

LEUCEMIA LINFATICA CRONICA:

L'INNOVATIVITÀ TERAPEUTICA ED
OLTRE...



Modalità diverse di resistenza

CIT BTKi BCL2i

- Genetic lesions and pathways
- Time of appearance
- Practical consequences

Antonio Cuneo



 università di ferrara
DA SEICENTO ANNI GUARDIAMO AVANTI.



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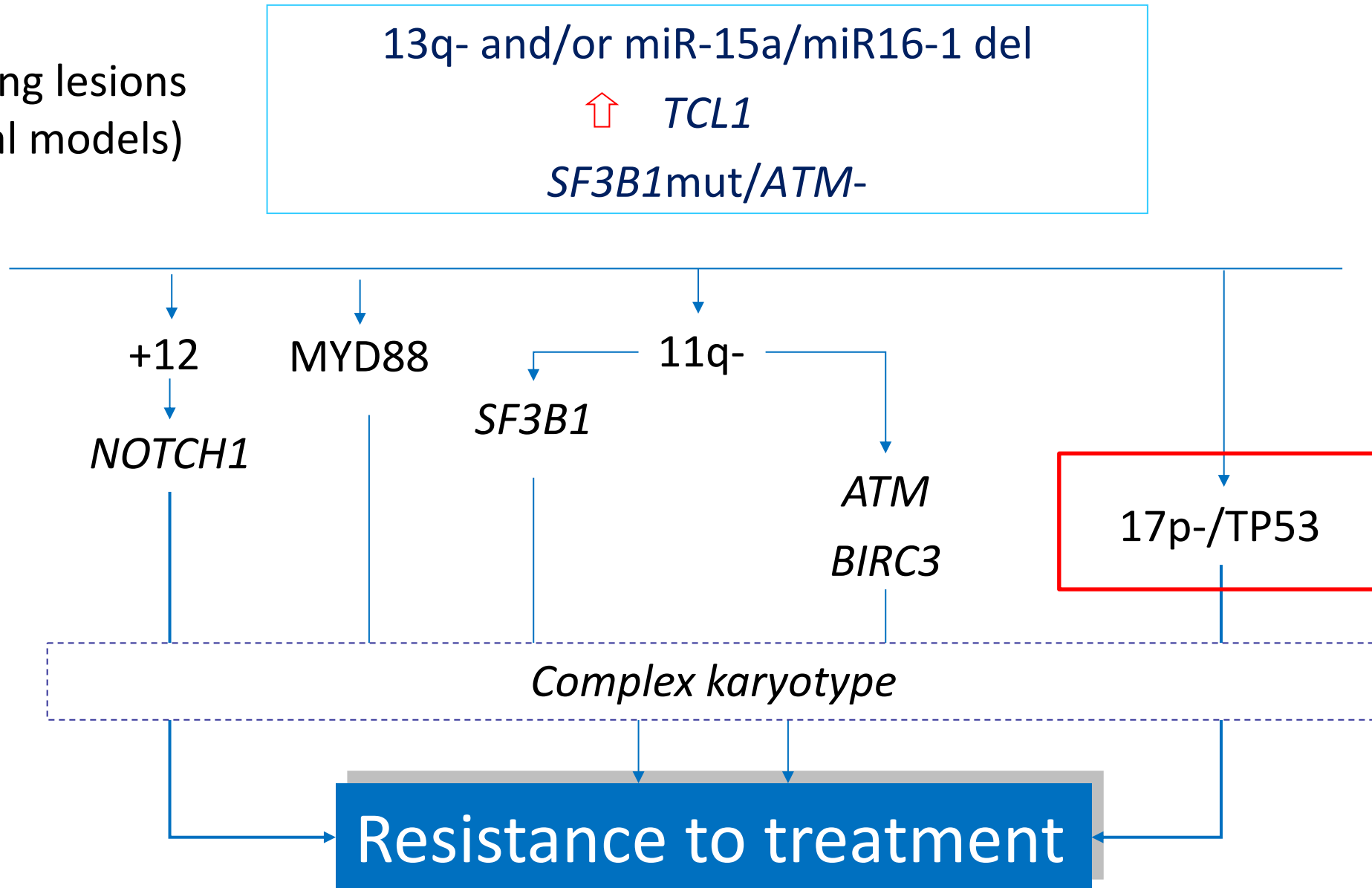


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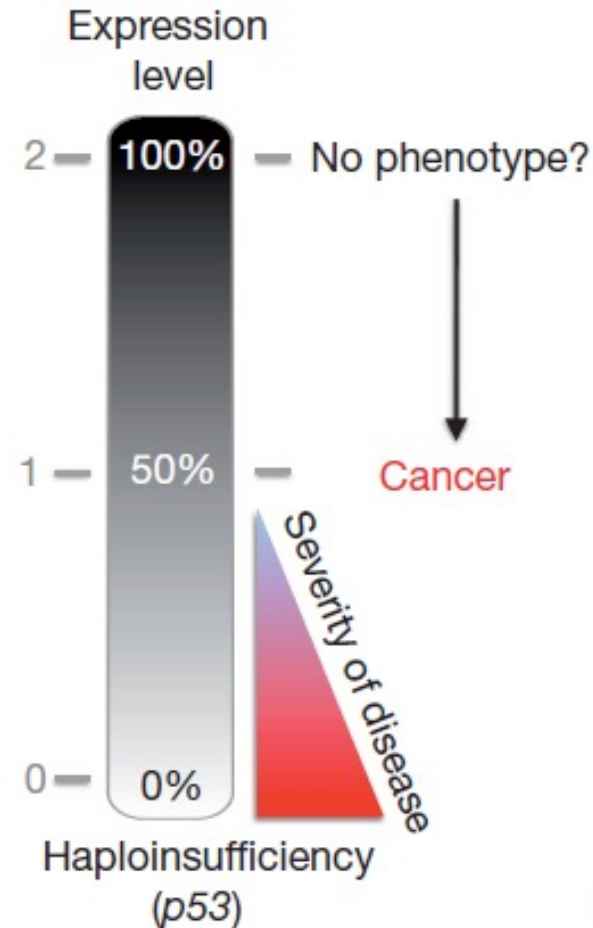
Sequential development of molecular cytogenetic lesions in CLL

Initiating lesions
(animal models)

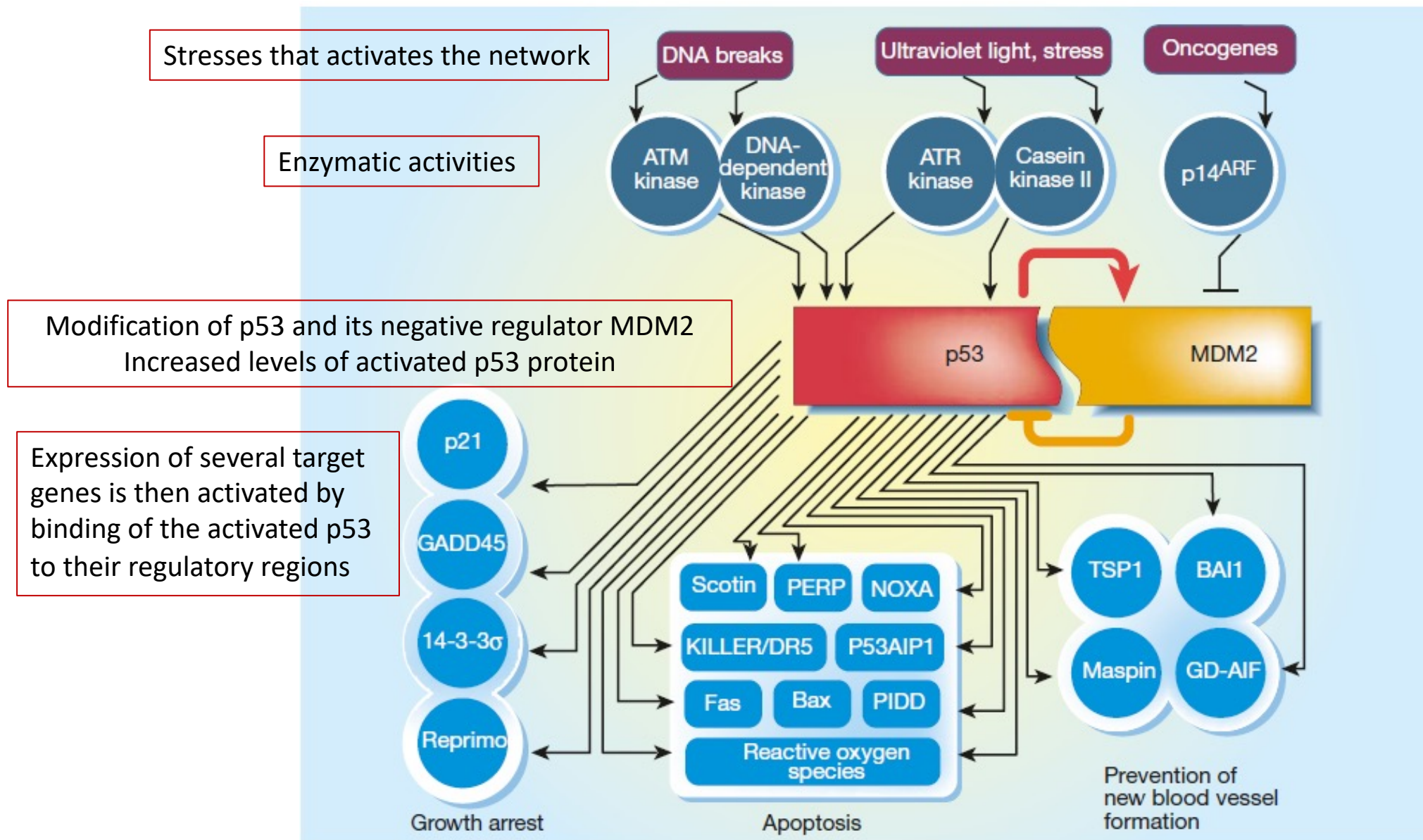


Paradigms of tumour suppression: Classical haploinsufficiency

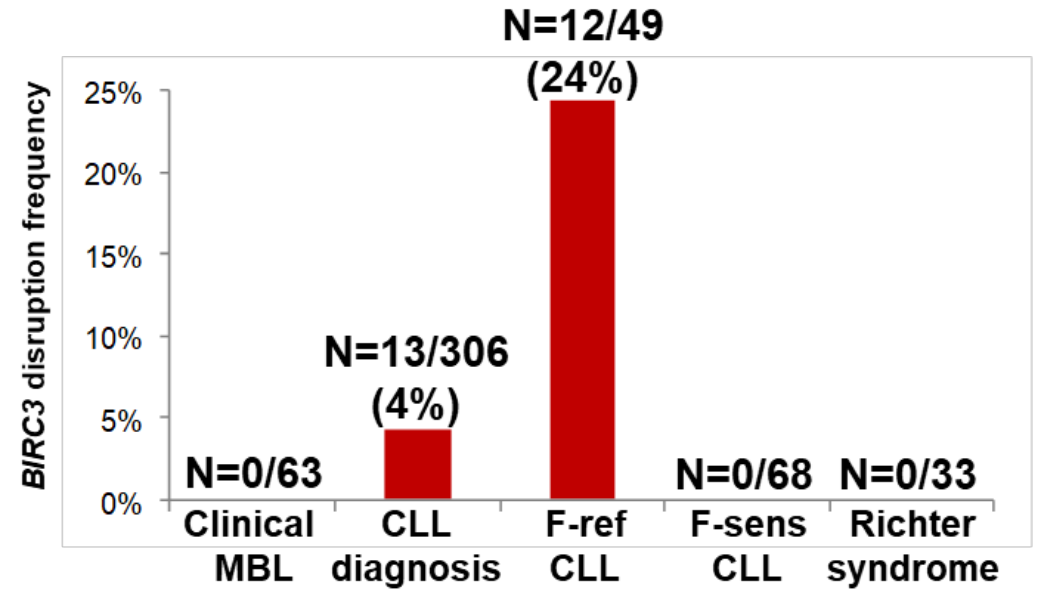
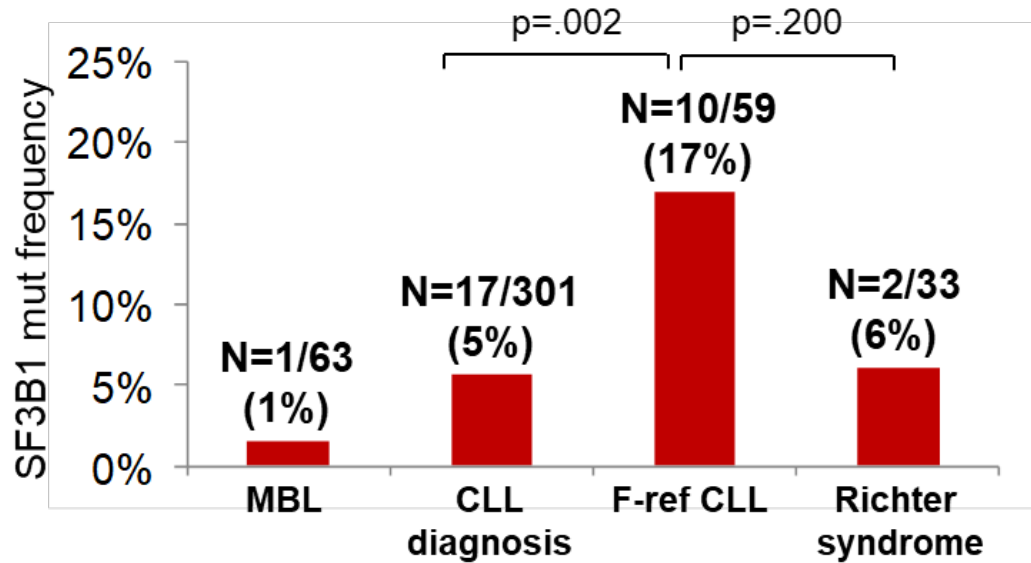
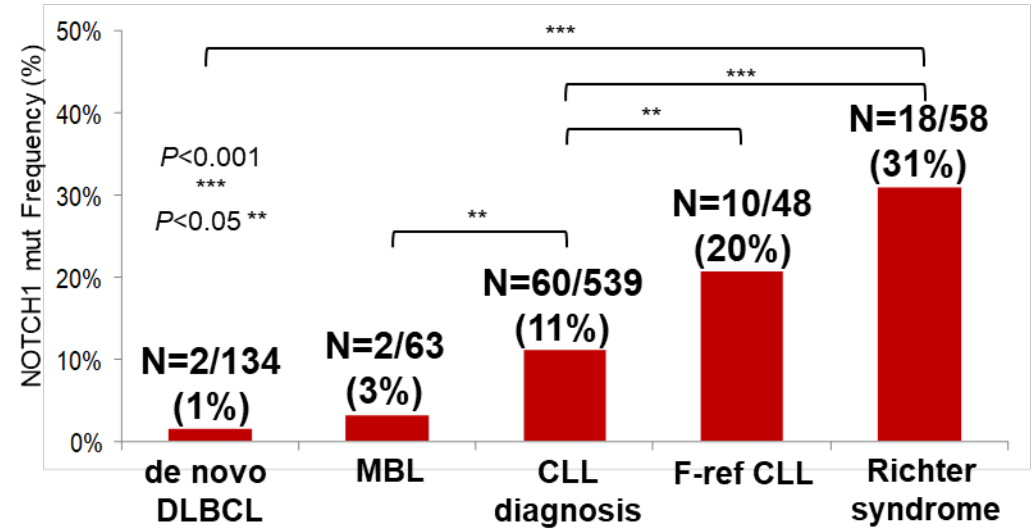
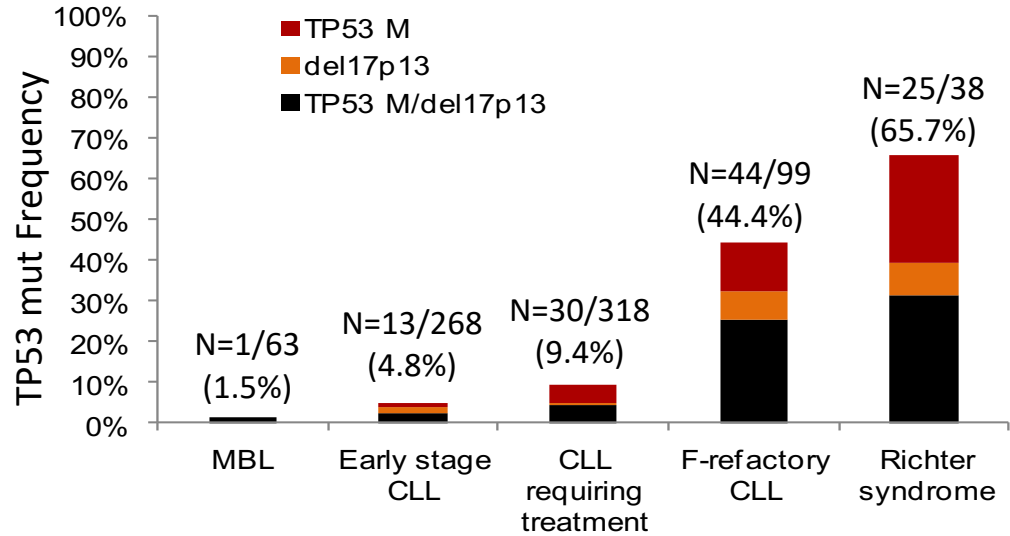
Loss of one TP53 allele is sufficient for induction of cancer.



Activation of the p53 network



TP53, NOTCH1, SF3B1 and BIRC3 abnormalities in CLL



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TP53, SF3B1, NOTCH1, BIRC3

Genomic complexity



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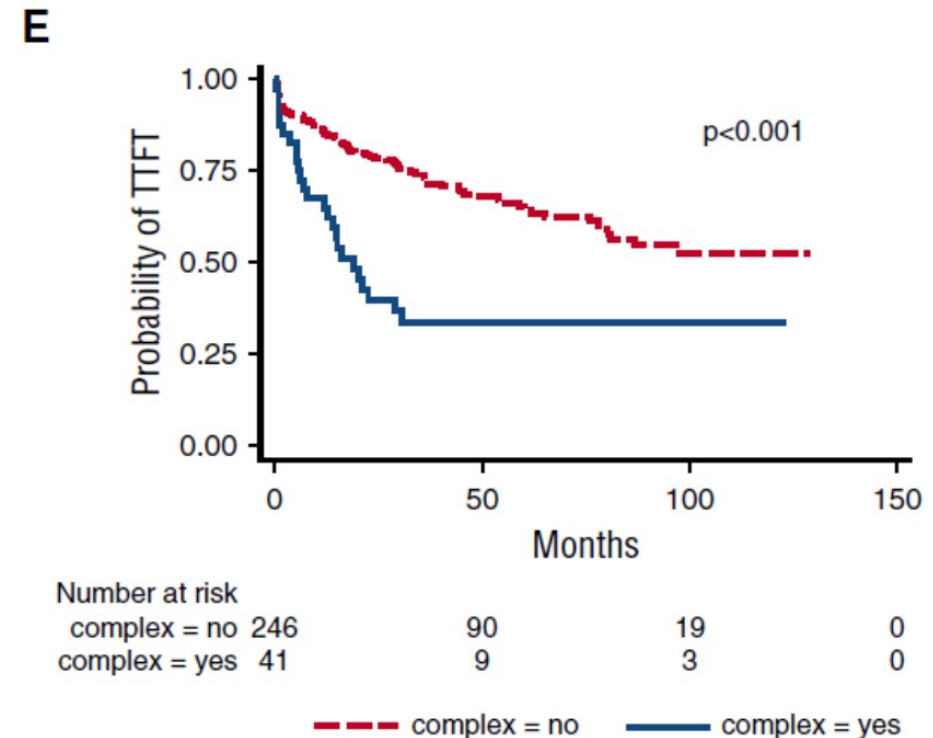
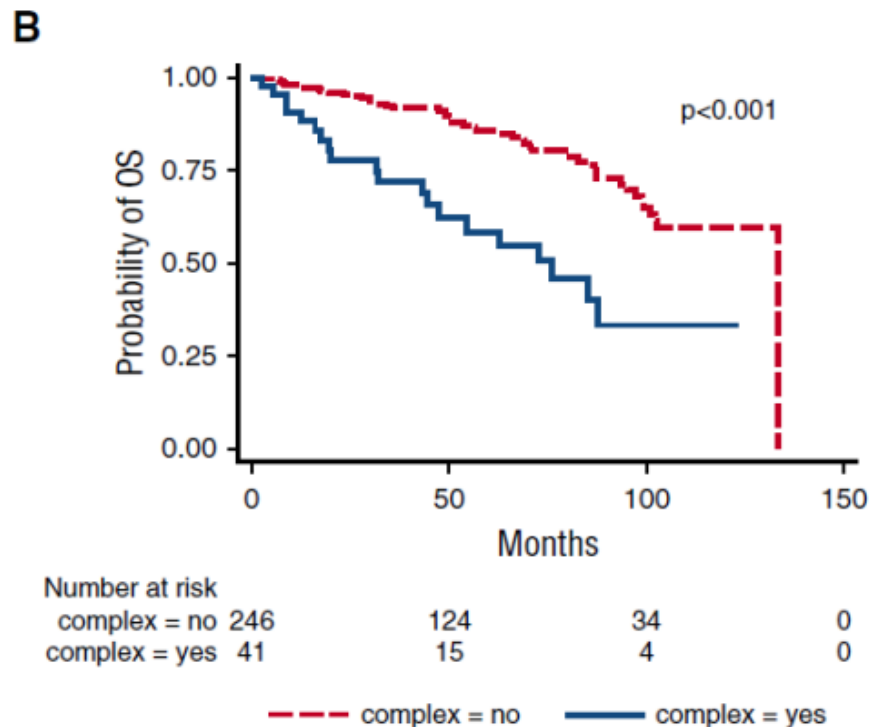


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In CLL the complex karyotype is associated with an inferior outcome

335 untreated CLL patients diagnosed and followed at our center between 2006 and 2016



At MVA, CK confirmed its negative prognostic impact both on OS ($p=0.002$) and TTFT ($p=0.012$),
independent of CLL-IPI

Practical consequences: options for first line treatment of CLL in 2023

no 17p-/no TP53 mutation

17p- and/or TP53 mutation

Finite duration

Continuous treatment

Venetoclax+O^^
(12 mos, oral and IV administration)

Ibrutinib + Venetoclax**
(15 mos., oral administration)

FCR only in «fit» and IGHV mutated
(6 mos., IV administration)

Chlor+O/BR only «unfit» and IGHV mutated
(6 mos, oral and IV administration)

Acalabrutinib
(take BID)

Ibrutinib
(take once a day)

Zanubrutinib**
(take BID)

Acalabrutinib
Ibrutinib
Zanubrutinib**

Ibrutinib + Venetoclax

Venetoclax+O

Idelalisib + R*

^^ In patients non-eligible to FCR in Italy; *only in patients with contra-indications for other therapies; **not reimbursed in Italia as of June 2023

O=Obinutuzumab; Chlor: Clorambucile; R=Rituximab; F: fludarabine; C: cyclophosphamide; BID: Bis in die

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Select known mechanisms of BTK inhibitor resistance

Gene or chromosome region affected	Mechanism of BTK inhibitor resistance	B-cell malignancies affected
BTK	Turns covalent bond into noncovalent	CLL, WM, MCL, MZL
PLC γ 2	Constitutive activation of BCR signaling pathway	CLL, MCL, MZL
Del(8p)	Downregulation of TRAIL-induced apoptosis	CLL, WM
CARD11	BTK-independent activation of BCR signaling pathway	CLL, DLBCL, FL, MCL, WM
TRAF2, TRAF3, BIRC3, MAP3K14	Constitutive activation of alternative NF- κ B pathway leading to cell survival independent of BCR signaling	MCL
ARID2, SMARCA2, SMARCA4	Increased BCL-XL, an antiapoptotic protein, limiting cell death	MCL
MYD88, KLHL14	Promotes assembly of multiprotein complex that constitutively activates NF- κ B pathway leading to cell survival independent of BCR signaling	DLBCL
TNFAIP3	Inactivation of negative regulator of NF- κ B, which constitutively activates NF- κ B pathway leading to cell survival independent of BCR signaling	DLBCL

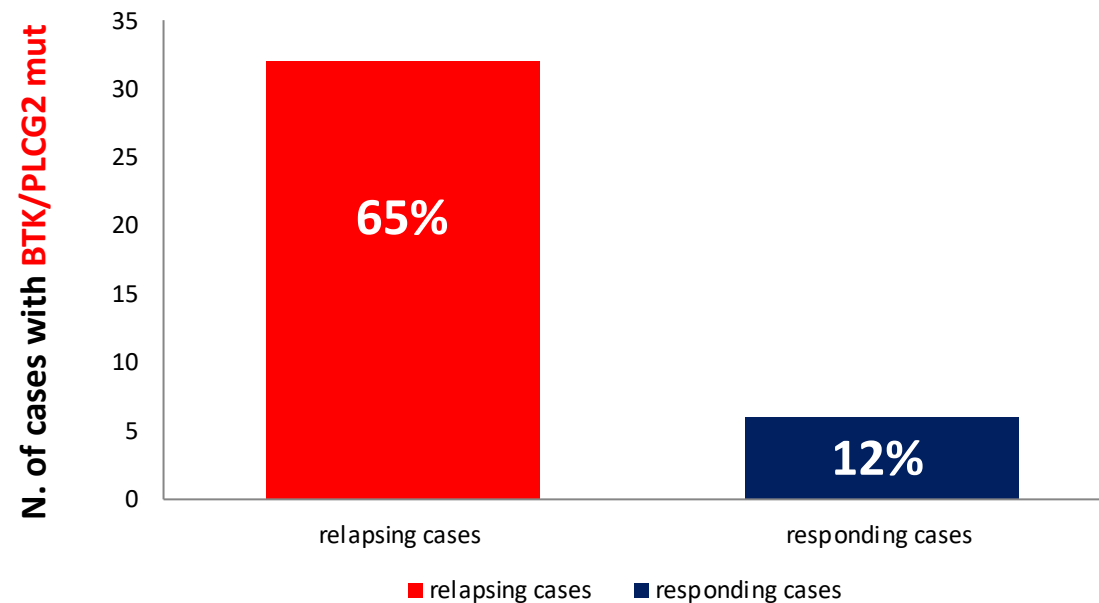
BTK and PLCG2 remain unmutated in one third of patients with CLL relapsing on ibrutinib

98 patients with CLL treated with ibrutinib

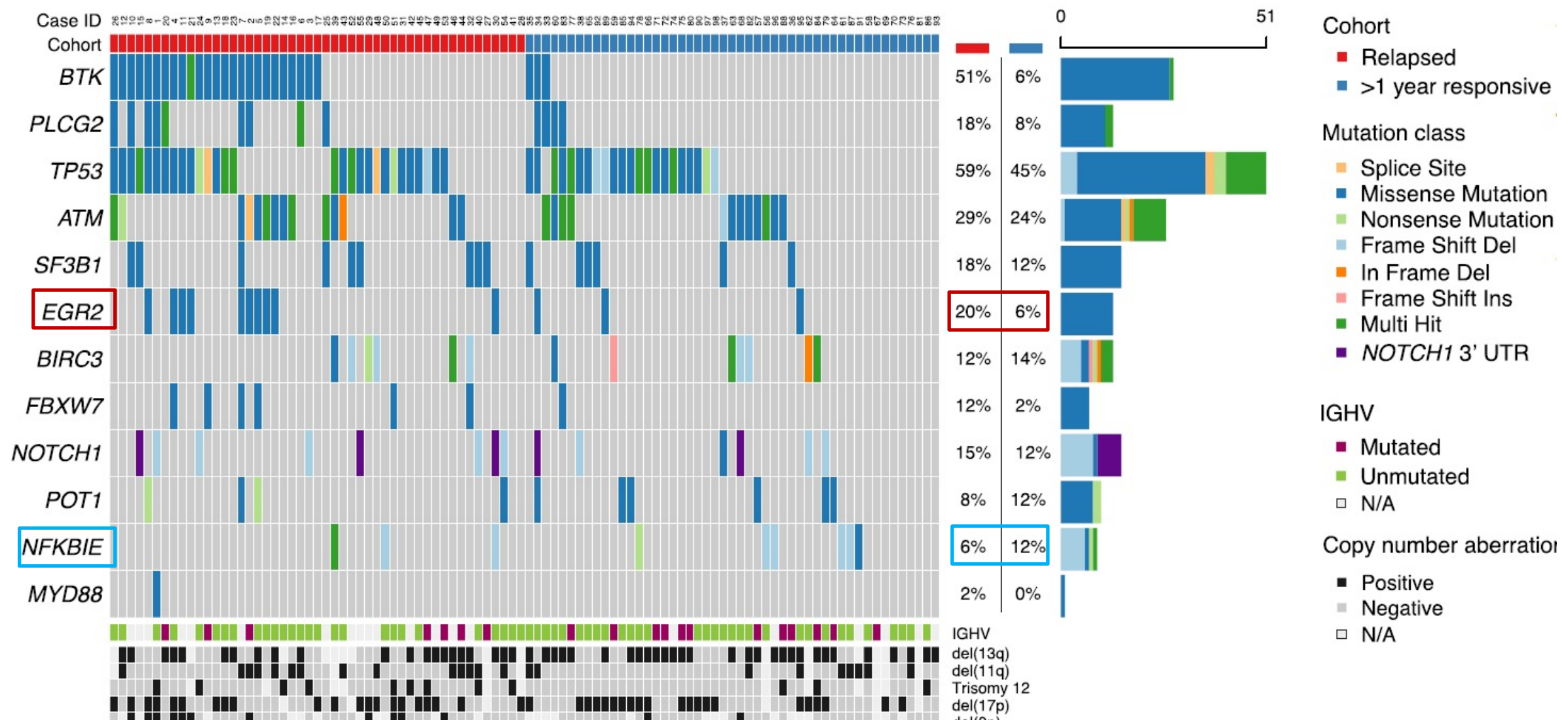
- NGS panel (1% sensitivity) comprising 13 CLL-relevant genes including BTK and PLCG2
- BTK hotspot mutations were validated by droplet digital PCR (0.1% sensitivity)

49 relapsing after an initial response

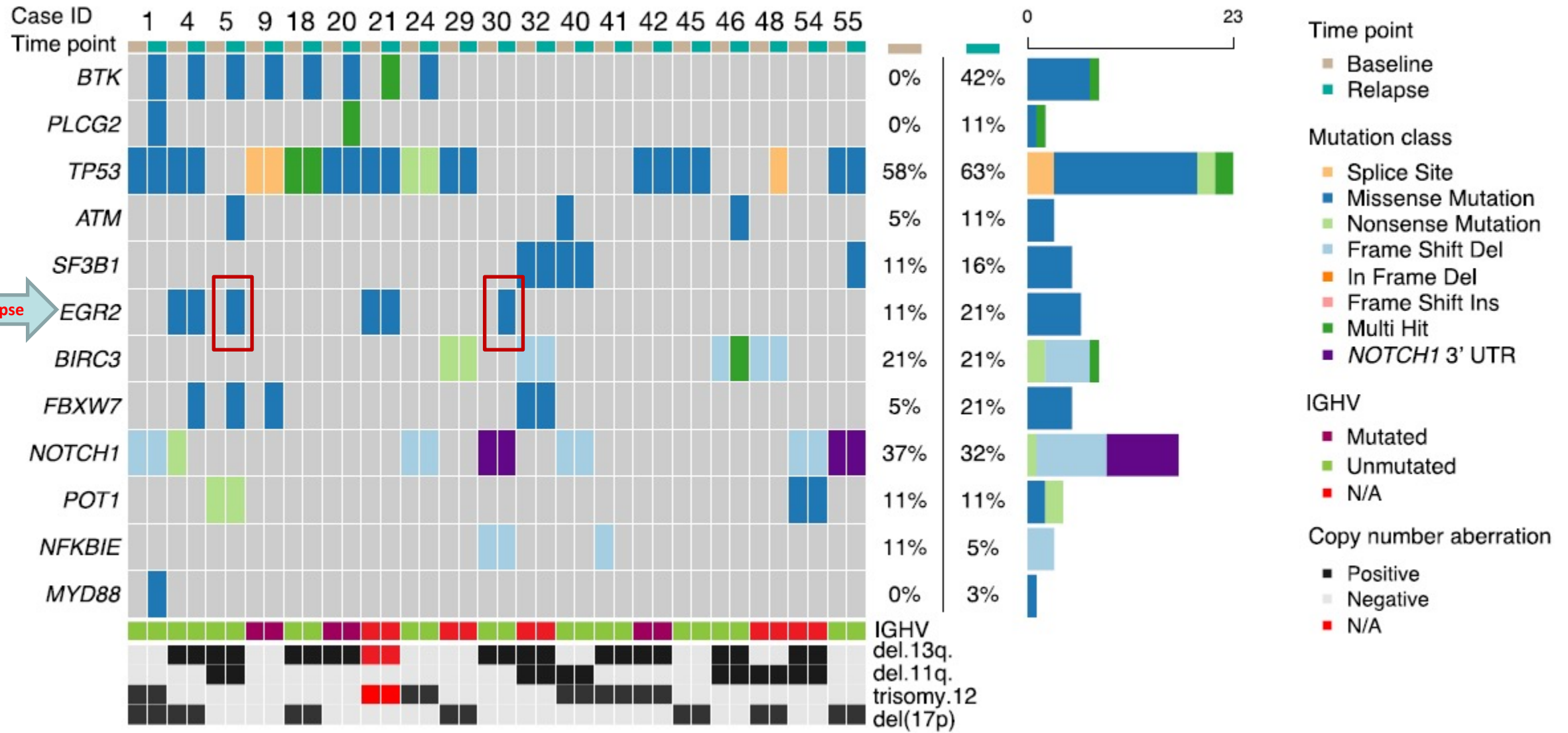
49 still responding after ≥ 1 year



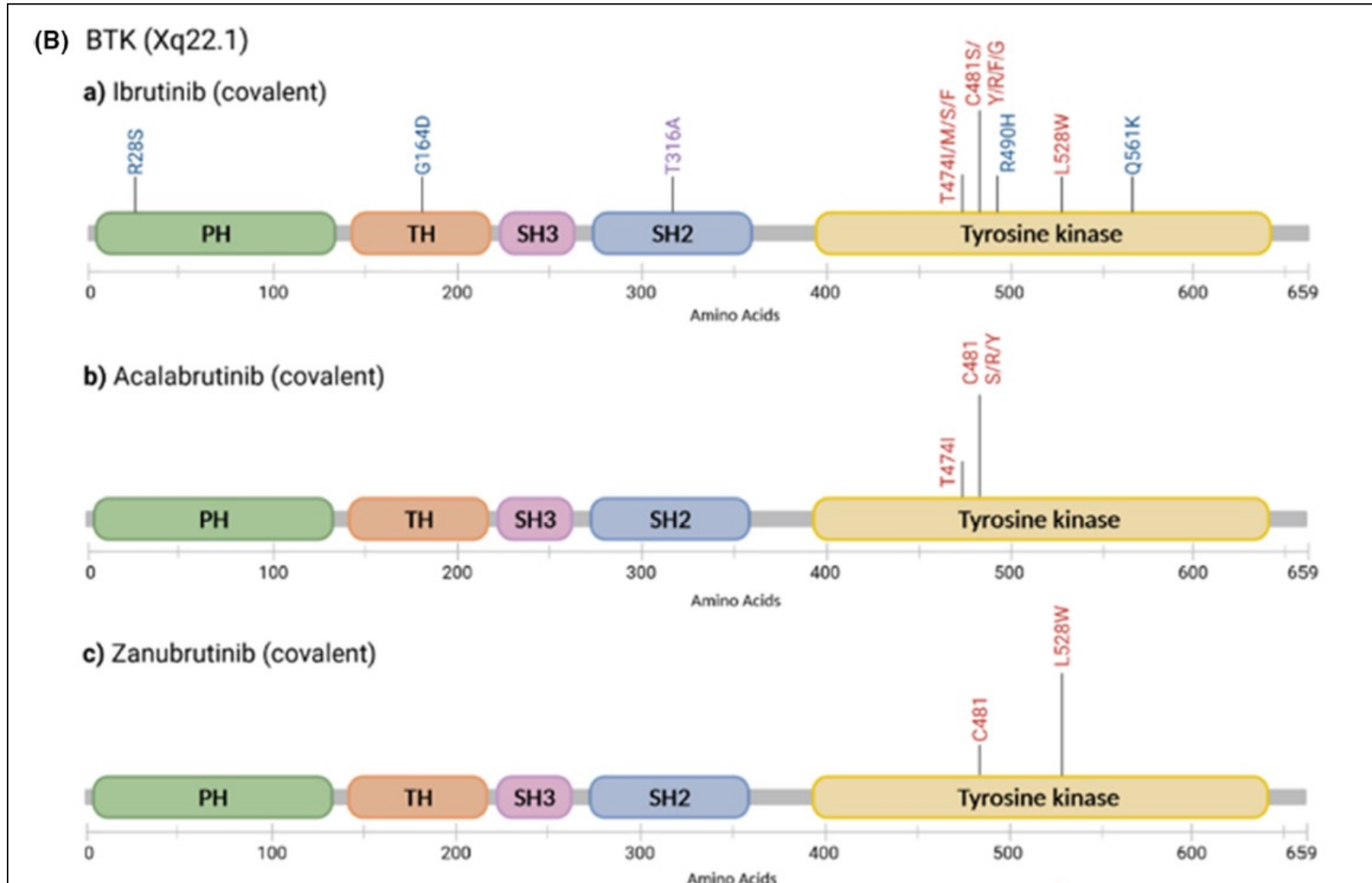
Somatic variants, IGHV mutational status, cytogenetic profile and the mutation frequency of each gene



Somatic variants in 19 patients with paired samples (at baseline and at relapse) of the relapsed cohort



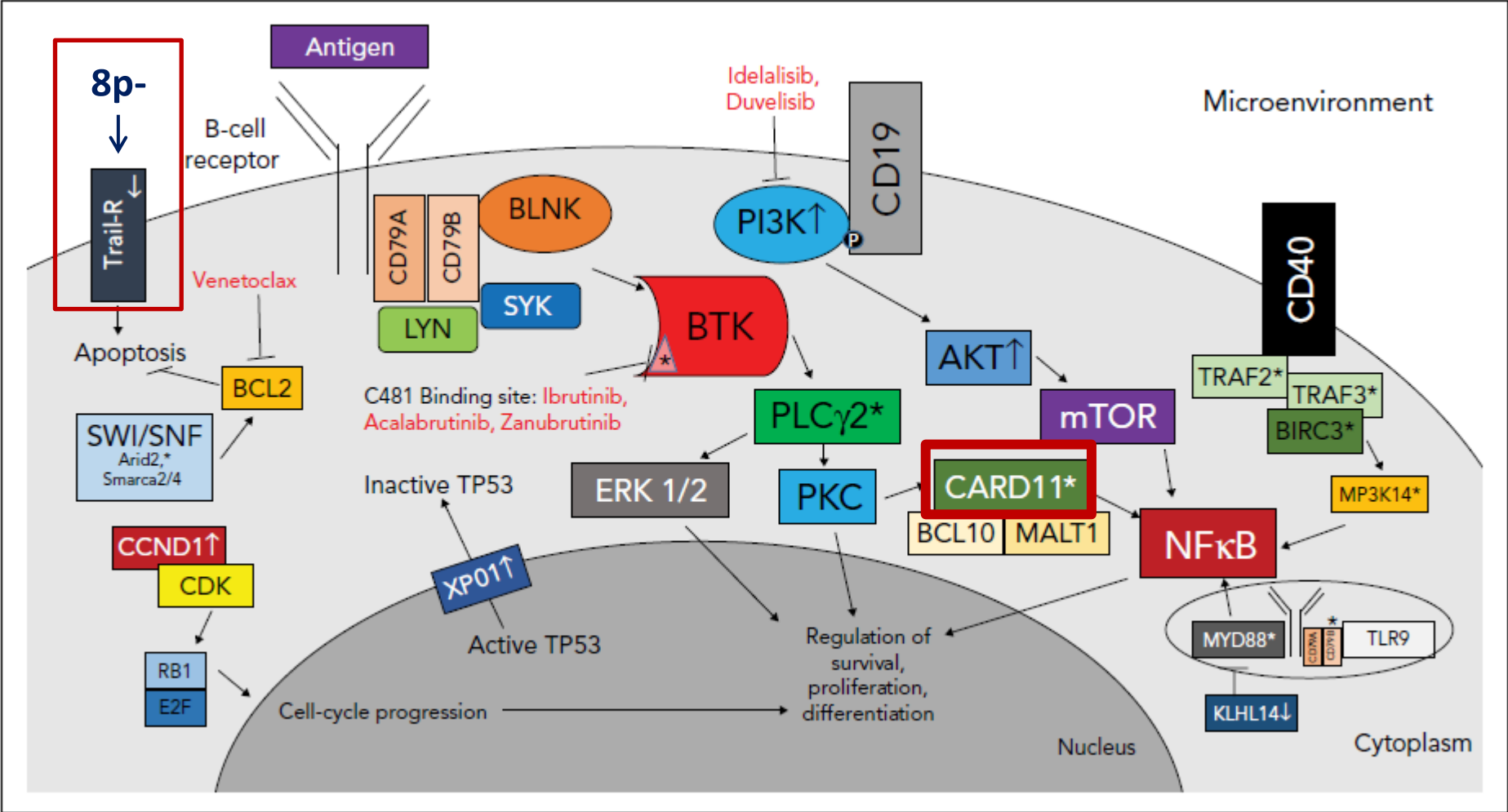
Clinically reported BTK mutations in patients treated with ibrutinib, acalabrutinib, zanubrutinib



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Overview of the BCR pathway with highlighted mechanisms of BTKi resistance



*Location of known BTKi resistance mutation

TRAIL: tumour necrosis factor related apoptosis-inducing ligand

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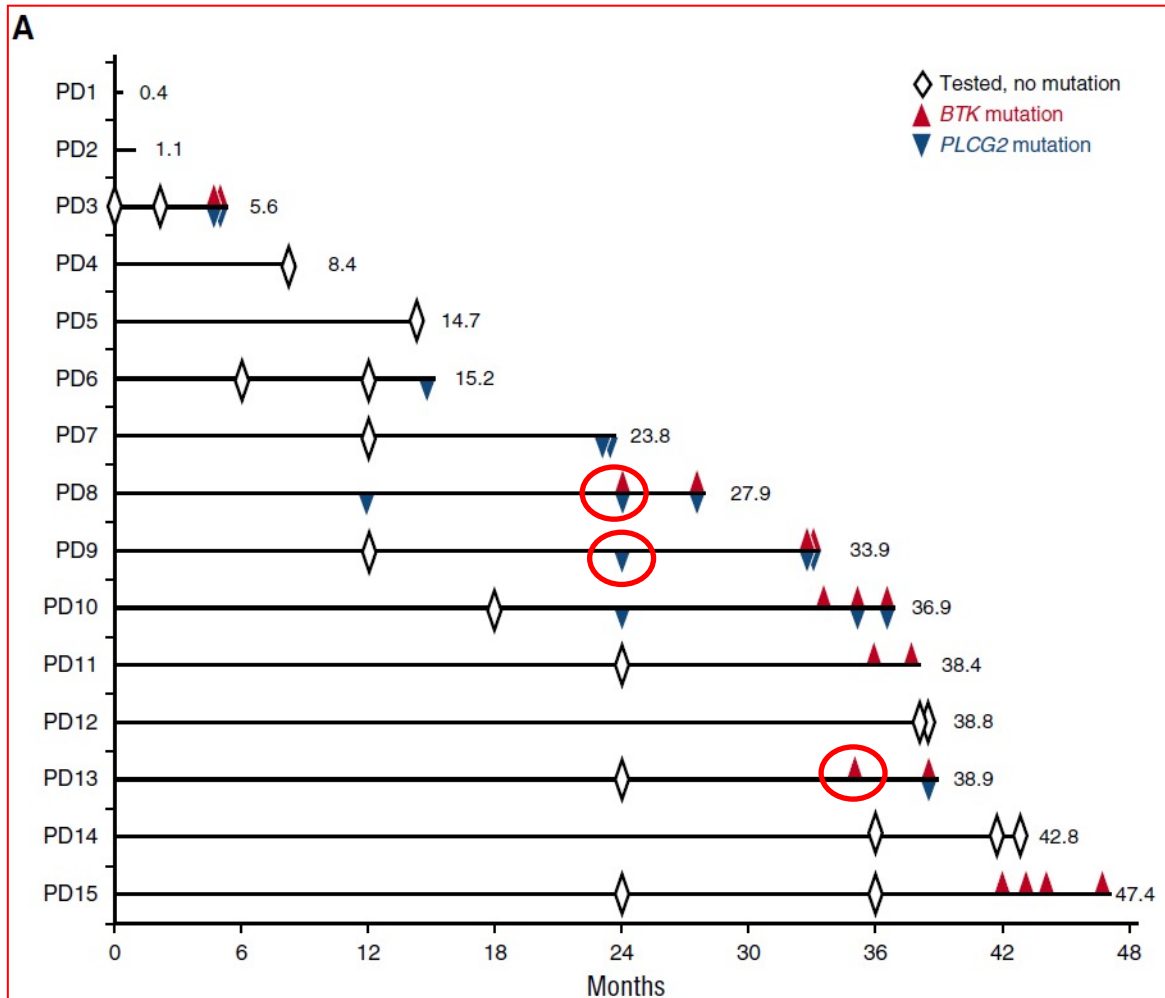


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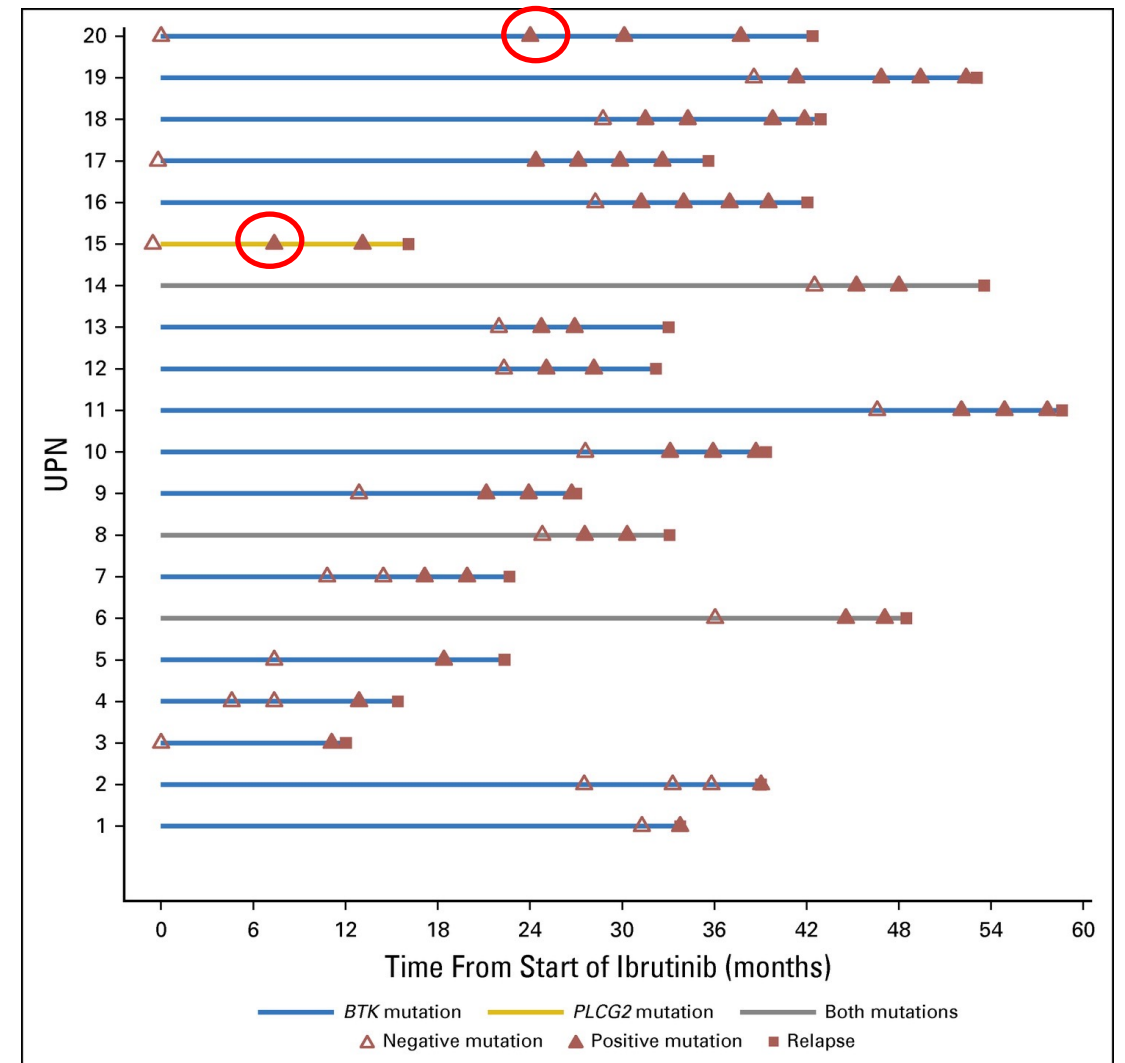


Clonal evolution during treatment with ibrutinib

15 patients who progressed on ibrutinib

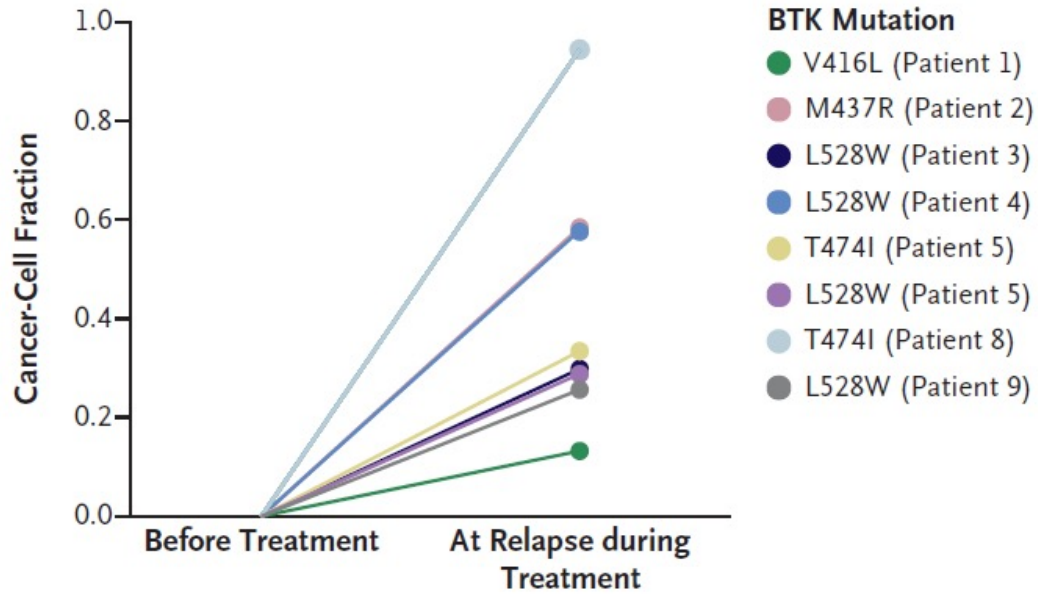


20 patients who progressed on ibrutinib

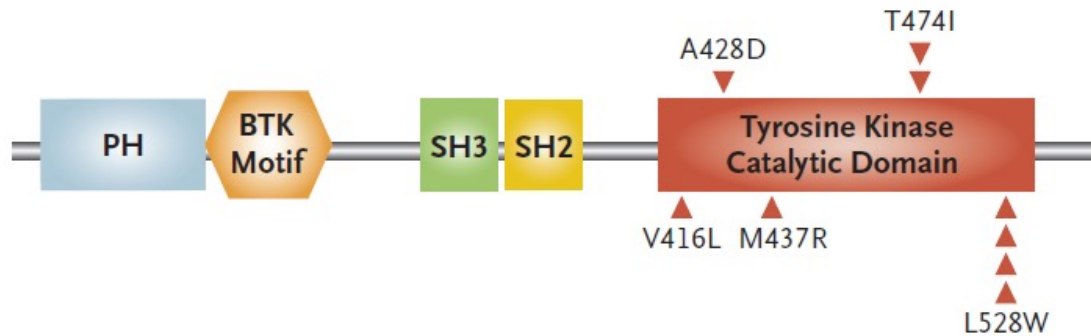


BTK Mutations in 9 CLL with Acquired Resistance to the Noncovalent BTK Inhibitor Pirtobrutinib

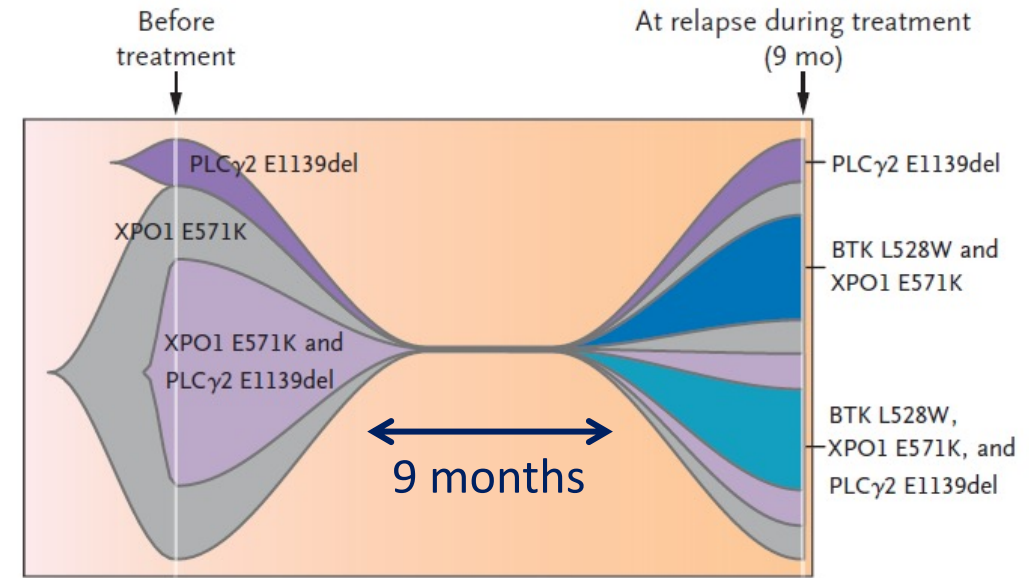
A Cancer-Cell Fraction of Non-C481 BTK Mutations



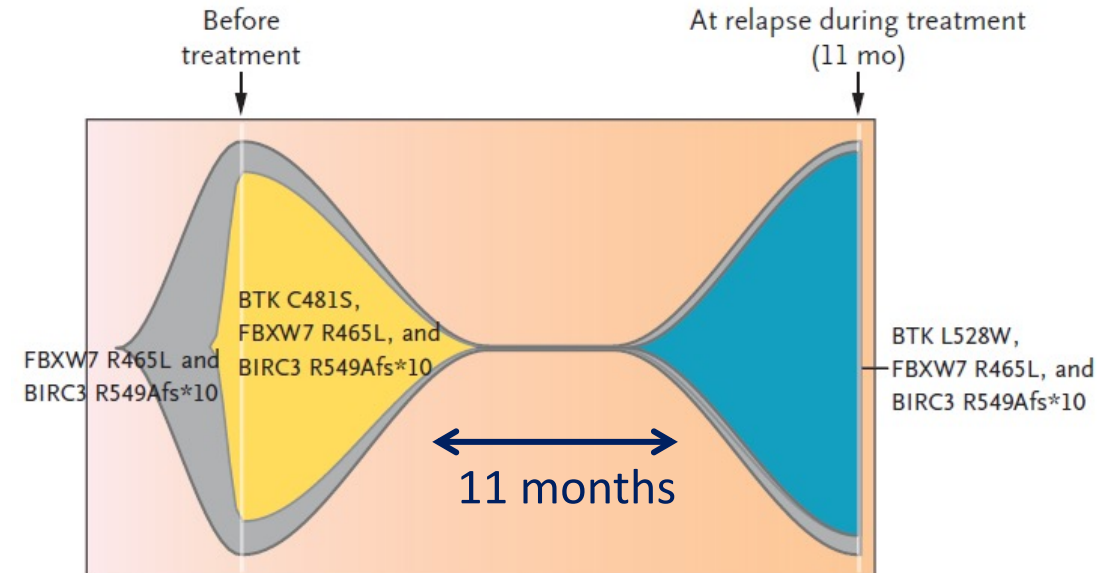
B Locations of BTK Mutations



C Mutations in Patient 3



D Mutations in Patient 4



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Members of the BCL-2 family and their role

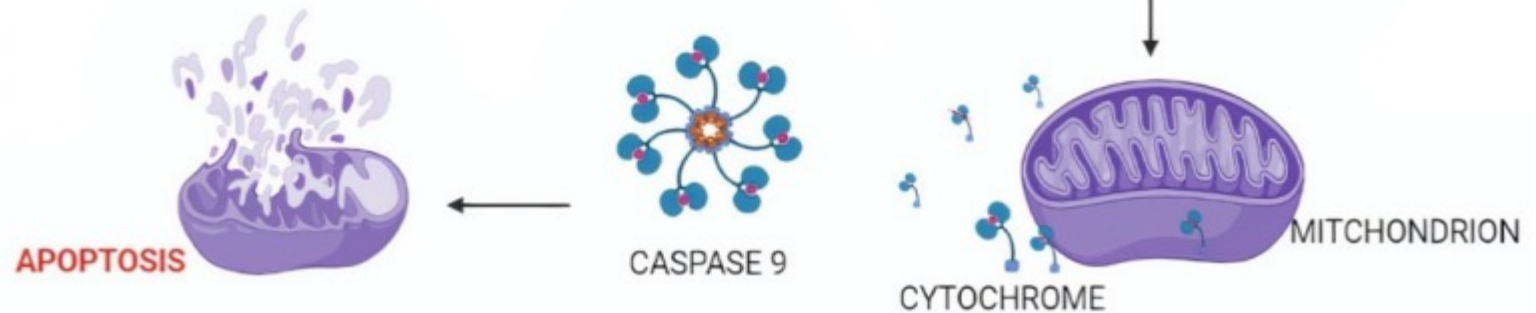
Schematic representation of the members of BCL-2 family and his subunits



BH: Bcl-2 Homology domain, necessary for protein function

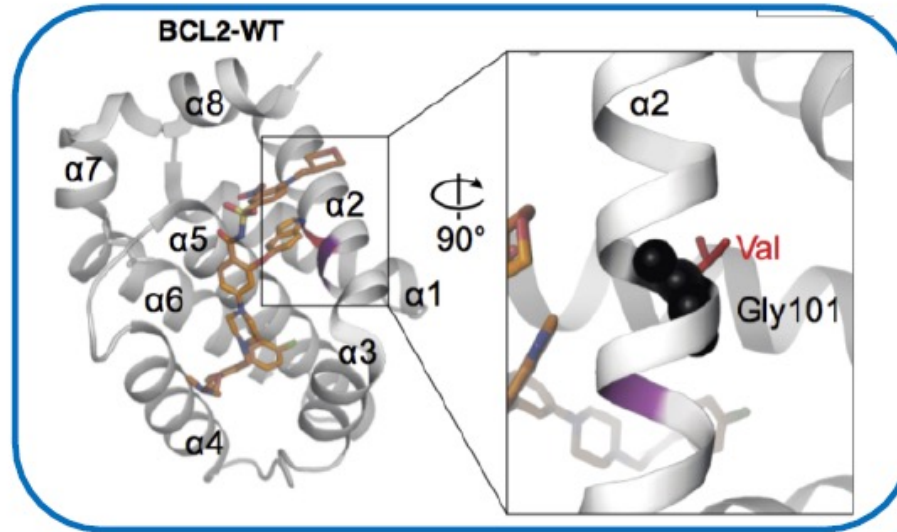
Targeting the intrinsic pathway of apoptosis

- Pro-apoptotic factors trigger BH3-only proteins
- Binding and inhibition of BCL2.
- Larger amounts of BAK and BAX rendered free.
- BAK and BAX dimerize
- Channel for Cytochrome-c leakage from the mitochondria
- Apoptosis



Mechanisms of Resistance to Venetoclax

BCL2 mutations



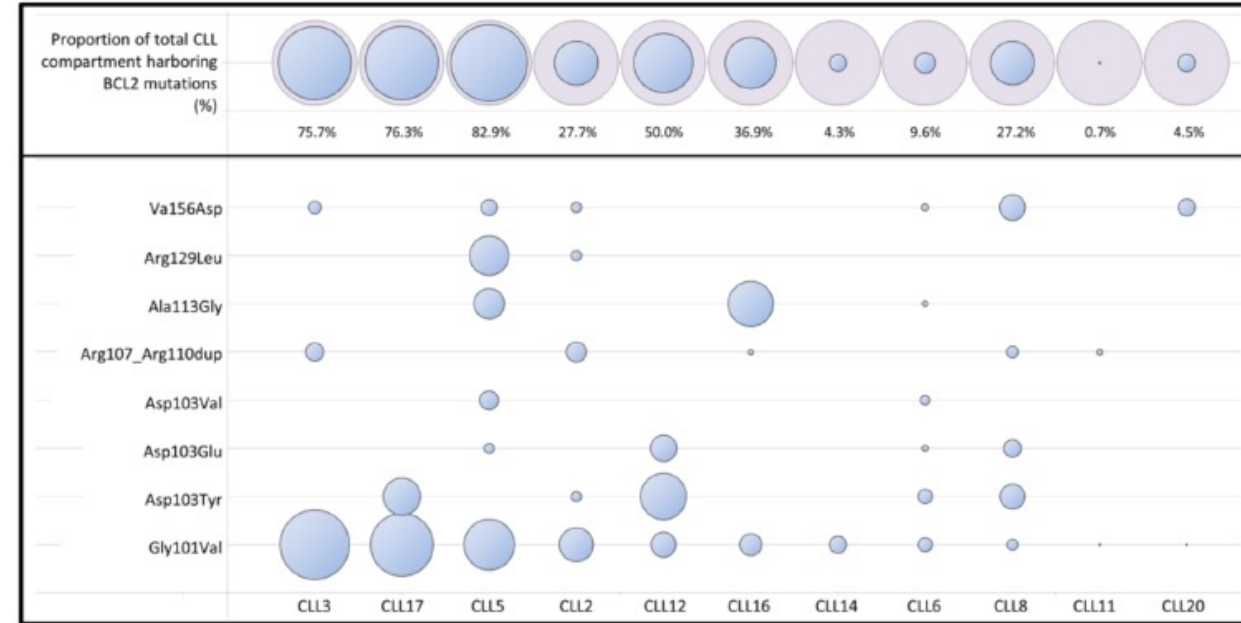
BCL2 Protein	Venetoclax K_i (nM \pm SD, n=3)	
Wildtype	0.018 \pm 0.014	180-fold reduction
Gly101Val	3.2 \pm 1.1	

Blombery *Cancer Discovery* 2019; Birkinshaw *Nat Comms* 2019

Mechanisms of Resistance to Venetoclax

BCL2 mutations

- Almost exclusively occur in context of ven exposure
- Maintain pro-survival function
- Reduce ven binding to BCL2
- Multiple sites, multiple clones



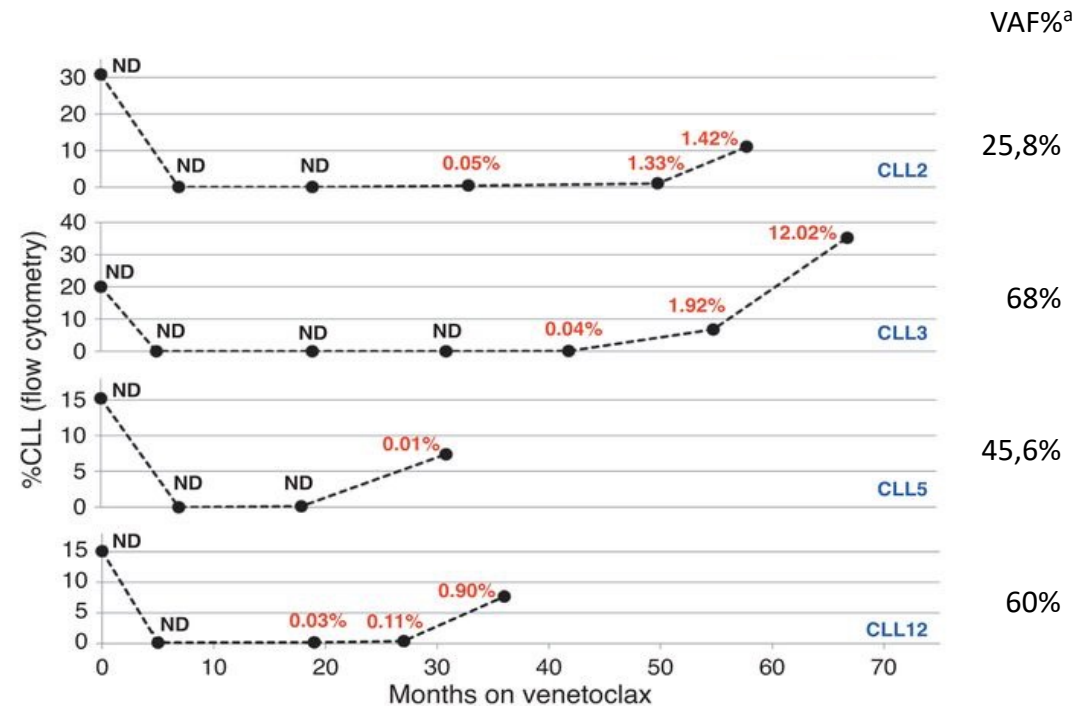
Blombery *Cancer Discovery* 2019; Birkinshaw *Nat Comms* 2019; Tausch *Haematologica* 2019; Blombery *Blood* 2020

BCL2 Gly101Val is specific for CLL with resistance to Venetoclax

Population	Number assessed	<i>BCL2</i> Gly101Val detected (%)	<i>BCL2</i> Phe104Leu detected (%)
Venetoclax-naïve CLL	96	0 (0%)	0 (0%)
CLL-type progression on venetoclax	15	7 (46.7%)	0 (0%)
Other B-cell malignancies			
- Follicular lymphoma	28	0 (0%)	0 (0%)
- Mantle cell lymphoma	28	0 (0%)	0 (0%)
- Diffuse large B-cell lymphoma	47	0 (0%)	0 (0%)
- Lymphoplasmacytic lymphoma	95	0 (0%)	0 (0%)
- Multiple myeloma	103	0 (0%)	0 (0%)
Cancer database (COSMIC ^a)	47,628	0 (0%)	2 (0.004%)
Population database (gnomAD ^b)	30,836	0 (0%)	0 (0%)

Time course of CLL response and subsequent emergence of Gly101Val mutation during venetoclax therapy

The CLL burden was measured by multi-parameter flow cytometry in serial BM aspirates from 4 patients from the initiation of venetoclax until the clinical diagnosis of progressive disease



^aCLL cells harboring G101V at progression; calculated by adjusting the measured VAF by the % of CLL cells in the bone marrow determined by flow cytometry.

Different mechanisms account for VEN resistance

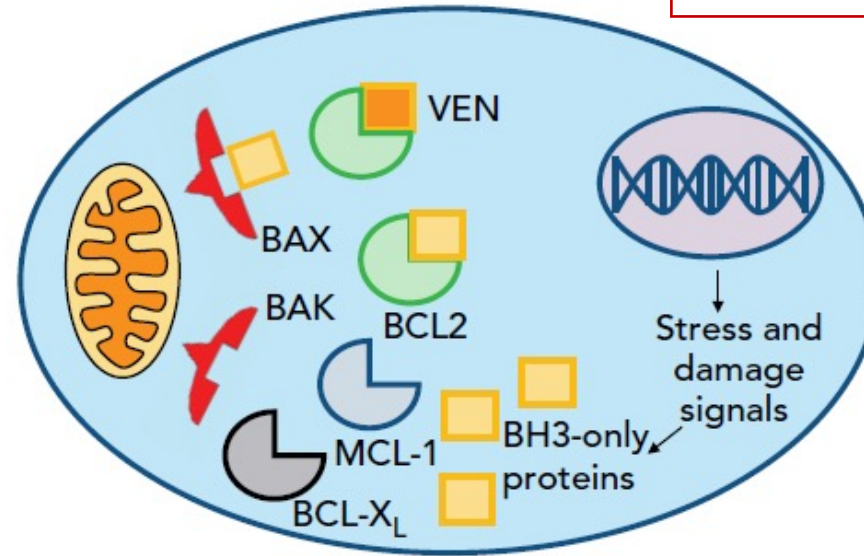
Sustained Ven exposure

BCL2 mutations

- Gly101Val/Ala
- Val156Asp
- Arg129Leu
- Ala113Gly
- Arg107_Arg110dup
- Asp103Glu/Tyr/Val
- Phe104Leu/Ser
- Leu119Val

Alternative BCL2 family proteins

- BCL-X_L upregulation
- Copy number gain *MCL-1*
- Amplification chromosome 1q23 (*MCL-1*)
- Microenvironment driven BCL-X_L, BLF-1, and *MCL-1* upregulation
- *BRAF* mutation, potentially upregulating *MCL-1*



Genomic instability

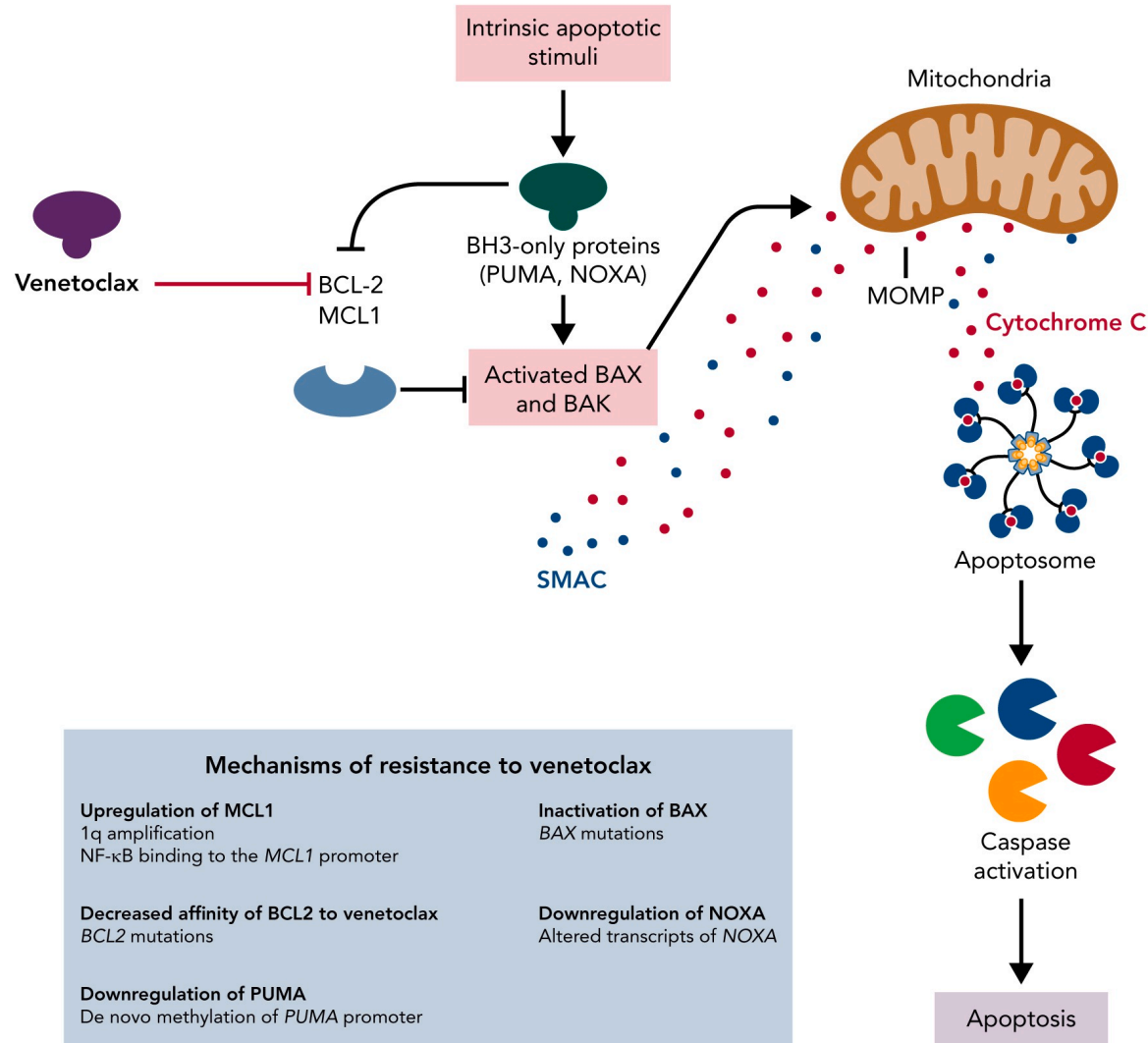
- Acquisition of *TP53* aberrations
- Evolution of complex karyotype

Other

- *BTG1* mutations
- *CDKN2A/B* homozygous deletions
- Amplification of *PD-L1*
- Amplification of *PRKAB2*

Early events?

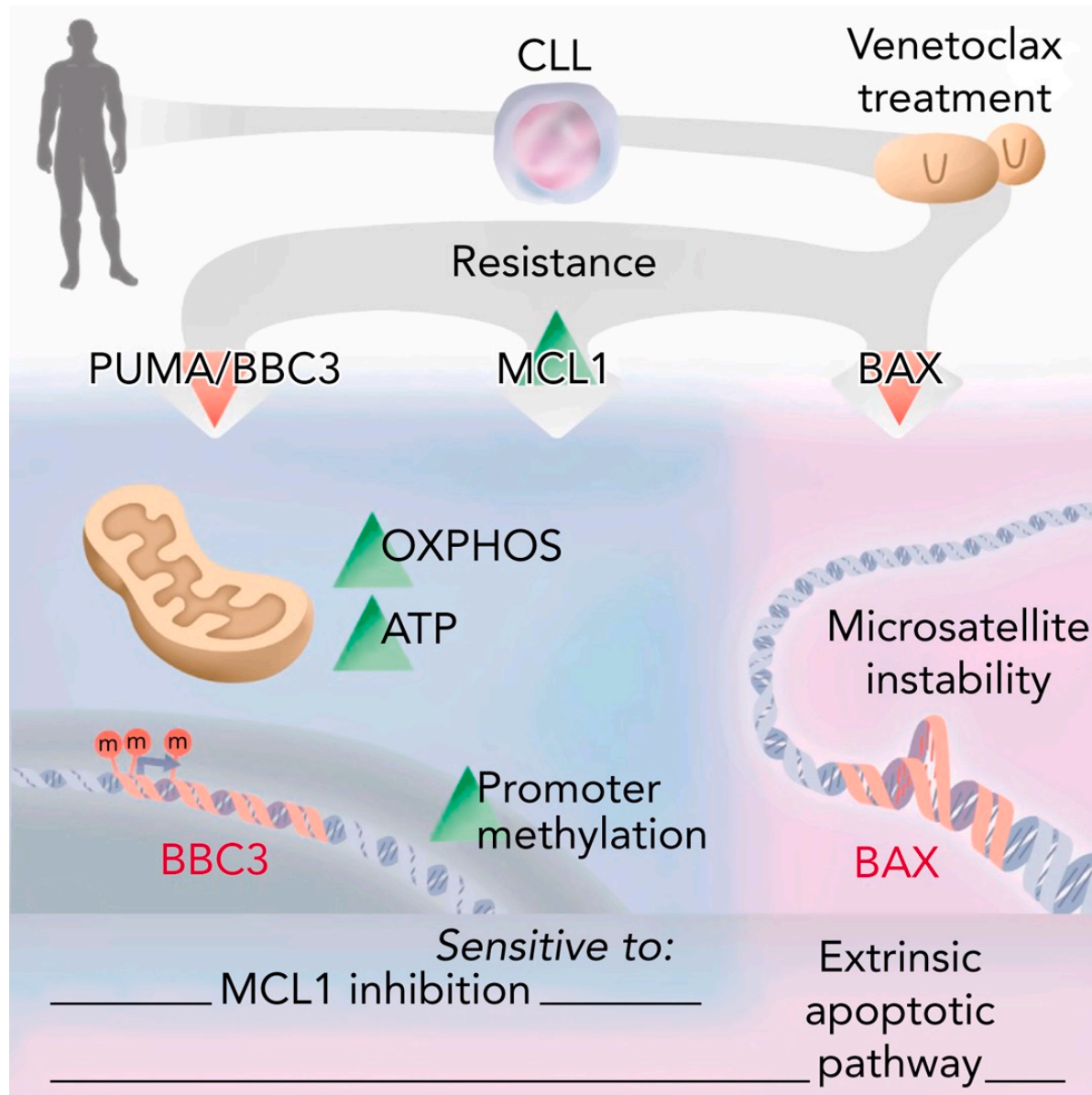
Mechanisms of resistance to venetoclax



MOMP, mitochondrial outer membrane permeabilization; SMAC, second mitochondria-derived activator of caspase

- De novo methylation of the PUMA promoter (downregulation of PUMA expression)
- MCL1 overexpression dominates in venetoclax-resistant clones
- Marked NF-κB activation and NF-κB binding to the MCL1 promoter resulted in increased MCL1 expression in relapses occurring on venetoclax therapy.
- Multiple mechanisms of escape (eg, 1q24 amplification, BCL2 mutations, BAX mutations, and altered transcript of proapoptotic NOXA) may coexist in the same tumor, usually restricted to different subclones
- Some of these escape mechanisms are unique, others are found in multiple patients

Deregulation and epigenetic modification of BCL2-family genes cause resistance to VEN in hematologic malignancies



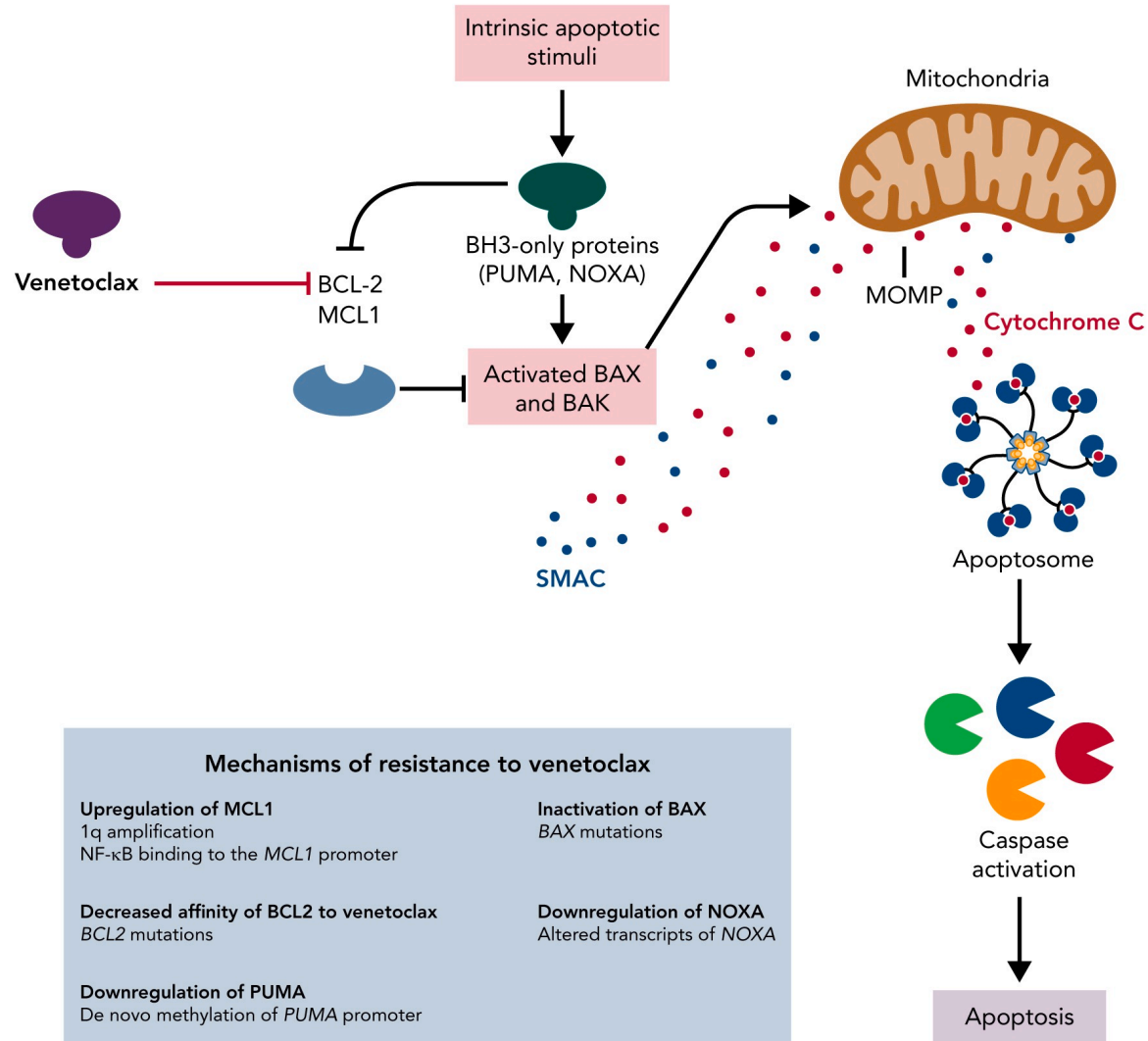
A CpG island within the PUMA promoter is methylated upon VEN treatment

Higher oxidative phosphorylation and adenosine triphosphate production, resembling the metabolic phenotype that is seen upon VEN resistance

PUMA loss is specific for acquired VEN resistance but not for acquired MCL1 resistance

BAX is essential for sensitivity toward both venetoclax and MCL1 inhibition

Mechanisms of resistance to venetoclax



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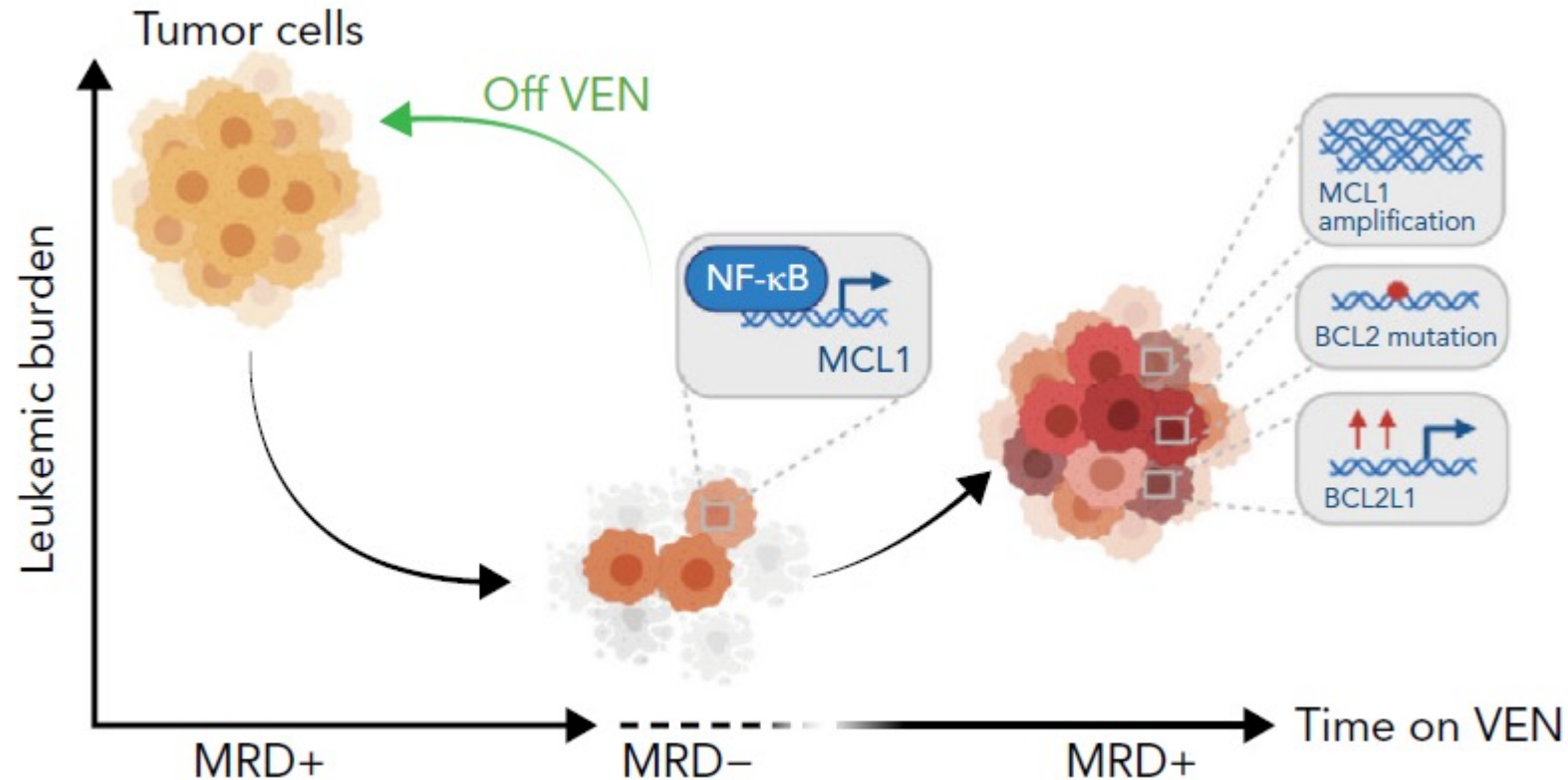
MOMP, mitochondrial outer membrane permeabilization;
 SMAC, second mitochondria-derived activator of caspase

Adalgisa Condoluci, Davide Rossi, Blood, 2022

Thijssen R, Blood. 2022; 140:2127-2141.

Mechanisms of resistance to venetoclax: study highlights

Epigenetic changes of resistance (ie, NF- κ B–promoted upregulation of MCL1) are driven and sustained by ongoing venetoclax therapy and they disappear once venetoclax therapy is stopped



Take home messages

Causes of resistance

- Selection of CIT resistant clones with TP53, SF3B1, NOTCH1, BIRC3 mutations and complex karyotype
- BTK and PLCG2 mutations account for $\approx 2/3$ of acquired resistance to covalent BTKi and were detected in patients with acquired resistance to non-covalent BTKi
- BTK/PCLG2 mutation may precede relapse by many months and may occur in multiple independent clones
- BCL2 mutations account for VEN resistance in $\approx 50\%$ of cases and anticipate disease progression by many months
- VEN resistance is multilayered and include epigenetic reprogramming

Implications

CIT is no longer an option in the vast majority of patients

Sequential studies to detect mutations are not necessary

The presence of BTK/PCLG2 mutations should prompt careful monitoring

Sequential studies to detect mutations are not necessary

Reversible epigenetic programming support fixed duration treatment