Characterization of leukemias with *ETV6-ABL1* fusion

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 doi:10.3324/haematol.2016.144345

Received: February 12, 2016

Accepted: May 18, 2016

Pre-published: May 26, 2016.

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Supplementary figures S1-S4, supplementary tables S1-S3

Figure S1

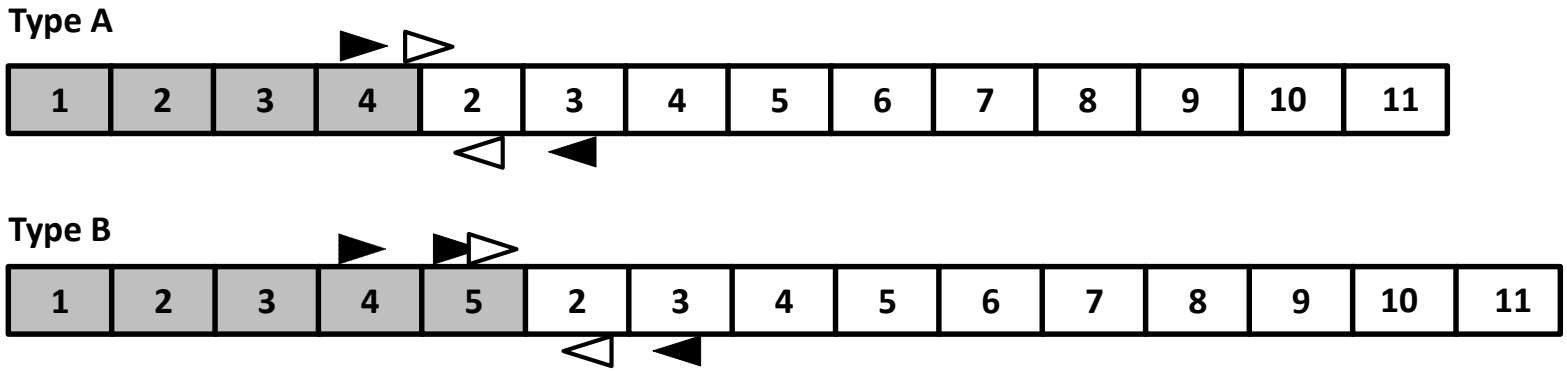

Fig S1 ETV6-ABL1 fusion transcript variants.
Schematic representation of two types of ETV6-ABL1 fusion transcript. Type A transcript differs from type B transcript by the absence of ETV6 exon 5. Grey boxes represent ETV6 and white boxes ABL1 exons. Black triangles represent primers used for detection 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

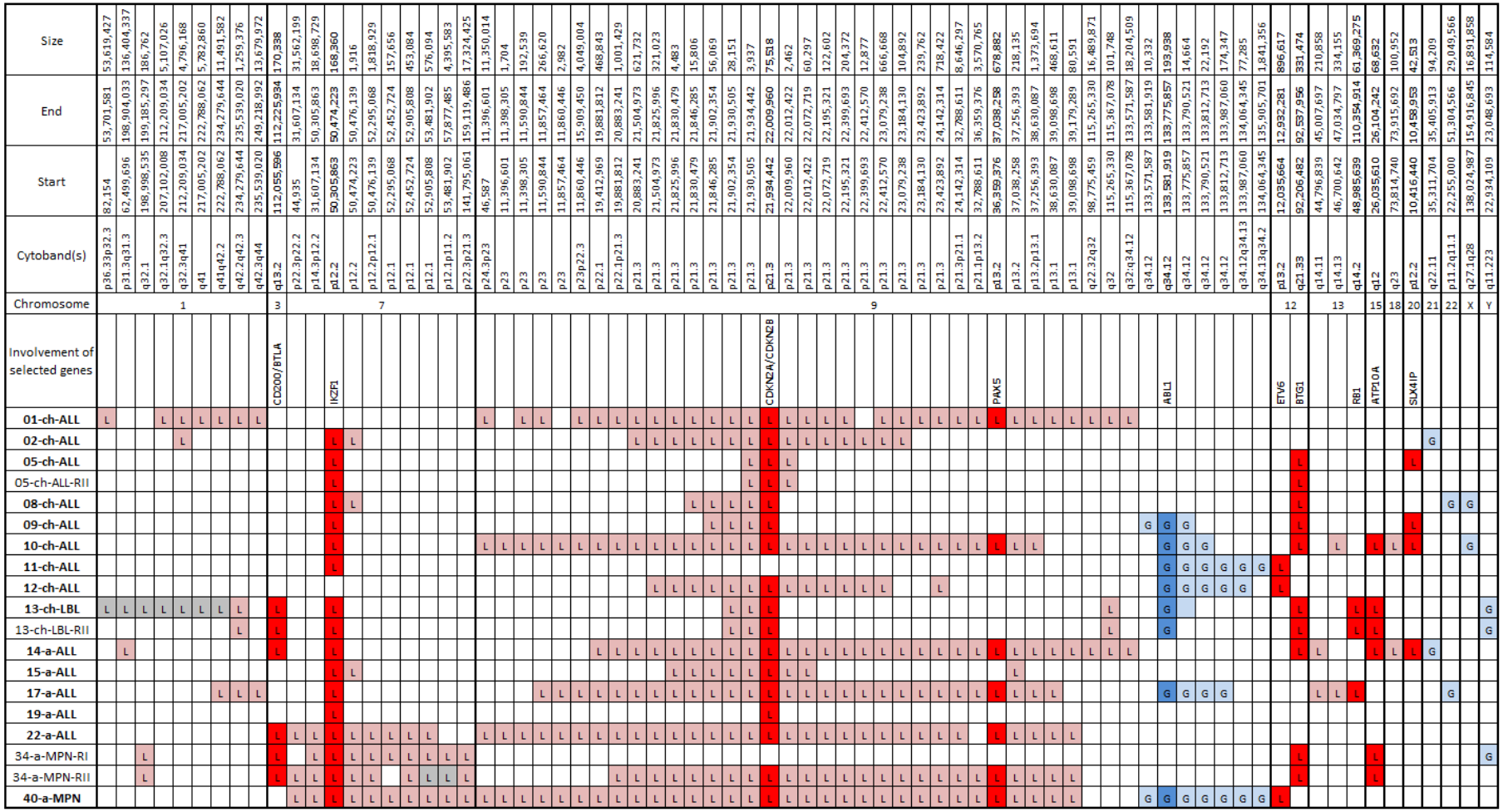

Fig S2 Genomic regions recurrently affected by CNA in ETV6/ABL1-positive malignancies.
All regions where losses (L) or gains (G) of at least 2 individual cases overlap are included. No regions of recurrent UPD were found. Regions which include selected important genes recurrently affected in human ALL 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

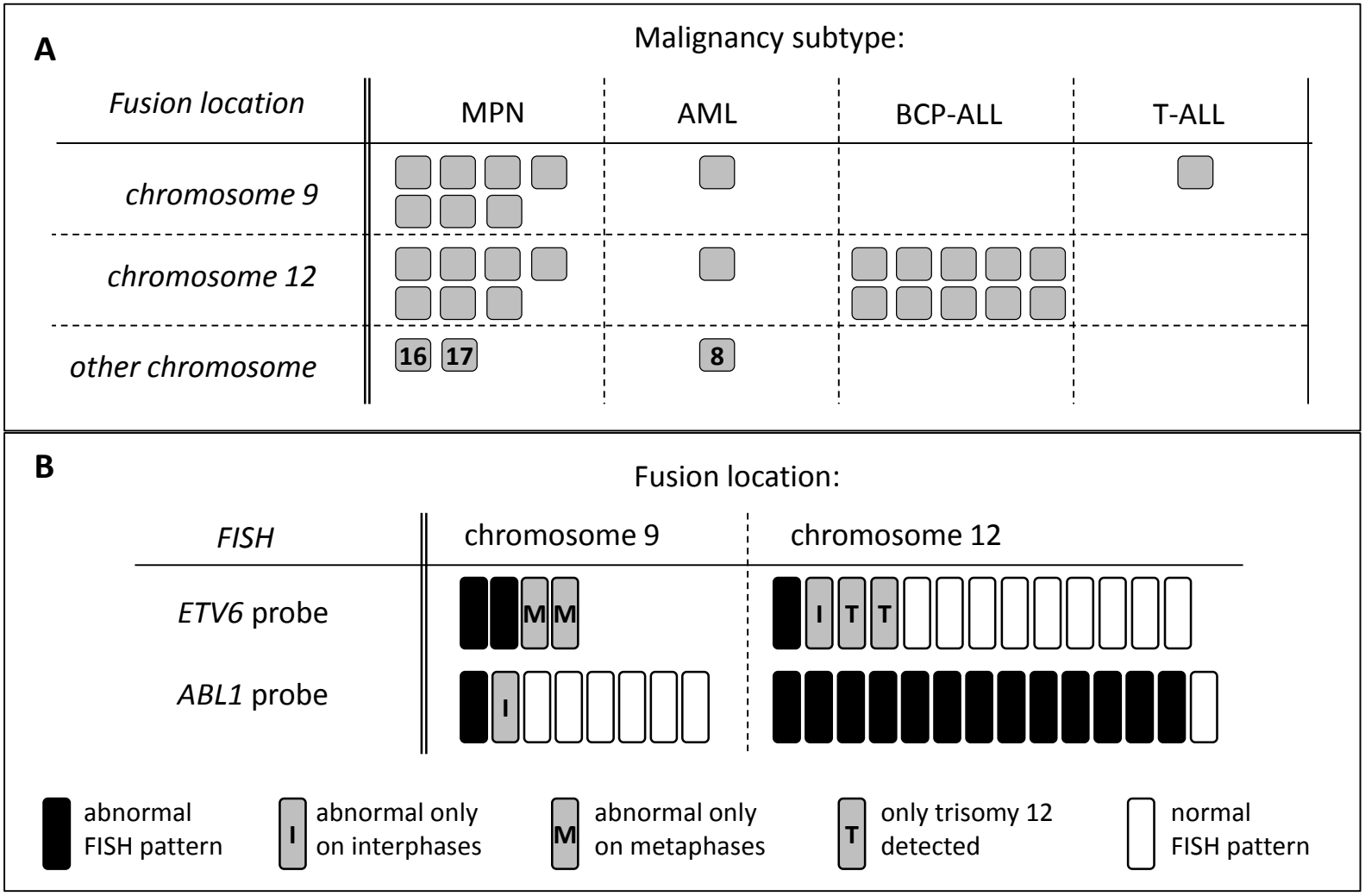

Fig S3: **Chromosomal localization of *ETV6-ABL1* fusion and results of FISH with commercial *ETV6* and *ABL1* probes.**
(A) Chromosomal localization of *ETV6-ABL1* fusion. In contrast to the even distribution of fusion location between chromosomes 12 and 9 in MPN/AML (8:8), in all 10 BCP-ALL cases where 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
ETV6-ABL1 (present study)	**total affected ALL/LBC cases**	**16**	**15**	**8**	**7**	**7**	**5**	**4**	**4**	**3**	**2**
	(%)	**94**	**88**	**47**	**41**	**41**	**29**	**24**	**24**	**18***	**12**
	total affected ch-ALL (%)	*90*	*80*	*30*	*50*	*50*	*40*	*20*	*10*	*20**	*10*
	total affected a-ALL (%)	*100*	*100*	*60*	*20*	*20*	*20*	*20*	*40*	*0*	*20*
literature data	**frequency in Ph^{pos} ALL[50] (%)**	**53&**	**84**	**51**	**14**	**n.r.**	**23**	**n.r.**	**n.r.**	**7**	**19**
	frequency in Ph^{pos} chALL[50] (%)	*48&*	*76*	*48*	*19*	*-*	*33*	*-*	*-*	*10*	*19*
	frequency in Ph^{pos} aALL[50] (%)	*59&*	*91*	*55*	*9*	*-*	*14*	*-*	*-*	*5*	*18*
	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**
	frequency in Ph^{neg} chALL[51] (%)	**25**	**8**	**23**	**6**	**n.r.**	**5**	**n.r.**	**n.r.**	**24**	**4**

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	Commercial ABL1 FISH probe used	Commercial ETV6 FISH probe used	Reference
01-ch-ALL	BCP-ALL	46,XX	n.r.	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)	*46,XY*	*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	Park et al. (2013)
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 3'TEL); 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	ES DC, BA	Zuna et al. (2010)
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	Park et al. (2013)
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)	*no karyotype*	*ETV6/ABL1 on 12p13*	*ES DC*	*DC DF*	
	2nd recurrence (MPN-LBC)	*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;p13p13)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	46,XY [20]	no FISH performed	n.r.	n.r.	Kelly et al. (2009)
	Recurrence (MPN-MBC)	*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	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	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)(p13q11t(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)
	Recurrence (MPN-MBC)	*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*	
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

Table S2. Full list of CNAs identified in ETV6/ABL1-positive cases identified by SNParray

Case ID	CNA type	Chromosome	Cytobands	Whole chromosome*	Start	End	Size	Genes
01-ch-ALL	Monoallelic loss	1	p36.33p32.3	no	82,154	53,701,581	53,619,427	> 5 genes
01-ch-ALL	Monoallelic loss	1	q32.1q44	no	207,102,008	249,218,992	42,116,984	> 5 genes
01-ch-ALL	Monoallelic loss	2	p22.1p15	no	39,497,758	62,629,315	23,131,557	> 5 genes
01-ch-ALL	Monoallelic loss	4	q32.1q35.2	no	160,594,757	190,915,650	30,320,893	> 5 genes
01-ch-ALL	Monoallelic loss	9	p24.3p23	no	46,587	11,396,601	11,350,014	> 5 genes
01-ch-ALL	Monoallelic loss	9	p23	no	11,398,305	11,857,464	459,159	no genes
01-ch-ALL	Monoallelic loss	9	p23p21.3	no	11,860,446	22,399,693	10,539,247	> 5 genes incl. **CDKN2A/CDKN2B**
01-ch-ALL	Monoallelic loss	9	p21.3p13.1	no	22,412,570	39,179,289	16,766,719	> 5 genes incl. **PAX5**
01-ch-ALL	Monoallelic loss	9	q22.32q34.12	no	98,775,459	133,571,587	34,796,128	> 5 genes
02-ch-ALL	Monoallelic loss	1	q32.3q41	no	212,209,034	217,005,202	4,796,168	> 5 genes
02-ch-ALL	Monoallelic loss	7	p12.2	no	50,350,267	50,476,139	125,872	**IKZF1**
02-ch-ALL	Monoallelic loss	9	p21.3	no	20,883,241	21,902,354	1,019,113	> 5 genes
02-ch-ALL	Biallelic loss	9	p21.3	no	21,902,354	22,004,153	101,799	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
02-ch-ALL	Monoallelic loss	9	p21.3	no	22,004,153	23,184,130	1,179,977	MTAP/CDKN2B-AS1/DMRTA1/LINC01239/**CDKN2B**
02-ch-ALL	Monoallelic loss	21	q22.11	no	35,311,704	35,405,913	94,209	LINC00649
05-ch-ALL	Monoallelic loss	7	p12.2	no	50,418,242	50,462,935	44,693	**IKZF1**
05-ch-ALL	Biallelic loss	9	p21.3	no	21,930,505	22,012,422	81,917	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
05-ch-ALL	Monoallelic loss	12	q21.33	no	92,284,255	92,536,826	252,571	C12orf79/**BTG1**
05-ch-ALL	Monoallelic loss	15	q26.1	no	92,076,959	92,575,841	498,882	SLCO3A1
05-ch-ALL	Monoallelic loss	20	p12.2	no	10,416,440	10,458,953	42,513	**SLX4IP**
05-ch-ALL	Monoallelic loss	X	p22.31	no	6,147,790	6,418,059	270,269	no genes
05-ch-ALL-RII	Monoallelic loss	7	p12.2	no	50,418,242	50,462,935	44,693	**IKZF1**
05-ch-ALL-RII	Biallelic loss	9	p21.3	no	21,930,505	22,012,422	81,917	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
05-ch-ALL-RII	Monoallelic loss	12	q21.33	no	92,284,255	92,536,826	252,571	C12orf79/**BTG1**
05-ch-ALL-RII	Monoallelic loss	15	q26.1	no	92,076,959	92,575,841	498,882	SLCO3A1
05-ch-ALL-RII	Monoallelic loss	X	p22.31	no	6,147,790	6,418,059	270,269	no genes
08-ch-ALL	Monoallelic loss	7	p12.2	no	50,350,267	50,476,139	125,872	**IKZF1**
08-ch-ALL	Monoallelic loss	9	p21.3	no	21,830,479	22,005,330	174,851	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
08-ch-ALL	Monoallelic loss	12	q21.33	no	92,206,482	92,537,956	331,474	C12orf79/**BTG1**
08-ch-ALL	Gain	17		yes	0	81,195,210	81,195,210	> 5 genes
08-ch-ALL	Gain	22		yes	0	51,304,566	51,304,566	> 5 genes
08-ch-ALL	Gain	X	q26.2q28	no	131,518,737	154,916,845	23,398,108	> 5 genes
09-ch-ALL	Monoallelic loss	2	q12.2	no	106,729,992	106,790,116	60,124	UXS1
09-ch-ALL	Monoallelic loss	2	q33.1	no	201,192,144	201,308,117	115,973	SPATS2L
09-ch-ALL	Monoallelic loss	7	p12.2	no	50,350,267	50,462,935	112,668	**IKZF1**
09-ch-ALL	Monoallelic loss	9	p21.3	no	21,846,285	21,865,842	19,557	MTAP
09-ch-ALL	Biallelic loss	9	p21.3	no	21,881,338	22,005,330	123,992	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
09-ch-ALL	Gain	9	q34.12	no	133,571,587	133,790,521	218,934	EXOSC2/**ABL1**/FIBCD1/QRFP
09-ch-ALL	Monoallelic loss	10	p15.1	no	3,836,471	3,868,226	31,755	no genes
09-ch-ALL	Monoallelic loss	12	q21.33	no	92,284,255	92,537,956	253,701	C12orf79/**BTG1**
09-ch-ALL	Monoallelic loss	15	q22.2	no	62,155,282	62,332,980	177,698	VPS13C
09-ch-ALL	Monoallelic loss	17	q21.32	no	45,187,429	45,499,396	311,967	MYL4/ITGB3/EFCAB13/CDC27/MIR4315-1
09-ch-ALL	Biallelic loss	19	p13.11p12	no	19,754,806	21,041,350	1,286,544	> 5 genes
09-ch-ALL	Monoallelic loss	19	p12	no	21,069,090	21,587,261	518,171	> 5 genes
09-ch-ALL	Biallelic loss	20	p12.2	no	10,416,440	10,443,064	26,624	**SLX4IP**
10-ch-ALL	Monoallelic loss	3	p14.2	no	60,066,610	60,559,240	492,630	FHIT
10-ch-ALL	Monoallelic loss	7	p12.2	no	50,350,267	50,457,188	106,921	**IKZF1**
10-ch-ALL	Gain	8	q13.1q24.3	no	66,354,675	146,298,143	79,943,468	> 5 genes
10-ch-ALL	Monoallelic loss	9	p24.3p21.3	no	46,587	21,833,000	21,786,413	> 5 genes
10-ch-ALL	Biallelic loss	9	p21.3	no	21,833,000	21,998,000	165,000	MTAP/CDKN2B-AS1/**CDKN2A**/C9orf53
10-ch-ALL	Monoallelic loss	9	p21.3p13.1	no	21,998,000	38,630,087	16,632,087	> 5 genes incl. **CDKN2B**/**PAX5**
10-ch-ALL	Gain	9	p13.1	no	38,631,767	39,778,619	1,146,852	CNTNAP3/ZNF658B
10-ch-ALL	Gain	9	q34.12	no	133,714,048	133,812,713	98,665	**ABL1**/FIBCD1/QRFP
10-ch-ALL	Monoallelic loss	11	q23.3	no	118,642,431	118,797,260	154,829	CXCR5/DDX6/BCL9L/MIR4492
10-ch-ALL	Monoallelic loss	12	q21.33	no	92,278,448	92,536,826	258,378	C12orf79/**BTG1**
10-ch-ALL	Monoallelic loss	13	q14.13	no	46,700,642	47,034,797	334,155	LCP1/KIAA0226L/LINC00563
10-ch-ALL	Monoallelic loss	15	q12	no	26,035,610	26,104,242	68,632	**ATP10A**/MIR4509-1/MIR4715
10-ch-ALL	Monoallelic loss	18	q23	no	73,597,826	73,915,692	317,866	LOC339298
10-ch-ALL	Monoallelic loss	20	p12.2	no	10,417,404	10,456,586	39,182	**SLX4IP**
10-ch-ALL	Gain	20	q11.22q11.23	no	32,576,128	37,262,128	4,686,000	> 5 genes
10-ch-ALL	Monoallelic loss	20	q11.23q13.33	no	37,267,729	62,956,141	25,688,412	> 5 genes
10-ch-ALL	Monoallelic loss	22	q11.22	no	22,517,826	23,294,984	777,158	> 5 genes
10-ch-ALL	Gain	X	q27.1q28	no	138,024,987	155,233,846	17,208,859	> 5 genes
11-ch-ALL	Monoallelic loss	3	p14.2p12.3	no	62,157,497	74,885,751	12,728,254	> 5 genes
11-ch-ALL	Monoallelic loss	7	p12.2	no	50,350,267	50,418,242	67,975	**IKZF1**
11-ch-ALL	Gain	9	q34.12q34.2	no	133,682,667	135,905,701	2,223,034	> 5 genes incl. **ABL1**
11-ch-ALL	Monoallelic loss	12	p13.2	no	12,039,551	12,156,322	116,771	**ETV6**
12-ch-ALL	Monoallelic loss	2	q14.1	no	117,373,537	117,566,409	192,872	no genes
12-ch-ALL	Monoallelic loss	9	p21.3	no	21,504,973	21,642,590	137,617	MIR31HG
12-ch-ALL	Biallelic loss	9	p21.3	no	21,651,620	22,189,716	538,096	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**
12-ch-ALL	Monoallelic loss	9	p21.3	no	22,195,321	23,079,238	883,917	DMRTA1/LINC01239
12-ch-ALL	Monoallelic loss	9	p21.3	no	23,423,892	24,142,314	718,422	ELAVL2
12-ch-ALL	Gain	9	q34.12q34.13	no	133,608,116	134,064,345	456,229	**ABL1**/LAMC3/AIF1L/NUP214/FIBCD1
12-ch-ALL	Monoallelic loss	12	p13.2p13.1	no	12,035,664	12,932,281	896,617	> 5 genes incl. **ETV6**
12-ch-ALL	Monoallelic loss	12	q24.32	no	128,703,350	128,747,854	44,504	no genes
12-ch-ALL	Monoallelic loss	19	q13.2	no	42,368,738	42,780,853	412,115	> 5 genes
13-ch-LBL	Uniparental disomy	1	p36.33p31.1	no	82,154	80,126,000	80,043,846	> 5 genes
13-ch-LBL	Monoallelic loss	1	p31.1p13.1	no	80,126,000	117,120,000	36,994,000	> 5 genes
13-ch-LBL	Monoallelic loss	1	q21.3	no	154,582,970	154,607,914	24,944	ADAR
13-ch-LBL	Monoallelic loss	3	q13.2	no	112,060,256	112,225,934	165,678	**CD200**/**BTLA**
13-ch-LBL	Monoallelic loss	4	q31.21q31.22	no	146,125,343	147,424,678	1,299,335	> 5 genes
13-ch-LBL	Monoallelic loss	5	q11.1	no	49,991,561	50,089,872	98,311	PARP8
13-ch-LBL	Monoallelic loss	6	p24.2	no	11,239,119	11,432,812	193,693	NEDD9
13-ch-LBL	Monoallelic loss	6	q23.3	no	136,648,627	136,753,218	104,591	MAP7
13-ch-LBL	Monoallelic loss	7	p12.2	no	50,350,267	50,417,522	67,255	**IKZF1**
13-ch-LBL	Biallelic loss	7	p12.2	no	50,417,522	50,462,935	45,413	**IKZF1**
13-ch-LBL	Monoallelic loss	7	p12.2	no	50,462,935	50,474,223	11,288	**IKZF1**
13-ch-LBL	Monoallelic loss	9	p21.3	no	21,902,354	22,003,367	101,013	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
13-ch-LBL	Monoallelic loss	9	q32	no	115,265,330	115,367,078	101,748	KIAA1958
13-ch-LBL	Gain	9	q34.12	no	133,593,939	133,775,857	181,918	**ABL1**/QRFP
13-ch-LBL	Monoallelic loss	10	q25.1	no	111,773,423	111,850,503	77,080	ADD3
13-ch-LBL	Monoallelic loss	12	q21.33	no	90,099,895	90,384,591	284,696	no genes
13-ch-LBL	Monoallelic loss	12	q21.33	no	92,206,482	92,539,590	333,108	C12orf79/**BTG1**
13-ch-LBL	Monoallelic loss	13	q14.2	no	48,985,639	49,079,503	93,864	**RB1**/LPAR6/RCBTB2
13-ch-LBL	Monoallelic loss	13	q33.3q34	no	110,299,924	110,354,914	54,990	no genes
13-ch-LBL	Monoallelic loss	15	q12	no	26,038,355	26,106,233	67,878	**ATP10A**/MIR4509-1/MIR4715
13-ch-LBL	Monoallelic loss	15	q26.1	no	90,461,129	90,574,591	113,462	ZNF710
13-ch-LBL	Monoallelic loss	18	q21.2	no	53,296,927	53,744,545	447,618	TCF4
13-ch-LBL	Monoallelic loss	Y	q11.223	no	22,934,109	23,048,693	114,584	RPS4Y2
13-ch-LBL-RII	UN	1	p36.33p31.1	no	82,154	80,126,000	80,043,846	> 5 genes
13-ch-LBL-RII	Monoallelic loss	1	p31.1p13.1	no	80,126,000	117,120,000	36,994,000	> 5 genes
13-ch-LBL-RII	Monoallelic loss	1	p12	no	119,068,677	119,146,085	77,408	no genes
13-ch-LBL-RII	Monoallelic loss	1	q21.3	no	154,582,970	154,607,914	24,944	ADAR
13-ch-LBL-RII	UN	1	q23.3q42.2	no	161,660,000	234,279,644	72,619,644	> 5 genes
13-ch-LBL-RII	Monoallelic loss	1	q42.2q42.3	no	234,279,644	235,539,020	1,259,376	> 5 genes
13-ch-LBL-RII	Monoallelic loss	3	q13.2	no	112,060,256	112,225,934	165,678	**CD200**/**BTLA**
13-ch-LBL-RII	Monoallelic loss	4	q31.21q31.22	no	146,125,343	147,424,678	1,299,335	> 5 genes
13-ch-LBL-RII	Monoallelic loss	5	q11.1	no	49,991,561	50,089,872	98,311	PARP8
13-ch-LBL-RII	Monoallelic loss	6	p24.2	no	11,239,119	11,432,812	193,693	NEDD9
13-ch-LBL-RII	Monoallelic loss	6	q23.3	no	136,648,627	136,753,218	104,591	MAP7
13-ch-LBL-RII	Monoallelic loss	7	p12.2	no	50,350,267	50,417,522	67,255	**IKZF1**
13-ch-LBL-RII	Biallelic loss	7	p12.2	no	50,417,522	50,462,935	45,413	**IKZF1**
13-ch-LBL-RII	Monoallelic loss	7	p12.2	no	50,462,935	50,474,223	11,288	**IKZF1**
13-ch-LBL-RII	Monoallelic loss	9	p21.3	no	21,902,354	22,003,367	101,013	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
13-ch-LBL-RII	Monoallelic loss	9	q32	no	115,265,330	115,367,078	101,748	KIAA1958
13-ch-LBL-RII	Gain	9	q34.12	no	133,593,939	133,775,857	181,918	**ABL1**/QRFP
13-ch-LBL-RII	Monoallelic loss	10	q25.1	no	111,773,423	111,850,503	77,080	ADD3
13-ch-LBL-RII	Monoallelic loss	12	q21.33	no	90,099,895	90,384,591	284,696	no genes
13-ch-LBL-RII	Monoallelic loss	12	q21.33	no	92,206,482	92,539,590	333,108	C12orf79/**BTG1**
13-ch-LBL-RII	Monoallelic loss	13	q14.2	no	48,985,639	49,079,503	93,864	**RB1**/LPAR6/RCBTB2
13-ch-LBL-RII	Monoallelic loss	13	q33.3q34	no	110,299,924	110,354,914	54,990	no genes
13-ch-LBL-RII	Monoallelic loss	15	q12	no	26,038,355	26,106,233	67,878	**ATP10A**/MIR4509-1/MIR4715
13-ch-LBL-RII	Monoallelic loss	15	q26.1	no	90,461,129	90,574,591	113,462	ZNF710
13-ch-LBL-RII	Monoallelic loss	18	q21.2	no	53,296,927	53,744,545	447,618	TCF4
13-ch-LBL-RII	Monoallelic loss	Y	q11.223	no	22,934,109	23,048,693	114,584	RPS4Y2
14-a-ALL	Monoallelic loss	1	p31.3	no	62,499,696	62,504,958	5,262	INADL
14-a-ALL	Monoallelic loss	1	q32.1	no	198,805,839	198,904,033	98,194	MIR181A1HG/MIR181B1/MIR181A1
14-a-ALL	Gain	3	p14.1	no	68,093,212	68,093,882	670	FAM19A1
14-a-ALL	Monoallelic loss	3	q13.2	no	112,055,596	112,215,558	159,962	**CD200**/**BTLA**
14-a-ALL	Monoallelic loss	4	q22.1	no	89,151,828	89,206,756	54,928	ABCG2/PPM1K
14-a-ALL	Monoallelic loss	5	q15	no	93,721,307	93,739,306	17,999	KIAA0825
14-a-ALL	Monoallelic loss	5	q21.1	no	102,167,708	102,454,941	287,233	PAM/GIN1
14-a-ALL	Biallelic loss	7	p12.2	no	50,350,267	50,418,949	68,682	**IKZF1**
14-a-ALL	Monoallelic loss	7	p12.2	no	50,423,963	50,457,188	33,225	**IKZF1**
14-a-ALL	Monoallelic loss	9	p22.1p21.3	no	19,412,969	21,956,331	2,543,362	> 5 genes
14-a-ALL	Biallelic loss	9	p21.3	no	21,956,914	21,999,228	42,314	MTAP/CDKN2B-AS1/**CDKN2A**/C9orf53
14-a-ALL	Monoallelic loss	9	p21.3	no	21,999,603	22,004,048	4,445	MTAP/CDKN2B-AS1/**CDKN2B**
14-a-ALL	Biallelic loss	9	p21.3	no	22,004,550	22,011,380	6,830	MTAP/CDKN2B-AS1/**CDKN2B**
14-a-ALL	Monoallelic loss	9	p21.3p13.1	no	22,011,477	40,619,209	18,607,732	> 5 genes incl. **PAX5**
14-a-ALL	Monoallelic loss	9	q21.11q34.12	no	70,940,583	133,581,919	62,641,336	> 5 genes
14-a-ALL	Monoallelic loss	10	q21.3	no	65,301,325	65,321,976	20,651	REEP3
14-a-ALL	Monoallelic loss	12	q12	no	46,148,733	46,159,838	11,105	ARID2
14-a-ALL	Monoallelic loss	12	q12	no	46,168,216	46,227,650	59,434	ARID2
14-a-ALL	Biallelic loss	12	q21.33	no	92,278,448	92,536,826	258,378	C12orf79/**BTG1**
14-a-ALL	Monoallelic loss	13	q14.11	no	44,796,839	45,007,697	210,858	SERP2/TSC22D1
14-a-ALL	Monoallelic loss	14	q32.2	no	98,130,332	98,138,102	7,770	LOC100129345
14-a-ALL	Monoallelic loss	15	q12	no	26,035,417	26,104,006	68,589	**ATP10A**/MIR4509-1/MIR4715
14-a-ALL	Monoallelic loss	15	q22.31	no	66,039,826	66,081,311	41,485	DENND4A
14-a-ALL	Monoallelic loss	15	q26.1	no	93,626,382	93,795,530	169,148	RGMA
14-a-ALL	Monoallelic loss	16	p13.13	no	12,190,002	12,279,574	89,572	SNX29
14-a-ALL	Monoallelic loss	16	q21	no	66,598,962	66,617,025	18,063	CKLF/CKLF-CMTM1/CMTM1/CMTM2
14-a-ALL	Monoallelic loss	18	q23	no	73,814,740	73,915,692	100,952	LOC339298
14-a-ALL	Monoallelic loss	20	p12.2	no	10,410,320	10,464,317	53,997	**SLX4IP**/MKKS
14-a-ALL	Monoallelic loss	21	q22.11	no	35,308,298	35,406,084	97,786	LINC00649
15-a-ALL	Monoallelic loss	7	p12.2	no	50,346,134	50,476,139	130,005	**IKZF1**
15-a-ALL	Monoallelic loss	9	p21.3	no	21,825,996	22,072,719	246,723	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
15-a-ALL	Monoallelic loss	9	p13.2	no	37,038,258	37,256,393	218,135	EBLN3/ZCCHC7
17-a-ALL	Monoallelic loss	1	q41q44	no	222,788,062	249,218,992	26,430,930	> 5 genes
17-a-ALL	Monoallelic loss	7	p12.2	no	50,305,863	50,366,637	60,774	**IKZF1**
17-a-ALL	Monoallelic loss	9	p23p22.3	no	11,590,844	15,909,450	4,318,606	> 5 genes
17-a-ALL	Biallelic loss	9	p22.3	no	15,909,450	15,942,765	33,315	CCDC171
17-a-ALL	Monoallelic loss	9	p22.3p21.3	no	15,942,765	21,974,218	6,031,453	> 5 genes incl. **CDKN2A**
17-a-ALL	Biallelic loss	9	p21.3	no	21,974,218	22,005,330	31,112	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**
17-a-ALL	Monoallelic loss	9	p21.3p13.1	no	22,005,330	39,098,698	17,093,368	> 5 genes incl. **CDKN2B**/**PAX5**
17-a-ALL	Gain	9	q34.12	no	133,670,874	133,987,060	316,186	**ABL1**/LAMC3/AIF1L/FIBCD1/QRFP
17-a-ALL	Monoallelic loss	12	p13.2p13.1	no	12,035,649	13,562,522	1,526,873	> 5 genes incl. **ETV6**
17-a-ALL	Monoallelic loss	13	q12.3q13.3	no	31,393,993	38,992,446	7,598,453	> 5 genes
17-a-ALL	Monoallelic loss	13	q14.11q34	no	43,549,782	115,103,529	71,553,747	> 5 genes incl. **RB1**/LCP1/KIAA0226L
17-a-ALL	Monoallelic loss	16	p13.3	no	88,165	2,440,033	2,351,868	> 5 genes
17-a-ALL	Gain	22	q11.22q13.33	no	22,255,000	51,304,566	29,049,566	> 5 genes
19-a-ALL	Monoallelic loss	7	p12.2	no	50,417,522	50,454,736	37,214	**IKZF1**
19-a-ALL	Monoallelic loss	9	p21.3	no	21,934,442	22,004,153	69,711	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
22-a-ALL	Monoallelic loss	3	q13.2	no	112,053,565	112,246,081	192,516	**CD200**/**BTLA**
22-a-ALL	Gain	6		yes	0	171,115,067	171,115,067	> 5 genes
22-a-ALL	Monoallelic loss	7	p22.3p12.1	no	44,935	53,481,902	53,436,967	> 5 genes incl. **IKZF1**
22-a-ALL	Monoallelic loss	9	p24.3p21.3	no	46,587	21,934,442	21,887,855	> 5 genes
22-a-ALL	Biallelic loss	9	p21.3	no	21,934,442	21,998,035	63,593	MTAP/CDKN2B-AS1/**CDKN2A**/C9orf53
22-a-ALL	Monoallelic loss	9	p21.3p21.1	no	21,998,035	32,788,611	10,790,576	> 5 genes incl. **CDKN2B**
22-a-ALL	Monoallelic loss	9	p13.2p13.1	no	36,359,376	39,179,289	2,819,913	> 5 genes incl. **PAX5**
22-a-ALL	Monoallelic loss	12	p13.31p13.2	no	9,823,553	11,728,337	1,904,784	> 5 genes
22-a-ALL	Monoallelic loss	12	p12.1	no	24,959,039	25,132,771	173,732	BCAT1
22-a-ALL	Uniparental disomy	20		yes	0	63,025,520	63,025,520	> 5 genes incl. **SLX4IP**
34-a-MPN-RI	Monoallelic loss	1	q32.1	no	198,998,535	199,185,297	186,762	no genes
34-a-MPN-RI	Monoallelic loss	2	p23.2	no	27,995,931	28,350,611	354,680	MRPL33/BRE/RBKS/BRE-AS1/MIR4263
34-a-MPN-RI	Monoallelic loss	3	q13.2	no	112,055,793	112,211,278	155,485	**CD200**/**BTLA**
34-a-MPN-RI	Monoallelic loss	6	p21.32	no	32,409,484	32,449,411	39,927	HLA-DRA
34-a-MPN-RI	Monoallelic loss	7	p14.3p12.2	no	31,607,134	50,417,522	18,810,388	> 5 genes incl. **IKZF1**
34-a-MPN-RI	Monoallelic loss	7	p12.2	no	50,417,522	50,462,935	45,413	**IKZF1**
34-a-MPN-RI	Monoallelic loss	7	p12.2p12.1	no	50,462,935	52,905,808	2,442,873	> 5 genes incl. **IKZF1**
34-a-MPN-RI	Monoallelic loss	7	p12.1p11.2	no	52,905,808	57,877,485	4,971,677	> 5 genes
34-a-MPN-RI	Monoallelic loss	8	q24.3	no	142,097,004	142,137,704	40,700	no genes
34-a-MPN-RI	Monoallelic loss	11	q23.3	no	116,746,718	117,003,749	257,031	SIK3
34-a-MPN-RI	Monoallelic loss	12	q21.33	no	92,284,255	92,537,956	253,701	C12orf79/**BTG1**
34-a-MPN-RI	Monoallelic loss	14	q22.1	no	52,570,719	52,734,092	163,373	no genes
34-a-MPN-RI	Monoallelic loss	15	q12	no	26,037,199	26,043,341	6,142	**ATP10A**/MIR4509-1
34-a-MPN-RI	Monoallelic loss	15	q26.1	no	93,387,339	93,441,907	54,568	LOC100507217/CHD2
34-a-MPN-RI	Monoallelic loss	19	q13.12	no	36,705,797	37,018,280	312,483	> 5 genes
34-a-MPN-RII	Monoallelic loss	1	q32.1	no	198,998,535	199,185,297	186,762	no genes
34-a-MPN-RII	Monoallelic loss	2	p23.2	no	27,995,931	28,350,611	354,680	MRPL33/BRE/RBKS/BRE-AS1/MIR4263
34-a-MPN-RII	Monoallelic loss	3	q13.2	no	112,055,793	112,211,278	155,485	**CD200**/**BTLA**
34-a-MPN-RII	Monoallelic loss	6	p21.32	no	32,409,484	32,449,411	39,927	HLA-DRA
34-a-MPN-RII	Monoallelic loss	7	p22.3p12.2	no	44,935	50,366,637	50,321,702	> 5 genes incl. **IKZF1**
34-a-MPN-RII	Biallelic loss	7	p12.2	no	50,417,522	50,462,935	45,413	**IKZF1**
34-a-MPN-RII	Monoallelic loss	7	p12.2p12.1	no	50,469,981	52,295,068	1,825,087	> 5 genes incl. **IKZF1**
34-a-MPN-RII	Monoallelic loss	7	p12.1	no	52,452,724	52,905,808	453,084	no genes
34-a-MPN-RII	UN	7	p12.1p11.2	no	52,905,808	57,877,485	4,971,677	> 5 genes
34-a-MPN-RII	Monoallelic loss	7	q34q36.3	no	141,795,061	159,119,486	17,324,425	> 5 genes
34-a-MPN-RII	Monoallelic loss	8	q24.3	no	142,097,004	142,137,704	40,700	no genes
34-a-MPN-RII	Monoallelic loss	9	p22.1p21.3	no	19,881,812	21,934,442	2,052,630	FOCAD/MTAP/MLLT3/PTPLAD2/MIR31HG
34-a-MPN-RII	Biallelic loss	9	p21.3	no	21,934,442	22,003,367	68,925	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
34-a-MPN-RII	Monoallelic loss	9	p21.3p13.1	no	22,003,367	39,179,289	17,175,922	> 5 genes incl. **CDKN2B**/**PAX5**
34-a-MPN-RII	Monoallelic loss	11	q23.3	no	116,746,718	117,003,749	257,031	SIK3
34-a-MPN-RII	Monoallelic loss	12	q21.33	no	92,284,255	92,537,956	253,701	C12orf79/**BTG1**
34-a-MPN-RII	Monoallelic loss	14	q22.1	no	52,570,719	52,734,092	163,373	no genes
34-a-MPN-RII	Monoallelic loss	15	q12	no	26,037,199	26,043,341	6,142	**ATP10A**/MIR4509-1
34-a-MPN-RII	Monoallelic loss	15	q26.1	no	93,387,339	93,441,907	54,568	LOC100507217/CHD2
34-a-MPN-RII	Monoallelic loss	16	q24.3	no	89,471,246	89,510,327	39,081	ANKRD11
34-a-MPN-RII	Monoallelic loss	19	q13.12	no	36,705,797	37,018,280	312,483	> 5 genes
34-a-MPN-RII	Monoallelic loss	Y		yes	0	59,373,566	59,373,566	> 5 genes
40-a-MPN	Monoallelic loss	4	p16.3p15.33	no	71,566	14,902,808	14,831,242	> 5 genes
40-a-MPN	Monoallelic loss	7	p22.3p22.2	no	44,935	3,396,065	3,351,130	> 5 genes
40-a-MPN	Biallelic loss	7	p22.2	no	3,400,463	3,434,275	33,812	SDK1
40-a-MPN	Monoallelic loss	7	p22.2q34	no	3,445,311	142,822,210	139,376,899	> 5 genes incl. **IKZF1**
40-a-MPN	Biallelic loss	7	q34	no	142,827,954	142,881,540	53,586	PIP/TAS2R39
40-a-MPN	Monoallelic loss	7	q34q36.3	no	142,899,393	159,119,486	16,220,093	> 5 genes
40-a-MPN	Monoallelic loss	9	p24.3p21.3	no	46,587	21,865,842	21,819,255	> 5 genes
40-a-MPN	Biallelic loss	9	p21.3	no	21,881,338	22,005,330	123,992	MTAP/CDKN2B-AS1/**CDKN2A**/**CDKN2B**/C9orf53
40-a-MPN	Monoallelic loss	9	p21.3p13.1	no	22,009,960	39,179,289	17,169,329	> 5 genes incl. **PAX5**
40-a-MPN	Gain	9	q21.11q34.3	no	70,984,372	141,066,491	70,082,119	> 5 genes incl. **ABL1**
40-a-MPN	Monoallelic loss	11	q22.2q23.2	no	102,514,861	114,451,355	11,936,494	> 5 genes
40-a-MPN	Gain	11	q23.2q25	no	114,456,874	134,934,063	20,477,189	> 5 genes

Abbreviations: CNA, copy number aberration; UN, uncertain - aberration with mosaic character (e.g. subclonal changes) with the small shift of copy number value which cannot be univocally called as losses/gains.

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

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.

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.