

Case 3



Multi-Institutional Hematopathology Interesting Case Conference

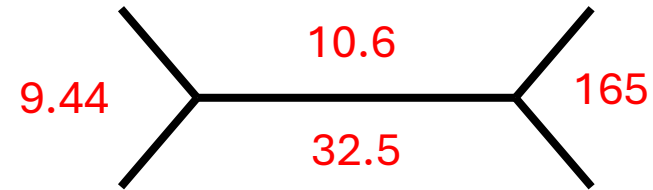
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Cleveland Clinic

PGY-5

History

- 82-year-old man
- Previously diagnosed B-cell lymphoma from an outside hospital, treatment unknown
- Presenting with visible right neck lymphadenopathy and 30-40 lb weight loss over the course of one year
- Lymph node biopsy performed



MCV: 101.9 fL

Differential:

Neutrophil: 87.5%

Lymphocytes: 3.4%

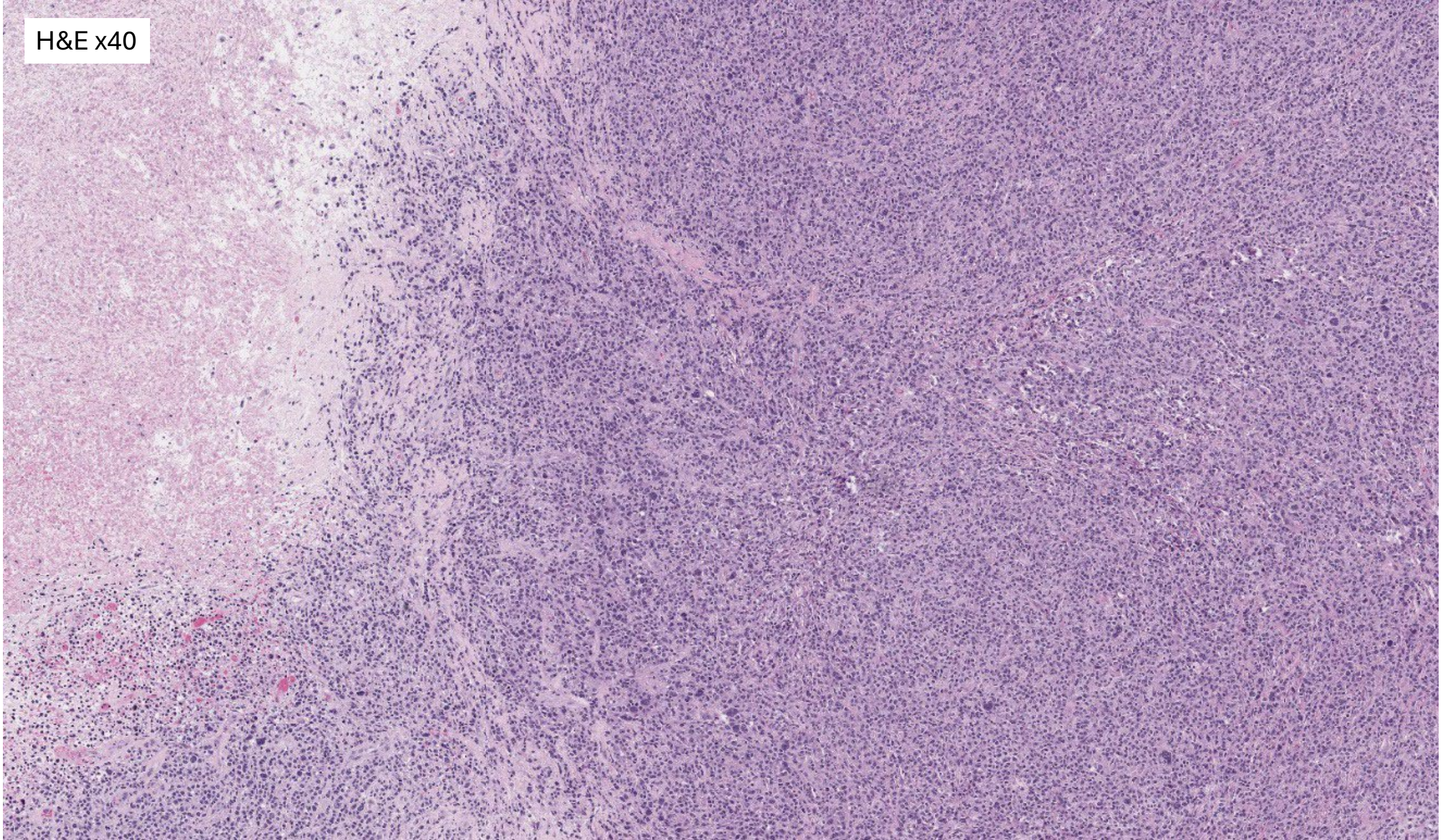
Monocytes: 7.8%

Eosinophils: 0.5%

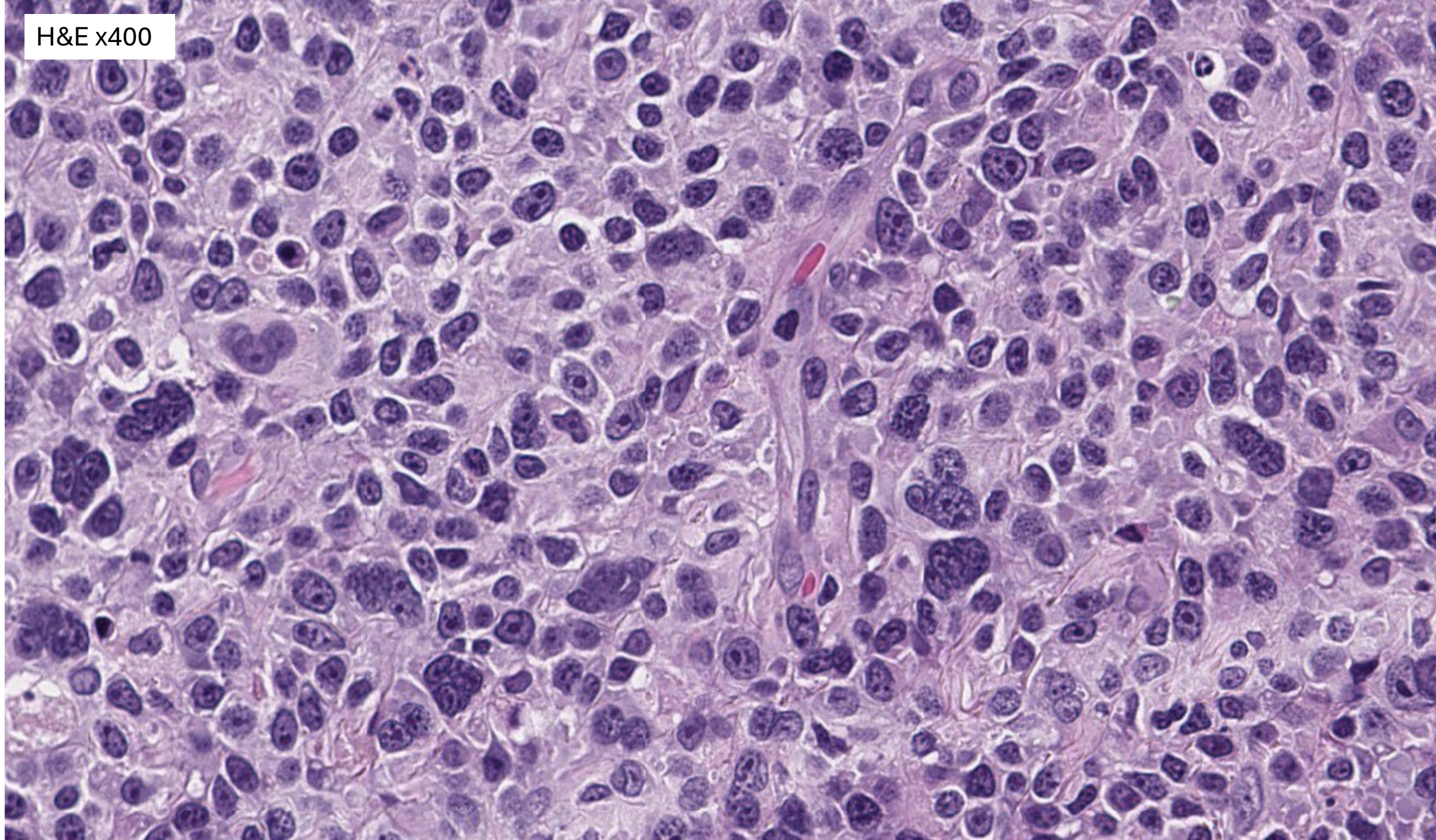
Basophils: 0.3%

LDH: 280 U/L

H&E x40

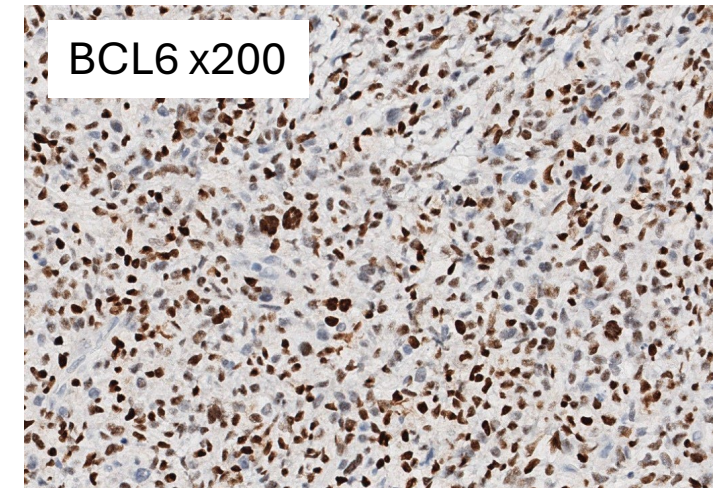
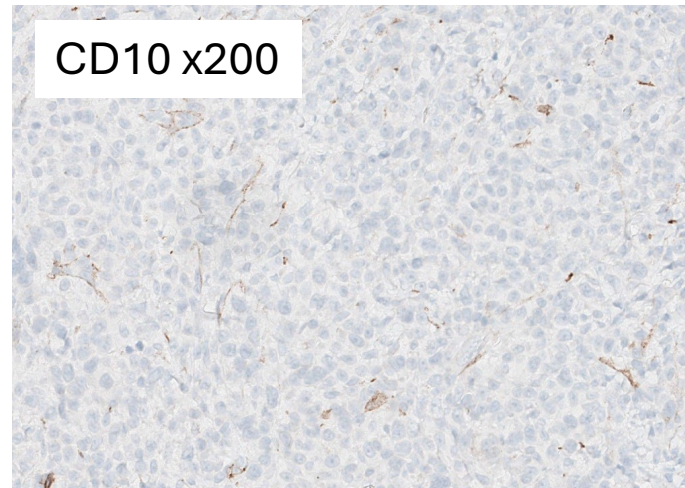
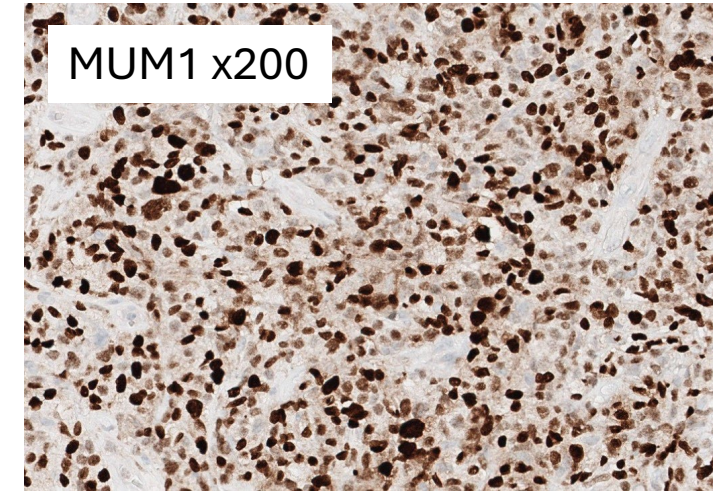
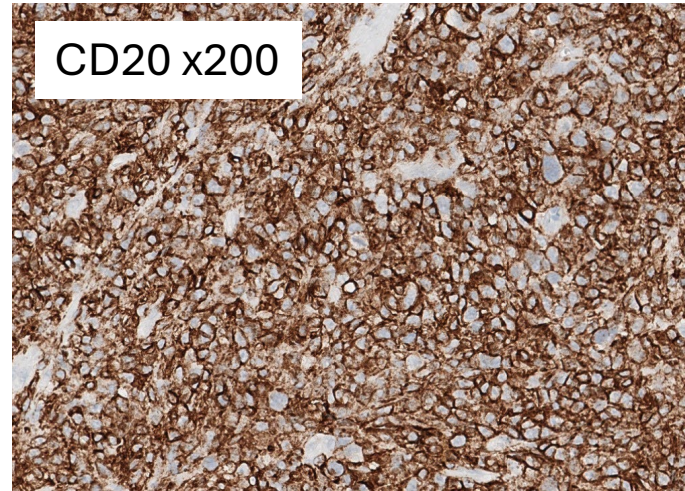


H&E x400



Immunophenotype

Marker	B-cell lymphoma
CD19	+
CD20	+
PAX5	+
CD5	-
CD10	-
BCL6	+
MUM1	+
BCL2	+ (greater than 90%)
C-MYC	+ (greater than 40%)
Cyclin D1	-
TdT	-
EBER ISH	-
KI-67	70-80%



FISH for Aggressive B-cell Lymphoma

	Result	Reference Range
<i>BCL6</i> Rearrangement	2%	(0-9%)
<i>MYC</i> Rearrangement	5%	(0-11%)
t(8;14)(q24.21;q32.33) <i>IGH::MYC</i>	3%	(0-7%)
<i>BCL2</i> Rearrangement	71%	(0-5%)

B-cell lymphoma NGS Results

- Pathogenic mutations detected:
 1. **B2M**: c.289G>T; p.Glu97* (81%)
 2. **KMT2D**: c.11800C>T; p.Gln3934* (55%)
 3. **TP53**: c.376-2_382delinsCCT; p.? (67%)
- Variants of unknown clinical significance detected:
 1. **ARID1A**: c.4918A>G; p.Thr1640Ala (13%)
 2. **ATM**: c.4564G>C; p.Gly1522Arg (3%)
 3. **BCL2**: Multiple variants in **BCL2** were detected (NM_000633.2)
 - c.-2G>A; p.? (24%)
 - c.66_67delinsAT; p.Lys22_Leu23= (48%)
 - c.95C>T; p.Ala32Val (48%)
 - c.103G>A; p.Val35Met (48%)
 - c.175C>G; p.Pro59Ala (52%)
 - c.179C>T; p.Ala60Val (25%)
 - c.386G>A; p.Arg129His (8%)
 - c.403G>A; p.Glu135Lys (26%)
 - c.493G>A; p.Glu165Lys (54%)
 4. **KMT2D**: c.176+3A>T; p.? (31%)
 5. **PIM1**: c.140G>C; p.Ser47Thr (29%)
 6. **TNFRSF14**: c.325C>T; p.Arg109Trp (80%)

Final Diagnosis

- Diffuse large B-cell lymphoma, NOS
 - Cell of origin (Hans classifier): non-Germinal center
- Can we subclassify more?

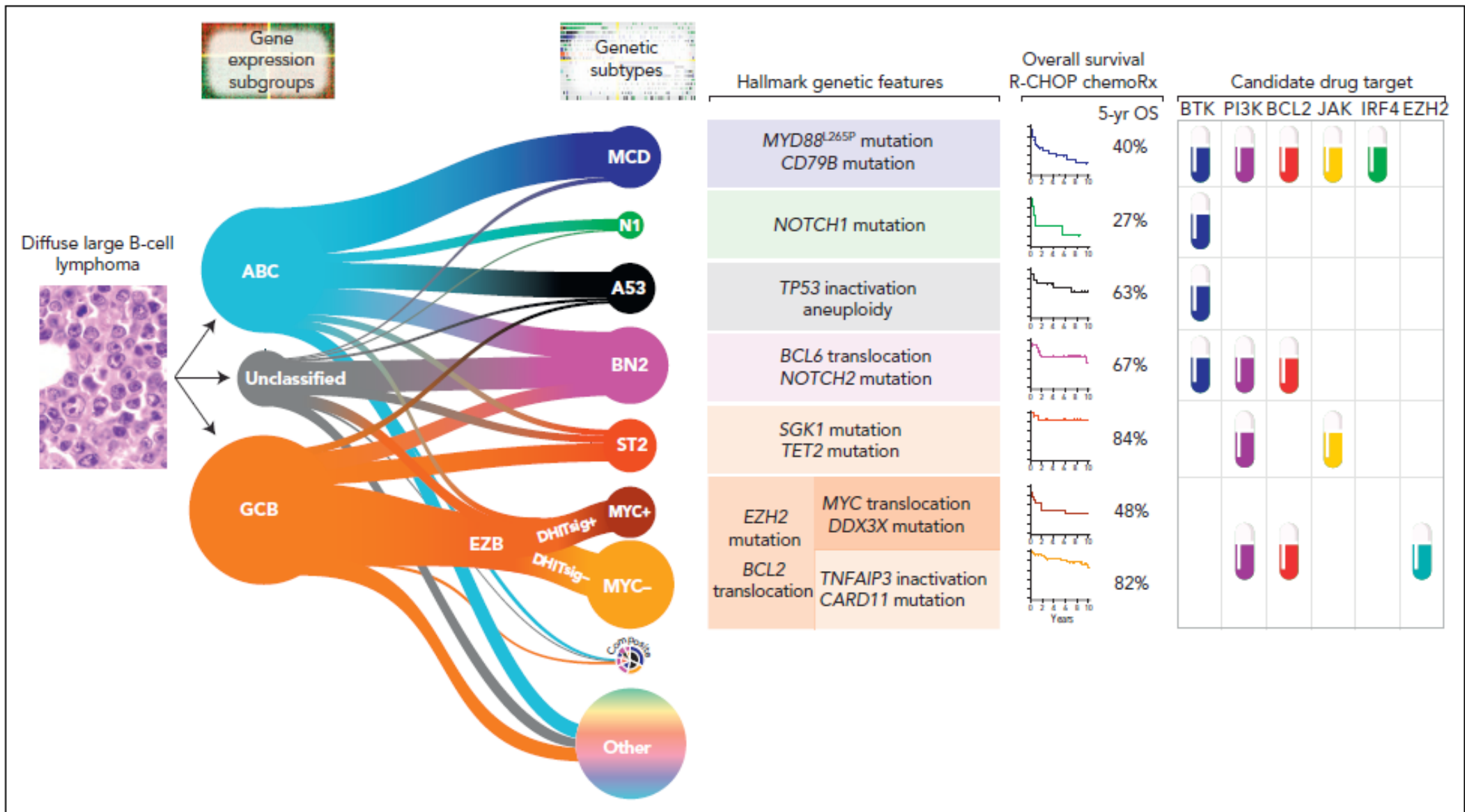
Molecular subclassification

A Probabilistic Classification Tool for Genetic Subtypes of Diffuse Large B Cell Lymphoma with Therapeutic Implications

George W. Wright,¹ Da Wei Huang,² James D. Phelan,² Zana A. Coulibaly,² Sandrine Roulland,² Ryan M. Young,² James Q. Wang,² Roland Schmitz,² Ryan D. Morin,³ Jeffrey Tang,³ Aixiang Jiang,³ Aleksander Bagaev,⁴ Olga Plotnikova,⁴ Nikita Kotlov,⁴ Calvin A. Johnson,⁵ Wyndham H. Wilson,² David W. Scott,⁶ and Louis M. Staudt^{2,7,*}

- Proposed molecular subclassification of DLBCL (3 independent studies)
- Diffuse large B cell lymphoma (DLBCL) consists of seven genetic subtypes

LymphGen	Modified HMRN	Harvard	Main Genetic Alterations	COO	Clinical Outcome	Related Lymphoma
MCD	MYD88	C5	<i>MYD88</i> ^{L265P} , <i>CD79B</i> , <i>PIM1</i> , <i>ETV6</i> , <i>CDKN2A</i>	ABC	Poor	Primary CNS lymphoma, Primary testis lymphoma
EZB	BCL2	C3	<i>BCL2</i> -R, <i>EZH2</i> , <i>CREBBP</i> , <i>KMT2D</i> , <i>TNFRSF14</i>	GCB	Good	Follicular lymphoma
EZB-MYC+	BCL2-MYC				Poor	Double hit lymphoma
BN2	NOTCH2	C1	<i>BCL6</i> -R, <i>NOTCH2</i> , <i>BCL10</i> , <i>SPEN</i> , <i>CD70</i> , <i>TNFAIP3</i>	ABC, GCB, UC	Intermediate	Marginal zone lymphoma
ST2	TET2/SGK1	C4	<i>TET2</i> , <i>SGK1</i> , <i>KLHL6</i> , <i>BRAF</i>	GCB	Good	Nodular lymphocyte predominant Hodgkin lymphoma
	SOCS1/SGK1		<i>SOCS1</i> , <i>SGK1</i> , <i>CD83</i> , <i>NFKBIA</i> , <i>NFKBIE</i> , <i>STAT3</i>	GCB	Very good	Primary mediastinal B cell lymphoma
Other	NEC	C0				
N1	NOTCH1	NA	<i>NOTCH1</i> , <i>ID3</i>	ABC	Poor	Chronic lymphocytic leukaemia
A53	NA	C2	<i>TP53</i> , aneuploidy	Mixed	Intermediate	

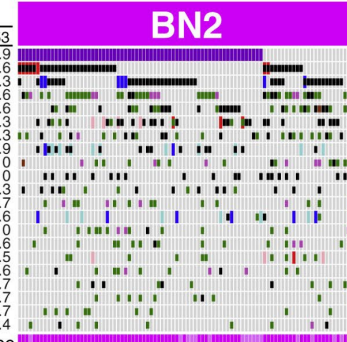


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2022

PMID: 36001803

Figure 3. Genetic subgroups of DLBCL illustrated using the LymphGen algorithm. The relationships between COO and the probabilistic assignments to genetics-based subgroups are shown. The size of the subgroup circles approximates the proportions of patients in each group, with the prevalence based on Schmitz et al,¹⁸⁵ adjusted for a population-based distribution of COO subgroups. Tumors assigned with high confidence to ≥ 2 subgroups are assigned to the composite group, while $\sim 37\%$ of tumors are not assigned to any subgroup with sufficient confidence (other). The hallmark genetic features are those frequent within that subgroup but are not required for that assignment. OS following R-CHOP chemoimmunotherapy along with inferred drug targets are shown. GCB, germinal center B-cell-like.

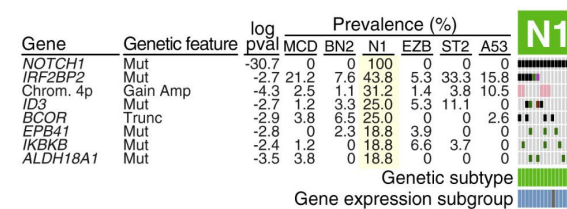
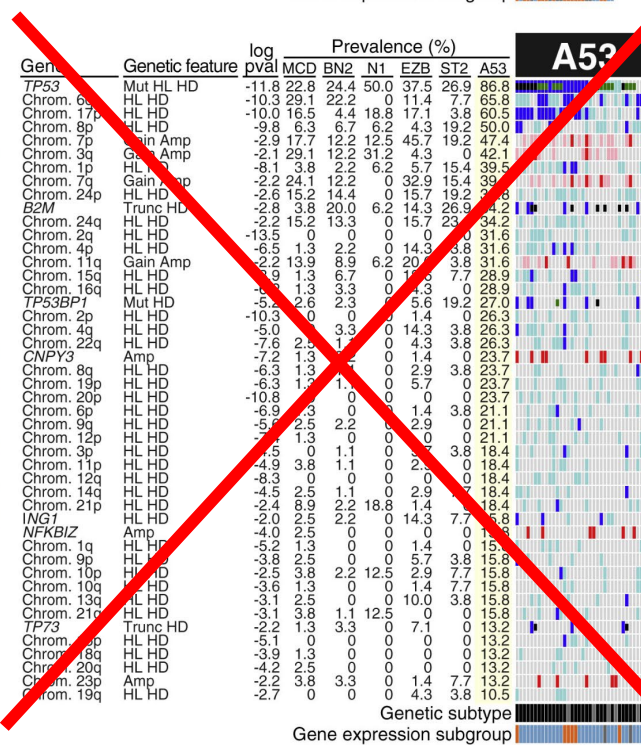
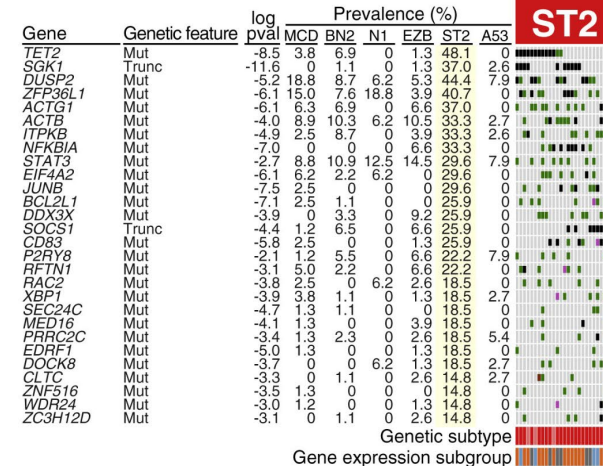
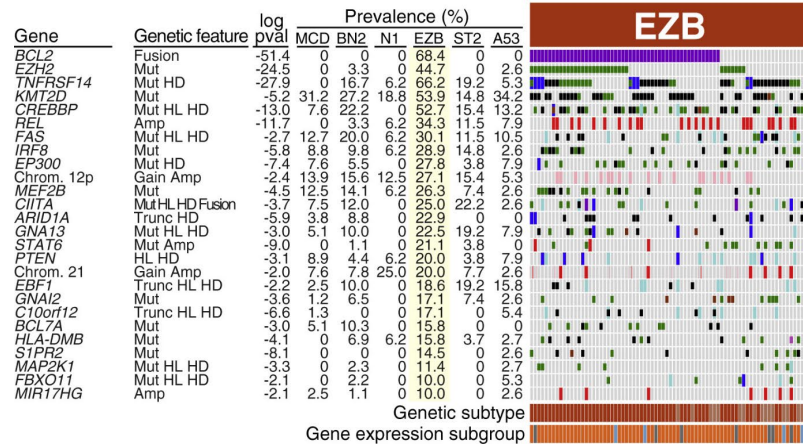
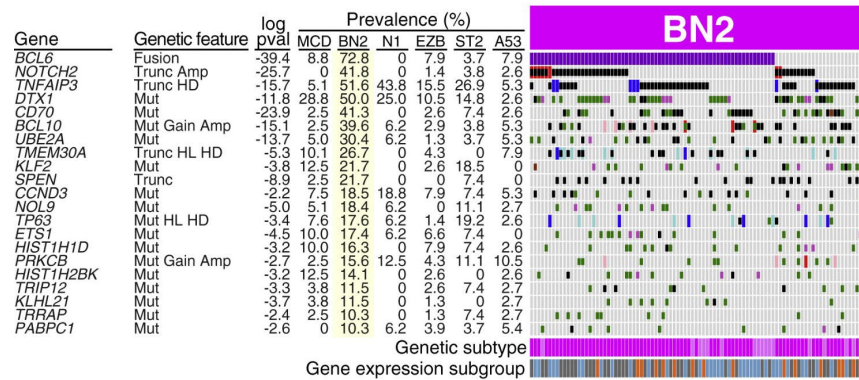
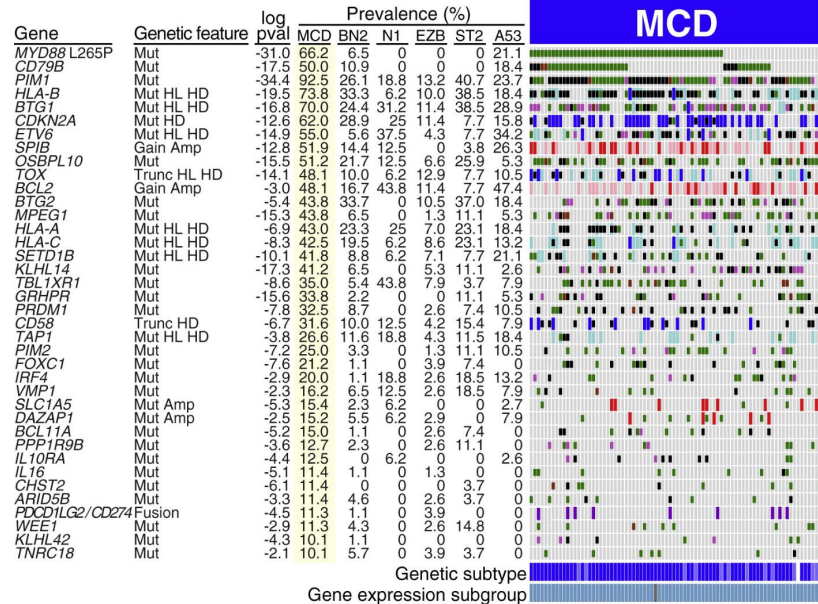
Gene	Genetic feature	log pval	Prevalence (%)						MCD
			MCD	BN2	N1	EZB	ST2	A53	
MYD88 L265P	Mut	-31.0	66.2	6.5	0	0	0	0	21.1
CD79B	Mut	-17.5	50.0	10.9	0	0	0	0	18.4
PIM1	Mut	-34.4	92.5	26.1	18.8	13.2	40.7	7.7	23.7
HLA-B	Mut HL HD	-19.5	73.8	33.3	6.2	10.0	38.5	18.4	
BTG1	Mut HL HD	-16.8	70.0	24.4	31.2	11.4	38.5	28.9	
CDKN2A	Mut HD	-12.6	62.0	28.9	25	11.4	7.7	15.8	
ETV6	Mut HL HD	-14.9	55.0	5.6	37.5	4.3	7.7	34.2	
SP1B	Gain Amp	-12.8	51.9	14.4	12.5	0	3.8	26.3	
OSBPL10	Mut	-15.5	51.2	21.7	12.5	0	25.9	5.3	
TOX	Trunc HL HD	-14.1	48.1	10.0	6.0	12.9	7.7	10.5	
BCL2	Gain Amp	-3.0	48.1	16.7	43.8	11.4	7.7	47.4	
BTG2	Mut	-5.4	43.8	33.7	0	10.5	37.0	18.4	
MPEG1	Mut	-15.3	43.8	6.5	0	1.3	11.1	5.3	
HLA-A	Mut HL HD	-6.9	43.0	23.3	25	7.0	23.1	18.4	
HLA-C	Mut HL HD	-8.3	42.5	19.5	6.2	8.6	23.1	13.2	
SETD1B	Mut HL HD	-10.1	41.8	8.8	6.2	7.1	7.7	21.1	
KLHL14	Mut	-17.3	41.2	6.5	0	5.3	11.1	2.6	
TBL1XR1	Mut	-8.6	35.0	5.4	43.8	7.9	3.7	7.9	
GRHPR	Mut	-15.6	33.8	2.2	0	0	11.1	5.3	
PRDM1	Mut	-7.8	32.5	8.7	0	2.6	7.4	10.5	
CD58	Trunc HD	-6.7	31.6	10.0	12.5	4.2	15.4	7.9	
TPA1	Mut HL HD	-3.8	26.6	11.6	18.8	4.3	11.5	18.4	
PIM2	Mut	-7.7	25.0	3.3	6.2	0	11.1	10.5	
FOXC1	Mut	-7.6	21.2	1.1	0	3.9	7.4	0	
IRF4	Mut	-2.9	20.0	1.1	18.8	2.6	18.5	13.2	
VMP1	Mut	-2.3	16.2	6.5	12.5	2.6	18.5	7.9	
SLC1A5	Mut Amp	-5.3	15.4	2.3	6.2	0	0	2.7	
DAZAP1	Mut Amp	-2.5	15.2	5.5	6.2	0	0	7.9	
BCL11A	Mut	-5.5	15.0	1.1	0	2.6	7.4	0	
PPP1R9B	Mut	-3.6	12.7	2.3	0	2.6	11.1	0	
IL10RA	Mut	-4.4	12.5	0	6.2	0	0	2.6	
IL16	Mut	-5.1	11.4	1.1	0	1.3	0	0	
CHST2	Mut	-6.1	11.4	0	0	0	3.7	0	
ARID5B	Mut	-3.3	11.4	4.6	0	2.6	3.7	0	
POU1LG2/CD274	Fusion	-4.5	11.3	1.1	0	3.9	0	0	
WEE1	Mut	-2.9	11.3	4.3	0	2.6	14.8	0	
KLHL42	Mut	-4.3	10.1	1.1	0	0	0	0	
TNRC18	Mut	-2.1	10.1	5.7	0	3.9	3.7	0	
Genetic subtype									
Gene expression subgroup									

Gene	Genetic feature	log pval	Prevalence (%)						
			MCD	BN2	N1	EZB	ST2	A53	
BCL6	Fusion	-39.4	8.8	72.8	0	7.9	3.7	7.9	
NOTCH2	Trunc Amp	-25.7	0	41.8	0	1.4	3.8	2.6	
TNFAIP3	Trunc HD	-15.7	5.1	51.6	43.8	15.5	26.9	5.3	
DTX1	Mut	-11.8	28.8	50.0	25.0	10.5	14.8	2.6	
CD70	Mut	-23.9	2.5	41.3	0	2.6	7.4	2.6	
BCL10	Mut Gain Amp	-15.8	13.0	41.3	0	2.6	3.8	3.3	
UBE2A	Mut	-13.7	5.0	30.4	6.2	1.3	3.7	5.3	
TMEM30A	Trunc HL HD	-5.3	10.1	26.7	0	4.3	0	7.9	
KLF2	Mut	-3.8	12.5	21.7	0	2.6	18.5	0	
SPEN	Trunc	-8.9	2.5	21.7	0	0	7.4	0	
CCND3	Mut	-2.2	7.5	18.5	18.8	7.9	7.4	5.3	
NOL9	Mut	-3.5	5.1	18.4	0	0	11.1	2.7	
TP63	Mut HL HD	-3.4	5.6	17.6	6.2	1.4	19.2	2.6	
ETS1	Mut	-4.5	10.0	17.4	6.2	6.6	7.4	0	
HIST1H1D	Mut	-3.2	10.0	16.3	0	7.9	7.4	2.6	
PRKCB	Mut Gain Amp	-2.7	2.5	15.6	12.5	4.3	11.1	10.5	
HIST1H2BK	Mut	-3.2	12.5	14.1	0	2.6	0	2.6	
TRIP12	Mut	-3.3	3.8	11.5	0	2.6	7.4	2.7	
KLHL21	Mut	-3.7	3.8	11.5	0	1.3	0	2.7	
TRRAP	Mut	-2.4	2.5	10.3	0	1.3	7.4	2.7	
PABPC1	Mut	-2.6	0	10.3	6.2	3.9	3.7	5.4	
Genetic subtype									
Gene expression subgroup									

Gene	Genetic feature	log pval	Prevalence (%)						
			MCD	BN2	N1	EZB	ST2	A53	
BCL2	Fusion	-51.4	0	0	0	68.4	0	0	EZB
EZH2	Mut	-24.5	0	3.3	0	44.7	0	2.6	
TNFRSF14	Mut HD	-27.9	0	16.7	6.2	66.2	19.2	5.3	
KMT2D	Mut	-5.2	31.2	27.2	18.8	53.9	14.8	34.2	
CREBBP	Mut HL HD	-13.0	7.6	22.2	0	19.2	15.4	13.2	
REL	Amp	-11.7	0	3.3	6.2	34.3	11.5	7.9	
FAS	Mut HL HD	-2.7	12.7	20.0	6.2	30.1	11.5	10.5	
IRF8	Mut	-5.8	8.8	9.8	6.2	28.9	14.8	2.6	
EP300	Mut HD	-7.4	7.6	5.5	0	27.8	3.8	7.9	
Chrom. 12p	Gain Amp	-2.4	13.9	15.6	12.5	27.1	15.4	5.3	
MEF2B	Mut	-4.5	12.5	14.1	6.2	26.3	7.4	2.6	
CIT4A	Mut HL HD Fusion	-3.7	7.5	12.0	0	25.0	22.2	2.6	
ARID1A	Trunc HD	-5.9	3.8	8.8	0	22.9	0	0	
GNA13	Mut HL HD	-3.0	5.1	10.0	0	22.5	19.2	7.9	
STAT6	Mut Amp	-9.0	0	1.1	0	21.1	3.8	0	
PTEN	HL HD	-3.1	8.9	4.4	6.2	20.0	3.8	7.9	
Chrom. 21	Gain Amp	-2.0	7.6	7.8	25.0	20.0	7.2	2.6	
EBF1	Trunc HL HD	-2.2	10.8	0	18.6	19.2	2.6	2.6	
GNAI2	Mut	-3.6	1.2	6.5	0	17.1	7.4	2.6	
C10orf12	Trunc HL HD	-6.6	1.3	0	0	17.1	0	5.4	
BCL7A	Mut	-3.0	5.1	10.3	0	15.8	0	0	
HLA-DMB	Mut	-4.1	0	6.9	6.2	15.8	3.7	2.7	
S1PR2	Mut	-8.1	0	0	0	14.5	0	2.6	
MAR2K1	Mut HL HD	-5.3	0	2.3	0	11.4	0	2.3	
FBXO11	Mut HL HD	-5.3	0	2.2	0	10.0	0	2.3	
MIR17HG	Amp	-2.1	2.5	1.1	0	10.0	0	2.6	
Genetic subtype									
Gene expression subgroup									

Gene	Genetic feature	log pval	Prevalence (%)						ST2
			MCD	BN2	N1	EZB	ST2	A53	
TET2	Mut	-8.5	3.8	6.9	0	1.3	48.1	0	
SGK1	Trunc	-11.6	0	1.1	0	1.3	37.0	2.6	
DUSP2	Mut	-5.5	18.8	6.7	6.2	5.3	34.4	7.9	
ZFP36L1	Mut	-6.1	15.0	7.6	18.8	3.9	40.7	0	
ACTG1	Mut	-6.1	6.3	6.9	0	6.6	37.0	0	
ACTB	Mut	-4.0	8.9	10.3	6.2	10.5	33.3	2.7	
ITPKB	Mut	-4.9	2.5	8.7	0	3.9	33.3	2.6	
NFKBIA	Mut	-7.0	0	0	0	6.6	33.3	0	
STAT3	Mut	-2.7	8.8	10.9	12.5	14.5	29.6	7.0	
EIF4A2	Mut	-6.1	6.2	2.2	6.2	0	29.6	0	
JUNB	Mut	-7.5	2.5	0	0	0	29.6	0	
BCL2L1	Mut	-7.1	2.5	1.1	0	0	25.9	0	
DDX3X	Mut	-3.9	0	3.3	0	9.2	25.9	0	
SOC3	Trunc	-4.4	1.2	6.5	0	6.6	25.9	0	
CD83	Mut	-5.8	2.5	0	0	1.3	25.9	0	
P2RY8	Mut	-2.1	1.2	5.5	0	6.6	22.2	7.9	
RFTN1	Mut	-3.1	5.0	2.2	0	6.6	22.2	0	
RAC2	Mut	-3.8	2.5	0	6.2	2.6	18.5	0	
XBP1	Mut	-3.9	3.8	1.1	0	1.3	18.5	2.7	
SEC24C	Mut	-4.7	1.3	1.1	0	0	18.5	0	
MED16	Mut	-4.1	1.3	0	0	3.9	18.5	0	
PRRC2C	Mut	-3.4	1.3	2.3	0	2.6	18.5	5.4	
EDRF1	Mut	-5.0	1.3	0	0	1.3	18.5	0	
DOCK8	Mut	-6.0	1.1	0	6.2	1.3	18.5	2.7	
CLTC	Mut	-3.3	0	1.1	0	2.6	14.8	2.7	
ZNF516	Mut	-3.5	1.3	0	0	0	14.8	0	
WDR24	Mut	-3.0	1.2	0	0	1.3	14.8	0	
ZC3H12D	Mut	-3.1	0	1.1	0	2.6	14.8	0	
Genetic subtype									
Gene expression subgroup									

Gene	Genetic feature	log pval	Prevalence (%)						
			MCD	BN2	N1	EZB	ST2	A53	
TP53	Mut HL HD	-11.8	22.8	24.4	50.0	37.5	26.9	86.8	
Chrom. 6q	HL HD	-10.3	29.1	22.2	0	11.4	7.7	65.8	
Chrom. 17p	HL HD	-10.0	16.5	4.4	18.8	17.1	3.8	60.5	
Chrom. 8p	HL HD	-9.9	6.3	4.3	19.2	50.0	0	50.0	
Chrom. 7p	Gain Amp	-2.9	17.7	12.2	12.5	45.7	19.2	47.4	
Chrom. 3q	Gain Amp	-2.1	29.1	12.2	31.2	4.3	0	42.1	
Chrom. 1p	HL HD	-8.1	3.8	2.2	6.2	5.7	15.4	39.5	
Chrom. 7q	Gain Amp	-2.2	24.1	12.2	0	32.9	15.4	39.5	
Chrom. 24p	HL HD	-2.6	15.2	14.4	0	15.7	19.2	36.8	
B2M	Trunc HD	-5.9	3.8	20.0	6.2	14.3	26.9	34.2	
Chrom. 24q	HL HD	-2.5	15.2	13.3	15.7	23.3	2.2	47.2	
Chrom. 2q	HL HD	-13.5	0	0	0	0	0	31.6	
Chrom. 4q	HL HD	-6.5	1.3	2.2	0	14.3	3.8	31.6	
Chrom. 11q	Gain Amp	-2.2	13.9	8.9	6.2	20.0	3.8	31.6	
Chrom. 15q	HL HD	-3.9	1.3	6.7	0	18.6	7.7	28.9	
Chrom. 16q	HL HD	-6.6	1.3	3.3	0	4.3	2.2	28.9	
TP53BP1	Mut HD	-2.2	2.6	2.2	0	0	19.2	28.9	
Chrom. 2p	HL HD	-10.3	0	0	0	1.4	0	26.3	
Chrom. 4q	HL HD	-5.0	0	3.3	0	14.3	3.8	26.3	
Chrom. 22q	HL HD	-7.6	2.5	1.1	0	4.3	3.8	26.3	
CNPY3	Amp	-7.2	1.3	2.2	0	1.4	0	23.7	
Chrom. 8q	HL HD	-6.3	1.3	1.1	0	2.9	3.8	23.7	
Chrom. 13p	HL HD	-6.3	1.3	1.1	0	0	0	23.7	
Chrom. 20p	HL HD	-10.8	0	0	0	5.7	0	23.7	
Chrom. 6p	HL HD	-6.9	1.3	0	0	1.4	3.8	21.1	
Chrom. 9q	HL HD	-5.6	2.5	2.2	0	2.9	0	21.1	
Chrom. 12p	HL HD	-7.4	1.3	0	0	0	0	21.1	
Chrom. 3p	HL HD	-4.9	0	1.1	0	5	3.8	18.4	
Chrom. 11p	HL HD	-4.9	3.8	1.1	0	2.9	0	18.4	
Chrom. 12q	HL HD	-8.3	0	0	0	0	0	18.4	
Chrom. 14q	HL HD	-4.5	2.5	1.1	0	2.9	7.7	18.4	
Chrom. 21p	HL HD	-2.4	8.9	2.2	18.8	1.4	0	18.4	
ING1	HL HD	-2.0	2.5	2.2	0	14.3	7.7	15.8	
NFKBIZ	Amp	-4.2	2.5	0	0	0	1.4	15.8	
Chrom. 1q	HL HD	-4.2	2.5	0	0	1.4	0	15.8	
Chrom. 9p	HL HD	-3.8	2.5	0	0	5.7	3.8	15.8	
Chrom. 10p	HL HD	-2.5	3.8	2.2	12.5	2.9	7.7	15.8	
Chrom. 10q	HL HD	-3.6	1.3	0	0	1.4	7.7	15.8	
Chrom. 13q	HL HD	-3.1	2.5	0	0	10.0	3.8	15.8	
Chrom. 21q	HL HD	-1.1	3.8	1.1	12.5	0	0	15.8	
TP73	Trunc HD	-2.2	1.3	3.3	0	7.7	0	13.2	
Chrom. 16p	HL HD	-5.1	0	0	0	0	0	13.2	
Chrom. 18q	HL HD	-3.9	1.3	0	0	0	0	13.2	
Chrom. 20q	HL HD	-4.2	2.5	0	0	0	0	13.2	
Chrom. 23p	Amp	-2.2	3.8	3.3	0	1.4	7.7	13.2	
Chrom. 19q	HL HD	-2.7	0	0	0	4.3	3.8	10.5	
Genetic subtype									
Gene expression subgroup									

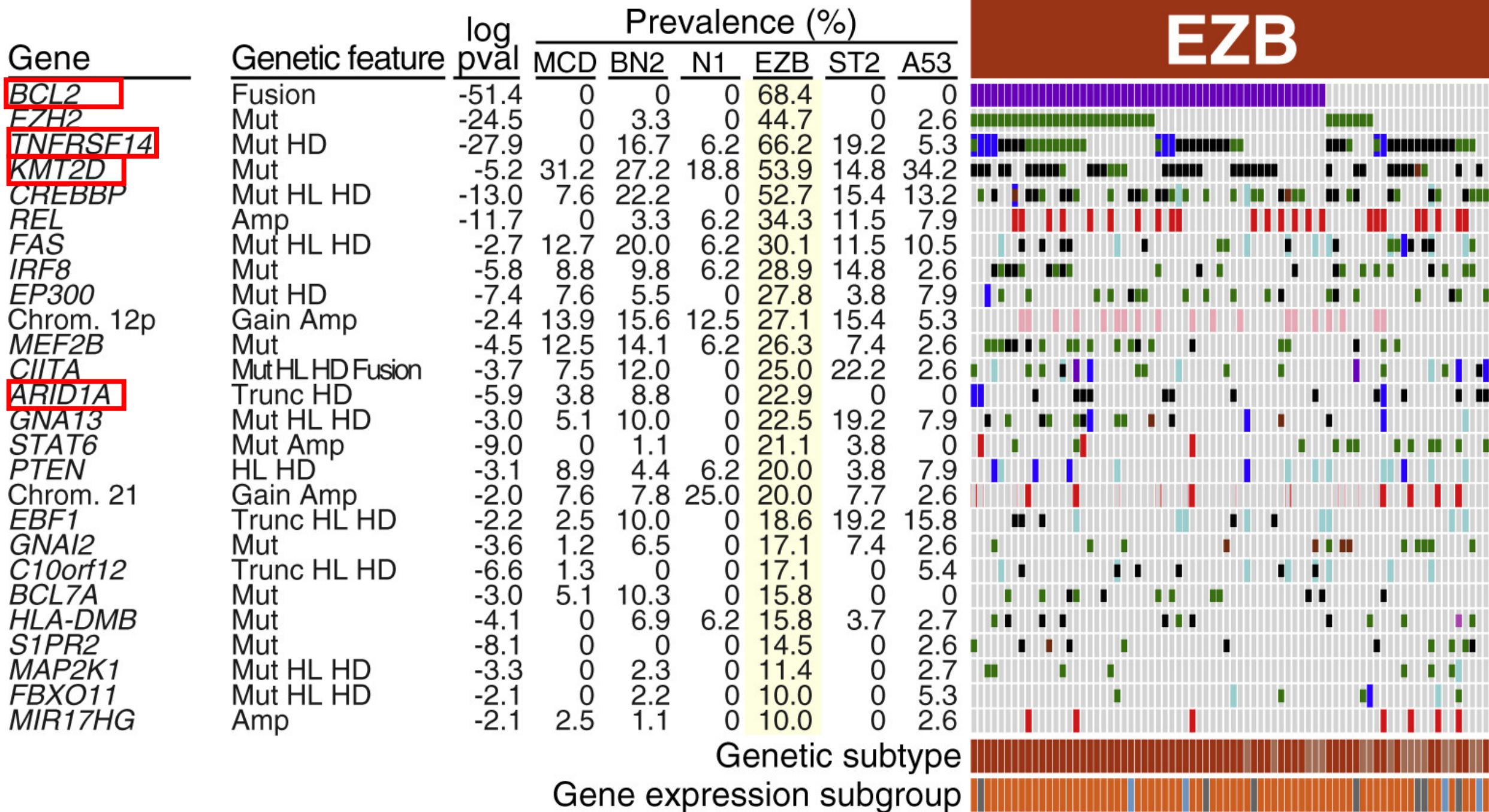


B-cell lymphoma NGS Results

- Pathogenic mutations detected:
 1. **B2M**: c.289G>T; p.Glu97* (81%)
 2. **KMT2D**: c.11800C>T; p.Gln3934* (55%)
 3. **TP53**: c.376-2_382delinsCCT; p.? (67%)
- Variants of unknown clinical significance detected:
 1. **ARID1A**: c.4918A>G; p.Thr1640Ala (13%)
 2. **ATM**: c.4564G>C; p.Gly1522Arg (3%)
 3. **BCL2**: Multiple variants in **BCL2** were detected (NM_000633.2)
 - c.-2G>A; p.? (24%)
 - c.66_67delinsAT; p.Lys22_Leu23= (48%)
 - c.95C>T; p.Ala32Val (48%)
 - c.103G>A; p.Val35Met (48%)
 - c.175C>G; p.Pro59Ala (52%)
 - c.179C>T; p.Ala60Val (25%)
 - c.386G>A; p.Arg129His (8%)
 - c.403G>A; p.Glu135Lys (26%)
 - c.493G>A; p.Glu165Lys (54%)
 4. **KMT2D**: c.176+3A>T; p.? (31%)
 5. **PIM1**: c.140G>C; p.Ser47Thr (29%)
 6. **TNFRSF14**: c.325C>T; p.Arg109Trp (80%)

Using the LymphGen Tool (2.0)

- 98% confidence that this belonged to the



Gene	Genetic feature	log pval	Prevalence (%)						A53
			MCD	BN2	N1	FZB	ST2	A53	
TP53	Mut HL HD	-11.8	22.8	24.4	50.0	37.5	26.9	86.8	
Chrom. 6q	HL HD	-10.3	29.1	22.2	0	11.4	7.7	65.8	
Chrom. 17p	HL HD	-10.0	16.5	4.4	18.8	17.1	3.8	60.5	
Chrom. 8p	HL HD	-9.8	6.3	6.7	6.2	4.3	19.2	50.0	
Chrom. 7p	Gain Amp	-2.9	17.7	12.2	12.5	45.7	19.2	47.4	
Chrom. 3q	Gain Amp	-2.1	29.1	12.2	31.2	4.3	0	42.1	
Chrom. 1p	HL HD	-8.1	3.8	2.2	6.2	5.7	15.4	39.5	
Chrom. 7q	Gain Amp	-2.2	24.1	12.2	0	32.9	15.4	39.5	
Chrom. 24p	HL HD	-2.6	15.2	14.4	0	15.7	19.2	36.8	
B2M	Trunc HD	-2.8	3.8	20.0	6.2	14.3	26.9	34.2	
Chrom. 24q	HL HD	-2.2	15.2	13.3	0	15.7	23.1	34.2	
Chrom. 2q	HL HD	-13.5	0	0	0	0	0	31.6	
Chrom. 4p	HL HD	-6.5	1.3	2.2	0	14.3	3.8	31.6	
Chrom. 11q	Gain Amp	-2.2	13.9	8.9	6.2	20.0	3.8	31.6	
Chrom. 15q	HL HD	-3.9	1.3	6.7	0	18.6	7.7	28.9	
Chrom. 16q	HL HD	-6.2	1.3	3.3	0	4.3	0	28.9	
TP53BP1	Mut HD	-5.2	2.6	2.3	0	5.6	19.2	27.0	
Chrom. 2p	HL HD	-10.3	0	0	0	1.4	0	26.3	
Chrom. 4q	HL HD	-5.0	0	3.3	0	14.3	3.8	26.3	
Chrom. 22q	HL HD	-7.6	2.5	1.1	0	4.3	3.8	26.3	
CNPY3	Amp	-7.2	1.3	2.2	0	1.4	0	23.7	
Chrom. 8q	HL HD	-6.3	1.3	1.1	0	2.9	3.8	23.7	
Chrom. 19p	HL HD	-6.3	1.3	1.1	0	5.7	0	23.7	
Chrom. 20p	HL HD	-10.8	0	0	0	0	0	23.7	
Chrom. 6p	HL HD	-6.9	1.3	0	0	1.4	3.8	21.1	
Chrom. 9q	HL HD	-5.6	2.5	2.2	0	2.9	0	21.1	
Chrom. 12p	HL HD	-7.4	1.3	0	0	0	0	21.1	
Chrom. 3p	HL HD	-4.5	0	1.1	0	5.7	3.8	18.4	
Chrom. 11p	HL HD	-4.9	3.8	1.1	0	2.9	0	18.4	
Chrom. 12q	HL HD	-8.3	0	0	0	0	0	18.4	
Chrom. 14q	HL HD	-4.5	2.5	1.1	0	2.9	7.7	18.4	
Chrom. 21p	HL HD	-2.4	8.9	2.2	18.8	1.4	0	18.4	
ING1	HL HD	-2.0	2.5	2.2	0	14.3	7.7	15.8	
NFKBIZ	Amp	-4.0	2.5	0	0	0	0	15.8	
Chrom. 1q	HL HD	-5.2	1.3	0	0	1.4	0	15.8	
Chrom. 9p	HL HD	-3.8	2.5	0	0	5.7	3.8	15.8	
Chrom. 10p	HL HD	-2.5	3.8	2.2	12.5	2.9	7.7	15.8	
Chrom. 10q	HL HD	-3.6	1.3	0	0	1.4	7.7	15.8	
Chrom. 13q	HL HD	-3.1	2.5	0	0	10.0	3.8	15.8	
Chrom. 21q	HL HD	-3.1	3.8	1.1	12.5	0	0	15.8	
TP73	Trunc HD	-2.2	1.3	3.3	0	7.1	0	13.2	
Chrom. 16p	HL HD	-5.1	0	0	0	0	0	13.2	
Chrom. 18q	HL HD	-3.9	1.3	0	0	0	0	13.2	
Chrom. 20q	HL HD	-4.2	2.5	0	0	0	0	13.2	
Chrom. 23p	Amp	-2.2	3.8	3.3	0	1.4	7.7	13.2	
Chrom. 19q	HL HD	-2.7	0	0	0	4.3	3.8	10.5	

Conclusion

- Molecular classification is expected to replace cell-of-origin subclassification
- LymphGen's results can inform the design and interpretation of clinical trials for DLBCL
- Currently, can be used for prognosis
- In the future, expected to affect management

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