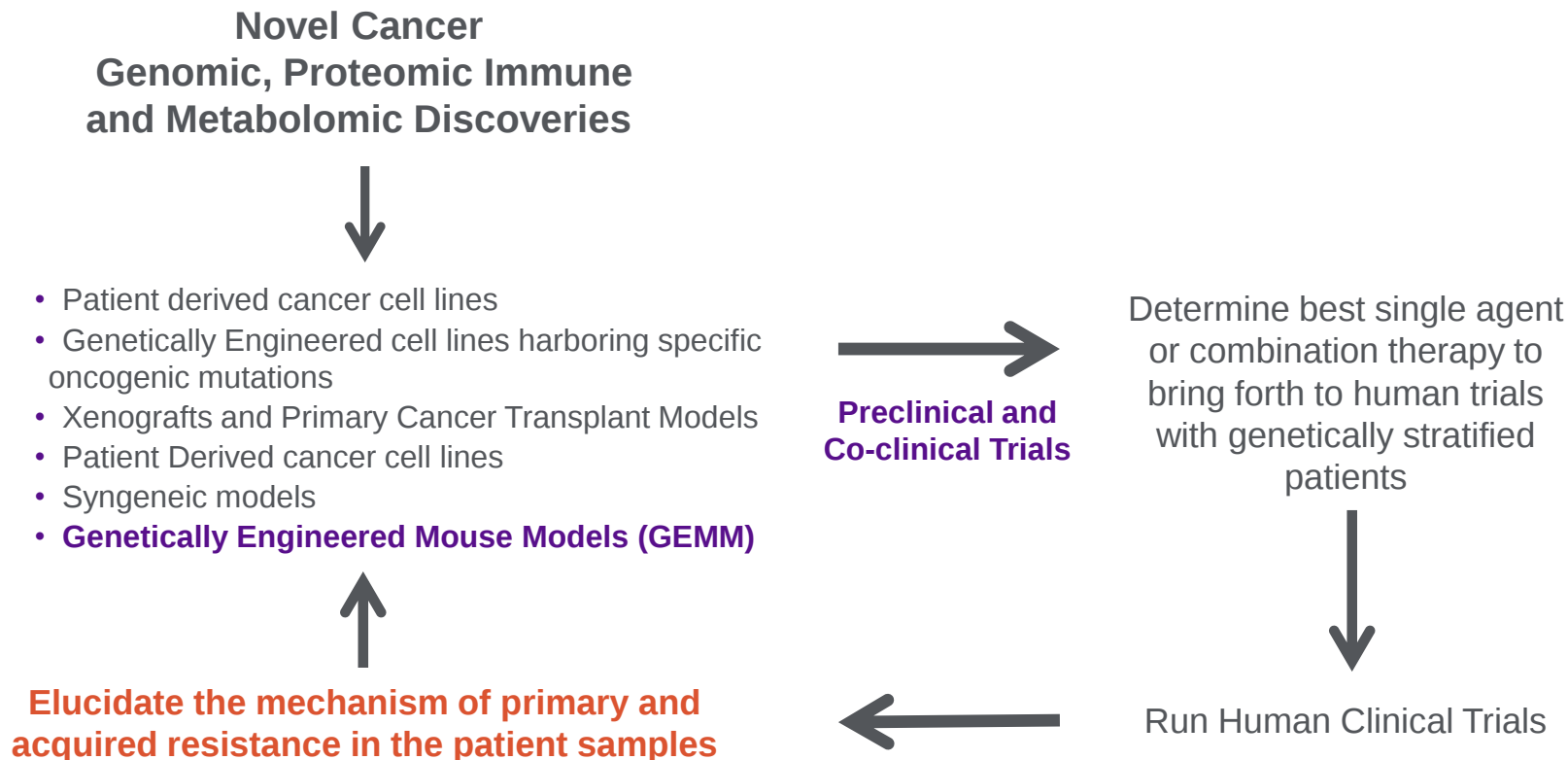


Preclinical Models to Elucidate Tumor Immune Microenvironment

Kwok-Kin Wong, MD, PhD

Division of Hematology and Medical Oncology

Integration of Bench and Bedside



Inducible Mouse Lung Cancer Models

KRAS G12D	C-MET	DDR2 mutants	IDH1 R132H
KRAS G12V	EGFR T790M-Del19/c-MET	FGFR 1	IDH2 R140Q
KRAS G12C	EGFR T790M-L858R/c-MET	FGFR 2 WT	IDH2 R172K
EGFR Del19	EGFR T790M-Del19	FGFR2 W290C	EZH2
EGFR L858R	EGFR T790M-L858R	FGFR2 S320C	EZH2 Y641N
EGFR T790M	EGFR T790M-L858R-C797S	FGFR2 K659N	RBP2
EGFR wild type	EGFR T790M-Del19-C797S	FGFR3 WT	LSD2
EGFR vIII	EGFR T790M-L858R-L718Q	FGFR3 K652E	LSD1
HER2 exon 20 insertion	EGFR T790M-Del19-L718Q	FGFR3 S249C	KDM5B
HER2 wild type	EML4-ALK F1174L	NRF2 WT	SETDB1
BRAF V600E	EML4-ALK L1196M	NRF2 G81S	MINA53
p110 exon 20 (H1047R)		SOX2	KDM2a
EML4-ALK		Pten/Lkb1	JMJD2C
KRAS G12D/Tbk1 mutant			Histone H3.3 G34R
			p53/Rb
			p53/Rb/p130
			p53/Rb/myc

Matching the right model to the right drug

Genetically engineered mouse cancer models for Immunotherapy

Current Conditional Mouse Lung Cancer Models

1. Genetically defined
2. Native Vasculature
3. Intact Immune System

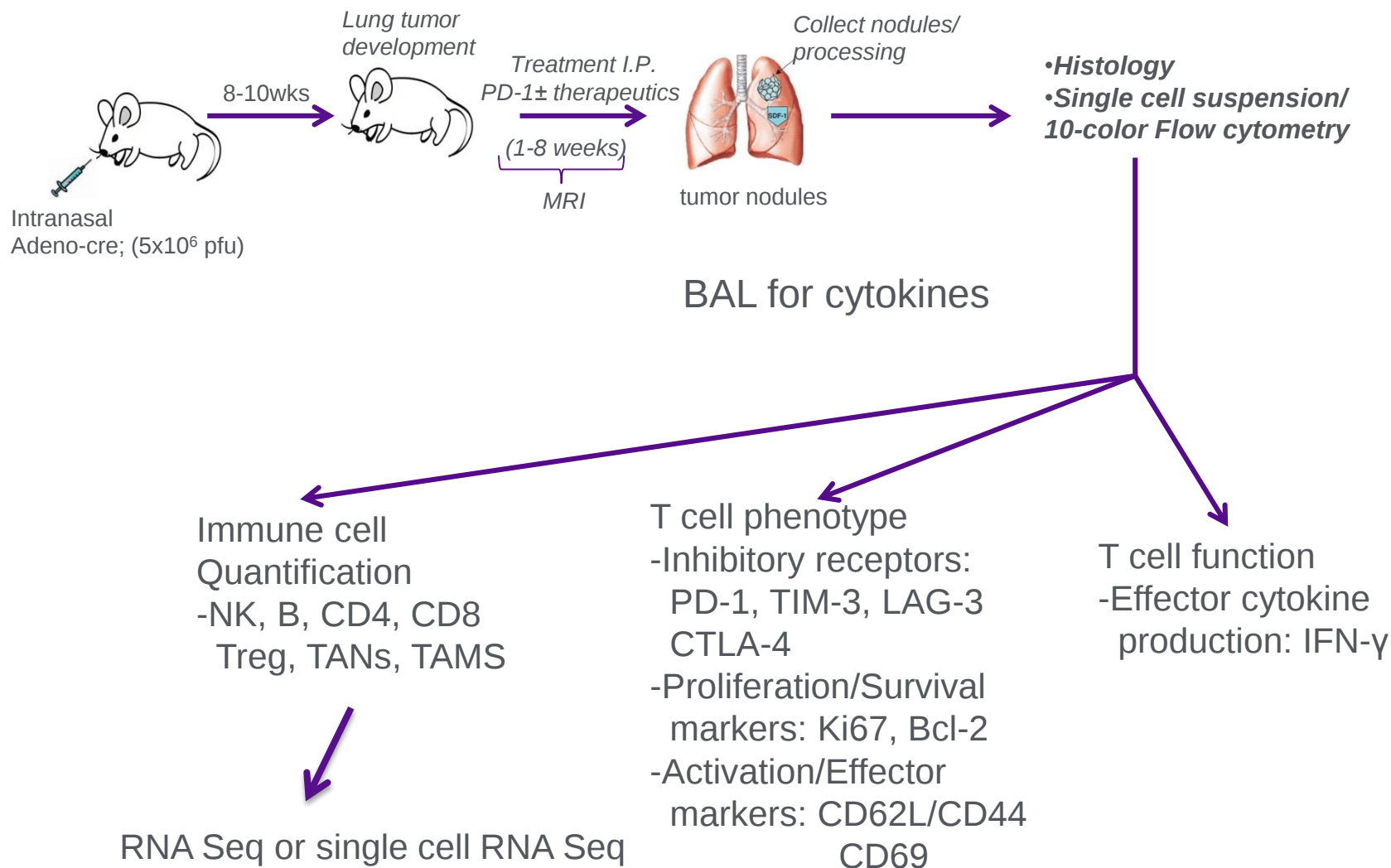
Potential limitations

1. Low Mutational Load (novel neo-antigens are present)
2. Low throughput for drug screening (large number of drug combinations)
3. Minor differences between mouse and human immune system

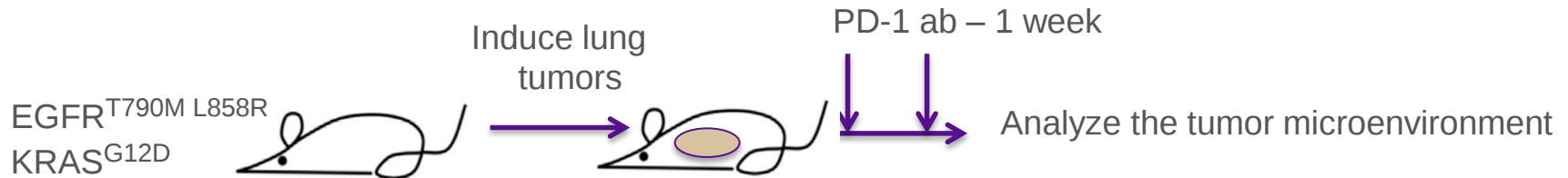
**LSL-
Kras^{G12D}**

**LSL-Kras^{G12D}
Lkb1^{f/f}**

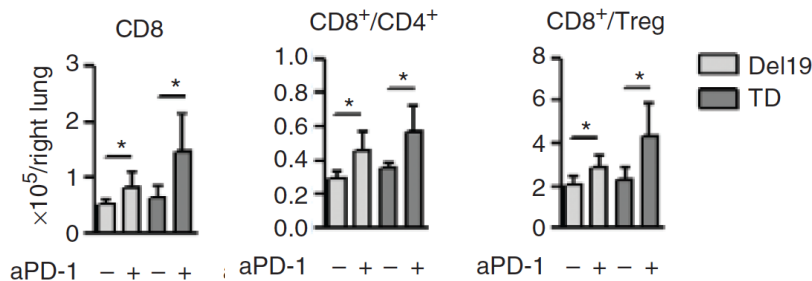
**LSL-
EGFR-TL**



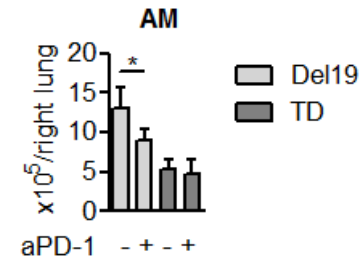
PD1 blockade decreases the immune suppressive factors in the microenvironment in EGFR driven tumors



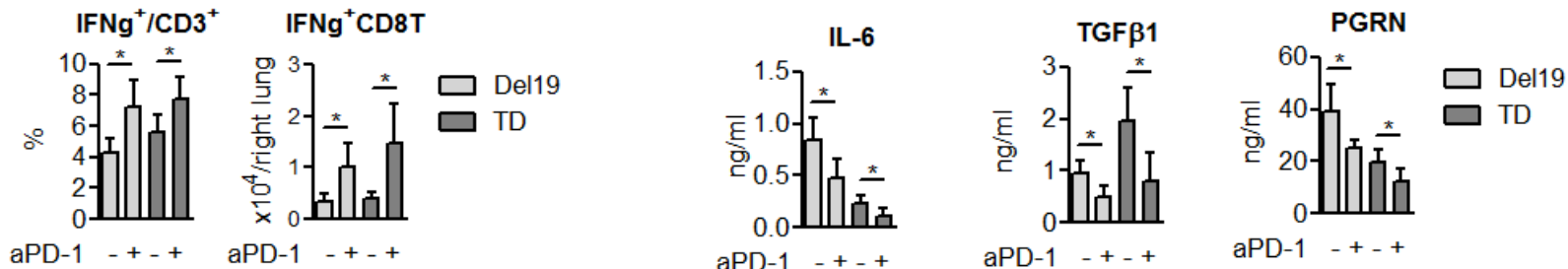
T CELLS



Macrophages

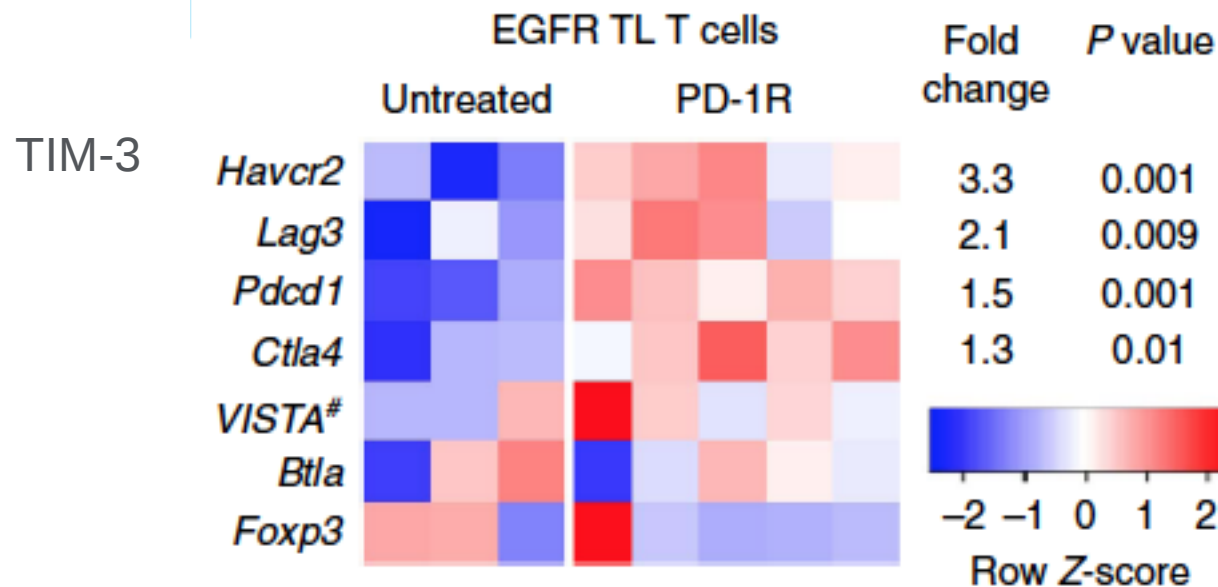
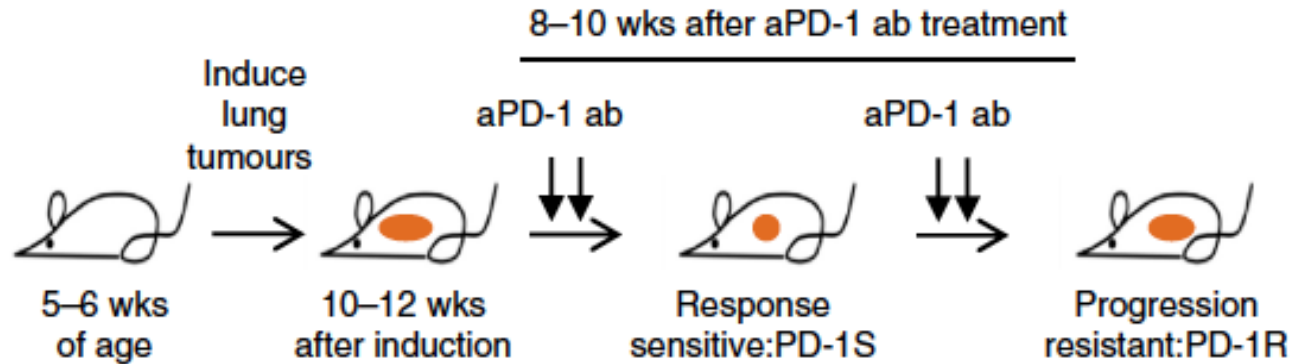


Cytokines

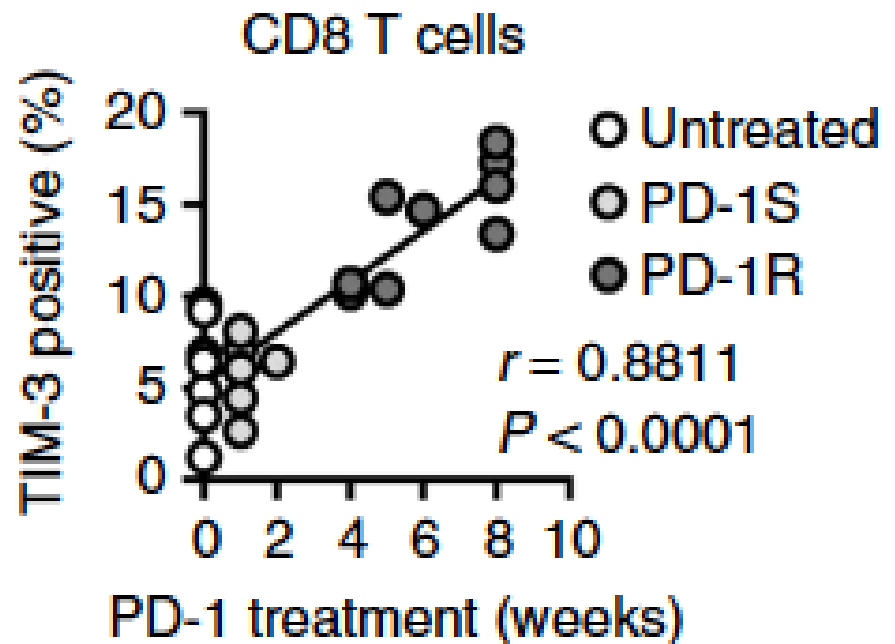
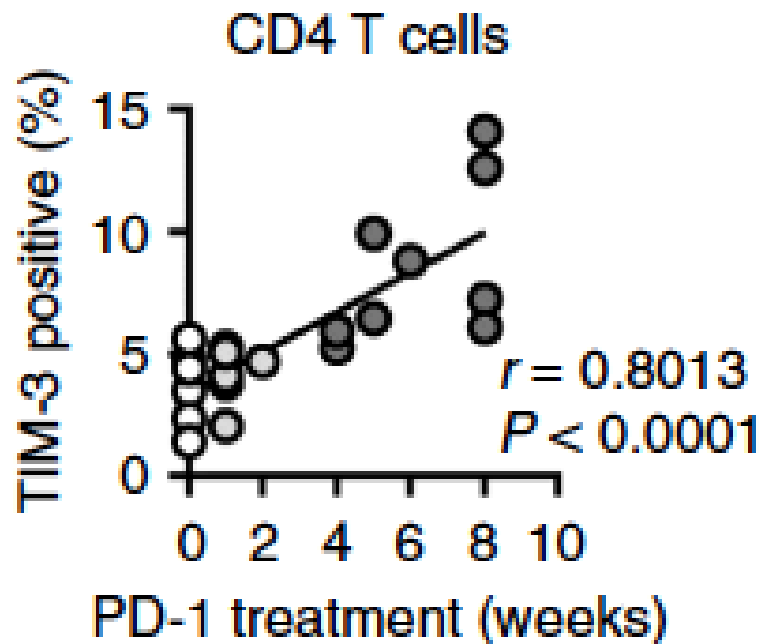


Adaptive Resistance to chronic PD1 Blockade

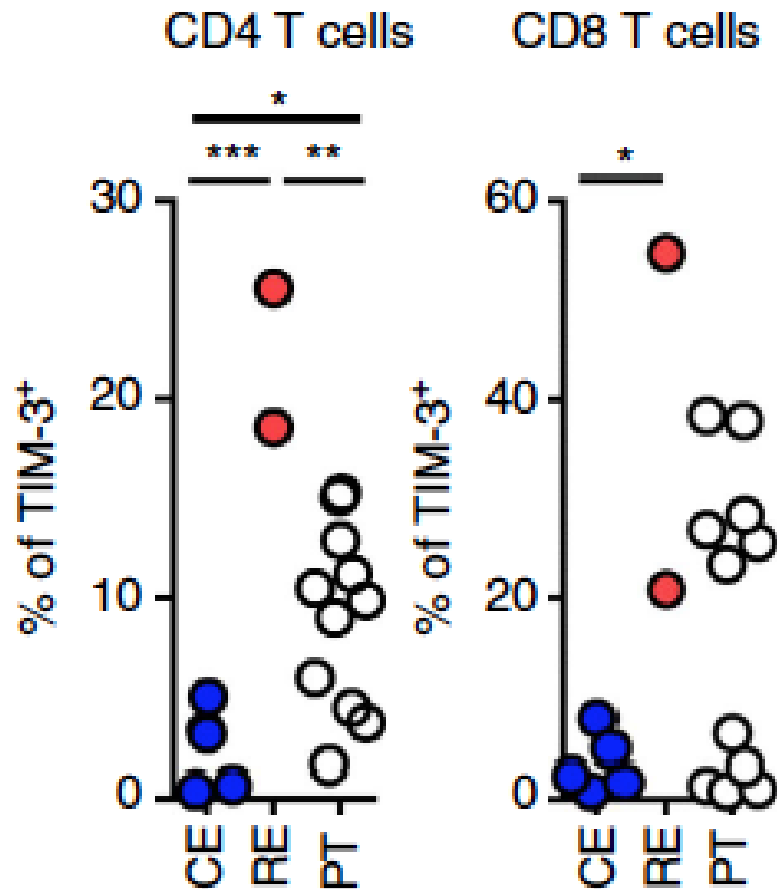
T cells in PD-1 resistant lung cancer



Increased TIM-3⁺ T cells in PD-1-resistant mouse lung cancer



Lung cancer patients that develop resistance to PD-1 therapy express higher levels of TIM-3



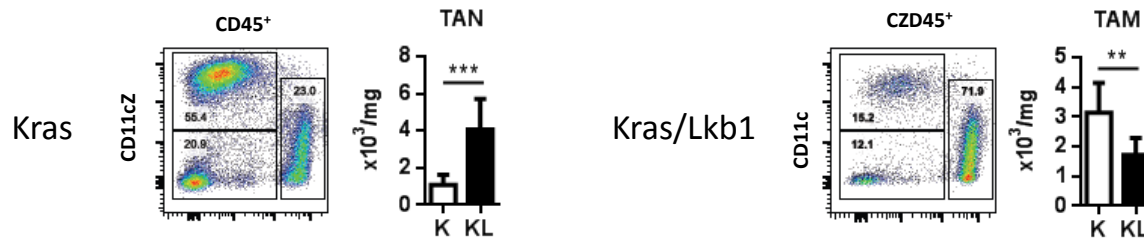
CE = control effusion

RE = resistant effusion

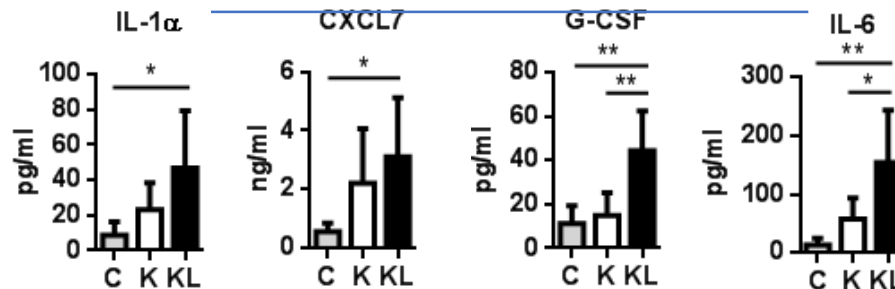
PT = primary tumor

Tumor Suppressor loss leads to altering of TME

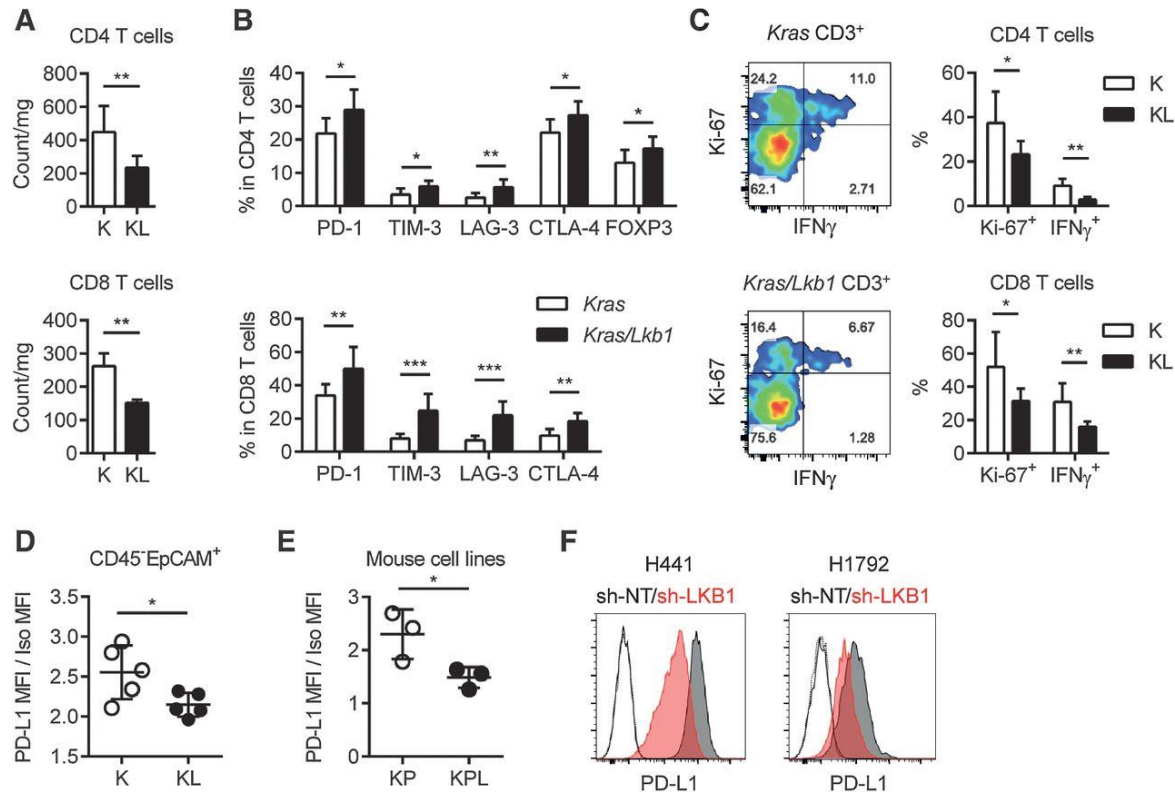
Lkb1 inactivation drives development of a distinct tumor immune microenvironment enriched with neutrophil inflammatory cytokines



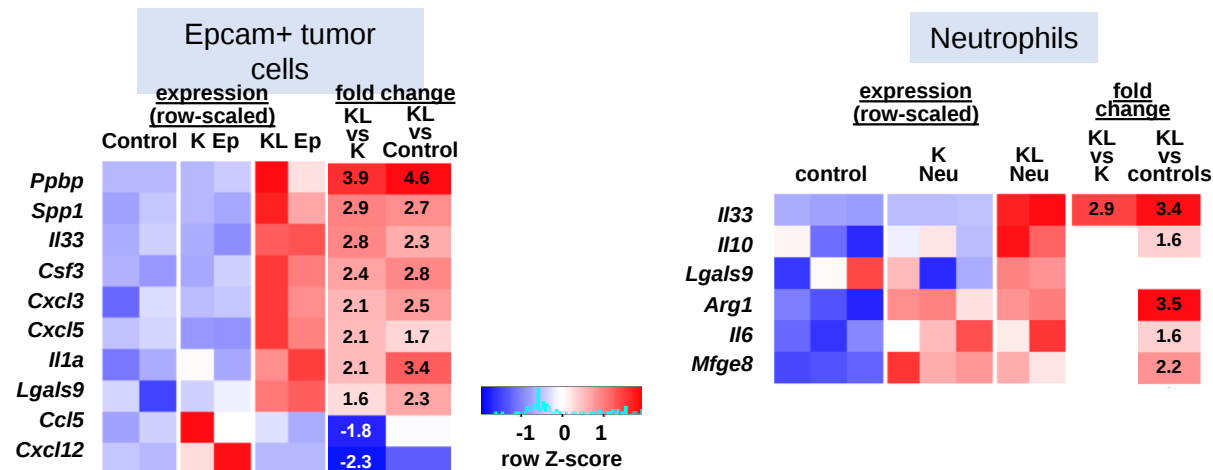
CYTOKINES IN BAL



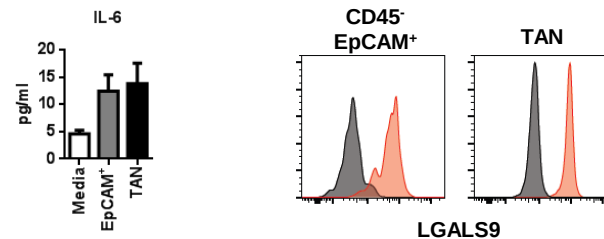
Lkb1 inactivation leads to a T-cell-suppressive tumor microenvironment with low PD-L1 expression in tumor cells.



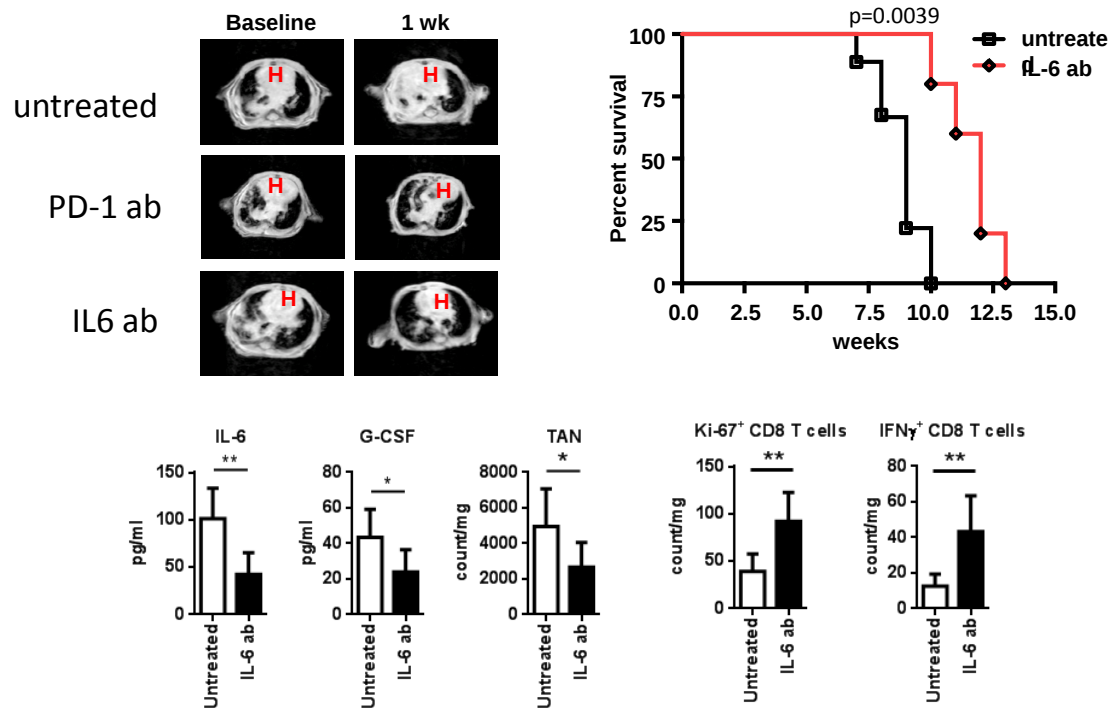
RNA sequencing of sorted tumor cell populations yields novel targets in different Kras vs Kras Lkb1 models



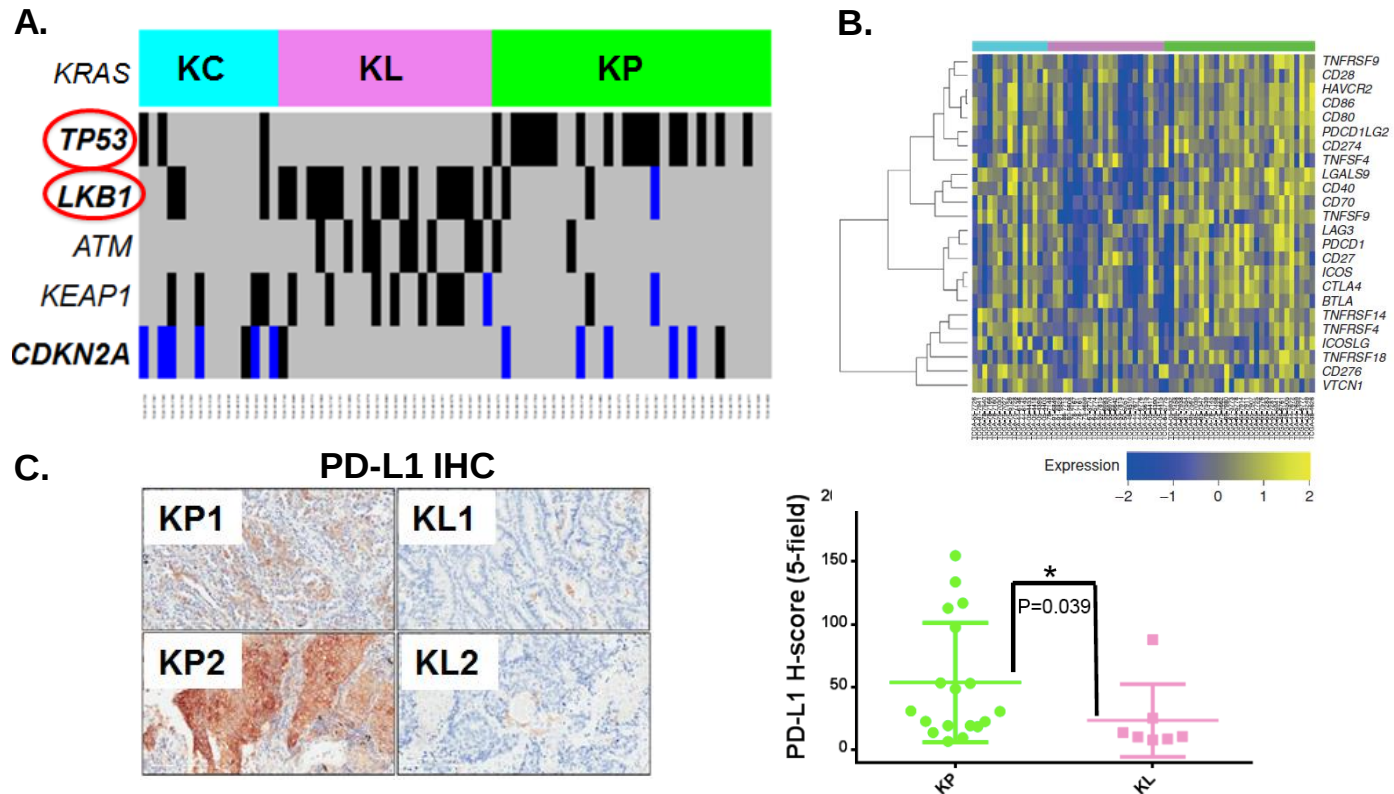
Validation of some targets at protein level in sorted tumor vs neutrophils



IL6 blockade but not PD-1 blockade is effective in Lkb1 mutant tumors

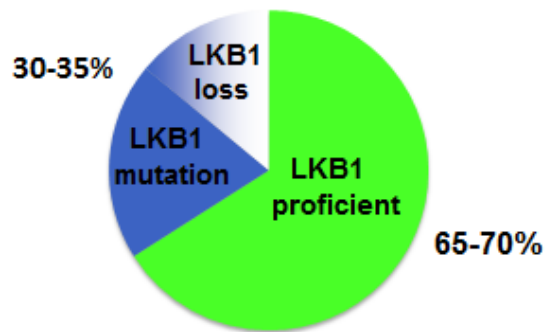


Co-mutations in *STK11/LKB1* (KL) and *TP53* (KP) define subgroups of *KRAS*-mutant LUAC with distinct immune profiles

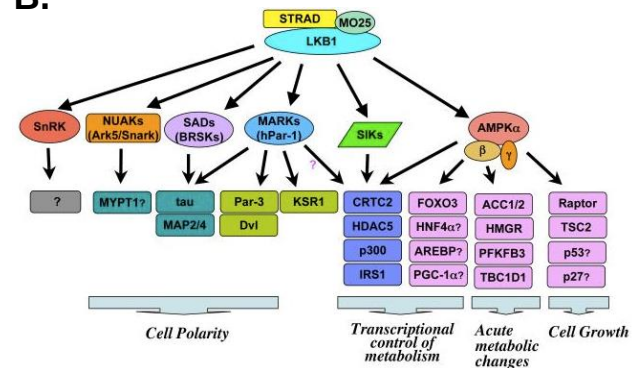


LKB1 inactivation is associated with a “cold” tumor immune microenvironment in LUAC

A. Lung adenocarcinoma

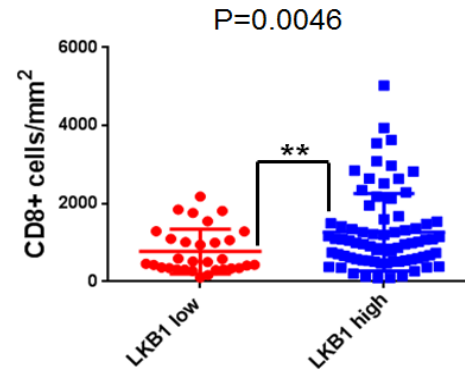
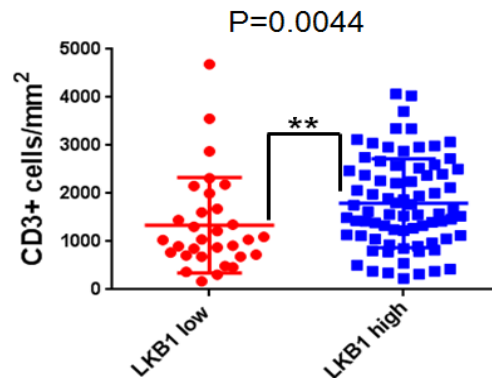


B.



Shackelford and Shaw, Nat Rev Cancer, 2009

C.



Skoulidis et al, ASCO Annual Meeting, 2015

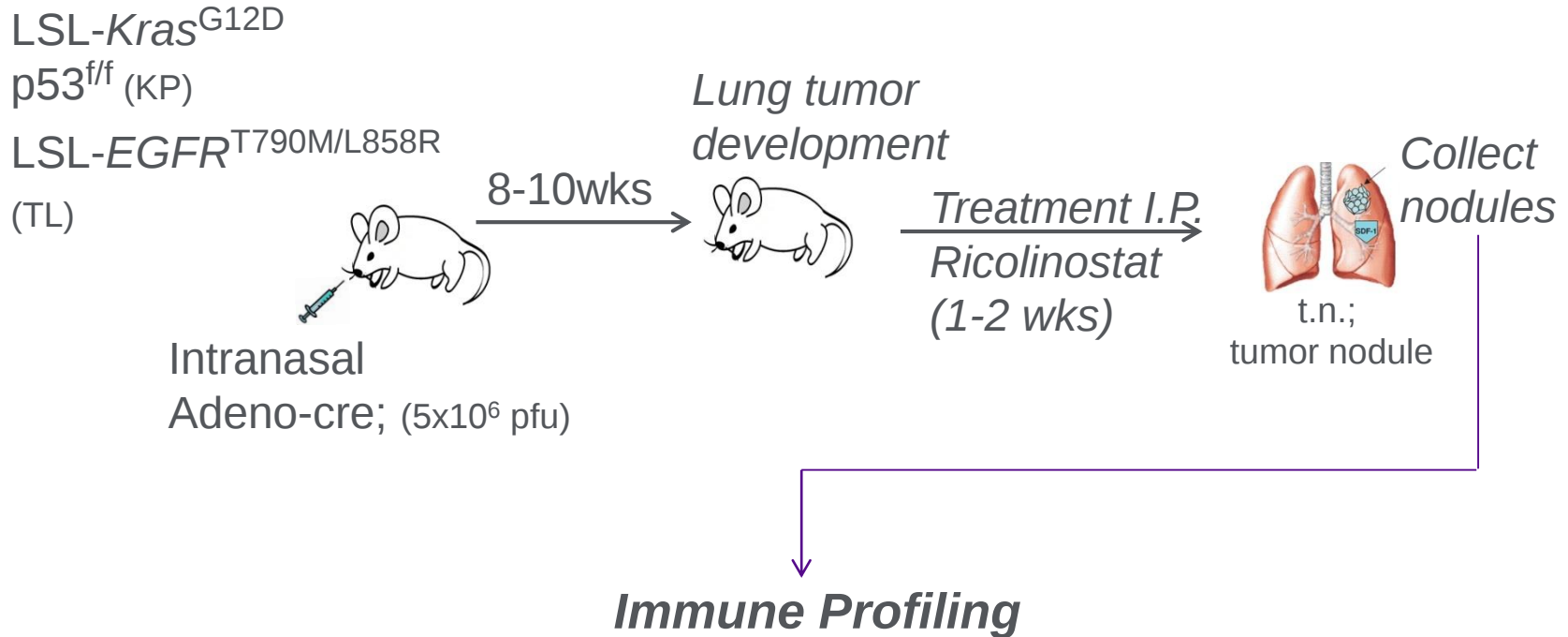
Preclinical Models to understand the impact of small molecules on the lung cancer tumor immune microenvironment

Epigenetics regulation in cancer: HDAC inhibitors

- Histone deacetylases (HDAC) catalyze the removal of acetyl groups from lysine residues in histones and non-histone proteins thereby regulating many cellular processes
- Pan or isozyme-specific HDACi have gained attention in oncologic applications due to their reported cytostatic effects in cancer models
- Emerging data highlight their immuno-regulatory properties in various inflammatory settings

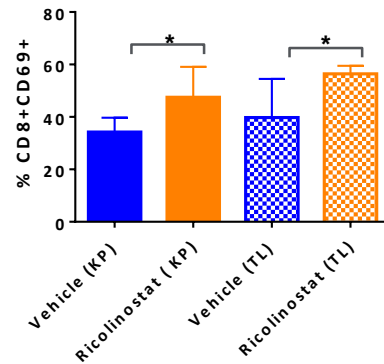
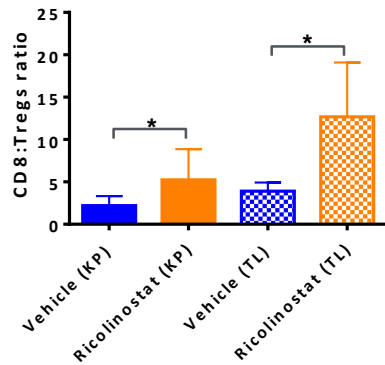
Immunomodulatory properties of ACY1215 (Ricolinostat) in genetically engineered mouse models of NSCLC

In vivo studies

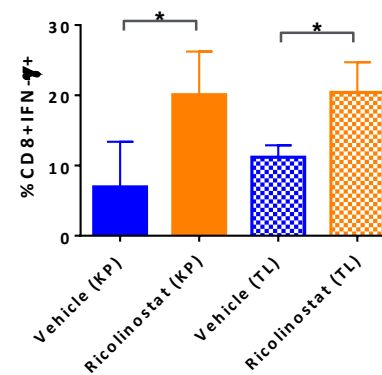


In vivo effects of ACY1215 in genetically engineered mouse models of NSCLC

Increased T cell activation

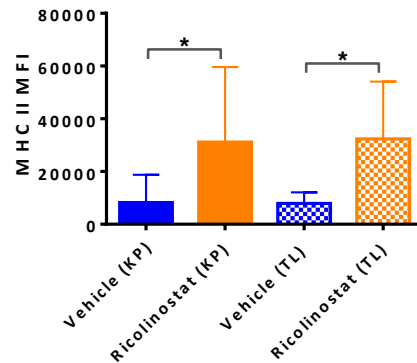


Increased T cell function

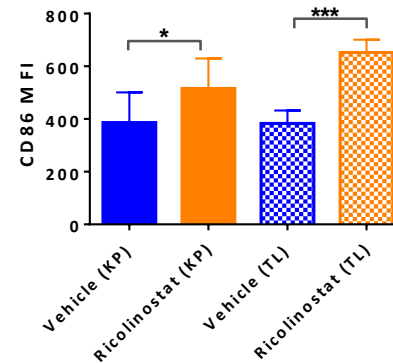


Effect on T cells

Increased MHC II

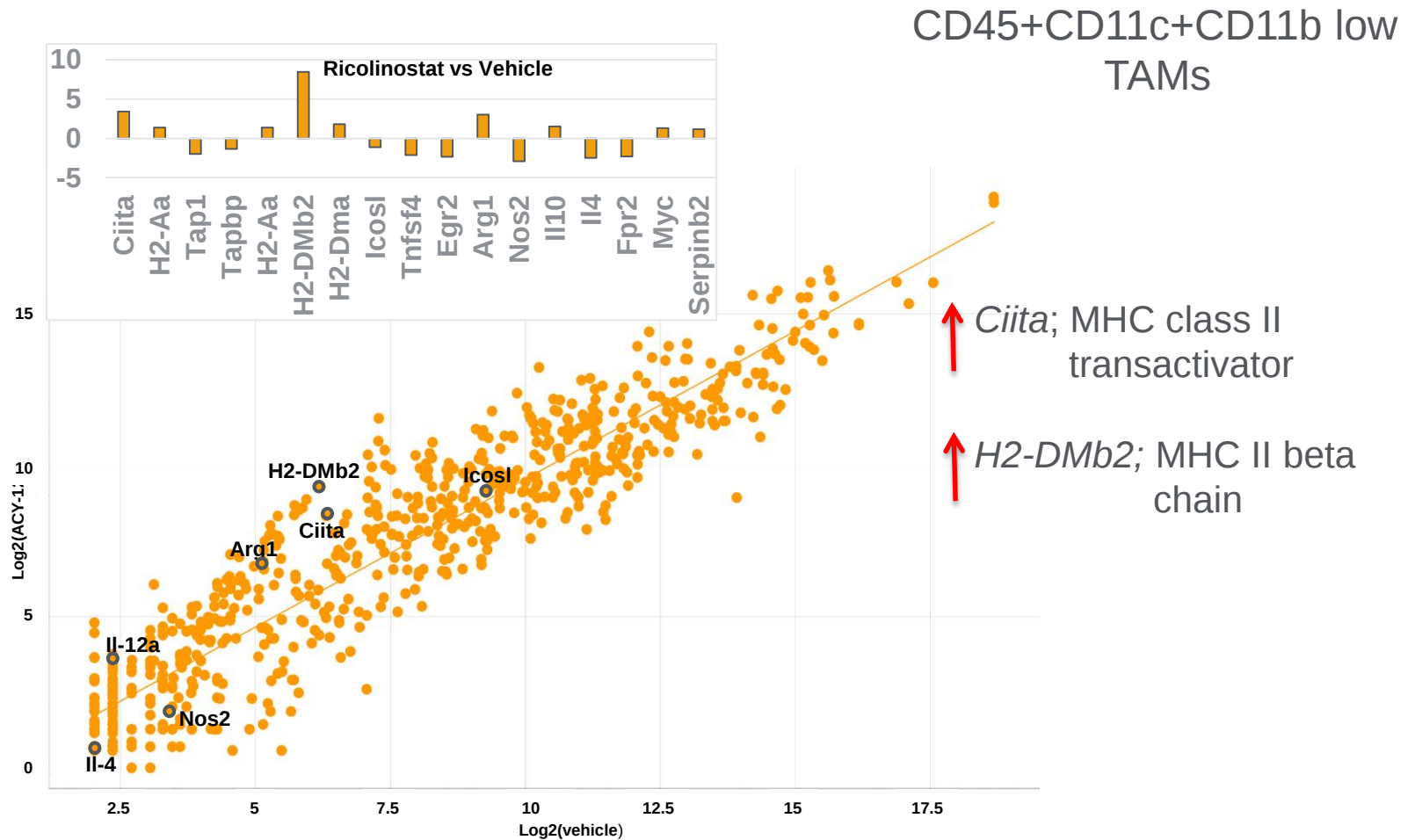


Increased CD86



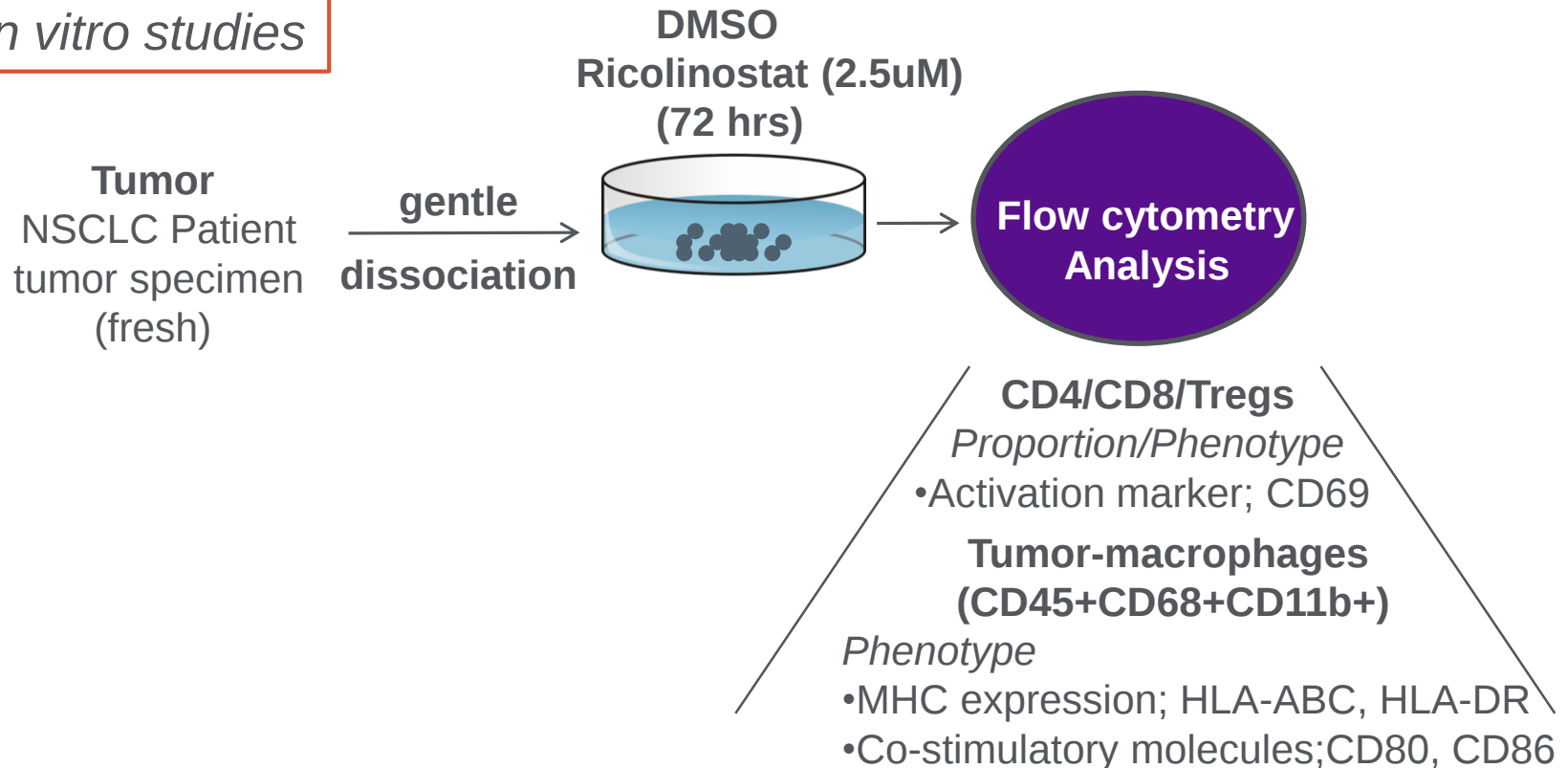
Effect on APC (macrophages)

Upregulation of MHC II assembly genes under ACY1215 treatment



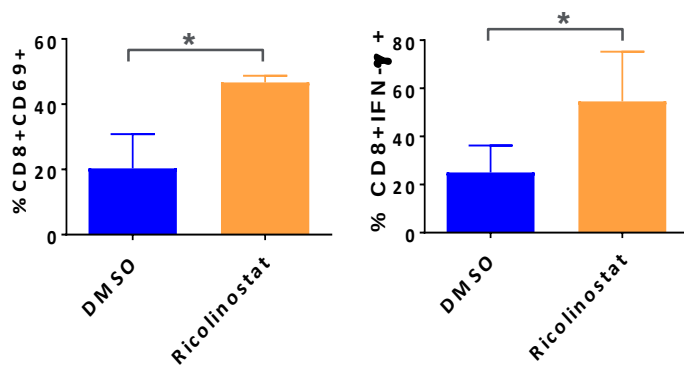
Human immunomodulatory properties of ACY1215

In vitro studies

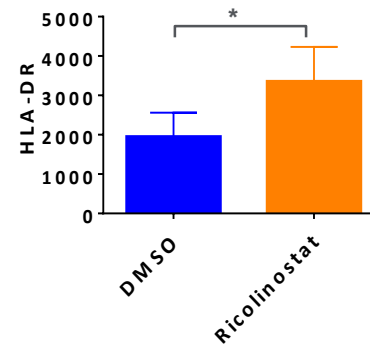


ACY1215 promotes immune-enhancing phenotypic and functional changes in human tumor-immune cell subsets

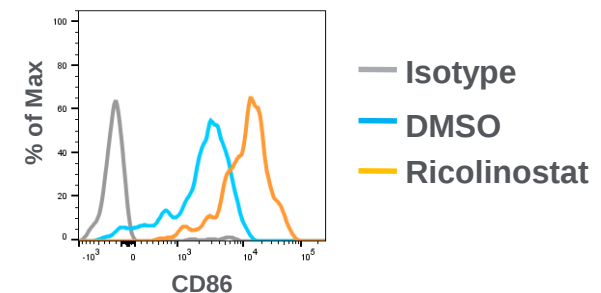
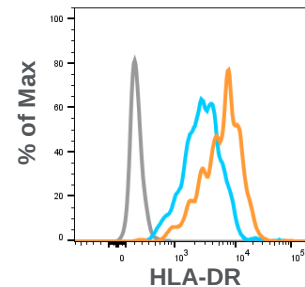
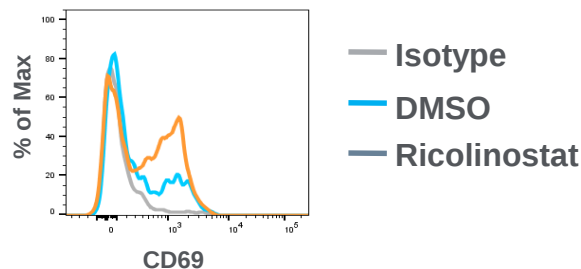
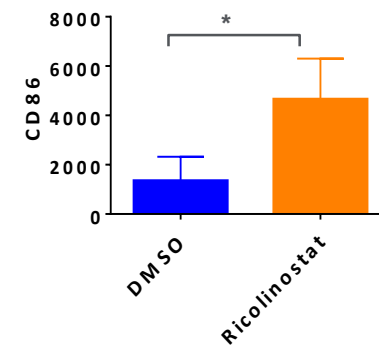
Increased T cell
Activation and function



Increased MHC II
(antigen presentation)



Increased CD86
(co-stimulation)

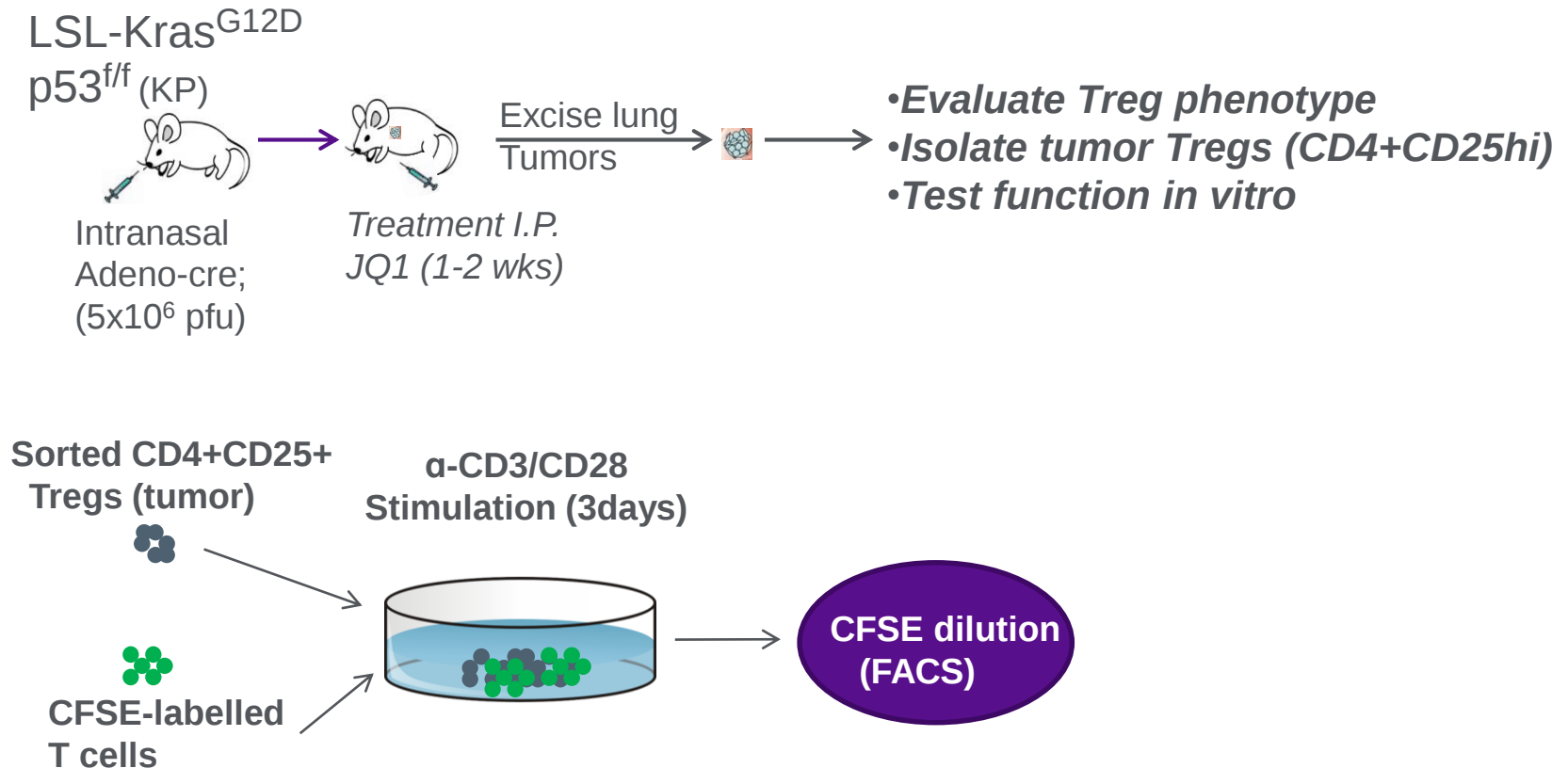


CD45+CD68+CD11b+
Tumor macrophages

Epigenetics regulation in cancer: Bromodomain inhibitors

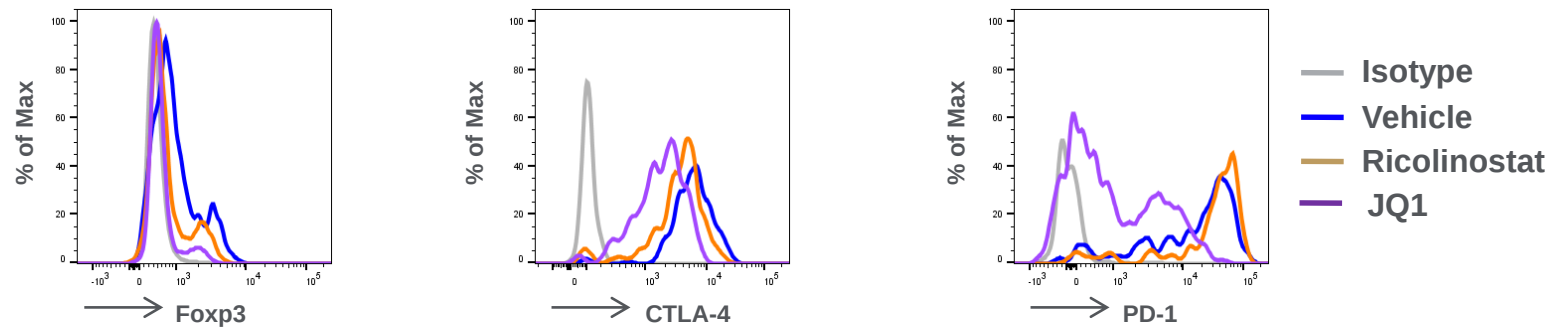
- Bromodomains are unique amino acid domains which act as readers of lysine acetylation thus are involved in epigenetic regulation
- The utility of inhibitors of bromodomain proteins (BrDi) are also being explored in many cancer indications
 - JQ1, an inhibitor of the BET family of bromodomain proteins (BRD2,3,4, and BRDT) has shown efficacy in hematologic malignancies such as AML and multiple myeloma
- A number of ongoing clinical trials are exploring therapeutic efficacy of BrDi in solid cancers
- There is paucity of data on their effects on tumor-associated immune cells

Evaluation of JQ1 effects on tumor-immune suppressive T cells

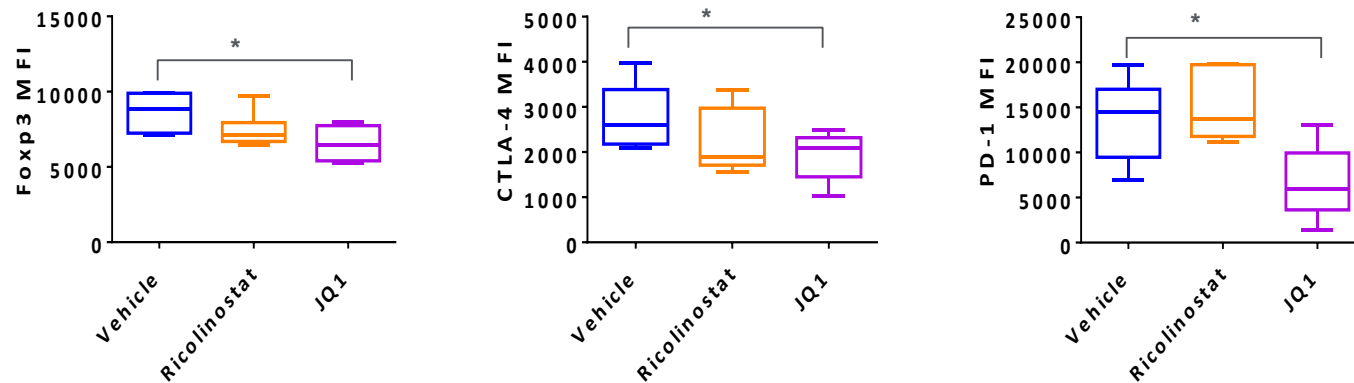


JQ1 alters the phenotype of suppressive Treg cells

A

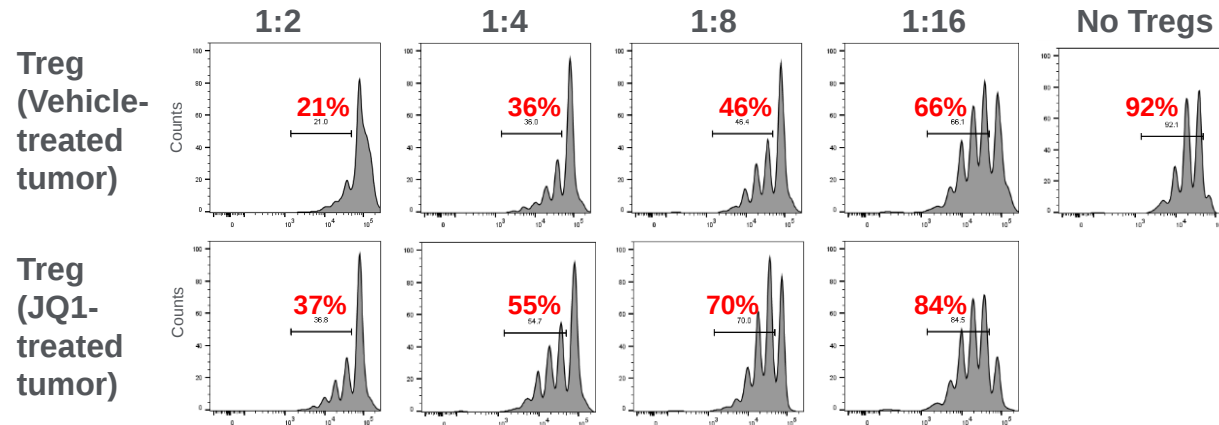


B

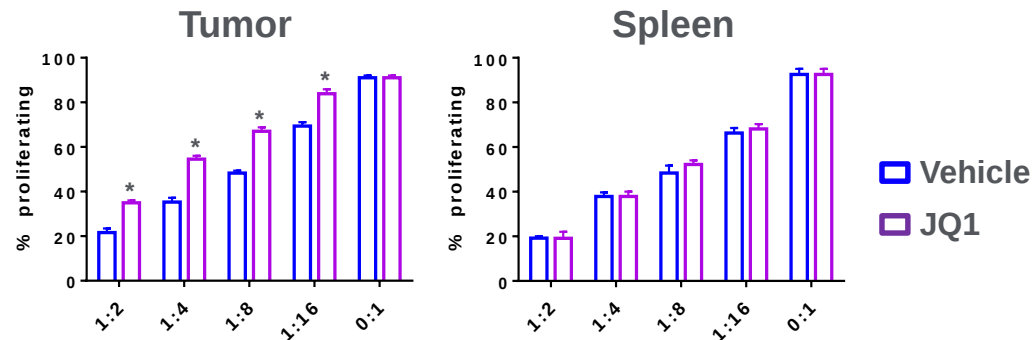


JQ1 disrupts the suppressive function of Tregs

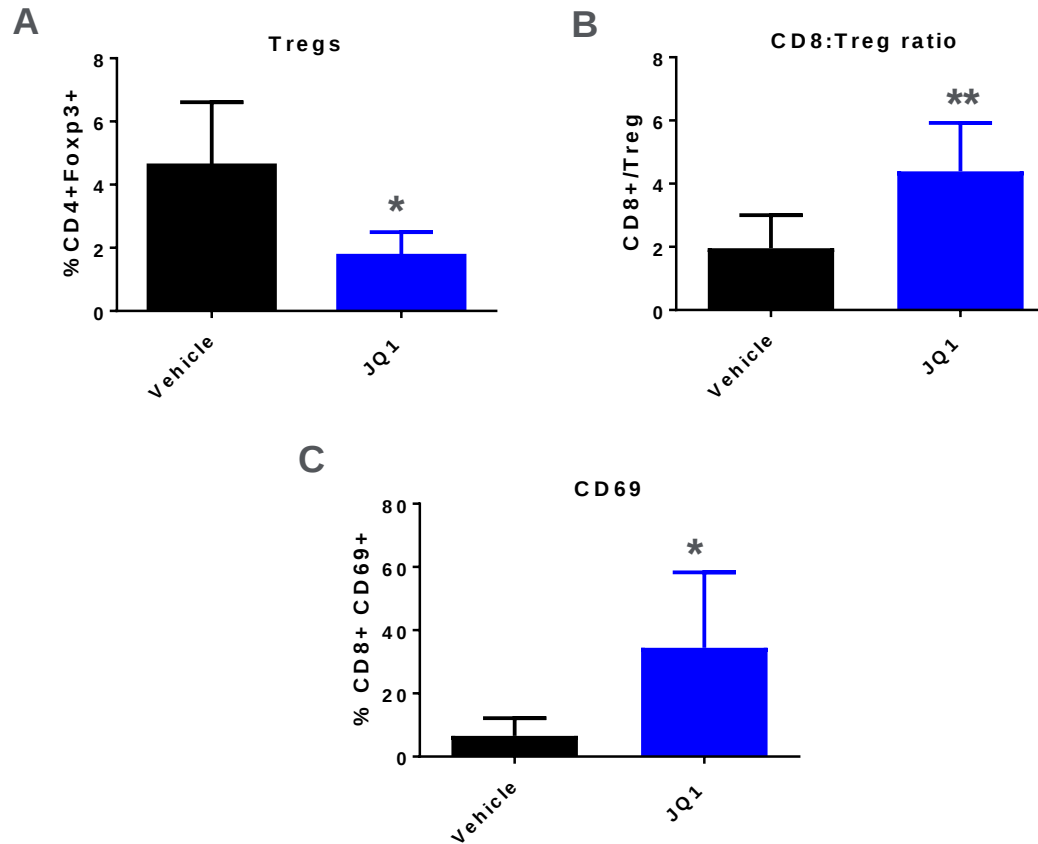
A



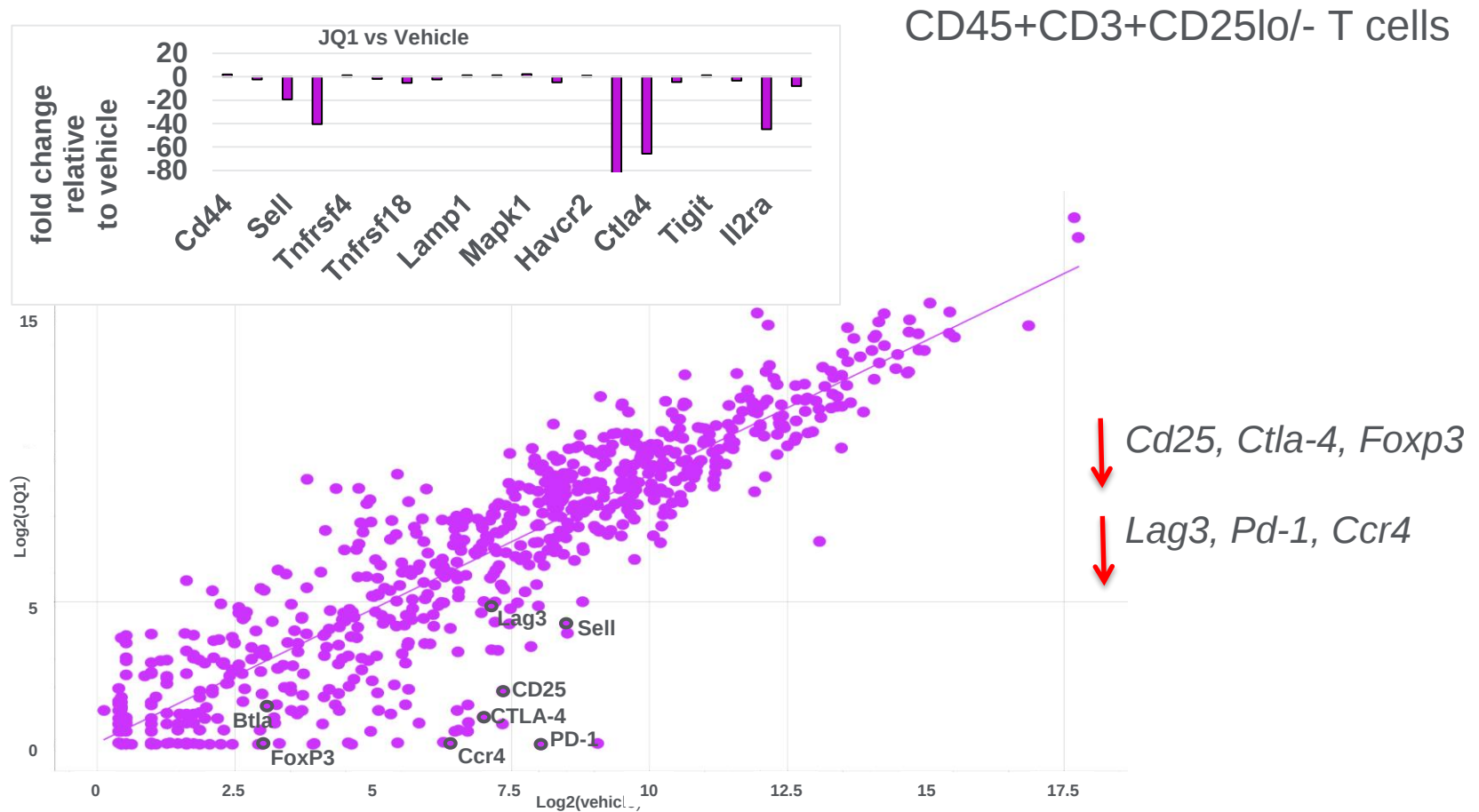
B



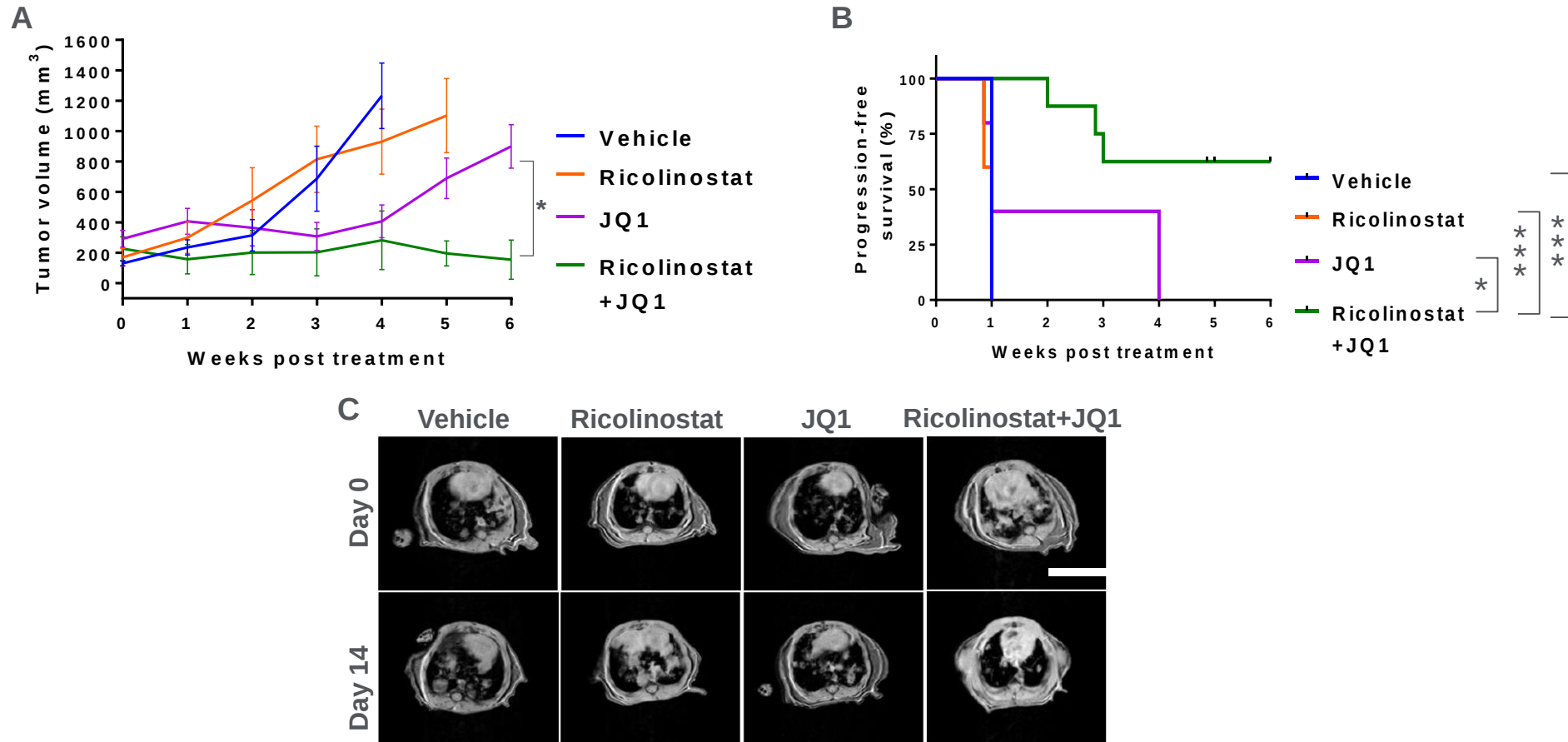
Effects of JQ1 on tumor-infiltrating immune cells in GEM (KP)



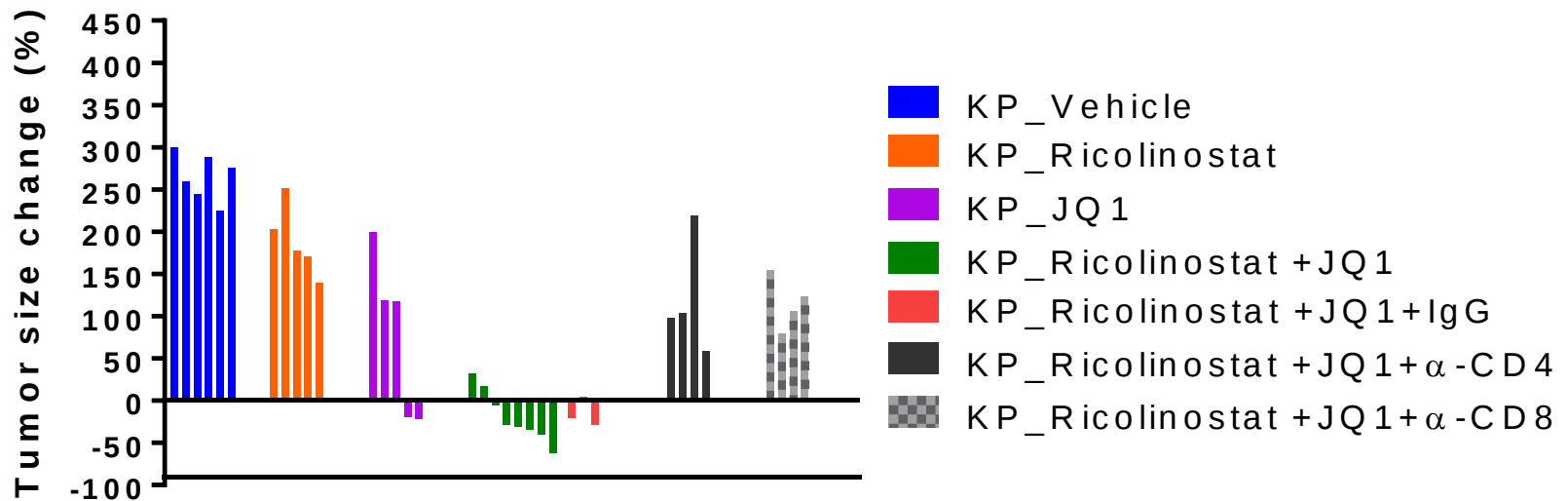
Down regulation of Treg-associated/immune checkpoint genes under JQ1 treatment



Combination of ACY1215 and JQ1 promotes durable anti-tumor response in GEM (KP)

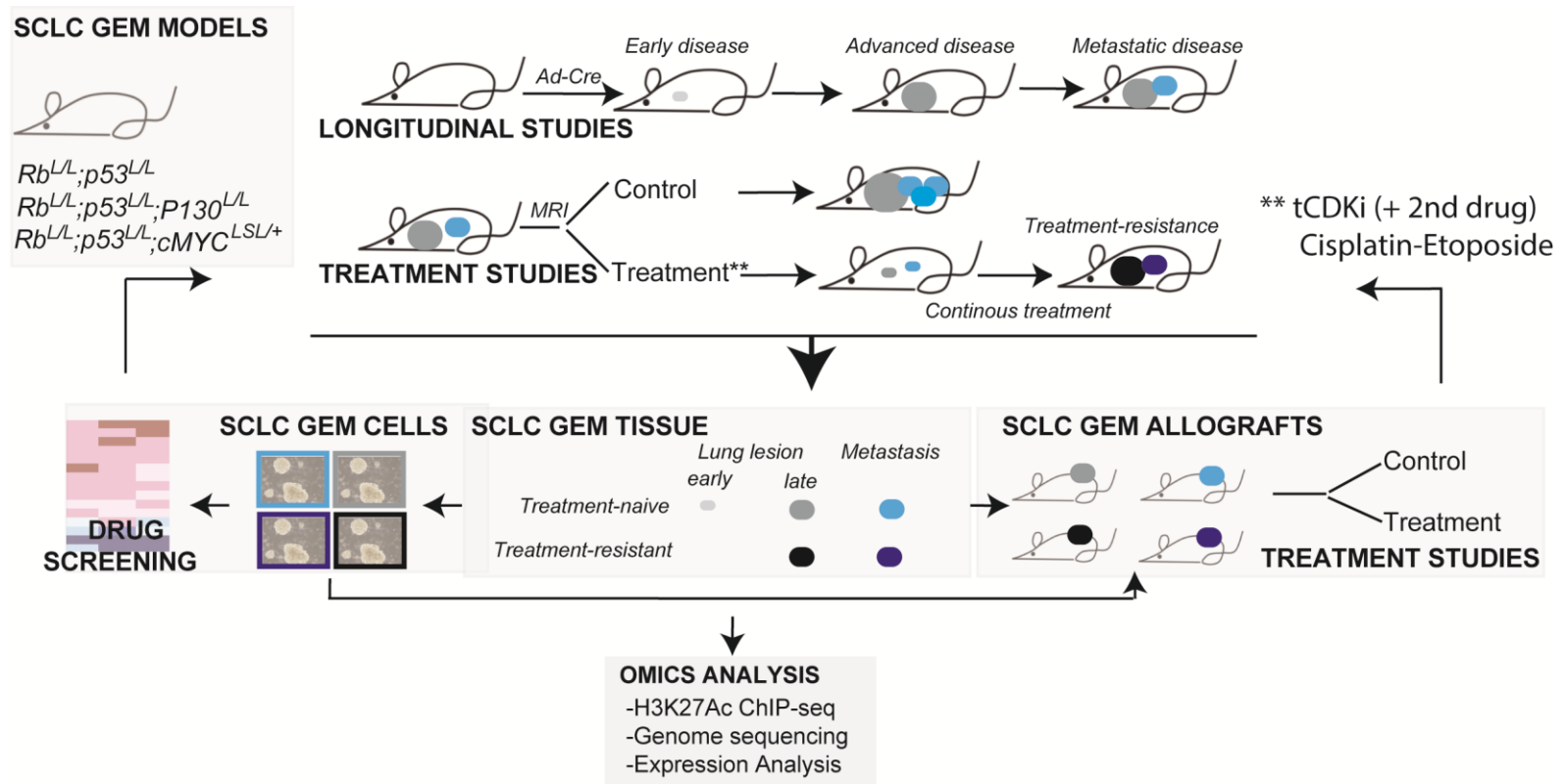


Immunotherapeutic effect of ACY1215 and JQ1 is dependent on both CD4+ and CD8+ T cell presence

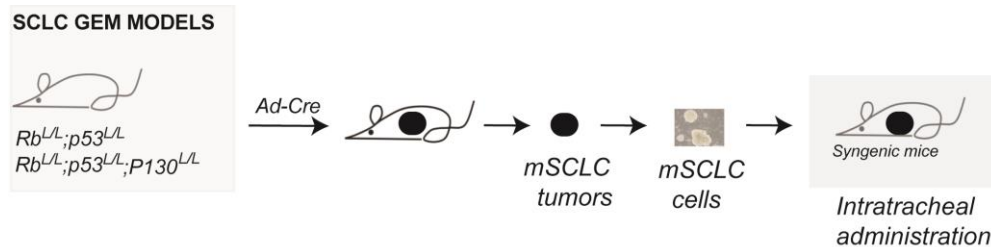


Metastatic murine small cell lung cancer preclinical models and new genomic technologies to interrogate TME

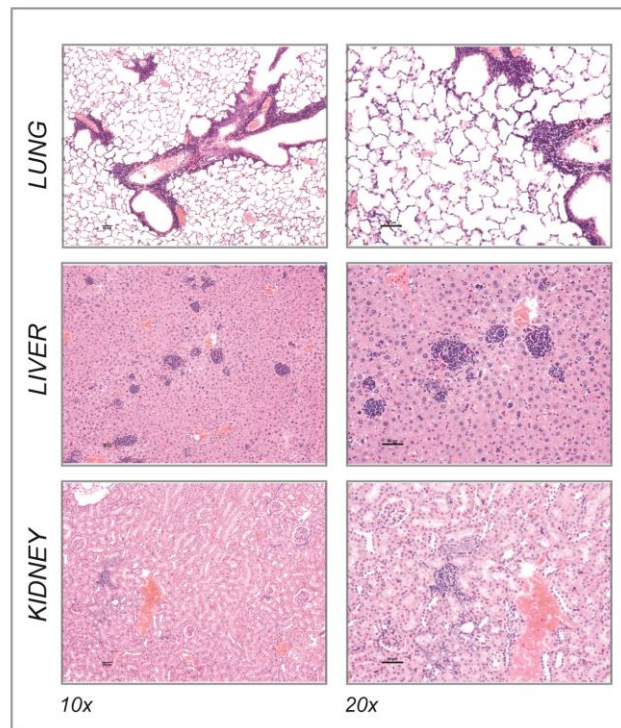
Investigation of the SCLC treatment-naïve and resistant tumor microenvironment - SCLC GEM model-based platform



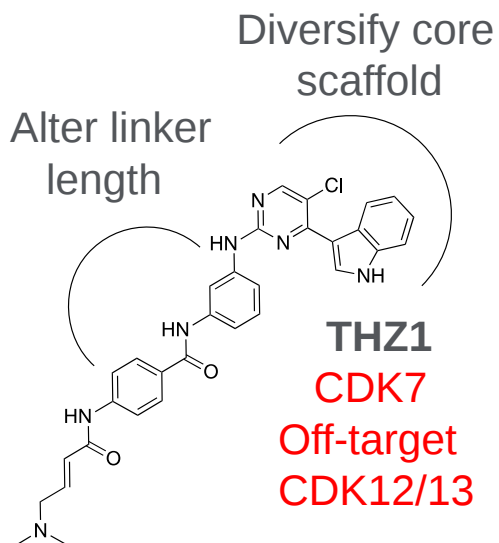
Investigation of the SCLC treatment-naïve and resistant tumor microenvironment - SCLC GEM model-based platform



16 weeks post cell administration

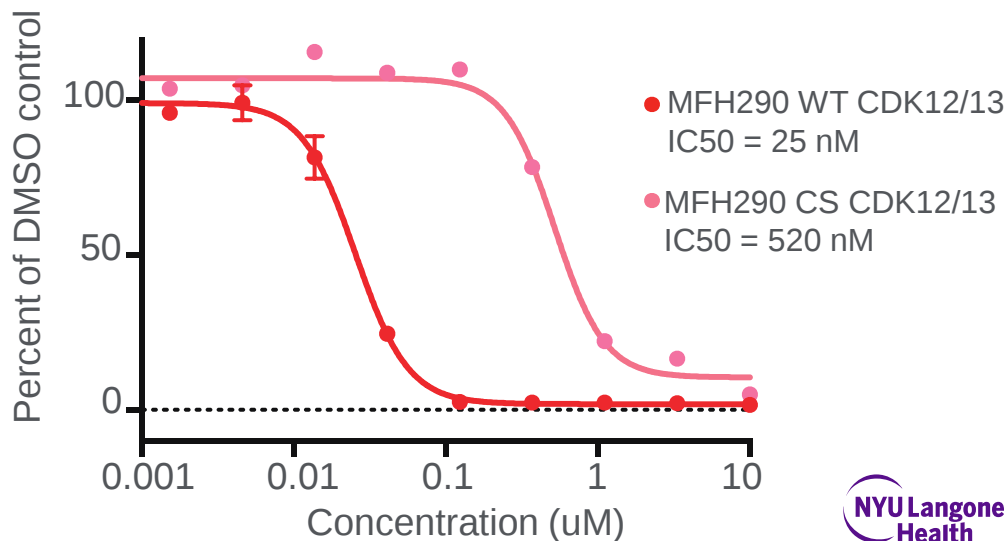
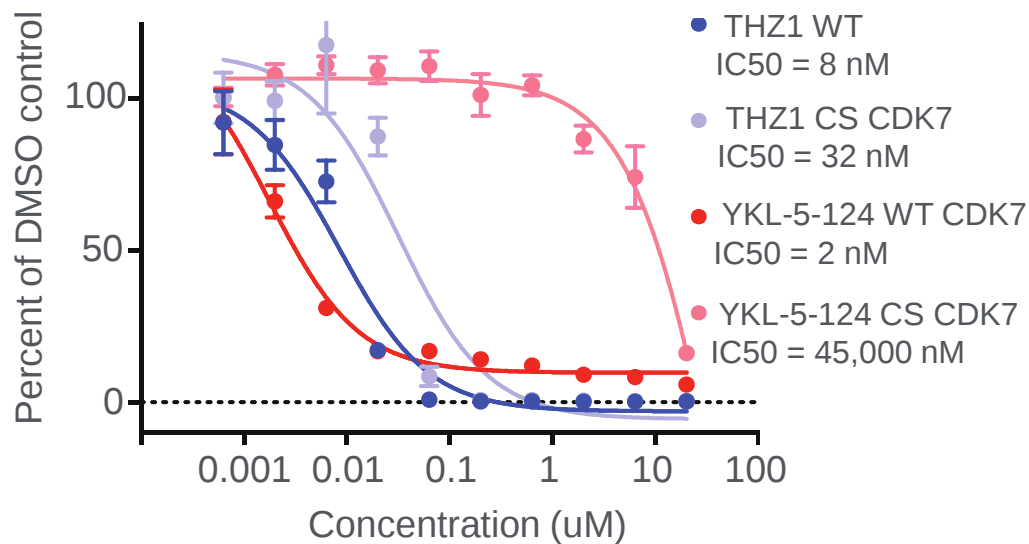


Medical chemistry beyond THZ1

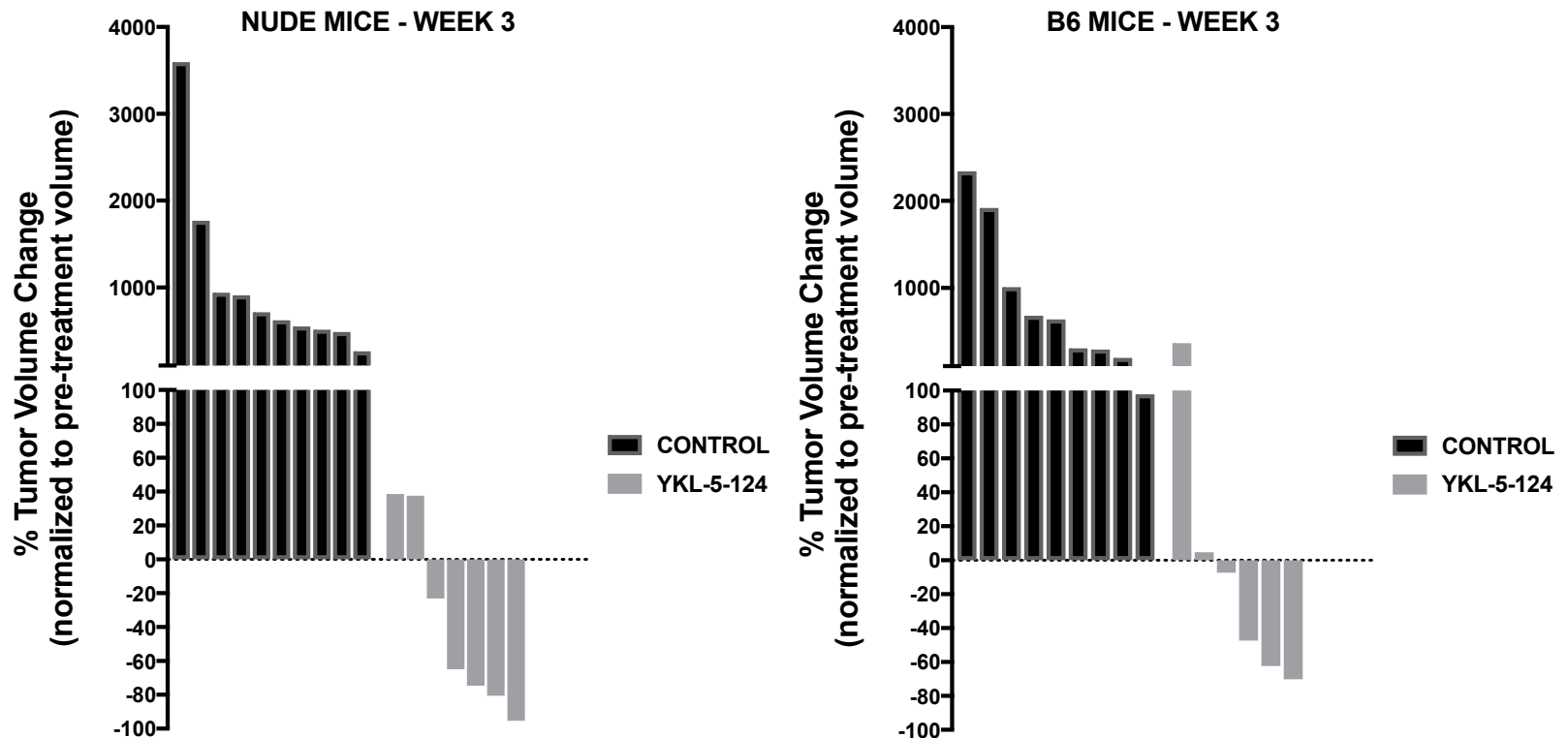


YKL-5-124
CDK7

MFH290
CDK12/13



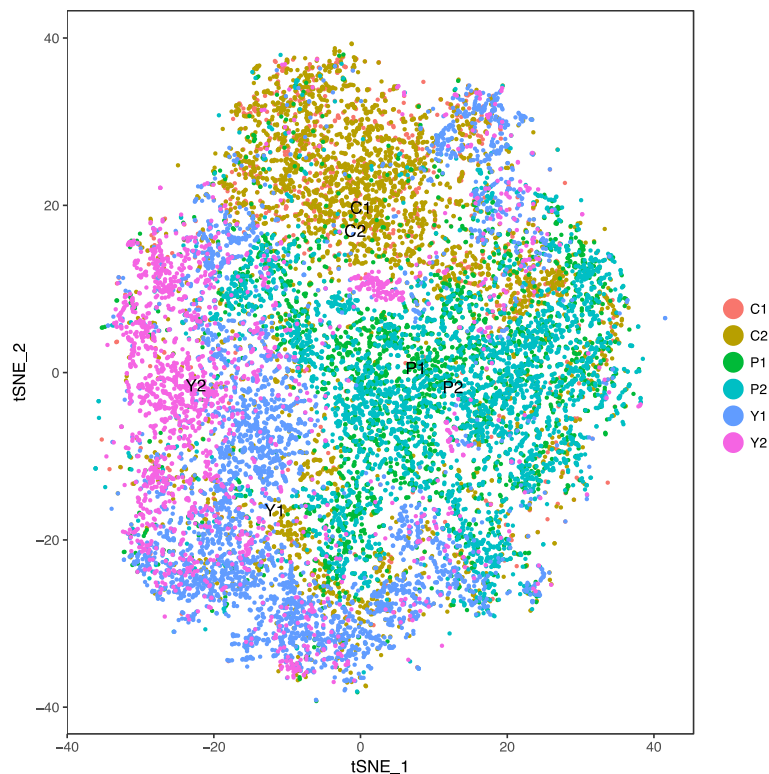
Investigation of the SCLC treatment-naïve and resistant tumor microenvironment - YKL5-124 treatment



Cancer Cells

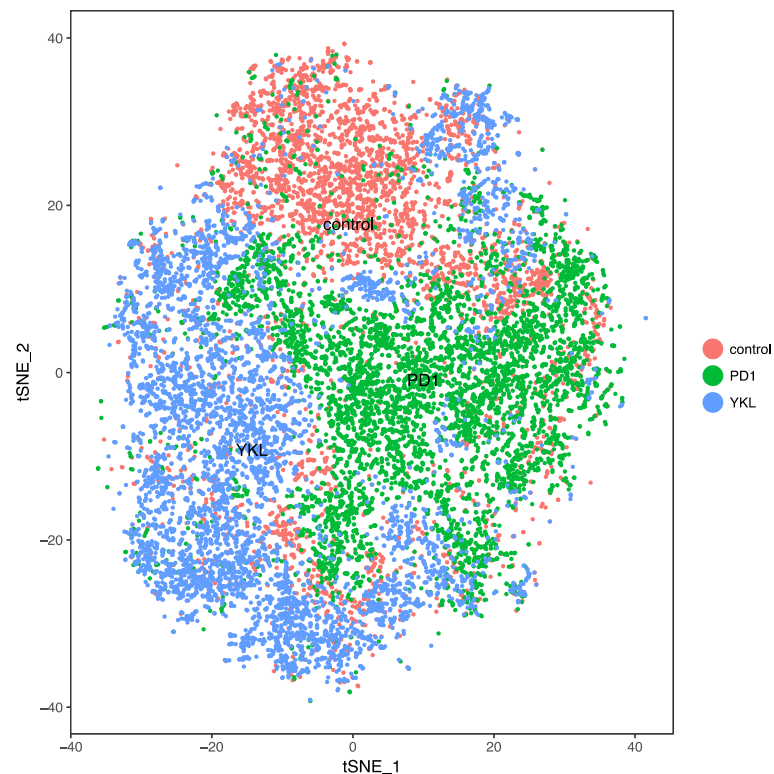
Biological replicates cluster together

- limited batch effects
- reproducible effects



Conditions (treatments + control) cluster together

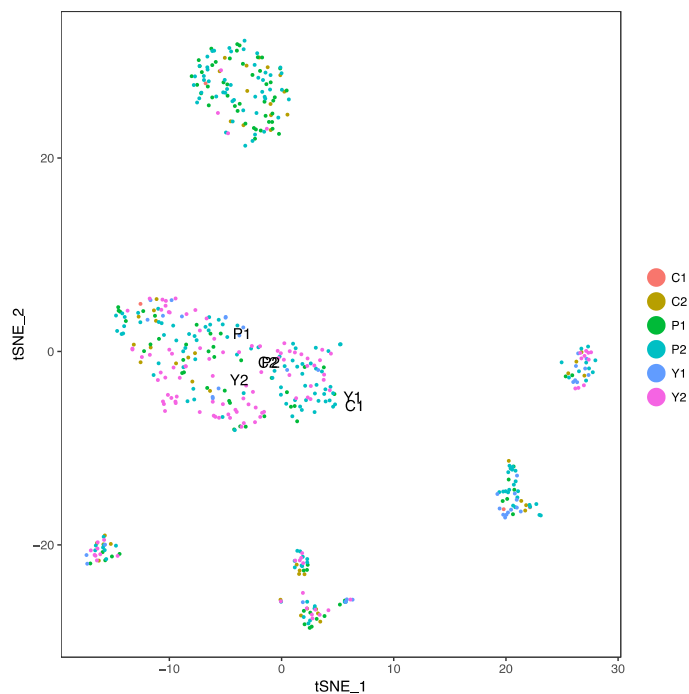
- treatment results in strong transcriptional effect



Immune Cells

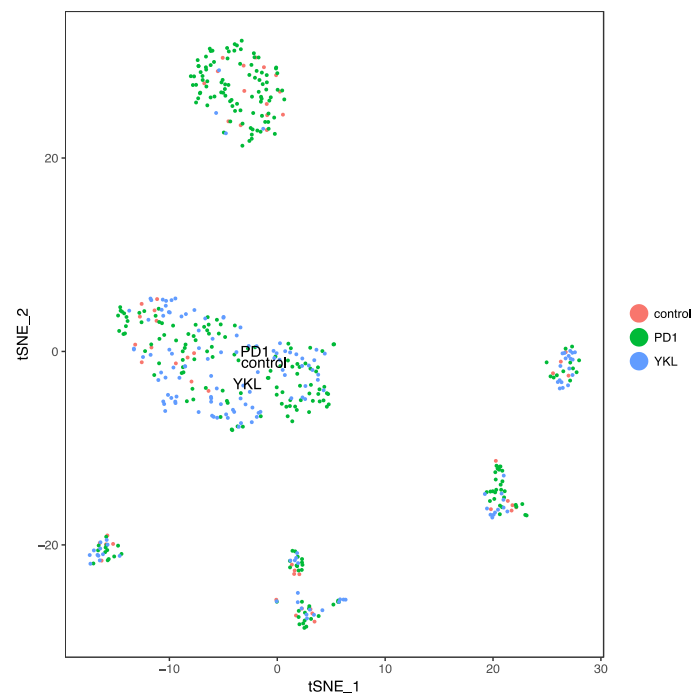
Biological replicates cluster together

- limited batch effects
- reproducible effects



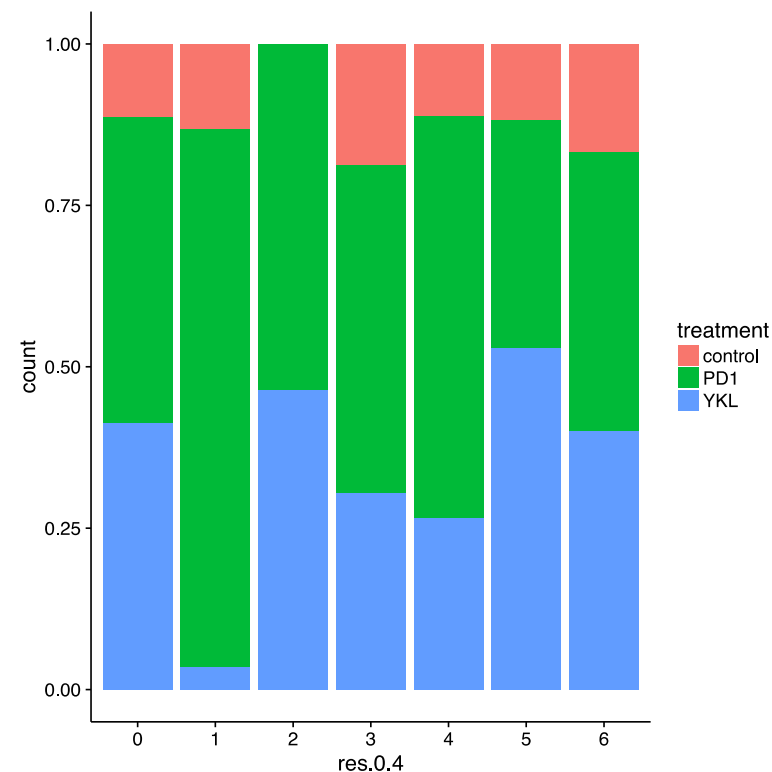
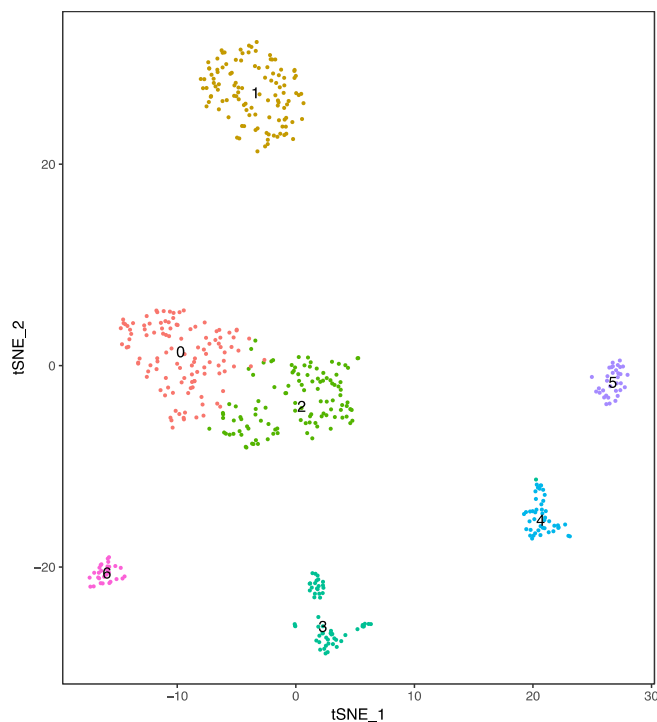
Conditions (treatments + control) do NOT cluster together

- major differences in mRNA abundance is due to different cell types



Immune Cells

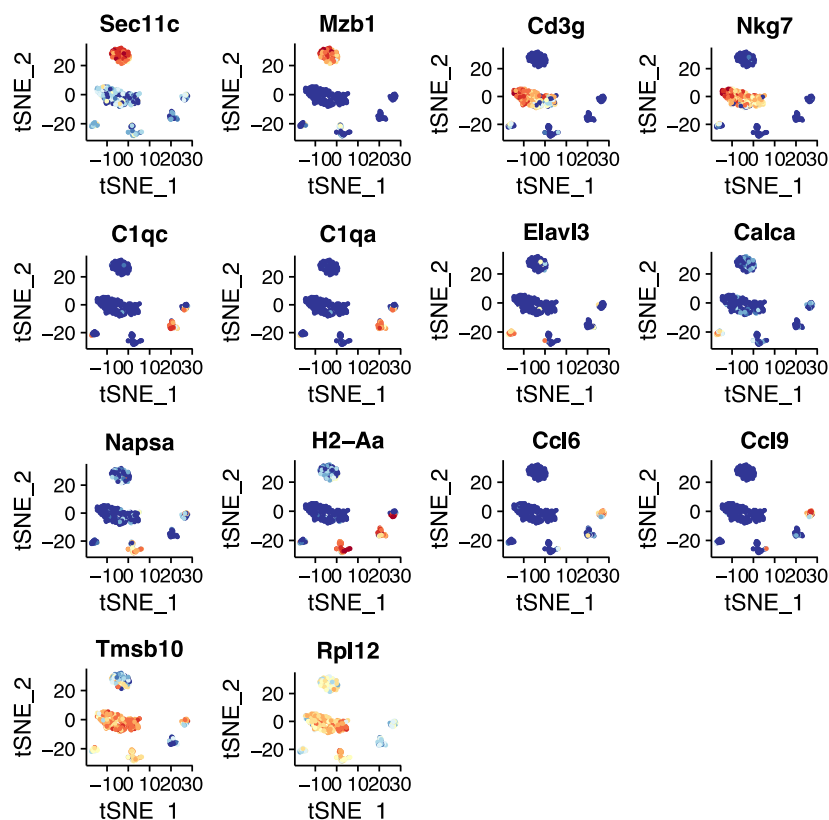
- Distribution of conditions in different identified clusters:
 - most clusters contain single-cells from all conditions, except cluster 2
 - cluster is enriched for single-cells from the PD1 treated samples



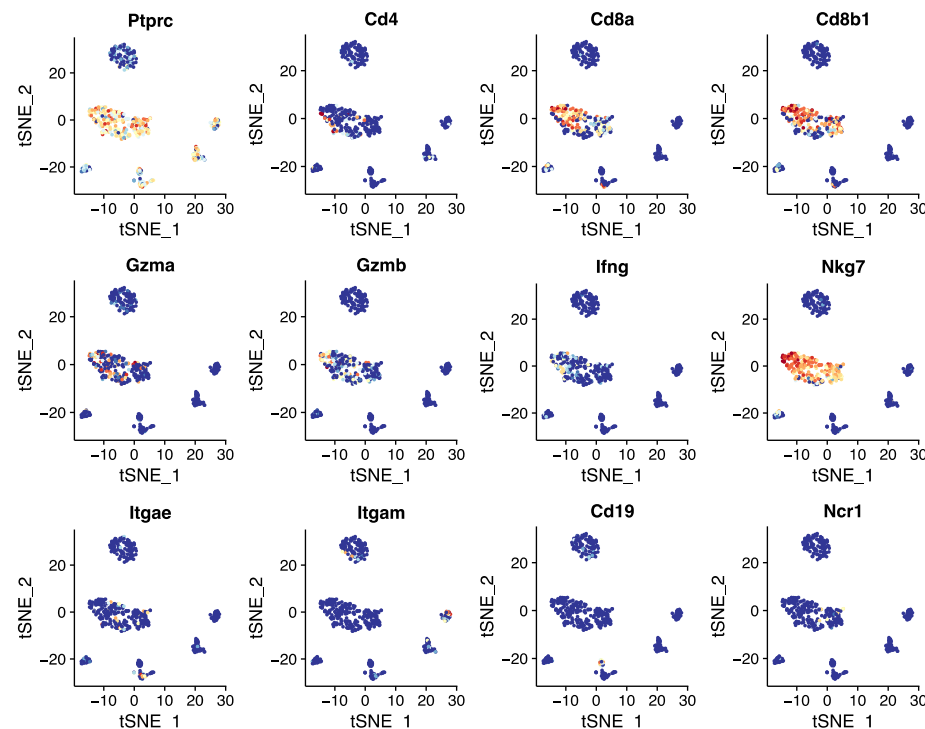
Immune Cells

- Based on New and Known markers, plus gene enrichment analysis, we could identify different types of immune cells: T cells, B cells, Dendritic cells, Macrophages, Monocytes, ... (fine-tuning in progress)

New markers



Known markers



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Cyril Benes MGH
Aaron Hata MGH

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