■ **Supplemental Table 1.** ■ Frequency and distribution of chromosomal aberrations in all patients detected by multiplex RT-PCR

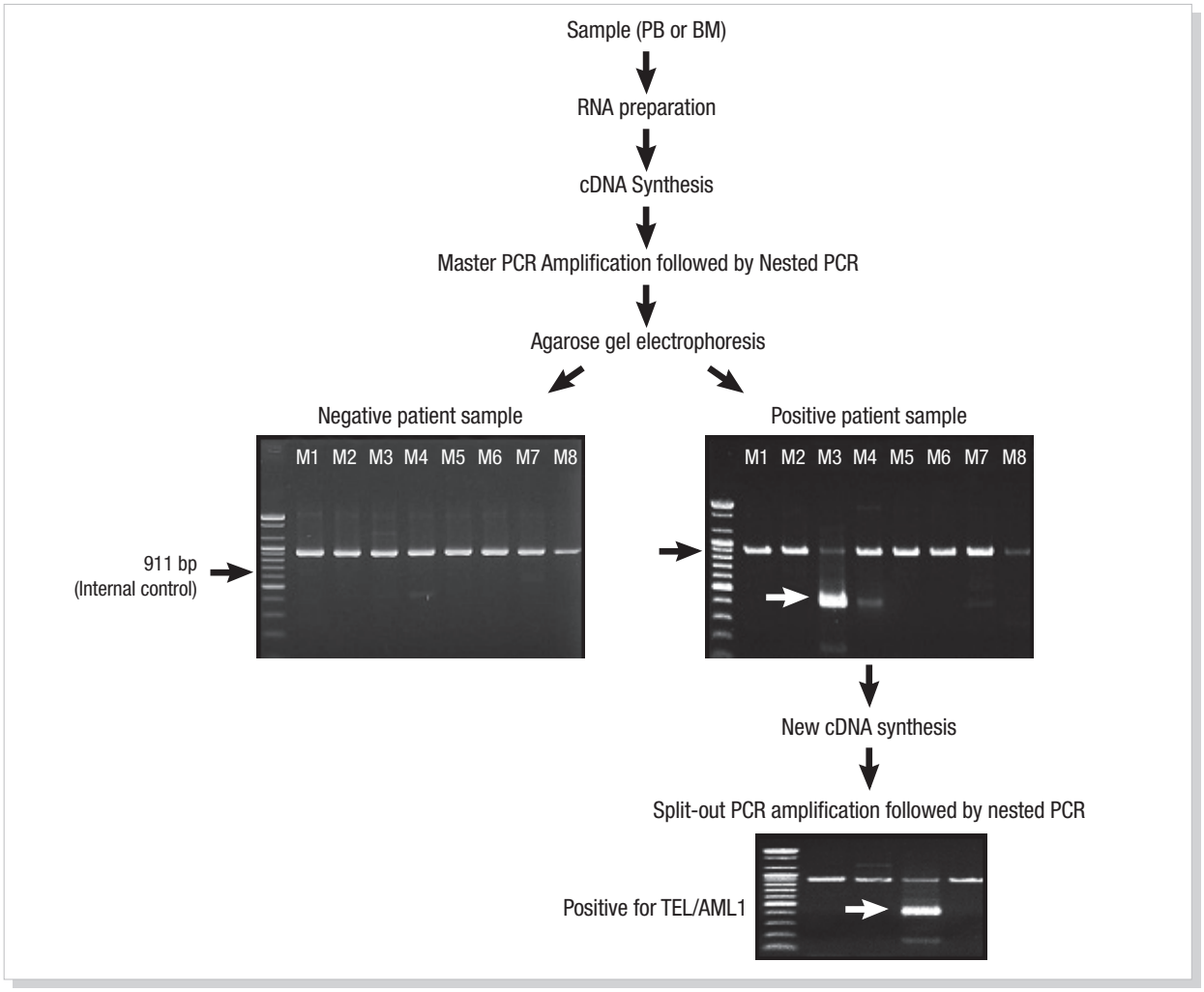
Genetic rearrangement detected by multiplex RT-PCR		AML (213)		ALL (104)		MPAL (8)	
		C (23)	A (190)	C (55)	A (49)	C (3)	A (5)
t(15;17)(q21;q22)	*PML/RARa*	4	31				
t(9;22)(q34;q11)	*BCR/ABL*	1*		4	17	1	3
t(8;21)(q22;q22)	*AML1/MGT8*	7	24				
11q23	*MLL*						
t(4;11)(q21.2;q23.2)	*MLL1/AF4*			3	2		
t(6;11)(q27;q23)	*MLL1/AF6*		2	1	1		
t(11;19)(q23;p13.1)	*MLL1/ELL*		3				
t(1;11)(p32;q23)	*MLL1/AF-1p*		1				
t(9;11)(p22;q23)	*MLL1/AF9*				1		
t(10;11)(p12;q23)	*MLL1/AF10*		1				
t(11;19)(q23;p13.3)	*MLL1/ENL*			1			
t(12;21)(p13;q22)	*TEL/AML1*			14	1		
t(1;19)(q23;p13)	*E2A/PBX*			4			
inv(16)(p13;q22)	*CBFb/MYH11*		3				
t(9;9)(q34:q34)	*SET/CAN*	1*	1		1		
t(9;12)(q34;p13)	*TEL/ABL*	1		1			
del(1p34)	*SIL1/TAL1*			1			
t(3;21)(q26;q22)	*AML1/MDS1*		1				
t(11;17)(q23;q21)	*PLZF/RARA*		1				
t(12;22)(p13;q11)	*TEL/MN1*		1				
t(16;21)(p11.2;q22.3)	*TLS/ERG*		1				
No. of positive cases (%)		13	70	29	23	1	3
		83 (39%)		52 (50%)		4 (50%)	

*Two fusion transcripts were detected by multiplex RT-PCR system in one sample; C, children; A, adults.

■ **Supplemental Table 2.** ■ Chromosomal alterations according to the type of malignancies and age group in all patients detected by conventional karyotyping including FISH

Genetic rearrangement detected by Conventional karyotyping		AML (213)		ALL (104)		MPAL (8)	
		C (23)	A (190)	C (55)	A (49)	C (3)	A (5)
t(15;17)(q21;q22)	*PML/RARa*	3	25				
t(9;22)(q34;q11)	*BCR/ABL*			3	14		3
t(8;21)(q22;q22)	*AML1/MGT8*	7	21				
11q23							
t(4;11)(q21.2;q23.2)	*MLL1/AF4*			2	2		
t(6;11)(q27;q23)	*MLL1/AF6*		1				
t(11;19)(q23;p13.1)	*MLL1/ELL*		1				
t(9;11)(p22;q23)	*MLL1/AF9*				1		
t(12;21)(p13;q22)	*TEL/AML1*			1			
t(1;19)(q23;p13)	*E2A/PBX*			1			
inv(16)(p13;q22)	*CBFb/MYH11*		2				
del(1p34)	*SIL1/TAL1*			1			
t(3;21)(q26;q22)	*AML1/MDS1*		1				
t(11;17)(q23;q21)	*PLZF/RARA*		1				
t(16;21)(p11.2;q22.3)	*TLS/ERG*		1				
Complex karyotype*		5	30	11	9	2	
Normal karyotype		6	102	28	20	1	2
Inappropriate specimen		1 (1†)	4 (4†)				
No mitotic cells			1 (1†)	8 (7†)	2 (2†)		
Not done		1 (1†)			1 (1†)		

*Complex karyotypes included chromosome abnormalities including numerical aberrations which were not detected by commercial multiplex RT-PCR system; †Genetic aberrations detected by FISH analysis, which was one of the genetic aberrations in 28 fusion genes list. C, children; A, adults.



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