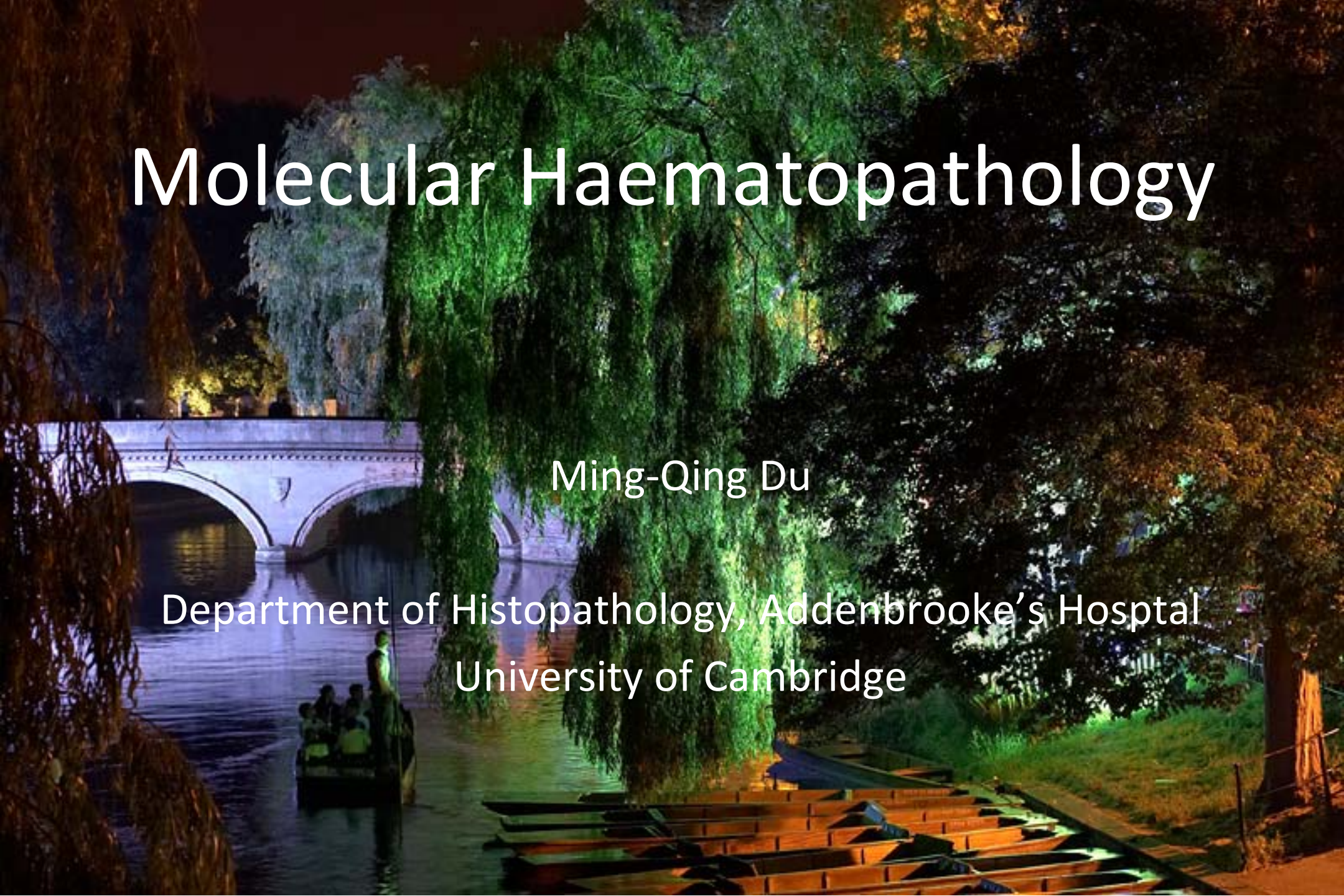


Molecular Haematopathology

A night photograph of a river scene. In the background, a stone bridge with multiple arches spans the river. A large, illuminated weeping willow tree hangs over the water from the right bank. Several small wooden boats are moored along the right bank in the foreground. The scene is lit with warm, golden light, likely from street lamps or bridge lights, creating a serene atmosphere.

Ming-Qing Du

Department of Histopathology, Addenbrooke's Hospital
University of Cambridge

Molecular Haematopathology: value

- o Diagnosis:

- Benign vs malignant
- Disease monitoring
- Sub-classification

- o Prognosis

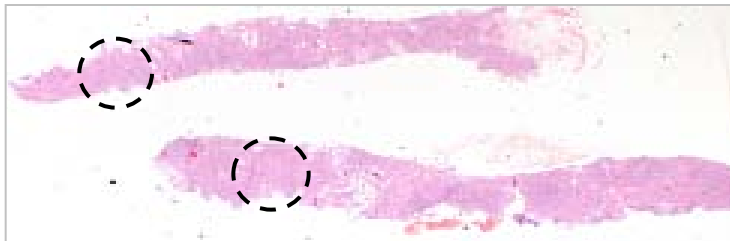
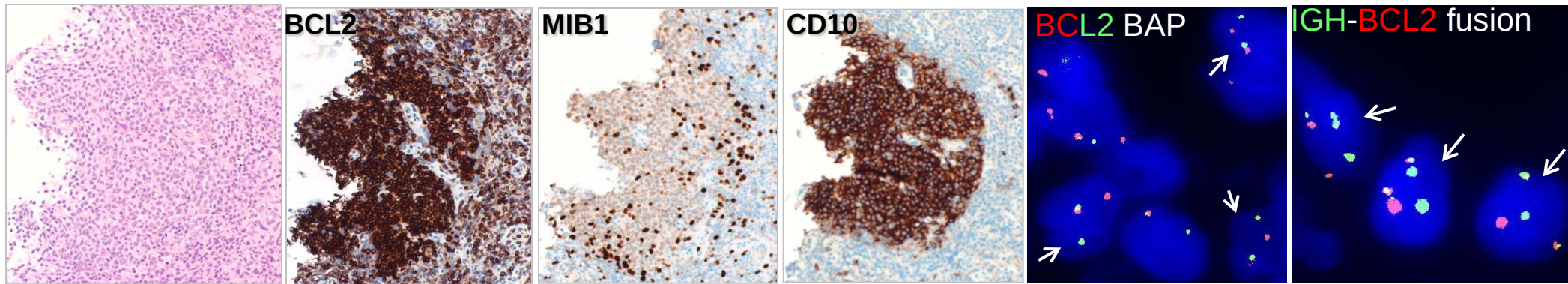
- o Treatment stratification

Molecular Haematopathology: **role of histopathologist**

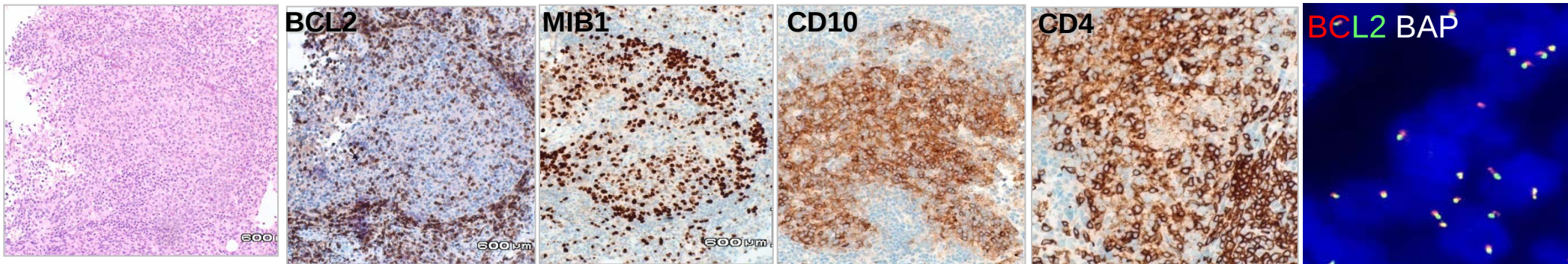
o Sample quality

- “tumour” content in remaining tissue blocks
 >10% for clonality analysis
 ? microdissection to enrich suspected cells
 preliminary histological opinion
- indicating area of lymphoma or suspected lesion
 interphase FISH & analysis of lymphoma cells

In situ follicular neoplasia



M1066,
46/female, left axillary LN core biopsy
B cell clonality analysis = polyclonal
(LN excision biopsy: a few follicles showing features of FL)



Molecular Haematopathology: **role of histopathologist**

o Appropriate molecular tests

- **clear need of molecular test**

 - suspicious, but not diagnostic lymphoma

 - cutaneous T-cell infiltrate suspected for T cell lymphoma

 - celiac disease refractory to gluten free diet

 - LPD associated with immunodeficiency

 -

- **clear impact if results informative**

 - diagnosis, classification, prognosis, treatment stratification

Molecular Haematopathology: **role of histopathologist**

Histopathologist



- o Sample quality
- o Appropriate molecular tests
- o Results interpretation in the context of clinicopathological findings
- o Integrated report

Clinical Scientist



- o Appropriate test & method
- o Test sensitivity
- o Test specificity
- o False negative
- o False positive

Molecular Haematopathology:

Diagnosis: benign vs malignant

- o B and T cell clonality
- o Somatic genetic changes

B & T cell clonality: BIOMED-2 protocol

IG gene rearrangements

locus	PCR reaction
IGH	5
IGK	2
IGL	1

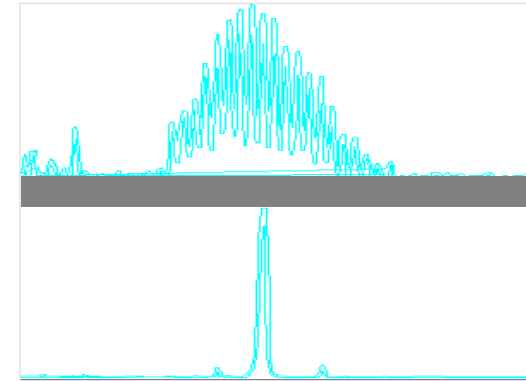
TCR gene rearrangement

locus	PCR reaction
TCRG	2
TCRB	3

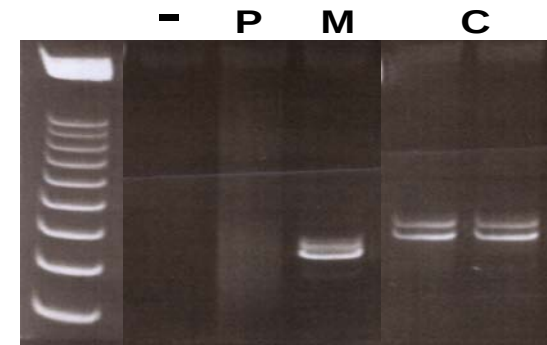
A single
PCR condition



GeneScan



Heteroduplex treatment
& PAGE



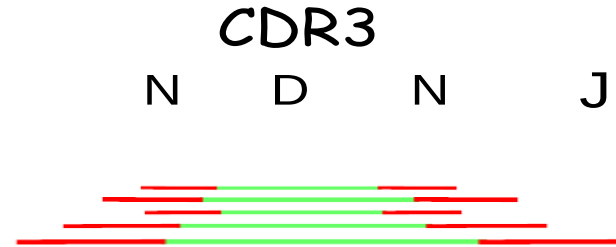
PCR Products analyses :

GeneScan or Heteroduplex analysis/PAGE?

IGH V_H-J_H

TCR β

TCR δ



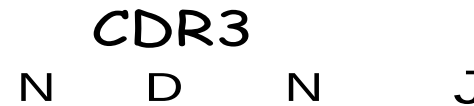
Heteroduplex & GeneScan are equally suitable, with the exception of TCR δ , which is better by heteroduplex

IGH D_H-J_H

IGK

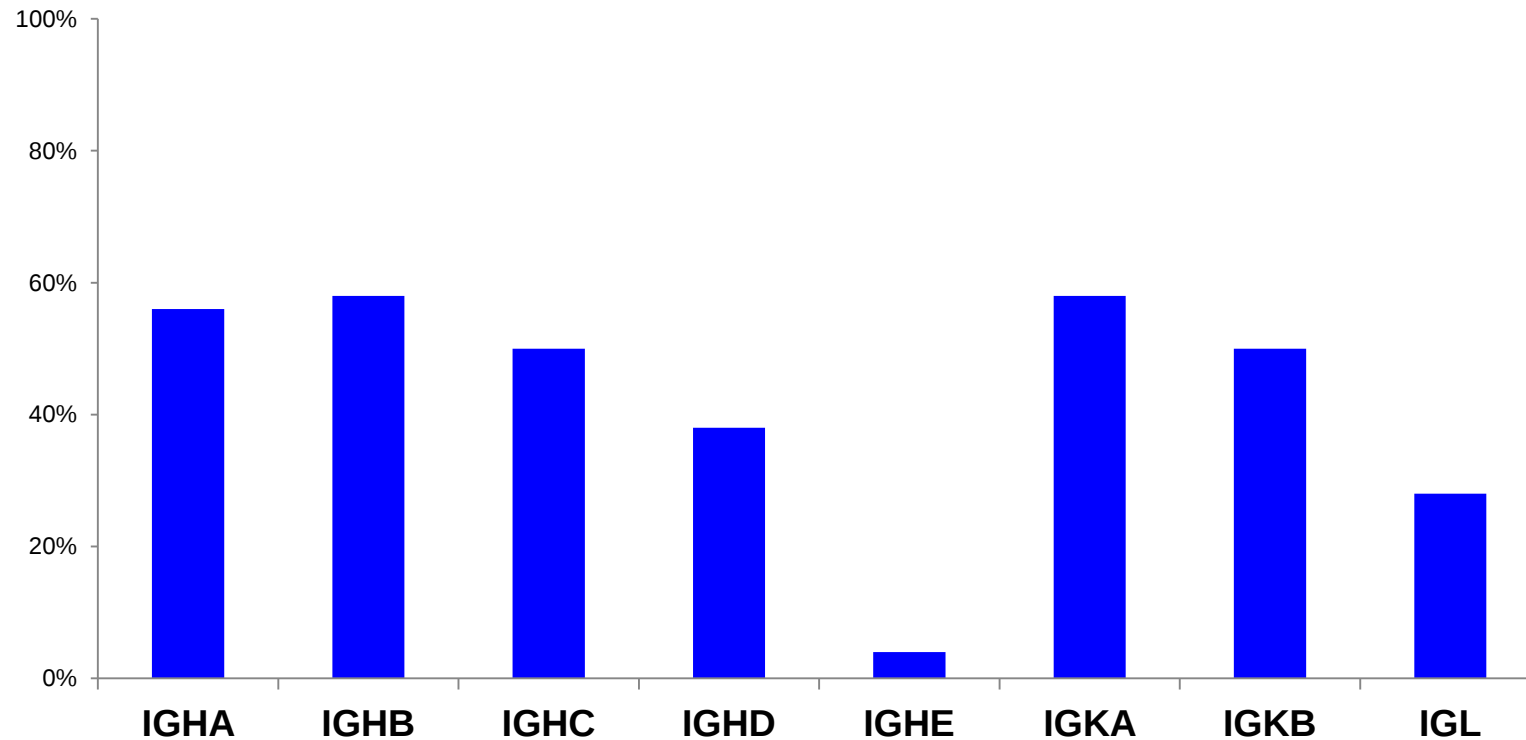
IGL

TCR γ



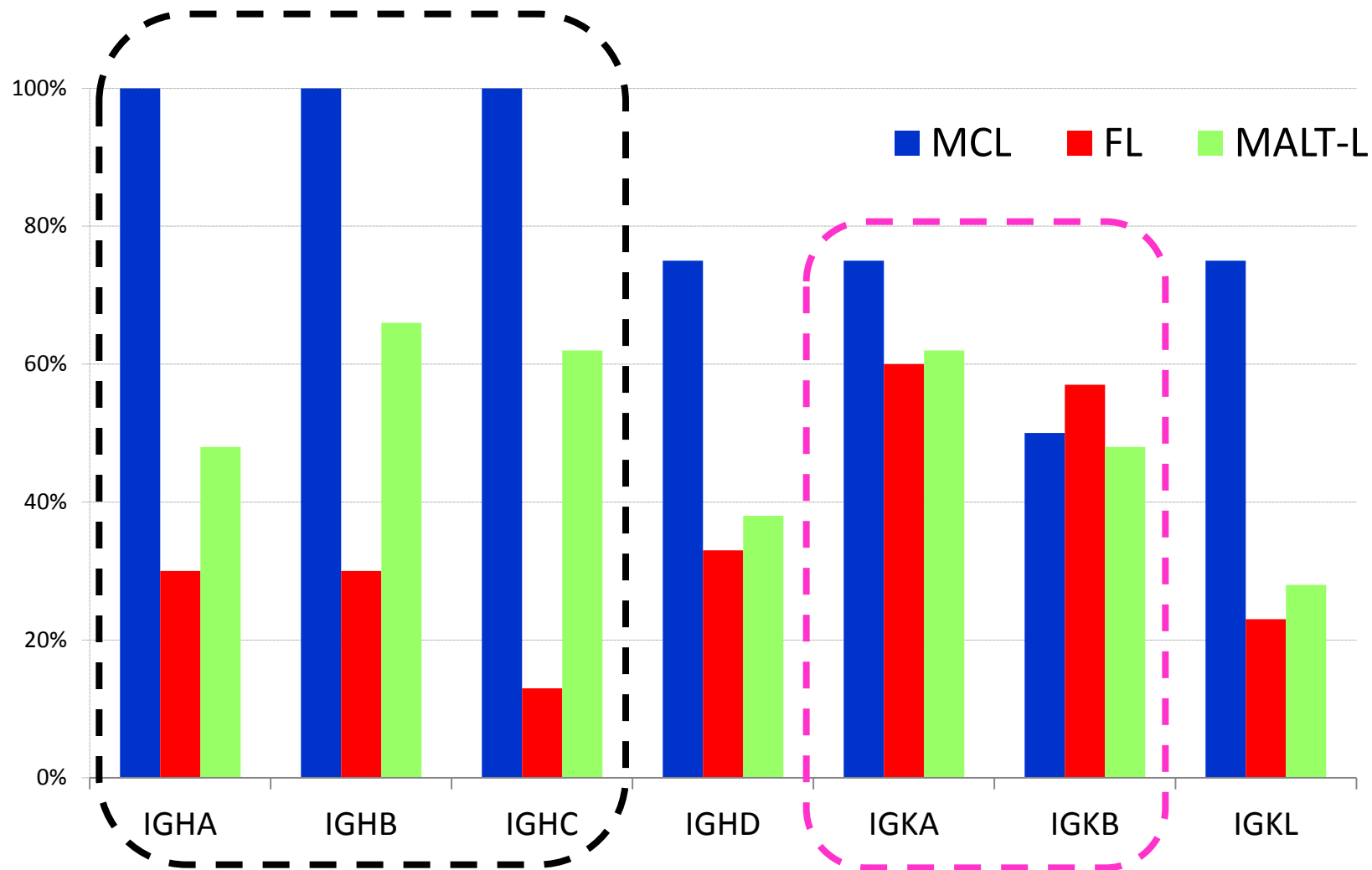
Heteroduplex better than GeneScan

BIOMED-2 B-cell clonality: efficacy depends on PCR reactions

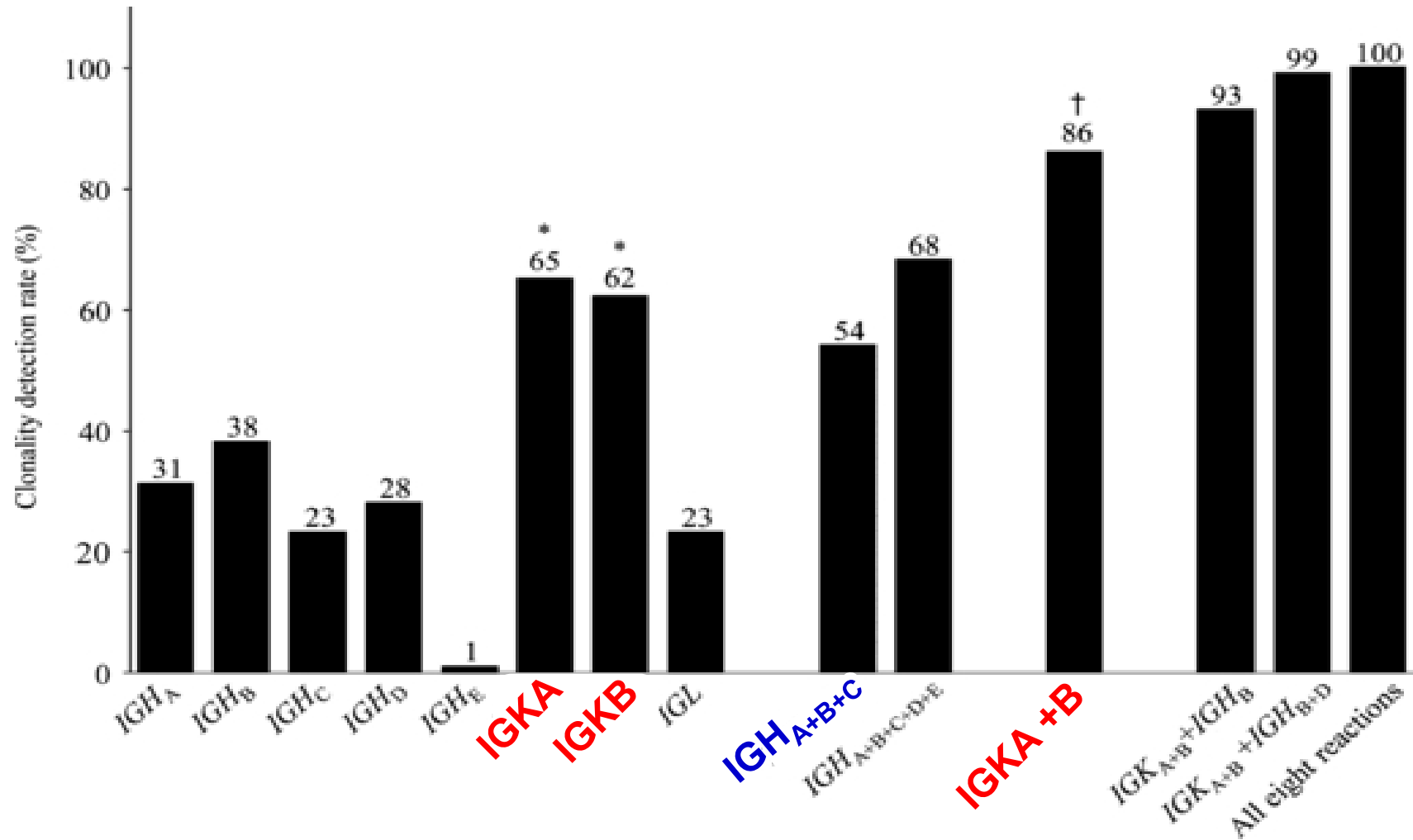


The sole use of any individual reaction is of limited value!

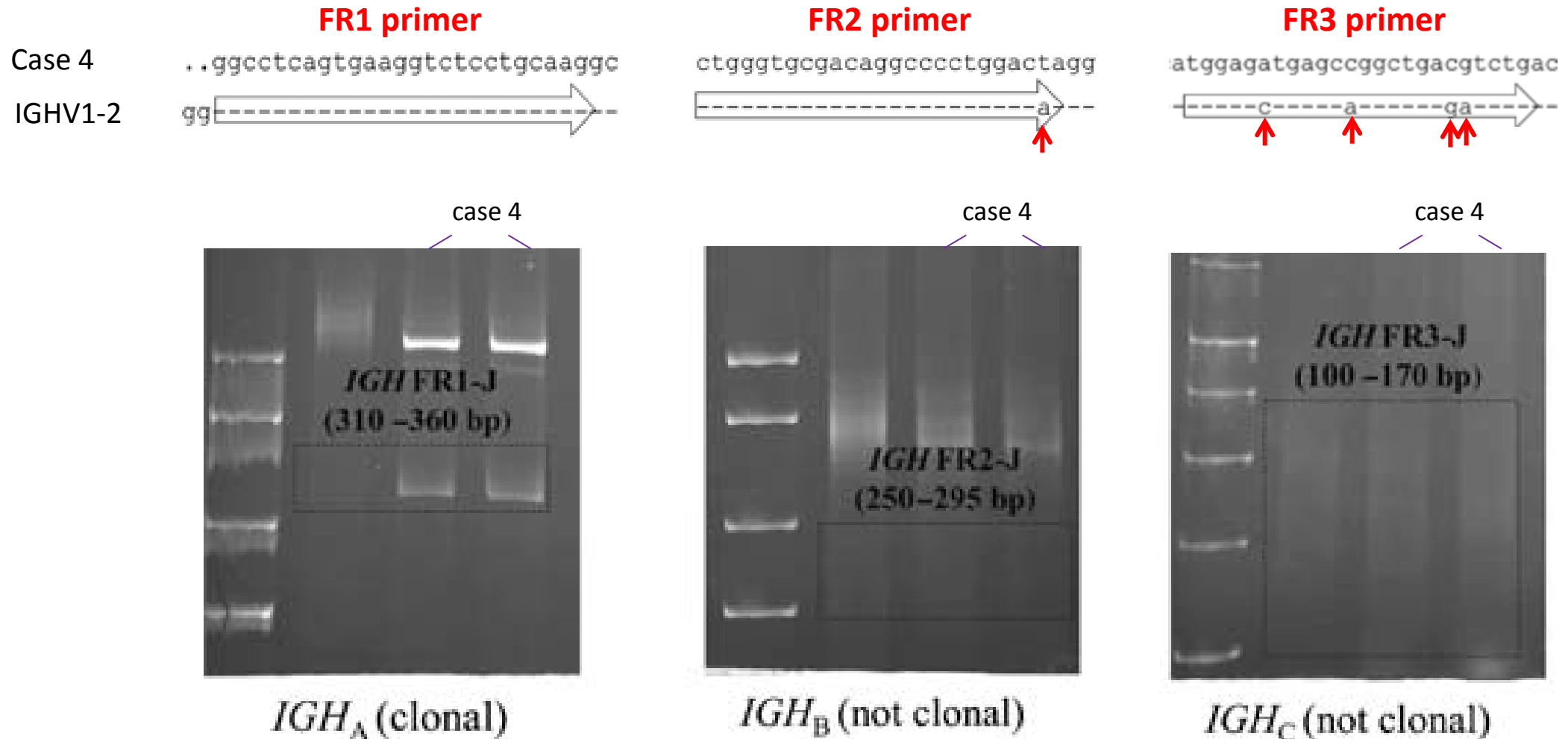
BIOMED-2 B-cell clonality: efficacy depends on lymphoma subtypes



IGK PCR essential for clonality analysis of FL



Failure of IGH PCR in FL due to mutations abolishing primer binding



BIOMED-2 B-cell clonality: strategy for routine application

PCR combination	Clonal rearrangement (%)	
	by >1 PCR	by ≥ 2 PCR
IGH _B + IGK _{A+B}	91%	58%
↓ If not clonal + IGH_{A+C+D} ↓ If not clonal + IGHL & IGH_E	99%	79%
	100%	80%

BIOMED-2 T-cell clonality: strategy for routine application

PCR combination	Clonal rearrangement (%)	
	by >1 PCR	by ≥ 2 PCR
TCRG _{A+B}	94%	30%
If not clonal ↓ + TCRB_{A+B}	98%	73%
If not clonal ↓ + TCRB_C + TCR_D	100%	82%

False negative

o Inadequate sample

- few lymphocytes
- poor DNA quality

o Technical limitations

- <10% clonal cells
- Inappropriate PCR combination
- Incomplete inclusion of all PCR tubes

o Nature of lymphoma

- Hodgkin's lymphoma
- GC and post-GC lymphoma
- NK cell lymphoma

False Positive

O Inadequate sample

- poor quality DNA
- limited lymphoid cells

O GI & skin biopsies: oligoclonal T-cells

O Technical issues

- Inadequate methods and inappropriate interpretation
- Occasional non-specific PCR product
- Cross lineage antigen receptor rearrangement

TCR gene rearrangement in B-ALL

IG gene rearrangement in T-ALL

O Reactive / inflammatory pathology:

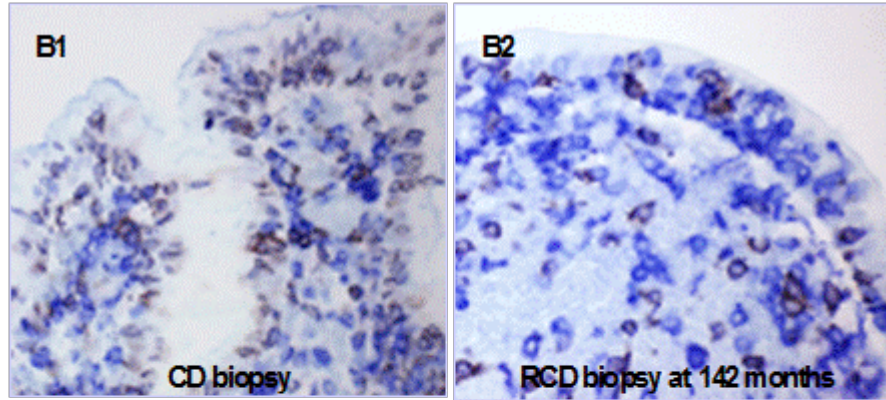
HP gastritis, EBV infection, active celiac disease, Sjogren's syndrome

Molecular Haematopathology:

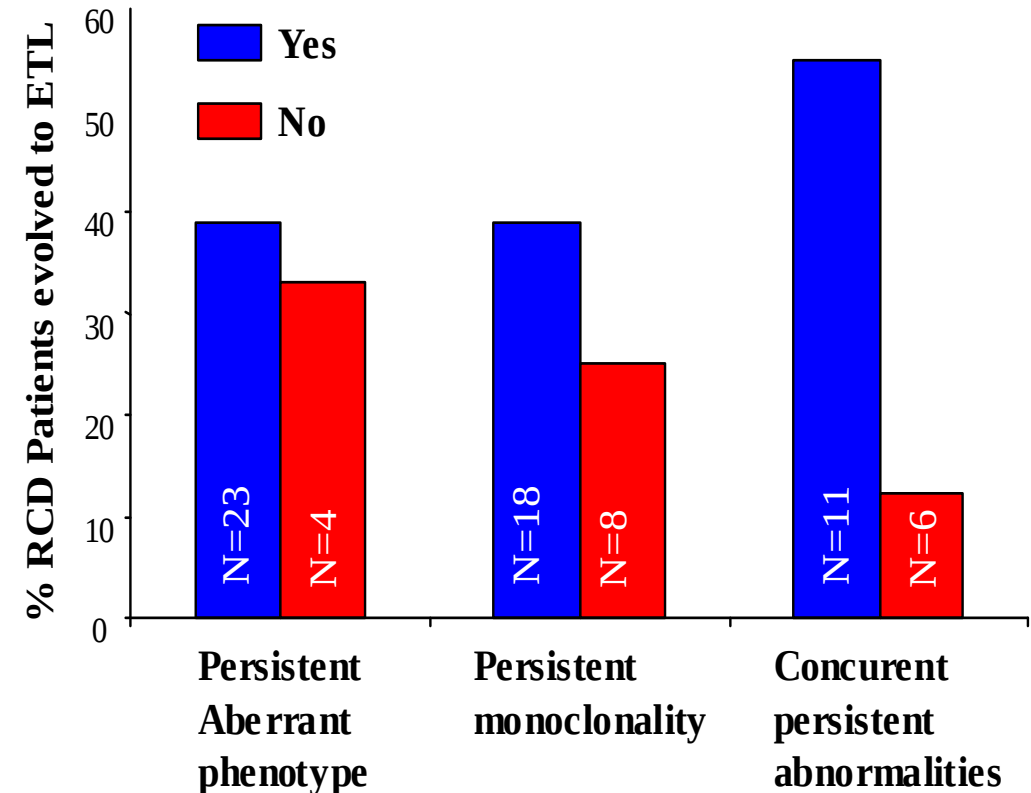
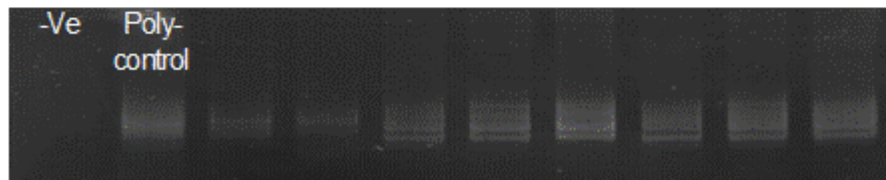
Diagnosis: disease monitoring

- o Persistent reactive lesions suspected lymphoma
 - CD-RCD-EATL sequence
 - Cutaneous T cell infiltrates
 - PTLD
 - ...
- o Clonal relationship of synchronous & metachronous lymphomas

Clonality analysis in RCD/EATL surveillance



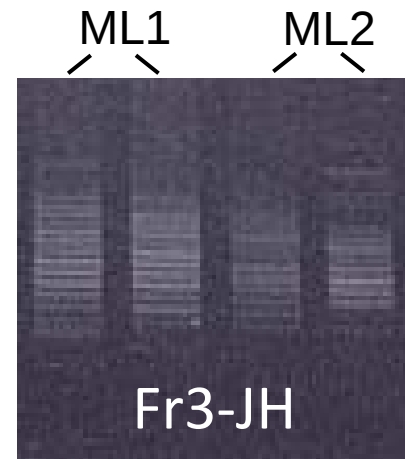
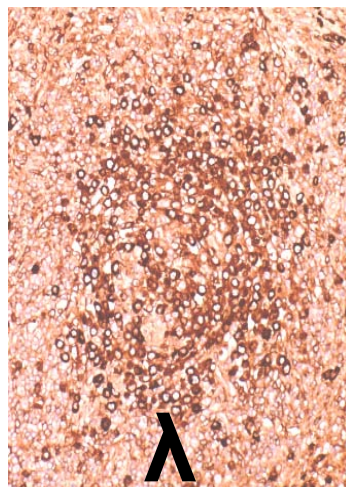
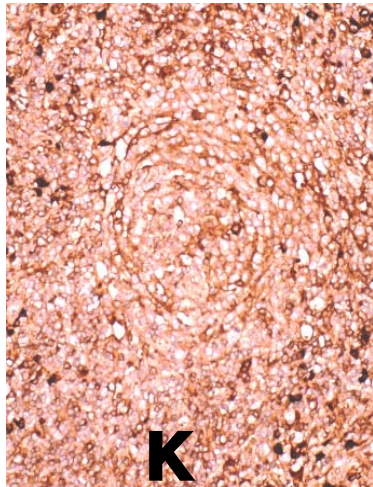
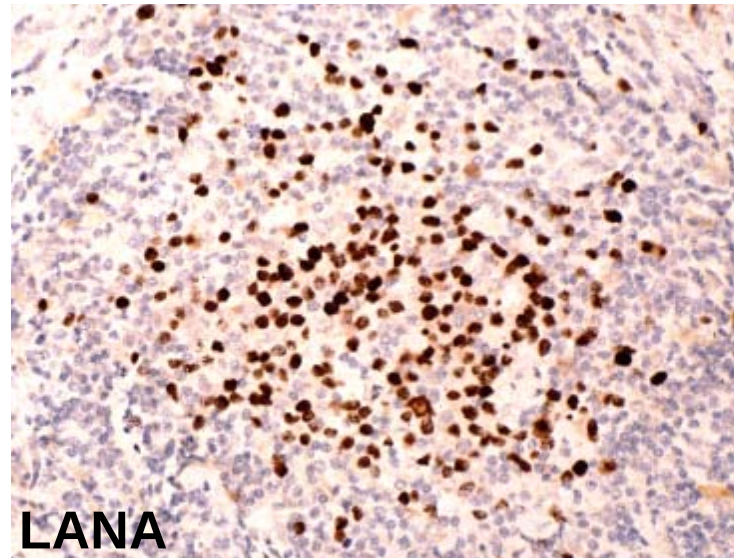
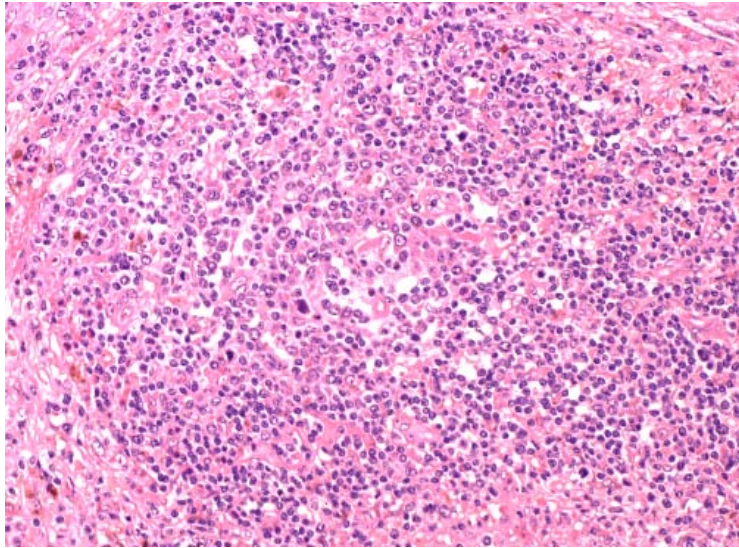
Diagnosis	CD			RCD				
Follow-up (months)	0	31	41	120	130	142	149	161
% CD3 ⁺ CD8 ⁺ IEL/T-cells	3	19	17	24	23	45	95	53
Clonality	P	P	C	C	C	C	C	C



- Transient monoclonality or aberrant IEL immunophenotype: **CD with GFD non-compliance**;
- Persistent identical monoclonality and aberrant IEL immunophenotype: **a feature of RCD**;
- Persistence of both the abnormalities in RCD: **high risk for EATL**.
- **Importance of continuous monitoring of both IEL immunophenotype and clonality in diagnosis and follow up of RCD.**

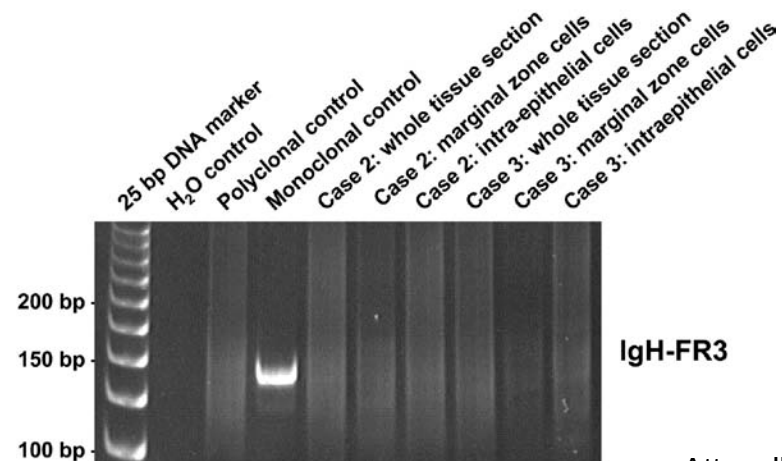
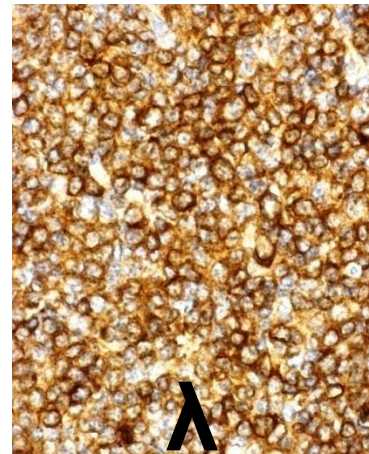
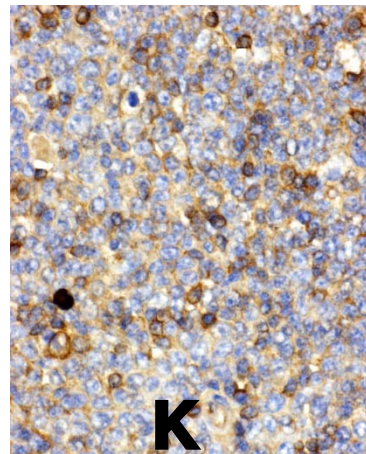
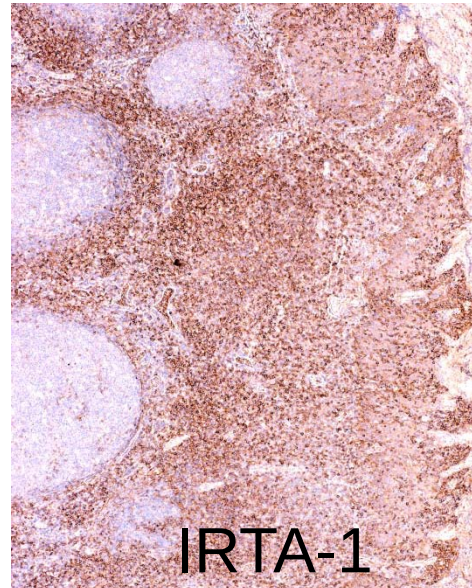
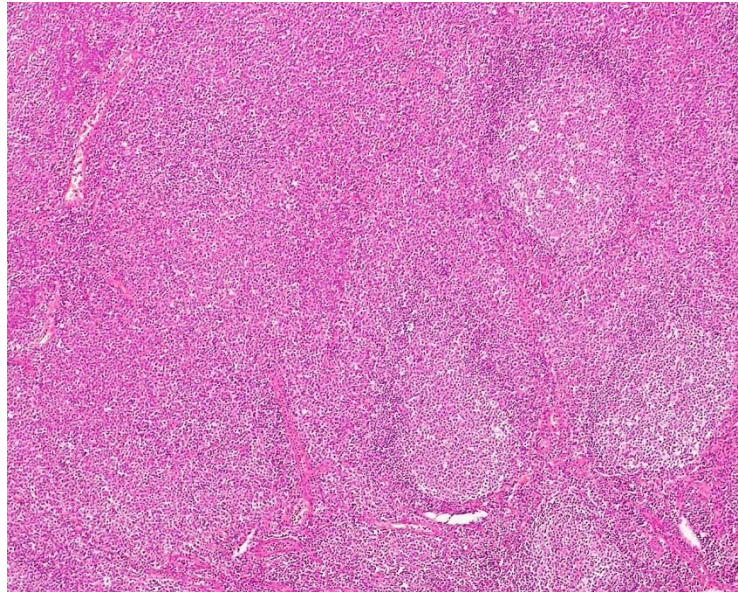
Paradoxical findings: light chain IHC vs IG PCR

KSHV associated LPD in MCD



Paradoxical findings: light chain IHC vs IG PCR

Atypical marginal zone hyperplasia in children



Molecular Haematopathology:

Diagnosis: sub-classification

o Chromosome translocation

- t(14;18)/IGH-BCL2: FL
- t(11;14)/CCND1-IGH: MCL
- t(8;14)/MYC-IGH BL
- t(11;18)/API2-MALT1: MALT lymphoma
- t(2;5)(p23;35)/NPM-ALK ALCL

o Genomic CNVs

- 7q32 deletion: SMZL

o Somatic mutations

- BRAF HCL
- MYD88 LPL

Incidence and specificity

Lymphoma type	Ch. translocation	Frequency	The gene involved
Follicular lymphoma	t(14;18)(q32;q21)	~90%	BCL2/IGH
Mantle cell lymphoma	t(11;14)(q13;q32)	~95%	CCND1/IGH
Burkitt lymphoma	t(8;14)(q24;q32)	100%	MYC/IGH
MALT lymphoma	t(11;18)(q21;q21)	0-40%	API2-MALT1
	t(1;14)(p22;q32)	5%	BCL10/IGH
	t(14;18)(q32;q21)	5%	MALT1/IGH
Anaplastic large cell lymphoma	t(2;5)(p23;35)	70-80%	NPM-ALK
	t(1;2)(q25;p23)	10-20%	TPM3-ALK
SMZL	7q32 deletion	30%	?

Burkitt lymphoma and DLBCL: differential diagnosis at genetic level

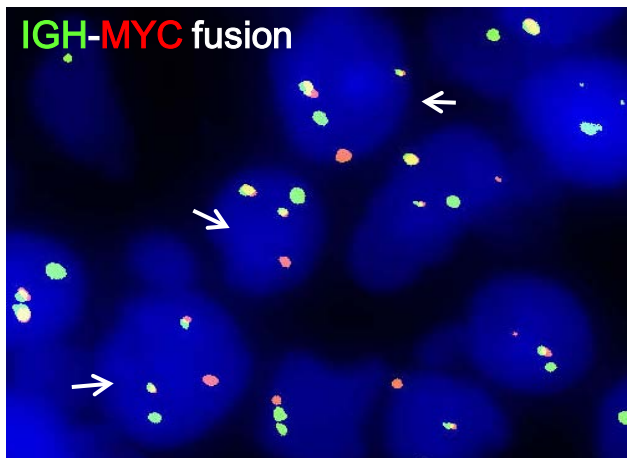
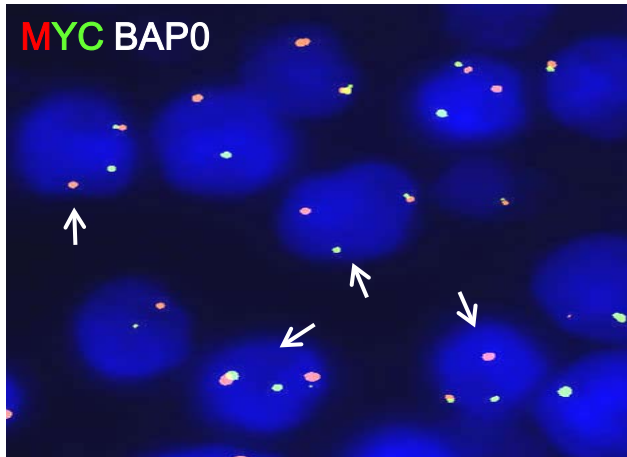
	BL	DLBCL (GC phenotype + high proliferation index)
Genetic changes	MYC translocation associated with IG gene MYC BAP +ve MYC-IG fusion +ve	-/+ MYC translocation frequently associate with non-IG genes MYC BAP +ve MYC-IG fusion often -ve
	Lack or simple cytogenetic/genomic changes BCL2 BAP: no CNV BCL6 BAP: no CNV	Presence of complex cytogenetic/genomic changes BCL2: often gain at 18q21 BCL6: often gain at 3q27
	Lack of other translocations BCL2 BAP: no translocation BCL6 BAP: no translocation	-/+ other translocations BCL2 BAP: -/+ translocation BCL6 BAP: -/+ translocation

M0911

6 year/male, small bowel

Diffuse infiltrate of intermediate sized cells, starry-sky,

CD20+, CD10+, BCL6+, **BCL2+**, Ki67~100%, TdT-



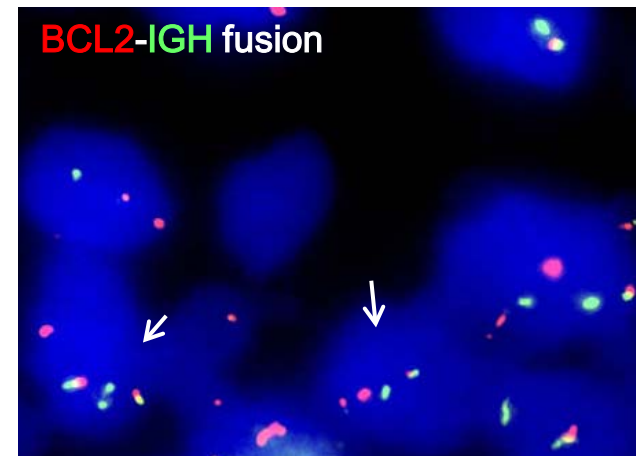
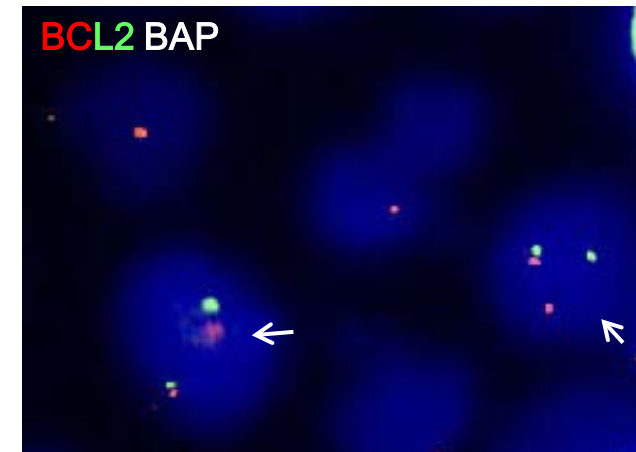
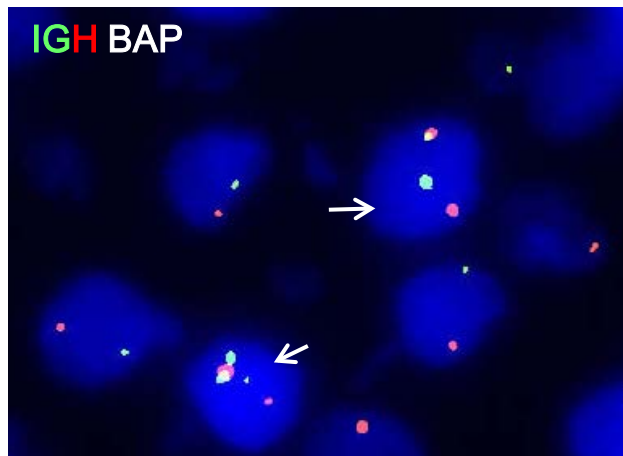
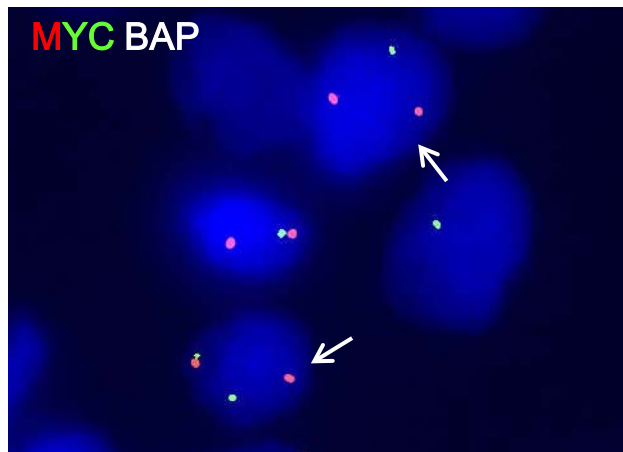
BCL2 BAP: no abnormalities
BCL6 BAP: no abnormalities

M1269

83/female, LN

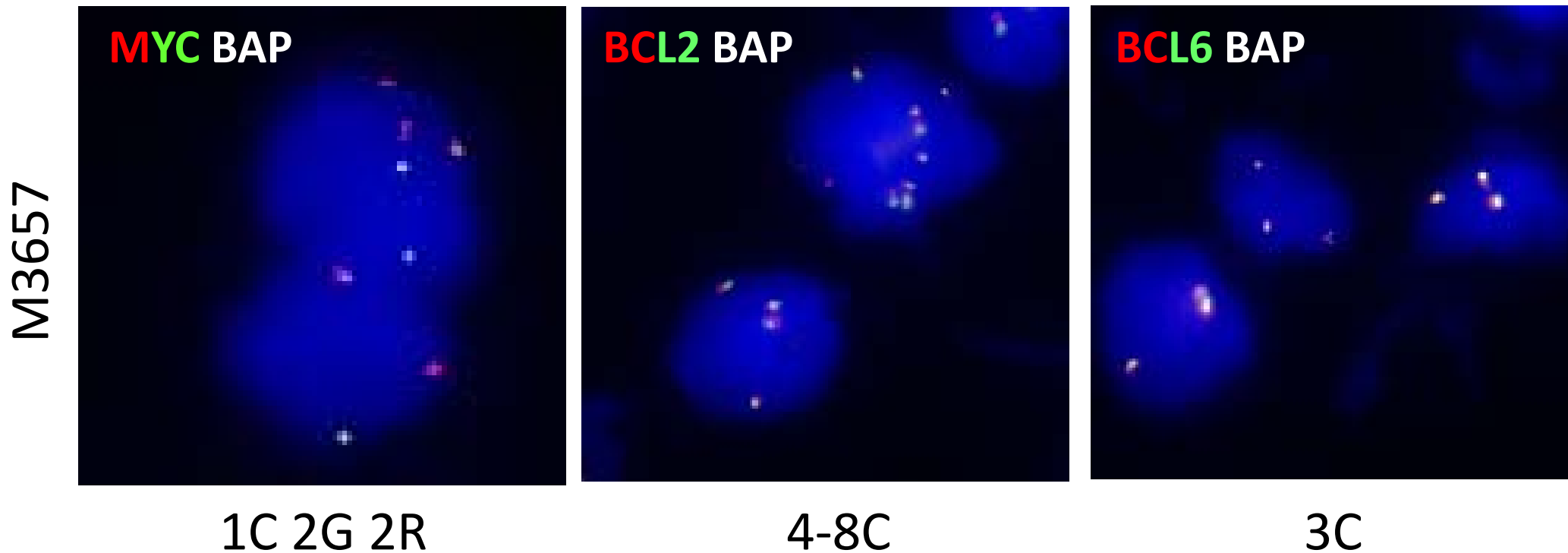
Diffuse infiltrate of large B cells,

CD20+, CD10+, BCL6+, BCL2+, Ki67~90%,



MYC-IGH fusion: no abnormalities

MYC translocation associates with CNV at BCL2 and BCL6 in a DLBCL



Molecular Haematopathology:

Prognosis and treatment stratification

- o MALT lymphoma

 - t(11;18)/API2-MALT1

 - t(1;14)/BCL10-IGH

- o CLL TP53 deletion/mutation

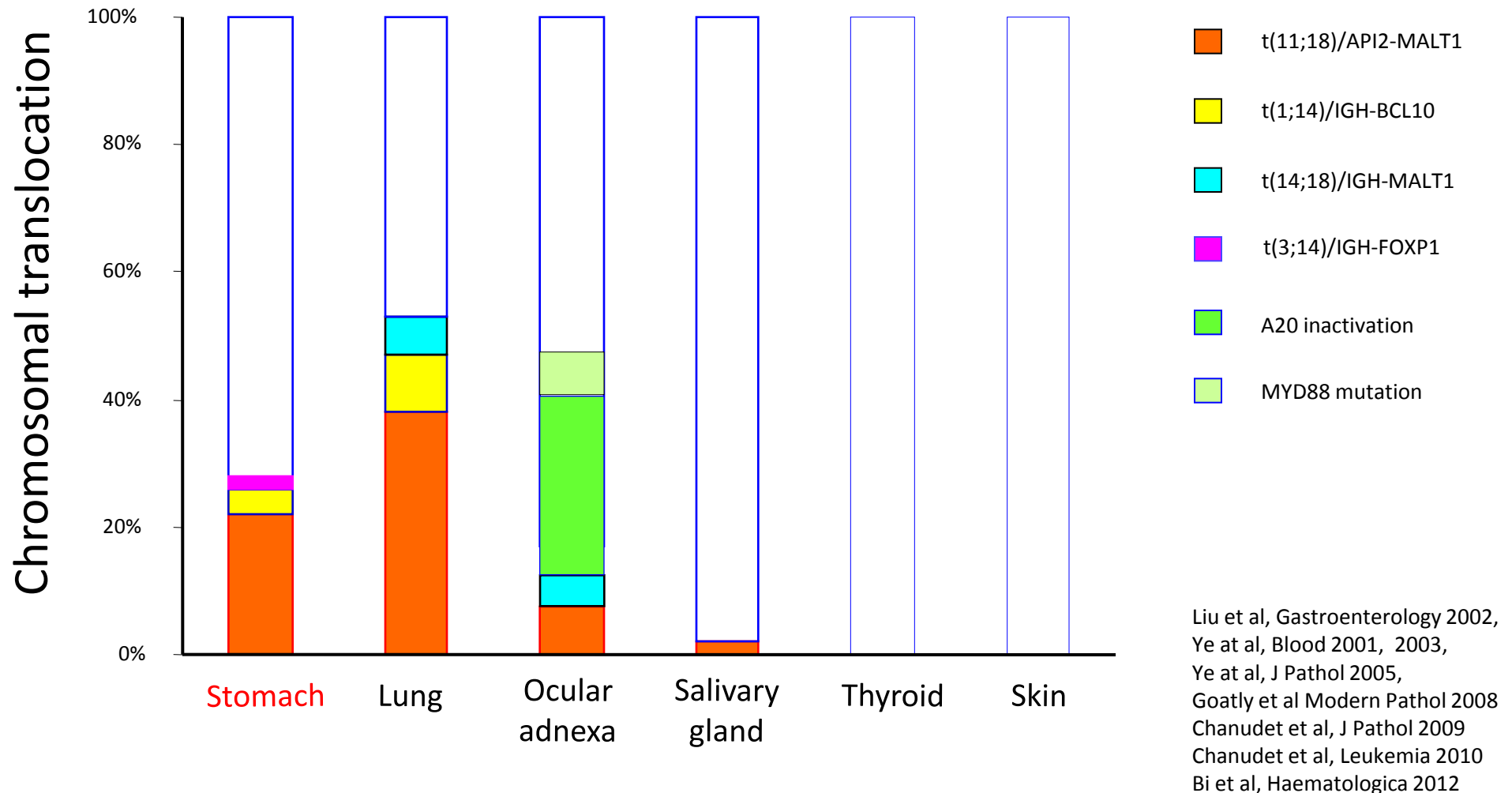
 - IGH mutation

- o DLBCL: MYC/BCL2 double hit

 - TP53 mutation

 - COO subtypes

Frequencies of known genetic abnormalities in MALT lymphoma

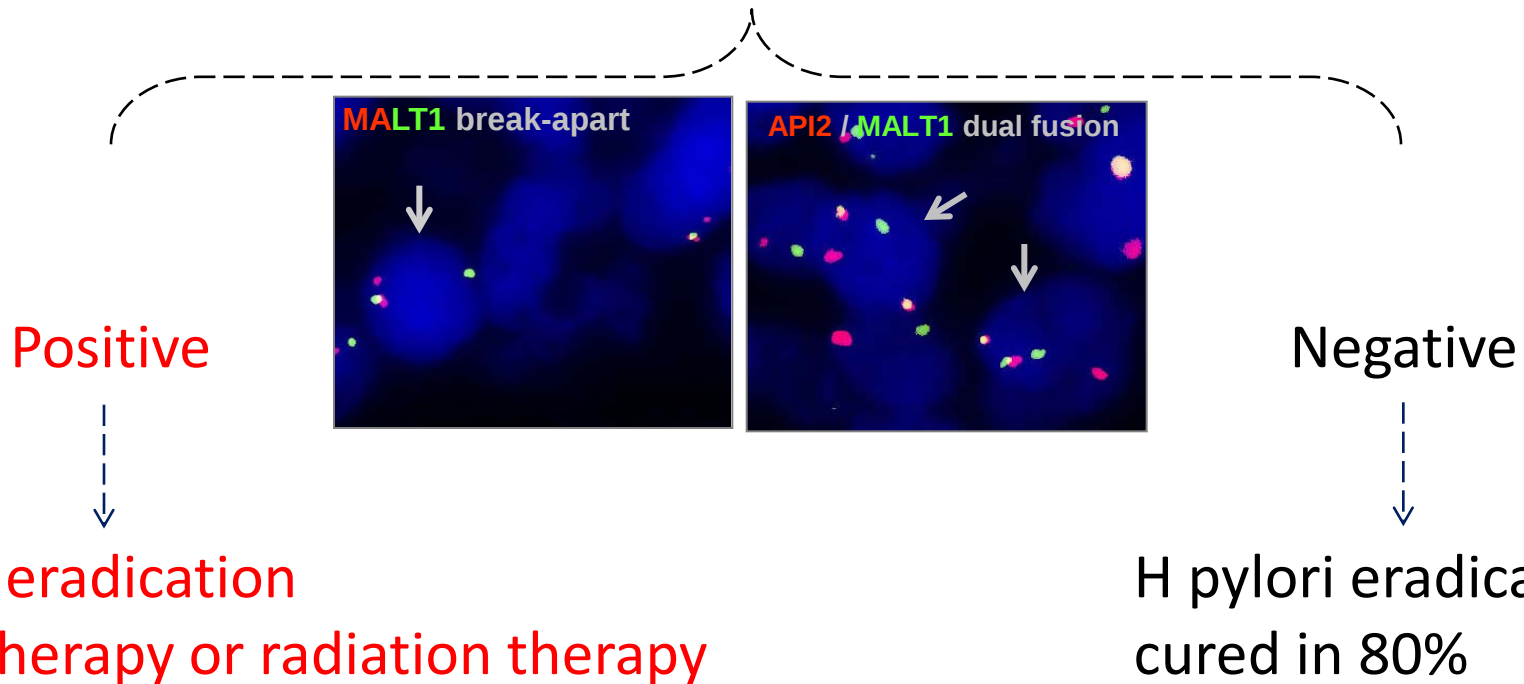


Gastric MALT lymphoma: treatment stratification by molecular subtyping

Gastric MALT lymphoma



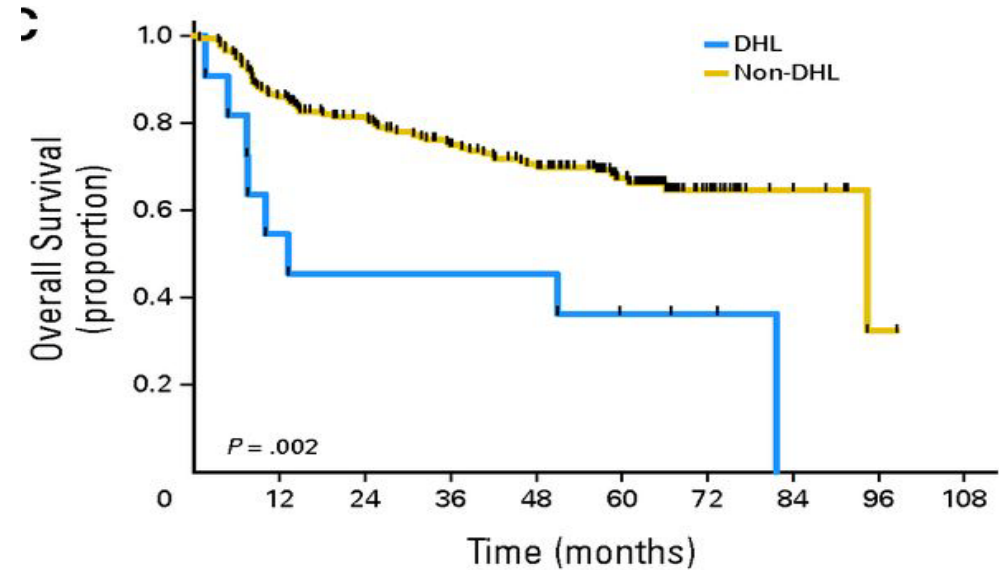
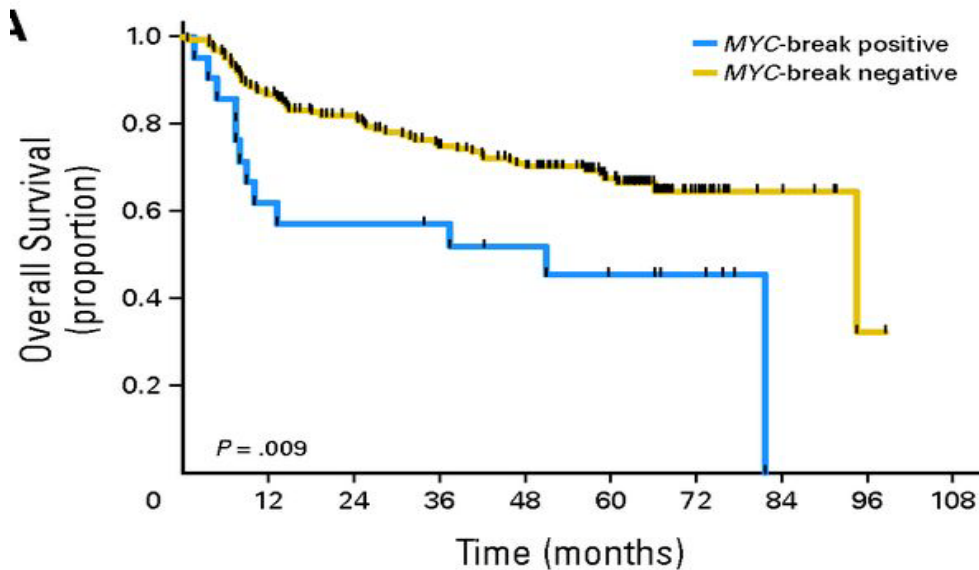
Analyses of MALT1 and BCL10 translocation



DLBCL: MYC translocation

~10%, associated with complex pattern of genomic profile

~5% being double-hit
(MYC + BCL2 trans)

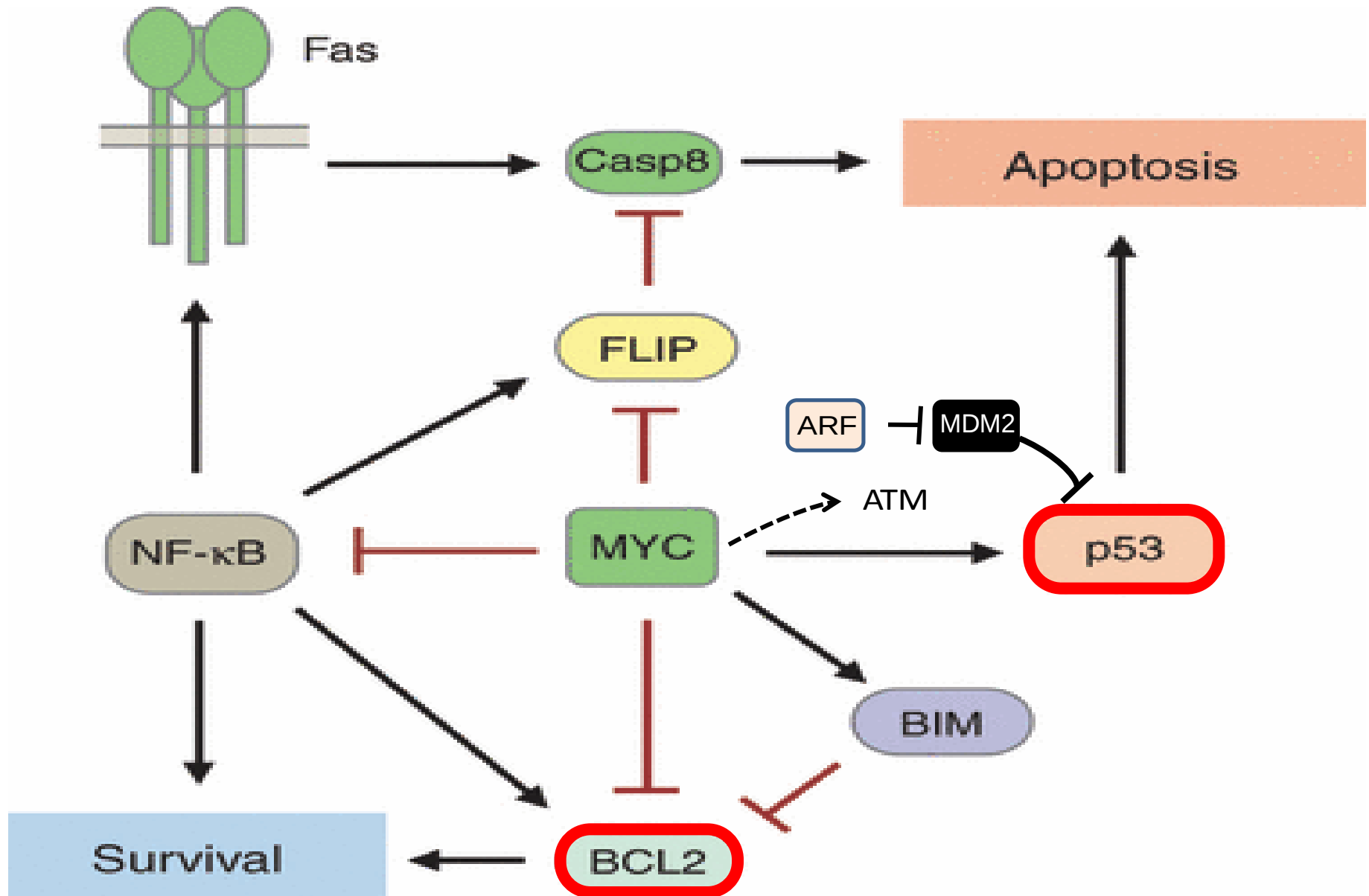


Green et al JCO 2012
Johnson et al JCO 2012
Barrans et al JCO 2010
Savage et al Blood 2009
Johnson et al Blood 2009

MYC: biological function

- Promoting cell-cycle progression
- Regulating ribosome biogenesis and protein synthesis
- Increase energy metabolism
- Regulating miRNA (miR 17-92) expression
- Increase stem cell renewal
- Inducing apoptosis

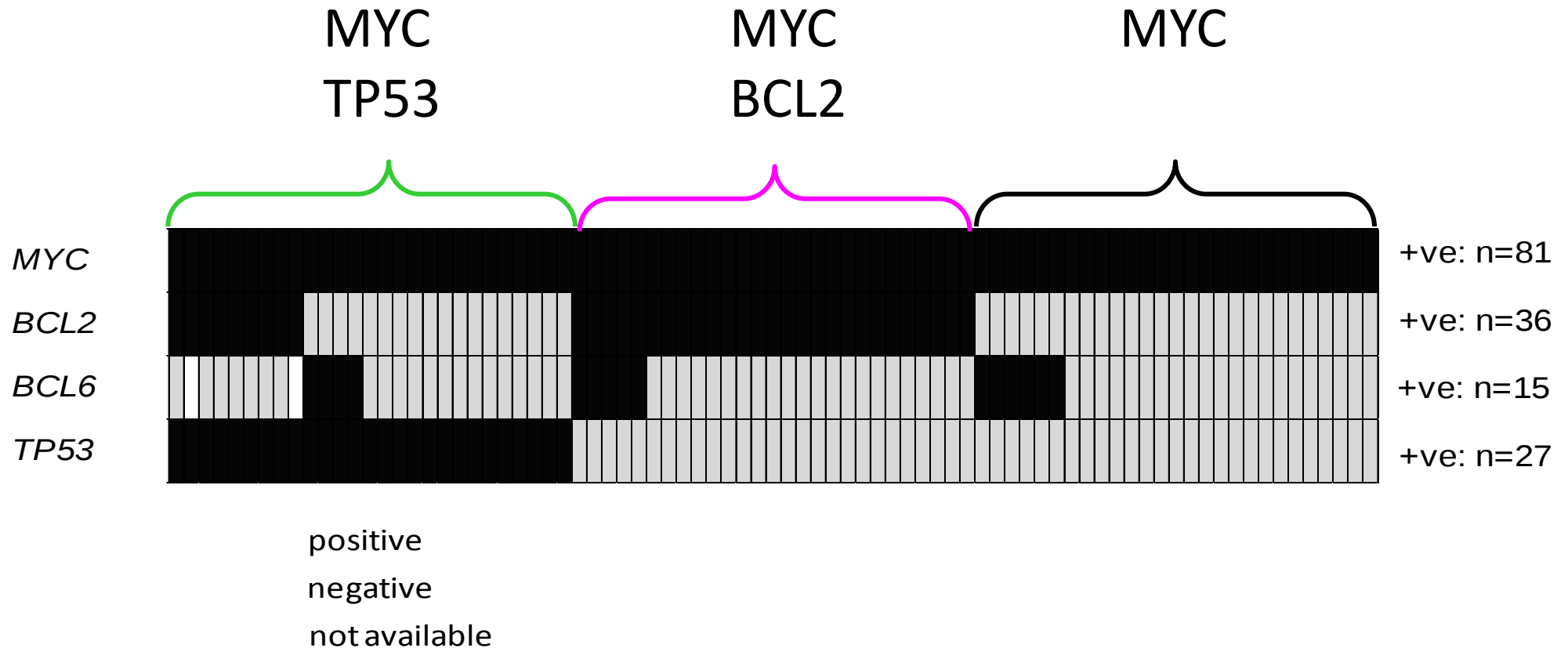
MYC and apoptosis



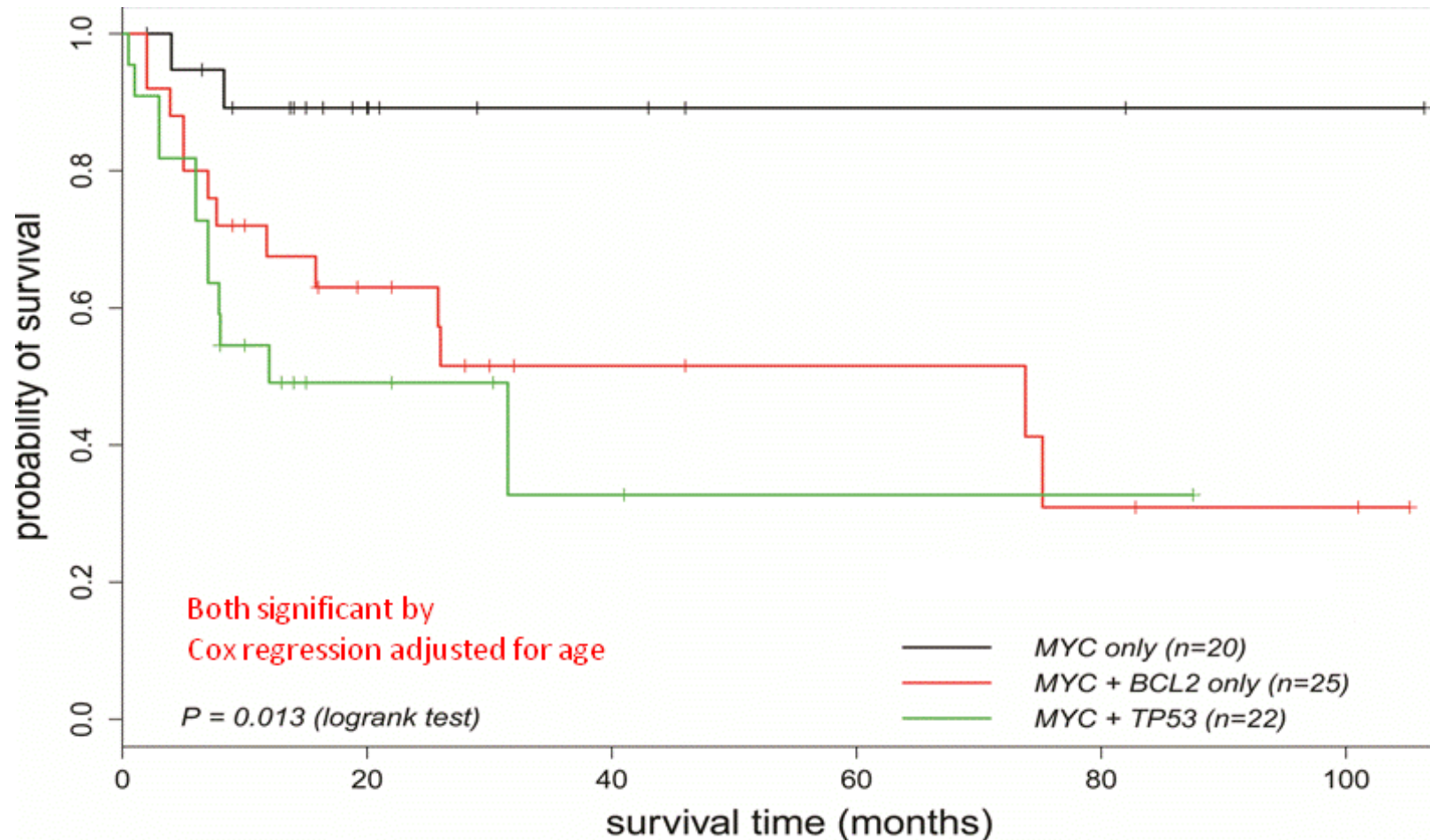
MYC and TP53: oncogenic cooperation

- o Majority of lymphomas in E μ -MYC mice harbour abnormalities in ARF1-MDM2-TP53
- o Rapid lymphoma development in double E μ -Myc and *p53*^{+/-} mice
- o Human Burkitt lymphoma
 - TP53 mutation in 40-50%
 - CDKN2A (INK4a/ARF) deletion in ~6%

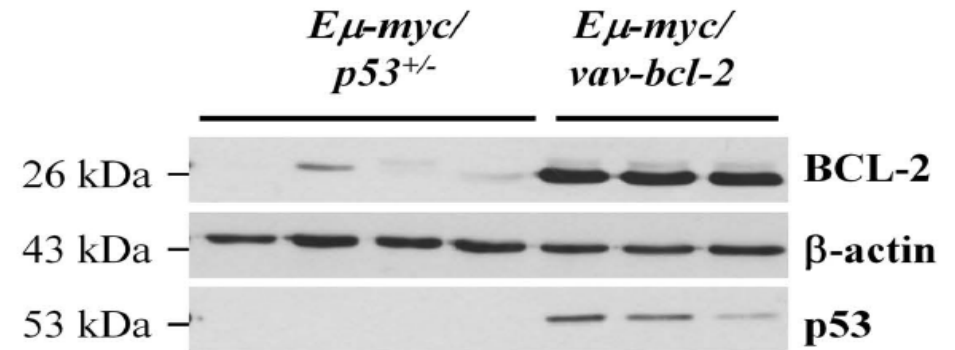
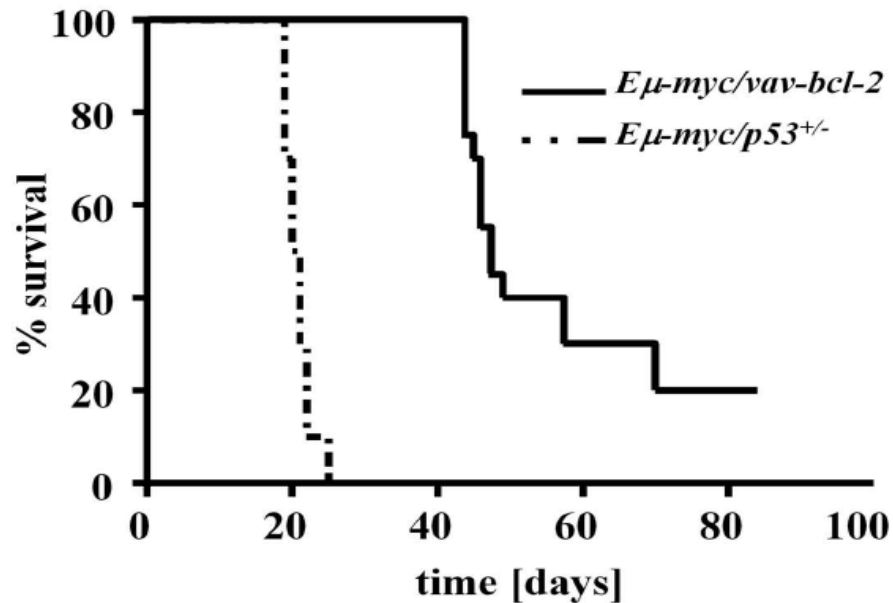
TP53 mutation, BCL2 and BCL6 translocation in MYC trans+ve DLBCL



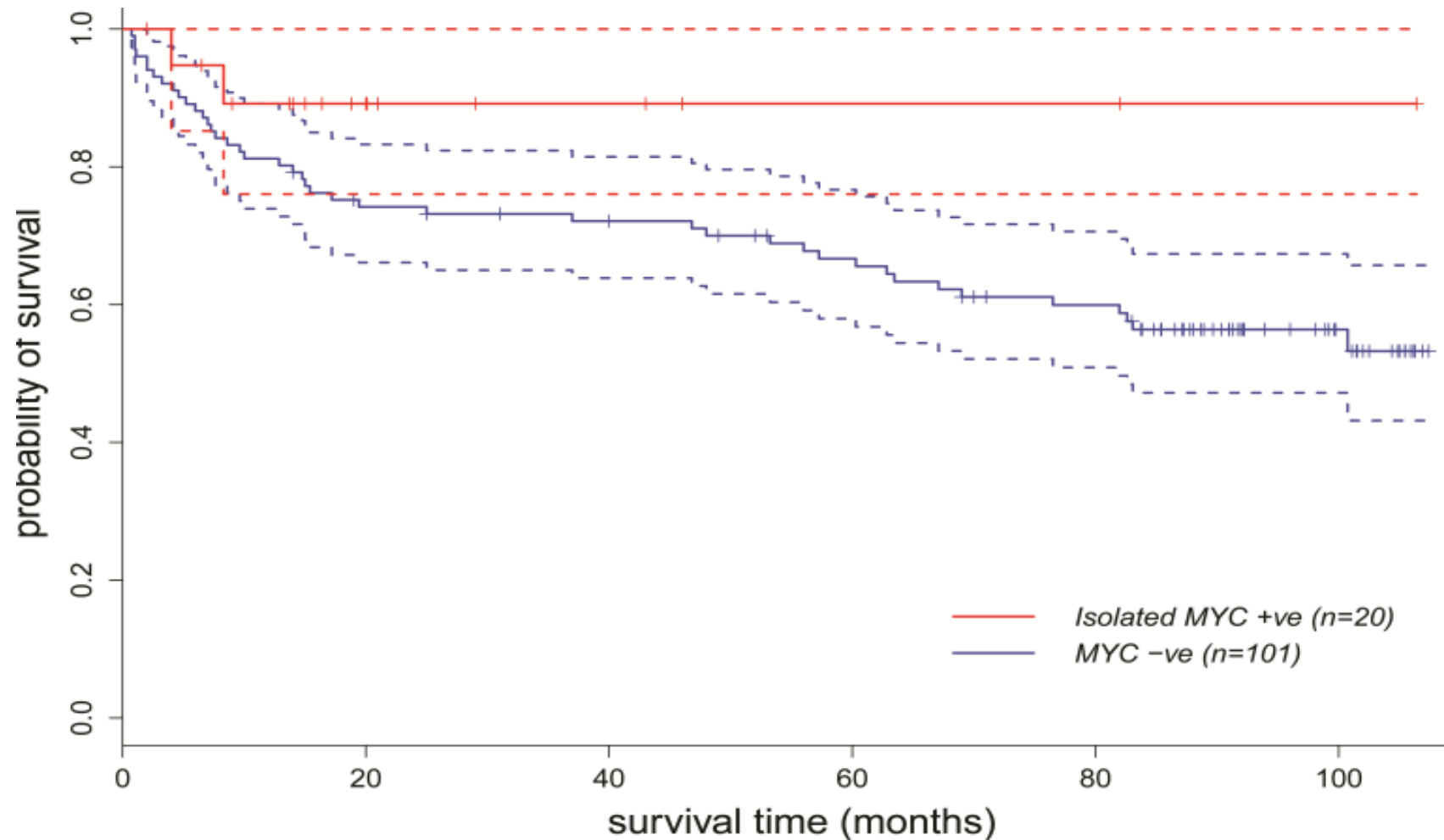
Prognosis of MYC trans+ve DLBCL according to the second genetic hit



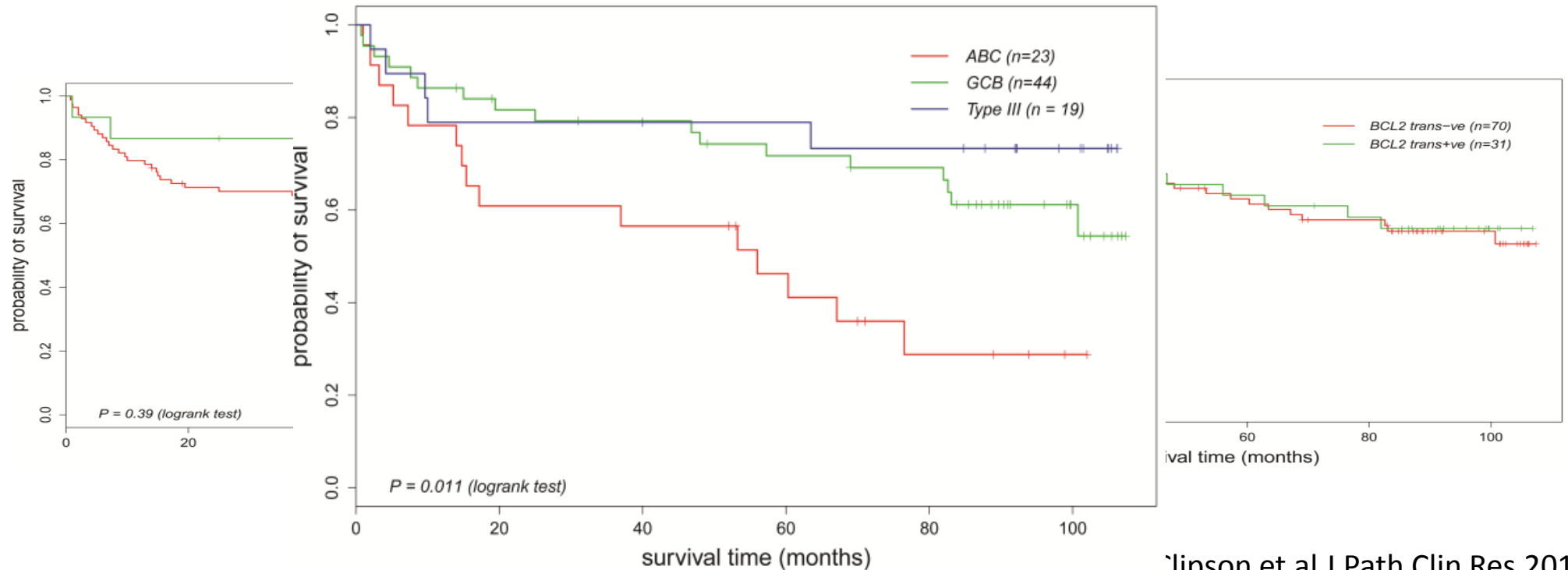
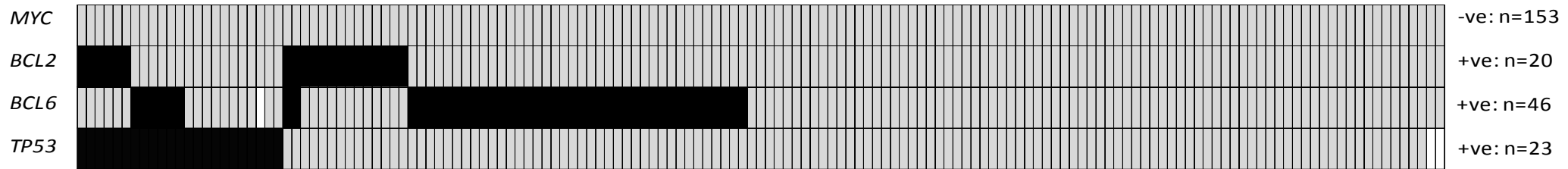
$E\mu$ -MYC mice: survival influenced by the second hit



Overall survival of DLBCL with isolated MYC translocation



TP53 mutation, BCL2 and BCL6 translocation in MYC trans-ve DLBCL



MYC translocation in prognosis of DLBCL

- o Double hit DLBCL
 - MYC translocation + TP53 mutation
 - MYC + BCL2 translocation
- o Double hit DLBCL show significant worse prognosis
- o Distinguish double-hit DLBCLs from those with an isolated *MYC* translocation.

Double hit DLBCL: detection by IHC?

o MYC & BCL2 IHC

- MYC/BCL2 double-hit
- MYC/BCL2 over-expression, but no translocation

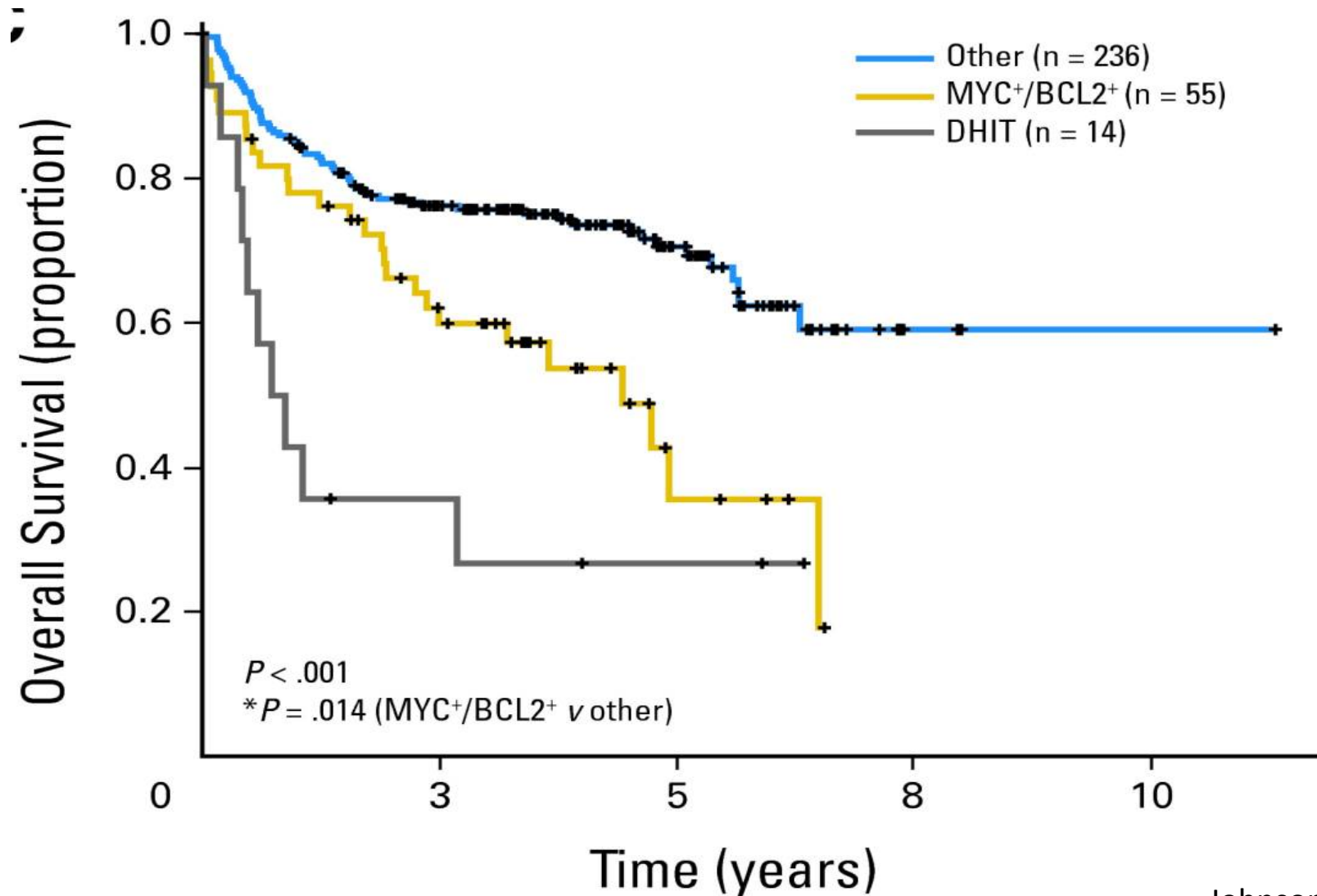
o MYC & TP53 IHC:

- Not detecting *TP53* frameshift/nonsense changes

Potential issues:

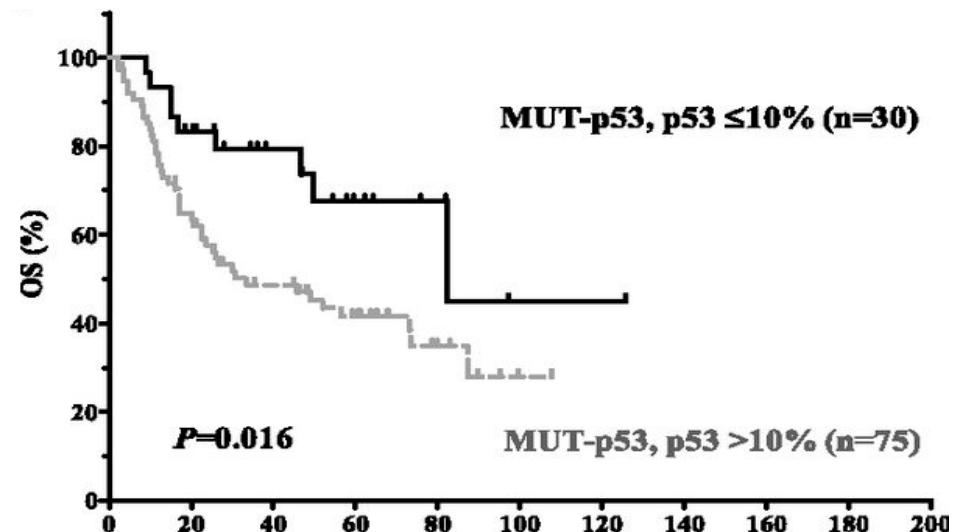
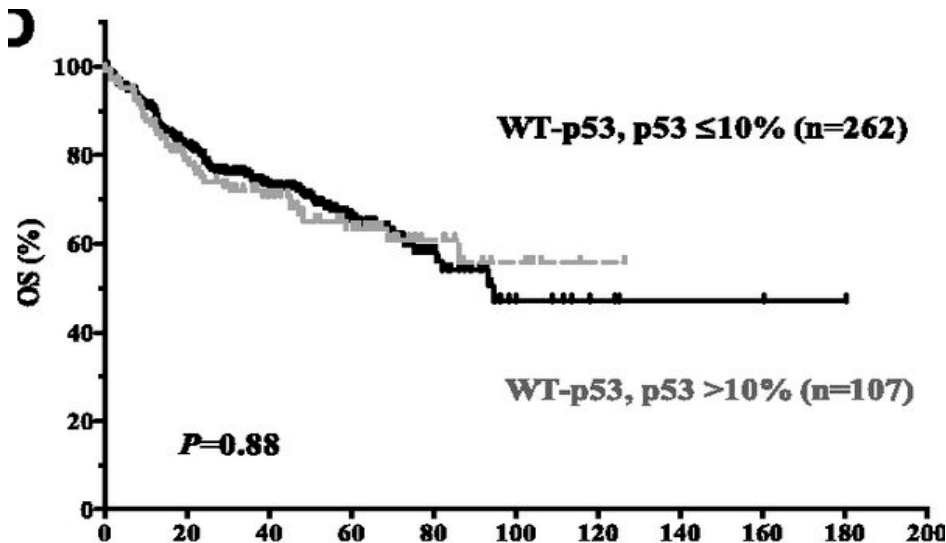
- variability in staining
- subjective
- cutoff value
- false negative / positive

MYC/BCL2 double-hit vs MYC/BCL2 co-expression

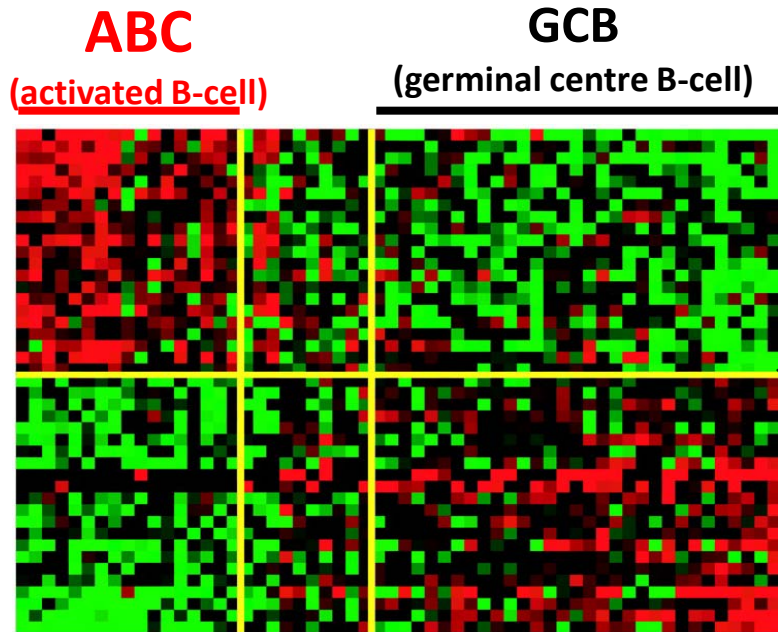


DLBCL: prognostic value of TP53 staining

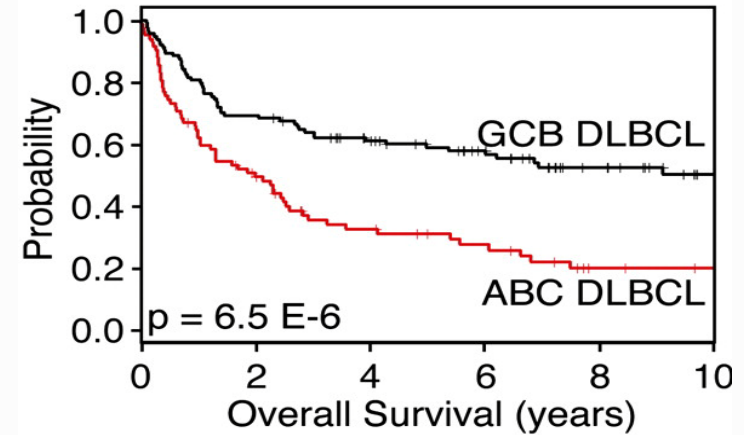
	Overall	WT-p53	MUT-p53
Number of MDM2 ⁻ patients	285	216	69
Number of MDM2 ⁺ patients	193	156	37
Mean MDM2 expression (% cells)	22%	24%	17%
Number of p53 ⁻ patients	292	262	30
Number of p53 ⁺ patients	182	107	75
Mean p53 expression (% cells)	23%	14%	54%



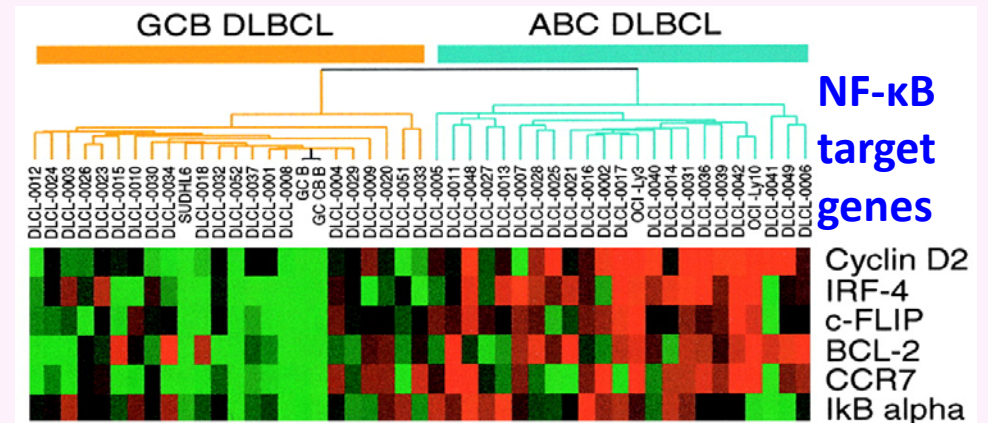
Diffuse large B-cell lymphoma (DLBCL)



Clinical utility



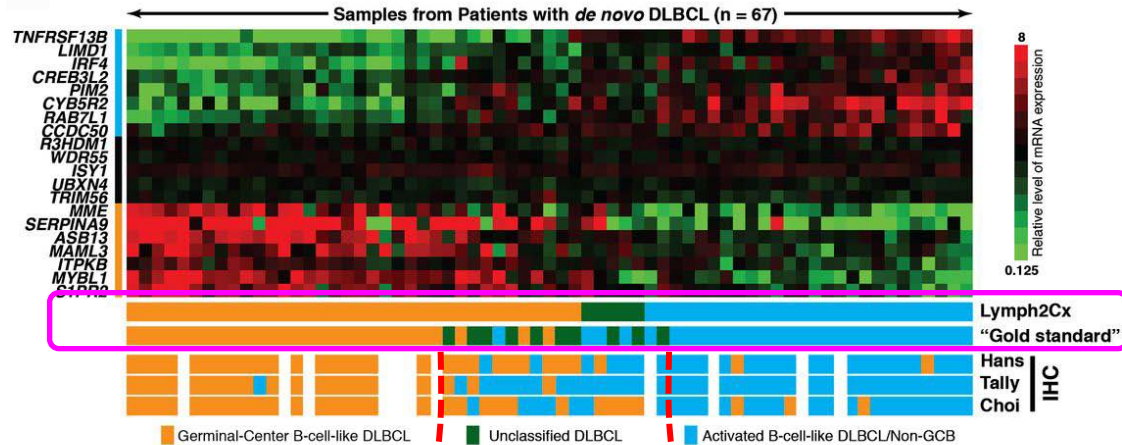
Molecular mechanism



COO subtyping using FFPE tissue

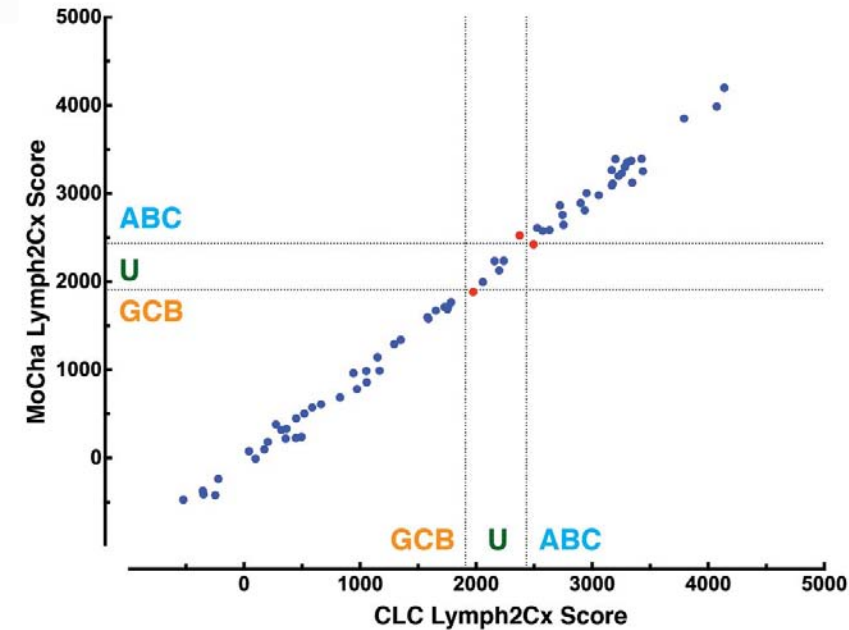
- o **IHC**: lacks reproducibility and low efficacy in survival separation;
- o **Quantitation of classifier gene mRNA expression**
 - Quantitative nuclease protection assay
 - Affymetrix HG133 plus 2 platform
 - Illumina DASL assay /DAC classifier
 - Nanostring technology
 - qRT-PCR with Fluidigm Biomark HD system

COO subtyping by GEP using FFPE tissue:



“molecular grey zone”

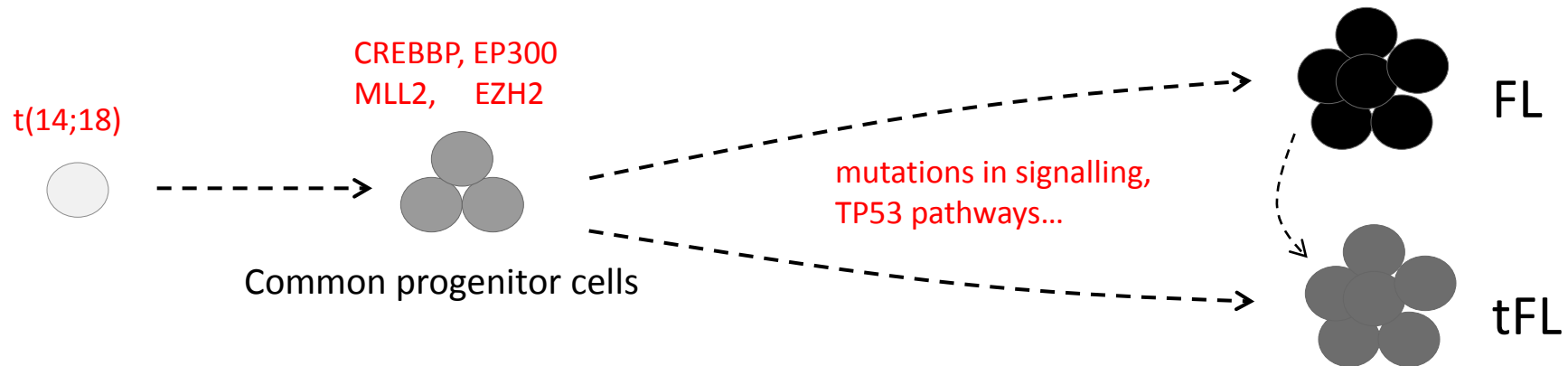
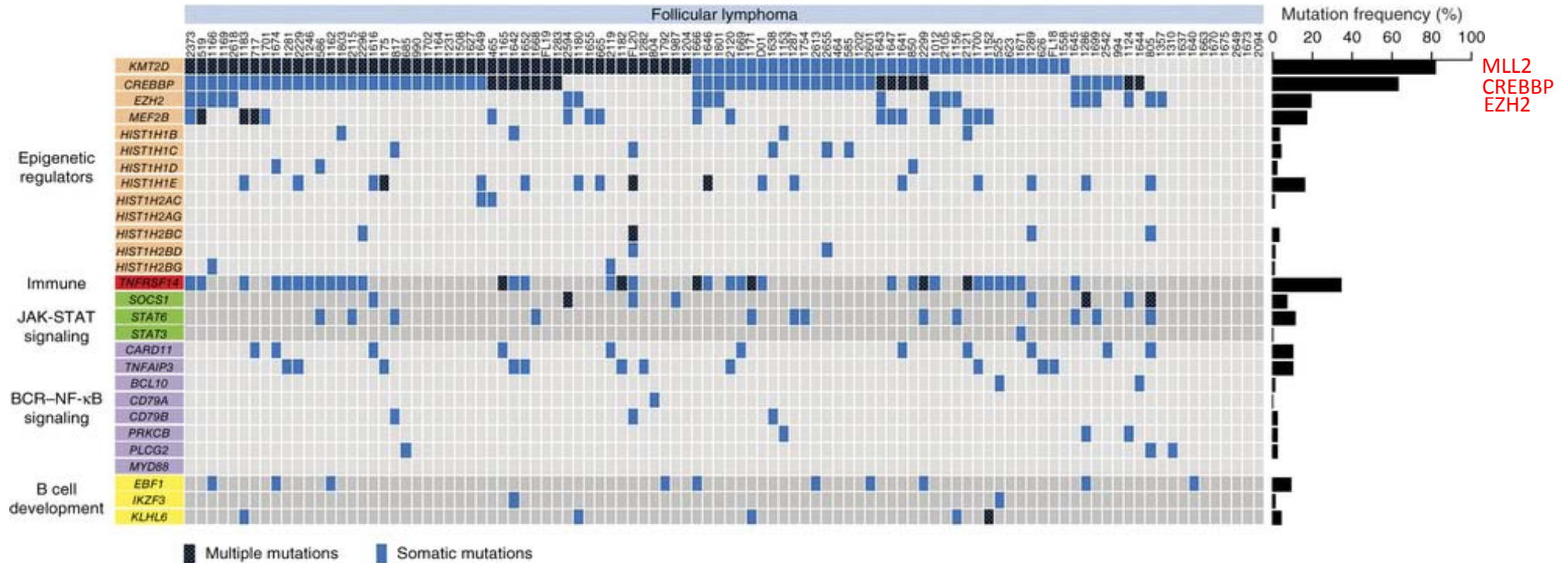
Concordance between
paired FFPE and FF
tissues = ~85%



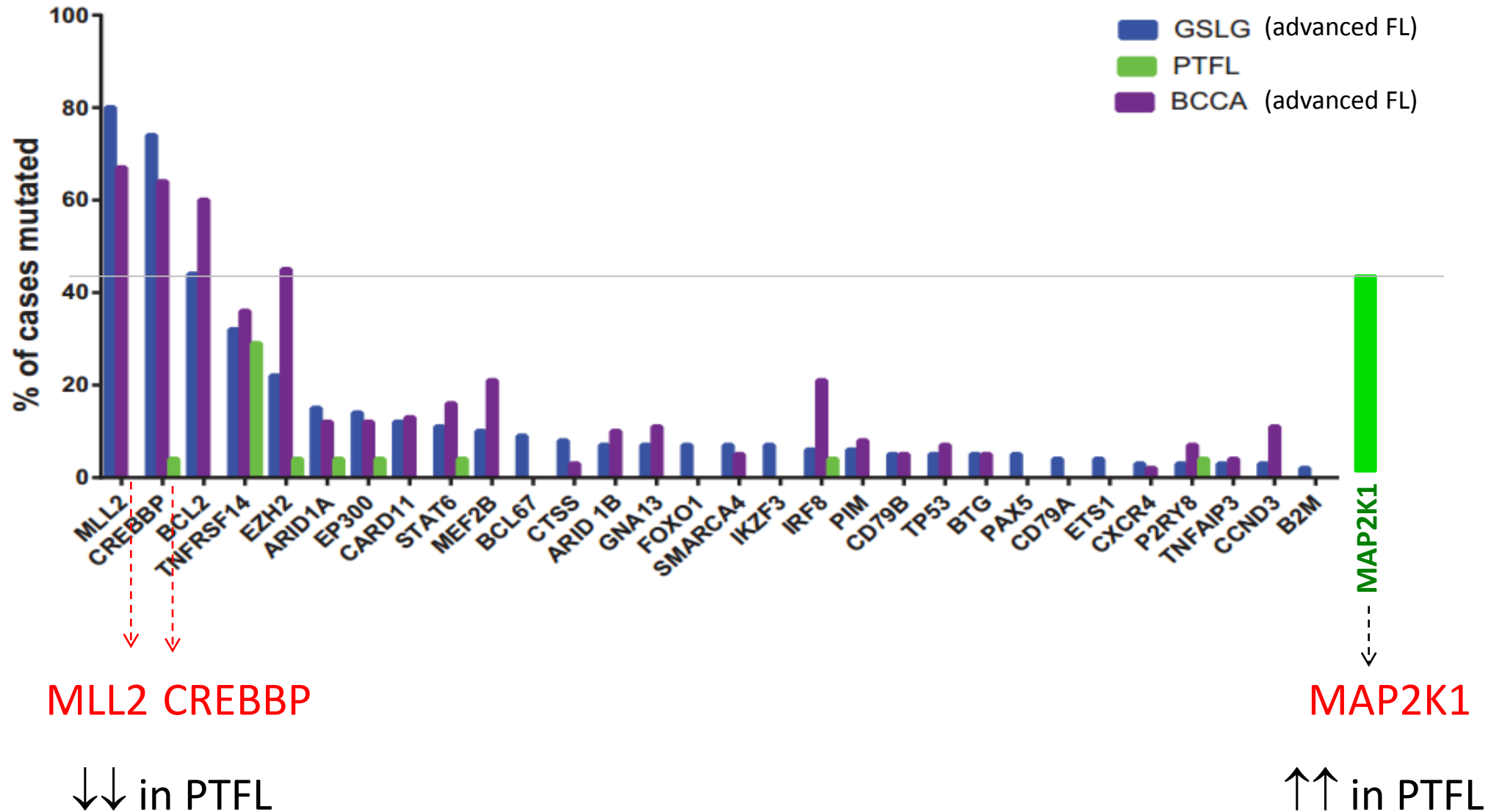
highly concordant
between labs = 98%

Mutation discoveries by NGS and their potential clinical utility

FL: mutation profile



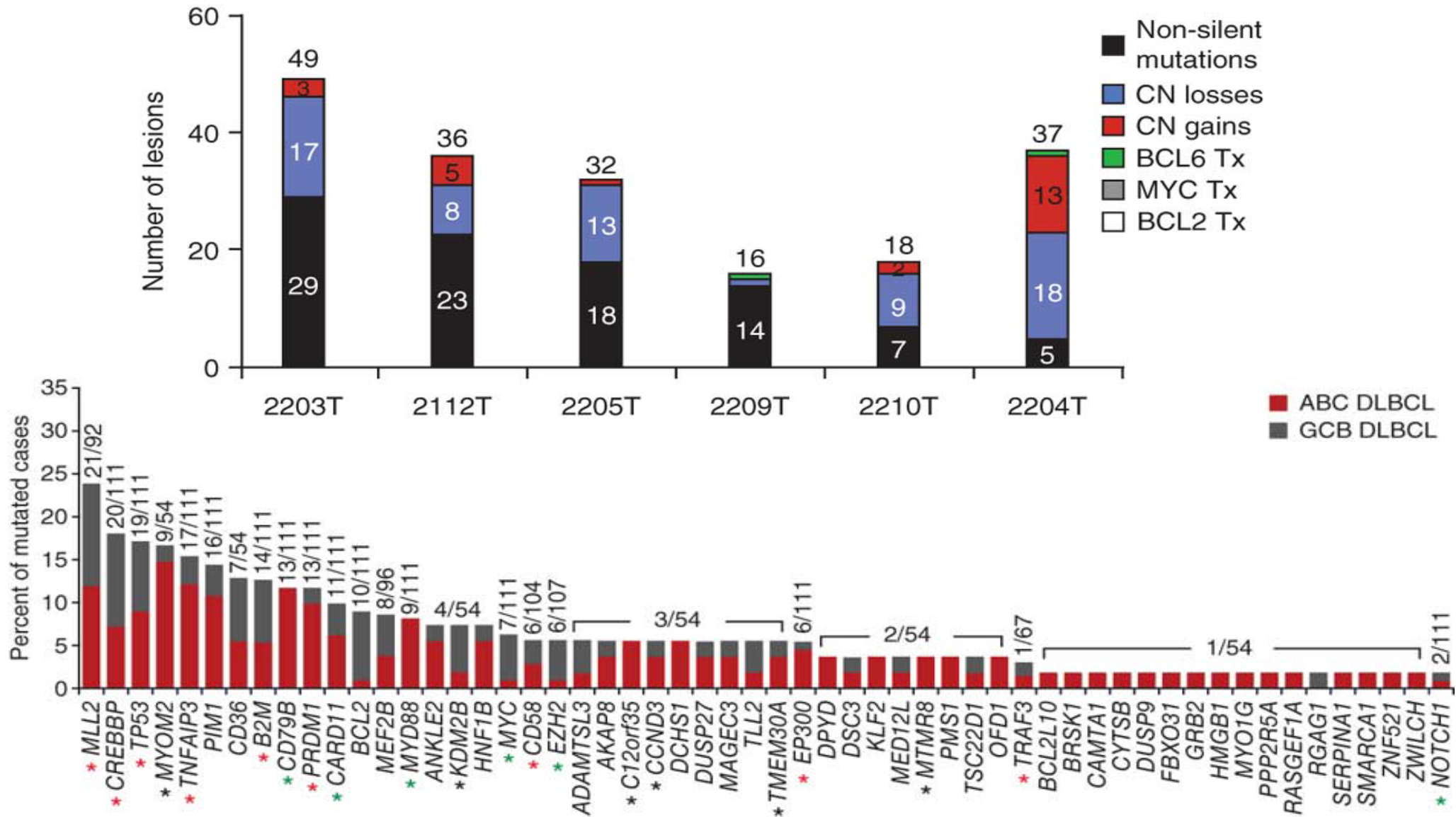
Paediatric-type nodal FL: mutation profile



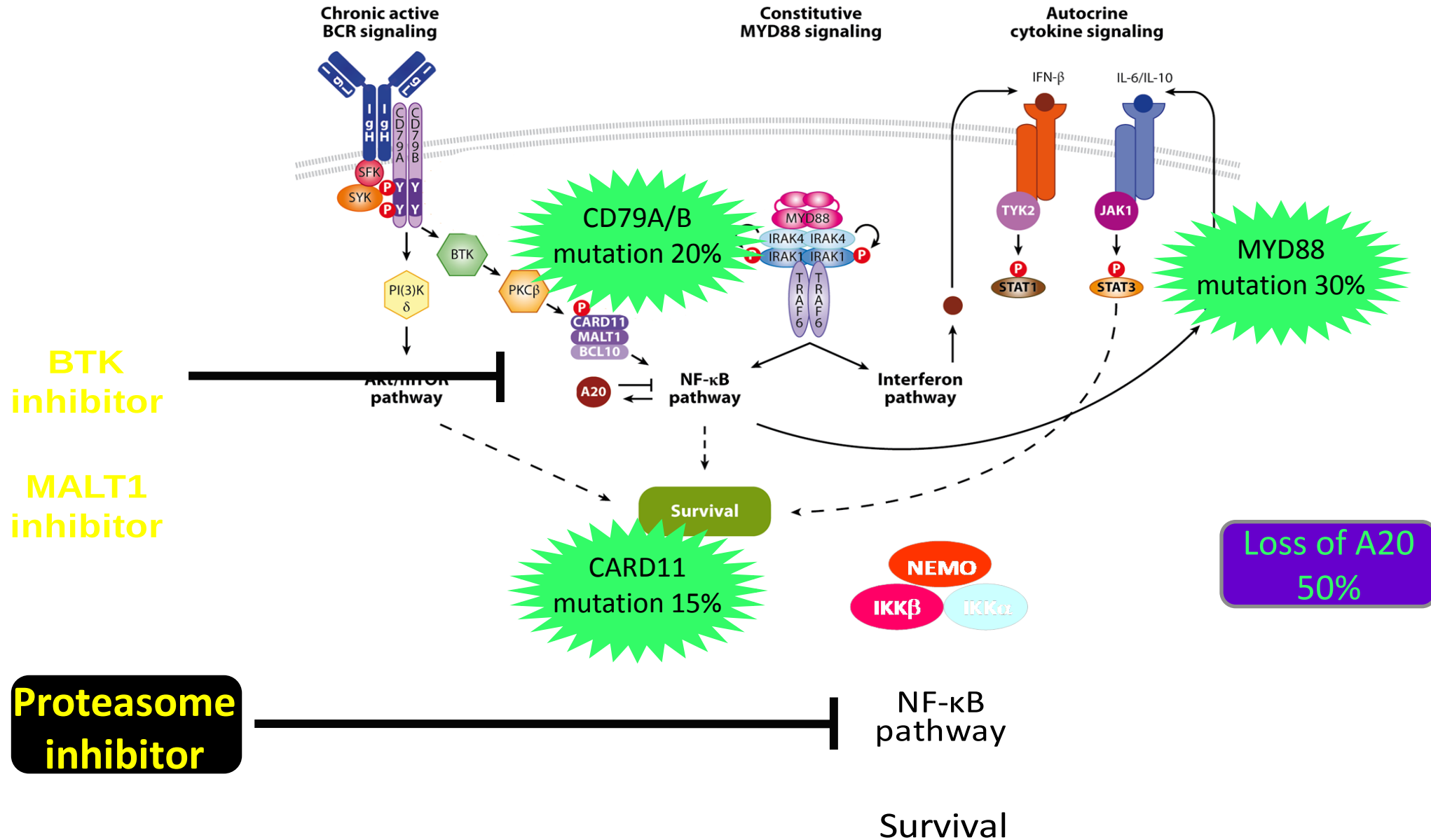
FL: genetic changes in differential diagnosis

Genetic changes	PTNFL	t(14;18)-ve FL	t(14;18)+ve FL
t(14;18)	-ve	-ve	+ve
MAP2K1	43%	n/a	?0
TNFRSF14	29-51%	36%	18-46%
KMT2D(MLL2)	0-16%	36%	67-82%
CREBBP	~3%	45%	33-64%
EZH2	0-3%	18%	7-20%

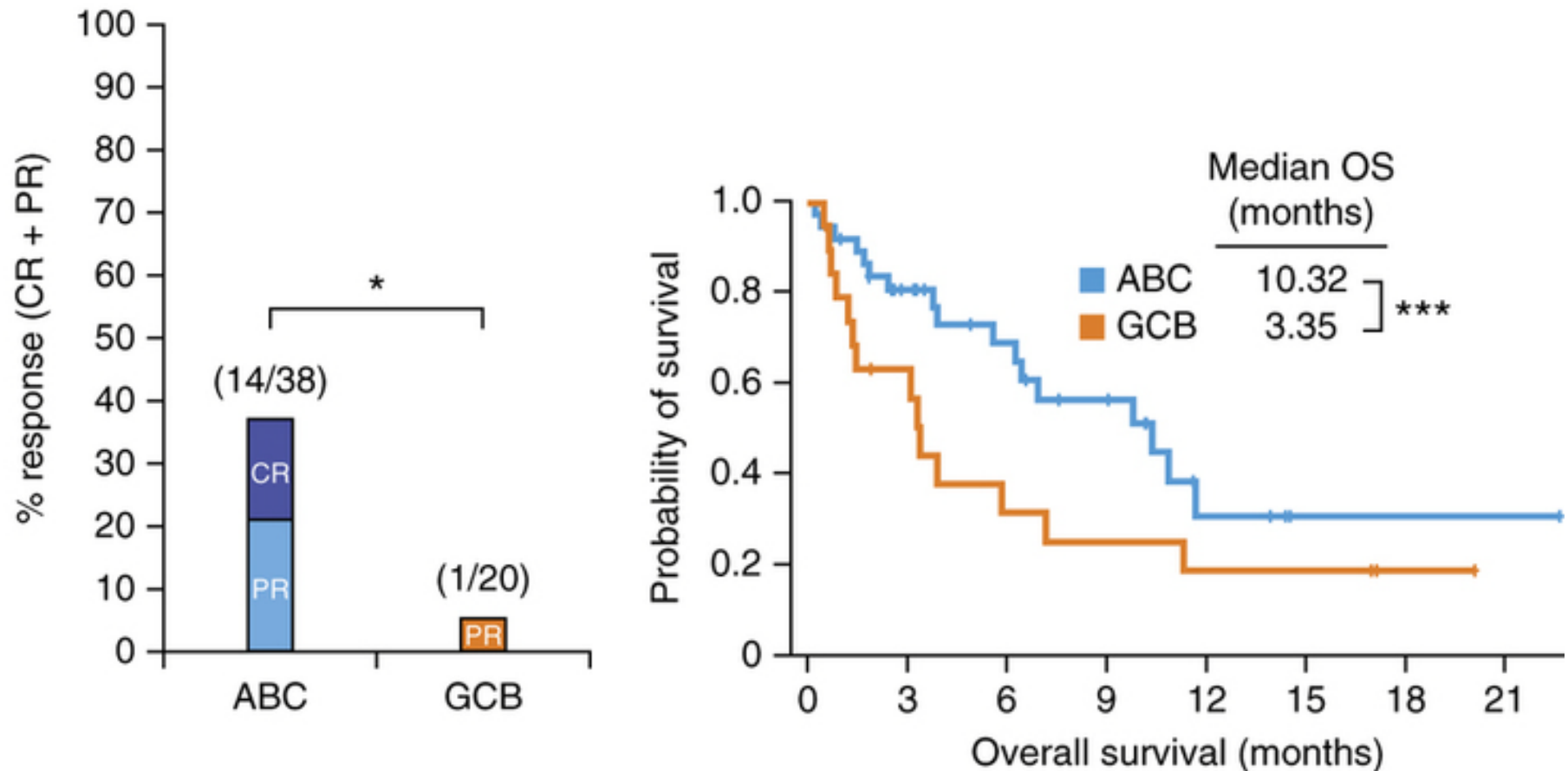
DLBCL: coding genome analyses



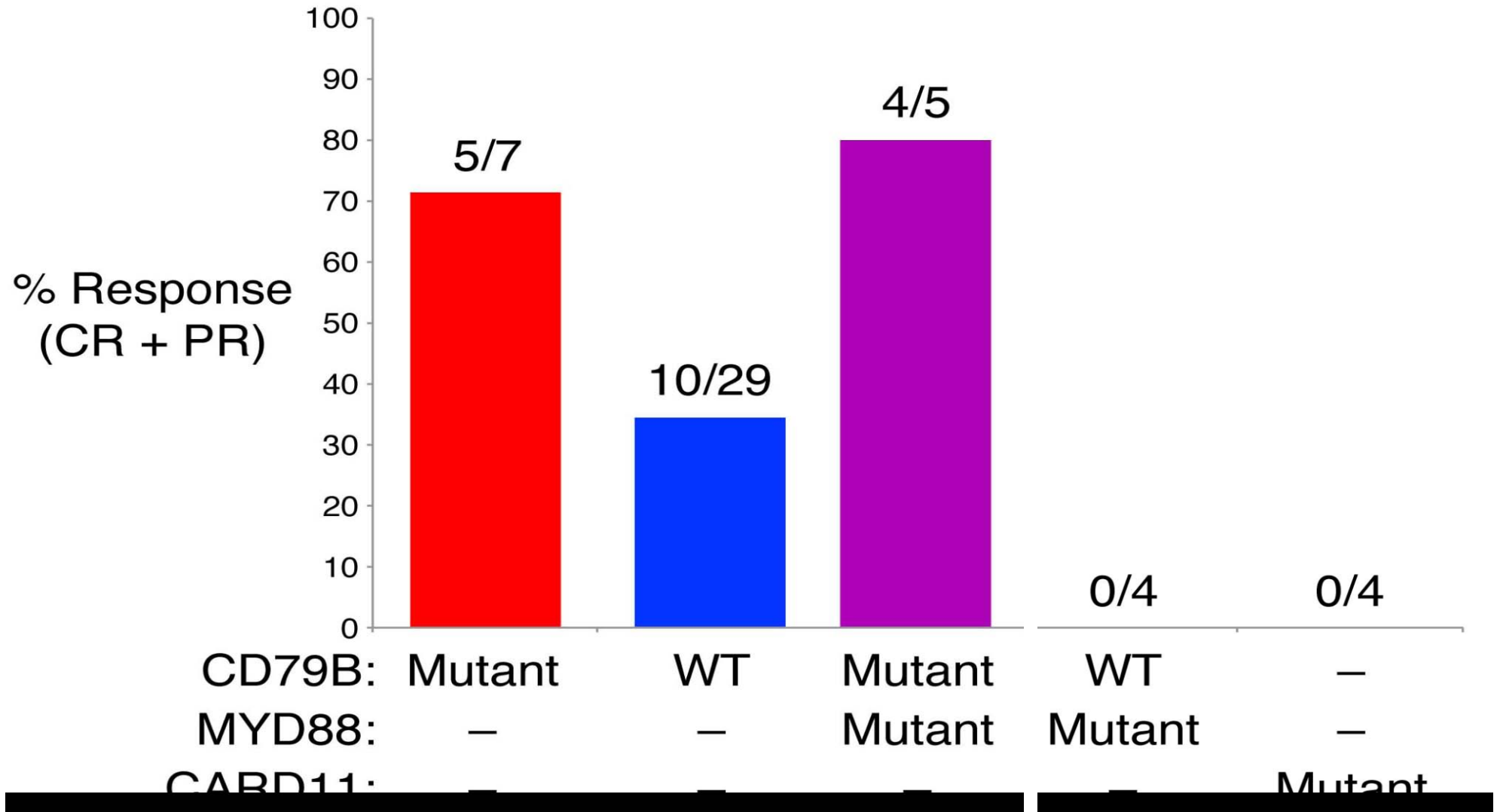
Targeted therapy in ABC-DLBCL



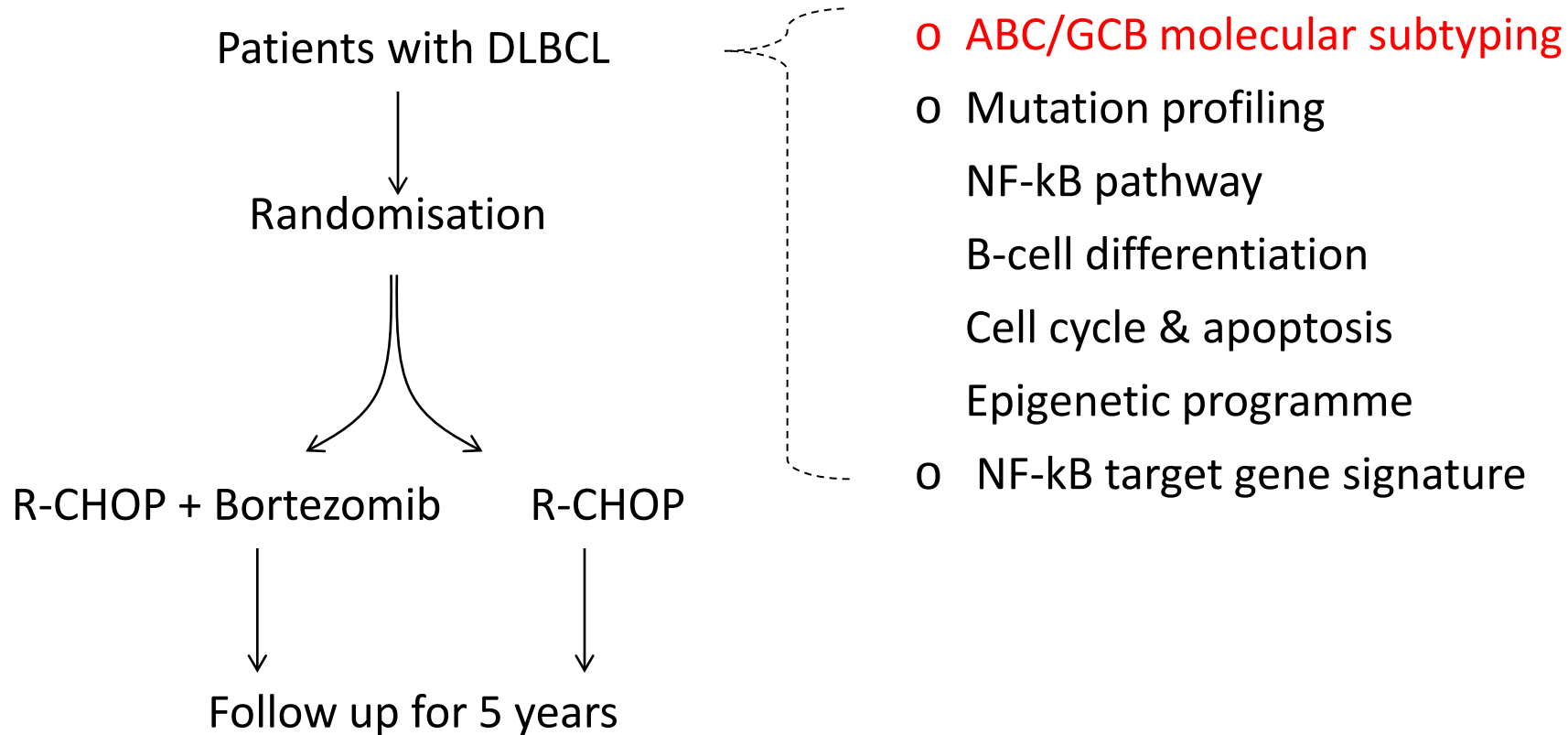
Phase I/II clinical trial of Ibrutinib in relapsed/refractory DLBCL



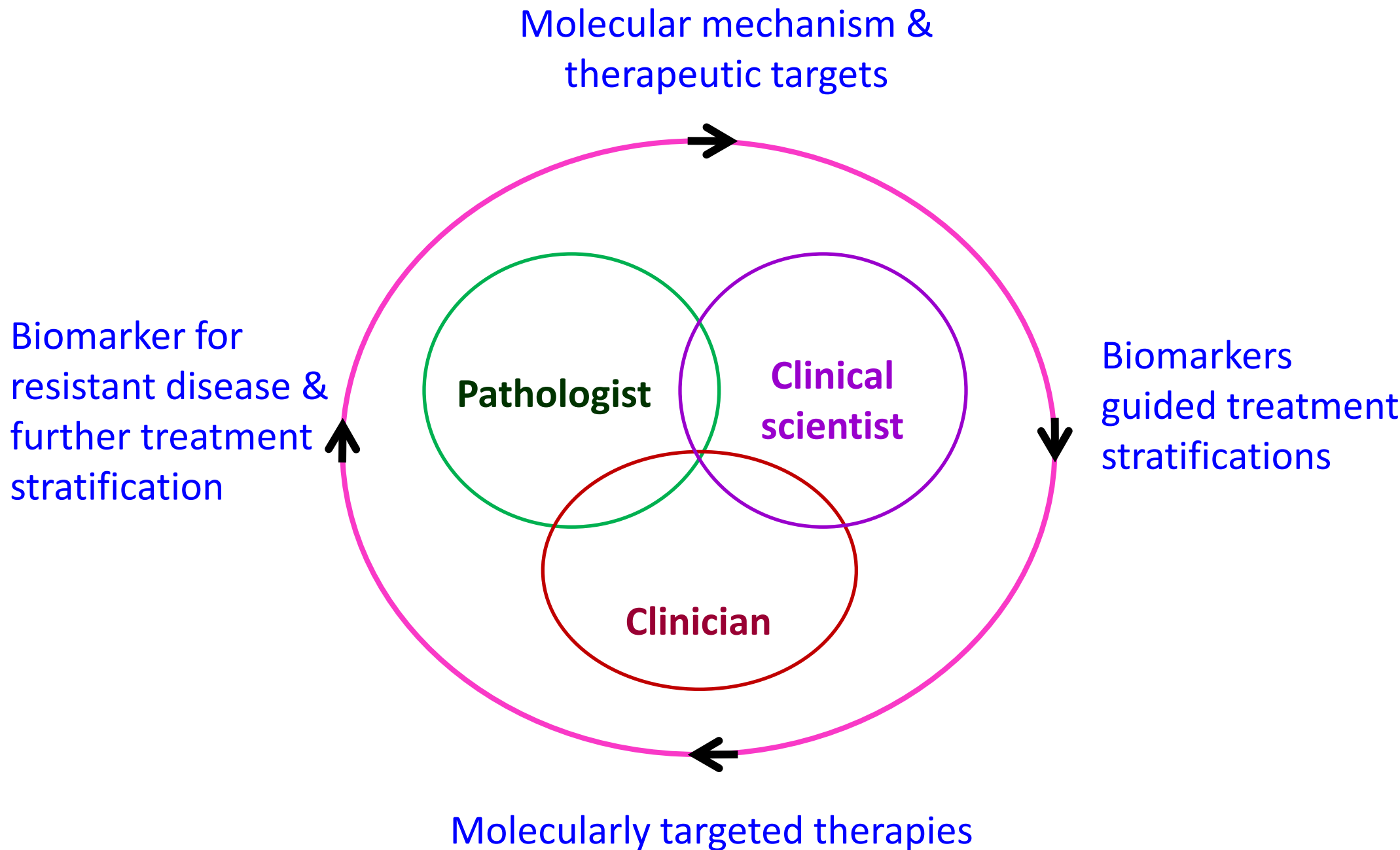
Impact of CD79B, MYD88 and CARD11 mutation on Ibrutinib treatment response in ABC-DLBCL



REMoDL-B phase-3 trial



- o Does the addition of bortezomib to R-CHOP improve progression free survival?
- o Does the molecular phenotype (either ABC or GCB) determine the benefit from the addition of bortezomib?



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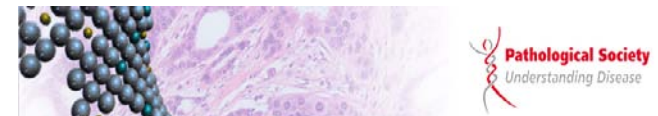
Michael Neat

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Bloodwise

Beating blood cancer since 1960



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