Myeloid Cell Populations (37 mAb Specificities)



# CyTOF Analysis Reveals Reordering of T3 Sarcoma Myeloid Populations During Immune Checkpoint Blockade Therapy



# Macrophage Remodeling As Detected By CyTOF: Cluster 10: (CX3CR1<sup>+</sup>/CD206<sup>+</sup>) vs Cluster 4: (iNOS<sup>+</sup>/CD38<sup>hi</sup>)



## Conclusions

- We have identified distinct subpopulations of lymphocytes and myeloid cells in progressively growing or therapeutically rejecting T3 sarcomas
- The subpopulations display distinct transcriptional profiles and functional markers
- The subpopulations display distinctive sensitivities to anti-PD-1 and anti-CTLA-4, when administered either alone or together
- Hypothesis to test: Do the subpopulations represent functional/dysfunctional or effector/inhibitory states of T cells (e.g., CD4<sup>+</sup> T cells or CD8<sup>+</sup> T cells or Treg) and macrophages
- Work is ongoing to isolate individual subpopulations and determine their positive or negative functional effects on the anti-tumor response

## Lessons and Take Home Messages

- scRNAseq and CyTOF each have unique advantages and their utility is maximized when used in concert
- Using high dimensional analysis approaches, we are identifying molecular and cellular changes that occur during successful cancer immunotherapy. We hope to apply what we learn from this work to human cancer immunotherapy thereby rendering it more effective

# High Dimensional Analysis of Immune Checkpoint Blockade-Mediated T3 Sarcoma Rejection

**Bob Schreiber**



**Max Artyomov**



**Katya  
Esaulova**

**Jeff  
Ward**

**Pamela  
Wong**

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**Evan Newell (SIgN)**  
**Michael Fehlings**

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**Ton Schumacher (Netherlands Cancer Institute)**

**Maxim Artyomov (Washington University)**  
**Katya Esaulova**

**Steve Oh (Washington University)**



**PARKER INSTITUTE**  
for CANCER IMMUNOTHERAPY



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ADVANCING CANCER IMMUNOTHERAPY WORLDWIDE

# Lessons and Take Home Messages

- Tumor neoantigen vaccines are safe, specific and effective in both preclinical tumor models and human cancer patients
- Clinical trials have begun at WUSTL to test the safety, specificity and efficacy of personalized cancer vaccines in cancer patients
- scRNAseq and CyTOF  
Using high dimensional analysis approaches, we are identifying molecular and cellular changes that occur during successful cancer immunotherapy. We hope to apply what we learn from this work to human cancer immunotherapy thereby rendering it more effective

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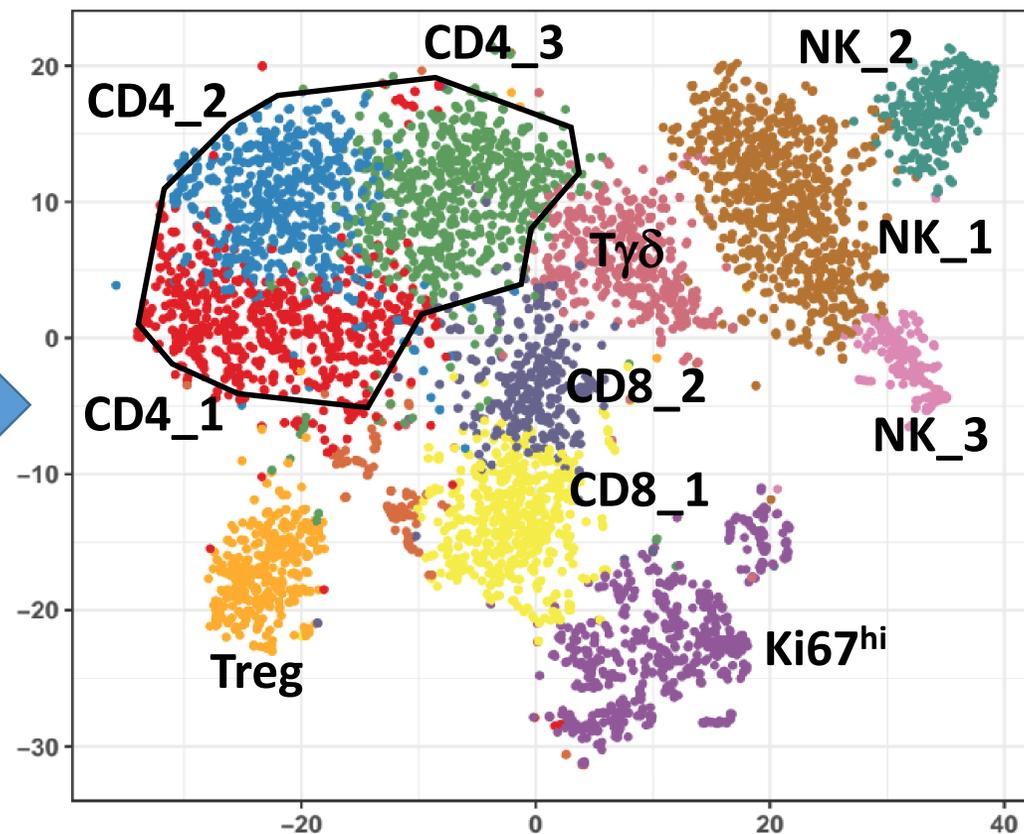
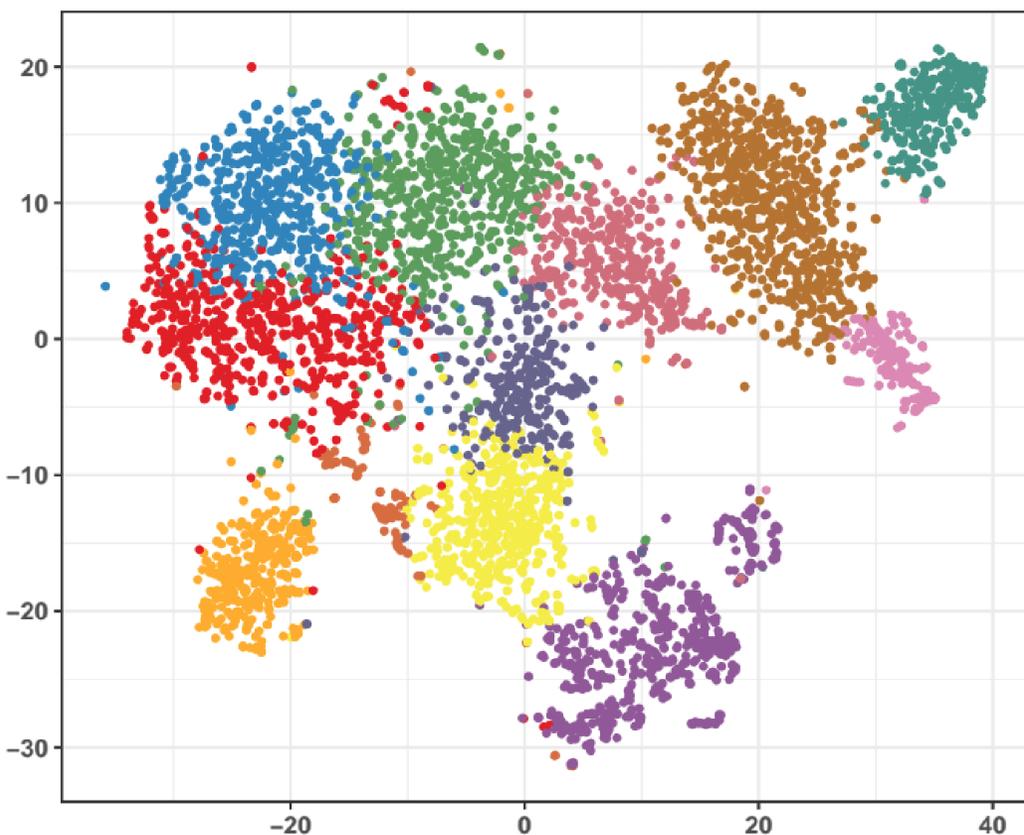
ADVANCING CANCER IMMUNOTHERAPY WORLDWIDE

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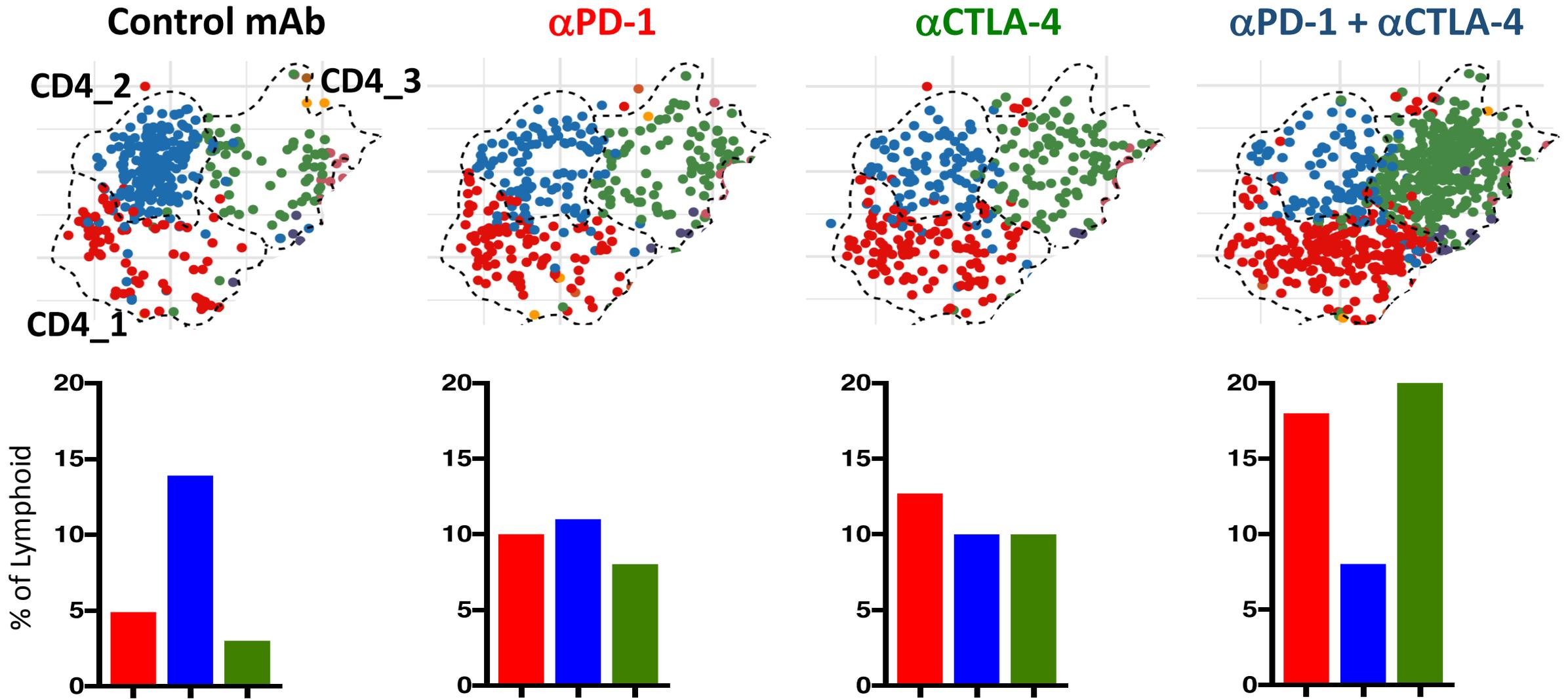
ADVANCING CANCER IMMUNOTHERAPY WORLDWIDE

# Identification of Three Major CD4<sup>+</sup> T Cell Subpopulations (scRNAseq)

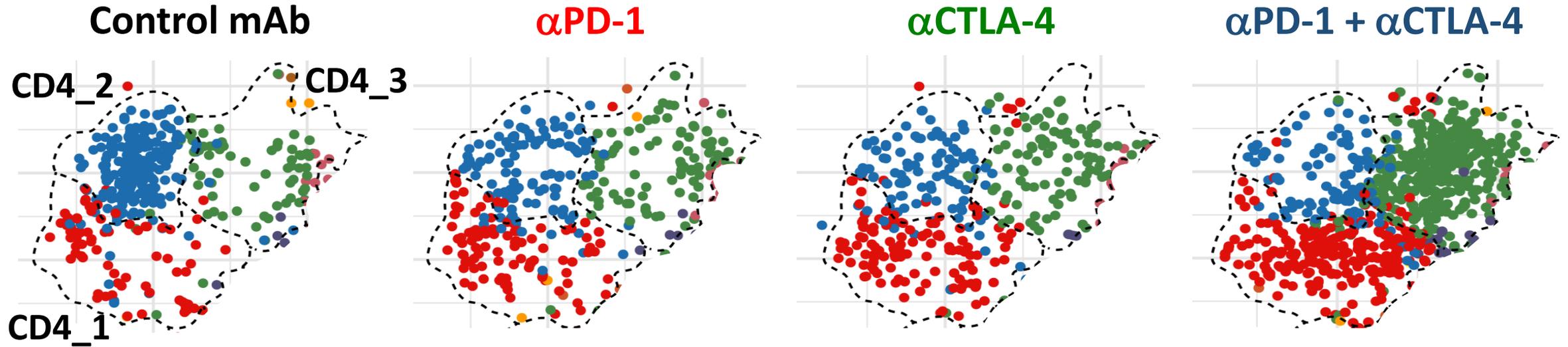
Lymphoid: 4989 cells



# Remodeling of Intratumoral CD4<sup>+</sup> T Cells Upon Immune Checkpoint Blockade Therapy (**scRNAseq**)



# Remodeling of Intratumoral CD4<sup>+</sup> T Cells Upon Immune Checkpoint Blockade Therapy (**scRNAseq**)



## CD4\_1

Upregulated pathways:

- Hypoxia
- TNF $\alpha$  signaling via NF- $\kappa$ B
- MAPK signaling
- TCR Signaling

## CD4\_2

Upregulated pathways:

- Peptide chain elongation
- Ribosome pathway

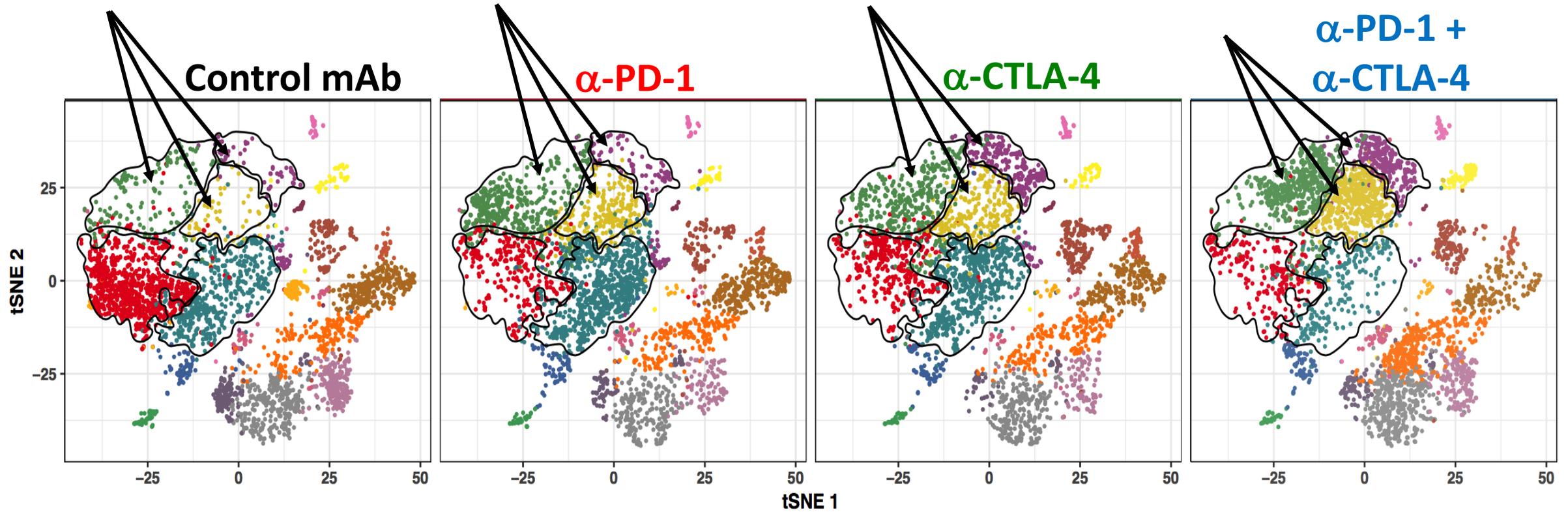
Downregulated pathways:

- Cell cycle
- G2M checkpoint

## CD4\_3

Less activated  
CD4<sup>+</sup> T Cells

# Clusters 2, 3 & 4 Show the Strongest Increases Upon Immune Checkpoint Blockade Treatment (**scRNAseq**)



# Immune Checkpoint Blockade Therapy Remodels the Tumor Infiltrating CD8<sup>+</sup> T Cell Compartment (CyTOF)

