



Genetic manipulation of antitumor T cells to elicit durable clinical response in adoptive immunotherapy

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Society for Immunotherapy of Cancer

#SITC2019

Disclosure Information

SITC 2019 World Immunotherapy Council's 3rd Young Investigator Symposium

Yuki Kagoya

I have the following financial relationships to disclose:

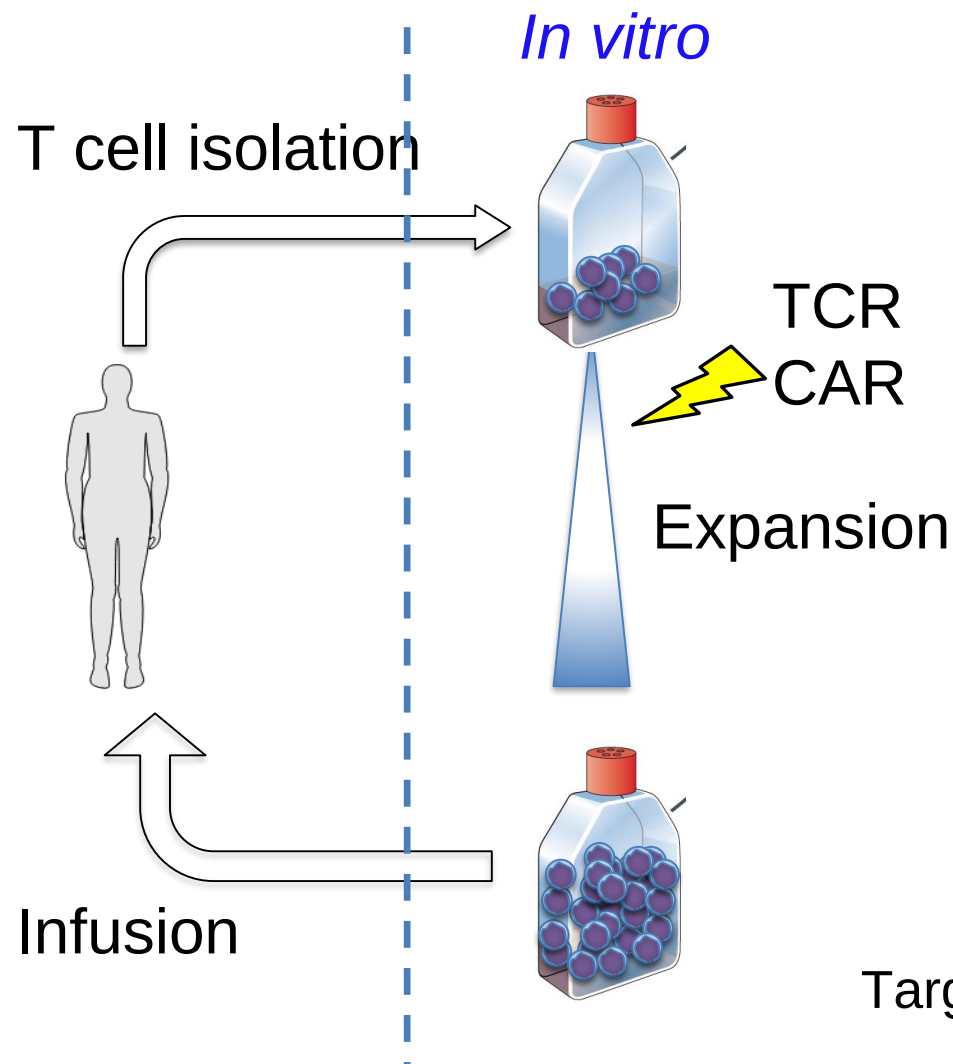
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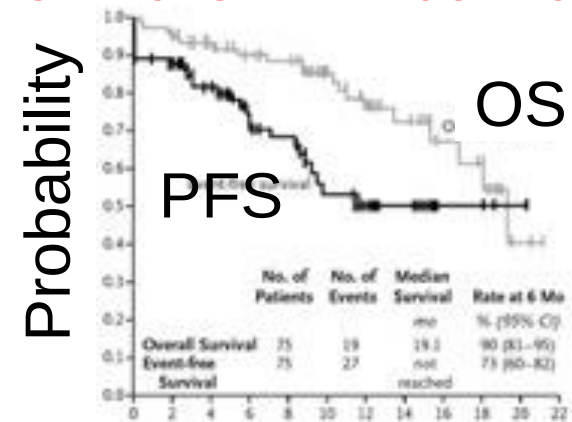
- and -

I will not discuss off label use and/or investigational use in my presentation.

Adoptive cancer immunotherapy

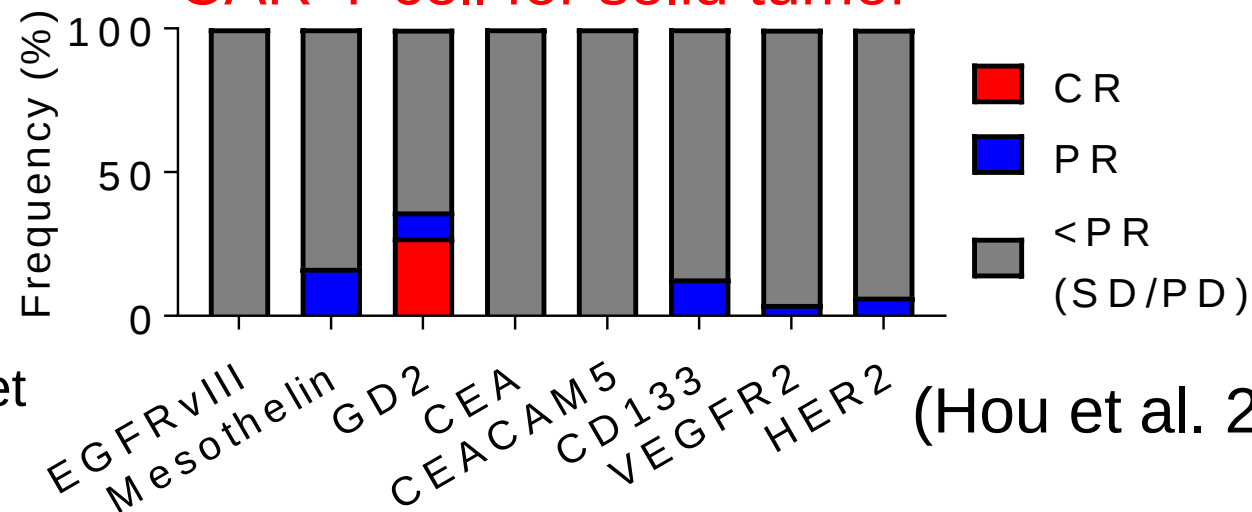


CD19 CAR-T cell for B-ALL



CR: 81%
OS: 90% (6 months)
(Maude et al. 2018)

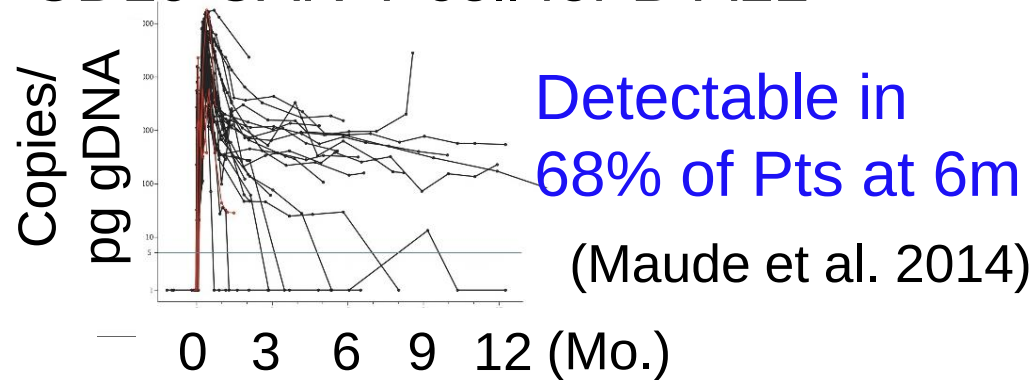
CAR-T cell for solid tumor



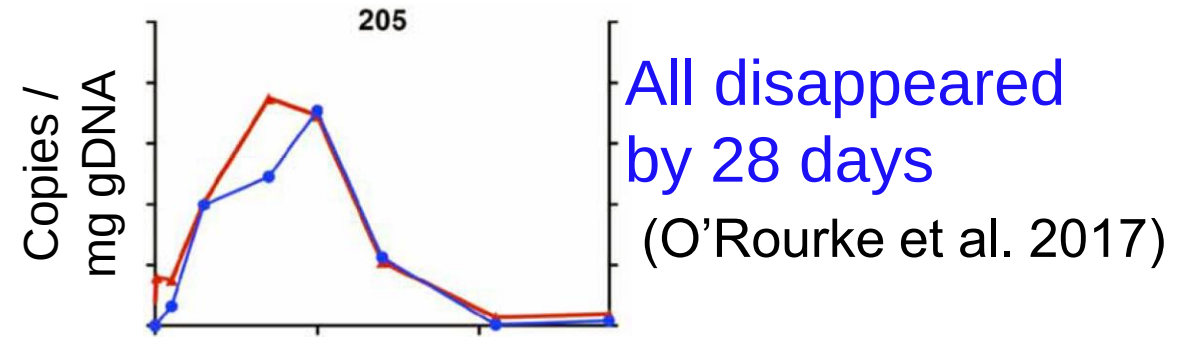
(Hou et al. 2019)

Poor persistence of infused antitumor T cells for solid tumor

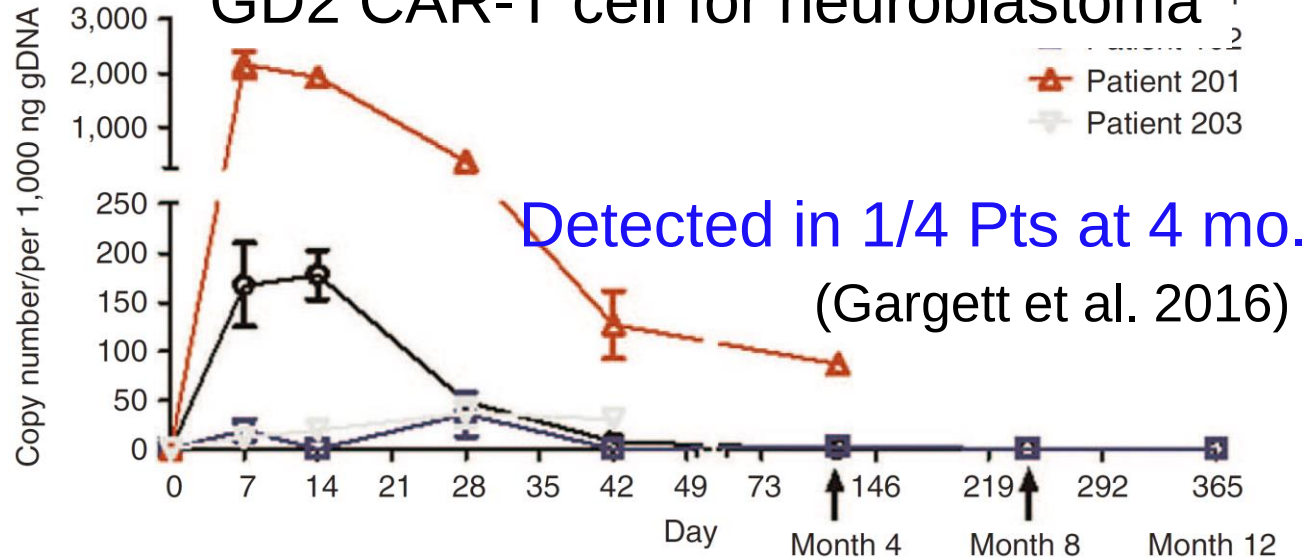
CD19 CAR-T cell for B-ALL



EGFRvIII CAR-T cell for glioblastoma

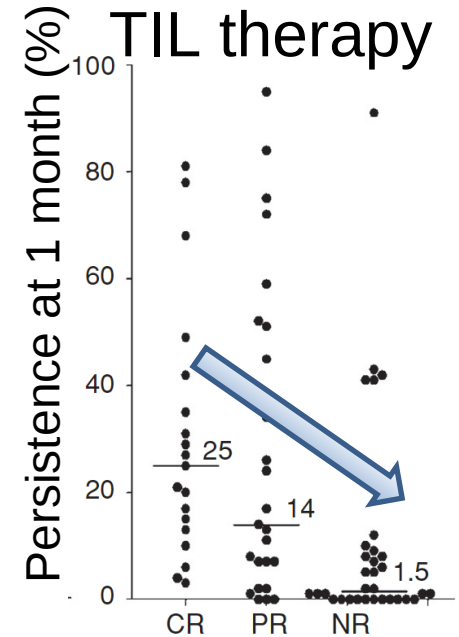


GD2 CAR-T cell for neuroblastoma

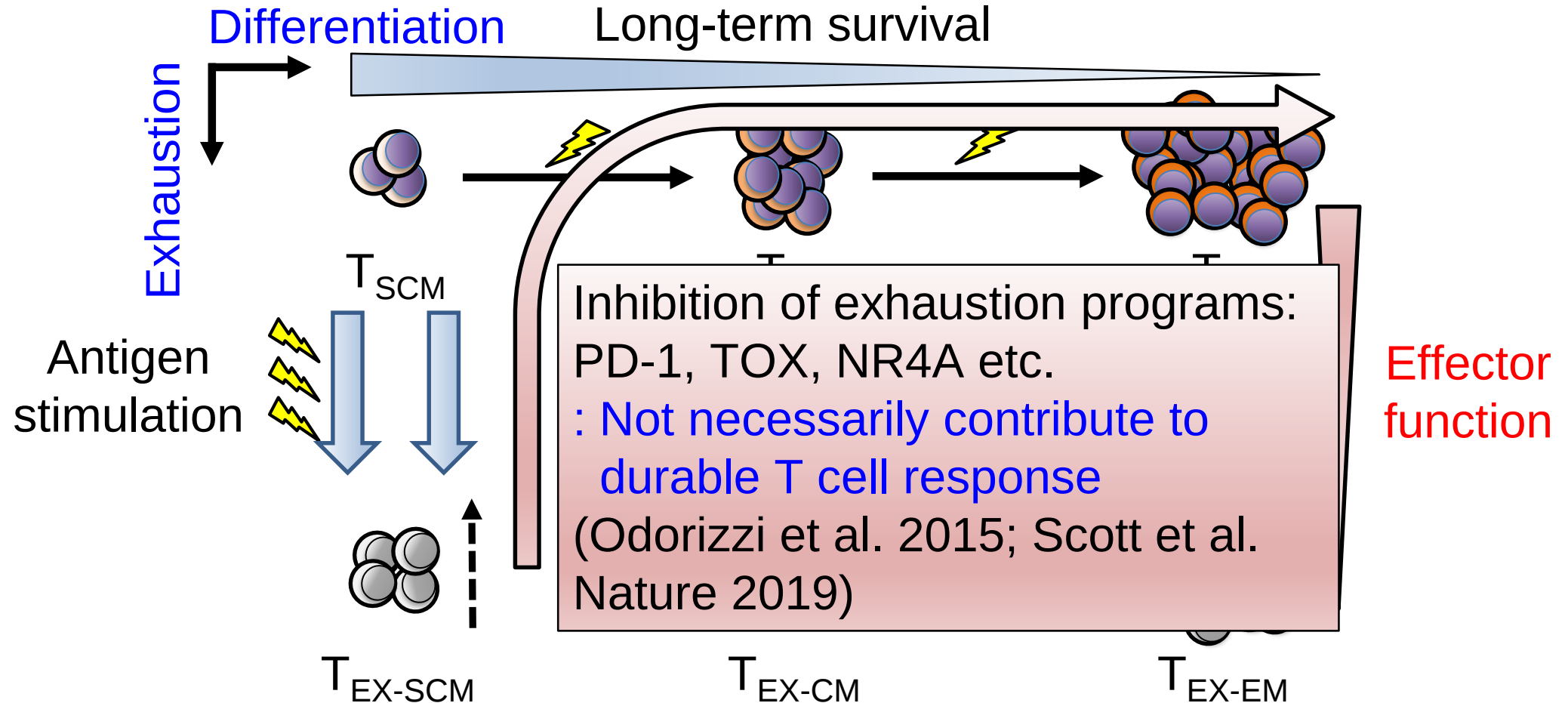


Persistence was correlated with treatment response

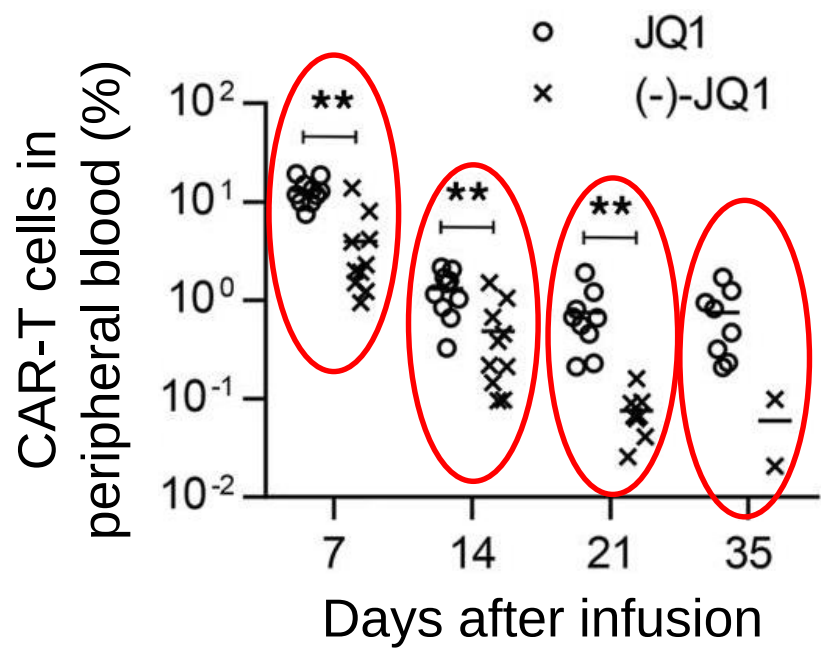
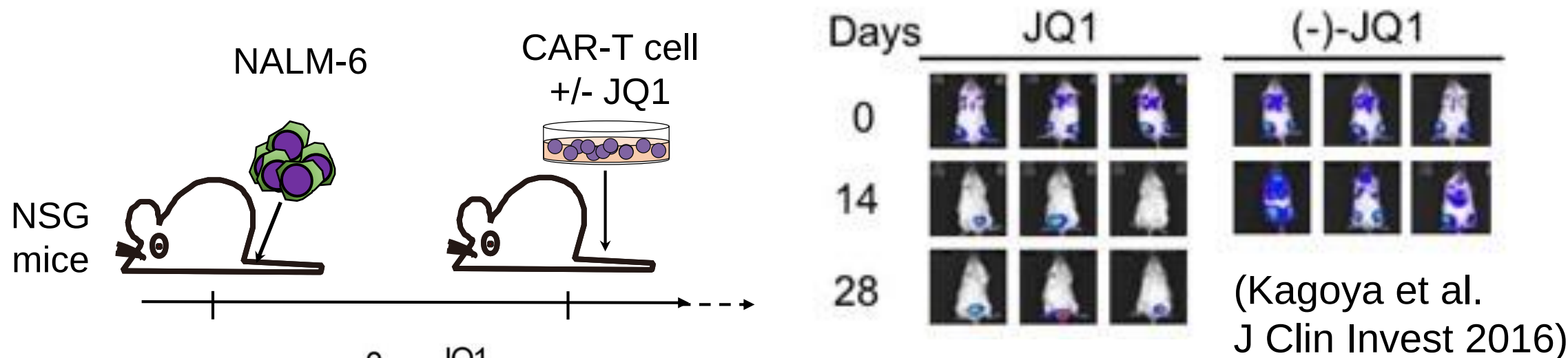
(Rosenberg et al. Clin Cancer Res 2011)



Factors to determine durable antitumor response: T cell differentiation and exhaustion



Suppression of effector programs *in vitro* enhances T cell persistence *in vivo*



JQ1 treatment increased CAR-T cell persistence early after infusion

→ Is it possible to enhance *in vivo* T cell persistence more sustainably?

TET2 ablation promotes T cell survival

LETTER

One of the most frequently mutated genes in T cell lymphoma

<https://doi.org/10.1038/s41586-018-0178-z>

Disruption of *TET2* promotes the therapeutic efficacy of CD19-targeted T cells

Joseph A. Fraietta^{1,2,3,4}, Christopher L. Nobles⁵, Morgan A. Sammons^{6,10}, Stefan Lundh^{1,2}, Shannon A. Carty^{2,11}, Tyler J. Reich^{1,2}, Alexandria P. Cogdill^{1,2}, Jennifer J. D. Morrisette³, Jamie E. DeNizio^{7,8}, Shantanu Reddy⁵, Young Hwang⁵, Mercy Gohil^{1,2}, Irina Kulikovskaya^{1,2}, Farzana Nazimuddin^{1,2}, Minnal Gupta^{1,2}, Fang Chen^{1,2}, John K. Everett⁵, Katherine A. Alexander⁶, Enrique Lin-Shiao⁶, Marvin H. Gee⁹, Xiaojun Liu^{1,2}, Regina M. Young^{1,2}, David Ambrose^{1,2}, Yan Wang^{1,2}, Jun Xu^{1,2}, Martha S. Jordan^{2,3}, Katherine T. Marcucci^{1,2}, Bruce L. Levine^{1,2,3}, K. Christopher Garcia⁹, Yangbing Zhao^{1,2}, Michael Kalos^{1,2,3}, David L. Porter^{1,2,7}, Rahul M. Kohli^{5,7,8}, Simon F. Lacey^{1,2,3}, Shelley L. Berger⁶, Frederic D. Bushman⁵, Carl H. June^{1,2,3,4*} & J. Joseph Melenhorst^{1,2,3,4*}

Fraietta et al. Nature 2018

Hypothesis: Genetic programs underlying T cell lymphoma development may enhance peripheral T cell survival

Recurrent genetic aberrations in T cell malignancies

PTCL-NOS

Genes	Freq (%)	Function
<i>TET2</i>	46-49	LoF
<i>DNMT3A</i>	27-36	LoF
<i>RHOA</i>	8-18	Complex
<i>FYN</i>	3	GoF
<i>VAV1</i>	11	Active (fusion)
<i>CDKN2A/2B</i>	9	Deletion

ALK-negative ALCL

Genes	Freq (%)	Function
<i>JAK1</i>	15	Active
<i>STAT3</i>	10	Active
<i>TET2</i>	33	LoF
<i>DNMT3A</i>	16	LoF
<i>DUSP22</i>	30	Downregulated
<i>PRDM1</i>	56	Deletion

Extranodal NK/T cell lymphoma

Genes	Freq (%)	Function
<i>TP53</i>	18-24	LoF
<i>JAK3</i>	35	Active
<i>DDX3X</i>	20	LoF
<i>STAT3</i>	6	Active
<i>STAT5B</i>	6	Active

AITL

Genes	Freq (%)	Function
<i>TET2</i>	76-83	LoF
<i>DNMT3A</i>	26-38	LoF
<i>RHOA</i>	50-71	LoF
<i>IDH2</i>	20-45	LoF/GoF

(Sandell et al. 2017)
(Keersmaecker et al. 2013)

Exploration of lymphoma genes to improve CAR-T cell function

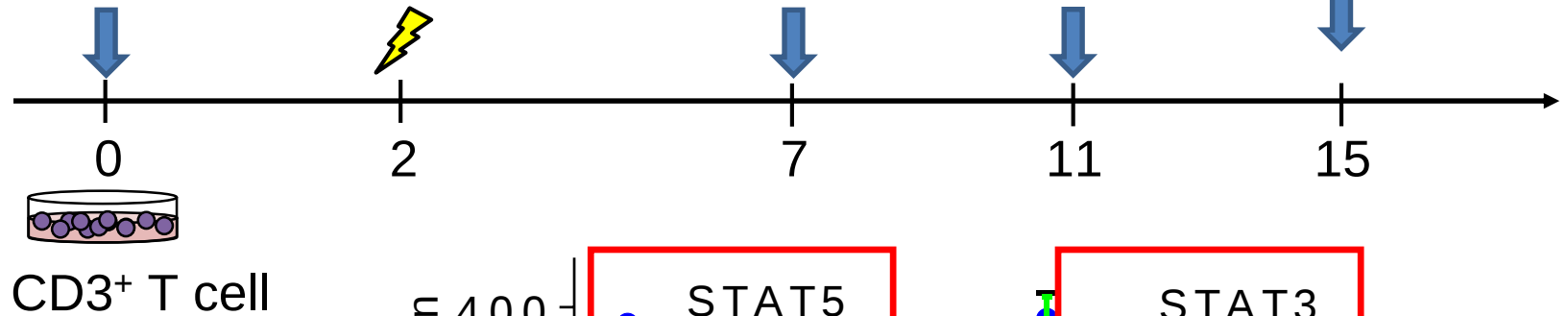
Lymphoma genes	P2A	Δ NGFR
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DNMT3A R882H
IDH2 R172K
JAK3 A572V
RHOA G17V
STAT3 Y640F
STAT5 N642H
VAV1 Δ aa778-786

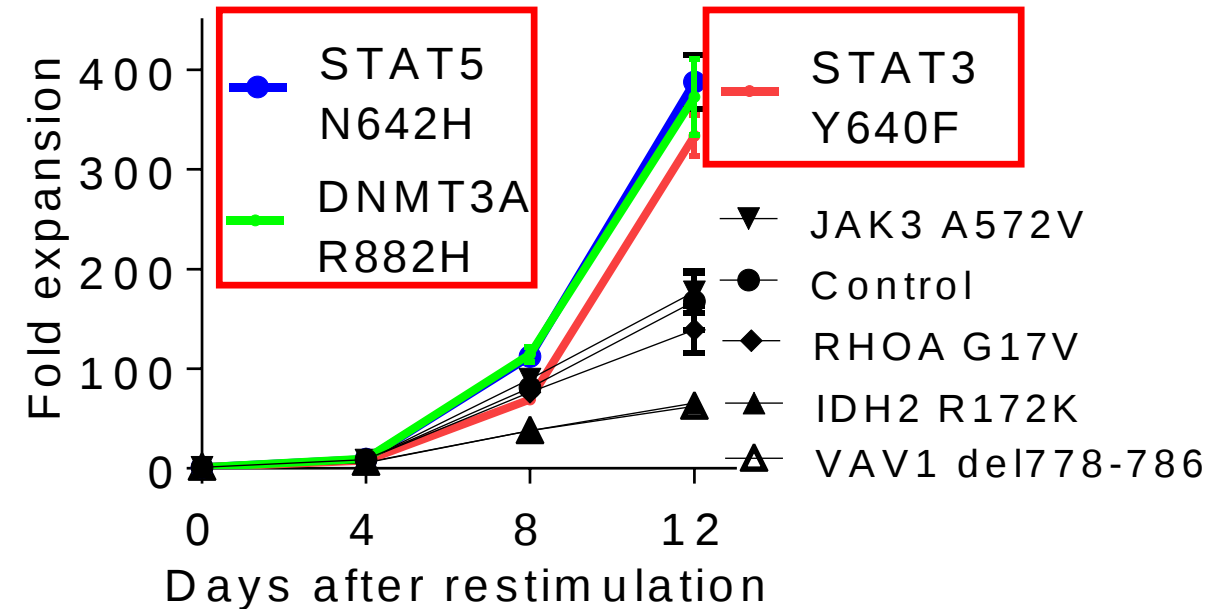
Stimulation
(α CD3/CD80)

Lymphoma
gene (RV)

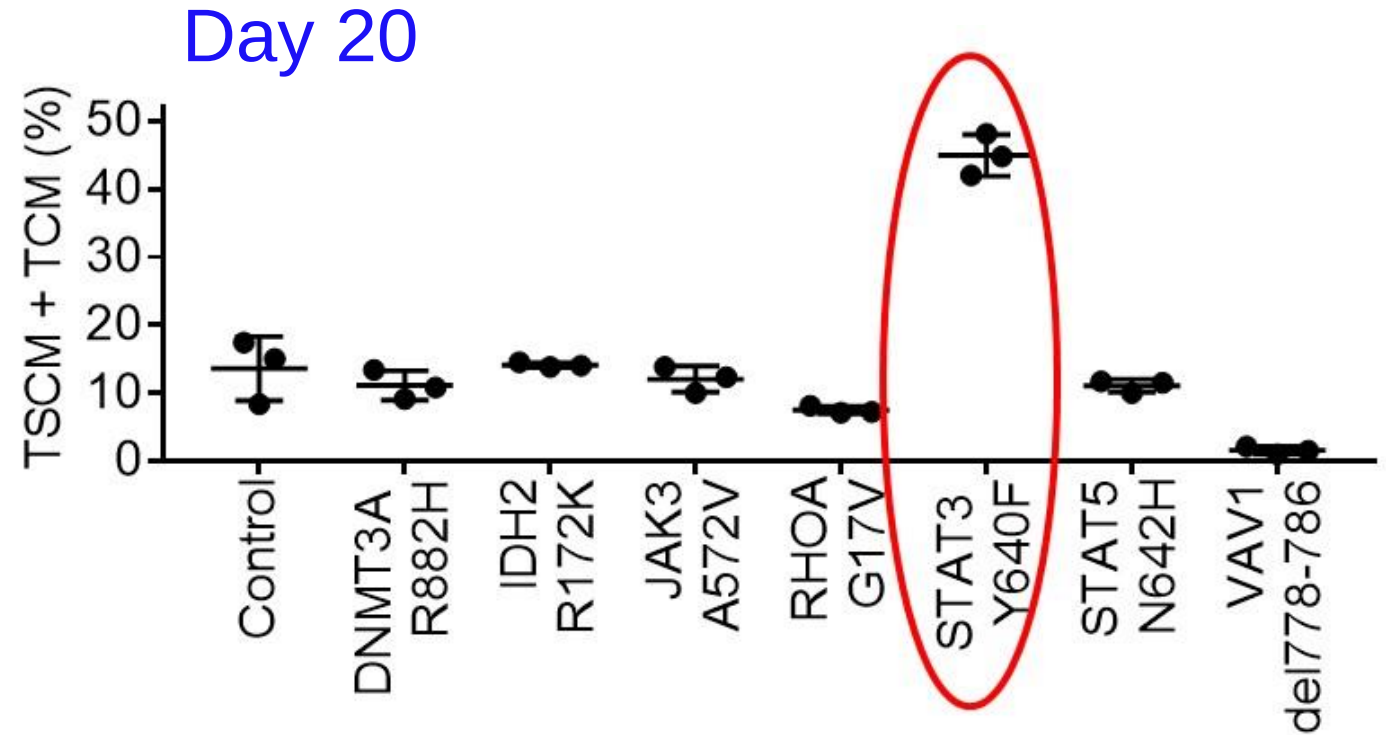
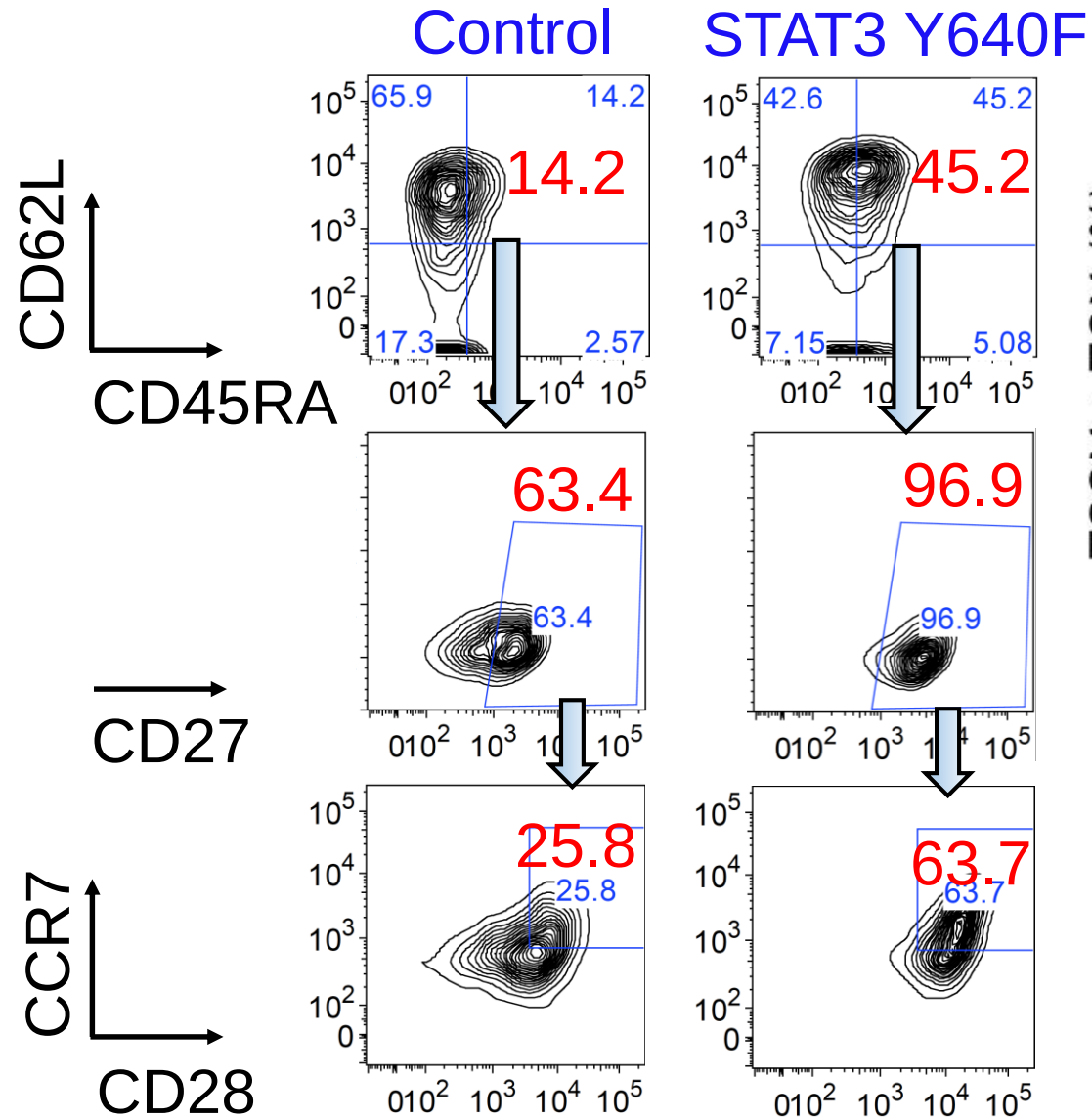
Restimulation
(α CD3/CD80)



**DNMT3A, STAT3, STAT5
mutations enhanced T cell
proliferation**

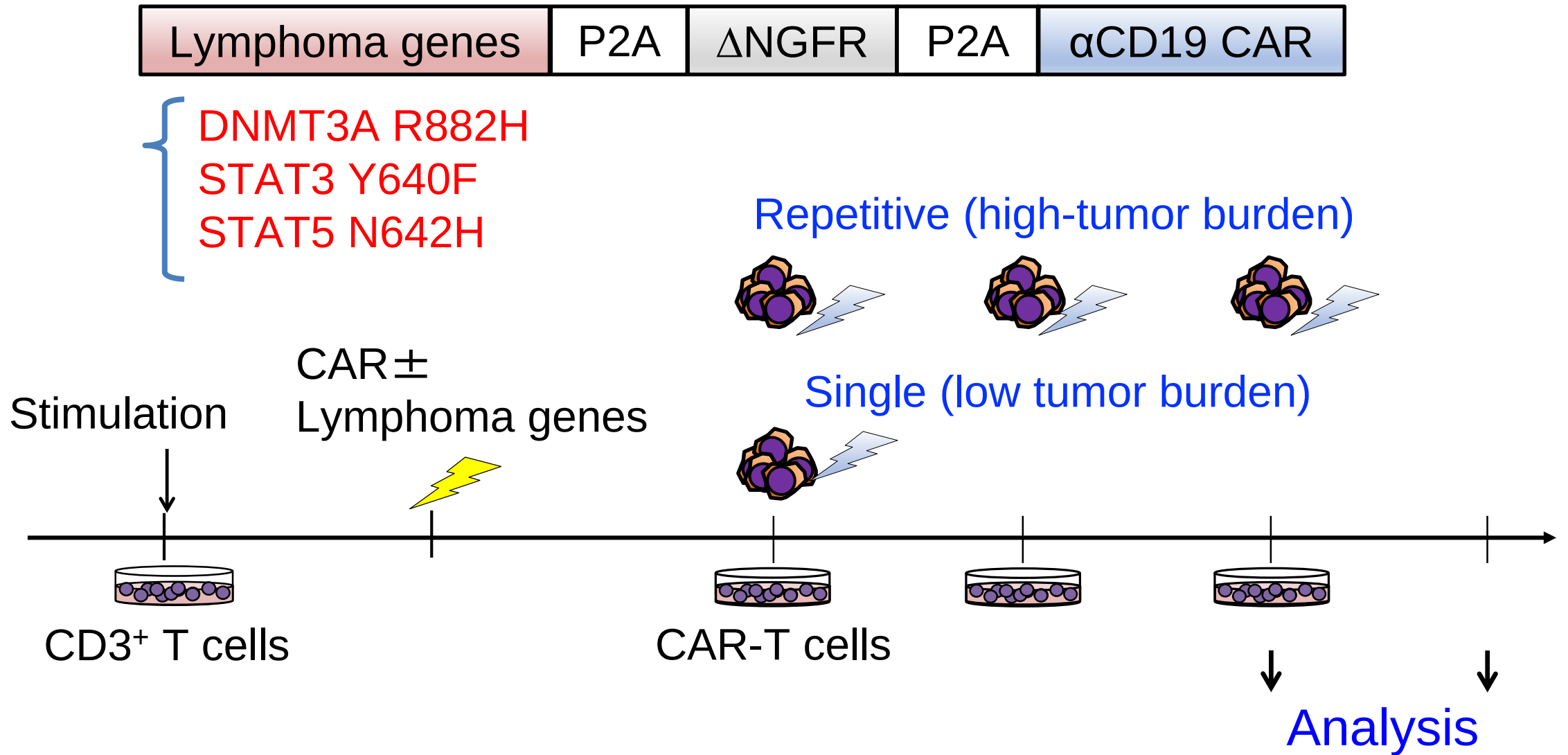


STAT3 activation helps maintain an early memory phenotype



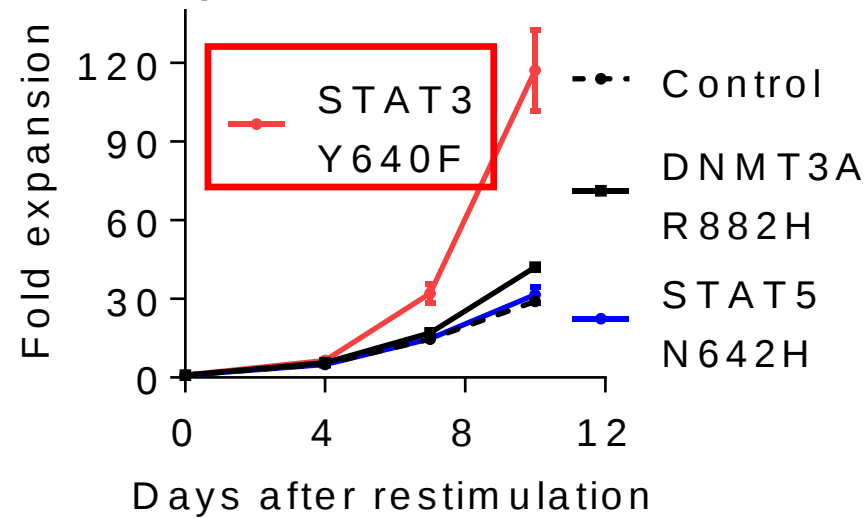
→ STAT3-activated memory T cells acquire enhanced self-renewal

Generation of CAR-T cells expressing oncogenes

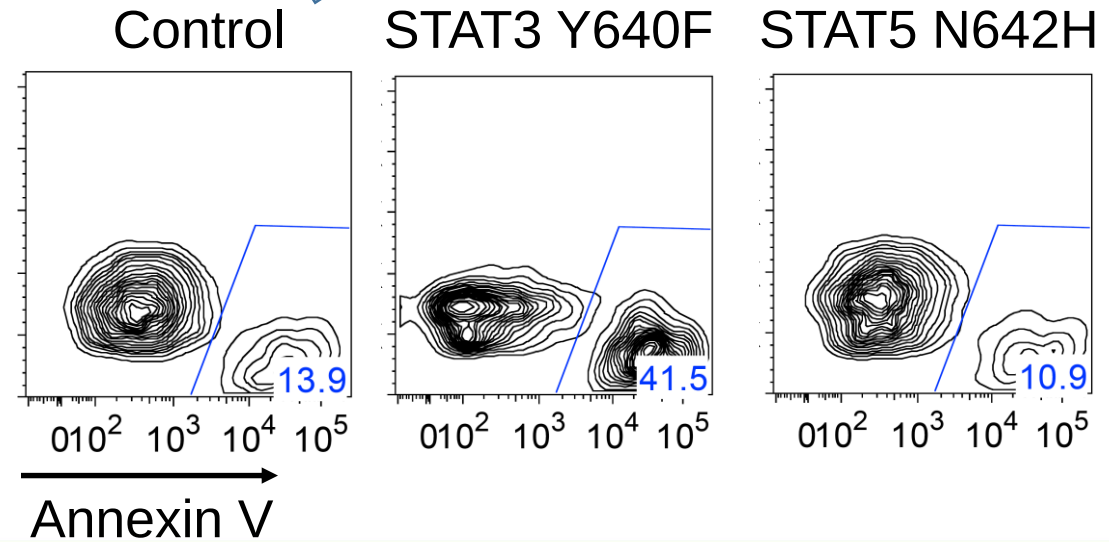
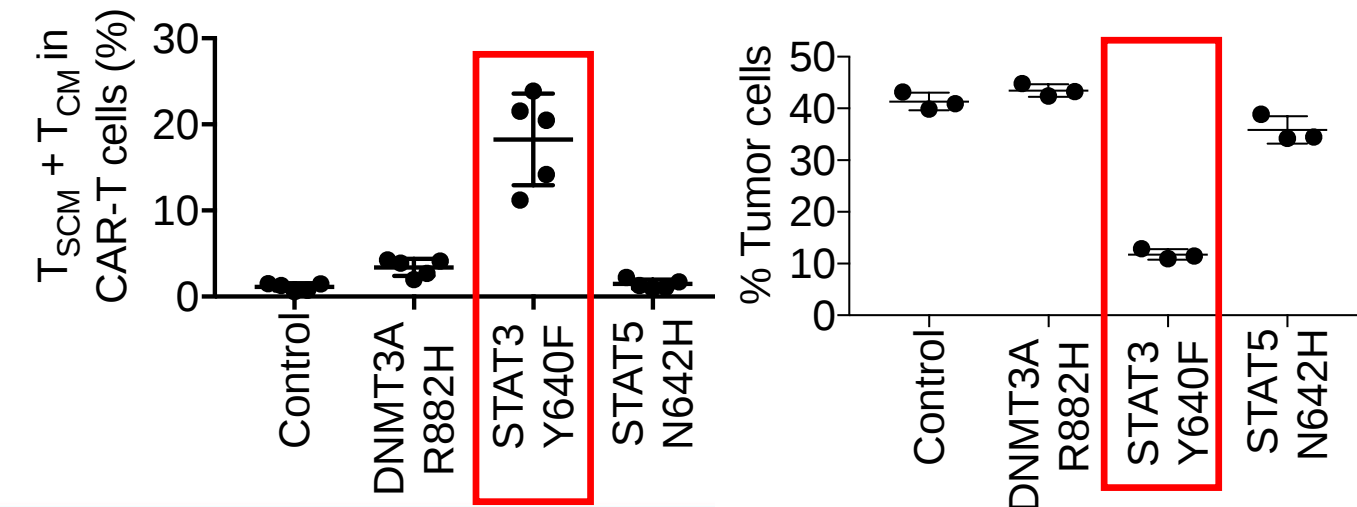
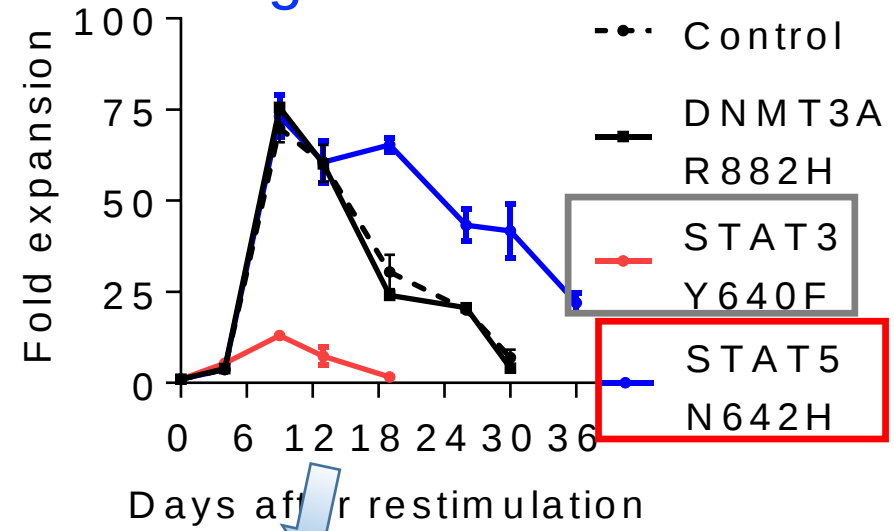


STAT3 and STAT5 differentially regulate T cell function

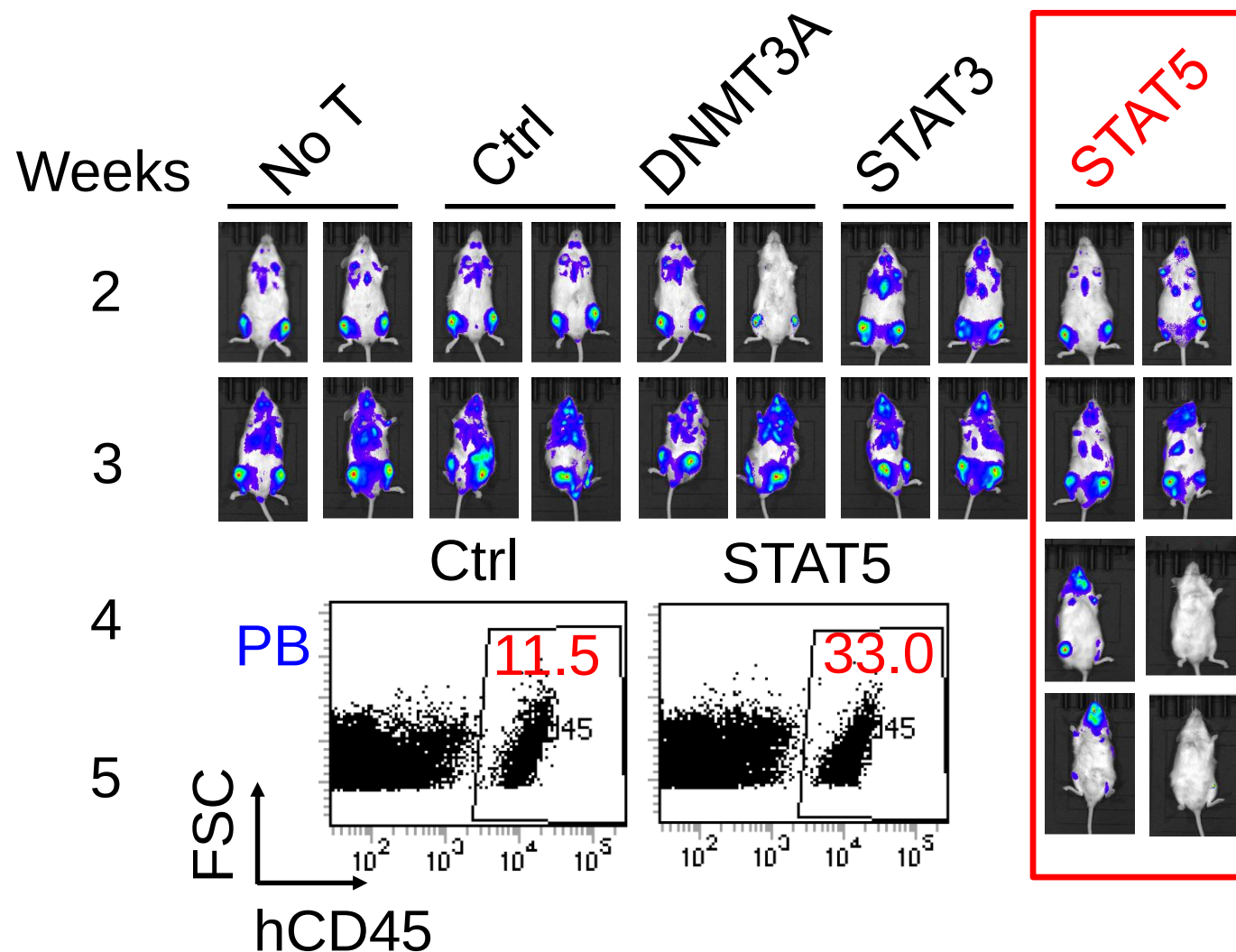
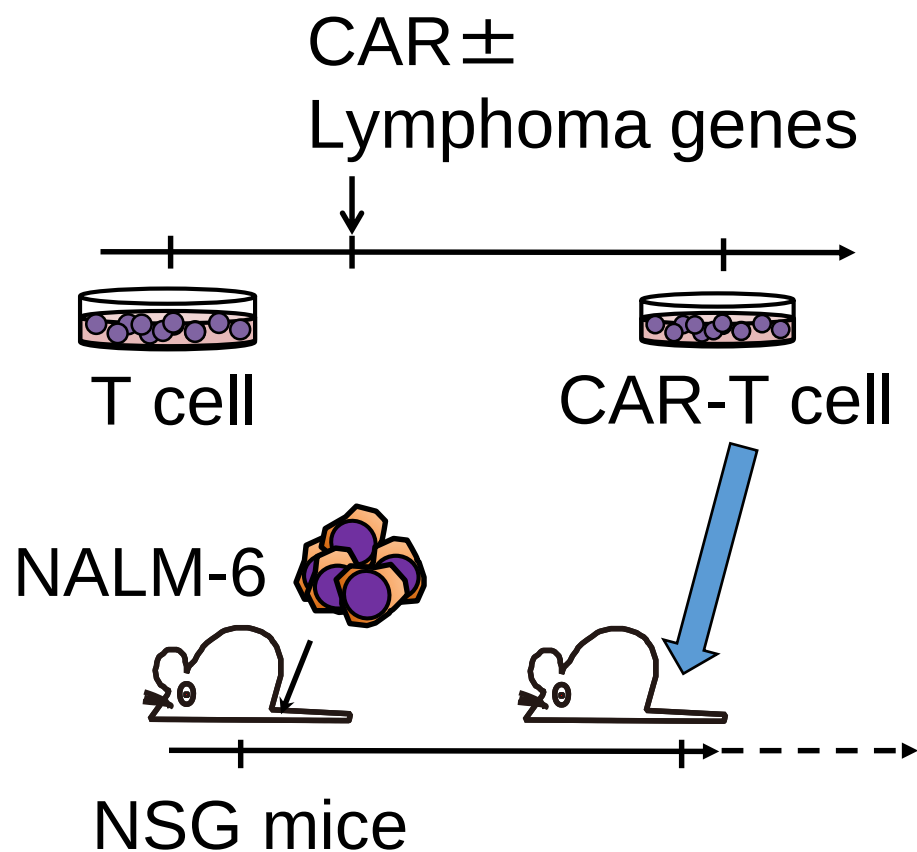
Repetitive stimulation



Single stimulation



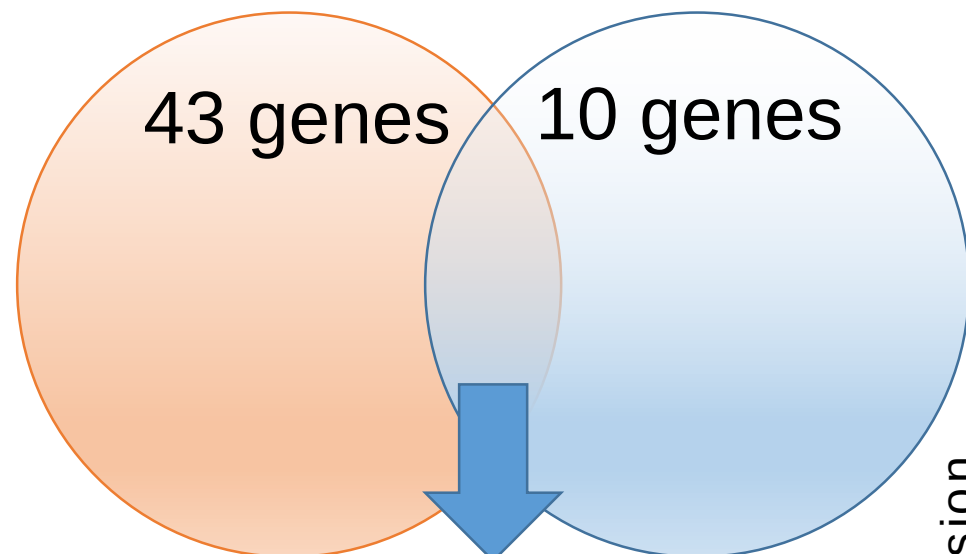
STAT5 activation elicits superior *in vivo* antitumor response



Downstream targets of STAT5

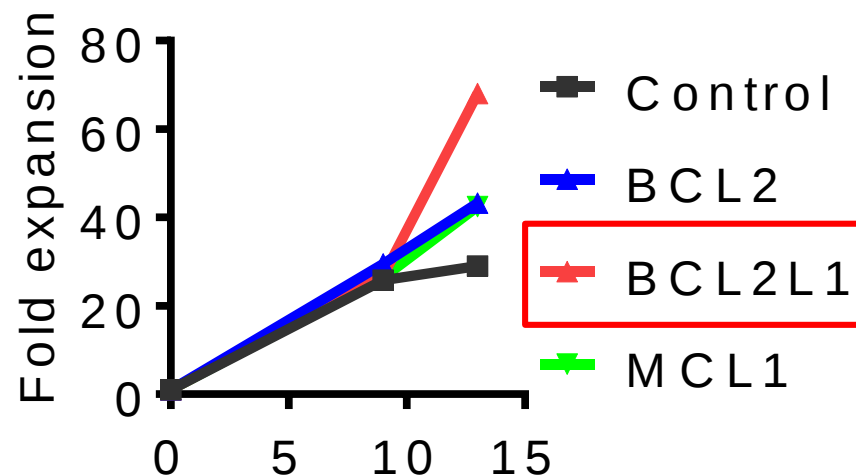
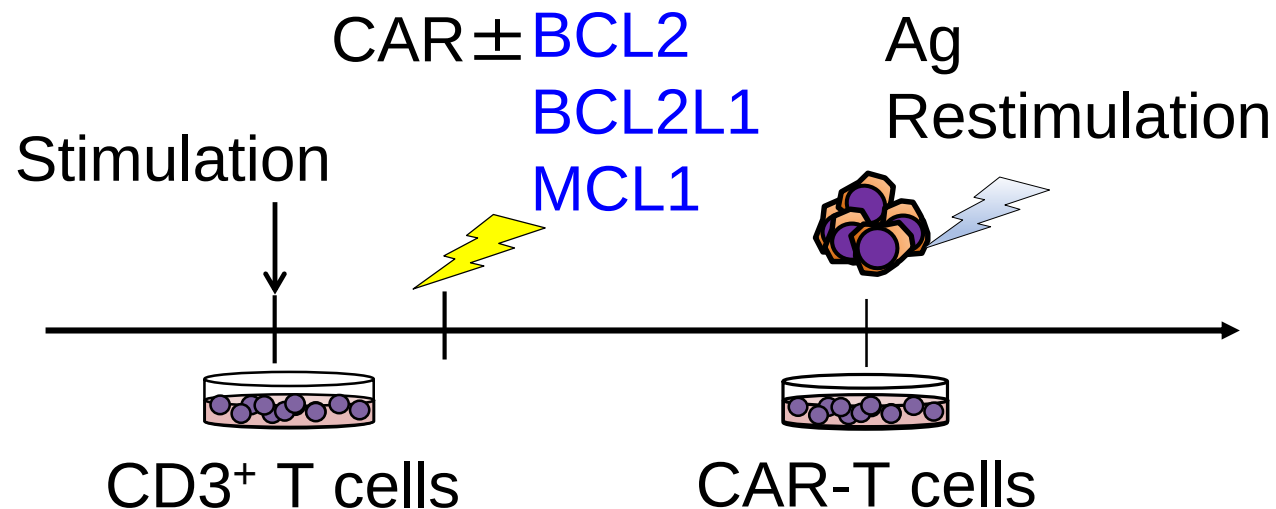
IL-2 induced IL-7 induced

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GSE58262

Nfil3
Prdm1
Bcl2
Bcl2l1



BCL2L1 was most effective to promote T cell proliferation

Summary and ongoing directions

- Genetic programs in T cell lymphoma enhance long-term CAR-T cell proliferation
 - STAT5 and its downstream genes (BCL2 family genes) are promising targets so far
- STAT3 activation confers unique properties to antitumor T cells
 - What are the responsible target genes?
 - Helpful in the context of high tumor-burden?

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