

L'ottimizzazione diagnostica del DLBCL

Stefano A. Pileri



MONDO
LINFOMI:
UN'INCREDIBILE DINAMICITÀ

7 NOVEMBRE 2023
Mercure Villa Romanazzi Carducci

Bari

Predominantly nodal

Diffuse large B-cell lymphoma, NOS

 Germinal center B-cell subtype

 Activated B-cell subtype

Large B-cell lymphoma with 11q aberration*

T cell/histiocyte-rich large B-cell lymphoma

Extranodal

Primary diffuse large B-cell lymphoma of the central nervous system

Primary diffuse large B-cell lymphoma of the testis*

Primary cutaneous diffuse large B-cell lymphoma, leg type

Intravascular large B-cell lymphoma

*HHV-8 and Epstein-Barr virus–negative primary effusion-based lymphoma**

Primary mediastinal large B-cell lymphoma

Mediastinal gray-zone lymphoma*

Epstein-Barr virus related

Epstein-Barr virus–positive diffuse large B-cell lymphoma, NOS

Diffuse large B-cell lymphoma associated with chronic inflammation

 Fibrin-associated diffuse large B-cell lymphoma

Large cell lymphoma with terminal B-cell differentiation

ALK-positive large B-cell lymphoma

Plasmablastic lymphoma

HHV-8–positive diffuse large B-cell lymphoma, NOS

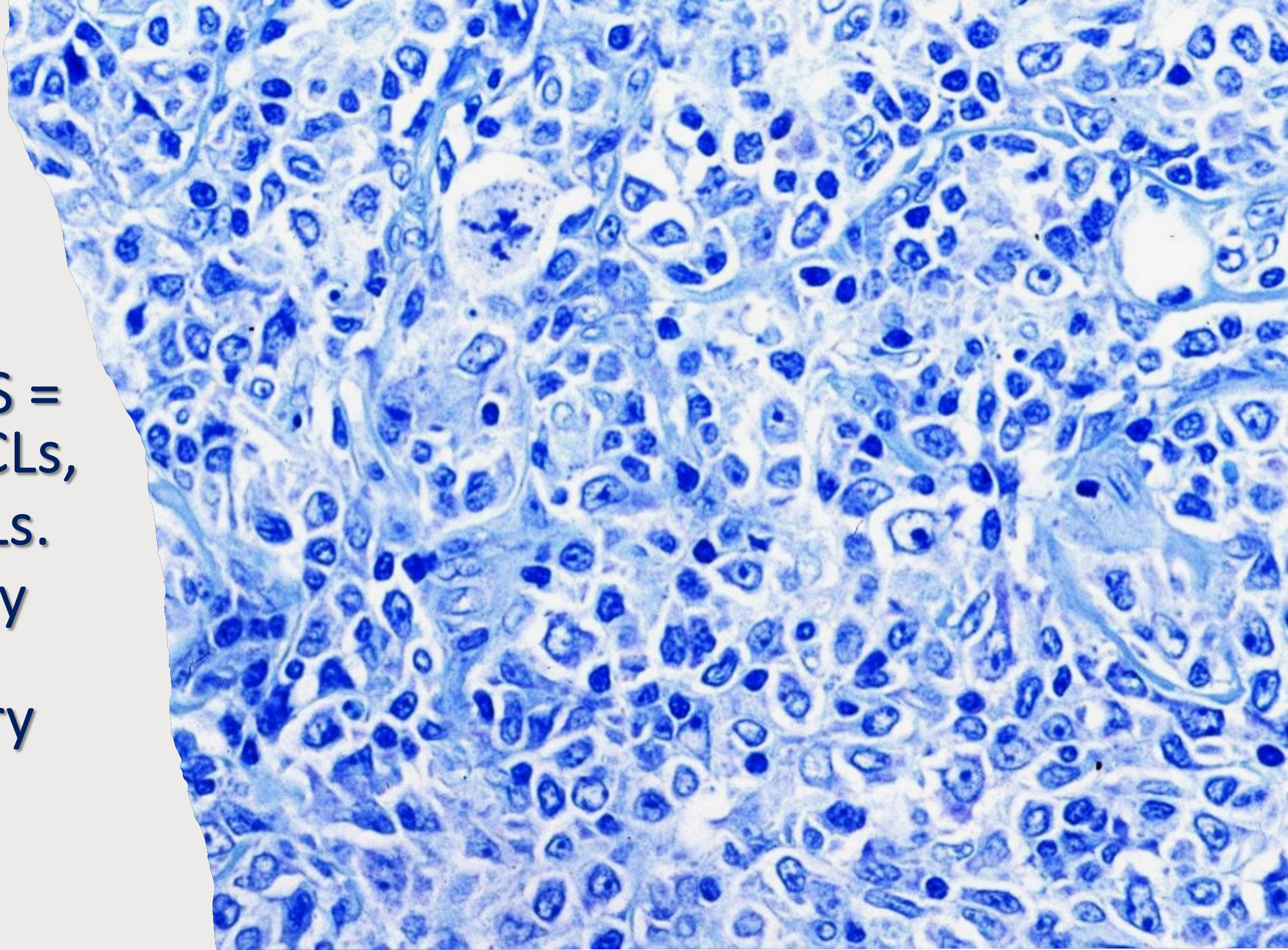
Primary effusion lymphoma

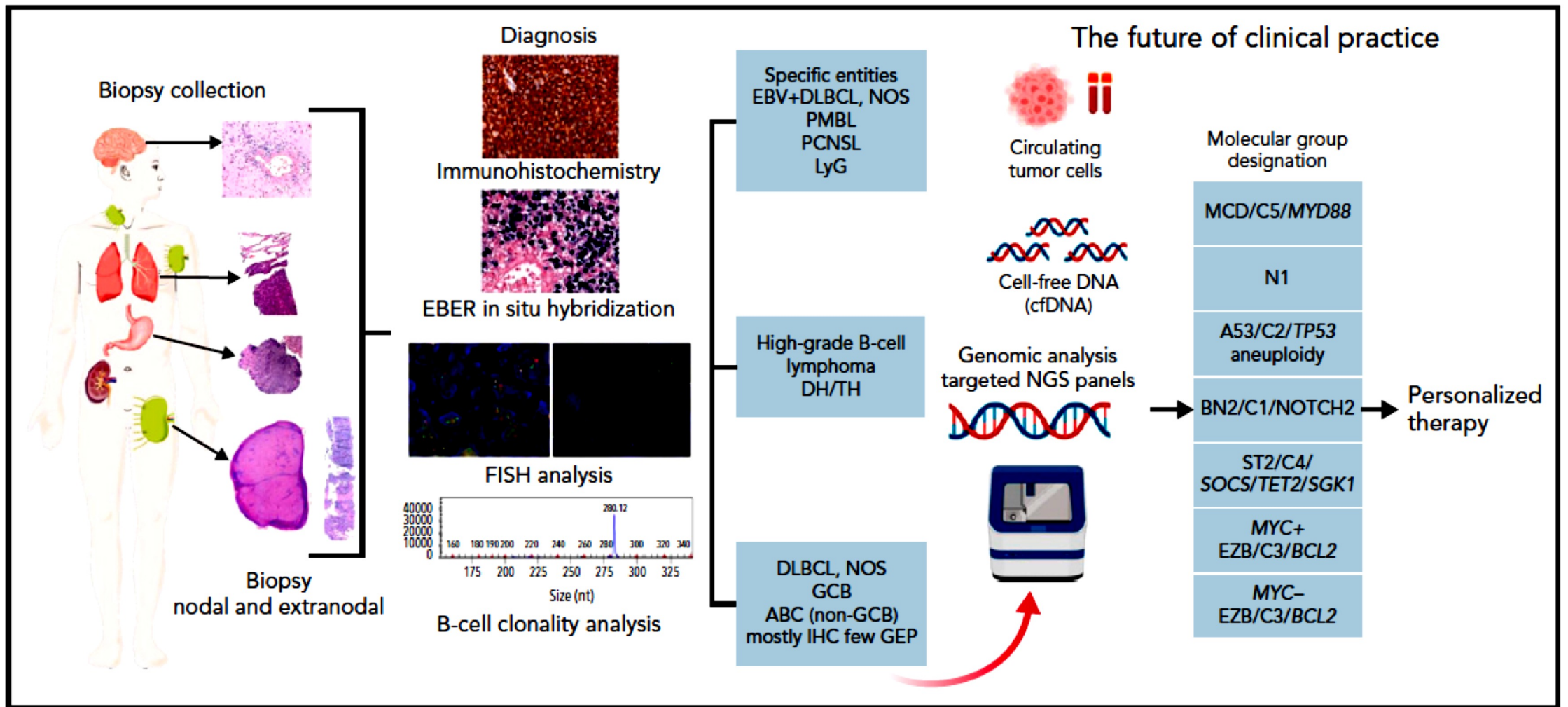
High grade B-cell lymphomas[¶]

High-grade B-cell lymphoma, with MYC and BCL2 rearrangements*

*High-grade B-cell lymphoma with MYC and BCL6 rearrangements**

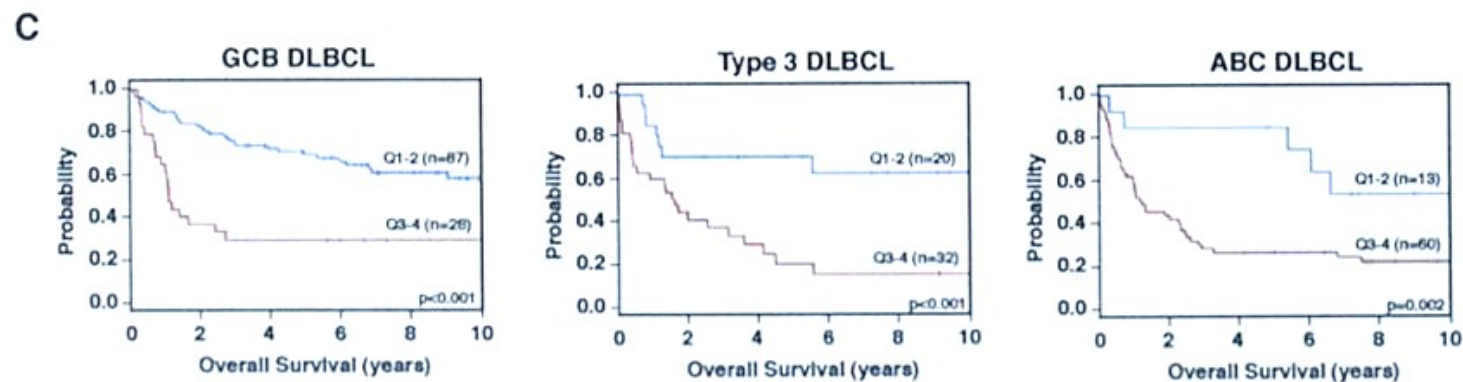
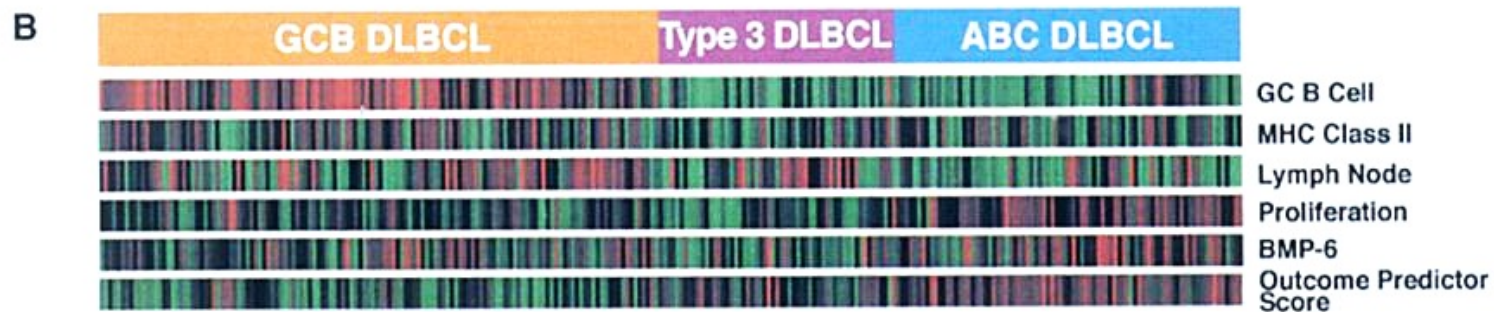
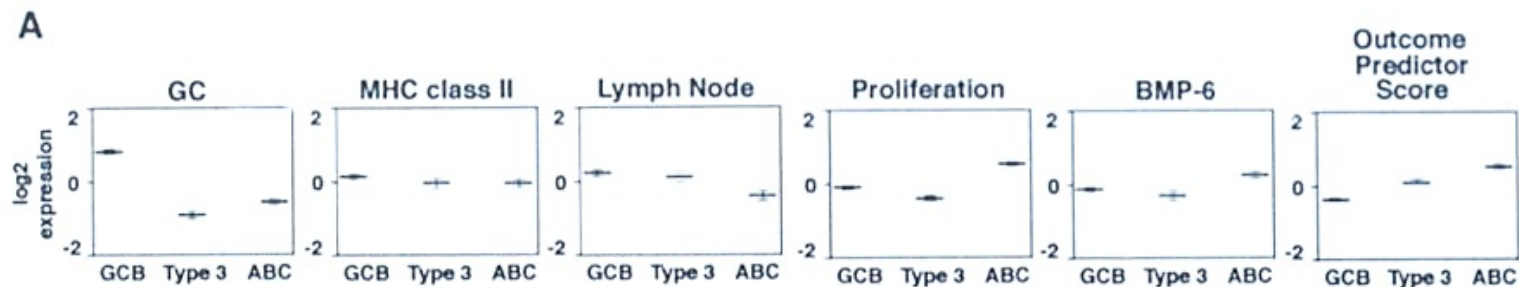
DLBCL, NOS =
80% of DBCLs,
40% of NHLs.
Morphology
not
contributory





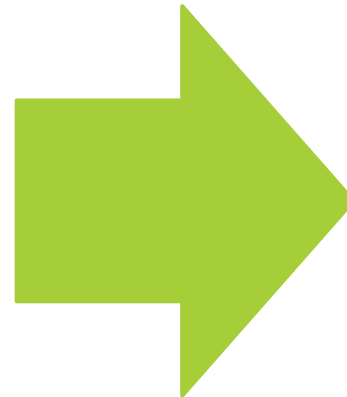
Cell of Origin (COO)

Rosenwald A et al. NEJM, 346:1937-47, 2002. Wright G et al. PNAS, 100:9991-6, 2003.



Targeted Digital Gene expression profiling

Smaller samples



Input
Lyse and Go
Protocols

More biology

Proteins	
• A β	• Iba1
• APOE	• HLA-DR

Genes	
• Apoe	• Anapc15
• Atm	• Pik3cb
• Akt1	• C3
• Bcl2	• Bax
• Crip1	• Ngfr
• Abcc3	• Bcas1
• Akt2	• Casp7
• Cx3cr1	• Agt
• Ago4	• Creb1
• Snca	• Csf1r
• Pik3r1	• Bmi1
• Mapk10	• Pten
• Casp3	• Fas
• Gria2	• Cd33
• Atp6v0e	• Pla2g4a
• Bid	• Casp8
• Il1r1	• Atp6v1a
• Anxa1	• Birc2
• Atg9a	• Cd69
• Bin1	• Mdm2
• Ptgs2	• Bad
• Grin2a	• Cldn5
• Pik3ca	• Jun

Cell-of-Origin Effect of Polatuzumab Vedotin in Diffuse Large B-Cell Lymphoma: No Ordinary Subgroup Analysis

Tracking no: BLD-2023-022048R1

David Russler-Germain (Washington University School of Medicine, United States) Edward Cliff (Brigham and Women's Hospital, United States) Nancy Bartlett (Washington University School of Medicine, United States)

Subgroup analysis from the POLARIX trial of polatuzumab vedotin plus chemotherapy for untreated large B-cell lymphoma suggests greater efficacy among patients with activated B-cell subtype disease. Both preclinical and additional clinical evidence support this interaction between cell-of-origin and polatuzumab efficacy.

FISH

MYC

BCL2

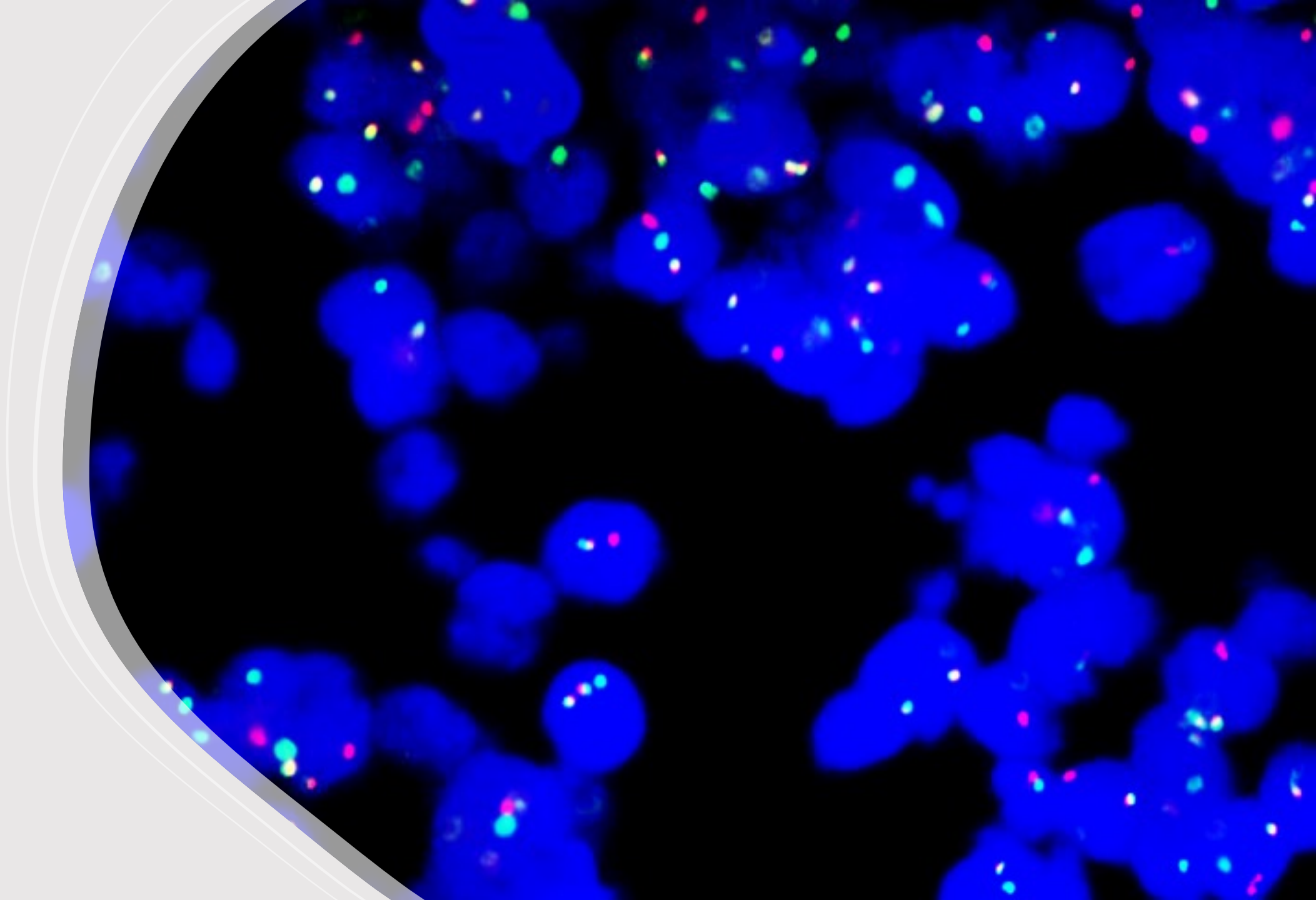
BCL6

IRF4

11q

EBER

ISH



REVIEW AND PERSPECTIVES



Emerging entities: high-grade/large B-cell lymphoma with 11q aberration, large B-cell lymphoma with *IRF4* rearrangement, and new molecular subgroups in large B-cell lymphomas. A report of the 2022 EA4HP/SH lymphoma workshop

Leticia Quintanilla-Martinez^{1,2} · Camille Laurent³ · Lorinda Soma⁴ · Siok-Bian Ng^{5,6} · Fina Climent⁷ · Sarah L. Ondrejka⁸ · Alberto Zamo⁹ · Andrew Wotherspoon¹⁰ · Laurence de Leval¹¹ · Stefan Dirnhofer¹² · Lorenzo Leoncini¹³

REVIEW AND PERSPECTIVES



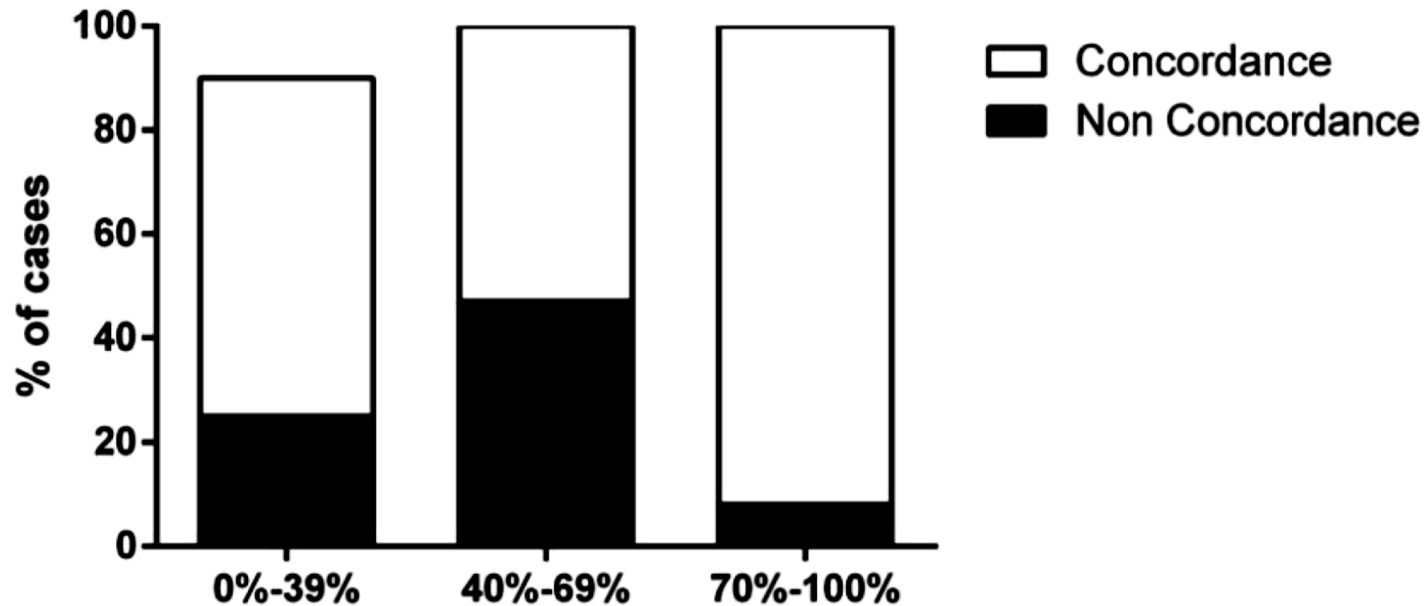
Cavity-based lymphomas: challenges and novel concepts. A report of the 2022 EA4HP/SH lymphoma workshop

Arianna Di Napoli¹ · Lori Soma² · Leticia Quintanilla-Martinez³ · Laurence de Leval⁴ · Lorenzo Leoncini⁵ · Alberto Zamo⁶ · Siok-Bian Ng⁷ · Sarah L. Ondrejka⁸ · Fina Climent⁹ · Andrew Wotherspoon¹⁰ · Stefan Dirnhofer¹¹

MYC protein expression scoring and its impact on the prognosis of aggressive B-cell lymphoma patients

by Maria R. Ambrosio, Stefano Lazzi, Giuseppe Lo Bello, Raffaella Santi, Leonardo Del Porro, Maria M. de Santi, Raffaella Guazzo, Lucia Mundo, Luigi Rigacci, Sofia Kovalchuck, Noel Onyango, Alberto Fabbri, Emanuele Cencini, Pier Luigi Zinzani, Francesco Zaja, Francesco Angrilli, Caterina Stelitano, Maria G. Cabras, Giuseppe Spataro, Roshanak Bob, Thomas Menter, Massimo Granai, Gabriele Cevenini, Kikkeri N. Naresh, Harald Stein, Elena Sabbatini, and Lorenzo Leoncini

Haematologica 2018 [Epub ahead of print]



Using Gene Expression Profiling to Move Beyond *MYC/BCL2* Rearrangements in High-Grade Lymphoma

Wing C. Chan, MD¹

rapid communication

Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma

Daisuke Ennishi, PhD¹; Aixiang Jiang, MSc^{1,2}; Merrill Boyle, BSc¹; Brett Collinge, BSc¹; Bruno M. Grande, BSc²; Susana Ben-Neriah, MSc¹; Christopher Rushton, BSc²; Jeffrey Tang, BSc²; Nicole Thomas, BSc²; Graham W. Slack, MD¹; Pedro Farinha, PhD¹; Katsuyoshi Takata, MD¹; Tomoko Miyata-Takata, MD¹; Jeffrey Craig, PhD¹; Anja Mottok, PhD³; Barbara Meissner, PhD¹; Saeed Saberi, PhD⁴; Ali Bashashati, PhD⁴; Diego Villa, MD¹; Kerry J. Savage, MD¹; Laurie H. Sehn, MD¹; Robert Kridel, PhD⁵; Andrew J. Mungall, PhD⁶; Marco A. Marra, PhD⁶; Sohrab P. Shah, PhD⁴; Christian Steidl, MD¹; Joseph M. Connors, MD¹; Randy D. Gascoyne, MD¹; Ryan D. Morin, PhD²; and David W. Scott, PhD¹

original report

Molecular High-Grade B-Cell Lymphoma: Defining a Poor-Risk Group That Requires Different Approaches to Therapy

Chulin Sha, PhD¹; Sharon Barrans, PhD²; Francesco Cucco, PhD³; Michael A. Bentley, DPhil¹; Matthew A. Care, PhD¹; Thomas Cummin, MD⁴; Hannah Kennedy, PhD³; Joe S. Thompson, MPhil³; Rahman Uddin, MSc¹; Lisa Worrillow, PhD²; Rebecca Chalkley, MPhil²; Moniek van Hoppe, MSc²; Sophia Ahmed, PhD¹; Tom Maishman, PhD⁴; Josh Caddy, BSc⁴; Anna Schuh, MD⁵; Christoph Mamot, MD⁵; Catherine Burton, MD²; Reuben Tooze, PhD¹; Andrew Davies, PhD⁴; Ming-Qing Du, PhD³; Peter W.M. Johnson, MD⁴; and David R. Westhead, DPhil¹

A 3-gene signature based on MYC, BCL-2 and NFKBIA improves risk stratification in diffuse large B-cell lymphoma

by Enrico Derenzini, Saveria Mazzara, Federica Melle, Giovanna Motta, Marco Fabbri, Riccardo Bruna, Claudio Agostinelli, Alessandra Cesano, Chiara Antonia Corsini, Ning Chen, Simona Righi, Elena Sabattini, Annalisa Chiappella, Angelica Calleri, Stefano Fiori, Valentina Tabanelli, Antonello Cabras, Giancarlo Pruneri, Umberto Vitolo, Alessandro Massimo Gianni, Alessandro Rambaldi, Paolo Corradini, Pier Luigi Zinzani, Corrado Tarella, and Stefano Pileri

Haematologica 2020 [Epub ahead of print]

Targeted Digital Gene Expression Profiling



RefSeq NCBI	Gene	Length NCBI	Protein aa
NM_002467.4	MYC	2379	454
NM_000633.2	BCL2	6492	239
NM_012452.2	TNFRSF13B	1377	293
NM_014240.2	LIMD1	6284	676
NM_001195286.1	IRF4	5329	451*
NM_194071.3	CREB3L2	7471	520*
NM_006875.3	PIM2	2234	311
NM_001302826.1	CYB5R	1713	276
NM_003929.2	RAB7L1	3324	203
NM_174908.3	CCDC50	8421	306
NM_015361.3	R3HDM1	4722	1099
NM_017706.4	WDR55	2580	383
NM_020701.3	ISY1	3778	285
NM_014607.3	UBXN4	4018	508
NM_030961.2	TRIM56	4723	755
NM_000902.3	MME	5643	750
NM_001284275.1	SERPINA9	1661	435*
NM_024701.3	ASB13	2736	278
NM_018717.4	MAML3	7086	1138
NM_002221.3	ITPKB	6162	946
NM_001080416.3	MYBL1	5192	752
NM_004230.3	S1PR2	3589	353
NM_020529.2	NFKBIA	1579	371
NM_139276.2	STAT3	4978	770
NM_000314.6	PTEN	8718	403*
NM_006218.2	PKI3CA	3724	1068

26-gene-panel for COO & key-genes Haematologica, 2020

224 DLBCL patients
FFPE specimens

DLCL04 (n = 130)
R-HDS (n = 94)

NanoString
insufficient mRNA n = 17

207 DLBCL patients

IHC
non-NOS n = 21

186 DLBCL patients

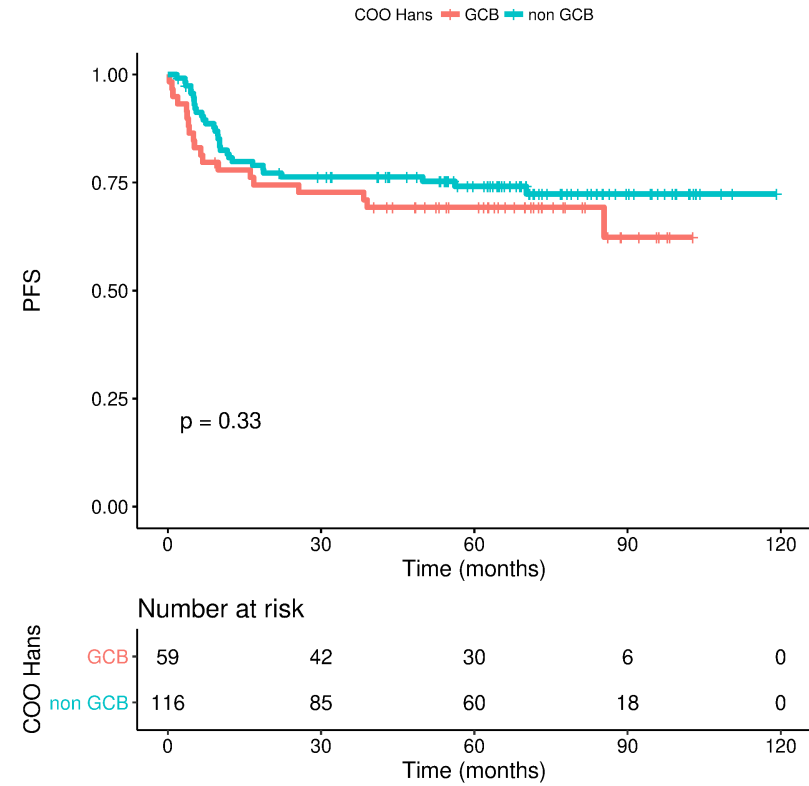
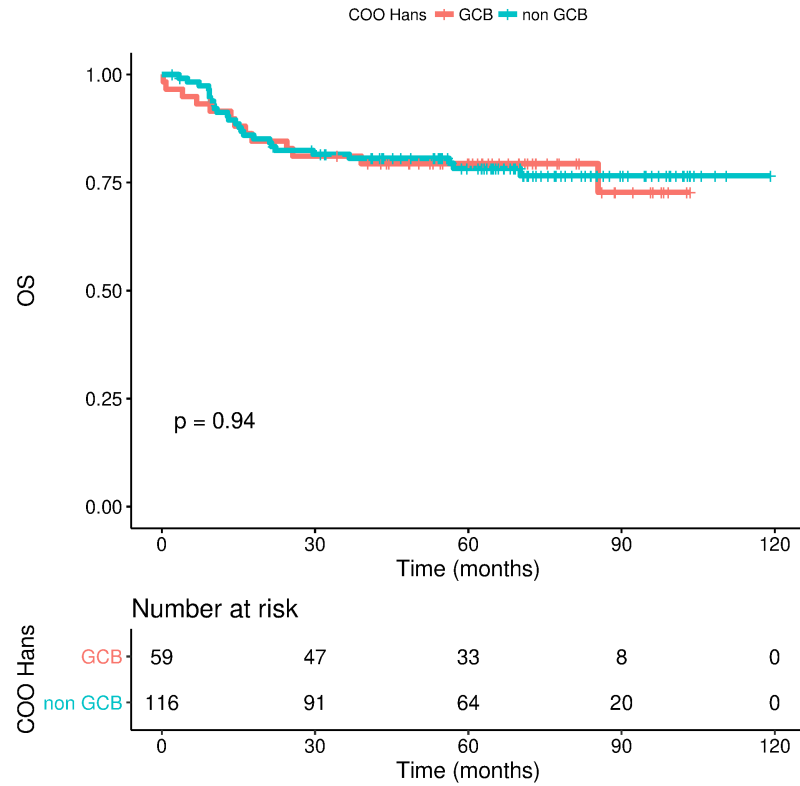
DLCL04 (n = 99)
R-HDS (n = 87)

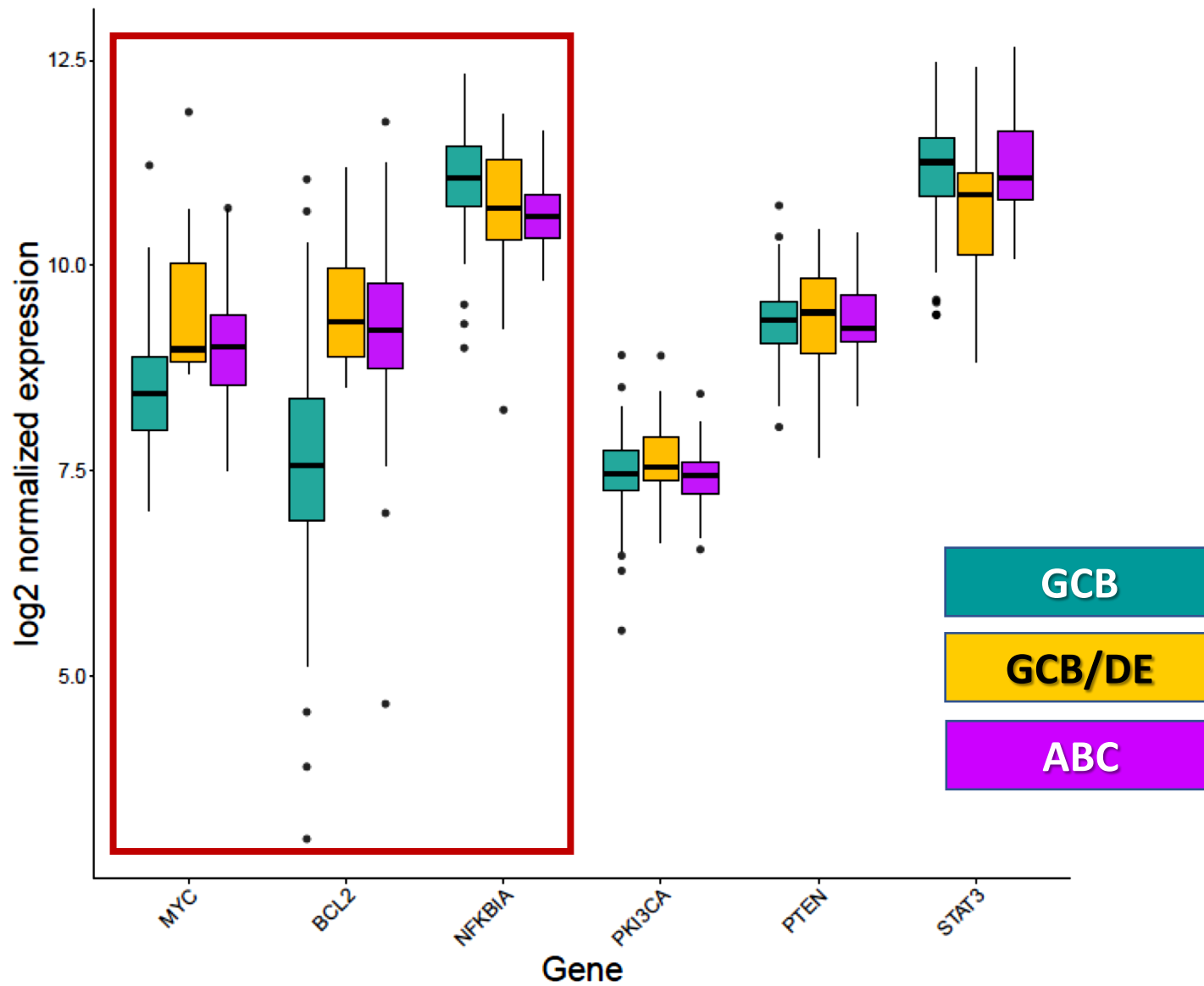
In both trials, only patients staged III-IV were enrolled, all treated with R-CHOP or R-CHOP-like therapies followed or not by Auto-SCT.

The mean age was 52 yr.s (18 – 65)

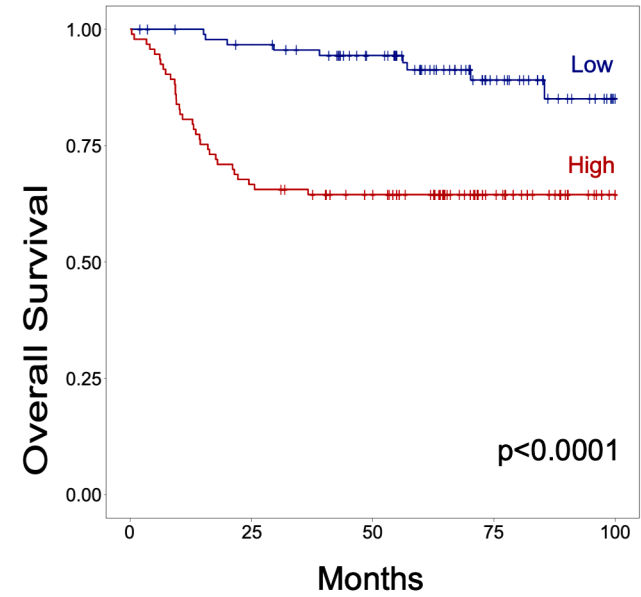
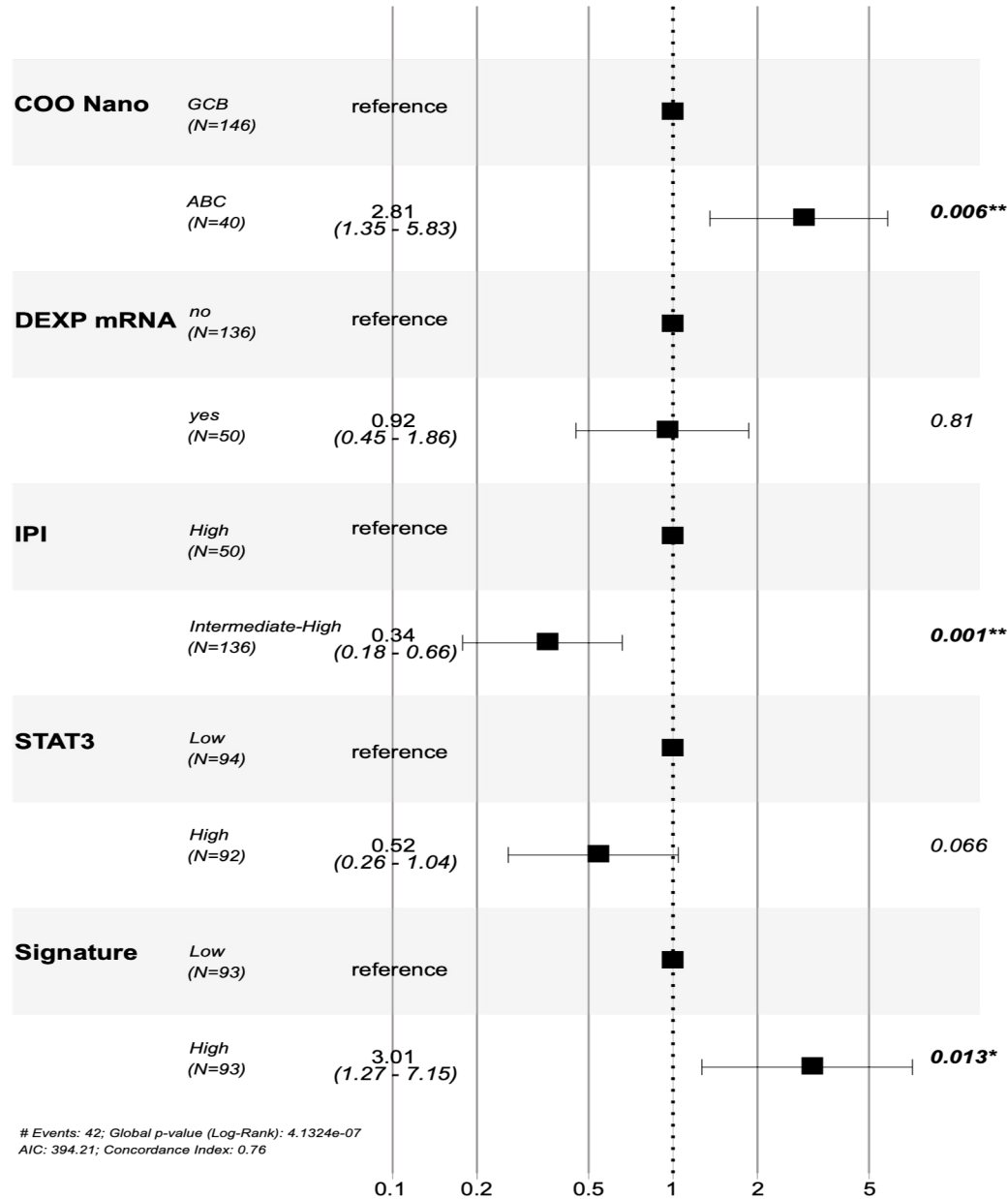
All the cases were studied by immunohistochemistry, targeted GEP and FISH (*BCL2*, *MYC* and *BCL6*).

COO according to Hans' classifier

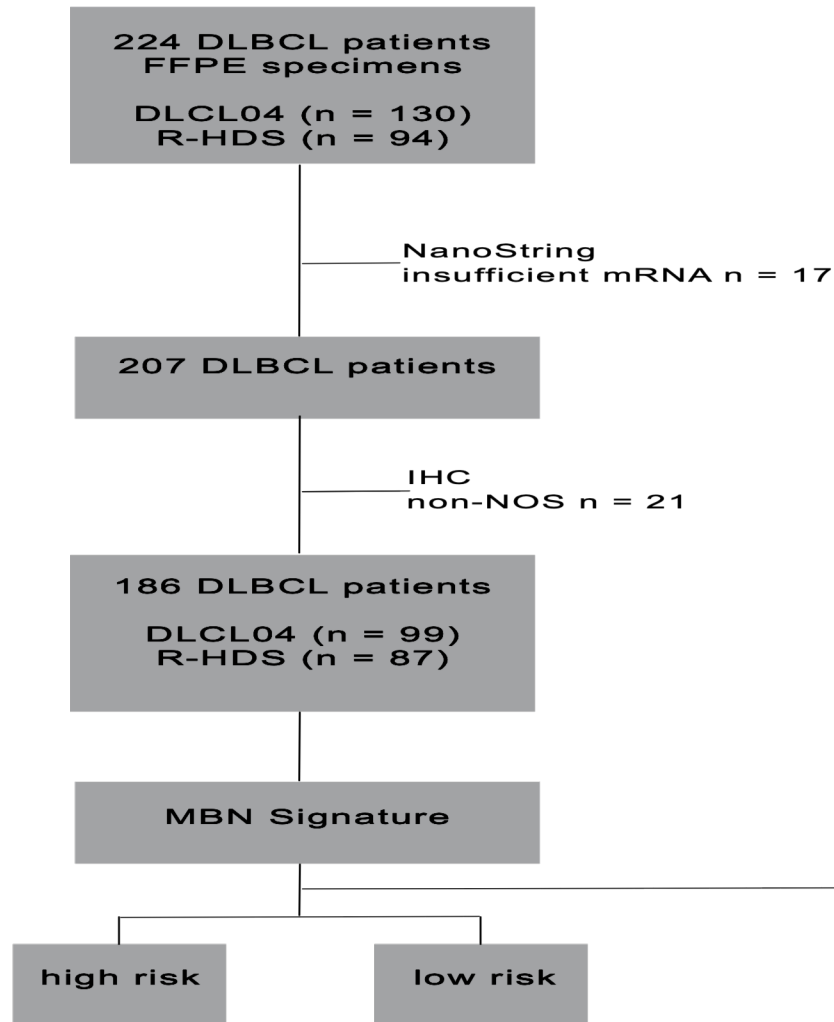




Variables **HR (95% CI)** **p-value**



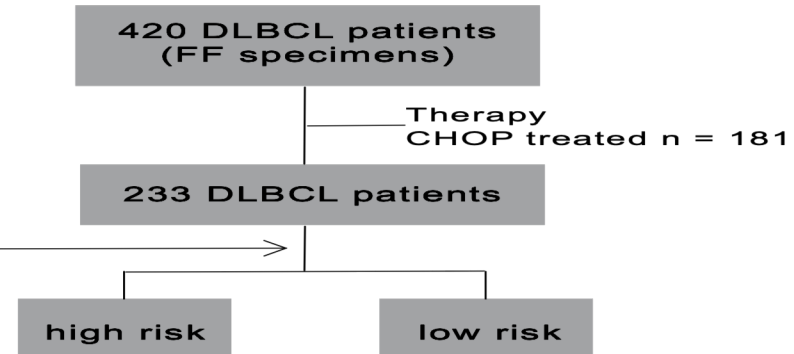
Groups	0	25	50	75	100
Low	93	86	70	34	10
High	93	62	52	23	3



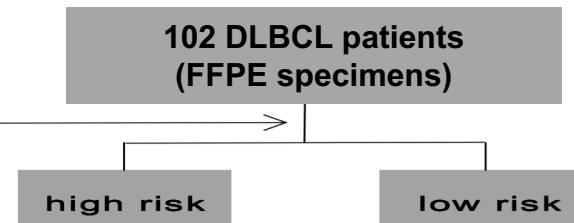
Molecular High-Grade B-Cell Lymphoma: Defining a Poor-Risk Group That Requires Different Approaches to Therapy

Chulin Sha, PhD¹; Sharon Barrans, PhD²; Francesco Cucco, PhD³; Michael A. Bentley, DPhil¹; Matthew A. Care, PhD¹; Thomas Cummin, MD⁴; Hannah Kennedy, PhD³; Joe S. Thompson, MPhil³; Rahman Uddin, MSc¹; Lisa WorriIlow, PhD²; Rebecca Chalkley, MPhil²; Moniek van Hoppe, MSc²; Sophia Ahmed, PhD¹; Tom Maishman, PhD⁴; Josh Caddy, BSc⁴; Anna Schuh, MD⁵; Christoph Mamot, MD⁶; Catherine Burton, MD²; Reuben Tooze, PhD¹; Andrew Davies, PhD⁴; Ming-Qing Du, PhD³; Peter W.M. Johnson, MD⁴; and David R. Westhead, DPhil¹

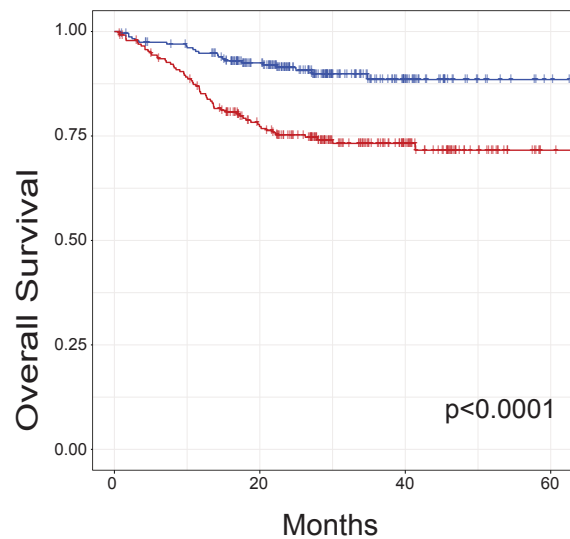
Validation Cohort (Lenz et al)



Validation Cohort (Real-life patients)

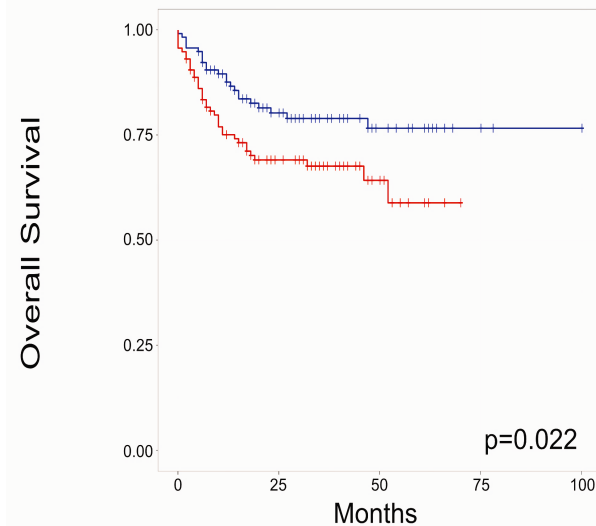


Sha's



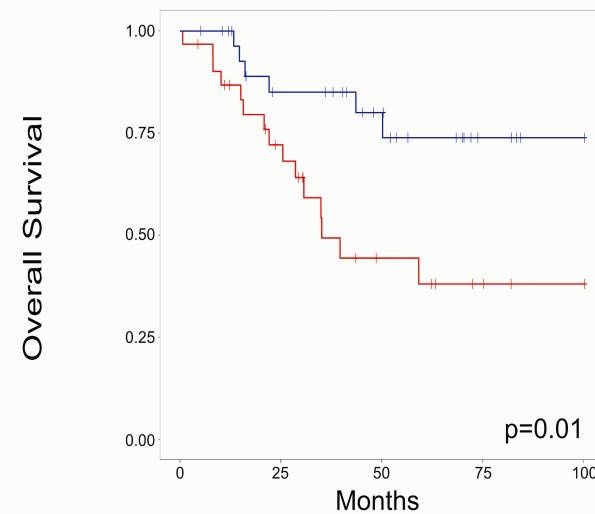
Groups	0	20	40	60
Low	235	174	40	2
High	234	156	54	2

Lenz's



Groups	0	25	50	75	100
MBN Low	117	66	25	4	2
MBN High	116	54	14	0	0

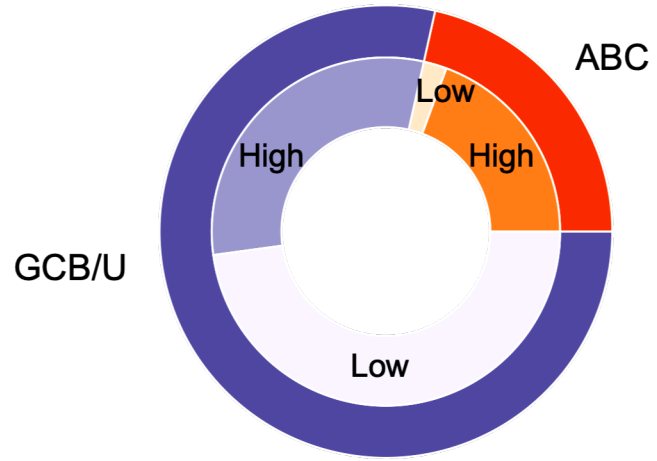
Real-life



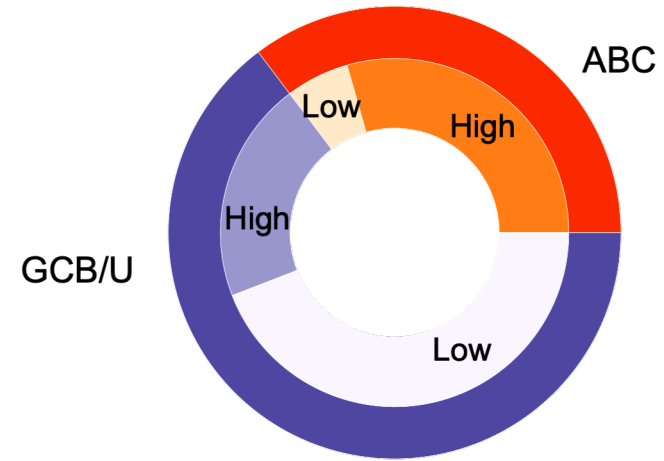
Groups	0	25	50	75	100
MBN Low	31	21	14	4	1
MBN High	31	18	7	3	1

R-CHOP

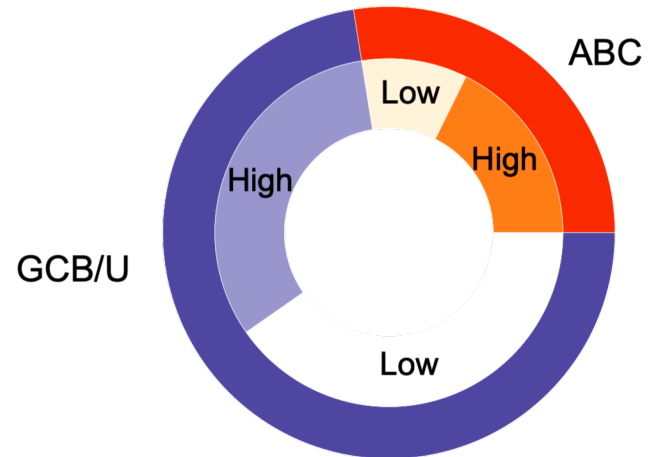
TRIALS n = 186

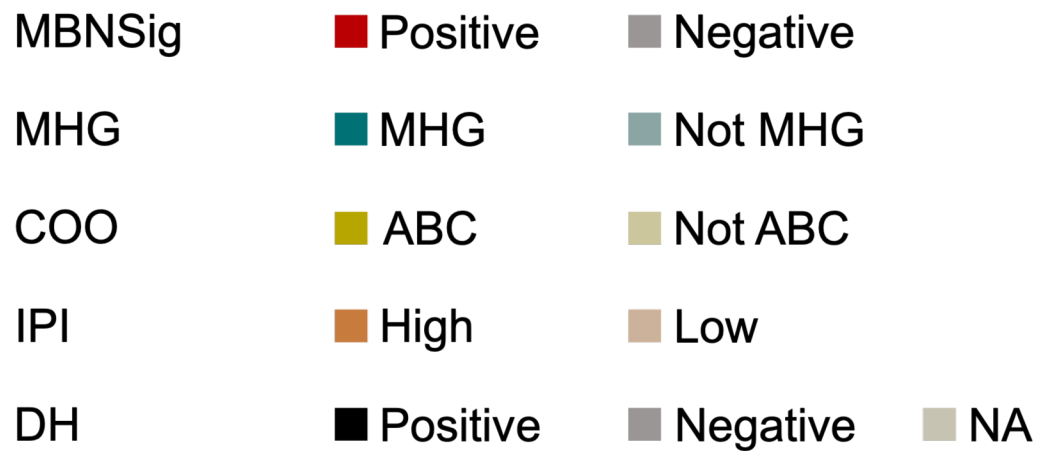
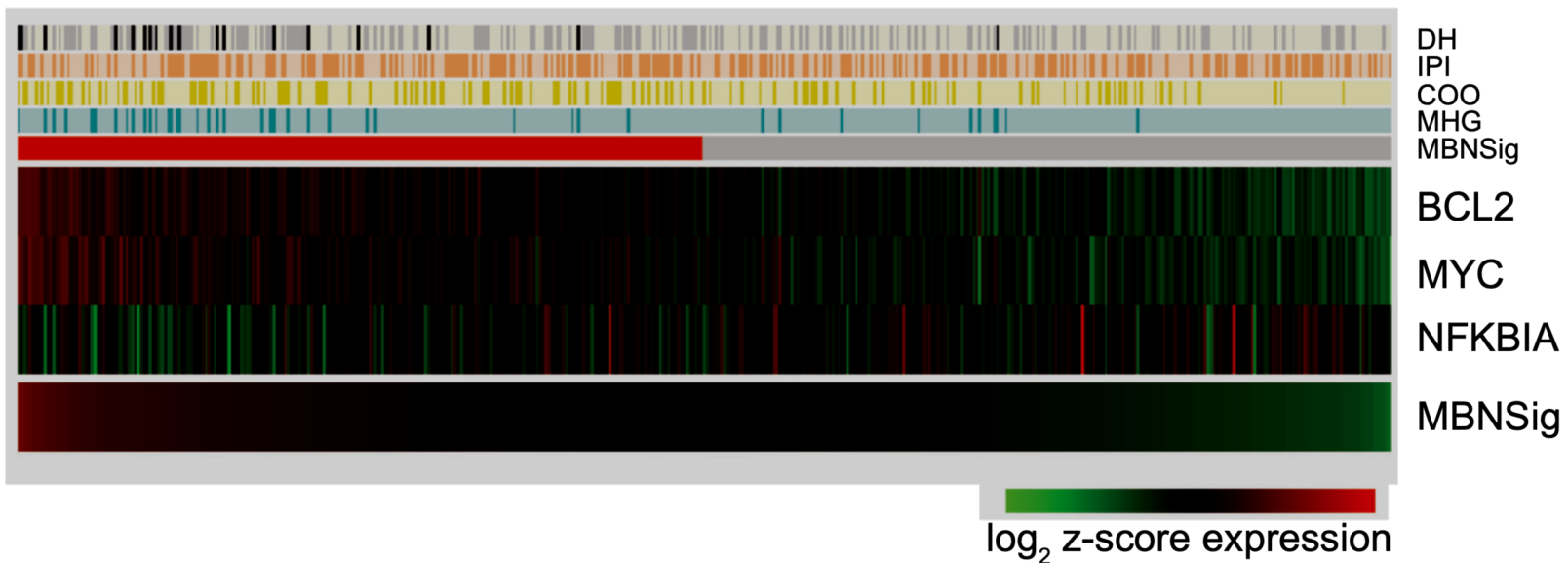


REAL-LIFE n = 102



SHA COHORT n = 469





Longitudinal expression profiling identifies a poor risk subset of patients with ABC-type diffuse large B-cell lymphoma

Submitted 18 March 2022; accepted 25 July 2022; prepublished online on *Blood Advances* First Edition 10 August 2022; final version published online 6 March 2023.

Findlay Bewicke-Copley,¹ Koorosh Korfi,¹ Shamzah Araf,¹ Brendan Hodgkinson,² Emil Kumar,¹ Thomas Cummin,³ Margaret Ashton-Key,⁴ Sharon Barrans,⁵ Suzan van Hoppe,⁵ Cathy Burton,⁵ Mohamed Elshiekh,⁶ Simon Rule,⁷ Nicola Crosbie,⁸ Andrew Clear,⁹ Maria Calaminici,⁹ Hendrik Runge,¹⁰ Robert K. Hills,¹¹ David W. Scott,¹² Lisa M. Rimsza,¹³ Geetha Menon,¹⁴ Chulin Sha,¹⁵ John R. Davies,¹⁵ Ai Nagano,¹ Andrew Davies,³ Daniel Painter,¹⁶ Alexandra Smith,¹⁶ John Gribben,⁹ Kikkeri N. Naresh,⁶ David R. Westhead,¹⁵ Jessica Okosun,⁹ Andrew Steele,¹⁷ Daniel J. Hodson,¹⁰ Sriram Balasubramanian,¹⁷ Peter Johnson,³ Jun Wang,^{1,*} and Jude Fitzgibbon^{1,*}

Microenvironment (ME)

ACCEPTED MANUSCRIPT

Dissection of DLBCL Microenvironment Provides a Gene Expression-Based Predictor of Survival Applicable to Formalin-Fixed Paraffin-Embedded Tissue

S Ciavarella, M C Vegliante, M Fabbri, S De Summa, F Melle, G Motta, V De Iuliis, G Opinto, A Enjuanes, S Rega, A Gulino, C Agostinelli, A Scattone, S Tommasi, A Mangia, F Mele, G Simone, A F Zito, G Ingravallo, U Vitolo, A Chiappella, C Tarella, A M Gianni, A Rambaldi, P L Zinzani, B Casadei, E Derenzini, G Loseto, A Pileri, V Tabanelli, S Fiori, A Rivas-Delgado, A López-Guillermo, T Venesio, A Sapino, E Campo, C Tripodo, A Guarini, S A Pileri ✉

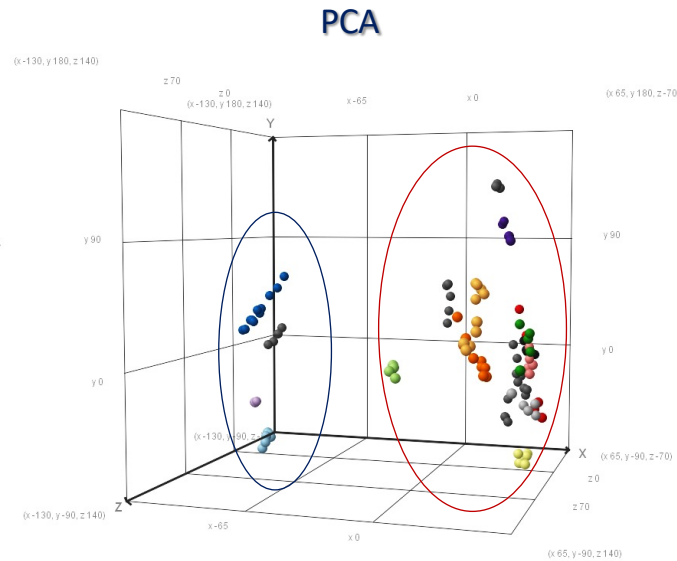
Annals of Oncology, mdy450, <https://doi.org/10.1093/annonc/mdy450>

Published: 11 October 2018

CIBERSORT analysis and selection of prognostic genes

A customized signature including 1,028 genes was generated to distinguish 17 cell types of both **stromal** and **immune** origin.

- Adipocites
- CD4-T cells
- CD8-T cells
- Dendritic cells
- Eosinophils
- Lymphatic endothelial cells
- Macrophages M2
- Memory_B_cells
- Monocytes
- Myofibroblasts
- NK_activated
- NK_resting
- Naive_B
- Neutrophils
- Pericytes
- Plasmacells
- Tgamma-delta



MF-related genes

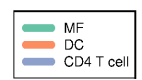
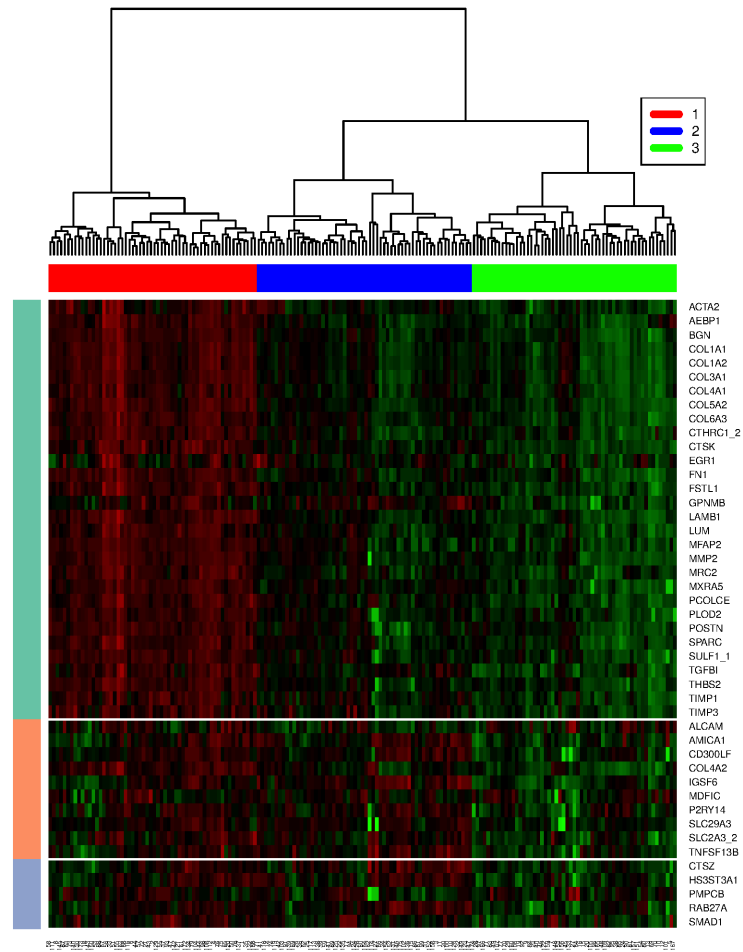
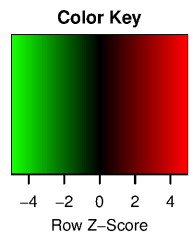
ACTA2 Actin, alpha 2, smooth muscle
 AEBP1 AE binding protein 1
 BGN Biglycan
 COL1A1 Collagen type I alpha 1
 COL1A2 Collagen type I alpha 2
 COL3A1 Collagen type III alpha 1
 COL4A1 Collagen type IV alpha 1
 COL5A2 Collagen type V alpha 2
 COL6A3 Collagen type VI alpha 3
 CTHRC1 Collagen triple helix repeat containing 1
 CTSK Cathepsin K
 EGR1 Early growth response 1
 FN1 Fibronectin 1
 FSTL1 Follistatin like 1
 GPNMB Glycoprotein nmb
 LAMB1 Laminin subunit beta 1
 LUM Lumican
 MFAP2 Microfibrillar associated protein 2
 MMP2 Matrix metalloproteinase 2
 MRC2 Mannose receptor, C type 2
 MXRAS Matrix-Remodelling Associated 5
 PCOLCE Procollagen C-endopeptidase enhancer
 PLOD2 Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2
 POSTN Periostin, osteoblast specific factor
 SPARC Secreted protein acidic and cysteine rich
 SULF1 Sulfatase 1
 TGFBI Transforming growth factor beta induced

DC-related genes

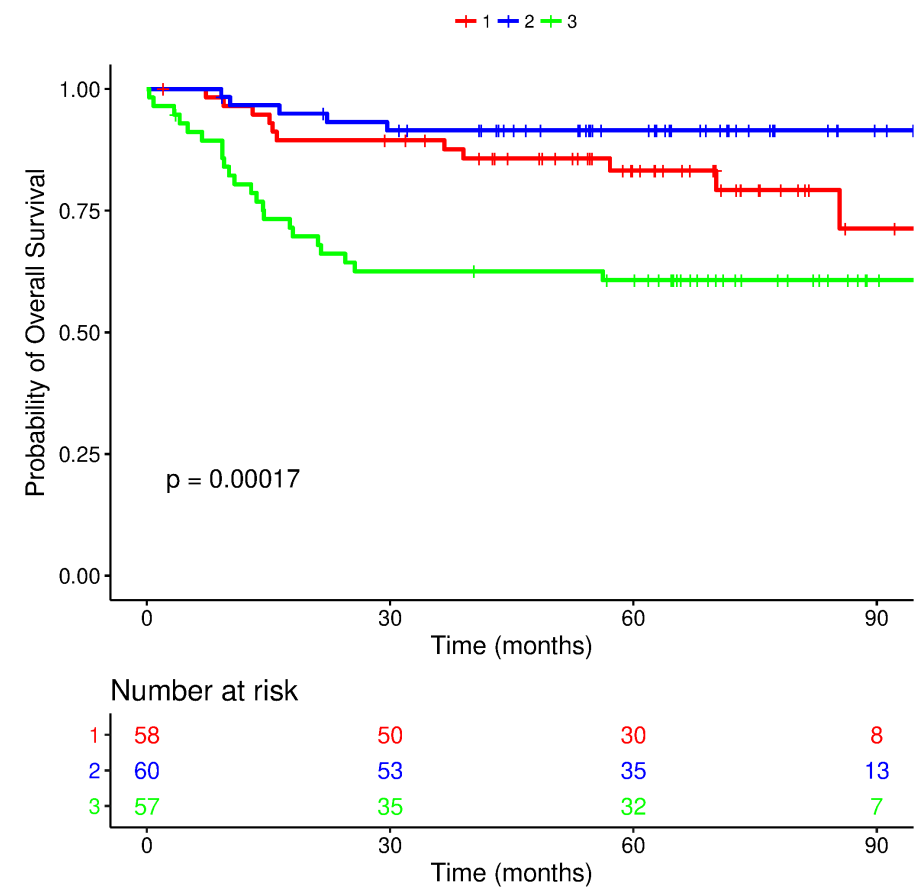
ALCAM Activated leukocyte cell adhesion molecule
 AMICA1 Adhesion molecule, interacts with CXADR antigen 1
 CD300LF CD300 molecule-like family member F
 COL4A2 Collagen, type IV, alpha 2
 IGSF6 Immunoglobulin superfamily, member 6
 MDIC MyoD Family Inhibitor Domain Containing
 P2RY14 Purinergic receptor P2Y, G-protein coupled, 14
 SLC29A3 Solute carrier family 29 (nucleoside transporters), member 3;
 SLC2A3 Solute carrier family 2 (facilitated glucose transporter),

CD4+ T cell-related genes

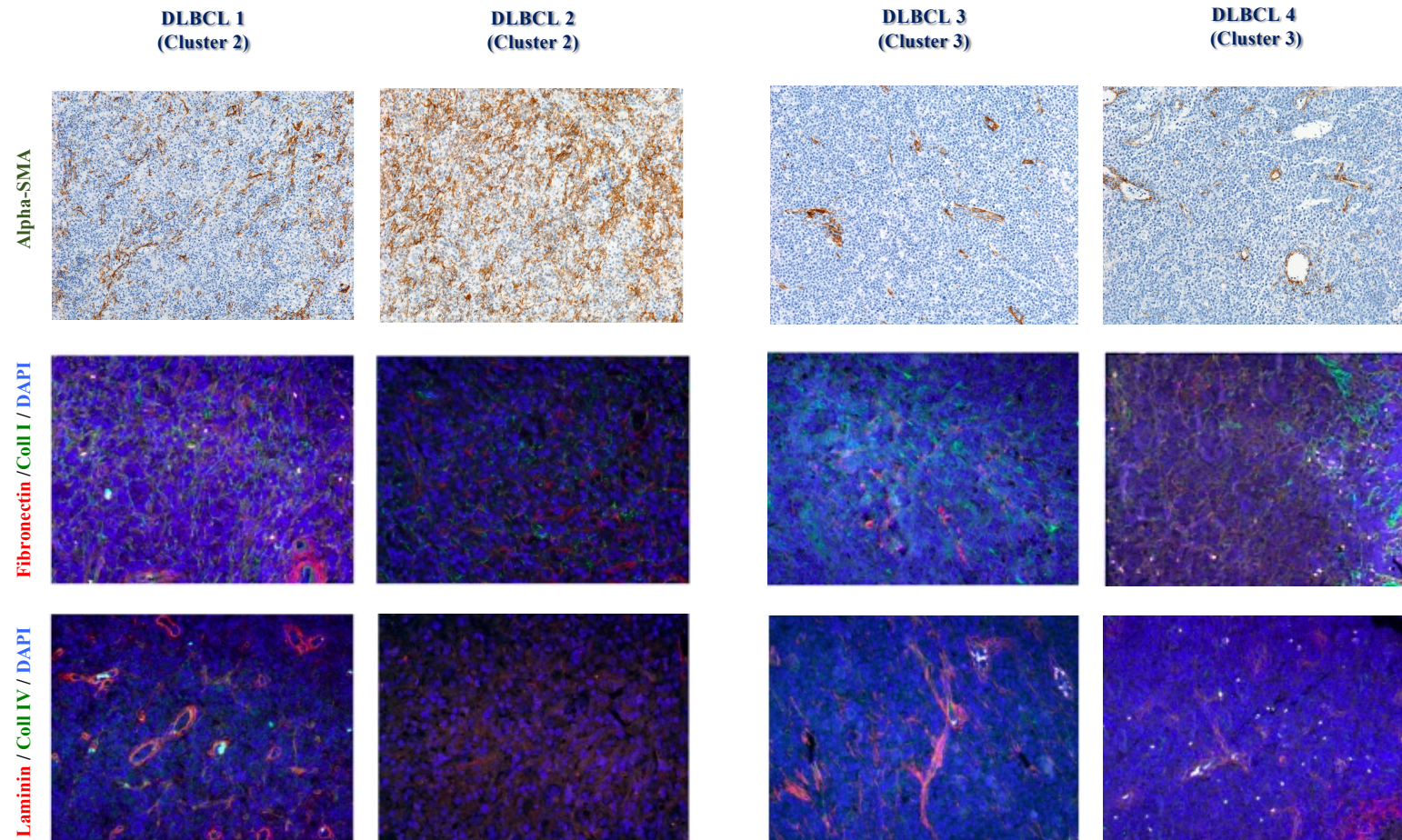
CTSZ Cathepsin 2
 HS3ST3A1 Heparan Sulfate-Glucosamine 3-Sulfotransferase 3A1
 PMPCB Peptidase, Mitochondrial Processing Beta Subunit
 RAB27A RAB27A, Member RAS Oncogene Family
 SMAD1 SMAD Family Member 1

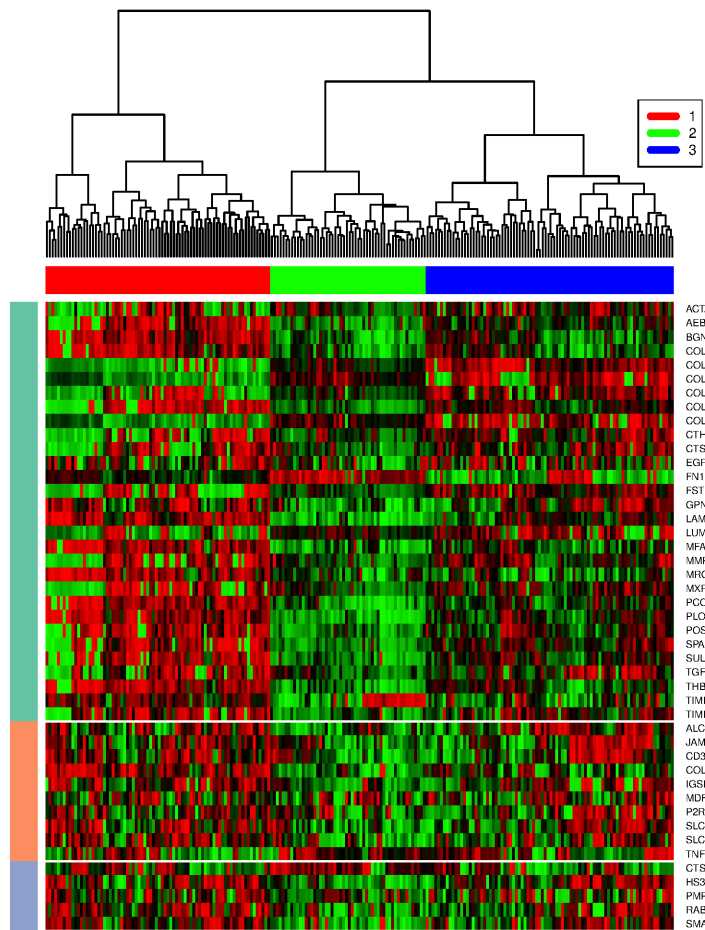
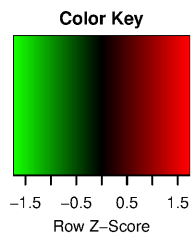


DLCL04 and R-HDS0305

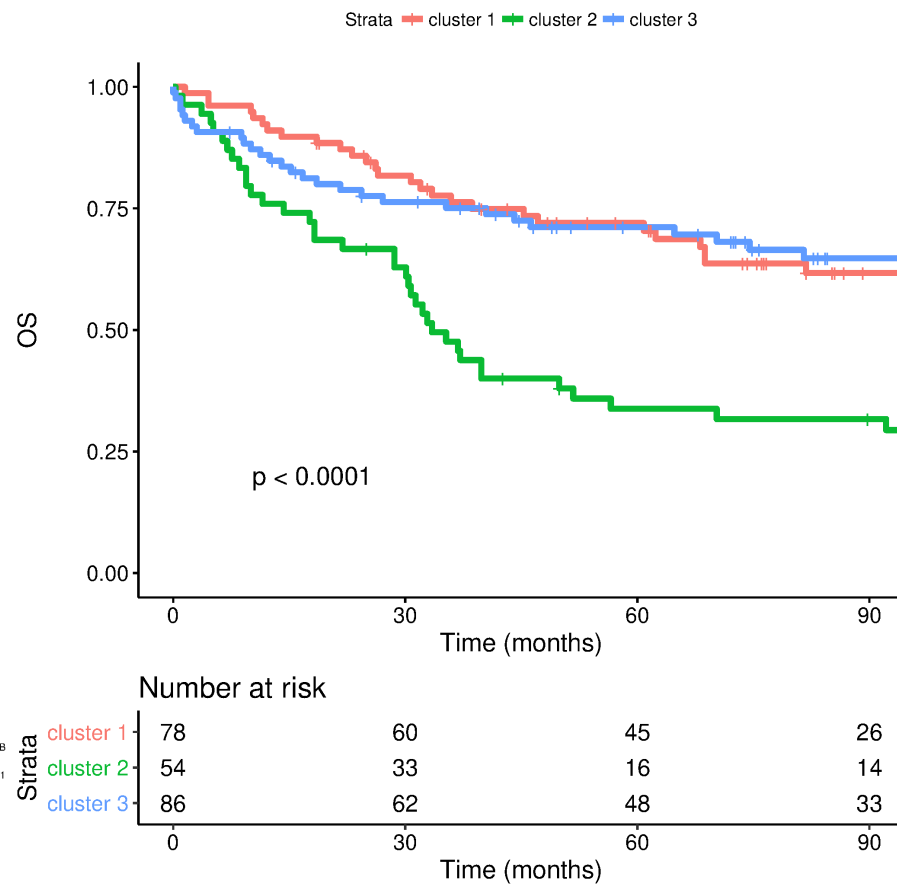


By *in situ* immunostaining we analyzed the expression of ECM proteins encoded by four of the fronting genes of the MF signature, namely Fibronectin, Collagen-I, Laminin, and Collagen-IV. However, the expression variability of these proteins does not support the use of immunohistochemistry as a reliable assay to provide insight on the prognostic gene expression patterns of DLBCL microenvironment determinants.





Lenz' series



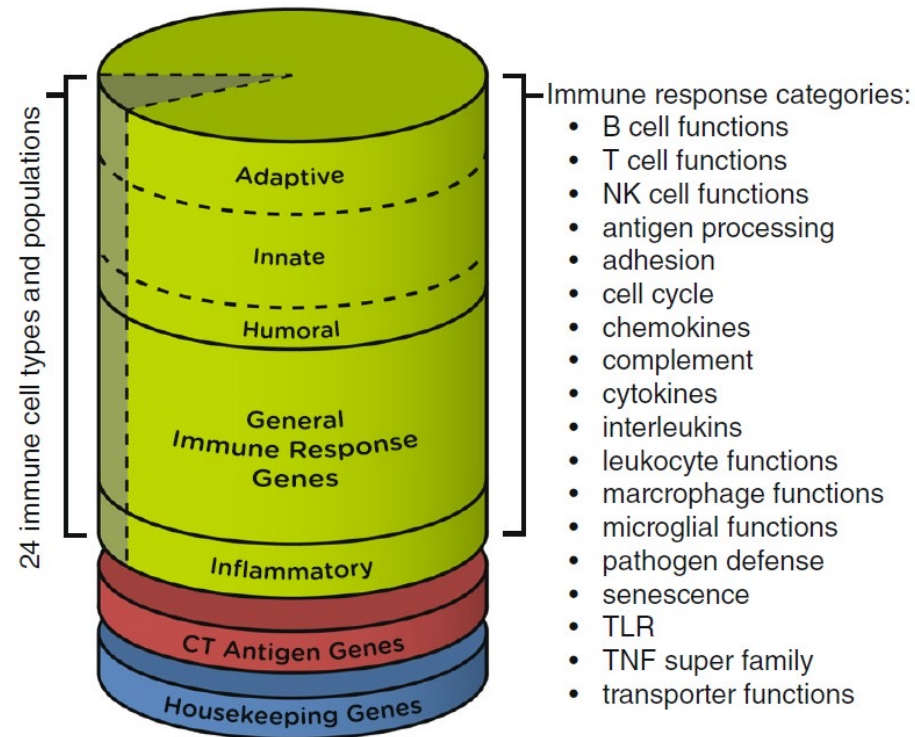
ORIGINAL ARTICLE

NR1H3 (LXR α) is associated with pro-inflammatory macrophages, predicts survival and suggests potential therapeutic rationales in diffuse large b-cell lymphoma

Maria Carmela Vegliante¹ | Saveria Mazzara² | Gian Maria Zaccaria¹ |
Simona De Summa³ | Flavia Esposito^{4,5} | Federica Melle² | Giovanna Motta² |
Maria Rosaria Sapienza²  | Giuseppina Opinto¹ | Giacomo Volpe¹ |
Antonella Bucci¹ | Grazia Gargano^{1,5} | Anna Enjuanes⁶ | Valentina Tabanelli² |
Stefano Fiori² | Carla Minoia¹ | Felice Clemente¹ | Antonio Negri¹ |
Alessandro Gulino⁷ | Gaia Morello⁸ | Anna Scattone⁹ | Alfredo F. Zito⁹ |
Stefania Tommasi³  | Claudio Agostinelli^{10,11} | Umberto Vitolo¹² |
Annalisa Chiappella¹³ | Anna Maria Barbui¹⁴ | Enrico Derenzini^{15,16} |
Pier Luigi Zinzani^{11,17} | Beatrice Casadei^{11,17} | Alfredo Rivas-Delgado¹⁸ |
Armando López-Guillermo¹⁸ | Elias Campo¹⁹ | Antonio Moschetta²⁰ |
Attilio Guarini¹ | Stefano A. Pileri² | Sabino Ciavarella¹ 

PanCancer Immune Profiling Panel (PCIP)

- A multiplexed gene expression approach to profiling cancer immunology
 - Quantify infiltrating immune cells in a tumor microenvironment
 - Assess immunological activity and response to therapeutic intervention
 - Identify tumor-specific antigens



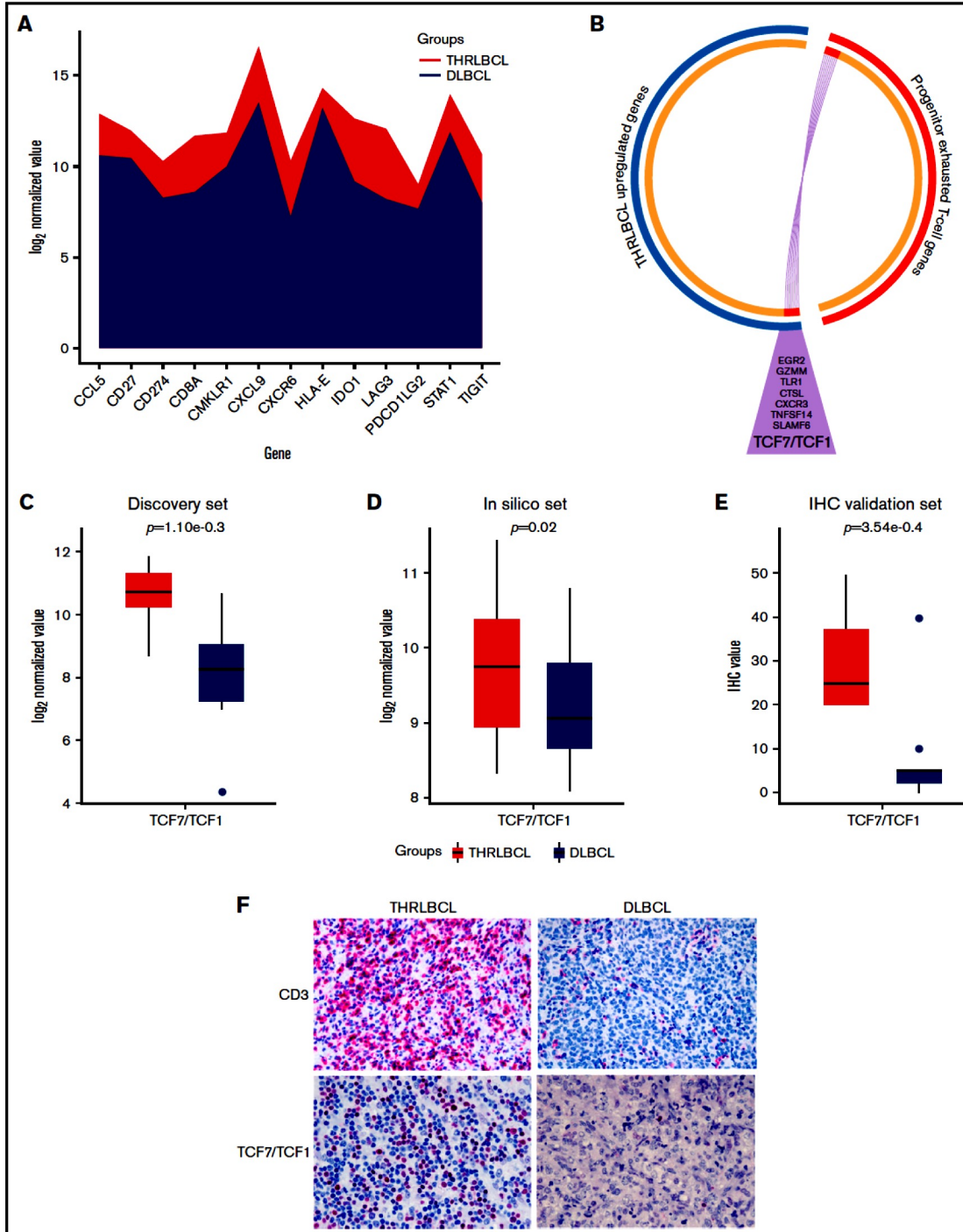
Discovery set: 12 THRBCLs vs. 10 DLBCLs, NOS

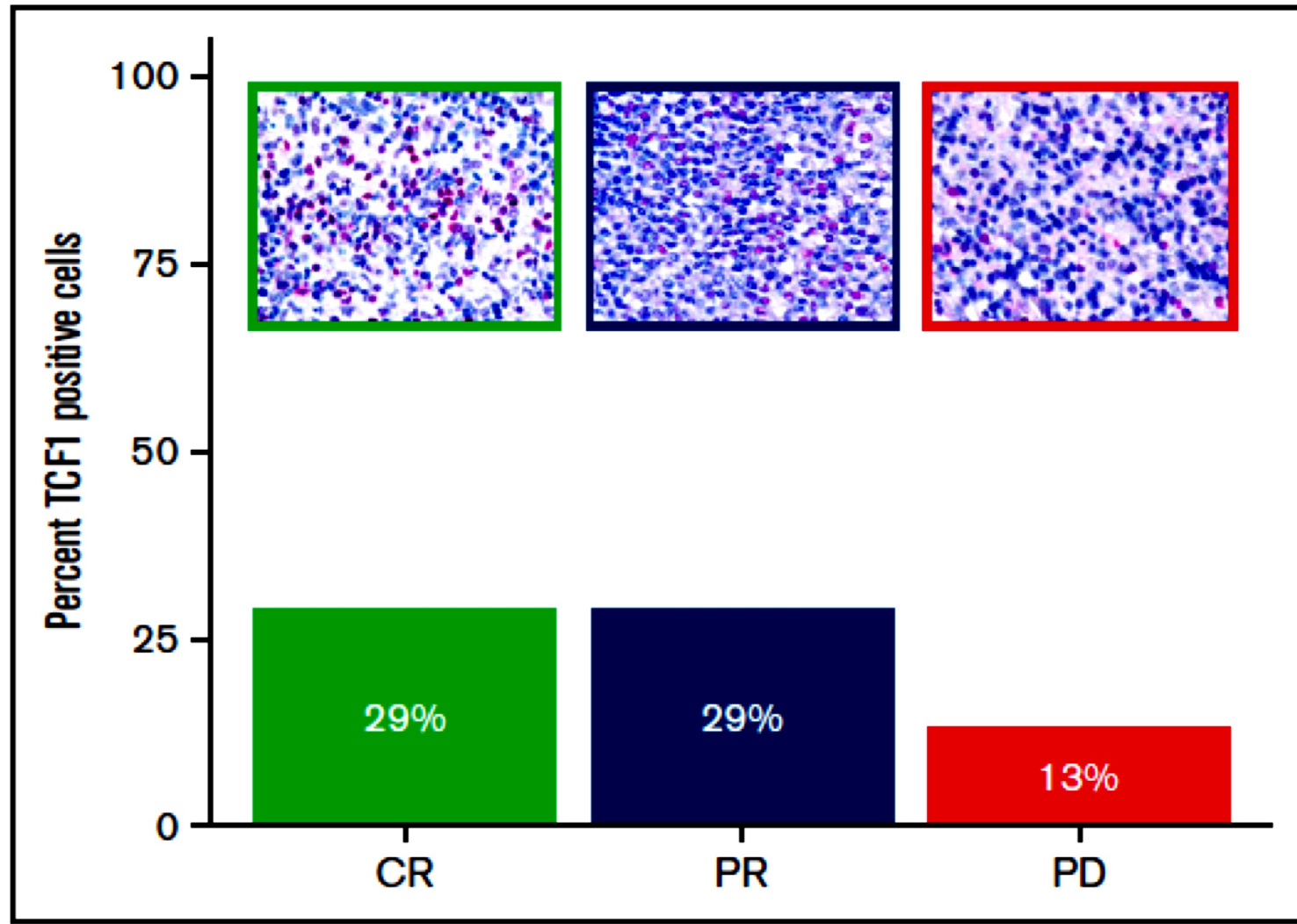
Key Points

- The interferon-driven inflammatory response and the PD-1 signaling were the most relevant modulators of the THRLBCL immune response.
- THRLBCL cases may be enriched in TCF1⁺ T cells, a subset of progenitor exhausted T cells associated with good response to immunotherapy.

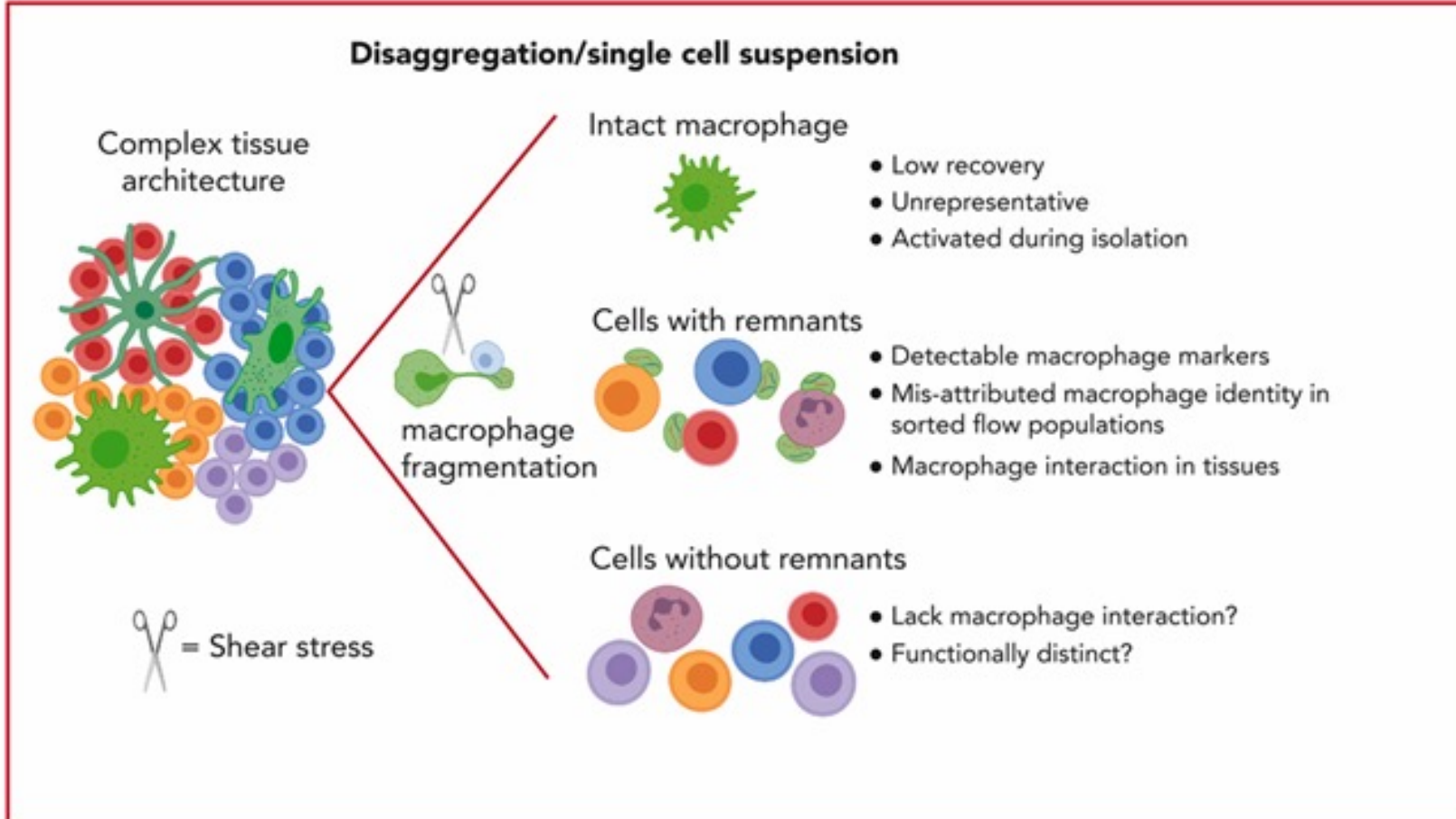
***In silico*: 31 THRBCLs vs.
473 DLBCLs, NOS**

**IHC: 15 THRBCLs vs.
26 DLBCLs, NOS**





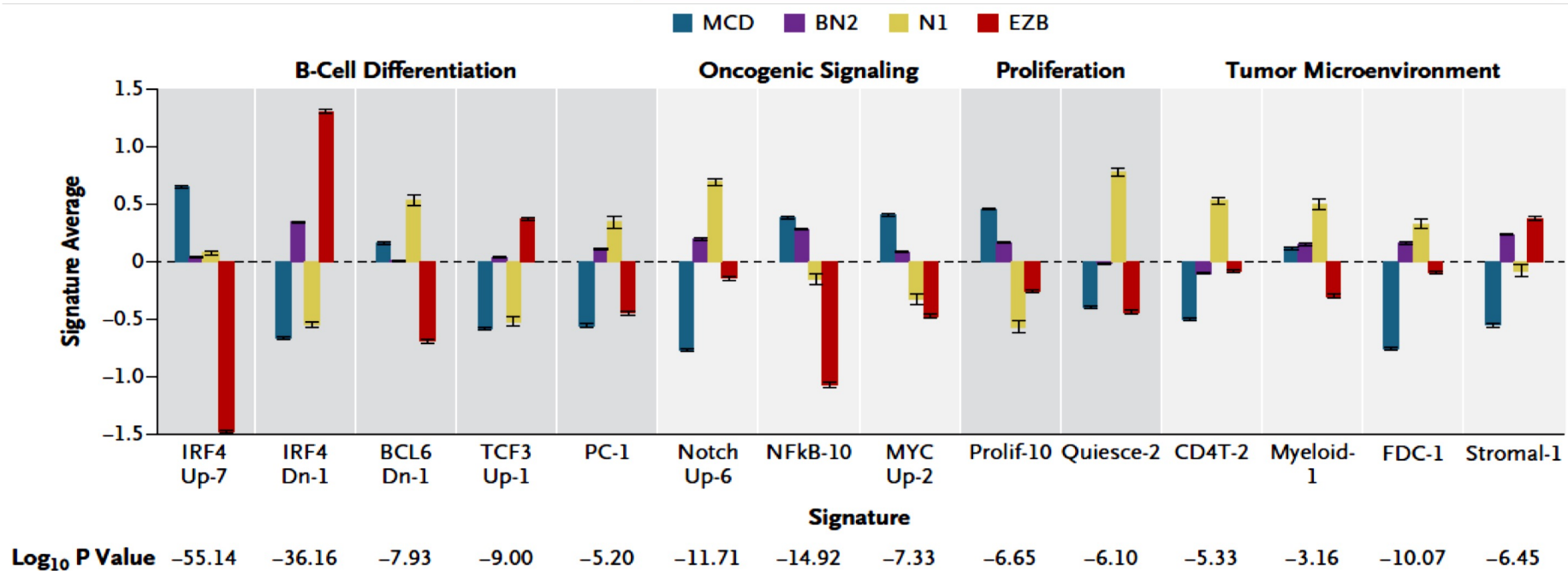
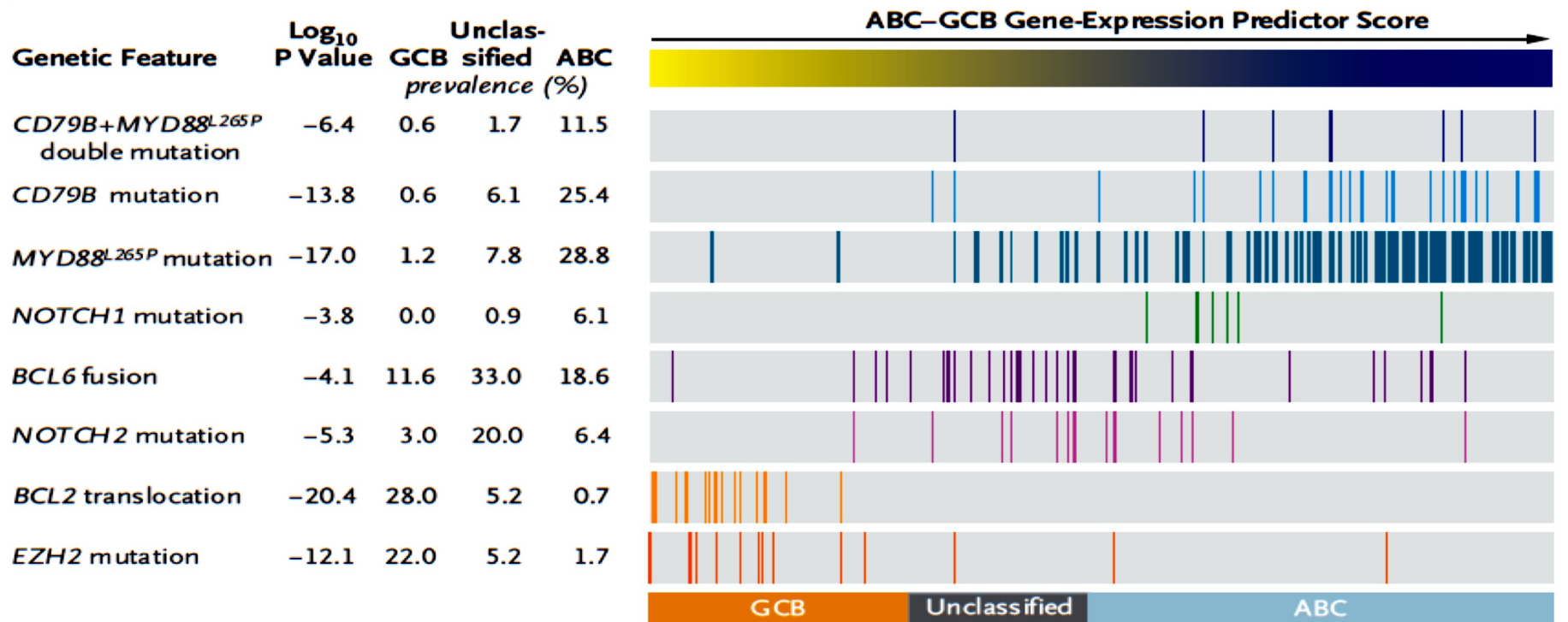
Macrophage heterogeneity in the single cell era: facts and artefacts

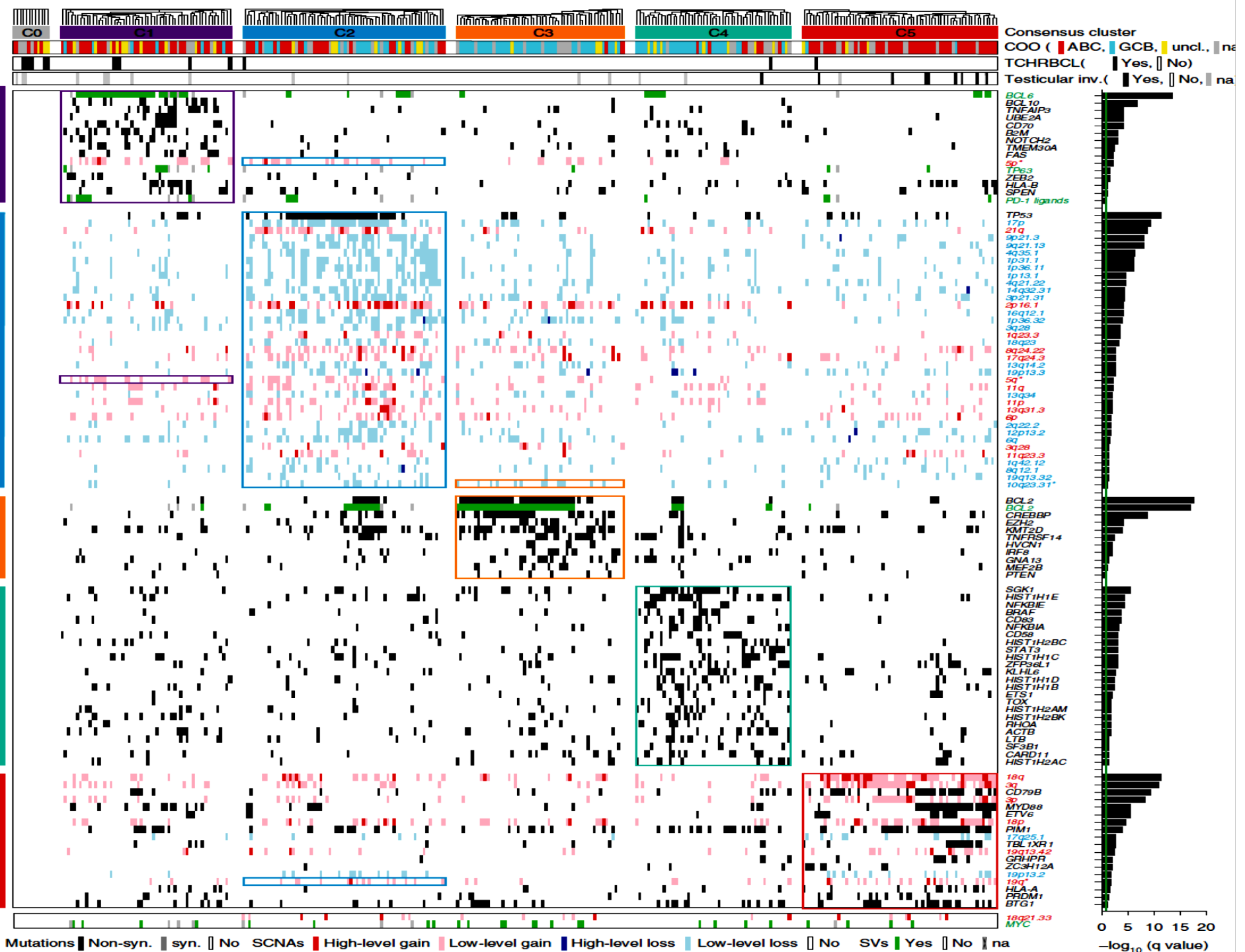


- **Macrophage fragmentation results in low yields of intact macrophage**
- **Macrophage remnants complicate ex vivo analysis**
- Hume et al. *Blood*, DOI: 10.1182/blood.2023020597

**Blood
Visual
Abstract**

Next generation sequencing (NGS)





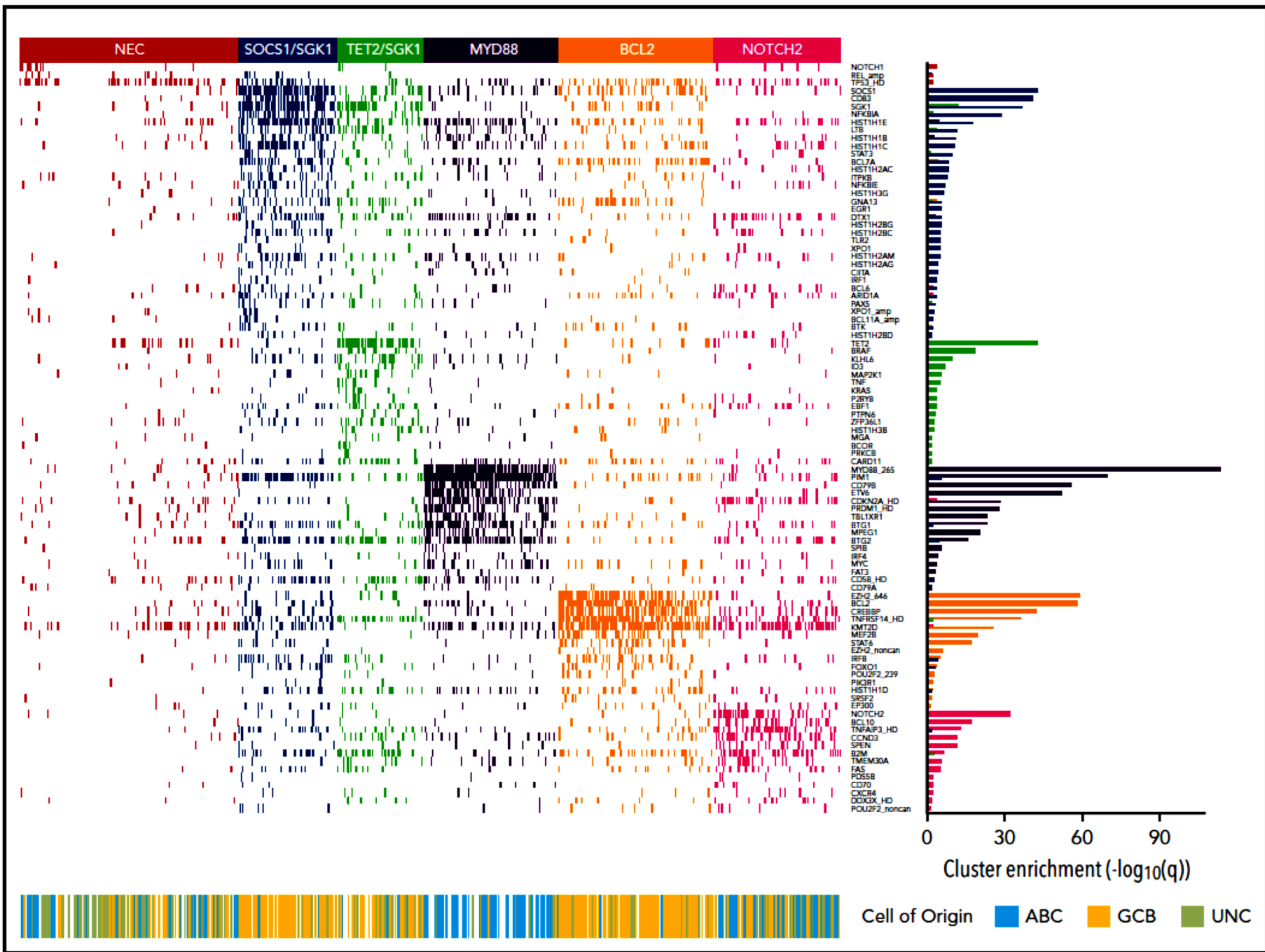


Table 2: Genomic subtypes of DLBCL

Wright 2020 ³⁰	Chapuy 2018 ²⁹	Lacy 2020 ³¹	Hallmark drivers	COO	% of cases	Outcome 5 yr OS (%)	Putative related small cell lymphoma
MCD	C5	MYD88	MYD88/CD79B	ABC	9-14-21	40-42	
BN2	C1	NOTCH2	tBCL6/ NOTCH2	GCB/ABC Unclassified	16-19	48-67	MZL
EZB-MYC-	C3	BCL2	EZH2 tBCL2	GCB	13-18	63-82	FL
EZB- MYC+			EZH2/tMYC	GCB/DZ	6	48	
A53	C2		TP53 Aneuploidy	All	7-21	63	
ST2	C4	SOCS1/SGK1 TET/SGK1	SOCS1/TET/ SGK1	GCB	5-17	65-84	NLPBL
N1			NOTCH1	ABC	2	27	CLL
UNCLASS		UNCLASS		Unclass, GCB,ABC	27-37	66	

ABC: Activated B-cell type; GCB: Germinal center B-cell type;
DZ: Dark zone signature; CLL: Chronic lymphocytic leukemia;
FL: Follicular lymphoma, MZL: Marginal zone lymphoma;
NLPBL: Nodular lymphocyte predominant B-cell lymphomat;
t: Translocation

LYMPHOID NEOPLASIA

MYD88^{L265P} augments proximal B-cell receptor signaling in large B-cell lymphomas via an interaction with DOCK8

Elisa Mandato,^{1,*} Qingsheng Yan,^{1,*} Jing Ouyang,^{1,2} Julia Paczkowska,¹ Yan Qin,^{1,3} Yansheng Hao,^{1,4} Kamil Bojarczuk,¹ Julia Hansen,^{1,5} Björn Chapuy,^{1,6} Scott J. Rodig,⁷ Sumbul Jawed Khan,¹ Robert A. Redd,⁸ and Margaret A. Shipp¹

KEY POINTS

- In DLBCLs with MYD88^{L265P} and CD79B^{Y196F} alterations, MYD88^{L265P} selectively increased proximal BCR signaling and survival via DOCK8.
- MYD88^{L265P}/DOCK8-enhanced proximal BCR signaling is a basis for the increased sensitivity of MYD88^{L265P}/CD79B^{Y196F} DLBCLs to BTK blockade.

 blood® 5 OCTOBER 2023 | VOLUME 142, NUMBER 14 1219



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2021 L Street NW, Suite 900,
Washington, DC 20036
Phone: 202-776-0544 | Fax 202-776-0545
editorial@hematology.org

DLBCL associated NOTCH2 mutations escape ubiquitin-dependent degradation and promote chemo-resistance

Tracking no: BLD-2022-018752R1

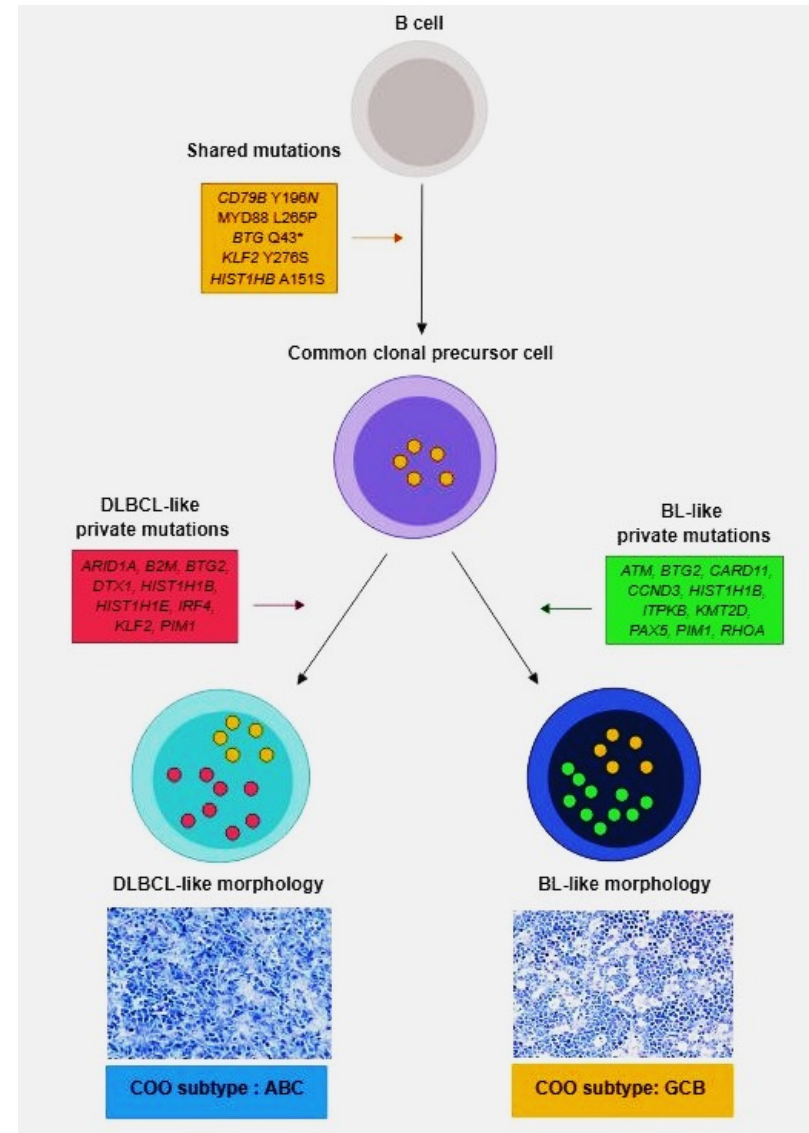
Nan Zhou (University of Pennsylvania, United States) Jaewoo Choi (University of Pennsylvania, United States) Grant Grothusen (University of Pennsylvania, United States) Bang-Jin Kim (University of Pennsylvania, United States) Diqiu Ren (University of Pennsylvania, United States) Zhendong Cao (University of Pennsylvania, United States) Qinglan Li (University of Pennsylvania, United States) Yiman Liu (University of Pennsylvania, United States) Arati Inamdar (University of Pennsylvania, United States) Thomas Beer (The Wistar Institute, United States) Hsin-Yao Tang (The Wistar Institute, United States) Eric Perkey (University of Pennsylvania, United States) Ivan Maillard (University of Pennsylvania, United States) Roberto Bonasio (University of Pennsylvania, United States) Junwei Shi (University of Pennsylvania, United States) Marco Ruella (University of Pennsylvania, United States) Liling Wan (University of Pennsylvania, United States) Luca Busino (University of Pennsylvania, United States)

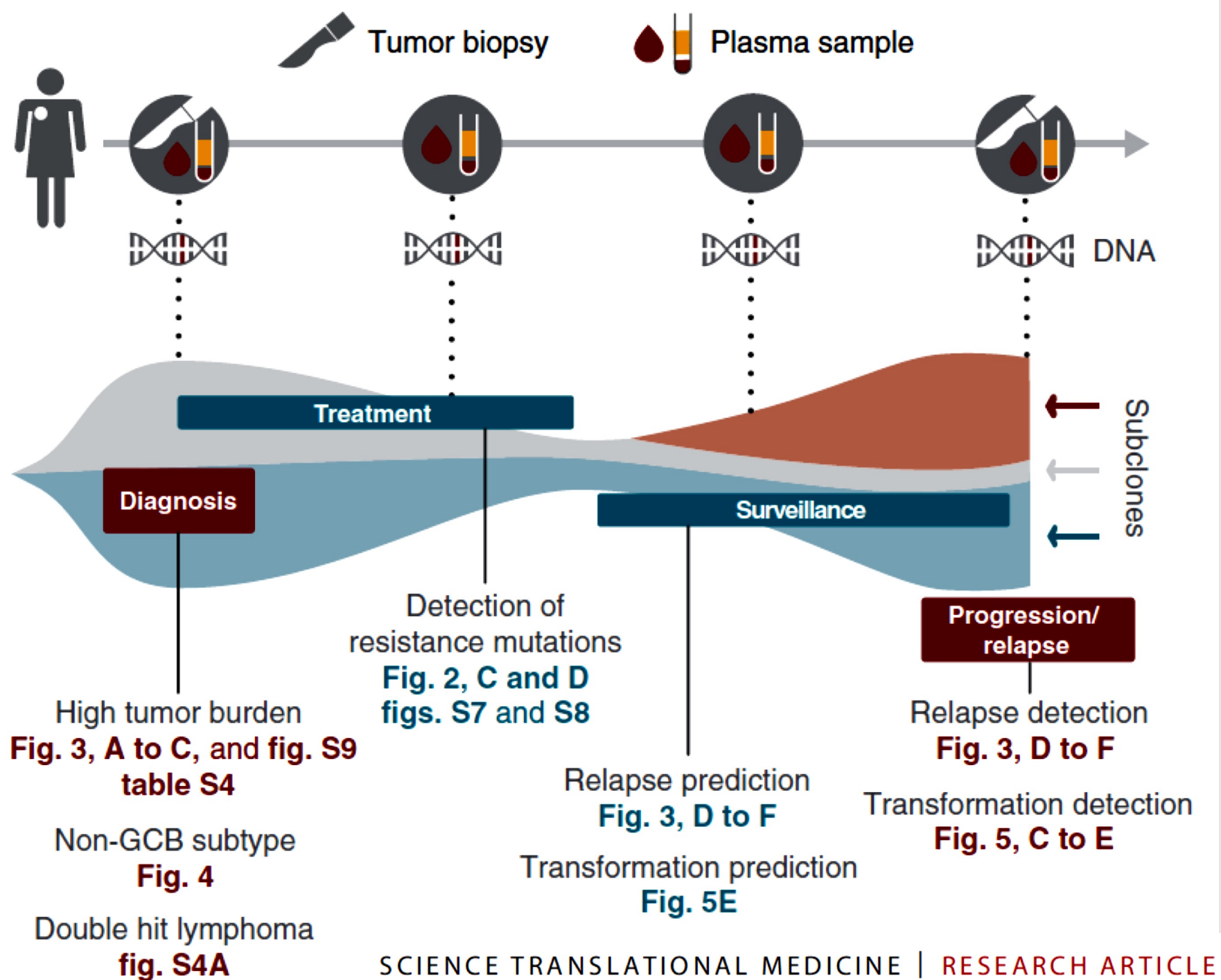


Evolutionary crossroads: morphological heterogeneity reflects divergent intra-clonal evolution in a case of high-grade B-cell lymphoma

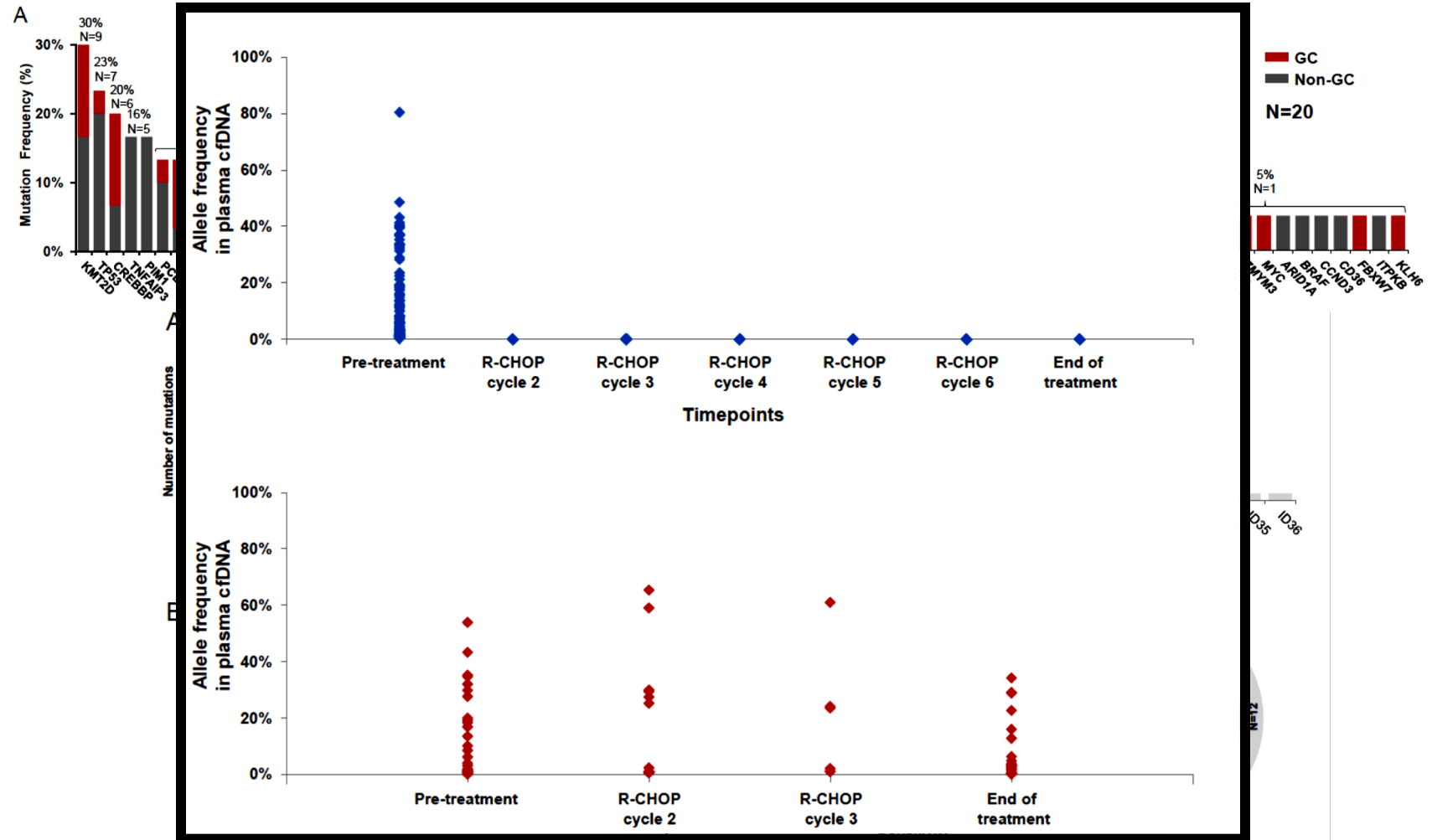
by Valentina Tabanelli, Federica Melle, Giovanna Motta, Saveria Mazzara, Marco Fabbri, Chiara Corsini, Elvira Gerbino, Angelica Calleri, Maria Rosaria Sapienza, Ignazio Abbene, Viviana Stufano, Massimo Barberis, and Stefano A. Pileri

Haematologica 2020 [Epub ahead of print]





DIFFUSE LARGE B-CELL LYMPHOMA GENOTYPING ON THE LIQUID BIOPSY





рахмат
danke

謝謝

ngiyabonga

teşekkür ederim

Баярлалаа
спасибо

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vinaka
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kam sah hamnida

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