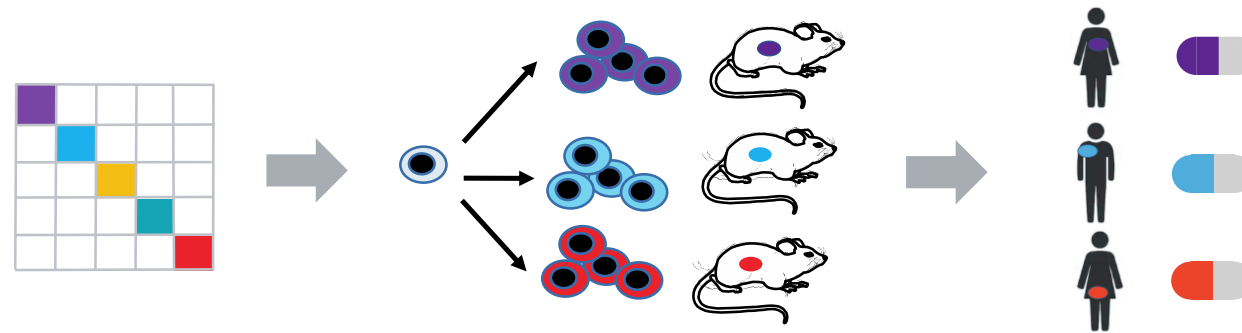


Bologna Aggressive Lymphoma Workshop

Precision Medicine in DLBCL – Molecular Predictors of Response



Björn Chapuy

Charité, University Medical Center Berlin

May 8, 2023

Disclosures

- I have the following financial relationships to disclose:

- *Research support from*

Gilead Sciences:

Gilead Oncology Award Winner 2021 (with S. Dietrich)

Gilead Oncology Award Winner 2018

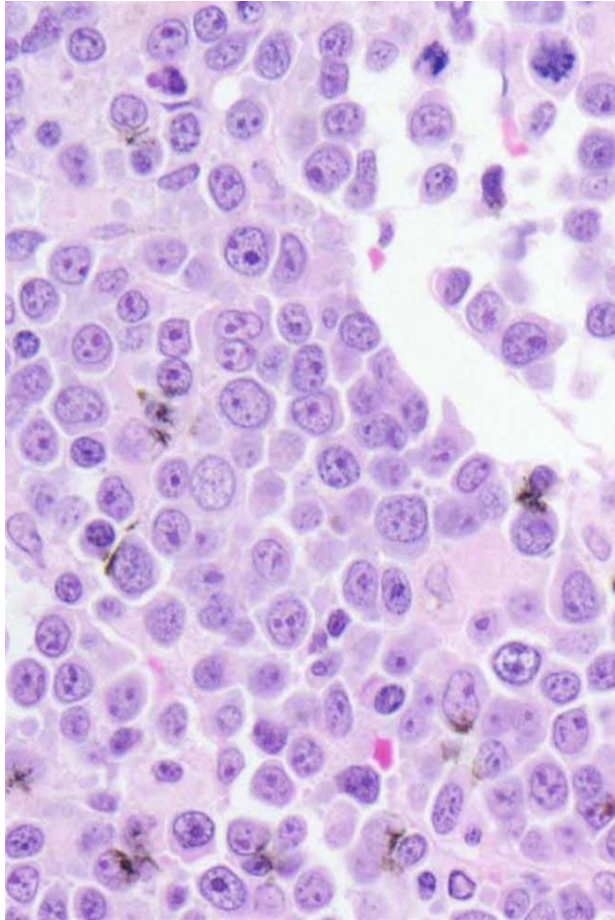
- *Honoraria for,
invited talks
advisory boards*

BMS, Astra Zeneca, Gilead, Roche, Sandoz, Incyte, Abbvie, Sobi
Regeneron, BMS, Roche, ADC, Incyte, Abbvie, Sobi

- *Patents*

I hold several patents on molecular subtyping of large B-cell lymphoma

Diffuse Large B-cell Lymphoma (DLBCL)

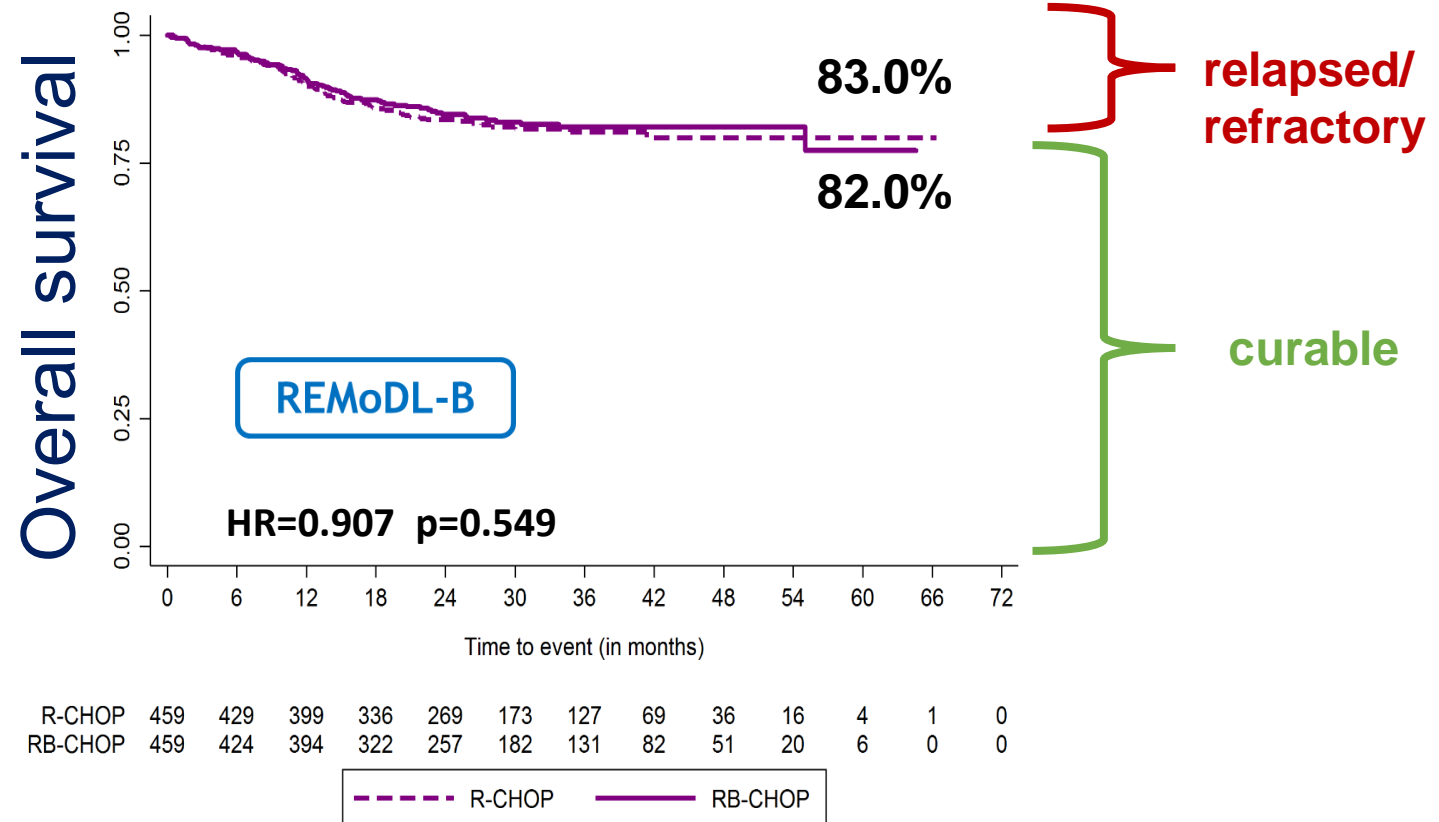
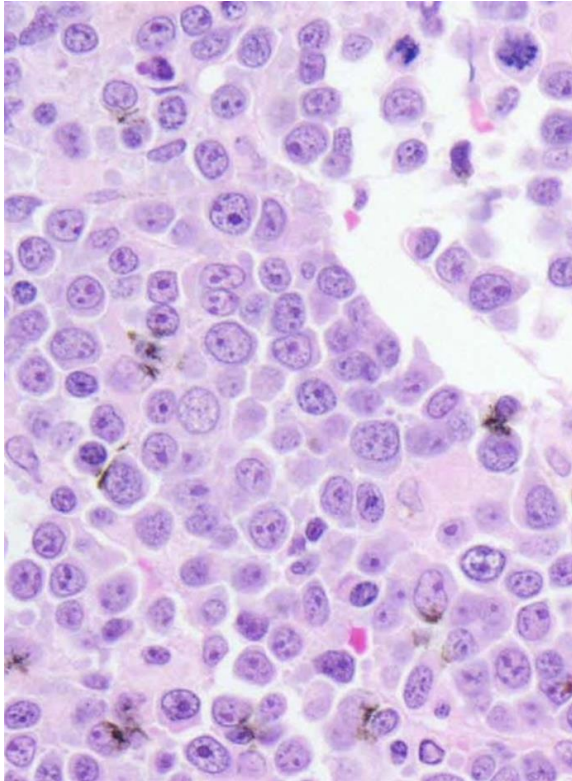


- Most common aggressive Non-Hodgkin lymphoma in adults.
- Arises from antigen-exposed germinal center B-cells.
- Separated from other LBCL such as high-grade B-cell lymphoma, PMBL and PCNSL.
- Molecular heterogenous disease with recognized transcriptionally subtypes with distinct functional characteristics.
- Genetically-defined DLBCL subtypes recently discovered.

→ Despite a more granular picture on the molecular insights of DLBCL have the perspectives of patients over the last 20 years only marginally changed.

DLBCLc

One disease, one treatment?



→ R-CHOP-like treatments is the established standard since decades.

Empirical Optimization of R-CHOP

5y-OS

50%

60%

65-70%

>90%

70-80

70

?

Optimal supportive care

CHOP

R-CHOP

6 x R-CHOP

IPI 0 - 4x R-CHOP +2R
IPI all - 6 x R-CHOP
IPI 2/3 - 8 x R-CHOEP

Pola + R-CHP
R-CHOP + XY

1993

2002

2008

2019

2023

“failed”

Longer treatment (8 vs 6)
Dose-density (14 vs. 21)
Higher doses (Mega)
Early Transplant
Infusional applications
New CD20 antibodies

R-CHOP + X 'all comer' designs
X = Bortezomib
X = Lenalidomide
X = Ibrutinib
X = other



Strategies Towards Precision Medicine (in Lymphoma)

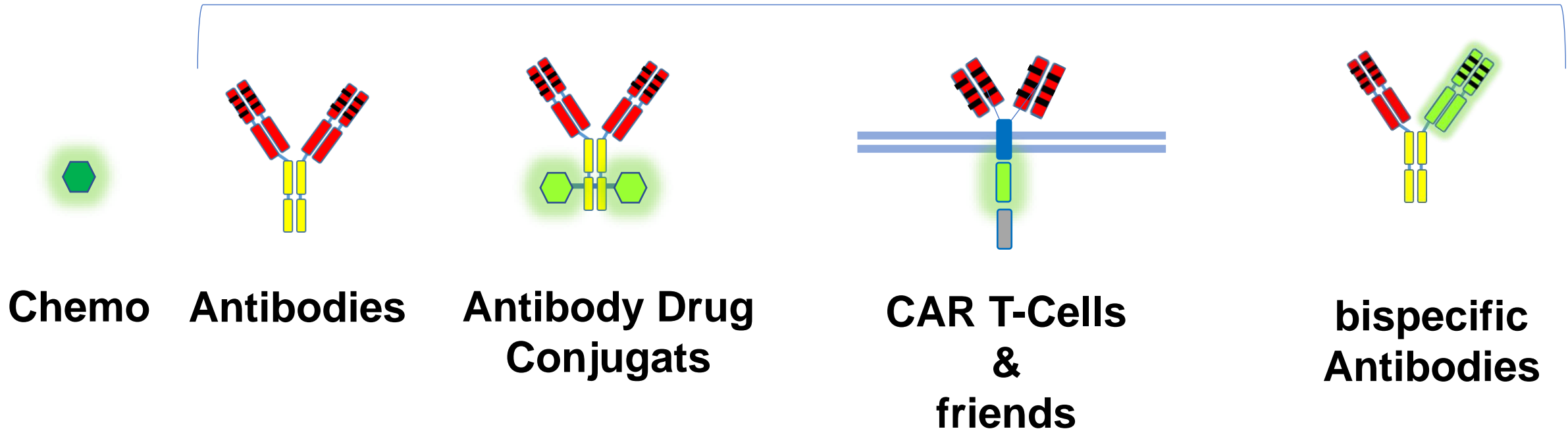
Molecular agnostic



“All comer” Studies
oriented towards surface epitopes

Precision Medicine in Lymphoma - New Bullets on the “Horizon” available

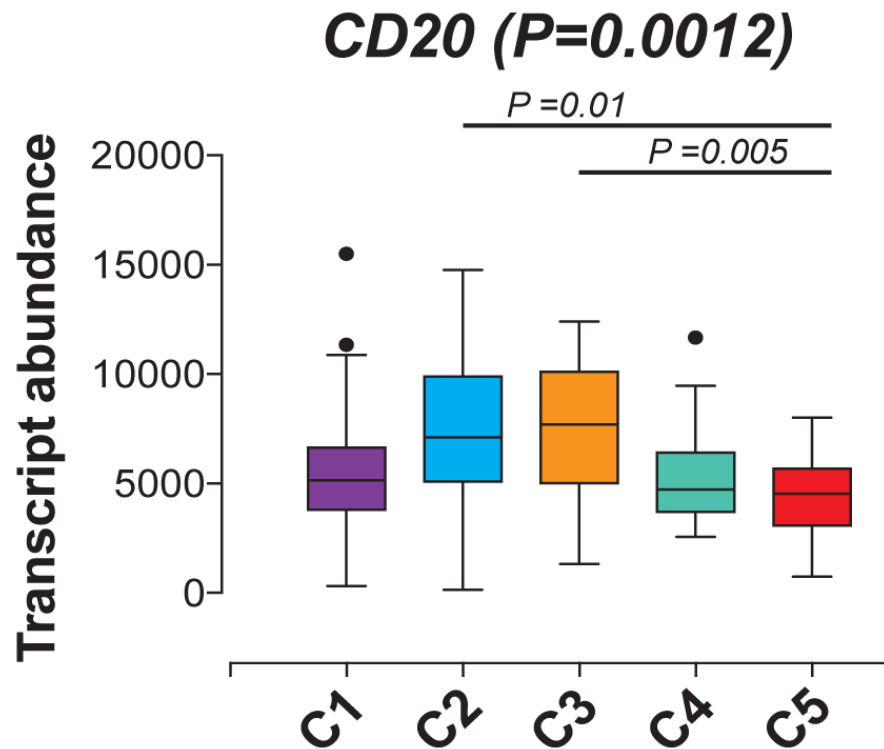
Targeting Surface Epitopes



Empirical Strategy

- Combine as single agent or smart combinations in all comer trials
- If needed (i.e. primary end point is failed) look for biomarkers and understand molecular heterogeneity

Heterogenous Abundance of CD20 in Genetic C1-C5 DLBCL Subtypes

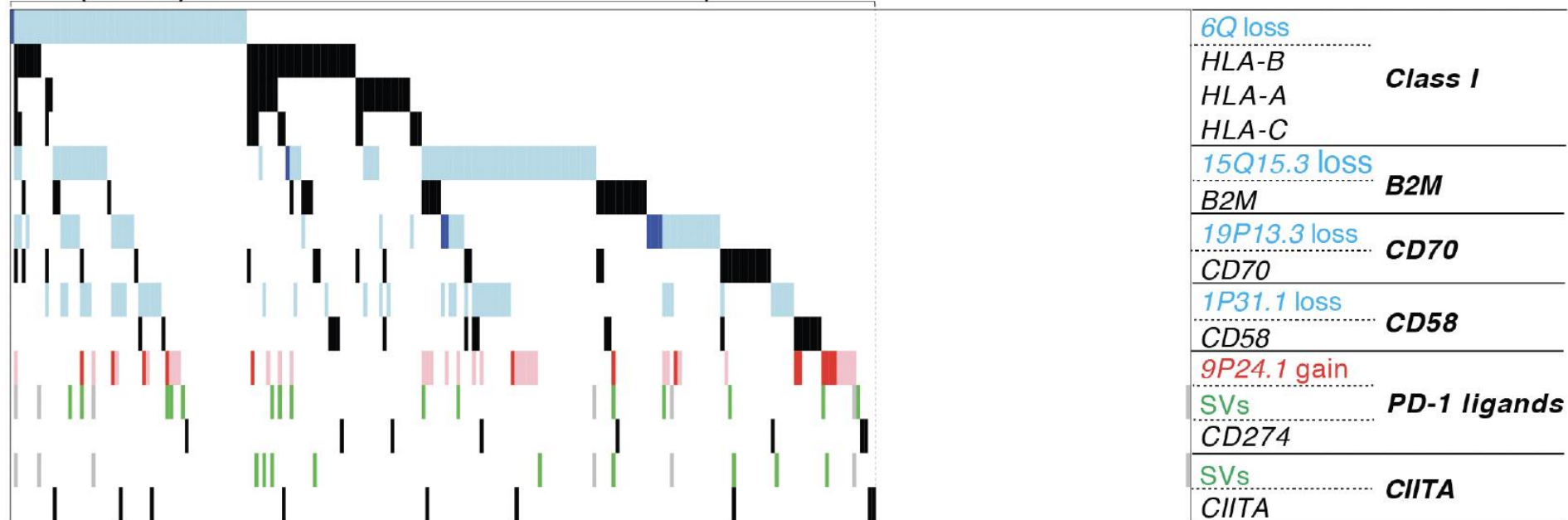


- CD20 transcript abundance is significantly different in genetically defined subtypes

➔ Highlights that epitope density varies for so called “agnostic” therapies

Frequent Immune Escape Pathways in DLBCL

74% (229/304) of DLBCLs harbor alterations in immune escape members



→ 2/3 of DLBCL patients have genetic alterations in a potent immune escape pathways

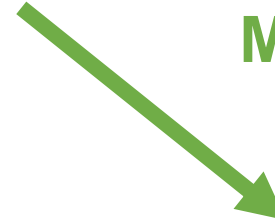
**Strategies Towards
Precision Medicine
(in Lymphoma)**

Molecular agnostic



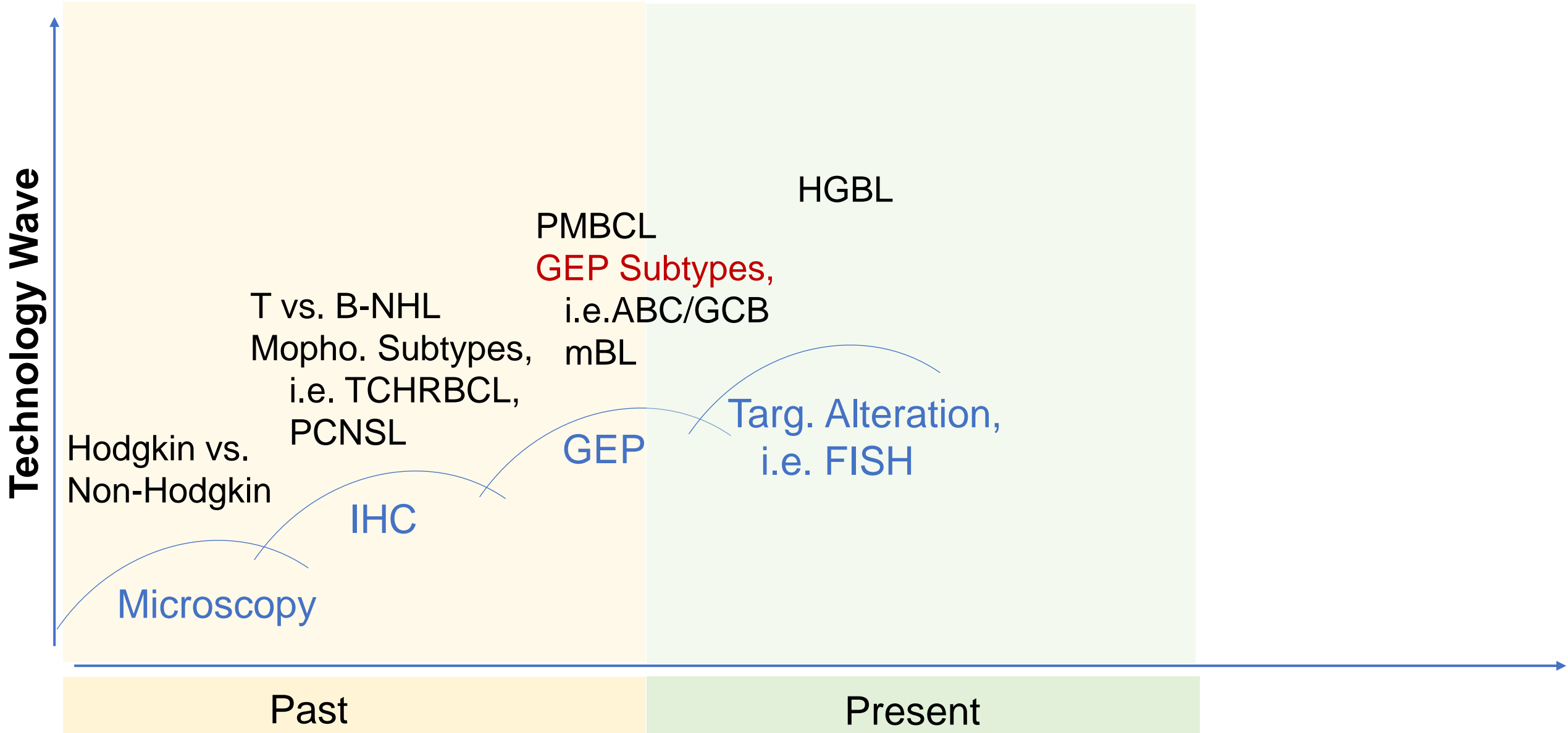
**“All comer” Studies
oriented towards surface epitopes**

Molecular affine



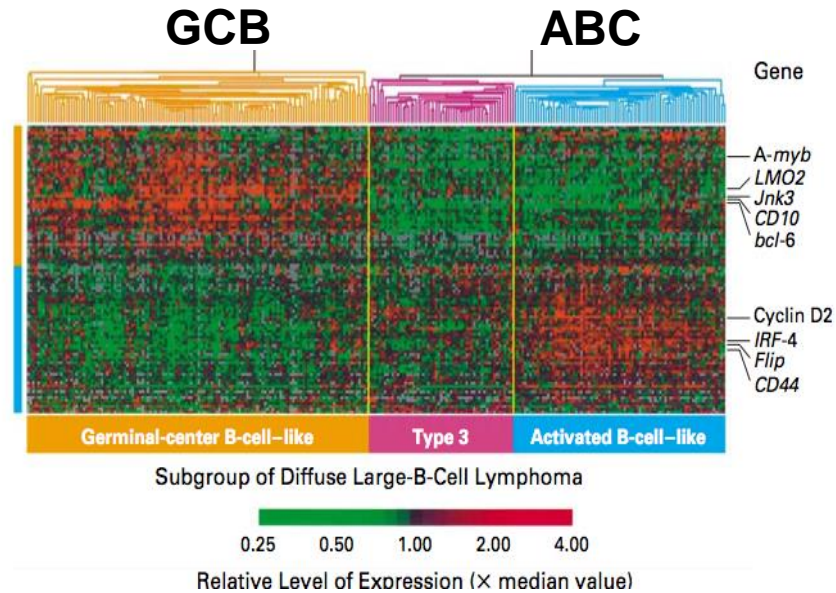
**Understanding Molecular Heterogeneity
&
Targeting Actionable Alterations**

Evolving Molecular Classification with Technology



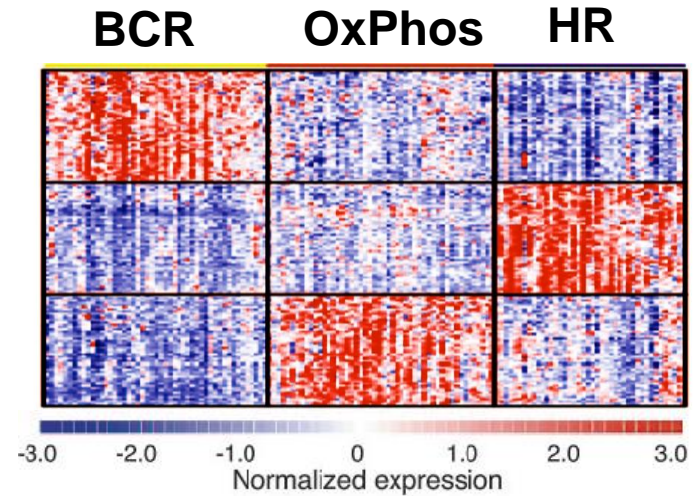
Transcriptional Heterogeneity in DLBCL

Cell of origin



Alizadeh et al, Nature 2000
Rosenwald et al, NEJM 2002
Lenz et al NEJM 2008
Lenz and Staudt NEJM 2010

Consensus Clusters



Monti et al, Blood 2005
Chen et al, Cancer Cell 2012
Caro et al, Cancer Cell 2013

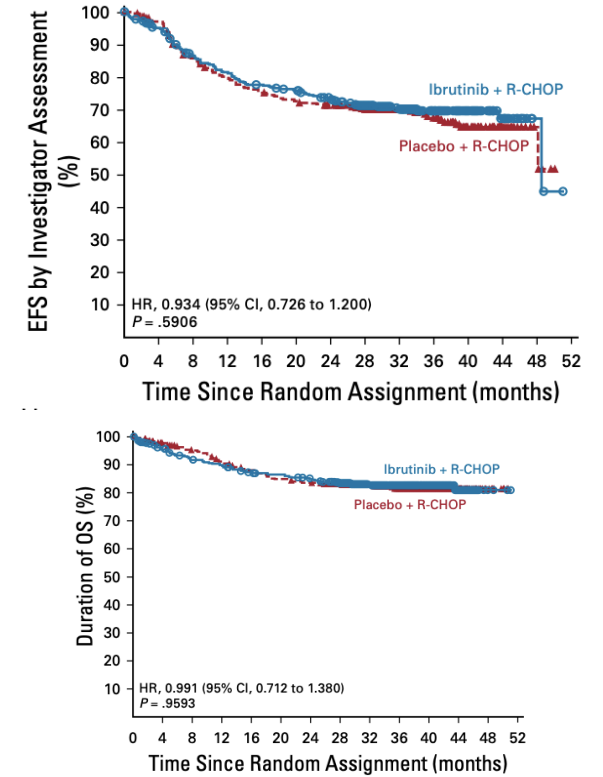
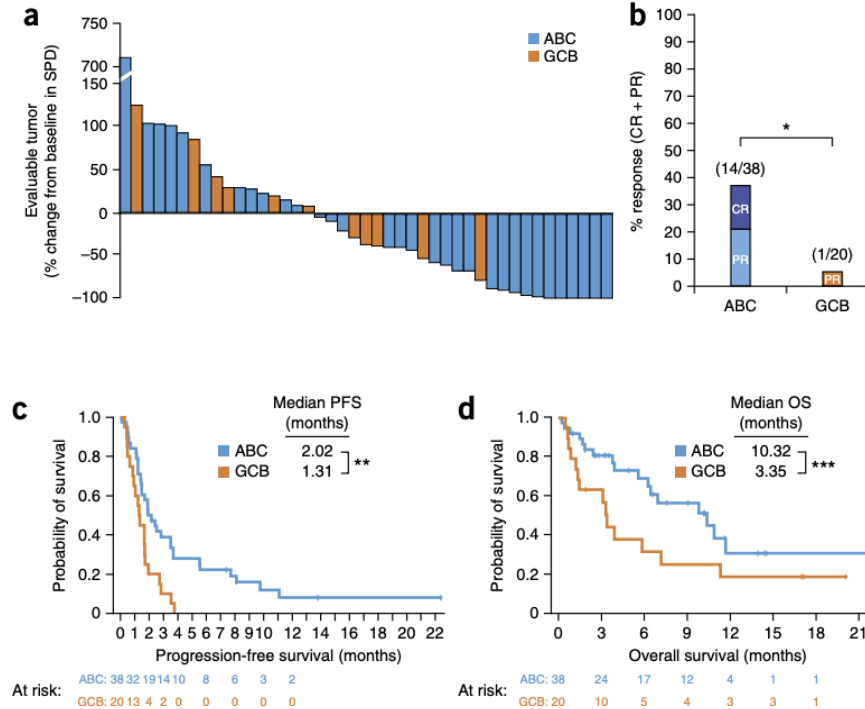
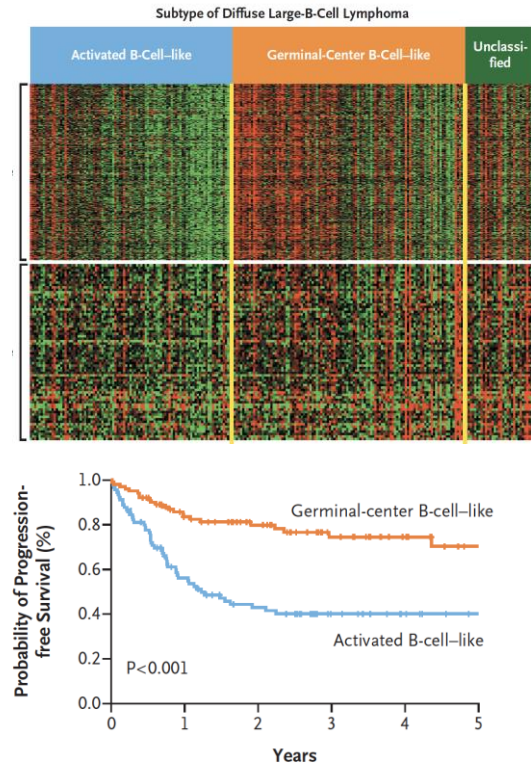
- Transcriptionally defined disease subtypes highlight specific aspects of DLBCL biology, suggest cancer cell dependencies and identify rational therapeutic targets.

Targeting ABC-type DLBCL

Transcriptional Heterogeneity of DLBCL

Vulnerability of ABC to BTK Inhibition

Phase III Trial Failed End Point



Lenz et al. *N Engl J Med* 2008;359:2313-23

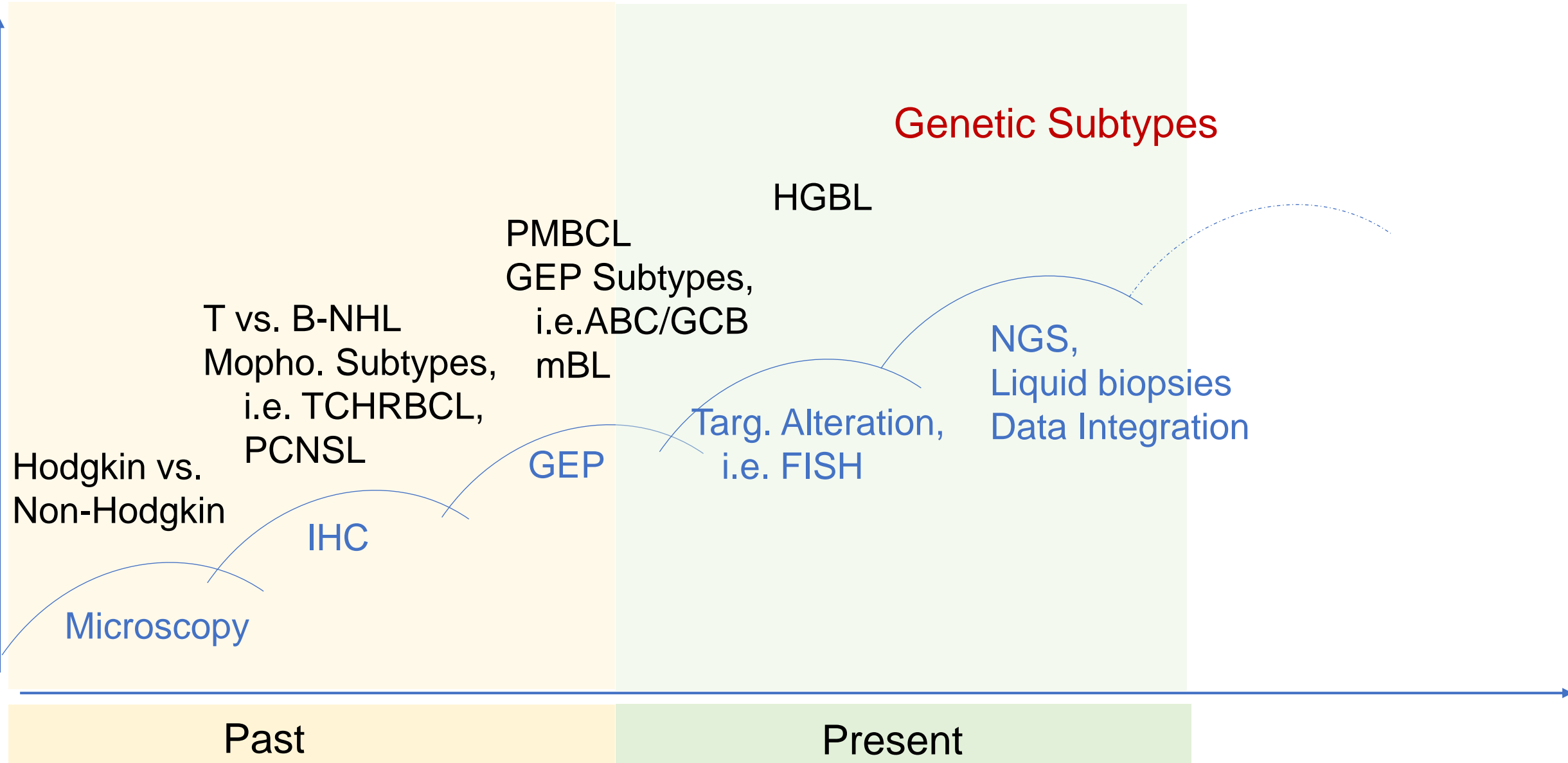
Wilson et al. *Nat Med*. 2015; 21, 922–926.

Younes et al. *JCO*. 2019; 20;37(15):1285-1295

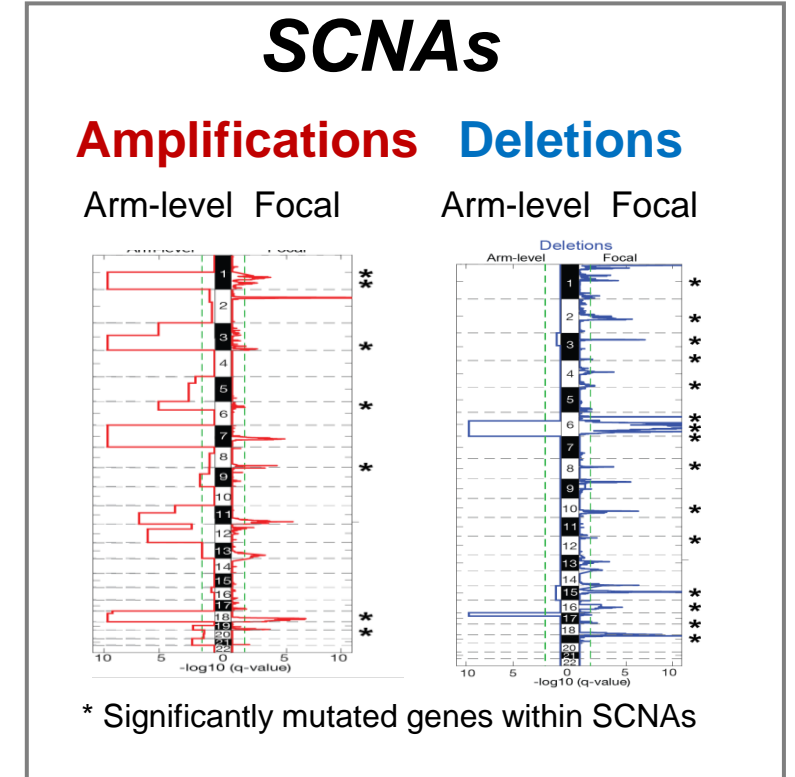
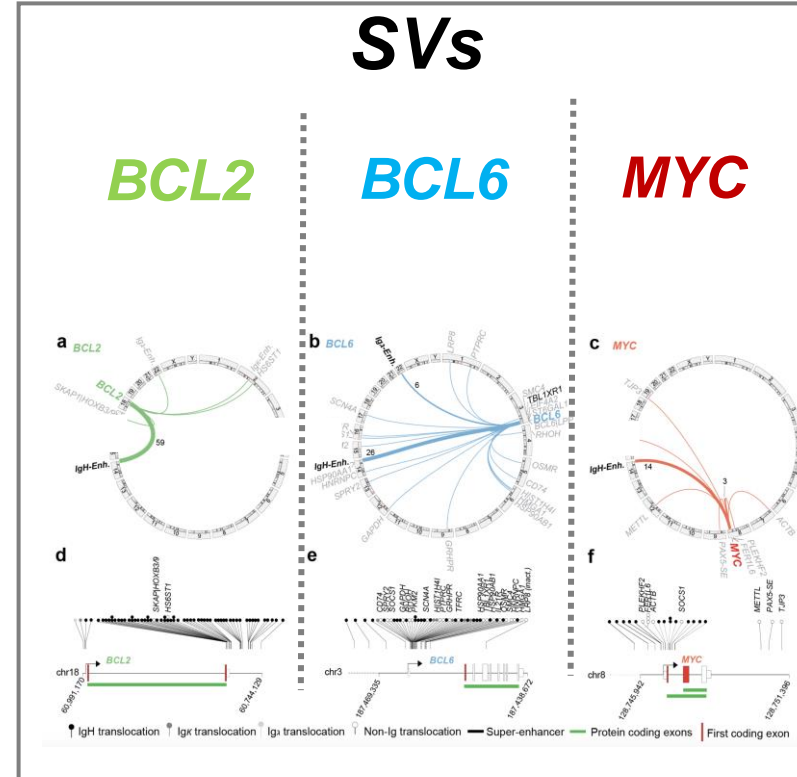
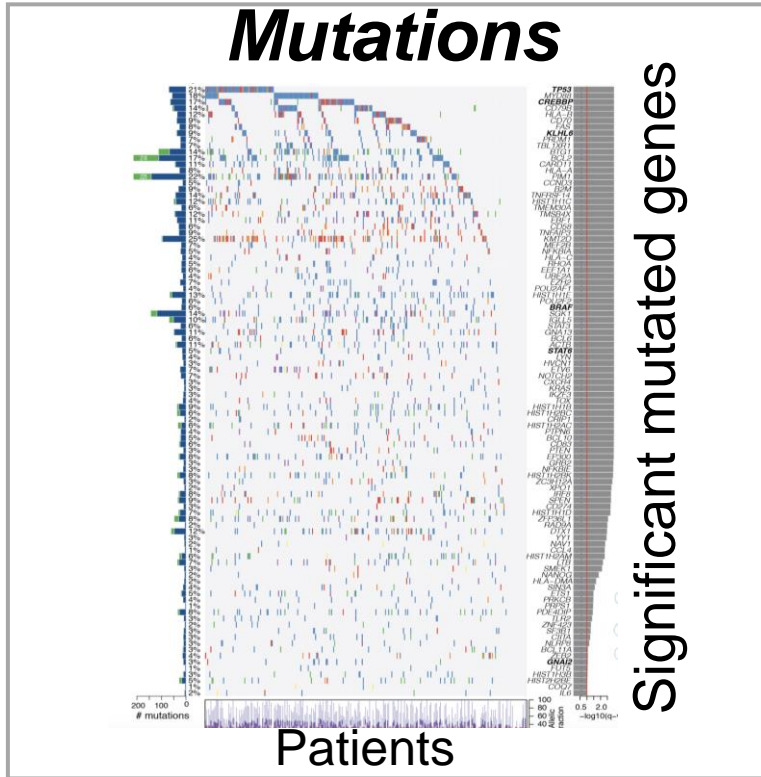
→ Suggested that there is additional molecular heterogeneity

Evolving Molecular Classification with Technology

Technology Wave



Comprehensive Genomic Analysis of Primary DLBCL



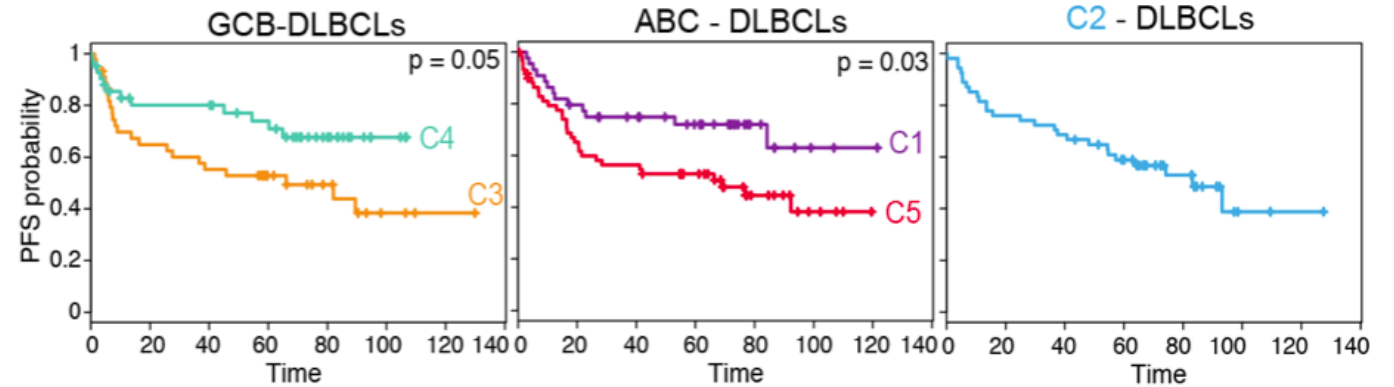
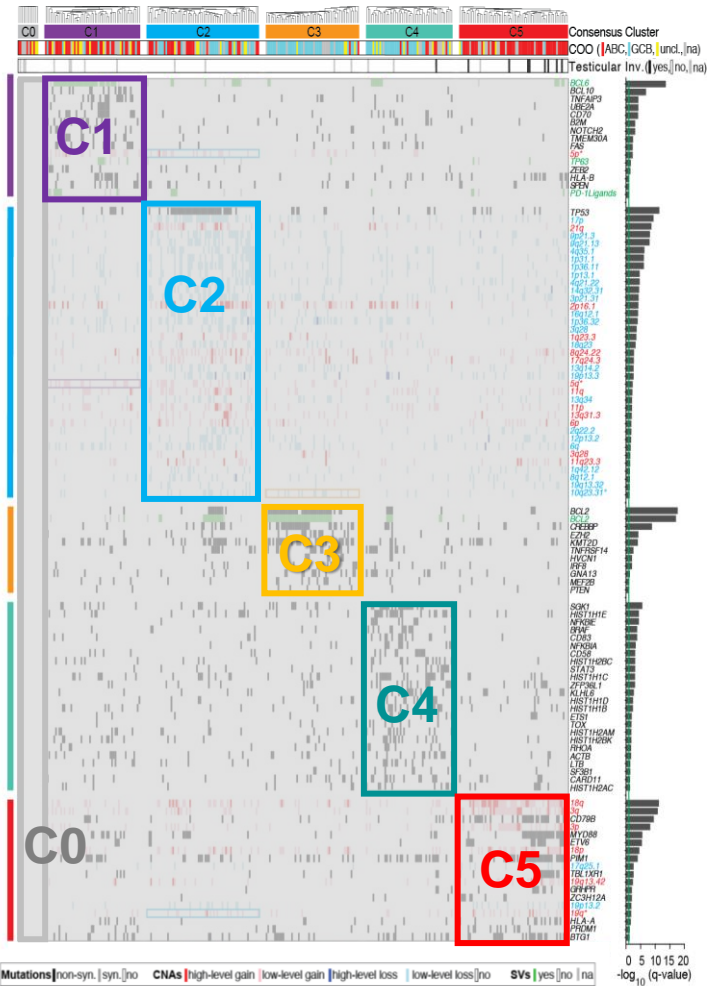
- Integration of recurrent mutations, somatic copy number alterations (SCNAs) and structural variants (SVs) in newly diagnosed DLBCLs.
- Median # of genetic driver alterations is **17 (1-48)**

GOAL: Define DLBCL genetic substructure

Genetic Signatures Predictive for Outcome Independent of the IPI

Genetically-distinct DLBCLs

Predictive for Outcome

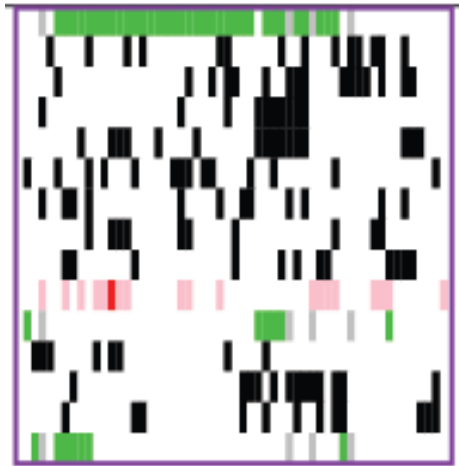


	Term	N	HR	p-value
IPI	Low	88	Reference	-
	Low-int.	56	1.90	0.027
	High-int.	74	2.59	< 0.001
	High	34	3.44	< 0.001
Clusters	C0/C1/C4	94	Reference	-
	C2	53	1.77	0.039
	C3/C5	105	2.01	0.003

HR (95% CI)

Genetically Distinct ABC-enriched DLBCLs

C1 DLBCLs

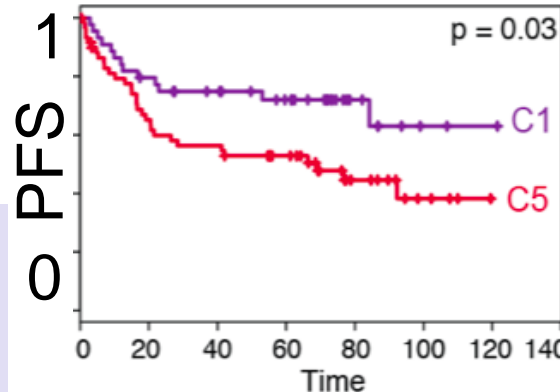
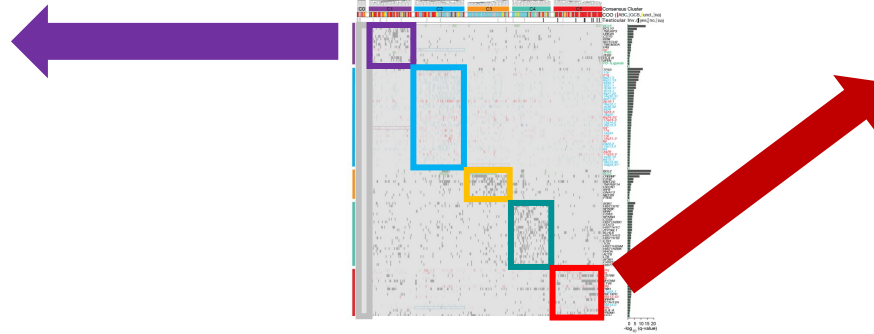


BCL6
BCL10
TNFAIP3
UBE2A
CD70
B2M
NOTCH2
TMEM30A
FAS
*5p**
TP63
ZEB2
HLA-B
SPEN
PD-1Ligands

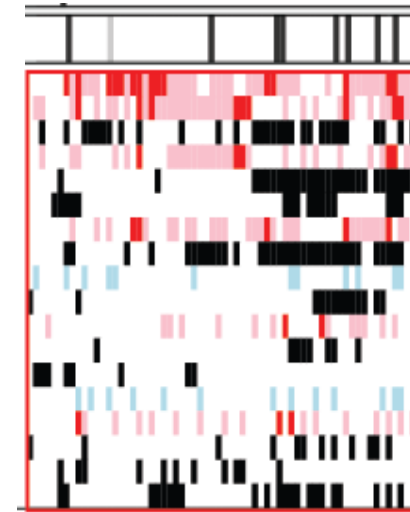
- Mutations as previously described in marginal zone lymphoma (**MZL**)¹⁻⁴
- *BCL6* SVs associated with **transformed MZL**⁵
- **Favorable** outcomes

→ **20% of DLBCLs occultly transformed MZL ?**

¹ Zhang et al., Nat. Gen 1999⁵ Flossbach et al., Int J Cancer 2011
² Rossi et al., JEM 2012
³ Kiel et al., JEM 2012
⁴ Spina et al., Blood 2016
⁶ Chapuy, Roemer et al., Blood 2016
⁷ Wright et al Cancer Cell 2020



C5 DLBCLs



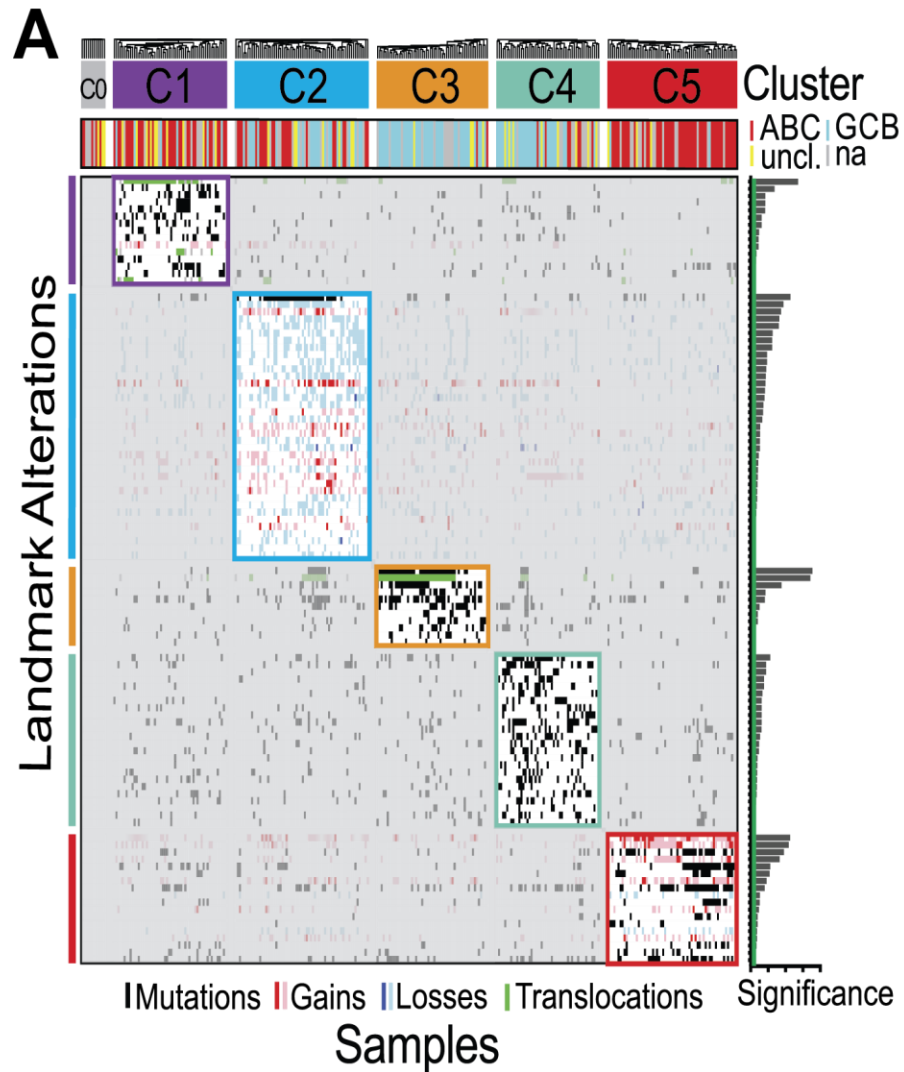
Testicular Involv.

18q
3q
CD79B
3p
MYD88
ETV6
18p
PIM1
17q25.1
TBL1XR1
19q13.42
GRHPR
ZC3H12A
19p13.2
*19q**
HLA-A
PRDM1
BTG1

- 18q/*BCL2* gain with concurrent mutations in *MYD88*^{L265P}/*CD79B*
- Resembled genetic sign. of **PCNSL** and **PTL**⁶ and **other extranodal lymphoma**⁷
- **8/9 DLBCL with testicular involvement**
- **Unfavorable** outcome
- **Coordinate genetic signature associated with extranodal tropism.**

Chapuy, Stewart, Dunford et al. Nat Med; 2018
 Wienand and Chapuy. Hem Oncol 2021

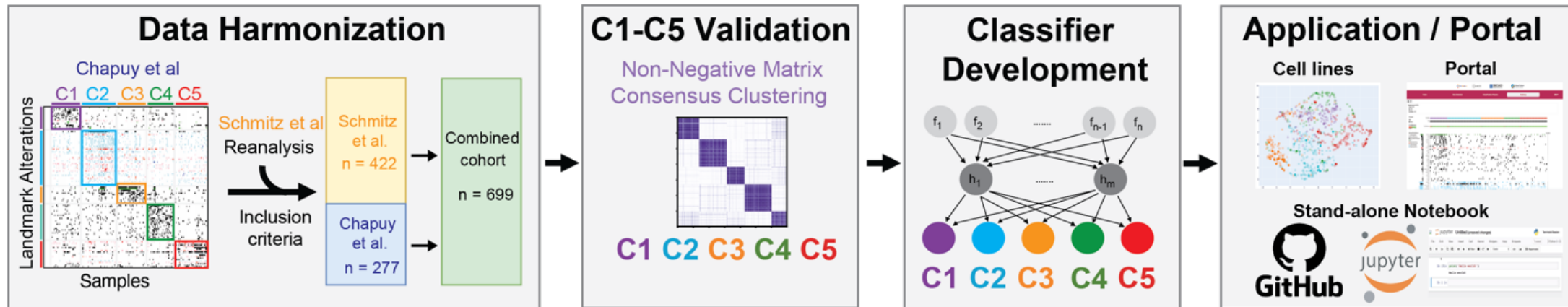
Genetically-distinct DLBCLs and their Associated Features



B

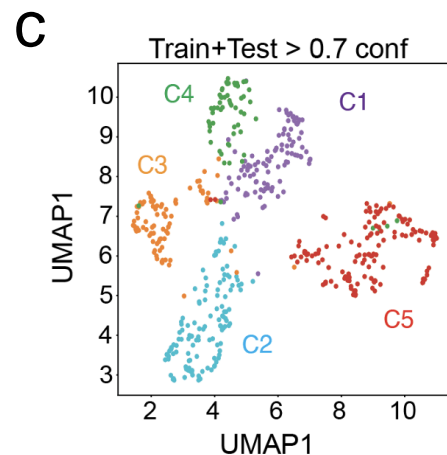
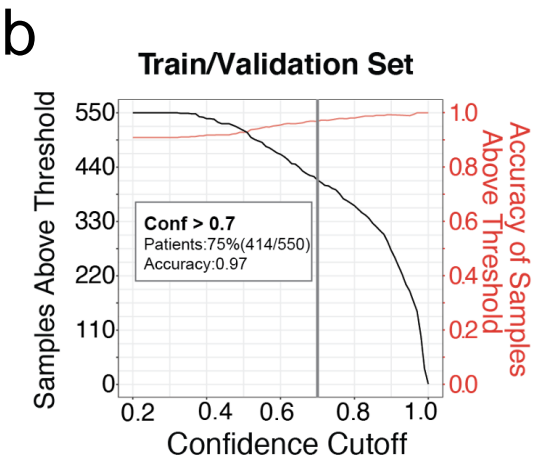
Genetic Subtype		Key Features	Transcriptional Subtype	Prognosis
DFCI	NCI			
C1	BN2	<i>BCL6</i> and <i>NOTCH2</i> - and <i>NF-κB</i> and immune escape pathway alterations; occulty transformed MZL	ABC	Favorable
C2	(A53 / TP53)	Biallelic inactivation of <i>TP53</i> , 9p21.3/ <i>CDKN2A</i> ; genomic instability	ABC/GCB independent	Steady rate of progression
C3	EZB	<i>BCL2</i> SVs, inactivating <i>PTEN</i> alterations and alterations of epigenetic enzymes	GCB	Unfavorable
C4	ST2	BCR/ <i>PI3K</i> -, <i>JAK/STAT</i> -, <i>RAS</i> -pathway and histone alterations	GCB	Favorable
C5	MCD	<i>BCL2</i> copy gain, activating <i>MYD88</i> and <i>CD79B</i> mutations; extranodal tropism	ABC	Unfavorable

Molecular Classifier for DLBclass



a

		Train/Validation Set					Test Set														
DLBclass		C1	C2	C3	C4	C5	C1	C2	C3	C4	C5	C1	C2	C3	C4	C5					
NMF labels	All cases	107	2	1	1	3	85	1	0	0	1	21	0	1	4	0					
	C1	1	117	1	5	3	0	97	1	0	1	1	39	0	2	2					
	C2	2	4	82	2	5	1	2	66	0	1	0	0	21	1	0					
	C3	3	2	2	64	4	2	0	2	44	1	1	0	1	19	1					
	C4	3	2	3	1	130	0	0	0	0	109	0	2	1	0	32					
C5	3	2	3	1	130	0	0	0	0	109	0	0	0	0	27						
Accuracy		91% (500/550)					97% (401/414)					89% (132/149)					98% (108/110)				



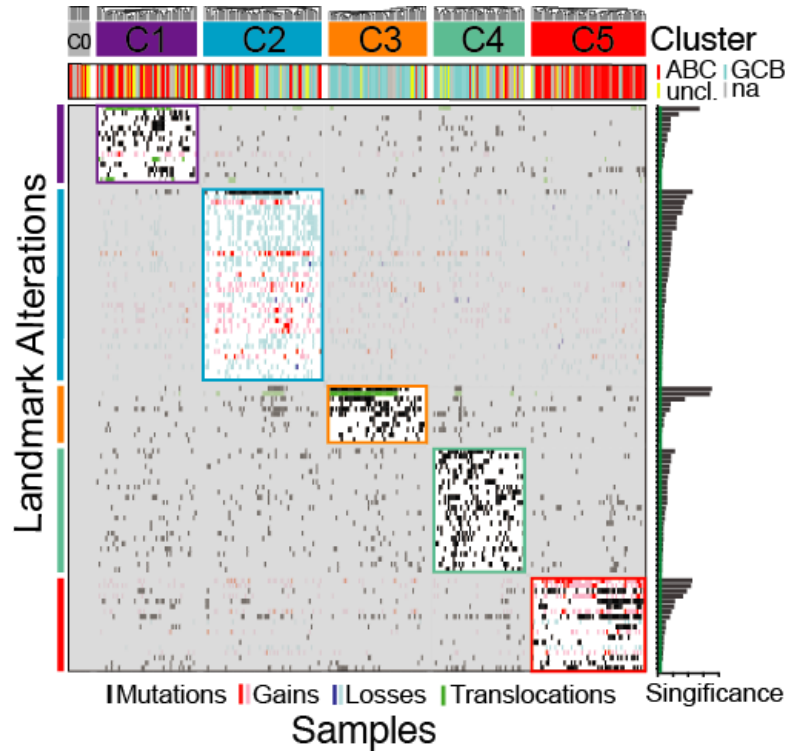
Properties

- Robust classification of single cases
- Output: C1-C5, probabilistic
- “easy-to-use” online tool

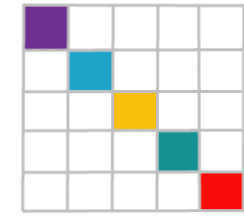


- ➔ Accurate identification of the C1-C5 DLBCL subtypes in newly diagnosed patients possible.
- ➔ Necessity for clinical translation.

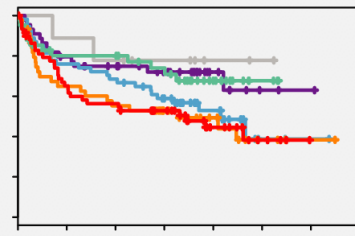
Genetically Distinct DLBCL Subtypes



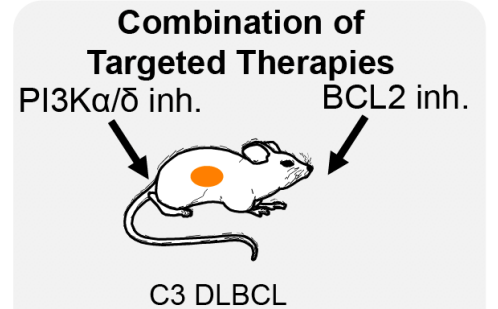
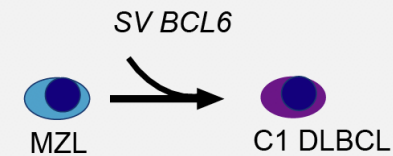
C1 C2 C3 C4 C5



Outcome Prediction



Novel Insight into Lymphomagenesis



➔ Genetically-defined DLBCL subsets (C1-C5) predict different outcomes, provide novel insights into lymphomagenesis and suggest certain combinations of targeted therapies.

Roadmap to Targeted Combination Therapies – PI3K $\alpha\delta$ /BCL2 Inhibition in C3 DLBCLs

A

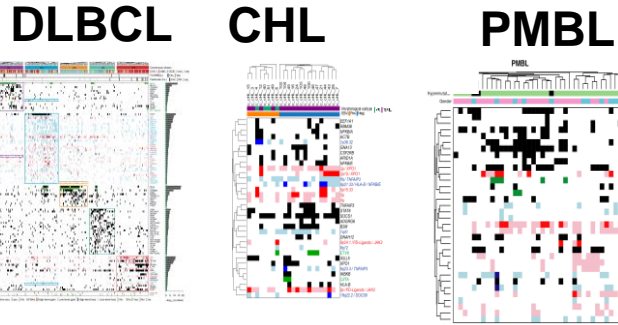


C3 DLBCLs

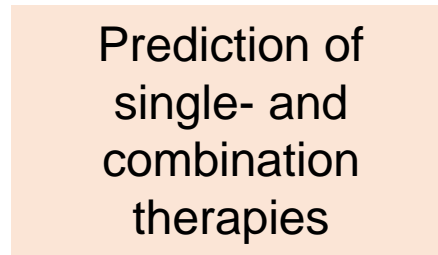
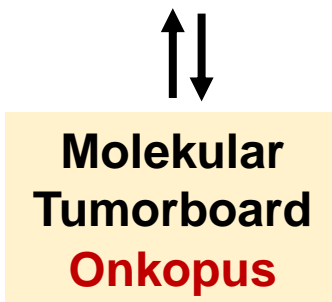
- Co-targeting of PI3K $\alpha\delta$ and BCL2 is highly synergistic in genetically-defined pre-clinical DLBCL models.
- ➔ Proof of concept that genetically-defined clusters provide a roadmap for rational (pre)clinical therapies

Molecular Lymphoma Board

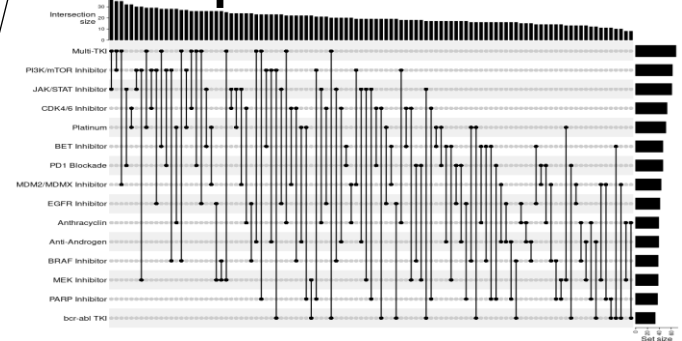
~800 primary lymphoma



Genomic Signature



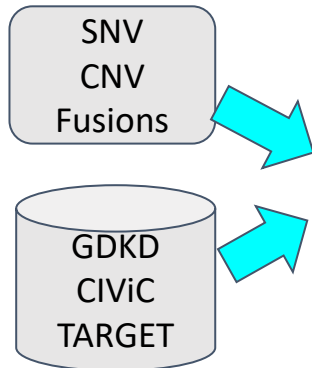
Upset Plots



Heatmaps



Vulcano Plots



Classification of therapy and evidence level

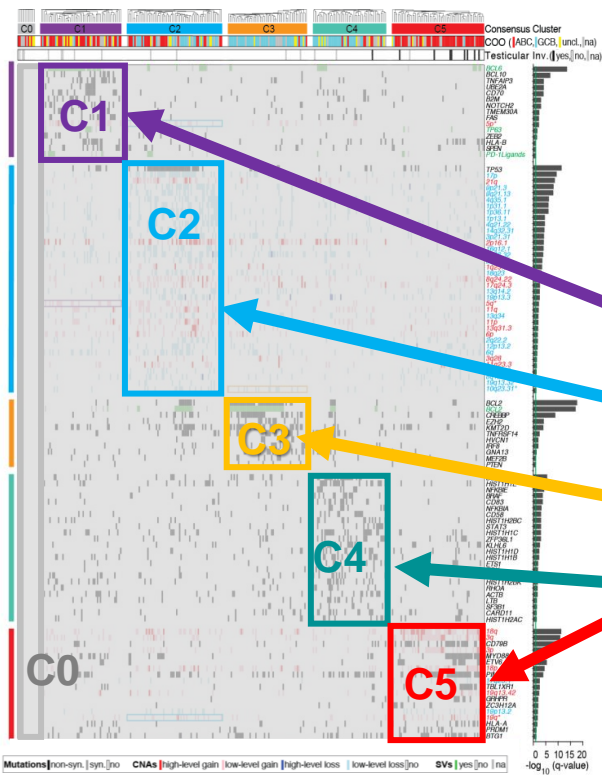
	Approved	Clinical	Preclinical
Same Cancer	A1	A2	A3
Other Cancer	B1	B2	B3

➔ Testable hypotheses are currently being evaluated in the wet-lab

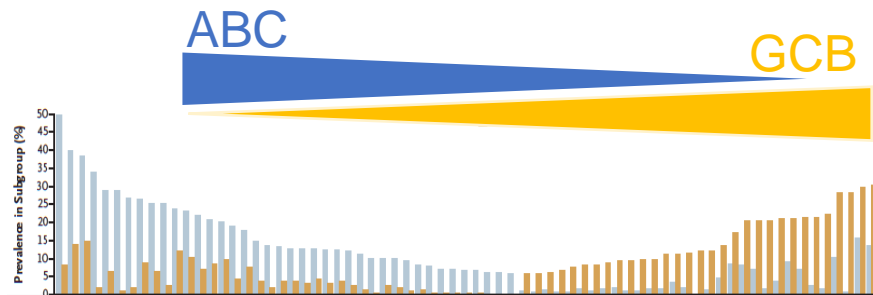
In collaboration mit T. Beißbarth (UMG) und dem CADS Program des BIH

Genetic DLBCL Classifications

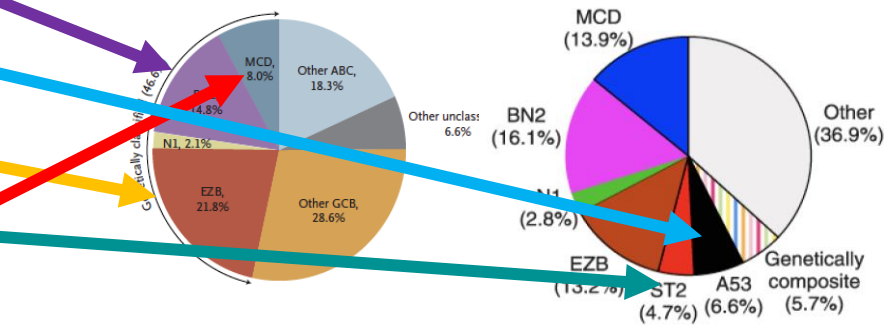
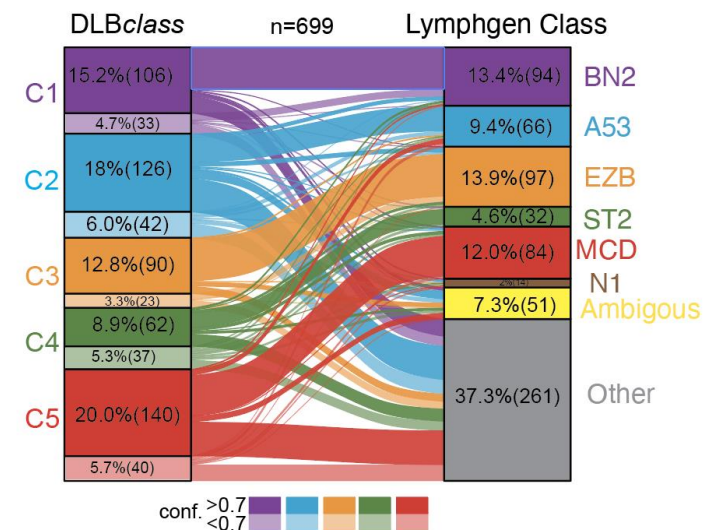
DLBclass



LymphGen



Comparisons



Schmitz, Wright, Huang, Johnson, et al. *NEJM* 2018

Wright et al. *Cancer Cell* 2020

Chapuy, Stewart, Dunford, et al. *Nat. Med.* 2018

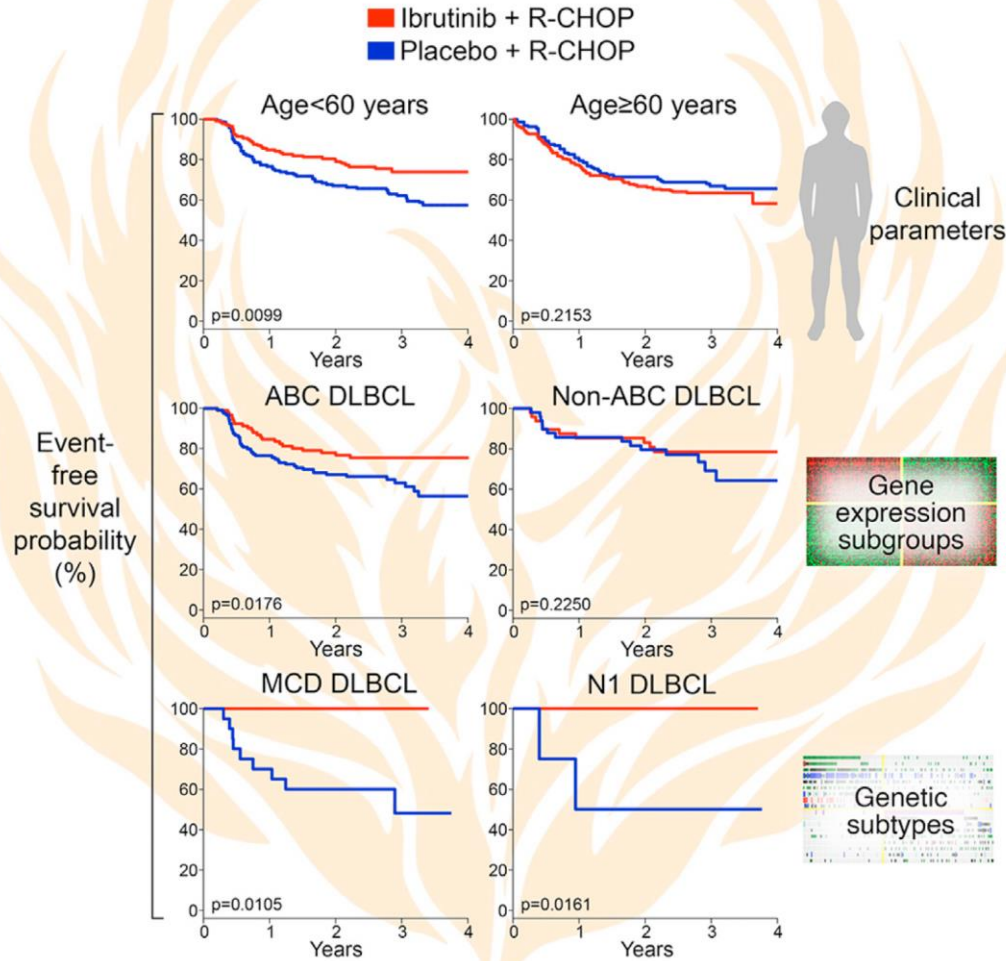
unpublished

→ DLBCL is genetically a heterogeneous disease with multiple genetic subtypes.
 → Major subtypes have been validated using targeted approaches¹.

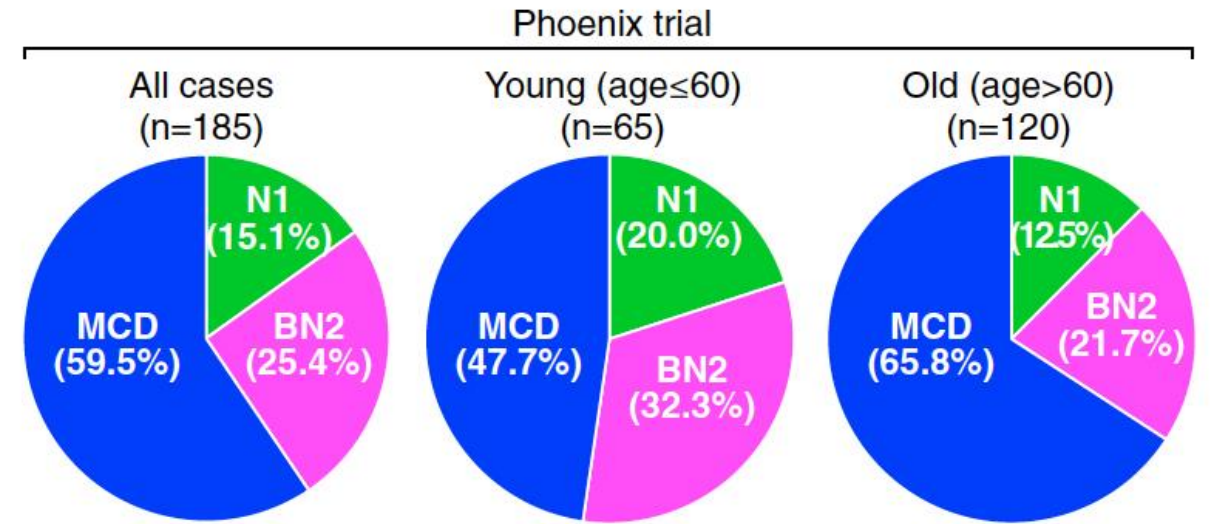
¹ Lacy et al *Blood* 2020

Effect of Ibrutinib with R-CHOP Chemotherapy in Genetic Subtypes of DLBCL

A Phoenix Phase III Clinical Trial in Previously Untreated Non-GCB Diffuse Large B Cell Lymphoma

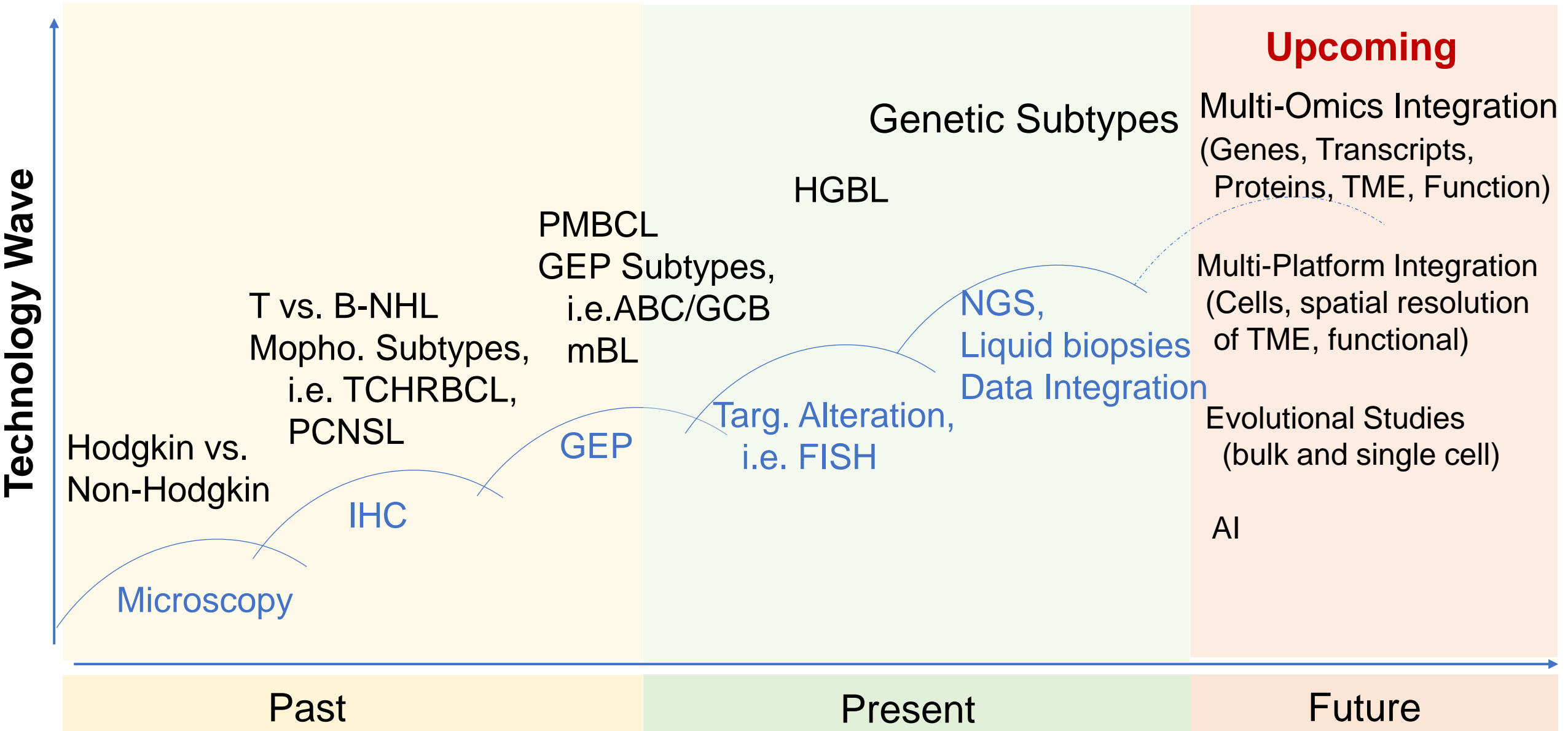


B

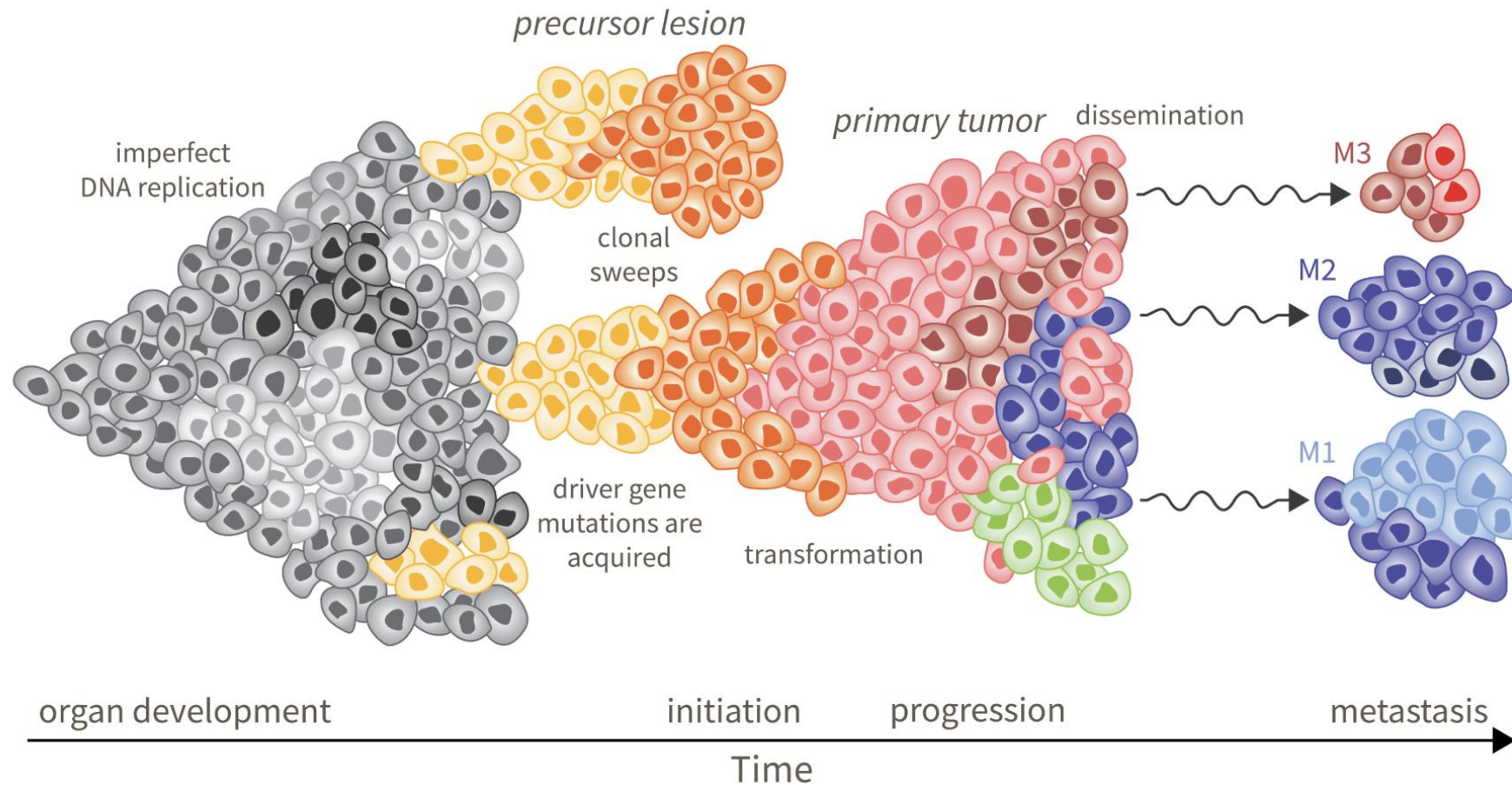


- BTK inhibitor ibrutinib plus R-CHOP is effective in younger patients with ABC DLBCL
- Patients with the MCD and N1 subtypes have 100% survival with ibrutinib plus R-CHOP

Evolving Molecular Classification with Technology



Intratatumoral Heterogeneity and Clonal Evolution

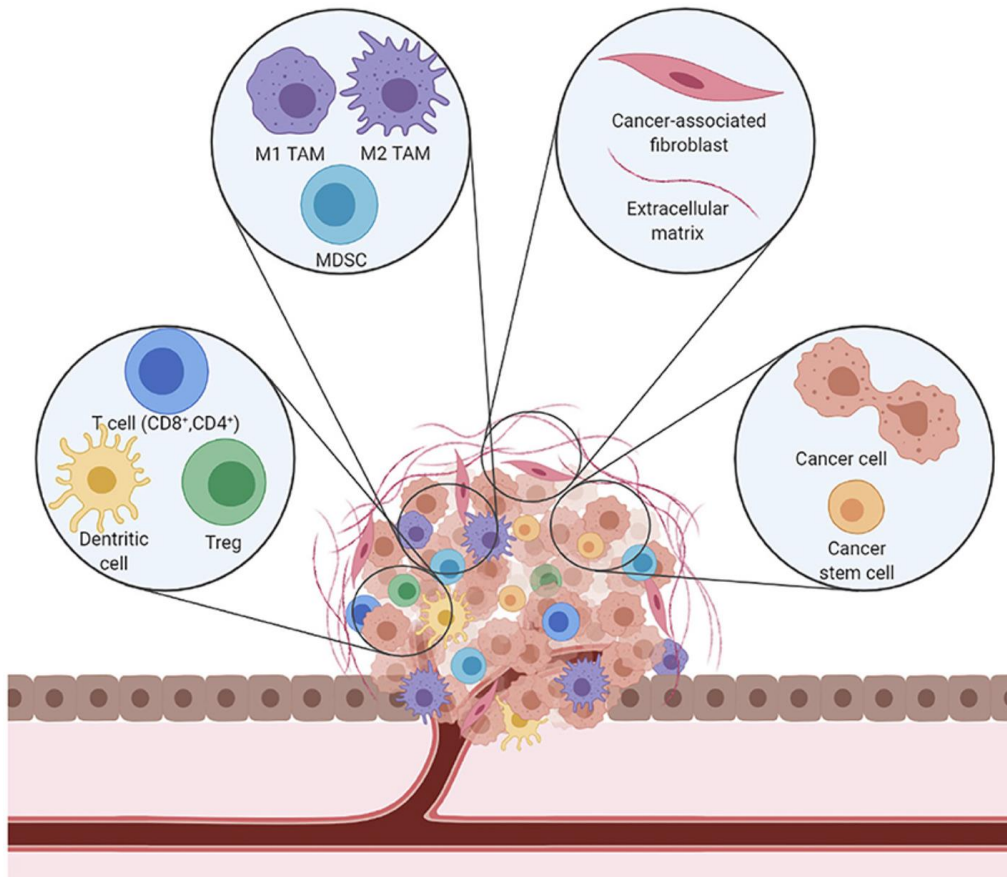


- DLBCL exhibit also intratumoral heterogeneity; Median of 17 genetic alterations.¹
- Treatment provides selection pressure.
- Systematic analyses are clinically warranted

¹ Chapuy, Stewart, Dunford, et al. Nat Med 2018

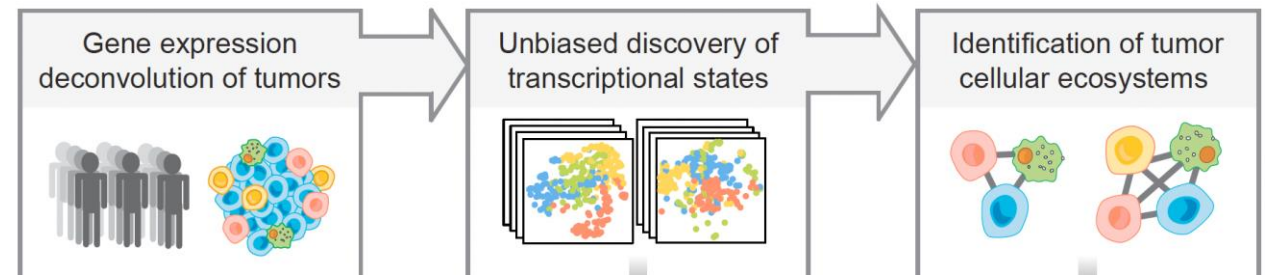
Beyond the Lymphoma Cell - Tumor as Organs

Lymphoma Microenvironment

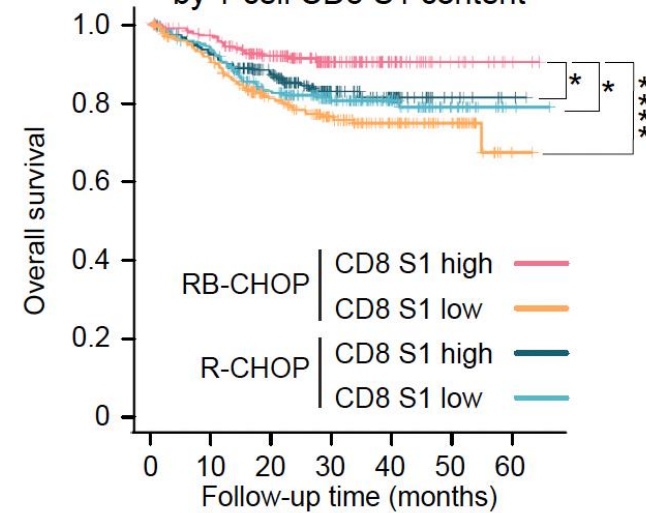


Benavente et al *Front in Oncol* 2020

"DLBCL Ecosystems"



Overall survival of patients stratified by T cell CD8 S1 content

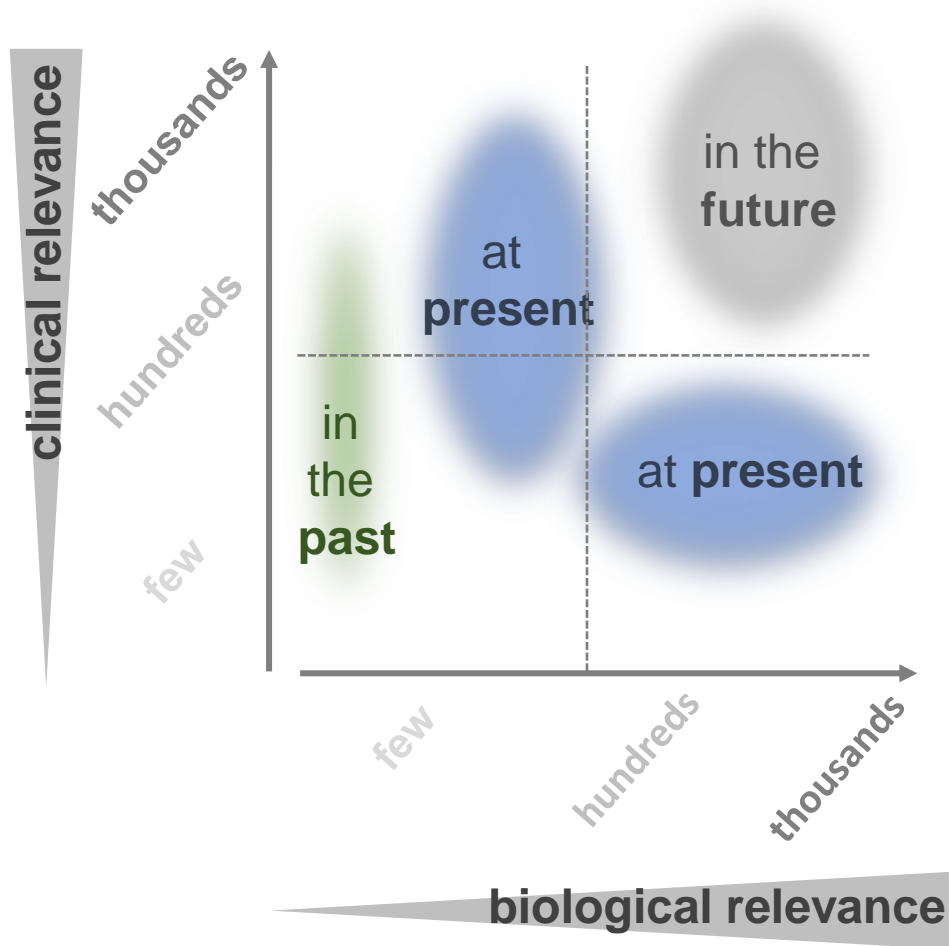


Steen, Luca et al *Cancer Cell* 2021

➔ Different lymphoma microenvironment signatures exist that might be relevant for treatment?

Current Challenges with Molecular Classifiers

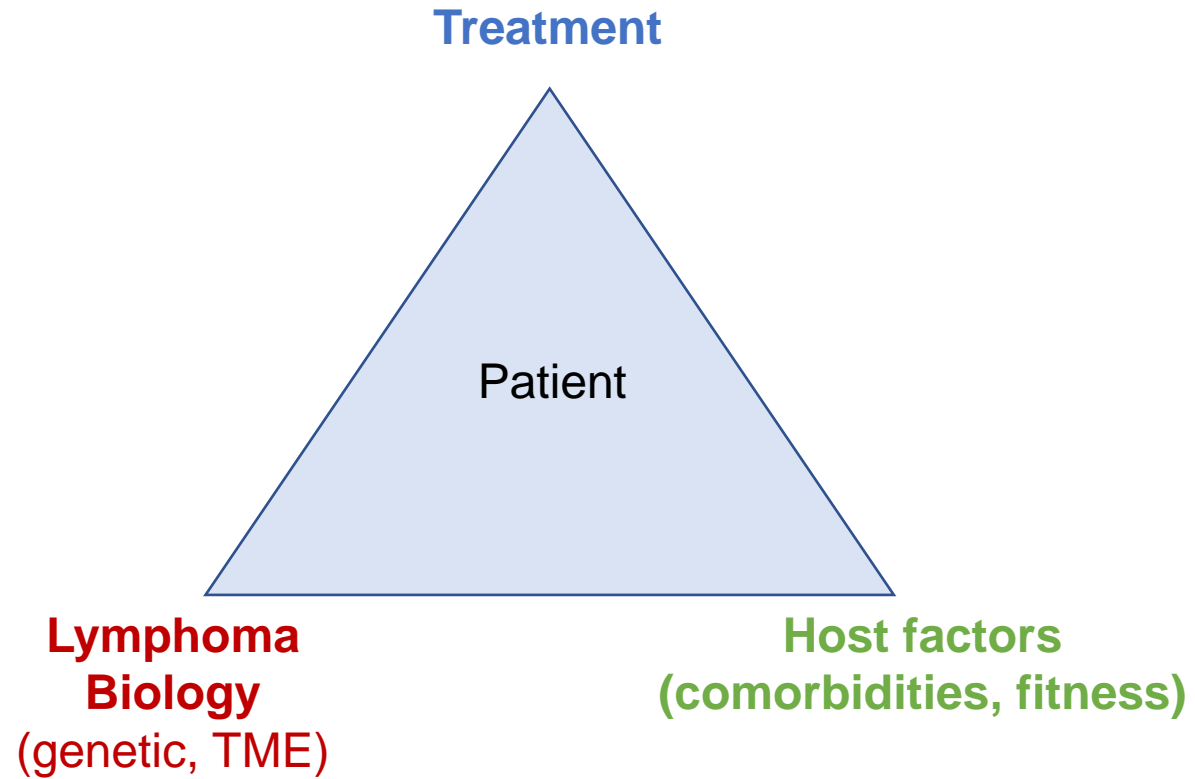
Evolving Approaches/"Moving Target"



Current Challenges

- (1) **Moving Target**
- (2) **Limited resources**
Biomaterial, people, funding
- (2) **Demanding/integrative computations**
Expertise in bioinformatics, statistics
- (3) **Translational/clinical impact**
Functional characterization
Translation into clinical trials

Understanding Response



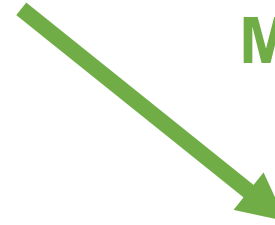
Strategies Towards Precision Medicine (in Lymphoma)

Molecular agnostic



**“All comer” Studies
oriented towards surface epitopes**

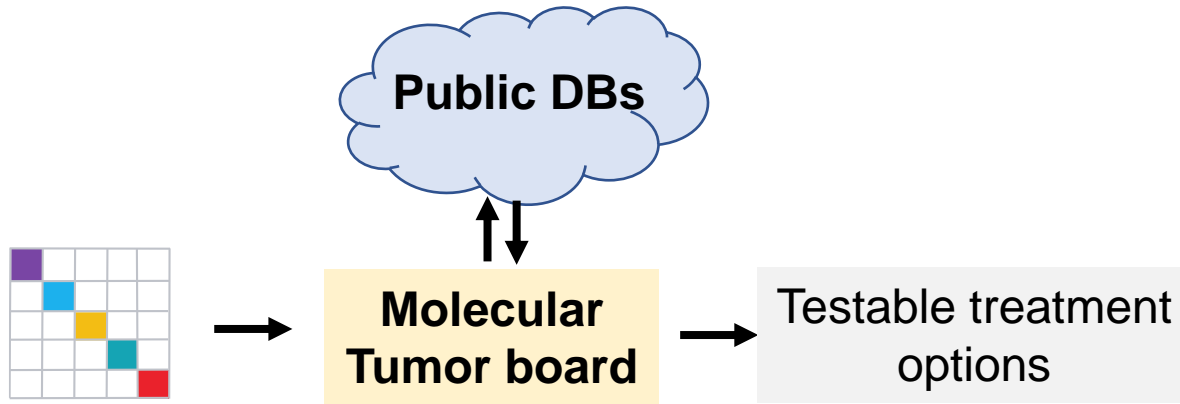
Molecular affine



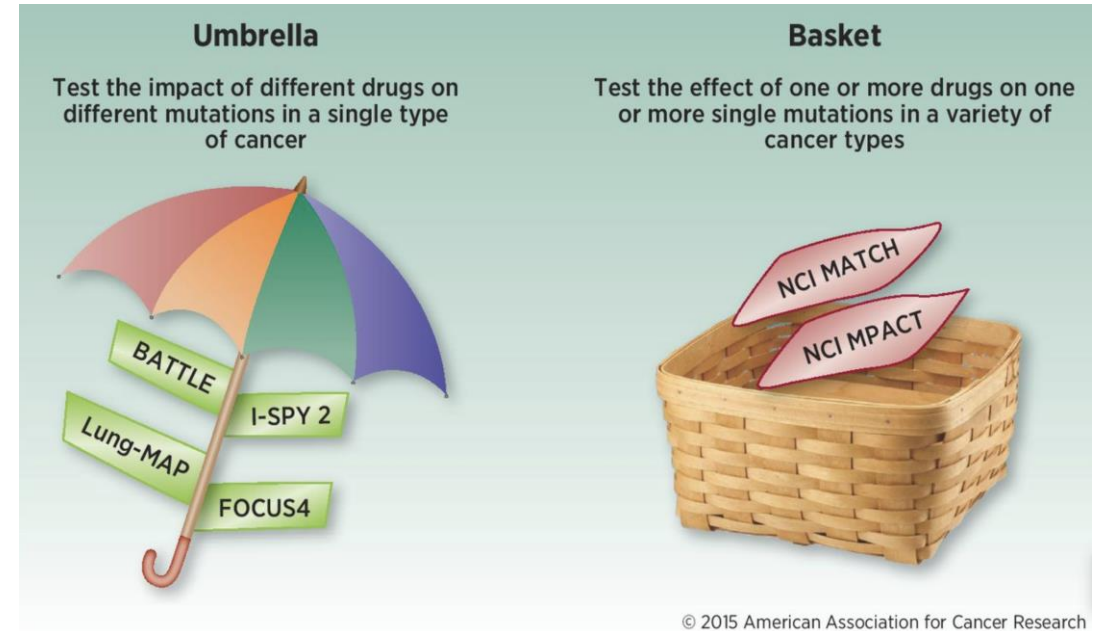
**Understanding Molecular Heterogeneity
&
Targeting Actionable Alterations**

Change in Patient Management and Trial Culture

Molecular Tumor Boards



All Comer Trials become problematic



- Complex biology demands molecularly trained physician and clinically trained biologists/computational biologists
- Need to rethink clinical trial designs

Biomarker-guided Targeted Therapy in DLBCL – R-CHOP+X

Study Design (NCT04025593)

- The study started from **July, 2019**.
- All patients were treated with ONE cycle of standard R-CHOP immediately at diagnosis.
- Patients were randomly assigned 1:1 and stratified by genetic subtype.
- Using targeted sequencing and FISH for BCL2, MYC translocation and BCL6 fusion to classify patients into six genetic subtypes MCD like, BN2 like, N1 like, EZB like, according to **NEJM classification (2018)**, TP53 mutation, and others.

Untreated DLBCL

- Age 18-80
- IPI ≥ 2



Stratified by K-medoids algorithm (PAM) simulated genetic subtyping using targeted sequencing panel of 18 genes:
BTG1, CD70, CD79B, CREBBP, DTX1, EP300, EZH2, MPEP1, MTOR, MYD88, NOTCH1, NOTCH2, PIM1, STAT6, TBL1XR1, TNFAIP3, TNFRSF14, and TP53



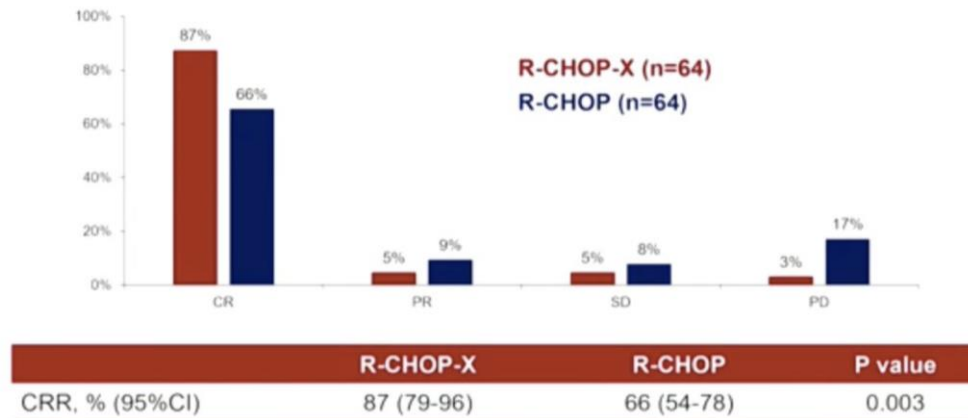
Ibrutinib¹	420mg po qd
Lenalidomide²	25mg d1-10 po
Tucidinostat³	20mg d1, 4, 8, 11 po
Decitabine⁴	10 mg/m ² d1-5
R-CHOP	Standard dose

G-CSF prophylaxis was given from the second cycle of chemotherapy if grade ≥ 3 neutropenia was present in the first cycle.

1. Younes et al., J Clin Oncol 2019. 2. Nowakowski et al., J Clin Oncol 2021. 3. Zhang et al., Clin Epigenet 2020. 4. Zhang et al., ICML 2019 abstract (NCT02951728)

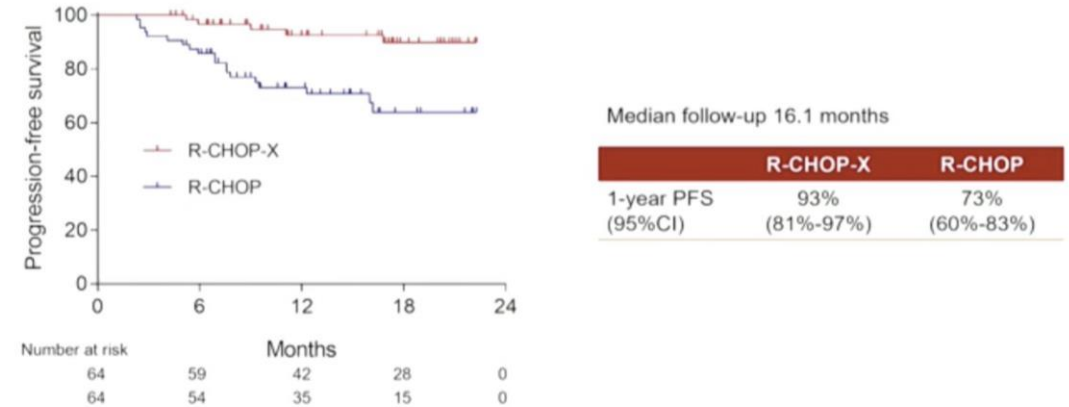
Biomarker-guided Targeted Therapy in DLBCL – R-CHOP+X

Primary Endpoint: CR rate



■ The study met the prespecified primary endpoint.

Secondary Endpoint: PFS



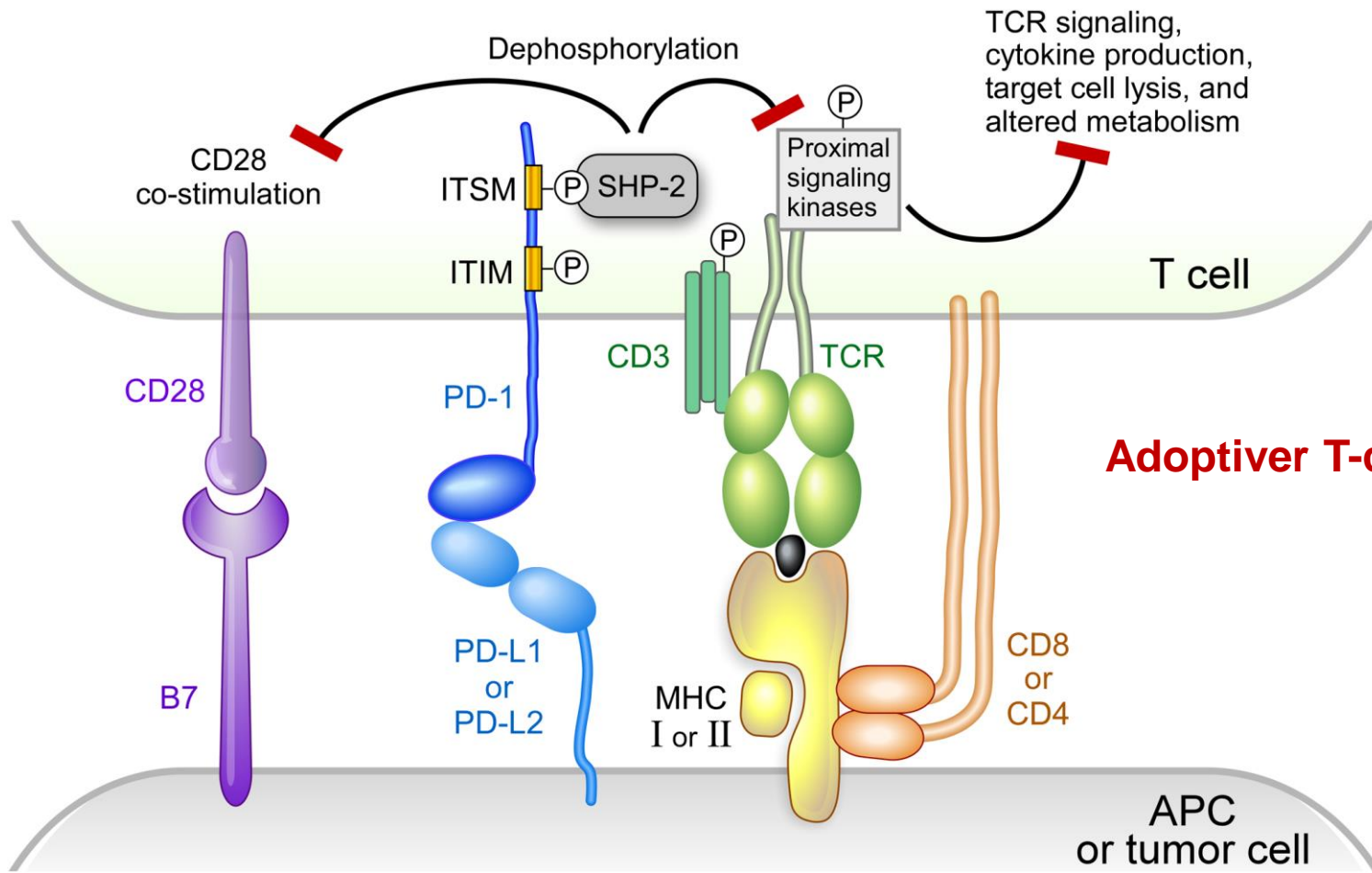
Adverse Events

Toxicity	R-CHOP-X	R-CHOP
Treatment related grade 3-4 AEs (%): Hematological		
Neutropenia	81%	75%
Thrombocytopenia	31%	11%
Anemia	25%	20%
Febrile neutropenia	20%	11%
Treatment related grade 3 AEs (%): Non-hematological		
Lung infection	6%	4%
Gastrointestinal bleeding	2%	3%
Interstitial lung disease	3%	2%
Sepsis	2%	0

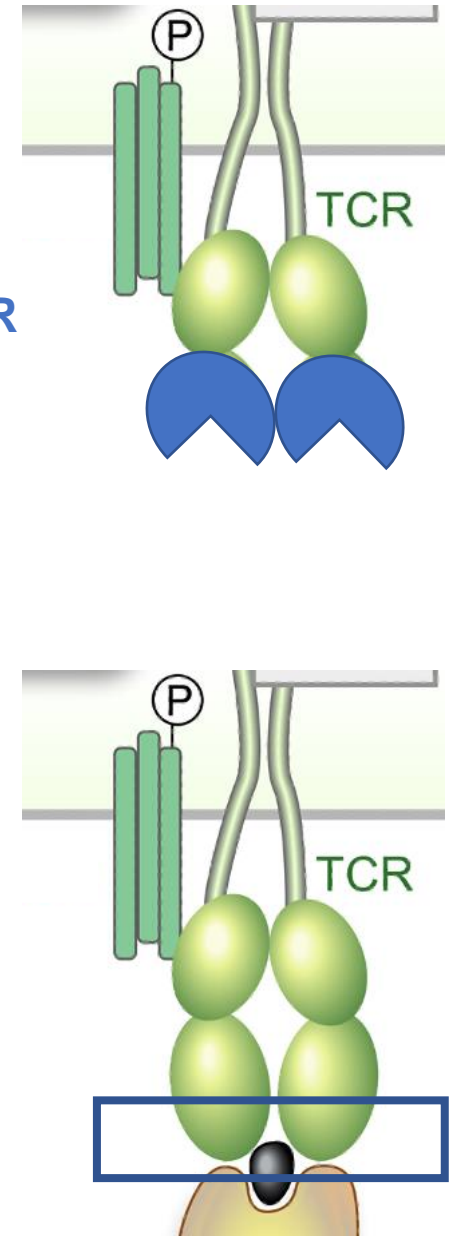
■ Cytopenia and thrombocytopenia were common in R-CHOP-X arm but manageable with supportive care and without treatment related mortality.

- ➔ Promising preliminary data
- ➔ Provides insights into feasibility of biomarker driven trials
- ➔ Follow up / full publication

Immunologic Synapse – T-cell Activation



Adoptive T-cell Transfer



Modified from Baumeister *et al.* 2016; *Annu. Rev. Immunol.* 34:539-73

Off-the-shelf TCRs in Development

Precision immunotherapy with a *MyD88 L265P* specific TCR für R/R lymphoma

Preclinical development

Clinical development

Isolation

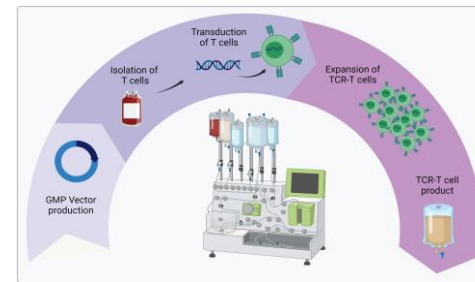
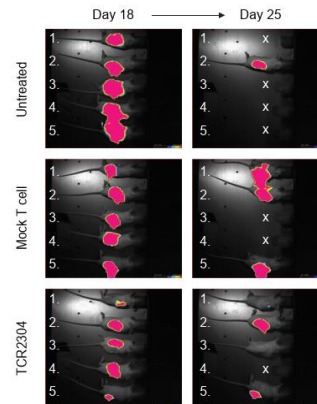
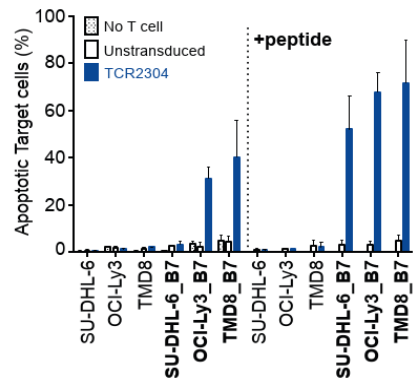
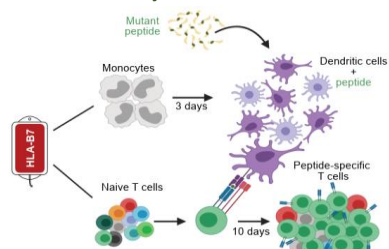
In vitro efficacy /
safety testing

In vivo
testing

Manufacturing
(Prodigy)

NCT
Multicenter Trial

Human, HLA-matched



Auto-TCR-T-cells
retroviral transduction

Charité-SCF

Berlin

Heidelberg

Würzburg

GLA

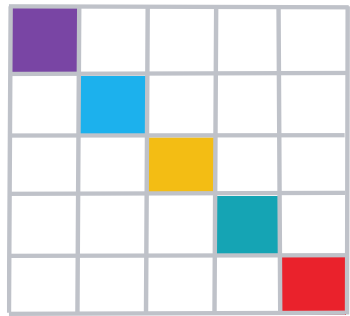
BMBF funding

First-patient-in Q1/2024

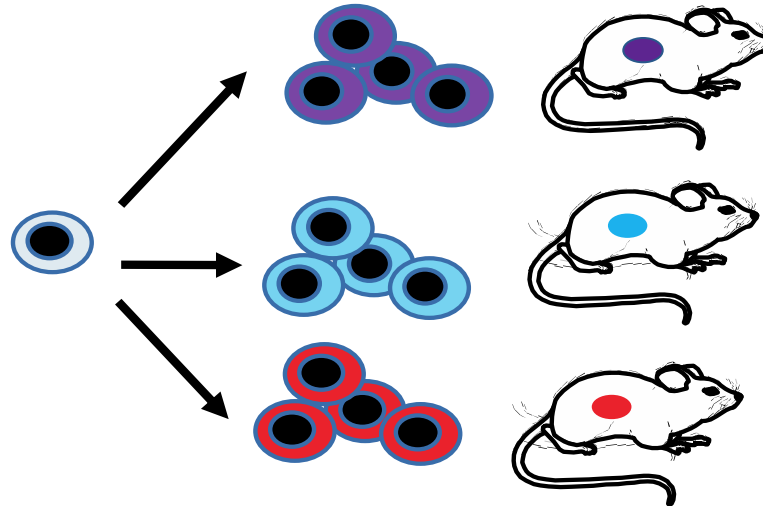
Antonia Busse

From Risk-Adapted to Biological-Informed Lymphoma Therapies

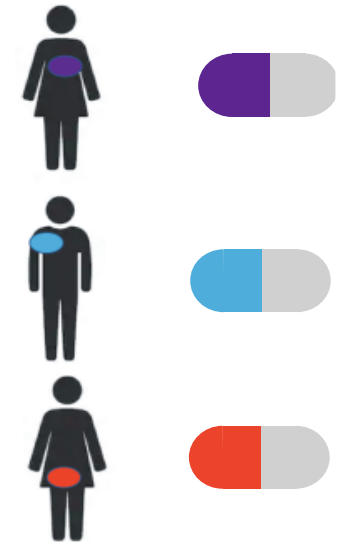
Identify Actionable Molecular Signatures



Exploit Associated Survival Pathways



Develop Rational Therapies and Biomarkers



Interested?

Contact

bjoern.chapuy@charite.de

More Info

<https://go.umg.eu/ag-chapuy>

Team Effort – The Chapuy Laboratory



Postdoctoral Fellows

Jens Löber

Joji Shimono

Manfred Konrad

Salaheddine Ali

Clinical Scientists

Hannes Treiber

Markus Maulhardt

Rebecca Wurm-Kuczera David Böckle

PhD

Nazli Serin

MTAs

Jennifer Günther

Debora Joopi

Vivian Grewe

Luisa Ohlmeier

Cand Meds/Master

Jonas Brandes

Adrian Meyer

Wiebke Feeken

Jan Arne Schrage

A. Hammerschmidt

Christopher Vierke

Julia Hansen

Katharina Wagner

Leonie Kröger

Jan Wehmeyer

Linda Lechner

Marek Werth

Hiring now! Open Positions for:

PhDs, Postdocs and Computational Biologists

Application: bjoern.chapuy@charite.de



More Info <https://go.umg.eu/ag-chapuy>

✉ bjoern.chapuy@charite.de

Thank you for your attention!

Looking forward to your questions?



Contact info:

Prof. Dr. B. Chapuy, Charité, CBF, bjoern.chapuy@charite.de