Tumor protein 53 mutations are enriched in diffuse large B-cell lymphoma with irregular CD19 marker expression

Authors and Affiliations

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Supplementary Table S1: Primary antibodies and criteria for interpreting staining for immunohistochemistry analyses.

Marker	Clone	Supplier	Staining interpretation (positive)
BCL2	124	Dako	>30% [1]
BCL6	PG-B6p	Dako	>50% [1]
BCL10	151	Dako	>20% nuclear [2]
CD19	LE-CD19	Dako	>30%
CD20	L26	Dako	>30% [3]
CD138	B-A38	Cell Marque	>25%[4]
c-MYC	Ep121	Cell Marque	>40% [5]
MUM1	MRQ-8	Cell Marque	>40% [6]
PAX5	24	Cell Marque	>50% [1]
TP53	DO-7	Dako	>50% [7]

Dako, Glostrup, Denmark; Cell Marque Corporation, Rocklin, CA, U S A).

Supplementary Table S2: Primer sequences using to amplify *TP53* exons.

Exon	Forward Primers	Reverse primers
1	5'-CTTGTCATGGCGACTGTCCAG-3'	5'-CGAGAGCCCGTGACTCAGAGAG-3'
2	5'-CAGGTGACCCAGGGTTGGAAG-3'	5'-GCCTGCCCTTCCAATGGATG-3'
3	5'-CAGAGACCTGTGGGAAGCGA-3'	5'-CAGGTCCCCAGCCCTCCAGG-3'
4	5'-CAACGTTCTGGTAAGGACAAG -3' 5'- CGATATTGAACAATGGTTCA -3'	5'- GGCATTCTGGGAGCTTCATC -3' 5'- CATTGAAGTCTCATCCAAG -3'
5	5'-CTTGTGCCCTGACTTTCAACTCTG -3' 5'-GTGCAGCTGTGGGTTGATTCC -3'	5'-CTGCTTGTAGATGGCCATGG -3' 5'- GACCCTGGGCAACCAGCCCT -3'
6	5'-CGACAGGGCTGGTTGCCCAG -3'	5'-CTCCCAGAGACCCCAGTTG -3'
7	5'-CAAGGCGCACTGGCCTCATCTTG -3'	5'-CAGGCCAGTGTGCAGGGTGG -3'
8	5'-AATGGGACAGGTAGGACCTG-3'	5'-CTGAGGCATAACTGCACCCT-3'
9	5'-AGGGTGCAGTTATGCCTCAG -3'	5'-CTGGAAACTTTCCACTTGATAAC -3'

10	5’-GTAGCTAACTAACTTCA GAAC -3’	5’-CAGGCTAGGCTAAGCTATGATG -3’
11	5’-AACTCAGGTACTGTGTAT ATAC-3’	5’-CCTATGGCTTTCCAACCTAG-3’
12	5’-CAGACCCTCTCACTCA TG TG -3’	5’CTGACGCACAGGTATTGCAAG-3’

Supplementary Table S3. Tumor and mutation details on the *TP53* mutations common to the to the amino acid positions substituted in either CD19 negative or positive DLBCL.

Cancer Study	Sample ID	Amino Acid Change	Type	AA change position common to DLBCL with CD19 status
Breast Invasive Carcinoma (BRCA)	TCGA-A1-A0SK-01	M133K	Missense	Negative
Head and Neck Squamous Cell Carcinoma (HNSC)	TCGA-CV-7415-01			
Breast Invasive Carcinoma (BRCA)	TCGA-A2-A3XV-01	C135F	Missense	
Lung Adenocarcinoma (LUAD)	TCGA-55-7573-01			

Stomach Adenocarcinoma (STAD)	TCGA-CD-5800-01			
Brain Lower Grade Glioma (LGG)	TCGA-RY-A845-01	L145P	Missense	
Bladder Urothelial Carcinoma (BLCA)	TCGA-DK-A1AB-01	E221*	Nonsense	Positive
Breast Invasive Carcinoma (BRCA)	TCGA-A7-A13D-01			
Liver Hepatocellular Carcinoma (LIHC)	TCGA-CC-A7IG-01			
Lung Squamous Cell Carcinoma (LUSC)	TCGA-22-5492-01			
Stomach Adenocarcinoma (STAD)	TCGA-CG-4477-01	E221Afs*2	Frameshift	
Stomach Adenocarcinoma (STAD)	TCGA-BR-8683-01	G226Afs*21	Frameshift	

Head and Neck Squamous cell carcinoma (HNSC)	TCGA-CV-7432-01	S240Gfs*20	Frameshift	
Bladder Urothelial Carcinoma (BLCA)	TCGA-DK-A3IS-01	S240Kfs*24	Frameshift	
Breast Invasive Carcinoma (BRCA)	TCGA-GM-A2DI-01	S261*	Nonsense	

Supplementary Table S4. List of Gene ontologies and Pathway downloaded from genesetdb [8] used to make the customize list of genes involved in differentiation.

Class	Set Name	Source DB	Gene #
GO	glial cell differentiation (GO:0010001)	GO_BP	15
GO	regulation of neuron differentiation (GO:0045664)	GO_BP	16
Pathway	Keratinocyte Differentiation	Biocarta	37
GO	macrophage differentiation (GO:0030225)	GO_BP	11
GO	negative regulation of neuron differentiation (GO:0045665)	GO_BP	47
GO	T cell differentiation (GO:0030217)	GO_BP	24
GO	keratinocyte differentiation (GO:0030216)	GO_BP	45
GO	neuron differentiation (GO:0030182)	GO_BP	81
GO	positive regulation of macrophage derived foam cell differentiation (GO:0010744)	GO_BP	14
GO	regulation of cell differentiation (GO:0045595)	GO_BP	24

GO	B cell differentiation (GO:0030183)	GO_BP	39
GO	mammary gland epithelial cell differentiation (GO:0060644)	GO_BP	13
GO	positive regulation of B cell differentiation (GO:0045579)	GO_BP	10
GO	epithelial cell differentiation (GO:0030855)	GO_BP	40
GO	positive regulation of cell differentiation (GO:0045597)	GO_BP	23

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