Characterization of leukemias with ETV6-ABL1 fusion

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Supplementary figures S1-S4, supplementary tables S1-S3

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Figure S1

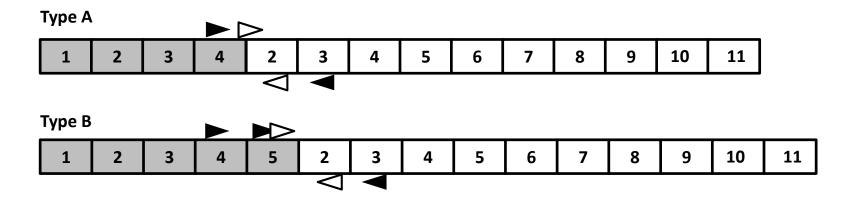


Fig S1 ETV6-ABL1 fusion transcript variants.

Schematic representation of two types of ETV6-ABL1 fusion transcript. Type A transcript differs from type B transcript by the absence of ETV6 exon 5. Grey boxes represent ETV6 and white boxes ABL1 exons. Black triangles represent primers used for detection of fusion transcript by RT-PCR. Primer pair annealing to exon 4 of ETV6 and to exon 3 of ABL1 was primarily designed to detect type A fusion (resulting in PCR product of 364 base pairs), however, using good quality cDNA it can also co-amplify type B fusion (resulting in PCR product of 910 base pairs). White triangles represent primers used for quantification of individual transcript types by qRT-PCR. For the primer sequences see the Methods.

Figure S2

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Size	53,619,427	136,404,337	5,107,026	4,796,168	5,782,860	1,259,376	13,679,972	170,338	31,562,199	168,360	1,916	1,818,929	157,656	576,094	4,395,583	17,324,425	11,350,014	192.539	266,533	2,982	4,049,004	468,843	1,001,429	621,732	321,023	4,483	56,069	28,151	3,937	75,518	2,462	60,297	122,602	204,372	666.668	104,892	239,762	718,422	8,646,297	3,570,765	218,135	1,373,694	468,611	80,591	16,489,871	18,204,509	10,332	193,938	14,664	22,192	174,347	1841356	896,617	331,474	210,858	334,155	61,369,275	100.952	42,513	94,209	29,049,566	16,891,858	114,584
End	01,5	198,904,033			222,788,062	235,539,020		-	31,607,134		П	890	52,452,724			159,119,486	11,396,601	11.590.844	\neg		15,909,450		=	\neg	9 5	\top		Т			П		T		23.079.238		23,423,892	24,142,314	32,788,611	35,359,376						133,571,587						701	12,932,281				4	73.915.692	10,458,953	35,405,913	995	154,916,845	23,048,693
Start	154	199 999 535	207,102,008	212,209,034	217,005,202	234,279,644	-	112,055,596	31 607 134	50,305,863	50,474,223	50,476,139	52,295,068	52,905,808	53,481,902	141,795,061	\neg	11,398,501	590,000	11,857,464	11,860,446	19,412,969	19,881,812	20,883,241	21,504,973	21,825,996	21.846.285	21,902,354	21,930,505	21,934,442	22,009,960	22,012,422	22,072,719	22,195,321	22.412.570	23,079,238	23,184,130	23,423,892	24,142,314	32,788,611	37,038,258		ΙI	39,098,698	98,775,459	115,367,078	133,571,587	133,581,919	133,775,857	133,790,521	133,812,713	133,367,000	12,035,664	$\overline{}$	П	46,700,642	48,985,639	73.814.740	10,416,440			138,024,987	22,934,109 23,048,693 114,584
Cytoband(s)	p36.33p32.3	p31.3q31.3	q32.1q32.3	q32.3q41	941	q42.2q42.3	q42.3q44	q13.2	p22.3p22.2	p12.2	p12.2	p12.2p12.1	p12.1	p12.1	p12.1p11.2	p22.3p21.3	p24.3p23	p23	p.2.3	p23	p23p22.3	p22.1	p22.1p21.3	p21.3	p21.3	p21.3	p21.3	p21.3	021.3	p21.3	p21.3	p21.3	p21.3p21.1	p21.1p13.2	p13.2	p13.2p13.1	p13.1	p13.1	q22.32q32	q32:q34.12	q34.12	q34.12	q34.12	q34.12	q34.12	934.12934.13	434.13434.2 p13.2	q21.33	q14.11	q14.13	914.2	q12 q23	p12.2	11	.1	q27.1q28	q11.223						
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40-a-MPN									LL	L	L	L	L L	L	L	L	L I	LL	. 1	L	L	L	L	L	L	LI	L	L	L	L	L	L	L	L I	L	L	L	L	L	LL	L	L	L	L			G	G	G	G	G (3 G	i L		Ш					L	Ш	丄	╝

Fig S2 Genomic regions recurrently affected by CNA in ETV6/ABL1-positive malignancies.

All regions where losses (L) or gains (G) of at least 2 individual cases overlap are included. No regions of recurrent UPD were found. Regions which include selected important genes recurrently affected in human ALL are displayed in bold font and bright colors. Samples from the first disease manifestation are displayed in bold, samples from disease recurrence are labeled by "R" and the order of recurrence in roman numerals. Regions of CNA with mosaic character (probably subclonal aberrations) with a small shift of copy number value which cannot be univocally called as losses/gains are in grey (considered as losses for this analysis). Sample 06-ch-ALL reffered on Figure 2 was not included in this analysis as exact genomic co-ordinates of identified CNA were not available. Abbreviations: CNA, copy number aberration; UPD, uniparental disomy.

Figure S3

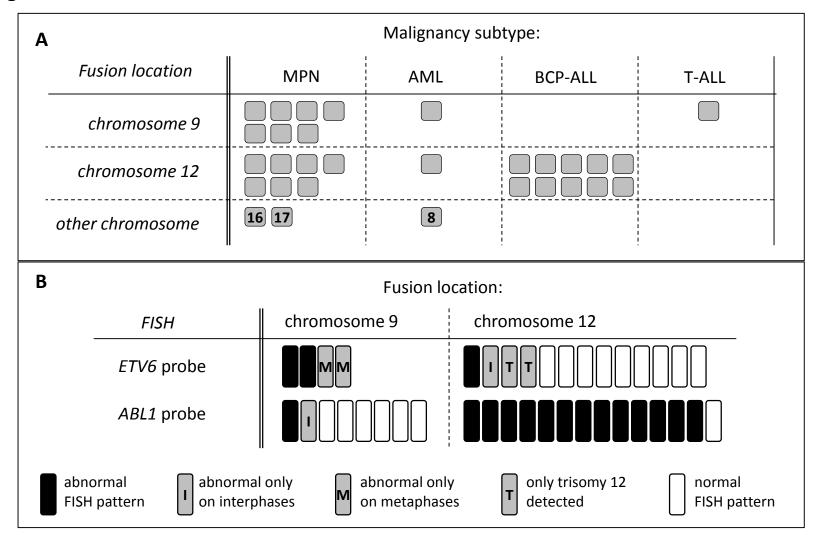


Fig S3: Chromosomal localization of ETV6-ABL1 fusion and results of FISH with commercial ETV6 and ABL1 probes.

- (A) Chromosomal localization of *ETV6-ABL1* fusion. In contrast to the even distribution of fusion location between chromosomes 12 and 9 in MPN/AML (8:8), in all 10 BCP-ALL cases where the chromosomal location could be identified, the *ETV6-ABL1* fusion was present on chromosome 12.
- (B) results of FISH with commercial *ETV6* and *ABL1* probes (used for *BCR-ABL1* and *ETV6-RUNX1* screening) in cases with the fusion localized on chromosomes 9 and 12. The *BCR-ABL1* commercial probes reliably detected the *ABL1* disruption in cases with fusion on chromosome 12 (13/14 results showed aberrant pattern), while most of the analyses looked normal in cases with fusion on chromosome 9 (6 normal, 2 aberrant (1 only on interphases)). Correspondingly, *ETV6* FISH with standard commercial probes showed aberrant pattern in all 4 cases with fusion on chromosome 9 (albeit 2 only on metaphases), while 9/13 cases with fusion on chromosome 12 looked normal, 2 showed just trisomy 12 and only 2 were aberrant (1 only on interphases).

Figure S4

		CDKN2A/ CDKN2B*	IKZF1	PAX5	BTG1	ABL1	SLX4IP	ATP10A	CD200/ BTLA	ETV6	RB1
	total affected ALL/LBC cases	16	15	8	7	7	5	4	4	3	2
ETV6-ABL1 (present	(%)	94	88	47	41	41	29	24	24	18*	12
(present study)	total affected ch-ALL (%)	90	80	30	50	50	40	20	10	20*	10
study)	total affected a-ALL (%)	100	100	60	20	20	20	20	40	0	20
	frequency in Ph ^{pos} ALL ⁵⁰ (%)	53 ^{&}	84	51	14	n.r.	23	n.r.	n.r.	7	19
literature	frequency in Ph ^{pos} chALL ⁵⁰ (%) frequency in Ph ^{pos} aALL ⁵⁰ (%)	48 ^{&} 59 ^{&}	76 91	48 55	19 9	-	33 14	-	-	10 5	19 18
data	frequency in Ph-like ALL ⁷ (%)	47	68	40	23	n.r.	n.r.	n.r.	23	14	5
	frequency in chALL ⁴⁹ (%)	26	12	18	7	n.r.	n.r.	n.r.	n.r.	21	6
	nequency in chart (10)	20	12	10	•		•		••••		

Fig S4 Frequency of selected aberrations in ETV6-ABL1 patients and in selected studies.

Frequency of selected aberrations reported in published studies^{7,49-51} is shown to illustrate similarity of CNA profiles between *ETV6-ABL1*-positive, *BCR-ABL1*-positive (Ph-positive) and *BCR-ABL1*-like (Ph-like) ALL.

Abbreviations: Ph, Philadelphia chromosome; a, adult; ch, childhood; neg, negative; pos, positive; n.r., not reported. & Frequency of *CDKN2A* deletions.

^{*} Relatively high frequency of *ETV6* deletions in *ETV6-ABL1*-positive cases compared to *BCR-ABL1*-positive ALL probably does not reflect frequency of genuine secondary *ETV6* loss but rather results from *ETV6* loss during primary genomic rearrangement.

Case ID	Cancer subtype	Karyotype / FISH	ABL1/ETV6 FISH details	ABL1 FISH	al Commercial ETV6 FISH d probe used	
01-ch-ALL	BCP-ALL	46,XX	n.r.	n.r.		present study
02-ch-ALL	BCP-ALL	46,XY,der(1)inv(1)(p11p34.2)t(1;9)(p11;p21)del(1)(q41),der(9)t(9;12)(q34.3;p13.3),der(9)t(1;9)(p11;p21),der(12)t(1;9;12)(q41?;q34.3;p13.3)[14]/46,XY)[5]	mFISH/mBAND: complex rearrangement, 12p on der(9)	ES DC	ES DC	Zuna et al. (2010)
03-ch-ALL	BCP-ALL	n.r.	n.r.	n.r.	n.r.	Papadopoulos et al. (1995)
04-ch-ALL	T-ALL	47,XXYc,del(6)(q15q23),der(9)ins(9;12)(q34;p13p13)inv(9)(q34q34)	extra copy of entire ETV6 inserted to 9q34; (translocated region mainly ETV6, distal to both ends retained on der(12)); 5'and 3'ABL1 retained on der(9)	ES DC	n.r.	Van Limbergen et al. (2001)
05-ch-ALL	BCP-ALL	46,XY[20]	BCR/ABL1 - 3x ABL1 (75%); BCR/ABL1, ETV6/RUNX1 and CEP12- insertion of part of the ABL1 into 12p13	DC DF	ES DC, BA	Zuna et al. (2010)
	1st recurrence (BCP-ALL)	46,XY[20]	BCR/ABL1 - 3x ABL1(59%)			
06-ch-ALL	BCP-ALL	46,XY,ins(12;9)(p13;q34q34)[20]	n.r.	n.r.	n.r.	Roberts et al. (2012), Roberts et al. (2014)
07-ch-ALL	BCP-ALL	46,XX,t(9;12)(q34;p13)[18]/46,XX[2]	n.r.	n.r.	n.r.	Roberts et al. (2014)
08-ch-ALL	BCP-ALL	no karyotype	n.r.	n.r.	n.r.	present study
09-ch-ALL	BCP-ALL	46,XX[20].ish der(12)ins(12;9)(p13;q34q34)(ETV6+, ABL1 dim)[8]	BCR/ABL1 - 3x ABL1	DC DF	ES DC	Malone et al. (2010)
10-ch-ALL	BCP-ALL	no karyotype	nuc ish 9q34(ABL1x2),22q11(BCRx2)	n.r.	n.r.	present study
11-ch-ALL	BCP-ALL	46,XY,?ins(12;9)(p13;q34q34)[20]	BCR/ABL1 – split ABL1 (60%); ETV6/RUNX1normal	DC DF	ES DC	present study
12-ch-ALL	T-ALL	46,XY	n.r.	n.r.	n.r.	present study
13-ch-LBL	B-LBL	46,XY	n.r.	n.r.	n.r.	present study
	2nd recurrence (BCP-ALL)	•	n.r.	n.r.	n.r.	
14-a-ALL	BCP-ALL	46XY[20]	n.r.	n.r.	n.r.	Roberts et al. (2014)
15-a-ALL	BCP-ALL	46,XX,del(9)(p22),der(10)t(9;10)(q22;p15)[12]/46,XX[8]	BCR/ABL1 - 3x ABL1; ETV6 BA - normal; ETV6/RUNX1 - normal; BCR/ABL1, ETV6/RUNX1- fusion on 12p (cryptic insertion of part of ABL1 into ETV6)	DC DF	DC DF; BA	` /
16-a-ALL	BCP-ALL	47,XX,+5. ish der(9)t(9;12)(q34;p13),der(12)t(9;12)(q34;p13)inv(12)(p13p13)	BCR/ABL1 - 3x ABL1; ETV6/RUNX1 - 3x ETV6 (small); ETV6 BA - 2x fusion + 1 orange (5' of ETV6); ETV6 on 9	DC DF	ES DC, BA	Song et al. (2014)
17-a-ALL	BCP-ALL	45,XY,del(1)(q42),-9,-13,add(16)(p1?3),mar [20]; COBRA-FISH: 45,XY,der(1)t(1;9),der(9)t(9;13),-13,der(16)t(16;22)	BAC FISH: loss of one 3' ETV6; insertion of duplicated 3' ABL1 into normal looking 12p (the one with loss of 3TEL); one intact ABL1 on 9, one intact ABL1 on der(1)t(1;9)	n.r.	n.r.	Baeumler et al. (2008)
18-a-ALL	BCP-ALL	46,XY,der(2)t(2;9)(p2?;q34),t(2;8)(p12;q24),der(9)t(2;9)(p2?;q34)ins(12;9)(p1?3;q34q34)[cp9]/ 46,XY[16]	ABL1 inserted into 12p; ETV6/RUNX1- normal	DC DF	ES DC	present study
19-a-ALL	BCP-ALL	46,XX,t(8;9;12)(p12;q34;p13)[22]	BCR/ABL1, ETV6/RUNX1 and CEP12 - insertion of part of the ABL1 into 12p13	ES DC		
20-a-ALL	BCP-ALL	46,XX,t(9;12)(q34;p13) [20]	n.r.	n.r.	n.r.	Zhou et al. (2012)
21-a-ALL	BCP-ALL	46,XY,t(9;12)(q34;p13)[2]/45,XY-2,-14,+17[2] /46,XY[16]	n.r.	n.r.	n.r.	Zhou et al. (2012)
22-a-ALL	BCP-ALL	complex rearrangements in 5 abnormal near-diploid clones (2 hyperdiploid, 1 diploid and 2 hypodiploid) involving chromosomes 1,6,7,9,11,13,19,20; t(9;12), ETV6/ABL1	t(9;12) with ETV6/ABL1 fusion	n.r.	n.r.	Yeung et al. (2014), Roberts et al. (2014)
23-a-AML	AML-M2	46,XY,t(8;12)(p21;p13)	BCR/ABL1 - 2x ABL1 on 9 and 1x on der(8)t(8;12); cosmids on ETV6 and ABL1 - ETV6 exons 3,4,5 on der(8), exon 8 on der(12); ETV6/ABL1 fusion signal on der(8)	DC DF	n.r.	La Starza et al. (2002)
24-a-AML	AML-M1	46,XY,t(9;12)(q34;p13) [18/20]/51,XY,+8,+9,t(9;12)(q34;p13),+12,+14,+17 [2/20]	BCR/ABL1 - normal; cosmids on ETV6 and ABL1 - fusion ETV6/ABL1 on der(9), ETV6 exon 8 on der(12)	DC DF	n.r.	La Starza et al. (2002)
25-a-AML	AML	46,XY [20]	BCR/ABL1 - 3x ABL1; ETV6 BA - normal; ETV6/RUNX1 - normal; BCR/ABL1, ETV6/RUNX1- fusion on 12p (cryptic insertion of part of ABL1 into ETV6)	DC DF	DC DF; BA	` ,
26-a-AML	AML-M6	45,add(X)(p11),Y,23,der(3)t(3;15)(q12;q15),t(4;7)(q21;q22),25,t(9;12;14)(q34;p13;q22),del(12)(p11p13),der(15)del(15)(q11q15),t(3;15)(q12;q15),der(18)t(3;18)(q11;q1?2),1mar	n.r.	n.r.	n.r.	Golub et al. (1996)
27-a-MPN	MPN	46,XX	BCR/ABL1 - normal but ASS (centromeric to ABL1) missing on one chromosome 9; metaphase FISH (ETV6, RUNX1, BCR, ABL1): ETV6/ABL1 fusion on chromosome 9	n.r.	n.r.	Kawamata et al. (2008)
28-a-MPN	MPN	46,XY,t(12;14)(p12;q11-13) [24]/46,XY [1]	YAC and cosmid probes: 5' end of ETV6 inserted into ABL1 on der(9); 3' ETV6 remained on der(12); part of 12p (behind ETV6) on 14	n.r.	n.r.	Andreasson et al. (1997)
29-a-MPN	MPN	46,XY,t(9;12)(q34;p13)	BCR/ABL1 - 3xABL1 (80%); ETV6/RUNX1 - 3xETV6	n.r.	n.r.	Perna et al. (2011)
30-a-MPN	MPN	46,XX,t(9;12)(q34;p13)[17]/46,XX[3]	BCR/ABL1 - normal; BCR/ABL1, ETV6/RUNX1 - fusion on 9q34; 9q subtelomeric on 12	ES DC	ES DC	Keung et al. (2002)
31-a-MPN	MPN	46,XX,t(9;12)(q34;p13)	BCR/ABL1 - 3x ABL1 (21%) visible only on interphases; ETV6 BA - split in all metaphases and 92% interphases; BAC probes - fusion on der(9)	DC DF	BA	Gancheva et al. (2013)
32-a-MPN	MPN	n.r.	Whole chromosome paints 9 and 12 do not evidence involvement of these chromosomes	n.r.	n.r.	Brunel et al. (1996)
33-a-MPN	MPN	46,XY	BCR/ABL1 - normal	n.r.	n.r.	Lin et al. (2002)
34-a-MPN	MPN	ETV6/ABL1	BCR/ABL1, ETV6/RUNX1 - ETV6/ABL1 on 12p13	ES DC	DC DF	Mozziconacci et al. (2007)
	1st recurrence (MPN-LBC)	, ,,	ETV6/ABL1 on 12p13	ES DC	DC DF	
		44,X,-Y,-7,?add(9)(p?1),del(9)(p12),add(12)(p13)[20]	ETV6/ABL1 on 12p13	ES DC	DC DF	
35-a-MPN	MPN	46,XY,del(6)(p21),der(9)inv(9)(q34q34)t(9;12)(q34;p13) or 46,XY,del(6)(p21),der(9)ins(9;12)(q34;p13)13)t(9;12)(q34;p13).	BCR/ABL1 - normal; 4-color FISH: translocation of distal ends of 12p and 9q; 5' and 3' ABL1 on der(9); YAC ETV6: part of the signal on der(9) near ABL1	ES DC	n.r.	Van Limbergen et al. (2001)
36-a-MPN	MPN	46,XX,ins(9,12)(q34;p13p13)	BCR/ABL1 - 3x ABL1 (47%); ETV6/ABL1 fusion (ins(9;12)(q34;p13p13)) (peripheral blood - 89%)	n.r.	n.r.	Nand et al. (2009)
37-a-MPN	MPN	46,XX,t(5;9)(q13;q34),add(17)(q2?1),del(5)(q13q34)/46,XX,t(5;9)(q13;q34),add(17)(q2?1),der(9)t(5;9)add(9)(q34)/51,XX,t(5;9)(q13;q34),add(17)(q2?1),(+8,+11,+12,+18,+19)	BCR/ABL1 - 5' of ABL1 on der(9), 3' of ABL1 on der(12p); cosmids: ETV6/ABL1 fusion on der(12); duplication of the der(12) in the hyperdiploid subclone	DC DF	n.r.	Meyer-Monard et al. (2005)
38-a-MPN	MPN	46,XY,t(5,12;16)(q34;p13;q2)	ETV6/ABL1 on 16q distal to MAF gene, which remains on 16q23 and the CBFA2T3 gene, which is transferred from 16q24 onto 12p	DC DF	n.r.	present study
39-a-MPN	MPN Decreases (MDN MBC)	46,XY [20]	no FISH performed	n.r.	n.r.	Kelly et al. (2009)
40 1451		46,XY,ins(12;9)(p13;q34q34)	BCR/ABL1- 3x ABL1 (92%), the additional on 12p; both ASS on 9q34; ETV6 BA - normal on metaphases, split on interphases; insertion of ABL1 into 12p13	DC DF	BA	
40-a-MPN	MPN-B-LBC	45,XY,7,der(9)t(9;9)(p11;q21).ishder(9)t(9;9)(ABL1++),t(9;12(q34;p13)(ABL1+;ETV6+,ABL1+)[8]/46,XY[12]	der(9)t(9;9) and cryptic t(9;12)(q34;p13) resulting in ETV6/ABL1 fusion POR(ABL1 and ETX) (ABL1 fusion and ar(N)(0)(12)(x34)(12)(x34)(12)(x34)(13)(x34)(x34)(x34)(x34)(x34)(x34)(x34)(x3	n.r.	n.r.	present study
41-a-MPN	MPN-e.m.T-LBC	46,XY,der(9)t(9;12)(q34;p13),del(12)(p13)[1]/46,sl,t(7;14)(p13;q11.2)[18]/47,sdl1,+19[1] (bone marrow); 46,XY,t(7;14)(p13;q11.2),der(9)t(9;12)(q34;p13),del(12)(p13)[4] (lymph node)	BCR/ABL1 and ETV6/RUNX1 - ETV6/ABL1 fusion on der(9)t(9;12)(q34;p13); der(9)inv(9)(q34q34)t(9;12)(q34;p13) (translocation of ETV6 into partly inverted ABL, telomeric part of 9q with rest of ABL1 deleted)	ES DC		Yamamoto et al. (2014)
42-a-MPN	MPN-MBC	45,XY,-7,t(9;12)(q34;q13)[18]/46,XY[6] [t(9;12)(q34;q13): der(9)t(9;12)(q34;q11), der(12)ins(12;9)(p13;q34q34)inv(12)(p13q11)t(9;12)(q34;q11)]	BCR/ABL1 - 3x ABL1 (9, der(9), der(12)); ETV6/ABL1 on der(12); der(9): break in ABL1, fusion with most of the 12q; ABL1 inserted into ETV6, followed by inv(12)(p13q11) and translocation between the 9q and 12q	ES DC	ES DC	Barbouti et al. (2003)
40 1451		45,XY,-7,t(9;12)[2]/45,idem,t(12;13)(p12;q13)[10]/46,XY[13]	BCR/ABL1 - 3x ABL1 (9, der(9), der(12)); ETV6/ABL1 on der(12); der(9): break in ABL1, fusion with most of the 12q; ABL1 inserted into ETV6, followed by inv(12)(p13q11) and translocation between the 9q and 12q	ES DC	ES DC	010 : (0000)
43-a-MPN	MPN-MBC	49,XY,+11,t(9;12)(q34;p1?),+der(12)t(9;12),+19,der(22)t(1;22)(q21;q11)	BCR/ABL1 - one ABL1 split between 9q34 and 12p (on 2 out of 3 chromosomes 12)	n.r.	n.r.	O'Brien et al. (2002)
44-a-MPN	MPN-B-LBC	46,XY,t(12;17)(p11.2;p11.2).ish der(17)(12ptel+,ETV6+,ABL1+,TP53+,RARA+),der(12)(LIS1+,ETV6-,12qtel+)	BCR/ABL1 - 3x ABL1 (additional on 17p); ETV6/RUNX1 - ETV6 on 17p; subtelomeric 12p on 17p; LIS1 (17p13.3) on 12p; TP53 (17p13.1) on 17	DC DF	DC DF	Tirado et al. (2005)

ES DC, extra signal dual color translocation probe DC DF, dual color dual fusion translocation probe

BA, break apart probe

0.4	CNA type		Whole chromosome. Start	о Ш	0 Siz	Genes
01-ch-ALL 01-ch-ALL 01-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss Monoallelic loss	1 q32.1q44 2 p22.1p15	82,154 5 no 207,102,008 24 no 39,497,758 6 no 160,594,757 19	2,629,315	53,619,427 42,116,984 23,131,557 30,320,893	> 5 genes > 5 genes > 5 genes > 5 genes
01-ch-ALL 01-ch-ALL 01-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	9 p24.3p23 9 p23	no 46,587 1	11,396,601 11,857,464		> 5 genes > 5 genes no genes > 5 genes incl. CDKN2A/CDKN2B
01-ch-ALL 01-ch-ALL	Monoallelic loss Monoallelic loss	9 p21.3p13.1 9 q22.32q34.12	no 22,412,570 3 no 98,775,459 13	39,179,289 33,571,587	16,766,719 34,796,128	> 5 genes incl. PAX5 > 5 genes
02-ch-ALL 02-ch-ALL 02-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	7 p12.2 9 p21.3	no 212,209,034 21 no 50,350,267 5 no 20,883,241 2	0,476,139	4,796,168 125,872 1,019,113	> 5 genes IKZF1 > 5 genes
02-ch-ALL 02-ch-ALL	Biallelic loss Monoallelic loss Monoallelic loss	9 p21.3 9 p21.3	no 21,902,354 2 no 22,004,153 2	22,004,153	101,799 1,179,977	MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 MTAP/CDKN2B-AS1/DMRTA1/LINC01239/CDKN2B
02-ch-ALL 05-ch-ALL 05-ch-ALL	Monoallelic loss Monoallelic loss Biallelic loss	7 p12.2	35,311,704 3 no 50,418,242 5 no 21,930,505 2	0,462,935	94,209 44,693 81,917	LINC00649 IKZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53
05-ch-ALL 05-ch-ALL 05-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	15 q26.1	no 92,284,255 9 no 92,076,959 9 no 10,416,440 1		252,571 498,882 42,513	C12orf79/BTG1 SLCO3A1 SLX4IP
05-ch-ALL 5-ch-ALL-RII	Monoallelic loss Monoallelic loss	X p22.31 7 p12.2	no 6,147,790 no 50,418,242 5	6,418,059 50,462,935	270,269 44,693	no genes IKZF1
5-ch-ALL-RII 5-ch-ALL-RII 5-ch-ALL-RII	Monoallelic loss	12 q21.33	no 21,930,505 2 no 92,284,255 9 no 92,076,959 9	2,536,826	81,917 252,571 498,882	MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 C12orf79/BTG1 SLCO3A1
5-ch-ALL-RII 08-ch-ALL 08-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	X p22.31 7 p12.2	no 50,350,267 5	6,418,059 60,476,139 22,005,330	270,269 125,872 174,851	no genes IKZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53
08-ch-ALL 08-ch-ALL	Monoallelic loss Gain	12 q21.33	no 92,206,482 9 es 0 8	92,537,956 81,195,210	331,474 81,195,210	C12orf79/BTG1 > 5 genes
08-ch-ALL 08-ch-ALL 09-ch-ALL	Gain Gain Monoallelic loss	X q26.2q28	es 0 5 no 131,518,737 15 no 106,729,992 10		51,304,566 23,398,108 60,124	> 5 genes > 5 genes UXS1
09-ch-ALL 09-ch-ALL	Monoallelic loss Monoallelic loss	2 q33.1 7 p12.2	no 201,192,144 20 no 50,350,267 5	01,308,117 50,462,935	115,973 112,668	SPATS2L IKZF1
09-ch-ALL 09-ch-ALL 09-ch-ALL	Monoallelic loss Biallelic loss Gain	9 p21.3	no 21,846,285 2 no 21,881,338 2 no 133,571,587 13	22,005,330	19,557 123,992 218,934	MTAP MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 EXOSC2/ABL1/FIBCD1/QRFP
09-ch-ALL 09-ch-ALL 09-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	12 q21.33	no 3,836,471 no 92,284,255 9 no 62,155,282 6		31,755 253,701 177,698	no genes C12orf79/BTG1 VPS13C
09-ch-ALL 09-ch-ALL	Monoallelic loss Biallelic loss	17 q21.32 19 p13.11p12	10 45,187,429 4 10 19,754,806 2	5,499,396	311,967 1,286,544	MYL4/ITGB3/EFCAB13/CDC27/MIR4315-1 > 5 genes
09-ch-ALL 09-ch-ALL 10-ch-ALL	Monoallelic loss Biallelic loss Monoallelic loss	20 p12.2	no 21,069,090 2 no 10,416,440 1 no 60,066,610 6	10,443,064	518,171 26,624 492,630	> 5 genes SLX4IP FHIT
10-ch-ALL 10-ch-ALL	Monoallelic loss Gain	7 p12.2 8 q13.1q24.3	50,350,267 5 no 66,354,675 14	50,457,188 16,298,143	106,921 79,943,468	IKZF1 > 5 genes
10-ch-ALL 10-ch-ALL 10-ch-ALL	Monoallelic loss Biallelic loss Monoallelic loss	9 p21.3	no 46,587 2 no 21,833,000 2 no 21,998,000 3		165,000	> 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 > 5 genes incl. CDKN2B/PAX5
10-ch-ALL	Gain Gain	9 p13.1 9 q34.12	38,631,767 3 no 133,714,048 13	33,812,713	1,146,852 98,665	CNTNAP3/ZNF658B ABL1/FIBCD1/QRFP
10-ch-ALL 10-ch-ALL 10-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	12 q21.33	no 118,642,431 11 no 92,278,448 9 no 46,700,642 4	2,536,826	154,829 258,378 334,155	CXCR5/DDX6/BCL9L/MIR4492 C12orf79/ BTG1 LCP1/KIAA0226L/LINC00563
10-ch-ALL 10-ch-ALL 10-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	18 q23		26,104,242 73,915,692 10,456,586	68,632 317,866 39,182	ATP10A/MIR4509-1/MIR4715 LOC339298 SLX4IP
10-ch-ALL 10-ch-ALL	Gain Monoallelic loss	20 q11.22q11.23 20 q11.23q13.33	no 32,576,128 3 no 37,267,729 6	37,262,128 52,956,141	4,686,000 25,688,412	> 5 genes > 5 genes
10-ch-ALL 10-ch-ALL 11-ch-ALL	Monoallelic loss Gain Monoallelic loss	X q27.1q28	no 22,517,826 2 no 138,024,987 15 no 62,157,497 7	55,233,846	777,158 17,208,859 12,728,254	> 5 genes > 5 genes > 5 genes
11-ch-ALL 11-ch-ALL	Monoallelic loss Gain	7 p12.2 9 q34.12q34.2	no 50,350,267 5 no 133,682,667 13	50,418,242 85,905,701	67,975 2,223,034	IKZF1 > 5 genes incl. ABL1
11-ch-ALL 12-ch-ALL 12-ch-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	2 q14.1 9 p21.3	no 12,039,551 1 no 117,373,537 11 no 21,504,973 2	17,566,409 21,642,590	116,771 192,872 137,617	ETV6 no genes MIR31HG
12-ch-ALL 12-ch-ALL 12-ch-ALL	Biallelic loss Monoallelic loss Monoallelic loss	9 p21.3 9 p21.3	21,651,620 2 22,195,321 2 23,423,892 2	23,079,238	538,096 883,917 718,422	MTAP/CDKN2B-AS1/CDKN2A/CDKN2B DMRTA1/LINC01239 ELAVL2
12-ch-ALL 12-ch-ALL	Gain Monoallelic loss	9 q34.12q34.13 12 p13.2p13.1	no 133,608,116 13 no 12,035,664 1	34,064,345 12,932,281	456,229 896,617	ABL1/LAMC3/AIF1L/NUP214/FIBCD1 > 5 genes incl. ETV6
12-ch-ALL 12-ch-ALL 13-ch-LBL	Monoallelic loss Monoallelic loss Uniparental disom	19 q13.2	no 128,703,350 12 no 42,368,738 4 no 82,154 8		44,504 412,115 80,043,846	no genes > 5 genes > 5 genes
13-ch-LBL	Monoallelic loss	1 p31.1p13.1 1 q21.3	no 80,126,000 11 no 154,582,970 15	54,607,914	24,944	> 5 genes ADAR CD200/BTLA
13-ch-LBL 13-ch-LBL 13-ch-LBL	Monoallelic loss Monoallelic loss Monoallelic loss	4 q31.21q31.22	no 112,060,256 11 no 146,125,343 14 no 49,991,561 5	7,424,678	165,678 1,299,335 98,311	> 5 genes PARP8
13-ch-LBL 13-ch-LBL 13-ch-LBL	Monoallelic loss Monoallelic loss Monoallelic loss	6 q23.3	no 11,239,119 1 no 136,648,627 13 no 50,350,267 5	86,753,218	193,693 104,591 67,255	NEDD9 MAP7 IKZF1
13-ch-LBL 13-ch-LBL	Biallelic loss Monoallelic loss	7 p12.2 7 p12.2	no 50,417,522 5 no 50,462,935 5	50,462,935 50,474,223	45,413 11,288	IKZF1 IKZF1
13-ch-LBL 13-ch-LBL 13-ch-LBL	Monoallelic loss Monoallelic loss Gain	9 q32	no 21,902,354 2 no 115,265,330 11 no 133,593,939 13	15,367,078	101,013 101,748 181,918	MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 KIAA1958 ABL1/QRFP
13-ch-LBL 13-ch-LBL 13-ch-LBL	Monoallelic loss Monoallelic loss Monoallelic loss	12 q21.33	no 111,773,423 11 no 90,099,895 9 no 92,206,482 9	0,384,591	77,080 284,696 333,108	ADD3 no genes C12orf79/BTG1
13-ch-LBL 13-ch-LBL	Monoallelic loss Monoallelic loss	13 q14.2	no 92,206,482 9 no 48,985,639 4 no 110,299,924 11	19,079,503	93,864 54,990	RB1/LPAR6/RCBTB2 no genes
13-ch-LBL 13-ch-LBL	Monoallelic loss Monoallelic loss Monoallelic loss	15 q26.1	no 26,038,355 2 no 90,461,129 9 no 53,296,927 5	0,574,591	67,878 113,462 447,618	ATP10A/MIR4509-1/MIR4715 ZNF710 TCF4
13-ch-LBL 3-ch-LBL-RII	Monoallelic loss UN	Y q11.223 1 p36.33p31.1	no 22,934,109 2 no 82,154 8	23,048,693 80,126,000	114,584 80,043,846	RPS4Y2 > 5 genes
3-ch-LBL-RII 3-ch-LBL-RII 3-ch-LBL-RII	Monoallelic loss	1 p12	no 80,126,000 11 no 119,068,677 11 no 154,582,970 15	19,146,085	36,994,000 77,408 24,944	> 5 genes no genes ADAR
3-ch-LBL-RII 3-ch-LBL-RII	UN Monoallelic loss	1 q23.3q42.2 1 q42.2q42.3	no 161,660,000 23 no 234,279,644 23	34,279,644 35,539,020	72,619,644 1,259,376	> 5 genes > 5 genes
3-ch-LBL-RII 3-ch-LBL-RII 3-ch-LBL-RII	Monoallelic loss	4 q31.21q31.22	no 112,060,256 11 no 146,125,343 14 no 49,991,561 5	7,424,678	165,678 1,299,335 98,311	CD200/BTLA > 5 genes PARP8
3-ch-LBL-RII 3-ch-LBL-RII 3-ch-LBL-RII	Monoallelic loss	6 q23.3	no 11,239,119 1 no 136,648,627 13 no 50,350,267 5	86,753,218	193,693 104,591 67,255	NEDD9 MAP7 IKZF1
3-ch-LBL-RII 3-ch-LBL-RII	Biallelic loss Monoallelic loss	7 p12.2 7 p12.2	no 50,417,522 5 no 50,462,935 5	50,462,935 50,474,223	45,413 11,288	IKZF1 IKZF1
3-ch-LBL-RII 3-ch-LBL-RII 3-ch-LBL-RII	Monoallelic loss	9 q32	no 21,902,354 2 no 115,265,330 11 no 133,593,939 13	15,367,078	101,013 101,748 181,918	MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 KIAA1958 ABL1/QRFP
3-ch-LBL-RII 3-ch-LBL-RII	Monoallelic loss	10 q25.1 12 q21.33	no 111,773,423 11	0,384,591	77,080 284,696	ADD3 no genes C12orf79/BTG1
3-ch-LBL-RII 3-ch-LBL-RII 3-ch-LBL-RII	Monoallelic loss Monoallelic loss	13 q14.2	no 92,206,482 9 no 48,985,639 4 no 110,299,924 11	19,079,503	333,108 93,864 54,990	RB1/LPAR6/RCBTB2 no genes
3-ch-LBL-RII 3-ch-LBL-RII 3-ch-LBL-RII	Monoallelic loss	15 q26.1	no 26,038,355 2 no 90,461,129 9 no 53,296,927 5	0,574,591	67,878 113,462 447,618	ATP10A/MIR4509-1/MIR4715 ZNF710 TCF4
3-ch-LBL-RII 14-a-ALL	Monoallelic loss	1 p31.3	22,934,109 2 no 62,499,696 6	2,504,958	114,584 5,262	RPS4Y2 INADL
14-a-ALL 14-a-ALL 14-a-ALL	Monoallelic loss Gain Monoallelic loss	3 p14.1	no 198,805,839 19 no 68,093,212 6 no 112,055,596 11	8,093,882	98,194 670 159,962	MIR181A1HG/MIR181B1/MIR181A1 FAM19A1 CD200/BTLA
14-a-ALL 14-a-ALL 14-a-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	5 q15	no 89,151,828 8 no 93,721,307 9 no 102,167,708 10	3,739,306	54,928 17,999 287,233	ABCG2/PPM1K KIAA0825 PAM/GIN1
14-a-ALL 14-a-ALL	Biallelic loss Monoallelic loss	7 p12.2 7 p12.2	no 50,350,267 5 no 50,423,963 5	50,418,949 50,457,188	68,682 33,225	IKZF1 IKZF1
14-a-ALL 14-a-ALL 14-a-ALL	Monoallelic loss Biallelic loss Monoallelic loss	9 p21.3	19,412,969 2 10 21,956,914 2 10 21,999,603 2	21,999,228	2,543,362 42,314 4,445	> 5 genes MTAP/CDKN2B-AS1/C DKN2A /C9orf53 MTAP/CDKN2B-AS1/C DKN2B
14-a-ALL 14-a-ALL 14-a-ALL	Biallelic loss Monoallelic loss	9 p21.3	no 22,004,550 2 no 22,011,477 4	22,011,380	6,830 18,607,732	MTAP/CDKN2B-AS1/CDKN2B > 5 genes incl. PAX5
14-a-ALL 14-a-ALL 14-a-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	10 q21.3	no 70,940,583 13 no 65,301,325 6 no 46,148,733 4	55,321,976	62,641,336 20,651 11,105	> 5 genes REEP3 ARID2
14-a-ALL	Monoallelic loss Biallelic loss	12 q12 12 q21.33	no 46,168,216 4 no 92,278,448 9	16,227,650 02,536,826	59,434 258,378	ARID2 C12orf79/BTG1
14-a-ALL 14-a-ALL 14-a-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	14 q32.2	44,796,839 4 no 98,130,332 9 no 26,035,417 2	8,138,102	210,858 7,770 68,589	SERP2/TSC22D1 LOC100129345 ATP10A/MIR4509-1/MIR4715
14-a-ALL 14-a-ALL 14-a-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	15 q26.1	no 66,039,826 6 no 93,626,382 9 no 12,190,002 1	3,795,530	41,485 169,148 89,572	DENND4A RGMA SNX29
14-a-ALL 14-a-ALL	Monoallelic loss Monoallelic loss	16 q21 18 q23	no 66,598,962 6 no 73,814,740 7	66,617,025 73,915,692	18,063 100,952	CKLF/CKLF-CMTM1/CMTM1/CMTM2 LOC339298
14-a-ALL 14-a-ALL 15-a-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	21 q22.11 7 p12.2	no 10,410,320 1 no 35,308,298 3 no 50,346,134 5	35,406,084 50,476,139	53,997 97,786 130,005	SLX4IP/MKKS LINC00649 IKZF1
15-a-ALL 15-a-ALL 17-a-ALL	Monoallelic loss Monoallelic loss Monoallelic loss	9 p21.3 9 p13.2	21,825,996 2 no 37,038,258 3 no 222,788,062 24	22,072,719 37,256,393	246,723 218,135 26,430,930	MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 EBLN3/ZCCHC7 > 5 genes
17-a-ALL 17-a-ALL	Monoallelic loss Monoallelic loss	7 p12.2 9 p23p22.3	50,305,863 5 no 11,590,844 1	50,366,637 15,909,450	60,774 4,318,606	IKZF1 > 5 genes
17-a-ALL 17-a-ALL 17-a-ALL	Biallelic loss Monoallelic loss Biallelic loss	9 p22.3p21.3 9 p21.3	15,909,450 1 15,942,765 2 10 21,974,218 2	21,974,218 22,005,330	33,315 6,031,453 31,112	CCDC171 > 5 genes incl. CDKN2A MTAP/CDKN2B-AS1/CDKN2A/CDKN2B
17-a-ALL 17-a-ALL	Monoallelic loss Gain Monoallelic loss	9 p21.3p13.1 9 q34.12	22,005,330 3 no 133,670,874 13 no 12,035,649 1	39,098,698 33,987,060	17,093,368 316,186 1,526,873	> 5 genes incl. CDKN2B/PAX5 ABL1/LAMC3/AIF1L/FIBCD1/QRFP > 5 genes incl. ETV6
17-a-ALL	Monoallelic loss		12,035,649 1 no 31,393,993 3 no 43,549,782 11	88,992,446	7,598,453	c @ wom
17-a-ALL 17-a-ALL 17-a-ALL	Monoallelic loss	13 q14.11q34		0.445	71,553,747	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L
17-a-ALL 17-a-ALL		13 q14.11q34 16 p13.3 22 q11.22q13.33			71,553,747 2,351,868 29,049,566 37,214	> 5 genes
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2	22,255,000 5 no 50,417,522 5 no 21,934,442 2 no 112,053,565 11	51,304,566 50,454,736 52,004,153 12,246,081	2,351,868 29,049,566 37,214 69,711 192,516	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 y 7 p22.3p12.1 9 p24.3p21.3	22,255,000 5 no 50,417,522 5 no 21,934,442 2 no 112,053,565 11 es 0 17 no 44,935 5 no 46,587 2	51,304,566 50,454,736 22,004,153 12,246,081 71,115,067 53,481,902 21,934,442	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes IKZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA > 5 genes > 5 genes incl. IKZF1 > 5 genes
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 y 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3p21.1	22,255,000 5 no 50,417,522 5 no 21,934,442 2 no 112,053,565 11 es 0 17 no 44,935 5	61,304,566 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 21,934,442 21,998,035 62,788,611	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes IKZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA > 5 genes > 5 genes KZF1
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3 9 p21.3 10 p13.2p13.1 11 p13.31p13.2 12 p12.1	22,255,000 5 50,417,522 5 10 21,934,442 2 112,053,565 11 110 44,935 5 110 44,935 5 110 21,934,442 2 110 21,938,035 3 110 36,359,376 3 110 9,823,553 1 110 24,959,039 2	61,304,566 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 21,934,442 21,998,035 82,788,611 89,179,289 11,728,337 25,132,771	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes incl. IKZF1 > 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 > 5 genes incl. CDKN2B > 5 genes incl. PAX5 > 5 genes BCAT1
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Gain Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3 12 p13.31p13.2 12 p12.1 12 p12.1 13 q32.1	22,255,000 5 50,417,522 5 10 21,934,442 2 112,053,565 11 110 44,935 5 110 44,935 5 110 21,934,442 2 1110 21,938,035 3 1110 36,359,376 3 1110 24,959,039 2	61,304,566 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 21,934,442 21,998,035 62,788,611 199,179,289 11,728,337 125,132,771 63,025,520 199,185,297	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA > 5 genes > 5 genes > 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 > 5 genes incl. IKZF1 > 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 > 5 genes incl. CDKN2B > 5 genes incl. PAX5 > 5 genes
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI 4-a-MPN-RI	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3p21.1 9 p13.2p13.1 12 p13.31p13.2 12 p12.1 12 p23.2 13 q13.2 6 p21.32	22,255,000 5 100 50,417,522 5 100 21,934,442 2 112,053,565 11 112,053,565 11 112,053,565 11 112,053,565 12 112,934,442 2 112,934,442 2 112,934,442 2 112,934,442 2 112,934,442 2 112,934,944 2 112,934,944 2 112,934,944 2 112,934,944 2 112,934,944 2 112,934,944 3	61,304,566 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 61,934,442 61,998,035 62,788,611 69,179,289 61,728,337 725,132,771 63,025,520 69,185,297 78,350,611 62,211,278 82,449,411	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes incl. IKZF1 5 genes incl. IKZF1 5 genes incl. CDKN2A/C9orf53 5 genes incl. CDKN2B 5 genes incl. CDKN2B 5 genes incl. PAX5 5 genes BCAT1 5 genes incl. SLX4IP no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 24-a-ALPN-RI 24-a-APN-RI	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3p21.1 9 p13.2p13.1 12 p13.31p13.2 12 p12.1 1y 20 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2 7 p12.2p12.1	22,255,000 5 50,417,522 5 10 50,417,522 5 10 21,934,442 2 112,053,565 11 112,053,565 11 113,053,565 11 114,935 5 115,053,565 12 115,934,442 2 115,934,442 2 115,938,035 3 115,053,576 3 115,053,576 3 115,055,793 1	61,304,566 60,454,736 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 61,934,442 61,998,035 82,788,611 89,179,289 11,728,337 725,132,771 83,025,520 89,185,297 88,350,611 12,211,278 82,449,411 60,417,522 60,462,935 62,905,808	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes incl. IKZF1 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 5 genes incl. CDKN2B 5 genes incl. CDKN2B 5 genes incl. PAX5 5 genes BCAT1 5 genes incl. SLX4IP no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA 5 genes incl. IKZF1 IKZF1 KZF1 S genes incl. IKZF1
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 24-a-MPN-RI 44-a-MPN-RI	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3 12 p13.2p13.1 12 p13.31p13.2 12 p12.1 14 q32.1 15 p23.2 16 p21.32 17 p14.3p12.2 18 p12.2 19 p12.2 19 p12.1 10 q32.1 2 p23.2 3 q13.2 10 p21.32 11 q32.1 2 p23.2 3 q13.2 11 q32.1 2 p23.2 3 q13.2 11 q32.1 2 p23.2 3 q13.2 12 p21.32 13 q13.2 14 q22.3	100 22,255,000 5 100 50,417,522 5 100 21,934,442 2 100 112,053,565 11 108 0 17 100 44,935 5 100 21,934,442 2 110,934,442 2 110,934,442 2 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 110,938,035 3 1112,055,793 11 112,055,793 11	61,304,566 60,454,736 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 61,934,442 61,998,035 62,788,611 69,179,289 11,728,337 62,520 11,728,337 12,211,278 13,025,520 19,185,297 18,350,611 12,211,278 12,211,278 13,025,520 14,449,411 150,417,522 150,462,935 152,905,808 157,877,485 12,137,704	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes incl. IKZF1 > 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 > 5 genes incl. CDKN2B > 5 genes incl. PAX5 > 5 genes BCAT1 > 5 genes BCAT1 > 5 genes incl. SLX4IP no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA > 5 genes incl. IKZF1 IKZF1 > 5 genes no genes No genes No genes No genes No genes No genes
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 24-a-MPN-RI 44-a-MPN-RI	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3 12 p13.31p13.2 12 p12.1 12 p12.1 14 p23.2 15 p23.2 16 p24.3p21.3 17 p12.2p12.1 18 p23.2 19 p23.2 19 p23.2 19 p23.2 10 q32.1 2 p23.2 2 q13.2 2 p21.32 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1	22,255,000 5 100 50,417,522 5 100 21,934,442 2 1012,053,565 11 108 0 17 10 44,935 5 10 46,587 2 21,934,442 2 10 21,934,442 2 10 21,938,035 3 10 36,359,376 3 10 24,959,039 2 10 198,998,535 19 24,959,039 2 10 198,998,535 19 10 27,995,931 2 112,055,793 11 10 32,409,484 3 10 31,607,134 5 10 50,417,522 5 10 50,462,935 5 10 52,905,808 5 10 142,097,004 14 10 116,746,718 11 10 92,284,255 9 10 52,570,719 5	61,304,566 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 21,934,442 21,998,035 62,788,611 69,179,289 11,728,337 725,132,771 63,025,520 69,185,297 78,350,611 12,211,278 62,449,411 60,417,522 60,462,935 62,905,808 67,877,485 12,137,704 17,003,749 12,537,956 12,734,092	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes incl. IKZF1 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 5 genes incl. CDKN2B 5 genes incl. PAX5 5 genes incl. PAX5 5 genes BCAT1 5 genes incl. SLX4IP no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA 5 genes incl. IKZF1 IKZF1 5 genes no genes SIK3 C12orf79/BTG1 no genes
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 24-a-MPN-RI 44-a	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3p21.1 9 p13.2p13.1 12 p13.31p13.2 12 p12.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q12 15 q26.1	22,255,000 5 100 50,417,522 5 100 21,934,442 2 1012,053,565 11 108 0 17 10 44,935 5 10 46,587 2 21,934,442 2 10 21,934,442 2 10 21,938,035 3 10 36,359,376 3 10 9,823,553 1 124,959,039 2 10 198,998,535 19 27,995,931 2 112,055,793 11 10 27,995,931 2 112,055,793 11 10 32,409,484 3 10 31,607,134 5 10 50,417,522 5 10 50,462,935 5 52,905,808 5 10 142,097,004 14 10 116,746,718 11 10 92,284,255 9	1,304,566 60,454,736 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 21,934,442 21,998,035 62,788,611 69,179,289 11,728,337 25,132,771 63,025,520 69,185,297 28,350,611 12,211,278 60,417,522 60,462,935 62,734,092 60,043,341 103,441,907	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes incl. IKZF1 5 genes MTAP/CDKN2B-AS1/CDKN2A/C9orf53 > 5 genes incl. CDKN2B 5 genes incl. PAX5 5 genes incl. PAX5 5 genes BCAT1 5 genes incl. SLX4IP no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA 5 genes incl. IKZF1 IKZF1 > 5 genes no genes SIK3 C12orf79/BTG1
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 24-a-MPN-RI 44-a-MPN-RI	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3p21.1 9 p13.2p13.1 12 p13.31p13.2 12 p12.1 12 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2	22,255,000 5 10 50,417,522 5 10 21,934,442 2 112,053,565 11 118	31,304,566 30,454,736 30,454,736 32,004,153 12,246,081 71,115,067 33,481,902 21,934,442 21,998,035 32,788,611 39,179,289 11,728,337 25,132,771 33,025,520 39,185,297 28,350,611 12,211,278 32,449,411 30,417,522 30,462,935 32,905,808 37,877,485 12,137,704 17,003,749 32,537,956 32,734,092 33,441,907 37,018,280 39,185,297 28,350,611	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes KZF1 6 genes KZF1 7 genes KZF1 1 KZF1 1 KZF1 5 genes KZF1 5 genes KZF1 5 genes KZF1 1 KZF1 5 genes KZF1 5 genes KZF1 1 KZF1 5 genes KZF1 6 GENES KZF1 7 GENES KZF1 8 GENES KZF1 9 GENES K
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17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 23-a-ALL 24-a-MPN-RI 24	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3 12 p13.31p13.2 12 p12.1 12 p12.1 13 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p42.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2p12.1	22,255,000 5 100 50,417,522 5 100 50,417,522 5 100 17,934,442 2 112,053,565 11 112,053,565 11 112,053,565 11 112,053,565 11 112,053,766 3 112,053,766 3 112,053,766 3 112,055,793 11	31,304,566 30,454,736 30,454,736 32,204,153 12,246,081 71,115,067 33,481,902 21,934,442 21,998,035 32,788,611 39,179,289 11,728,337 25,132,771 33,025,520 39,185,297 28,350,611 12,211,278 32,449,411 30,417,522 30,462,935 32,905,808 37,877,485 12,137,704 17,003,749 12,537,956 32,734,092 32,60,43,341 33,441,907 37,018,280 39,185,297 28,350,611 12,211,278 30,449,411 30,441,907 37,018,280 39,185,297 38,350,611 12,211,278 39,185,297 30,449,411 30,441,907 37,018,280 39,185,297 38,350,611 12,211,278 39,185,297 30,462,935	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA > 5 genes 5 genes KZF1 6 genes KZF1 7 genes KZF1 8 genes KZF1 9 genes KZF1 1 kZF1 1 kZF1 5 genes KZF1 1 kZF1
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3p21.1 12 p13.31p13.2 12 p12.1 12 p12.1 13 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2 7 p12.2 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2 7 p12.1 7 p12.1 7 p12.1	22,255,000 5 100 50,417,522 5 100 21,934,442 2 1012,053,565 11 108 0 17 10 44,935 5 10 21,934,442 2 10 21,934,442 2 10 21,934,442 2 10 21,938,035 3 10 36,359,376 3 10 9,823,553 1 124,959,039 2 10 198,998,535 19 27,995,931 2 112,055,793 11 32,409,484 3 31,607,134 5 50,417,522 5 10 50,462,935 5 52,905,808 5 142,097,004 14 1016,746,718 11 10 92,284,255 9 10 52,570,719 5 26,037,199 2 93,387,339 9 10 36,705,797 3 10 198,998,535 19 27,995,931 2 112,055,793 11 32,409,484 3 44,935 5 50,417,522 5	31,304,566 30,454,736 30,454,736 32,204,153 12,246,081 71,115,067 33,481,902 21,934,442 21,998,035 32,788,611 39,179,289 11,728,337 25,132,771 33,025,520 39,185,297 28,350,611 12,211,278 32,449,411 30,417,522 30,462,935 32,905,808 37,877,485 32,449,411 33,441,907 37,018,280 39,185,297 28,350,611 33,441,907 37,018,280 39,185,297 28,350,611 33,441,907 37,018,280 39,185,297 28,350,611 30,2537,956 32,734,092 32,6043,341 33,441,907 37,018,280 39,185,297 28,350,611 32,211,278 32,449,411 30,366,637 30,462,935 32,295,068 32,295,068 32,295,068 32,295,068 32,787,485	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087 453,084 4,971,677	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA 5 genes 5 genes incl. IKZF1 5 genes incl. IKZF1 5 genes incl. CDKN2B/C9orf53 > 5 genes incl. CDKN2B/C9orf53 > 5 genes incl. CDKN2B 5 genes incl. CDKN2B 5 genes incl. PAX5 5 genes BCAT1 5 genes incl. SLX4IP no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA 5 genes incl. IKZF1 KZF1 5 genes no genes SIK3 C12orf79/BTG1 no genes ATP10A/MIR4509-1 LOC100507217/CHD2 5 genes no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA 5 genes no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA 5 genes incl. IKZF1 IKZF1 IKZF1
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 22-a-ALL 24-a-MPN-RI 34-a-MPN-R	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3p21.1 12 p13.31p13.2 12 p12.1 14 p13.31p13.2 15 p12.1 16 p23.2 17 p12.2 18 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2 7 p12.1 7 p12.1p11.2 7 q34q36.3 8 q24.3 9 p22.1p21.3	22,255,000 5 50,417,522 5 10 21,934,442 2 112,053,565 11 113,053,565 11 114,053,565 11 114,053,565 11 115,053,565 11 115,053,565 11 115,053,766 3 116,053,766 3 117,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 116,746,718 11 116,746,718 11 117,055,793 11 116,746,718 11 117,055,793 11 116,746,718 11 117,055,793 11 116,746,718 11 117,055,793 11 117,055,793 11 118,093,387,339 9 119,387,339 9 110,338,7339 9 110,338,7339 9 110,338,7339 9 1112,055,793 11 112,055,793 11	31,304,566 30,454,736 30,454,736 30,454,736 32,204,153 32,246,081 71,115,067 33,481,902 21,934,442 21,998,035 32,788,611 39,179,289 31,728,337 25,132,771 33,025,520 39,185,297 28,350,611 32,241,278 32,449,411 30,417,522 30,462,935 32,734,092 32,734,092 32,734,092 32,734,092 32,734,092 33,441,907 37,018,280 39,185,297 28,350,611 30,417,522 31,211,278 32,449,411 33,441,907 37,018,280 39,185,297 38,350,611 39,127,048 30,462,935 30,462	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087 453,084 4,971,677 17,324,425 40,700 2,052,630	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 24-a-MPN-RI 44-a-MPN-RI	Monoallelic loss Monoallelic loss Gain Monoallelic loss Monoallelic loss Monoallelic loss Gain Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3p21.1 12 p13.2p13.1 12 p13.31p13.2 12 p12.1 14 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2 7 p12.2p12.1 7 p12.1p11.2 7 q34q36.3 8 q24.3 9 p22.1p21.3 9 p21.3p13.1	22,255,000 5 50,417,522 5 10 21,934,442 2 112,053,565 11 112,053,565 11 112,053,565 11 112,053,565 11 112,053,565 11 112,053,563 12 112,934,442 2 113,934,442 2 113,934,442 2 113,934,442 2 113,934,353 11 113,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 112,055,793 11 113,055,793 11 114,097,004 14 116,746,718 11 115,225 15 114,097,004 14 116,746,718 11 117,055,793 11	31,304,566 30,454,736 30,454,736 32,004,153 12,246,081 71,115,067 33,481,902 21,934,442 21,998,035 32,788,611 39,179,289 11,728,337 25,132,771 33,025,520 39,185,297 28,350,611 12,211,278 32,449,411 30,417,522 30,462,935 32,784,092 32,449,411 33,441,907 37,018,280 39,185,297 28,350,611 12,211,278 32,449,411 33,441,907 37,018,280 39,185,297 38,350,611 12,211,278 32,449,411 33,441,907 37,018,280 39,185,297 38,350,611 12,211,278 32,449,411 33,441,907 37,018,280 39,185,297 38,350,611 12,211,278 32,449,411 30,366,637 30,462,935 32,295,068 32,295,288 32,295,288 33,295,288 34,412 34,412 34,412 34,412 34,413 34,442 34,411 34,442 34,411 34,442 34,411 34,442 34,941 34,941 34,442 34,941 34,442 34,941	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087 453,084 4,971,677 17,324,425 40,700 2,052,630 68,925	> 5 genes
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 22-	Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3p21.1 12 p13.31p13.2 12 p12.1 14 p23.2 15 p24.3 11 q23.2 17 p12.1p11.2 18 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2p12.1 7 p12.1p11.2 7 q34q36.3 8 q24.3 9 p22.1p21.3 9 p21.3p13.1 11 q23.3 12 q21.33 14 q22.1	22,255,000 5 100 50,417,522 5 101 50,417,522 5 101 21,934,442 2 101 12,053,565 11 108	1,304,566 60,454,736 60,454,736 60,454,736 62,004,153 12,246,081 71,115,067 63,481,902 61,934,442 61,998,035 62,788,611 69,179,289 61,728,337 725,132,771 63,025,520 69,185,297 78,350,611 78,12211,278 78,2449,411 78,2449,411 78,2449,411 78,247,485 78,734,092 78,350,611 78,7018,280 78,734,092 78,350,611 78,7018,280 78,734,092 78,350,611 78,7018,280 78,734,092 78,350,611 78,7018,280 78,734,092 78,350,611 78,7018,280 78,734,092 78,366,637 78,718,280 78,718,280 78,718,297 78,366,637 78,718,280 78,366,637 78,485 78,774,485 78,719,486 78,77,485 78,77,485 78,77,485 78,77,485 78,77,485 78,77,485 78,77,485 78,77,966	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087 453,084 4,971,677 17,324,425 40,700 2,052,630 6,8925 17,175,922 257,031 253,701 163,373	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 23-a-ALL 24-a-MPN-RI 34-a-MPN-RI 34-a-MPN-	Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3p21.1 12 p13.31p13.2 12 p12.1 13 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2 7 p12.2p12.1 7 p12.1p11.2 7 q34q36.3 8 q24.3 9 p22.1p21.3 9 p21.3 11 q23.3 12 q22.1 15 q12 15 q26.1 16 q24.3	22,255,000 5 50,417,522 5 10 21,934,442 2 112,053,565 11 112,053,565 11 113,053,565 11 114,053,565 11 115,053,765 11 115,053,765 11 115,053,765 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 116,746,718 11 117,055,793 11 116,746,718 11 117,055,793 11 116,746,718 11 117,055,793 11 116,746,718 11 117,055,793 11 116,746,718 11 117,055,793 11 117,055,793 11 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 118,998,535 19 119,998,535 19 119,998,535 19 110,055,793 11 110,055,7	31,304,566 30,454,736 30,454,736 30,454,736 31,2246,081 31,115,067 33,481,902 31,934,442 31,998,035 32,788,611 39,179,289 31,728,337 33,025,520 39,185,297 38,350,611 32,211,278 32,449,411 30,417,522 30,462,935 32,905,808 37,877,485 32,137,704 31,704,341 31,441,907 37,018,280 39,185,297 38,350,611 39,179,289 30,462,935 30,46	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087 45,3084 4,971,677 17,324,425 40,700 2,052,630 68,925 17,175,922 257,031 253,701 163,373 6,142 54,568 39,927	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 24-a-MPN-RI 4-a-MPN-RI	Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3p21.1 12 p13.2p13.1 12 p13.31p13.2 12 p12.1 14 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2 7 p12.2 7 p12.2 7 p12.1 7 p12.1p11.2 7 q34q36.3 8 q24.3 9 p22.1p21.3 9 p21.3p13.1 11 q23.3 12 q21.33 14 q22.1 15 q12 17 p12.1p11.2 7 q34q36.3 8 q24.3 9 p22.1p21.3 9 p21.3p13.1 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 16 q24.3 19 q13.12 Y	22,255,000 5 50,417,522 5 10 21,934,442 2 112,053,565 11 es	31,304,566 30,454,736 30,454,736 30,454,736 32,204,153 12,246,081 71,115,067 33,481,902 21,934,442 21,998,035 32,788,611 39,179,289 11,728,337 25,132,771 33,025,520 39,185,297 28,350,611 12,211,278 32,449,411 30,417,522 30,462,935 32,905,808 37,877,485 42,137,704 17,003,749 12,237,956 32,734,092 32,449,411 33,441,907 37,018,280 39,185,297 28,350,611 22,211,278 32,449,411 30,446,935 32,295,661 32,211,278 32,449,411 30,462,935 32,295,668 32,295,668 32,295,668 32,295,668 32,295,668 32,295,808 37,877,485 39,119,486 42,137,704 41,934,442 42,003,367 49,179,289 47,037,956 62,734,092 62,643,341 43,441,907 47,037,956 62,734,092 62,643,341 48,941 49,179,289 47,037,956 62,734,092 62,637,956 62,734,092 62,643,341 63,441,907	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087 453,084 4,971,677 17,324,425 40,700 2,052,630 68,925 17,175,922 257,031 253,701 163,373 6,142 54,568	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L
17-a-ALL 17-a-ALL 17-a-ALL 17-a-ALL 19-a-ALL 19-a-ALL 19-a-ALL 22-a-ALL 24-a-MPN-RI 4-a-MPN-RI 4-a-MP	Monoallelic loss	13 q14.11q34 16 p13.3 22 q11.22q13.33 7 p12.2 9 p21.3 3 q13.2 6 7 p22.3p12.1 9 p24.3p21.3 9 p21.3 9 p21.3 9 p21.3p21.1 12 p13.31p13.2 12 p12.1 12 p12.1 12 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p14.3p12.2 7 p12.2p12.1 7 p12.1p11.2 8 q24.3 11 q23.3 12 q21.33 14 q22.1 15 q12 15 q26.1 19 q13.12 1 q32.1 2 p23.2 3 q13.2 6 p21.32 7 p22.3p12.2 7 p12.2 7 p12.2p12.1 7 p12.1p11.2 7 q34q36.3 8 q22.3 9 p22.1p2.3 9 p21.3 9 p22.3p12.2 7 p12.2 7 p12	22,255,000 5 10 50,417,522 5 112,053,565 11 112,053,565 11 113,053,565 11 114,053,565 11 114,053,565 11 115,053,766 11 115,053,766 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 115,055,793 11 116,746,718 11 116,746,718 11 116,746,718 11 116,746,718 11 116,746,718 11 116,746,718 11 116,746,718 11 116,746,718 11 116,746,718 11 116,746,718 11 117,055,793 11	1,304,566 60,454,736 60,454,736 60,454,736 62,2004,153 12,246,081 71,115,067 63,481,902 61,934,442 61,998,035 62,788,611 69,179,289 61,728,337 725,132,771 63,025,520 69,185,297 78,350,611 61,211,278 62,449,411 60,417,522 60,462,935 62,734,092 62,734,092 62,734,092 62,734,092 63,441,907 67,018,280 69,185,297 68,350,611 61,211,278 62,449,411 60,417,522 60,462,935 62,734,092 62,734,092 62,734,092 63,441,907 67,018,280 69,185,297 68,350,611 60,462,935 62,734,092 62,734,092 62,734,092 63,441,907 67,018,280 67,877,485 67,877,485 67,877,485 67,919,486 62,734,092 62,905,808 67,877,485 69,19,486 62,137,704 61,934,442 62,003,367 69,19,289 67,003,749 69,179,289 67,003,749 69,179,289 67,003,749 67,003,	2,351,868 29,049,566 37,214 69,711 192,516 171,115,067 53,436,967 21,887,855 63,593 10,790,576 2,819,913 1,904,784 173,732 63,025,520 186,762 354,680 155,485 39,927 18,810,388 45,413 2,442,873 4,971,677 40,700 257,031 253,701 163,373 6,142 54,568 312,483 186,762 354,680 155,485 39,927 50,321,702 45,413 1,825,087 453,084 4,971,677 17,324,425 40,700 2,052,630 68,925 17,175,922 257,031 253,701 163,373 6,142 54,568 39,927 50,321,702 45,413 1,825,087 453,084 4,971,677 17,324,425 40,700 2,052,630 68,925 17,175,922 257,031 253,701 163,373 6,142 54,568 39,081 312,483 59,373,566 14,831,242 3,351,130 33,812	> 5 genes > 5 genes incl. RB1/LCP1/KIAA0226L > 5 genes > 5 genes KZF1 MTAP/CDKN2B-AS1/CDKN2A/CDKN2B/C9orf53 CD200/BTLA > 5 genes 5 genes incl. IKZF1 > 5 genes incl. IKZF1 > 5 genes incl. CDKN2B > 5 genes incl. SLX4IP no genes MRPL33/BRE/RBKS/BRE-AS1/MIR4263 CD200/BTLA HLA-DRA > 5 genes incl. IKZF1 KZF1 > 5 genes incl. IKZF1 KZF1 > 5 genes incl. IKZF1 > 5 genes incl. IKZF1 IKZF1 > 5 genes incl. IKZF1 > 5 genes incl. IKZF1 Department of the property of
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Selected genes recurrently deleted in human ALL or genes found frequently affected in ETV6/ABL1-positive ALL within the present study are highlighted in bold.

 $Samples \ from \ disease \ recurrences \ are \ labeled \ by \ "R" \ within \ the \ case \ ID, \ the \ order \ of \ recurrence(s) \ is \ displayed \ in \ roman \ numerals.$

Table S3. Total numbers of CNA and particular CNA subtypes in *ETV6-ABL1*-positive cases analyzed by SNParray

Case ID	total	Losses	Gains	UPDs	UN
01-ch-ALL	9	9	-	-	-
02-ch-ALL	5	5	-	-	-
05-ch-ALL	6	6	-	-	-
05-ch-ALL-RII*	5	5	-	-	-
08-ch-ALL	6	3	3	-	-
09-ch-ALL	13	12	1	-	-
10-ch-ALL	18	13	5	-	-
11-ch-ALL	4	3	1	-	-
12-ch-ALL	9	8	1	-	-
13-ch-LBL	23	21	1	1	-
13-ch-LBL-RII*	26	23	1	-	2
14-a-ALL	29	28	1	-	-
15-a-ALL	3	3	-	-	-
17-a-ALL	13	11	2	-	-
19-a-ALL	2	2	-	-	-
22-a-ALL	10	8	1	1	-
34-a-MPN	0	-	-	-	-
34-a-MPN-RI*	15	15	-	-	-
34-a-MPN-RII*	22	21	-	-	1
38-a-MPN	0	-	-	-	-
40-a-MPN	12	10	2	-	-

Abbreviations: CNA, copy number aberration; UPD, uniparental disomy; UN, uncertain - aberration with mosaic character (e.g. subclonal change) with a small shift of copy number value which cannot be univocally called as loss/gain.

^{*} Disease recurrences; the order of recurrence(s) is displayed in roman numerals.