

Molecular Genetics of Small Mature B-cell Lymphomas

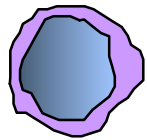
Elias Campo

Hospital Clinic, University of Barcelona

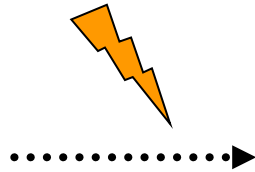
Barcelona, Spain

Genetic Drivers in Lymphomagenesis

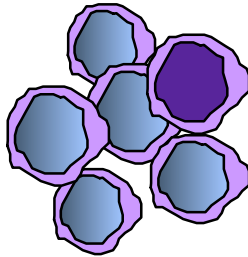
Clonal Population



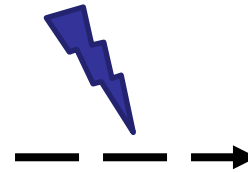
Primary Genetic Alterations



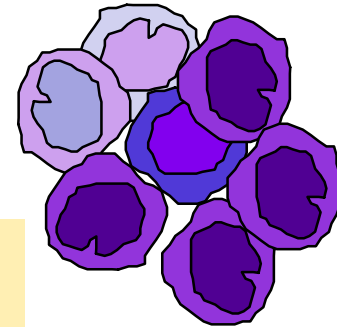
Overt Lymphoid Neoplasia



Secondary Genetic Alterations



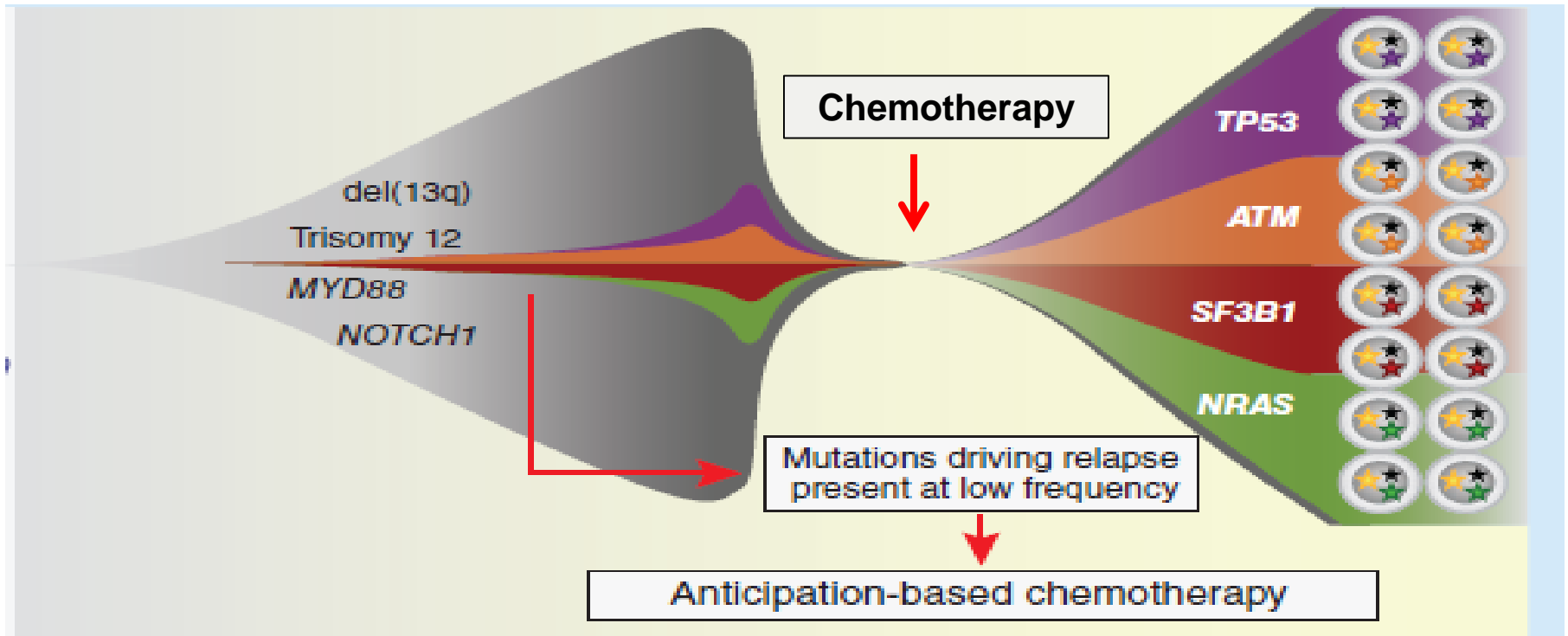
Progression/
Transformation



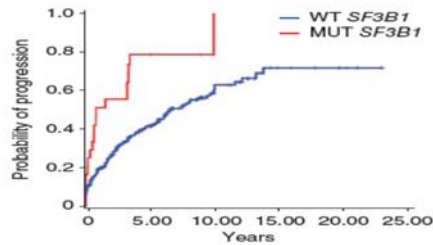
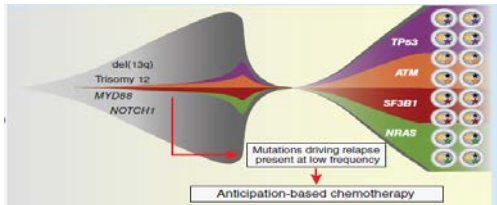
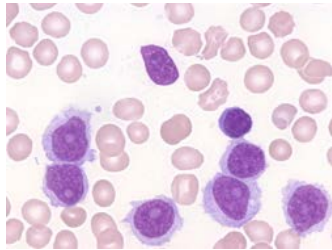
Microenvironment

Genetic alterations

The mutational profile is a dynamic process

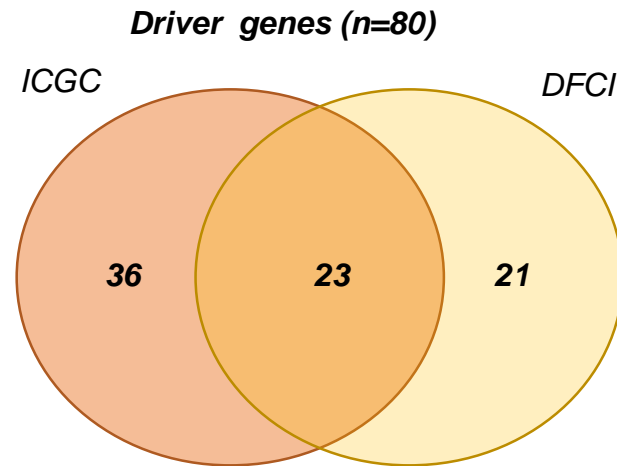
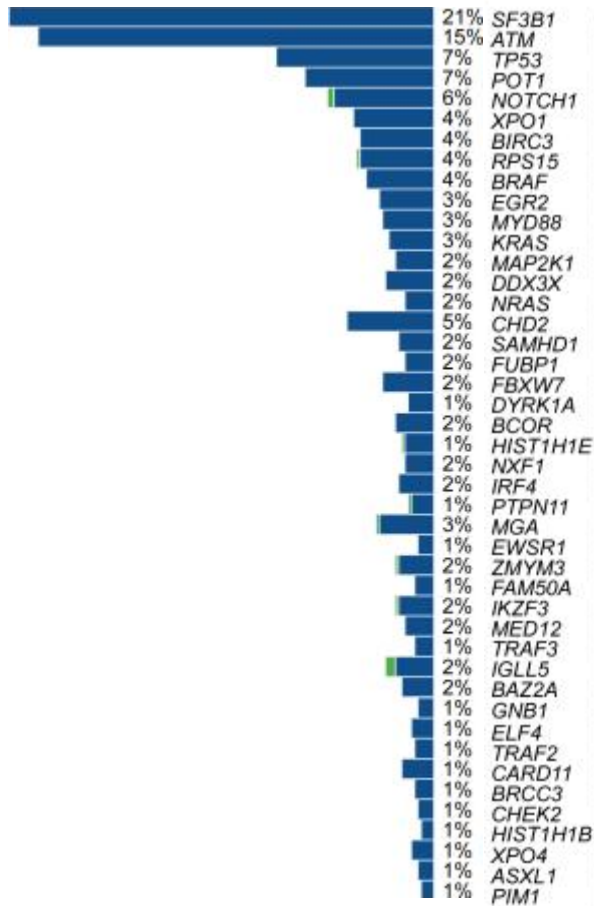


Impact of NGS in Small B-cell Neoplasms

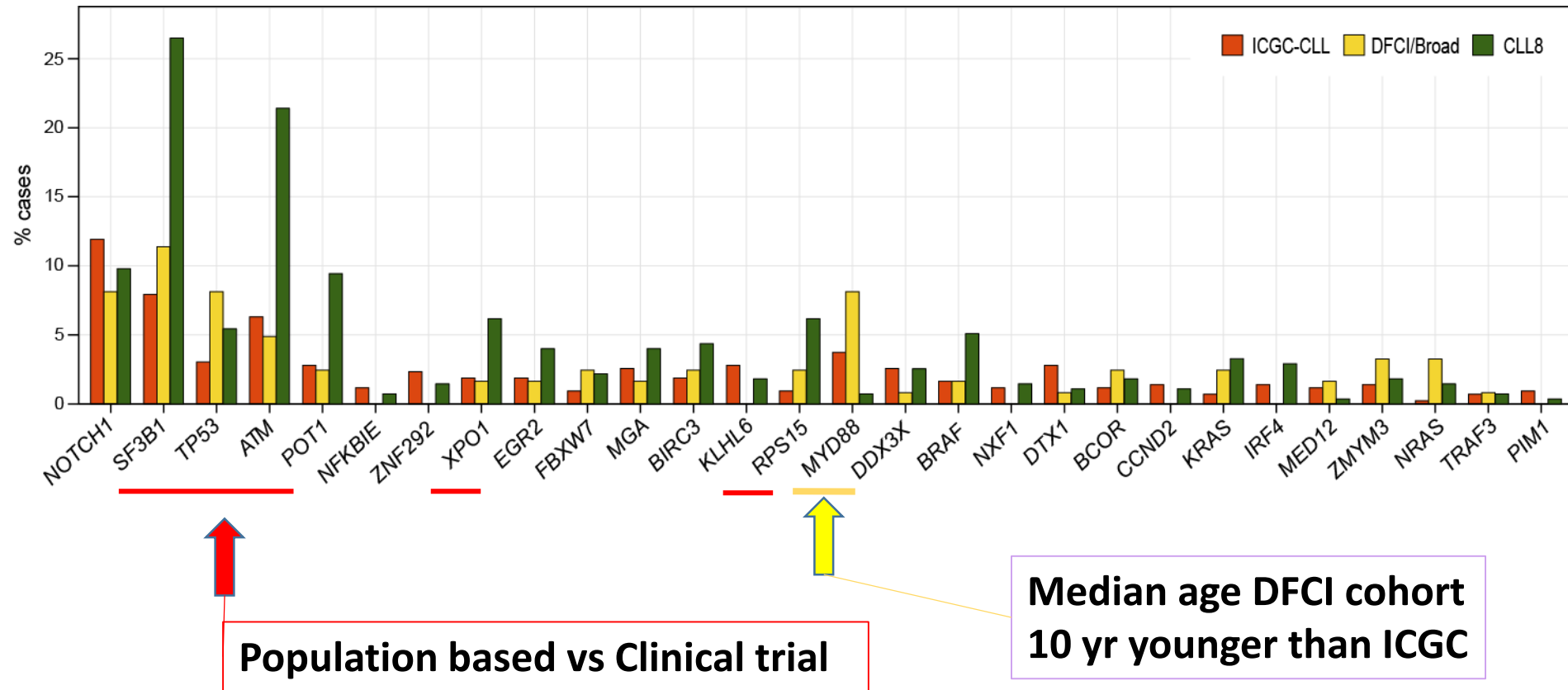


- Disease specific profiles
- Understanding evolution of the disease
- Prognostic groups and risk stratification
- Orient management strategies

Driver mutated Genes and CNA in CLL ICGC & Danna-Farber (DFCI)



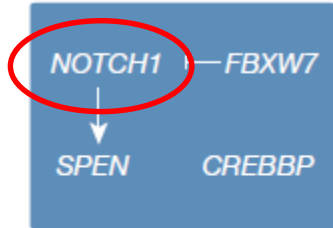
Driver mutated Genes in CLL genomes (ICGC vs Dana Farber (DFCI))



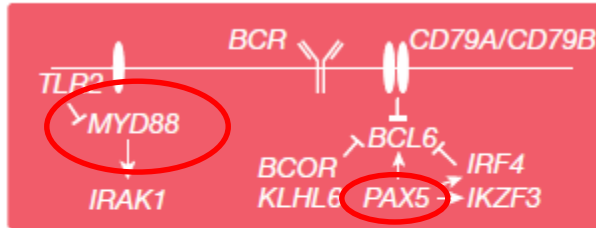
ICGC (n=428): (Puente *et al.* Nature 2015).
 DFCI/Broad (n=123) Only pretreatment cases considered
 CLL8 (n=278): Clinical trial (Landau *et al.* Nature 2015)

Mutated Pathways in CLL

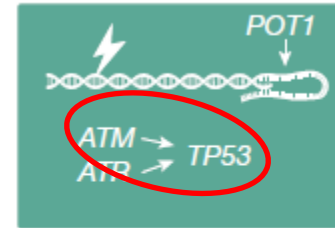
NOTCH1 signalling



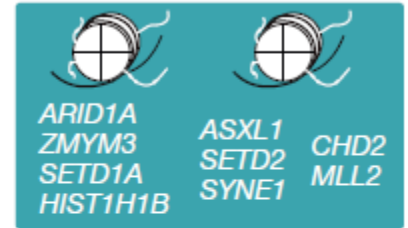
B-cell signalling



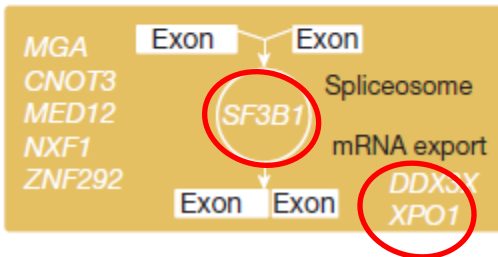
DNA damage response



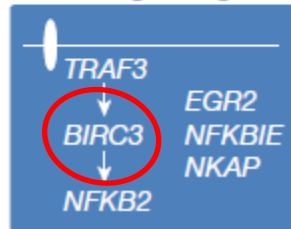
Genome/chromatin structure



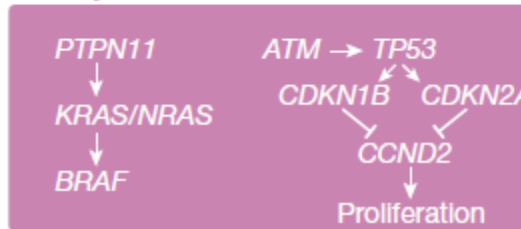
RNA metabolism



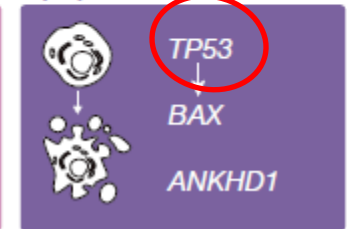
NF-κB signalling



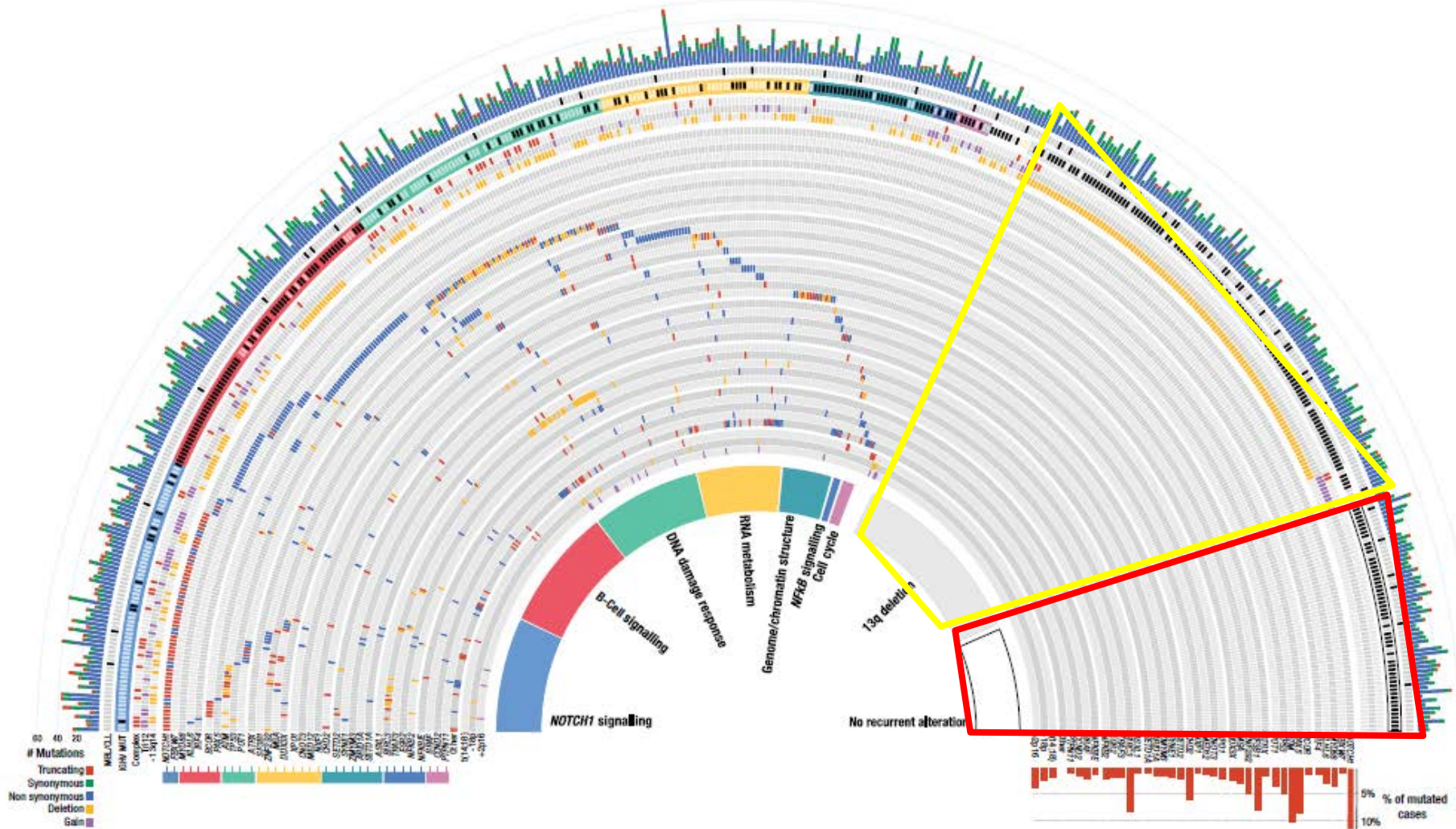
Cell cycle



Apoptosis

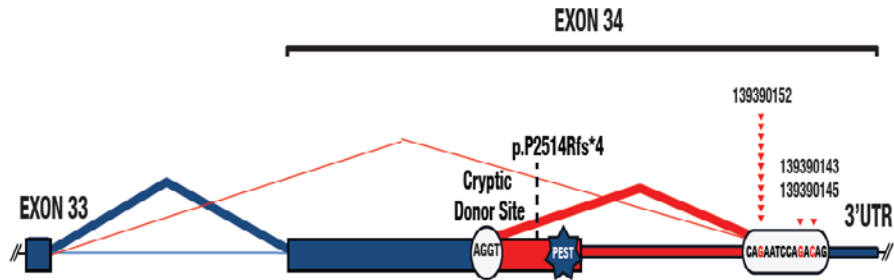


Genomic Heterogeneity and Driverless in CLL

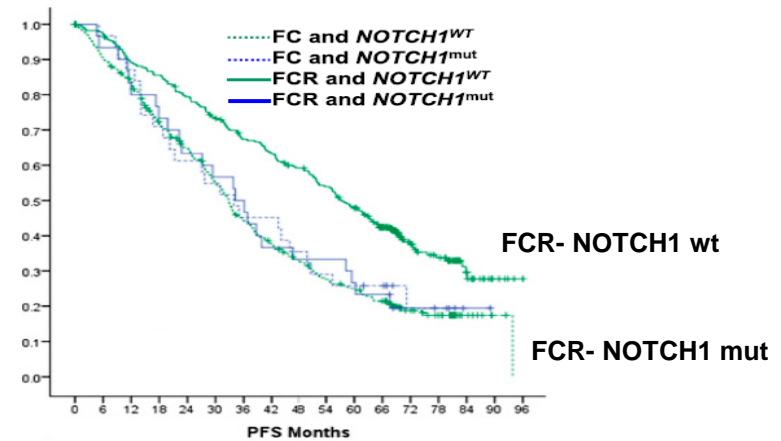
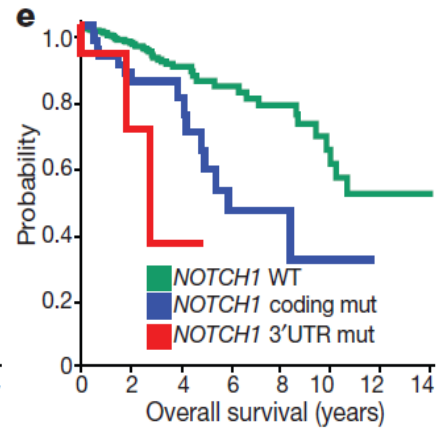
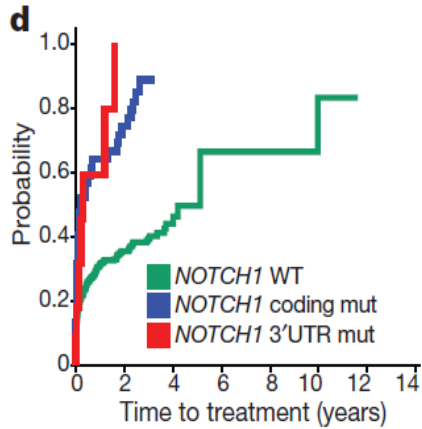
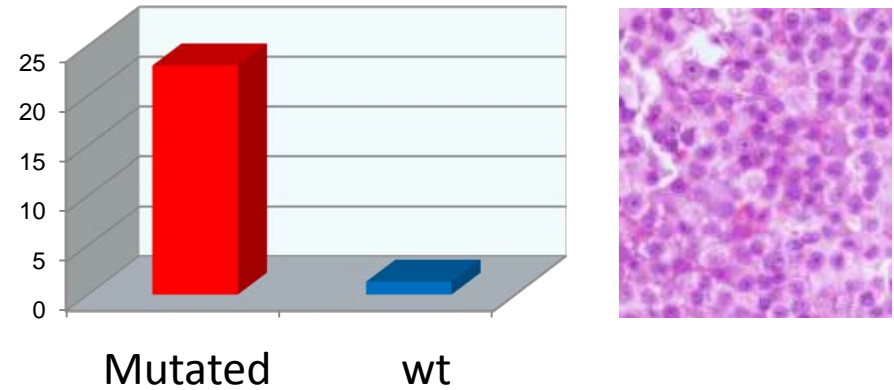


452 CLL & 54 MBL (150 whole genomes)
 13.631 mut in coding genes: 27 per tumor
 951 CNA (2 per tumor)
 59 driver genes

NOTCH1 Mutations in CLL

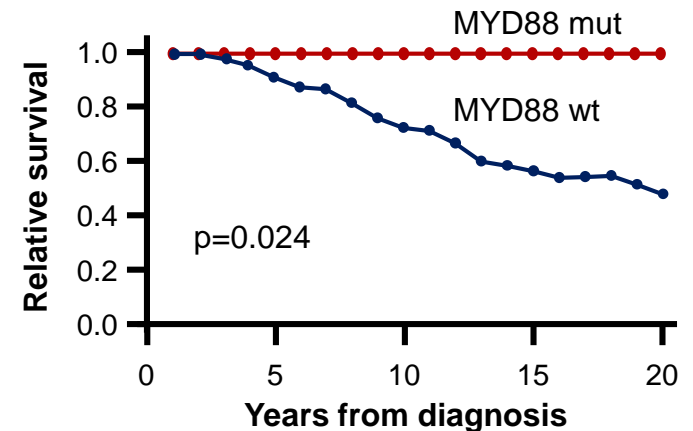
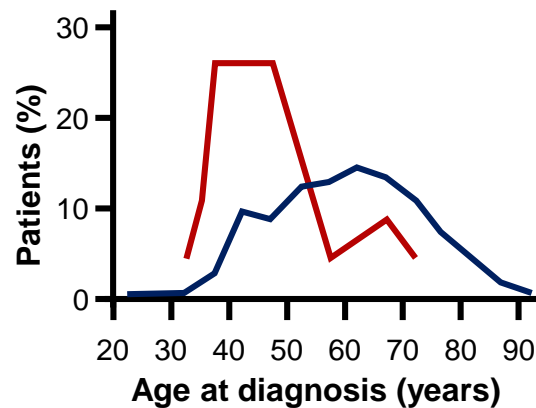
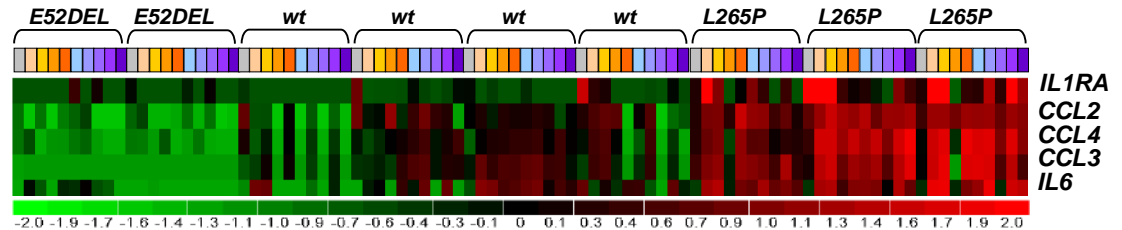
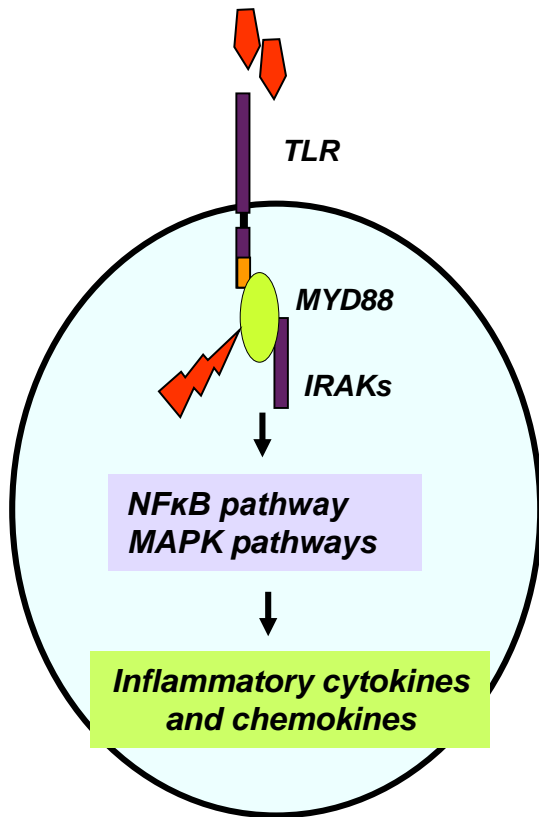


Richter Transformation



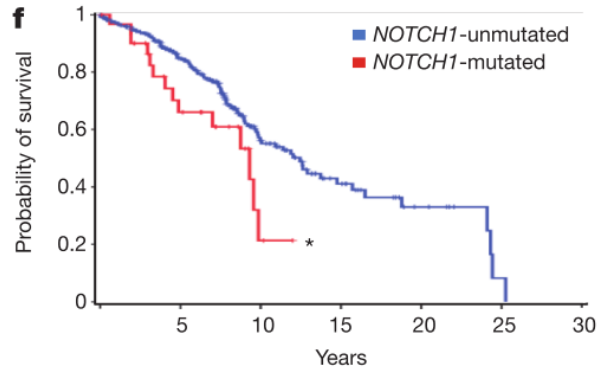
TLR/MYD88 mutated pathway in CLL

A specific subgroup of patients?



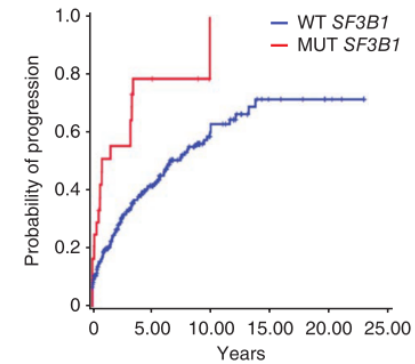
Clinical relevance of individual mutated genes in CLL

NOTCH1



Puente *et al.* 2011, Nature

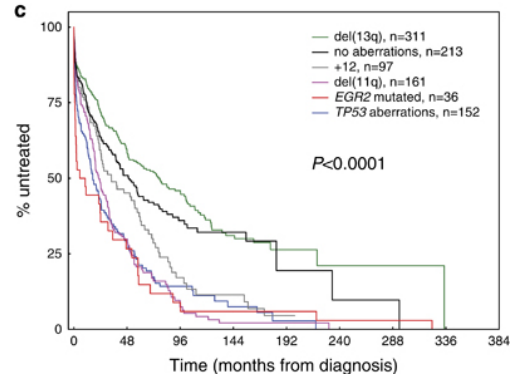
SF3B1



Quesada *et al.* 2011, Nat Genetics

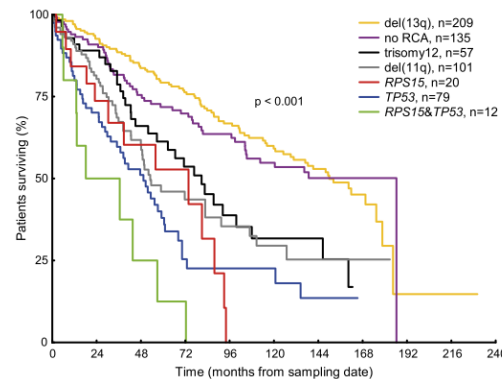


EGR2



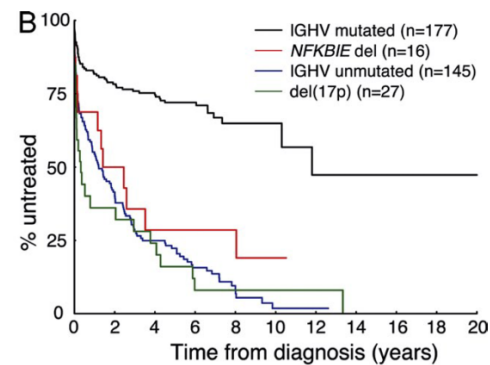
Young *et al.* 2017, Leukemia

RPS15



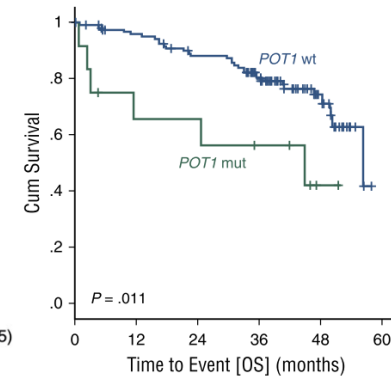
Ljungström *et al.* 2015, Blood

NFKBIE



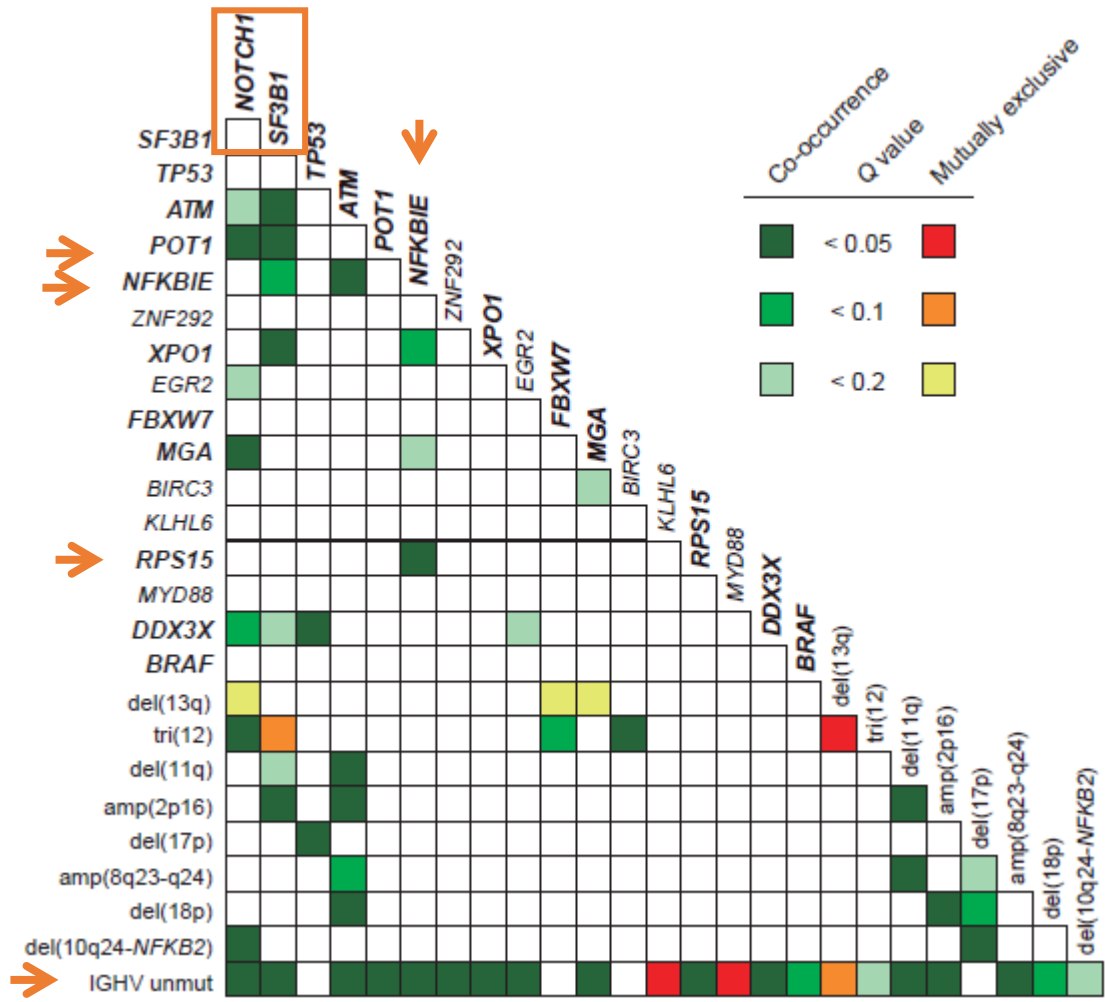
Mansouri *et al.* 2015, JEM

POT1



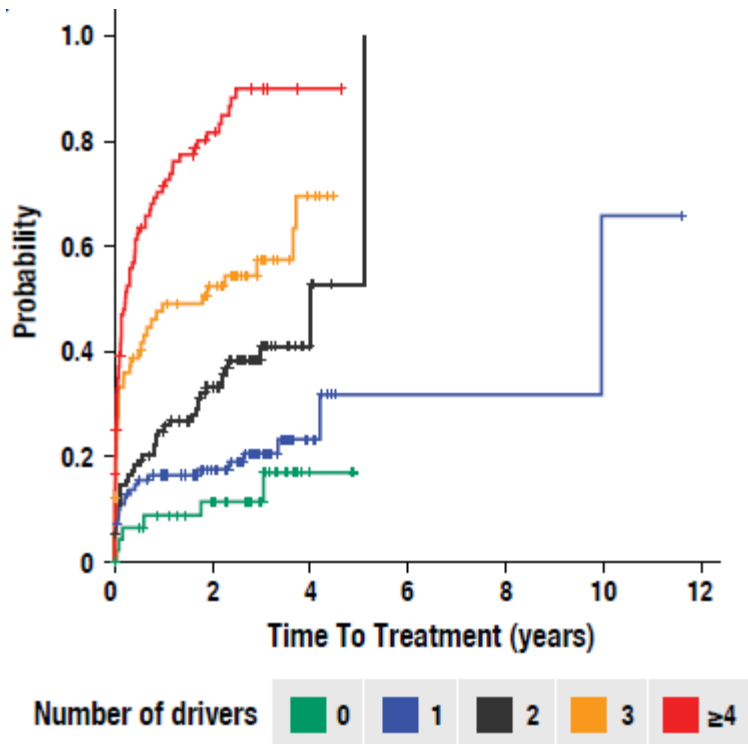
Herling *et al.* 2016, Blood

Co-occurrence of driver alterations in CLL



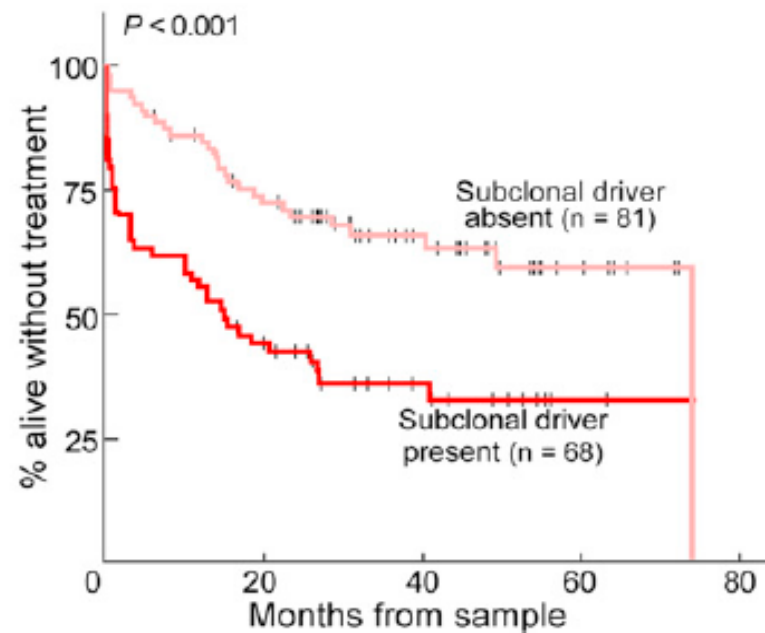
Prognostic impact of number of mutated drivers and subclonal alterations in CLL

Number of drivers

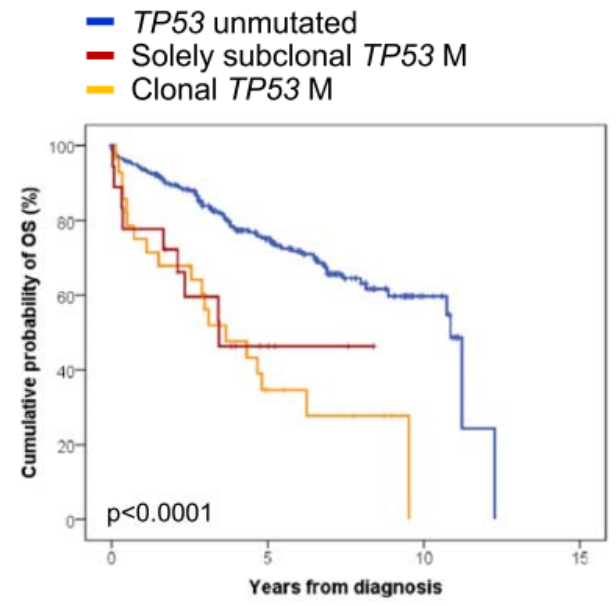
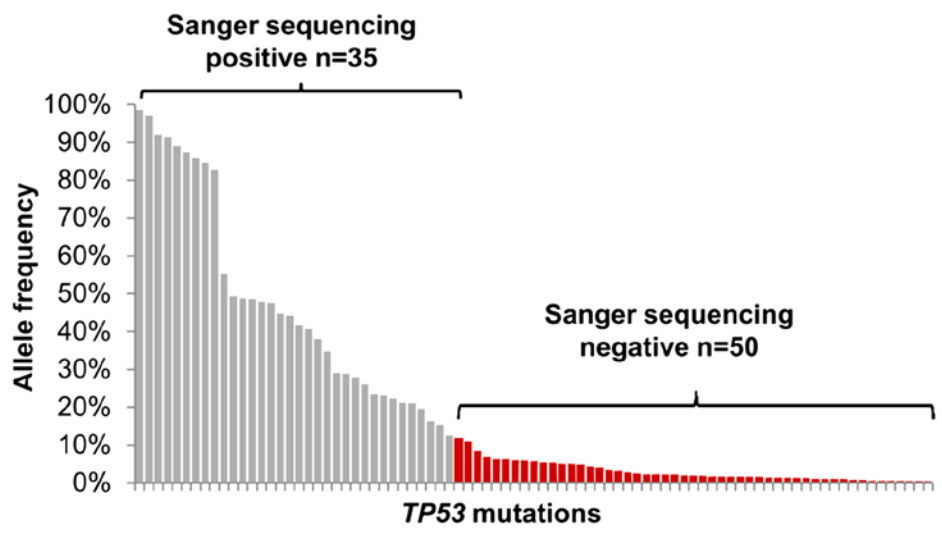
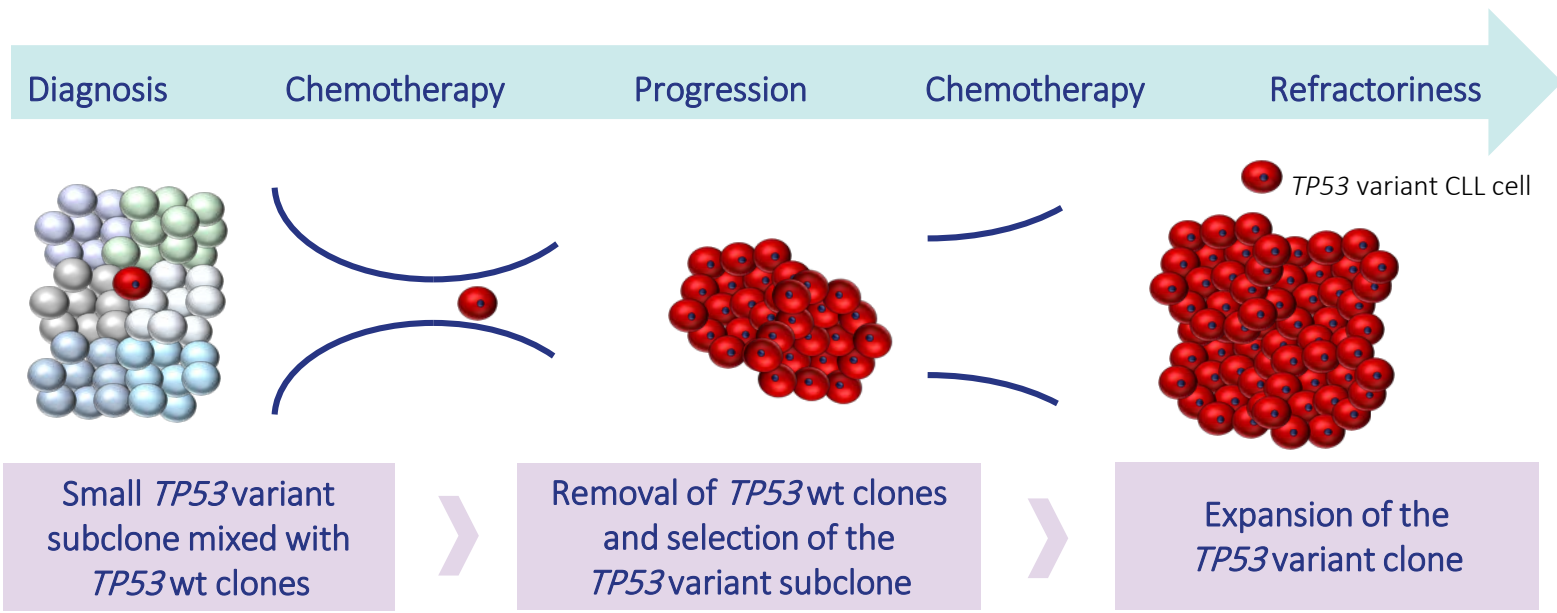


Puente X et al Nature 2015

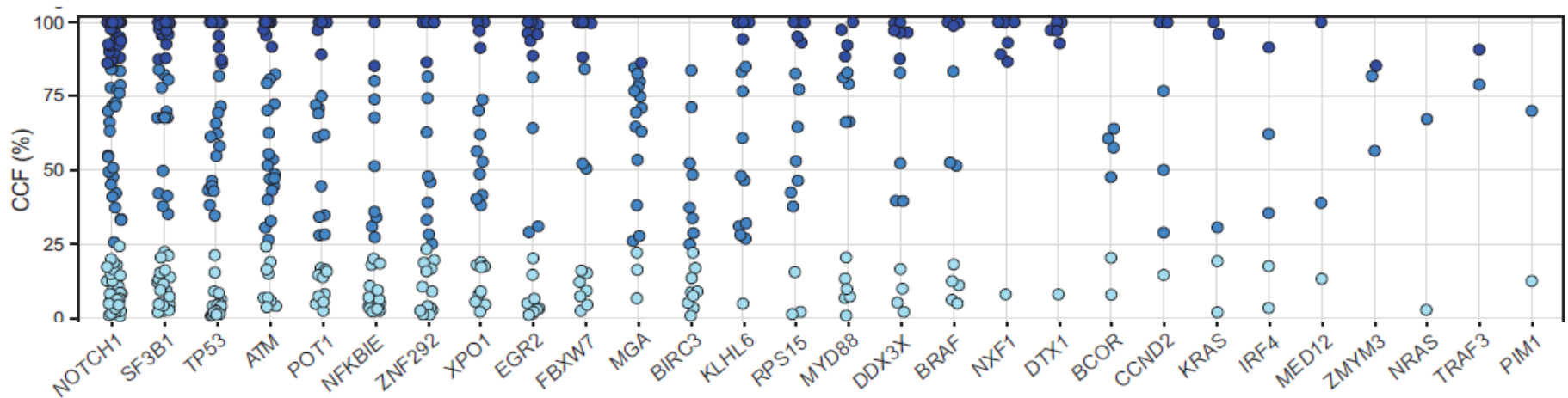
Clonal/subclonal heterogeneity



Landau DA et al Cell 2013

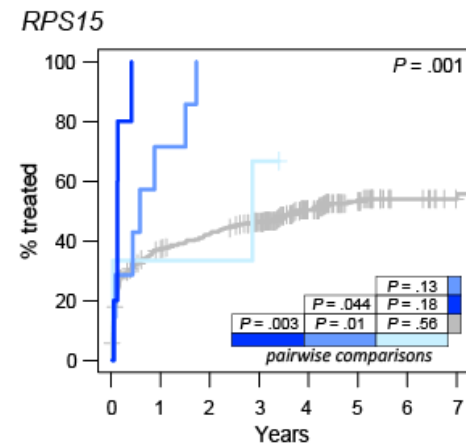
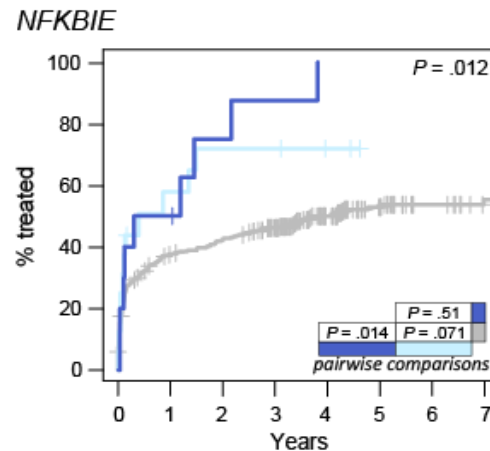
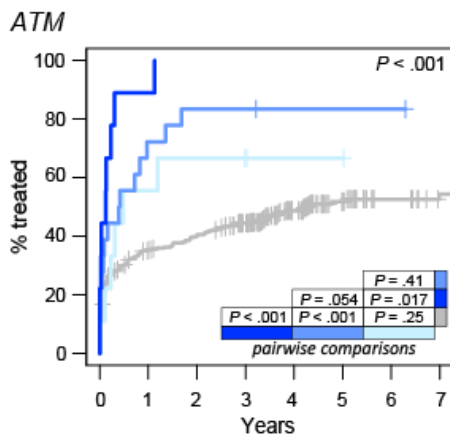
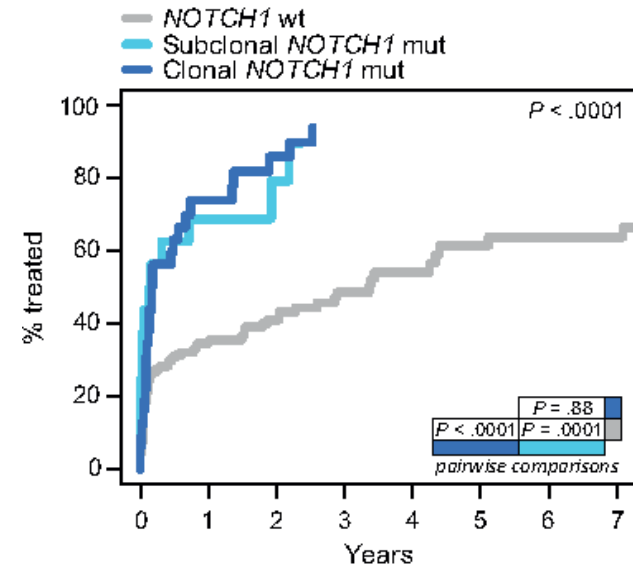
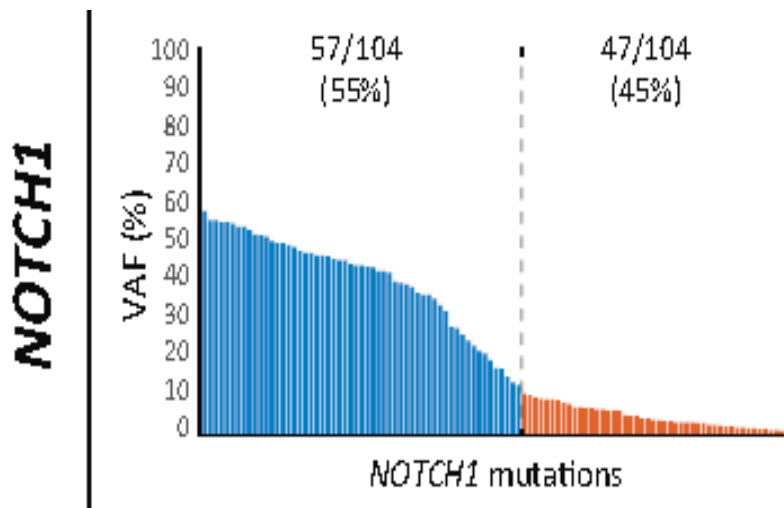


Small mutated subclones are identified in virtually all genes

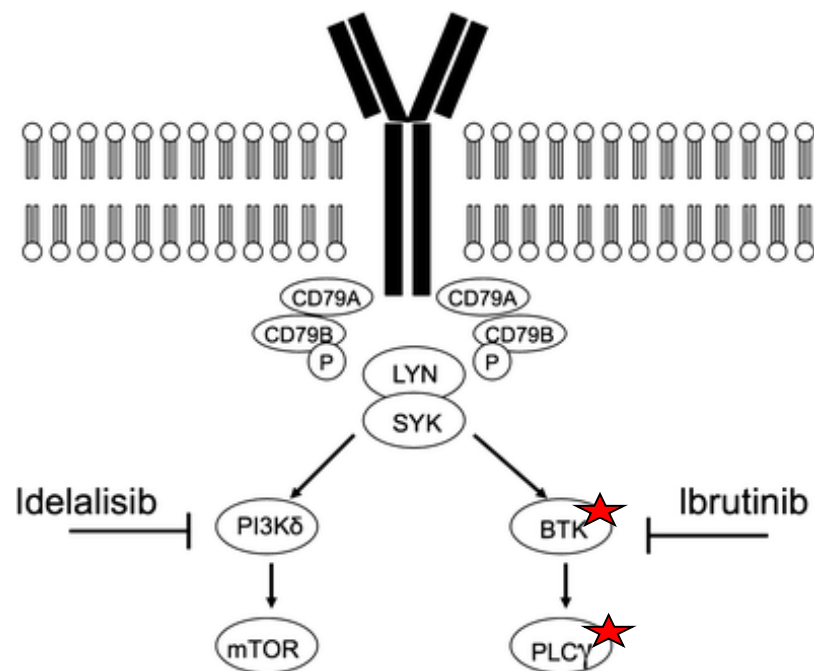


- 406 untreated patients
- 28 CLL driver genes
- Mean coverage 1500x NGS
- Sensitive pipeline 0.1% allelic frequency

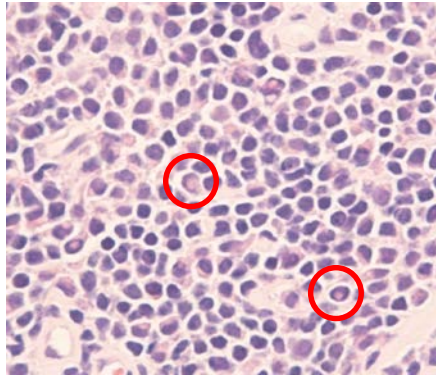
Clinical Impact of clonal and subclonal mutations in CLL



Ibrutinib-resistant mutations may be detected before clinical relapse



Detection of mutated subclones may precede treatment
Median 8-9 months (3-15 months)



Somatic Mutations in Lymphoplasmacytic Lymphoma

MYD88 L265P

- **95% WM/LPL**
- 29% DLBCL-ABC
- 6% MZL
- 3% CLL

CXCR4

- **25-35% WM/LPL**
- Associated with MYD88
- More active disease
- Less lymphadenopathy
- More resistant disease to new drugs

BTK

Patients treated with Ibrutinib

Mutations before clinical progression

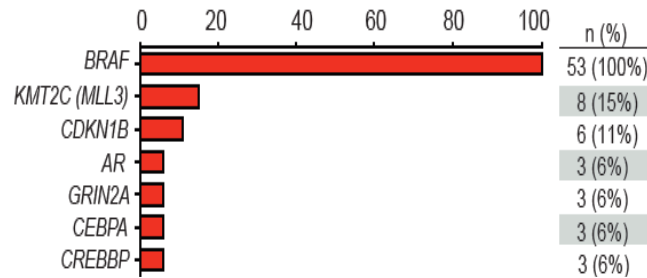
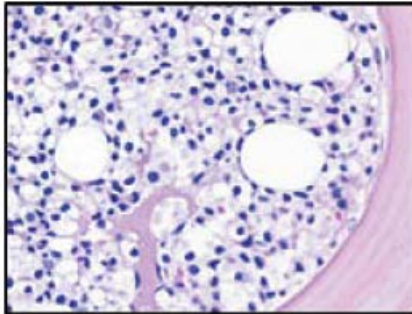
- **Useful information in the differential diagnosis of LPL**
- **Need to be interpreted in the global context of the disease**

When should *MYD88* L265P mutations be studied in small B-cell neoplasms?

- Differential diagnosis of LPL strongly considered but findings not conclusive
- Differential diagnosis between LPL and IgM PCM
- If LPL is not in the differential diagnosis *MYD88* mutations may not be useful

Somatic Mutations in HCL and HCLv

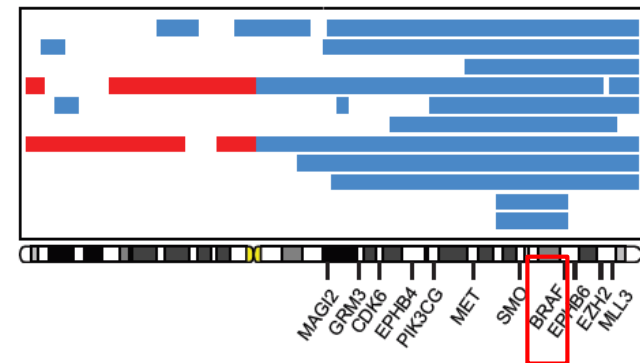
Hairy Cell Leukemia



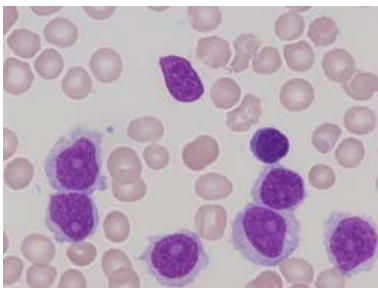
Vemurafenib Resistance

- NF1/NF2 downregulation
- KRAS mutation

7q deletion



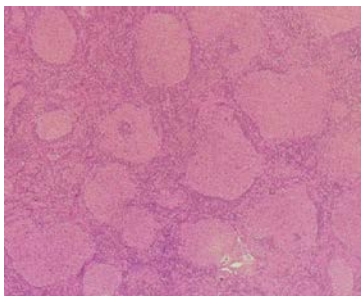
HCL-v



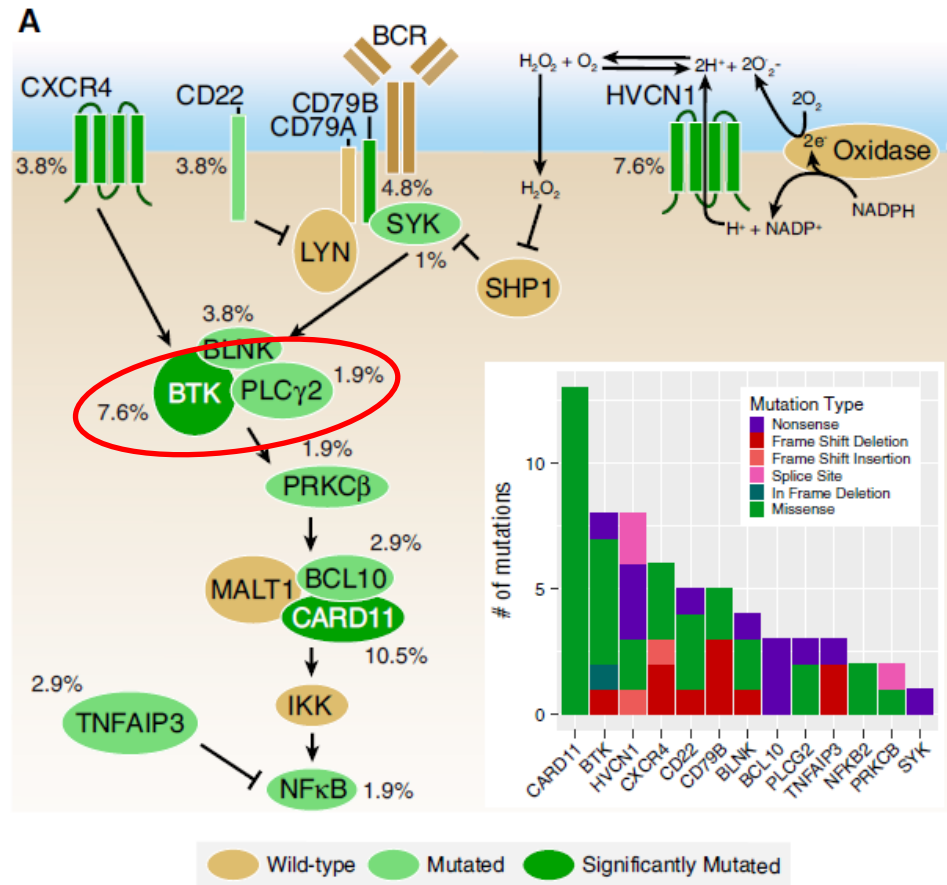
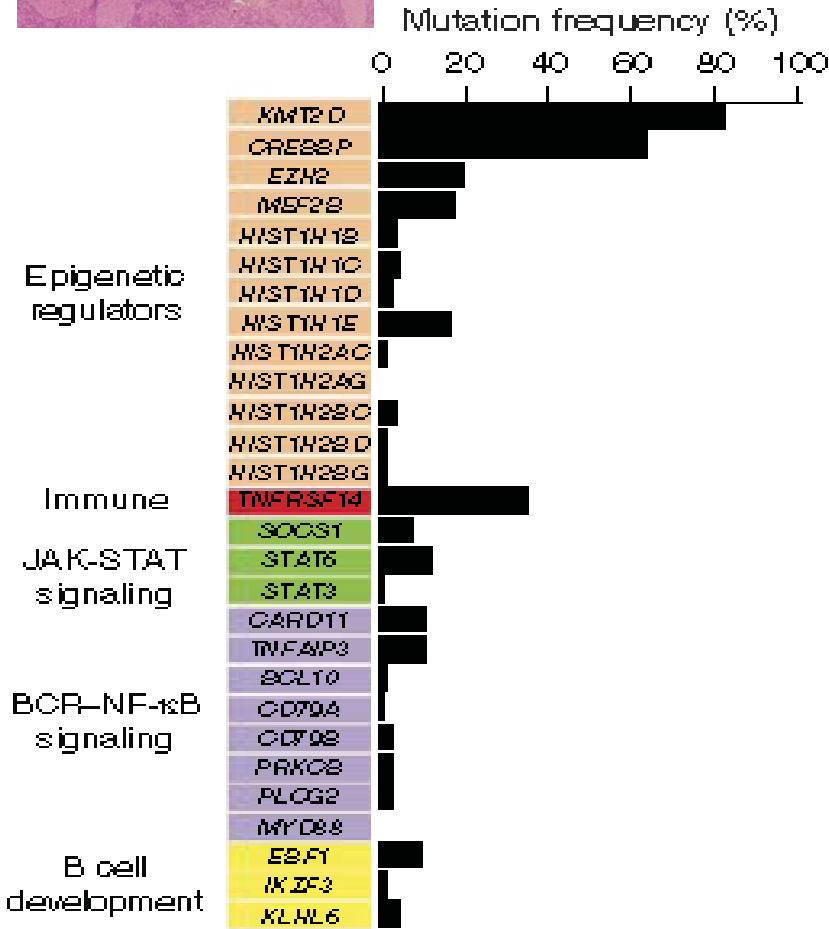
MAP2K1

- **50 % HCLv**
- 50% HCL IgH V4-34
- 50% Pediatric Type FL

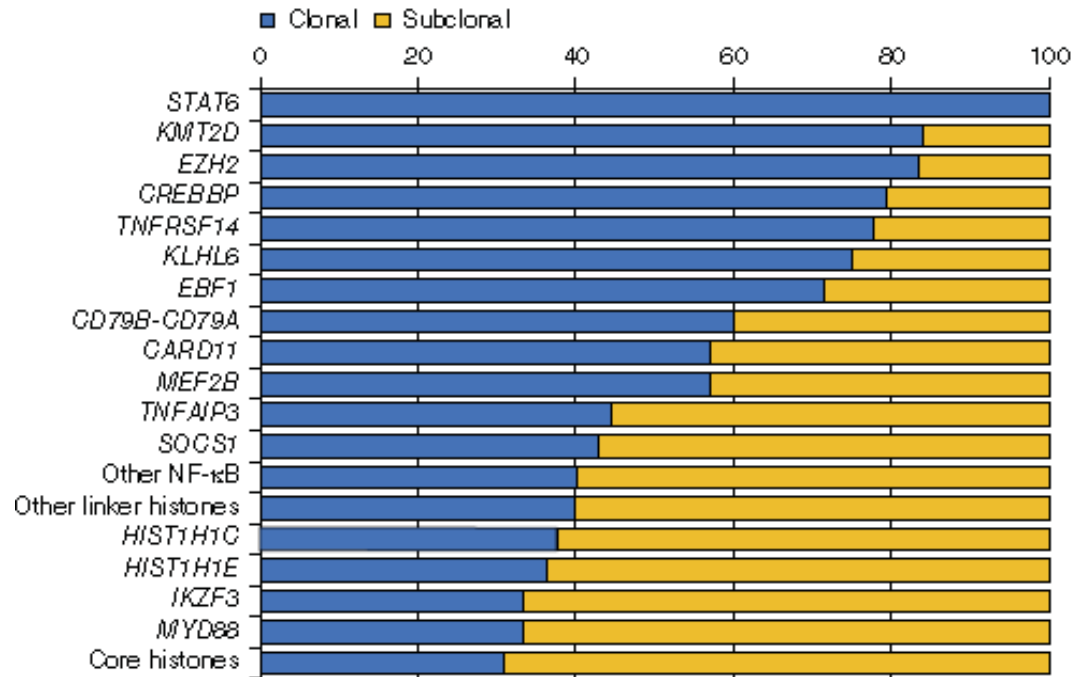
CCND3, U2AF1



Follicular lymphoma Mutational Landscape



Early and Late Mutations in Follicular Lymphoma



Early driver mutations in chromatin regulator genes

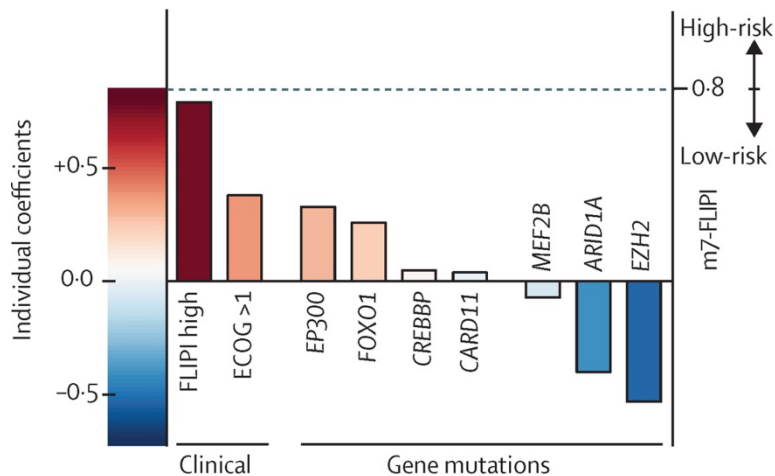
(*CREBBP*, *EZH2* and *KMT2D* (*MLL2*)),

Gained at transformation : *EBF1* and regulators of NF-κB signaling

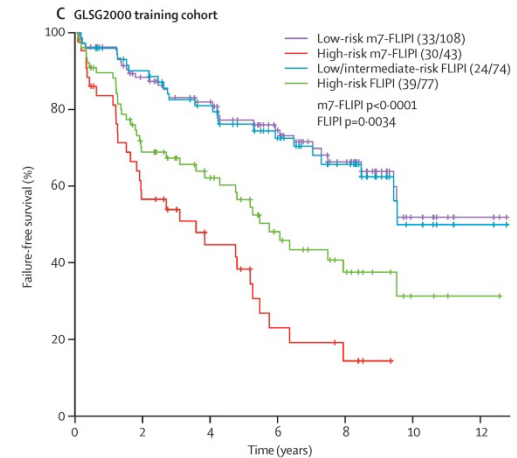
(*MYD88* and *TNFAIP3*)

Clinical Impact of FL Mutations

Risk Stratification



Pastore et al Lancet Oncol. 2015 Sep;16(9):1011-1012



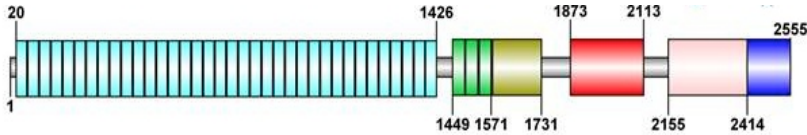
Target Therapy

EZH2 inhibitor (Tazemetostat) in Refractory/Relapsed FL

- OR: 63% in patients with EZH2 mutations ($N = 8$)
28% in with wild type EZH2 ($N = 46$)

Morschhauser F et al Hematol Oncol 2017; 35, S2: 24–25

NOTCH1/2 Mutations in FL

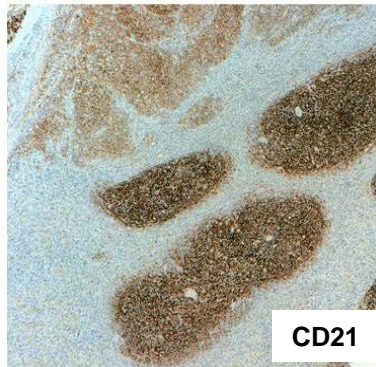
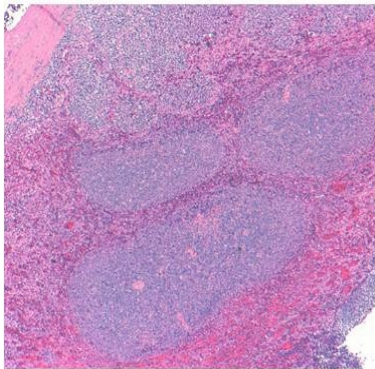


PEST/TADD domain
Truncating mutations

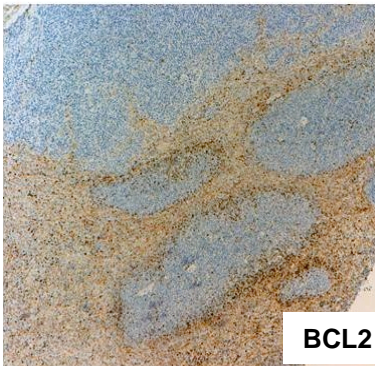
7/112 FL cases (6.3%)

5 *NOTCH1*
2 *NOTCH2*

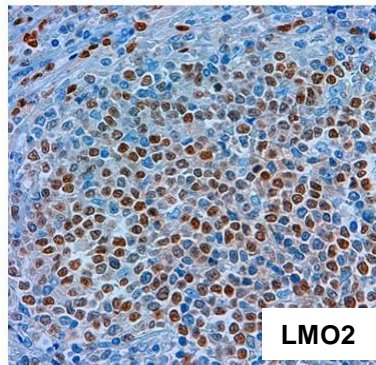
NOTCH3/4 (4%)



CD21



BCL2

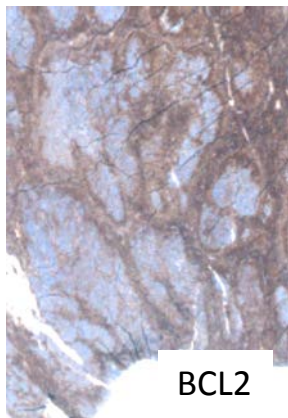
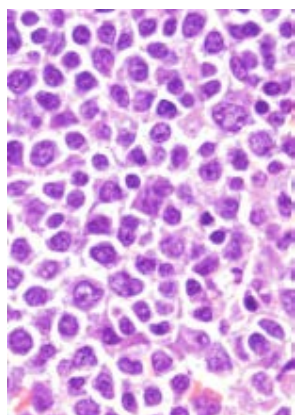


LMO2

Female
Splenic/extranodal involvement
Negative for t(14;18)
DLBCL component

Karube K et al J Pathol 2014; 234:423-30
Krysiak K et al Blood 2017; 129: 473-483

Pediatric Type Follicular Lymphoma

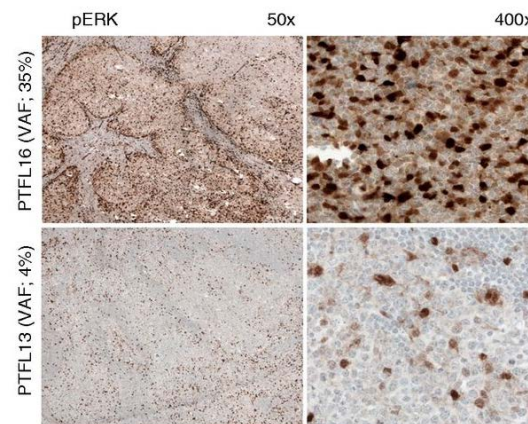


BCL2

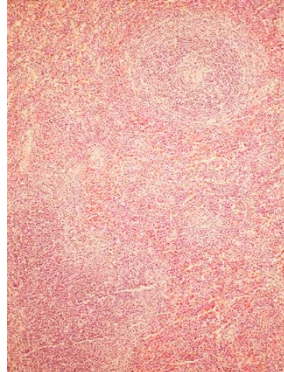
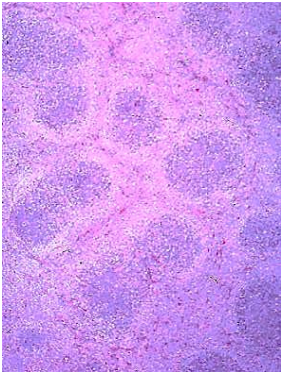
Genes	PTFL (n=71) (%)	t(14;18)-neg FL (%)	t(14;18)-pos FL (%)	P-value
<i>TNFRSF14</i>	33-51	36	18-46	Ns
<i>KMT2D</i>	14-16	36	67-82	Ns
<i>CREBBP</i>	3*	45	33-64	0.001
<i>FOXO1</i>	5	27	-	Ns
<i>GNA13</i>	11	0	-	Ns
<i>EZH2</i>	3*	18	7-20	0.0049

* >18yr

Genes	PTFL
<i>MAP2K1</i>	38-49%
<i>MAPK1</i>	10%
<i>IRF8</i>	15-50%

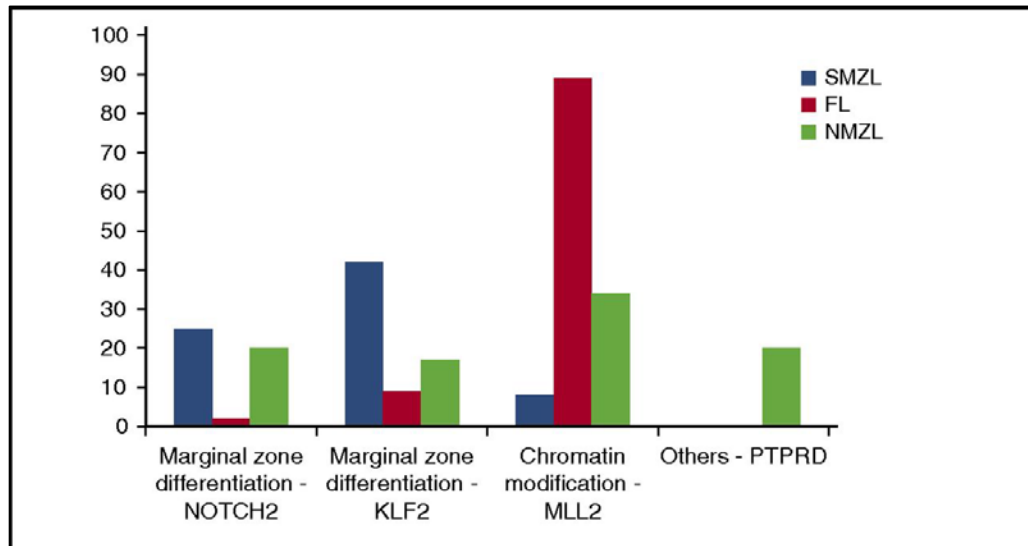


Mutational Profile of Nodal and Splenic Marginal Zone Lymphoma

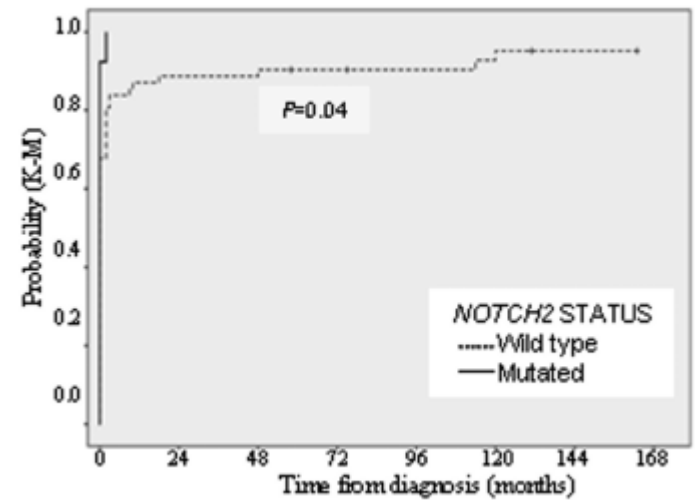
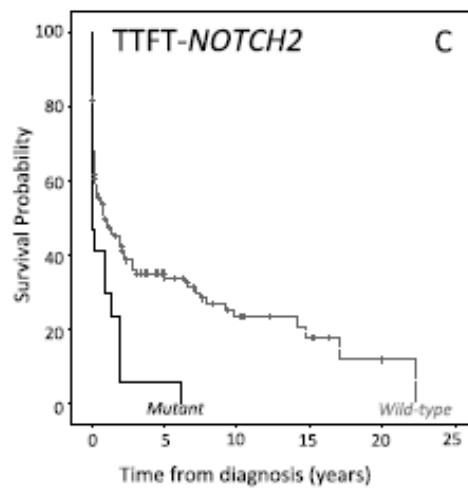
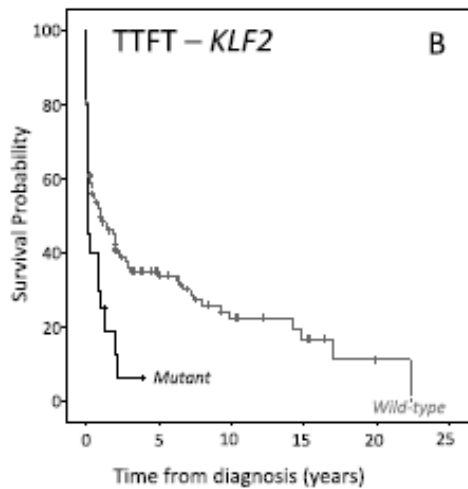


Targeted Pathways

- **KLF2, NOTCH2, activation** (40-25%)
- **NFκB activation** (36-51%)
- **BCR signaling** (SMZL 8%)
- **PTPRD** (NMZL 20%)



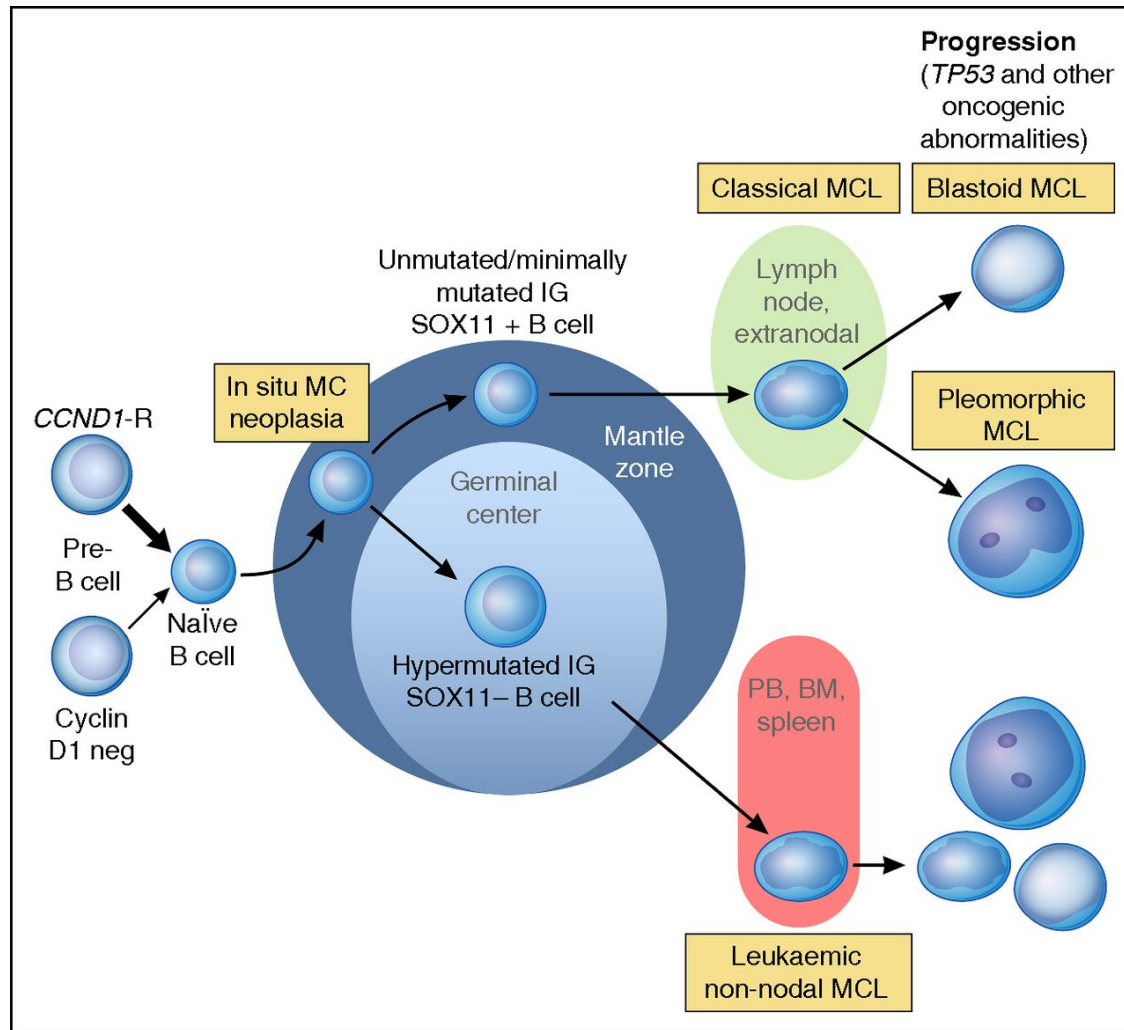
Clinical Impact of Somatic Mutations in SMZL



Parry et al Clin Cancer Res 2015

Campos-Martin Y et al Haematologica 2017

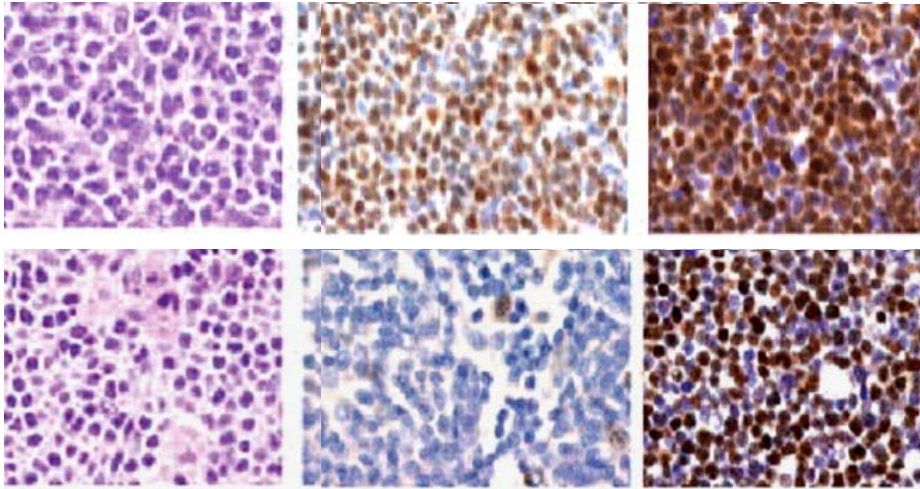
Molecular Pathogenesis and Clinical Subtypes of MCL



Mantle cell lymphoma

CCND1-negative variant

Classic MCL

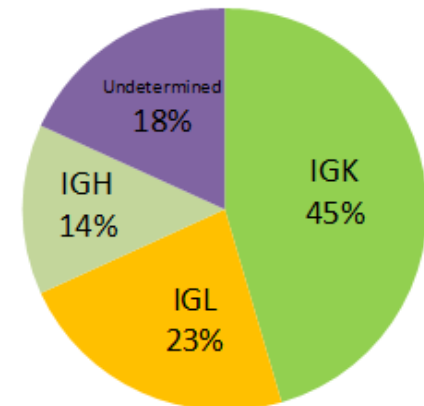
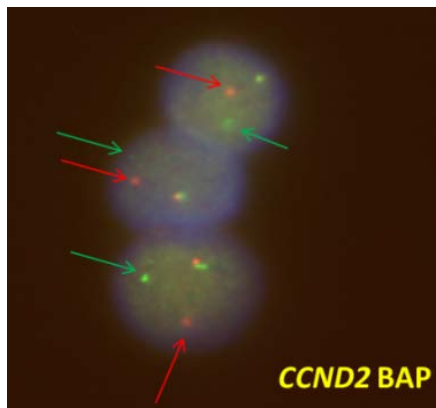


Rearrangements	No. (%)
<i>CCND2</i>	22 (55%)
<i>CCND3</i>	0
No <i>Cyclin D</i> gene translocation	18 (45%)

CCND1 neg MCL

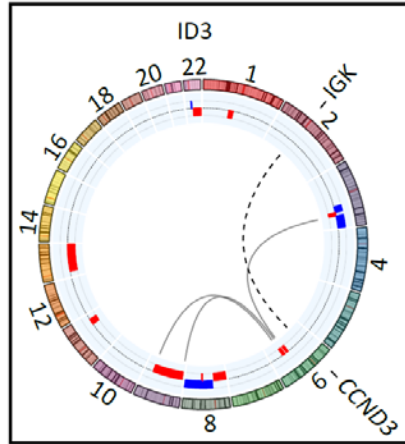
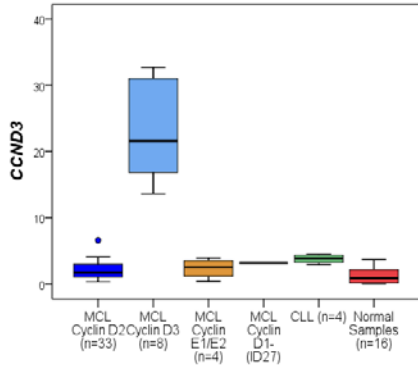
Cyclin D1

Sox11

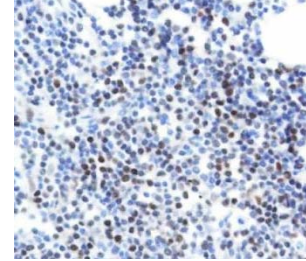


Cryptic IG-CCND1/2/3 rearrangements in MCL

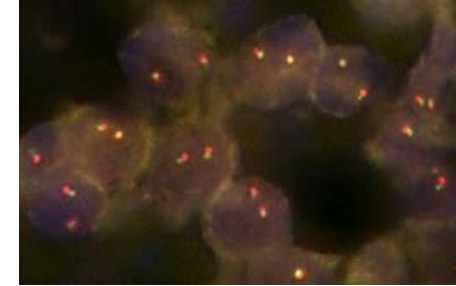
CCND1/2 neg MCL



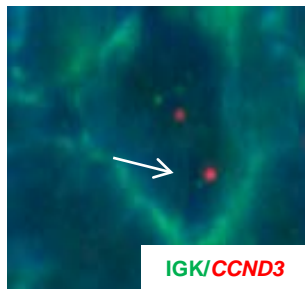
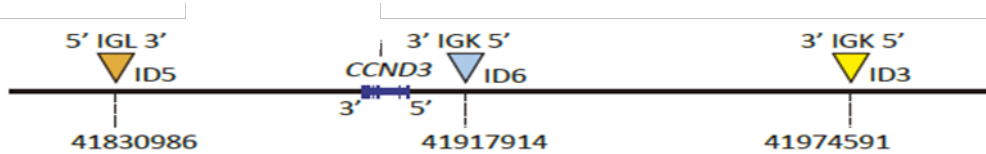
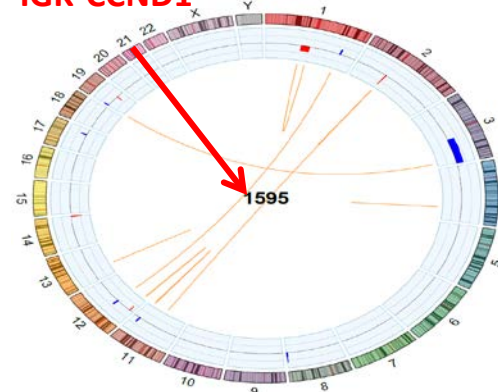
IHC CCND1+



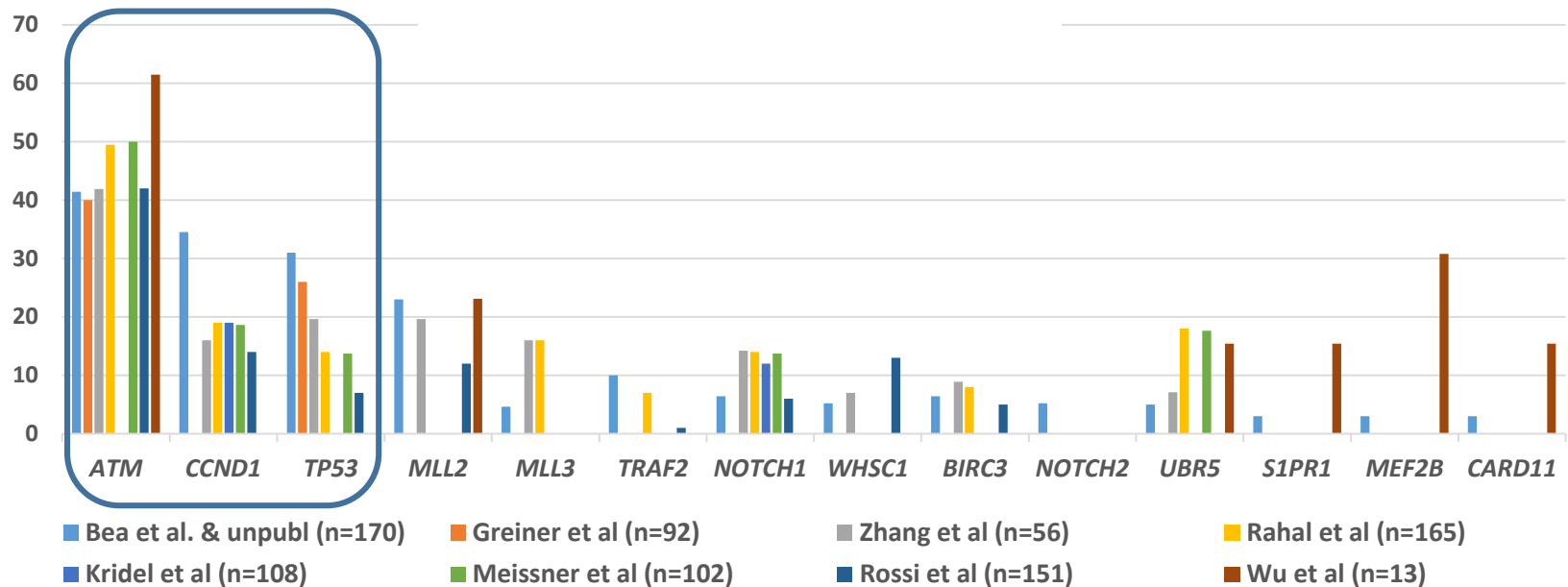
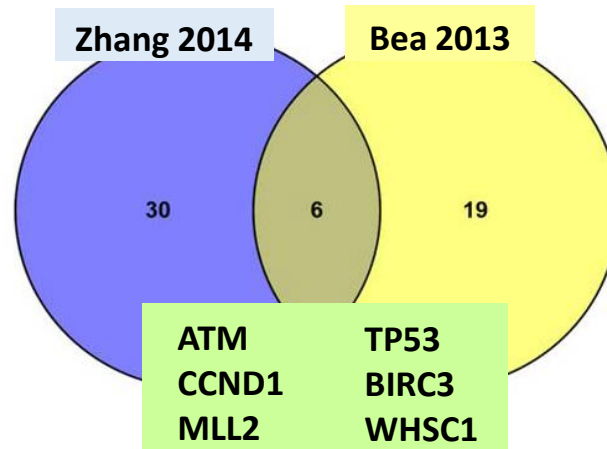
Break apart CCND1 neg



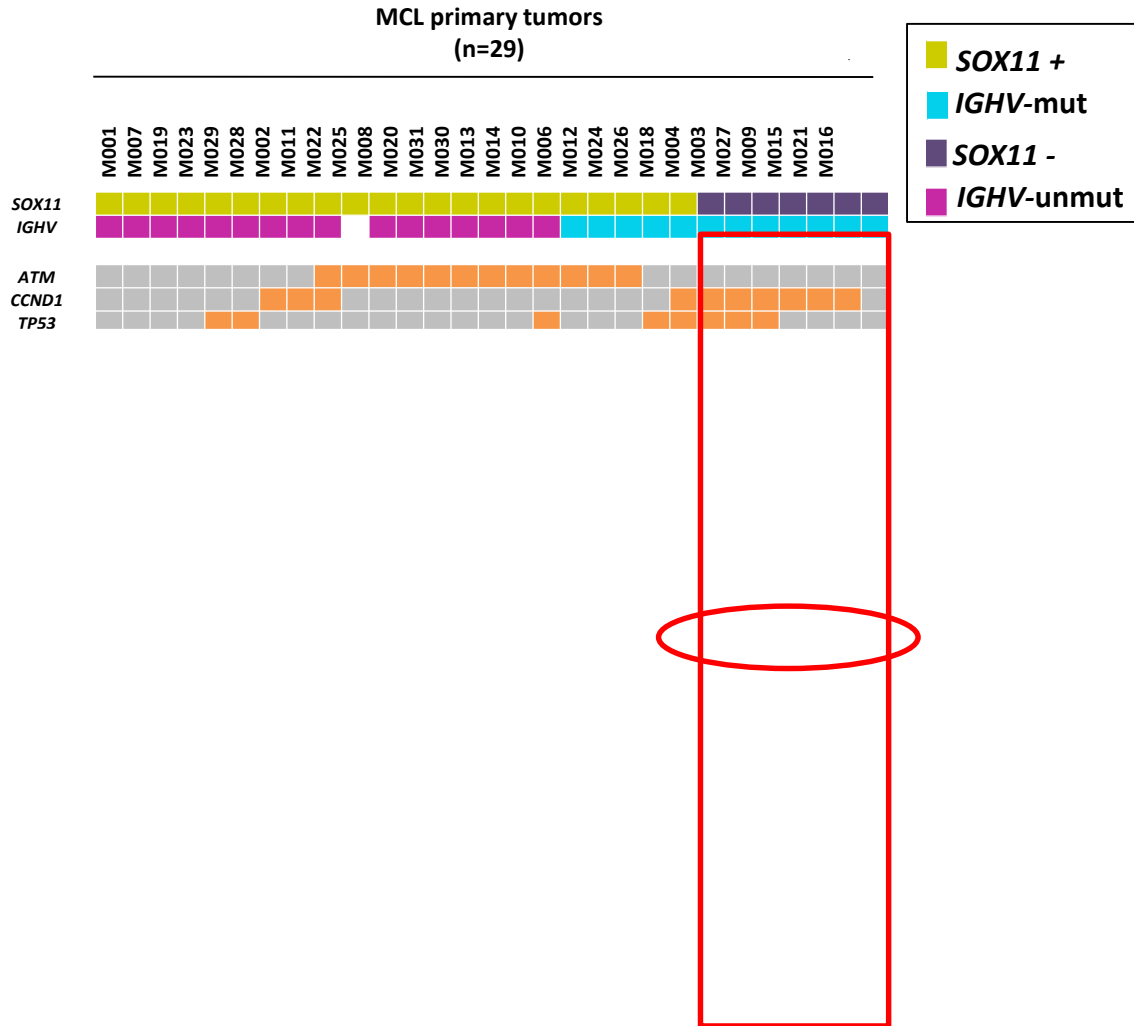
Cryptic IGK-CCND1



Recurrent gene mutations in MCL



Somatic Mutations in MCL



SOX11 +
ATM (55%)
Chromatin (10%)

NOTCH1/2 (5%)
 TP53 23%)
 BIRC3 (7%)

High CNA

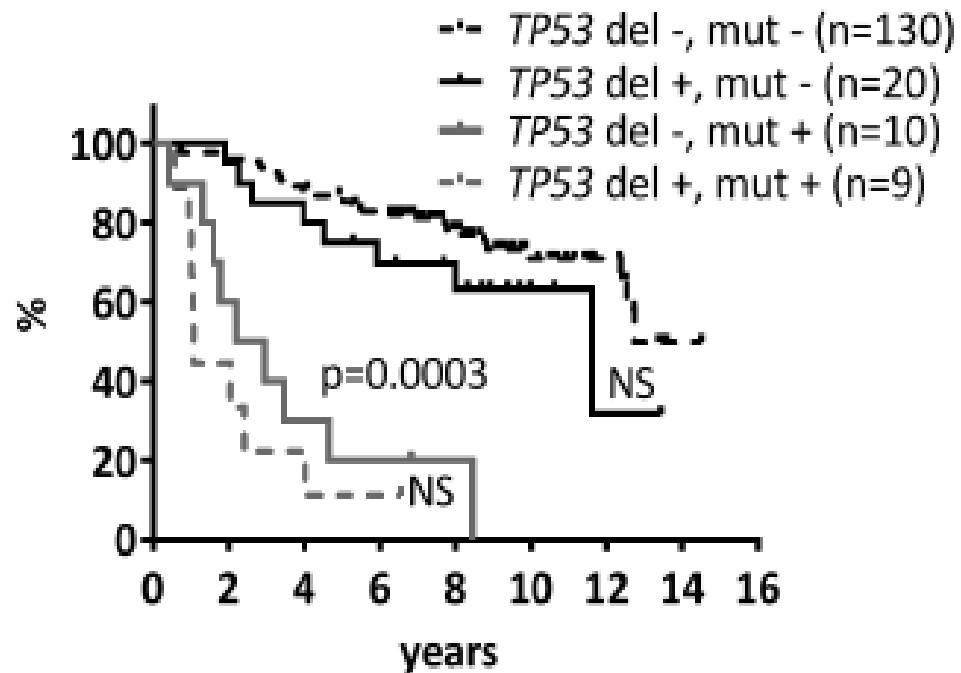
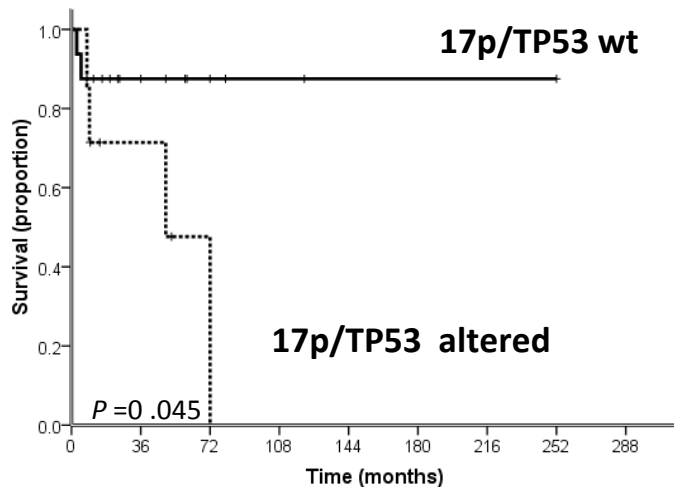
SOX11 -
TLR2 (29%)

NOTCH1/2 (5%)
 TP53 23%)
 BIRC3 (14%)

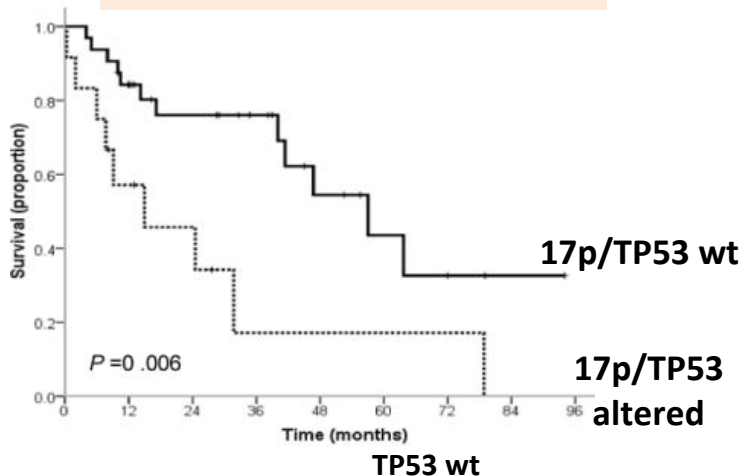
Low CNA

Prognostic impact of 17p *TP53* aberrations in MCL

SOX11-negative MCL



SOX11 +



Eskelund CW et al Blood 2017

Royo C et al, Leukemia 2012

Clinical Relevance of Mutational Profiles in Lymphoid Neoplasms

- **Diagnostic criteria to refine entities**
- **Identification of subsets of patients**
- **Prognostic and predictive significance**
- **Monitoring disease evolution: Dynamic evolution of mutational landscape**
- **Targets for therapy decisions:**
 - **Selection of patients**
 - **Actionable mutations**



M Chagall, Tossa de Mar, 1933

Recurrently Mutated Pathways in Small B-cell Neoplasms

Pathway	U-CLL	M-CLL	cMCL	nnMCL	FL	PTFL	LPL	MZL	HCL
DNA-damage	+		+						
SF3B1	+	+/-							
NOTCH1/2	+	+/-	+		+/-			+	
Chromatin Remodeling			+		+				
BCR-signaling					+			+/-	
NFkB	+		+					+/-	
TLR/MYD88		+/-		+/-			+		
MAPK						+			+