

Figure S1. Relative contribution of the most common base exchanges within our angioimmunoblastic T-cell lymphoma samples to the mutational profiles.

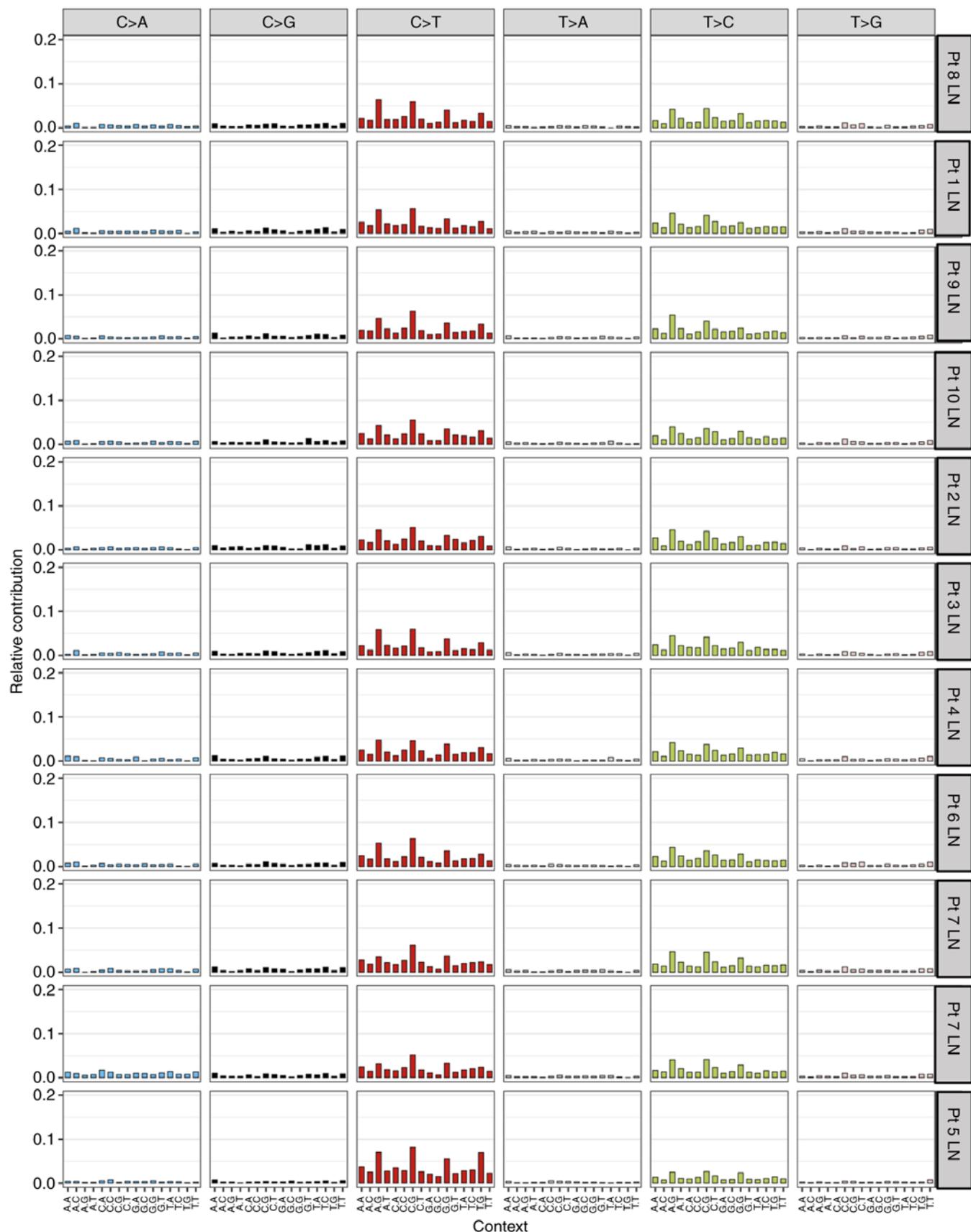


Figure S2. Kaplan-Meier survival plot of patients with angioimmunoblastic T-cell lymphoma. Red, EBV negative cases. Blue, EBV positive cases. EBV, Epstein Barr Virus; pos, positive; neg, negative.

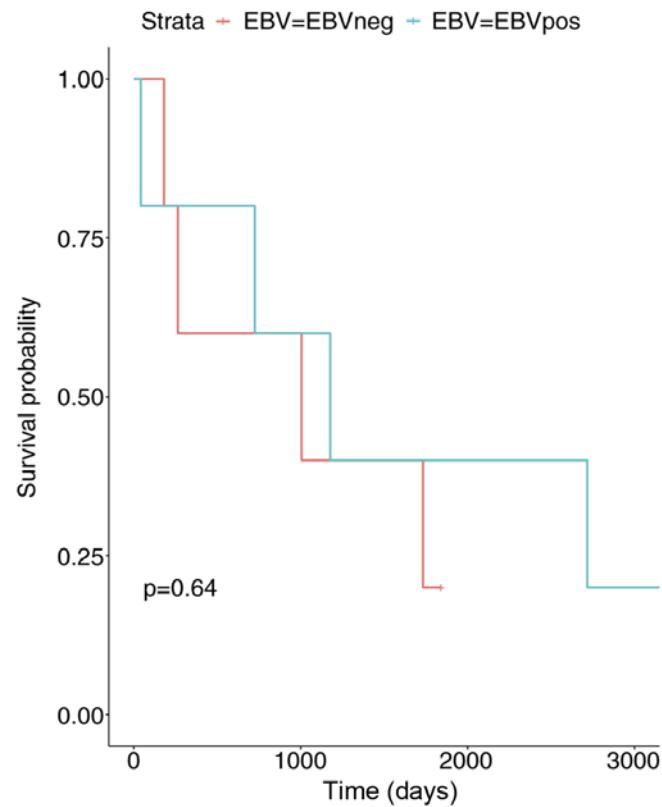


Figure S3. Principal component analysis of gene expression profile of angioimmunoblastic T-cell lymphoma. Shown is the PCA for *RHOA* mutational status and EBV infection status determined by NGS (see color key). EBV, Epstein Barr Virus; NGS, next generation sequencing; RHOA, ras homolog family member A.

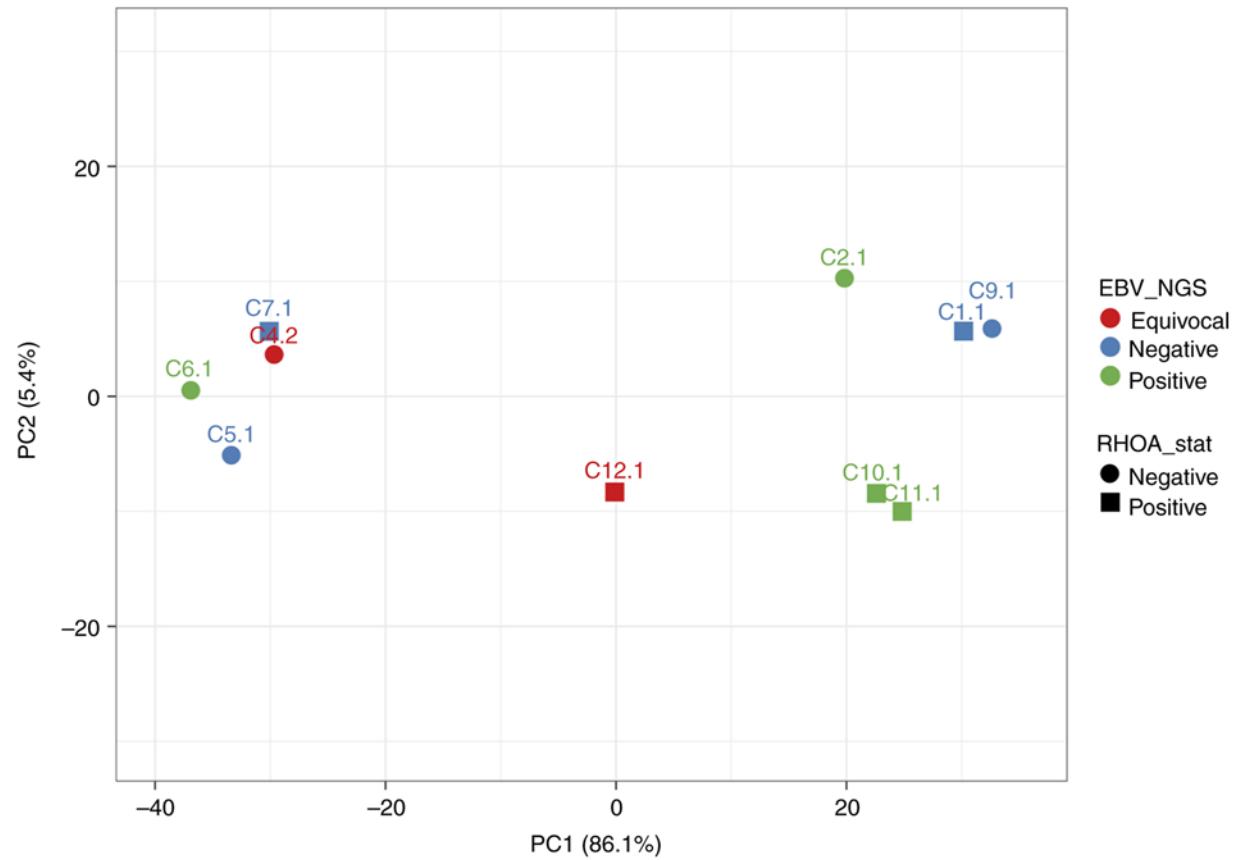


Figure S4. Heatmaps with hierarchical clustering by Euclidean distance for the relative contribution of cosmic signatures within the mutational pattern of angioimmunoblastic T-cell lymphoma cases. A, bone marrow tissues.

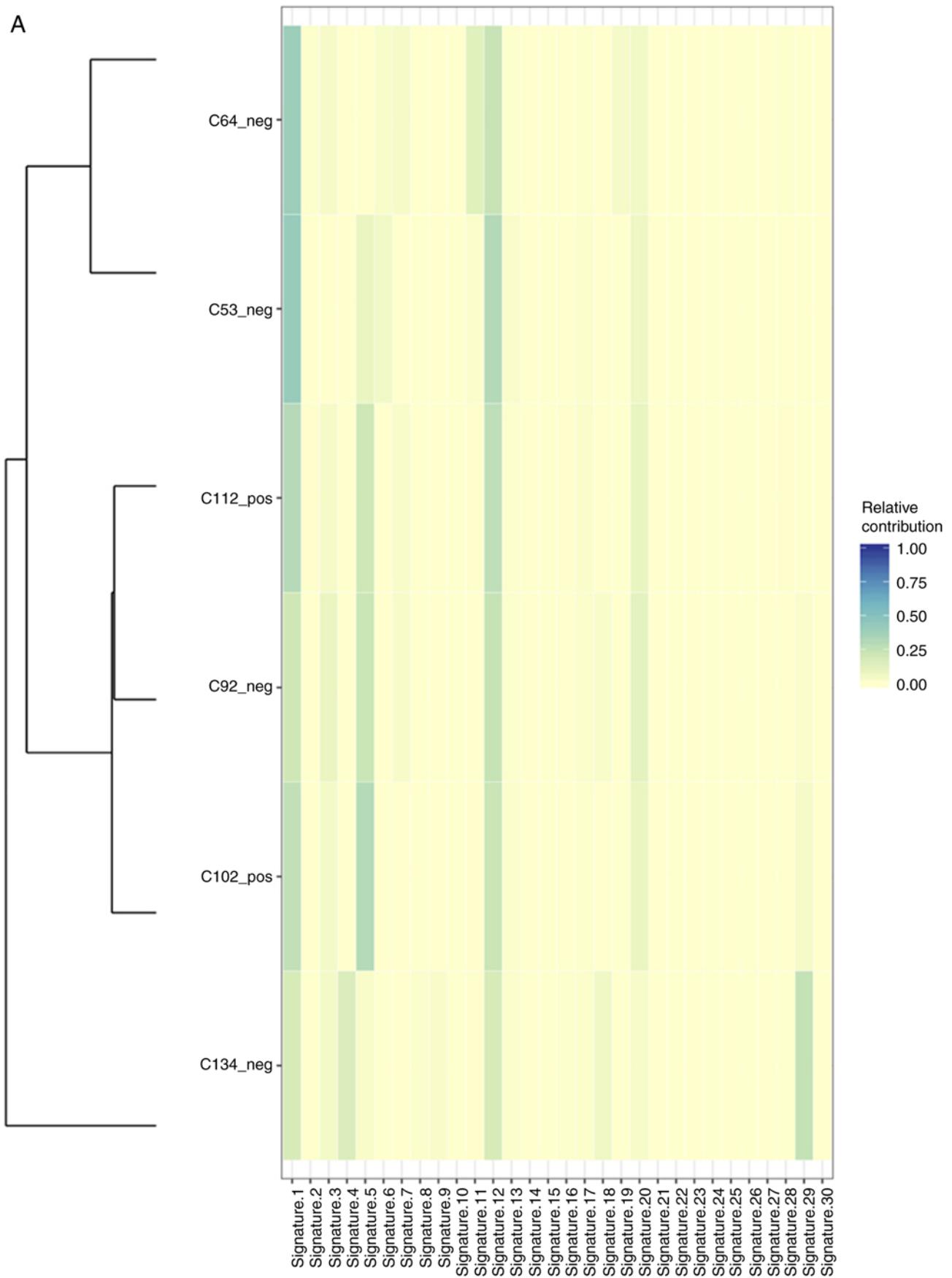


Figure S4 (Continued). Heatmaps with hierarchical clustering by Euclidean distance for the relative contribution of cosmic signatures within the mutational pattern of angioimmunoblastic T-cell lymphoma cases. B, lymph node tissues. Case numbers are tagged with ‘pos’ for *RHOA* positive mutational status and ‘neg’ for *RHOA* negative status. *RHOA*, ras homolog family member A.

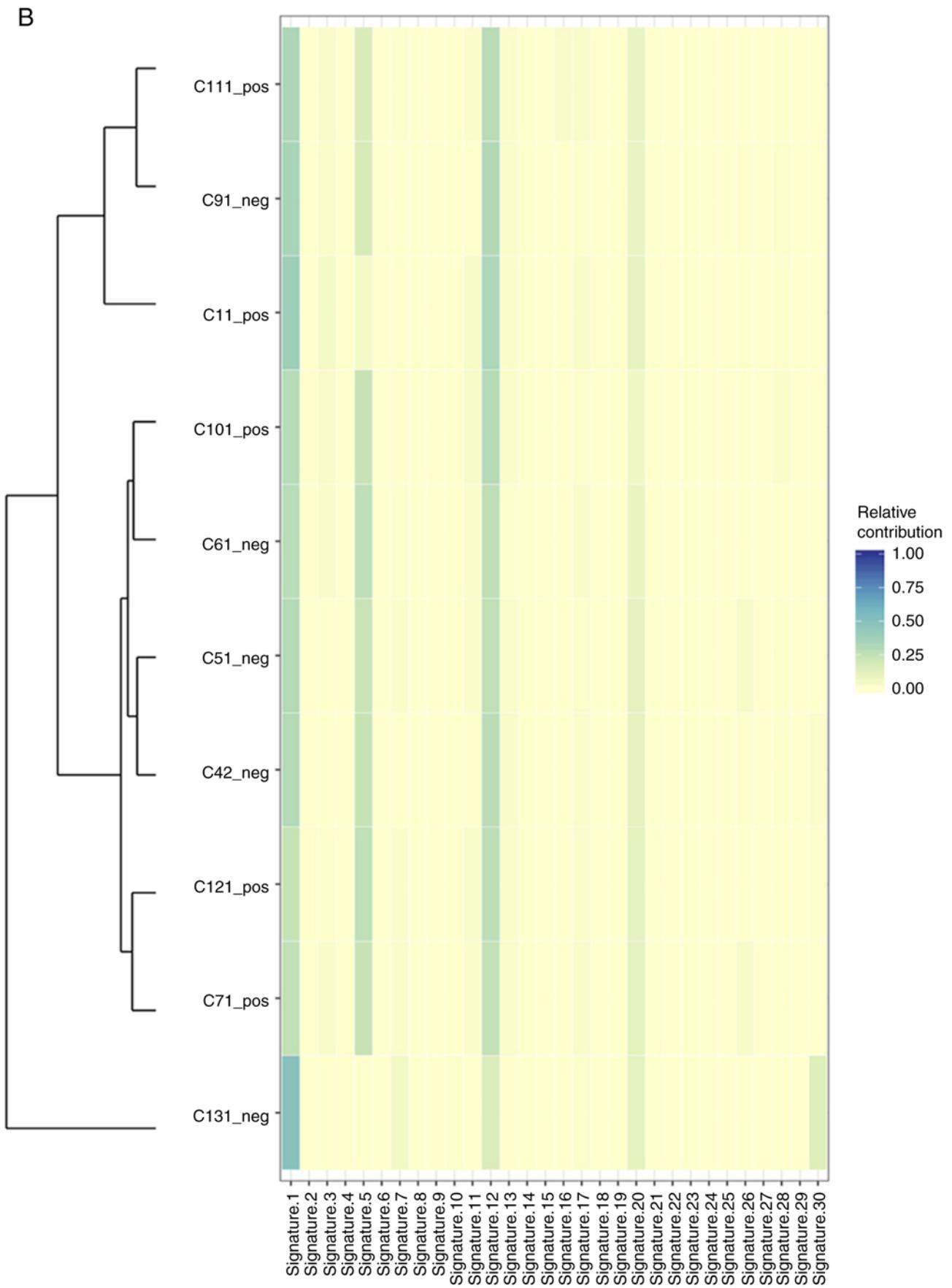


Table SI. Genes and microbes in Heme Malignancy Evaluation and Infectious Disease panel (HeME-ID).

ABL1	CCND2	DNAH5	GATA3	IRF4	MKL1	PHF6
ABL2	CCND3	DNAH9	GNA13	IRF8	MPL	PIGA
AKT1	CCR4	DNM2	GNAI2	IRS4	MSH4	PIK3CA
ALK	CCR7	DNMT1	GNAS	ITK	MSN	PIK3CD
ANKRD11	CD274/PDL1	DNMT3A	GNB1	JAK1	MTOR	PIK3R4
APLNR	CD28	DUSP22	GPRC5D	JAK2	MYC	PIK3R5
ARID1A	CD58	ECT2L	GRM1	JAK3	MYD88	PIM1
ARID1B	CD79A	EED	GTF2I	JAKMIP2	MYH11	PIM3
ARID2	CD79B	EIF4A1	HMCN1	KCNH5	MYH9	PLCG1
ARID5B	CDH10	ELN	HNRNPA1	KCNH8	NAV2	PLCG2
ASXL1	CDH11	EP300	HNRNPR	KDM6A	NCKAP5	PML
ASXL3	CDH18	EPHA8	HRAS	KDM6B	NCOR1	POLE
ATM	CDKN2A	EPHB3	HSD17B13	KIF23	NF1	POT1
ATP2B3	CDKN2B	EPHB4	ICOS	KIT	NFKB1	PRDM1
ATRX	CDKN2C	EPOR	ID3	KLF2	NFKB2	PRF1
B2M	CELSR2	EPS8	IDH1	KLHL6	NFKBIE	PRKCB
BANK1	CEPBA	ERBB4	IDH2	KMT2A	NKD1	PTEN
BCL11A	CHD2	ETNK1	IGHA1	KMT2C	NLRP12	PTPN1
BCL11B	CHD8	ETV6	IGHA2	KMT2D	NOL4	PTPN11
BCL2	CIITA	EZH2	IGHG1	KRAS	NOTCH1	PTPN2
BCL6	CNOT1	FAS	IGHG2	LAMB1	NOTCH2	PTPRM
BCOR	CNOT3	FAT1	IGHG3	LAMB2	NPHS1	PTPRT
BCORL1	COL22A1	FAT2	IGHG4	LCK	NPM1	RAD21
BCR	CREBBP	FAT4	IGHJ1	LCT	NR4A3	RARA
BIRC3	CRLF2	FBXW10	IGHJ2	LIMCH1	NRAS	RB1
BRAF	CSF3R	FBXW7	IGHJ3	LMO1	NRP1	RBM15
BTG1	CSMD3	FGFR3	IGHJ4	LMO2	NRSN1	RELN
BTK	CTCF	FLG2	IGHJ5	LPA	NT5C2	RHOA
CACNA1C	CTLA4	FLT3	IGHJ6	LYL1	NTRK3	RHOB
CACNA2D1	CTNNB1	FMNL2	IGHM	MALT1	NUP214	RHOT2
CALR	CUX1	FOXA3	IKZF1	MAP2K1	NUP98	RIMS1
CARD11	CXCR4	FOXO1	IKZF2	MAPK1	PAX5	RPL10
CBL	DCC	FOXO3	IKZF3	MBNL1	PCLO	RPN1
CBLB	DDX31	FOXO4	IL7R	EVI1/MECOM	PCM1	RPS15
CBLC	DDX3X	FYN	INO80	MEF2B	PDCD1	RTF1
CCDC85A	DDX58	GATA1	INTS8	MEGF6	PDGFRA	RUNX1
CCND1	DDX60	GATA2	IQGAP2	MGA	PDGFRB	RUNX1T1
RYR3	SIL1					
S1PR1	TRGV1					
S1PR2	TRGV2					
SALL3	TRGV8					
SAMD9	TRGV11					
SCN2A	TRAF1					
SEC24D	U2AF1					
SEPT5	U2AF2					
SEPT6	UBP1					
SEPT9	UBR5					
SET	ULK4					
SETBP1	UNC5D					
SETD2	VAV1					
SF3B1	WAS					
SGK1	WHSC1/NSD2					
SH2B3	WT1					
SLFN5	XPO1					
SMARCA2	YTHDF2					
SMARCB1	ZAP70					
SMC1A	ZEB1					
SMC3	ZFHGX2					
SOCS1	ZFHGX3					

Table SI. Continued.

SOCS3	ZRSR2
SPEG	
SPEN	
SRF	
SRGAP3	
SRSF2	
STAG1	
STAG2	
STAG3	
STAT1	
STAT3	
STAT5A	
STAT5B	
STAT6	
Microbe	
EBV	
HHV8	
HTLV-1	
HTLV-2	
CMV	
HIV1	
HIV2	
HSV1	
HSV2	
B19	
Helicobacter Pylori	
Bartonella henselae	
Treponema pallidum	

Table SII. Quantitative sequencing results showing Epstein Barr Virus detection only.

Case	Tissue	Region	Coverage, %	Sequencing depth
Case 1	LN	1	11.5	0.8
		2	0	0.07
		3	5.7	0.5
Case 2	LN	1	64.1	4.0
		2	13.2	1.4
		3	39.6	2.8
Case 3	LN	1	0	0.13
		2	0	0.13
		3	0	0.19
	BM	1	0	0.06
		2	0	0.06
		3	0	0.07
Case 4	LN	1	100	448
		2	100	402
		3	100	406
	BM	1	8.5	0.5
		2	0	0.2
		3	6	0.5
	LN	1	0	0.03
		2	0	0
		3	5.3	0.85
Case 6	LN	1	0	0.15
		2	5.4	0.53
		3	0	0.2
	BM	1	0	0
		2	0	0
		3	0	0
	LN	1	87	9.2
		2	88	9.2
		3	87	10.2
Case 7	BM	1	0	0
		2	0	0
		3	0	0
	LN	1	99.7	18.8
		2	78.3	12.6
		3	89.4	13.8
	BM	1	0	0
		2	0	0
		3	0	0
Case 9		1	51.8	3.8
		2	46.8	3.4
		3	53.8	3.5
Case 10	LN	1	100	2117
		2	89.7	1643
		3	100	1842
	BM	1	8.8	0.5
		2	6.7	0.4
		3	8.6	0.7
	BM	1	63.3	12.7
		2	49.5	7
		3	59.4	10.6
	BM	1	10.2	0.6
		2	12.9	0.7
		3	6.6	0.5

LN, lymph node; BM, bone marrow.