

# Clonal hematopoiesis in diffuse large B-cell lymphoma: clinical impact and genetic relatedness to lymphoma and therapy-related myeloid neoplasm

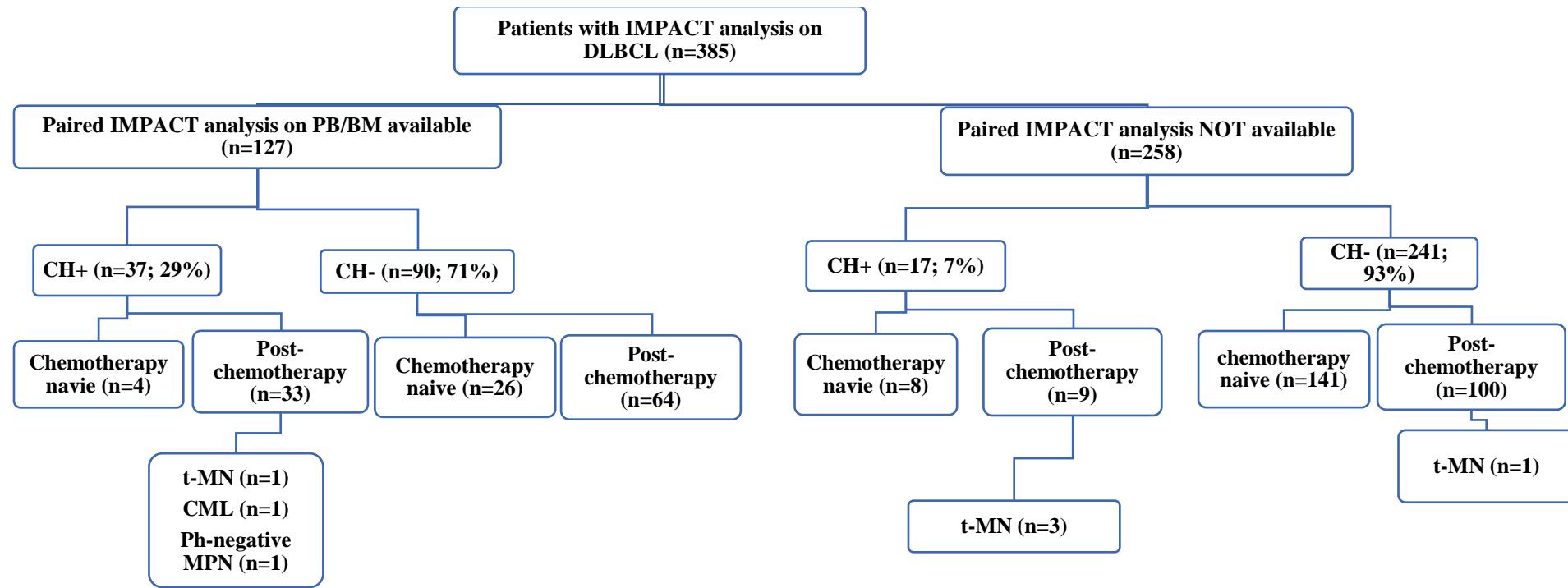
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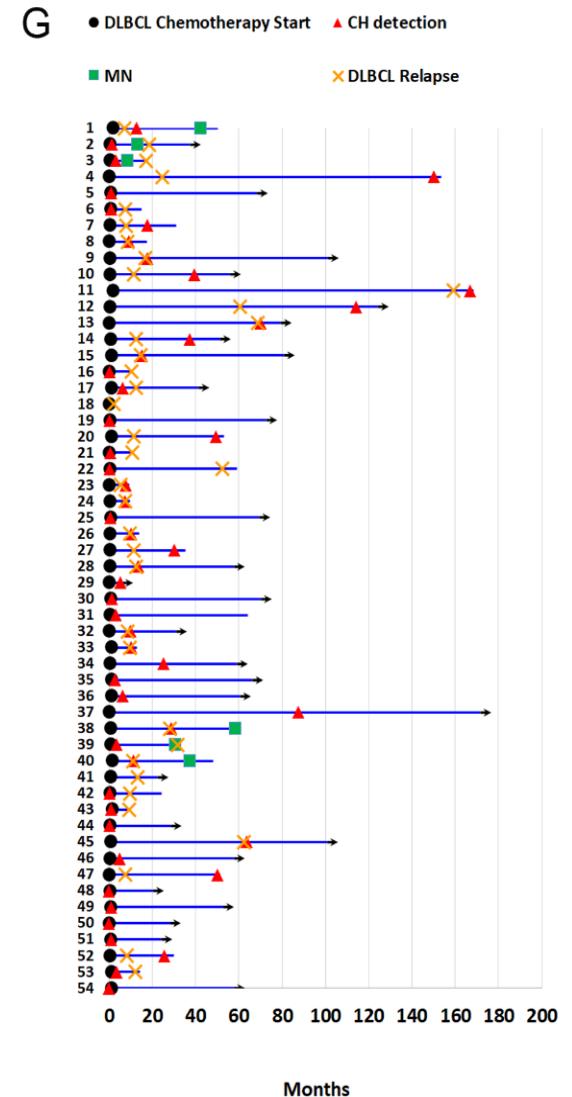
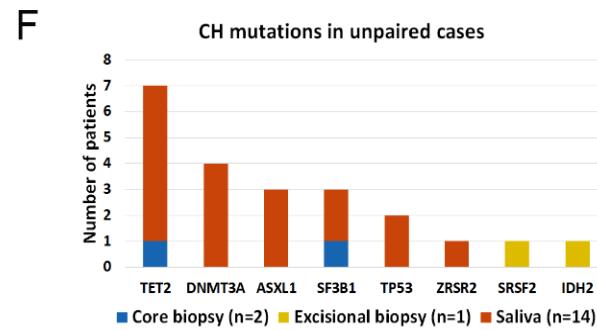
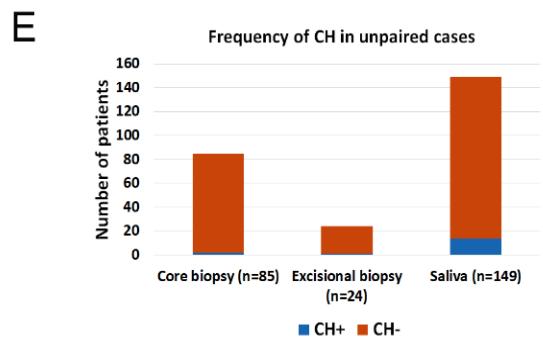
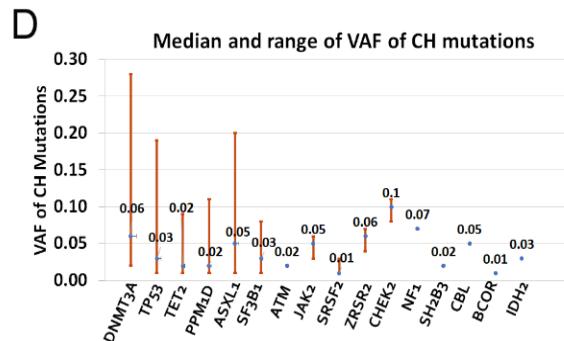
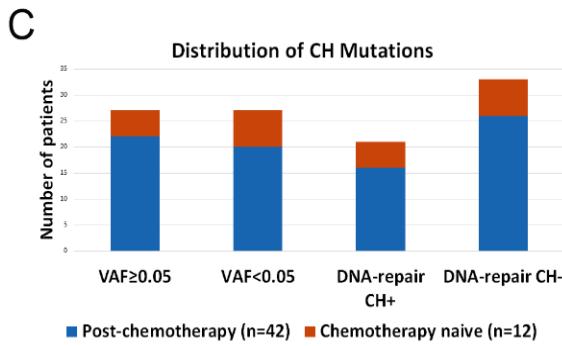
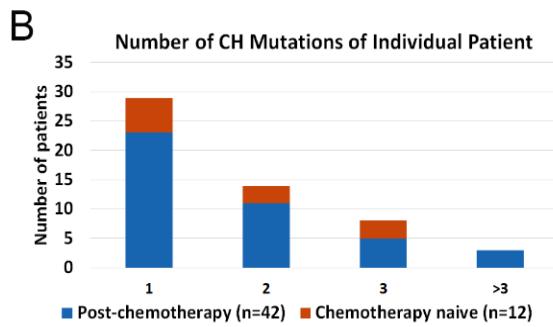
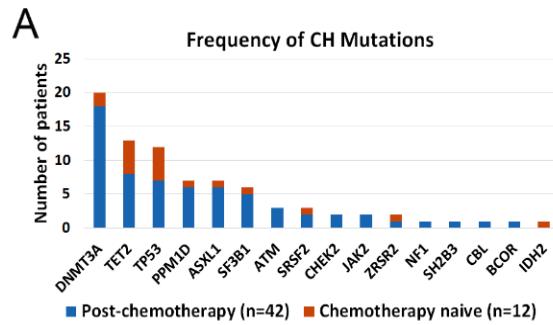
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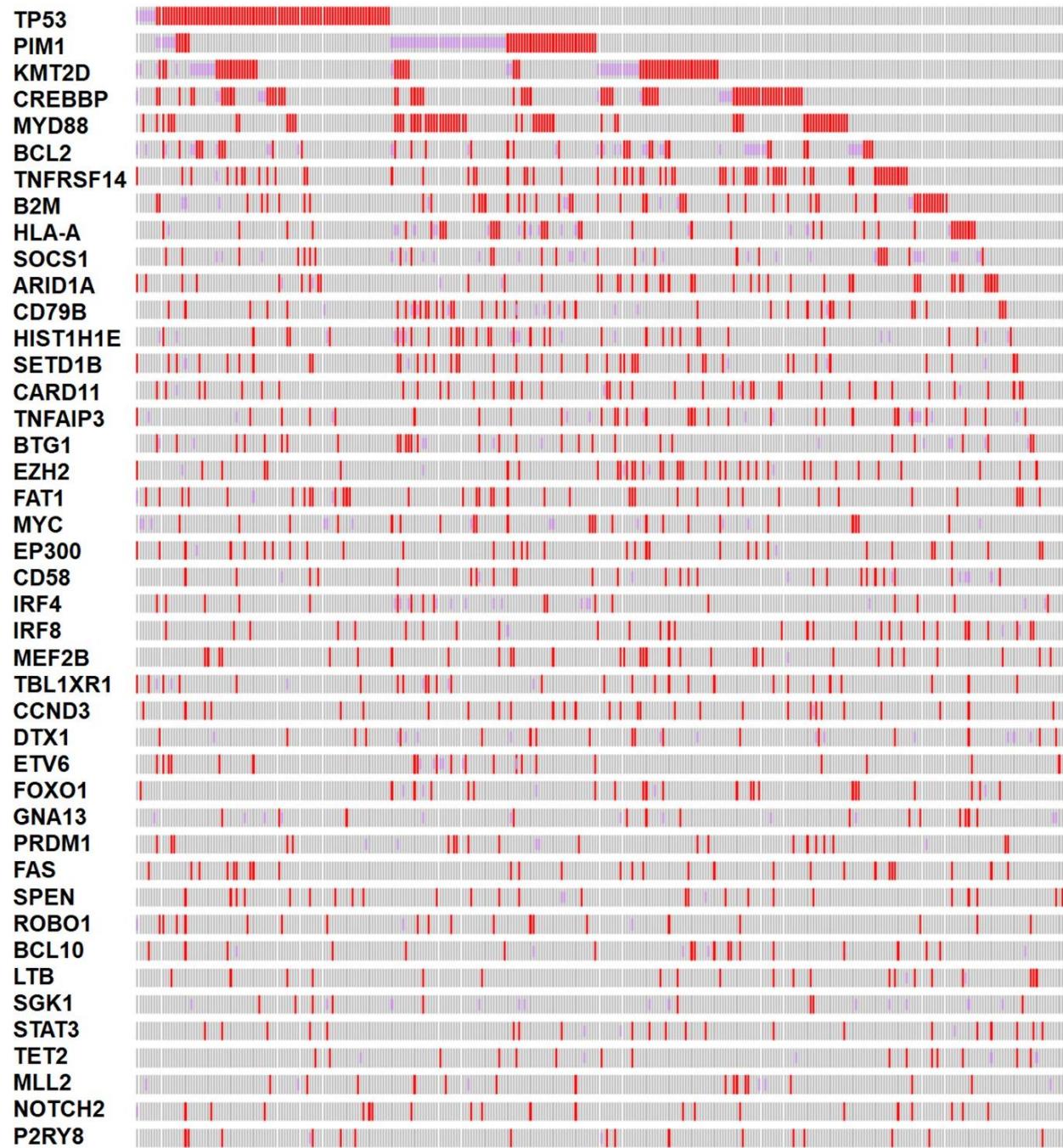
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**Supplementary Figure 1:** Distribution of CH, chemotherapy history and MN development of the cases included in the cohort.



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**Supplementary Figure 2. Characterization of CH mutations, swimmer plot of 54 CH+ patients and mutational profiles of DLBCL in CH- patients.** 2A. Frequency of CH mutations in entire cohort. 2B. Number of CH mutations in individual patients of entire cohort. 2C. Distribution of CH mutations in entire cohort. 2D. Median and range of VAFs of CH mutations in entire cohort. 2E. Frequency of CH mutations detected in lymphoma tissue (core or excisional biopsies) and/or saliva in patients without paired PB/BM analysis. No significant difference for CH assignment ( $p=0.1$ ) seen among sample types: core biopsy (2/85), excisional biopsy (1/24) and saliva (14/149). 2F. CH mutations detected in lymphoma tissue and saliva in patients without paired PB/BM analysis. 2G. Swimmer plot indicating the time points at which DLBCL chemotherapy was initiated, CH testing was performed, myeloid neoplasms were detected and occurrence of DLBCL relapse for the 54 CH+ patients. 2H: Mutational profiles of DLBCL of 331 CH- patients. Red: single mutation; Purple: double or multiple mutations.

**Supplementary Table 1.** Mutational profiles and VAF of CH and lymphoma clones

	MN	CH clones				Lymphoma clones		Evidence of Clonal relatedness
		CH Mutations	VAF (CH)	VAF (MN)	VAF (lymphoma)	Lymphoma Mutations	VAF	
<b>CH-</b>	t-MDS	TP53 p.R248Q	<0.005	0.97	<0.005	KMT2D, ATM, SH2B3, SETD1A, WHSC1	0.41-0.83	None
<b>CH+</b>	t-MDS	TP53 p.H179D	0.01	0.35	<0.005	MYD88, PIM1, CD79B, ARID5B, MSH6, HIST1H1E, SP140, TBL1XR1	0.27-0.35	None
	t-MDS	TET2 p.S1284F	0.02	0.31	0	KMT2D, BCL6, CDNK2A, CTCF, P2RY8	0.11-0.46	None
		KMD5C p.S1215L	0.03	0.07	0			
		TET2 p.K1094*	0.02	0.03	0			
		SF3B1 p.K666N	0.01	0.03	0			
	t-MDS	DNMT3A p.R326C	0.02	0.46	<0.005	KMT2D, SOCS1, DTX1, FOXO1, CYLD, STAT5A, ACTG1, TYK2, HIST1H1E, HIST1H1C	0.16-0.47	None
	t-AML	TP53 p.C141Y	0.01	0.03	<0.005	CDKN1B, MYD88, CD79B, PIM, IRF8	0.11-0.24	None

	CML	TET2 p.P1419H	0.03	0.51	<0.005	BCL6, MYC, PIM1, NOTCH2, SRSF2, EGFR, MDM2, DTX1, GNA13, PLCG2, FANCA	0.35-0.41	None
		TET2 p.A1341Gfs*3	0.02	0.45	<0.005			
		SF3B1 p.W658G	0.03	0.48	0			
	MPN	JAK2 p.V617F	0.06	0.48	0	TET2	0.44	None
		SF3B1 p.K666N	0.08	0.47	<0.005			