

# Clinical, immunophenotypic, cytogenetic, and molecular genetic features in 117 adult patients with mixed-phenotype acute leukemia defined by WHO-2008 classification

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Online Supplementary Table S1. Copy number variations identified by array-CGH in 12 patients.

Case	Aberration	Cytoband	Start locus	End locus	Genes in the aberrant region
1	duplication trisomy	8q24 chromosome 21	131070296	131104859	ASAP11T1 multiple
2	deletion	1q31.1	184848595	184950328	FAM129A
	deletion	2p15	61538962	61762873	USP34, XPO1
	deletion	5q14.3	88128258	88812408	MEF2C
	deletion	7p13	0	43972490	UBE2D4 (disrupted)
	deletion	9p21.3	21902814	22008167	CDKN2A
	deletion	9p24.3-9p13.2	0	36899524	PAX5 (disrupted)
	deletion	9q33.3	128517633	128615510	PBX3 (disrupted)
	deletion	10q25.1	111772794	111872558	ADD3
	deletion	12p12.1	25416767	25529976	KRAS
	deletion	12q21.33	92328436	92532791	BTG1
	deletion	12q24.11	110740756	111692399	ATP2A2, CUX2, TCTN1, GPN3, MYL2
	deletion	22q11.2	22745368	22962941	PRAME
3	duplication	1p21.1	104067184	104155244	RPCN3, AMY2B
	deletion	12p13.3	8031207	8117977	SLC2A14, SLC2A3
	deletion	20p12.1	14721866	14808927	MACROD2
4	deletion	5q21.3	107178284	107487408	FBXL17
	deletion	7p22	5806358	5889565	ZNF815
	deletion	9p21	19726199	22512565	CDKN2A, CDKN2B, MLLT3
	duplication	11q24.2-11q25	125290934	132497189	ETS1, FLI1, FEZ1, SNX19, NTM, OPCML (disrupted)
	deletion	12q14.3-12q15	67708304	69065506	CAND1 (disrupted), DYRK2, IL22, IL26, MDM1, RAPIA
	deletion	16p13.13	11081965	11467971	CLEC16A, SOCS1, PRM3, PRM2, PRM1, C16orf75,
5	duplication trisomy duplication	5q35.2 chromosome 8 11p15.4	176671264 3766491	176879431 3973762	NSD1 (NUP98-NSD1 fusion) NUP98 (NUP98-NSD1 fusion)
6	trisomy deletion duplication deletion deletion deletion deletion	chromosome 4 7p12.2 7q11.23 9p 11p 17q11.2 Xp11.4	50023023 72726578 0 0 29084332 38707324	50076720 74142268 39167302 43363699 30374582 40303082	multiple ZPBP (disrupted) ELN, LIMK1, BCL7B, TBL2, EIF4H, RFC2, LAT2, CLIP2 multiple multiple NF1, RAB11FIP4, C17orf79, UTP6, C17orf42, ADAP2, RNF135 BCOR
7	deletion deletion deletion deletion deletion duplication	5q14.3 6q26 6q25.3 6q23.3 7p12.2 11q24.1	88184587 162493994 158725303 135375146 50367431 122738079	88812408 162552319 158873681 135429926 50455015 122909318	MEF2C (disrupted) PARK2 (disrupted) TULP4 (disrupted) HBS1L (disrupted) IKZF1 CRTAM, C11orf63, BSX
8	deletion trisomy	11q14.1 chromosome 21	81397072	81768536	BC041900 multiple
9	deletion deletion deletion deletion deletion duplication	5q33.3 6q23.3 7p12.2 7q11 9q21.11 12q24.31	158445552 135375146 50367431 64679717 70984481 123223418	158517178 135456365 50459333 64974722 71497249 123350783	EBF1 (disrupted) HBS1L (disrupted) IKZF1 INTS4L1, ZNF92, INTS4L2 PGM5, C9orf71, FAM122A (disrupted) HIP1R, CCDC62, DENR

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10	deletion	3p22.3	35695821	35768588	ARPP21(disrupted)
	deletion	3q13.2	112068548	112224778	CD200,BTLA
	duplication	3q21.1	123212761	123259089	PTPLB
	deletion	3q25.1	151951166	152055052	MBNL1(disrupted)
	deletion	4q25	109010394	109089344	LEF1(disrupted)
	deletion	5q35.1	172271401	172300904	ERG1C1(disrupted)
	deletion	7p12.2	50427655	50459333	IKZF1
	deletion	7q22.3	104592257	104666801	MLL5(disrupted)
	duplication	8q12.1	58006167	58488946	C8ORF71
	deletion	9p21.3	21983069	22008596	CDKN2A
	deletion	10p13	14555157	14784688	FAM107(disrupted)
	deletion	11q22.3	104643704	104852147	CASP12,CASP4
	deletion	12q21.33	92274591	92539427	BTG1
	deletion	19p13.11-19p12	19764889	21591409	multiple
deletion	20p12.1	14685390	14983888	MACROD2(disrupted)	
11	deletion	5q14.2-5q35.3	81868013	180712204	multiple
	duplication	6q16.1-6q27	95831585	170921030	multiple
	duplication	10p12.31	21634368	21982346	miR-1915,C10orf140,MLLT10(disrupted)
	duplication	12q15	70610813	70718596	CNOT2(disrupted)
	duplication	Xq27.2	140705348	141008991	MGAEC3,MGAEC1,SPANXA1,SPANXA2,SPANXD,SPANXE
12	deletion	21q22.12	36208820	36354450	RUNX1(disrupted)