



1404

# *Animal models*

2012...2015.

T-Cell Lymphomas: We are illuminating the darkest of tunnels

April 27-29, 2015

Bologna

GIORGIO INGHIRAMI

Weill Cornell Medical College, New York, NY

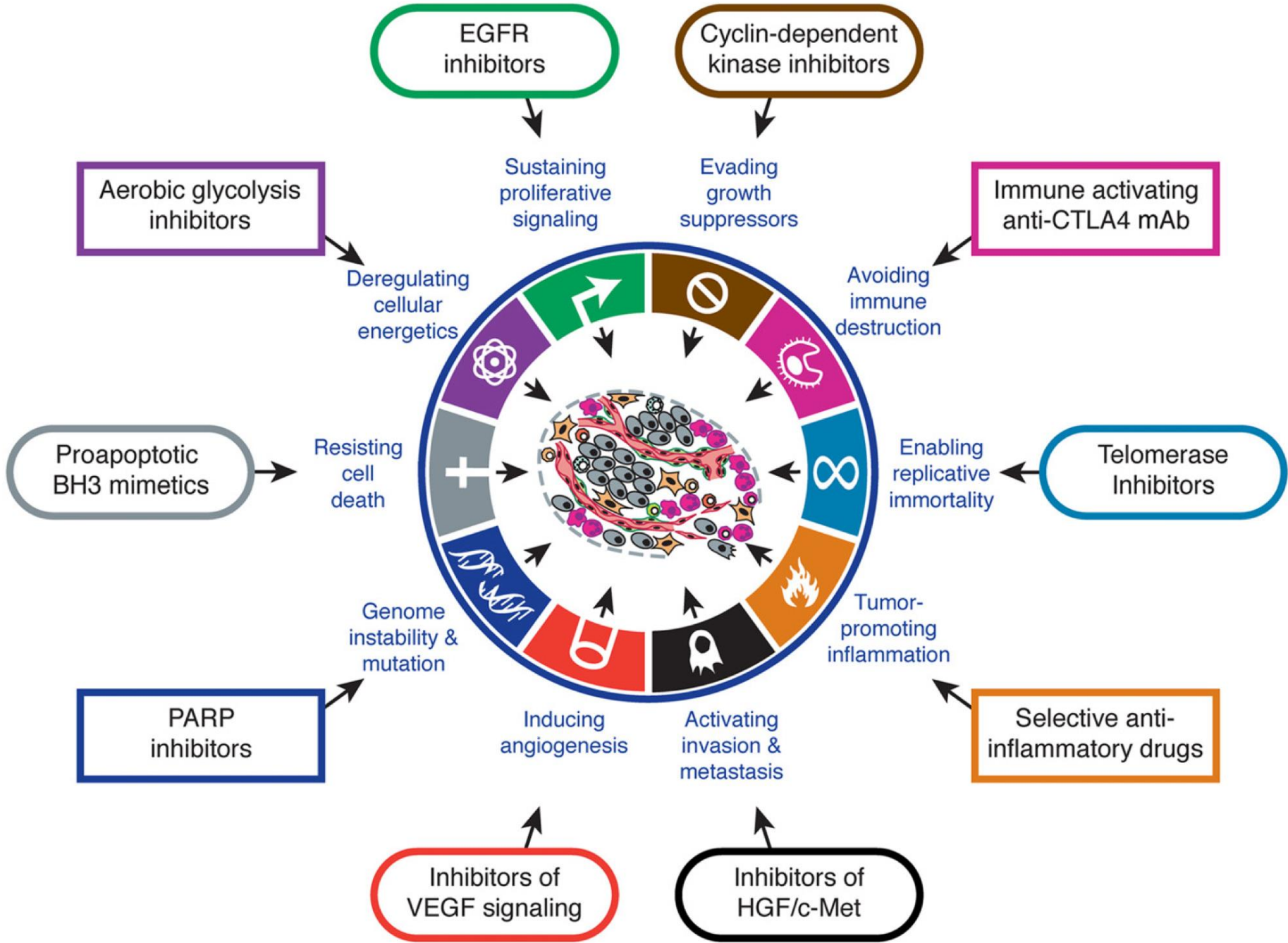
Center of Experimental Medicine and Research (CeRMS) University of Turin

# *Why we need reliable pre-clinical models?*

- Only a **handful number of compounds** reaches the clinical arena (1 of 10,000).
- **Small numbers of poorly characterized tumor cell lines** that inadequately recapitulate human disease
- ‘Xenografts do not predict for human effects’, with **90% of novel antineoplastic drugs failing** despite antitumor efficacy in classical preclinical models.
- Conventional **GEM mouse models** express/loose target genes in all cells under ectopic/forced promoters/enhancer, often with a constitutive modality
- Xenograft and/or **GEM, PDX models do not fully recapitulate the human tumour environment**
- **Erroneous use and misinterpretation of preclinical data** from cell lines and animal models.
- A poor appreciation of pharmacokinetics and pharmacodynamics, and the use of problematic endpoints and testing strategies.
- **Preclinical testing rarely includes predictive biomarkers** that, when advanced to clinical trials, will help to distinguish those patients who are likely to benefit from a drug.

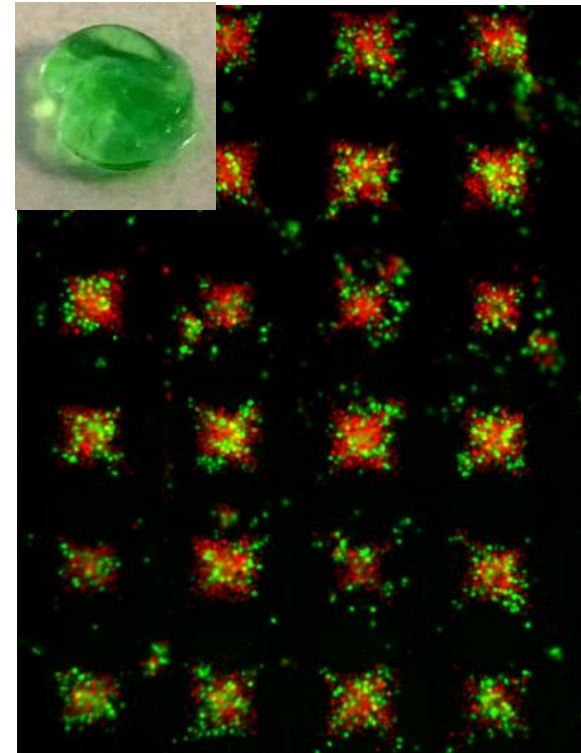
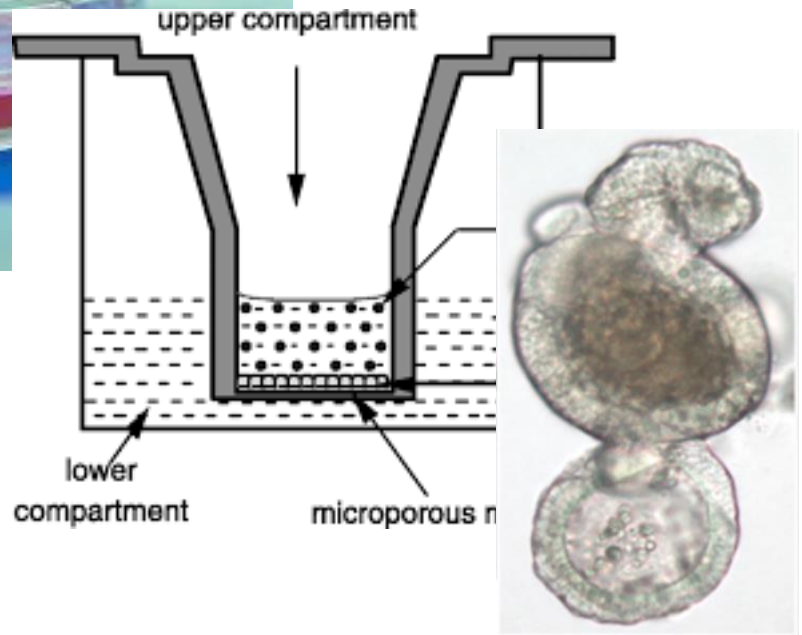
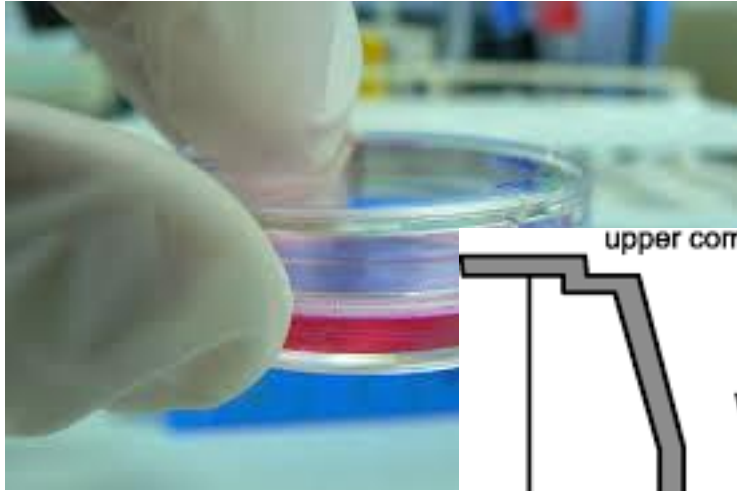
# *What about reproducible PTCL models?*

- Although several cell lines derived from T-ALL exist. Rare in vitro models for neoplastic post-thymic lymphocytes are available, with HTLV-I+, CTCL and ALK+ ALCL lines representing the exception.
- Few spontaneous (Roquinsan) or engineered (i.e. ITK-SYK, NPM-ALK) mouse models, faithfully reproducing their corresponding human counterparts, have been successfully used to define the pathogenetic mechanisms leading to T-cell transformation and/or design and validate therapeutic protocols.

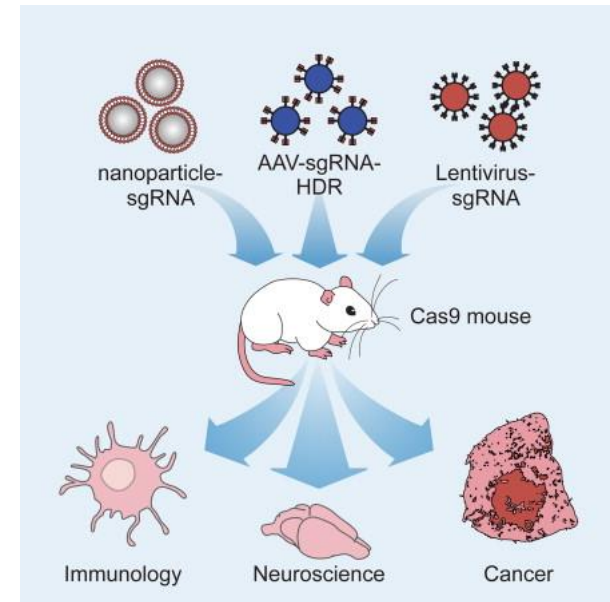
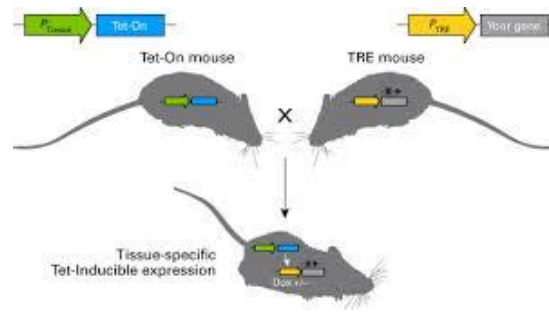
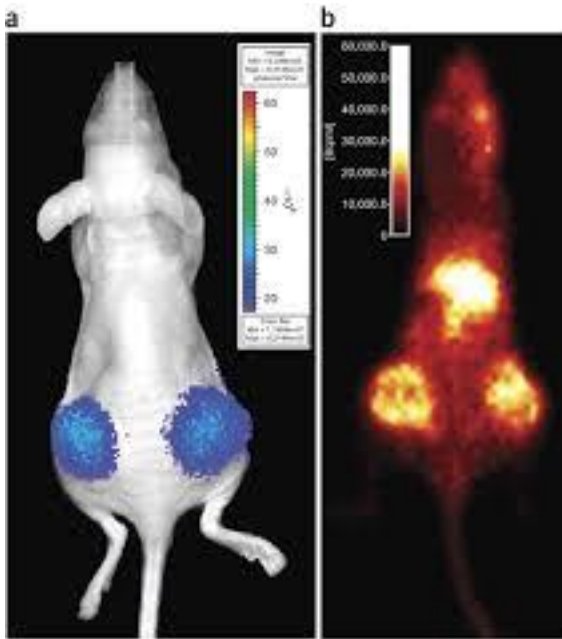


Douglas Hanahan and Robert A. Weinberg Cell. 2011, 44(5):646-74

# *Have we the right models ?:* *“2D versus 3D in vitro”*

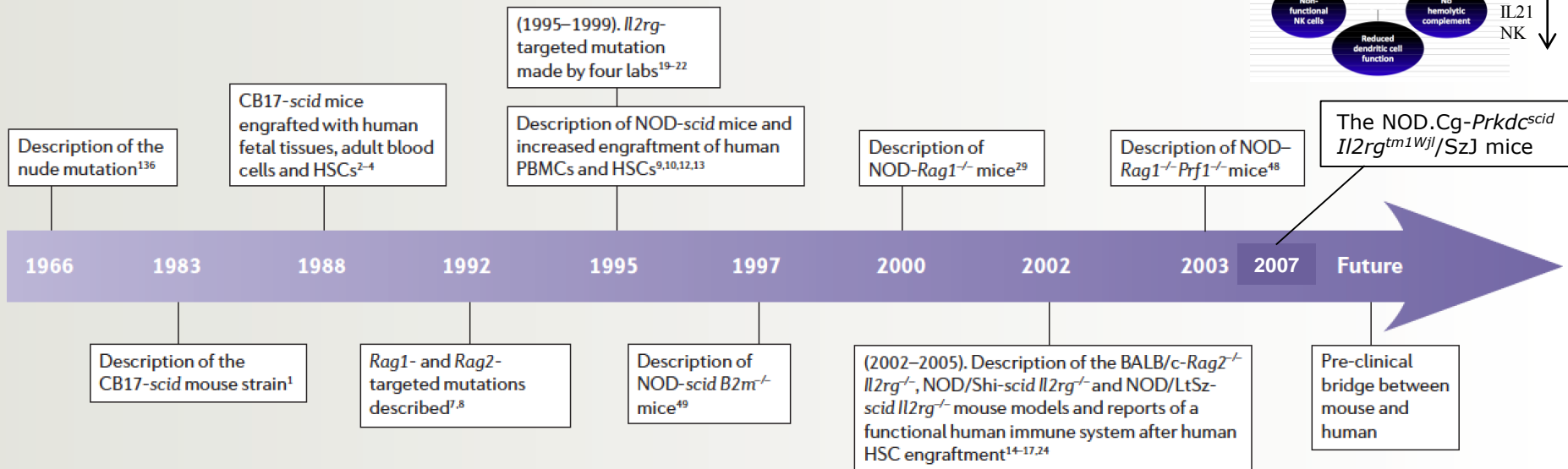


# *Rapidly evolving strategies for new mouse models*



# Humanized mouse models

## Timeline | Important events in the development of humanized mice

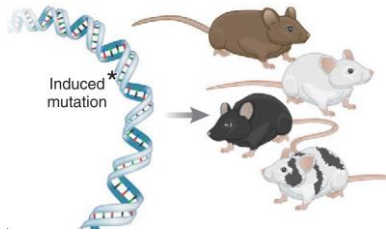


*B2m*,  $\beta_2$ -microglobulin; HSC, haematopoietic stem cell; *Il2rg*, interleukin-2 receptor  $\gamma$ -chain; NOD, non-obese diabetic; PBMC, peripheral-blood mononuclear cell; *Prf1*, perforin 1; *Rag*, recombination-activating gene; *scid*, severe combined immunodeficiency.

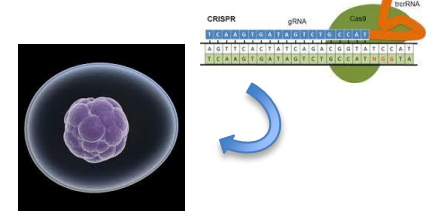
# The PDTX models



Humanized NSG mice



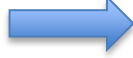
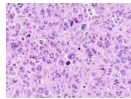
MHC-I ko  
IL-6  
IL-3, CSF2, Kit ligand  
Class II  
BAFF



MHC-IA2 NSG mice



Sub-Q



Organoids





# NOD/scid and NSG mice have been successfully used to study human CTL



*Meyer L.H. et al 2011*

Cancer Cell  
**Article**

**Early Relapse in ALL Is Identified by Time to Leukemia in NOD/SCID Mice and Is Characterized by a Gene Signature Involving Survival Pathways**

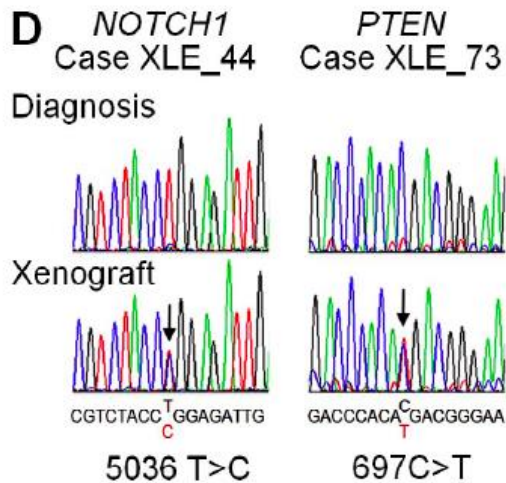
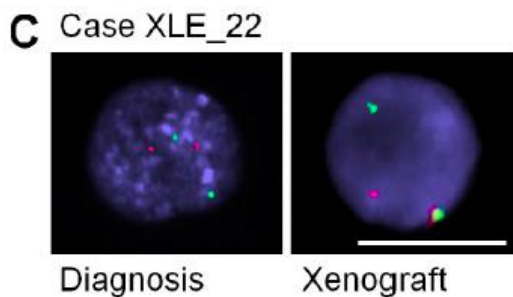
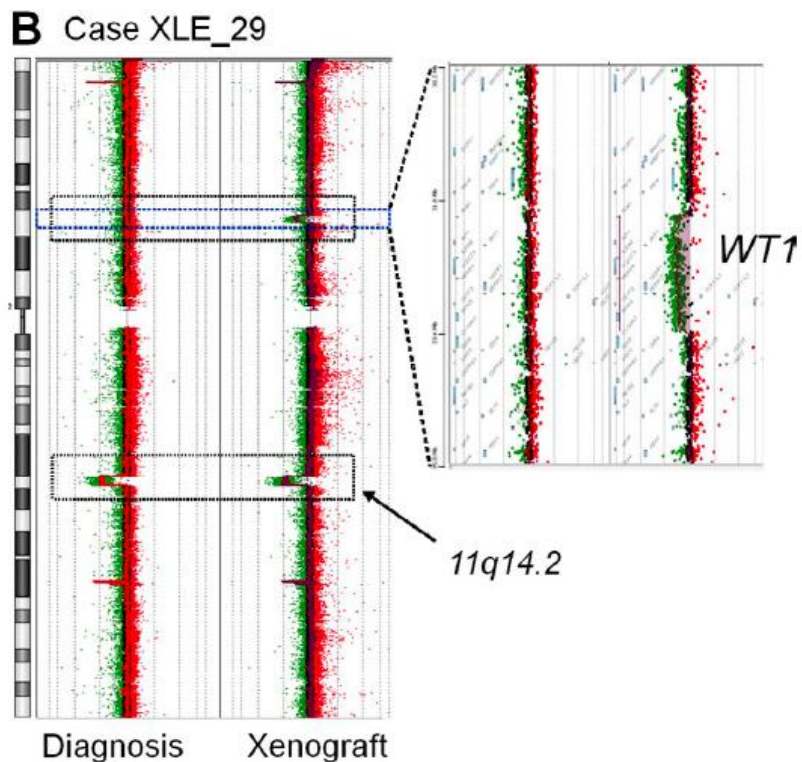
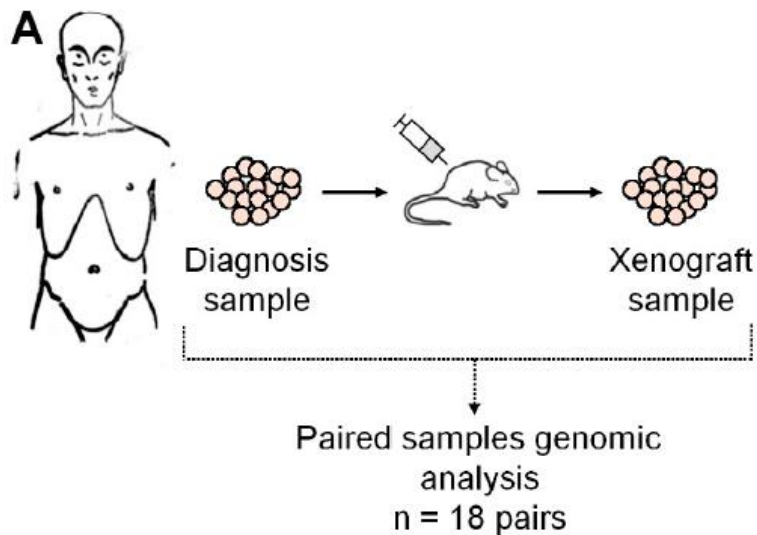
Brief Definitive Report

**JEM** *Clappier E. et al 2011*

Clonal selection in xenografted human T cell acute lymphoblastic leukemia recapitulates gain of malignancy at relapse

*Experimental Dermatology, Krejsgaard T. et al 2010*

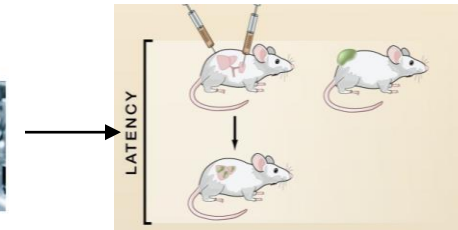
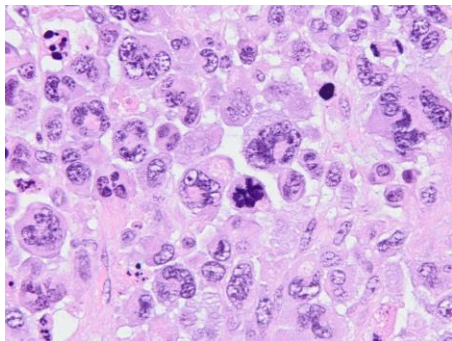
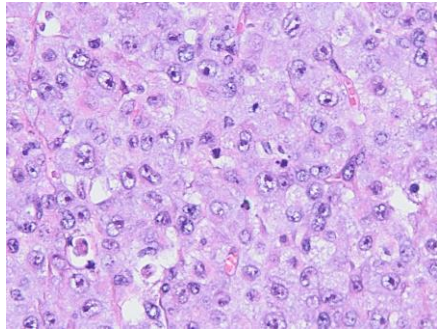
**A novel xenograft model of cutaneous T-cell lymphoma**



**E**

Gene	Change in xenograft
<i>PTEN</i>	Deletion or mutation
<i>CDKN2A/B</i>	Deletion
<i>WT1</i>	Deletion
<i>DLEU7</i>	Deletion
<i>MYB</i>	Gain
<i>MYC</i>	Translocation
<i>NOTCH1</i>	Mutation
<i>FBXW7</i>	Mutation

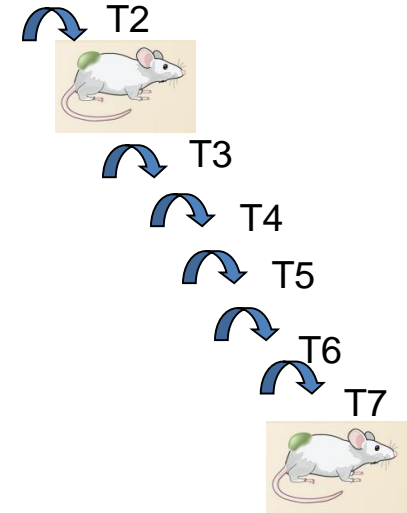
# Patient Derived Tumor Graft from fresh and/or cryopreserved tissue samples



Tumor fragment implants  
in NSG mice

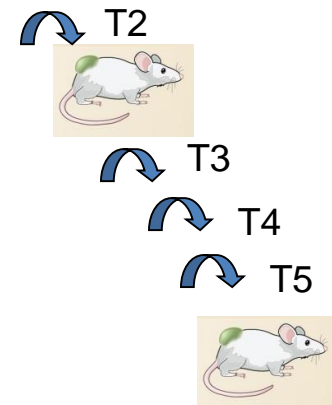
6 wks

Serial tumorgrafts ALK+ ALCL

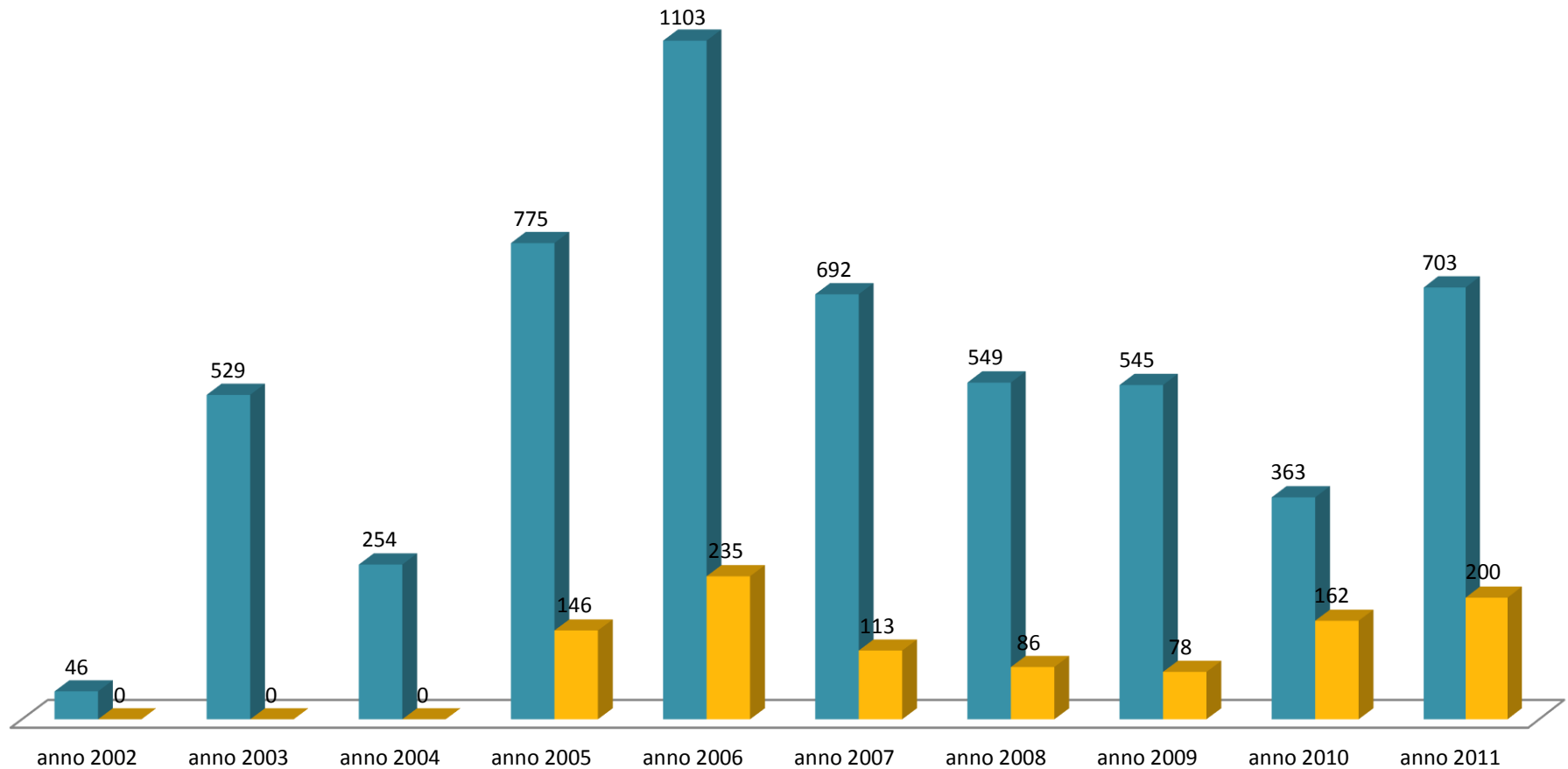


Serial Tumorgrafts ALK- ALCL

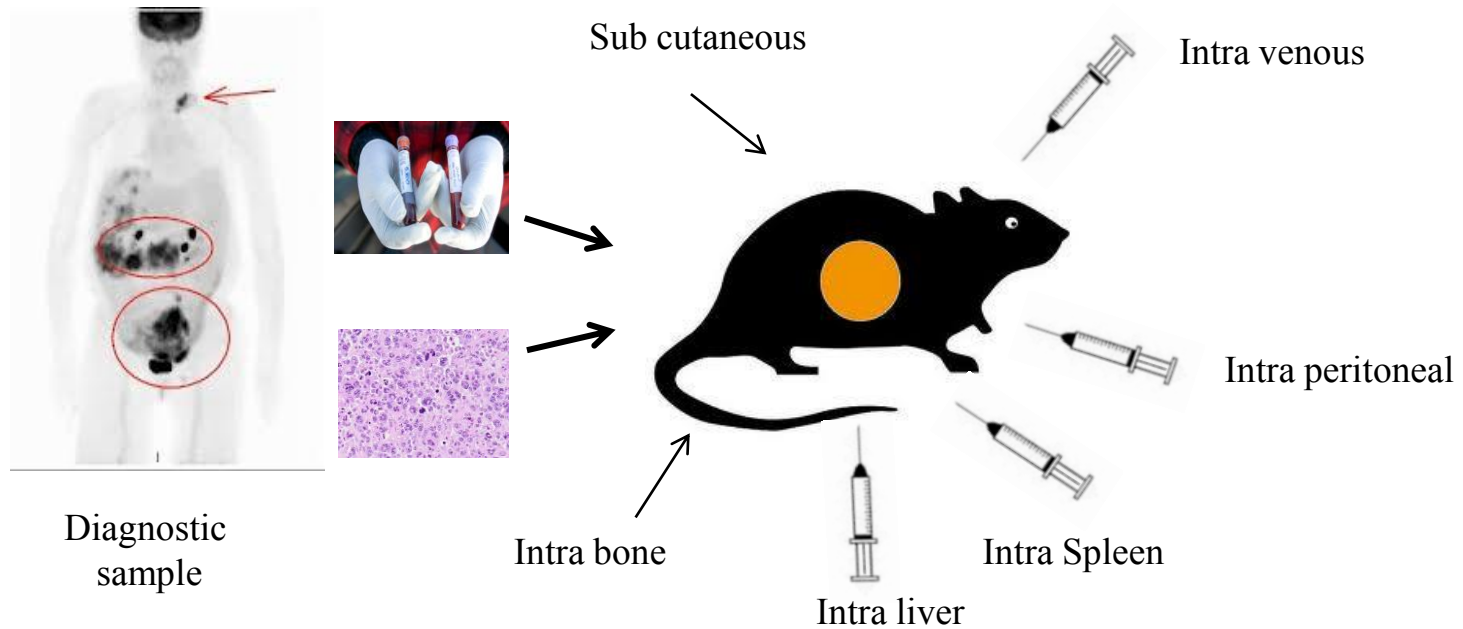
8 wks



# *Source of cancer samples: Fresh versus viable frozen tissues?*



# *Can different implantation routes improve PDTX grafting?*



# Precision Therapeutic Medicine: new ideas at work



Biorepository



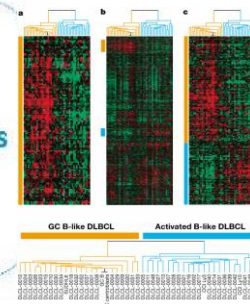
Molecular stratifiers



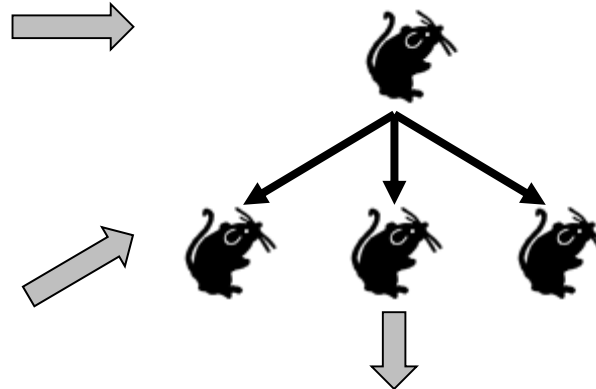
5

**Results**

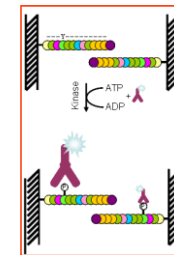
Tumor growth inhibition results delivered to oncologist



Tumor expansion



HTP molecular stratification

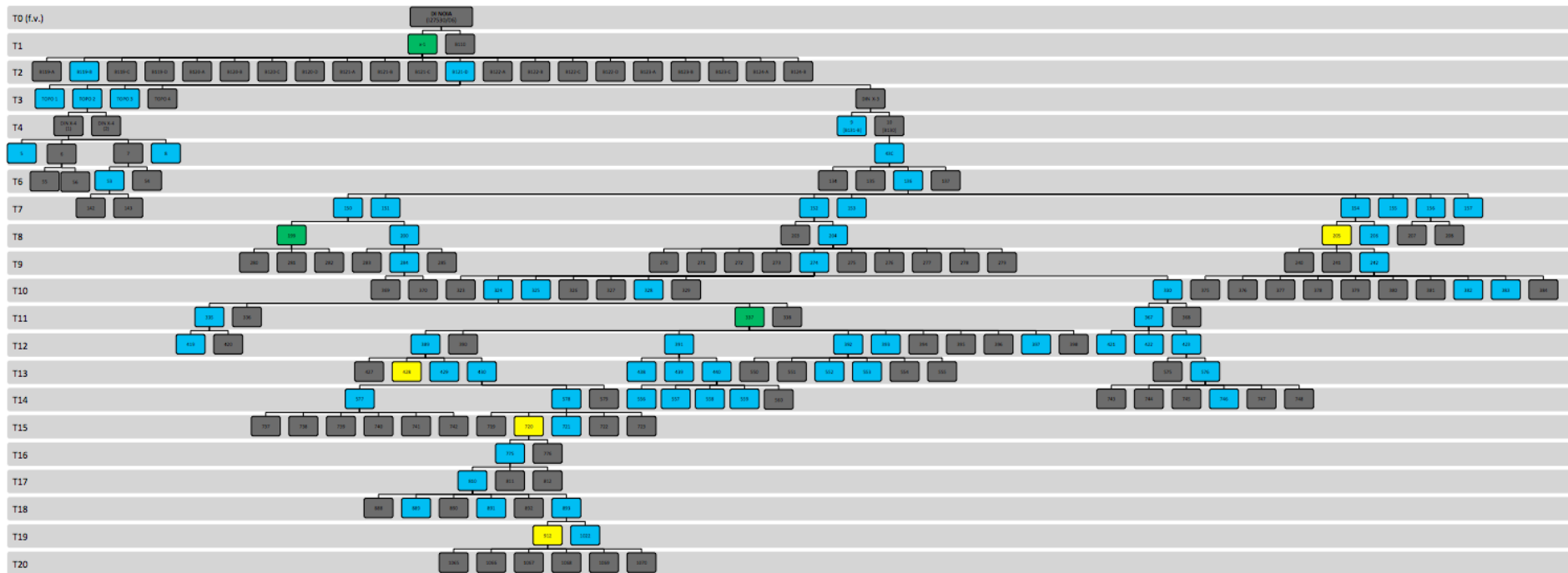


- WES
- RNAseq
- RRBs
- Proteomics

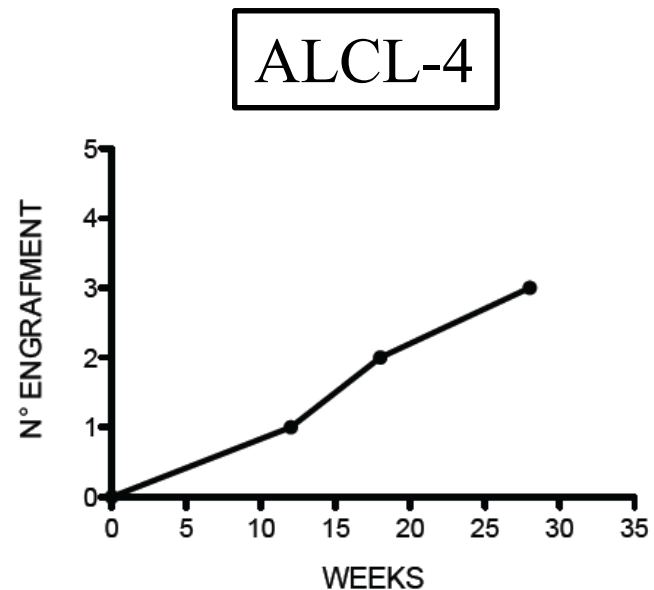
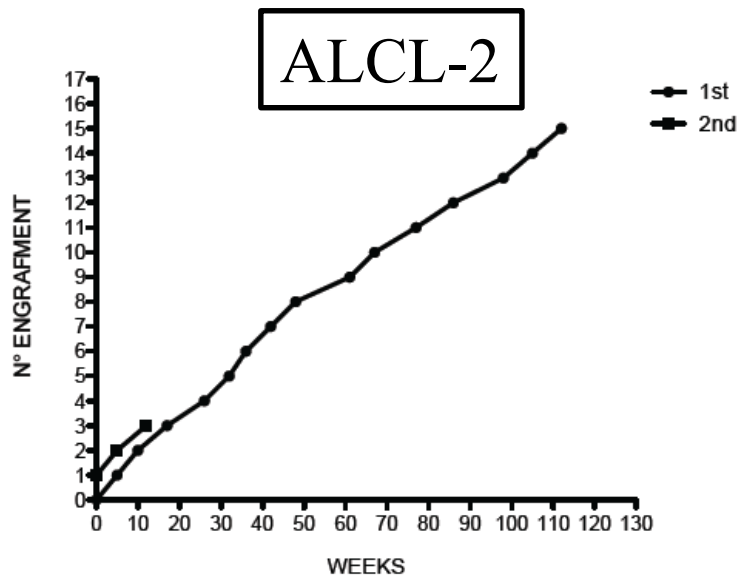
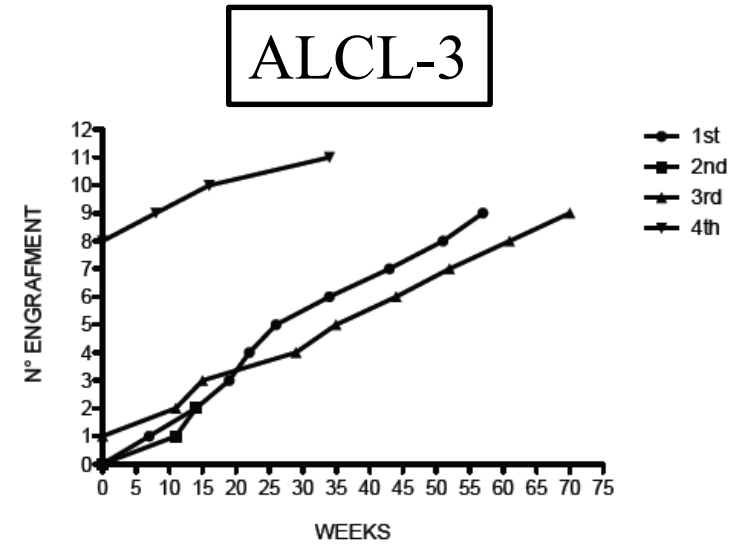
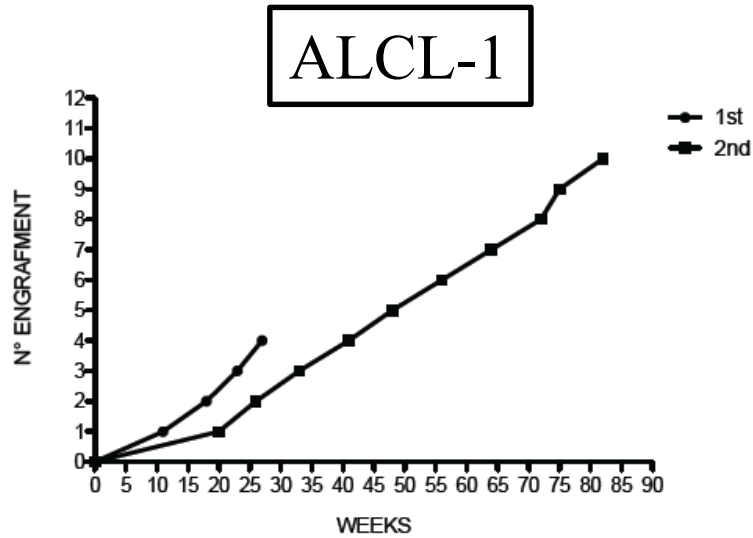


# Representative ALCL tumorgraft expansion

## ALCL-1

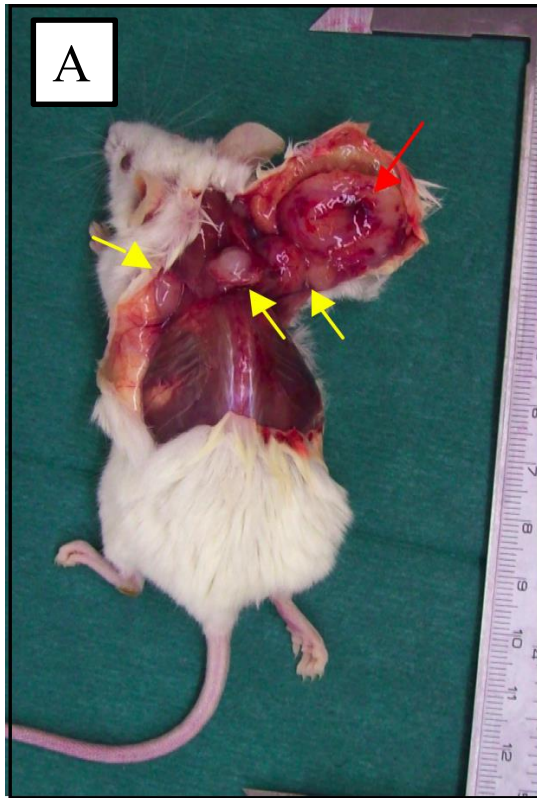


# ALCL time curves along serial tumorgraft passages

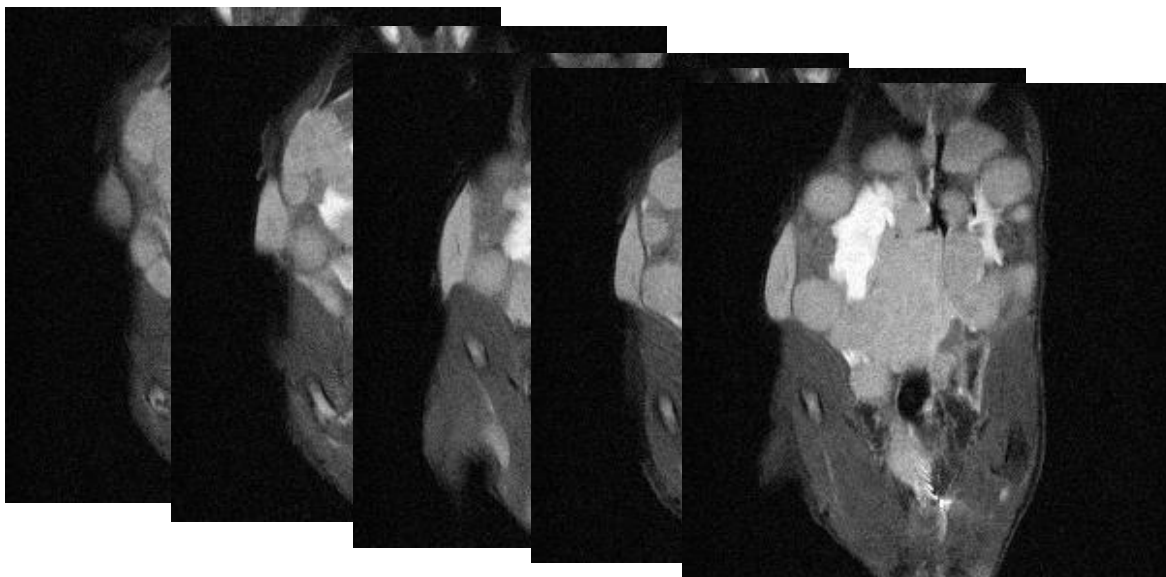




# ALCL tumorgraft on disseminate to secondary lymphoid and parenchymal organs

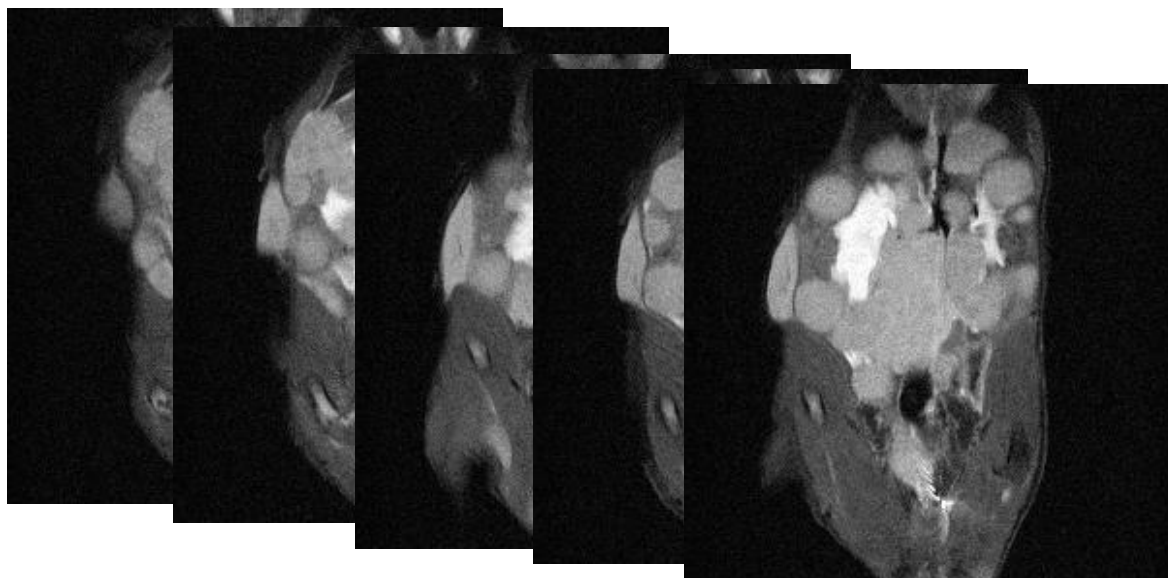


# *Total body MRI scanning and therapeutic response assessments*



 aspectimaging

# *Total body MRI scanning and therapeutic response assessments*

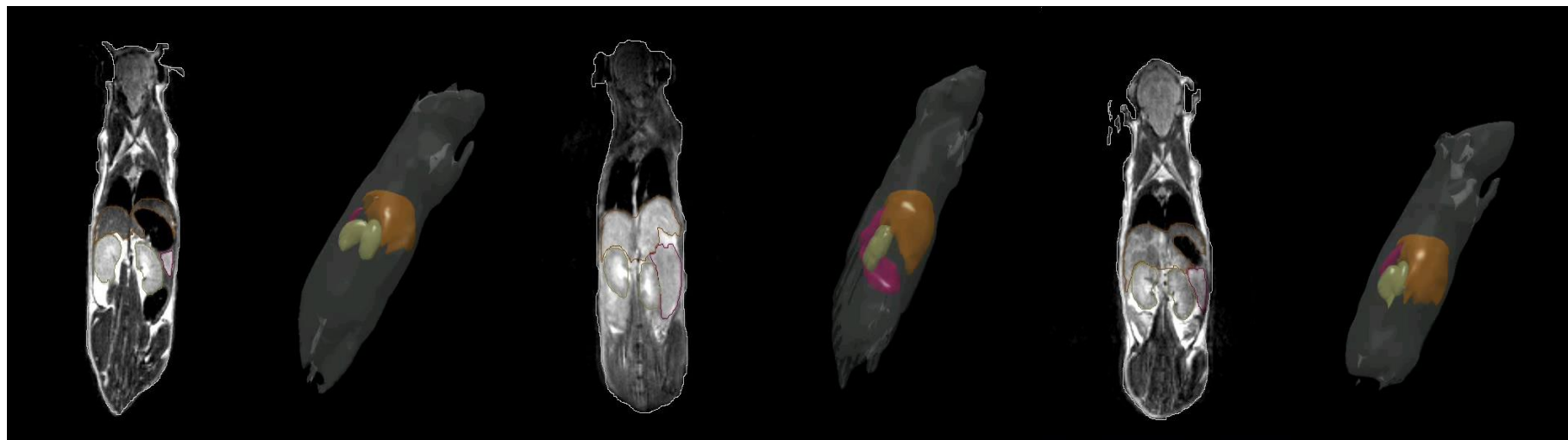


 aspectimaging

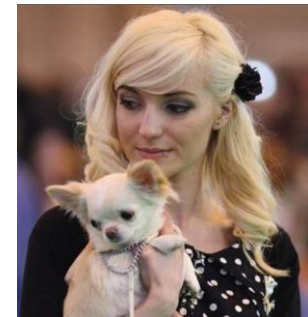
ALCL-PDT Day 0

ALCL-PDT day 14

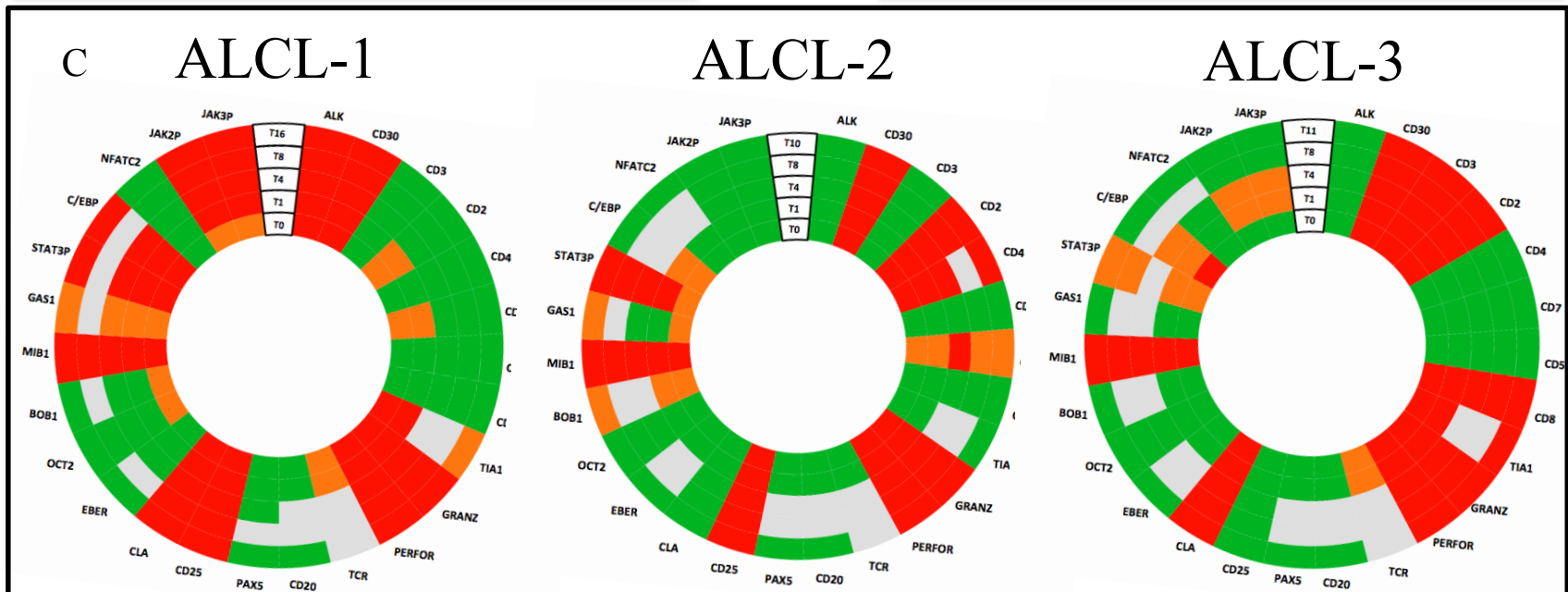
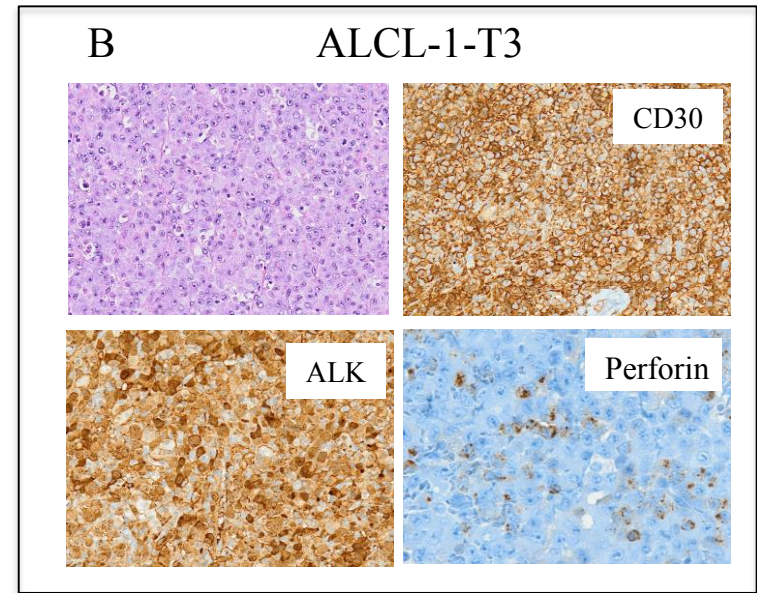
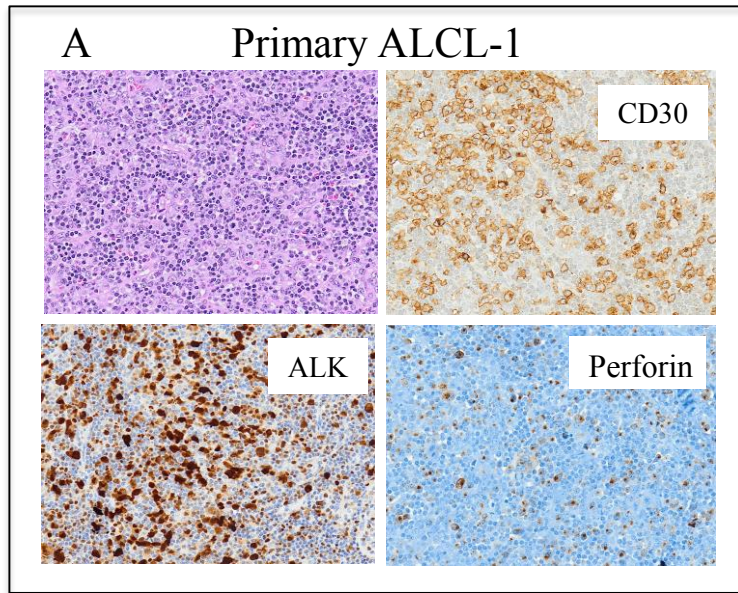
ALCL-PDT day 14 treated



# ***Do PDTX fully recapitulate their corresponding primary lesions***

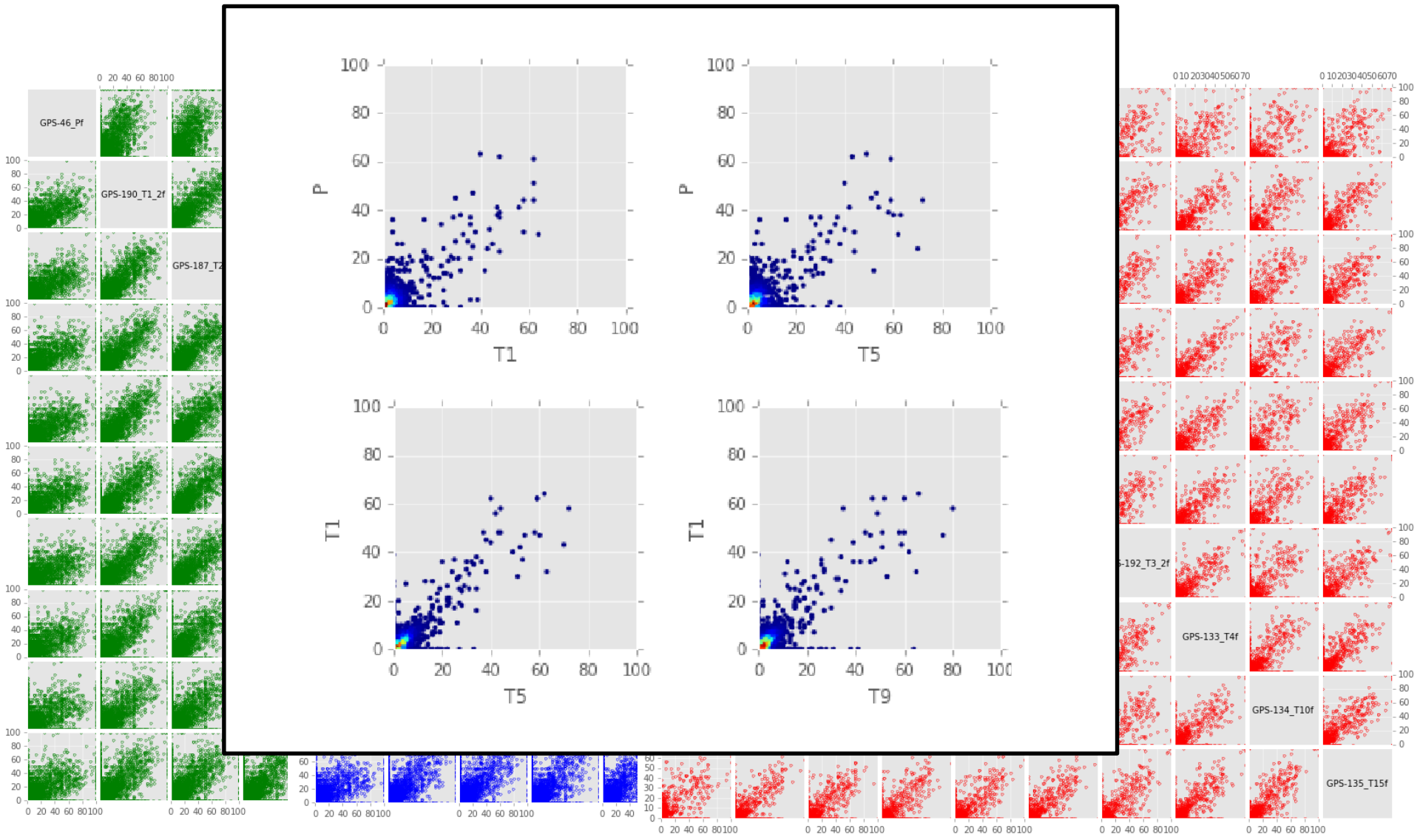


# Primary ALCL and matched ALCL tumorgrafts display identical immuno-profiles

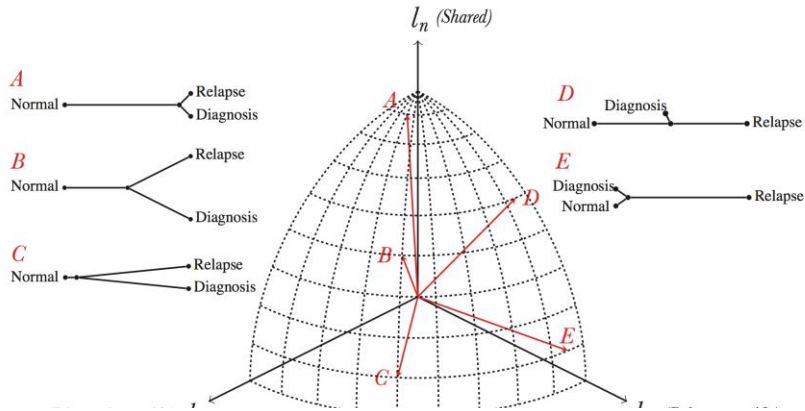




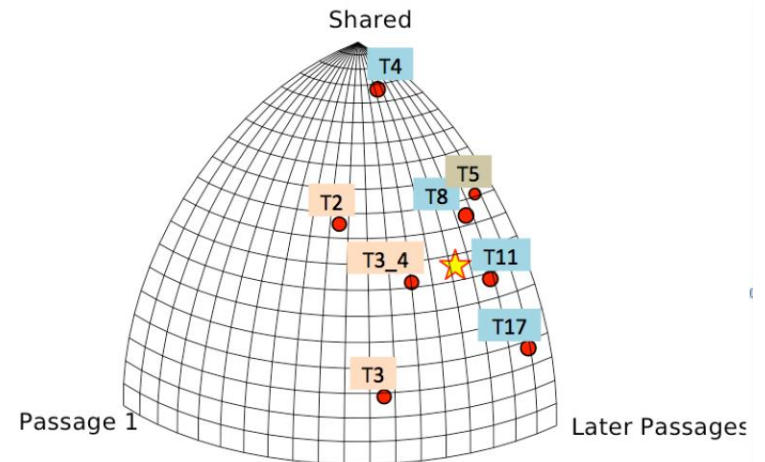
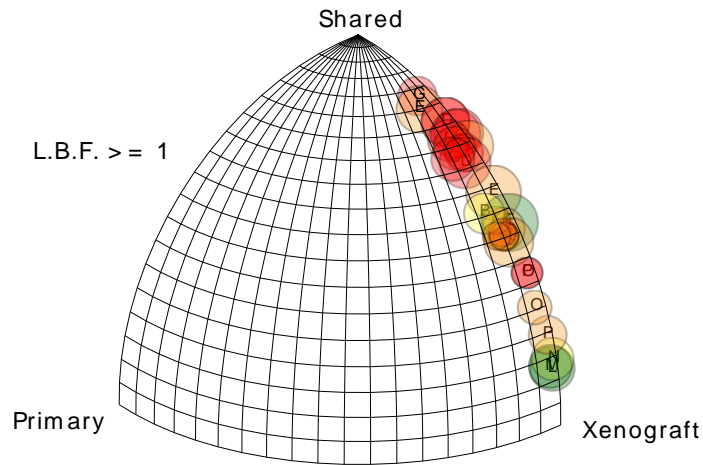
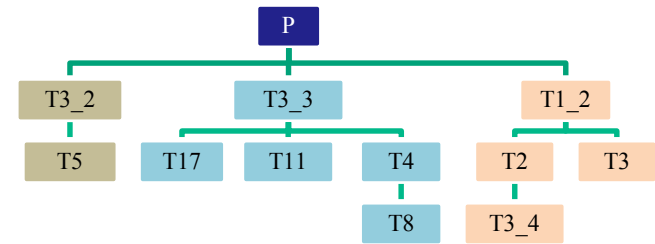
# *Does clonal evolution take place in NSG models?*



# Evolutionary modes in $P\Sigma^3$ .



## ALCL-3-PDT

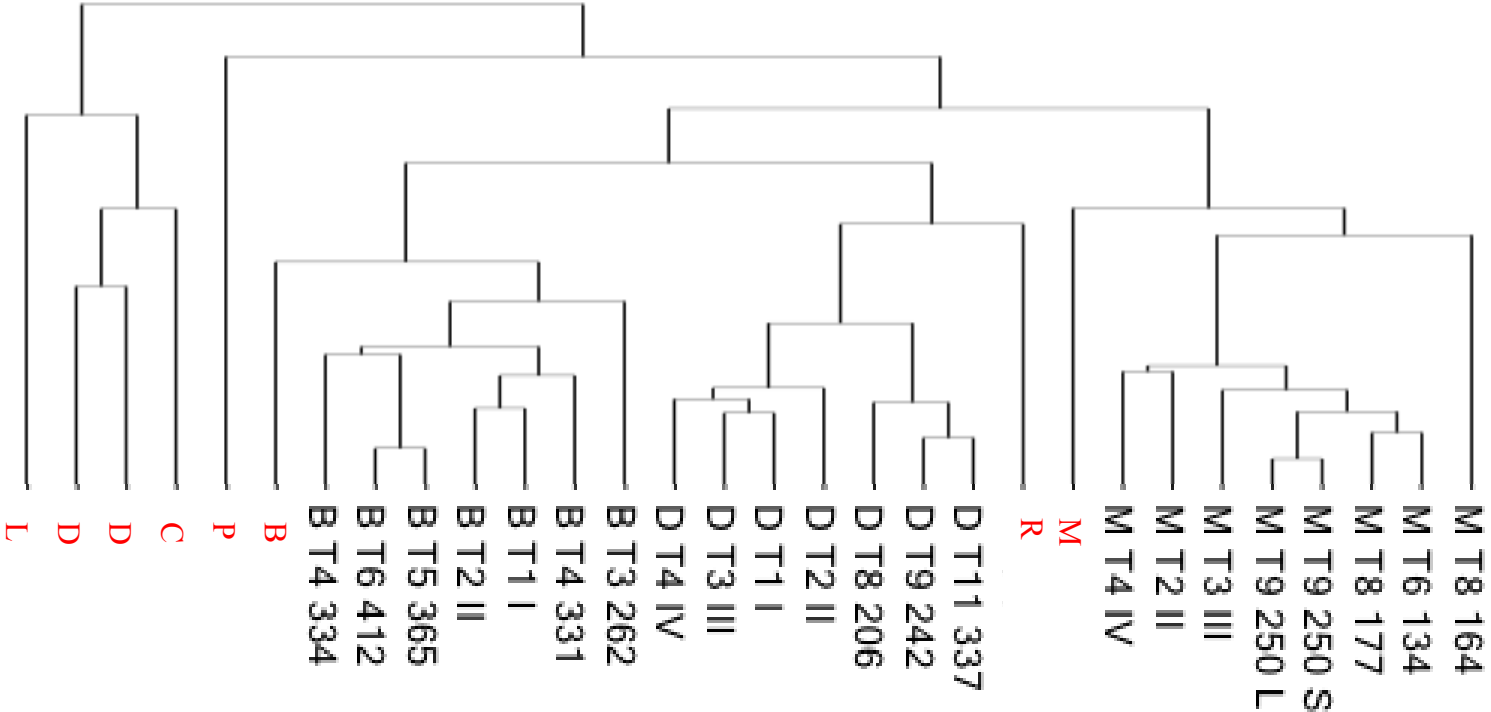




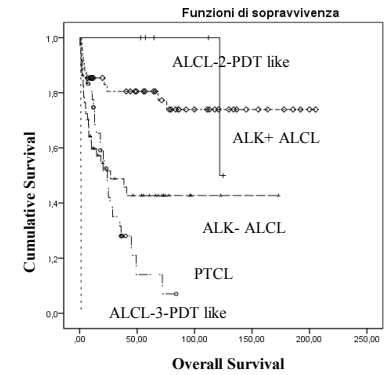
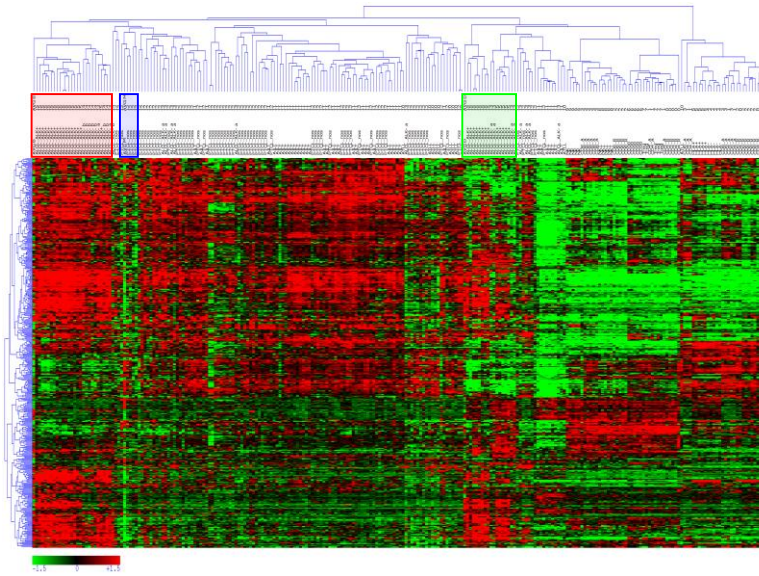
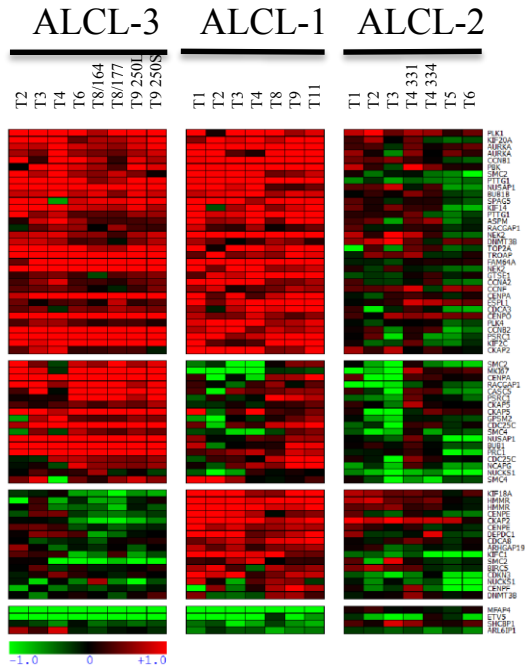
# Can we discover novel hits?

The image displays a large, multi-page data table, likely a spreadsheet or a database export, with a prominent red border. The table is organized into three distinct sections, each with its own set of headers and data rows. The columns are densely packed and contain a variety of data types, including chemical structures (SMILES strings), names, and numerical values. The data is color-coded, with rows alternating between light green and light red backgrounds. The table is organized into three distinct sections, each with its own set of headers and data rows. The columns are densely packed and contain a variety of data types, including chemical structures (SMILES strings), names, and numerical values. The data is color-coded, with rows alternating between light green and light red backgrounds. The table is organized into three distinct sections, each with its own set of headers and data rows. The columns are densely packed and contain a variety of data types, including chemical structures (SMILES strings), names, and numerical values. The data is color-coded, with rows alternating between light green and light red backgrounds.

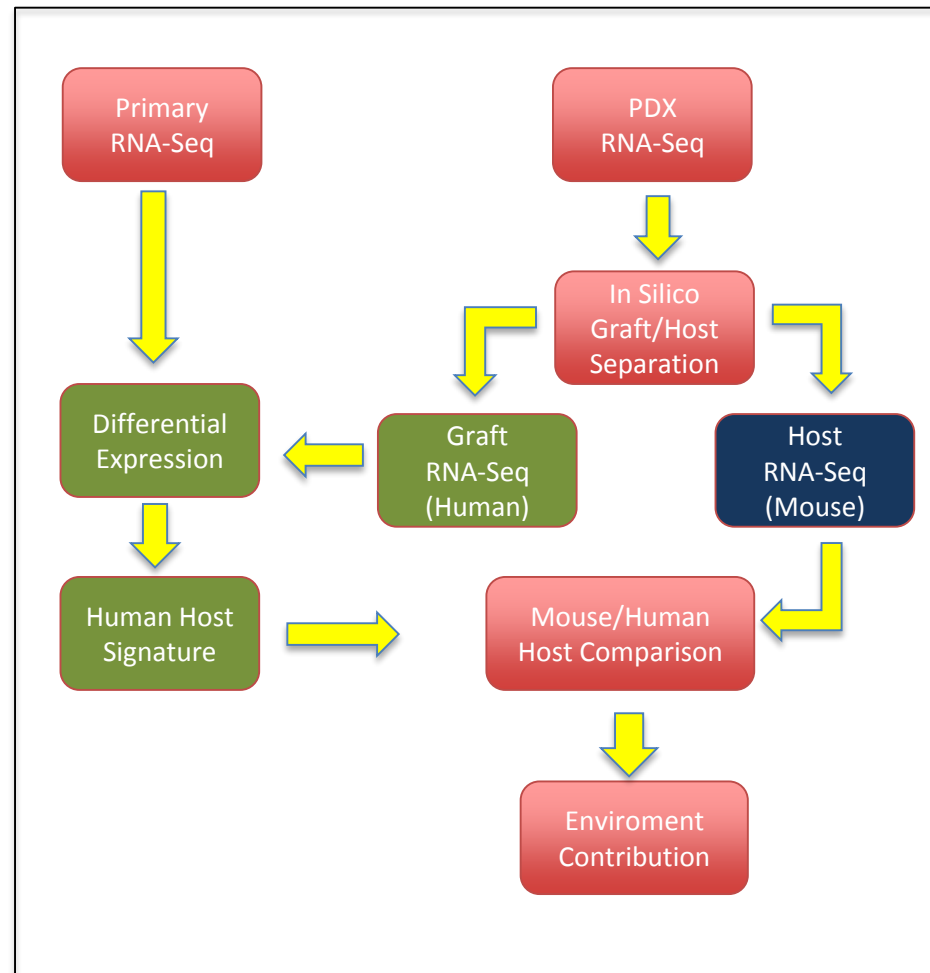
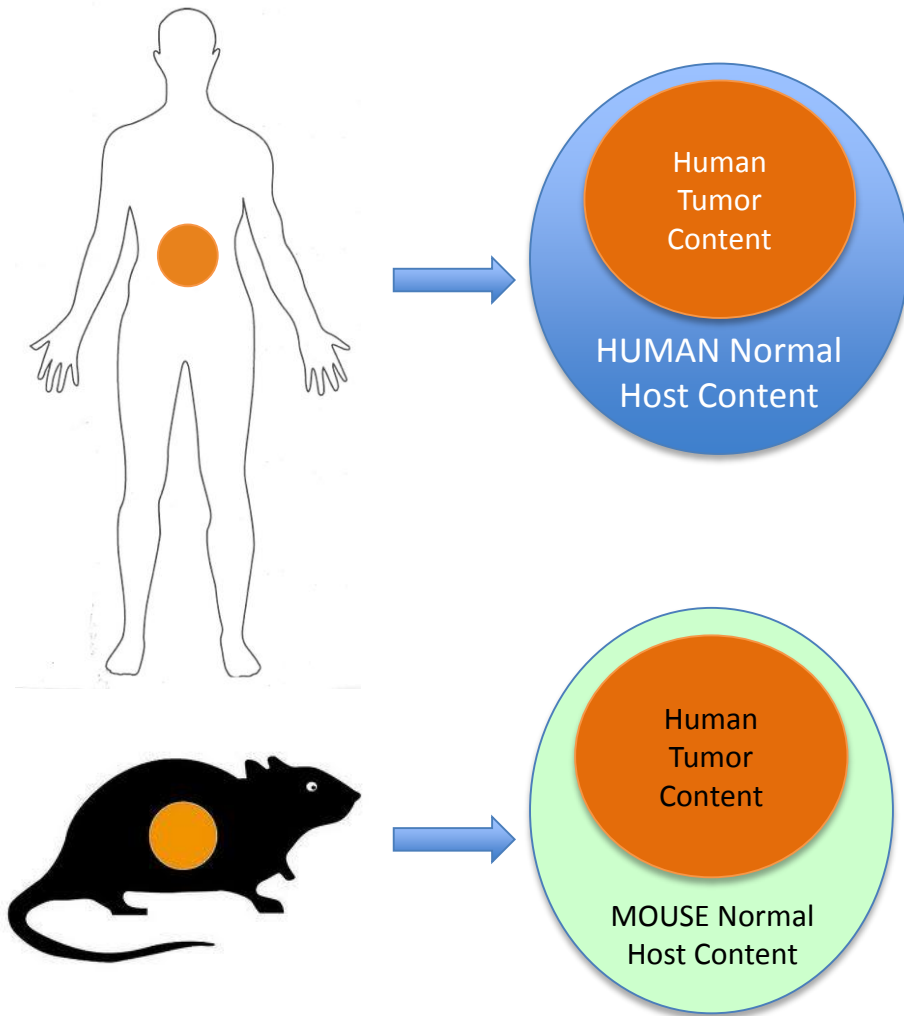
# Gene expression profiling shows unique signature for each individual tumorgraft ALCL line

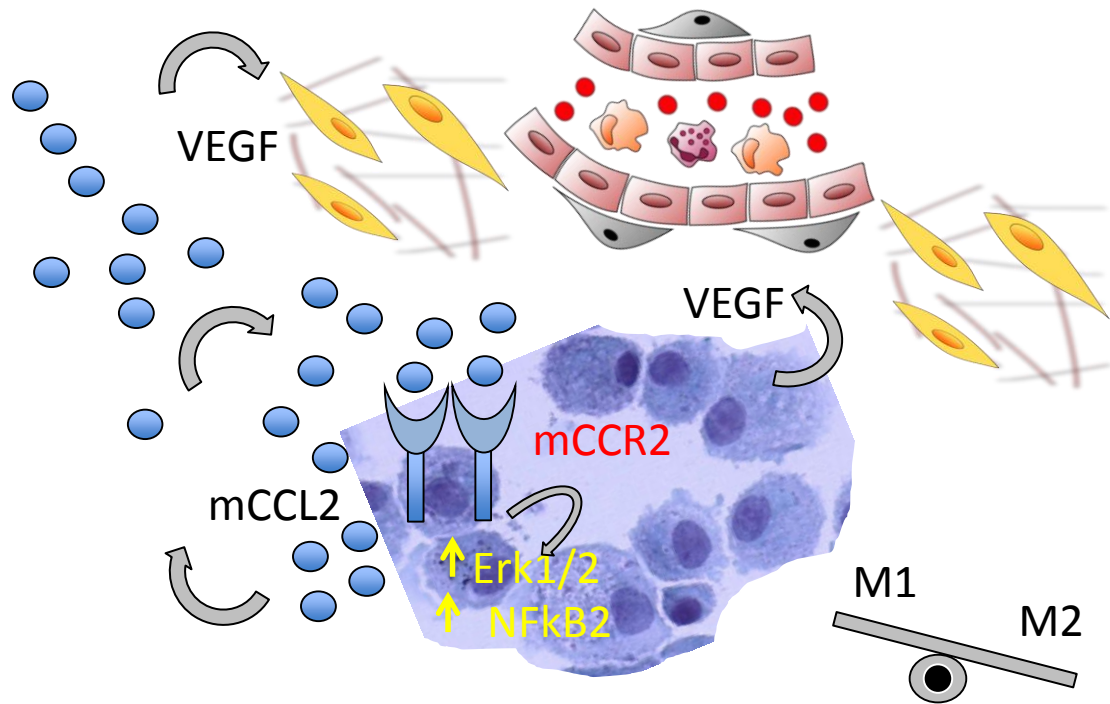
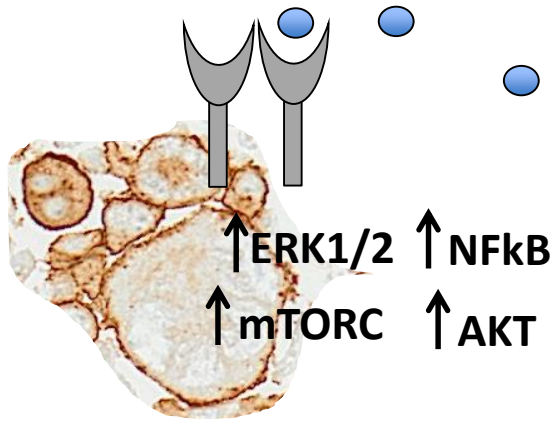
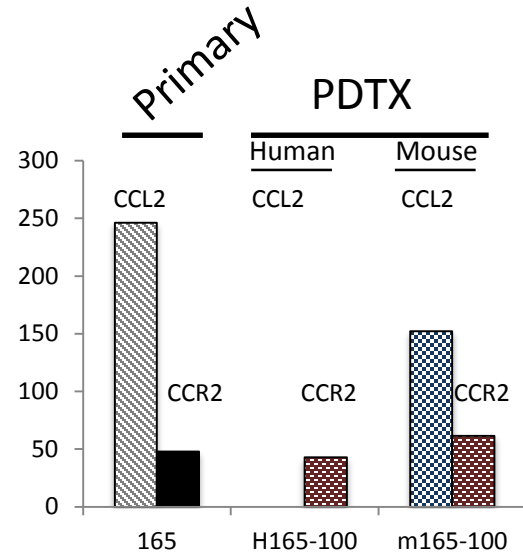
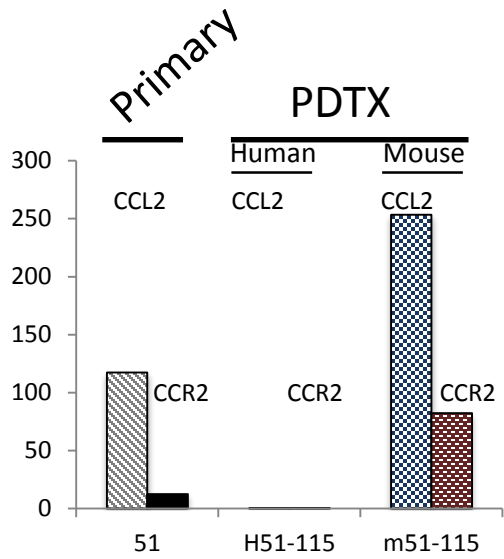


# Gene expression signatures of ALCL-PDT identified unique subsets among PTCL patients



# Host-lymphoma Interactions

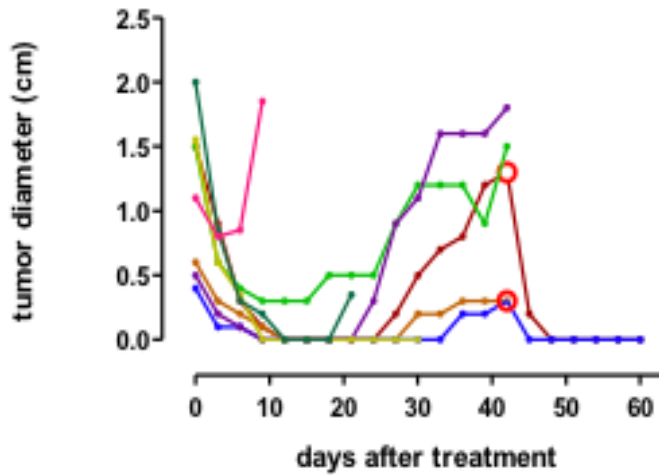




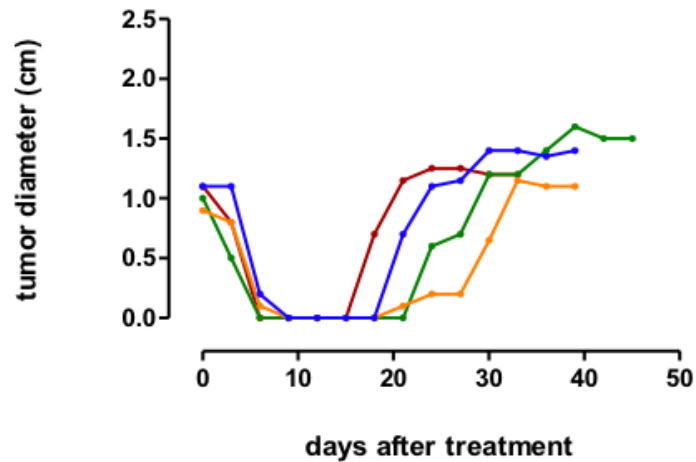
↑ Migration

# *NSG tumorgrafts respond to conventional treatments as matched primary ALCL*

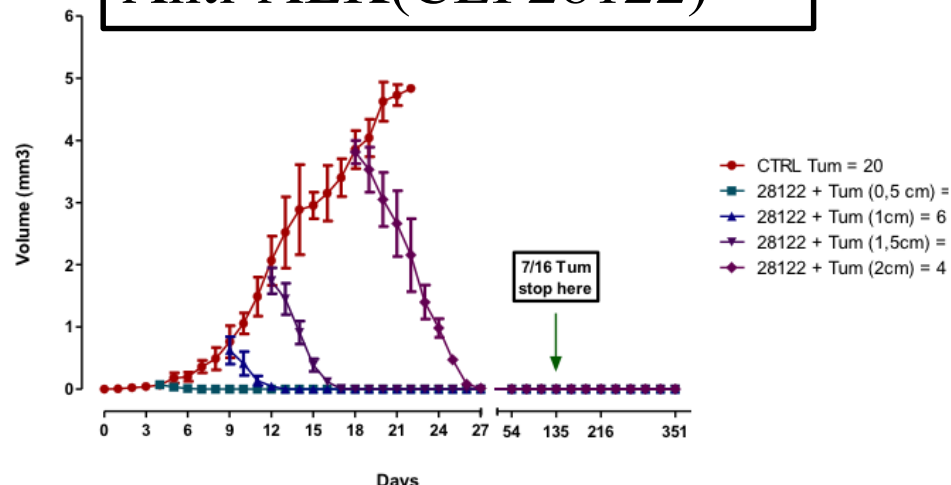
1th line CHOP



2nd line CHOP



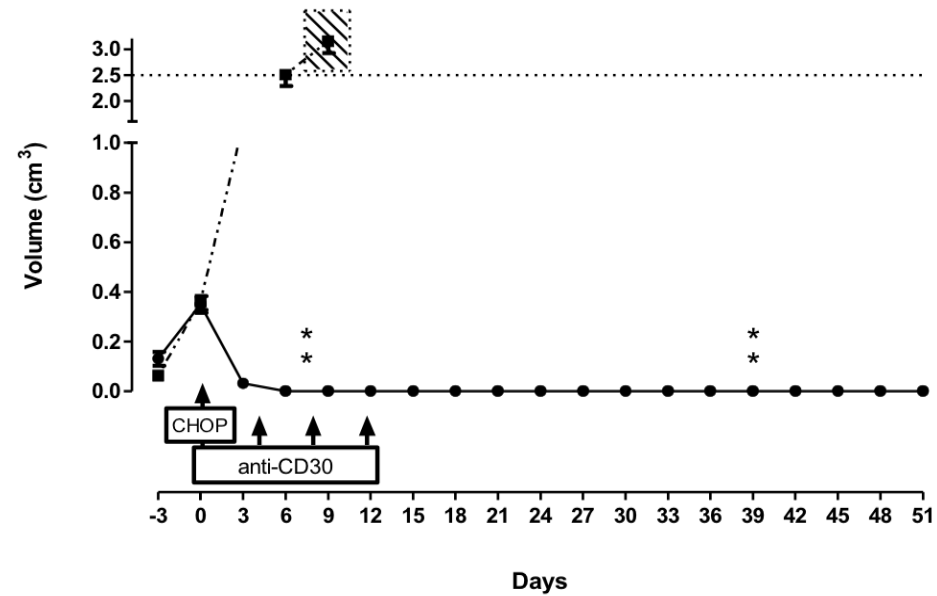
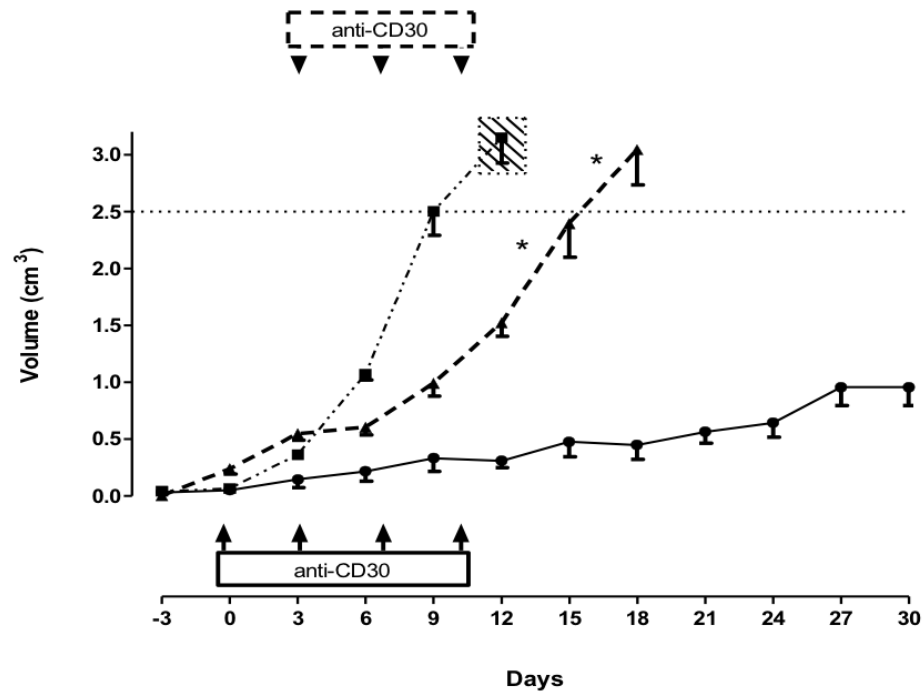
Anti-ALK(CEP28122)



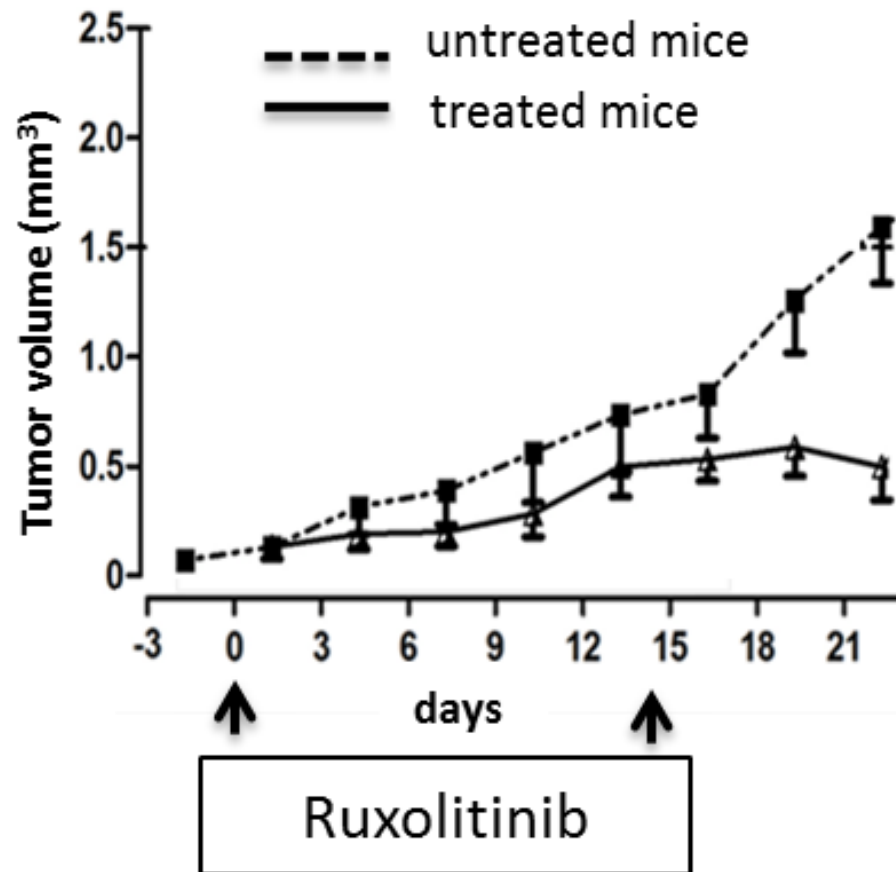
ALCL-1

# The efficacy of SGN-35 is related on the tumor burden

## ALCL-1

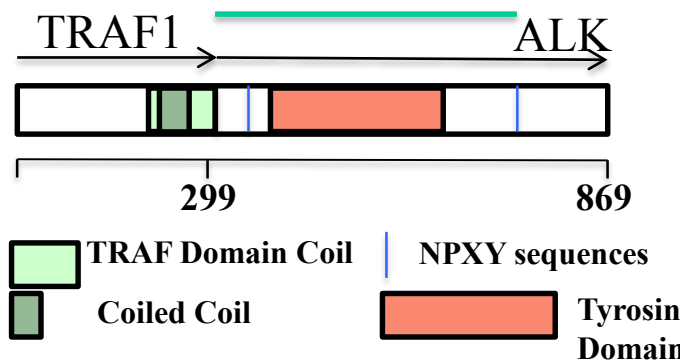


# ***Anti JAK1/2 inhibitors represent an alternative approach for pSTAT3+ ALK- ALCL***

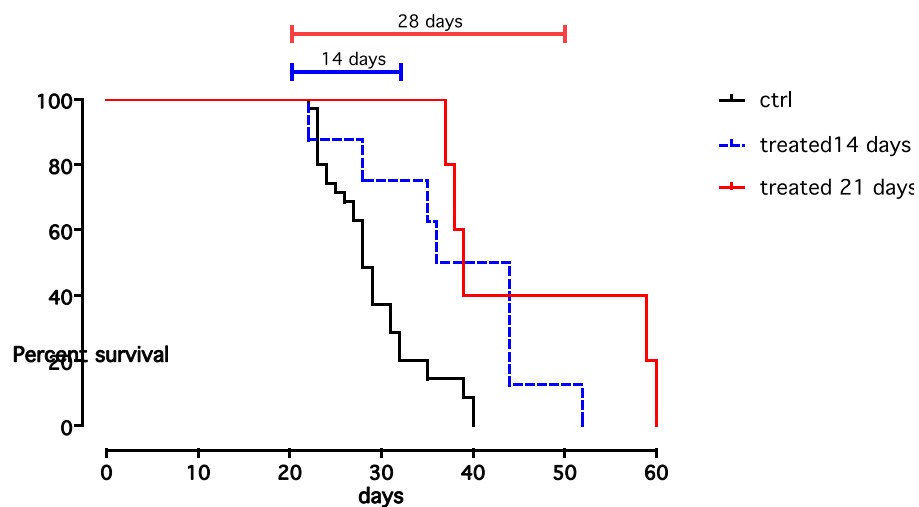
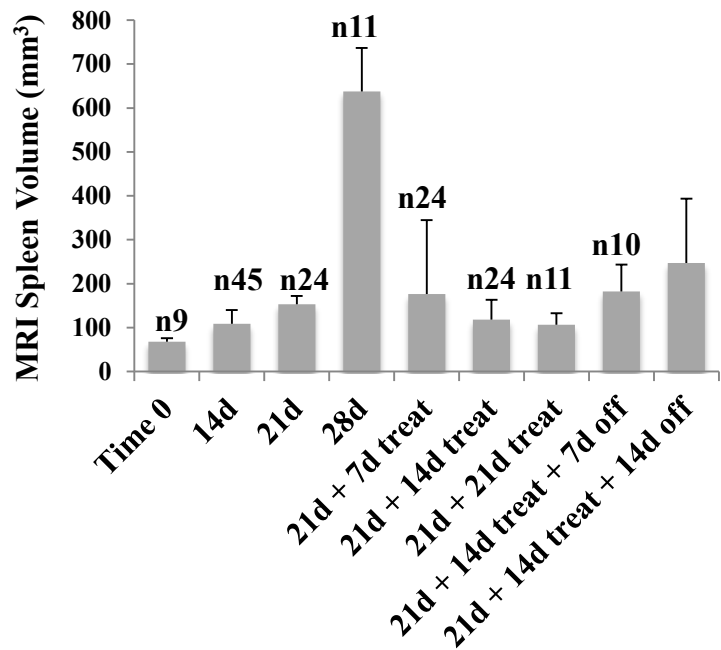
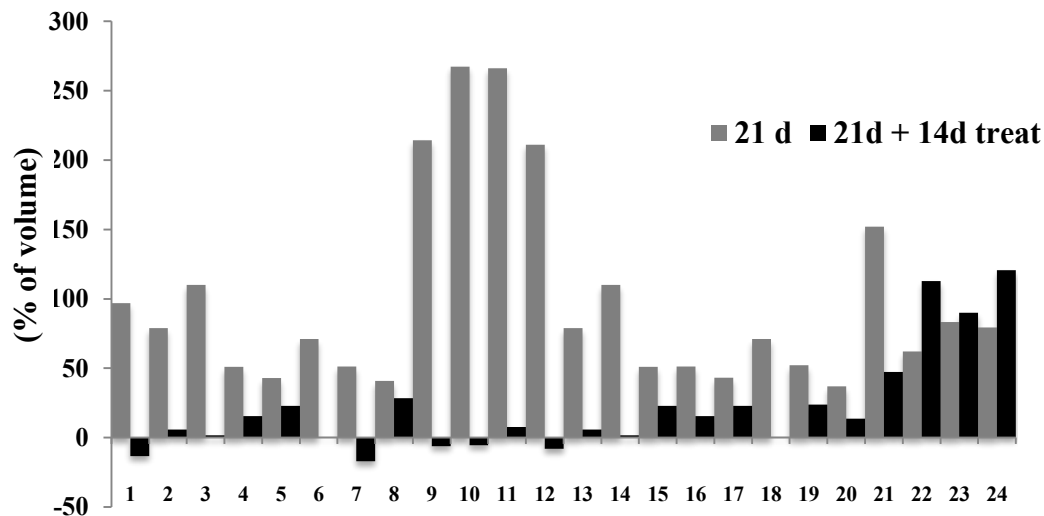




# Treatment of ALK+ ALCL PDXT predicts clinical responses



Variation from base line



## ***Conclusions: hurdles and problems***

- Low grade lymphoma do not successful implant
- Time of engraftment can be exceedingly long
- Many lymphoma require host support
- The relationship with the immune system is hardly reproducible in human reconstituted mice
- PDTX do not propagate successfully *in vitro*

## *Conclusions: advantages and benefits*

- Lymphoma derived PDT represent novel and powerful tools for investigating high-grade/end stage processes
- Humanized NSG mice should facilitate the creation of broad PDT libraries
- Lymphoma derived PDT need extensive genetic and functional analyses
- Molecularly annotated PDT are powerful models for testing new compounds/therapeutic strategies which can be provided to selected cohorts of cancer patients.

# Acknowledgements

## WCMC

Fabrizio Tabbo'

Maria Todaro

Ramona Crescenzo

Marcello Gaudiano

Michela Boi

Leandro Cerchietti

## CeRMS

Roberto Piva

Cristina Abele

Rodolfo Marchiorlatti

Katia Messana

Indira Landra

Nicoletta Chiesa

## Columbia University

Raul Rabadan

Francesco Abate

Sakellarios Zairis

## Policlinico di Milano

Antonino Neri

Luca Agnelli

## Hugef, Torino

Sivia Deaglio

Tiziana Vaisitti

## IOSI

Francesco Bertoni

Michela Boi

Ivo Kwee

## IRCC-Candiolo

Enzo Medico

Barbara Martinoglio

## The European T-cell Lymphoma Study Group

Genetics-driven targeted  
management of lymphoid  
malignancies

AIRC 5x1000