

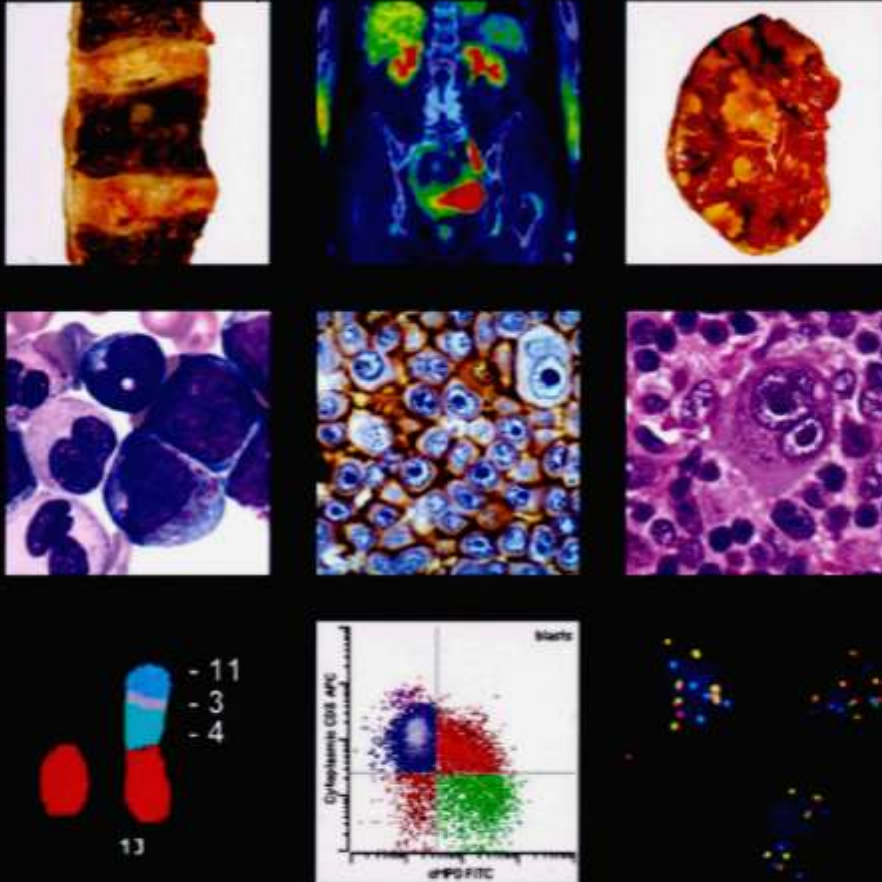


ANATOMIA PATOLOGICA DEL LINFOMA A CELLULE DEL MANTELLO

Prof. Alberto Zamò – Dipartimento di Oncologia
Università di Torino

WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues

Steven H. Swerdlow, Elias Campo, Nancy Lee Harris, Elaine S. Jaffe, Stefano A. Pileri, Harald Stein, Jürgen Thiele, Daniel A. Arber, Robert P. Hasserjian, Michelle M. Le Beau, Attilio Orazi, Reiner Siebert



Definition

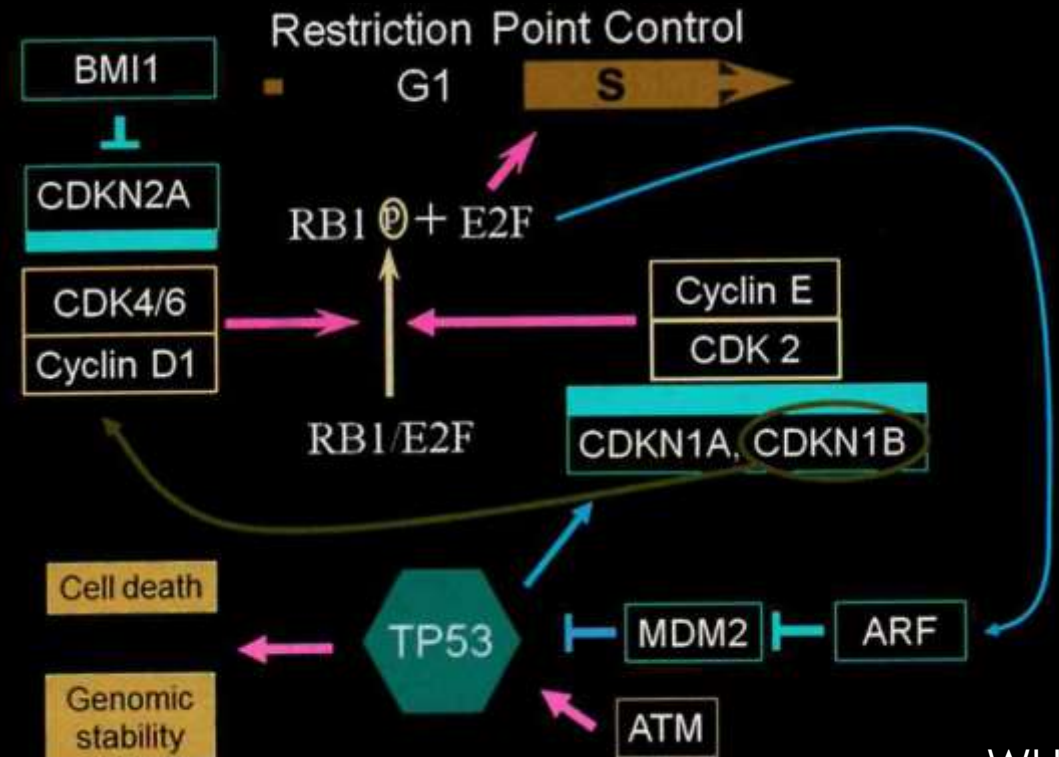
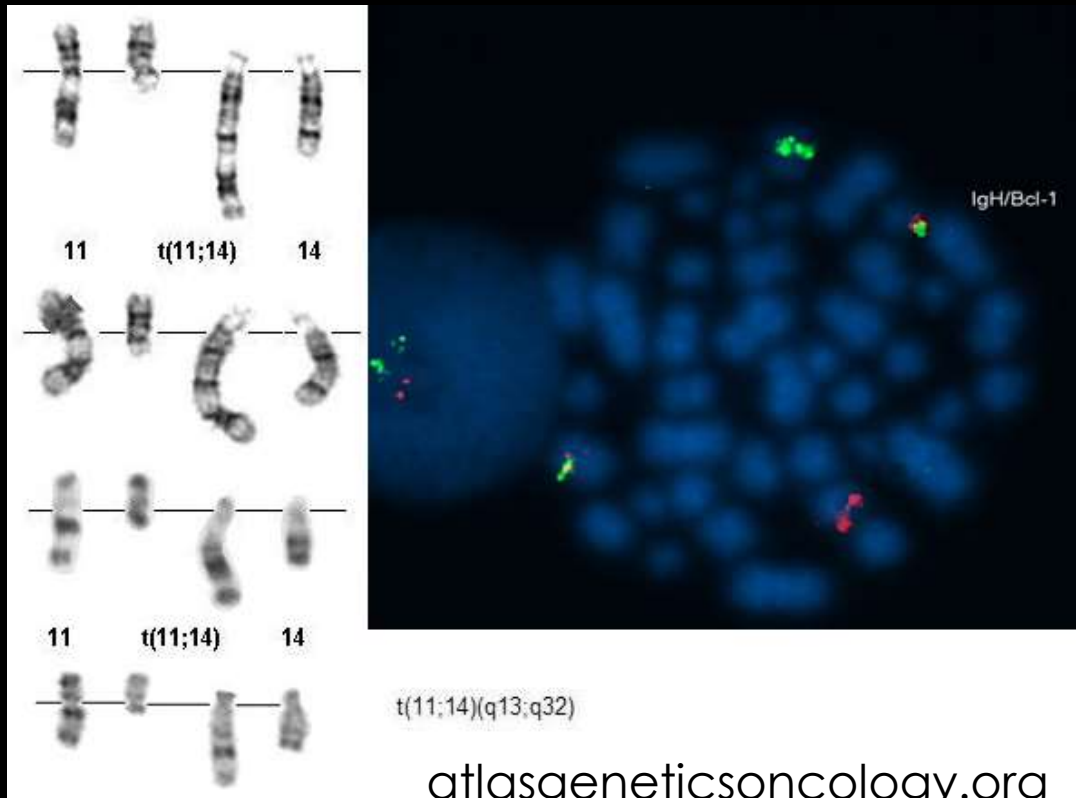
Mantle cell lymphoma is a mature B-cell neoplasm usually composed of monomorphic small to medium-sized lymphoid cells with irregular nuclear contours; in >95% of cases, there is a *CCND1* translocation {245,543,2219,2269,3849,4018}. Neoplastic transformed cells (centroblasts), paraimmunoblasts, and proliferation centres are absent. Mantle cell lymphoma has traditionally been considered a very aggressive and incurable lymphoma, but more indolent variants, including leukaemic non-nodal mantle cell lymphoma and in situ mantle cell neoplasia, are now also well recognized.

PATOGENESI

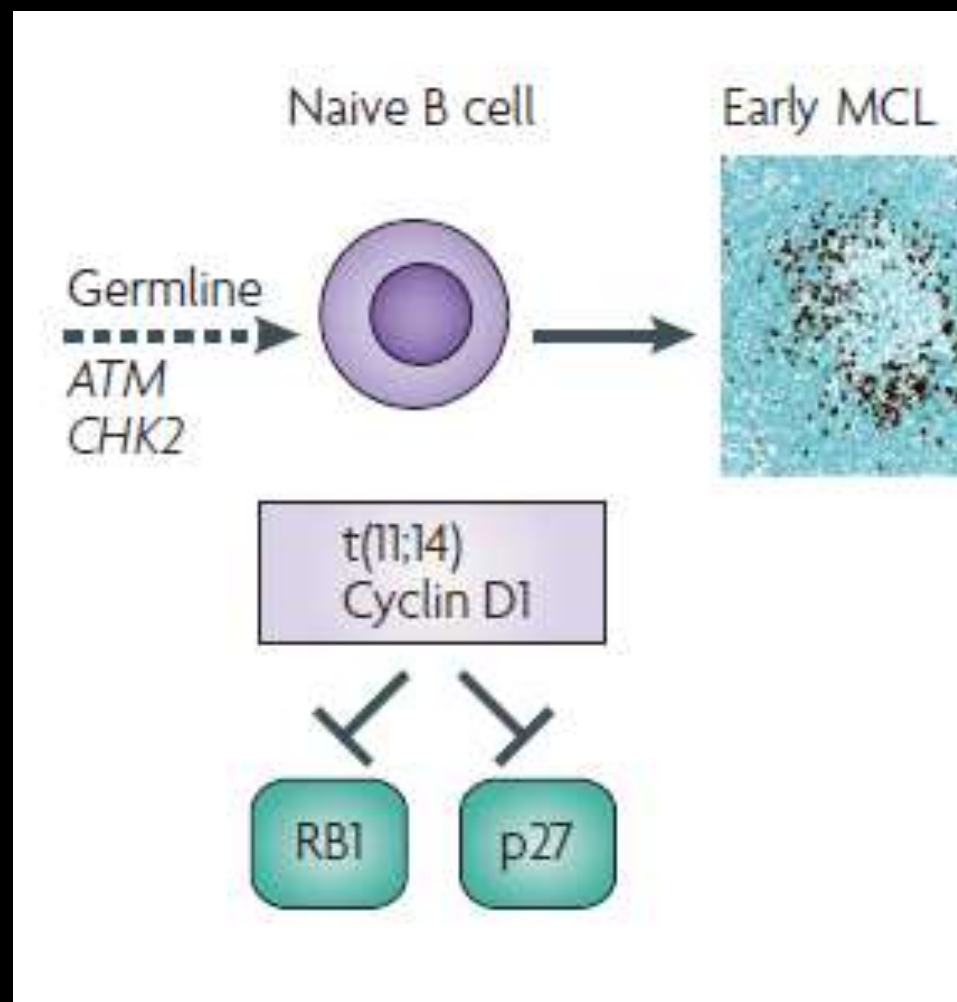


LINFOMA A CELLULE DEL MANTELLO

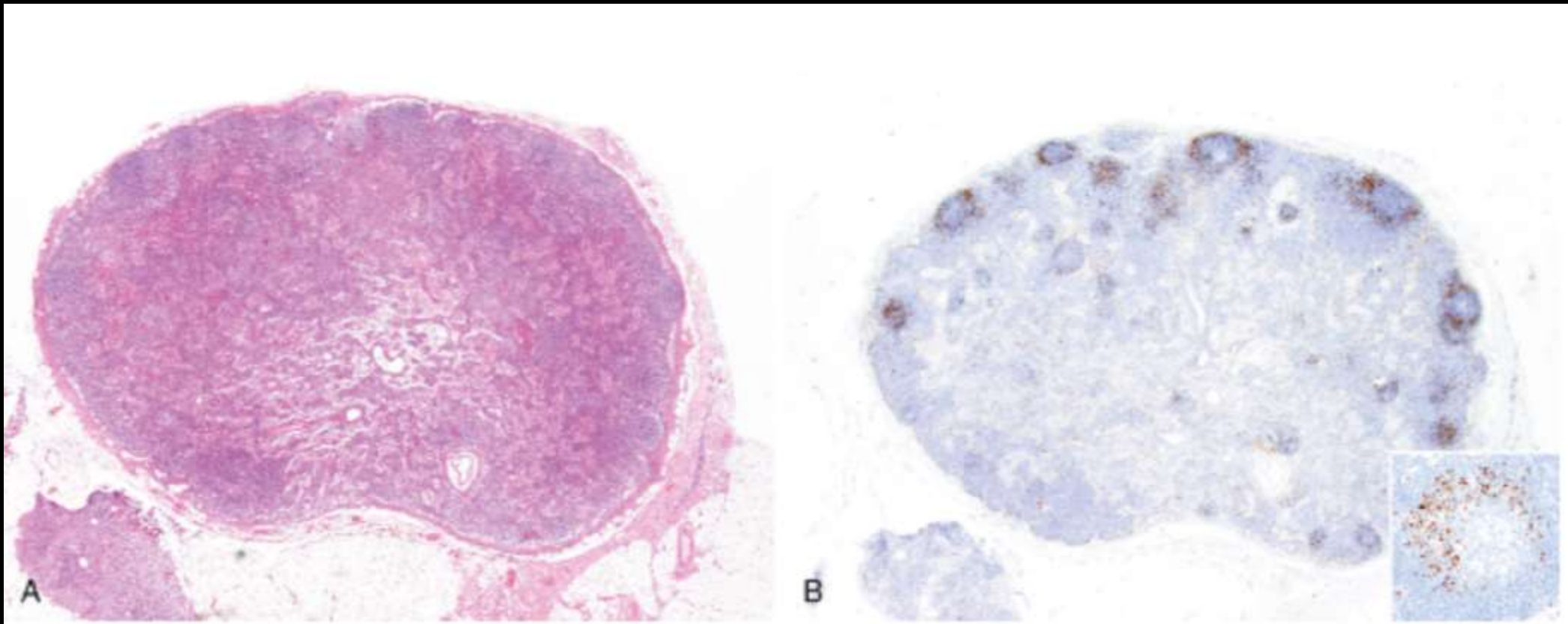
- Deriva da una cellula pre-B che acquisisce una traslocazione a carico del locus di ciclina D1



WHO BB



NEOPLASIA MANTELLARE IN SITU

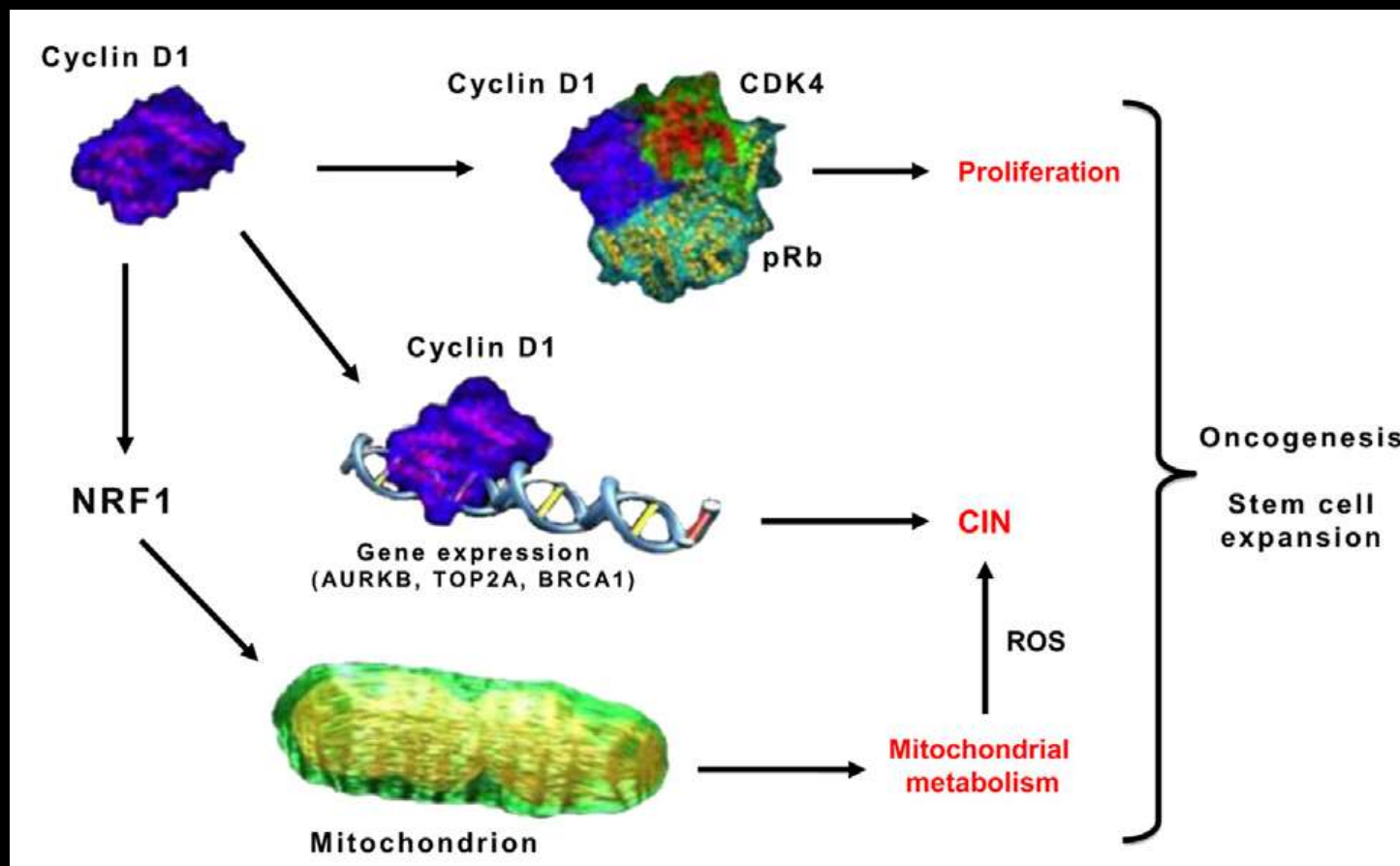


CICLINA D1

- Funzioni classiche
 - Interazione con CDK4/6
- Funzioni alternative
 - Regolazione della trascrizione
 - DNA damage response
 - Inibizione di BAX



CICLINA D1 E CIN



MCL T(11;14) NEGATIVO

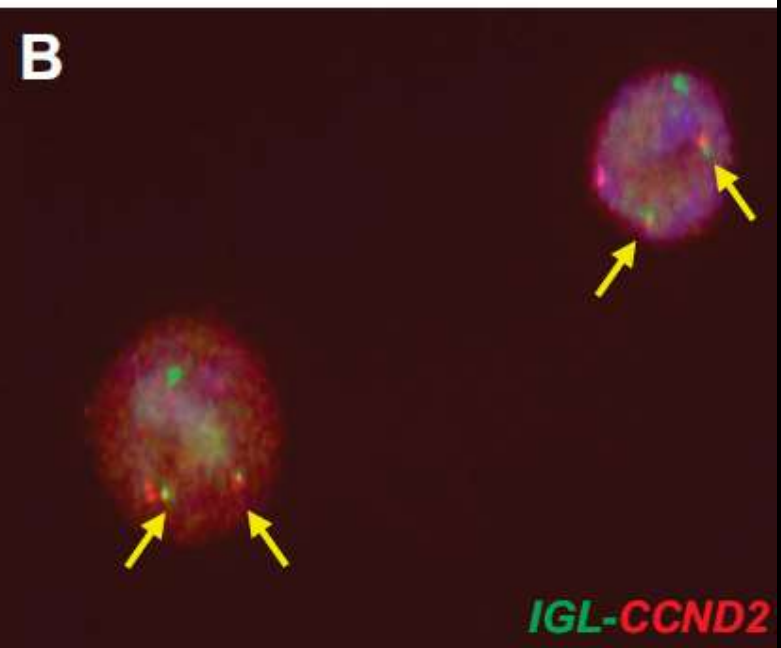
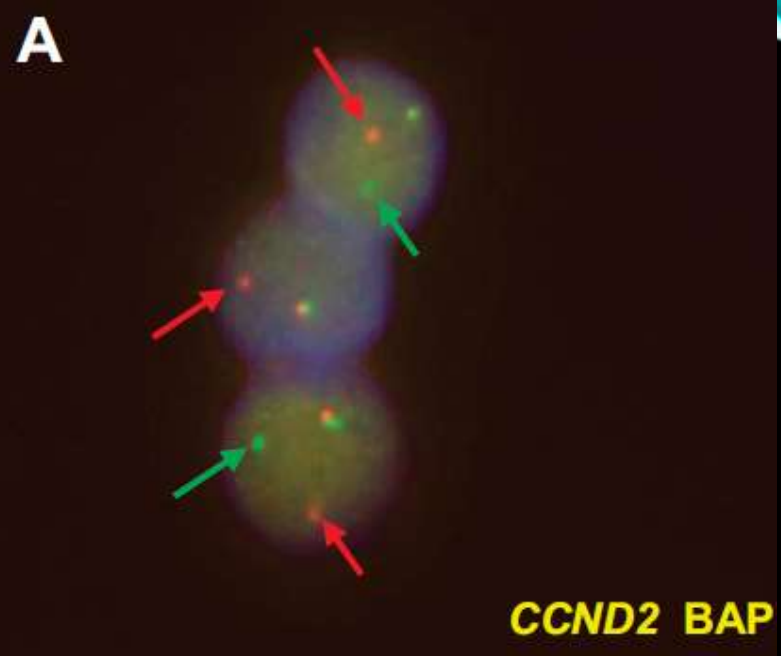
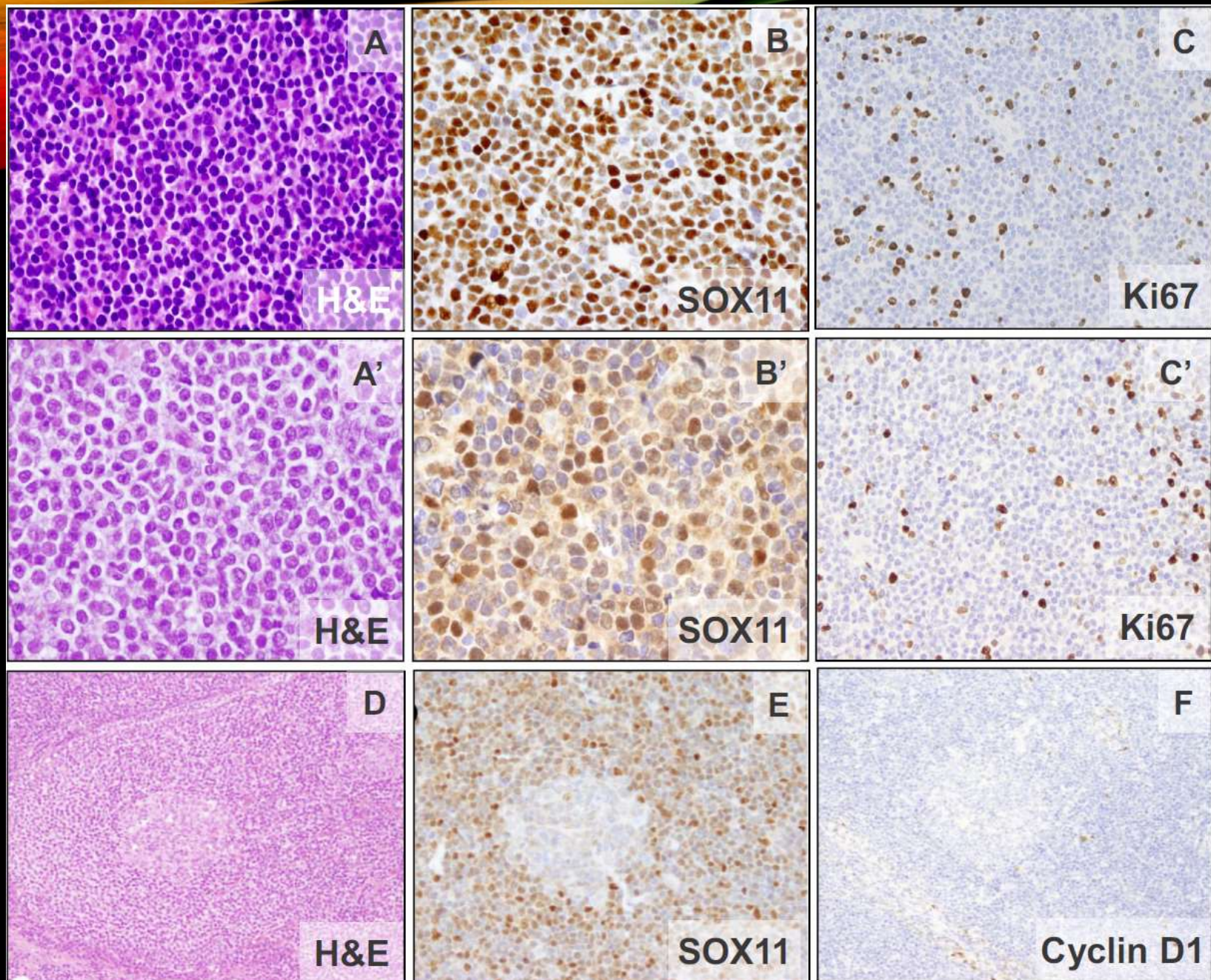
***CCND2* rearrangements are the most frequent genetic events in cyclin D1[−] mantle cell lymphoma**

*Itziar Salaverria,^{1,2} *Cristina Royo,¹ Alejandra Carvajal-Cuenca,¹ Guillem Clot,¹ Alba Navarro,¹ Alejandra Valera,¹ Joo Y. Song,³ Renata Woroniecka,⁴ Grzegorz Rymkiewicz,⁵ Wolfram Klapper,⁶ Elena M. Hartmann,⁷ Pierre Sujobert,⁸ Iwona Wlodarska,⁹ Judith A. Ferry,¹⁰ Philippe Gaulard,⁸ German Ott,¹¹ Andreas Rosenwald,⁷ Armando Lopez-Guillermo,¹² Leticia Quintanilla-Martinez,¹³ Nancy L. Harris,¹⁰ Elaine S. Jaffe,³ Reiner Siebert,² Elias Campo,¹ and Silvia Beà¹

BLOOD, 21 FEBRUARY 2013 • VOLUME 121, NUMBER 8

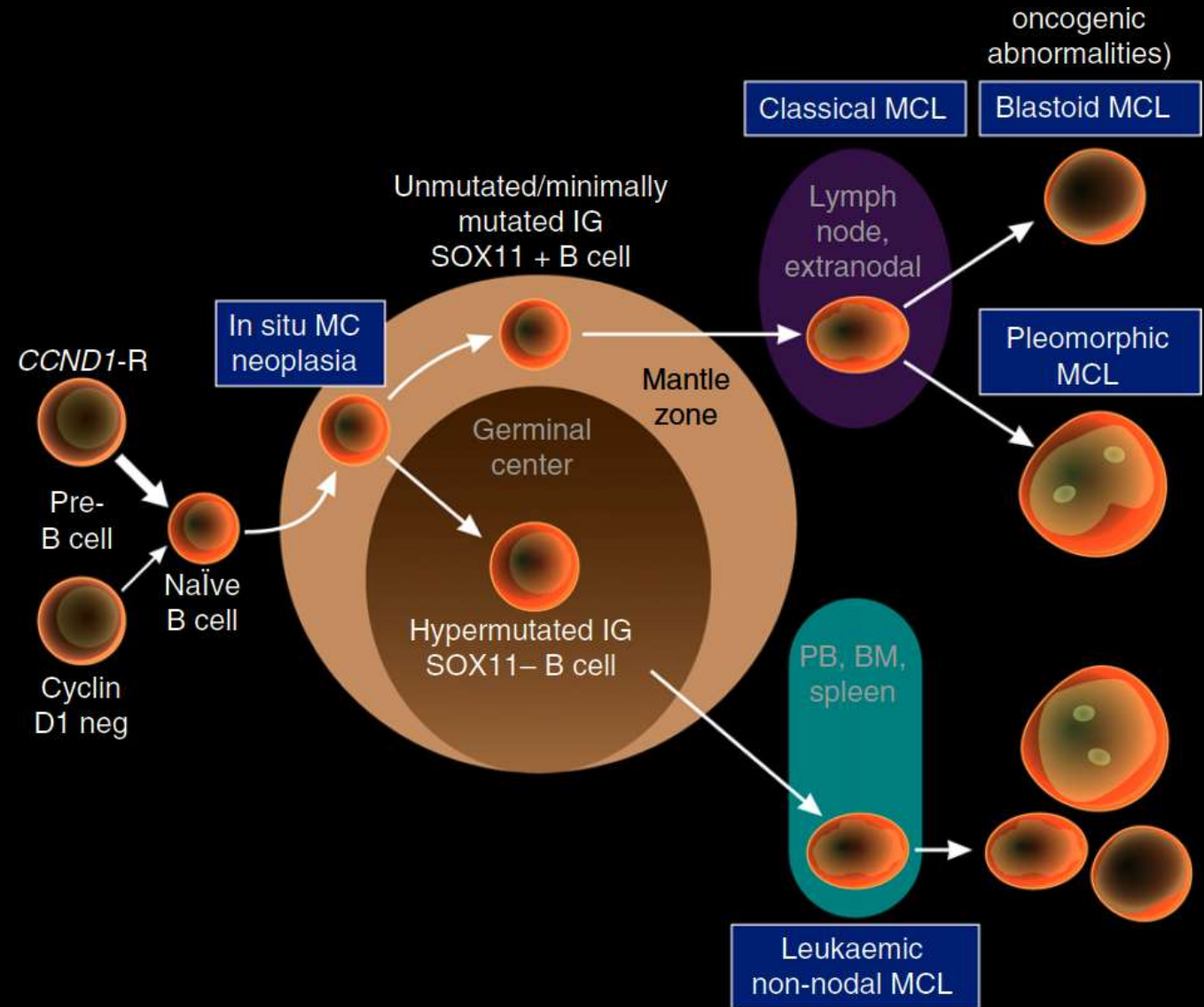
Table 1. Genetic, morphologic, and immunophenotypical parameters of 40 cyclin D1[−]/SOX11⁺ MCL patients

Parameter	n	%
<i>CCND2</i> translocation		
<i>IGH-CCND2</i>	3/40	8
<i>IGK-CCND2</i>	10/40	25
<i>IGL-CCND2</i>	5/40	13
<i>CCND2</i> -break*	2/40	5
<i>CCND2</i> -?†	2/40	5
Negative	18/40	45



PATOGENESI

- Successivamente due vie patogenetiche
- >> Bypass de centro germinativo (cellule naive)
- < Esperienza del centro germinativo (cellule memoria)



I DUE SOTTOTIPI DIFFERISCONO

- Ipermutazione somatica dei geni delle IG
- Profili di espressione genica
- microRNA
- Pattern di metilazione
- Alterazioni genomiche
- Comportamento clinico

CLASSIFICAZIONE WHO 2016-7

Large B-cell lymphoma with IRF4 rearrangement

Primary cutaneous follicle centre lymphoma

Mantle cell lymphoma

In situ mantle cell neoplasia

Diffuse large B-cell lymphoma (DLBCL), NOS

Germinal centre B-cell subtype

Activated B-cell subtype

- Two MCL subtypes recognized with different clinicopathological manifestations and molecular pathogenetic pathways: one largely with unmutated/minimally mutated IGHV and mostly SOX11⁺ and the other largely with mutated IGHV and mostly SOX11⁻ (indolent leukemic nonnodal MCL with PB, bone marrow (BM), $\pm$ splenic involvement, may become more aggressive).

MCL TIPO NAIVE

- Più frequente
- Sox11 molto trascritto, proteina elevata
- Geneticamente instabile
- Mutazioni multiple in regolatori del ciclo cellulare, geni del DNA-damage-response, modificatori della cromatina e geni che regolano l'apoptosi



MCL TIPO MEMORY

- Poco frequente
- RNA e proteina di SOX11 bassi
- Geneticamente stabile (inizialmente)
- Ipermutazione somatica IG e non-IG
- Leucemico non-nodale





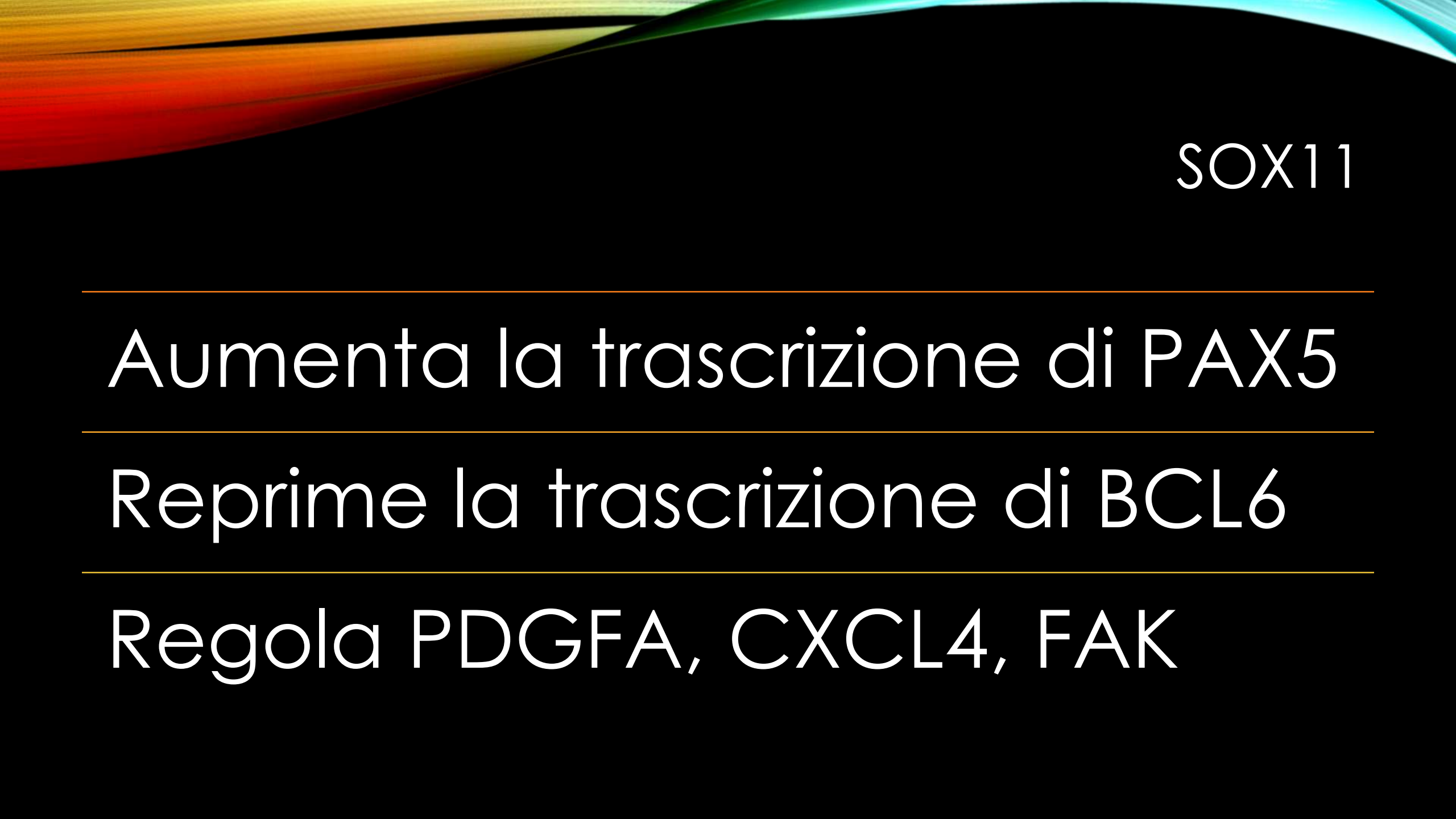
SOX11

Fattore di trascrizione

Assente nelle cellule linfoidi normali

Espressione nel 25-50% dei linfomi di Burkitt

Altri linfomi con eccezione del MCL negativi

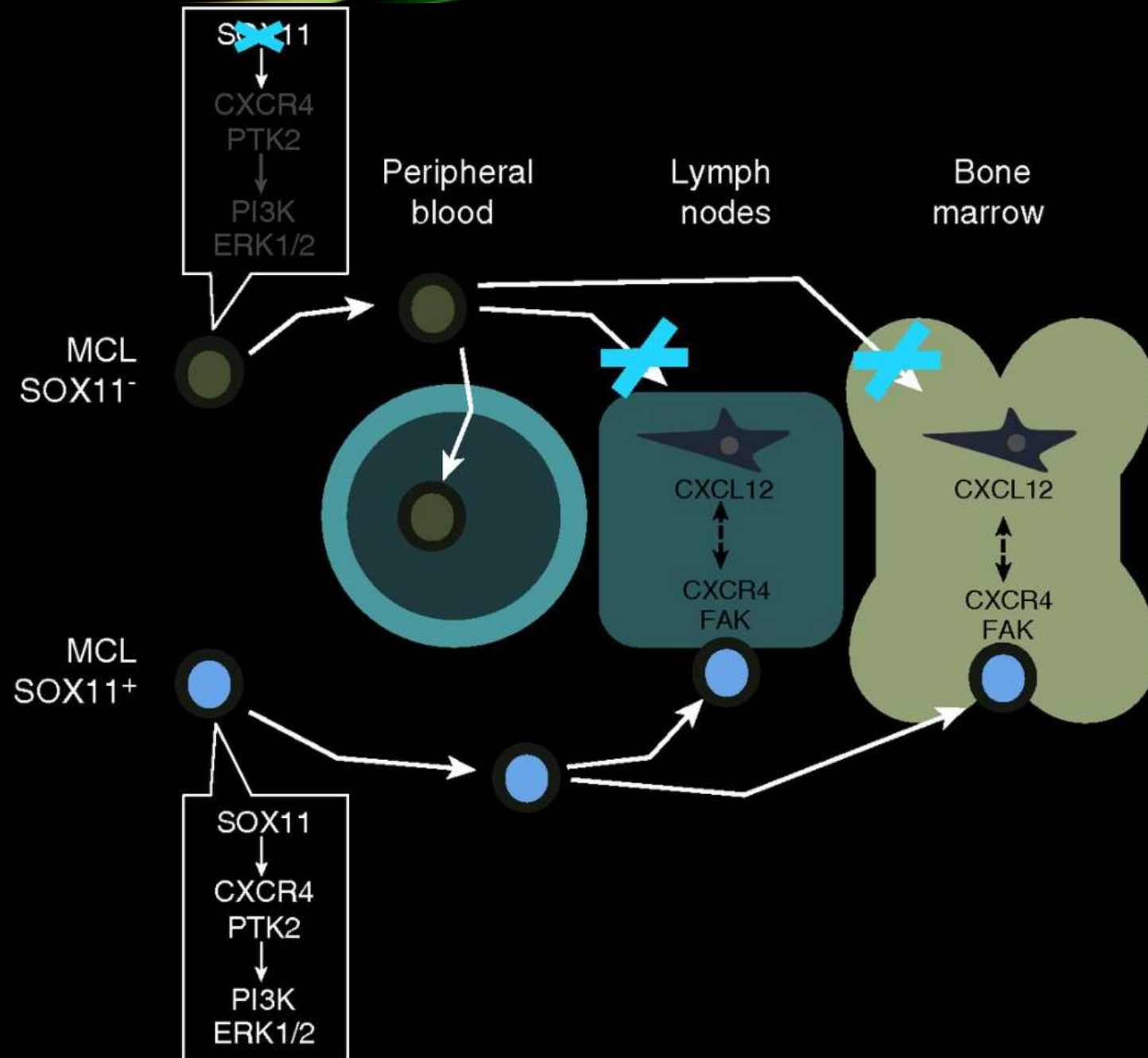


SOX11

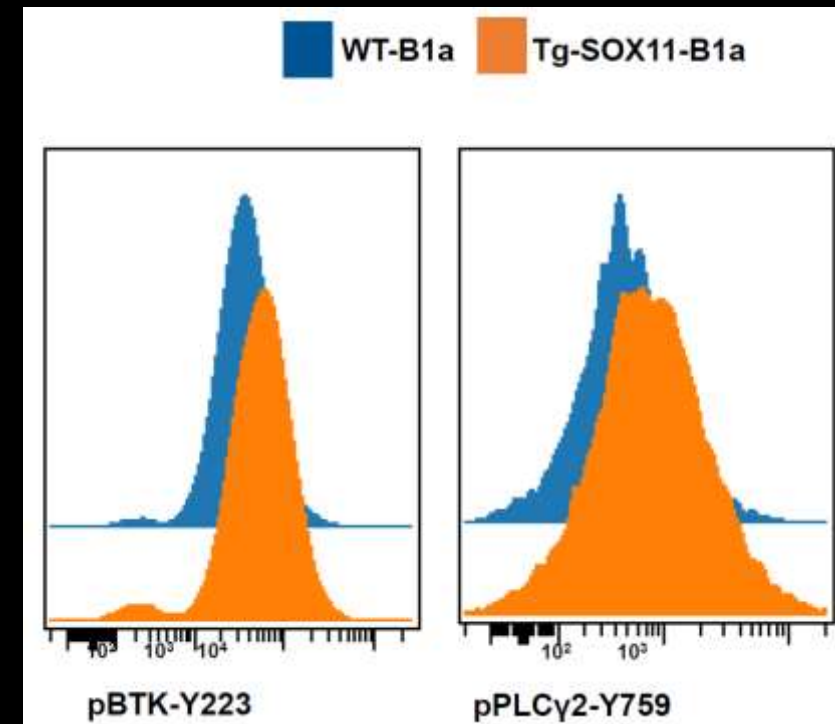
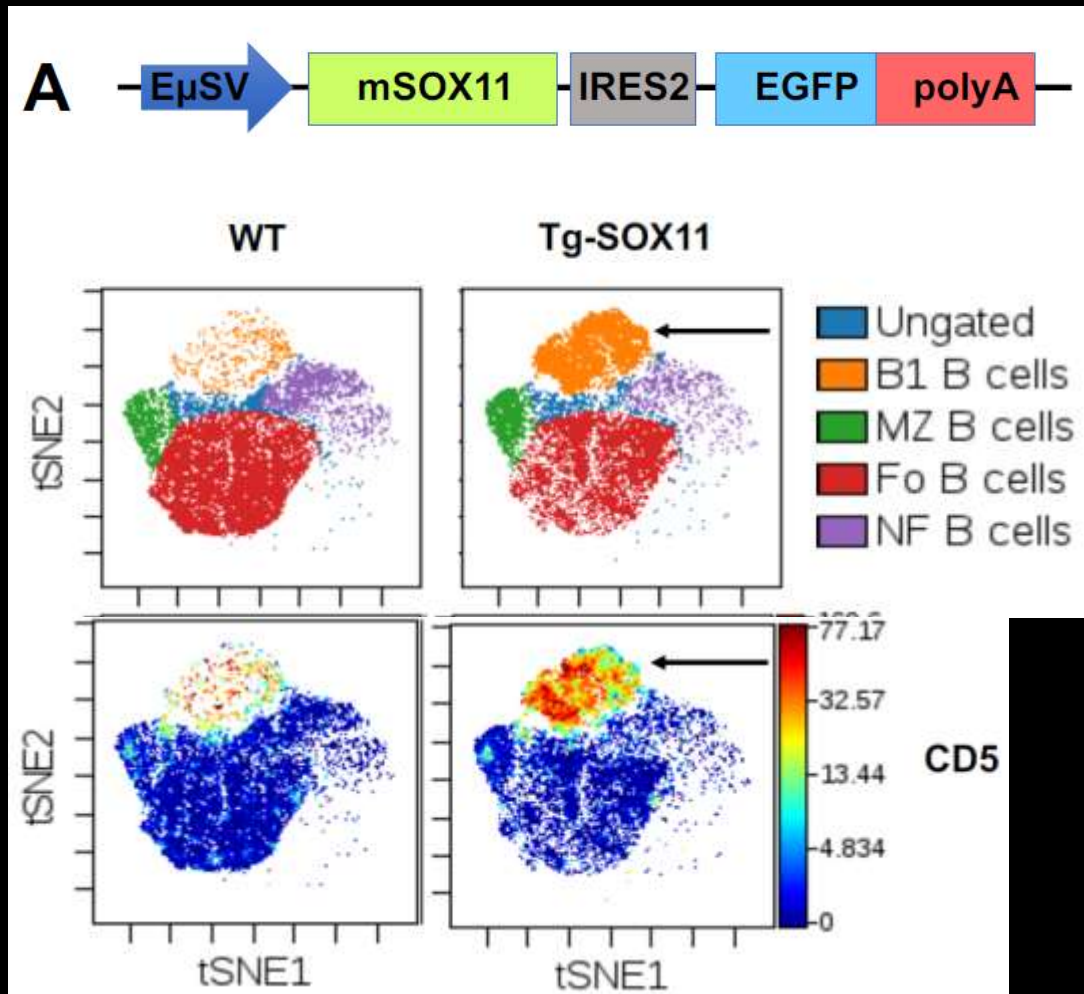
Aumenta la trascrizione di PAX5

Reprime la trascrizione di BCL6

Regola PDGFA, CXCL4, FAK



MODELLO TRANSGENICO



Kuo et al. Blood 2018



RUOLO DEL B-CELL RECEPTOR

VH Bias e stereotipi

Lambda bias

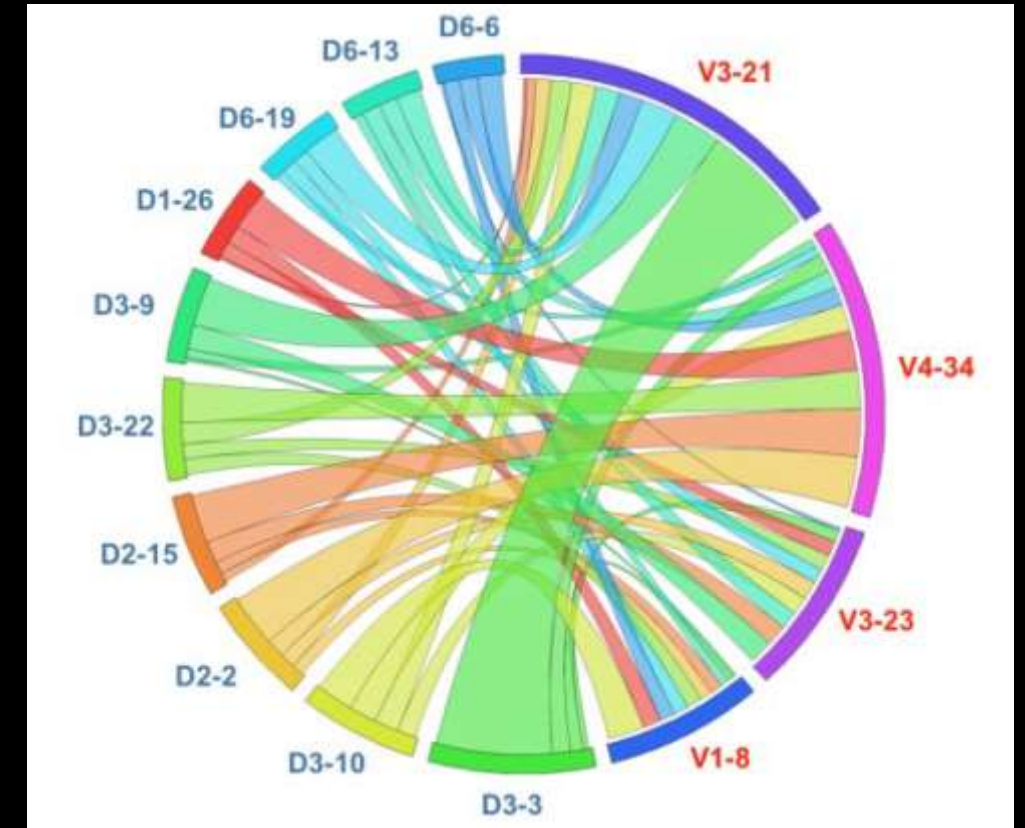
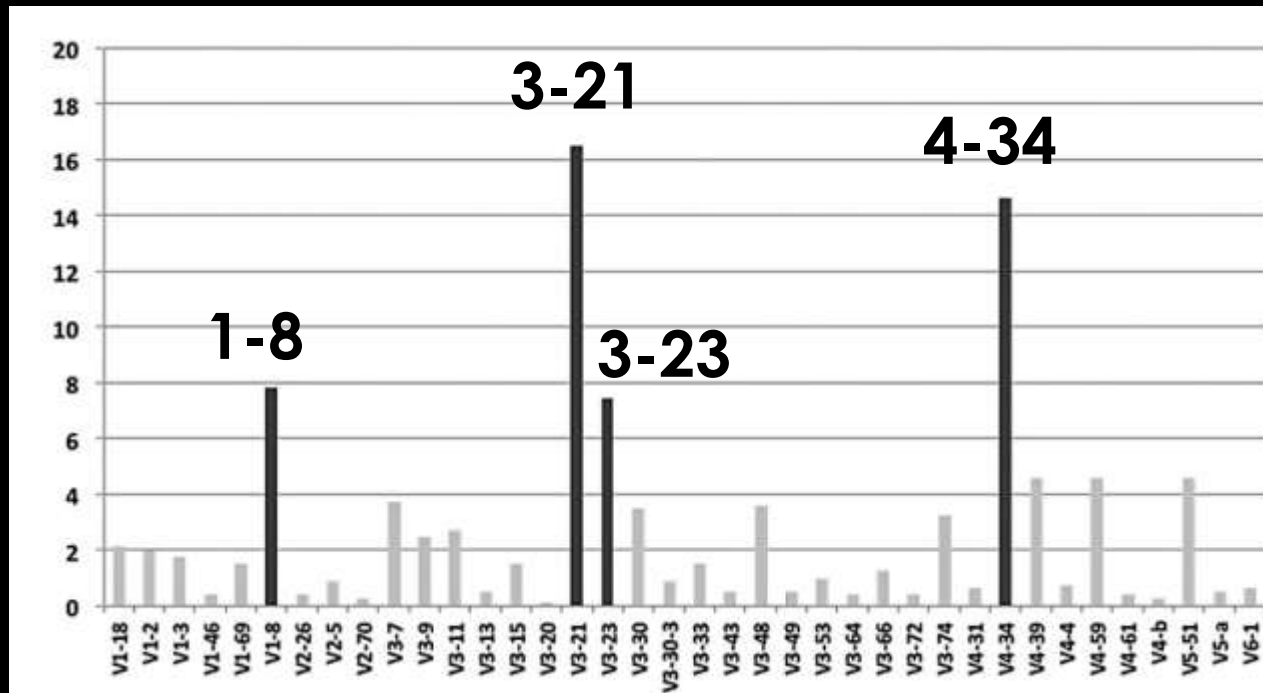
Attivazione cronica attiva in vitro e in vivo

Antigeni

Is there a role for antigen selection in mantle cell lymphoma? Immunogenetic support from a series of 807 cases

*Anastasia Hadzidimitriou,¹ *Andreas Agathangelidis,^{1,3} Nikos Darzentas,¹ Fiona Murray,⁴ Marie-Helene Delfau-Larue,^{5,6} Lone Bredo Pedersen,⁷ Alba Navarro Lopez,⁸ Antonis Dagklis,⁹ Paul Rombout,¹⁰ Kheira Beldjord,¹¹ Arne Kolstad,¹² Martin H. Dreyling,¹³ Achilles Anagnostopoulos,² Athanasios Tsaftaris,¹ Penelope Mavragani-Tsipidou,³ Andreas Rosenwald,¹⁴ Maurilio Ponzoni,¹⁵ Patricia Groenen,¹⁰ Paolo Ghia,⁹ Birgitta Sander,¹⁶ Theodora Papadaki,¹⁷ Elias Campo,⁸ †Christian Geisler,⁷ Richard Rosenquist,⁴ Frederic Davi,¹⁸ Christiane Pott,¹⁹ and Kostas Stamatopoulos^{1,2}

BLOOD, 15 SEPTEMBER 2011 • VOLUME 118, NUMBER 11



10,4% DEI CDR3 SONO STEREOREOTIPATI

A

V3-21/D6-6/J6	V	D6-6		J6	
GERMLINE	AR	EYSSSS		YYYYYGMDV	
07-5780	..				
MC45-2	..				
MC57	..	T			
04-2198	..	.WD...		G.....	
MCL-DK-01-0013	..			A.....	
MCL-SE-01-0036	..			N.....	
V3-21/D3-9/J4	V	N1	D3-9	N2	J4
GERMLINE	AR	YYDILTGYYN			YFDY
06-8174	..	DDT		Y	
08-9994	..	..R		PD	
FRA-MCL054	..	EGQ		T.	
FRA-MCL111	..	.SS	H.....	NS.	
FRA-MCL139	..	.SR		S.	

B

V4-34/D2-2/J6	V	N1	D2-2	N2	J6
GERMLINE	AR		DIVVVPAAI		YYYYYYMDV
04-0309	..	G		AVF	
05-2890	..	.		LSGF	
59812389	..	.	.L.....	G	L..
MCL-DK-01-0038	..	DS		KVI	
MCL-SE-01-0028	..	.		A	
MCL-SE-01-0083	..	.	E.....	S	
MCL-SE-01-0113	..	.T	V..	NS	
V4-34/D1-26/J6	V		D1-26	N2	J6
GERMLINE	AR		GIVGAT		YYYYYYMDV
05-2651	.S			TA	
07-1996	..		.D....	.	D...
MCL-DK-01-0150	..		.E.A..	QS	
MCL-DK-01-0158	..		.E....	.A	..F.....

STEREOTIPIA DELLE CATENE LEGGERE

Table IV. LCDR3 alignment of MCL cell lines and published sequences.

Sequence ID	<i>IGLV</i> gene	<i>IGLJ</i> gene	LCDR3 sequence
MC45-2 [†]	<i>IGLV3-19*01</i>	<i>IGLJ2*01</i>	CNSRDSSGN-HLVF
MC57 [†]	<i>IGLV3-19*01</i>	<i>IGLJ2*01</i>	CNSRDSSGN-HVVF
SE-01-0036-L1 [†]	<i>IGLV3-19*01</i>	<i>IGLJ2*01</i>	CNSRDSSGN-HVVF
Mino	<i>IGLV3-19*01</i>	<i>IGLJ2*01/IGLJ3*01</i>	CNSRDSSGNPHVVF
Jeko-1	<i>IGKV3-20*01</i>	<i>IGKJ2*01</i>	CQQYGSSPNTF
UPN-2	<i>IGKV3-20*01</i>	<i>IGKJ4*01</i>	CQQYGSSP-AF
JVM-2	<i>IGLV2-14*01</i>	<i>IGLJ2*01/IGLJ3*01</i>	CSSYTSSS-V-VF
JVM-13	<i>IGLV2-14*01</i>	<i>IGLJ2*01/IGLJ3*01</i>	CSSYTSSSTLMIF

[†]Data from ref. [18].

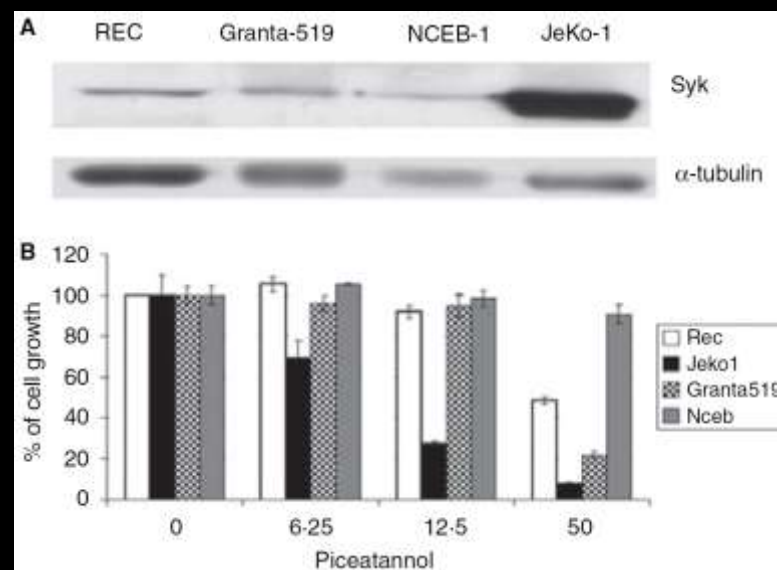
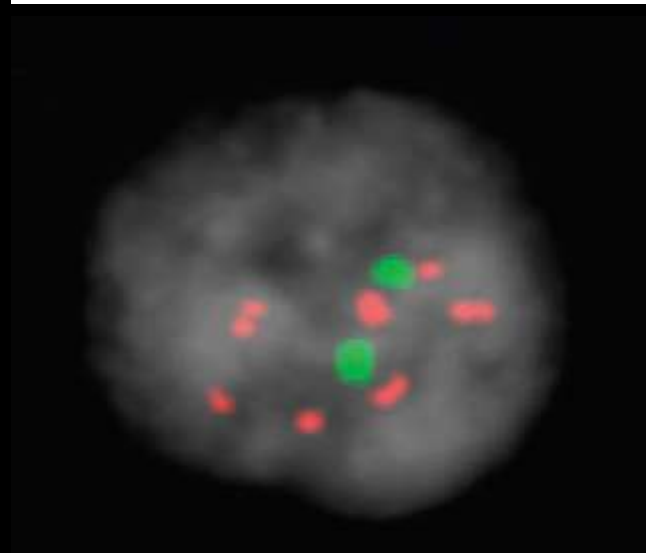
Genomic and expression profiling identifies the B-cell associated tyrosine kinase Syk as a possible therapeutic target in mantle cell lymphoma

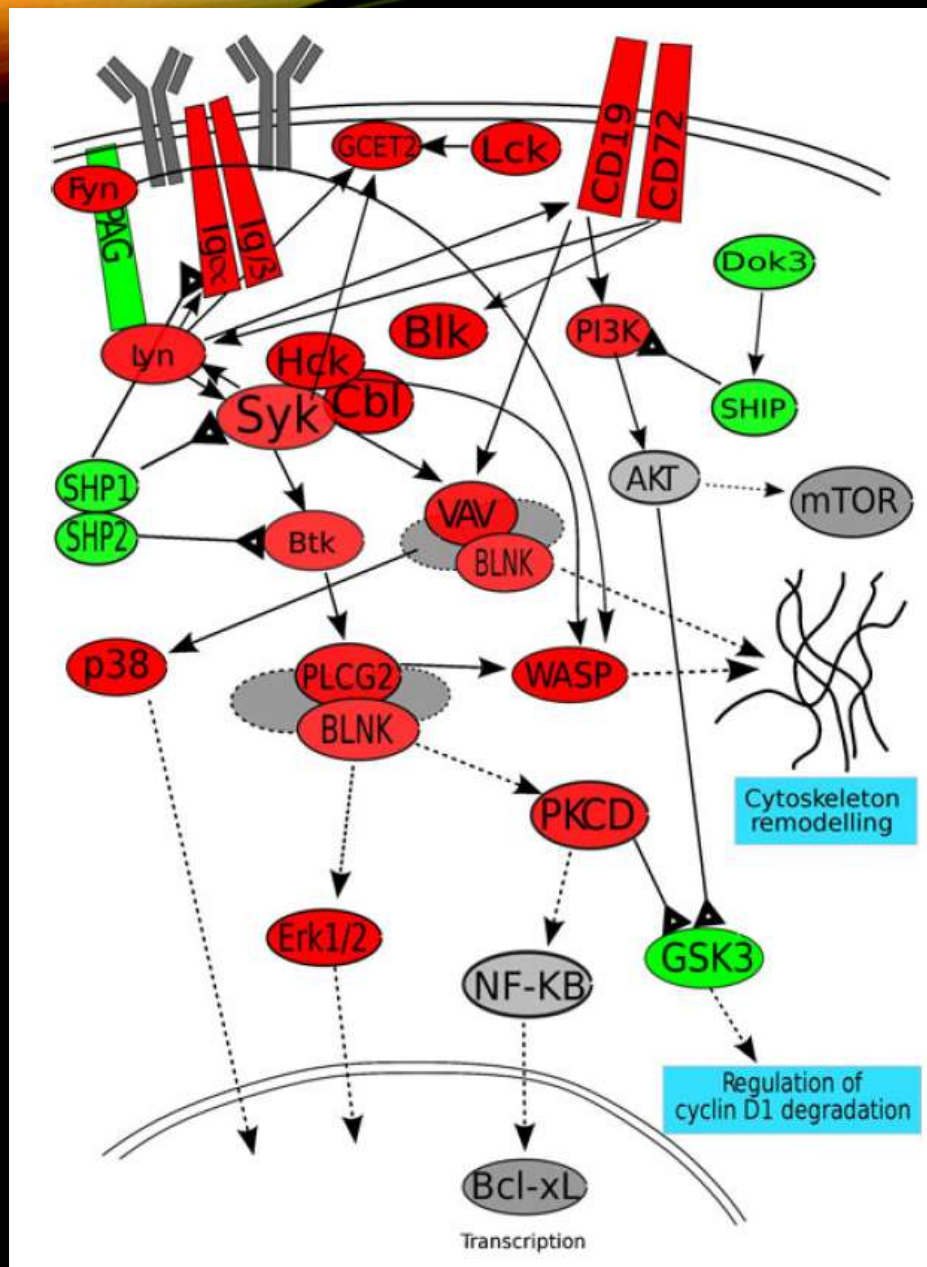
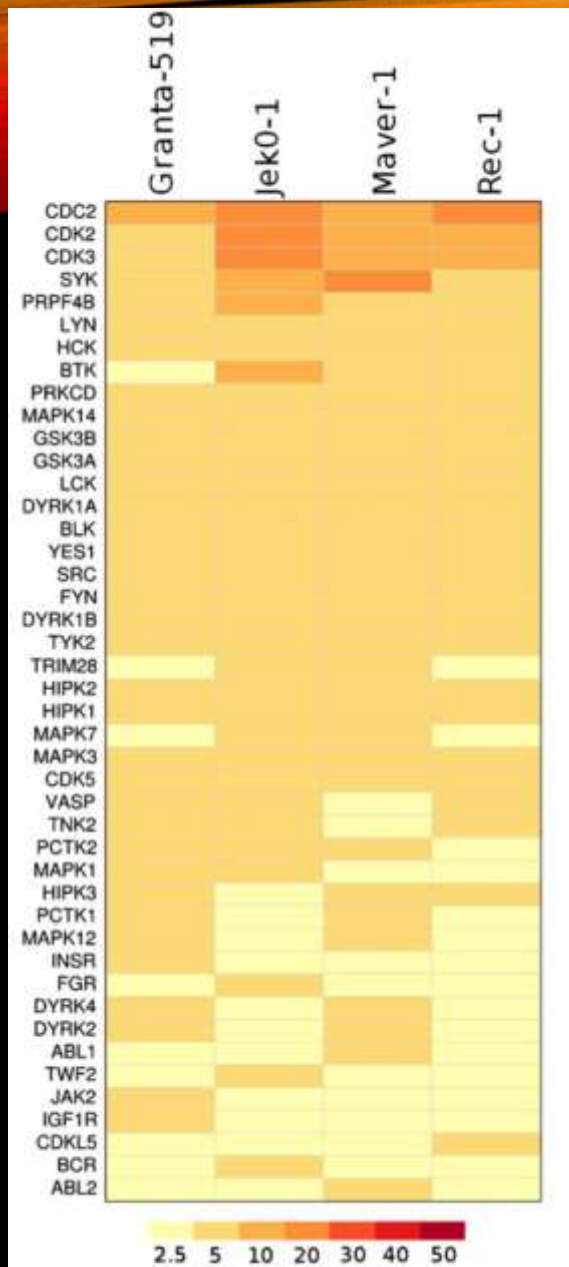
British Journal of Haematology, **132**, 303–316

Andrea Rinaldi,¹ Ivo Kwee,^{1,2} Monica Taborelli,¹ Cristina Largo,³ Silvia Uccella,⁴ Vittoria Martin,⁴ Giulia Poretti,¹ Gianluca Gaidano,⁵ Giuseppe Calabrese,⁶ Giovanni Martinelli,⁷ Luca Baldini,⁸ Giancarlo Pruneri,⁹ Carlo Capella,⁴ Emanuele Zucca,¹⁰ Finbarr E. Cotter,¹¹ Juan C. Cigudosa,³ Carlo V. Catapano,¹ Maria G. Tibiletti⁴ and Francesco Bertoni^{1,11}

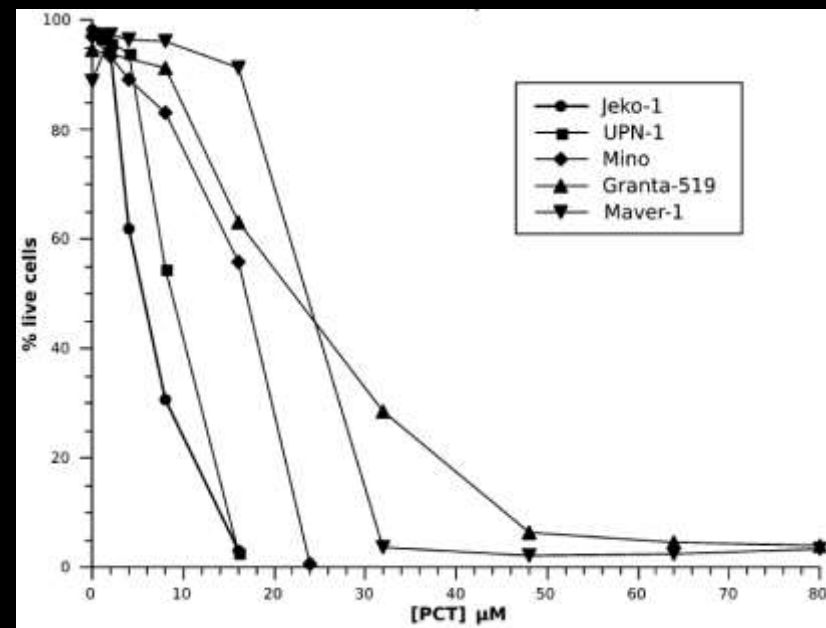
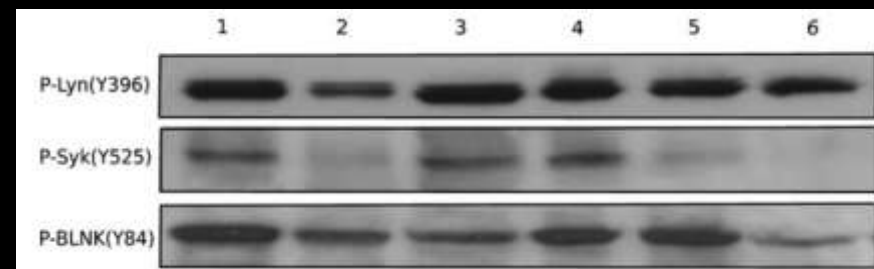
Table II. Genes showing a positive correlation between increased DNA copy number and gene expression in mantle cell lymphoma cell lines.

Gene symbol	Localisation
<i>GYG, SSR3, LAMP3, PLR2H, HES1, EST</i>	3q24–3q29
<i>FGD2, FLJ11236, MRPL2, C6ORF89, MTCH1, EST</i>	6p21-ter
<i>SYK, BICD2, PHF2, PTCH, TGFBR1, SEC61B, TMEFF1, CDW92, ENDOG</i>	9q22–9q31.2
<i>ABAT, CARHSP1, USP7, PROO149, MHC2TA, LOC51760, ESTs</i>	16p12.3–16p13.2
<i>NEDD4L, ZNF532, LMAN1, BCL2, FVT1, VPS4B, TXNDC10, RTTN, SOCS6</i>	18q21–18q22.2

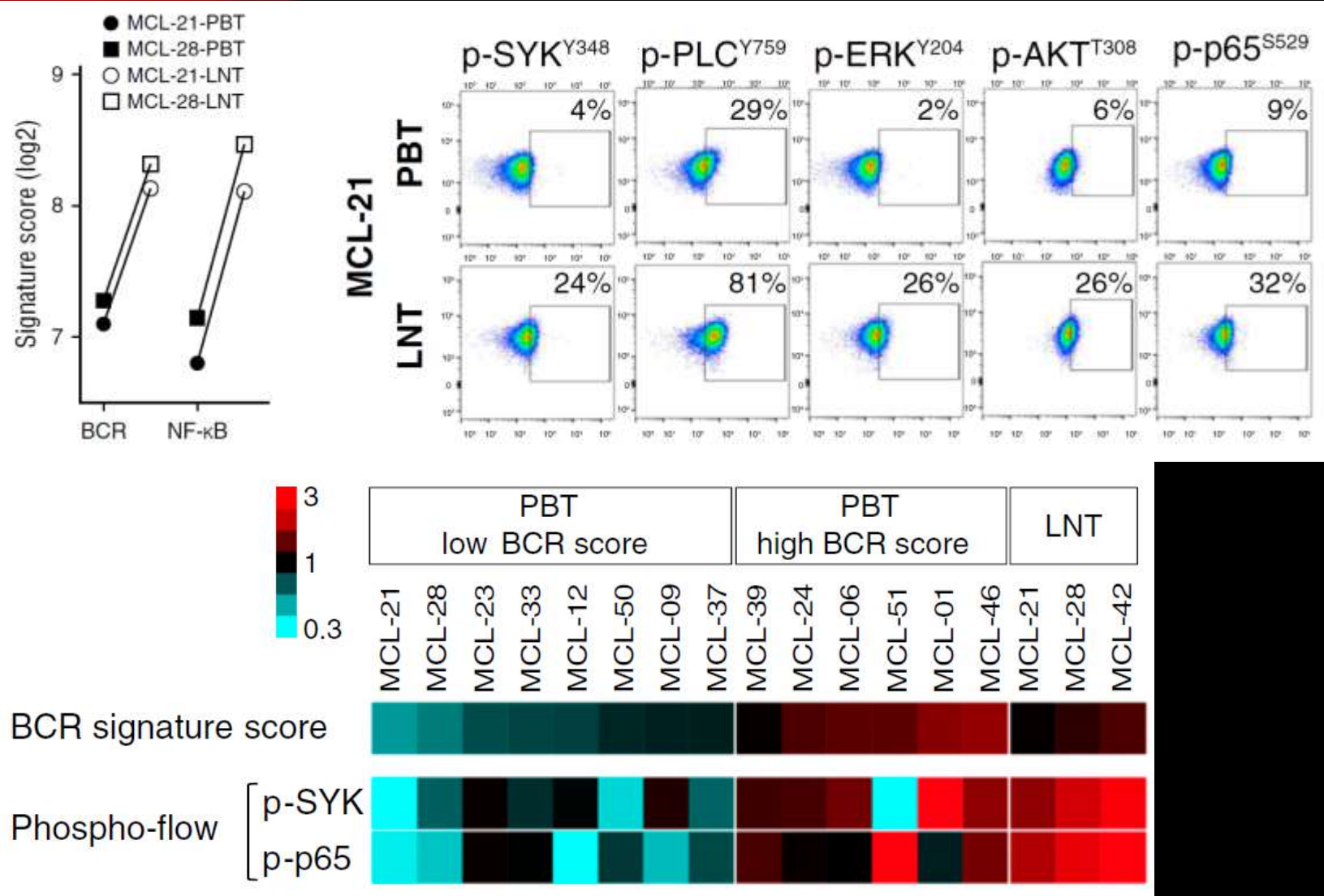




MCL primary tissues



Pathogenic role of B-cell receptor signaling and canonical NF-κB activation in mantle cell lymphoma

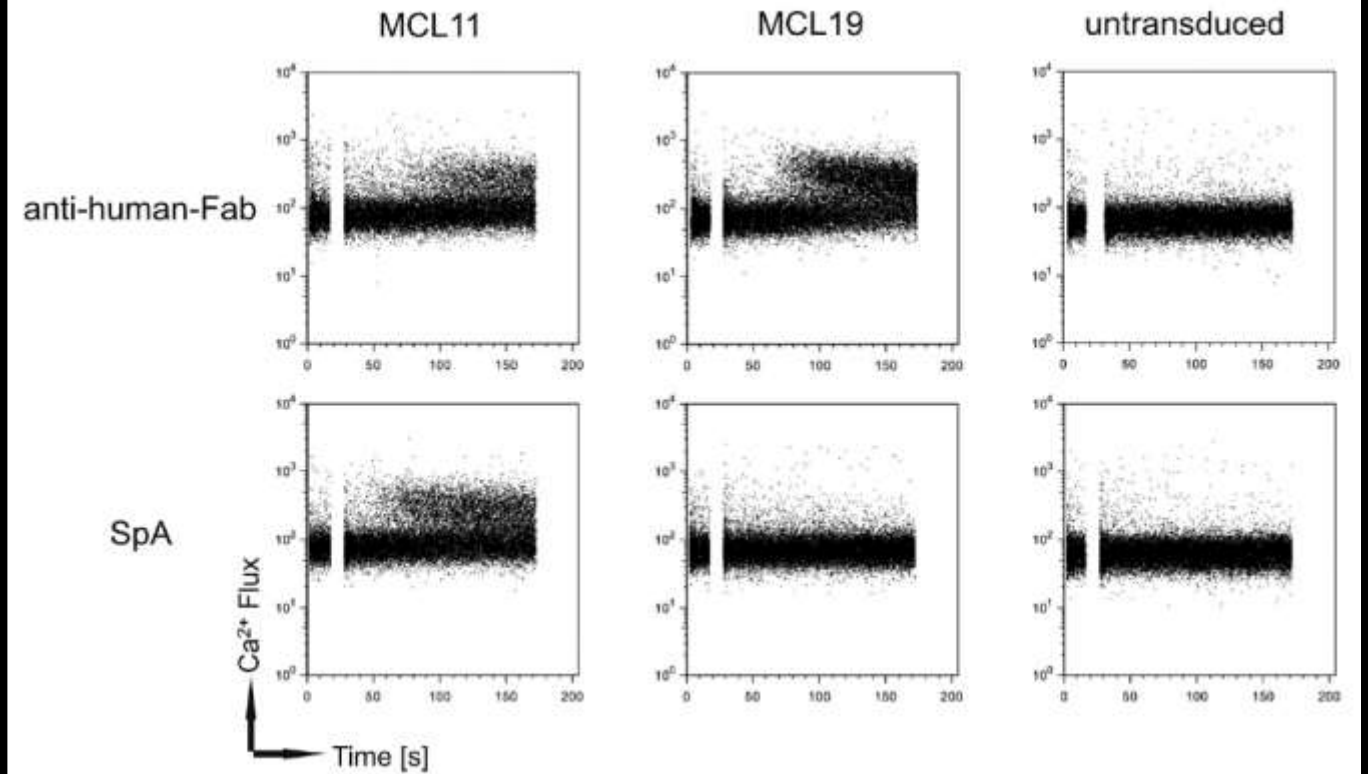


Saba et al.

SUPERANTIGEN – S.AUREUS PROTEIN A MOTIF

A

	Motif	G	S	R/K	K/I/T	Y	K	G	R	T	S	Q	N/G	S
Sample	IGHV-gene segment	16	18	20	65	67	72	74	75	77	79	90	92	93
MCL23	IGHV3-9	G	S	R	I	Y	K	G	R	T	S	Q	N	S
MCL1	IGHV3-21	G	S	R	I	Y	K	G	R	T	S	Q	N	S
MCL8	IGHV3-21	G	S	R	I	Y	K	G	R	T	S	Q	N	S
MCL11	IGHV3-21	G	S	R	I	Y	K	G	R	T	S	Q	N	S
MCL20	IGHV3-21	G	S	R	I	Y	K	G	R	T	S	Q	N	S
MCL28	IGHV3-21	G	S	R	I	Y	K	G	R	T	S	Q	N	S
MCL2	IGHV3-23	G	S	R	T	Y	K	G	R	T	S	Q	N	S
MCL10	IGHV3-23	G	S	R	T	Y	K	G	R	T	S	Q	N	S
MCL22	IGHV3-30	G	S	R	K	Y	K	G	R	T	S	Q	N	S
MCL13	IGHV3-48	G	S	R	I	Y	K	G	R	T	S	Q	N	S
MCL5	IGHV3-49	G	S	R	T	Y	K	G	R	T	S	Q	N	S
MCL31	IGHV3-74	G	S	R	T	Y	K	G	R	T	S	Q	N	S
FL6	IGHV3-11	G	S	R	T	Y	K	G	R	T	S	Q	N	S
FL10	IGHV3-11	G	S	R	T	Y	E	G	R	F	S	Q	N	N
FL8	IGHV3-11	G	S	R	T	Y	K	G	R	T	S	Q	N	S
FL101	IGHV3-15	G	S	R	T	Y	R	G	R	T	S	H	S	N
FL11	IGHV3-23	G	S	R	T	Y	K	G	R	S	S	H	N	R
FL5	IGHV3-53	G	S	R	T	Y	K	G	R	T	S	Q	N	T
CLL149	IGHV3-7	G	S	R	K	F	K	G	R	S	S	Q	N	S
CLL172	IGHV3-7	G	T	R	K	Y	R	G	R	T	S	Q	N	S
CLL024	IGHV3-9	G	S	R	I	Y	K	G	R	T	S	Q	N	S
CLL83	IGHV3-21	G	S	R	M	Y	K	G	R	T	S	Q	N	S
CLL173	IGHV3-23	G	A	R	T	Y	E	G	R	T	S	Q	N	S
CLL003	IGHV3-30	G	S	R	K	Y	K	G	R	T	S	Q	N	S
CLL145	IGHV3-30	G	S	R	K	Y	K	G	R	T	S	Q	N	S



Fichtner et al. Haematologica. 2016 Sep;101(9):e378-81

LESIONI GENETICHE

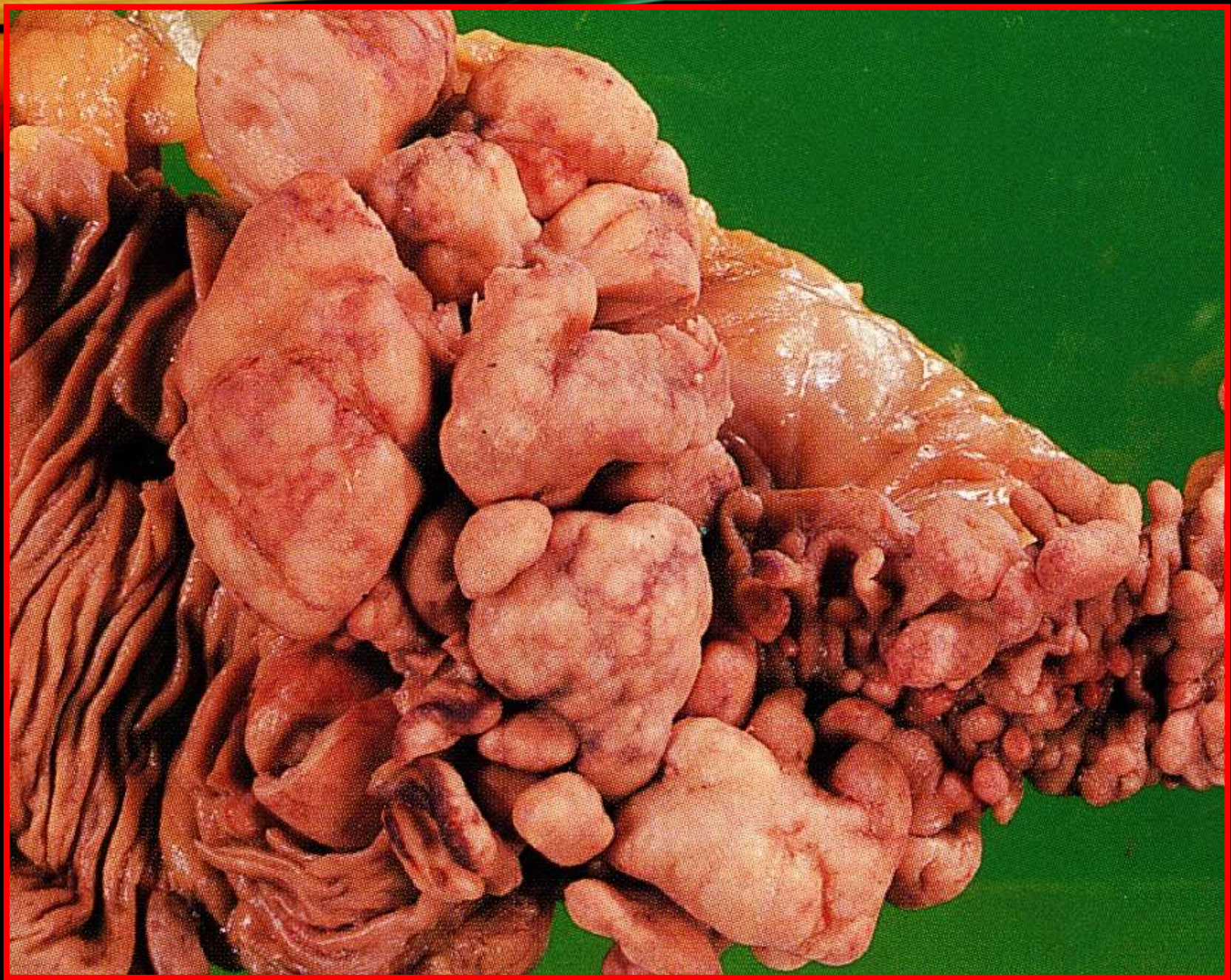
- Elevato numero di lesioni genetiche per caso
- Instabilità genetica
- Frequente cromotripsi/cromoplessia
- Traslocazione di MYC possibile ma rara
- MYC CNA relativamente più frequenti

LESIONI GENETICHE RICORRENTI

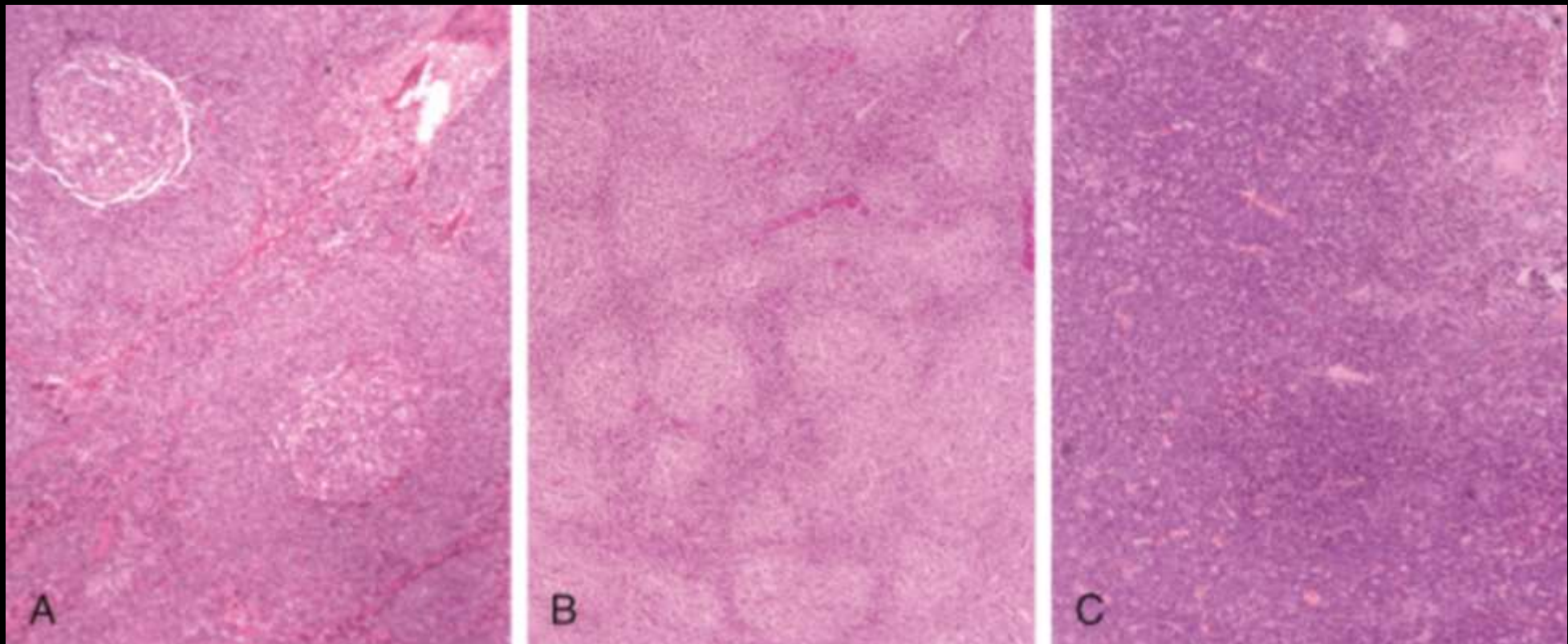
	Naive MCL	Memory MCL
ATM	55%	0%
TP53	25%	25%
CDKN2A deletion	20%	0%
CCND1	18%	86% (SHM)
KMT2D	18%	0%
NSD2/WHSC1	15%	0%
UBR5	14%	0%
BIRC3	7%	7%
NOTCH2	6%	4%
NOTCH1	4%	0%
TLR2	0%	3%

MORFOLOGIA



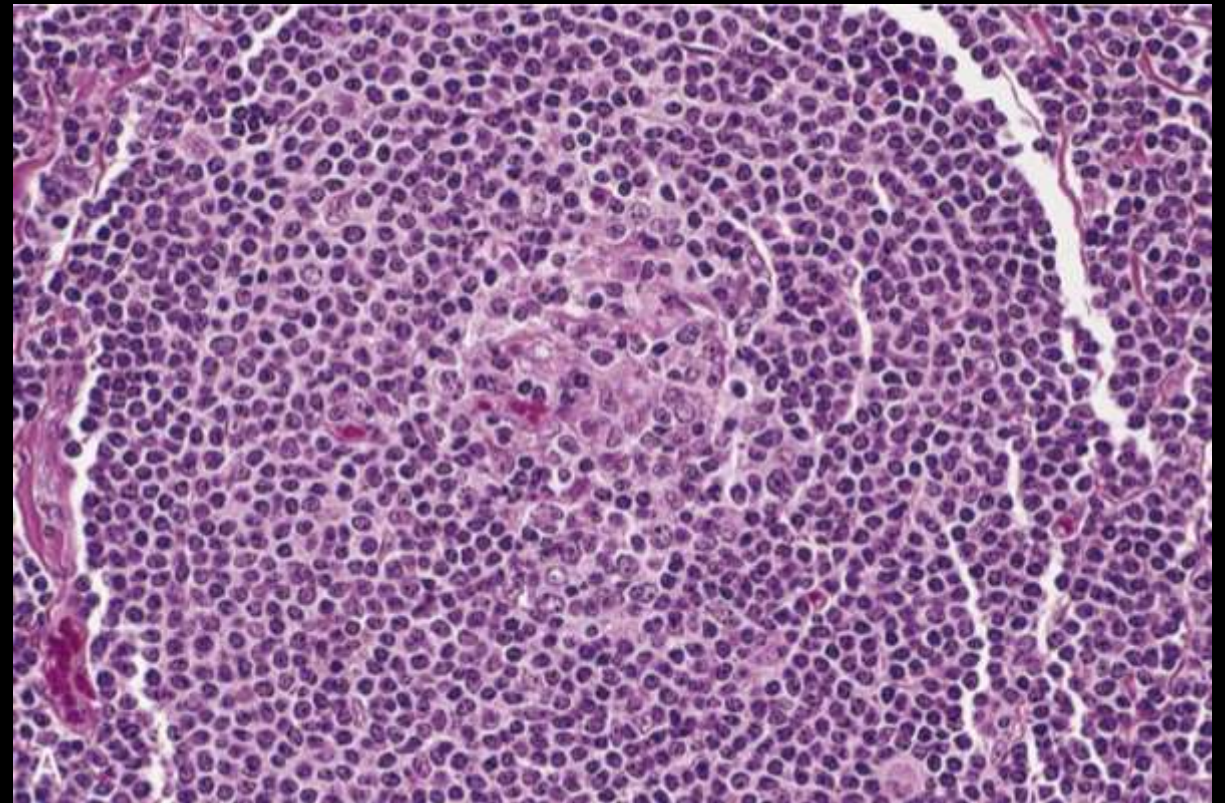


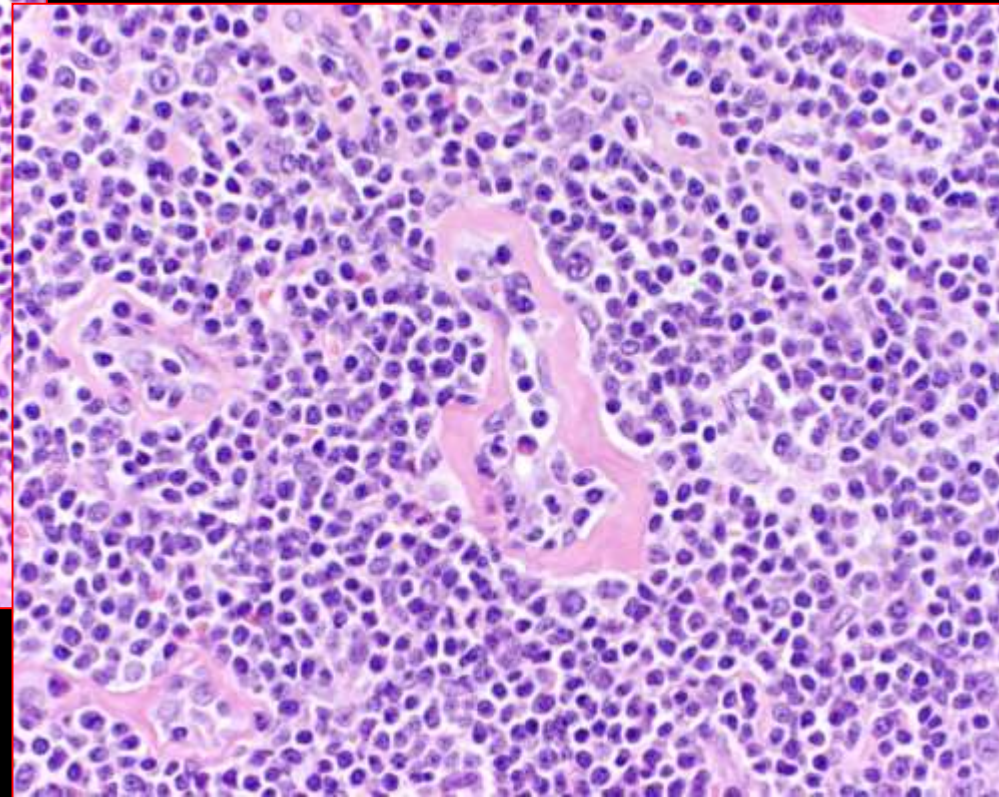
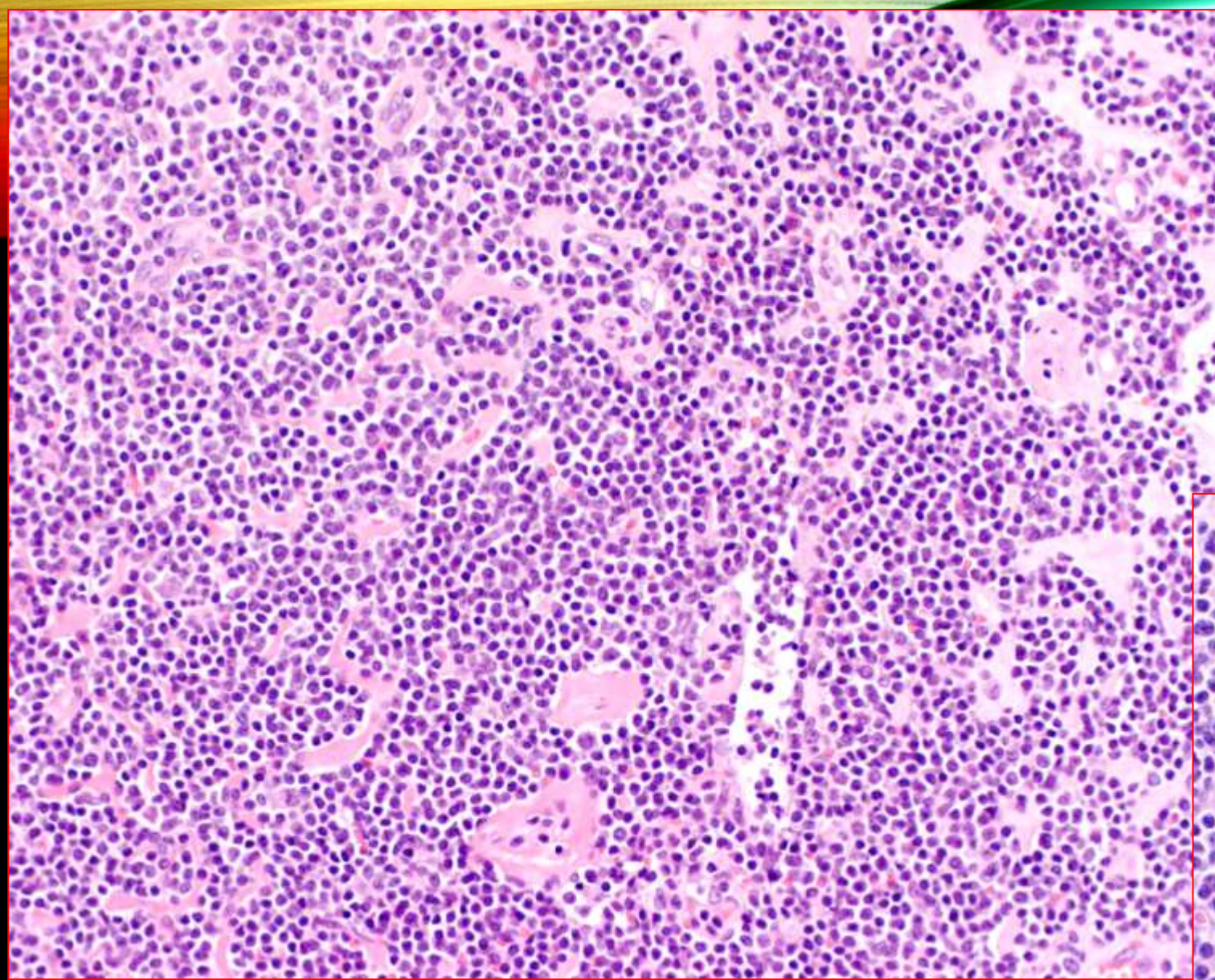
PATTERN LINFONODALI

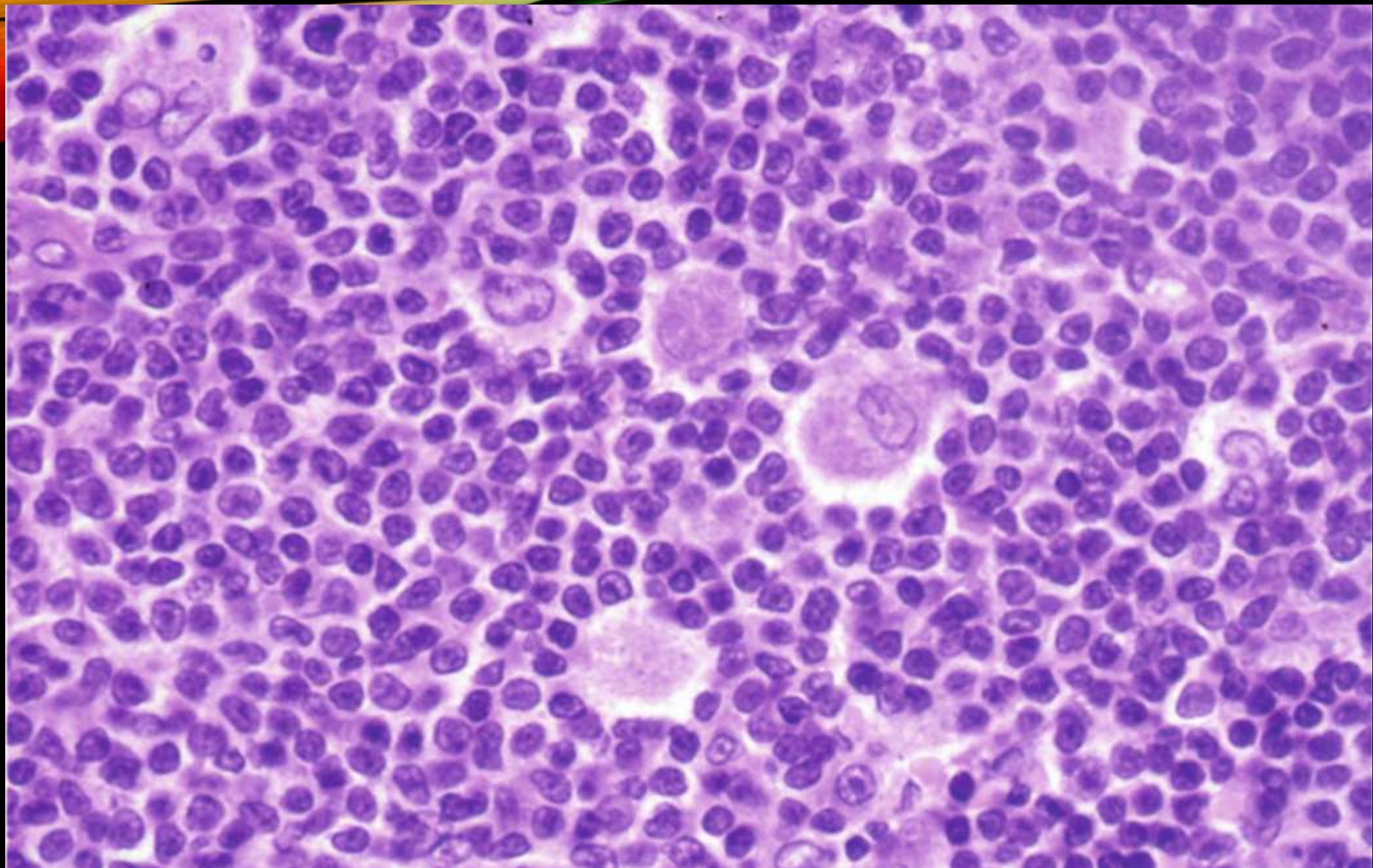


MORFOLOGIA CLASSICA

- Proliferazione nodulare o diffusa
- Elementi medio-piccoli, monotoni

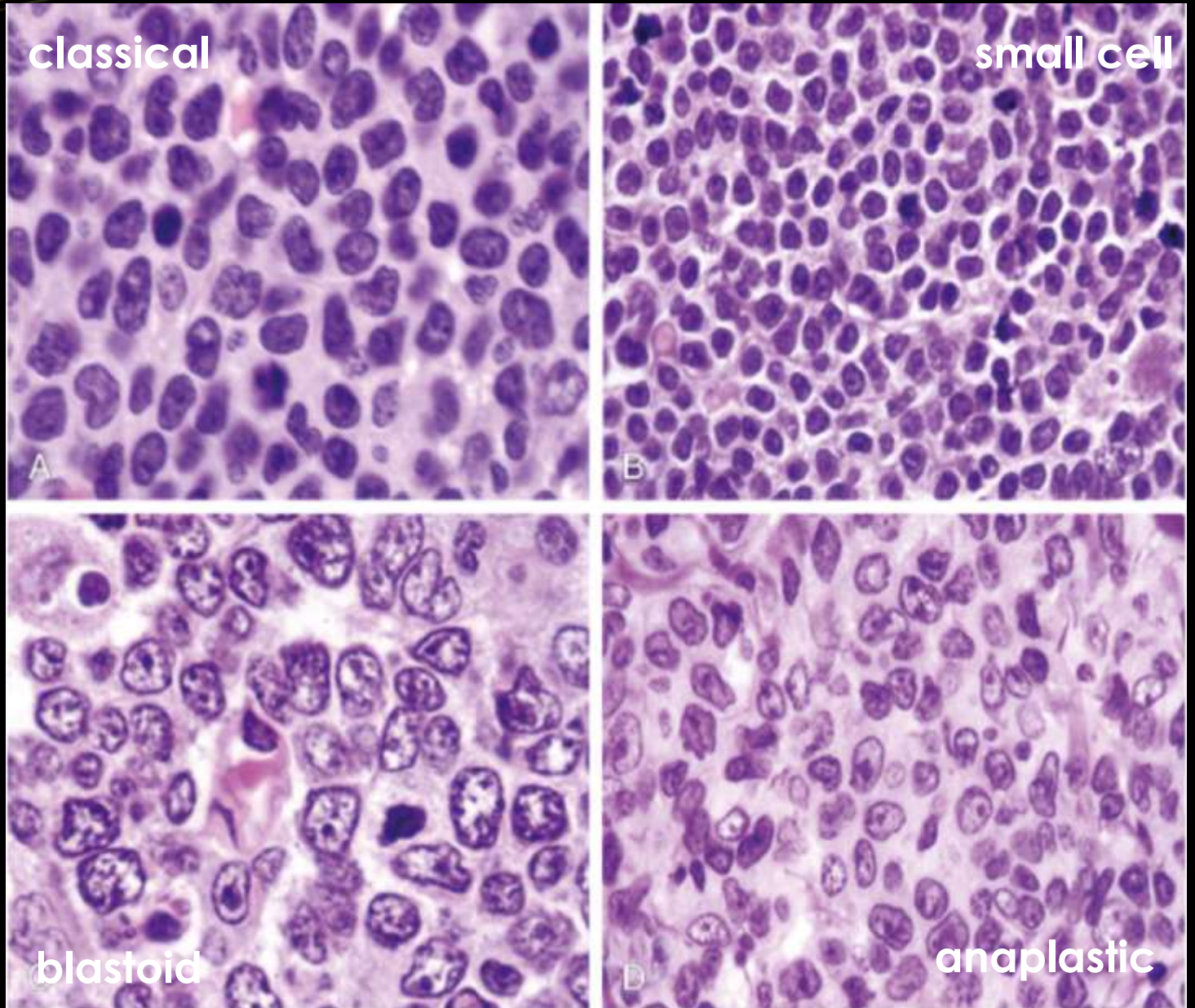






MORFOLOGIA VARIANTE

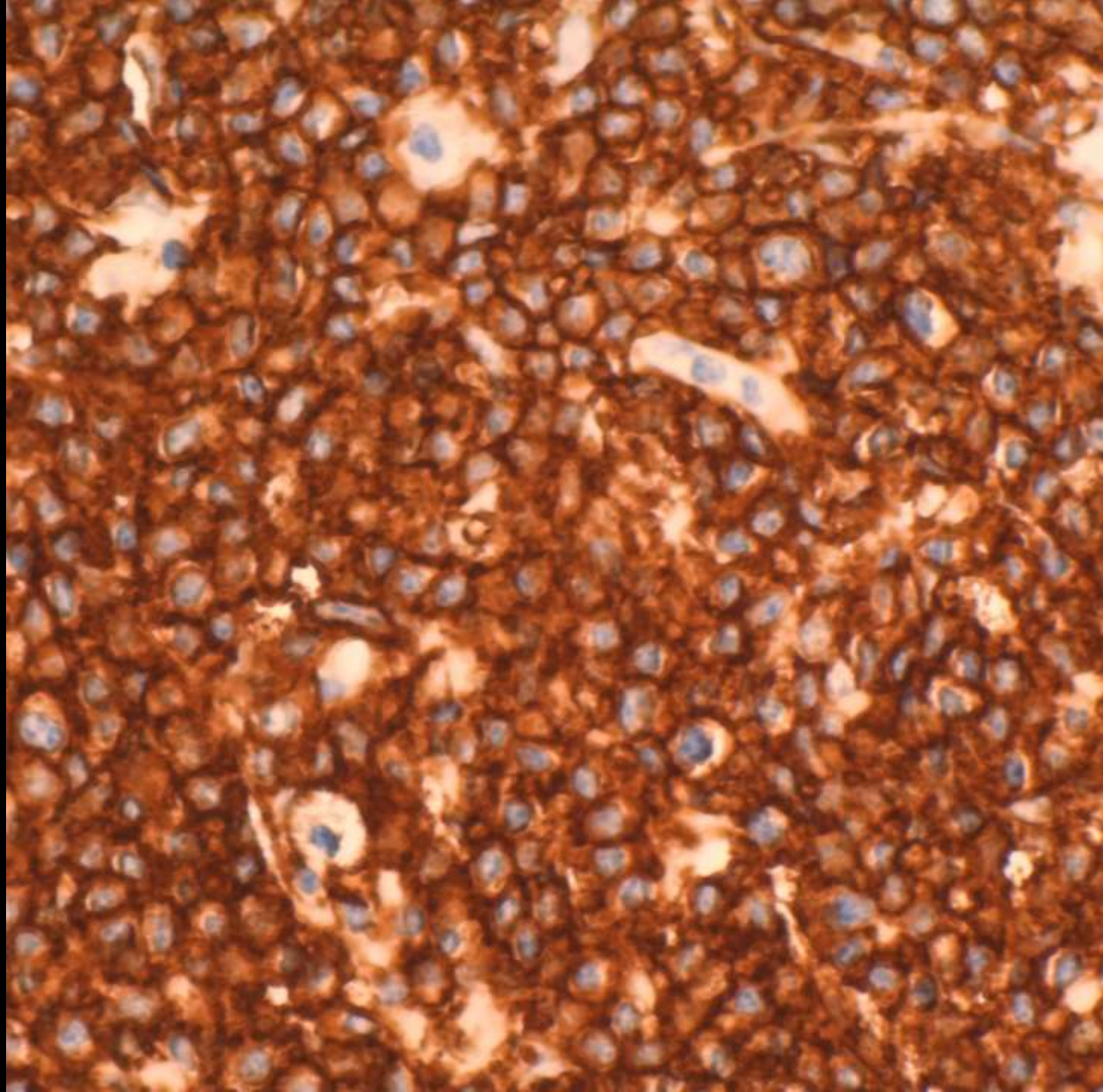
- Piccole cellule
- Blastoidi
- Anaplastico
- (Monocitoide)



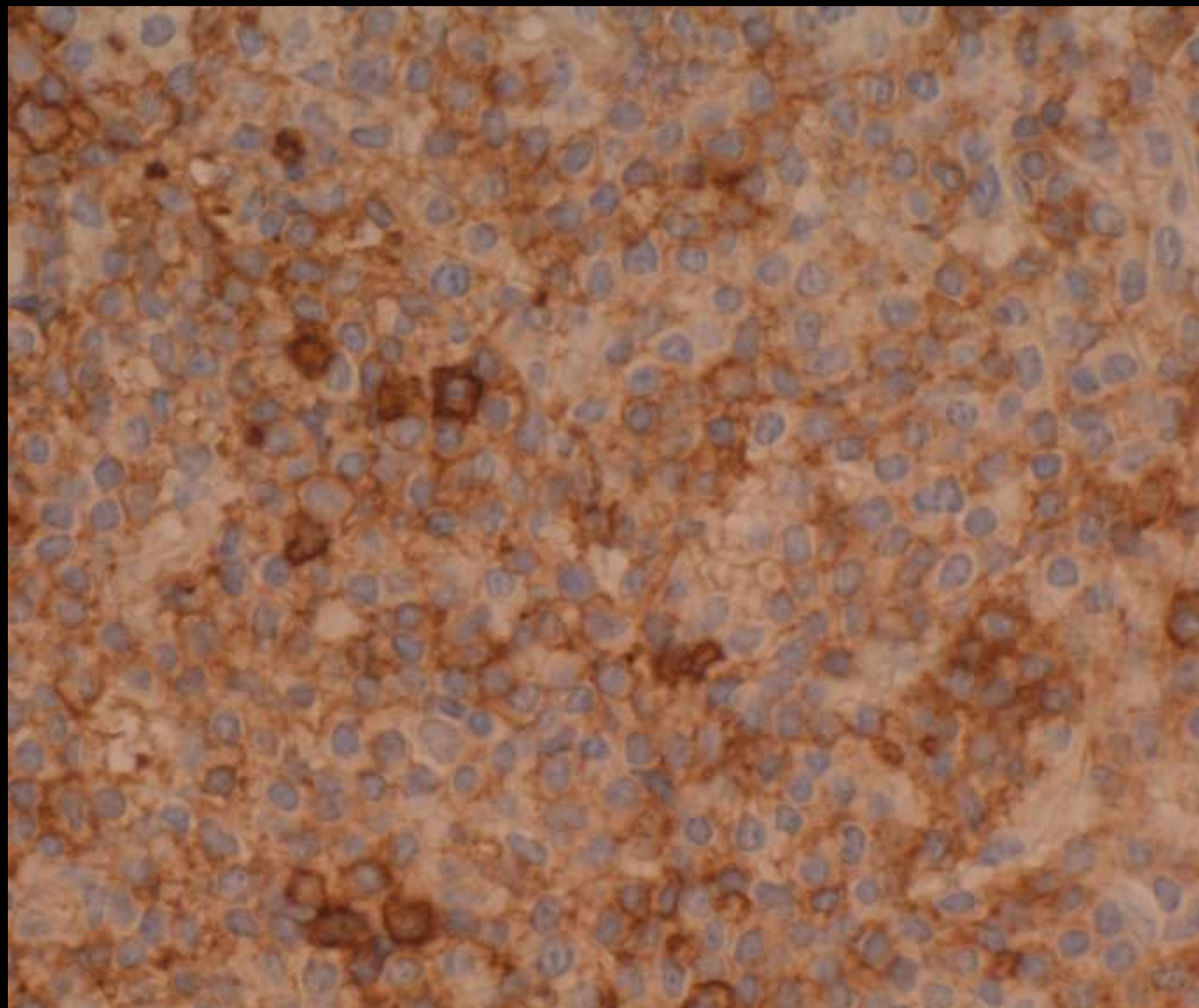
IMMUNOFENOTIPO

- Marcatori B positivi (alta intensità in citometria a flusso)
- CD5 positivo
- Ciclina D1 positivo (90%)
- SOX11 positivo (marcatore più specifico)
- LEF1-negativo (DD B-CLL)

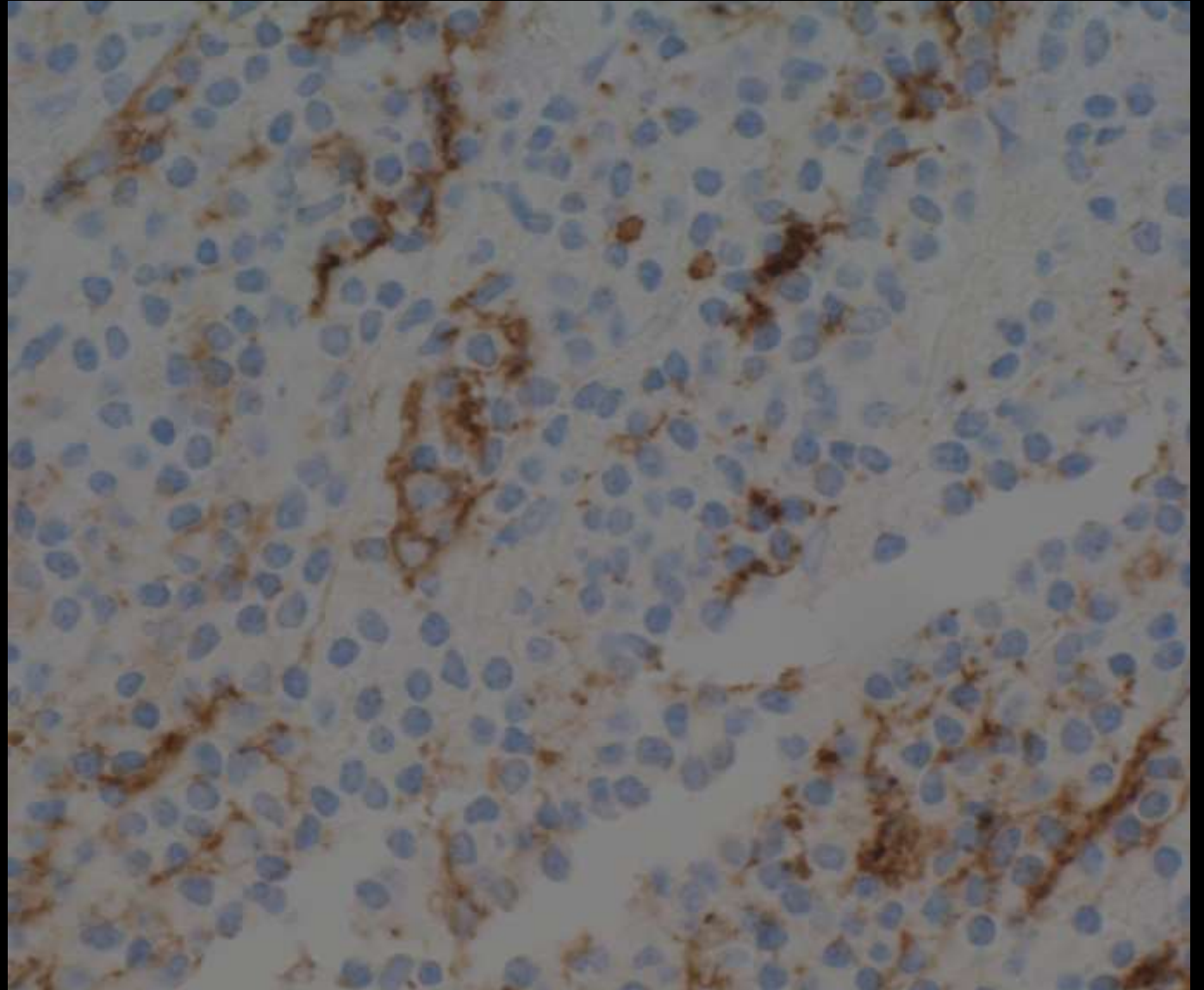
CD20



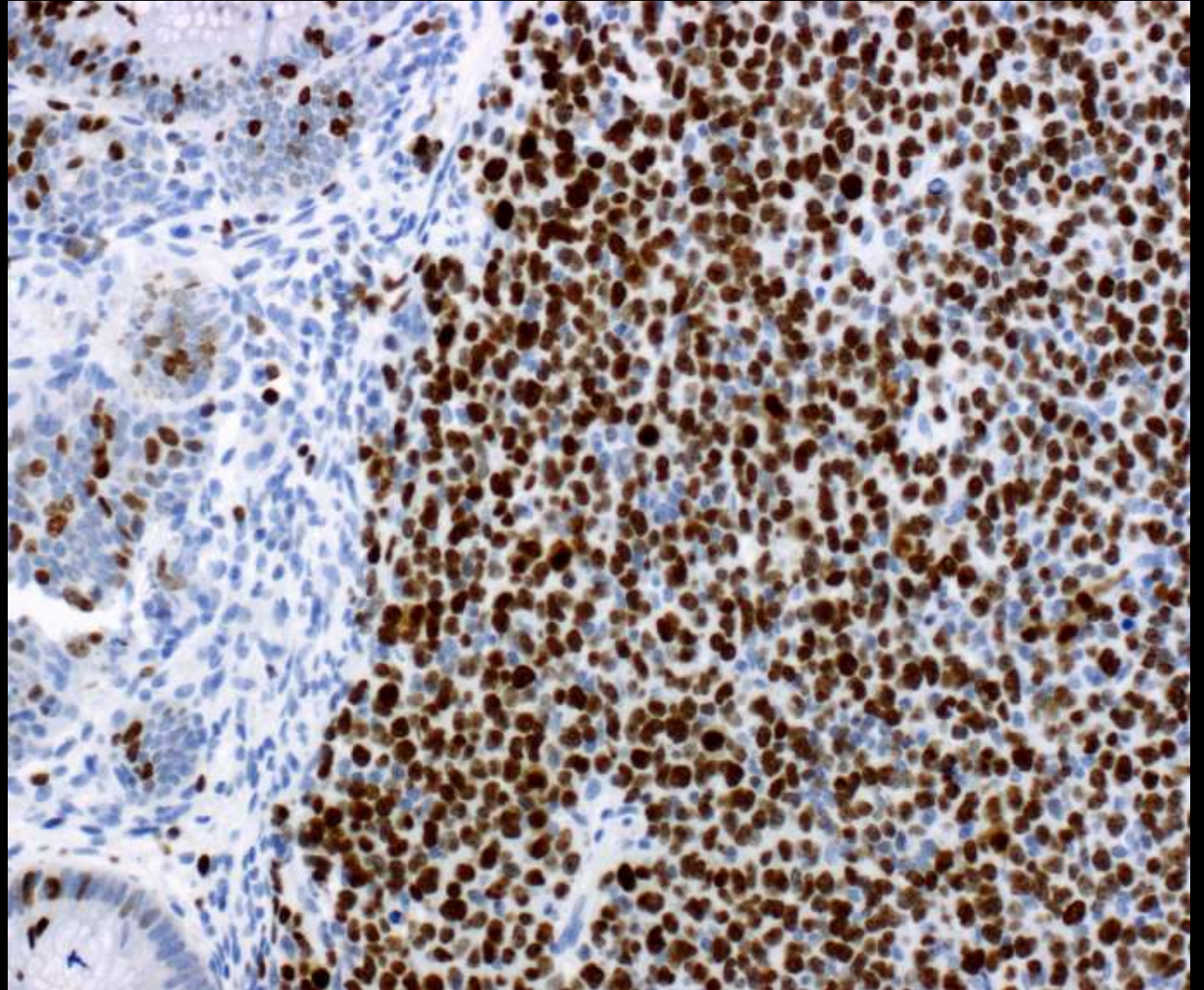
CD5



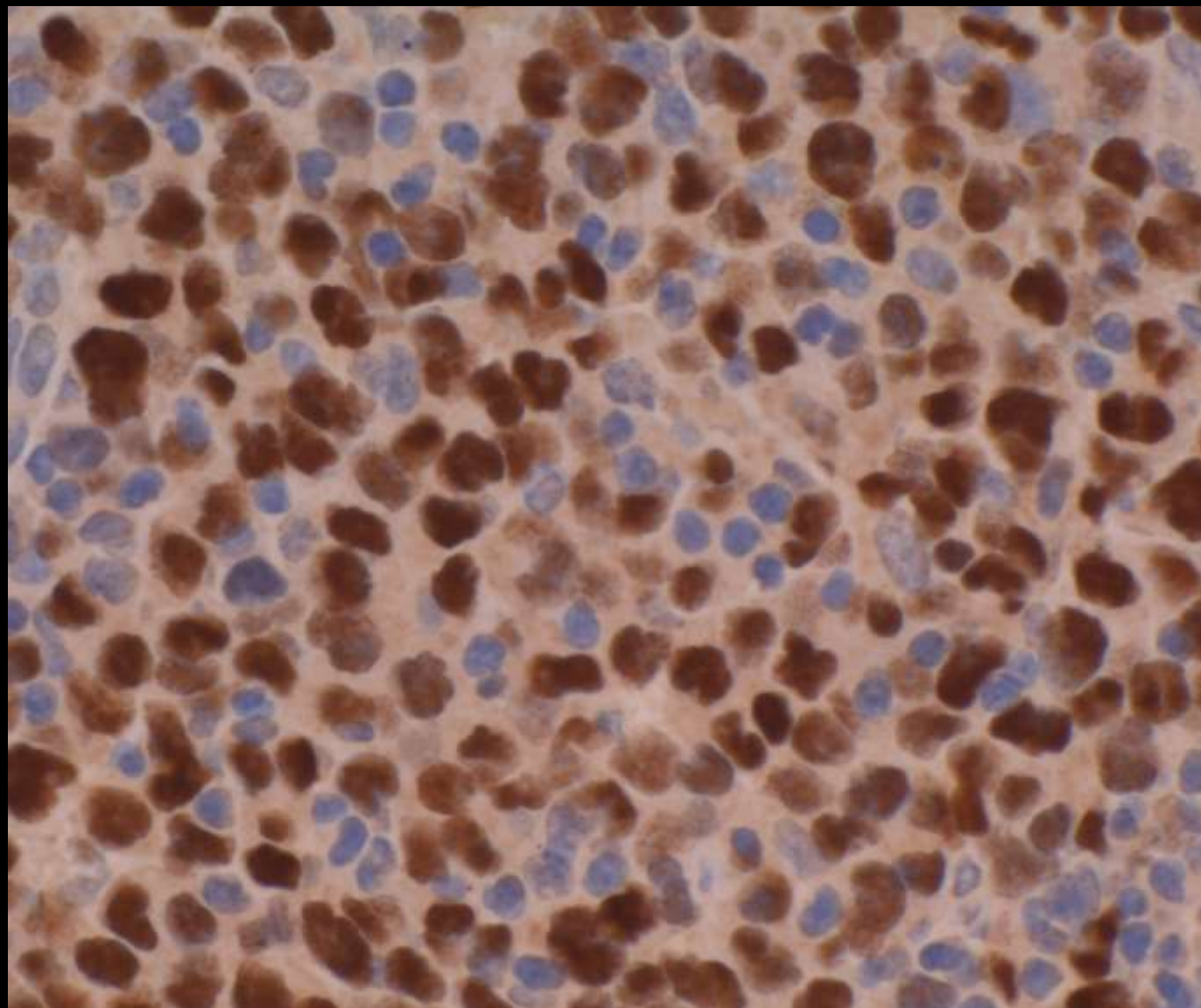
CD23



CCND1



SOX11

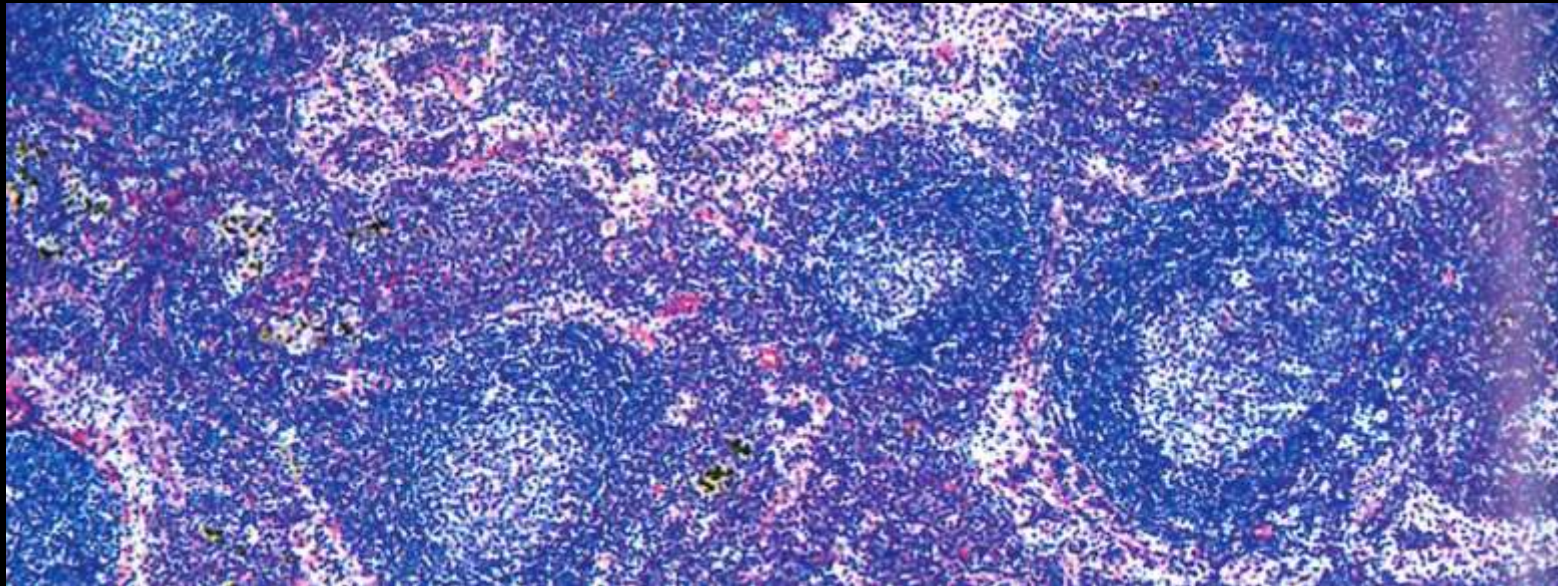


FATTORI PROGNOSTICI PATOLOGICI

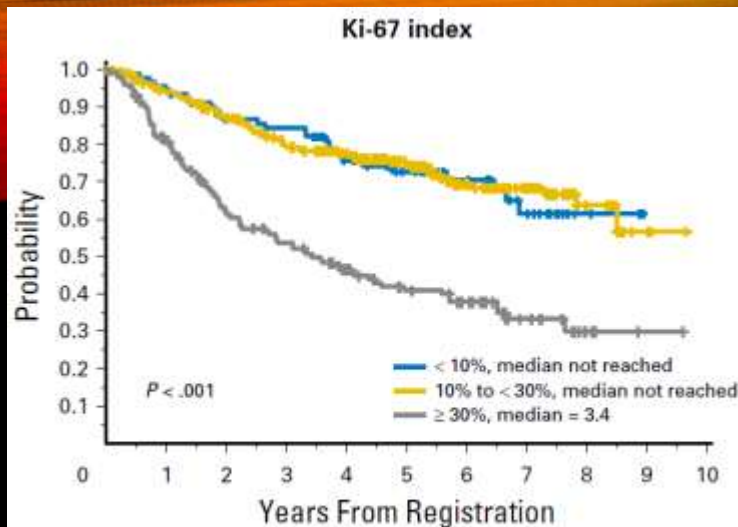


VARIANTI MORFOLOGICHE

- Blastoide (prognosi peggiore, forse non indipendente)
- A piccole cellule (migliore, correlata a variante leucemica non-nodale)
- Pattern mantellare (migliore)

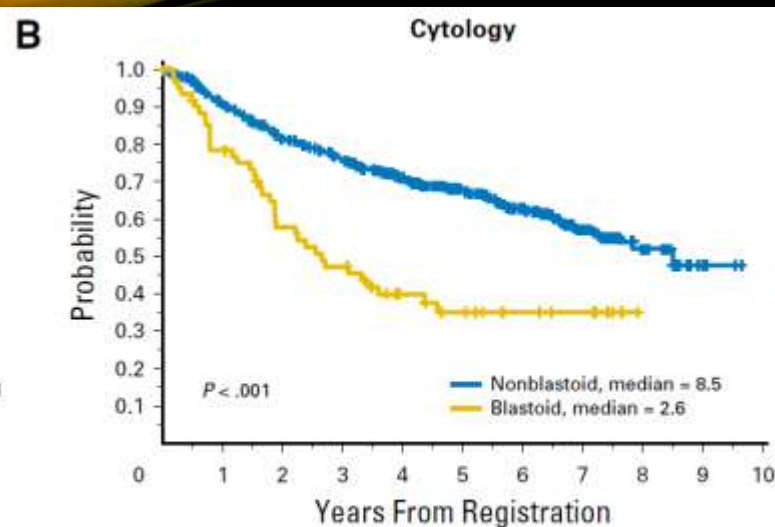


KI-67



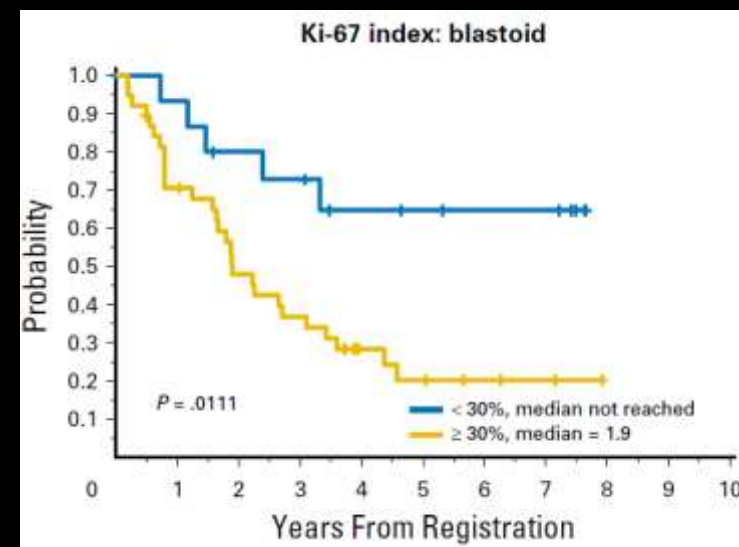
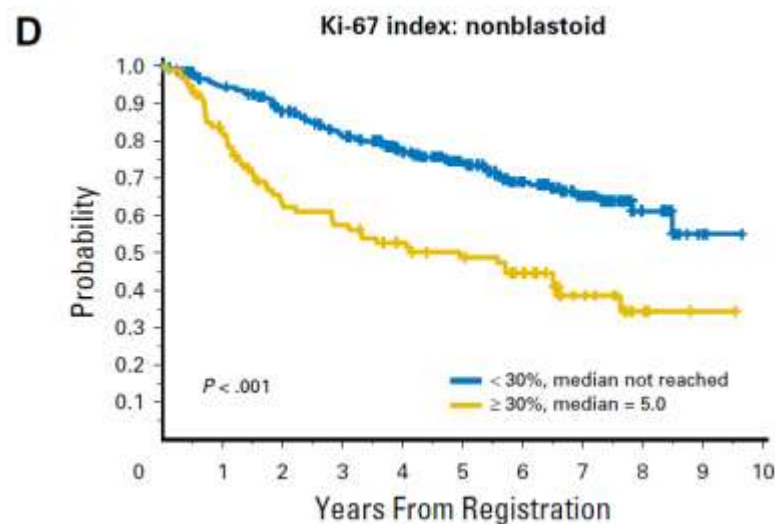
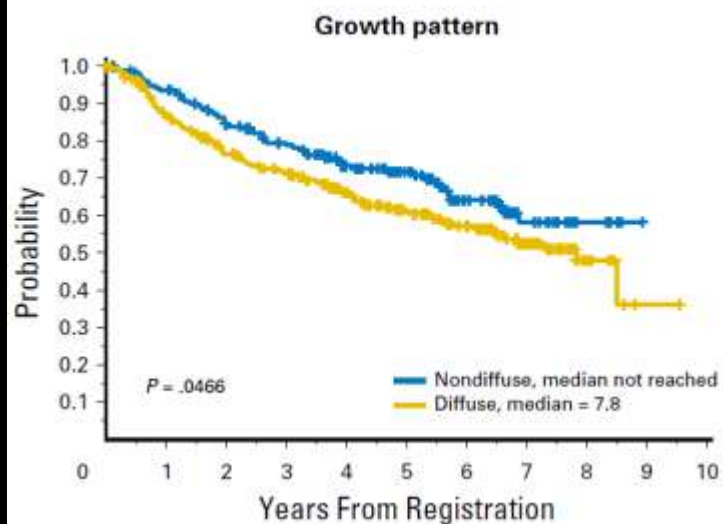
No. at risk

	95	87	75	73	55	45	31	17	3	0
< 30%	261	232	207	177	143	108	73	49	16	2
≥ 30%	152	116	83	71	52	42	31	17	4	1

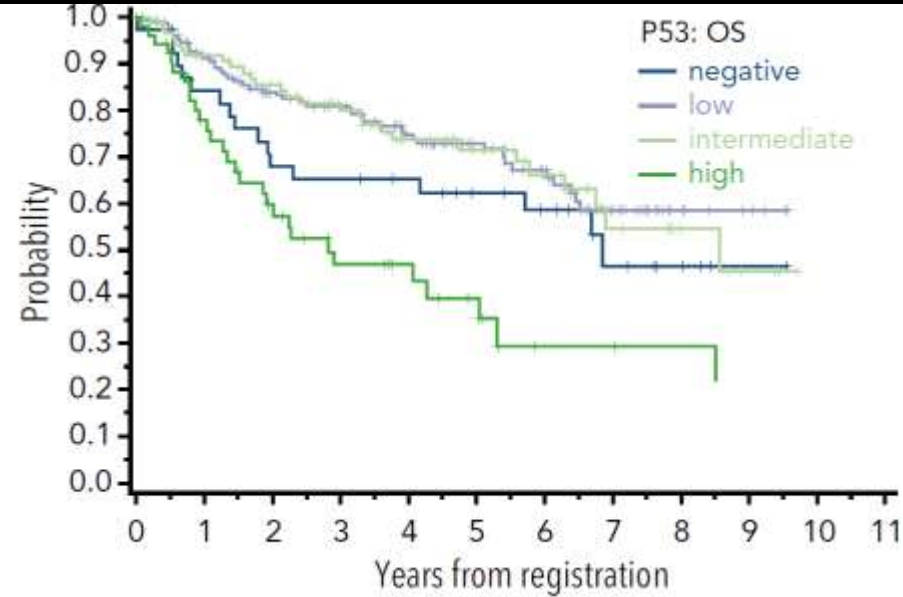
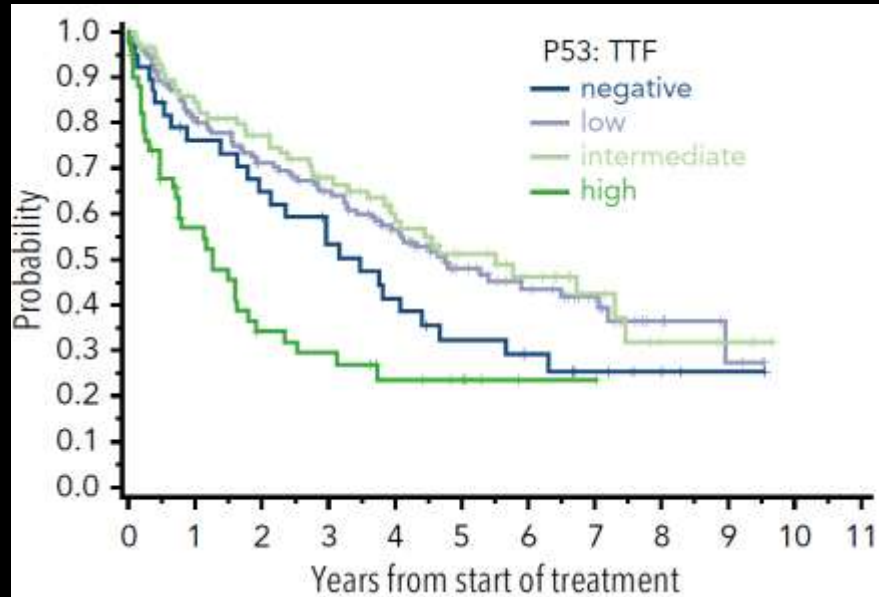


No. at risk

	558	483	416	370	293	219	153	89	22	3	0
Nonblastoid	558	483	416	370	293	219	153	89	22	3	0
Blastoid	62	47	33	27	17	13	9	7	0		



TP53 EXPRESSION



Expression of TP53 is associated with the outcome of MCL independent of MIPI and Ki-67 in trials of the European MCL Network

Sietse M. Aukema,^{1,*} Eva Hoster,^{2,3,*} Andreas Rosenwald,^{4,5} Danielle Canoni,⁶ Marie-Hélène Delfau-Larue,^{7,9} Grzegorz Rymkiewicz,¹⁰ Christoph Thorns,¹¹ Sylvia Hartmann,¹² Hanneke Kluin-Nelemans,¹³ Olivier Hermine,^{14,15} Martin Dreyling,^{2,*} and Wolfram Klapper^{1,*}

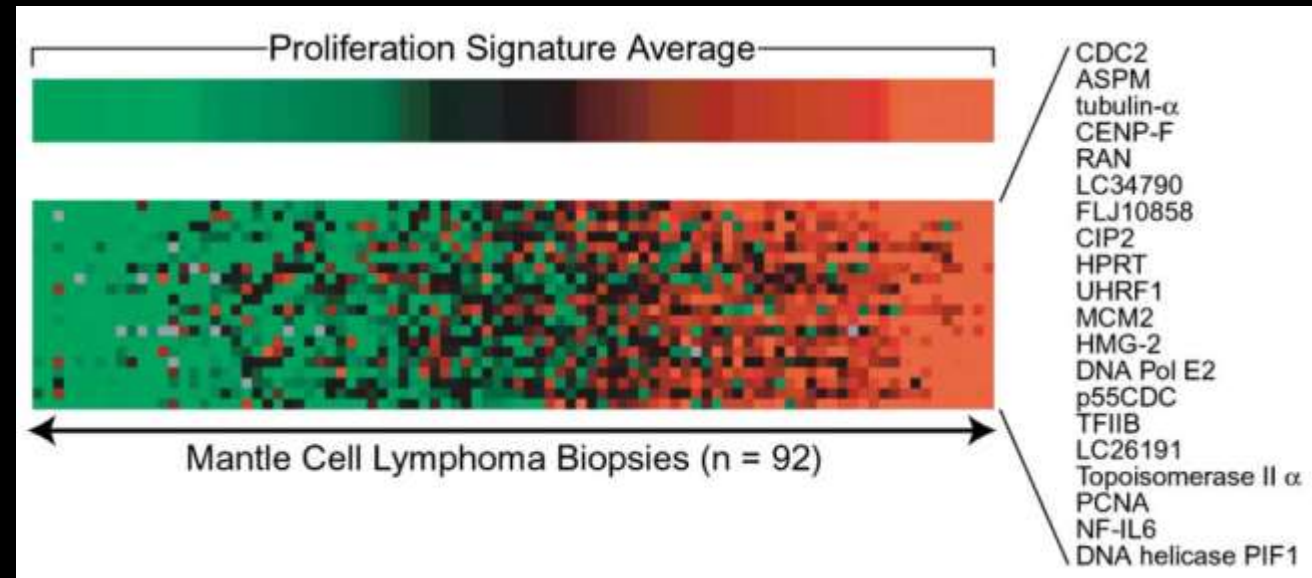
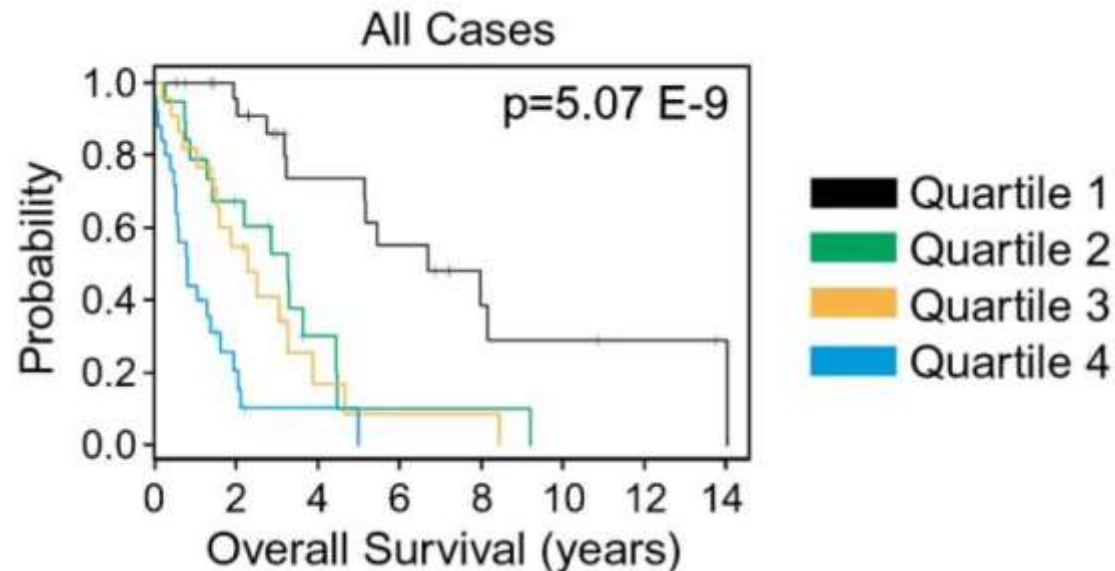
FATTORI PROGNOSTICI MOLECOLARI



PROLIFERATION SIGNATURE

The proliferation gene expression signature is a quantitative integrator of oncogenic events that predicts survival in mantle cell lymphoma

Andreas Rosenwald,^{1,2} George Wright,^{1,5} Adrian Wiestner,^{1,2} Wing C. Chan,^{1,9}
Joseph M. Connors,^{1,18} Elias Campo,^{1,8} Randy D. Gascoyne,^{1,18} Thomas M. Grogan,^{1,13,17}
H. Konrad Müller-Hermelink,^{1,19} Erlend B. Smeland,^{1,22} Michael Chiorazzi,^{1,2} Jena M. Giltman,^{1,2}
Elaine M. Hurt,^{1,2} Hong Zhao,^{1,2} Lauren Averett,^{1,2} Sarah Henrickson,^{1,2} Liming Yang,^{1,7} John Powell,^{1,7}
Wyndham H. Wilson,^{1,3} Elaine S. Jaffe,^{1,4} Richard Simon,^{1,5} Richard D. Klausner,^{1,6} Emilio Montserrat,^{1,8}
Francesc Bosch,^{1,8} Timothy C. Greiner,^{1,9} Dennis D. Weisenburger,^{1,9} Warren G. Sanger,^{1,10}
Bhavana J. Dave,^{1,9} James C. Lynch,^{1,11} Julie Vose,^{1,12} James O. Armitage,^{1,12} Richard I. Fisher,^{1,16,17}
Thomas P. Miller,^{1,14,17} Michael LeBlanc,^{1,15,17} German Ott,^{1,19} Stein Kvaloy,^{1,20} Harald Holte,^{1,20}
Jan Delabie,^{1,21} and Louis M. Staudt^{1,2,*}

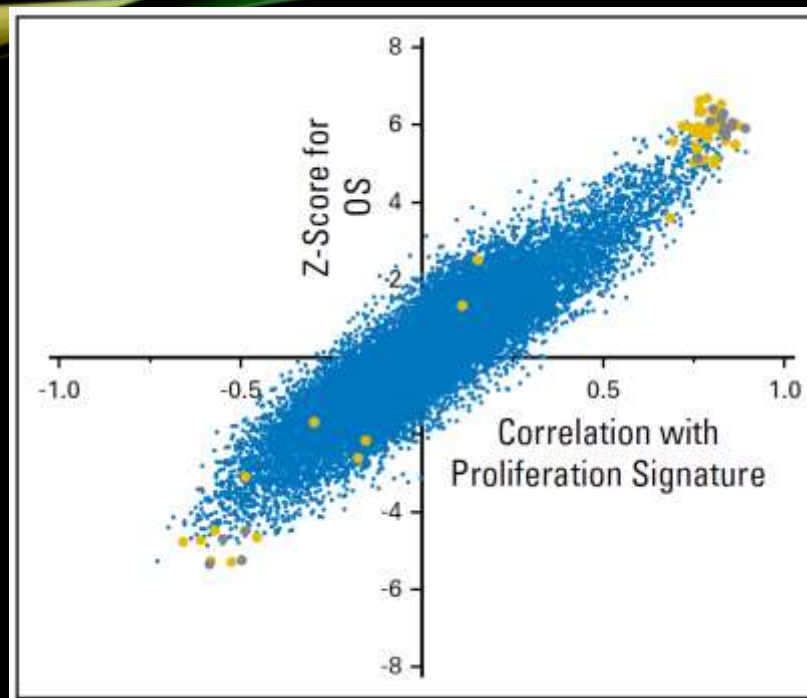


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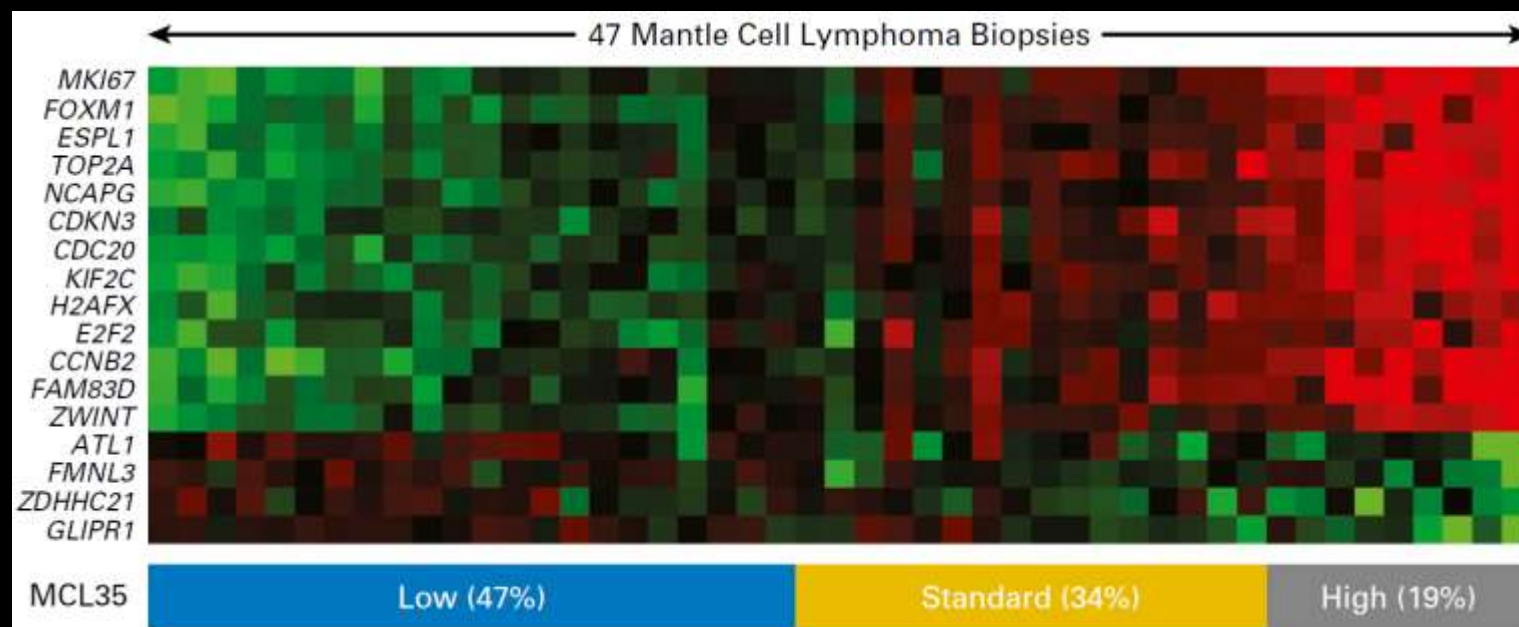
JOURNAL OF CLINICAL ONCOLOGY

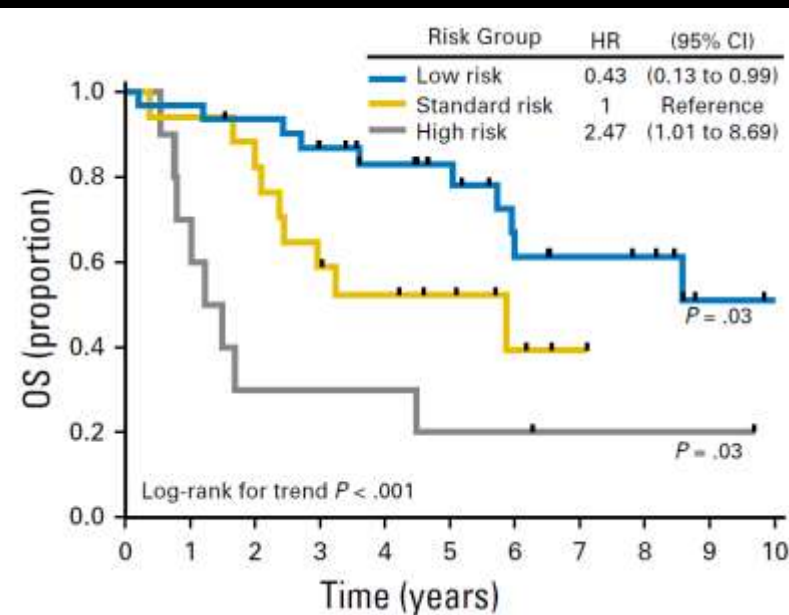
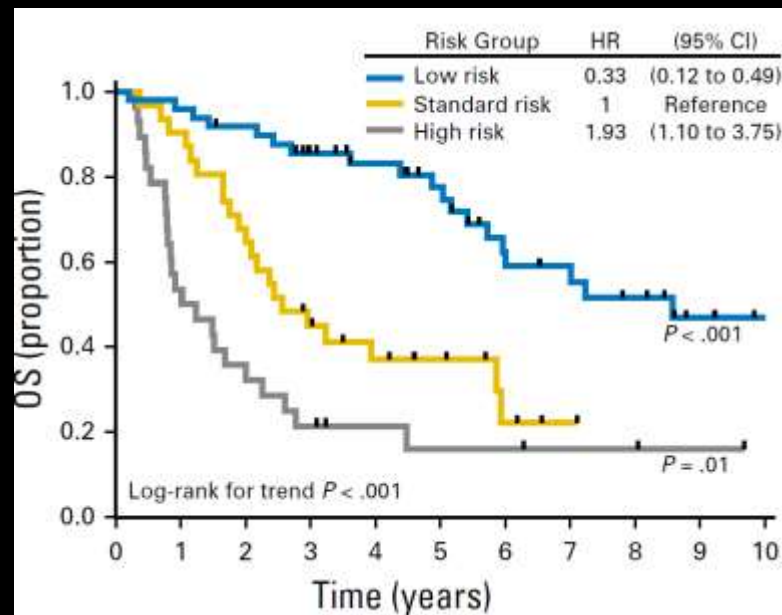
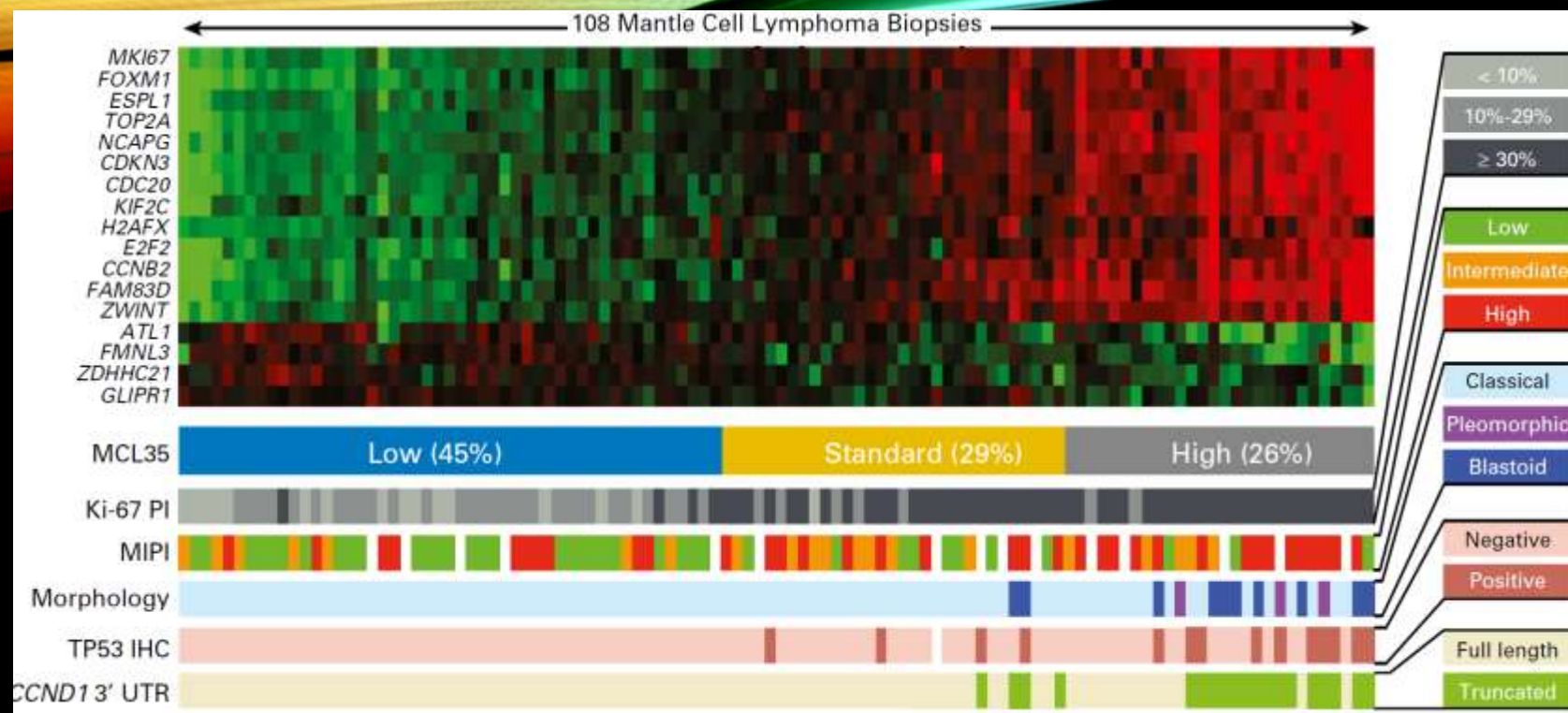
New Molecular Assay for the Proliferation Signature in Mantle Cell Lymphoma Applicable to Formalin-Fixed Paraffin-Embedded Biopsies

David W. Scott, Pau Albrisqueta, George W. Wright, Graham W. Slack, Anja Mottok, Diego Villa, Pedro Jares, Hilka Rauer-Wunderlich, Cristina Rojo, Guillem Clot, Magda Pinyol, Merrill Boyle, Fong Chun Chan, Rita M. Brazier, Wing C. Chan, Dennis D. Weisenburger, James R. Cook, Timothy C. Greiner, Kai Fu, German Ott, Jan Delabie, Erlend B. Simelund, Harald Holte, Elaine S. Jaffe, Christian Steidl, Joseph M. Connors, Randy D. Gascoyne, Andreas Rosenwald, Louis M. Staudt, Elias Campo, and Lisa M. Rimsza, for the Lymphoma/Leukemia Molecular Profiling Project



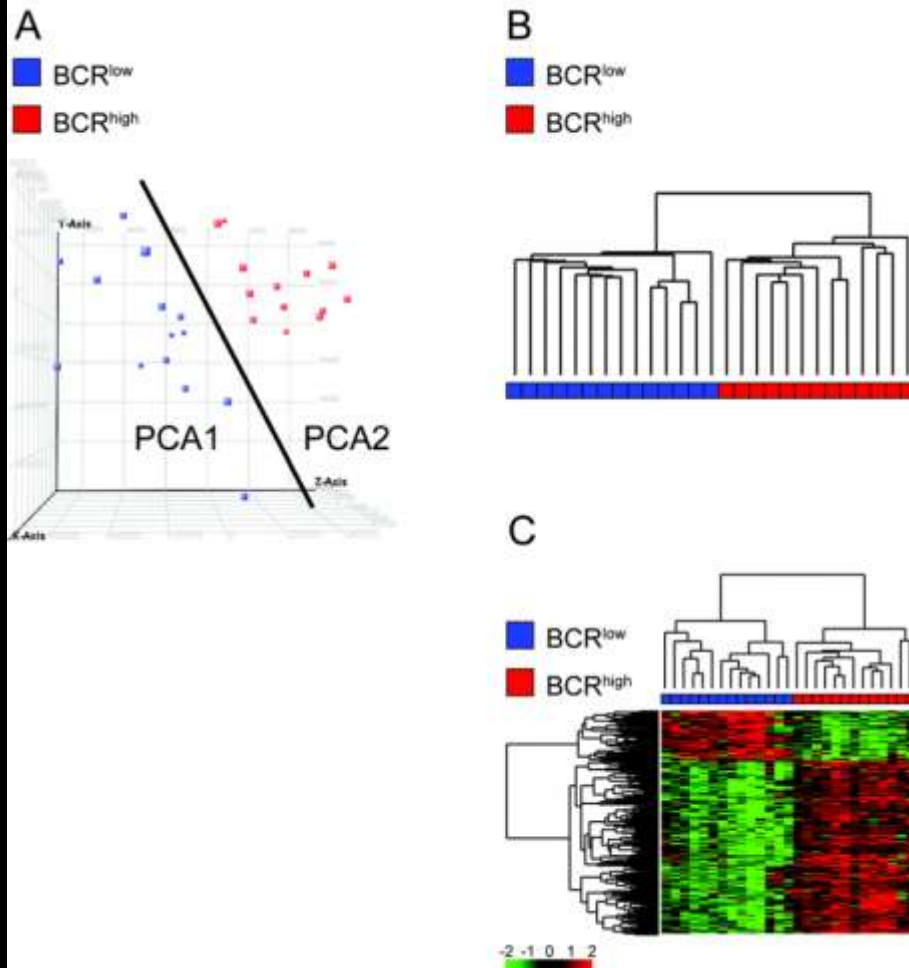
MCL35





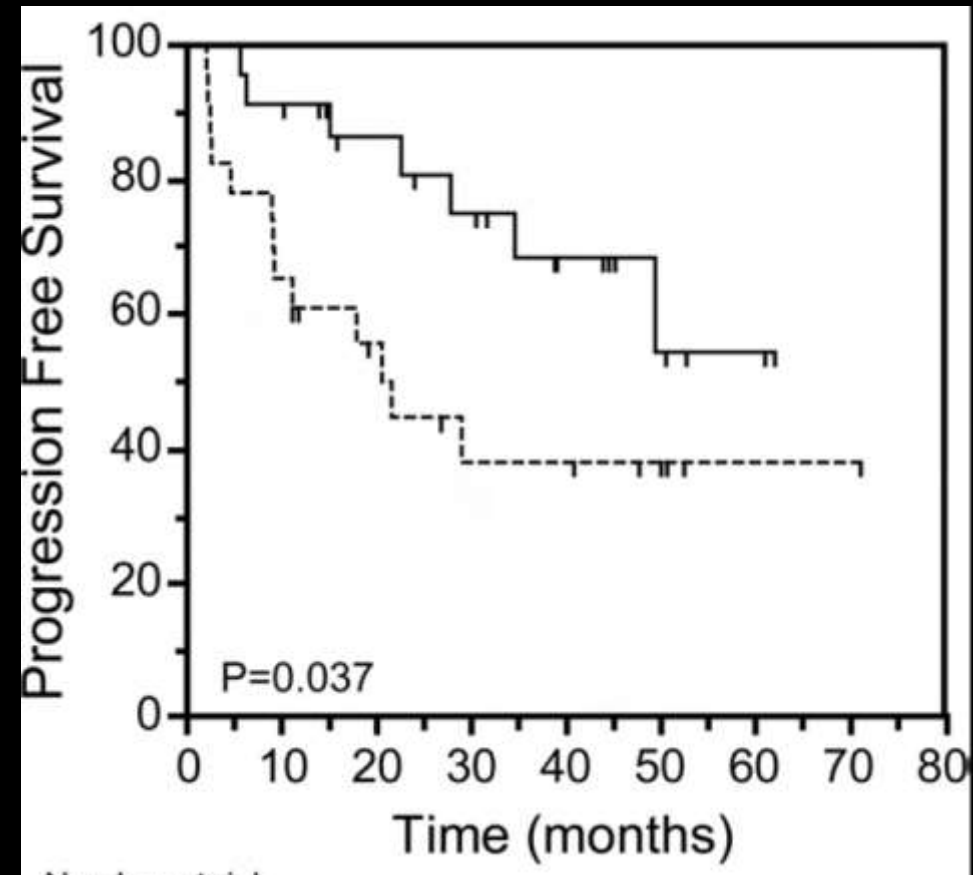
A B-cell receptor-related gene signature predicts survival in mantle cell lymphoma: results from the “Fondazione Italiana Linfomi” MCL-0208 trial

by Riccardo Bomben, Simone Ferrero, Tiziana D'Agaro, Michele Dal Bo, Alessandro Re, Andrea Evangelista, Angelo Michele Carella, Alberto Zamò, Umberto Vitolo, Paola Omedè, Chiara Rusconi, Luca Arcaini, Luigi Rigacci, Stefano Luminari, Andrea Piccin, Delong Liu, Adrien Wiestner, Gianluca Gaidano, Sergio Cortelazzo, Marco Ladetto, and Valter Gattei

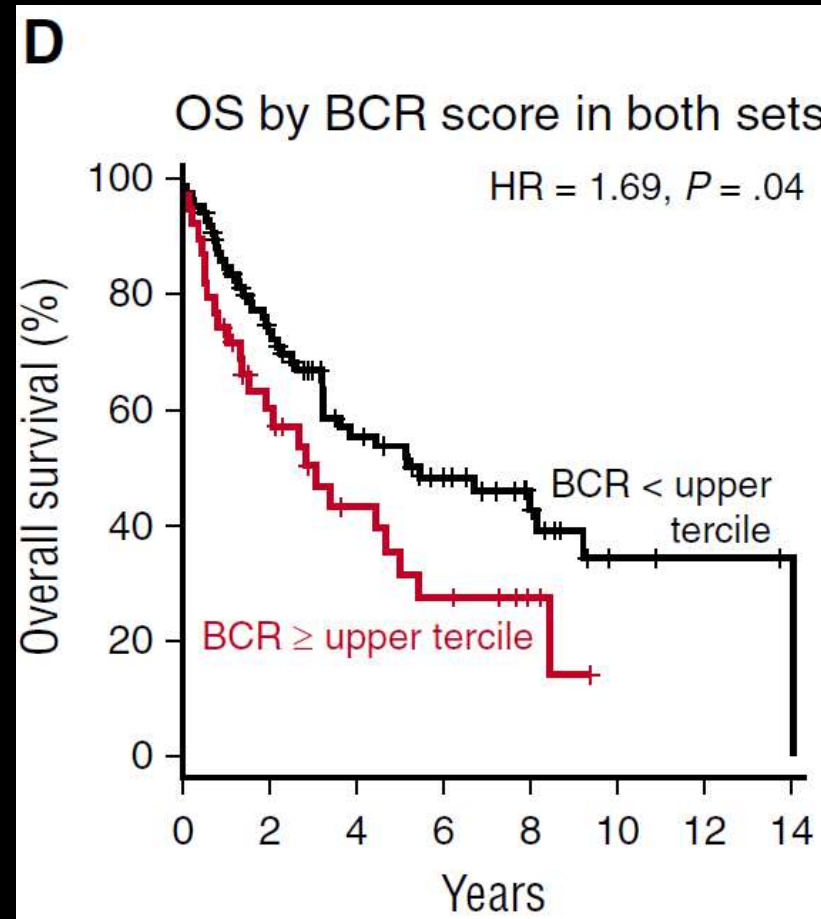


Haematologica 2018 [Epub ahead of print]

BCR INDEX



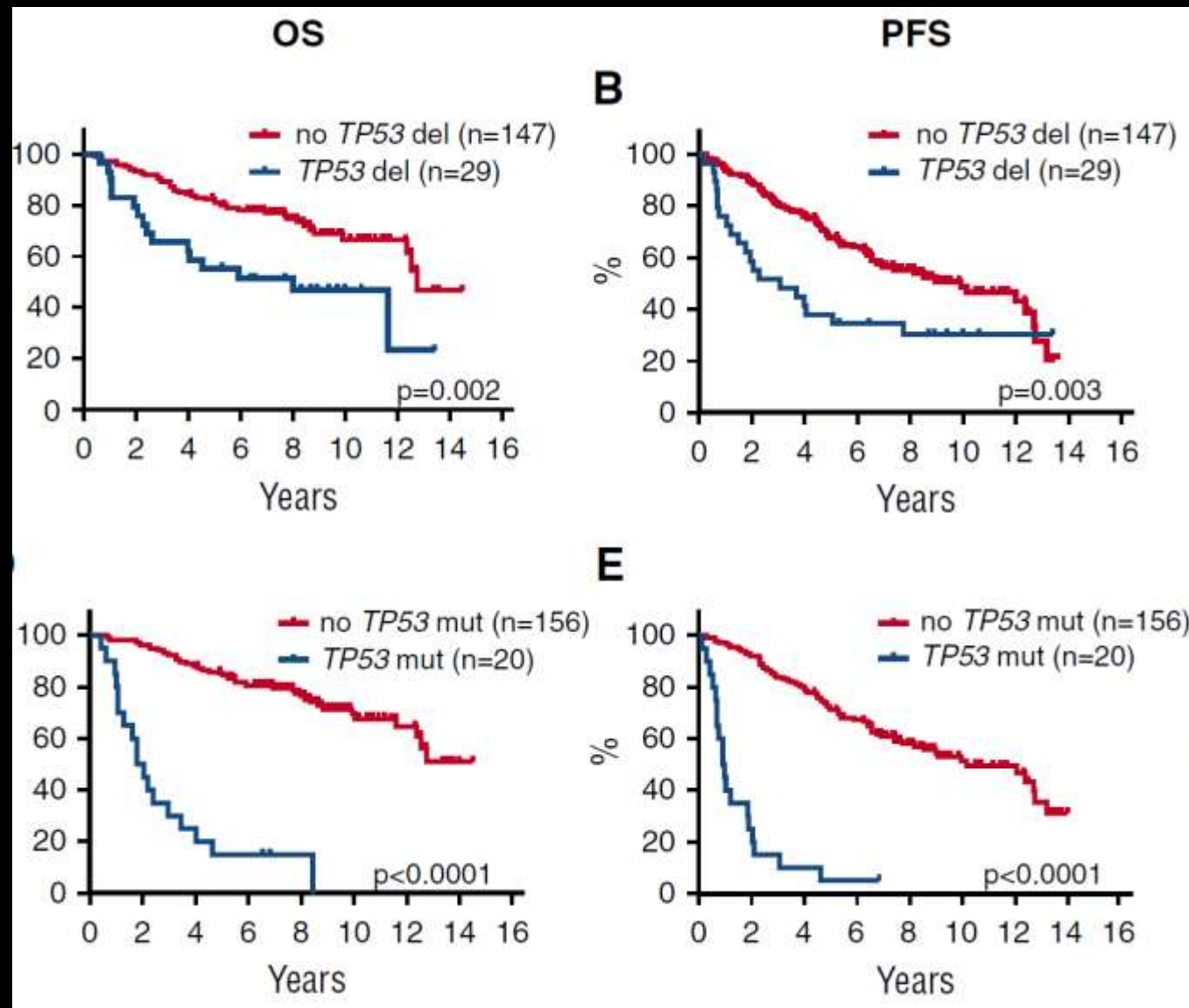
BCR SCORE



Saba et al. 2016

MUTAZIONI/DELEZIONI DI TP53

Eskelund et al., Blood. 2017 Oct
26;130(17):1903-1910

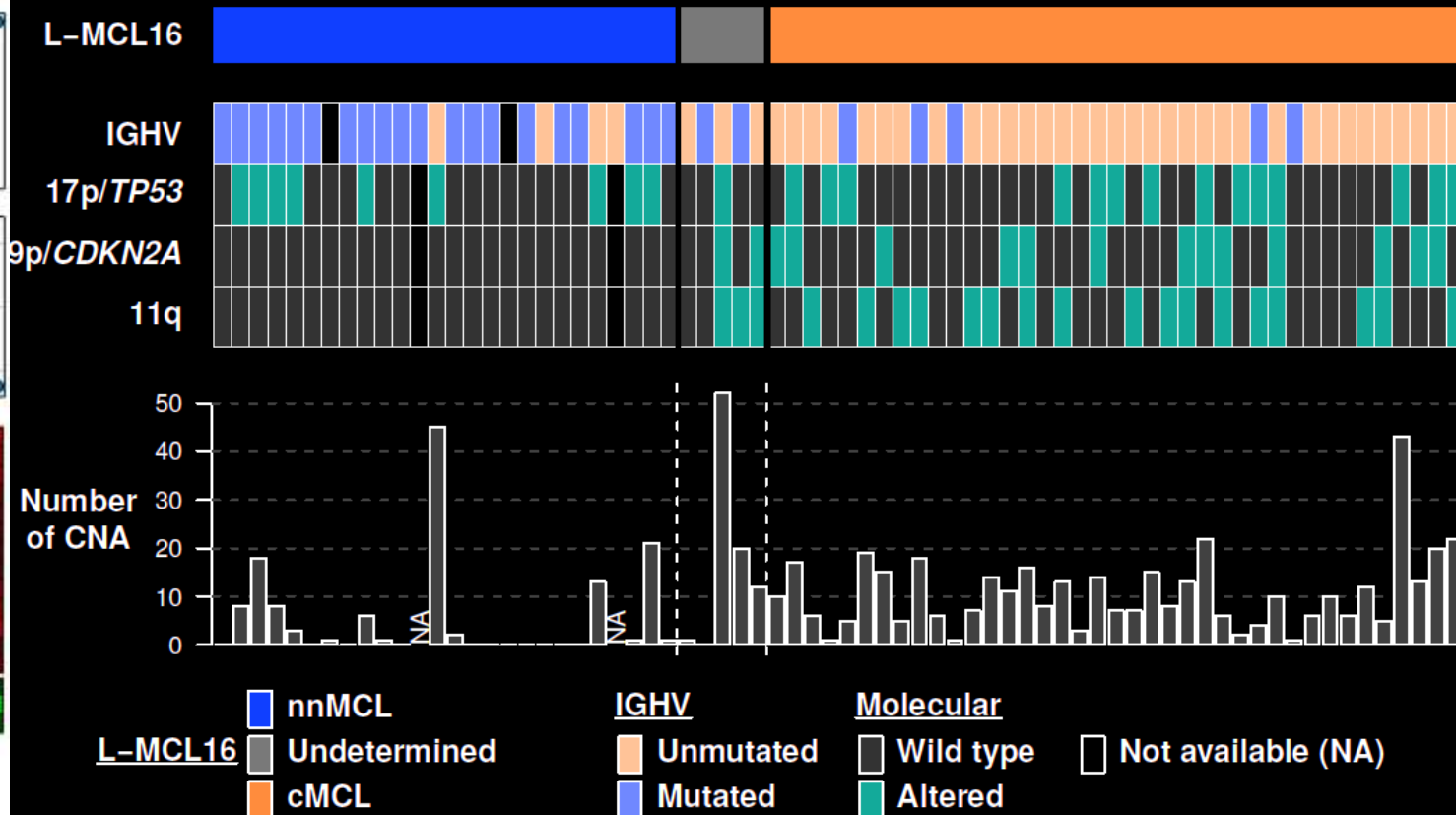
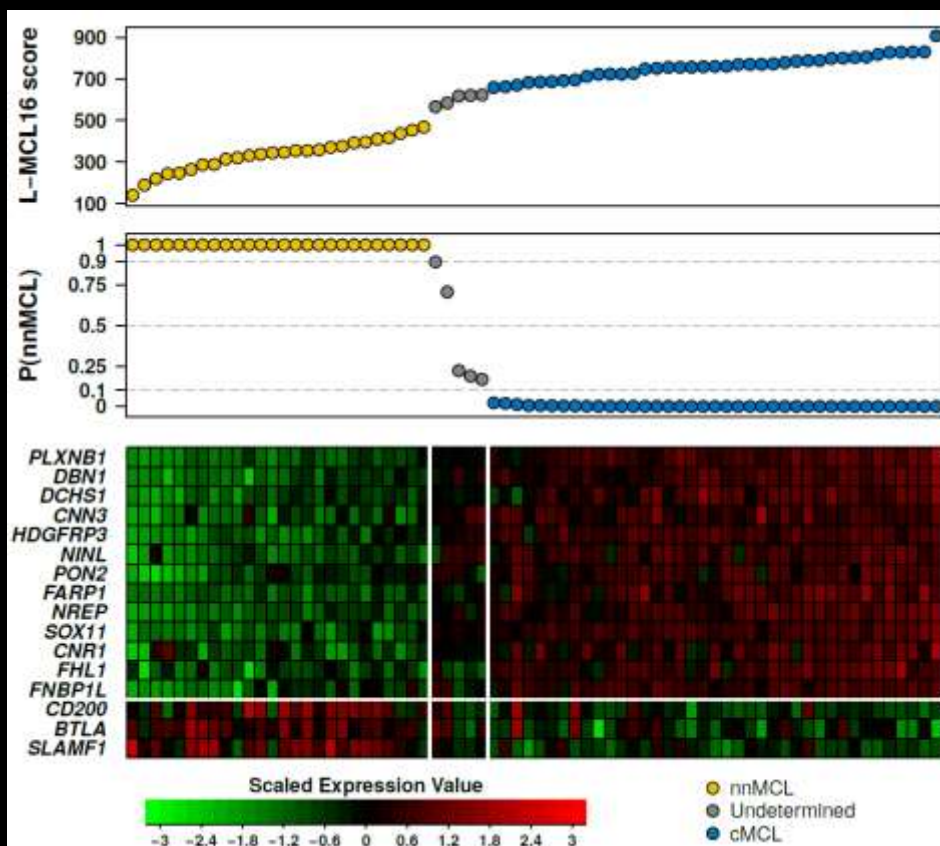


Blood. 2018 May 16. pii: blood-2018-03-838136. doi: 10.1182/blood-2018-03-838136. [Epub ahead of print]

A new molecular assay and genomic complexity predict outcome in conventional and leukemic non-nodal mantle cell lymphoma.

Clot G¹, Jares P², Giné E³, Navarro A¹, Royo C¹, Pinyol M¹, Martín-García D¹, Demajo S¹, Espinet B⁴, Salar A⁴, Ferrer A⁴, Muntanola A⁵, Aymerich M⁶, Rauert-Wunderlich H⁷, Jaffe ES⁸, Connors JM⁹, Gascoyne RD⁹, Delabie J¹⁰, López-Guillermo A¹, Ott G¹¹, Wright GW⁸, Staudt LM⁸, Rosenwald A⁷, Scott DW⁹, Rimsza LM¹², Beà S¹, Campo E¹³.

L-MCL16



WHAT'S IN THE FUTURE?

- Separazione del MCL "memory"
- Signatures molecolari
- Sequenziamento genico/CNA



