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Use of circulating tumor DNA to genotype aggressive lymphoma

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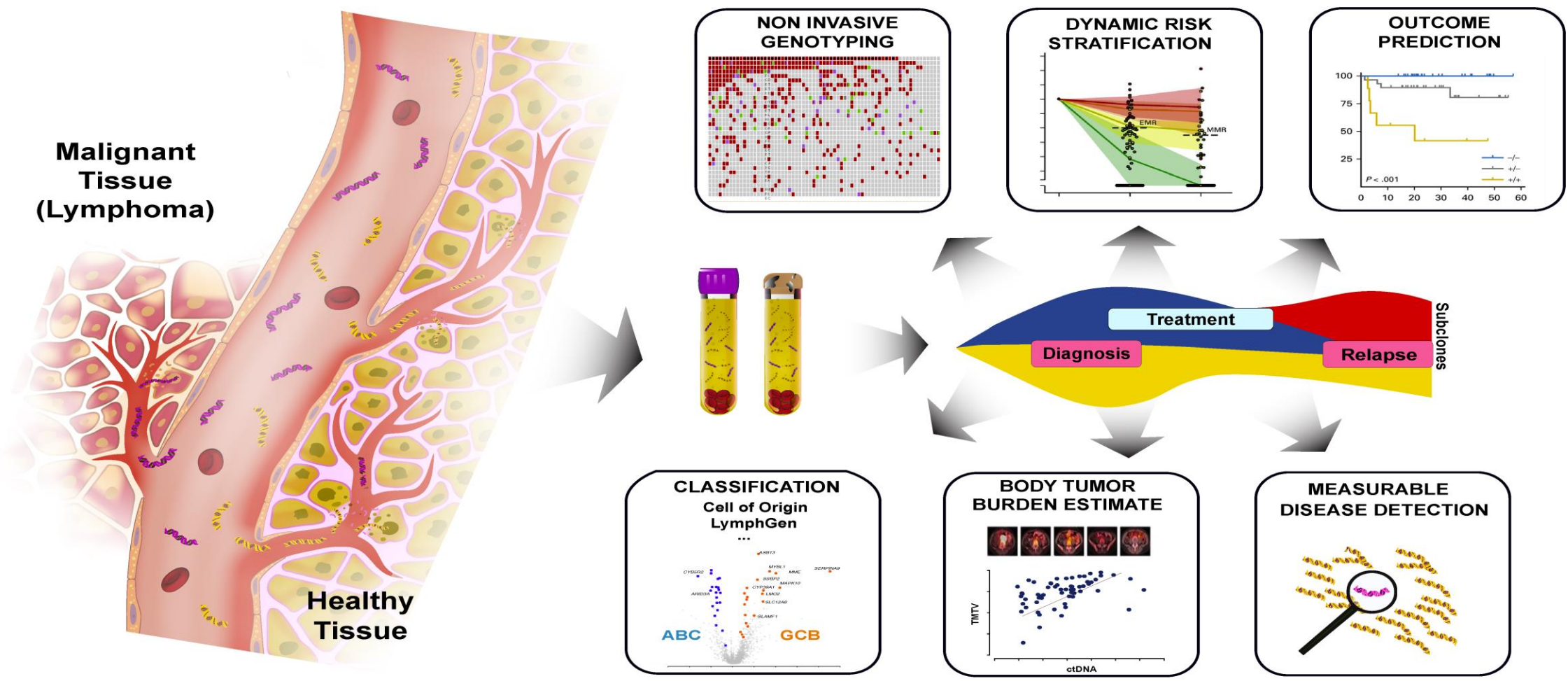
Bellinzona - Switzerland

DISCLOSURES OF COMMERCIAL SUPPORT

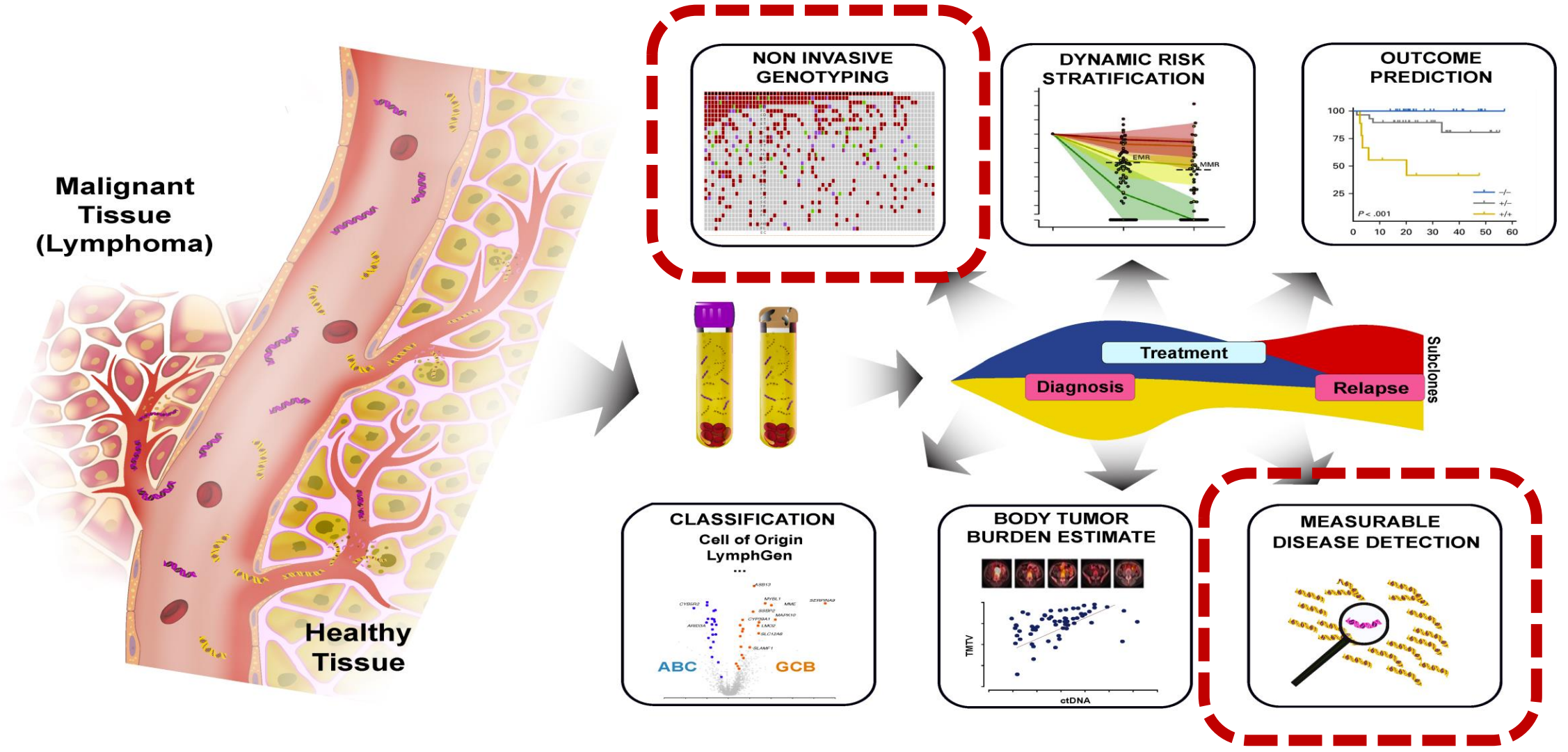
Name of Company	Research support	Employee	Consultant	Stockholder	Speaker's Bureau	Scientific Advisory Board	Other
AbbVie	X					X	
AstraZeneca	X					X	
BeiGene	X					X	
BMS						X	
Janssen	X					X	
MSD	X						

Background

Cell free DNA (cfDNA) - Circulating tumor DNA (ctDNA)

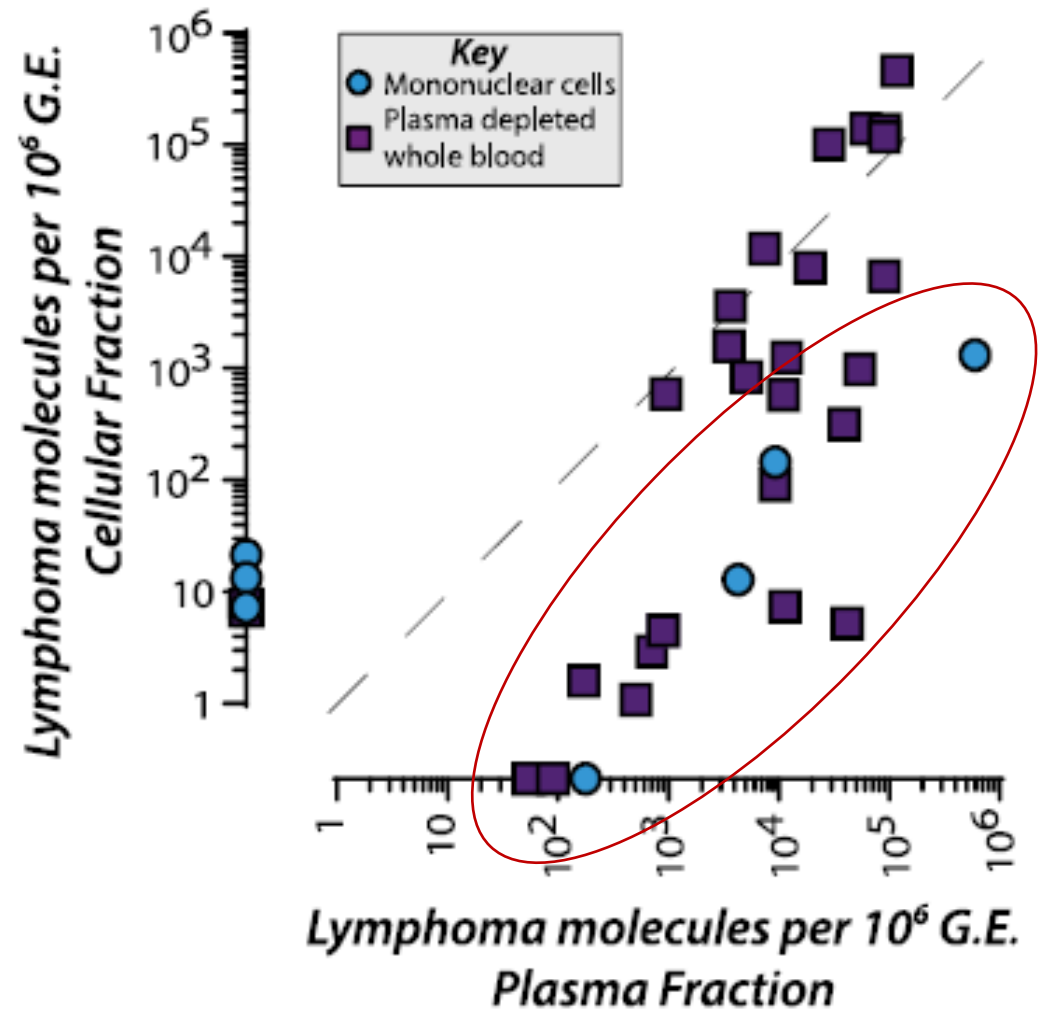


Cell free DNA (cfDNA) - Circulating tumor DNA (ctDNA)



Why and how assessing ctDNA in DLBCL?

Lymphoma DNA is 150-fold more abundant in plasma than PBMC



ctDNA detection in lymphomas across common methodologies



Challenges for ctDNA in lymphomas

Low total amounts of ctDNA

Plasma:
~2,000 genomes/mL

PBMC:
~5,000,000 genomes/mL

Low fractional tumor abundance

Diverse mutational profiles of lymphomas

ctDNA methodologies applied to lymphomas

PCR-based

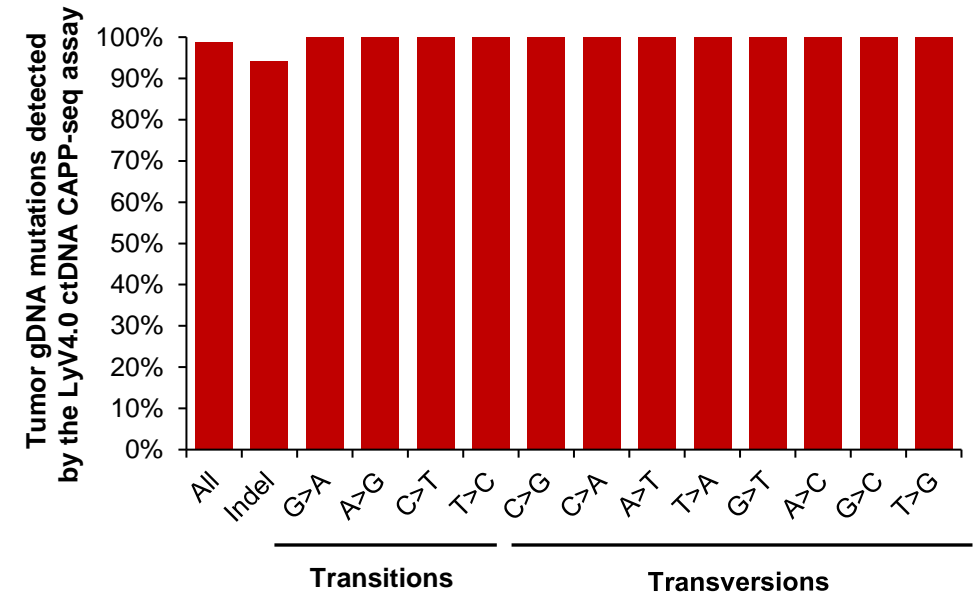
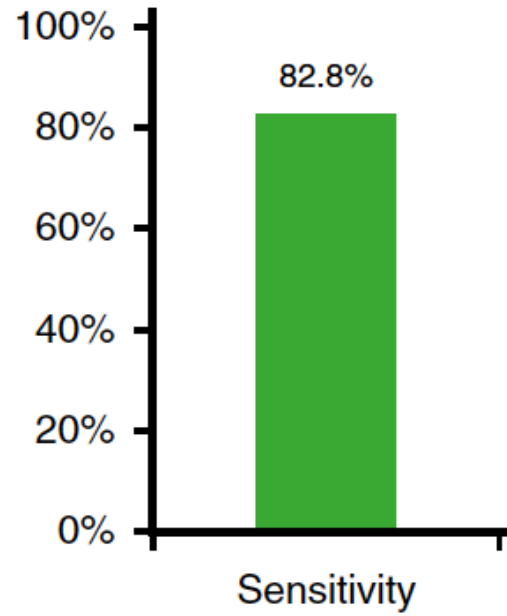
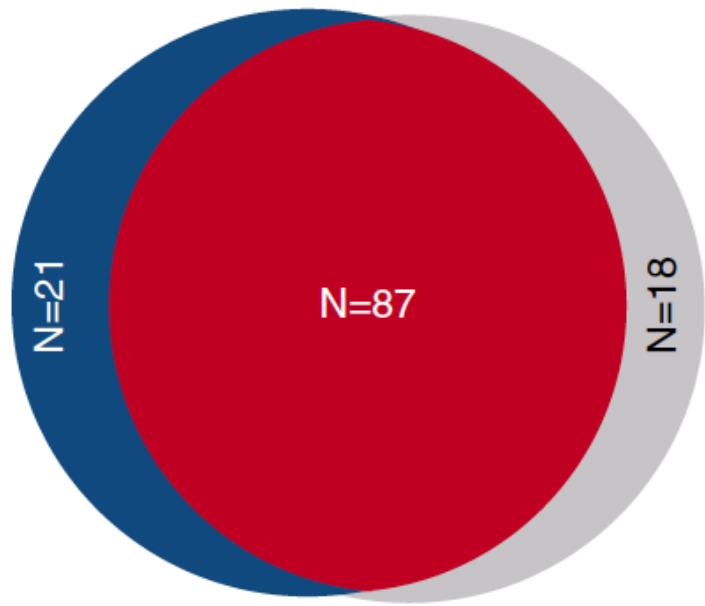
Sequencing-based

	dPCR	Ig sequencing	CAPP-seq	Lymphopanel	WGS
Disease detection	+	++	++	+	+
Mutational genotyping	+	-	++	+	+

Identification of genetic lesions

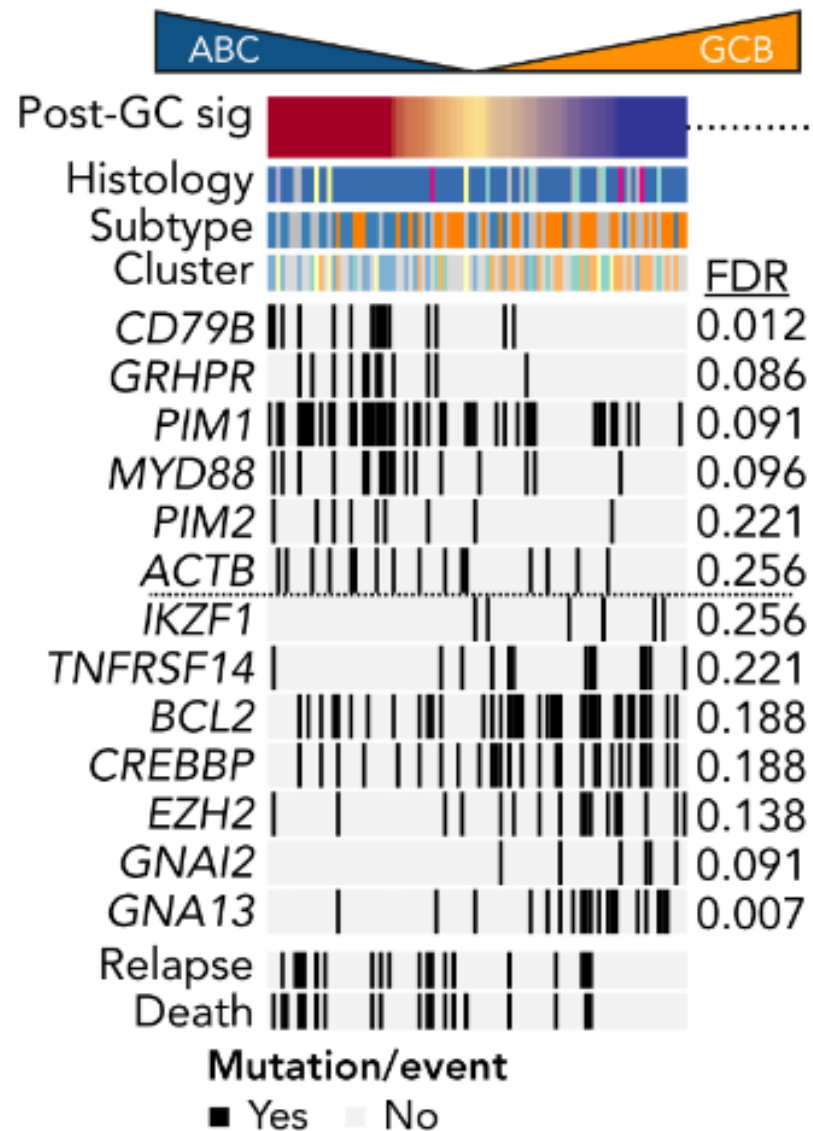
Diagnostic performance of DLBCL mutation profiling on ctDNA

- Mutation identified both in gDNA and in cfDNA
- Mutation identified in gDNA only
- Mutation identified in cfDNA only



Scherer F, Sci Transl Med. 2016
 Rossi D, Blood. 2017
 Bruscaggin A, et al. Blood Adv. 2021
 Meriranta L, Blood. 2022

DLBCL subtype identification by mutation analysis of ctDNA

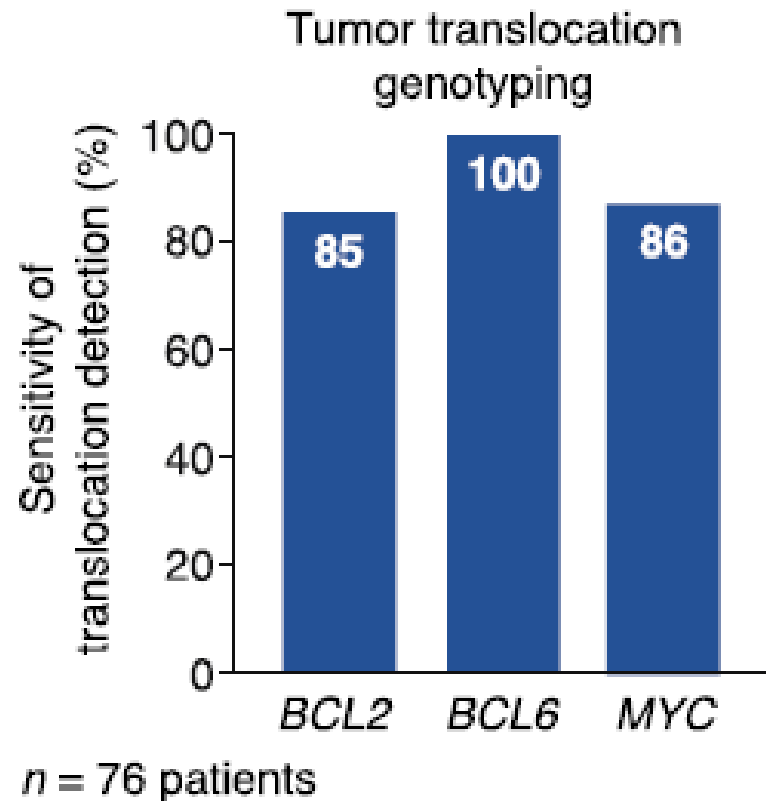


Identification of SV by using CAPP-seq

BN2/C1 subtype includes BCL6 translocation among biomarkers

EZB/C3 subtype includes BCL2 translocation among biomarkers

EZB-MYC subtype includes BCL2 and MYC translocations among biomarkers



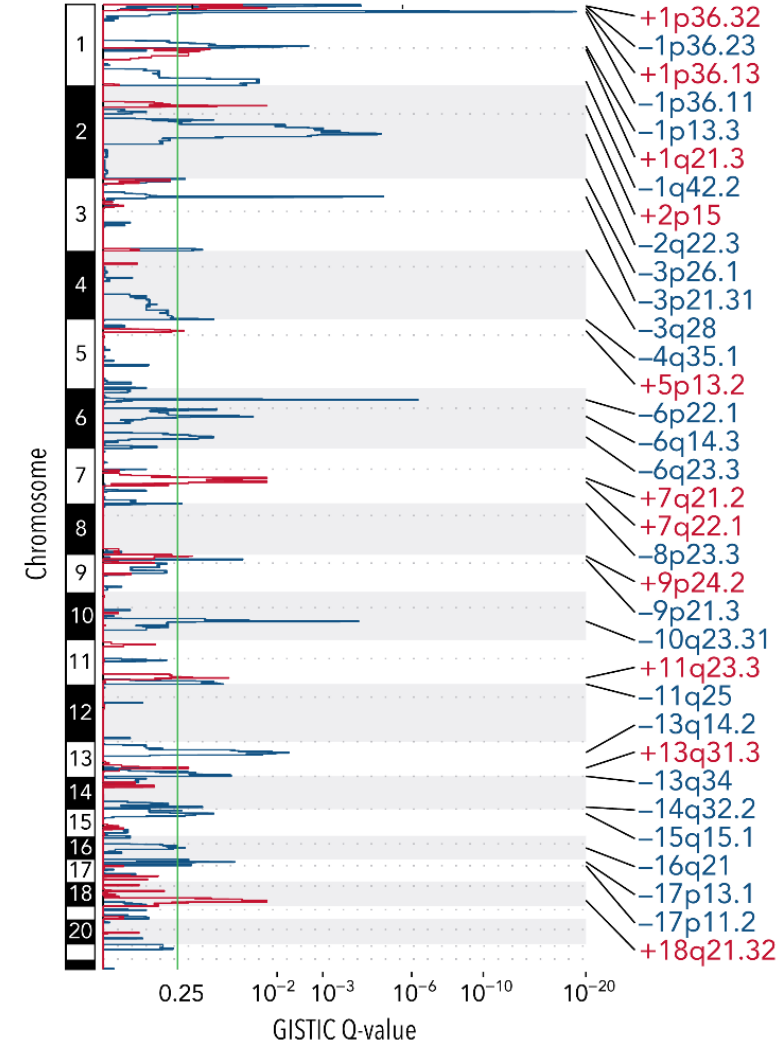
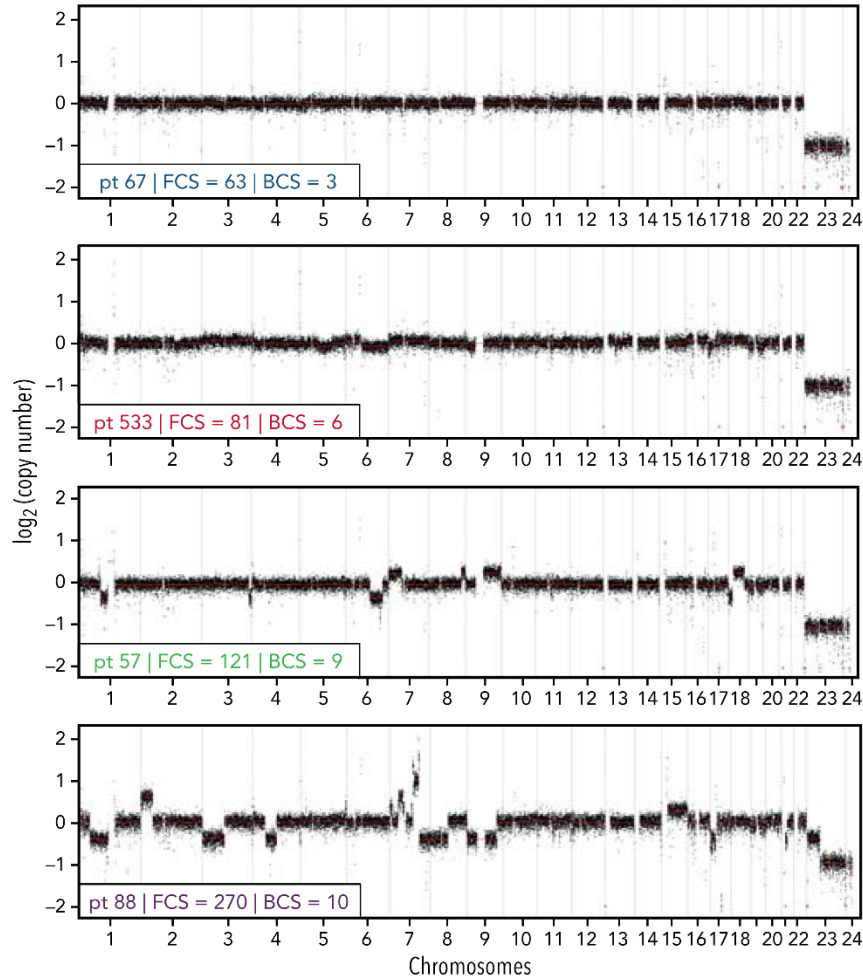
BCL2/IGH breakpoint coverage: 70%

BCL6 breakpoint translocation coverage: 85%

MYC breakpoint coverages: 90%

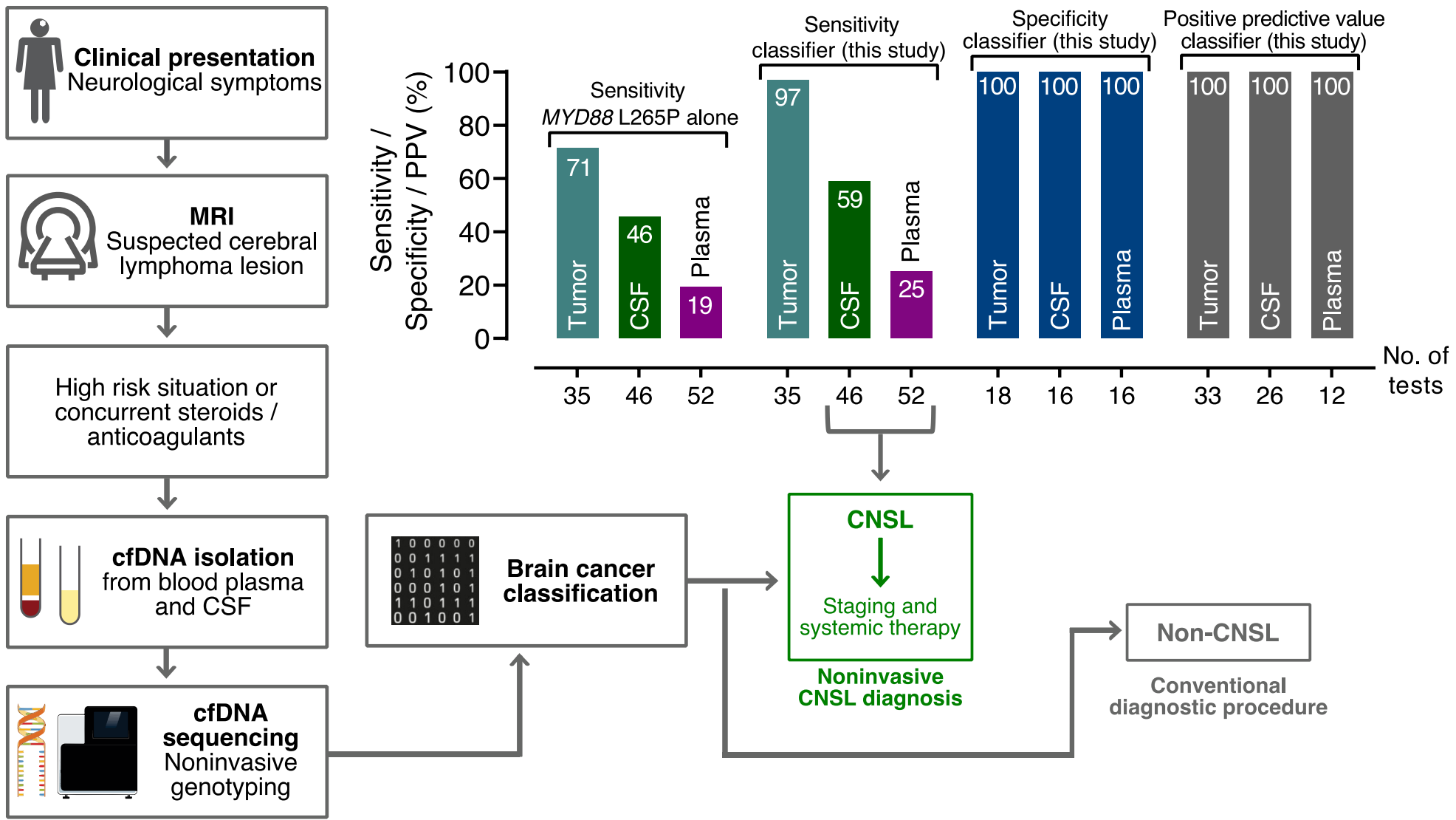
Identification of tumor copy number abnormalities by using low pass WGS

A53/C2 subtype includes multiple CNA among biomarkers

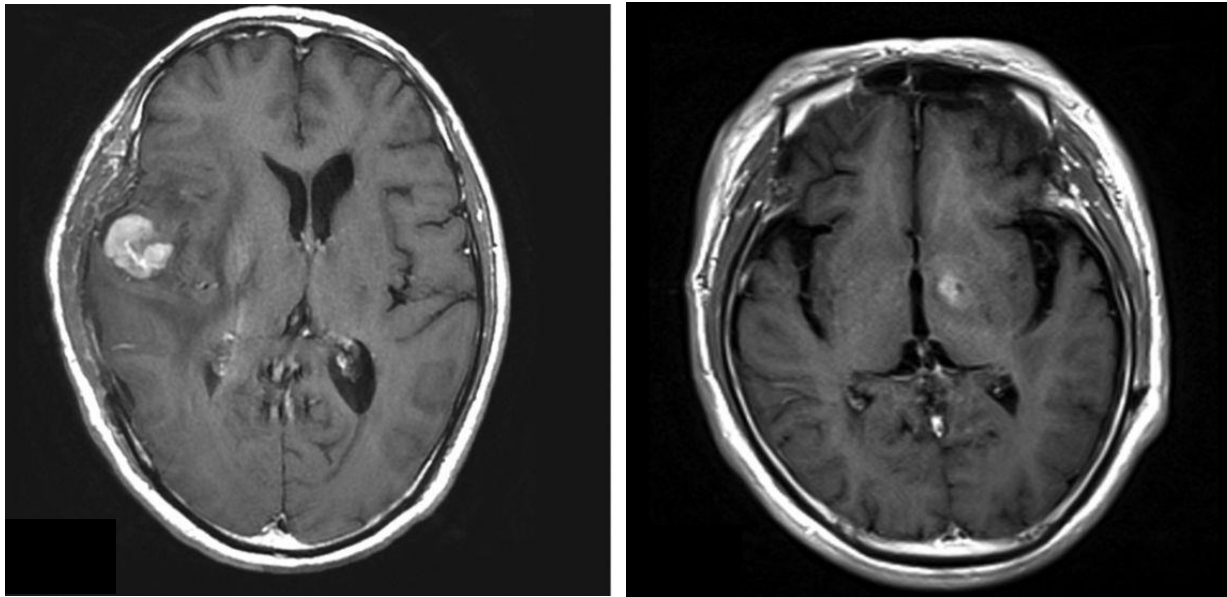


Clinical applications in LBCL: diagnosis

Biopsy-free CNSL classification

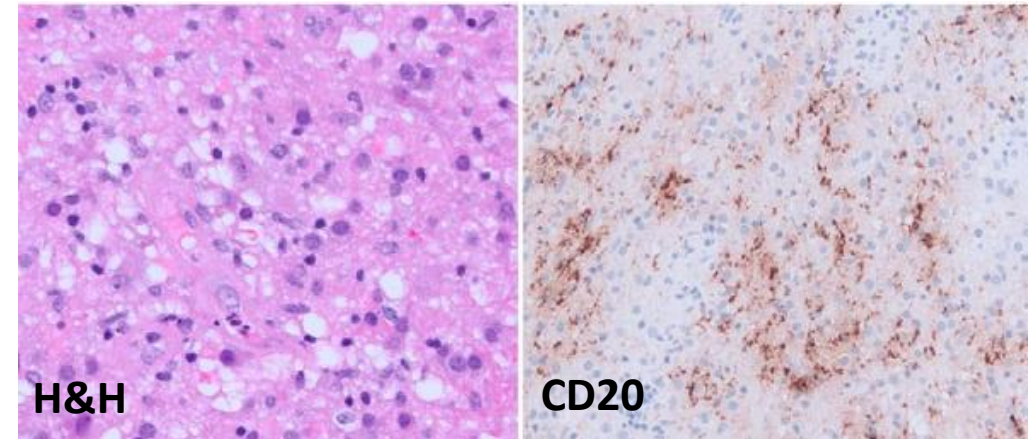


Accessibility of the lesion

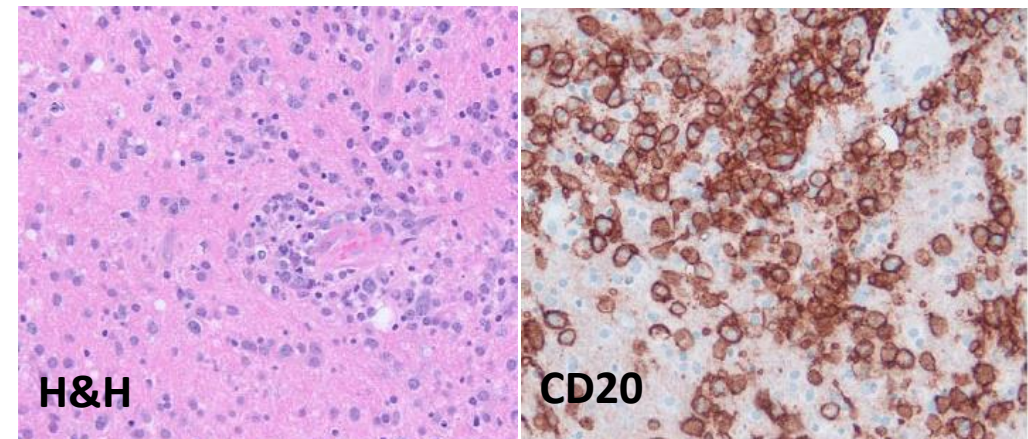


PCNSL vanishing after steroid pre-treatment

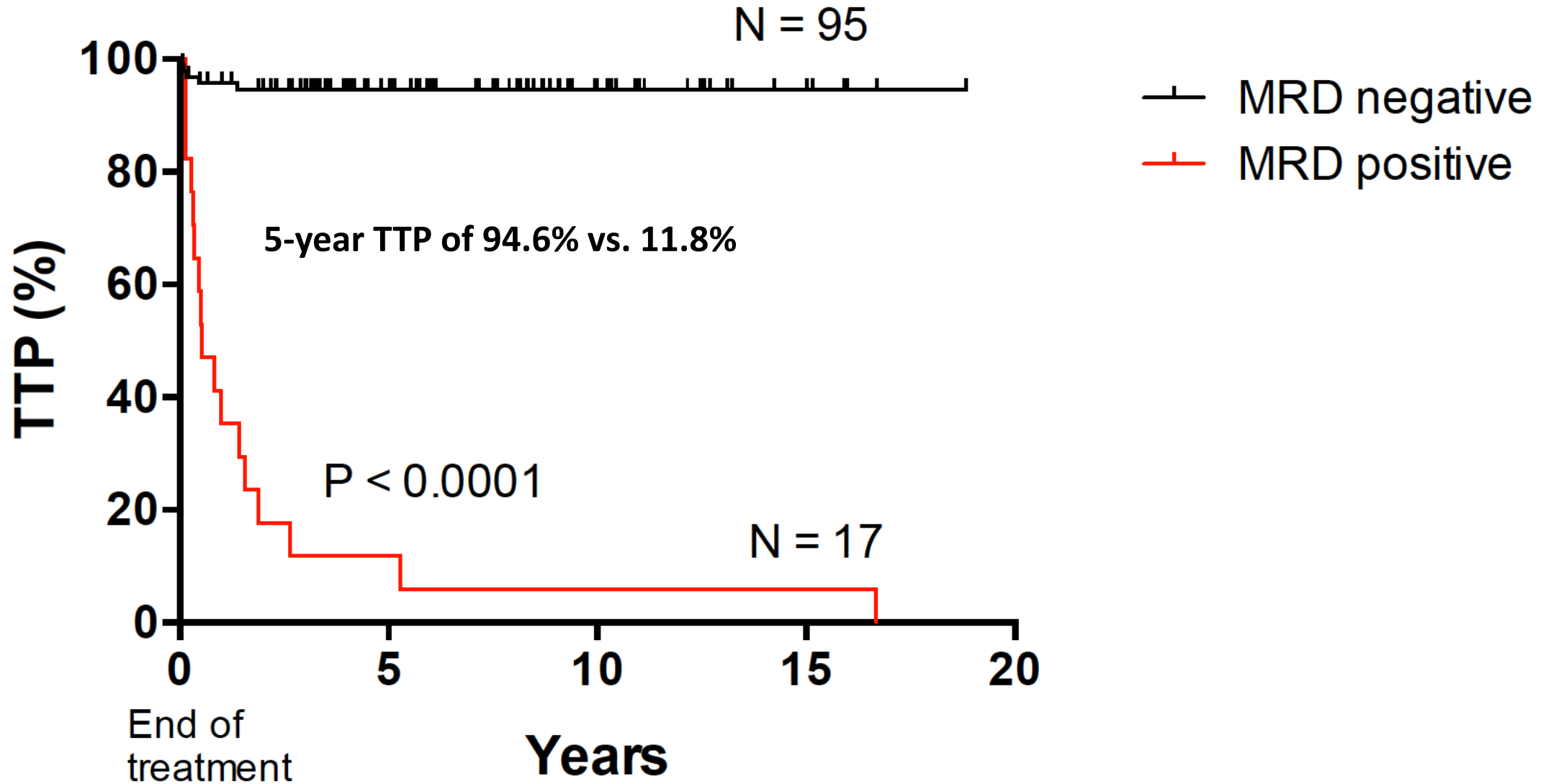
Pre-steroid Tx

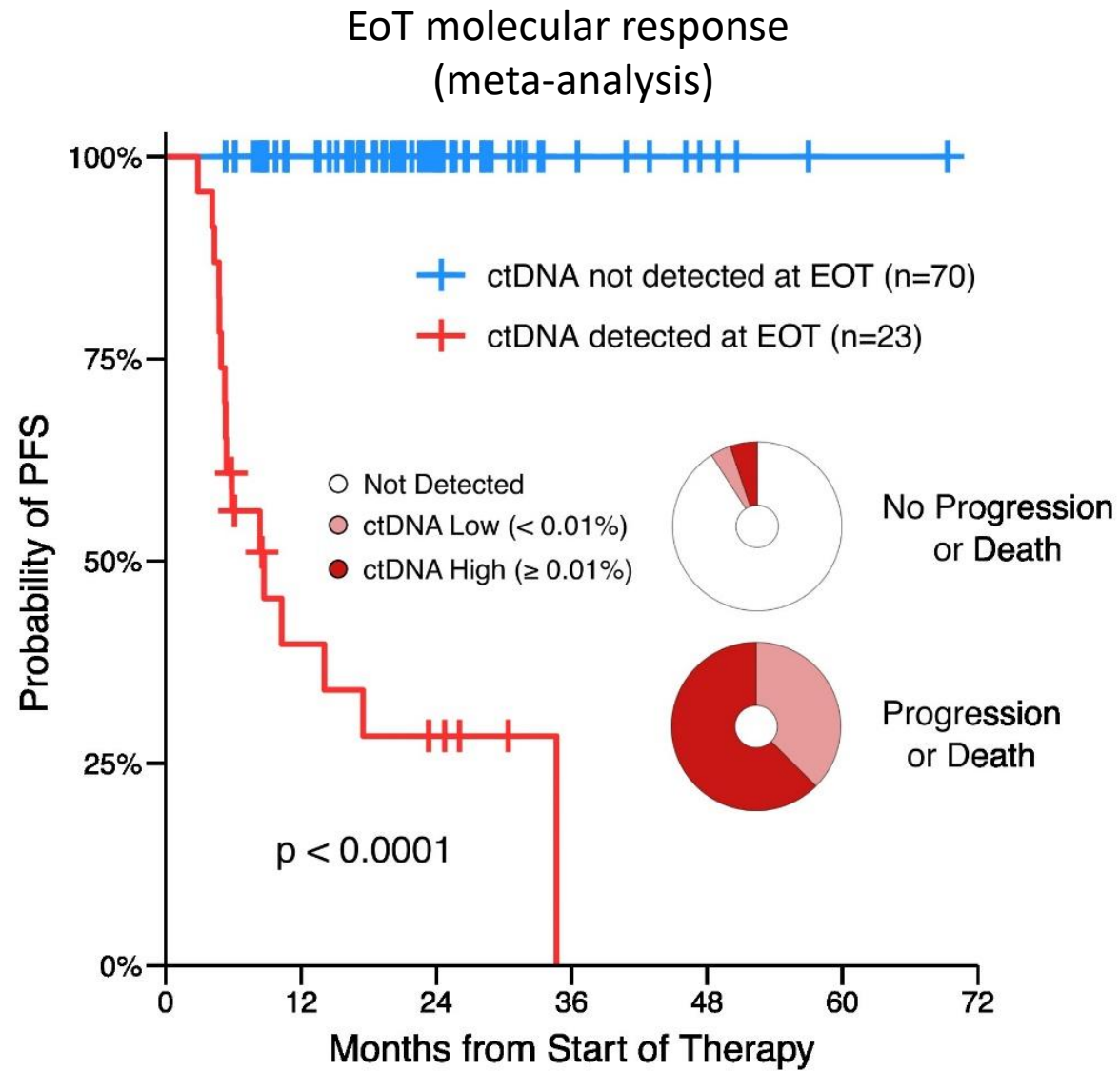


No pre-steroid Tx

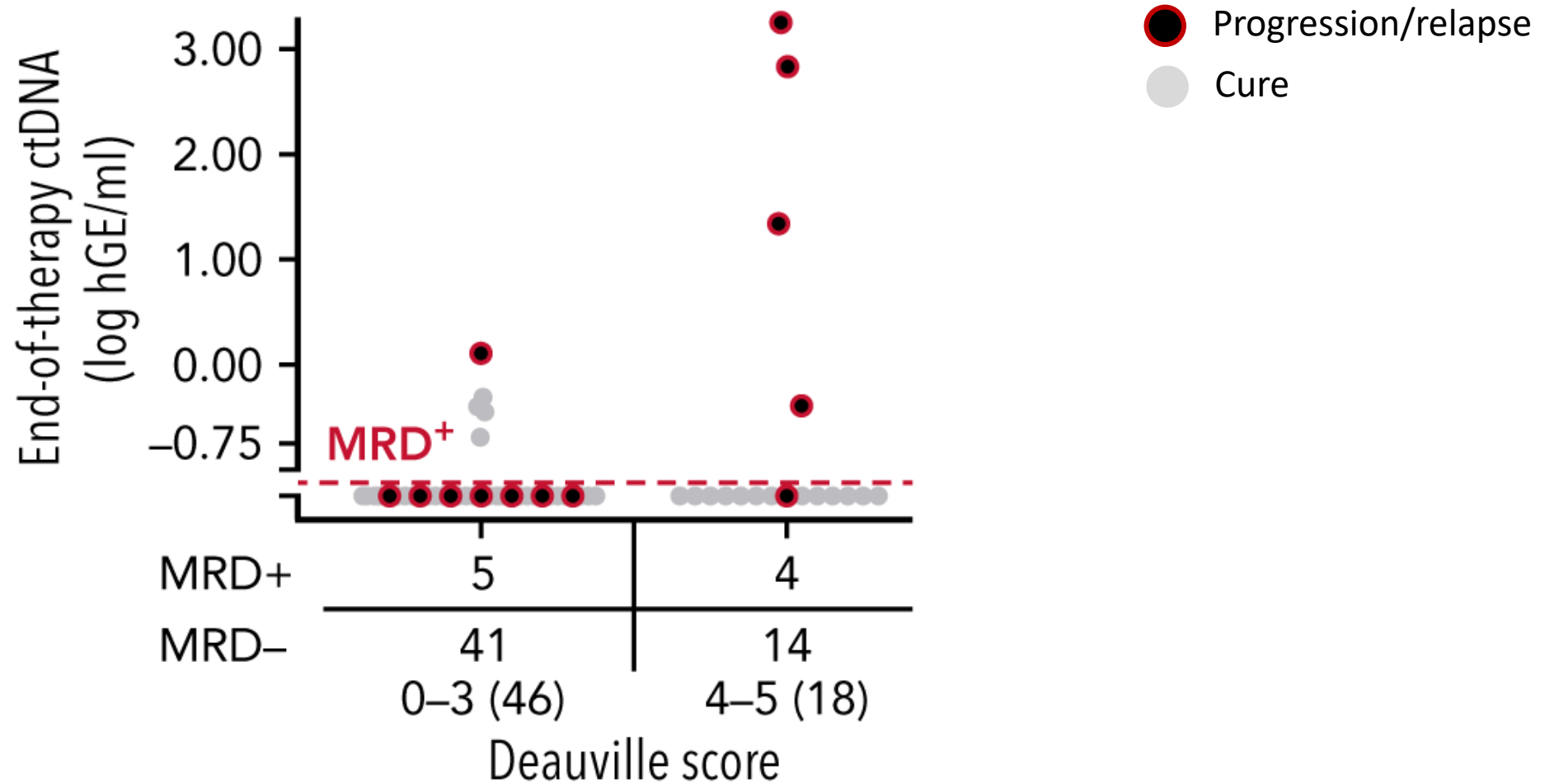


Clinical applications in LBCL: monitoring





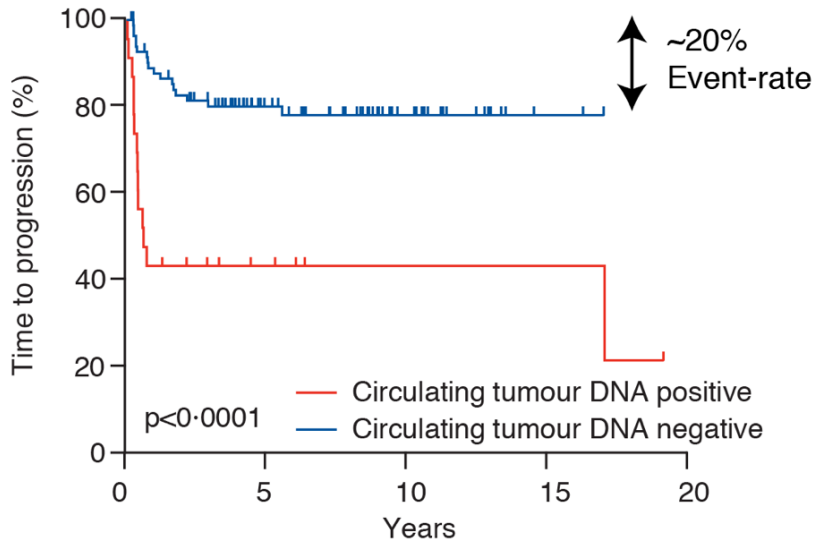
MRD after therapy identify false positive PET/CT



Surveillance MRD at the interim timepoint predicts progression

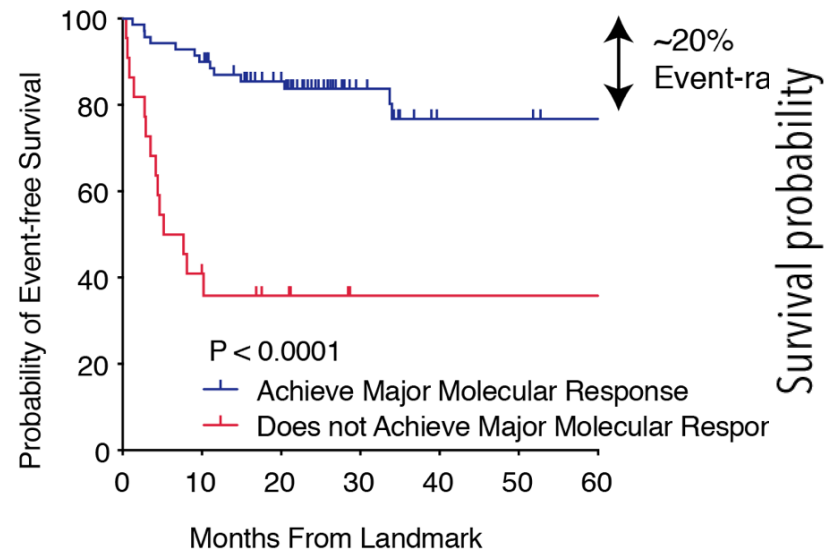


Ig-HTS (ClonoSEQ) Detectable at Cycle 3



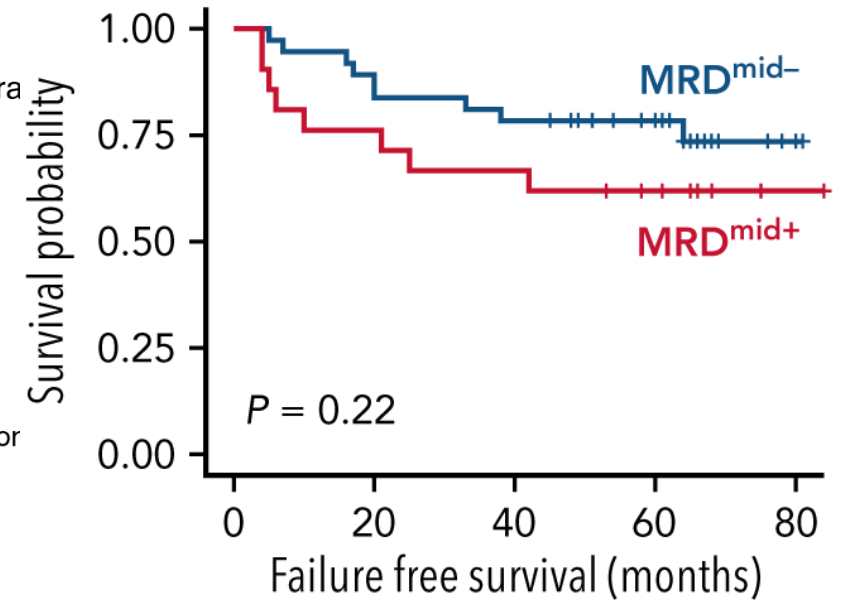
Roschewski MR et al. *Lancet Oncology*. 2015.

CAPP-Seq Major Molecular Response



Kurtz et al, *JCO*. 2018

MRD at mid-staging (n = 58)



Number at risk

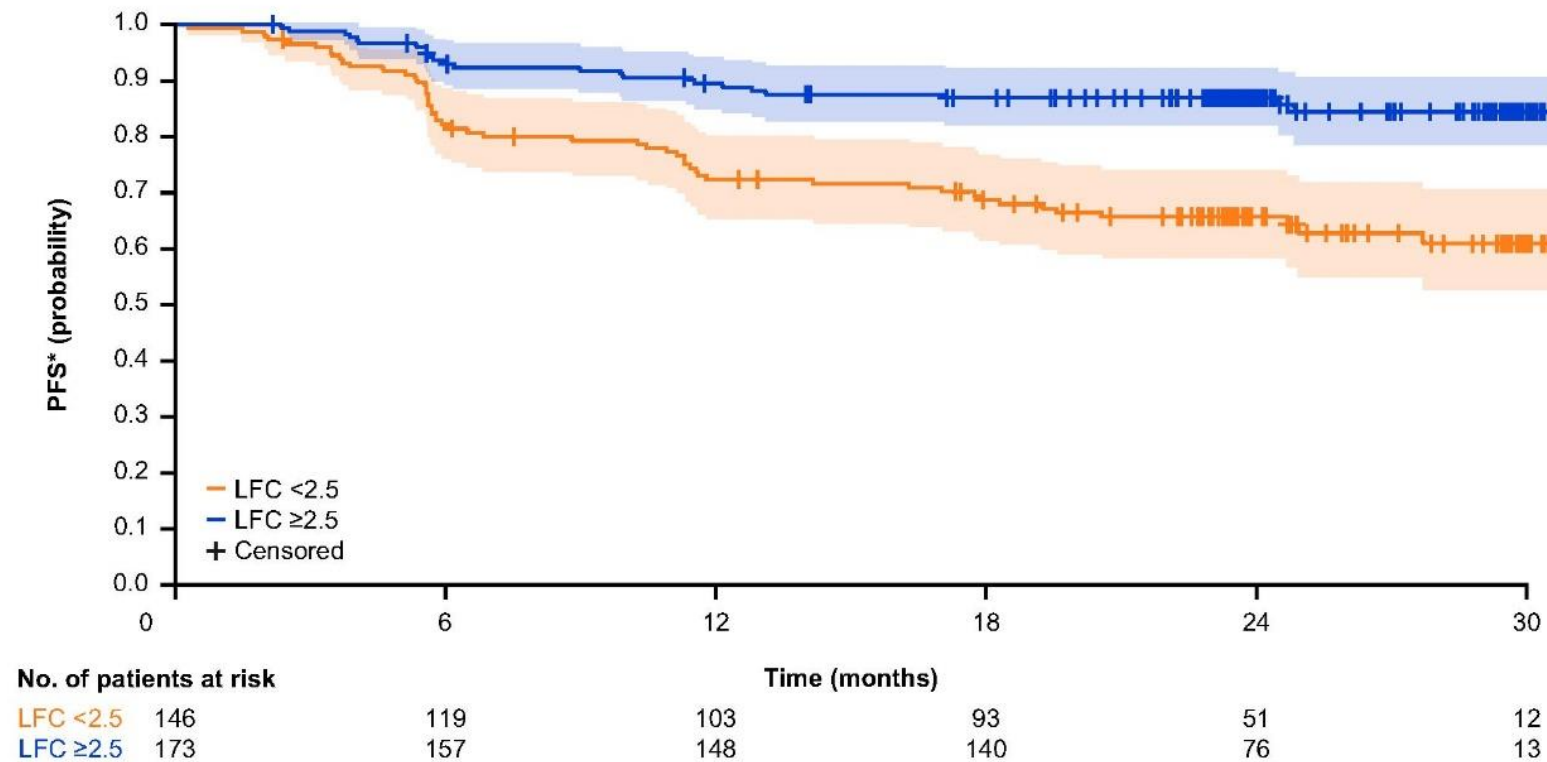
Neg	37	33	29	20	2
Pos	21	16	14	11	1
	0	20	40	60	80

Meriranta L, *Blood*. 2022

Interim molecular response (POLARIX trial)

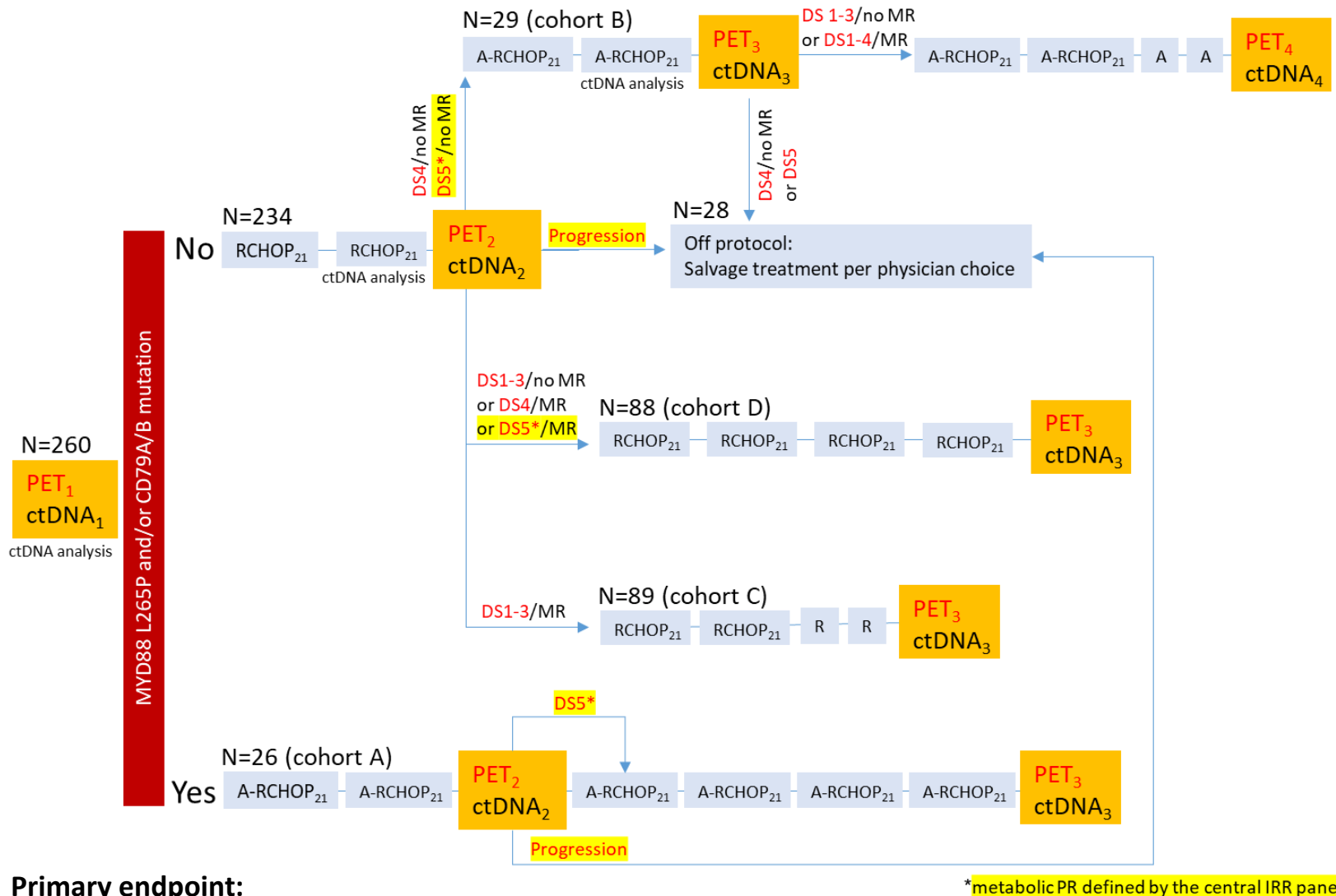
Figure. PFS of Pola-R-CHP-treated patients (LFC <2.5 vs LFC ≥2.5)

A)



- Baseline ctDNA in CSF aids in the diagnosis of PCNSL
- Baseline ctDNA profile can capture genetic subtypes of DLBCL, but accuracy should be improved
- EOT MRD measured by ctDNA corrects false positive EOT PET/CT
- Interim MRD measured by ctDNA needs further studies (best time-point, assay sensitivity, threshold)

SAKK 38/19 PEDRO: Trial Design



Timely delivery of **ctDNA** samples (analysis 10-14 days) at:

1. Baseline
2. C2D8 for non-mutated patients
3. C4D8 for cohort B

Upload **PET/CT** scans to WIDEN (42-1 day prior to registration)

Primary endpoint:

- Progression free survival according to the Lugano criteria (Cohorts A, C and D)
- Complete remission rate according to the Lugano criteria (Cohort B)

*metabolic PR defined by the central IRR panel

SAKK 38/19 PEDRO

Main inclusion criteria

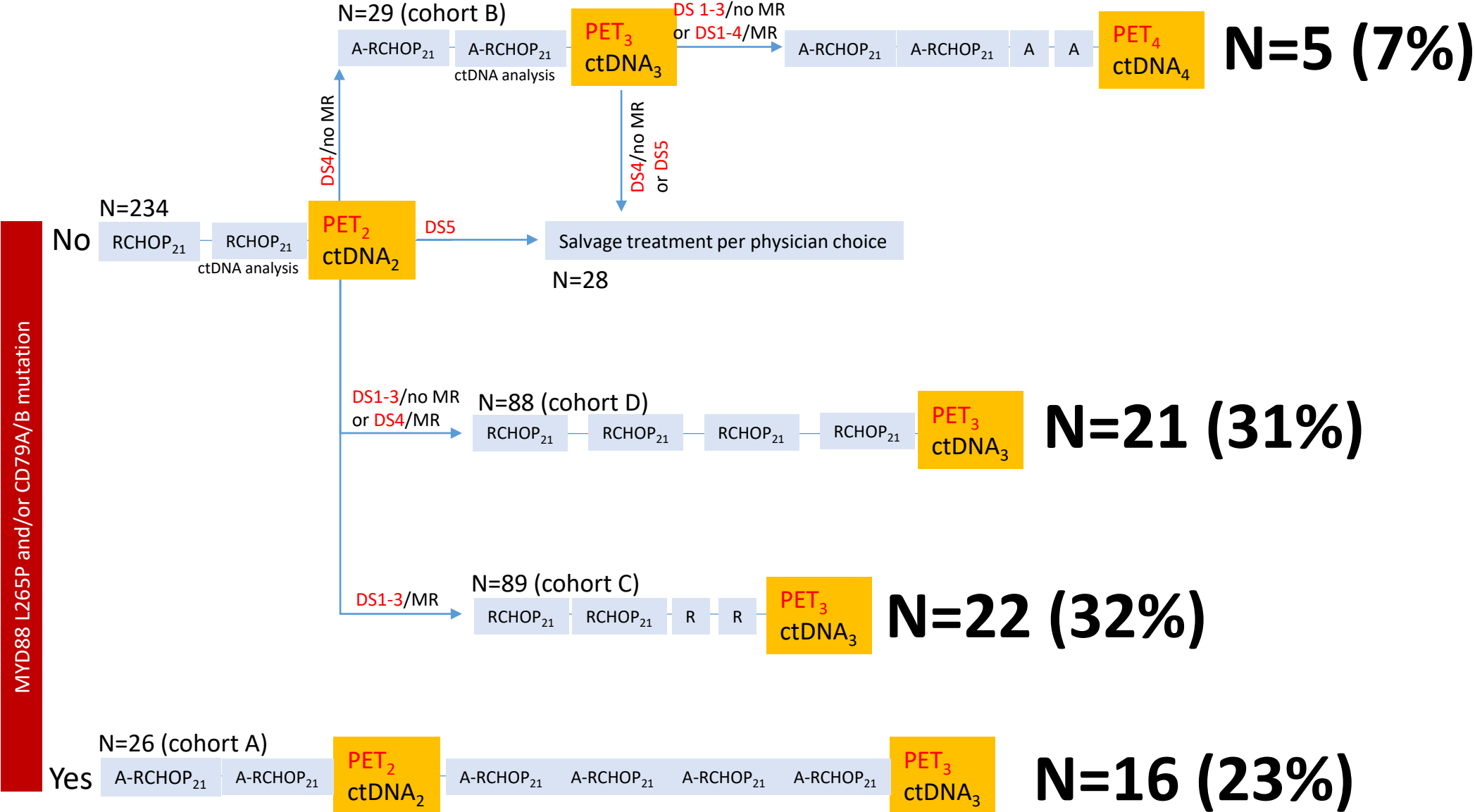
- Histologically confirmed, treatment-naïve DLBCL NOS
- Ann Arbor stage I-IV
- Eligible for 6 cycles of R-CHOP;
- Metabolically active measurable disease by 18FDG PET-CT
- At least 1 measurable site of disease
- Quantifiable and qualifiable circulating tumor DNA

ctDNA-driven therapy of DLBCL: SAKK 38/19



N=69

N=260
PET₁
 ctDNA₁
 ctDNA analysis



SAKK 38/19 PEDRO: Screening Failures

Incl./Excl. criteria	n	Details (n)
6.1.2	29	<ul style="list-style-type: none"> • Not DLBCL, NOS (16) <ul style="list-style-type: none"> • Transformed lymphoma (4) • Hodgkin lymphoma (3) • High-grade B-cell lymphoma (1) • Follicular Lymphoma (1) • Other (6) • No detectable ctDNA (10) • No measurable disease (3)
6.1.6	1	<ul style="list-style-type: none"> • Platelet count too low
6.1.7	1	<ul style="list-style-type: none"> • Bilirubin and ALAT too high
6.1.8	1	<ul style="list-style-type: none"> • Creatinine clearance
6.2.10	1	<ul style="list-style-type: none"> • Testis involvement
Physician's decision / Other	18	<ul style="list-style-type: none"> • PI decision: no further reason (6) • Patient's withdrawal of consent (4) • Not in need of / not fit for 6 cycles of R-CHOP (3) • Missing info (3) • Worsening of condition / in need of therapy (2)
Total	51	

Acknowledgment



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