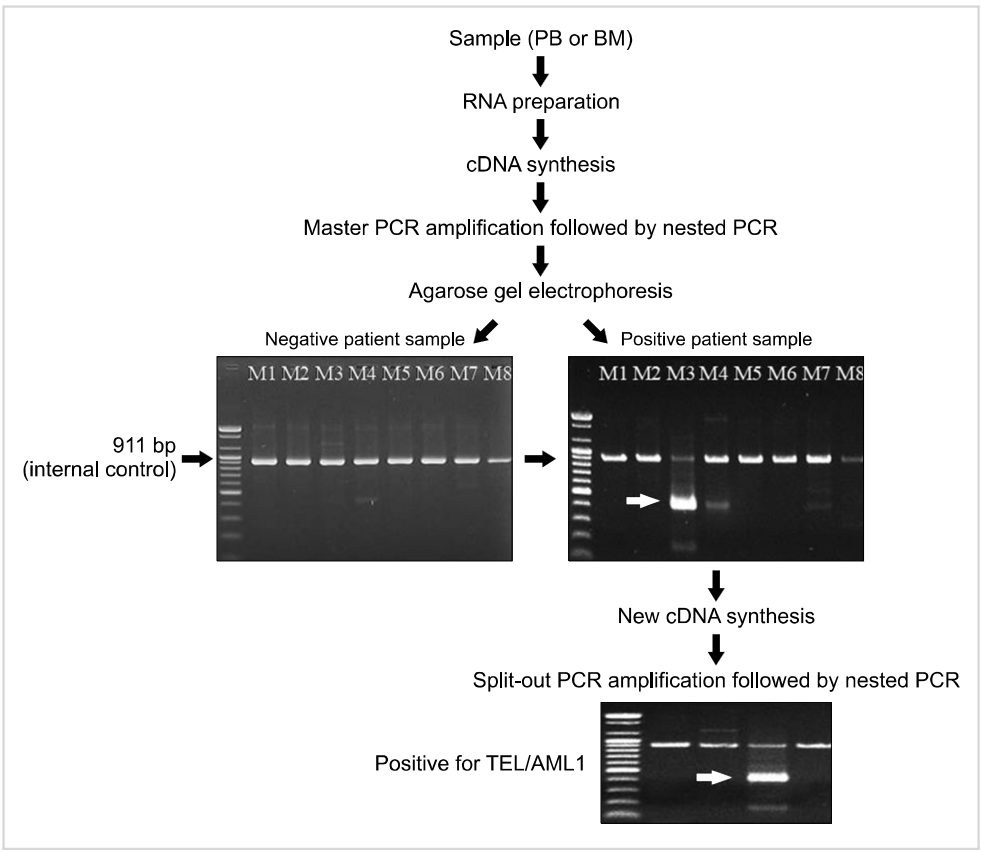
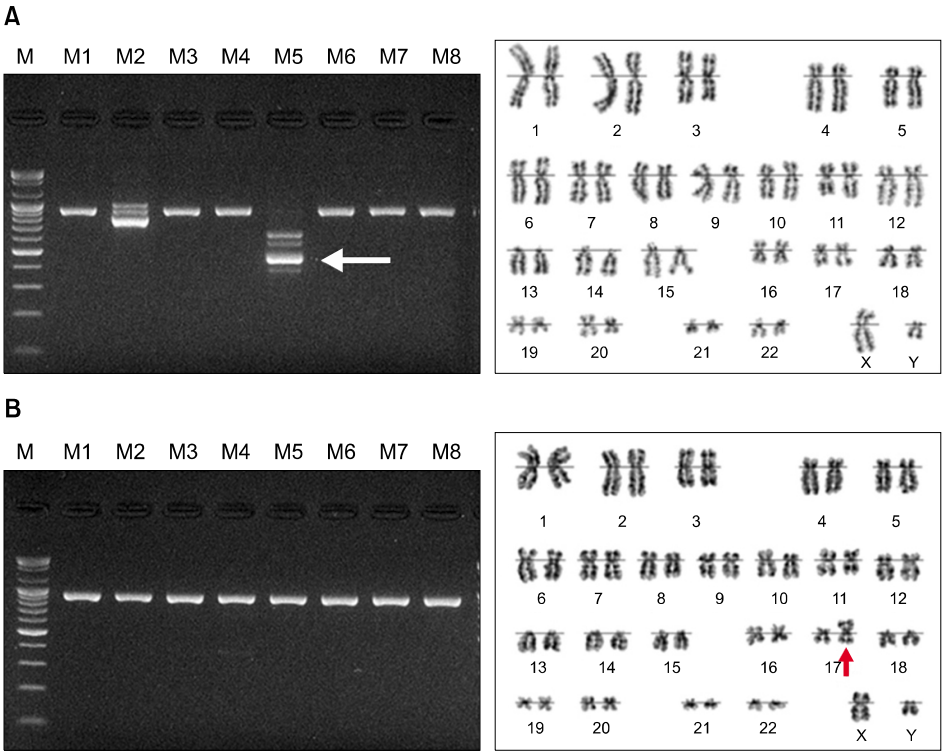


Supplementary Fig. 1. Flow diagram illustrating the multiplex RT-PCR system and the split-out analysis with a negative patient (left) and a positive patient (right) exhibiting a band in reaction M3 (lane 3; arrow). Abbreviations: BM, bone marrow; IC, internal control; PB, peripheral blood.



Supplementary Fig. 2. Representative chromosomal aberrations were detected using only multiplex RT-PCR or conventional cytogenetics. **(A)** Cryptic cytogenetic abnormalities, which usually disclose a normal karyotype using conventional cytogenetics, were detected only using the multiplex RT-PCR system. The positive band at the 454 base pair (arrow) in the master PCR step was the *KMT2A/MLLT3* gene rearrangement based on multiplex RT-PCR. **(B)** Some chromosomal aberrations, such as i(17)(q10), t(3;3), or t(8;14), should be included in the multiplex RT-PCR system, which were not covered by the commercially available multiplex RT-PCR system. The arrows indicate i(17)(q10), which was detected only using conventional cytogenetics.
Abbreviation: M, molecular weight marker.

Supplementary Table 1. Types and distribution of acute leukemia cases in this study.

Diagnosis	Adult	Childhood	Total
AML			
De novo	400	38	438
Secondary	81	2	83
ALL			
De novo			
Early preB cell type	14	2	16
PreB cell type	66	66	132
B cell type	10	4	14
T cell type	14	8	22
Secondary	3	0	3
MPAL	4	5	9
N of cases	592	125	717
N of cases (%)	83	17	100

Abbreviations: ALL, acute lymphoid leukemia; AML, acute myeloid leukemia; MPAL, mixed phenotype acute leukemia.

Supplementary Table 2. Frequency and spectra of chromosomal aberrations according to the age group in patients with hematologic malignancies, detected using the multiplex RT-PCR system.

Chromosomal aberration using multiplex RT-PCR system	Fusion transcript	Adult	Childhood	Total
t(15;17)(q24;q21)	*PML/RARA*	59	8	67
t(9;22)(q34;q11)	*BCR/ABL1*	40	7	47
t(8;21)(q22;q22)	*RUNX1/RUNX1T1*	29	5	34
11q23				
t(4;11)(q21;q23)	*KMT2A/AFF1*	1	2	3
t(6;11)(q27;q23)	*KMT2A /AFDN*	5		5
t(11;19)(q23;p13.3)	*KMT2A /ELL*	2		2
t(9;11)(p22;q23)	*KMT2A /MLLT3*	5	4	9
t(10;11)(p12;q23)	*KMT2A /MLLT10*	3	3	6
t(11;19)(q23;p13.3)	*KMT2A /MLLT1*		1	1
t(12;21)(p13;q22)	*ETV6/RUNX1*		15	15
t(1;19)(q23;p13)	*TCF3/PBX1*	4	1	5
inv(16)(p13;q22)	*CBFB/MYH11*	20	3	23
t(9;9)(q34;q34)	*SET/NUP214*	2		2
del(1p32)	*STIL/TAL1*	1	3	4
t(16;21)(p11;q22)	*FUS/ERG*	2	1	3
t(6;9)(p23;q34)	*DEK/NUP214*	1	1	2
N of positive cases		174	54	228
Total cases		592	125	717
NT		72	8	80
Cases excluding 'NT'		520	117	637
Positive cases excluding 'NT' (%)		33	46	36

Abbreviation: NT, not tested.

Supplementary Table 3. Frequency and spectra of chromosomal aberrations according to the age group in patients with hematologic malignancies, detected using conventional cytogenetics, including FISH.

Chromosomal aberrationusing conventional cytogenetics	Fusion transcript	Adult		Childhood		Total
		K	F	K	F	
t(15;17)(q24;q21)	*PML/RARA*	49	10	5	3	67
t(9;22)(q34;q11)	*BCR/ABL1*	25	9	4	3	41
t(8;21)(q22;q22)	*RUNX1/RUNX1T1*	30		6		36
11q23						
t(4;11)(q21;q23)	*KMT2A /AFF1*	1				1
t(6;11)(q27;q23)	*KMT2A /AFDN*	5				5
t(11;19)(q23;p13.3)	*KMT2A /ELL*					0
t(9;11)(p22;q23)	*KMT2A /MLLT3*	4		3		7
t(10;11)(p12;q23)	*KMT2A /MLLT10*	3		2		5
t(11;19)(q23;p13.3)	*KMT2A /MLLT1*			1		1
t(12;21)(p13;q22)	*ETV6/RUNX1*			5	7	12
t(1;19)(q23;p13)	*TCF3/PBX1*	1				1
inv(16)(p13;q22)	*CBFB/MYH11*	18	1	3		22
t(9;9)(q34;q34)	*SET/NUP214*					0
del(1p32)	*STIL/TAL1*					0
t(16;21)(p11;q22)	*FUS/ERG*	1		1		2
t(6;9)(p23;q34)	*DEK/NUP214*	1		1		2
Extra-aberration[a)]		125	8	33	4	170
Positive cases excluding extra-aberration		158		44		202
Positive cases		291		81		372
Total cases		592		125		717
NT		21		6		27
Cases excluding 'NT'		571		119		690
Positive cases excluding 'extra-aberration' & 'NT'(%)		28		37		29
Positive cases excluding 'NT' (%)		51		68		54

[a)]Extra-aberration is the numerical abnormality or structural rearrangements, excluding 28 fusions of multiplex RT-PCR system.
Abbreviations: F, fluorescence in situ hybridization; K, karyotype; NT, not tested.

Supplementary Table 4. Chromosomal aberrations according to the type of acute leukemia and age group in all patients using conventional cytogenetics, including FISH.

Chromosomal aberrationusing conventional cytogenetics	Fusion transcript	AML		ALL		MPAL		Total
		C	A	C	A	C	A	
t(15;17)(q24;q21)	*PML/RARA*	8	59					67
t(9;22)(q34;q11)	*BCR/ABL1*	1	6	5	25	1	3	41
t(8;21)(q22;q22)	*RUNX1/RUNX1T1*	6	30					36
11q23								
t(4;11)(q21;q23)	*KMT2A /AFF1*				1			1
t(6;11)(q27;q23)	*KMT2A /AFDN*		5					5
t(11;19)(q23;p13.3)	*KMT2A /ELL*							0
t(9;11)(p22;q23)	*KMT2A /MLLT3*	2	4			1		7
t(10;11)(p12;q23)	*KMT2A /MLLT10*	1	3	1				5
t(11;19)(q23;p13.3)	*KMT2A /MLLT1*			1				1
t(12;21)(p13;q22)	*ETV6/RUNX1*			12				12
t(1;19)(q23;p13)	*TCF3/PBX1*				1			1
inv(16)(p13;q22)	*CBFB/MYH11*	3	19					22
t(9;9)(q34;q34)	*SET/NUP214*							0
del(1p32)	*STIL/TAL1*							0
t(16;21)(p11;q22)	*FUS/ERG*	1	1					2
t(6;9)(p23;q34)	*DEK/NUP214*	1	1					2
Extra-aberration[a)]		9	109	26	24	2		170
Normal karyotype		7	196	20	37	1	1	262
Inappropriate specimen			27	7	8			42
No mitotic cells			7	3	4			14
Not tested		1	14	5	7			27
Positive cases excluding extra-aberration		23	128	19	27	2	3	202
Positive cases		32	237	45	51	4	3	372
Total cases		40	481	80	107	5	4	717
NT		1	14	5	7	0	0	27
Cases excluding 'NT'		39	467	75	100	5	4	690
Positive cases excluding 'extra-aberration' & 'NT'(%)		59	27	25	27	40	75	29
Positive cases excluding 'NT' (%)		82	51	60	51	80	75	54

[a)]Extra-aberrations are numerical abnormalities or structural rearrangements, excluding 28 fusions of the multiplex RT-PCR system.
Abbreviations: A, adult; C, childhood; NT, not tested.

Supplementary Table 5. Frequency and spectra of chromosomal aberrations according to the type of acute leukemia and age group in all patients, detected using multiplex RT-PCR system.

Chromosomal aberration using multiplex RT-PCR system	Fusion transcript	AML		ALL		MPAL		Total
		C	A	C	A	C	A	
t(15;17)(q24;q21)	*PML/RARA*	8	59					67
t(9;22)(q34;q11)	*BCR/ABL1*	1	8	5	29	1	3	47
t(8;21)(q22;q22)	*RUNX1/RUNX1T1*	5	29					34
11q23								
t(4;11)(q21;q23)	*KMT2A /AFF1*			2	1			3
t(6;11)(q27;q23)	*KMT2A /AFDN*		5					5
t(11;19)(q23;p13.3)	*KMT2A /ELL*		2					2
t(9;11)(p22;q23)	*KMT2A /MLLT3*	3	5			1		9
t(10;11)(p12;q23)	*KMT2A /MLLT10*	2	3	1				6
t(11;19)(q23;p13.3)	*KMT2A /MLLT1*			1				1
t(12;21)(p13;q22)	*ETV6/RUNX1*			15				15
t(1;19)(q23;p13)	*TCF3/PBX1*			1	4			5
inv(16)(p13;q22)	*CBFB/MYH11*	3	20					23
t(9;9)(q34;q34)	*SET/NUP214*		1		1			2
del(1p32)	*STIL/TAL1*			3	1			4
t(16;21)(p11;q22)	*FUS/ERG*	1	2					3
t(6;9)(p23;q34)	*DEK/NUP214*	1	1					2
Positive cases		24	135	28	36	2	3	228
Total cases		40	481	80	107	5	4	717
NT		3	58	5	14	0	0	80
Cases excluding 'NT'		37	423	75	93	5	4	637
Positive cases excluding 'NT' (%)		65	32	37	39	40	75	36

Abbreviations: A, adult; C, childhood; NT, not tested.

Supplementary Table 6. Comparison of chromosomal aberrations detected using multiplex RT-PCR system and conventional cytogenetics.

Comparison	Multiplex RT-PCR system	Conventional cytogenetics	Cases (N=553)	Cases (%)
Concordant, 71%	Positive	Positive	105	19
		Positive with extra-aberrations[a)]	61	11
	Negative	Negative	228	41
Discordant, 29%	Positive	Negative	19	5
		Numerical abnormalities	2	
		Structural rearrangements	7	
	Negative	Numerical abnormalities	43	24
		Structural rearrangements	88	

[a)]Positive with extra-aberrations refers to a fusion transcript in the multiplex RT-PCR system with numerical abnormalities or structural rearrangements.

Supplementary Table 7. Distribution of chromosomal aberrations which were not covered by multiplex RT-PCR system.

Age (yr)	Sex	Diagnosis	Karyotype	FISH
0	F	AML, M0	47,XX,+19/40~45,XX,-11,+19,-21	
1	M	AML, M7	46,XY,add(14)(q32)/46,idem,t(2;11)(q32;q23)	
1	M	ALL, L2, early precursor B-cell type	47,XY,+8,del(11)(q23)	MLL
2	M	ALL, L2, precursor B-cell type	46,XY,del(13)(q12)	
2	M	AML, M4	46,XY,t(2;7)(p13;p14)	
2	M	ALL, L1, precursor B-cell type	46,XY,inv(9)(p12q13)	
3	M	ALL, L2, precursor B-cell type	52,XY	
3	M	ALL, L1, precursor B-cell type	54,XY,+8,+9,+10,+11,+21,+3~4mar,inc	MLL
3	M	ALL, L2, T-cell type	46,XY,t(1;7)(p36.2;p15)	MLL
3	F	ALL, precursor B-cell type	45,XX,+3,-6,add(7)(p22),-9,-20,+mar	
4	M	AML, M7	49,XY,+8,+14,-21,+2mar	IGH
4	M	ALL, precursor B-cell type	46,X,add(Y)(q12),del(21)(p11)	
4	M	ALL, L2, precursor B-cell type	46,XY,add(11)(q24),dup(13)(q14q22),add(14)(q32)	
5	F	ALL, L2, precursor B-cell type	55~58,XX,+3,+4,+5,+6,+8,+9,+10,+12,+13,+14,+16,+18,+21,+22	
5	M	ALL, L2, precursor B-cell type	47,XY,+21c	
5	F	ALL, precursor B-cell type	55~56,XX,+4,+8,+10,+17,+21,+2mar,inc	
6	F	ALL, L2, precursor B-cell type	54<2n>,XX	
7	M	ALL, L2, B-cell type	46,XY,del(16)(q22q24)	
8	F	Relapse status of known AML, M5	46,XX,-4,-22,+1~2mar	MLL
10	M	AML, M2	47~49,XY,+4,+14,+21	
11	F	Mixed phenotype acute leukemia, B/myeloid	44~47,XX,add(1)(p36),add(3)(q28),add(4)(q34),-8,-9,del(9)(q23),dup(14)(q12q32),+1~2mr	
11	M	ALL, precursor B-cell type	46,XY,add(1)(p36.2)	
11	M	ALL, L2, precursor B-cell type	49~55,XY,+X,dup(1)(q22q42),+4,+5,+6,+13,+19,+21	
12	M	ALL, L2, precursor B-cell type	55~56,XY,+5,+6,+11,+12,+21,+22,+1~3mar	
13	F	ALL, L2, precursor B-cell type	60~65,XXXX,+1,+1,+4,+6,+6,+8,+9,+10,+11,+14,+19,+19,+21,+21	
13	M	AML, M1	51~54,XY,+2,+5,+6,+10,+11,+14,+19,-20,-21,+1~3mar	
13	F	ALL, L2, precursor B-cell type	40~43,XX,-3,i(7)(q10),+11,-12,-15,-17,+1~2mar	
13	M	ALL, L3, B-cell type	46,XY,t(8;14)((q24.1;q32)	MYC/IGH
14	F	Mixed phenotype acute leukemia, B/myeloid, NOS	46,XX,t(1;5)(p36;p13)	
18	F	AML, M2	48,XX,+8,+11	MLL
19	F	ALL, L2, precursor B-cell type	47,XX,del(6)(q23),add(12)(p13),+21	MLL
19	M	AML, M0	46,XY,dup(2)(q21q33),dup(6)(q23q25)/47,idem,+22	
20	F	ALL, L2, precursor B-cell type	54,XX,+4,+6,+10,+14,+17,+18,+21,+22	
28	M	BM involvement of T cell lymphoma	46,XY,t(2;19)(p12;q13)	
30	F	AML, M4	43~47,XX,+5,del(5)(q12q33),-8,-20	
30	F	ALL, early precursor B-cell type	46,XX,del(9)(p21)	
31	M	AML with myelodysplasia-related change	44,X,-Y,-7	CEP (7)
31	F	AML, M4	46,XX,del(12)(q13)	
33	M	AML, M6	47,XY,+8	CEP (8)
33	M	AML, M1	46,XY,add(1)(p36.2),der(6)t(1;6)(q21;p24),add(7)(p22),del(11)(q14)	
34	M	ALL, L2, early precursor B-cell type	46,XY,t(3;7)(p21;p22),t(8;12)(q22;p13)	
36	F	AML, M1	46,XX,+13,der(13;13)(q10;q10)	
36	M	AML, M5	46,XY,inv(11)(p15q22)/42~45,idem,-9,-16,-18,-19	
36	F	AML, M2	46,XX,inv(9)(p12q13),t(11;22)(q24;q12)	
43	F	AML with myelodysplasia-related change	47,XX,+19	
44	F	AML, M2	47,XX,+22	
47	M	AML, M7	81~88,XXYY,…/44~48,XY,-11,-14,-18,+3~6mar	MLL
48	F	ALL, L2, early precursor B-cell type	94~95<4n>,XXXX.	MLL
48	F	AML with myelodysplasia-related change	46,X,inv(X)(p22q13)/46,X,del(X)(p22.1)	
49	F	AML, M2	42,XX,del(1)(q42),+2,-4,-5,+6,del(6)(q23),+8,add(9)(q34),-13,-13,-14,-15,-20,-21,+mar	MLL
52	F	AML, M2	47,XX,+mar	
52	F	AML, M2	46,XX,t(7;11)(p15;p15)	
52	M	AML, M1	46,XY,del(5)(q22)	

Supplementary Table 7. Continued 1.

Age (yr)	Sex	Diagnosis	Karyotype	FISH
53	M	ALL, L2, precursor B-cell type	46,XY,t(3;9)(q25;p21),add(17)(p13),i(17)(q10)	
55	M	AML, M2	49,XY,+8,+10,+13	
55	F	AML, M1	47,XX,+21	
56	F	ALL, precursor B-cell type	45~46,XX,add(7)(p22),-9,+mar	
56	F	ALL, L2, precursor B-cell type	43~46,XX,+1,der(1;8)(q10;q10),+8,add(22)(q13.2)	
57	F	AML, M2Eo	47~49,XX,+9,+11,+18,+21,+22	
57	M	AML, M2	47,XY,+11	MLL
57	F	AML with myelodysplasia-related change	46,XX,t(3;3)(q21;q26)	
58	M	AML with myelodysplasia-related change	44,XY,-5,add(5)(q35),t(6;17)(p21;p13),-13,-13,add(16)(q24), -17,-18,-21,+4mar	
59	F	AML, M0	47,XX,+8	
59	M	AML, M2	55~57<2n>,XY,inc	
59	M	AML with myelodysplasia-related change	45,XY,dup(1)(q21q32),add(4)(q34),del(5)(p15),inv(9)(p12q13),-15,-18,+1~2mar	
59	F	AML with myelodysplasia-related change	46,XX,+1,dic(1;15)(p11;p11)/46,idem,del(7)(q22q34)	
59	M	AML, M2	43~44,XY,inv(3)(p12q26),-5,-7,-10,add(17)(p13),-20,+1~2mar	
59	M	AML, M2	42,XY,add(3)(q28),+5,add(5)(q35.2),-8,-10,-15,-16,-17,-18, +mar	
60	F	AML, M2	47,XX,+8	
60	M	AML, M1	47,XY,+11	MLL
60	F	Hypocellular AML	47,XX,+mar	
60	F	ALL, L2, precursor B-cell type	46,XX,dup(1)(q12q43),+5,add(5)(p15.2)	
61	F	AML, M2	46,XX,+14,-16	
61	F	ALL, L2, precursor B-cell type	36,XX,-2,-3,-6,-7,-9,-13,-15,-16,-17,-19,+mar/69~71,XXX,-3, +4,+5,+6,+11,-13,-15,+21,+22,+1~2mar	MLL
62	M	AML with myelodysplasia-related change	94~95<4n>,XXYY.	
62	M	AML with myelodysplasia-related change	47,XY,+11	
63	M	AML, M2	39~45,XY,-9,-15,-18,-20,-21,-22	
63	M	ALL, precursor B-cell type	47,XY,dup(1)(q21q32),+20/48,XY,idem,+21	
65	F	AML, M2	47,XX,+8	
65	M	AML, M6	47,XY,+8/48,idem,+15	MLL
65	F	Therapy related myeloid neoplasms, AML	43~47,XX,-8,-12,-17,-18,-19,+1~8mar	MLL
66	M	ALL, L2, B-cell type, Mature B-cell Neoplasm expressing CD5	48,XY,del(6)(q23),+16,+17,i(18)(q10),-19	
67	F	AML, M4	47,XX,+10	
67	F	ALL, B-cell type	49,XX,+3,+13,+mar	
67	M	AML, M2	44,X,add(Y)(q12),dic(1;7)(p11;q11),-22/45,idem,+20	
67	M	Acute panmyelosis with myelofibrosis	44~45,XY,del(3)(q26),-7,- 8,-17,-18,+1~4mar	
69	M	AML, M2	41~46,XY,-5,-6,-7,-15,-17,-17,-18,-22,+2~4mar	
69	M	AML with myelodysplasia-related change	42~46,XY,-6,-7,-8,-9,+13,-21,-22,+1~3mar	
69	F	ALL, L2, precursor B-cell type	45,X,-X,add(7)(p22),add(17)(p13)	
69	M	AML, M0	48,XY, +6,-7,+18,+mar/49,idem,+10	CEP (7)
69	F	AML, M2	58~65,XXX,+1,+3,+6,+7,+8,+10,+11,+12,+13,+14,+15, +16,+17,+19,+21,+22,+1~3mar	
70	M	AML, M1	47,XY,+8	
70	M	AML with myelodysplasia-related change	46,XY,add(21)(q22)	
71	M	AML with myelodysplasia-related change	43~47,XY,-22,+mar	
71	M	AML, M1	43,XY,del(2)(q35),del(4)(p?),+11,del(11)(q23),-15,-16,-17,-18, -19,-20,+2mar,inc	MLL
72	F	AML, M2	47,XX,+21	
72	M	AML, M4	47,XY,+8	
72	M	AML, M2	44~46,XY,+4,-7,del(7)(q33),-9,+mar	
73	M	AML, M2	46,XY,+8	
73	F	Secondary AML	44~46,XX,add(1)(p36.3),-6,-11,-13,+3~5mar	
73	M	AML, M2	45,XY,-11,add(13)(q33),del(15)(q21)	
74	M	AML, M1	47,XY,+8	
74	M	ALL, L2, precursor T-cell type	47,XY,+mar	
74	M	AML, M4	46,XY,del(12)(p11.2),i(17)(q10)	
75	M	AML, M2	42~45,XY,-7,-13,-17,-18	

Supplementary Table 7. Continued 2.

Age (yr)	Sex	Diagnosis	Karyotype	FISH
75	M	AML, M2	47,XY,+8	
75	M	AML, M2	42~46,XY,del(5)(q33),dic(12;17)(p11.2;p11.2),-18,+1~2mar	MLL
75	M	Secondary AML from known atypical CML	46,XY,i(17)(q10)/47,idem,+13	
76	M	AML, M2	45,X,-Y	
76	M	AML, M2	47,XY,+10	
76	M	AML with myelodysplasia-related change	45~46,XY,-11,-12,-13,add(15)(q26),-18,+2~3mar/92,XXYY,…	
76	M	AML, M2	47,XY,+4/49,XY,idem,i(17)(q10),+2mar	
76	F	AML, M2	45~48,XX,-10,-12,+1~5mar	
76	M	AML, M1	46,XY,del(7)(q22)	
76	F	AML, M2	46,XX,-3,-9,-12,+21,+1~3mar	
76	F	AML, M6a	43~46,X,-X,-3,-5,-7,-10,del(12)(p11.2),add(21)(p11.2), +1~3mar	
77	M	AML, M2	45,X,-Y	
77	F	AML, M4	70~80<3n+>,XXX.	PML/RARA
77	F	AML, M2	69~79,XXX.	
77	F	ALL, L1, precursor B-cell type	46,XX,dup(2)(q24q36)	
77	M	AML, M2	46,XY,t(7;11)(p15;p15)	
77	F	AML, M1	56,XX,+3,t(5;21)(p11;q11),+7,del(7)(q32)x2,+8,+9,+10,+11, +15,+16,+20	MLL
79	M	AML converted from MPN, Secondary AML	47,XY,+9/47,idem,i(17)(q10)	
79	F	AML, M0	46~47,XX,-8,+21,+mar	
80	F	AML, M2	45,XX,-7/44,XX,-7,-10	
81	M	AML, M2	43~45,XY,-3,-5,-9,-12,-22,+1~3mar	MLL
81	F	AML, M2	46,XX,del(7)(q22)	
82	F	AML, M1	44,XX,-5,-7,add(12)(p11.2),-21,+mar	
83	M	AML transformation of post-ET MF	47,XY,+21	
84	M	AML, M0	46,XY,i(17)(q10)/46,idem,+13,-21	PML/RARA
84	F	AML, M2	41~45,XX,del(5)(p13),del(5)(q22q34),t(12;21)(q13;q22),-15, -16,-17,-19,-22,+mar	

Supplementary Table 8. List of chromosomal aberrations which were or were not detected using multiplex RT-PCR system.

Chromosomal aberrations covered by multiplex RT-PCR system			
t(9;22)(q34;q11)	*BCR/ABL1*	t(9;11)(p22;q23)	*KMT2A /MLLT3*
inv(16)(p13;q22)	*CBFB/MYH11*	t(6;11)(q27;q23)	*KMT2A /AFDN*
t(6;9)(p23;q34)	*DEK/NUP214*	t(15;17)(q24;q21)	*PML/RARA*
t(12;21)(p13;q22)	*ETV6/RUNX1*	t(8;21)(q22;q22)	*RUNX1/RUNX1T1*
t(16;21)(p11;q22)	*FUS/ERG*	t(9;9)(q34;q34)	*SET/NUP214*
t(4;11)(q21;q23)	*KMT2A /AFF1*	TAL1 40 kb deletion	*STIL/TAL1*
t(11;19)(q23;p13.3)	*KMT2A /MLLT1*	t(1;19)(q23;p13)	*TCF3/PBX1*
t(10;11)(p12;q23)	*KMT2A /MLLT10*	t(11;19)(q23;p13.3)	*KMT2A /ELL*
Chromosomal aberrations not covered by multiplex RT-PCR system			
add(1)(p36)	add(Y)(q12)	del(7)(q22q34)	i(18)(q10)
add(1)(p36.2)	del(1)(q42)	del(7)(q32)x2	inv(11)(p15q22)
add(1)(p36.3)	del(11)(q14)	del(7)(q33)	inv(3)(p12q26)
add(11)(q24)	del(11)(q23)	del(9)(p21)	inv(9)(p12q13)
add(12)(p11.2)	del(12)(p11.2)	del(9)(q23)	inv(X)(p22q13)
add(12)(p13)	del(12)(q13)	del(X)(p22.1)	t(1;5)(p36;p13)
add(13)(q33)	del(13)(q12)	der(1;8)(q10;q10)	t(1;7)(p36.2;p15)
add(14)(q32)	del(15)(q21)	der(13;13)(q10;q10)	t(11;22)(q24;q12)
add(15)(q26)	del(16)(q22q24)	der(6)t(1;6)(q21;p24)	t(2;11)(q32;q23)
add(16)(q24)	del(2)(q35)	dic(1;7)(p11;q11)	t(2;19)(p12;q13)
add(17)(p13)	del(21)(p11)	dic(1;15)(p11;p11)	t(2;7)(p13;p14)
add(21)(p11.2)	del(3)(q26)	dic(12;17)(p11.2;p11.2)	t(3;3)(q21;q26)
add(21)(q22)	del(4)(p?)	dup(1)(q12q43)	t(3;7)(p21;p22)
add(22)(q13.2)	del(5)(p13)	dup(1)(q21q32)	t(3;9)(q25;p21)
add(3)(q28)	del(5)(p15)	dup(1)(q22q42)	t(5;21)(p11;q11)
add(4)(q34)	del(5)(q12q33)	dup(13)(q14q22)	t(6;17)(p21;p13)
add(5)(p15.2)	del(5)(q22)	dup(14)(q12q32)	t(7;11)(p15;p15)
add(5)(q35)	del(5)(q22q34)	dup(2)(q21q33)	t(8;12)(q22;p13)
add(5)(q35.2)	del(5)(q33)	dup(2)(q24q36)	t(8;14)(q24.1;q32)
add(7)(p22)	del(6)(q23)	dup(6)(q23q25)	
add(9)(q34)	del(7)(q22)	i(17)(q10)	
Chromosomal aberrations which should be covered by multiplex RT-PCR system			
t(3;3)(q21;q26.2)		i(17)(q10)	
t(8;14)(q24;q32)			

Supplementary Table 9. Frequency and spectra of chromosomal aberrations according to the type of leukemia in childhood acute leukemia patients.

Chromosomal aberration	Fusion transcript	AML (N=40)			ALL (N=80)			MPAL (N=5)		
		C	P	COM	C	P	COM	C	P	COM
t(15;17)(q24;q21)	*PML/RARA*	8	8	8						
t(9;22)(q34;q11)	*BCR/ABL1*	1	1	1	5	5	5	1	1	1
t(8;21)(q22;q22)	*RUNX1/RUNX1T1*	6	5	6						
11q23										
t(4;11)(q21;q23)	*KMT2A /AFF1*					2	2			
t(6;11)(q27;q23)	*KMT2A /AFDN*									
t(11;19)(q23;p13.3)	*KMT2A /ELL*									
t(9;11)(p22;q23)	*KMT2A /MLLT3*	2	3	3				1	1	1
t(10;11)(p12;q23)	*KMT2A /MLLT10*	1	2	2	1	1	1			
t(11;19)(q23;p13.3)	*KMT2A /MLLT1*				1	1	1			
t(12;21)(p13;q22)	*ETV6/RUNX1*				12	15	15			
t(1;19)(q23;p13)	*TCF3/PBX1*					1	1			
inv(16)(p13;q22)	*CBFB/MYH11*	3	3	3						
t(9;9)(q34;q34)	*SET/NUP214*									
del(1p32)	*STIL/TAL1*					3	3			
t(16;21)(p11;q22)	*FUS/ERG*	1	1	1						
t(6;9)(p23;q34)	*DEK/NUP214*	1	1	1						
NT		1	3		5	5		0	0	

Abbreviations: C, conventional cytogenetics including FISH; COM, combined cytogenetics or PCR; NT, not tested; P, multiplex RT-PCR system.

Supplementary Table 10. Frequency and spectra of chromosomal aberrations according to the type of leukemia in adult acute leukemia patients.

Chromosomal aberration	Fusion transcript	AML (N=481)			ALL (N=107)			MPAL (N=4)		
		C	P	COM	C	P	COM	C	P	COM
t(15;17)(q24;q21)	*PML/RARA*	59	59	59						
t(9;22)(q34;q11)	*BCR/ABL1*	6	8	8	25	29	29	3	3	3
t(8;21)(q22;q22)	*RUNX1/RUNX1T1*	30	29	30						
11q23										
t(4;11)(q21;q23)	*KMT2A /AFF1*				1	1	1			
t(6;11)(q27;q23)	*KMT2A /AFDN*	5	5	5						
t(11;19)(q23;p13.3)	*KMT2A /ELL*		2	2						
t(9;11)(p22;q23)	*KMT2A /MLLT3*	4	5	5						
t(10;11)(p12;q23)	*KMT2A /MLLT10*	3	3	3						
t(11;19)(q23;p13.3)	*KMT2A /MLLT1*									
t(12;21)(p13;q22)	*ETV6/RUNX1*									
t(1;19)(q23;p13)	*TCF3/PBX1*				1	4	4			
inv(16)(p13;q22)	*CBFB/MYH11*	19	20	20						
t(9;9)(q34;q34)	*SET/NUP214*		1	1		1	1			
del(1p32)	*STIL/TAL1*					1	1			
t(16;21)(p11;q22)	*FUS/ERG*	1	2	2						
t(6;9)(p23;q34)	*DEK/NUP214*	1	1	1						
NT		14	58		7	14		0	0	

Abbreviations: C, conventional cytogenetics including FISH; COM, combined cytogenetics or PCR; NT, not tested; P, multiplex RT-PCR system.