Supporting Information

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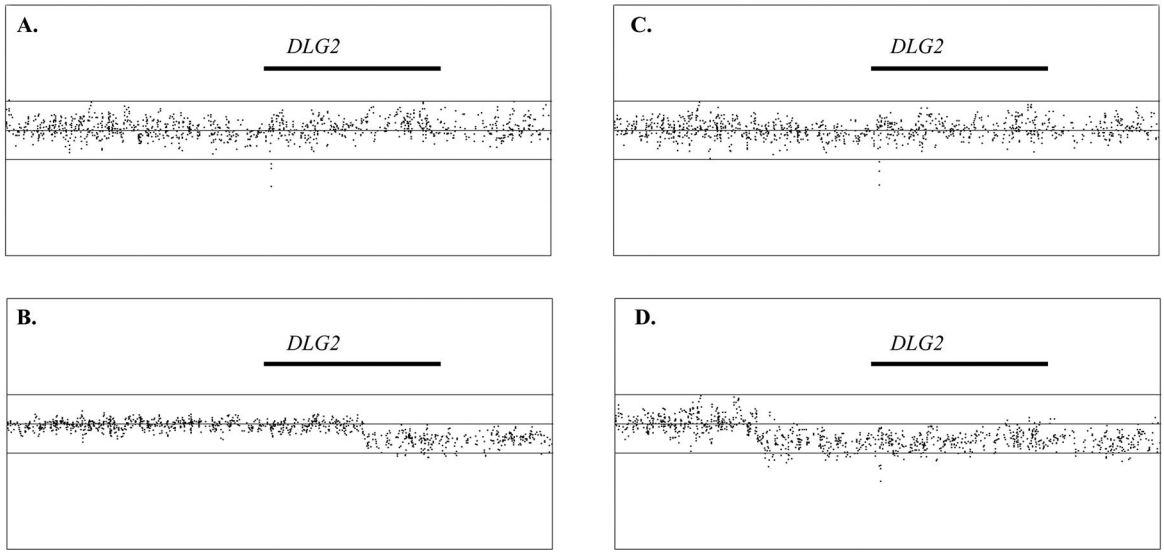

Fig. S1. SNP array analysis results from the 250K Nsp and the 250K Sty arrays showing deletions in the region 80,095,773–85,771,543 bp at 11q14.1, including the *DLG2* gene, in cases 36 (*A*), 20 (*B*), 22 (*C*), and 18 (*D*). Each dot represents the $\log_2$ ratio of one SNP with a moving average of three SNPs. The top line represents a $\log_2$ ratio of 1, the middle line a $\log_2$ ratio of 0, and the lower line a $\log_2$ ratio of -−1. Homozygous deletions involving three SNPs are seen in *A* and *C*, whereas *B* and *D* display larger hemizygous deletions with different breakpoints. All three deleted SNPs in *A* and *B* showed low $\log_2$ ratios without moving average being used; however, the $\log_2$ ratio of the middle SNP was lowest, resulting in the deletion involving three SNPs also when a moving average of three was used.

Table S1. Recurrent copy-number changes in 45 cases of adult ALL

Chr	Type	Minimum overlapping region (bp)	Cases	Gene(s) in region
1	G	152959805–154321968	1, 11, 13, 16–18, 22	>20 genes
2	G	24069–33871421	6, 10, 17	>20 genes
2	G	45269745–45813464	6, 9, 10, 17	*SIX2*, *Q6UXP8_HUMAN*, *SRBD1*, *PRKCE*
2	G	70434818–70671402	6, 10, 17, 31	*TGFA*
2	G	96024027–102842030	6, 10, 17	>20 genes
2	G	113287052–113837255	6, 10, 17, 38	*IL1B*, *Q96RW6_HUMAN*, *IL1F7*, *IL1F9*, *IL1F8*, *IL1F6*, *IL1F10*, *IL1F5*, *IL1RN*, *PSD4*, *PAX8*, *Q7Z3M5_HUMAN*
2	G	120938965–121350605	6, 17, 25, 38	*XR_017842.1*, *GLI2*
4	G	95058442–191167888	5, 6, 10, 11, 17	>20 genes
6	G	54908833–57334141	5, 10, 17	*FAM83B*, *HCRTR2*, *GFRAL*, *HMGCLL1*, *BMP5*, *COL21A1*, *DST*, *C6orf65*, *KIAA1586*, *ZNF451*, *RAB23*, *BAG2*, *PRIM2A*
6	G	58398624–58835794	5, 10, 17	No gene
6	G	62335171–64390812	5, 10, 17	*KHDRBS2*, *Q5VVH2_HUMAN*, *GLULD1*, *PTP4A1*
8	G	68109495–95881160	2, 5, 6, 11, 17	>20 genes
8	G	128742289–146263538	2, 5, 6, 13, 17, 42	>20 genes
9	G	76313209–77347450	5, 8, 15	*RORB*, *TRPM6*, *Q6ZU26_HUMAN*, *C9orf40*, *C9orf41*, *C9orf95*, *OSTF1*
9	G	132722573–132737555	2, 5, 6, 8, 15, 37	*ABL1*
10	G	21948809–24410943	6, 17, 27, 29	*MLLT10*, *DNAJC1*, *COMMD3*, *BMI1*, *SPAG6*, *PIP5K2A*, *ARMC3*, *MSRB2*, *PTF1A*, *C10orf67*, *OTUD1*, *KIAA1217*
17	G	41006823–41711411	1, 42	*LOC644172*, *Q76N56_HUMAN*, *Q49A53_HUMAN*, *C17orf69*, *CRHR1*, *NP_787078.1*, *MAPT*, *KIAA1267*, *LOC644253*
17	G	50913698–78599918	28, 42	>20 genes
19	G	212033–7947700	5, 18	>20 genes
21	G	9984282–14824157	6, 10, 11, 18, 26	*TPTE*, *BAGE*, *Q9NSJ1_HUMAN*, *FGF7P2*, *Q9NSI9_HUMAN*, *ANKRD21*, *NP_001013751.1*, *C21orf15*, *Q14180_HUMAN*, *LIPI*, *Q14179_HUMAN*, *RBM11*, *STCH*, *SAMSN1*
21	G	24240731–29938657	6, 10, 11, 18, 26	>20 genes
21	G	30142181–36165999	6, 10, 11, 18, 26	>20 genes
22	G	21916945–21957369	2, 5, 6, 8	*BCR*
X	G	50754108–51454911	3, 5, 10, 11, 17	*NUDT10*, *NUDT11*
X	G	86572549–100680651	3, 5, 10, 11, 17	>20 genes
X	G	122822542–139908341	3, 5, 10, 11, 25	>20 genes
X	G	143325548–143947901	3, 5, 7, 10, 11, 25	No gene
X	G	144936361–154500683	3, 5, 17, 10, 11, 25	>20 genes
2	L	212781980–212889560	39, 40	*ERBB4*
3	L	1737407–1747270	4, 15, 22	No gene
3	L	22540900–22541550	3, 4, 15, 37, 44, 45	*Q5T7C0_HUMAN*
3	L	31477964–31478724	4, 14	No gene
3	L	46870380–47292669	4, 34	*MYL3*, *PTHR1*, *CCDC12*, *NBEAL3*, *SETD2*, *KIF9*
3	L	57303907–64754696	3, 4	>20 genes, includes *FHIT*
3	L	65713504–68660540	3, 4	*MAGI1_HUMAN*, *SLC25A26*, *LRIG1*, *KBTBD8*, *SUCLG2*, *FAM19A1*
3	L	68846707–86665129	3, 4	>20 genes
3	L	90346746–96684332	3, 4	>20 genes
3	L	97145031–97673844	3, 4	No gene
3	L	113941777–114057770	3, 4, 21	*NP_001008784.1*
3	L	178446215–180805079	4, 25	*KCNMB2*, *ZMAT3*, *PIK3CA*, *KCNMB3*, *ZNF639*, *MFN1*, *GNB4*, *ACTL6A*, *MRPL47*
5	L	158212216–158445390	1, 7	*EBF1*, *Q9UHV1_HUMAN*
6	L	72163343–73052051	5, 17	*C6orf155*, *RIMS1*
6	L	77496587–77497656	5, 11, 17, 18, 29	No gene
6	L	79325534–89324095	5, 17, 41	>20 genes
6	L	103242724–103537117	5, 17, 34, 45	No gene
6	L	108863061–109313107	5, 17, 18, 34, 45	*LACE1*, *FOXO3A*, *Q5R3E8_HUMAN*, *ARMC2*
6	L	109328539–109429247	5, 17, 34, 45	*ARMC2*, *SESN1*
6	L	109441151–109610493	5, 17, 18, 34, 45	*SESN1*, *C6orf182*

Chr	Type	Minimum overlapping region (bp)	Cases	Gene(s) in region
6	L	111647065–112403213	5, 17, 18, 34, 45	*SLC16A10, KIAA1919, Q6ZMM1_HUMAN, REV3L, TRAF3IP2, FYN*
6	L	132321497–132563205	1, 17	No gene
6	L	135318389–135574497	9, 17	*HBS1L, MYB*
6	L	166513701–167478691	4, 17	*NP_787118.2, SFT2D1, BRP44L, RPS6KA2, Q8N719_HUMAN, RNASET2, CCR6*
6	L	168580479–170716684	4, 17	*SMOC2, THBS2, WDR27, C6orf120, TCTE3, PHF10, C6orf70, C6orf122, C6orf208, DLL1, FAM120B, PSMB1, TBP*
7	L	3092123–3122339	2, 3, 32, 35, 44	No gene
7	L	28928705–28960965	2–5, 14, 35	No gene
7	L	46161255–46708961	2–5, 35	No gene
7	L	50148762–50305027	2–5, 8, 15, 35	No gene
7	L	50386119–50458852	2–5, 15, 25, 35	*IKZF1*
7	L	52748967–52938074	2–4, 15, 35	No gene
7	L	53647659–53656839	2, 4, 35, 45	No gene
7	L	69939282–69975878	4, 39	No gene
7	L	157919888–157920856	7, 35	*PTPRN2*
9	L	19776217–20520136	2–5, 8, 15, 17, 19, 23, 37, 38,	*SLC24A2, MLLT3*
9	L	21935605–21978896	2–5, 8, 10, 15–17, 19, 23, 24, 26, 27, 32, 36–39, 41, 42	*MTAP, CDKN2A*
9	L	27008020–27826571	2–5, 8, 15, 17, 23, 33, 37, 38, 41, 42	*IFT74, TEK, C9orf11, MOBKL2B, IFNK, C9orf72*
9	L	31749826–32932226	2–5, 8, 15, 17, 23, 33, 37, 38, 41, 42	*ACO1, DDX58, TOPORS, C9orf133, NDUFB6, TAF1L, NP_997723.1*
9	L	36868774–36922342	2–5, 7, 8, 15–17, 23, 24, 33, 37, 38, 41	*PAX5*
9	L	77380889–77815460	5, 42	*PCSK5*
9	L	102395933–105160491	37, 42	*NP_060223.2, BAAT, MRPL50, ZNF189, ALDOB, C9orf125, RNF20, GRIN3A, PPP3R2, C9orf107, CYLC2*
9	L	132594866–132698182	2, 6	*ABL1*
10	L	19684689–19685245	11, 17, 40	No gene
11	L	82856041–82856909	18, 20, 36	*DLG2*
11	L	83813054–91470306	18, 22	>20 genes
11	L	99026041–99070312	18, 39	No gene
11	L	107451612–108051787	18, 44	*CUL5, ACAT1, NPAT, ATM, C11orf65, KDELC2, EXPH5, DDX10*
11	L	109321017–111421334	18, 44	>20 genes
11	L	117873875–118270810	18, 28	*MLL, NP_001073910.1, TMEM25, ARCN1, C11orf60, PHLDB1, TREH, DDX6, BLR1*
12	L	11698451–11884405	9, 19, 26, 33, 34, 42, 45	*ETV6*
12	L	12740508–13171749	9, 19, 33, 37, 42, 45	*CDKN1B, APOLD1, XR_01683.7, hCG_27695, GPRC5A, GPRC5D, Q6ZMM7_HUMAN, HEBP1, Q8IXE5_HUMAN, KIAA1467, GSG1*
12	L	14986429–15060729	26, 42, 45	*ARHGDIB, PDE6H*
12	L	16132922–17981926	37, 42, 45	*LOC729025, MGST1, LMO3*
13	L	30338555–30521993	17, 44	*C13orf33, C13orf26*
13	L	47885033–48052038	17, 18, 37, 40, 44	*RB1, P2RY5, RCBTB2, Q96DJ9_HUMAN*
13	L	62577464–62608954	17, 24	No gene
13	L	98206541–102272032	17, 44	*DOCK9, UBAC2, Q9BYX6_HUMAN, GPR18, EBI2, TM9SF2, CLYBL, ZIC5, ZIC2, PCCA, Q9BVM4_HUMAN, TMTC4, NALCN, ITGBL1, FGF14, TPP2, NP_001010977.1, C13orf27, KDELC1, BIVM, Q8NDH2_HUMAN, Q8N800_HUMAN*
15	L	32718656–32765105	17, 34, 37	No gene
15	L	34257086–41538368	17, 18, 37	>20 genes
15	L	57683100–57806956	6, 18, 37	*GCNT3, GTF2A2, BNIP2*
15	L	74531357–74573896	11, 18	*ZNF291*
15	L	98211579–98252586	17, 35	No gene
16	L	48001470–61794355	1, 17	>20 genes
16	L	81742548–81759394	1, 42	*CDH13*
17	L	7142477–12416952	11, 17, 20	>20 genes
18	L	62058576–62062341	17, 39	No gene
20	L	14694326–15050827	17, 20	*C20orf133*
20	L	35515209–38695901	4, 8, 23	>20 genes

Chr	Type	Minimum overlapping region (bp)	Cases	Gene(s) in region
20	L	40341490–57703423	4, 8, 23	>20 genes
21	L	14830513–15087868	26, 44	*SAMSN1*
22	L	14441016–15665049	8, 41	*LOC649486*, *OR11H13P*, *NP_055221.1*, *XKR3*
X	L	29163088–29163277	17, 27	*IL1RAPL1*
X	L	86245971–86291201	44, 45	No gene
X	L	117831542–117831838	17, 40	No gene
X	L	140049338–140082296	10, 17, 45	*LDOC1**

ALL, acute lymphoblastic leukemia; Chr, chromosome; bp, base pairs; G, copy number gain; L, copy number loss. All positions are according to NCBI Build 36.
*Within maximally deleted region.

Table S2. *CDKN2A* (*P16*) deletions detected in 45 adult ALL cases

Start position* (Mb)	End position* (Mb)	Size Mb (max Mb)†	Type	Including *CDKN2B* (*P15*)	Associated change	Case	Comment
19.776217 (19.750153)	22.420804 (22.474016)	2.644587 (2.723863)	HoD	Yes	HeD	37	
21.836327 (21.823659)	21.978896 (21.981752)	0.142569 (0.158093)	HoD	No	pUPD	36	
21.880326 (21.859079)	22.088619 (22.093813)	0.208293 (0.234734)	HoD	Yes	pUPD	39	
21.047062 (21.045413)	22.742380 (22.747714)	1.695318 (1.702301)	HoD	Yes	HeD	16	
21.968443 (21.948524)	22.021005 (22.031998)	0.052562 (0.083474)	HoD	Yes	HeD	2	
21.968443 (21.948524)	21.999960 (22.007836)	0.031517 (0.059312)	HoD	Yes	HeD	3	
21.669152 (21.663608)	22.571260 (22.582589)	0.902108 (0.918981)	HoD	Yes	HeD	15	
21.899000 (21.880326)	21.978896 (21.988733)	0.079896 (0.108407)	HoD	No	HeD	4	*CDKN2B* (*P15*) hemizygously deleted
21.935605 (21.944953)	22.008781 (22.018801)	0.073176 (0.073848)	HoD	Yes	HeD	27	
21.823659 (21.818110)	22.152238 (22.158128)	0.328579 (0.340018)	HoD	Yes	HeD	5	
21.248474 (21.225216)	22.197037 (22.209365)	0.948563 (0.984149)	HoD	Yes	HeD	23	
21818110 (21797994)	25.577832 (25.581948)	3.759722 (3.783954)	HoD	Yes	HeD	42	
19.463612 (19.458614)	22.420804 (22.474016)	2.957192 (3.015402)	HoD	Yes	pUPD	19	
21.899000 (21.880326)	21.995330 (21.999960)	0.09633 (0.119634)	HoD	Yes	HeD	8	
21.823659 (21.818110)	21.981752 (21.988733)	0.158093 (0.170623)	HoD	No	pUPD	32	
21.763167 (21.757404)	21.999960 (22.007836)	0.236793 (0.250432)	HoD	Yes	pUPD	10	
20.833841 (20.824837)	23.413785 (23.430715)	2.579944 (2.605878)	HoD	Yes	HeD	38	
0.030910 (0)	45.028875 (66.266293)	44.997965 (66.266293)	HeD	Yes	N/A	17	
20.629801 (20.615875)	45.028875 (66.266293)	24.399074 (45.650418)	HeD	Yes	N/A	41	
21.225442 (21.218285)	22.402948 (22.420804)	1.177506 (1.202519)	HeD	Yes	N/A	24	
21.248474 (21.228127)	22.209365 (22.227321)	0.960891 (0.981238)	HeD	Yes	N/A	26	

ALL, acute lymphoblastic leukemia; Mb, megabases; HoD, homozygous deletion; HeD, hemizygous deleton; N/A, not applicable.
*Positions are given for first abnormal SNP and in brackets for first normal neighboring SNP. All positions are according to NCBI Build 36.
†Distance between first and last abnormal SNPs, in parentheses between normal neighboring SNPs.

Table S3. Clinical and karyotypic features of the 45 adolescent and adult ALL cases included in the study

Case no.	Gender/ age	WCC	Immuno-phenotype	Karyotype	Group*
1	F/25	340	B	46,XX,t(9;22)(q34;q11.2),add(16)(q1–2)	Ph+
2	M/47	131	B	46,XY,t(9;22)(q34;q11.2)	Ph+
3	M/82	136	B	47,XY,+X,add(1)(q21),?add(2)(q3),-3,der(7;9)(q10;q10)t(9;22)(q34;q11.2), der(22)t(9;22)(q34;q11.2),+der(22)t(9;22),+der(?)t(1;?)(q21;?)[cp9]	Ph+
4	F/63	87	B	46,XX,t(9;22)(q34;q11.2)	Ph+
5	F/40	5	B	46,XX,t(9;22)(q34;q11)/ 53,idem,+?5,+22,+der(22)t(9;22),+mar1,+mar2x2,inc	Ph+
6	F/58	49	B	55,XX,+X,+2,+4,+8,t(9;22)(q34;q11),+10,+14,+21,+21,+der(22)t(9;22)	Ph+
7	M/66	219	B	46,XY,t(9;22)(q34;q11)	Ph+
8	M/45	74	B	45,XY,t(9;22)(q34;q11),-13/ 45,XY,der(9)t(9;22)(q34;q11)add(9)(p11),add(14)(p11),-20,der(22)t(9;22)	Ph+
9	M/27	169	B	46,XY,t(9;22)(q34;q11)	Ph+
10	F/41	80	B	52,XX,+X,+4,+6,t(9;22)(q34;q11),+18,+21,+mar	Ph+
11	F/45	80	B	51,XX,+X,+1,+4,t(4;11)(q21;q23),+8,der(17)t(17;?)(q10;?),+21	11q23/*MLL*
12	F/54	638	B	46,XX,t(4;11)(q21;q23)	11q23/*MLL*
13	M/46	71	B	46,XY	**t(8;14)**
14	F/69	95	B	46,XX,t(8;14)(q24.1;q32)	t(8;14)
15	M/16	49	B	46,XY/nuc ish 9q34(ABLx3)[89/ 100],4cen(CEP4x2),10cen(CEP10x2),11q23(MLLx2),12p13(TELx2), 17cen(CEP17x2),18cen(CEP18x2),21q22(AML1x2),22q11(BCRx2)[100]	other
16	M/25	18	B	46,XY,inv(14)(q11.2q32)	other
17	M/62	16	B	80,<4n>,-X,-X,-Y,-Y,add(1)(q2?),?add(5)(q3?),-6,-6,-8,-9,-9,-10,-10,-10,-11,-11,-13,-13,-14, -14,-15,-15,-16,-16,-17,-17,-19,+13mar,inc[cp5]	other
18	M/69	48	B	45,X,?Y,del(1)(p21),der(8),der(11),-1,-4,- 5,-7,-13,-20,+21,+mar[cp]	other
19	M/18	51	B	46,XY	NK
20	F/19	58	B	46,XX/nuc ish 4cen(CEP4x2),9p21(P16x2),9q34(ABLx2),10cen(CEP10x2), 11q23(MLLx2),12p13(TELx2),14q32(IGHx2), 19p13(E2Ax2),21q22(AML1x2),22q11(BCRx2)[100]	NK
21	M/57	6	B	46,XY	NK
22	M/59	24	B	46,XY/nuc ish 8q24(MYCx2),9q34(ABLx2),11q23(MLLx2),14q32(IGHx2),22q11(BCRx2)[100]	NK
23	F/21	40	B	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	N/A
24	F/24	24	B	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	N/A
25	M/45	11	B	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	N/A
26	F/18	77	B	N/A	**iAMP21**
27	M/13	279	T	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	T-ALL
28	M/15	182	T	46,XY	T-ALL
29	M/16	304	T	47,XY,+20	T-ALL
30	M/17	96	T	46,XY	T-ALL
31	M/19	105	T	46,XY/nuc ish 9q34(ABLx2),11q23(MLLx2),22q11(BCRx2)[100]	T-ALL
32	M/19	458	T	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	T-ALL
33	M/21	192	T	46,XY/nuc ish 9q34(ABLx2),11q23(MLLx2),22q11(BCRx2)[100]	T-ALL
34	M/21	27	T	46,XY,del(6)(q1?q2?)	T-ALL
35	M/22	295	T	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	T-ALL
36	M/29	136	T	46,XY	T-ALL
37	M/33	328	T	45,XY,add(7)(q3?),-9/ 46,XY,add(7)(q3?),del(9)(q22),?del(9)(p13p24),del(15)(q1?q22)/47,XY,add(7)(q3?), del(9)(q22),?(del(9)(p13p24),del(15)(q1?q22),+mar	T-ALL
38	M/36	303	T	46,XY,der(9)t(2;9)(q14;p13)	T-ALL
39	M/38	148	T	46,XY	T-ALL
40	F/67	84	T	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	T-ALL
41	M/14	136	T	46,XY,del(6)(q15q16),del(9)(p21)	T-ALL
42	M/22	138	N/A	46,XY	N/A
43	M/33	88	N/A	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	N/A
44	F/66	9	N/A	nuc ish 9q34(ABLx2),22q11(BCRx2)[100]	N/A
45	F/35	15	N/A	46,XX,t(9;11)(p22;q23)	N/A

WCC, white blood cell count; F, female; M, male; NK, normal karyotype; iAMP21, intrachromosomal amplification of chromosome 21; N/A, not available.
*Aberrations identified with SNP array only are marked by bold text.

Table S4. Gains of 1q detected in 45 adult ALL cases

Start position, Mb (max Mb)*	End position Mb (max Mb)*	Size Mb (max Mb)†	Case	Expected cytogenetic aberration	Comment
0.742429 (0.775852)	247.110269 (247.110269)	246.367840 (246.334417)	11	+1	Trisomy 1
141.510591 (120.953314)	146.292286 (147.216118)	4.781695 (26.262804)	16	dup(1)(q12q21.1)	Possibly CNP‡
141.510591 (120.953314)	247.110269 (247.110269)	105.599678 (126.156955)	22	dup(1)(q12q44)	All of 1q
141.510591 (120.953314)	247.110269 (247.110269)	105.599678 (126.156955)	1	dup(1)(q12q44)	All of 1q
141.510591 (120.953314)	215.402418 (215.407074)	73.891827 (94.453760)	18	dup(1)(q12q41)	Three consecutive gains
215.516892 (215.509261)	216.223617 (216.241657)	0.706725 (0.732396)	18	dup(1)(q41q41)	Three consecutive gains
216.555832 (216.241657)	247.110269 (247.110269)	30.554437 (30.868612)	18	dup(1)(q41q44)	Three consecutive gains
141.510591 (120.953314)	195.393272 (195.482842)	53.882681 (74.529528)	13	dup(1)(q12q31.3)	
152.959805 (152.950730)	154.321968 (154.326774)	1.362163 (1.376044)	17	dup(1)(q22q22)	Minimally gained region

ALL, acute lymphoblastic leukemia; Mb, megabases; CNP, copy number polymorphism.

*Positions are given for first abnormal SNP and in brackets for first normal neighbouring SNP. All positions are according to NCBI Build 36.

†Distance between first and last abnormal SNPs, in brackets between normal neighbouring SNPs.

‡Overlapping with reported known CNP (Database of Genomic Variants; http://projects.tcag.ca/variation/).

Table S5. Minimally deleted 6q regions involved in more than two adult ALL cases

Start position* (Mb)	End position* (Mb)	Cases	Genes in region	Comment
77.496587	77.497656	5, 11, 17, 18, 29	*MYO6*	Possible CNP†
79.325534	89.324095	5, 17, 41	≈40 genes	
103.242724	103.537117	5, 17, 34, 45	No genes	
108.863061	109.313107	5, 17, 18, 34, 45	*LACE1*, *FOXO3*, *ARMC2*	
109.328539	109.429247	5, 17, 34, 45	*ARMC2*, *SESN1*	
109.441151	109.610493	5, 17, 18, 34, 45	*SESN1*, *KIF6*	
111.647065	112.403213	5, 17, 18, 34, 45	*KIAA1919*, *REV3L*, *TRAF3IP2*, *FYN*	

ALL, acute lymphoblastic leukemia; Mb, megabases; CNP, copy number polymorphism.
*Positions are given for first abnormal SNP. All positions are according to NCBI Build 36.
‡Overlapping with reported known CNP (Database of Genomic Variants; http://projects.tcag.ca/variation/).

Other Supporting Information Files

Dataset S1