



Terapia a durata fissa: fitness e stato mutazionale

Gianluca Gaidano, M.D., Ph.D.

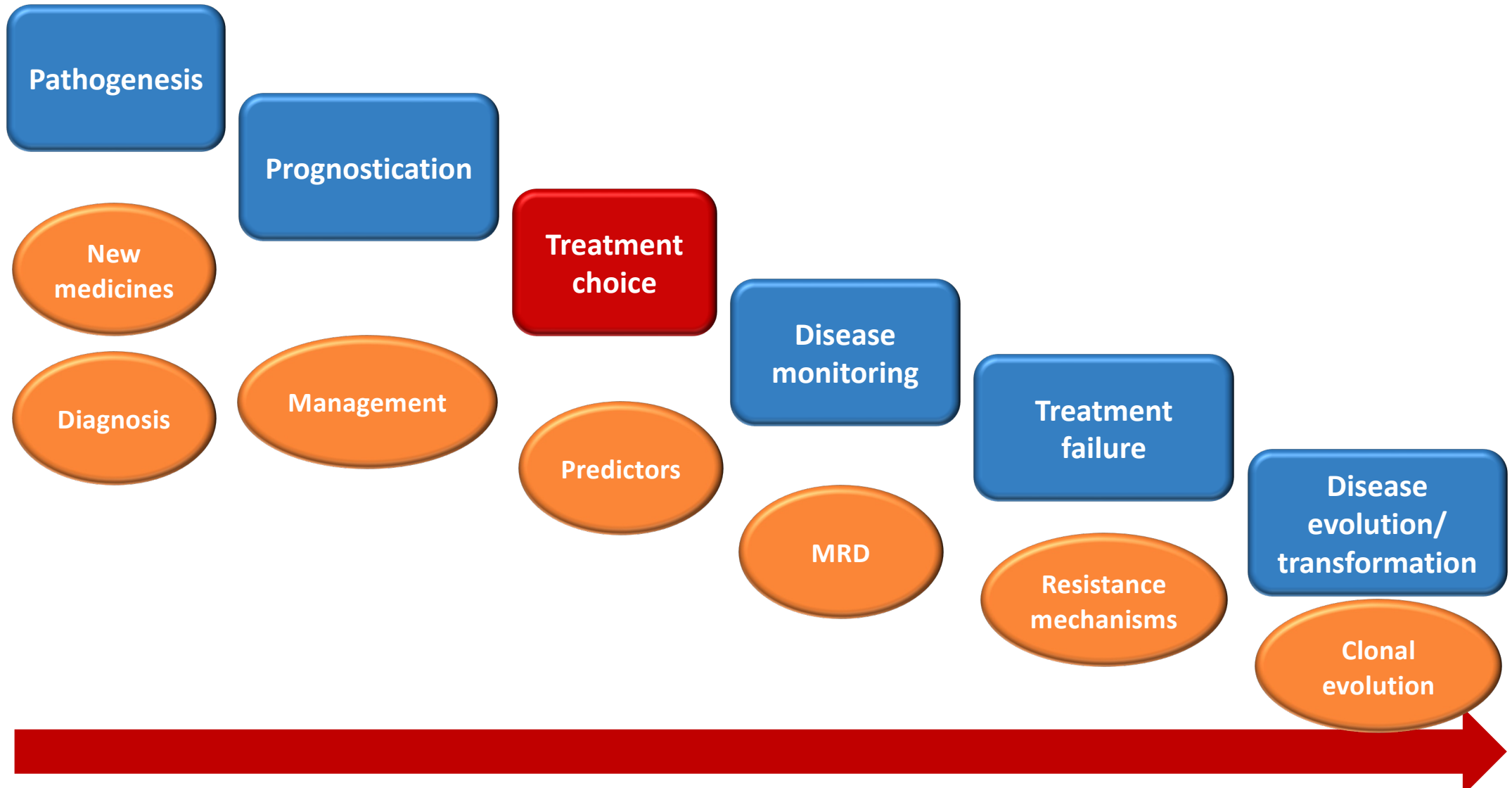


**Division of Hematology
Department of Translational Medicine
Università del Piemonte Orientale
Novara, Italy**


Disclosures

Company name	Research support	Employee	Consultant	Stockholder	Speakers bureau	Advisory board	Other
Abbvie					√	√	
AstraZeneca					√	√	
BeiGene					√	√	
Hikma					√		
Incyte					√	√	
Johnson & Johnson					√	√	
Lilly					√	√	

Applications of molecular biology in CLL



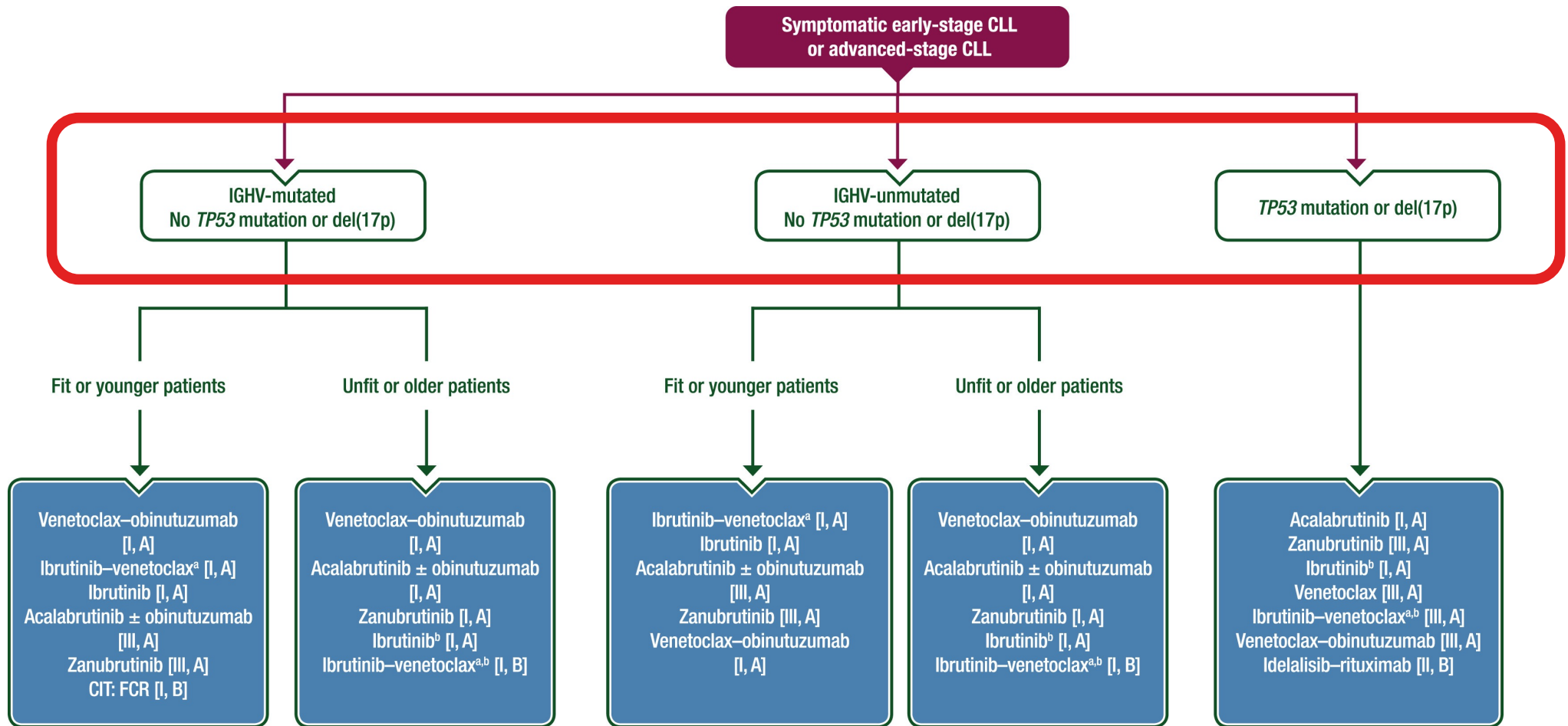
Baseline evaluation of CLL: “Always” only tests in the clinical practice

				
	Diagnosis	Monitoring	Treatment	Richter
History + Physical	✓	✓	✓	✓
CBC + Differential	✓	✓	✓	✓
PB phenotyping*	✓			
Serum chem, Ig, DAT			✓	✓
Ches X-ray			✓	
FISH			✓	+ additional tests <i>Kittai et al., Blood 2025</i>
TP53 mutation			✓	
IGHV mutation			✓	
				*kappa/lambda, CD19, CD20, CD5, CD23, CD10, CD200

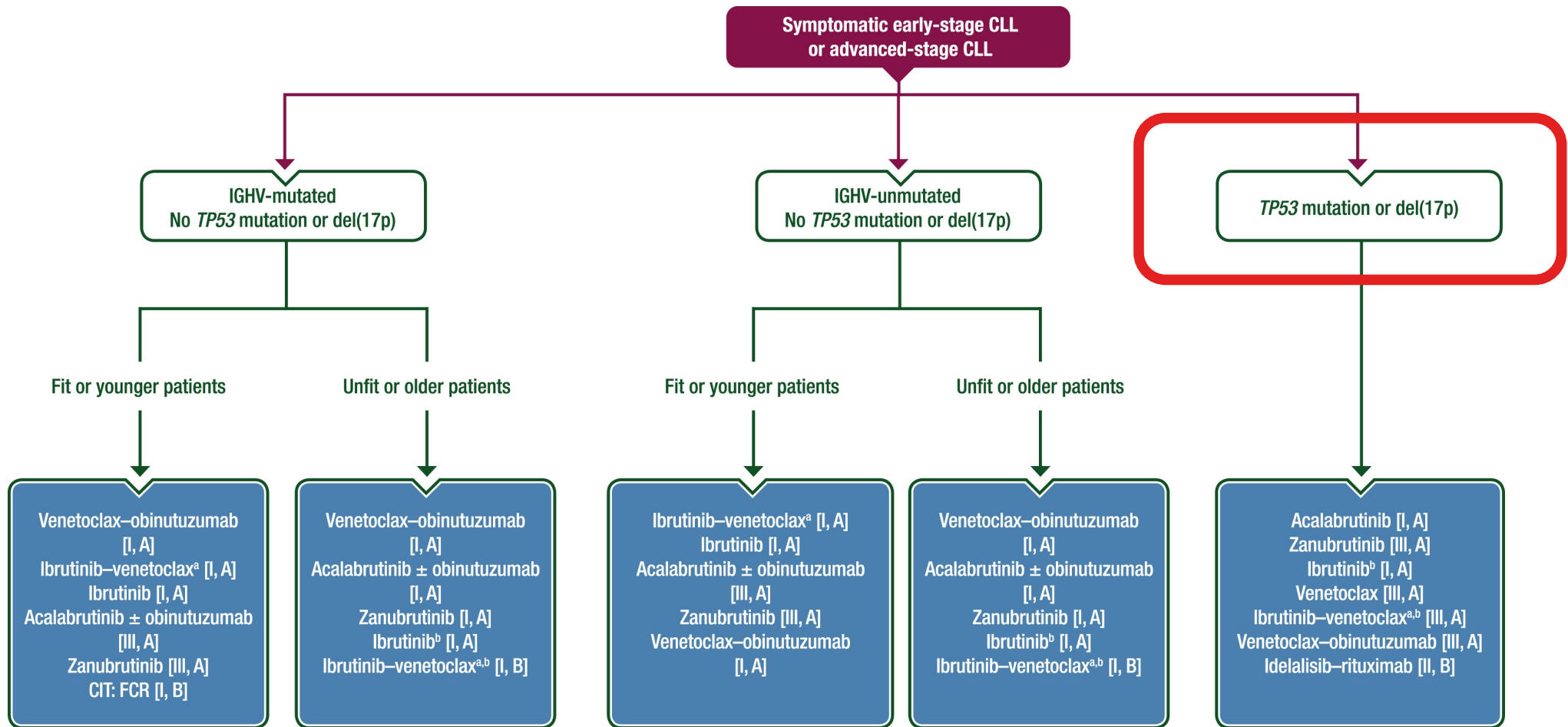
Molecular tests at treatment requirement according to iwCLL guidelines

FISH	del(13q)	no predictive value / not useful for choosing treatment
	del(11q)	no predictive value / not useful for choosing treatment
	del(17p)	
	add(12)	no predictive value / not useful for choosing treatment
DNA seq	TP53 mut	TP53 mutation only is rare; in general coupled with del(17p)
	IGHV mut	Predictive value in ESMO but not in NCCN guidelines

CLL biomarkers in the ESMO guidelines for 1L treatment



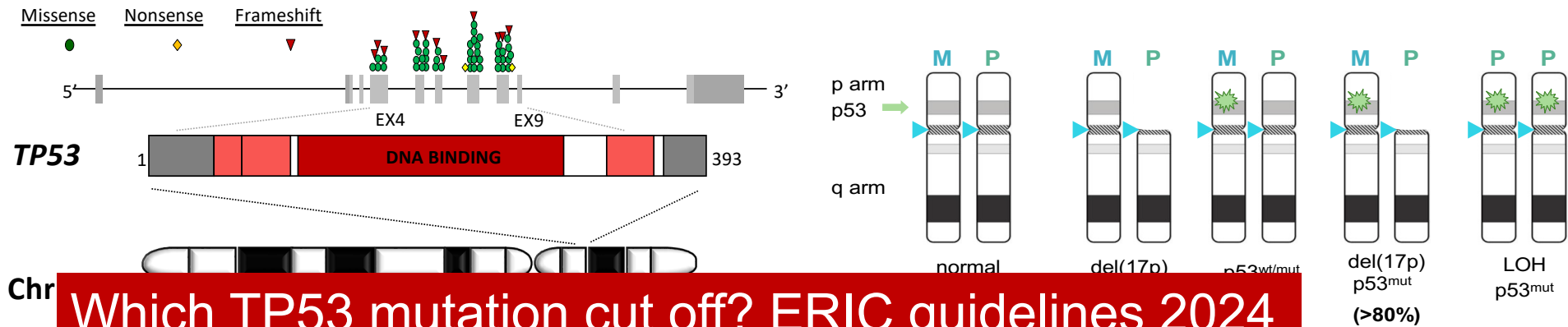
CLL biomarkers in the ESMO guidelines for 1L treatment



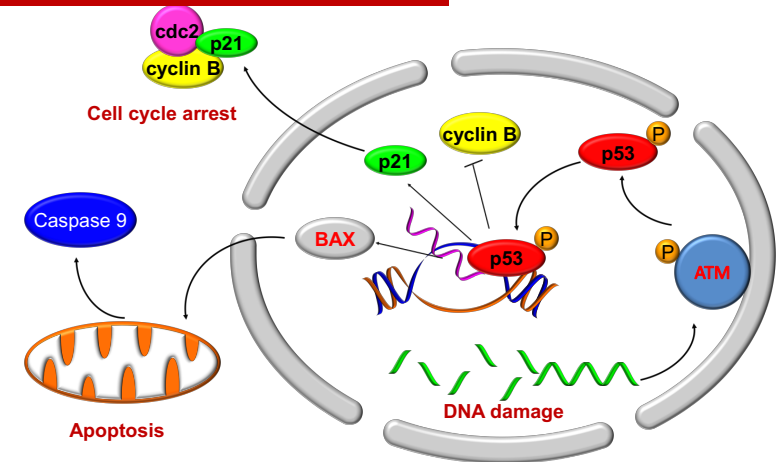
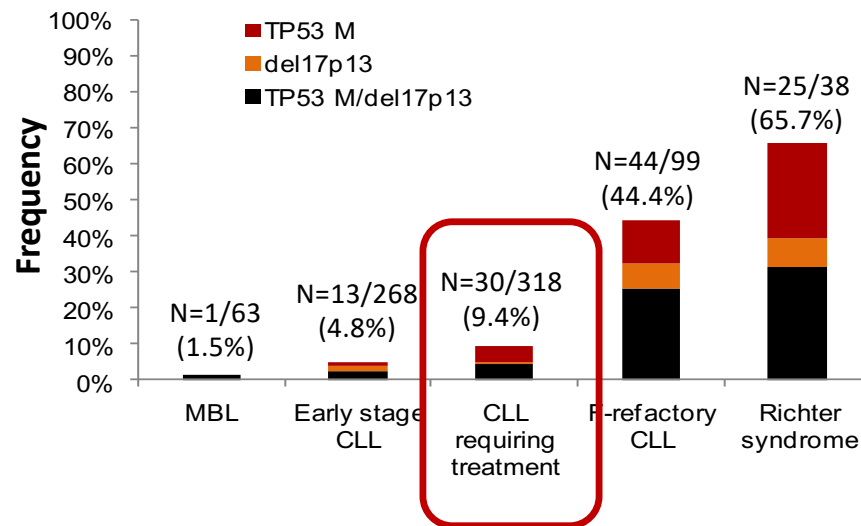
Clinical applications of predictive and prognostic biomarkers in CLL: Guideline recommendations

	General practice	Clinical trial
FISH for del(13q), del(11q), del(17p), add(12)	Always	Always
<i>TP53</i> mutations	Always	Always
IG genes	Always	Always

TP53 abnormalities in CLL

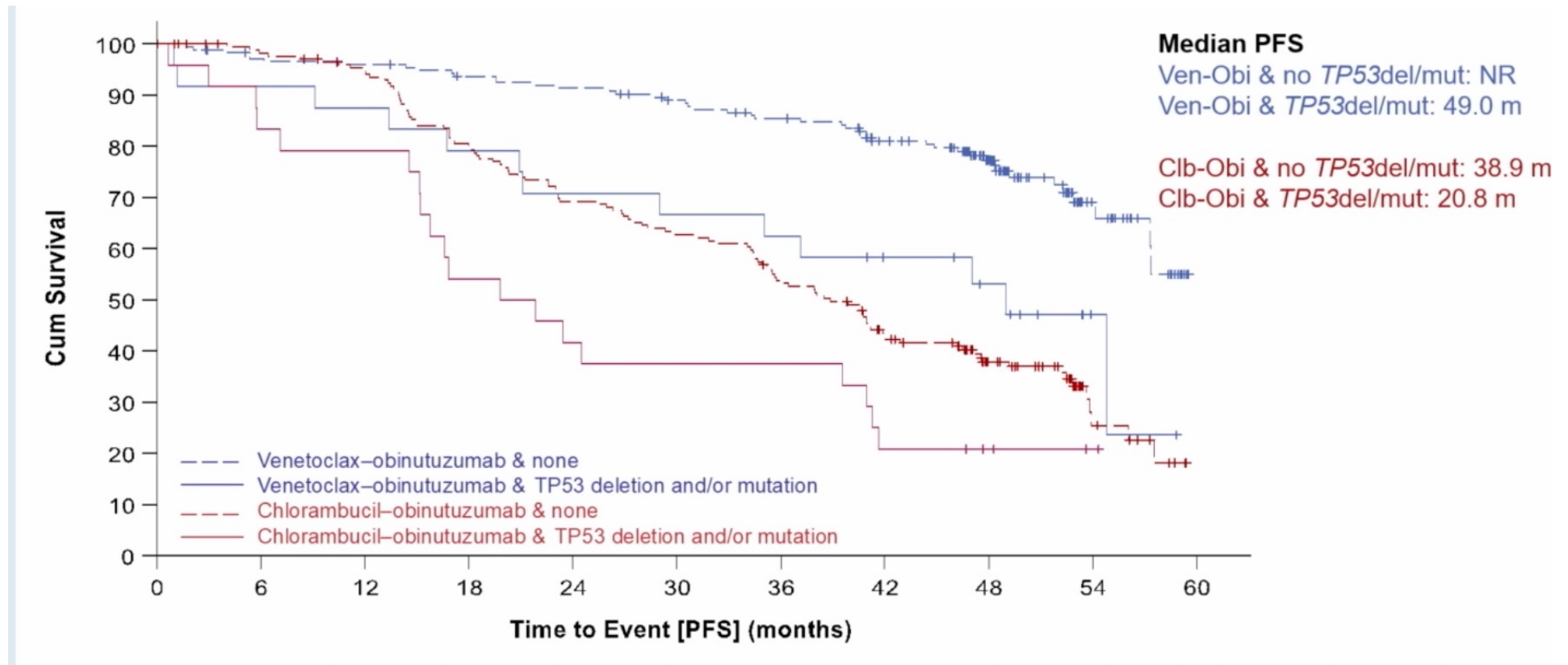


Which TP53 mutation cut off? ERIC guidelines 2024



Dohner et al, New Engl J Med 2000 ; Zenz et al J Clin Oncol 2010; Rossi et al Blood 2011; Zainuddin et al, Leuk Res 2011; Rossi et al Blood 2014

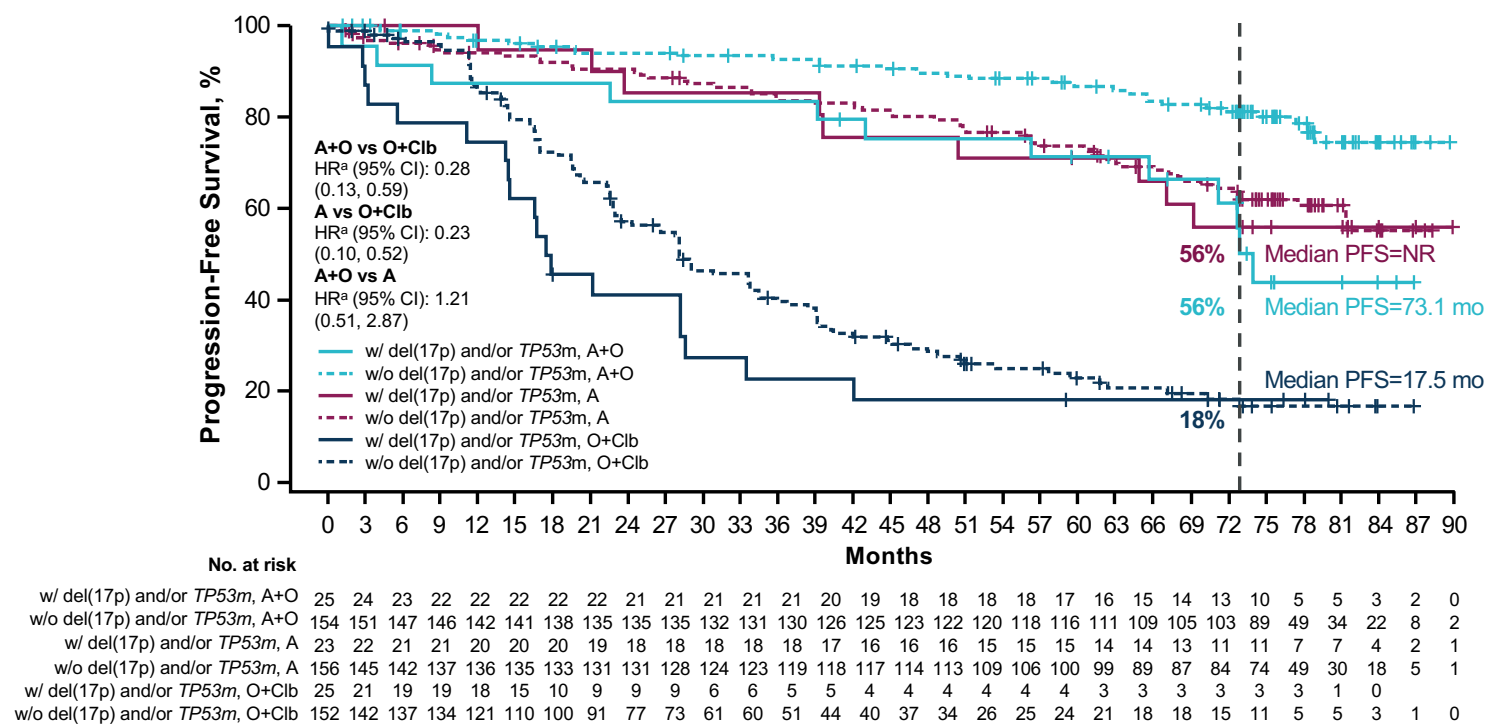
Clinical impact of *TP53* in the CLL14 trial



Ven-Obi mitigates, but does not abolish, the negative prognostic impact of *TP53* disruption

ACALABRUTINIB: combination of longest follow up + best safety profile

Investigator-Assessed PFS in Patients With Del(17p) and/or Mutated *TP53*

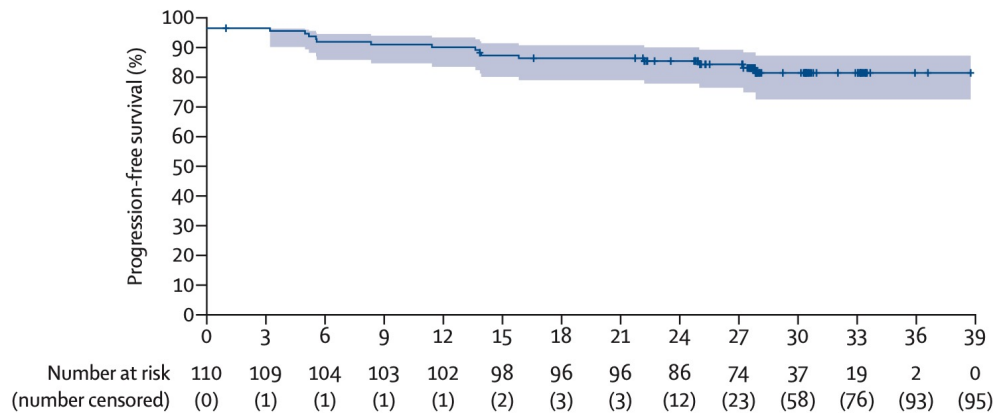


^aHazard ratio based on unstratified Cox proportional-hazards model.

A = acalabrutinib; CI = confidence interval; Clb = chlorambucil; HR = hazard ratio; NR = not reached; O = Obinutuzumab; PFS = progression free survival; *TP53* = tumour protein p53; vs = versus.

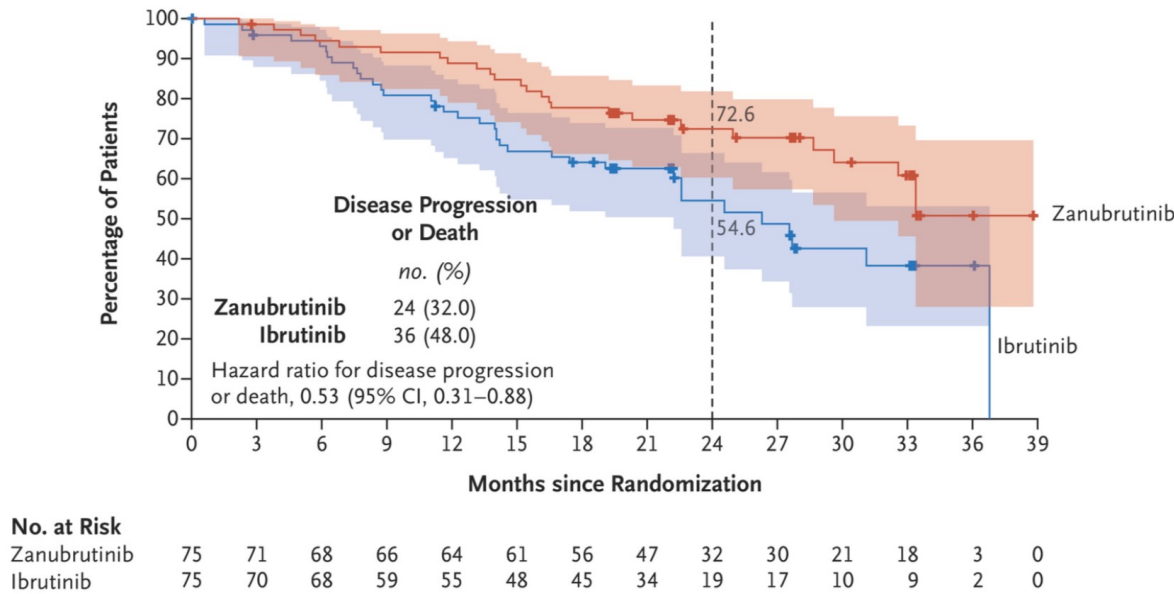
Zanubrutinib activity in *TP53* disrupted patients

ARM C SEQUOIA TRIAL



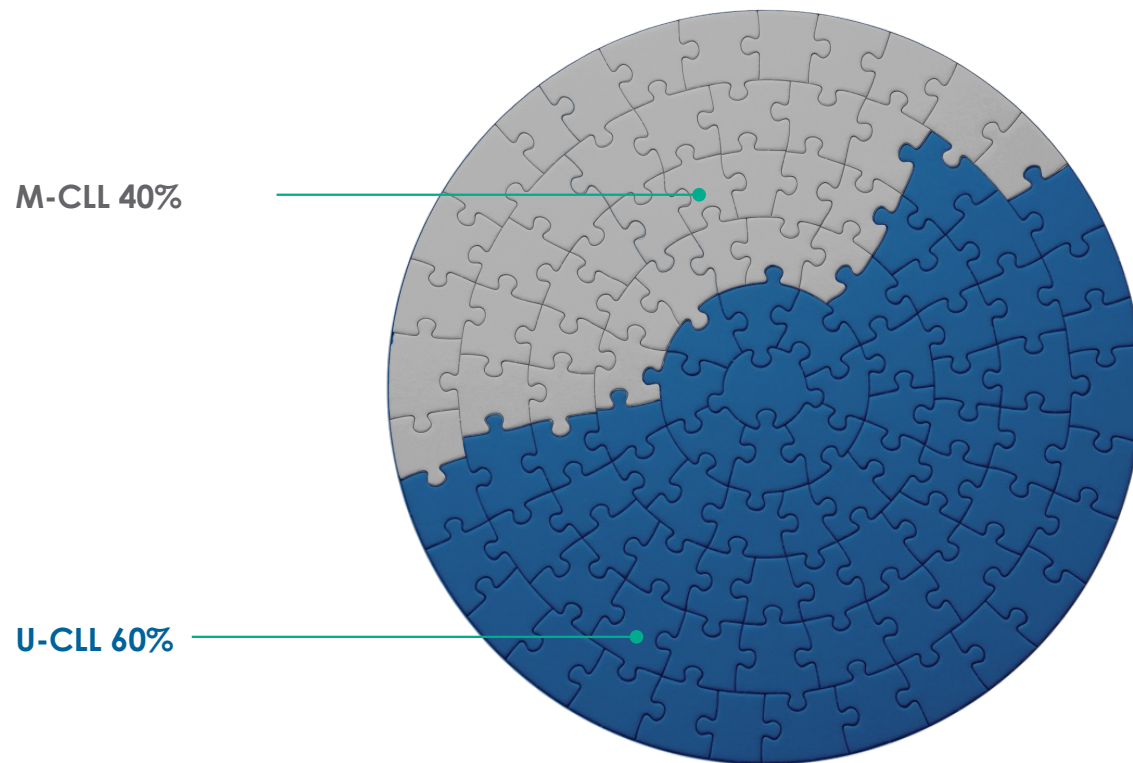
In the ARM C of the SEQUOIA trial the 24 months of *TP53* disrupted patients was 88.9%

ALPINE TRIAL



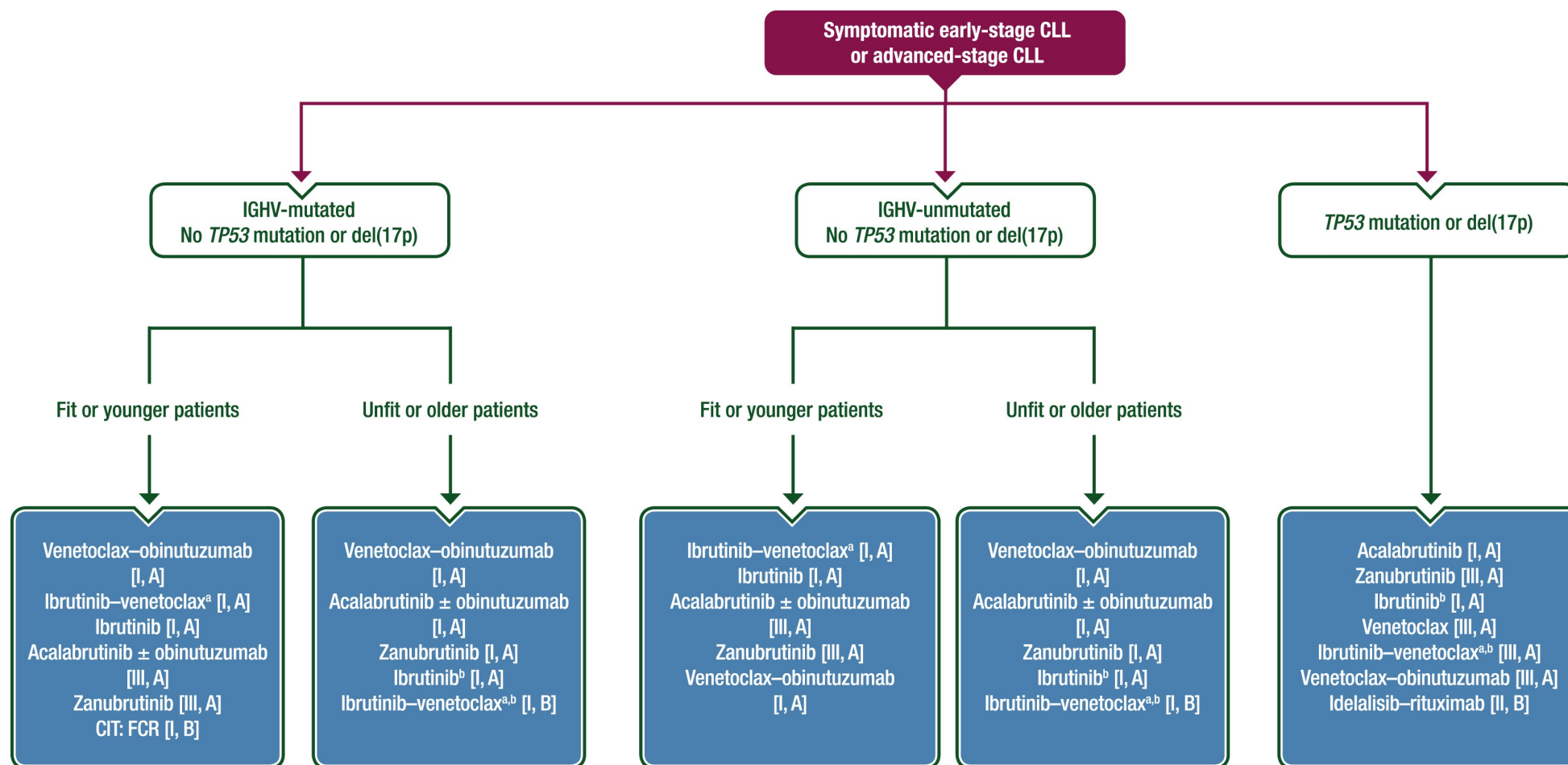
In the ALPINE trial zanubrutinib was more effective compared to ibrutinib in *TP53* disrupted patients

Around 60% of CLL patients requiring treatment have an unmutated IGHV mutational status (U-CLL)

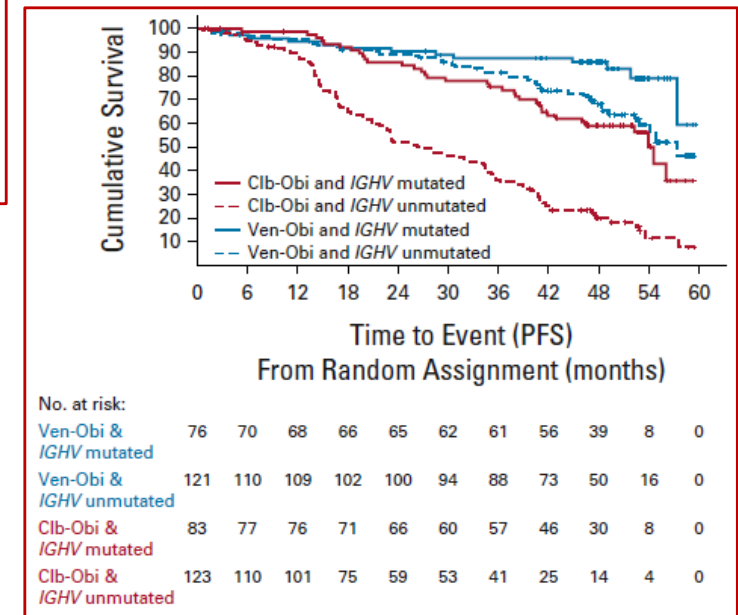
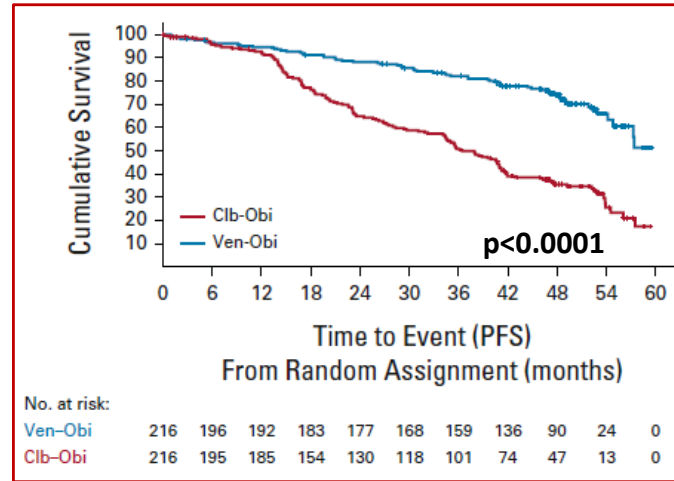
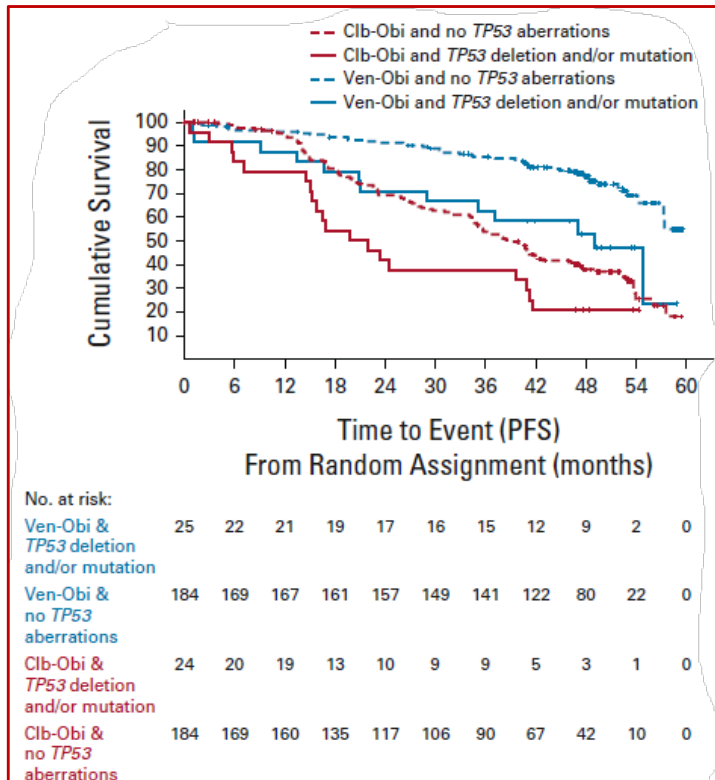


Performing IGHV testing and treating appropriately will have a significant impact on patients' outcomes¹

CLL biomarkers in the ESMO guidelines for 1L treatment



Venetoclax-obinutuzumab vs Clb-Obi in previously untreated CLL (CLL14)



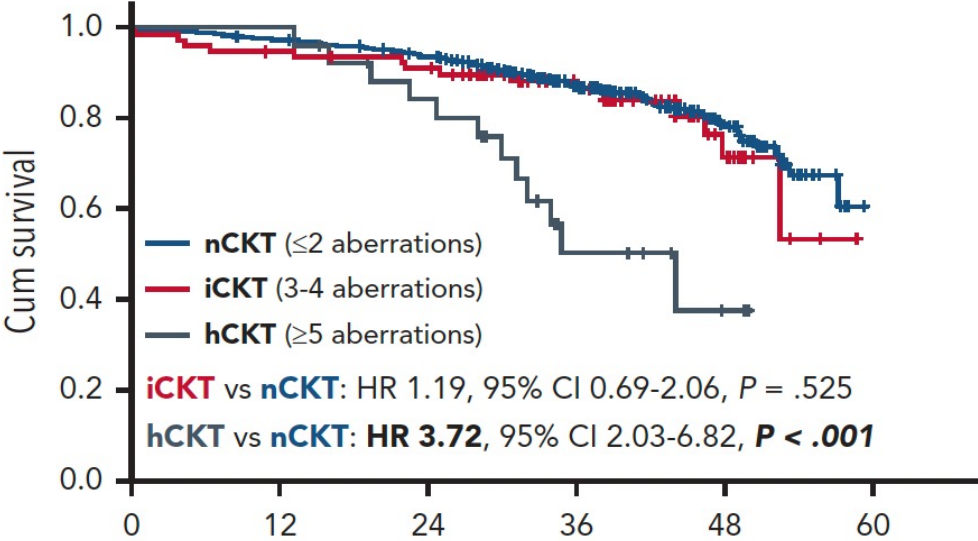
Ven-Obi mitigates, but does not completely overcome, the negative prognostic impact of *TP53* abnormalities and of unmutated *IGHV* genes

Molecular predictors of PFS in CLL with venetoclax-based combinations in the CLL13/GAIA trial

iii) CK

hCKT → poor PFS

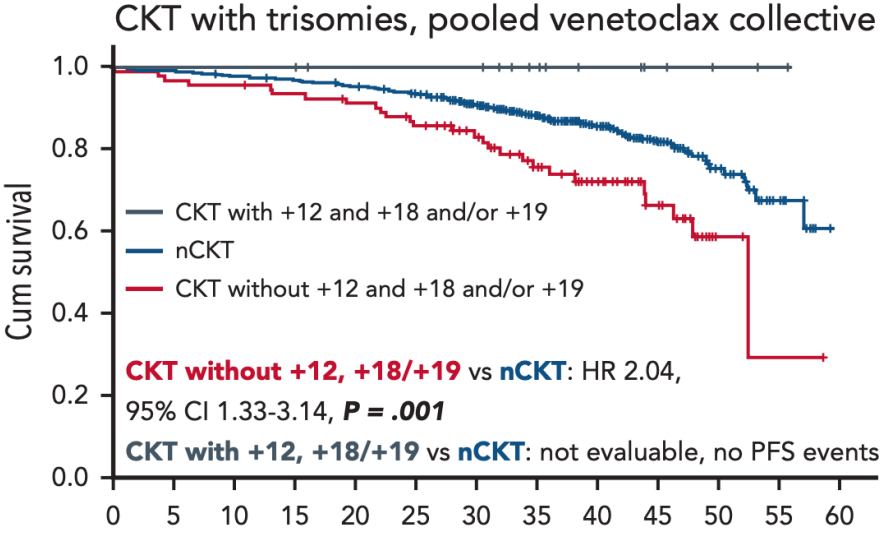
Pooled venetoclax collective



Patients at risk		Time to event [PFS] (months)				
		0	12	24	36	48
nCKT	565	547	522	308	99	
iCKT	80	75	71	44	14	
hCKT	27	27	21	8	2	

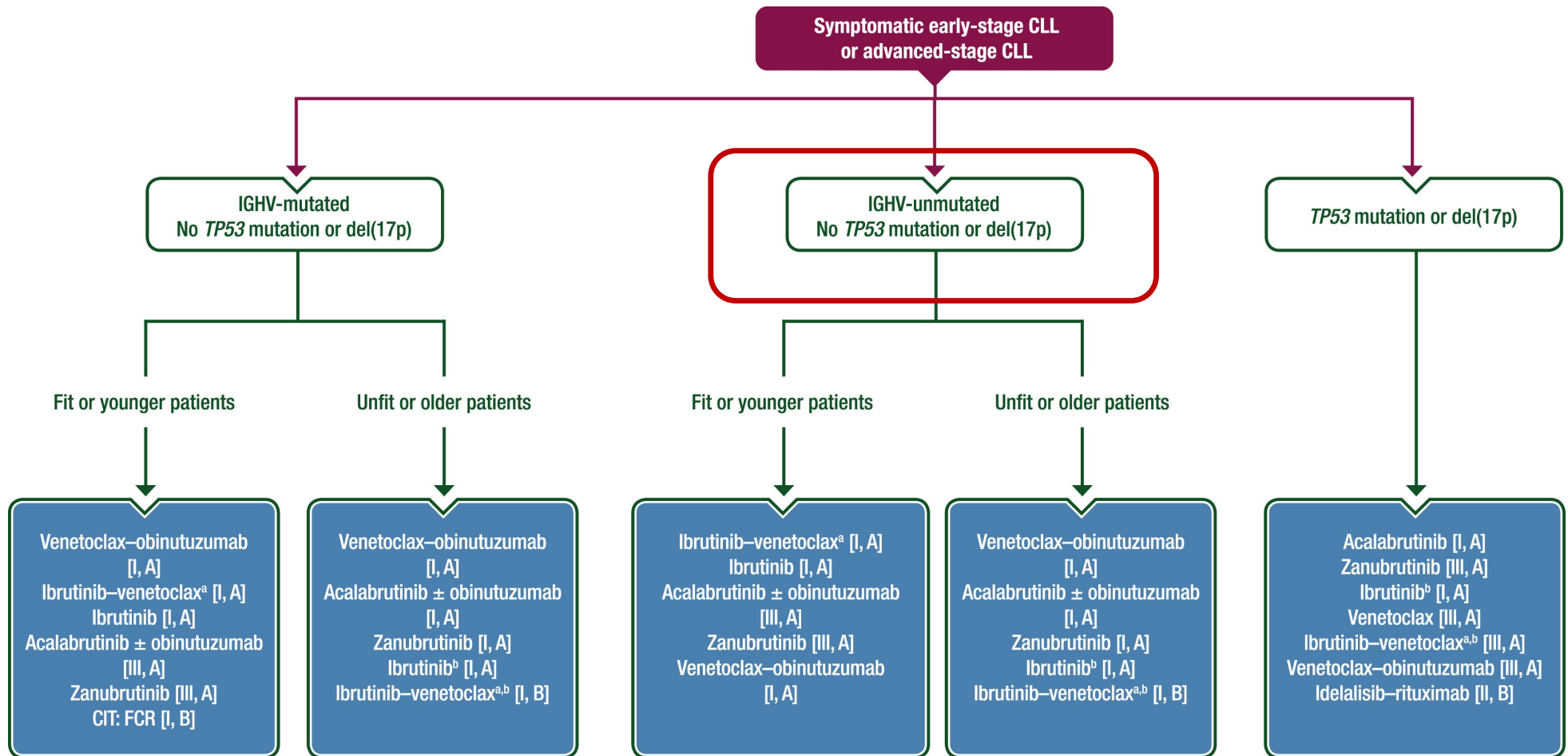
+12, +18, +19 → excellent PFS

D



Patients at risk		Time to event [PFS] (months)				
		0	5	10	15	20
nCKT	565	547	522	308	99	
CKT without +12, +18/19	92	87	79	45	13	
CKT with +12, +18/19	15	15	13	7	3	

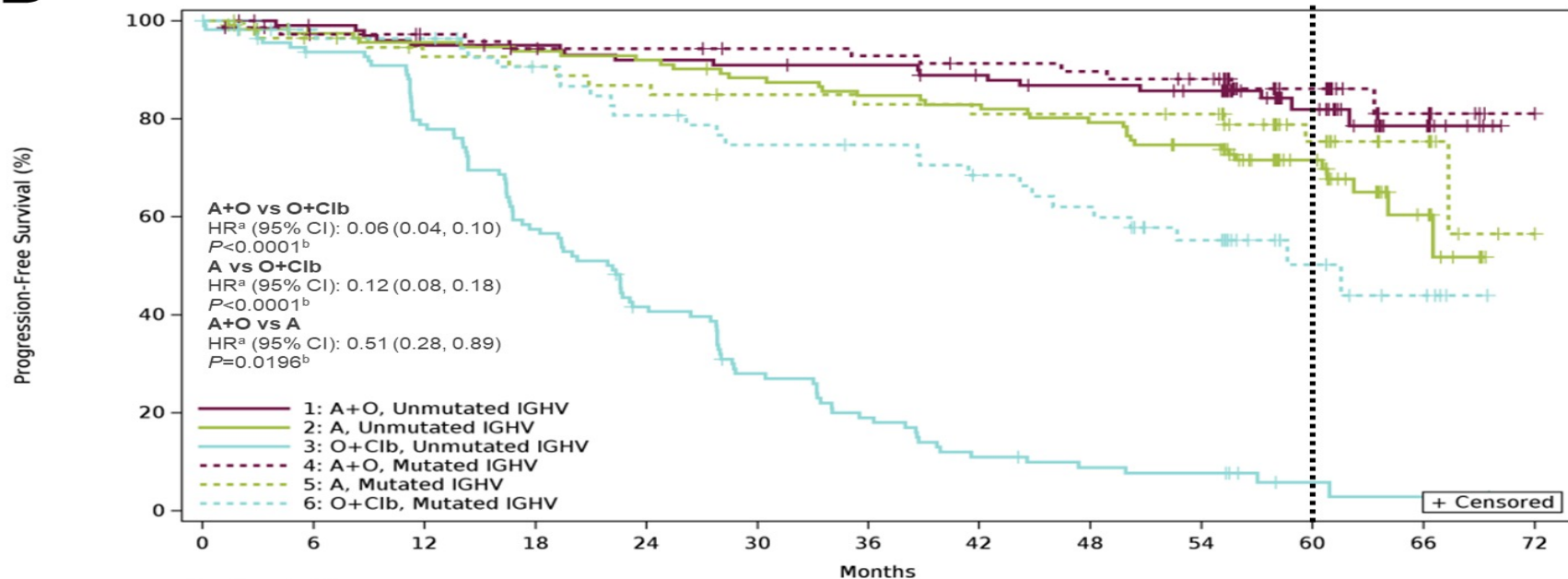
CLL biomarkers in the ESMO guidelines for 1L treatment



ELEVATE-TN 5-year follow-up: Inv PFS in patients with uIGHV & IGHVm

B

Investigator-assessed progression-free survival in patients with uIGHV & IGHVm (B):

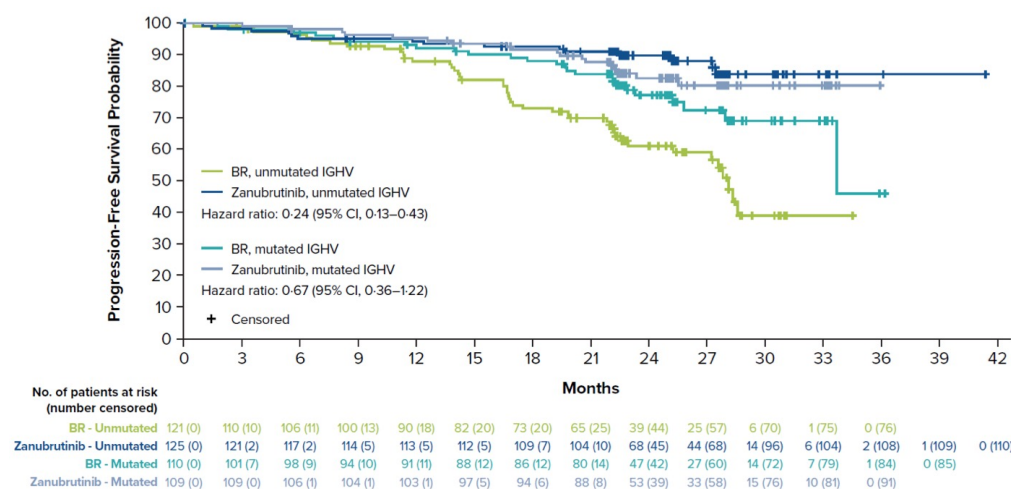


Number at risk

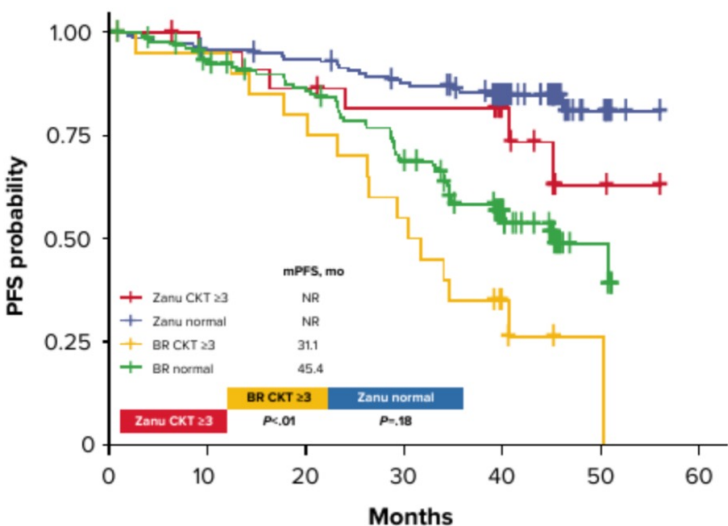
A+O, Unmutated IGHV	103	101	99	97	95	95	94	92	91	91	90	89	89	85	84	81	81	80	77	57	36	22	14	4	0
A, Unmutated IGHV	118	111	108	106	106	105	104	103	102	100	97	96	93	92	91	88	87	82	79	60	41	24	12	4	0
O+Clb, Unmutated IGHV	116	105	101	99	85	75	62	55	43	41	28	27	19	14	11	9	8	7	7	4	2	1	1	1	0
A+O, Mutated IGHV	74	72	69	69	67	66	64	63	63	63	61	61	60	59	58	58	57	56	54	40	28	17	13	3	1
A, Mutated IGHV	59	54	53	50	48	48	47	45	45	44	43	43	42	42	41	41	41	41	40	33	22	15	10	2	1
O+Clb, Mutated IGHV	59	56	53	52	52	48	46	43	41	39	37	37	36	34	32	30	29	23	22	15	10	6	5	1	0

Sharman et al, Lancet 2020; Sharman et al, ASCO 2022

Zanubrutinib activity according to IGHV mutational status and complex karyotype



Zanubrutinib overcomes the prognostic impact of IGHV mutational status

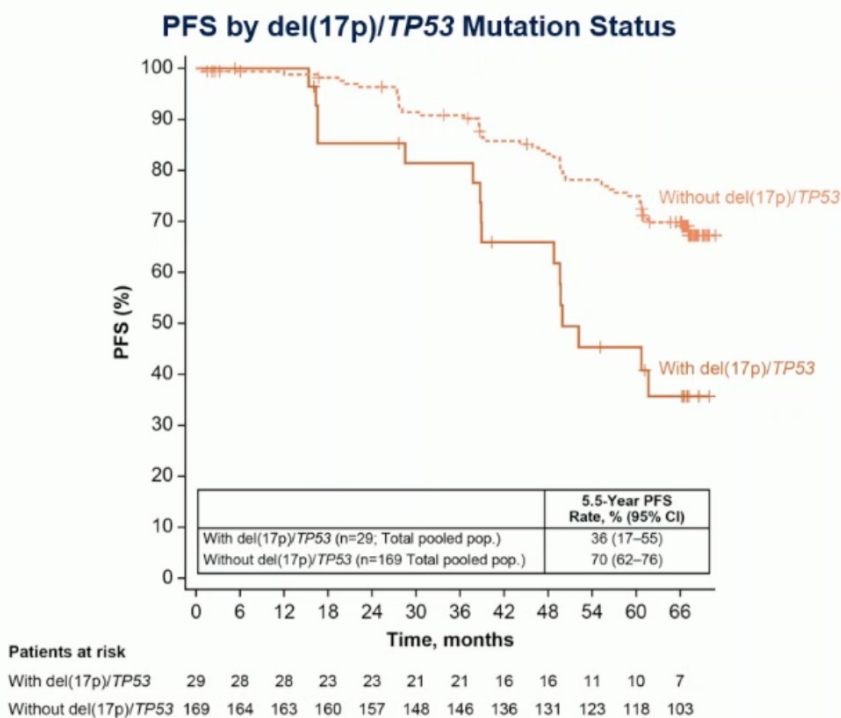


Zanubrutinib overcomes the prognostic impact of complex karyotype

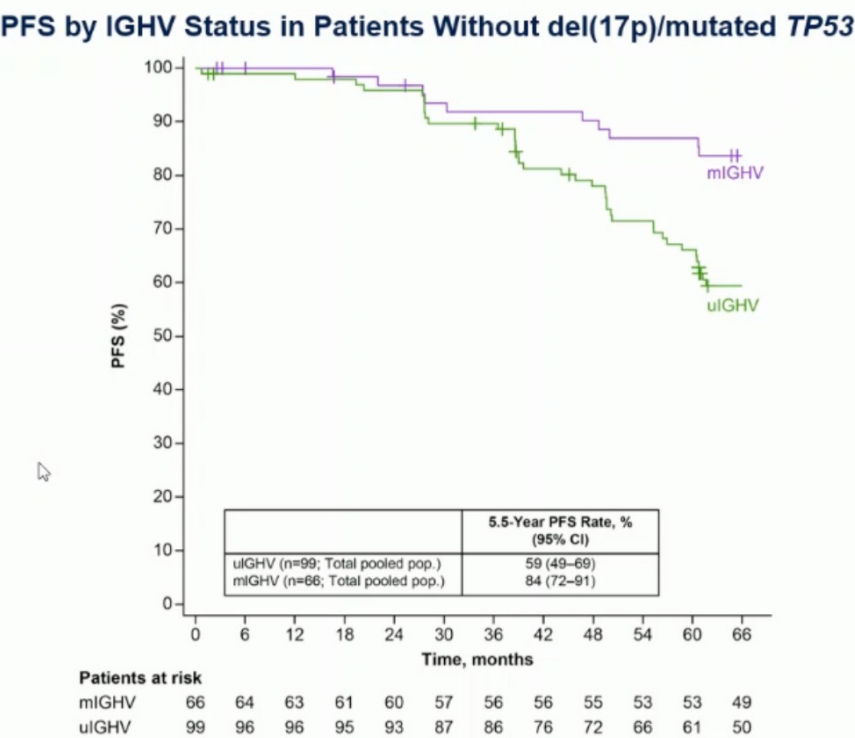
Tam *et al.*, *Lancet Oncol.* 2022; Xu *et al.*, ASH2023 #1092.

Captivate: Impact of biomarkers

Impact of del(17p)/mutated *TP53* and IGHV Status On Long-Term PFS (Total Pooled Population)



FD Cohort ^a	5.5-Year PFS Rate, % (95% CI)
With del(17p)/ <i>TP53</i> (n=27; FD cohort only)	30 (12–49)
Without del(17p)/ <i>TP53</i> (n=129; FD cohort only)	66 (57–74)

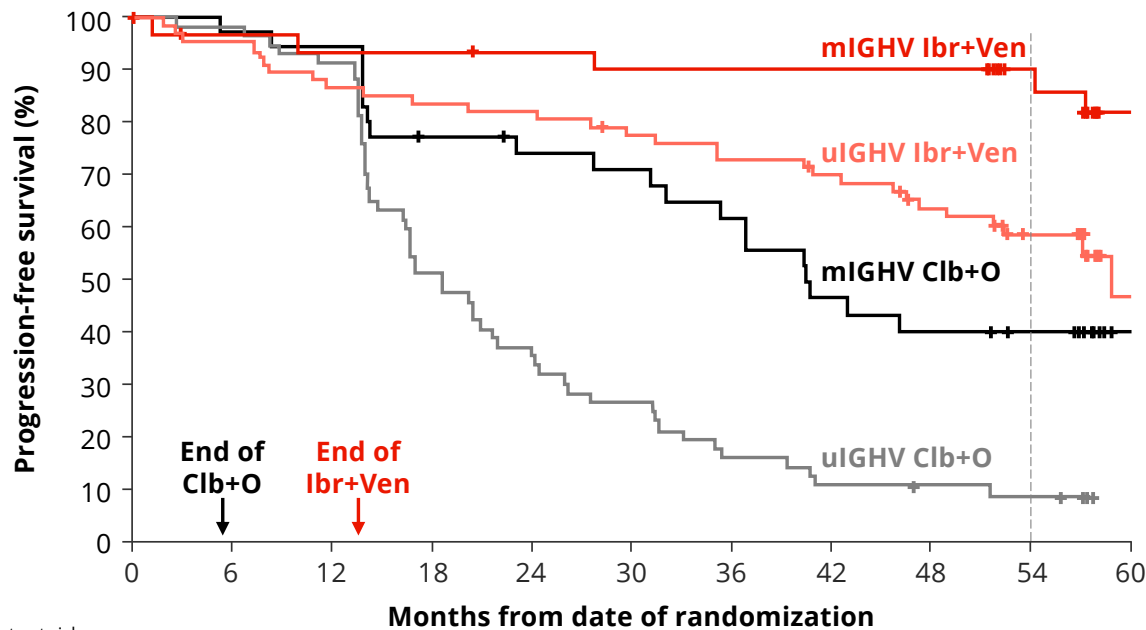


FD Cohort ^a	5.5-Year PFS Rate, % (95% CI)
uIGHV (n=71; FD cohort only)	53 (40–64)
mIGHV (n=55; FD cohort only)	80 (66–89)

^aSee Supplementary Information for details. mIGHV, mutated IGHV.

GLOW: At 57 Months of Follow-up, Ibr+Ven Improved PFS Versus Clb+O Regardless of IGHV Status

Progression-Free Survival (ITT) by IGHV Status



Patients at risk											
mIGHV Ibr+Ven	32	29	28	28	27	26	26	26	26	22	5
uIGHV Ibr+Ven	67	64	58	56	55	51	48	45	39	30	6
mIGHV Clb+O	35	34	33	26	24	23	20	15	13	9	2
uIGHV Clb+O	57	56	52	29	21	15	9	6	5	4	0

Results based on updated IGHV reclassifications
Investigator-assessed progression-free survival was analyzed

- Estimated 54-month PFS rates:
 - **Ibr+Ven:**
 - 90% for patients with mIGHV
 - 59% for patients with uIGHV
 - **Clb+O:**
 - 40% for patients with mIGHV
 - 8% for patients with uIGHV



Considerations for 1L treatment choice

Comorbidities

Disease biology

Pharmacology

Duration

Sustainability

Cardio
vascular
safety

Biomarkers
(TP53
disruption)

Resistance
mutations
(after 1st
line BTKi)

Covalent

Non-
covalent

Continuous
single agent
treatment?

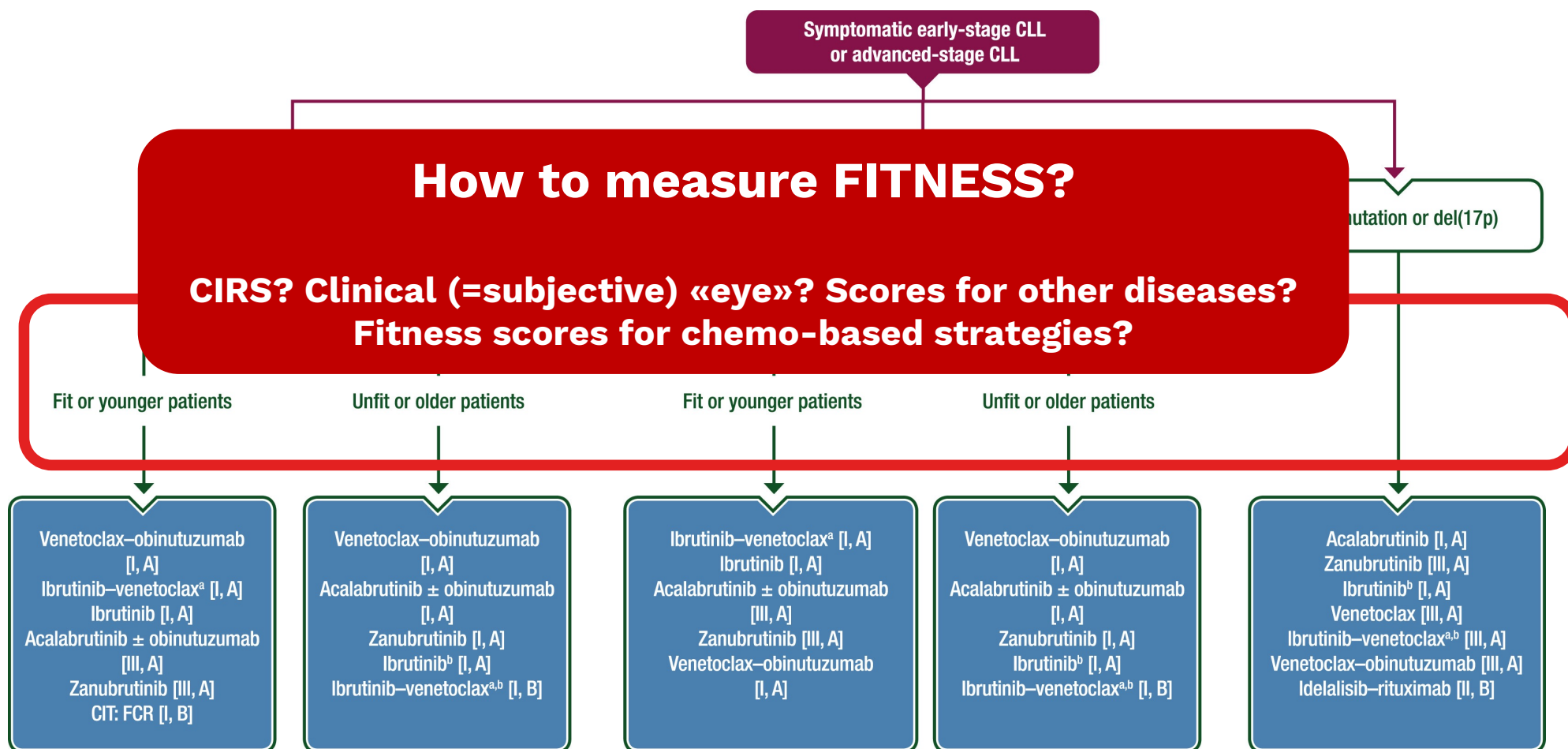
Fixed
duration
combo?

Financial
toxicity

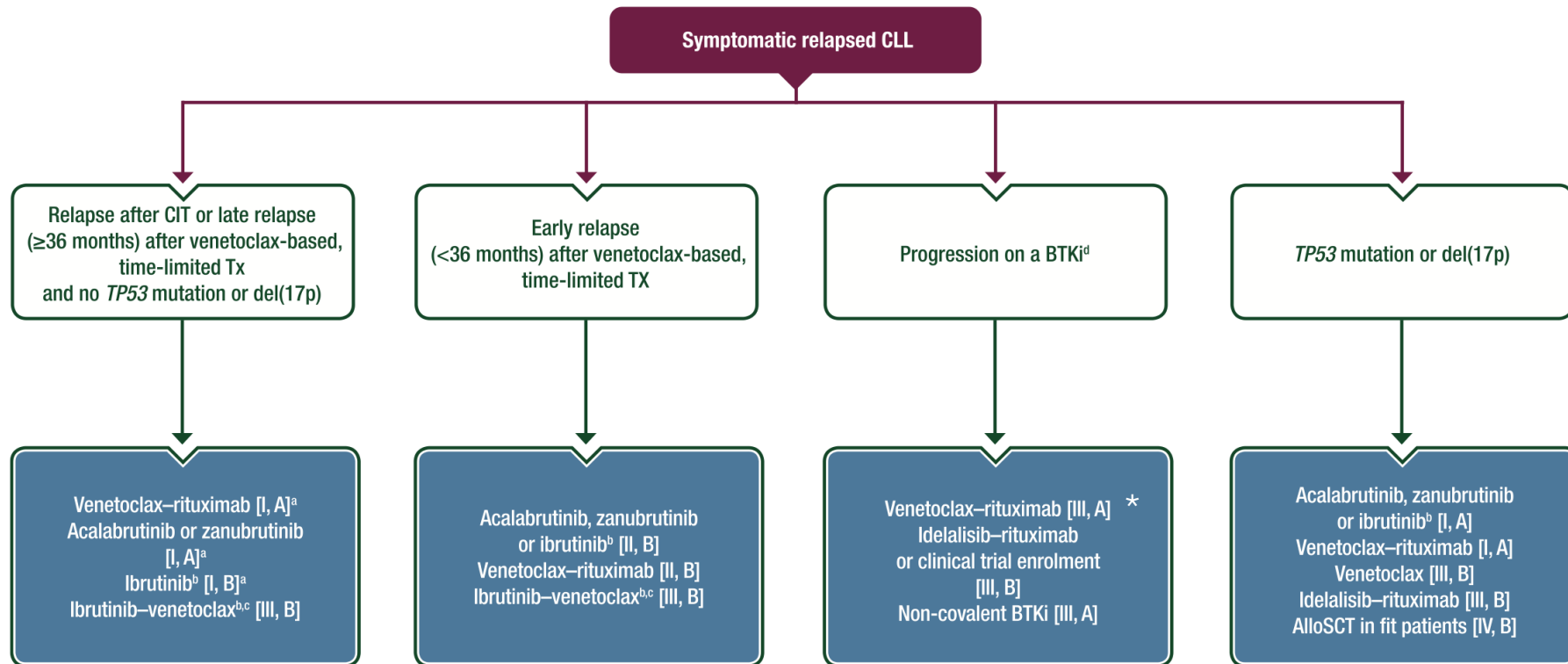
Accessibility
Affordability

Patient's preferences

CLL biomarkers in the ESMO guidelines for 1L treatment



ESMO guidelines for R/R CLL (2024)



^aFor relapse after CIT, BTKis or venetoclax–rituximab should be considered equally, depending on comorbidities, comedication, access and preference.

^bIbrutinib should be considered carefully particularly in older patients with cardiac comorbidities.

^cNot EMA approved, not FDA approved in relapse.

^dIf a patient relapses after prior treatment with a BTKi, which was stopped due to side-effects, changing to a different BTKi or rechallenge could be considered [III, B].

* *not an option in double refractory patients (refractory to both BTKi and BCL2i)*

Eichorst et al., Ann Oncol. 2024

Biomarkers in CLL in the era of pathway inhibitors

Progression of
early stage CLL

IGHV

XPO1

Treatment
choice

TP53

IGHV

CK

NOTCH1

Treatment
monitoring

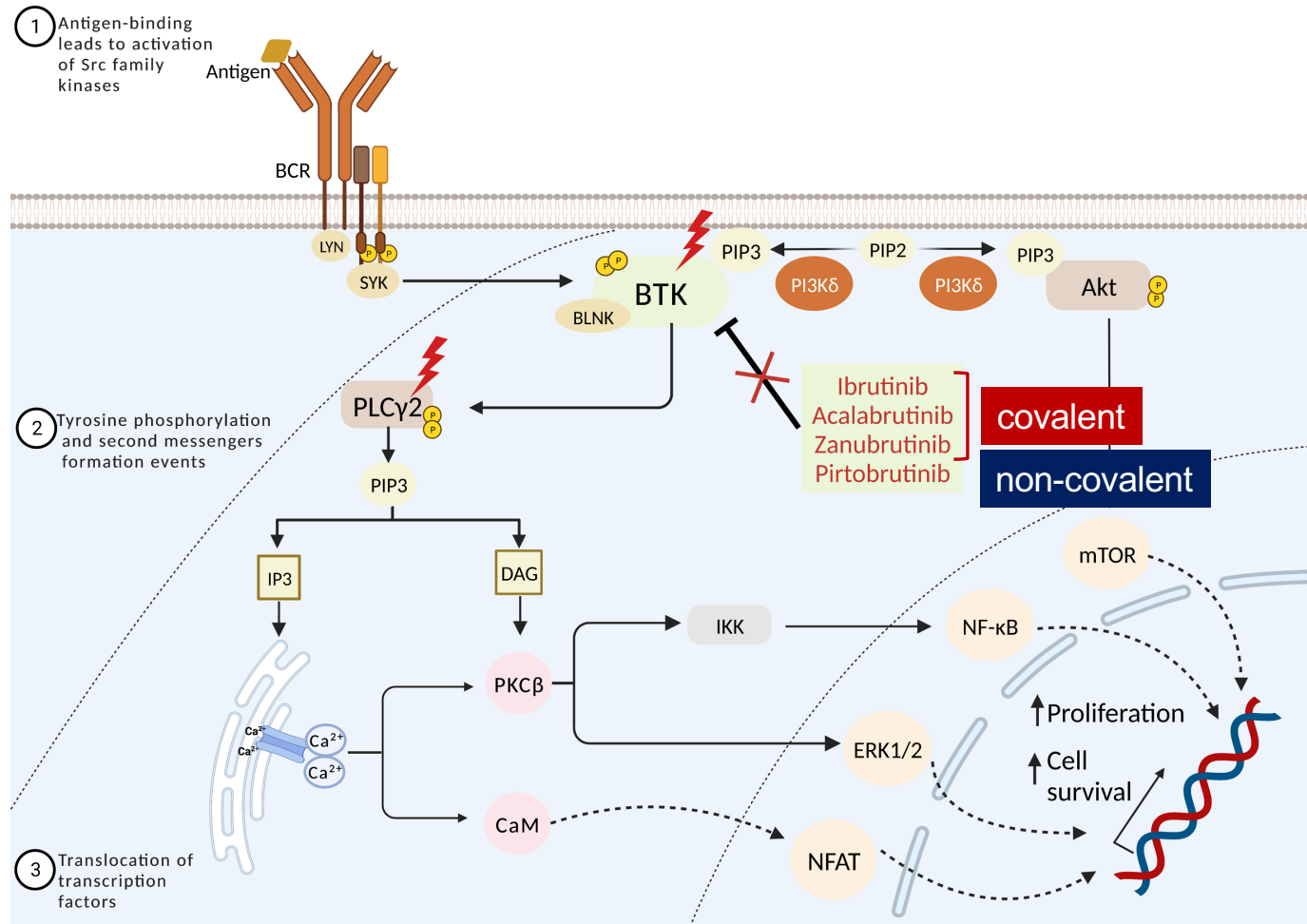
MRD

Refractoriness
mutations

BTK

BCL2

BTK targeting by covalent and non-covalent BTK inhibitors



BTK mutations are not the sole responsible for BTKi resistance

IBRUTINIB TREATMENT

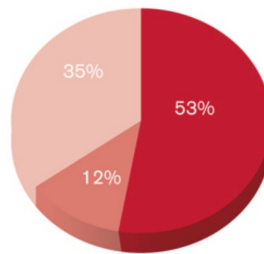


Relapsed patients



n = 49

BTK/PLCG2 mutated by
NGS and ddPCR



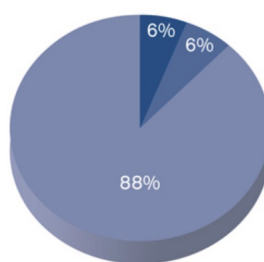
■ mutated (NGS&ddPCR)
■ mutated (ddPCR)
■ wild type

Responding patients



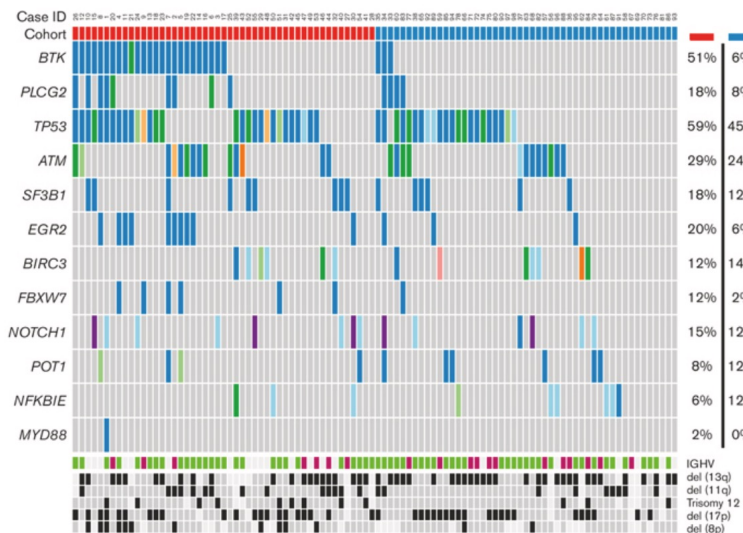
n = 49

BTK/PLCG2 mutated by
NGS and ddPCR



■ mutated (NGS&ddPCR)
■ mutated (ddPCR)
■ wild type

Genomic landscape



- One-third of patients with CLL relapsing on ibrutinib do not carry *BTK/PLCG2* mutations, even with a 0.1% sensitivity
- Additional mechanisms, such as del(8p), *EGR2* and NF-κB pathway mutations, may be cooperating in determining progression on ibrutinib.

BTK targeting by covalent and non-covalent BTK inhibitors

Biomarker	Prevalence before treatment	Prevalence at progression	Mechanism of resistance	Predictive value
BTK point mutations of C481: C481S/R/Y/G	N/A	~50%	Reduced affinity for covalent BTKi	Poor response to covalent BTKi
BTK point mutations of the tyrosine kinase domain: L528W, V416L, T474I, M437R, A428D	N/A	~16%	Binding impairment of non-covalent BTKi	Poor response to covalent and non-covalent BTKi
PLCG2 mutations: R665W, L845G, C849R, D993H	N/A	13%	Constitutively active PLCγ2	Poor response to BTKi
BCL2 mutations: G101V, D103Y, F104I	N/A	~15%	Binding impairment of BCL2i	Poor response to BCL2i
Upregulation of MCL-1 and/or BCL-xL	N/A	N/A	Enhanced apoptosis evasion	Poor response to BCL2i
High serum [IL-10]	N/A	N/A	Reduced T cell response through IL-10R stimulation	Poor response to PD-1/PD-L1 immune checkpoint inhibitors
Low serum [IL-6]	N/A	N/A	CAR-T cell exhaustion due to defective IL-6R stimulation	Poor response to CAR-T cells
Low levels of CD27 ⁺ CD45RO ⁺ CD8 ⁺ T cells	N/A	N/A	Reduced population of active CAR-T cells	Poor response to CAR-T cells

Mutations of resistance to BTKi

BTK C481 mutations

- preclude irreversible binding of covalent BTKi to BTK
- result in a greatly reduced drug potency

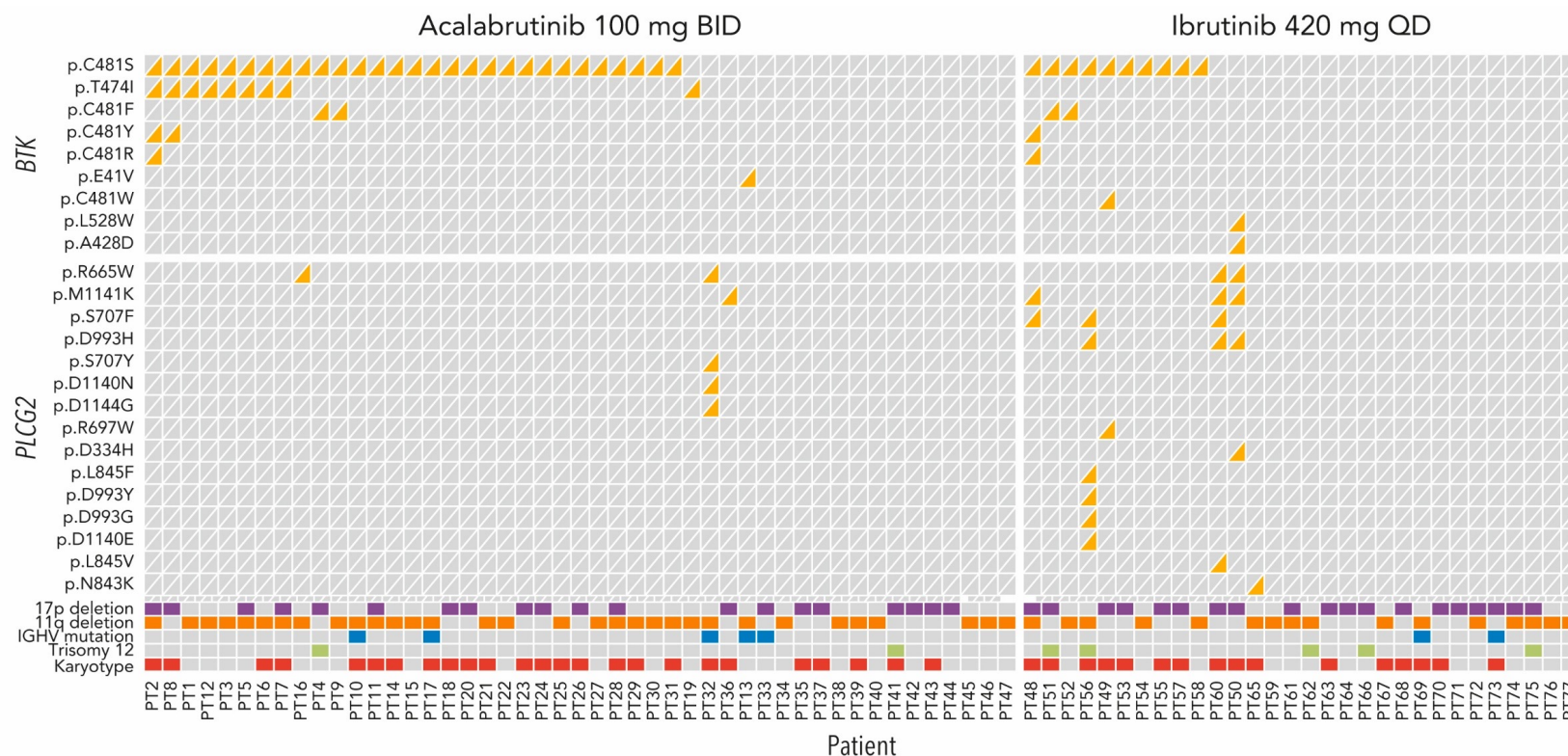
BTK T474 gatekeeper

- interfere with BTKi (both covalent and noncovalent) binding to BTK
- allow for normal B-cell signaling

BTK L528W kinase-dead

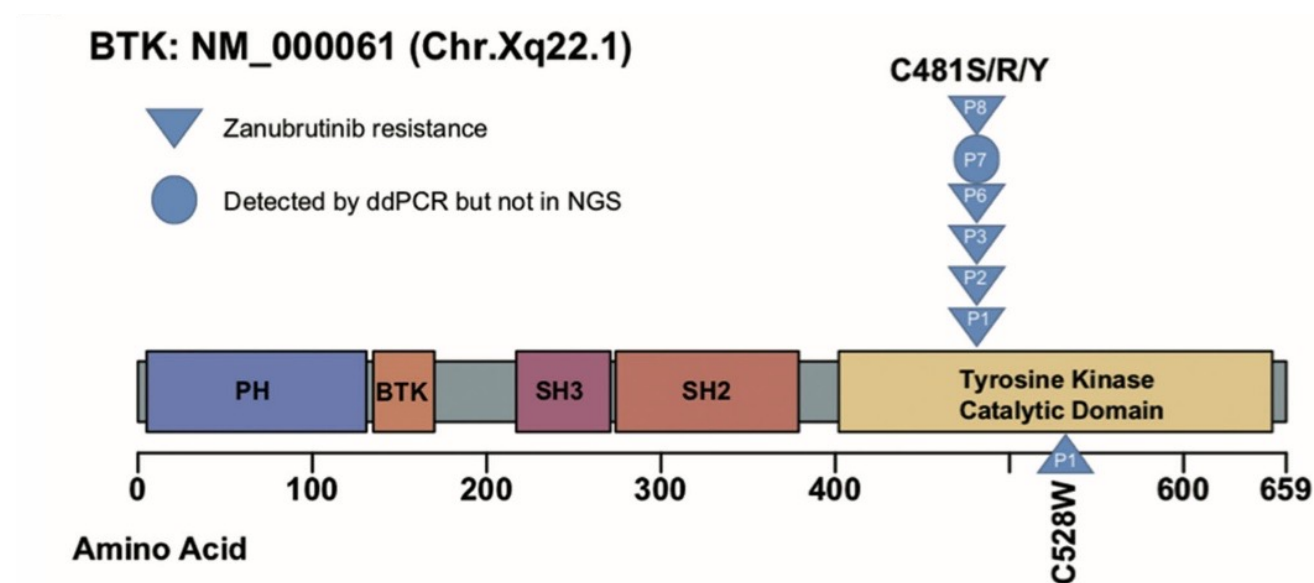
- hinder BTK catalytic activity
- B-cell signaling is thought to continue via a BTK scaffolding

Genetic resistance to Ibrutinib and Acalabrutinib



- *BTK* C481 is the most common
- *BTK* Gatekeeper T474I is observed with A but not I
- *BTK* Kinase-dead mutation L528W rare
- *PLCG2* M co-occur with *BTK* M in I but not A

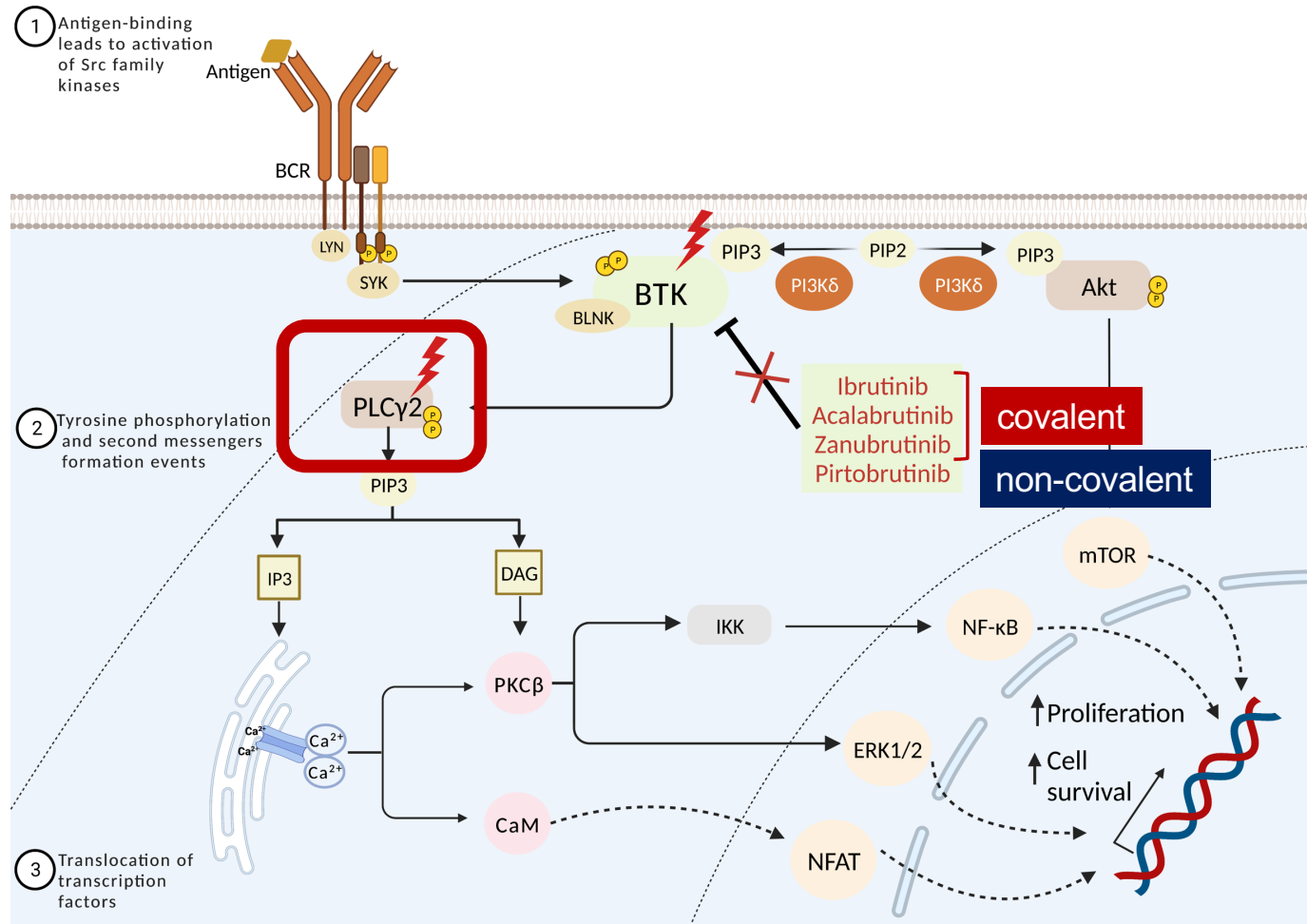
Genetic resistance to Zanubrutinib



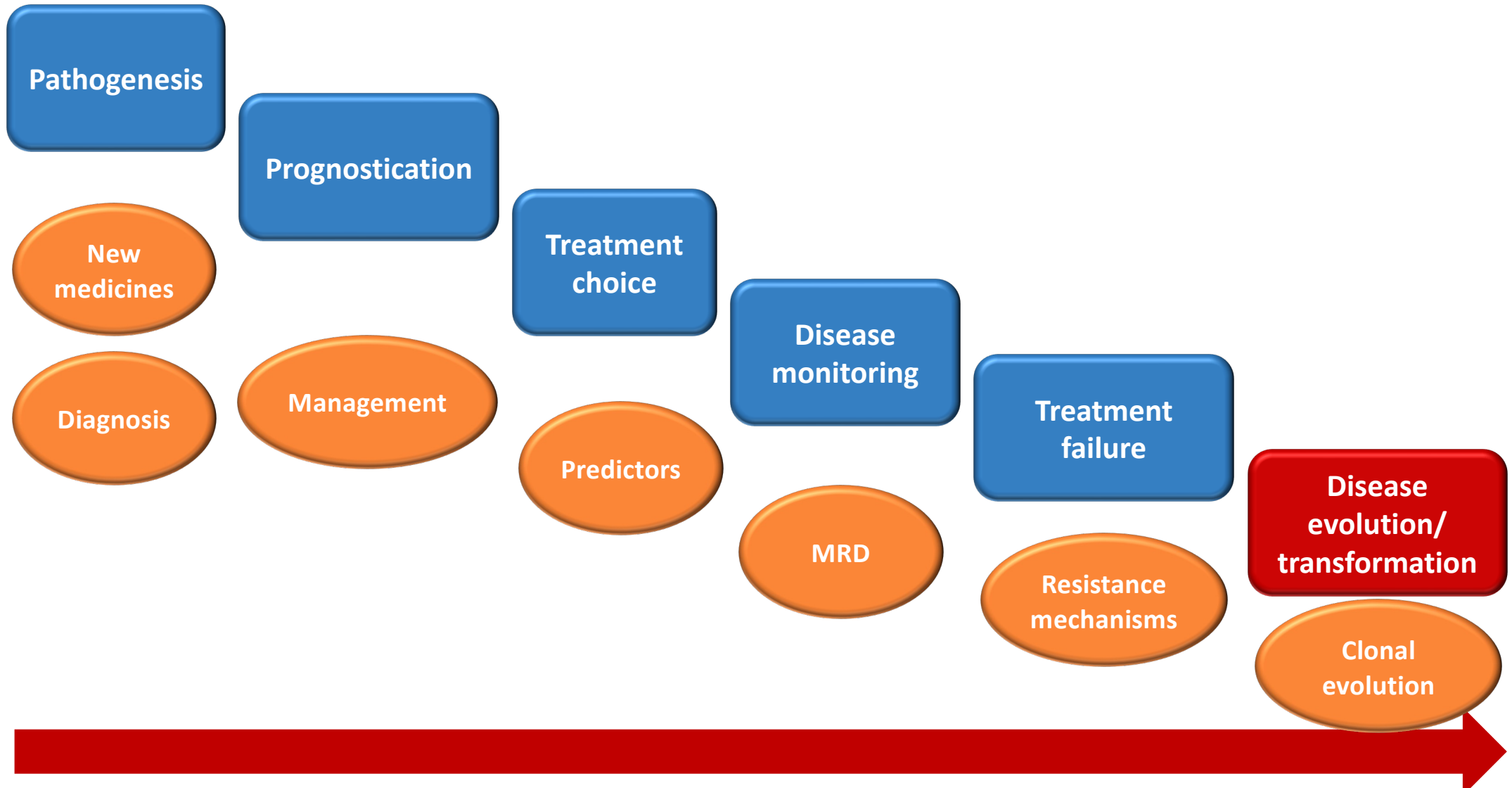
- *BTK* C481 is the most common
- *BTK* Kinase-dead mutation L528W in 50%
- *BTK* Gatekeeper T474I not observed
- *PLCG2* M exclusive with *BTK* M
- Small numbers (23 cases from 3 cohorts)

Blombery P, Blood Adv. 2022
Zhu H, Blood. 2022
Brown JR, Blood. 2023

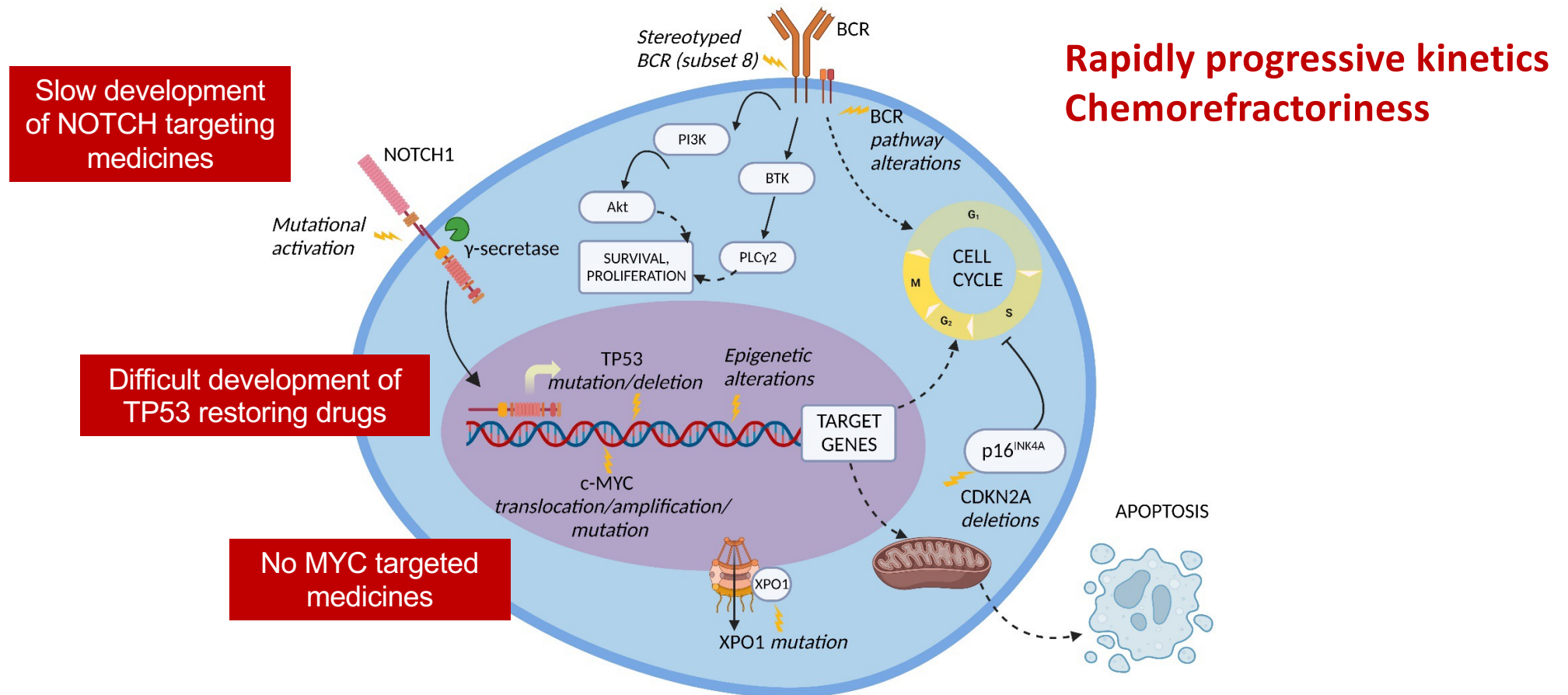
Gain of Function PLC γ 2 mutations bypass BTK targeting and constitutively activate BCR signaling



Applications of molecular biology in CLL



Reasons for treatment failure in Richter syndrome





Title: International Consensus Statement on Diagnosis, Evaluation, and Research of Richter Transformation: ERIC Recommendations

Short Title: Consensus Statements for Richter Transformation

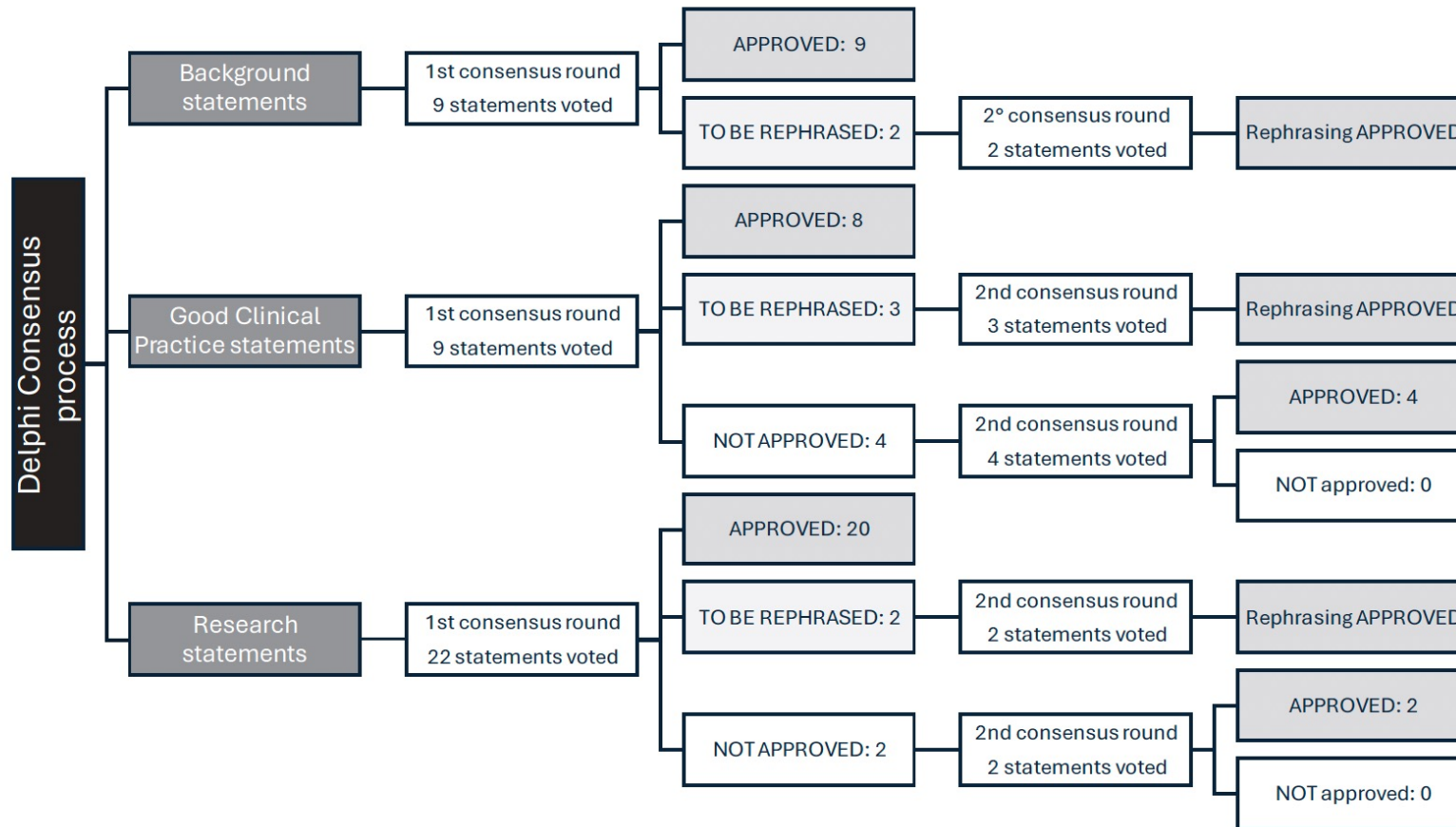
Authors: Adam S Kittai^{*1}, Monia Marchetti^{*2}, Othman Al-Sawaf³, Ohad Benjamini⁴, Alexey V Danilov⁵, Matthew S Davids⁶, Barbara Eichhorst³, Toby A Eyre⁷, Anna Maria Frustaci⁸, Michael Hallek³, Paul J. Hampel⁹, Yair Herishanu¹⁰, Rodney J Hicks¹¹, Arnon P Kater¹², Rebecca L King¹³, Jose Martin-Subero^{14,15}, Carolyn Owen¹⁶, Erin Parry⁶, Maurilio Ponzoni^{17,18}, Davide Rossi¹⁹, Tanya Siddiqi⁵, Stephan Stilgenbauer²⁰, Constantine S Tam²¹, Elisa ten Hacken²², Philip A Thompson^{23,24}, William Wierda²⁵, Gianluca Gaidano^{#26}, Jennifer A Woyach^{#27}, and Paolo Ghia^{#18,28}

*ASK, MM – Contributed equally to this study

#GG, JAW, and PG – Contributed equally to this study

Kittai A, Marchetti M et al. 2025 Apr 16; doi: 10.1182/blood.2024028064

The Delphi process



Statements pertinent to RT diagnosis

1.2.1. RT should be **suspected** in patients with clinical decline, B-symptoms, elevated LDH, rapidly enlarging lymphadenopathy, and/or discordant response to CLL treatment

There should be strong consideration for RT in patients with discordant enlarging lymphadenopathy (e.g. one nodal group growing rapidly compared to others)

1.2.2. In patients with a clinical suspicion of RT, a **PET-CT** should be attained

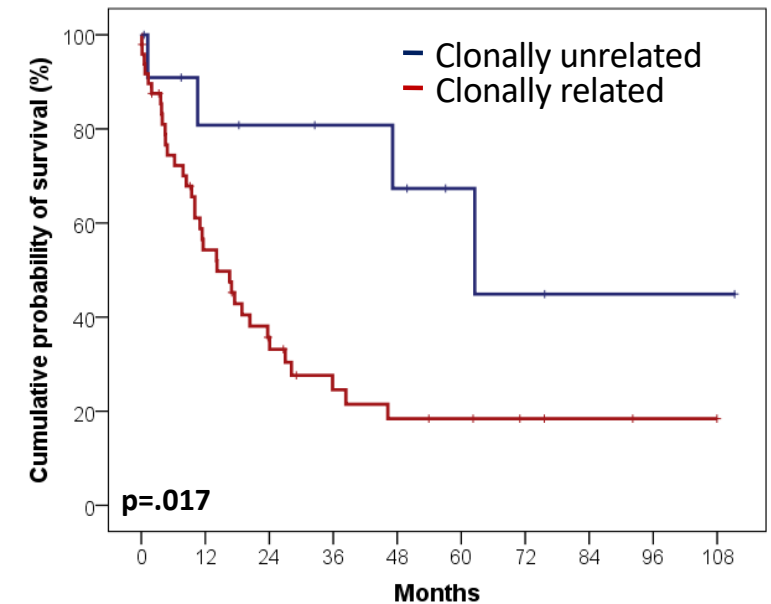
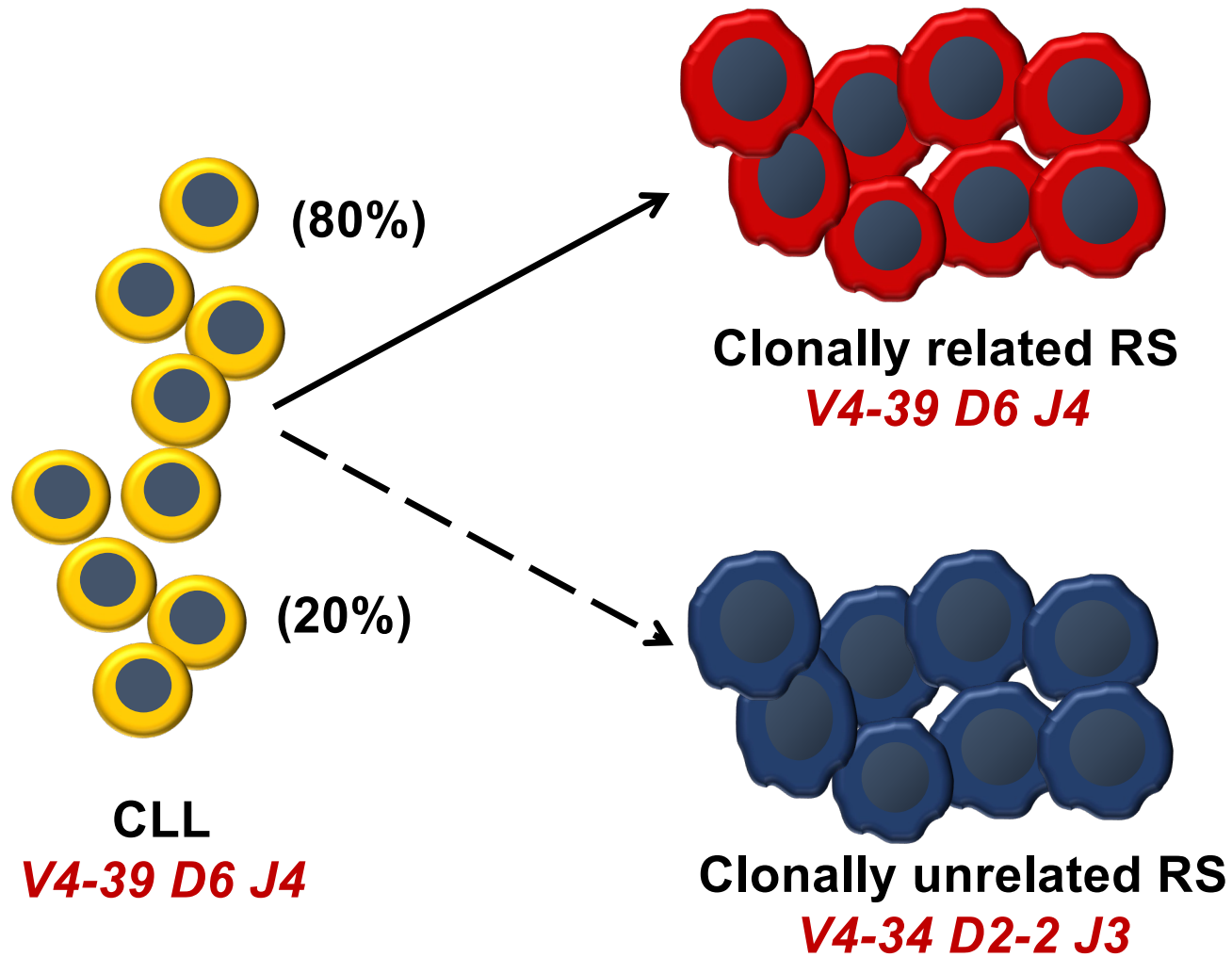
1.2.3. The **most accessible lesion with the highest avidity** should be targeted for biopsy
SUV avidity of <5 suggests a low likelihood of RT

1.2.4. **Biopsy** of the affected tissue for histology assessment **is needed to diagnose RT**

1.2.5. We strongly recommend attaining an excisional biopsy for diagnosis

1.2.6. All efforts should be made to have pathology reviewed by an **expert hemopathologist**

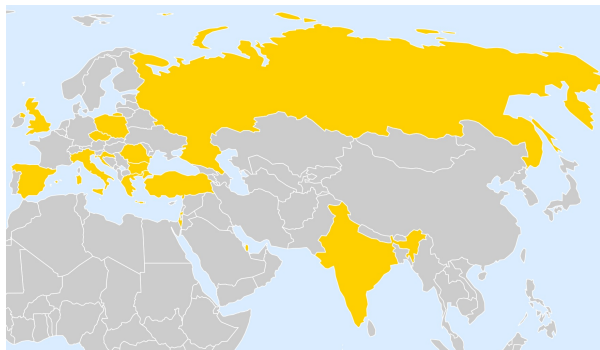
Clonal relationship in Richter transformation



ERIC Richter study: Patient characteristics



A total of 316 Richter transformation cases were collected from 24 hematological centers in 14 countries



ERIC countries involved till now in the project

Patients characteristic at the time of CLL

Variables	N (%)
Median age at CLL diagnosis	61 years (IQR 52-67)
Gender	
Female	121 (34.4%)
Male	231 (65.6%)
Binet stage	
A	161 (51.3%)
B	110 (35.0%)
C	43 (13.7%)
IGHV mutational status	
Mutated	52 (25.5%)
Unmutated	152 (74.5%)
TP53 mutated	
Yes	32 (23.2%)
No	106 (76.8%)
Median number of CLL lines of therapy	3 (IQR 2-4)
Treated with BTKi at any line of treatment	
Yes	124 (40.7%)
No	181 (59.3%)
Treated with BCL2i at any line of treatment	
Yes	62 (22.1%)
No	218 (77.9%)

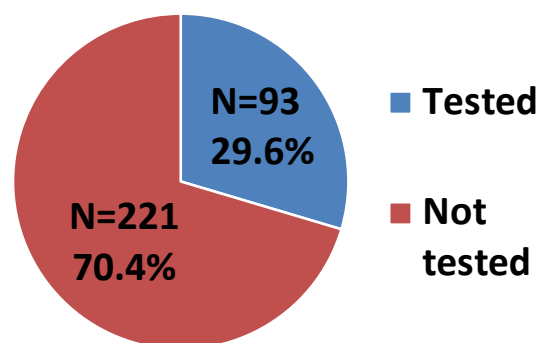
Patients characteristic at the time of RT

Variables	N (%)
Median age at Richter	68 years (IQR 60-74)
Median time from CLL diagnosis to Richter transformation	5.6 years (IQR 2.3-9.1)
TP53 mutated	
Yes	28 (41.8%)
No	39 (58.2%)
Histology of Richter	
DLBCL	268 (84.8%)
Hodgkin lymphoma	28 (8.9%)
Other	20 (6.3%)

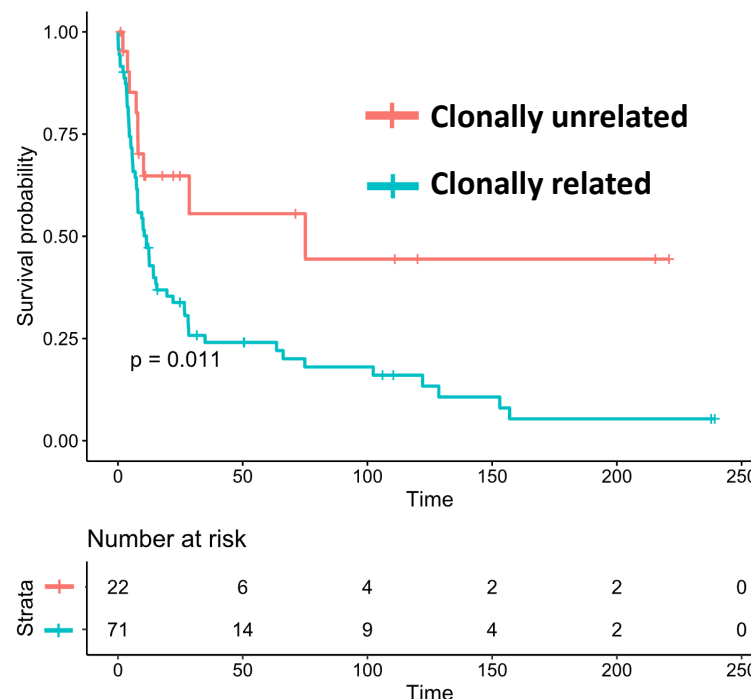
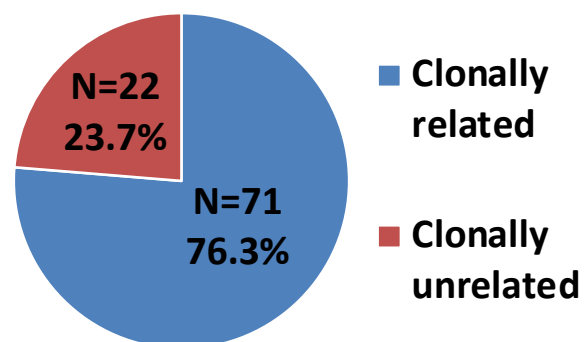
Moia et al, ERIC 2024

ERIC Richter study: Clonal relationship represents the most important prognostic/predictive factor in Richter transformation

Clonal relationship assessment



Clonal relationship results



Clonally related Richter significantly associated with shorter survival

Moia et al, ERIC 2024

Statements pertinent to RT diagnosis

1.2.7. Clonal relationship of the RT tissue and antecedent CLL cells should be tested, as it is one of the strongest prognostic factors for RT survival: patients with clonally unrelated RT have a markedly better prognosis

2.2.1. Clonality should be determined by comparing IG gene rearrangement from the RT tissue to the IG gene rearrangement in the CLL cells

International Consensus Statement on Diagnosis, Evaluation, and Research of Richter Transformation

Context of Research

Richter transformation (RT) remains a rare entity and is associated with dismal outcomes. There is no consensus on the study or management of RT currently published.

Aim of This Study

We convened a group of 29 international experts on RT to establish consensus recommendations on the diagnosis, evaluation, and research of RT.

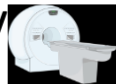
Findings

Diagnosis/ Prognosis



- We strongly recommend attaining an excisional biopsy on the most metabolically active, accessible lymph node for diagnosis.
- Current standard of care treatment with RCHOP-like regimens has poor efficacy.

Prognostication/ Staging



- Clonality should be determined by comparing IG gene rearrangements from the RT tissue and the CLL cells.
- We recommend using a pre-treatment PET-CT to establish the extent of the disease.

Clinical Trial Recommendations



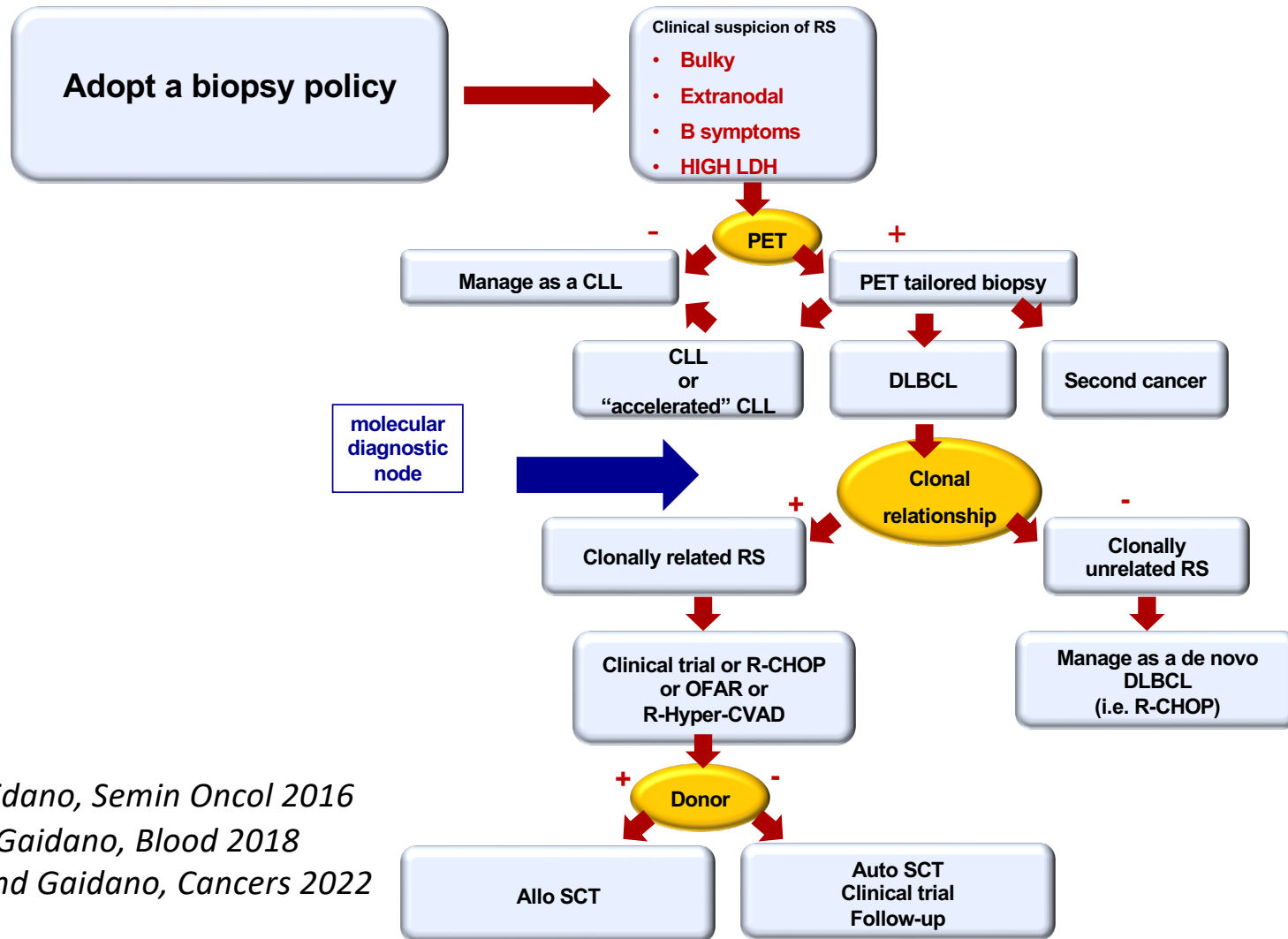
- If at all possible, patients with RT should be treated on clinical trials.
- Response of RT and CLL should be objectively assessed and reported based on both Lugano criteria as well as iwCLL guidelines.

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Conclusions: Given the poor outcomes associated with RT, participation in clinical trials should be encouraged. Prospective clinical studies along with collection of primary longitudinal samples are needed to develop rational therapeutic strategies for this disease.

Kittai A, Marchetti M et al. 2025 Apr 16; doi: 10.1182/blood.2024028064

Clinical algorithm for managing Richter transformation



Rossi and Gaidano, *Semin Oncol* 2016
Rossi, Spina, Gaidano, *Blood* 2018
Mouhssine and Gaidano, *Cancers* 2022

Conclusions

- BCR signaling pathway and BCL2-mediated inhibition of apoptosis represent the mainstay of CLL pathogenesis and provide actionable therapeutic targets
- Biomarkers are relevant in 1L treatment choice also in the era of pathway inhibitors
- Chemoimmunotherapy has no longer a role in CLL treatment if pathway inhibitors are accessible
- Continuous therapy with BTKi overcomes the adverse prognostic impact of disrupted *TP53*
- Multiple chemo-free options are available for 1L treatment according to molecular predictors, fitness, age and patient preferences
- Treatment sequencing of R/R patients highly depends on 1L therapy
- Richter transformation should be appropriately suspected and diagnosed, also considering the new therapeutic developments