



Prognostication for Follicular Lymphoma in 2026

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Disclosures

- Consultancy and honoraria: AbbVie, BMS, Genentech/Roche, Genmab, Incyte
- Research funding: Genentech, Genmab, Gilead, Lymphoma Research Foundation
- Leadership: American Society of Hematology, Lymphoma Research Foundation

The Paradox of Follicular Lymphoma in 2026

- Most patients have OS comparable to age-matched population
- 15–20% experience POD24
- FLIPI high-risk \neq POD24 (30% never progress early)
- FLIPI low-risk \neq safe (20% experience POD24)
- Instruments designed for a disease that no longer exists at the same scale of lethality; insensitive at capturing high risk

Three Destinies Define Follicular Lymphoma

~20%
POD24

*Progression within
24 months of 1L therapy*

5-yr OS: 29–54%
vs ~90% in non-POD24
Drives ~80% of lymphoma
mortality

~15%
Transformation

*Histologic transformation
to DLBCL over lifetime*

5-yr OS post-tFL: ~40%
Majority of remaining
lymphoma deaths in FL

~42%
Functional Cure

*OS comparable to age-matched
general population after EFS24*

S0016: 15-yr follow-up
No excess lymphoma mortality
after landmark

Old, New and Emerging Tools

Next-generation clinical scoring: FLIPI24, FLIPI-C

Biological / genomic prognostication: m7-FLIPI, FOXO1, gene signatures

Liquid biopsy and MRD

Imaging: TMTV, radiomics

Predicting transformation risk?

Current Clinical Prognostic Calculators: low vs. high

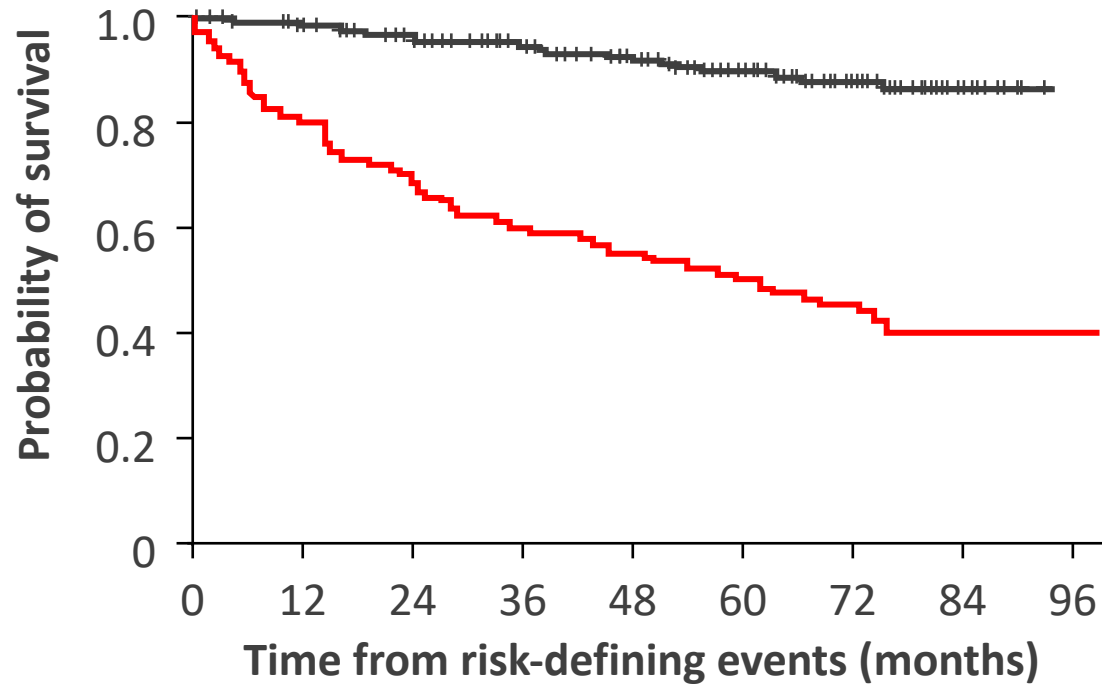
	FLIPI ^{1,2}	FLIPI ^{2,3-5}	PRIMA PI ⁶	M7-FLIPI ⁷
Components	Age, stage, hemoglobin, LDH, nodal sites	β 2M, diameter lymph node, BMI, hemoglobin, age	β 2M, BMI	FLIPI, ECOG PS, mutation status of seven genes
5 yr OS by risk group	Low: 91% High: 53%	Low: 96% High: 67%	Low: 93% High: 81%	Low: 84–90% High: 42–65%
	FLEX score⁸	POD24-PI²		
Components	Male sex, sum of lesion dimension, Grade 3a, extranodal sites, ECOG PS, hemoglobin, β 2M, NK cell count, LDH	High-risk FLIPI, mutation status of three genes		
5 yr OS by risk group	Low: 97% (3-year) High: 87% (3-year)	Low: 89–91% High: 48–71%		



1. Solal-Céligny P, et al. Blood 2004;104:1258–65; 2. Jurinovic V, et al. Blood 2016;128:1112–20;
 3. Terol MJ, et al. Blood 2010;116:3128; 4. Rodríguez-Sevilla JJ, et al. Blood Adv 2023;7:1606–14;
 5. Federico M, et al. J Clin Oncol 2009;27:4555–62; 6. Bachy E, et al. Blood 2018;132:49–58;
 7. Pastore A, et al. Lancet Oncol 2015;16:1111–22; 8. Mir F, et al. Am J Hematol 2020;95:1503–10;
 9. Casulo C, et al. ASH 2023; Abstract (abstract #1657);

Narrowing Focus to Predict Who Will Have Early Progression Given Unmet Need

OS according to POD24* (N=588)



	Patients, n	5-year OS, %
— POD24*	110	50
— Reference	420	90

POD24

- 15% to 20% after 1L
- High risk of transformation (30-70%)
- FL histology still does worse
- Chemorefractoriness
- Rapidly gets to 3L+ of therapy

FLIPI24: Finally Asking The Right Question?

Clinical Prediction Model Built for EFS24

- Developed and internally validated to predict 24-month event rates
- Captures POD24, transformation, death in one pre-treatment metric

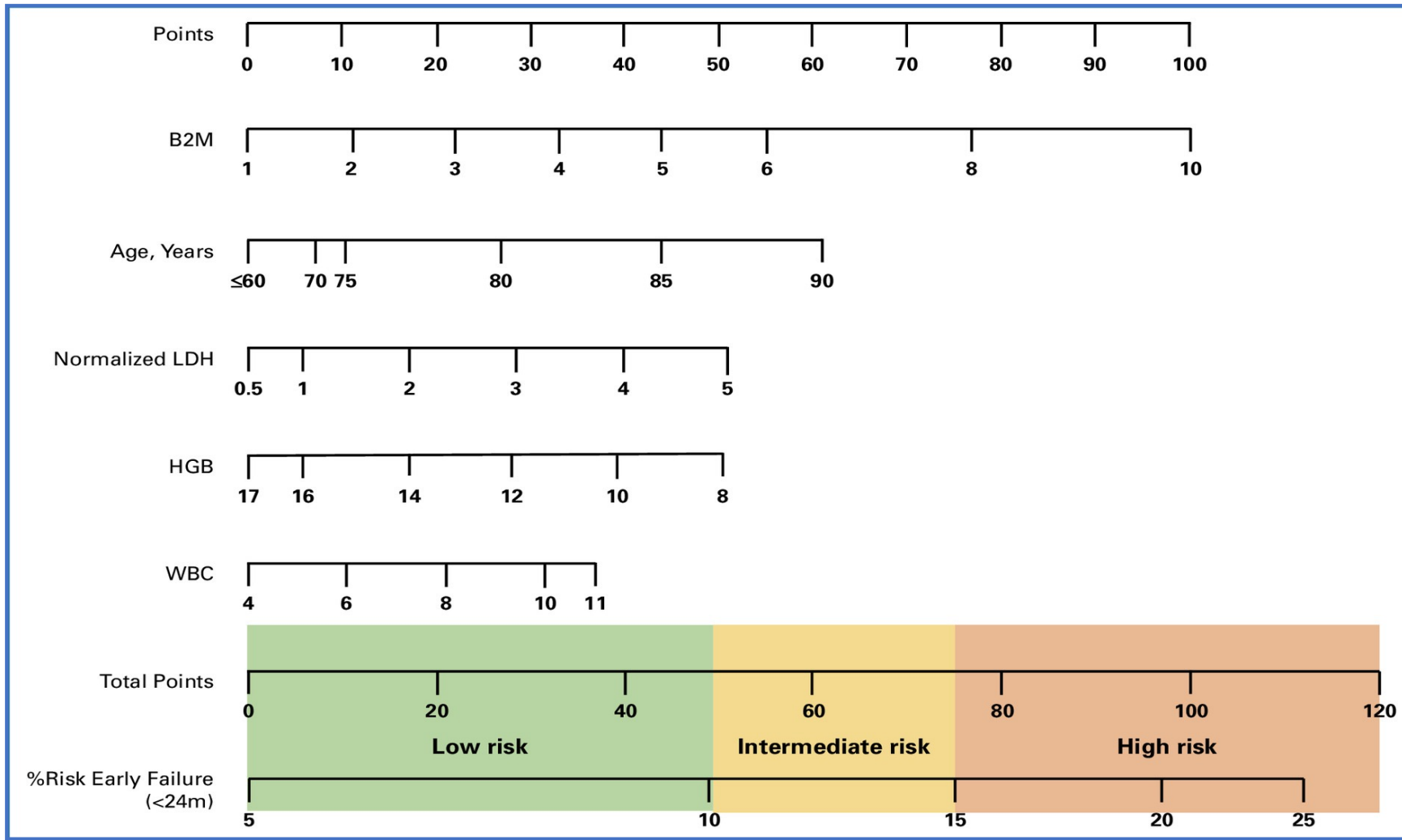
Validated across 10 cohorts, N = 4,485

- Any 1L chemoimmunotherapy (some R maintenance)

Outperforms FLIPI, FLIPI2, PRIMA-PI

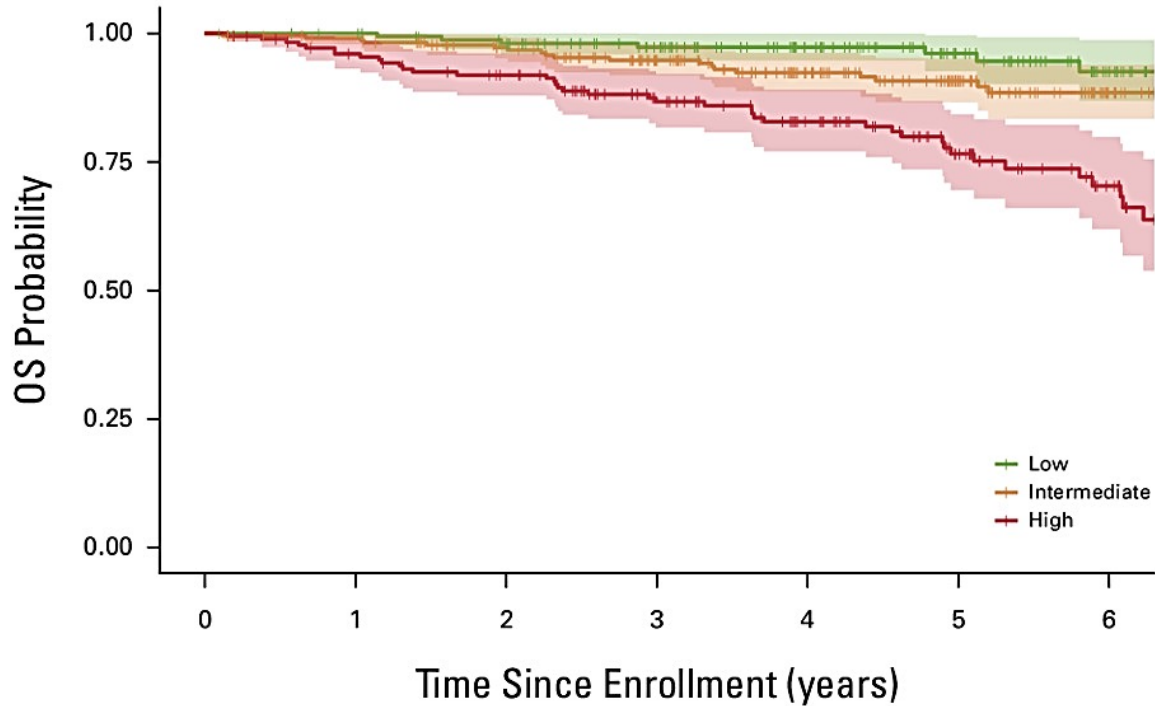
- For EFS24, OS

FLIPI24 Nomogram Estimates Early Event Probability



Corresponding 5-year Survival Based on FLIPI24 Risk Score

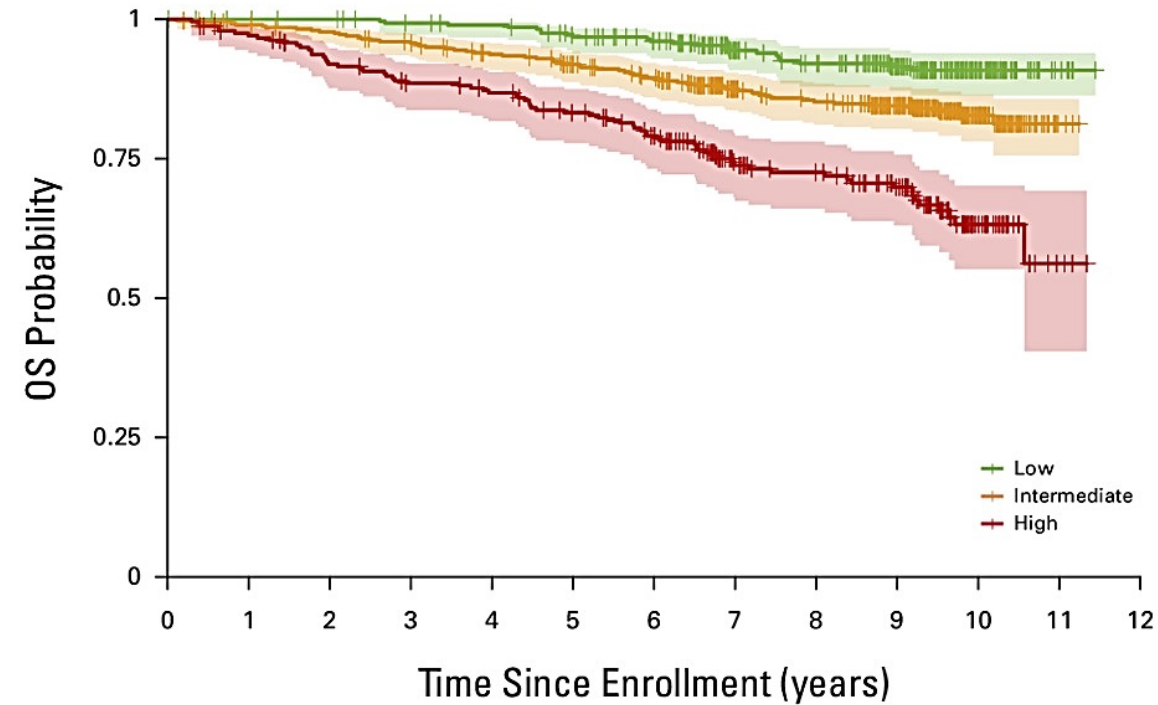
Original LEO Cohort



Number at risk (number censored)

	0	1	2	3	4	5	6
Low	160 (0)	157 (3)	149 (8)	130 (26)	98 (58)	66 (89)	36 (117)
Intermediate	226 (0)	218 (6)	200 (20)	170 (45)	129 (82)	88 (121)	45 (162)
High	179 (0)	165 (7)	152 (13)	120 (37)	96 (56)	63 (83)	37 (105)

PRIMA Validation Cohort



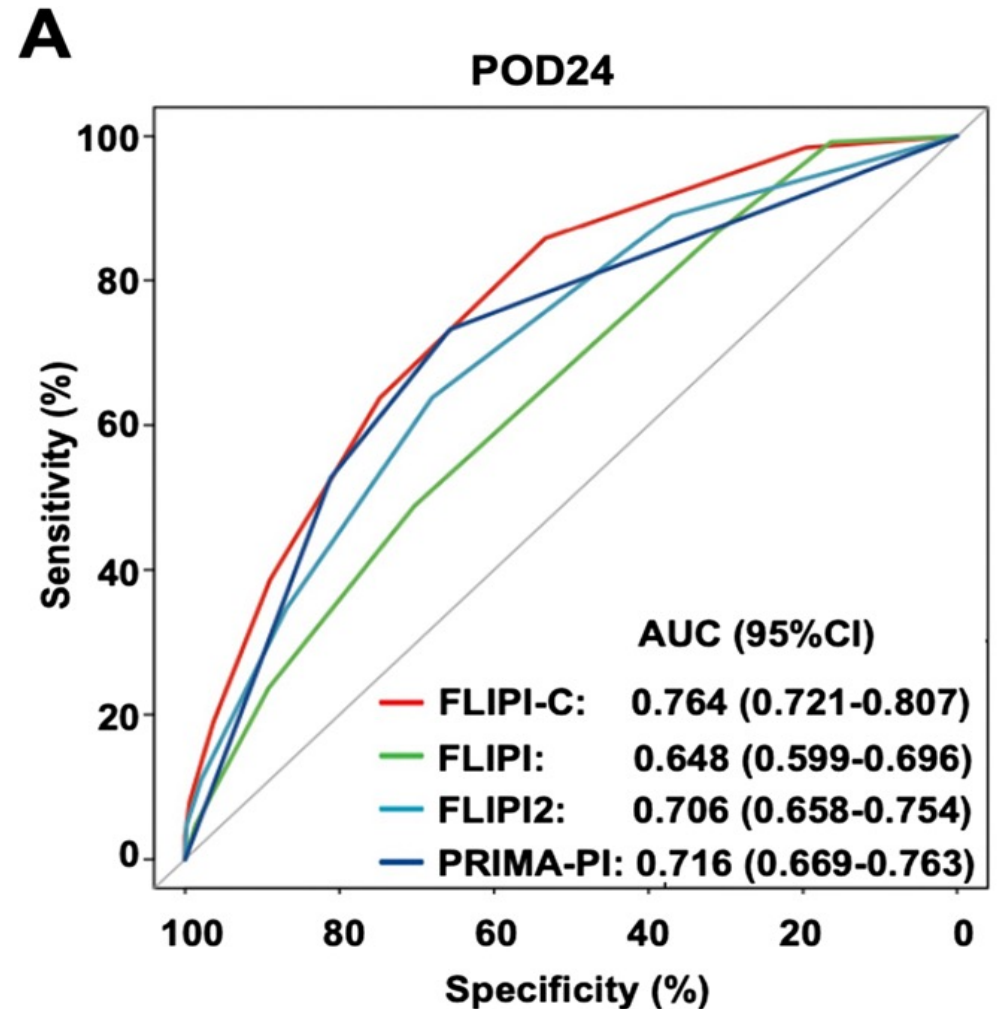
Number at risk (number censored)

	0	1	2	3	4	5	6	7	8	9	10	11	12
Low	294 (0)	290 (4)	288 (6)	282 (10)	279 (12)	268 (17)	256 (27)	210 (69)	193 (81)	156 (117)	60 (212)	7 (265)	0 (272)
Intermediate	406 (0)	397 (5)	390 (7)	379 (10)	364 (17)	349 (25)	332 (33)	272 (86)	257 (94)	219 (130)	83 (263)	3 (342)	0 (345)
High	242 (0)	231 (4)	215 (8)	204 (11)	198 (13)	185 (18)	167 (27)	124 (60)	114 (68)	96 (82)	31 (140)	3 (167)	0 (170)

█ Low-risk 96%-97%
 █ Intermediate-risk 91%-92%
 █ High-risk 77%-83%

FLIPI-C: Using AI For Prognostication

- Machine learning-based model to predict POD24 using AI algorithms
- 17 Chinese centers across 20 years, N= 1,938, external validation GALLIUM (N=1,145)
- Outperformed FLIPI, FLIPI2, PRIMA-PI, and FLEX



Old, New and Emerging Tools

Next-generation clinical scoring: FLIPI24, FLIPI-C

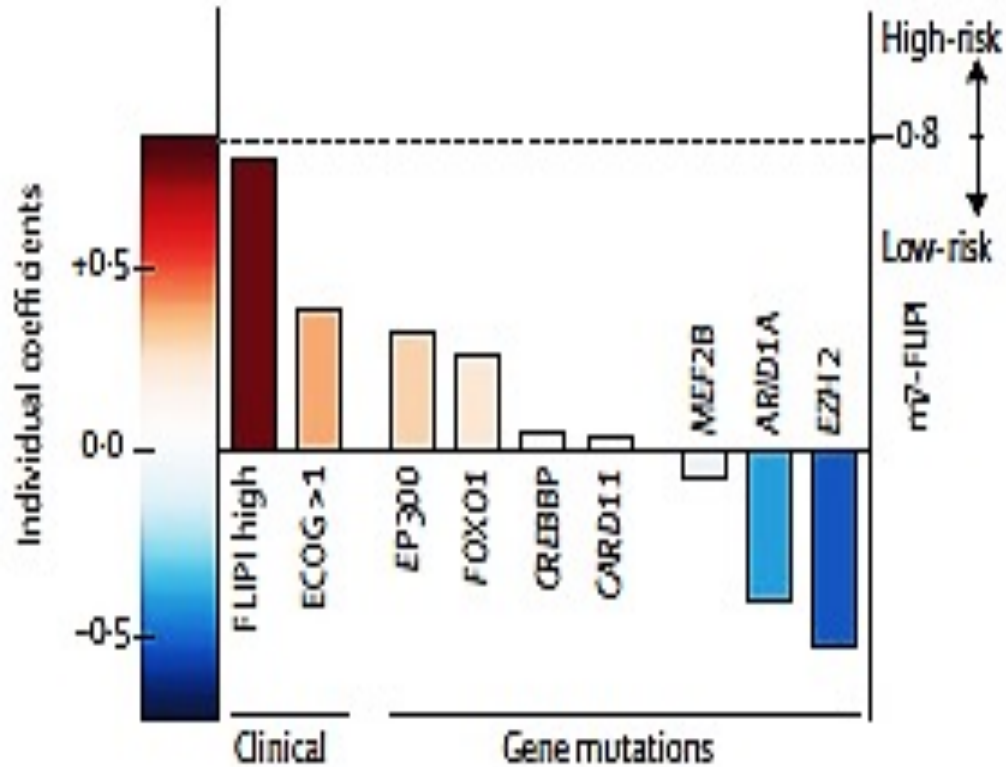
Biological / genomic prognostication: m7-FLIPI, FOXO1, gene signatures

Liquid biopsy and MRD

Imaging: TMTV, radiomics

Predicting transformation risk?

Biologic Classifiers: Promises and Limitations of m7FLIPI



What it integrates
 7 mutations: EZH2, ARID1A, EP300
 FOXO1, MEF2B, CREBBP, CARD11
 + FLIPI score + ECOG PS

Reclassification
 Downgrades ~50% of FLIPI
 high-risk patients to low-risk
 with consistent outcomes

Treatment-dependent
 Prognostic in R-CHOP only
 Not validated in bendamustine
 or other regimens

Incomplete risk capture
 ~50% of POD24 cases
 classified as low-risk by m7-FLIPI

Not validated to adapt or intensify therapy

■ strengths ■ limitations

Pastore et al. *Lancet Oncol* 2015; Bantilan and Zelenetz *ASH* 2023

FOXO1 mutation independently predicts shorter PFS, OS after adjusting for FLIPI, ECOG

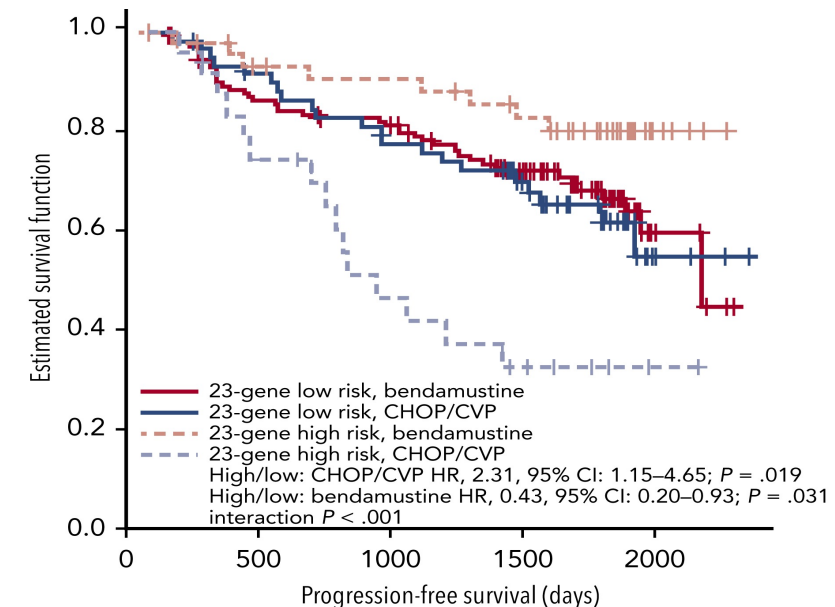
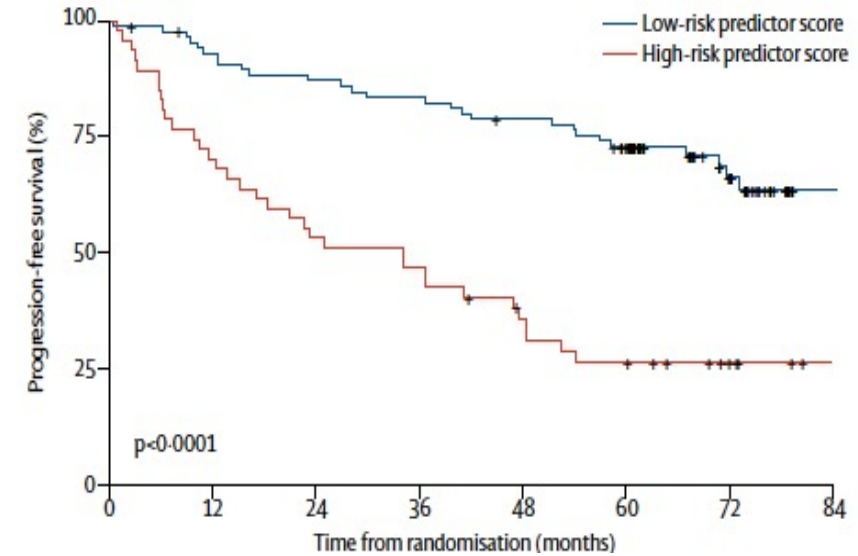
Gene Expression Signatures in FL Predict Outcome But Depend on Treatment

23-gene score in PRIMA trial

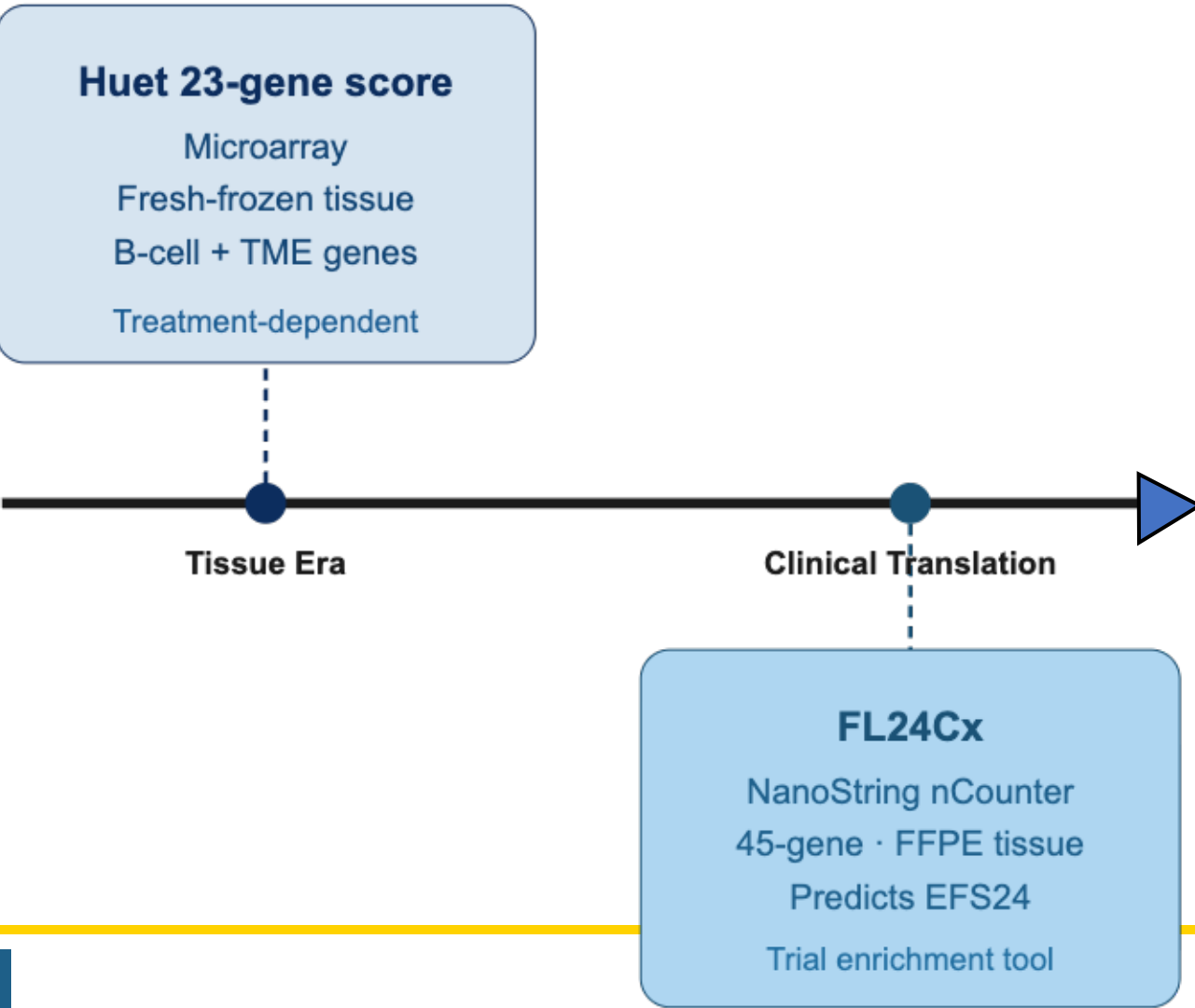
- Fresh-frozen tumor biopsies from 149 patients
- Independently predicts PFS
- High-risk patients 3.7× greater risk of progression vs. low-risk (HR 3.68)

23-gene score in GALLIUM trial

- Performance validated in 274 patients
- Does not hold with Bendamustine treatment
- ~50% of gene interactions treatment-dependent



Moving From Fresh Tissue to FFPE For Clinical Use



Gene Expression Signature To Identify POD24

FL24Cx

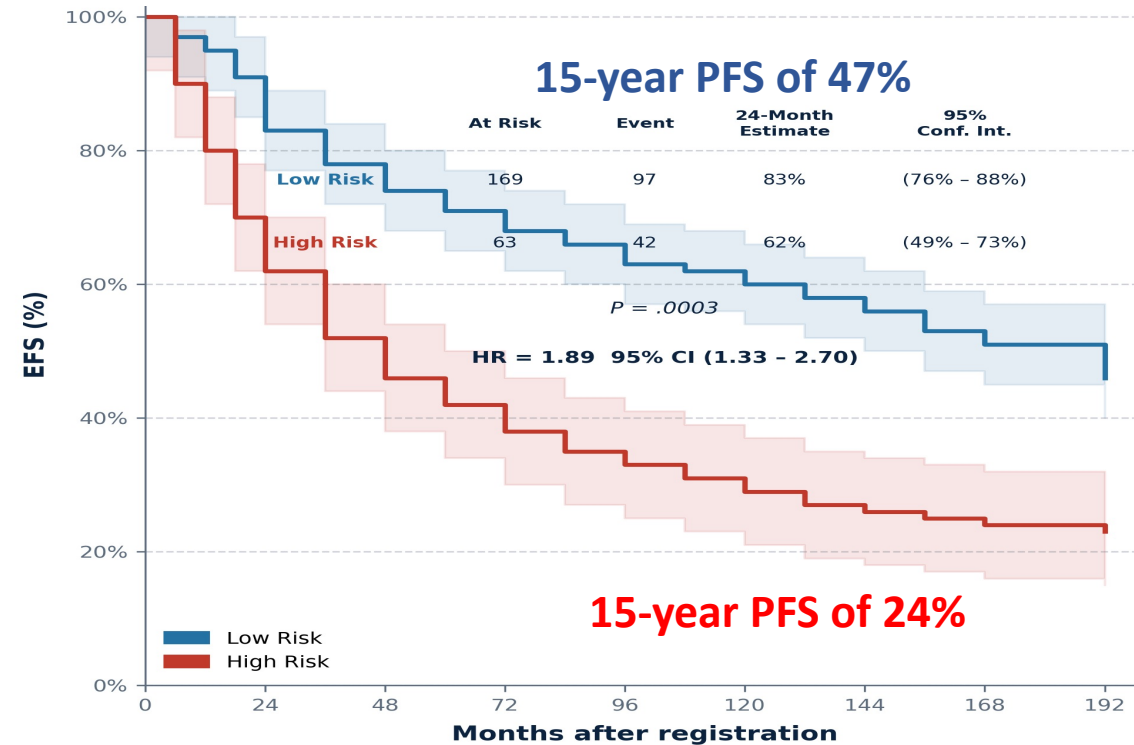
- 45-gene expression assay using FFPE
- NanoString platform
- Patients from PRIMA, multiple registries
- Logistic regression model predicting EFS24

Built on Prior Signatures

- Incorporated IR1+ IR2 immune response gene sets¹
- Extended and refined the 23-gene framework
- Validated in SWOG S0016 (n=232)
- R-CHOP, chemoimmunotherapy treatment

Outcomes

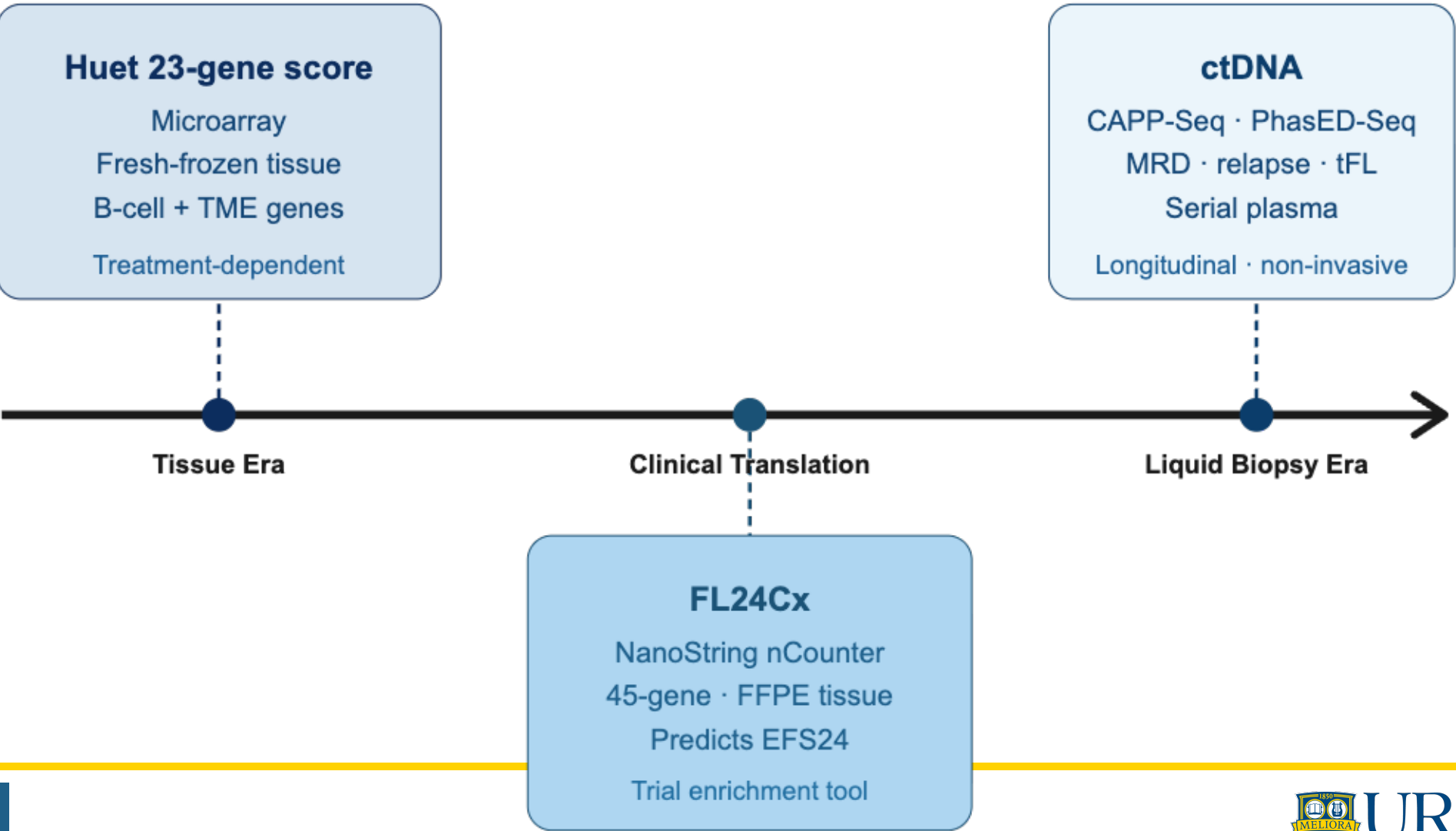
- High and low risk of POD24 gene signature
- Risk of POD24 twice as high in high-risk group
- Not validated to guide therapy adaptation



at Risk

Low Risk 169	137	120	112	100	86	75	67	42
High Risk 63	39	31	24	23	19	18	15	11

Moving From Fresh Tissue to Blood Based Markers



MRD Assessment: A Powerful Prognostic Signal in FL

- Longitudinal, non-invasive
- Baseline prognostication, early treatment resistance, disease kinetics, monitor disease burden and clonal evolution

PCR and Flow Cytometry Assays

- PCR primers for *IGH:BCL2*
- Cannot be identified in up to 50% of FL

Cell free DNA (cfDNA)

- DNA released during apoptosis
- Lymphoma derived: ctDNA
- Low in FL

NGS Based

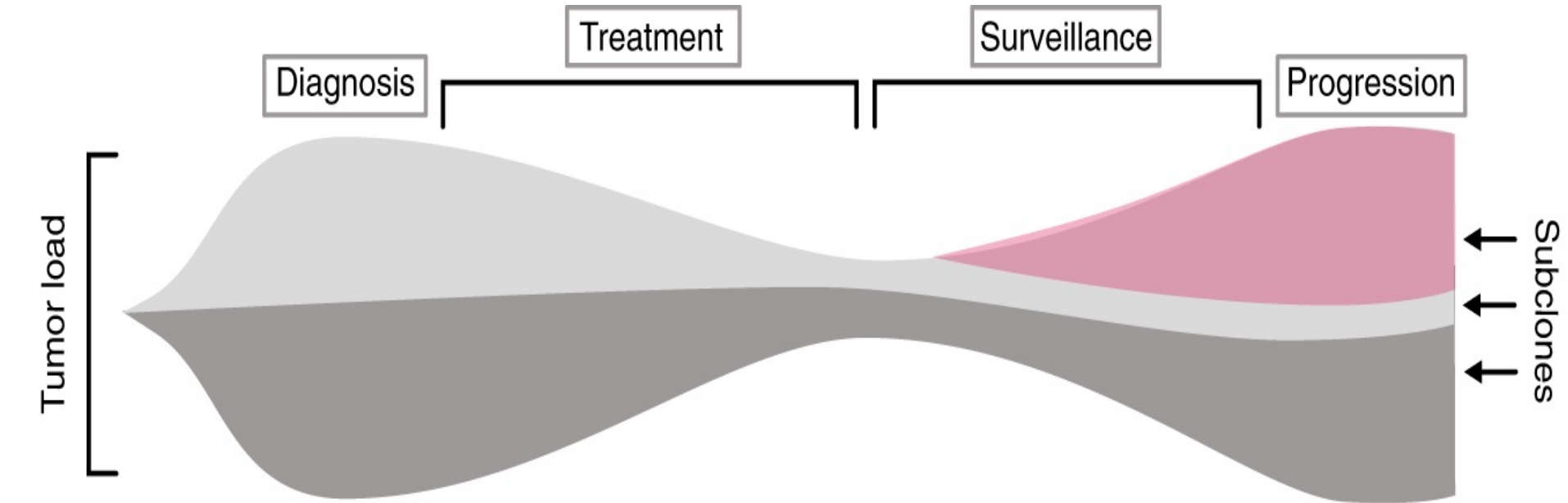
CAPP Seq

- Tracks individual single nucleotide variants (SNVs)
- Background error rate 10^{-4}

PhasED Seq

- Tracks multiple somatic mutations on same DNA
- Background error rate 10^{-7}

Potential Applications of MRD/ctDNA in FL

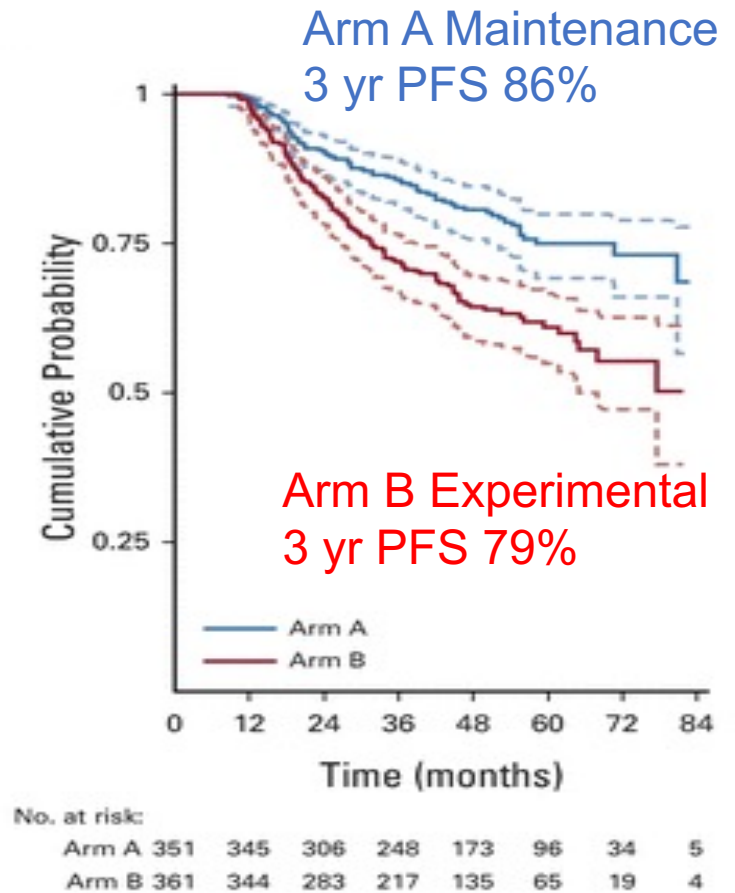
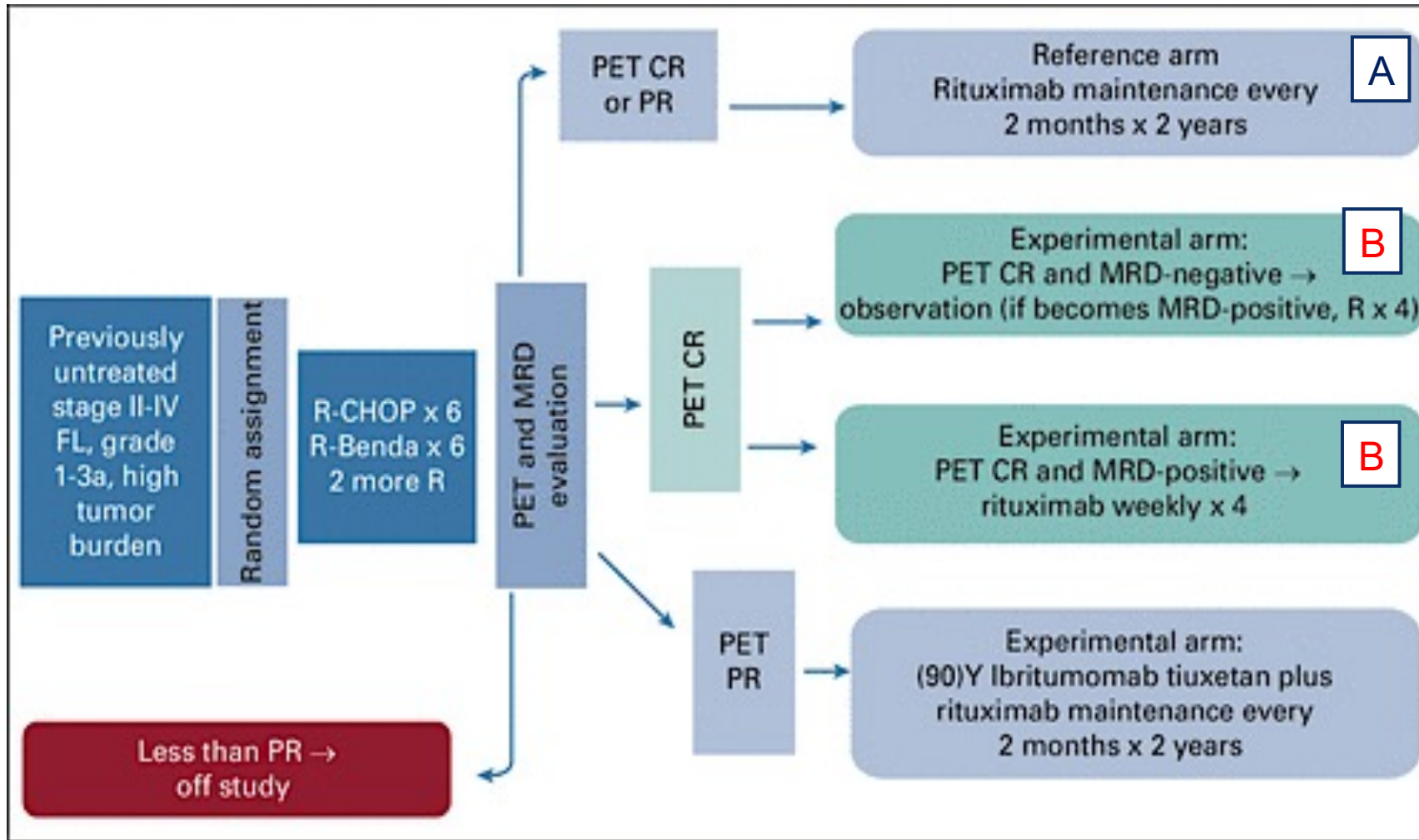


Potential clinical applications / translational research perspectives of ctDNA in B-cell lymphomas

ctDNA quantification/ monitoring	Tumor burden quantification	Early prediction of treatment failure	Relapse prediction	
	Prediction of clinical outcomes	Dynamic and personalized outcome prediction	MRD monitoring	Relapse detection

Lauer et al.
Leukemia 2022

Can you Response-Adapt Treatment Based on MRD at End of Therapy? FOLL 12 Study



Old, New and Emerging Tools

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Liquid biopsy and MRD

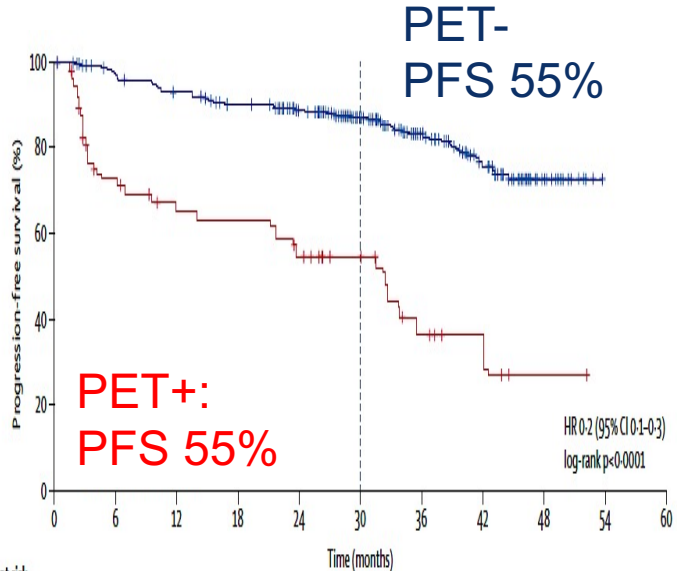
Imaging: TMTV, radiomics

Predicting transformation risk?

Using PET as Platform to Identify High Risk Groups

Positive End Treatment PET

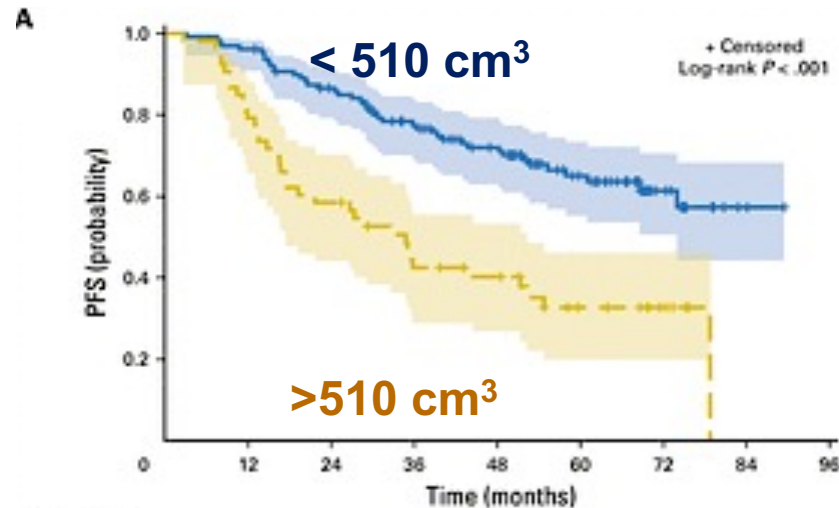
Inferior PFS, OS, in GALLIUM



Number at risk (number censored)	0	6	12	18	24	30	36	42	48	54	60
Complete response	448 (0)	414 (21)	393 (26)	373 (33)	329 (72)	247 (149)	161 (225)	88 (288)	23 (349)	0 (349)	0 (349)
No complete response	60 (0)	39 (5)	32 (9)	31 (9)	26 (10)	20 (16)	9 (22)	4 (27)	1 (29)	0 (29)	0 (29)

Total Metabolic Tumor Vol. (TMTV)

Identifies patients at risk for POD24, worse PFS

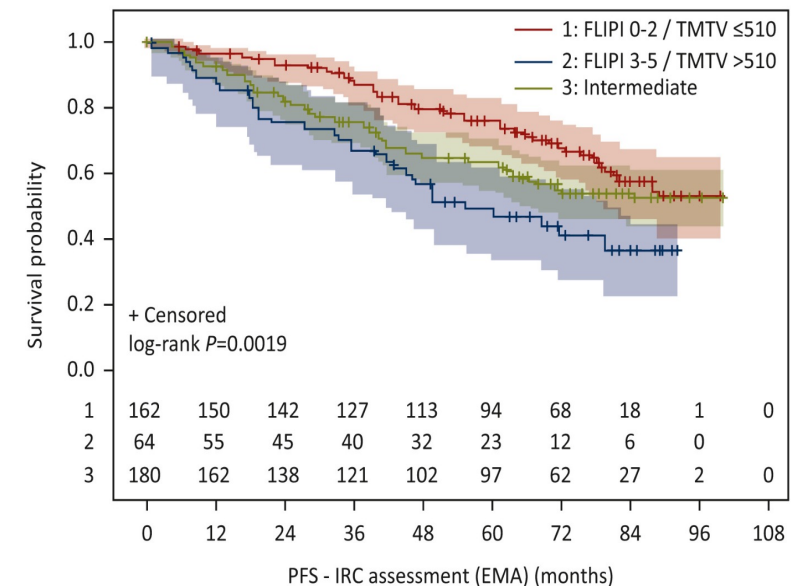


No. at risk	0	12	24	36	48	60	72	84	96
≤ 510 cm ³	128	123	107	89	74	45	17	2	0
> 510 cm ³	53	42	31	21	18	10	5	0	0

	No. of Patients	Event	Censored	Median Survival (95% CI)
≤ 510 cm ³	128	33.6% (43)	66.4% (85)	NR (74 to NR)
> 510 cm ³	53	66% (35)	34% (18)	34.8 (17.4 to 52.2)

TMTV + FLIPI

PFS by classified FLIPI and TMTV - biomarkers set with number of patients at risk and 95% confidence limits



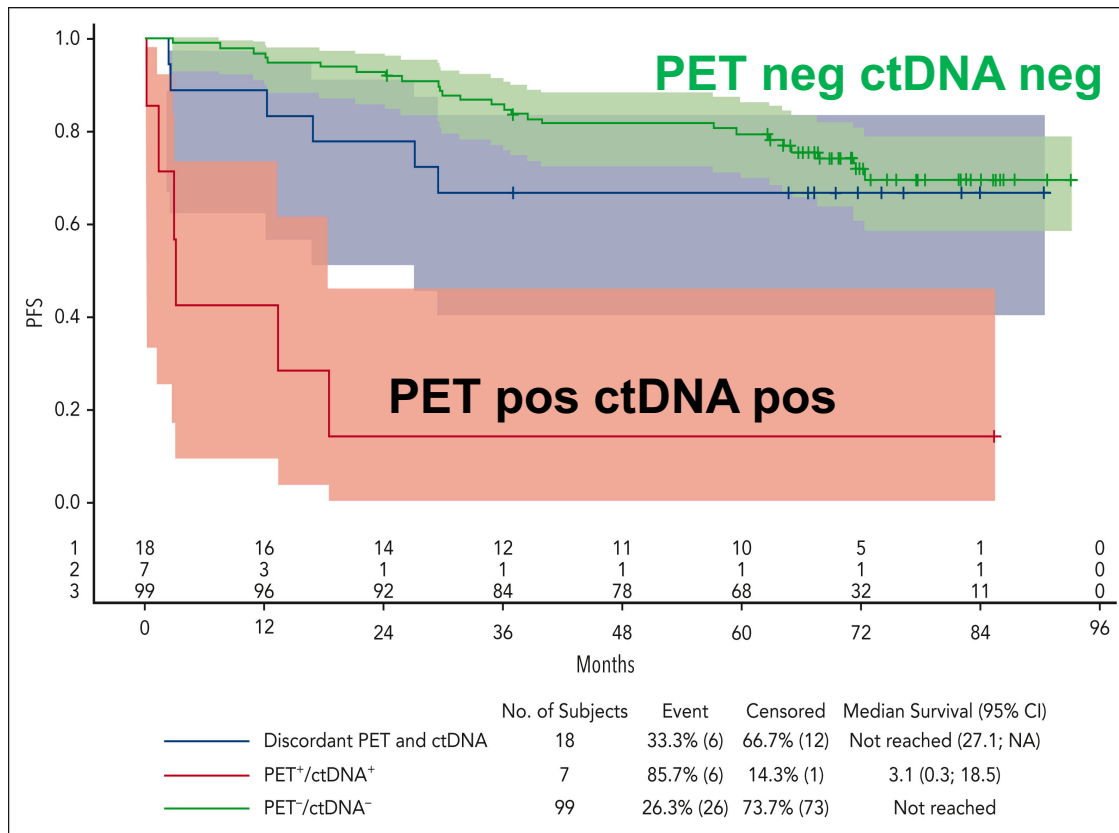
	0	12	24	36	48	60	72	84	96	108
1	162	150	142	127	113	94	68	18	1	0
2	64	55	45	40	32	23	12	6	0	0
3	180	162	138	121	102	97	62	27	2	0

PFS - IRC assessment (EMA) (months)

	No. of patients	Event	Censored	Median survival (95% CL)
FLIPI 0-2 / TMTV ≤ 510	162	32.1% (52)	67.9% (110)	Not reached (79.1-NA)
FLIPI 3-5 / TMTV > 510	64	53.1% (34)	46.9% (30)	55.4 (42.4-NA)
Intermediate	180	41.1% (74)	58.9% (106)	Not reached (66.3-NA)

Can We Identify POD24 Patients Before Progression Using Combination of PET and ctDNA?

- RELEVANCE Trial R-chemo vs. R², 124 patients with PET/ctDNA images and paired serum



12% of patients had POD24			
Marker	PPV POD24	NPV POD24	Median PFS neg vs pos
ctDNA alone	58%	>90%	NR vs. 17.7 mos (p=0.0038)
PET alone	45%	>90%	NR vs. 28.3 mos (p=0.002)
Combined (+)	86%	>90%	

Old, New and Emerging Tools

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Biological / genomic prognostication: m7-FLIPI, FOXO1, gene signatures

Liquid biopsy and MRD

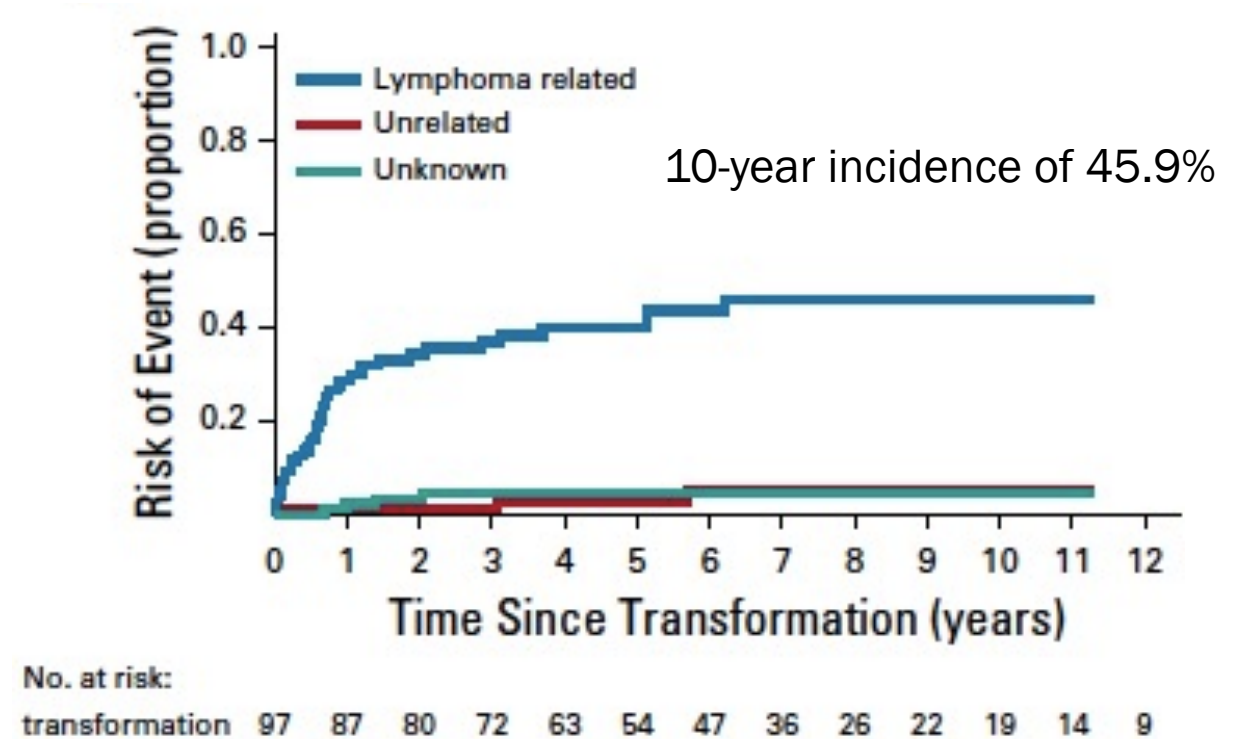
Imaging: TMTV, radiomics

Predicting transformation risk?

Predicting Histologic Transformation

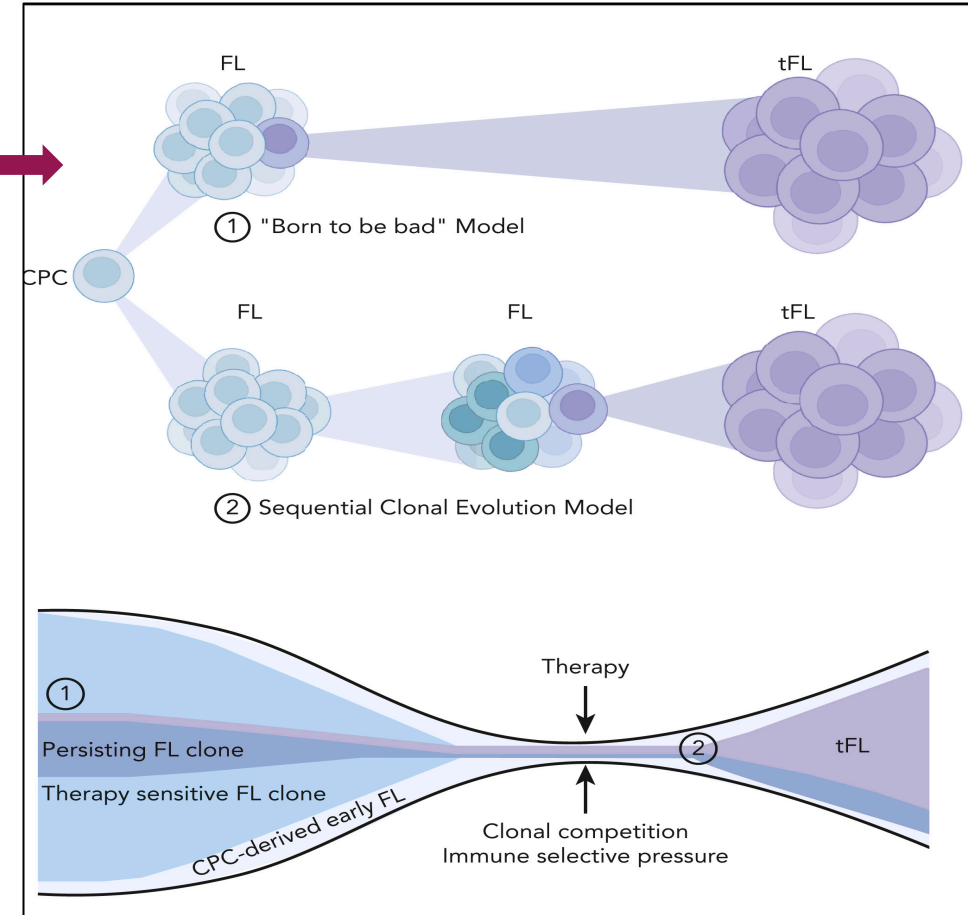
- Factors**
- High risk FLIPI
 - Elevated LDH
 - Grade 3a histology
 - Poor PS
 - B symptoms
 - Use of rituximab?
 - Prior therapy?
 - Time from diagnosis

Mortality Following Transformation



Biologic Origins of Transformation

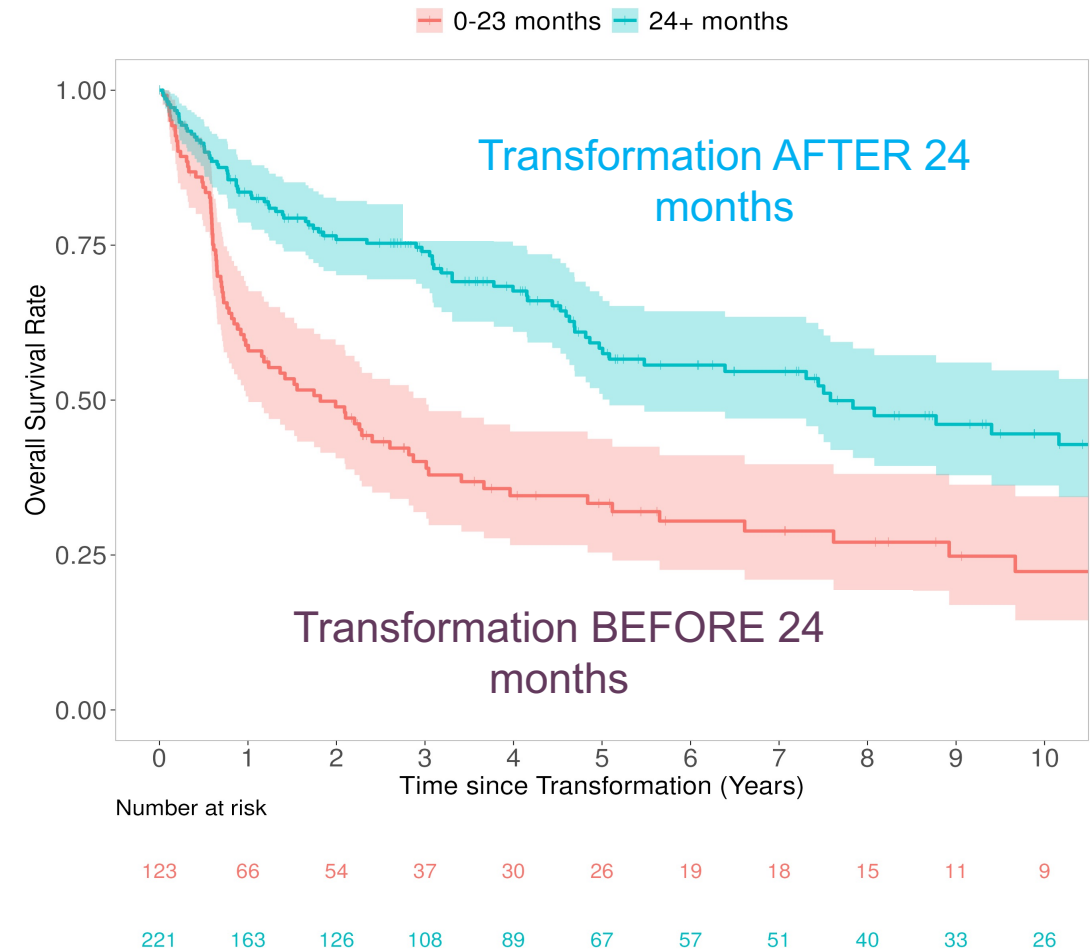
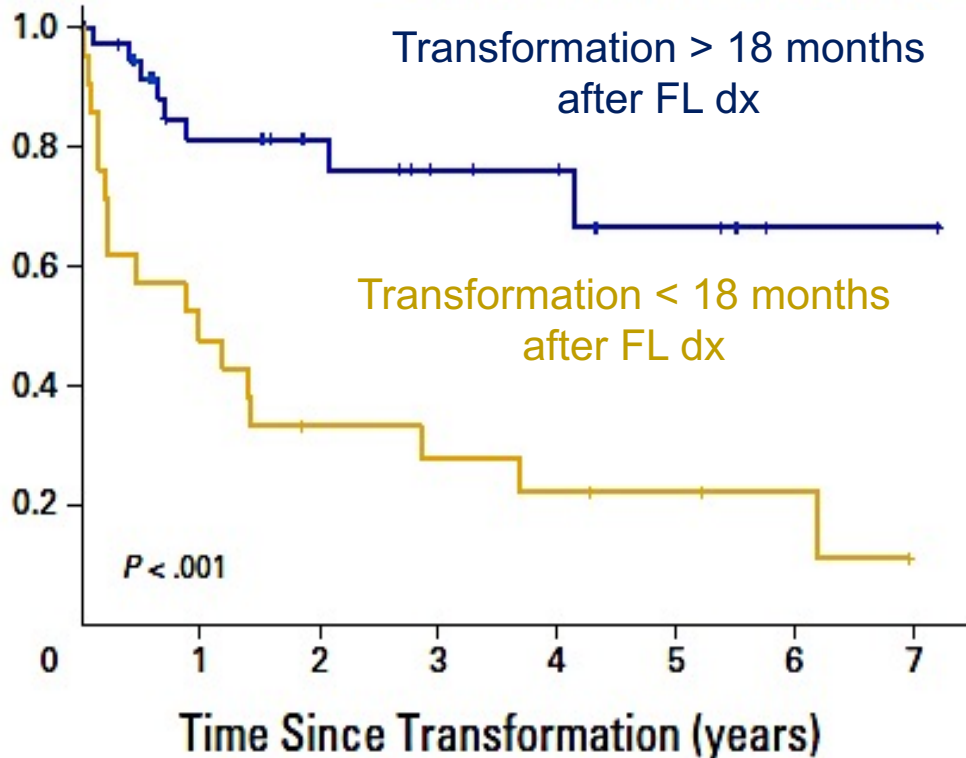
Category	Lower Transformation Risk	Higher Transformation Risk
Clonal origin	Early CPC divergence <ul style="list-style-type: none"> Short branch from common precursor Fewer private DLBCL mutations May present as composite lymphoma 	Sequential clonal evolution <ul style="list-style-type: none"> Late divergence from common precursor Shaped by therapy and immune pressure
Genetic subtype	"Constrained FL" <ul style="list-style-type: none"> Lower mutational burden CREBBP KAT missense mutations mTORC1 pathway mutations Less aberrant somatic hypermutation 	"DLBCL-like FL" <ul style="list-style-type: none"> Higher mutational burden CREBBP nonsense mutations Elevated aberrant somatic hypermutation
Phenotypic B-cell state	GC-like FL <ul style="list-style-type: none"> Germinal center B-cell state Lower intratumoral diversity Lower transformation risk 	MEM-like FL <ul style="list-style-type: none"> Memory B-cell differentiation state Higher intratumoral diversity
Tumor Micro-environment	Intact immune support <ul style="list-style-type: none"> T follicular helper cells preserved Follicular dendritic cell meshworks intact Low CD8⁺LAG3⁺ exhausted T cells 	Immune exhaustion <ul style="list-style-type: none"> Loss of Tfh cells and FDC meshworks CD8⁺LAG3⁺PD1⁺ T cell expansion near tumor Correlates with time to transformation



Chemotherapy backbones may select for transformation-prone clones

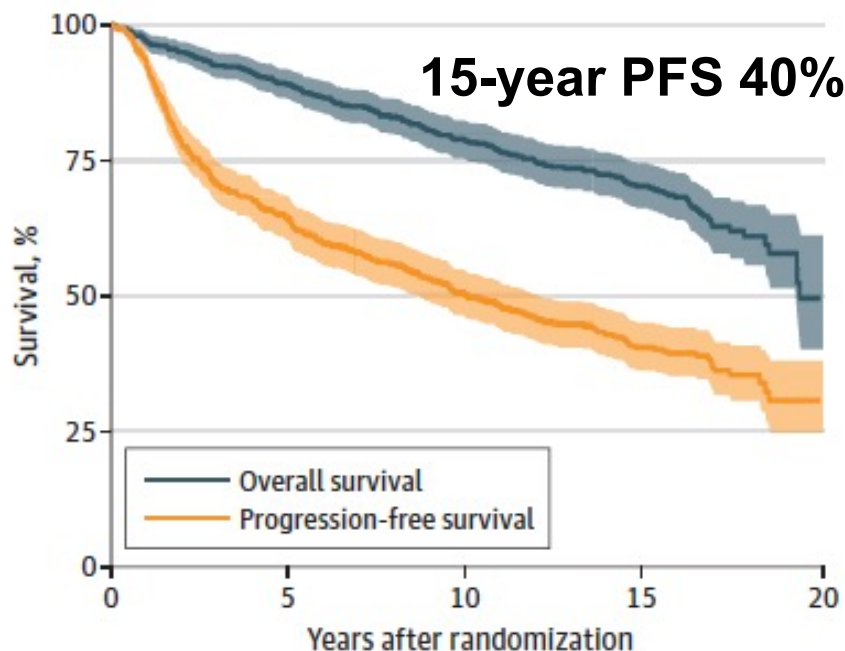
Histologic Transformation: MER/LEO Real-World

- Early vs late HT worse outcomes

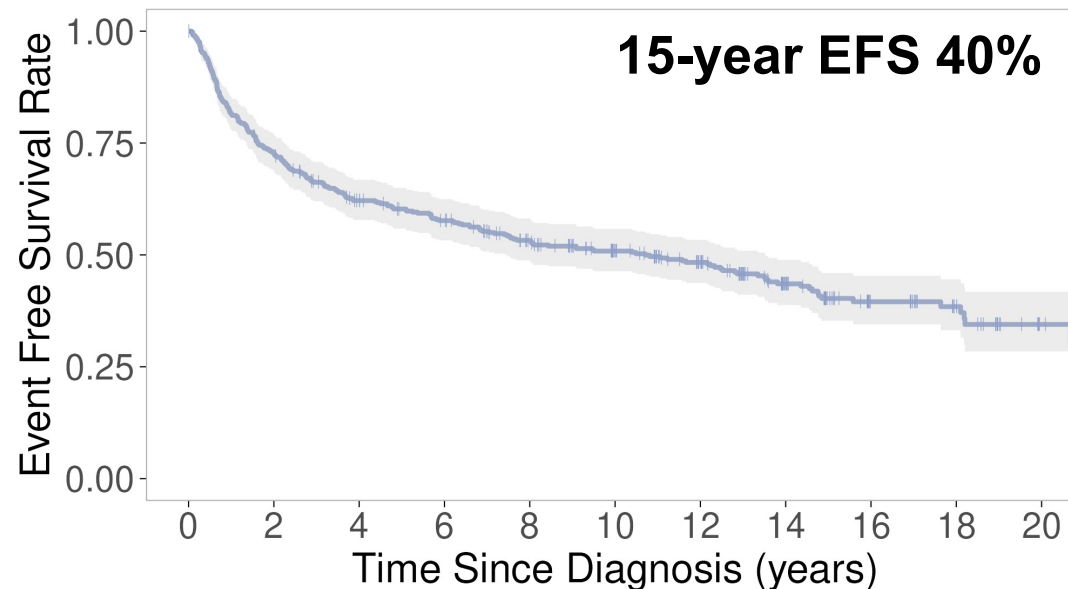


Predicting Who is Cured: Long term follow up SWOG0016 and Mayo/Iowa MER

Cure rates highest with low risk FLIPI and low $\beta 2$ microglobulin



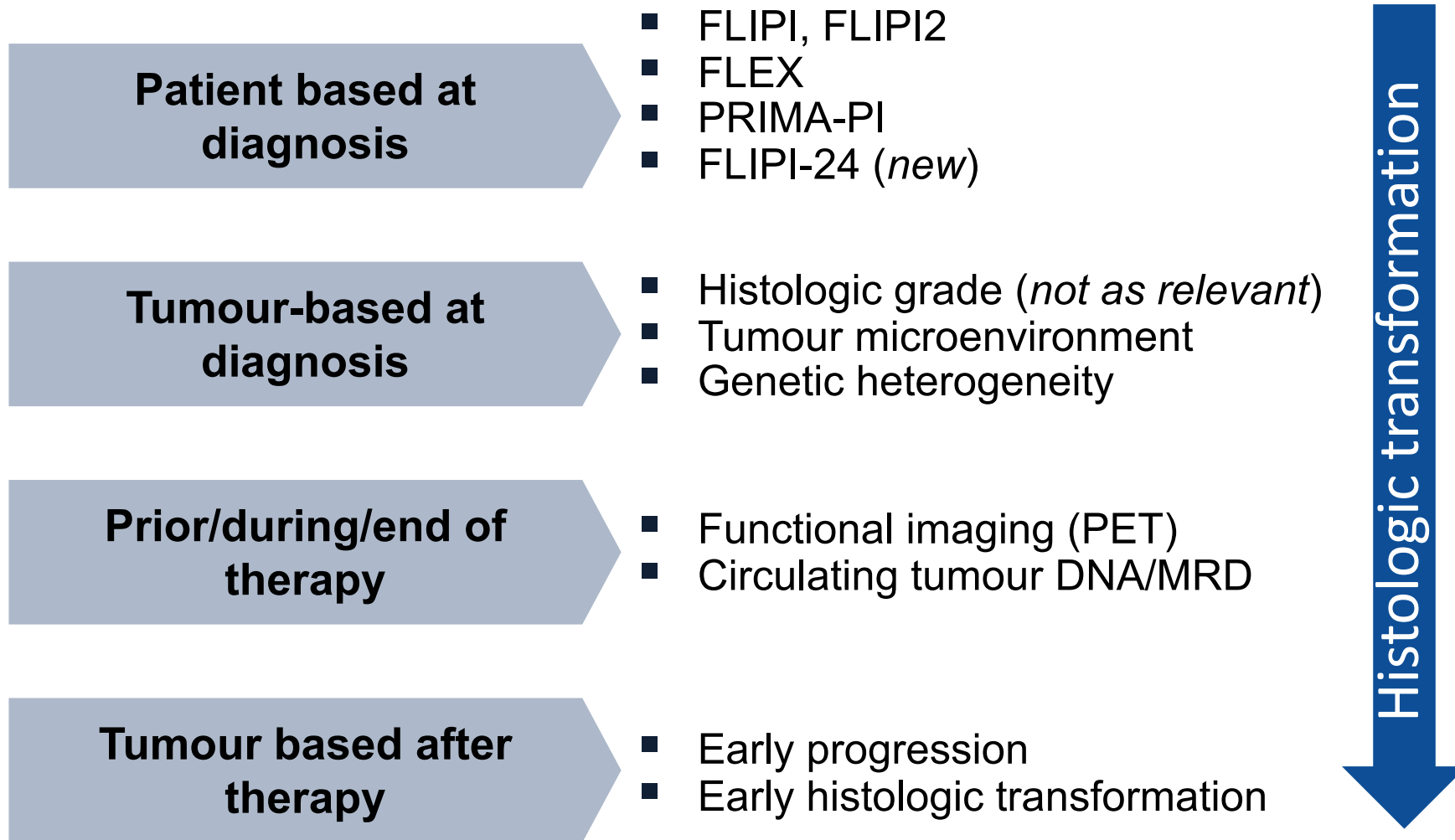
No. at risk	0	5	10	15	20
Overall survival	531	459	382	239	9
Progression-free survival	531	333	243	139	4



Number at risk	0	2	4	6	8	10	12	14	16	18	20
IC	453	327	269	243	207	171	139	87	45	31	9

Relapse rates decrease over time, 7% 1st 5 years → >1% between years 15-20

Summary of Prognostic Marker Continuum



What Can Change Clinical Practice Tomorrow?

FLIPI24 and MRD-directed Treatment Decisions at Diagnosis

- High risk FLIPI24 and TMTV at diagnosis → clinical trial?
- Multi-modal score + TME to predict histologic transformation and cure?

De-escalate

Intensify

End of Treatment and Surveillance

- In MRD-negative low-risk FL, blood-based surveillance replacing imaging?
- ctDNA+ end of treatment → maintenance vs. novel agent?
- Retreatment vs. observation with MRD recurrence?

Thank you!

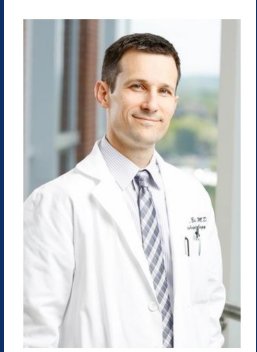


Jonathan Friedberg



UR
MEDICINE

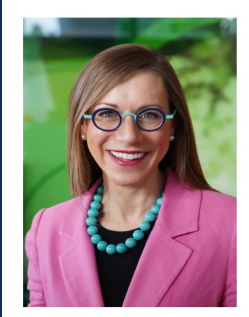
WILMOT
CANCER INSTITUTE



Paul Barr



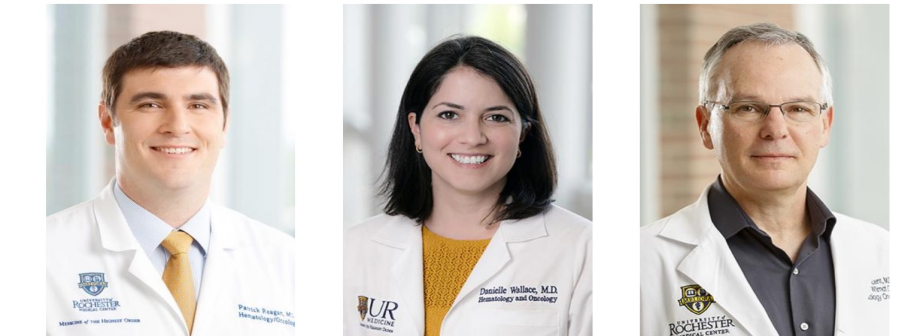
A Cancer Center Designated by the National Cancer Institute



Jaime Flerlage



Sandy Constine



Pat Reagan

Danielle Wallace

Clive Zent