
4th POSTGRADUATE

CLL Conference

Bologna
November 13-14
2023

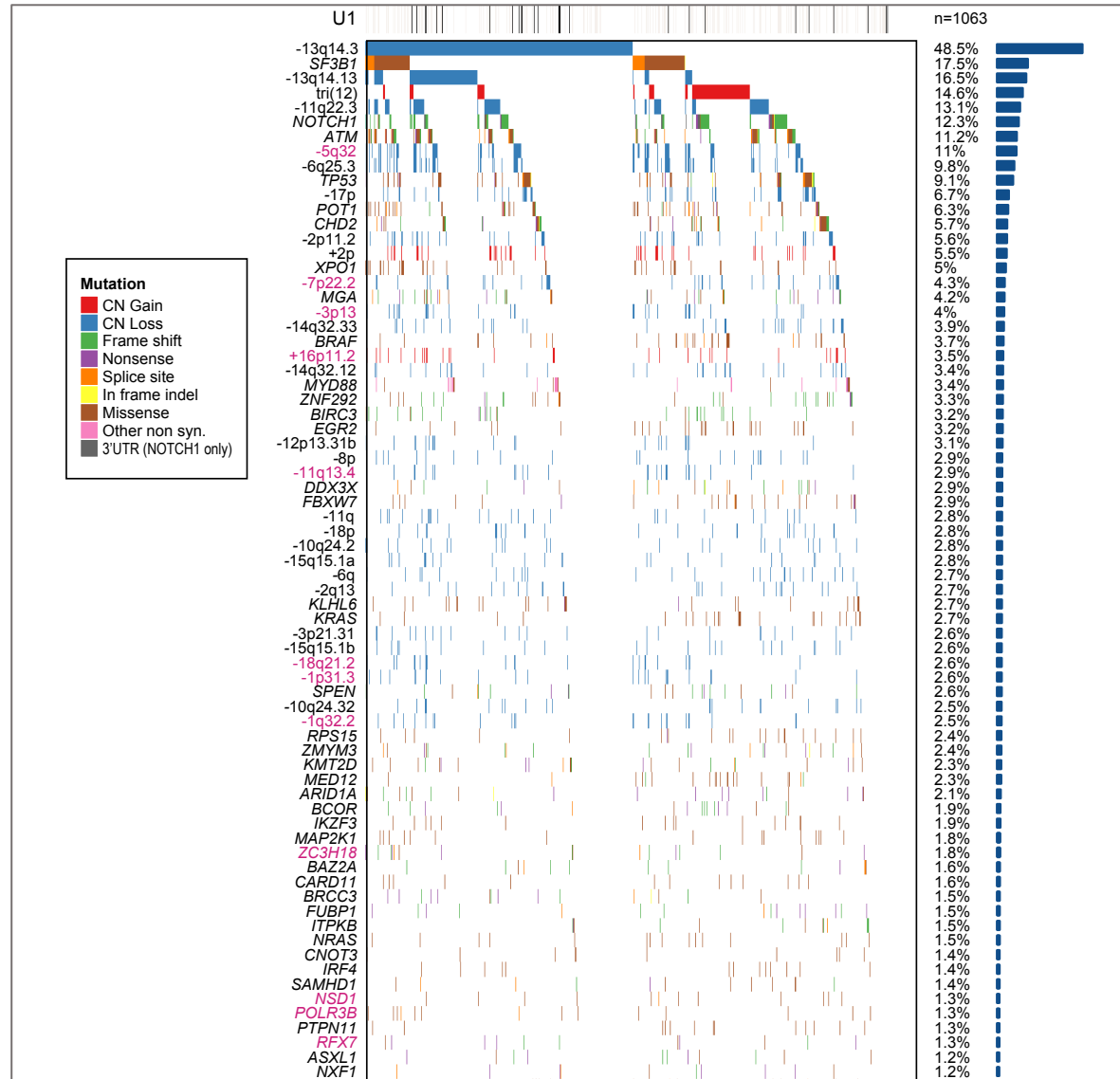
Royal Hotel Carlton

President:
Pier Luigi Zinzani

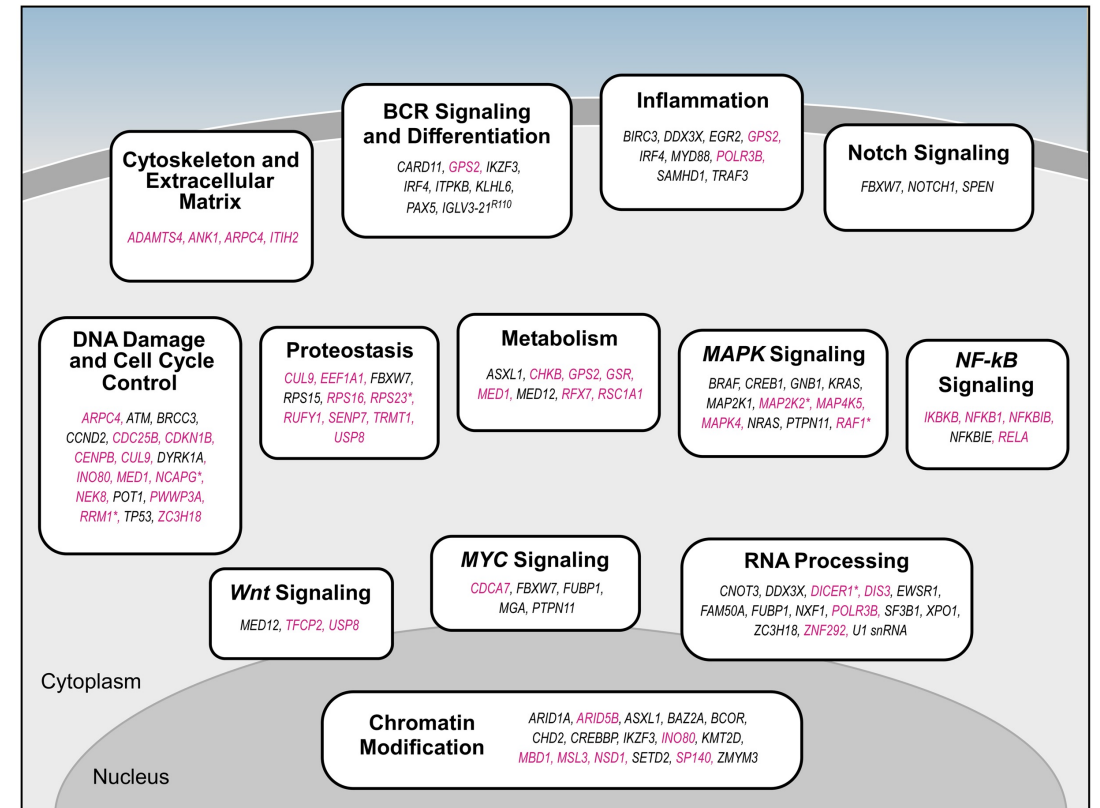
**Genetic portrait of CLL:
insights from mouse models**

Dimitar Efremov, MD, PhD
Molecular Hematology Unit
ICGEB, Trieste, Italy

Chronic Lymphocytic Leukemia – Genetic Lesions



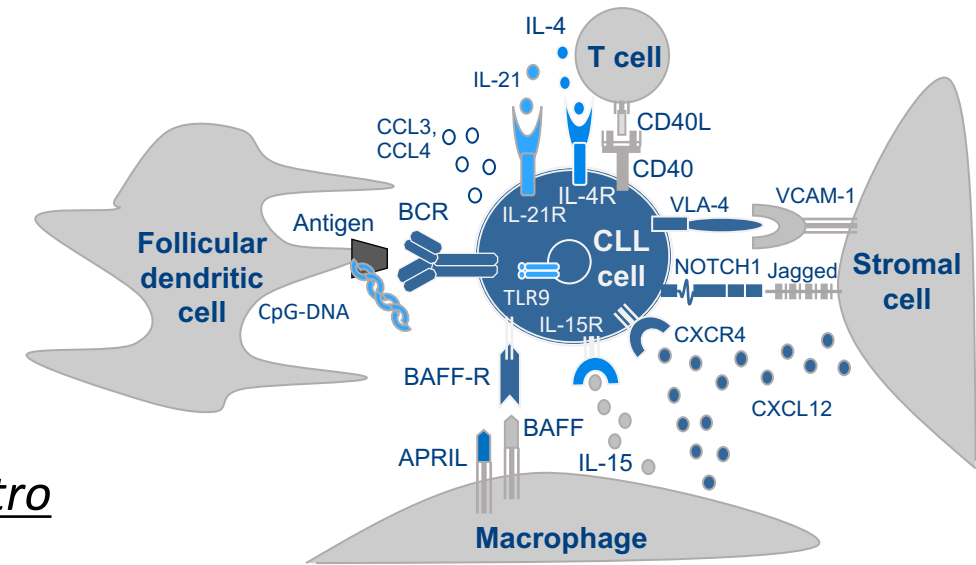
- *sSNV/indel* in 82 putative CLL driver genes (59 mutated in <2% of patients)
- *sCNA* in 130 genomic regions



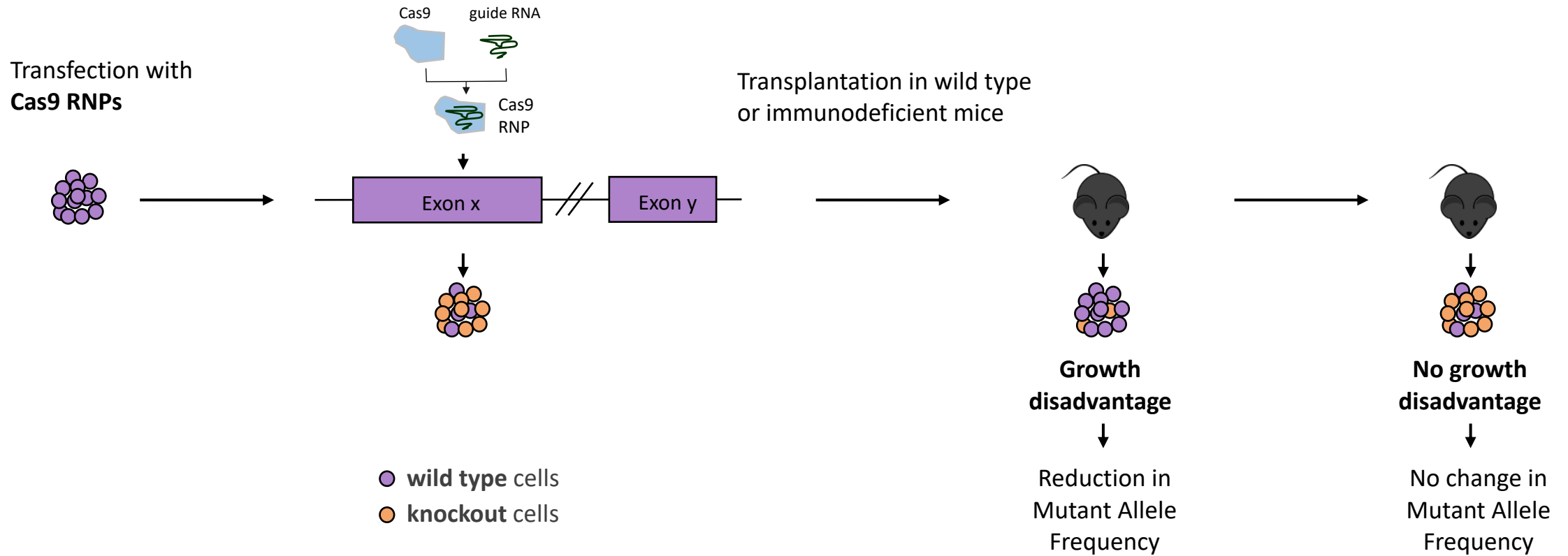
Knisbacher BA et al. Molecular map of chronic lymphocytic leukemia and its impact on outcome. Nat Genet. 2022

Chronic Lymphocytic Leukemia – Microenvironmental signals

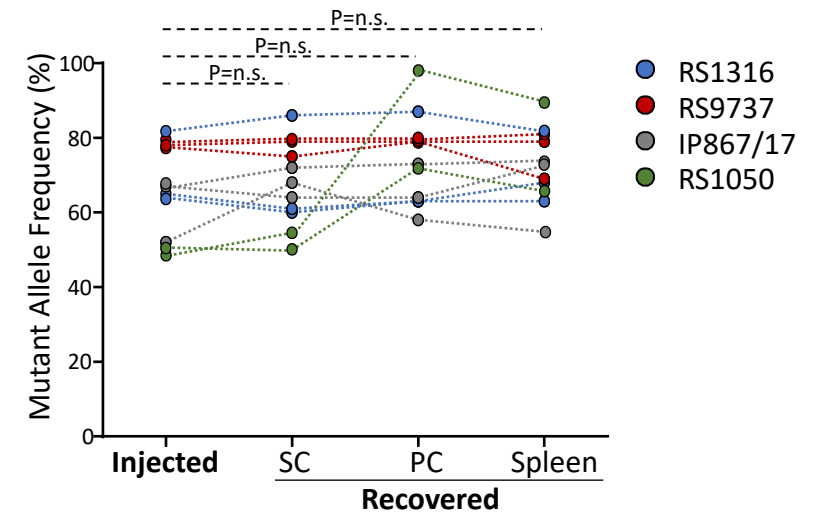
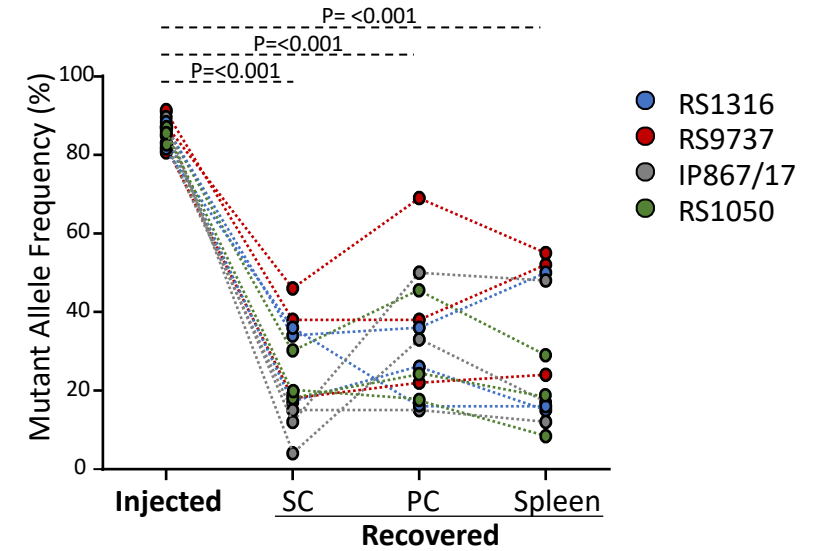
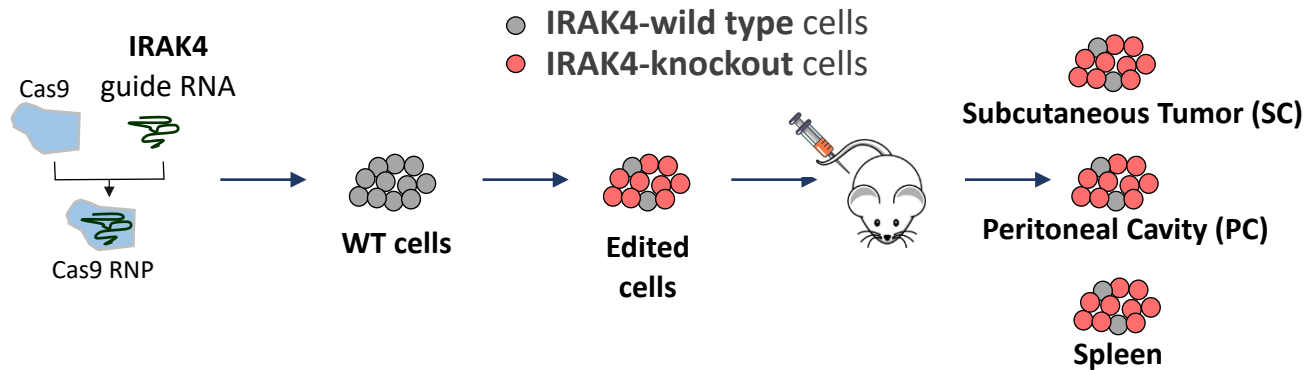
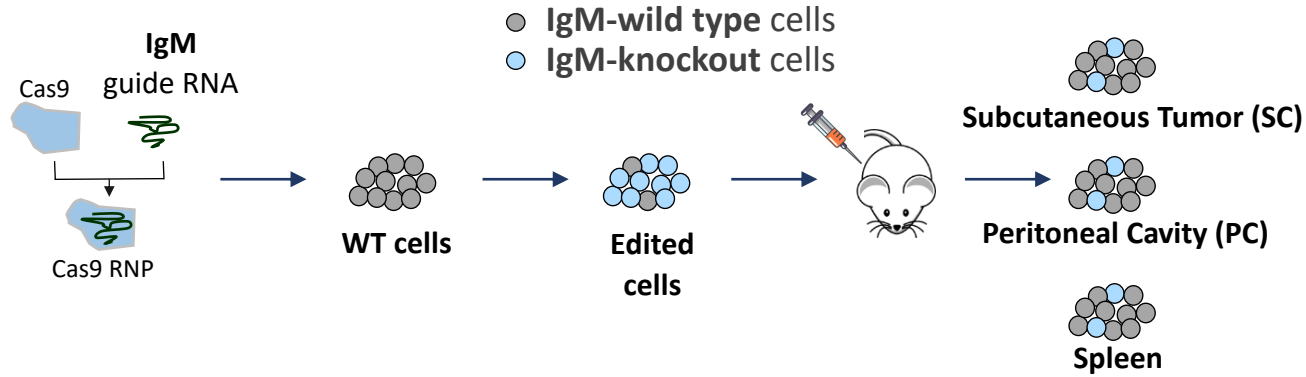
- Microenvironmental stimuli that increase CLL cell **survival** *in vitro*
 - T cells (CD40L, IL-4)
 - Mesenchymal stromal cells (Jagged, VCAM-1, CXCL12)
 - Macrophages (BAFF, APRIL, IL-15, CXCL12, Wnt5a)
 - B-cell receptor (BCR) ligands (apoptosis-associated autoantigens)
 - Toll-like receptor (TLR) ligands (CpG-unmethylated mitochondrial DNA)
- Microenvironmental stimuli that induce CLL cell **proliferation** *in vitro*
 - T cell derived (CD40L + IL-4 + IL-21)
 - Toll-like receptor ligands (CpG-DNA) + IL-15/IL-2
- Microenvironmental stimuli that induce **resistance** to the **novel drugs** *in vitro*
 - B cell receptor stimulation (venetoclax resistance)
 - Toll-like receptor ligands (CpG-DNA) (venetoclax resistance)
 - T cell coculture (CD40 stimulation) (venetoclax resistance)
 - Macrophage coculture (venetoclax resistance)
 - IL4 (ibrutinib resistance)
 - Integrin VLA-4 stimulation (ibrutinib resistance)



Genome editing of intracellular signaling pathways in primary murine CLL or patient-derived Richter Syndrome cells to study *in vivo* the role of microenvironmental signals in CLL cell growth, survival and treatment resistance



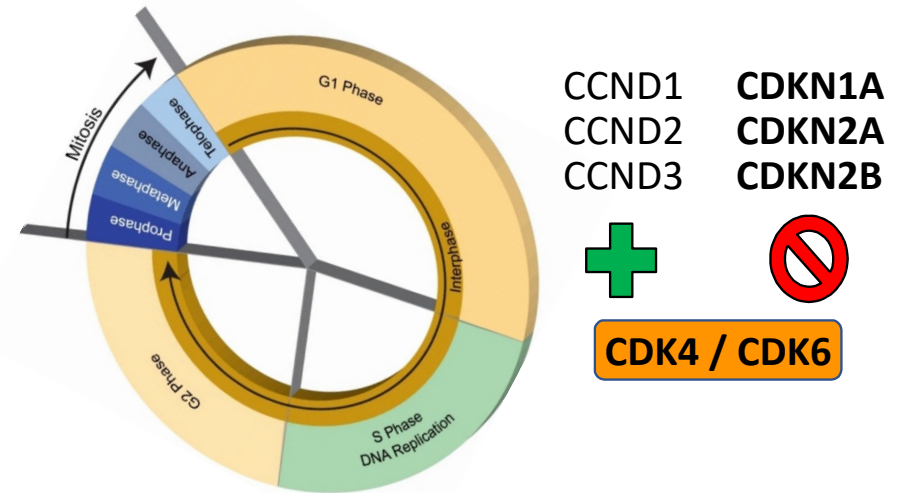
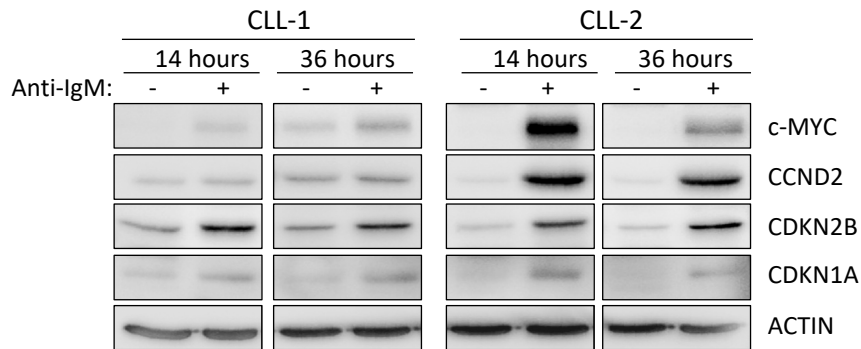
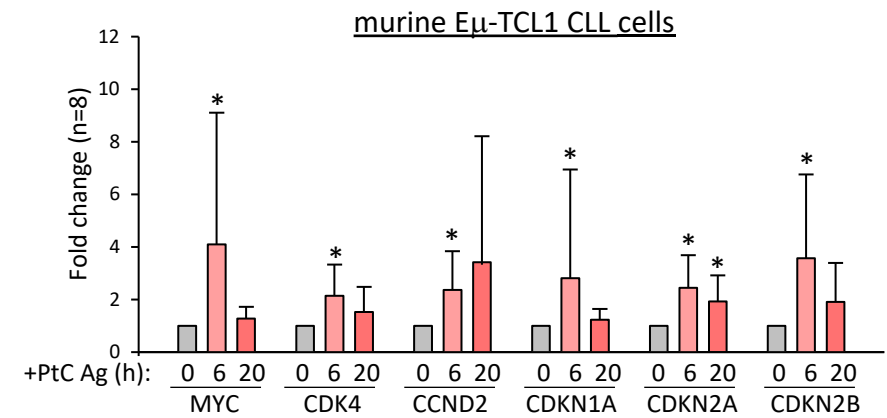
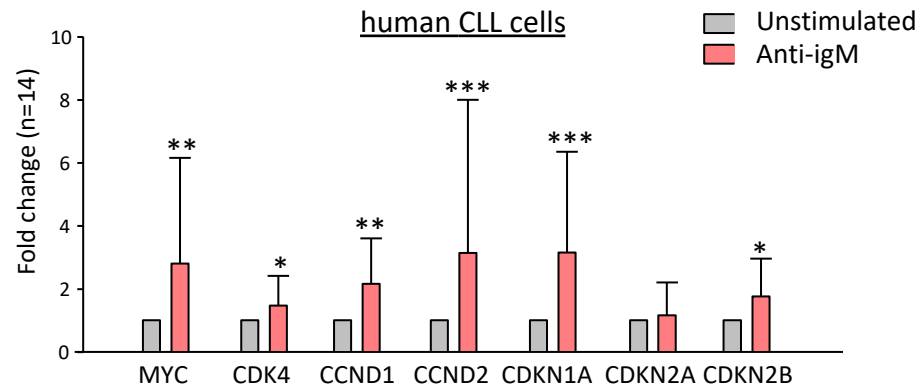
Genetic disruption of B cell receptor (BCR) but not Toll-like receptor (TLR) signaling suppresses the growth of xenografted human Richter syndrome cells *in vivo*



Martines C et al. Macrophage- and BCR-derived but not TLR-derived signals support the growth of CLL and Richter syndrome murine models *in vivo*. *Blood* 2022; 140:2335-2347

Cooperation between microenvironmental signals and genetic lesions during CLL transformation

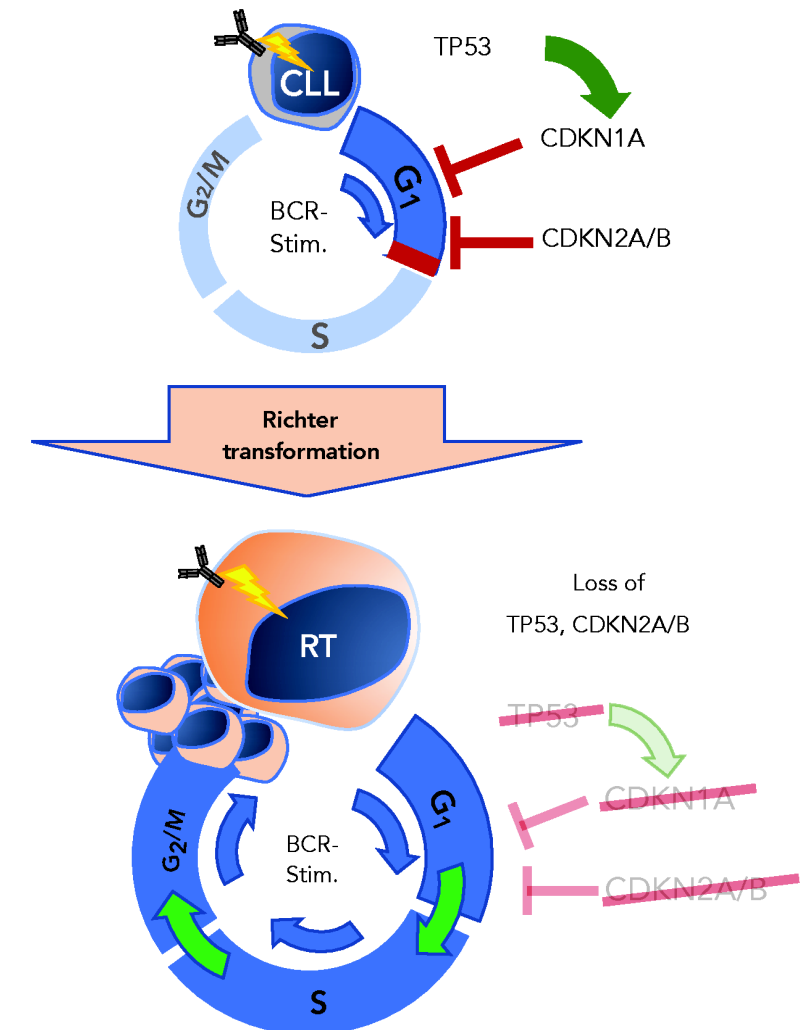
BCR signaling induces both **positive** (CCND1, CCND2, CDK4, MYC) and **negative** (CDKN1A, CDKN2A, CDKN2B) cell cycle regulators in human and murine CLL B cells



Common genetic lesions in clonally-related Richter Transformation

Genetic lesion	Frequency in CLL	Frequency in RT	Cellular Pathway
TP53 mutation and/or deletion (del17p13)	10% - 15%	>80%	DNA damage response and cell cycle (induces CDKN1A)
CDKN2A/CDKN2B deletion (del9p21)	1.5%	40 - 50%	Cell cycle
MYC abnormalities: t(8;14), amp(8q24)	5 - 7%	15 - 30%	MYC signaling
MGA deletion (del15q)	4%	20%	MYC signaling
NOTCH1 mutation	10% - 15%	30%	NOTCH1 signaling

Parry EM et al. Nat Med. 2023; 29(1):158-169
 Nadeu F et al. Nat Med. 2022; 28(8):1662-1671
 Klintman J et al. Blood. 2021;137(20):2800-2816.
 Fabbri G. J Exp Med. 2013; 210(11):2273-2288
 Chigrinova E et al. Blood. 2013; 122(15):2673-2682
 Leeksma AC et al. Haematologica. 2021; 106(1):87-97.
 Knisbacher BA et al. Nat Genet. 2022; 54(11):1664-1674

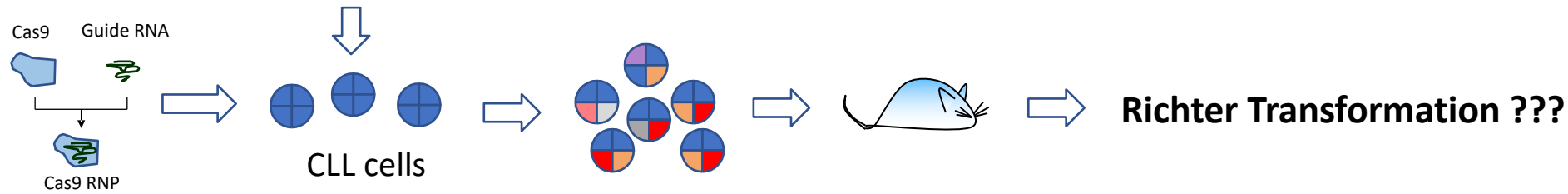


Adapted from Pallasch CP, Blood. 2021; 138:1005-1007

Can combined introduction of TP53, CDKN2A and CDKN2B loss-of-function genetic lesions in autoreactive murine E μ -TCL1-derived CLL cells result in Richter Transformation?

CRISPR/Cas9
genome editing

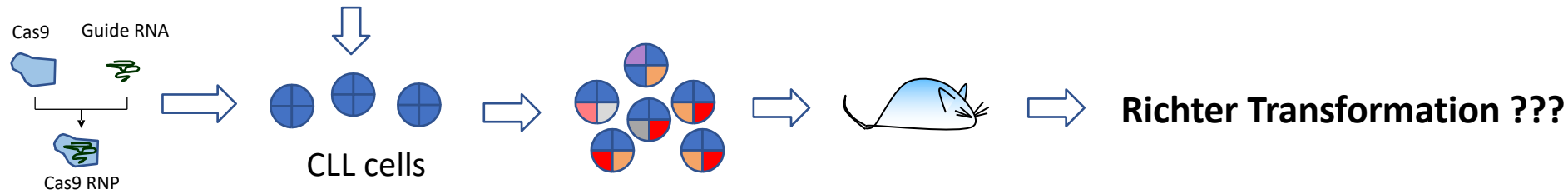
Targeted genes:
TP53; CDKN2A; CDKN2B



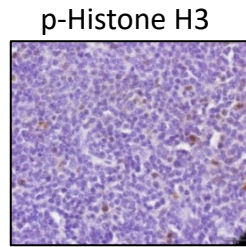
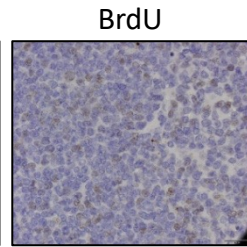
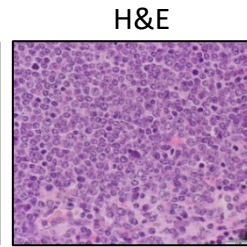
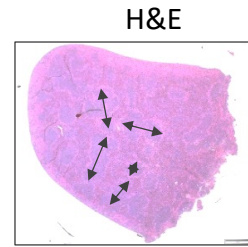
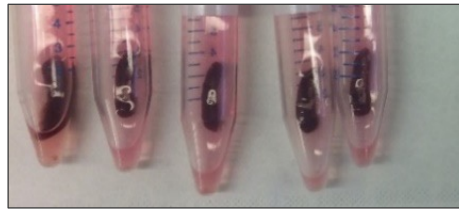
Combined introduction of TP53/CDKN2A/CDKN2B genetic lesions in murine E μ -TCL1-derived CLL cells results in development of aggressive tumors with features of Richter's Transformation

CRISPR/Cas9
genome editing

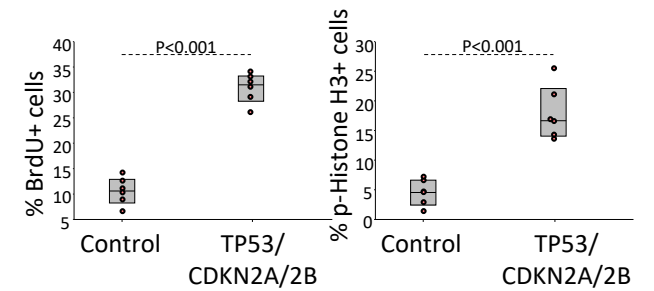
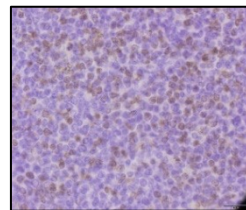
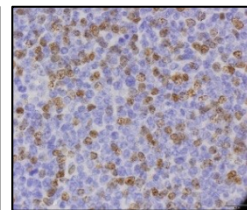
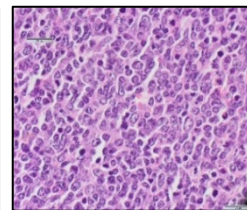
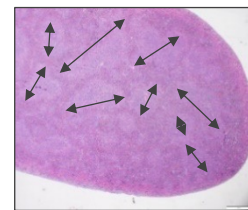
Targeted genes:
TP53; CDKN2A; CDKN2B



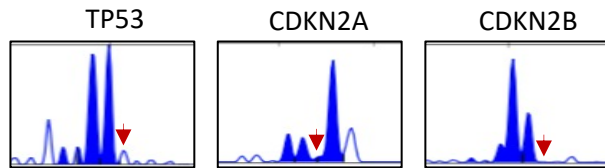
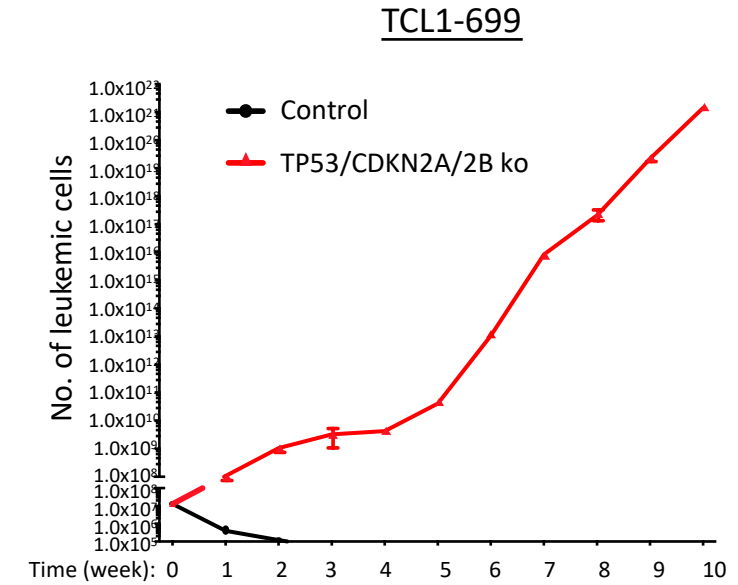
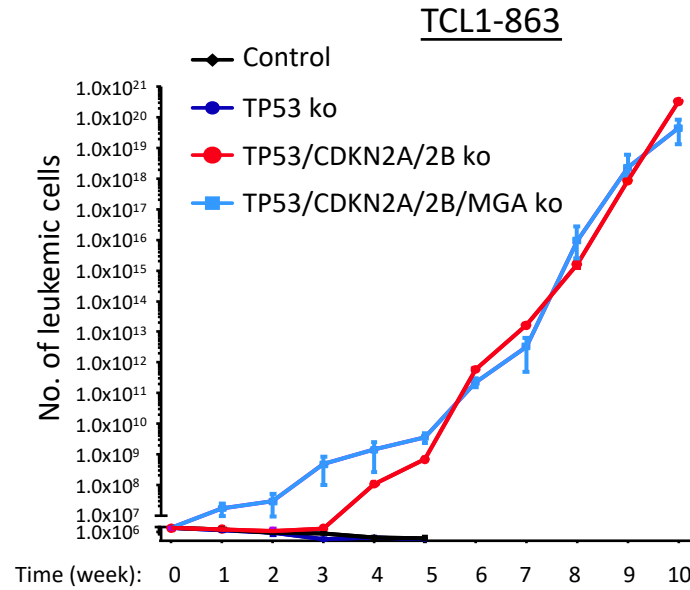
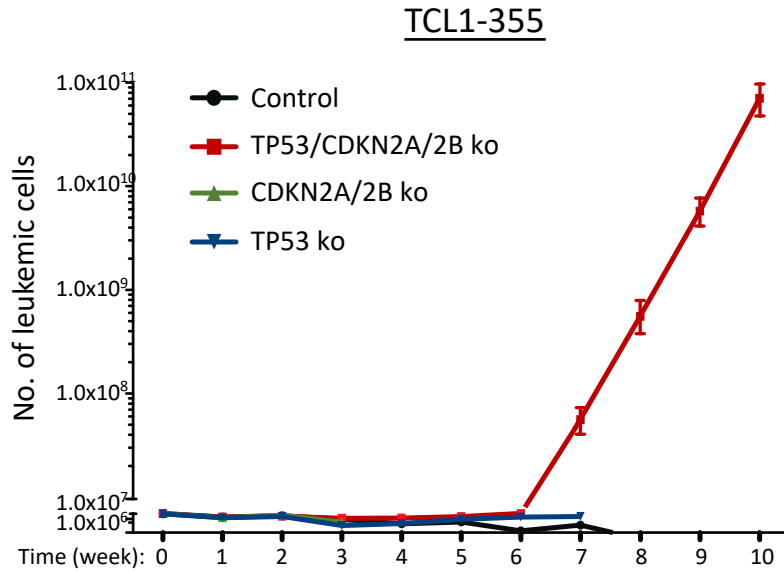
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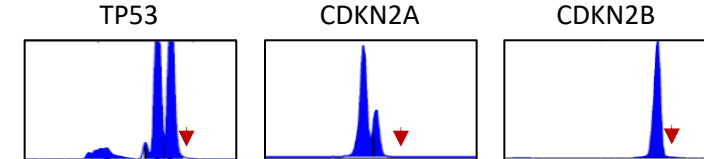
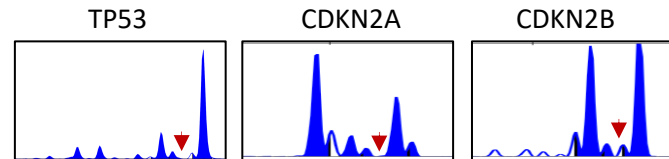
CDKN2A/2B
/TP53 ko



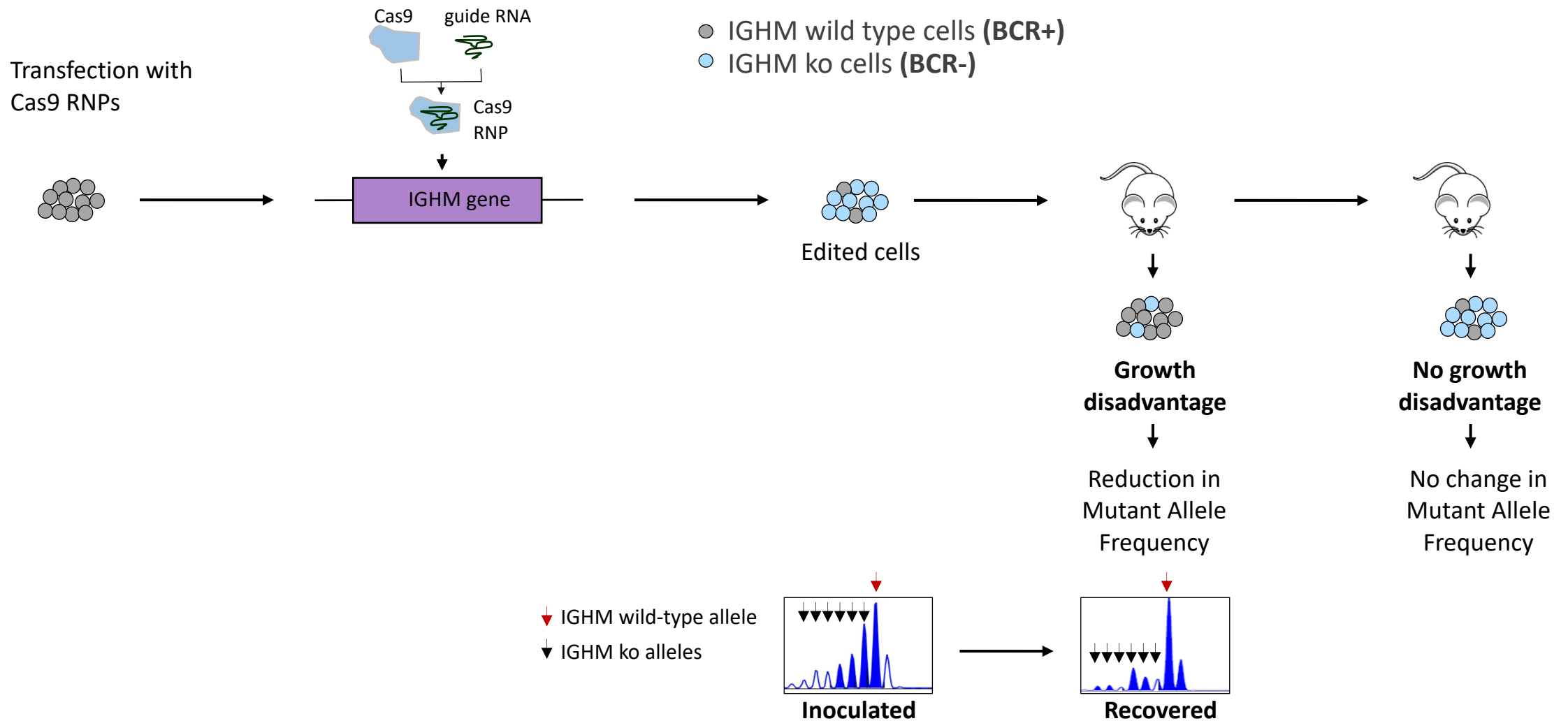
Biallelic disruption of TP53, CDKN2A and CDKN2B in murine E μ -TCL1-derived CLL cells results in spontaneous leukemia cell proliferation *in vitro*



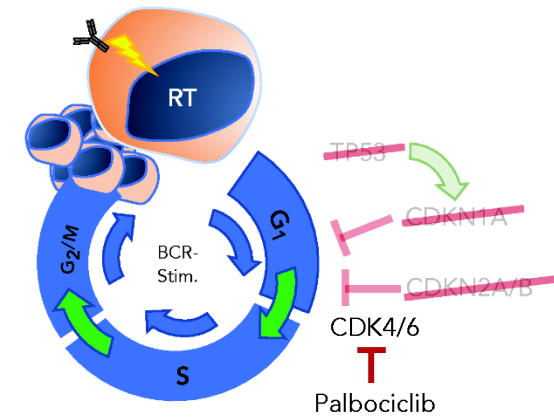
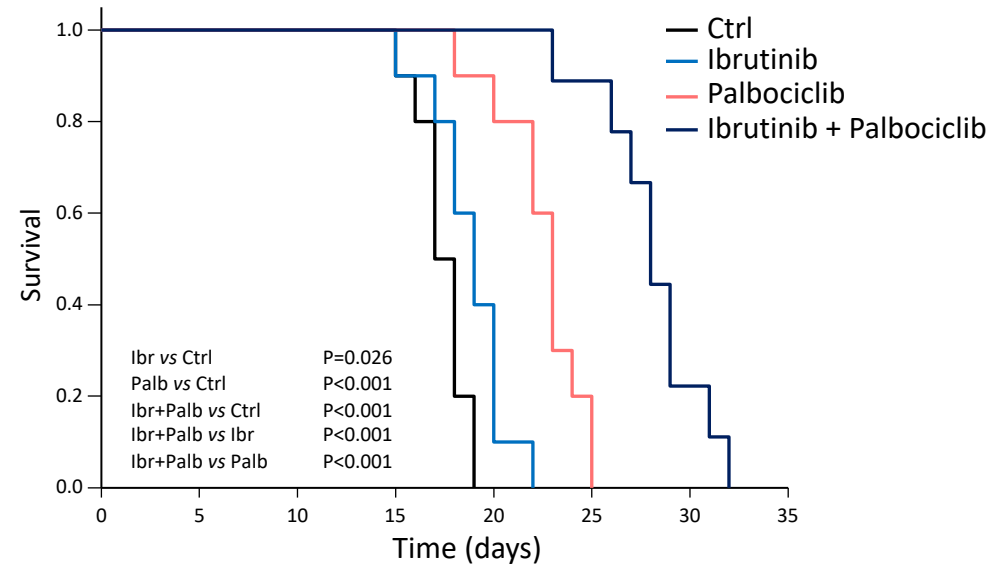
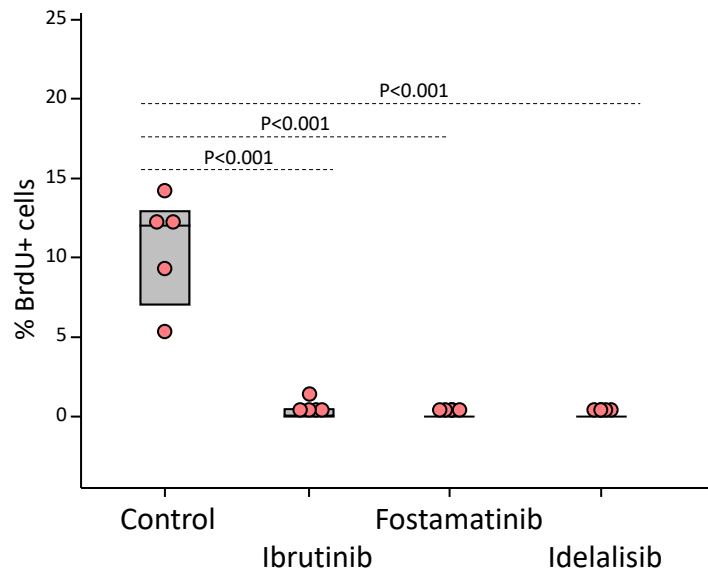
↓ Wild Type allele



Murine E μ -TCL1-derived RS cells with IGHM knockout are negatively selected in vivo

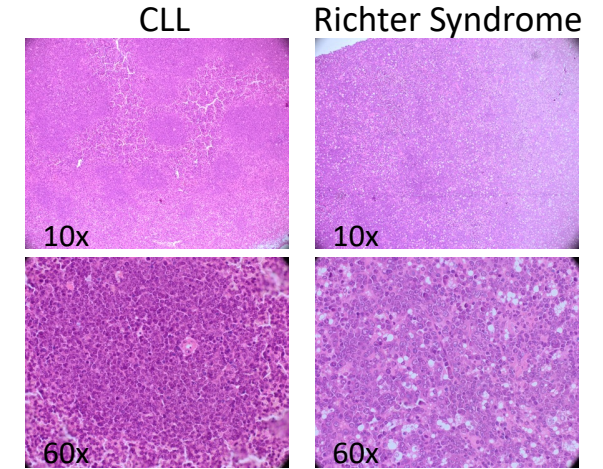
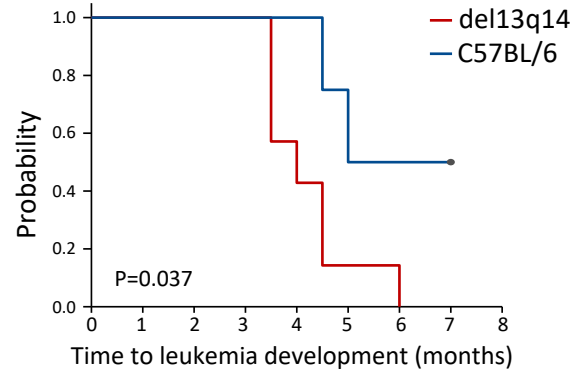
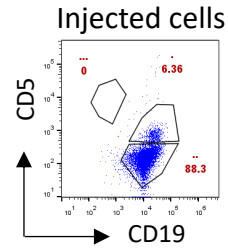
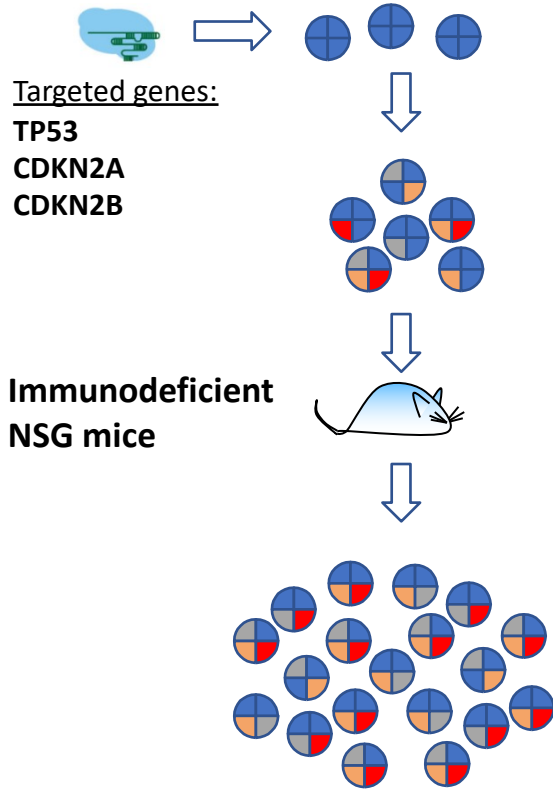


Murine E μ -TCL1-derived Richter Syndrome cells with TP53/CDKN2A/2B genetic lesions are sensitive to combination treatment with a BCR and CDK4/6 inhibitor

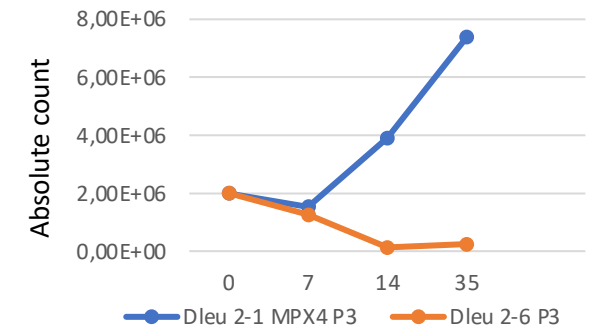
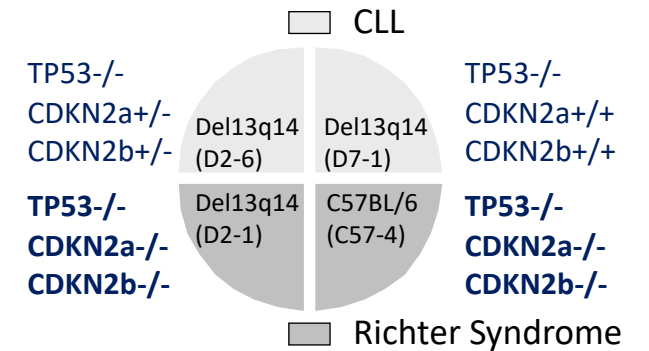
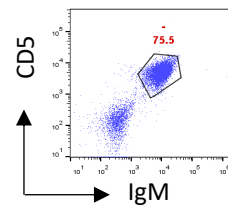
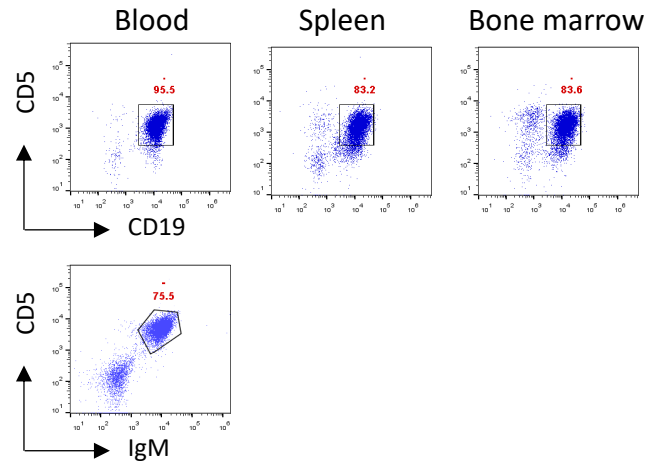


Biallelic disruption of TP53, CDKN2A and CDKN2B in non-leukemic B cells from del13q14 or C57BL/6 mice results in development of CD5+/IgM+ B cell tumors with features of Richter's Transformation

non-leukemic murine B cells
(del13q14 n=7, C57BL/6 n=4)



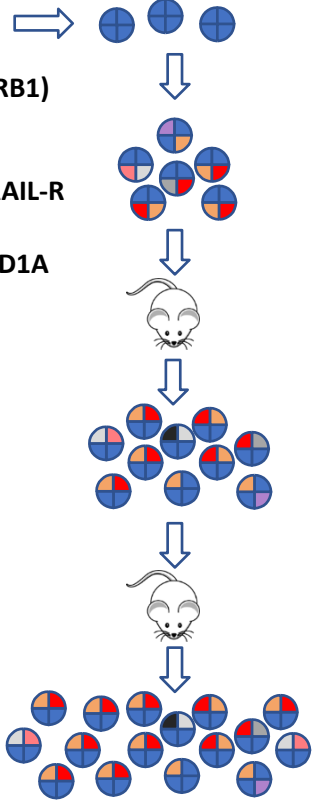
Immunodeficient NSG mice



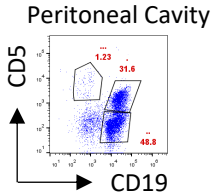
Generation of murine CLL/RS models by multiplexed CRISPR/Cas9 editing of TP53 and 12-14 CLL driver genes other than CDKN2A/CDKN2B

non-leukemic murine B cells
(del13q14 n=8)

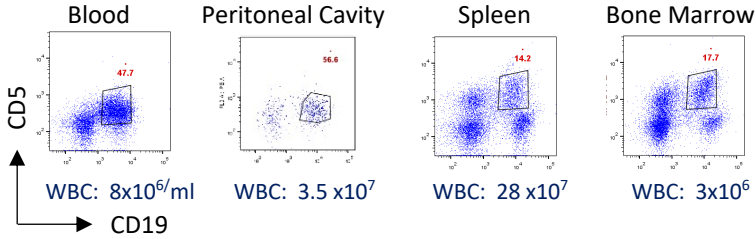
- Targeted genes:
 TP53, ATM, POT1
 Retinoblastoma (RB1)
 SAMHD1
 FBXW7, NOTCH1
 BIRC3, NFKBIE, TRAIL-R
 MGA
 CHD2, SETD2, ARID1A



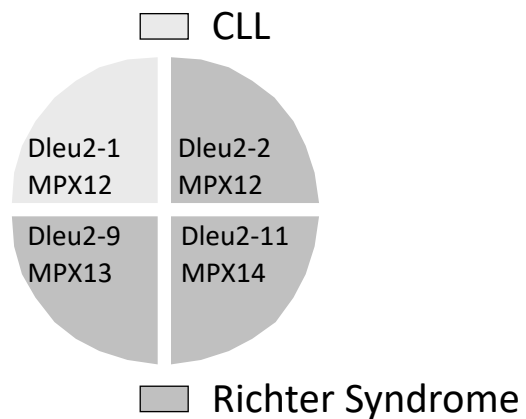
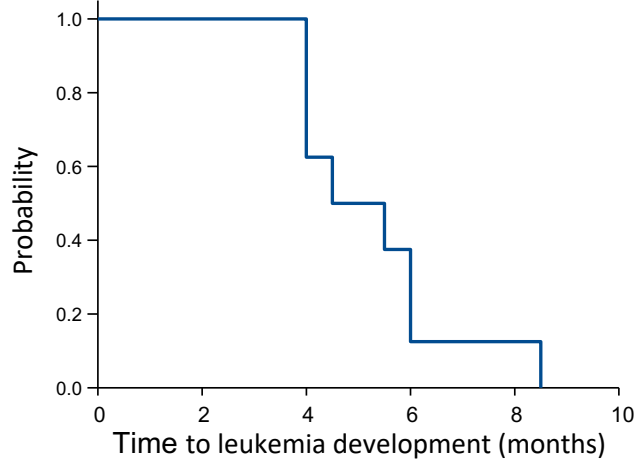
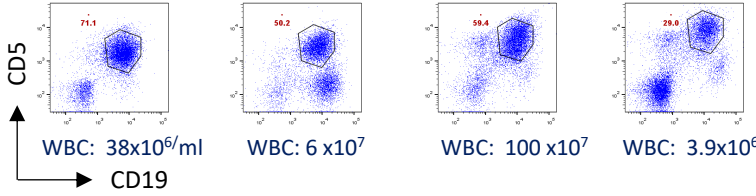
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Month 4



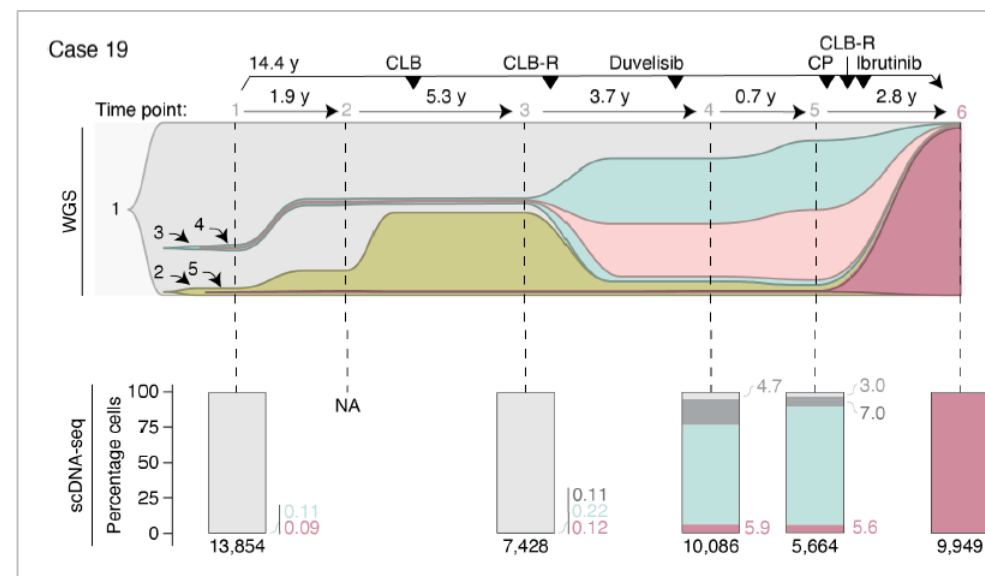
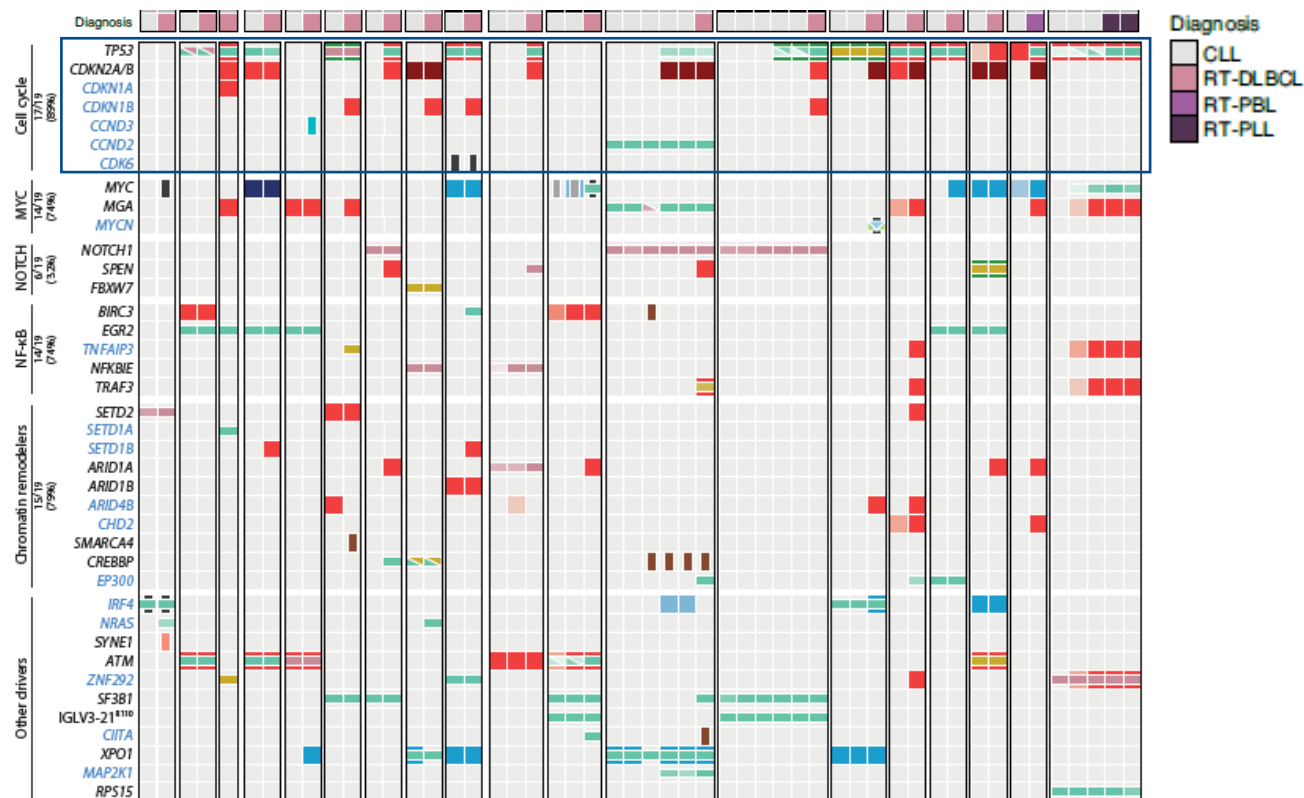
Month 6



Can events in the tumor microenvironment contribute to Richter Transformation?

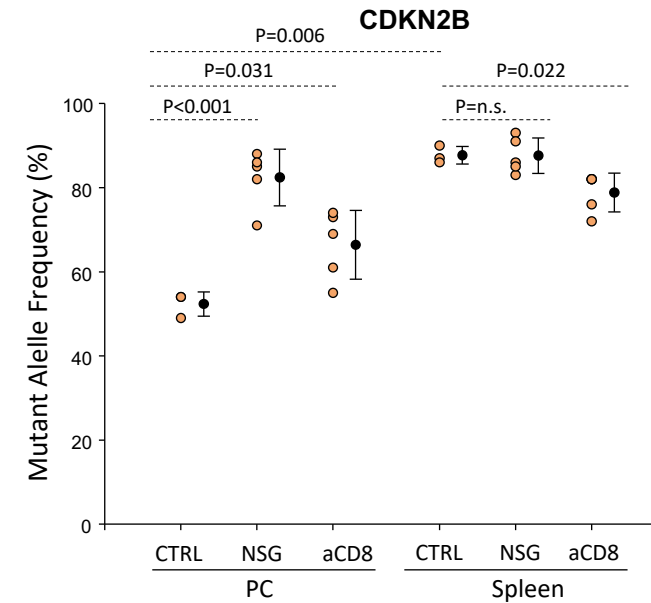
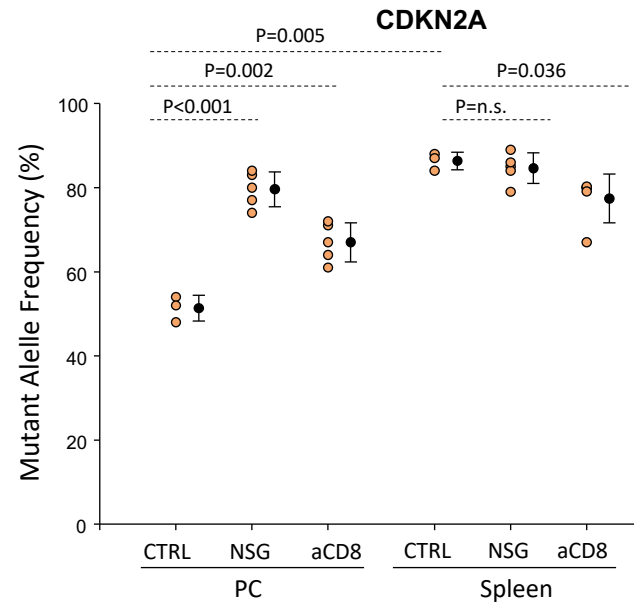
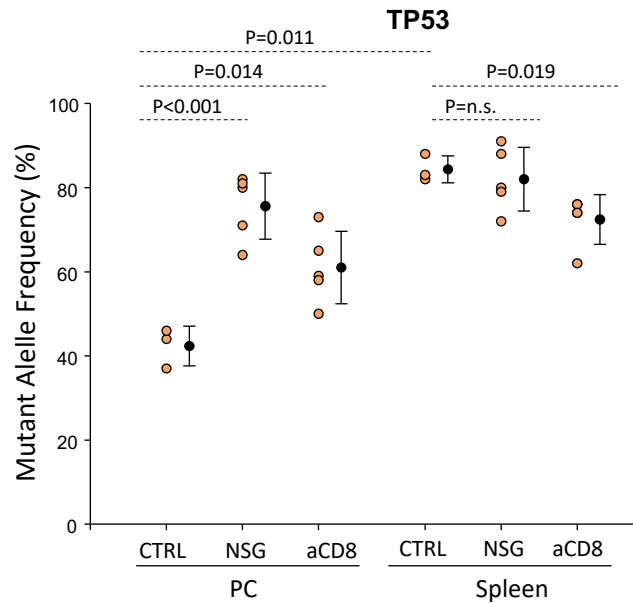
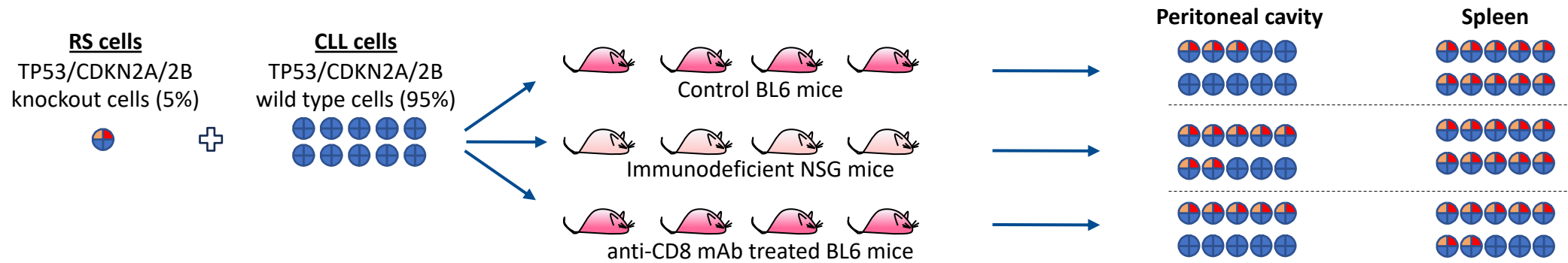
Early seeding of Richter transformation: early acquisition of driver alterations

- Deletions or inactivating mutations in cell cycle inhibitors or activating mutations in positive cell cycle regulators present in >90 of Richter Syndrome cases
- Small subclones of cells with genomic features of RS may be present for many years prior to the appearance of the clinical manifestations of Richter Syndrome



Nadeu F et al. *Detection of early seeding of Richter transformation in chronic lymphocytic leukemia. Nat Med.* 2022; 28:1662-1671

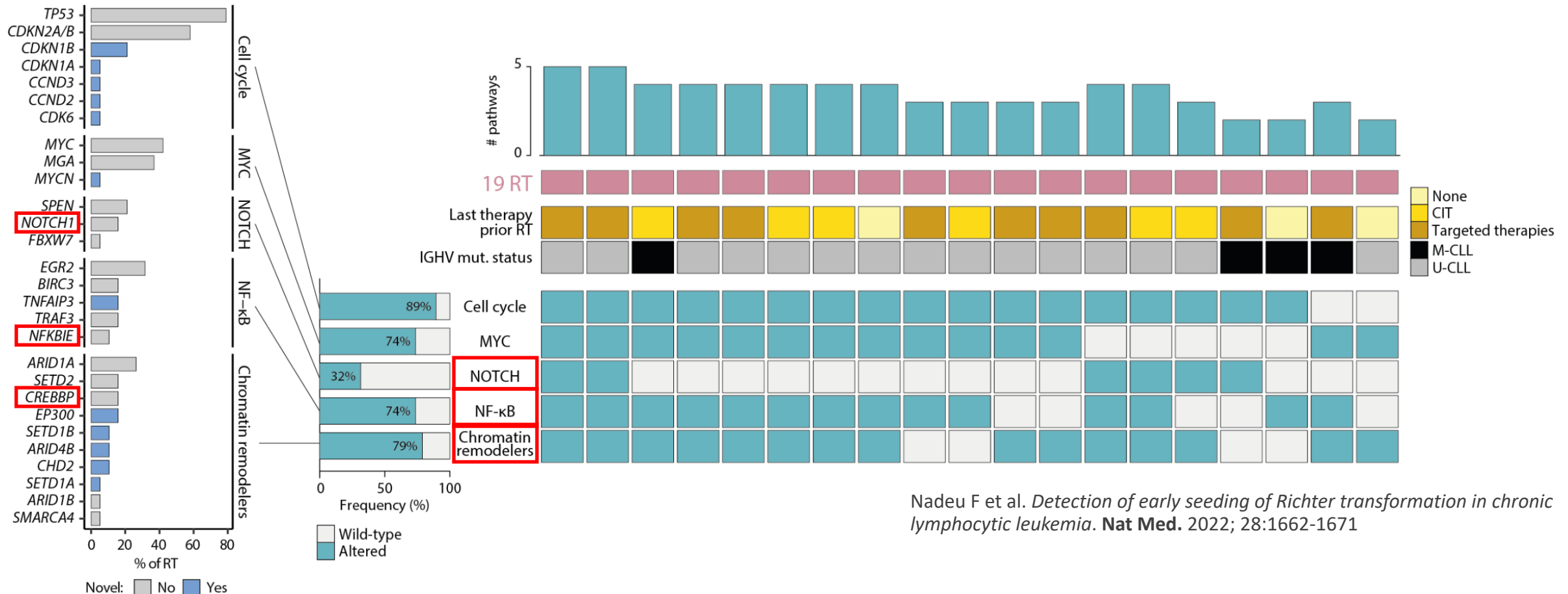
Murine RS cells with TP53/CDKN2A/2B lesions are differently selected in peritoneal cavity vs spleen and in immunodeficient vs immunocompetent mice



Potential mechanisms that can cause loss of immune control in Richter Syndrome

- Mutations in NOTCH1 and certain chromatin modifiers contribute to immune evasion by downregulating expression of MHC class II genes and upregulating PD-L1 expression on the malignant B cells

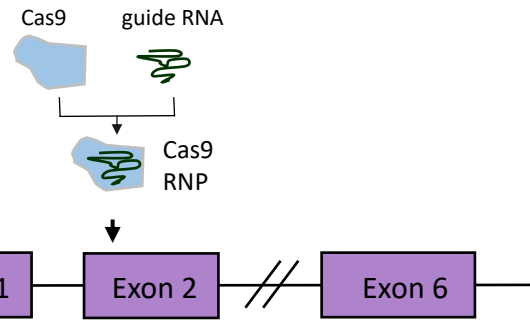
Mangolini M et al. Nat Commun. 2022; 13:6220
 Fontes JD et al, Mol Cell Biol. 1999; 19(1):941-7
 Green MR et al, Proc Natl Acad Sci U S A. 2015; 112(10):E1116-25



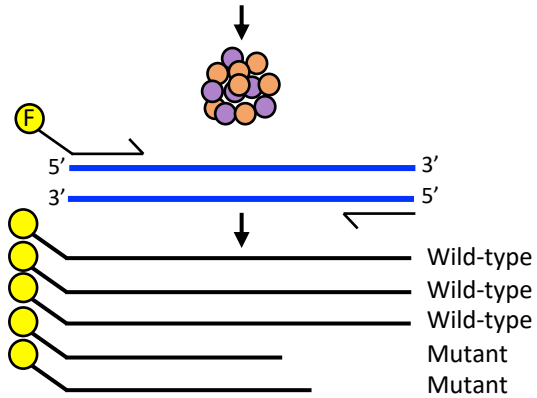
Nadeu F et al. *Detection of early seeding of Richter transformation in chronic lymphocytic leukemia.* Nat Med. 2022; 28:1662-1671

Introduction of loss-of-function NFKBIE mutations in TCL1-derived Richter Syndrome cells by CRISPR/Cas 9 editing

Transfection of murine E μ -TCL1 RS cells with Cas9 RNP targeting Nfkbie exon 2

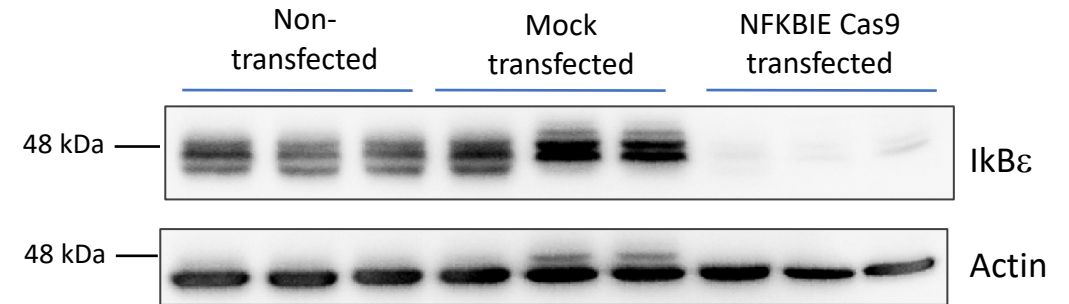
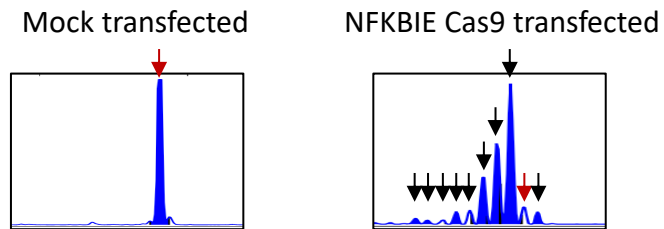


PCR amplification

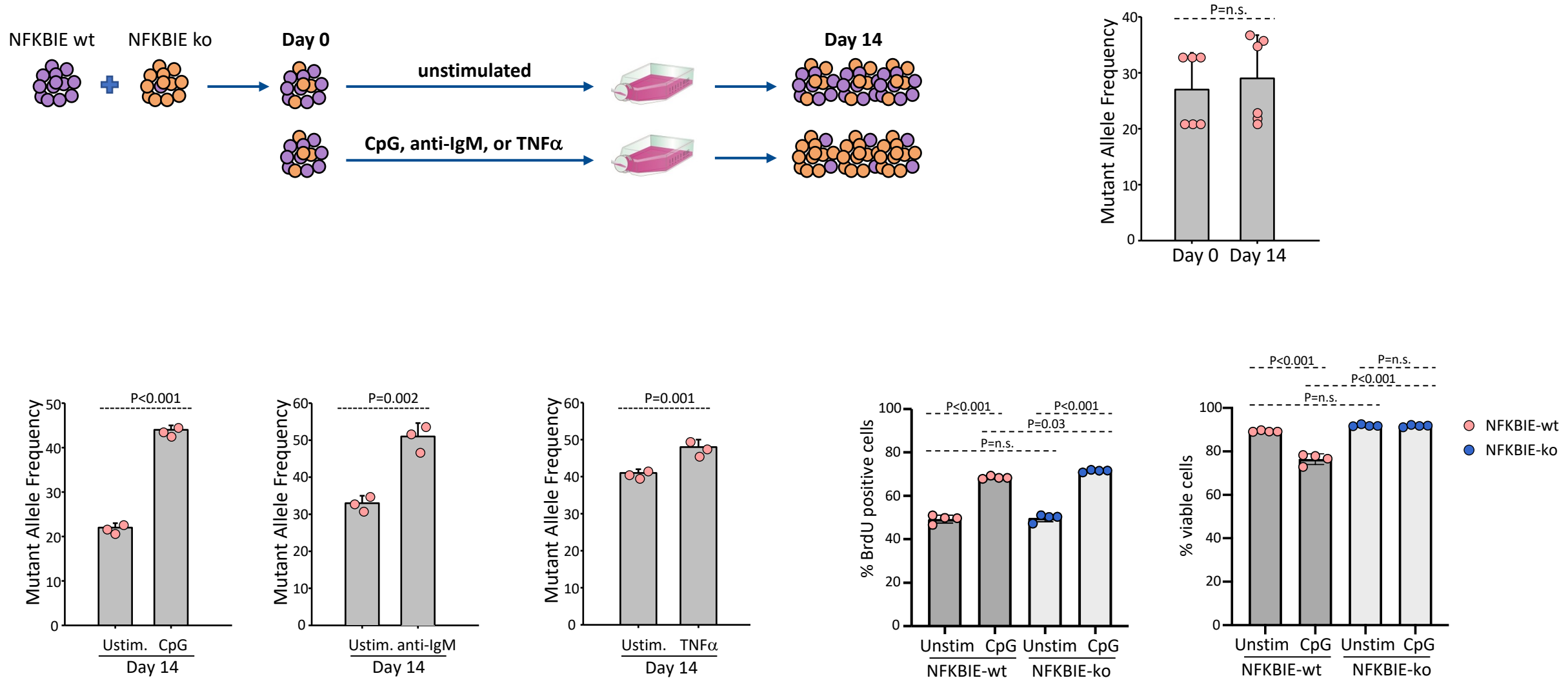


Amplicon capillary electrophoresis

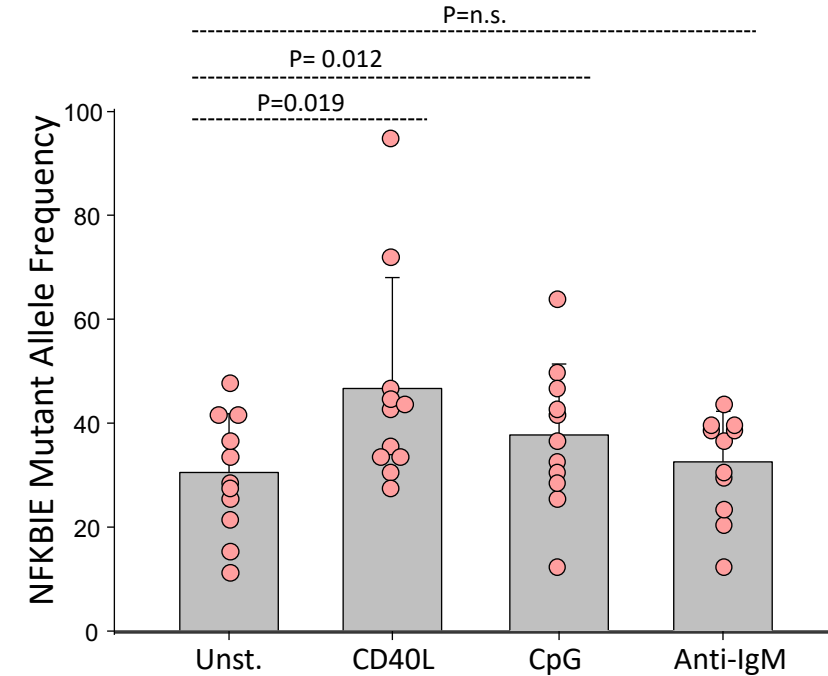
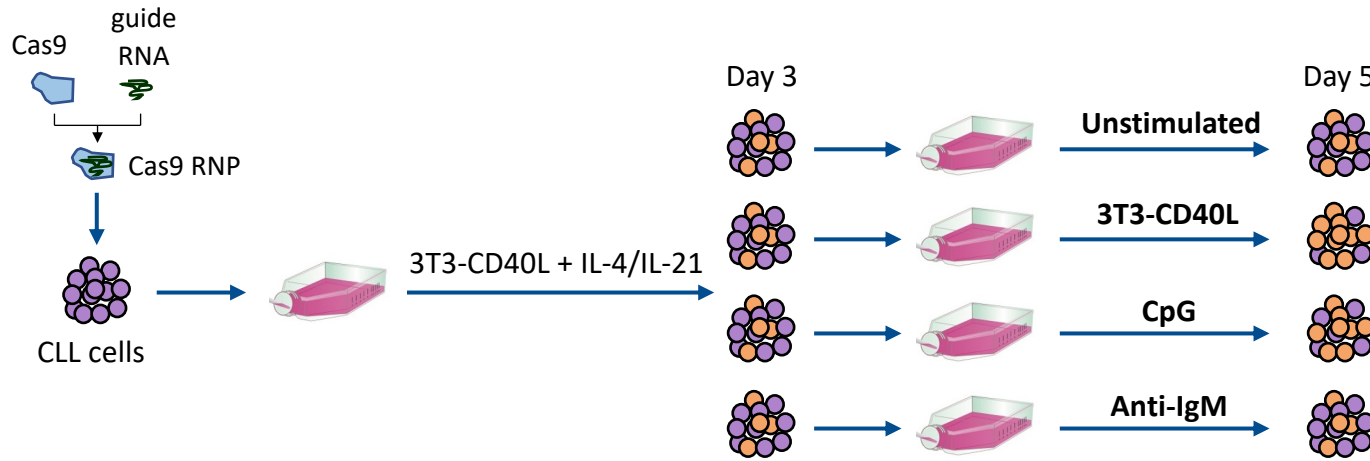
↓ Wild-type allele
↓ Mutant alleles



Murine RS cells with NFKBIE-mutations are positively selected by microenvironmental signals that activate the NF- κ B pathway

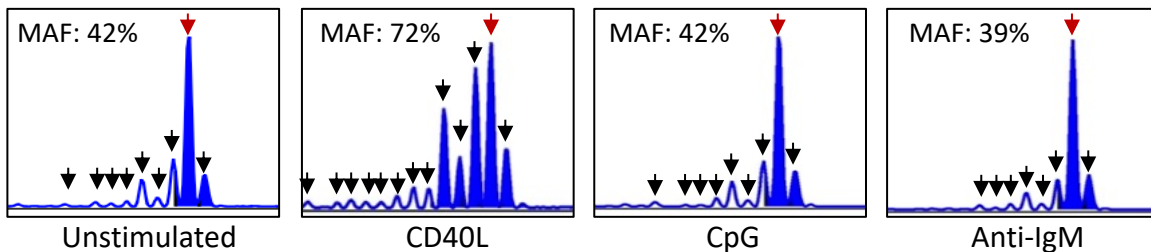


Human CLL cells with NFKBIE-mutations are positively selected by microenvironmental signals that activate the NF- κ B pathway

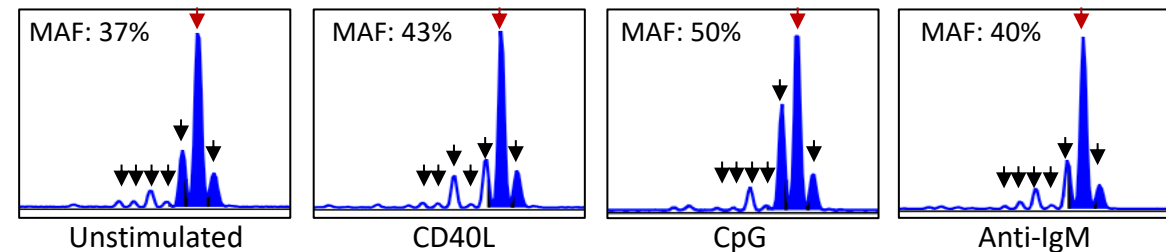


▼ Wild-type allele
▼ Mutant alleles

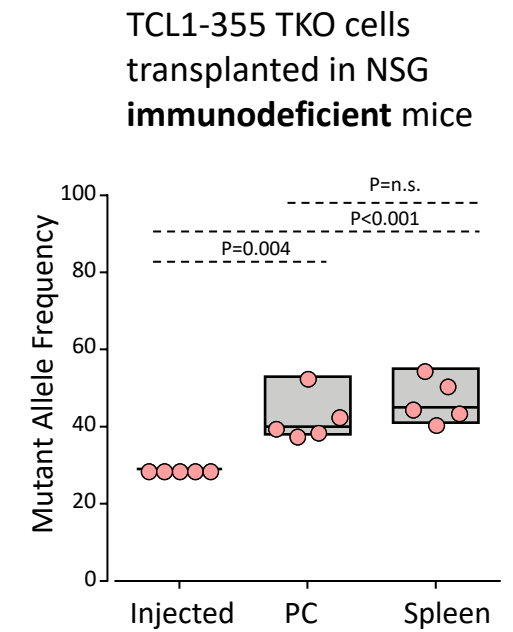
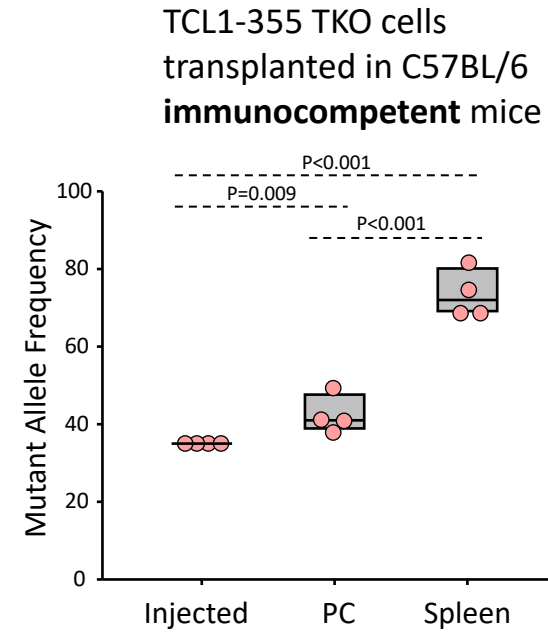
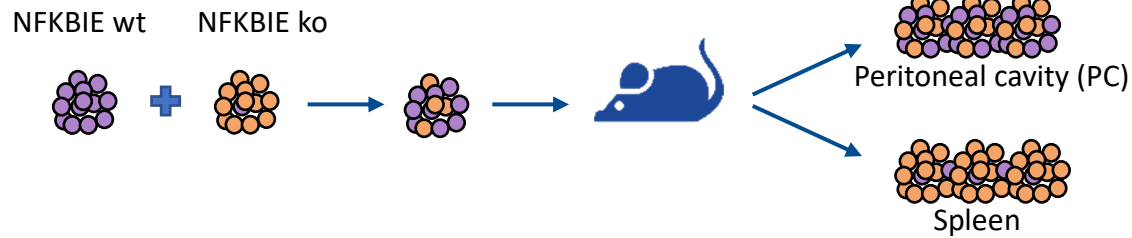
CLL G398



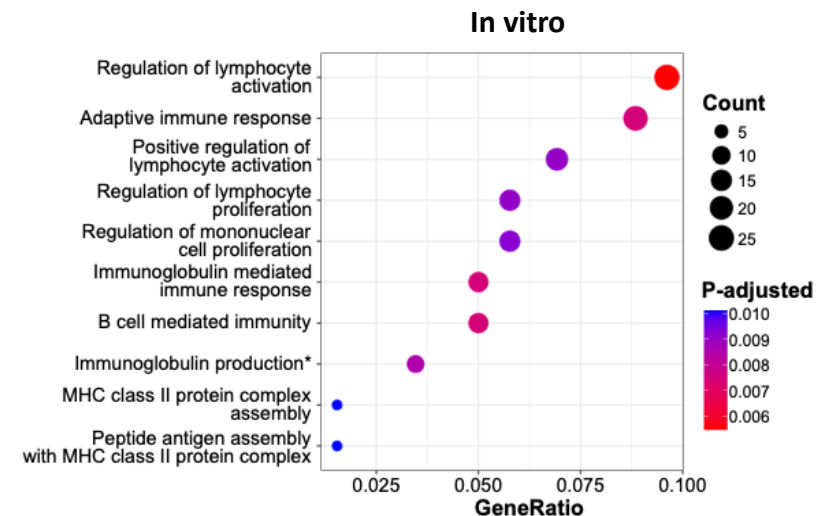
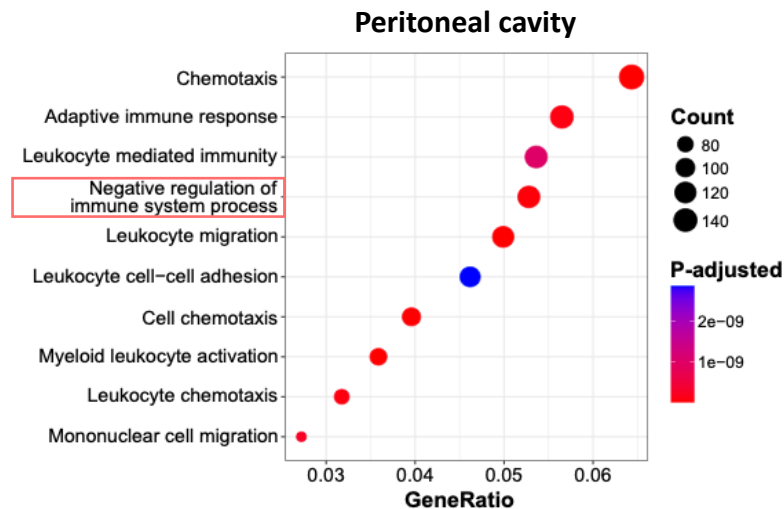
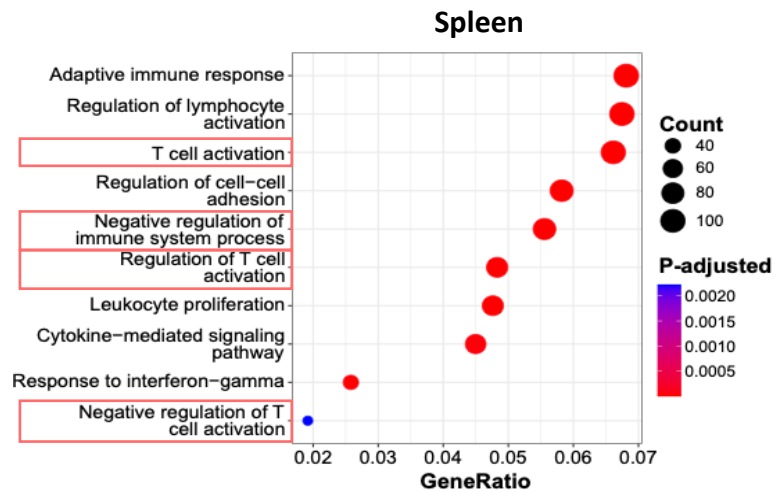
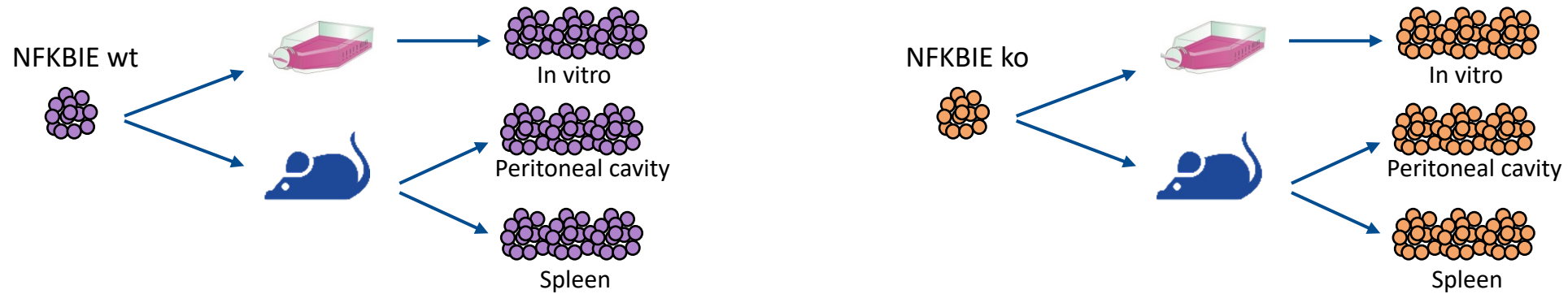
CLL G392



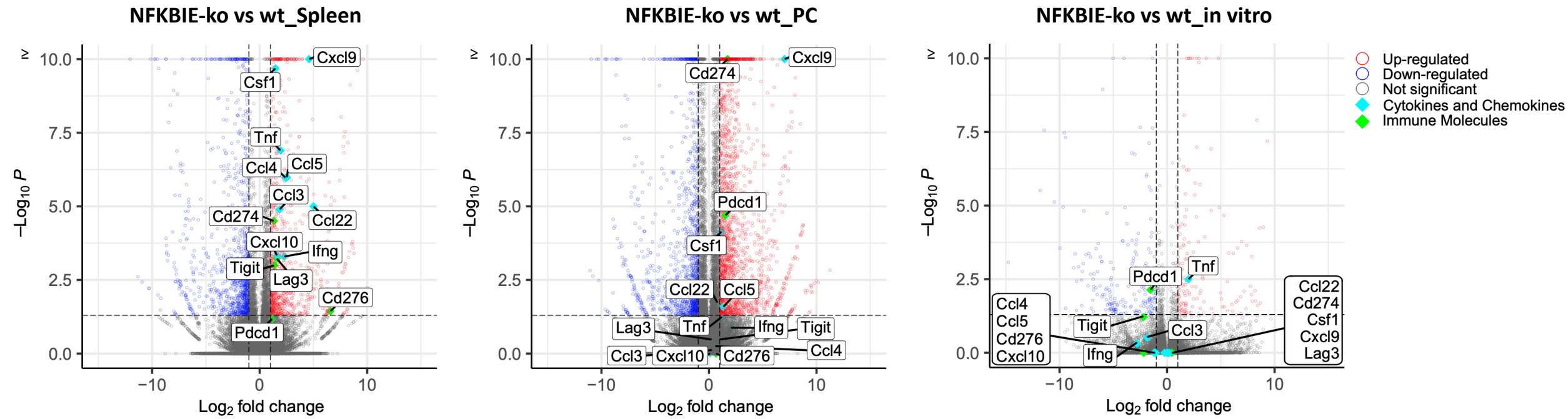
NFKBIE-mutated murine RS cells are differently selected in different anatomical compartments of immunocompetent and immunodeficient mice



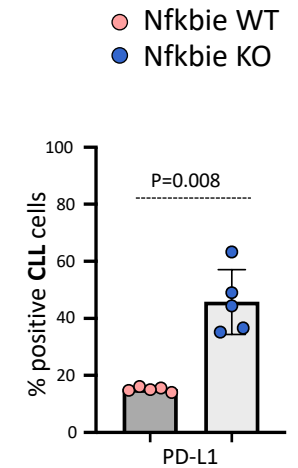
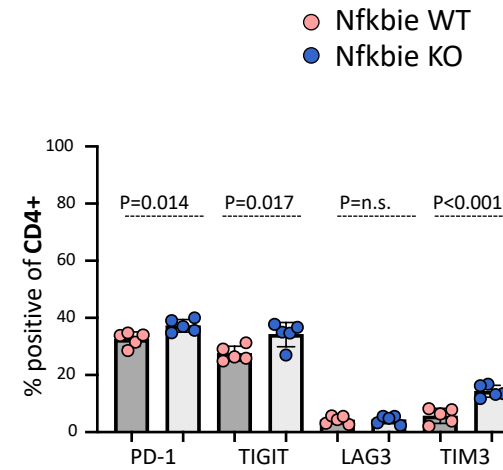
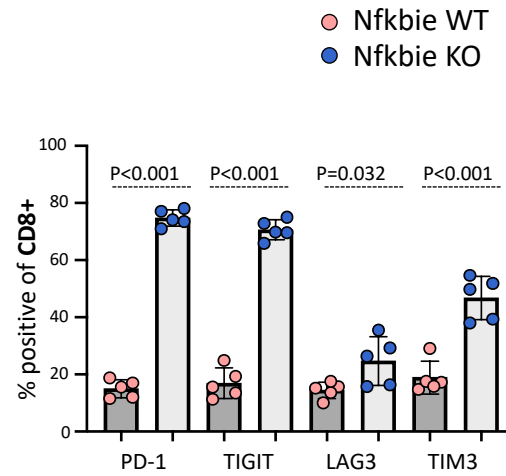
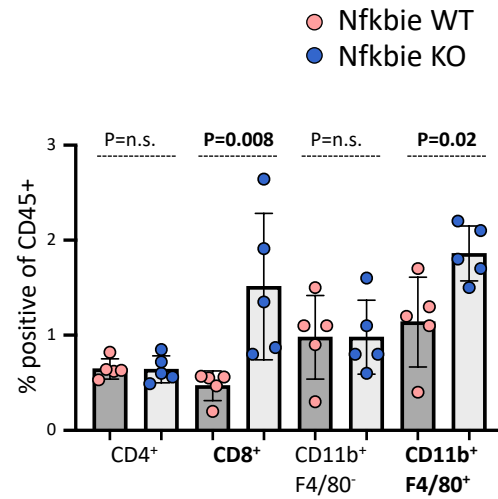
NFKBIE-mutated murine RS cells induce changes in the tumor immune microenvironment



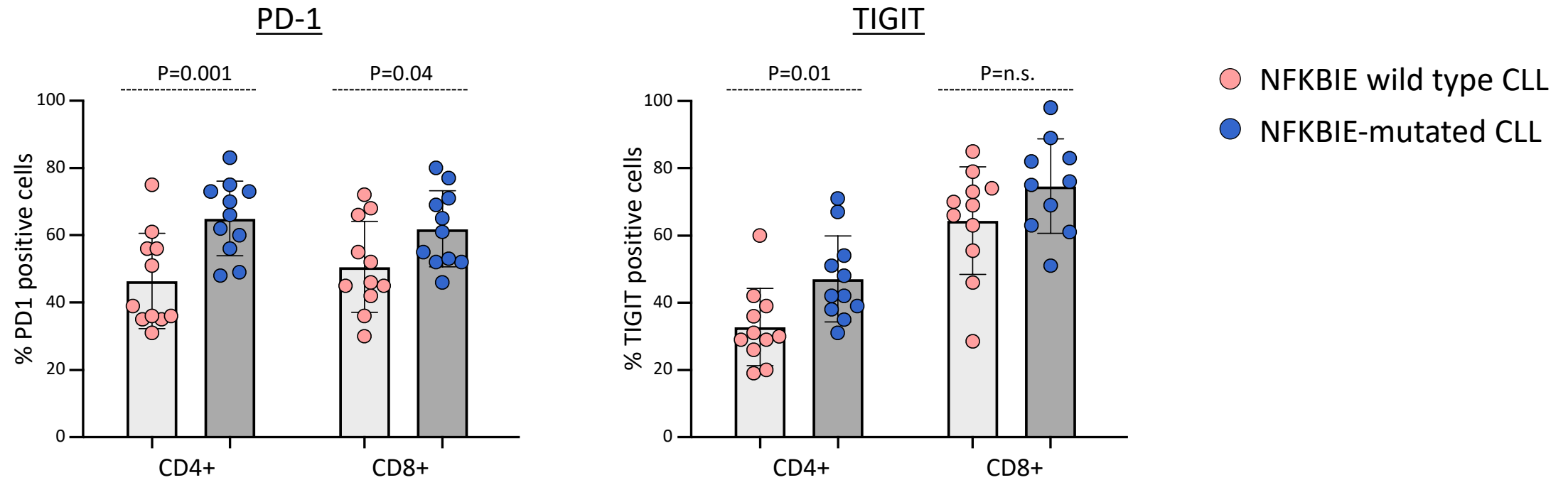
Cytokines and chemokines involved in recruitment of T cells and macrophages and inhibitory immune checkpoint molecules are enriched in spleens of mice receiving NFKBIE-mutated RS cells



Spleens of mice receiving NFKBIE-mutated CLL cells show increased expression of inhibitory checkpoint molecules on CD4+ and CD8+ T cells



TIGIT and PD-1 expression by CD4+ and CD8+ T cells in NFKBIE-mutated CLL (VAF >0.2) vs NFKBIE-wild type CLL patients



Take-home messages

- *In vivo* murine CLL and RS models with patient-specific genetic lesions can be rapidly generated by CRISPR/Cas9 editing and can be used to study the mechanisms underlying CLL progression and Richter transformation
- Cell cycle deregulation caused by combined loss of TP53 and CDKN2A/2B represents one mechanism of Richter transformation
- Genetic lesions in some CLL driver genes may contribute to Richter transformation by facilitating immune escape of the malignant B cells

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