



# **BIOPSIA LIQUIDA**

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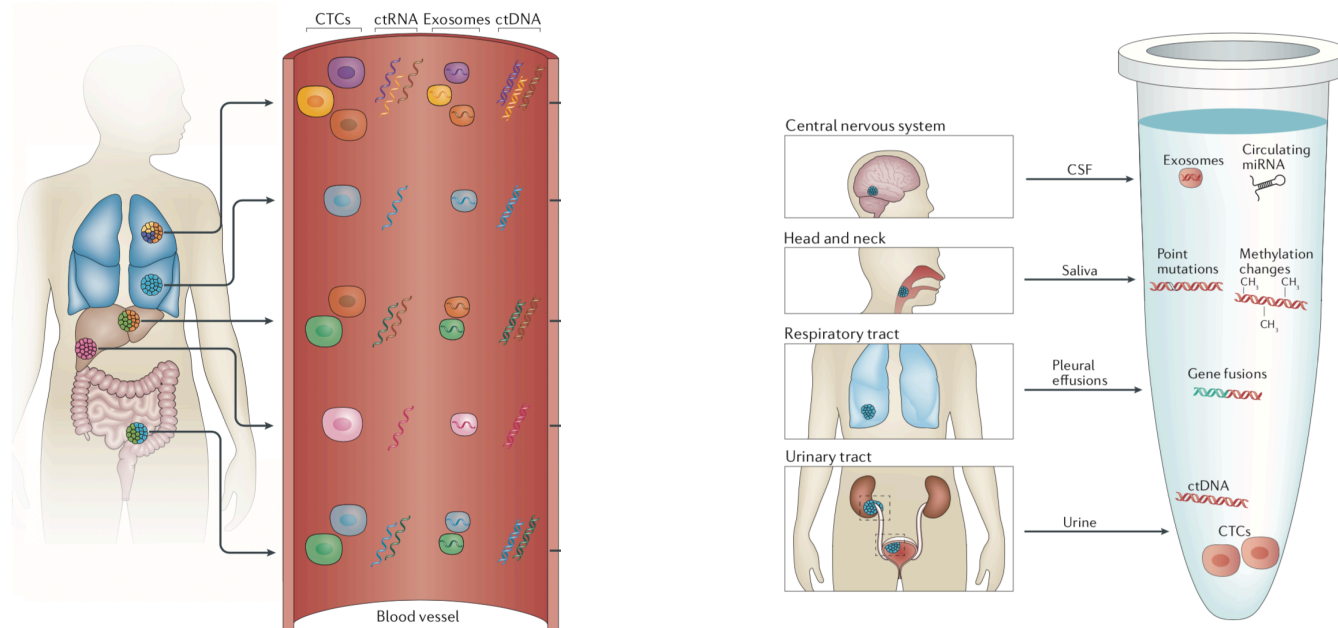


# **DISCLOSURES: GIANLUCA GAIDANO**

- **Advisory boards, Speakers' bureau:** Janssen, Gilead, Abbvie, Roche, Morphosys, Amgen
  
- **Non-financial interests:** Chair of EHA Global Outreach Program, Board Member of Società Italiana di Ematologia, Fondazione Italiana Linfomi

# The liquid biopsy

- A broad category of minimally invasive tests done on a sample of blood or other biological fluids
- Liquid biopsy can be used to analyze cell-free DNA (cfDNA), cells and vesicles such as exosomes that can originate from different healthy tissues and also from cancers



Merker JD, et al., *JCO*. 2018; Siravegna G, et al., *Nat Rev Clin Oncol*. 2017

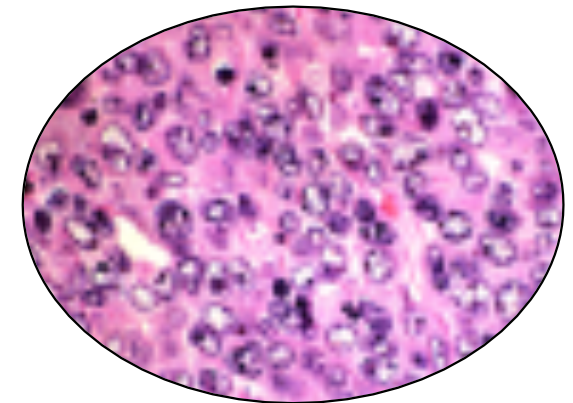
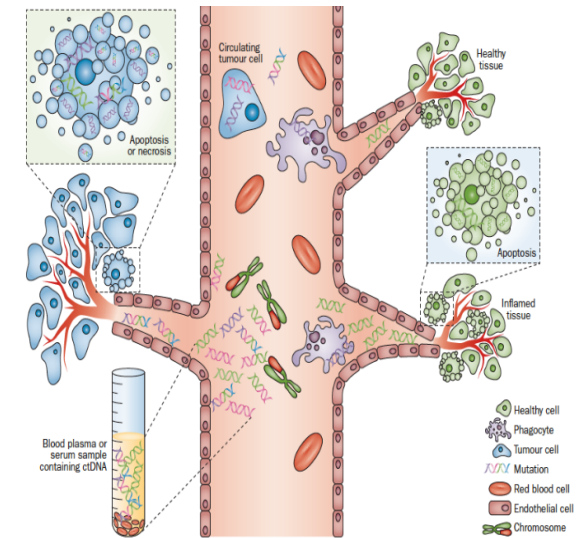
# Liquid Biopsy vs Tissue Biopsy in hematology

## LIQUID biopsy during the clinical course:

- enables assessment of tumor heterogeneity and evaluation of all/most tumor localizations in real-time (“global view”)
- allows monitoring of tumor dynamics and of treatment response

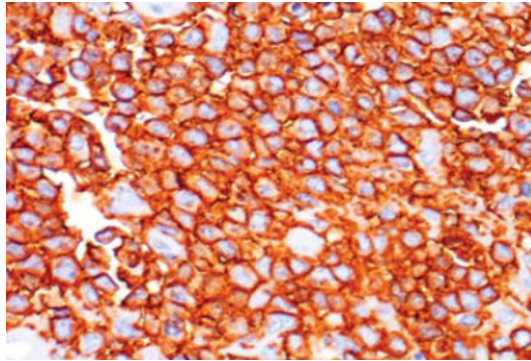
## TISSUE biopsy during the clinical course:

- may not reflect the whole genetic picture of the disease
- may not be feasible based on patient conditions or tumor accessibility
- is unethical/impractical for *periodic* monitoring of disease progression/recurrence



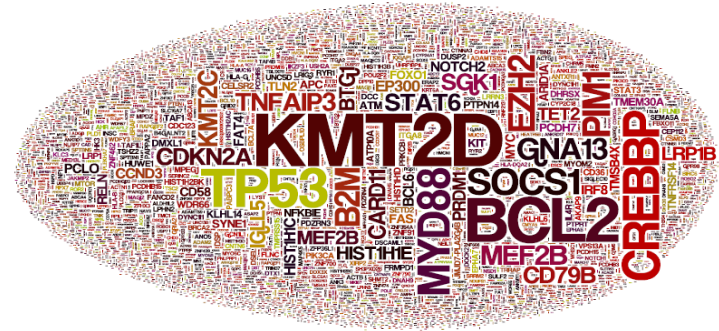
# Diffuse large B-cell lymphoma vs Hodgkin lymphoma

Tumor cells are enriched in the mass

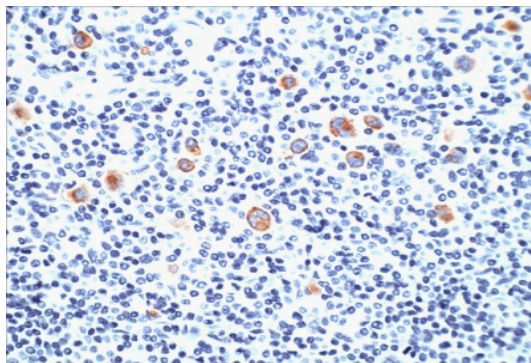


**DLBCL**

Exome sequencing data from >1000 cases



Tumor cells are rare in the mass



**CHL**

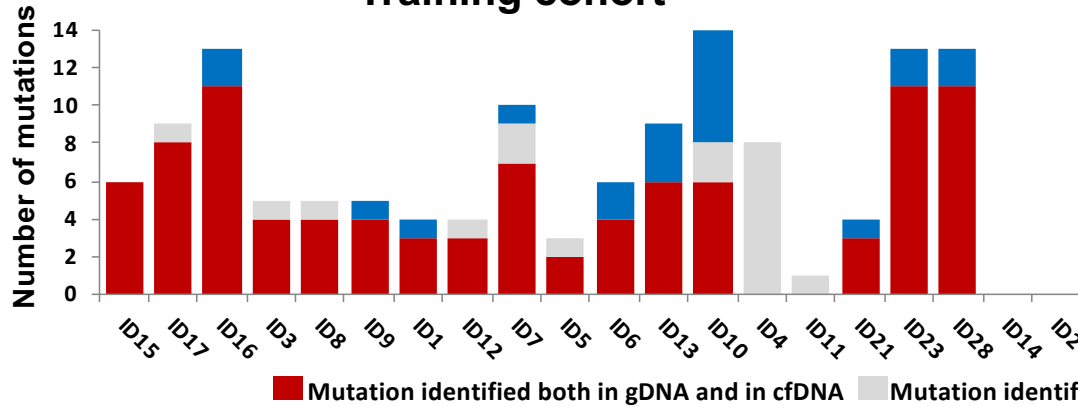
Exome sequencing data from only 10 cases



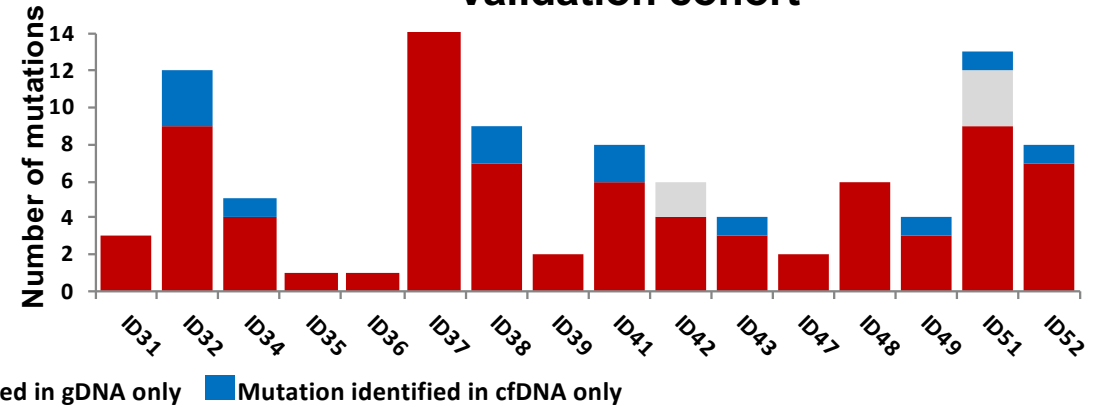
- **Genotyping**
- Clonal evolution
- Outcome prediction and MRD monitoring

# Plasma cfDNA genotyping vs tumor gDNA genotyping

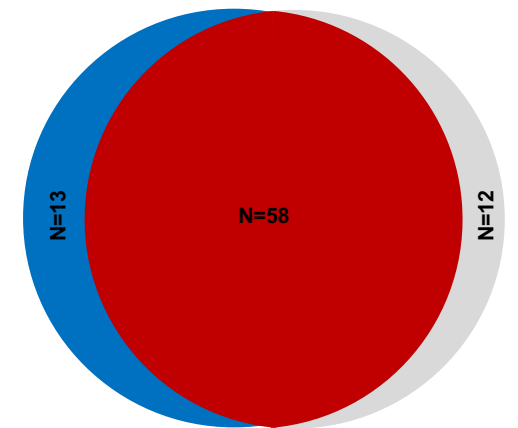
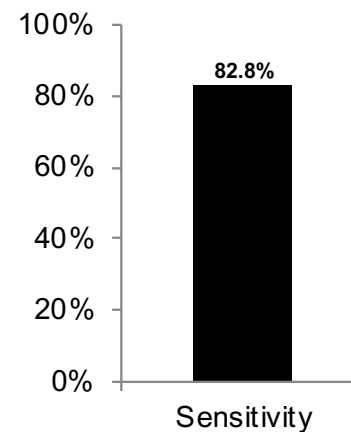
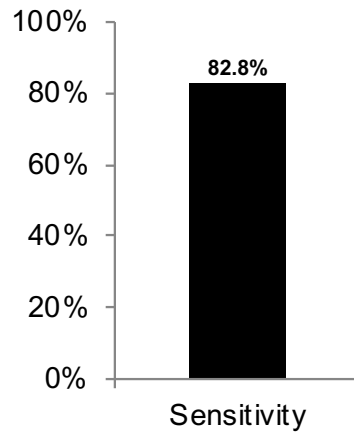
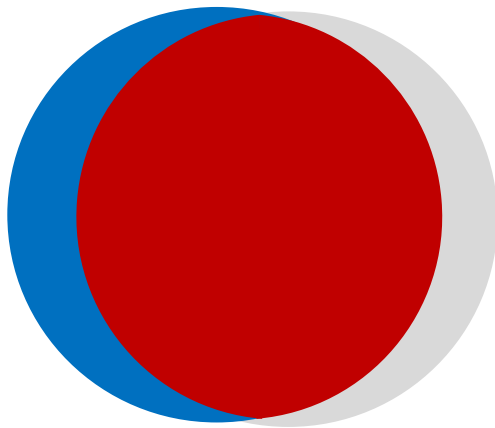
**Training cohort**



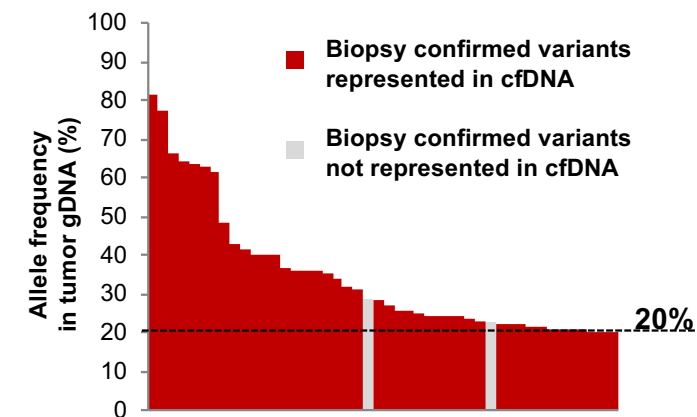
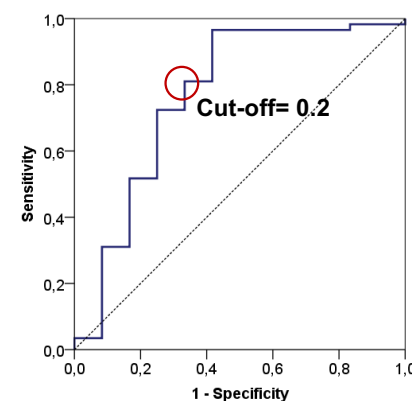
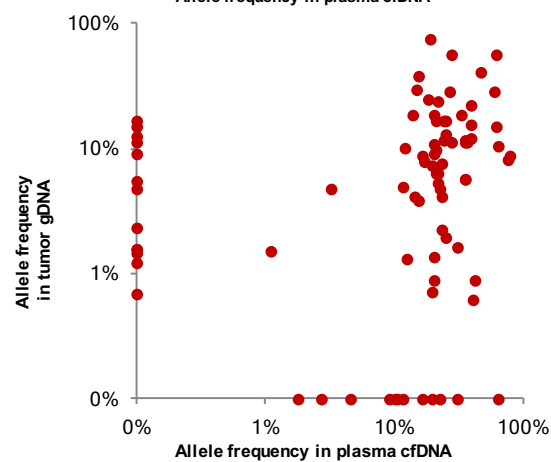
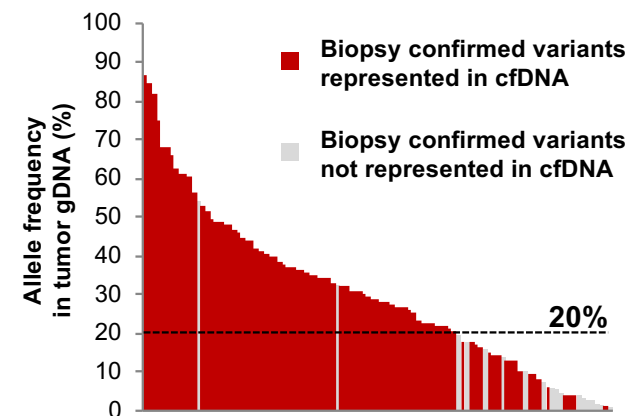
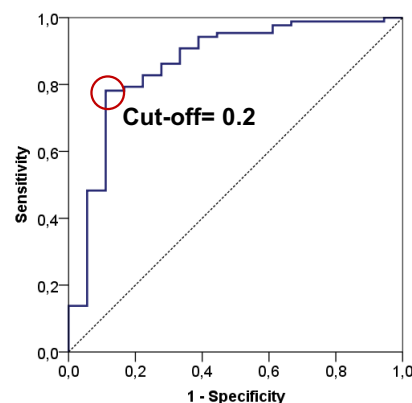
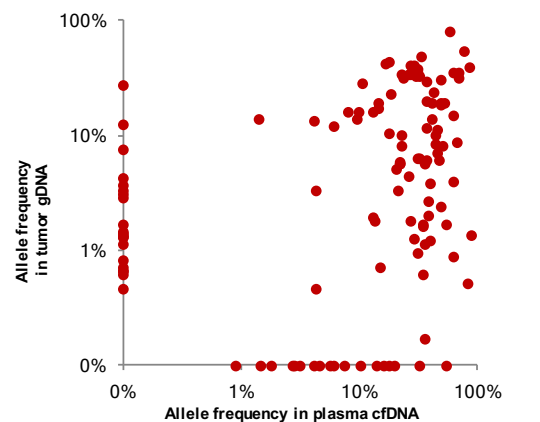
**Validation cohort**



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

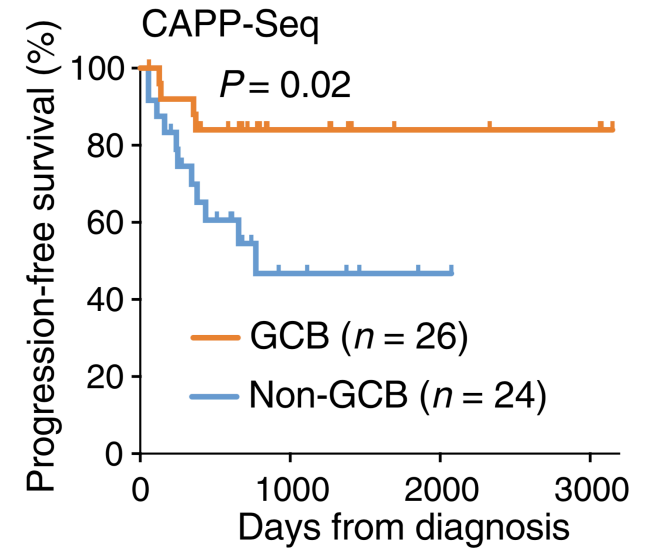
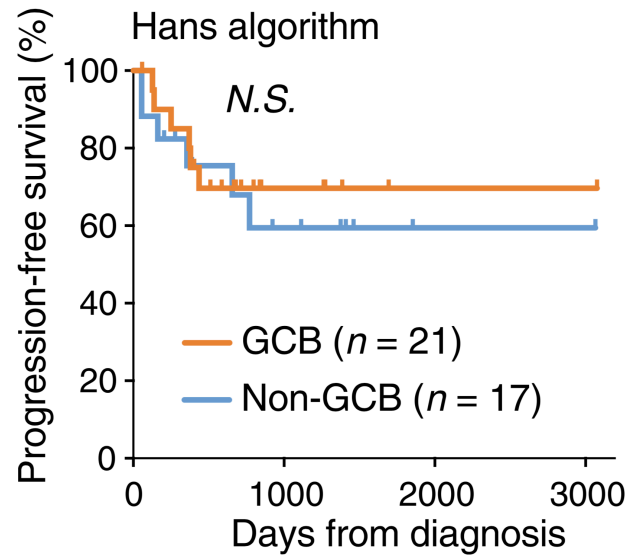
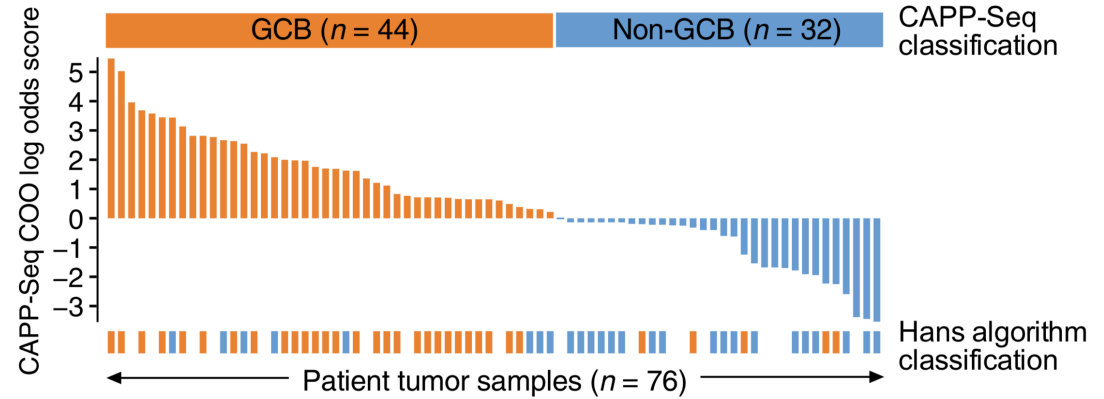
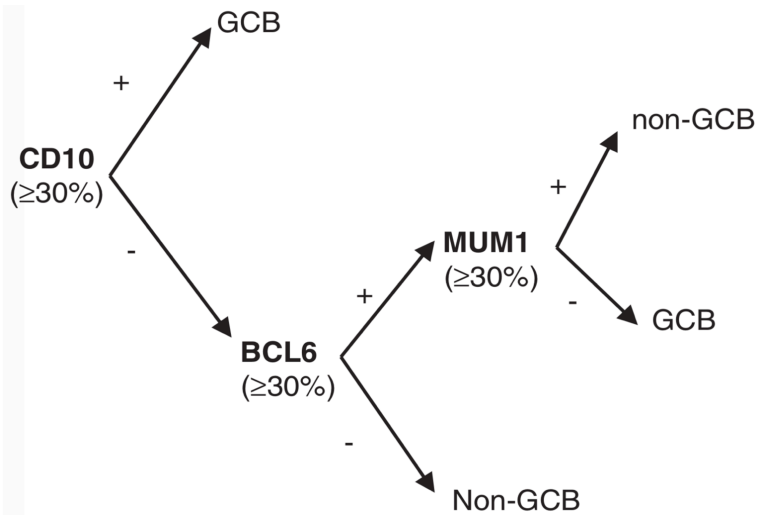


# cfDNA genotyping has an optimal sensitivity for mutations represented in >20% of the tumor alleles





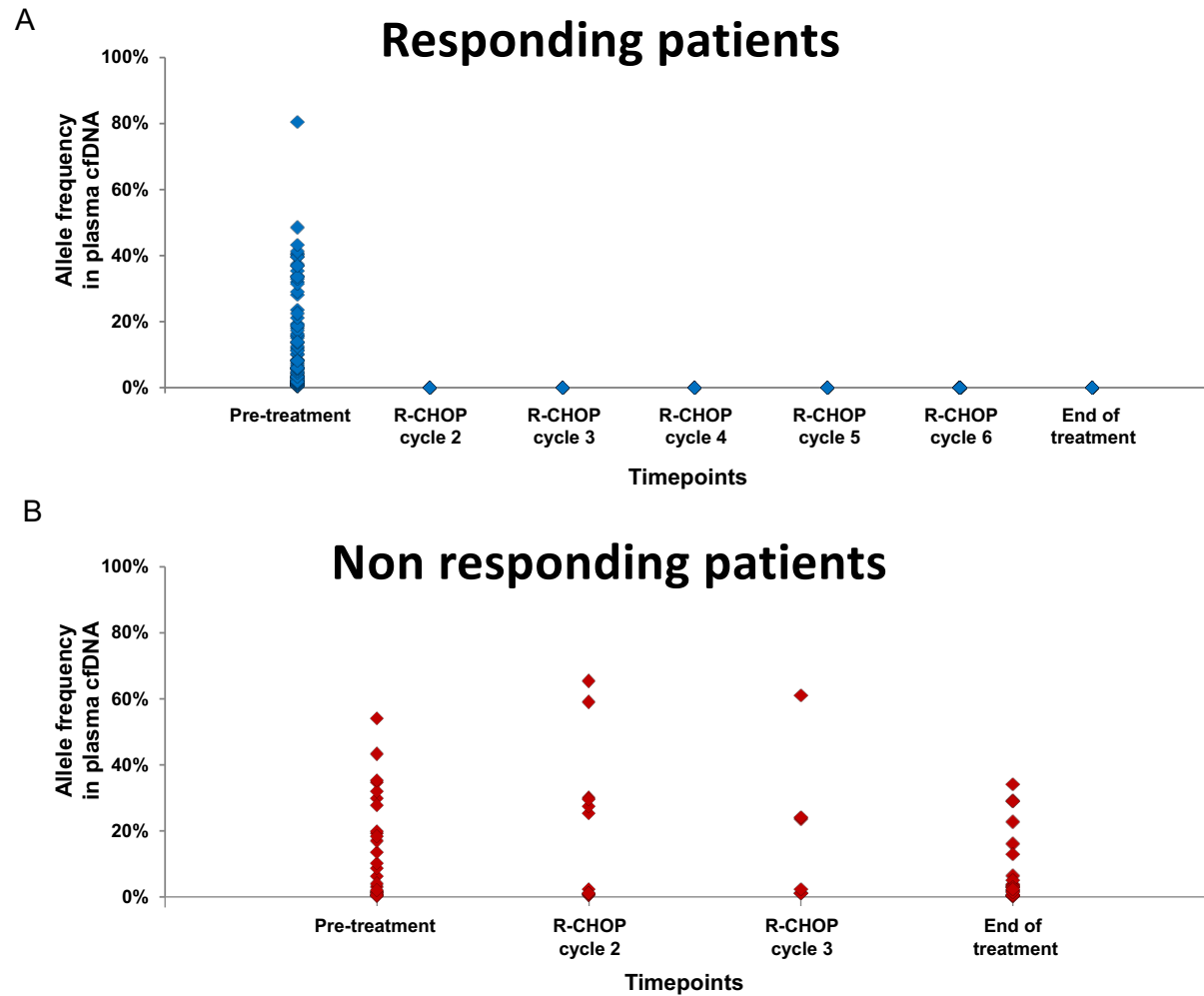
# COO classification with cfDNA



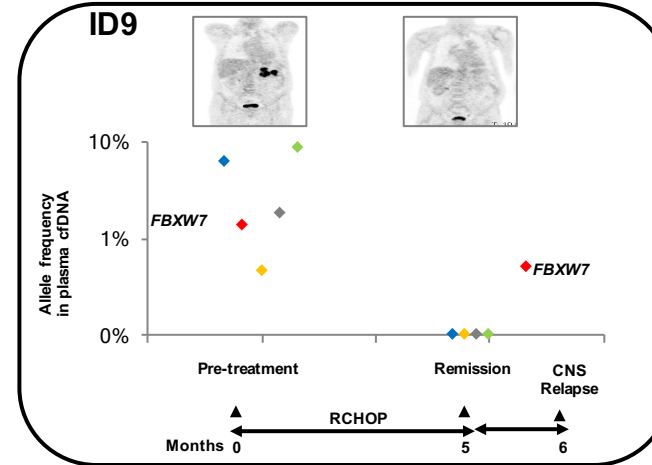
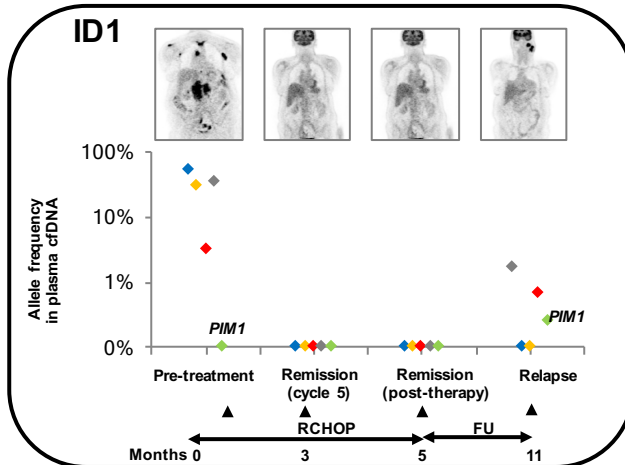
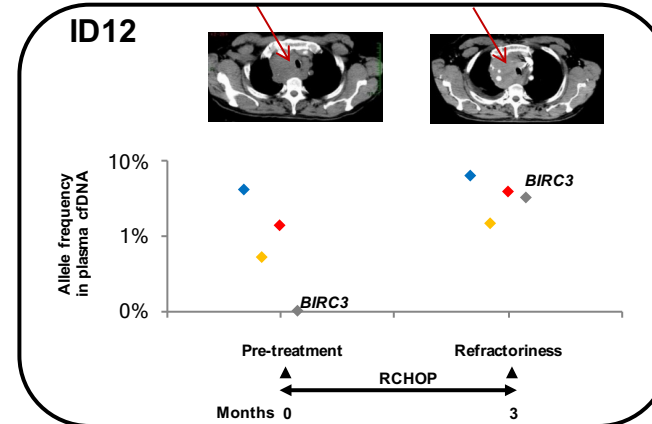
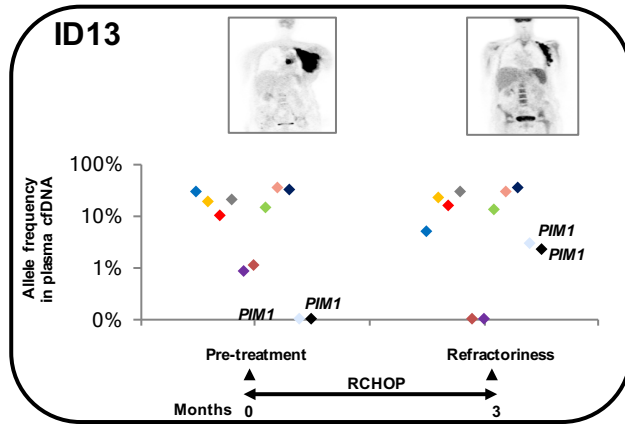
Hans C et al., *Blood*, 2004; Scherer F et al., *Sci. Transl. Med* 2016

- Genotyping
- **Clonal evolution**
- Outcome prediction and MRD monitoring

# Mutations are cleared from plasma cfDNA in responding DLBCL patients but not in refractory patients treated with R-CHOP

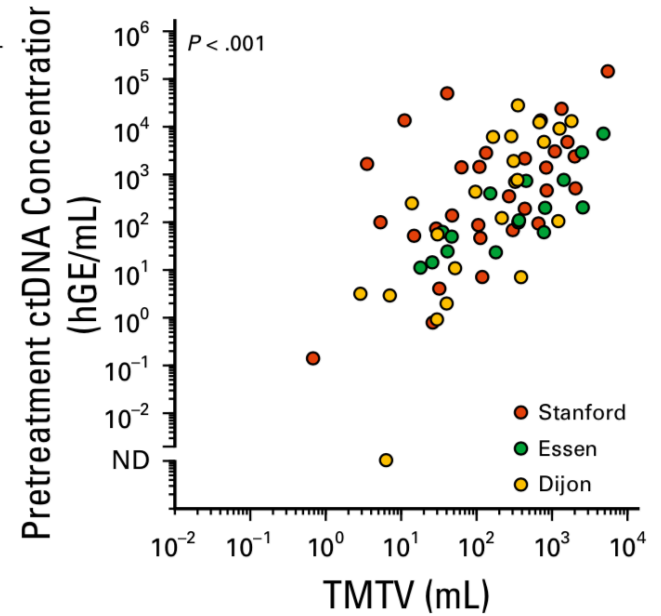
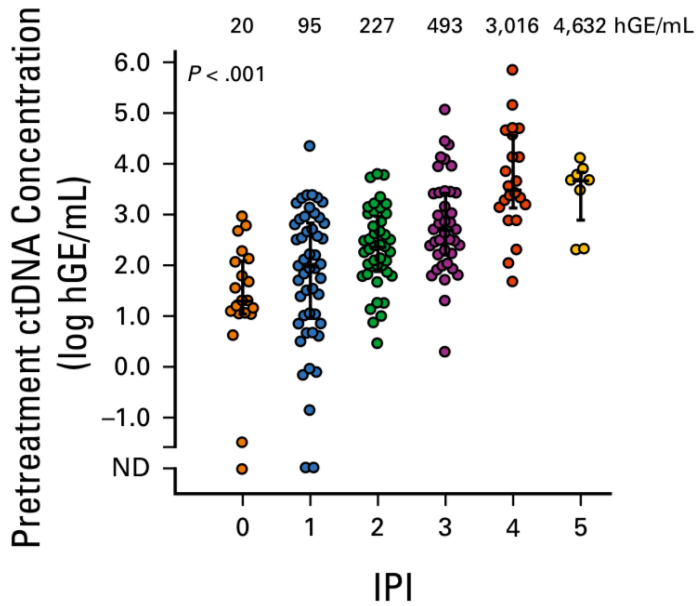
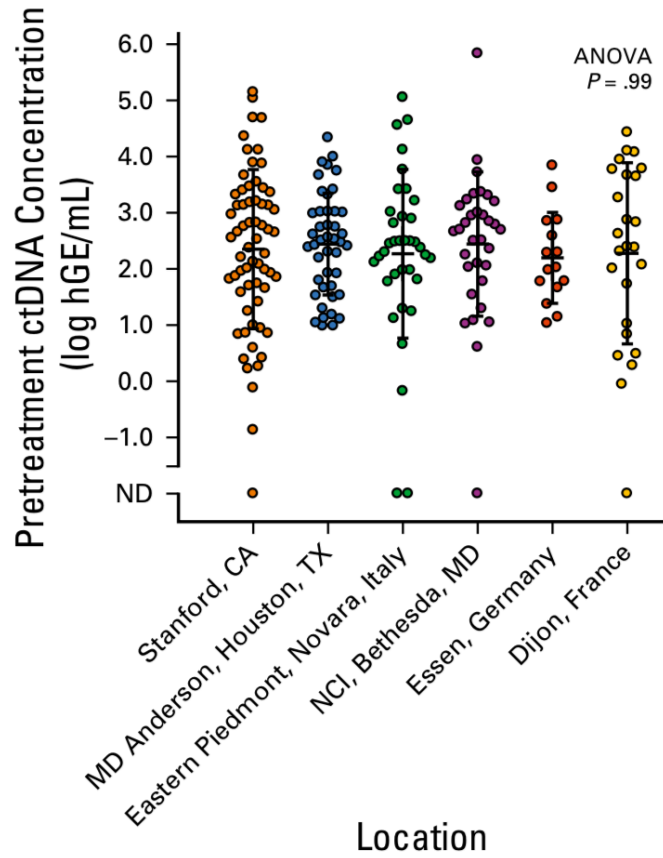


# Longitudinal cfDNA genotyping allows real-time monitoring of clonal evolution of DLBCL

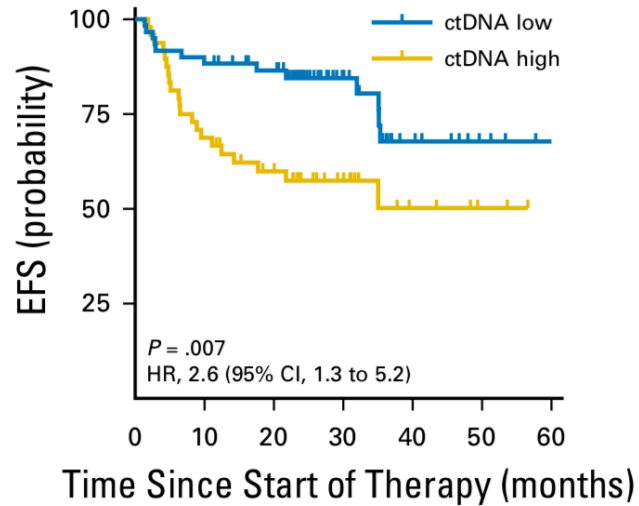
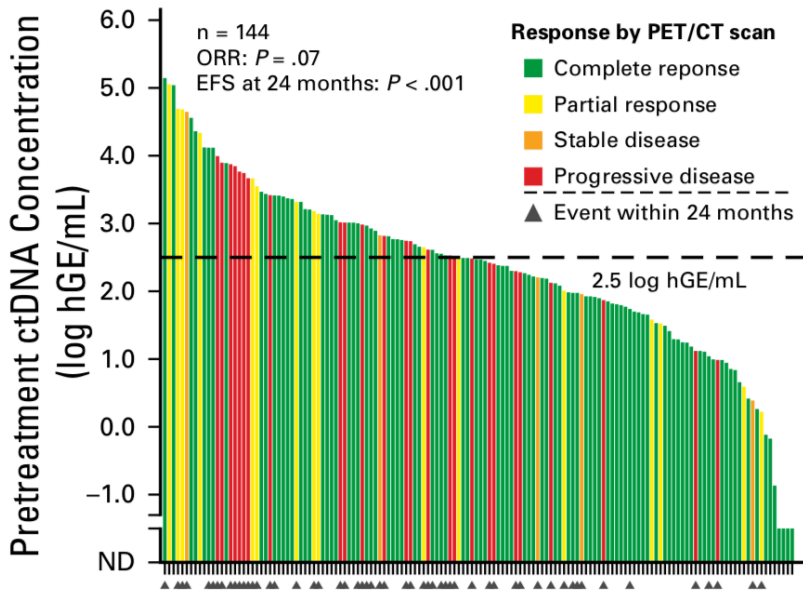


- Genotyping
- Clonal evolution
- **Outcome prediction and MRD monitoring**

# Correlation of ctDNA with IPI and Total Metabolic Tumor Volume (TMTV) in DLBCL

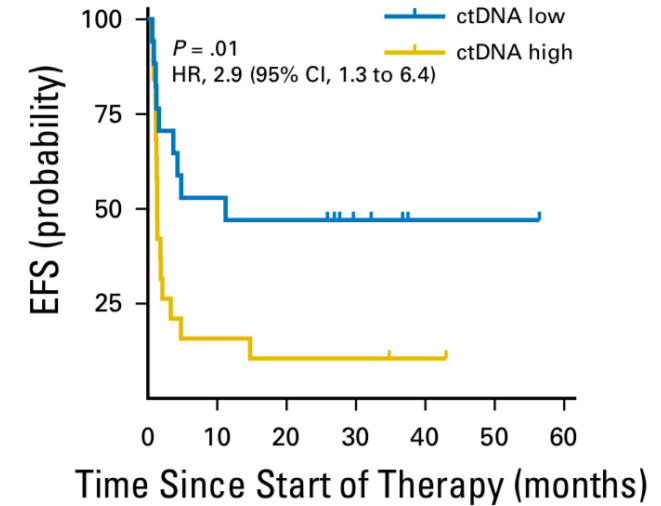


# Pretreatment ctDNA is a robust biomarker in DLBCL



No. at risk:

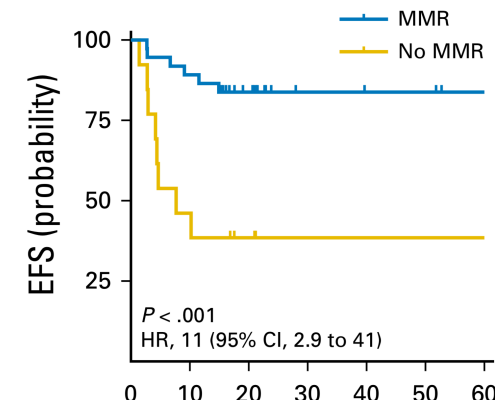
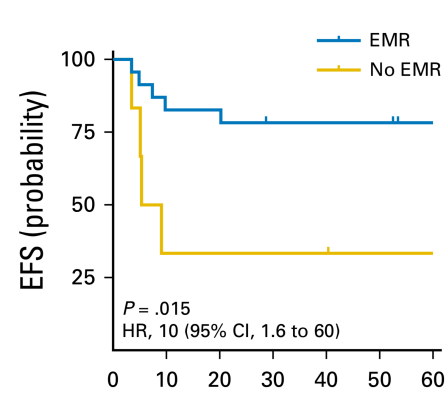
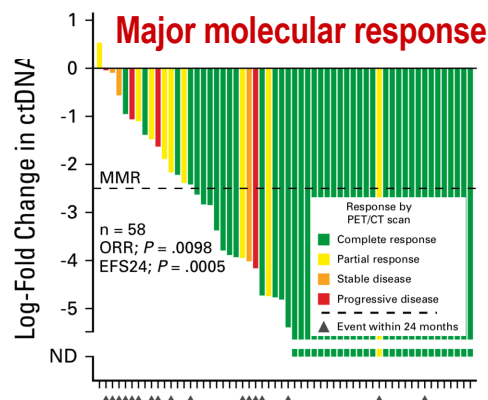
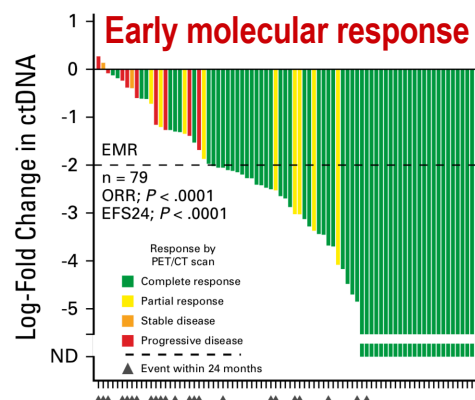
ctDNA low	60	53	47	23	10	4	1
ctDNA high	48	33	25	13	5	2	0



No. at risk:

ctDNA low	17	9	8	4	1	1	0
ctDNA high	19	3	2	2	1	0	0

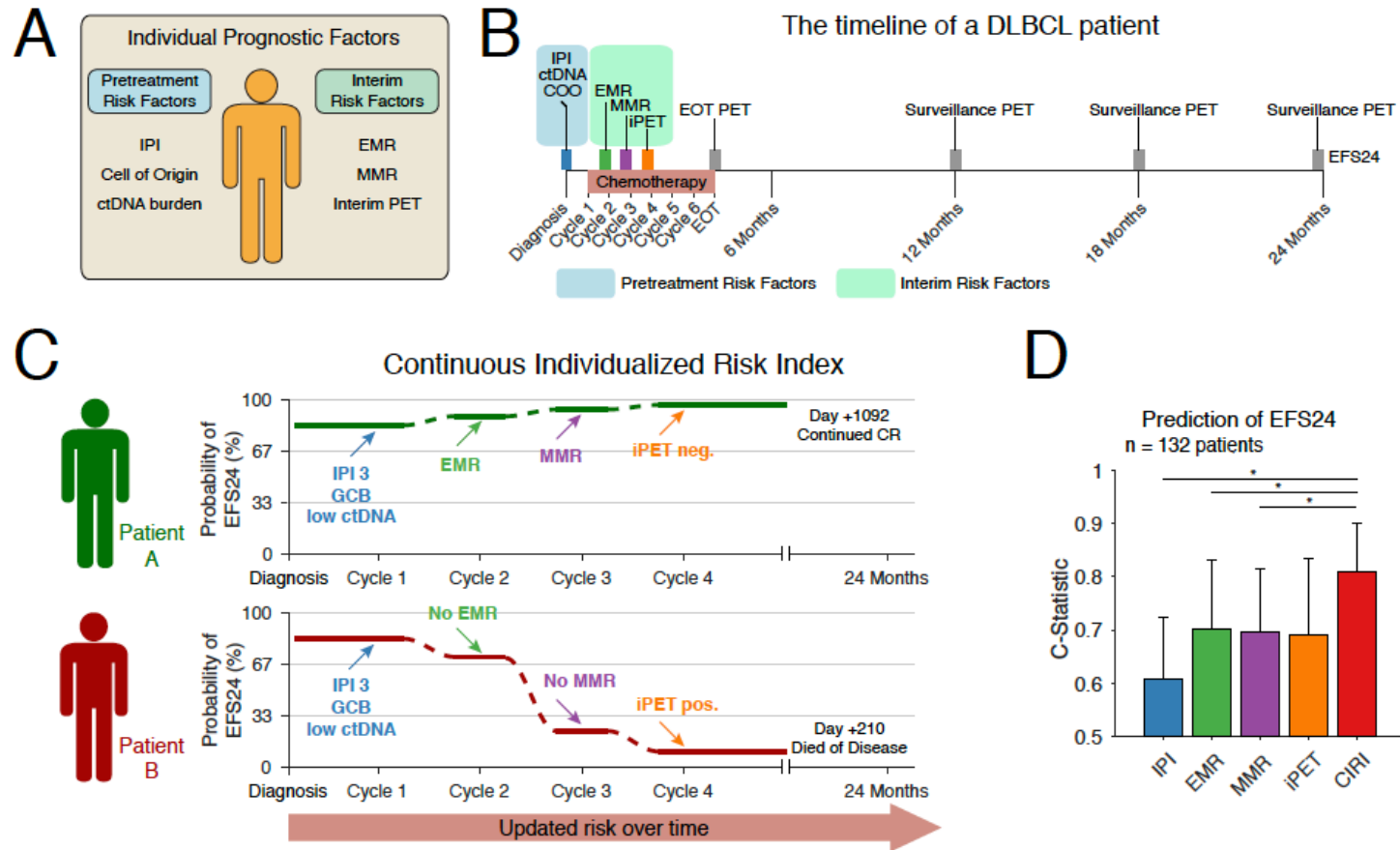
# ctDNA monitoring during therapy predict outcomes in DLBCL



Parameter	HR (95% CI)	<i>P</i>	HR (95% CI)	<i>P</i>
<b>EFS</b>				
IPI (0 to 5)	1.21 (0.87 to 1.69)	.25	0.93 (0.63 to 1.37)	.71
Pretreatment ctDNA (low v high)	2.77 (1.08 to 7.13)	.034*	2.97 (0.92 to 9.62)	.070
Molecular response†	5.93 (2.52 to 13.95)	< .001*	8.58 (3.3 to 22.32)	< .001*
Interim PET (positive v negative)	3.74 (1.46 to 9.57)	.006*	3.45 (1.27 to 9.34)	.015*
<b>OS</b>				
IPI (0 to 5)	1.36 (0.82 to 2.23)	.23	1.14 (0.63 to 2.25)	.670
Pretreatment ctDNA (low v high)	3.12 (0.65 to 15.05)	.16	1.13 (0.16 to 8.21)	.899
Molecular response†	5.27 (1.41 to 19.78)	.014*	4.15 (1.17 to 15.57)	.029*
Interim PET (positive v negative)	22.35 (2.83 to 2868)	< .001*	16.87 (1.96 to 2214)	.005*

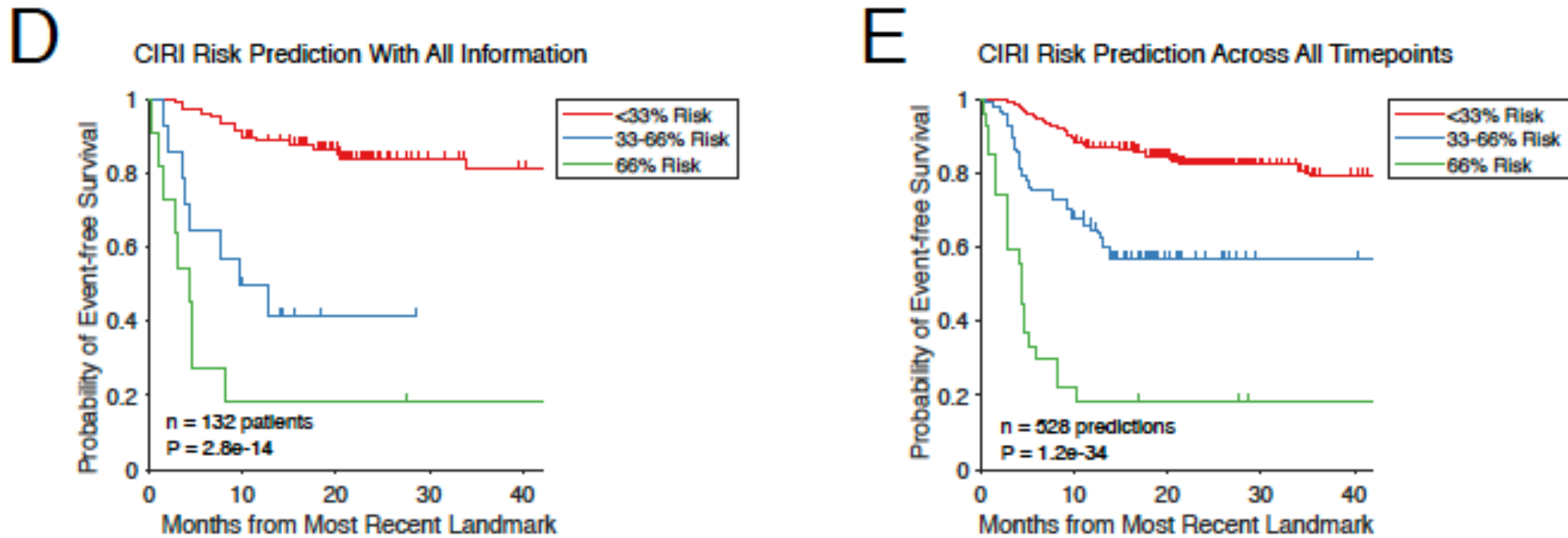


# CIRI integrated model in DLBCL



Kurtz et al, Cell 2019

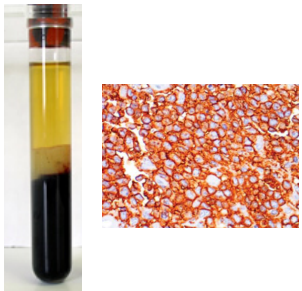
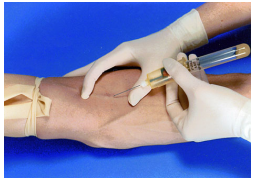
# CIRI integrated model in DLBCL



*Kurtz et al, Cell 2019*

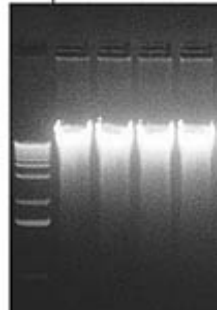
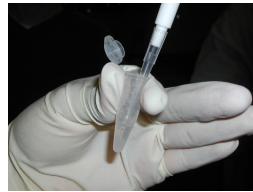
# LymphoSIGHT™ platform

1) Collect 10cc peripheral blood



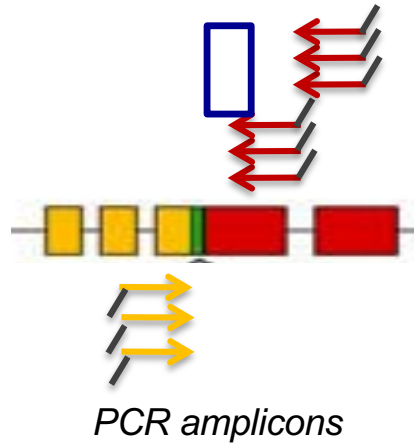
*Serum or FFPE biopsy*

2) Extract DNA



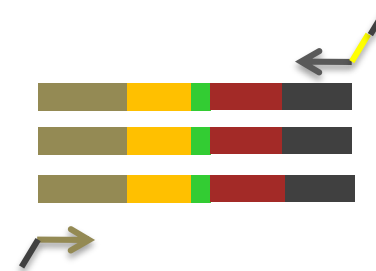
*Genomic DNA*

3) Amplify VDJ with multiplex PCR



*PCR amplicons*

4) Prepare for sequencing with common PCR



*Sequencing library*

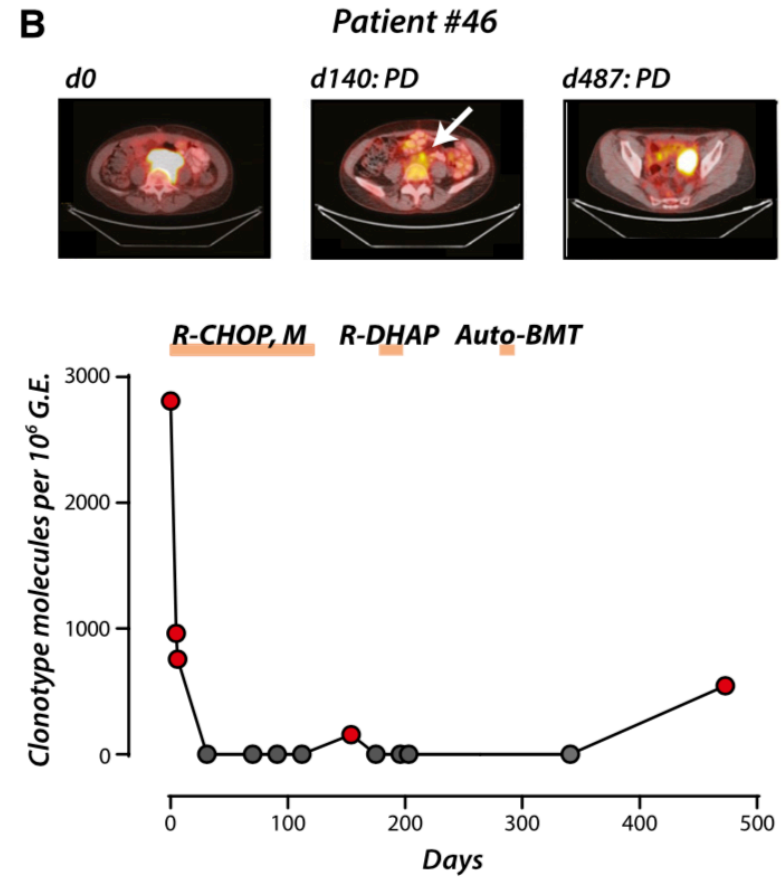
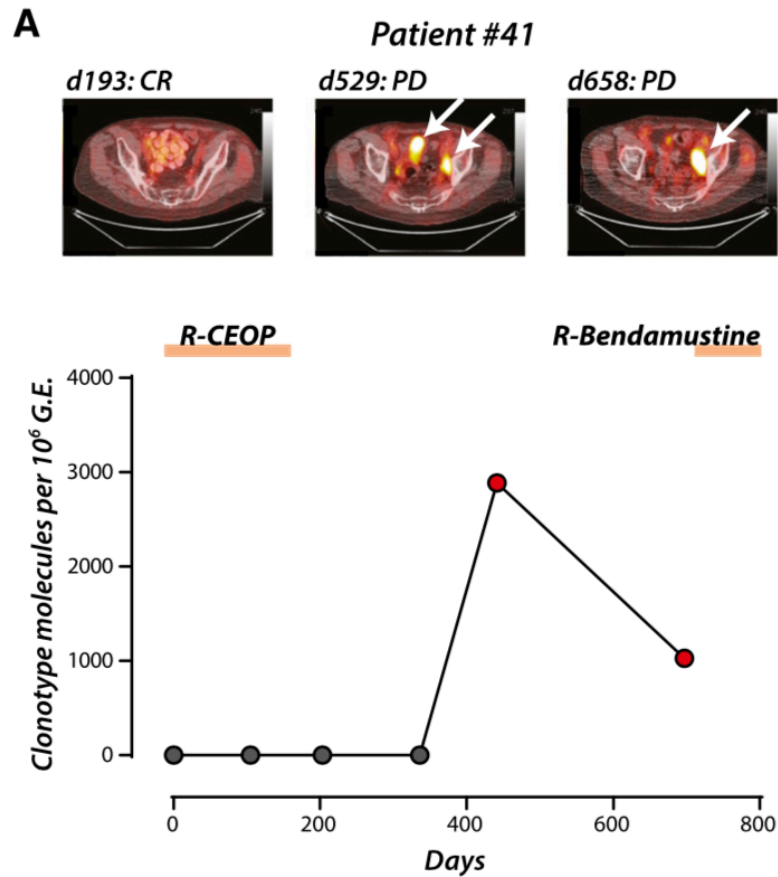
5) Sequence ~1M 100bp reads



```
CTGGCCCCAGTAGTCATACCAACTAGCG  
TTGGCCCCAGAAATCAAGACCATCTAAA  
ACGGCCCCAGAGATCGAAGTACCAGTGT  
TTGGCCCCAGACGTCATATTGTAGTAG  
CTGGCCCCAGAAGTCAGACCGGCTAACA
```

*Sequence data*

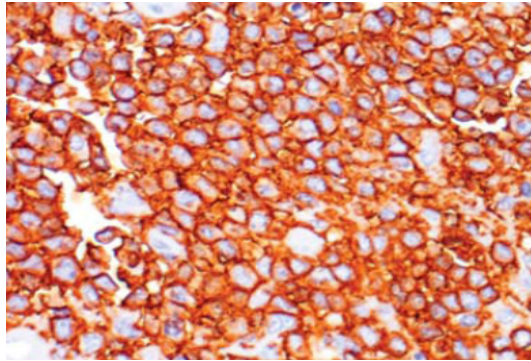
# Noninvasive monitoring of DLBCL by immunoglobulin high-throughput sequencing



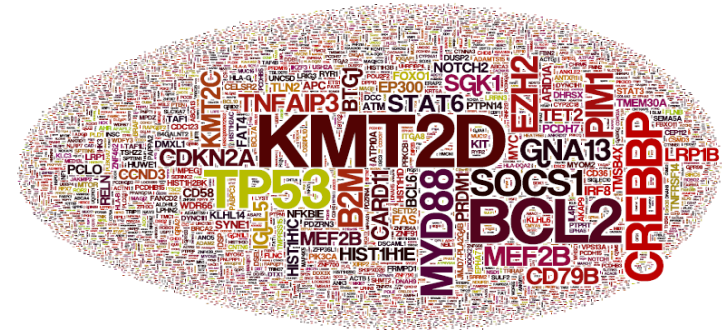
# Diffuse large B-cell lymphoma vs Hodgkin lymphoma

Tumor cells are enriched in the mass

**DLBCL**

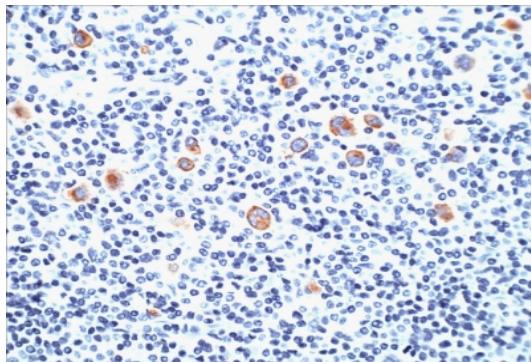


Exome sequencing data from >1000 cases



Tumor cells are rare in the mass

**CHL**

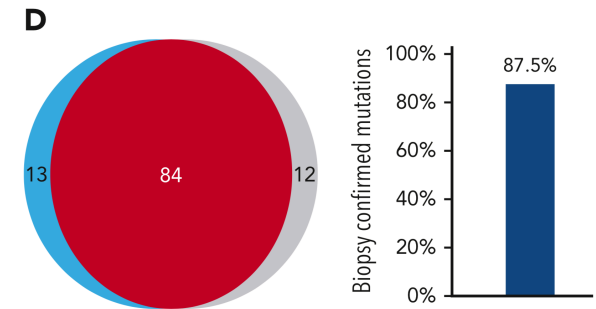
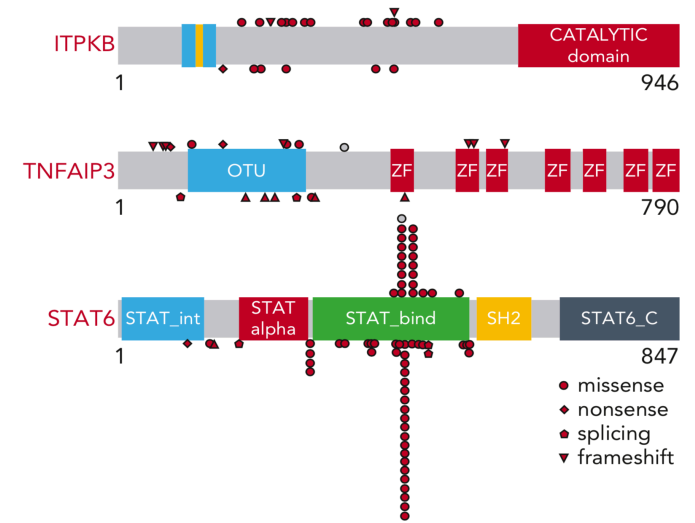
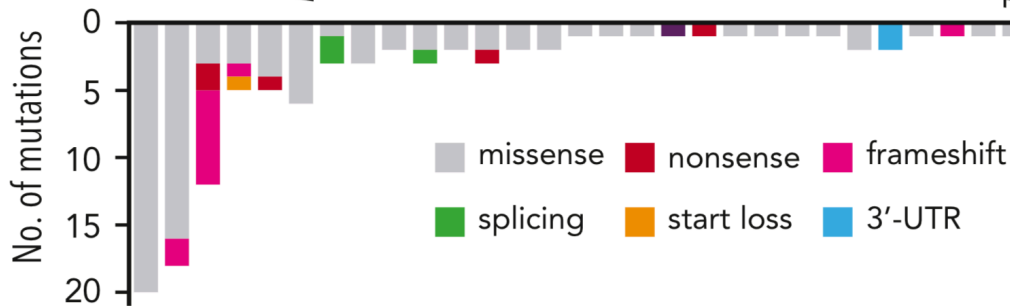
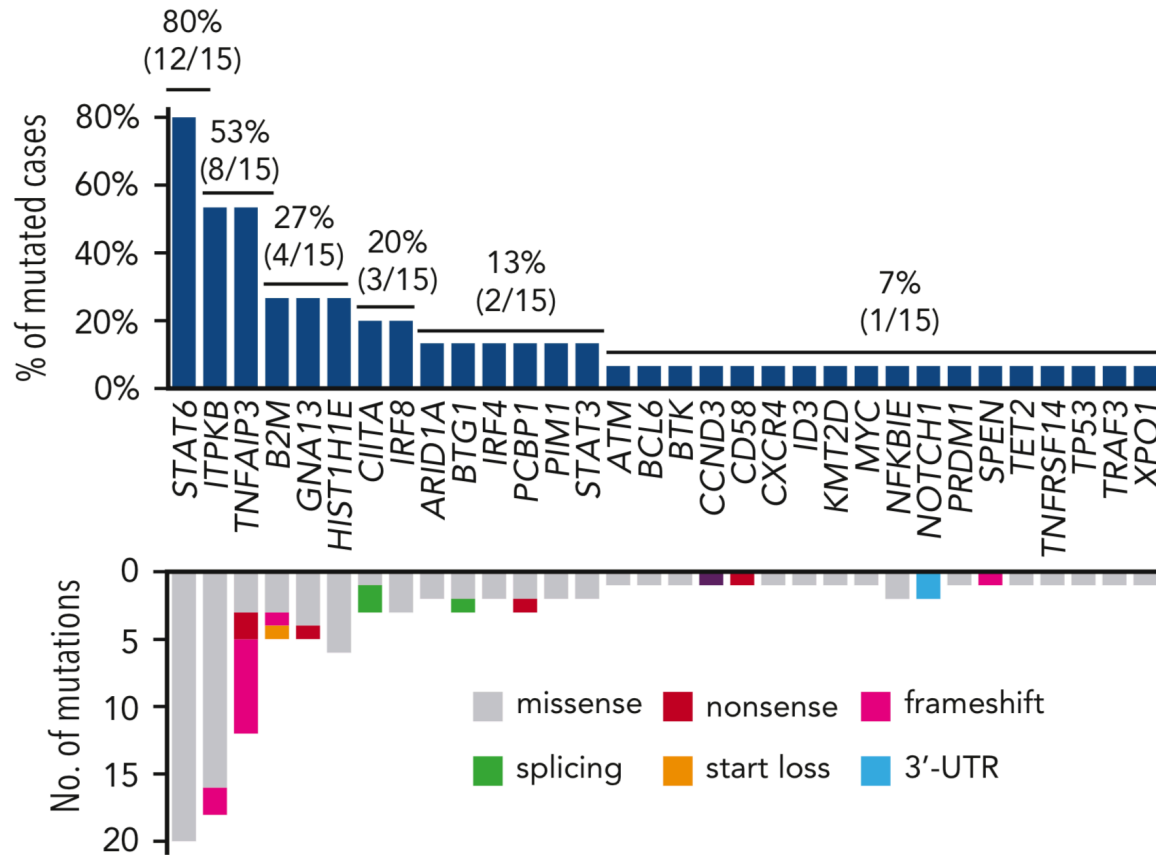


Exome sequencing data from only 10 cases



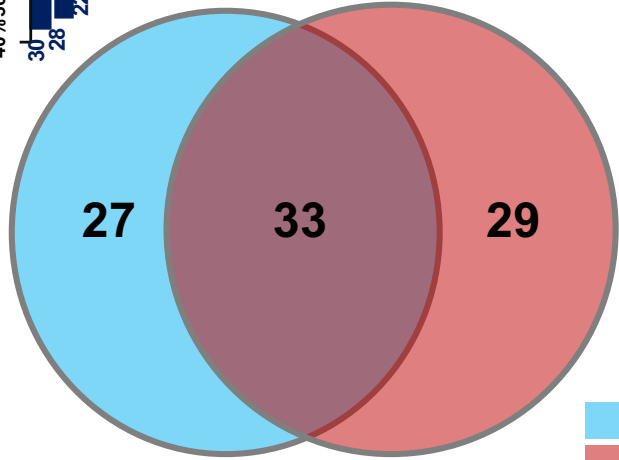
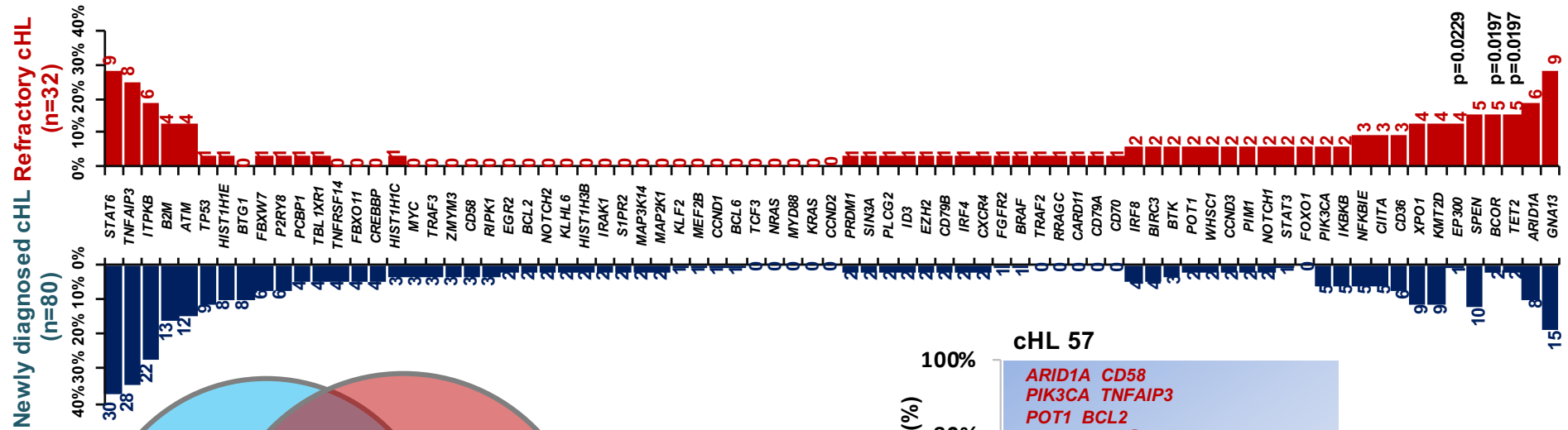
- Genotyping
- Clonal evolution
- Outcome prediction and MRD monitoring

# The liquid biopsy mirrors the genetics of cHL

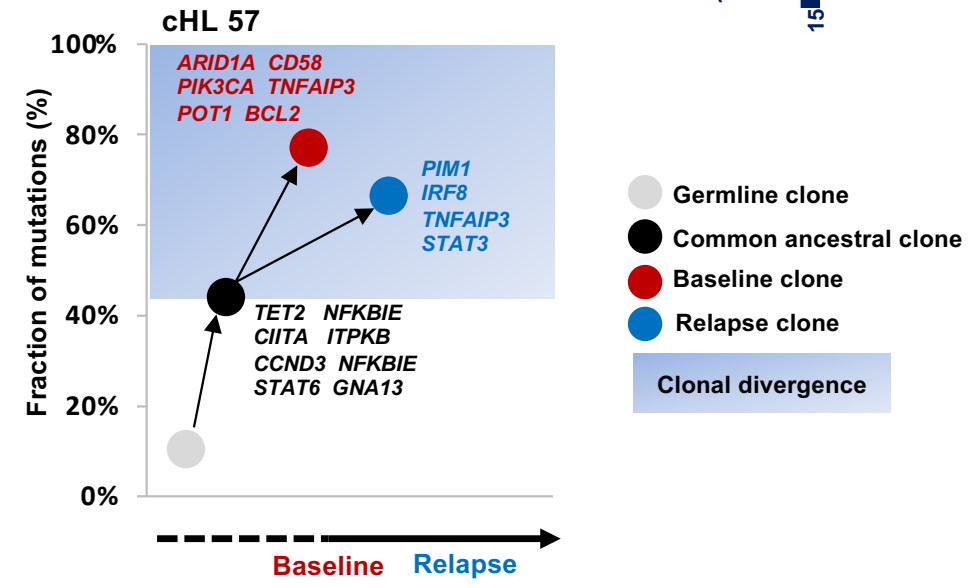


- Mutation identified both in gDNA and in ctDNA
- Mutation identified in ctDNA
- Mutation identified in gDNA

# Non invasive monitoring of clonal evolution in refractory cHL

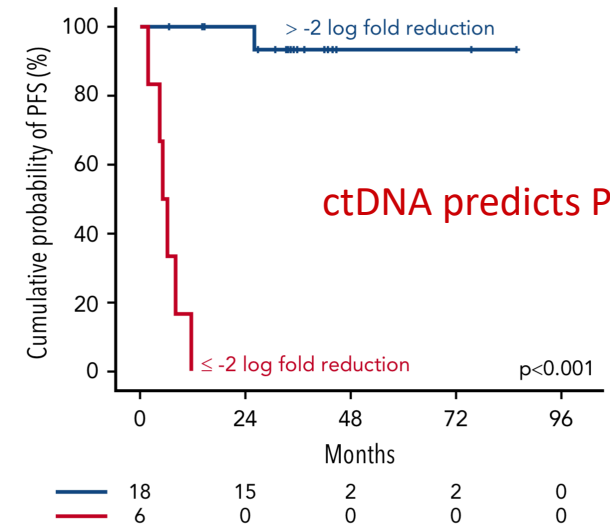
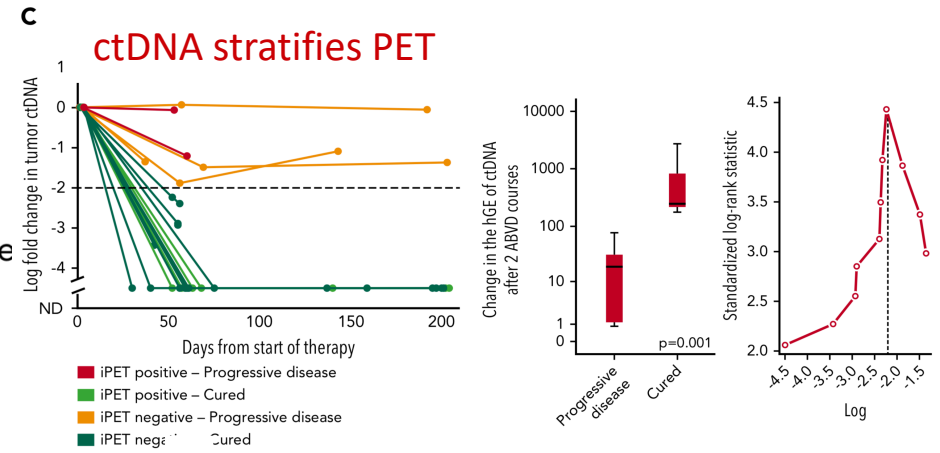
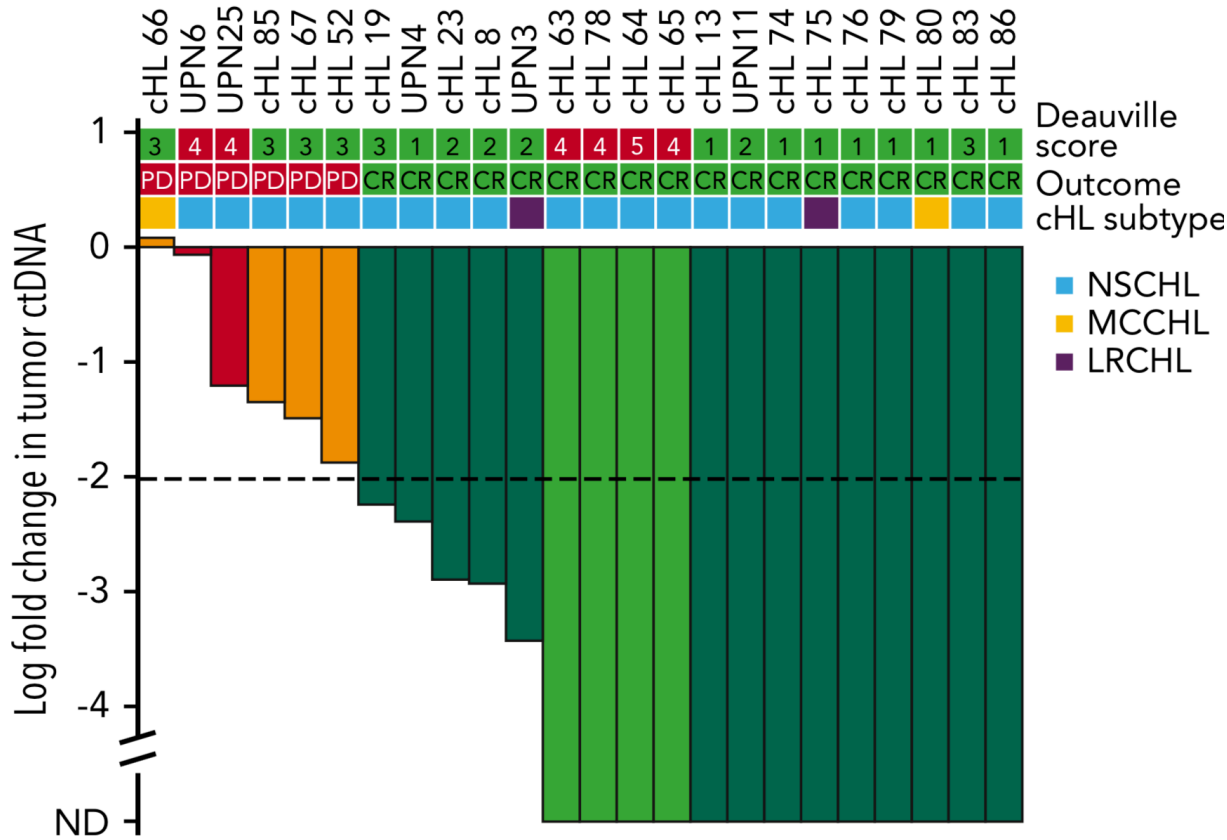


■ Tumor specific at baseline  
■ Tumor specific at relapse  
■ Shared





# Changes in tumor cfDNA complement iPET in cHL



ctDNA predicts PFS

Spina V, et al., *Blood*, 2018

# Conclusions (i): Genotyping and clonal evolution

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- ctDNA is as accurate as genotyping of the diagnostic biopsy to detect somatic mutations both in DLBCL and cHL
- ctDNA genotyping allows the identification of mutations that are otherwise absent in the tissue biopsy conceivably because restricted to clones that are anatomically distant from the biopsy site
- Liquid biopsy may provide a real-time and non-invasive approach to track clonal evolution and emergence of treatment resistant clones in lymphoma
- In the perspective of “precision medicine”, liquid biopsy may allow dynamic monitoring and targeting of DLBCL and cHL

## Conclusions (ii): Outcome prediction and MRD monitoring

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- Changes in ctDNA correlate with outcome in DLBCL treated with R-CHOP and in cHL treated with ABVD
- In cHL treated with ABVD, ctDNA MRD analysis may be useful to complement and refine the prognostic value of iPET
- A comprehensive comparison between MRD monitoring by IgH analysis and by CAPP-seq genotyping is needed



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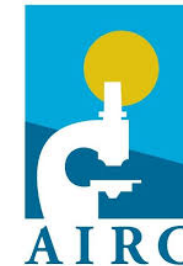


**Hematology**

**Annarosa Cuccaro**  
**Stefan Hohaus**

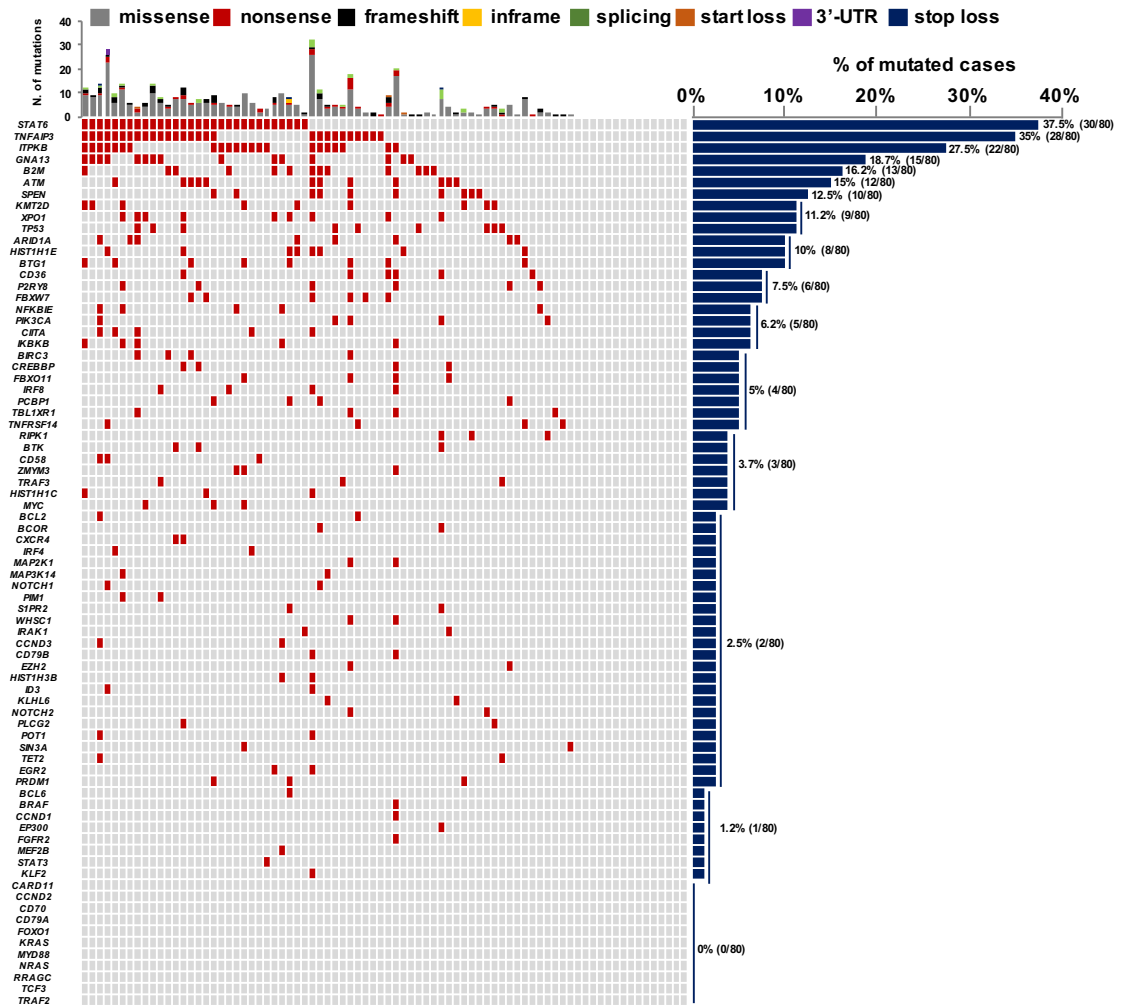
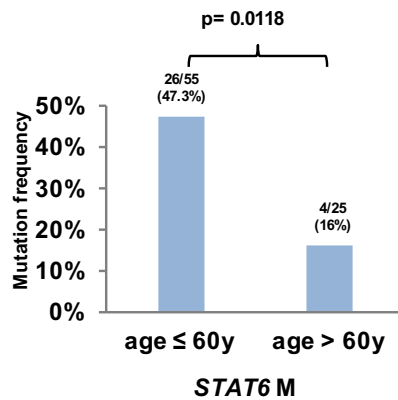
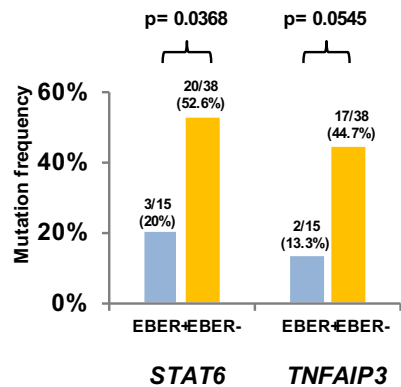
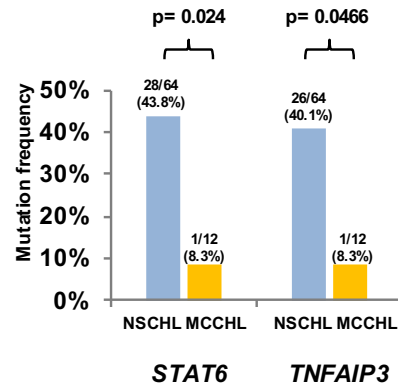
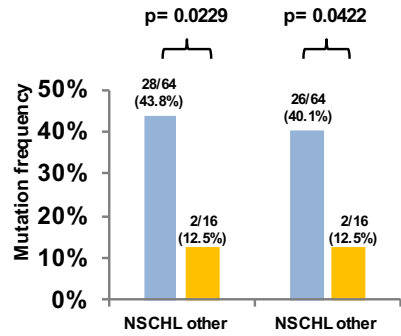
**Pathology**

**Maurizio Martini**  
**Luigi Larocca**



**5x1000**  
**x AIRC = RICERCA**

# Mutational landscape of newly diagnosed cHL



# “One size fits all” versus Precision Medicine

