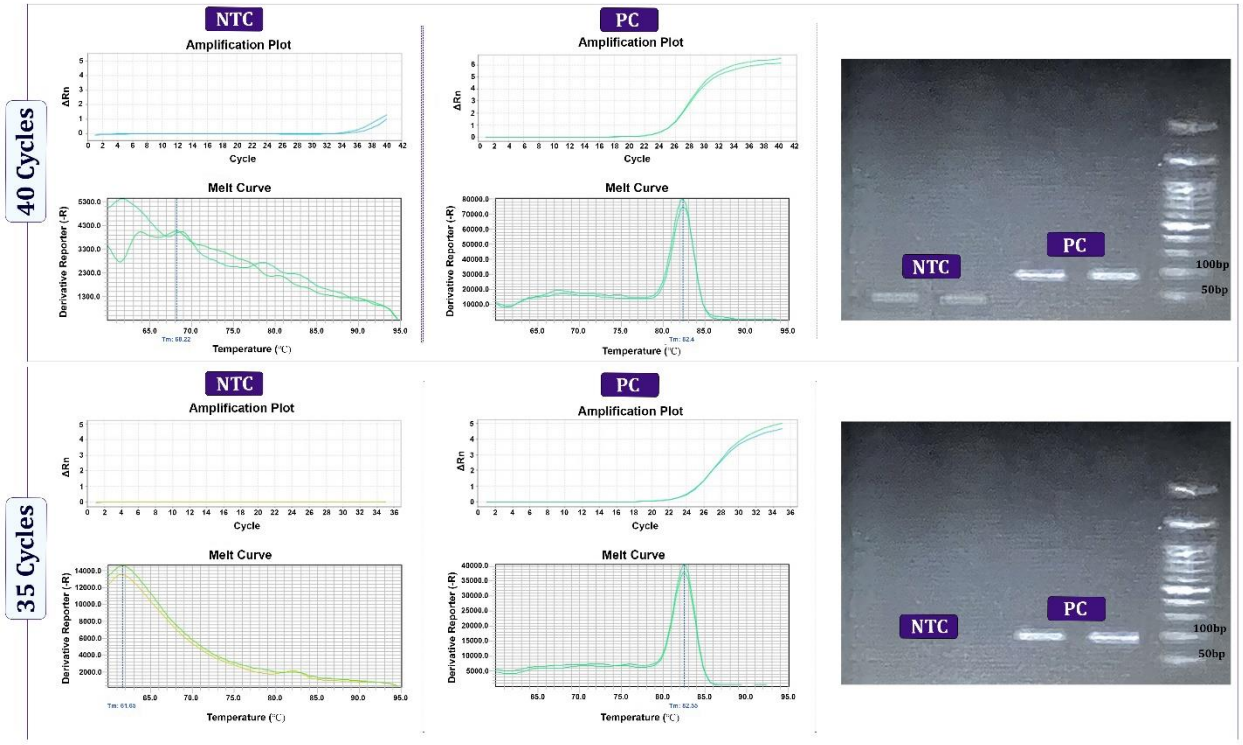
Supplementary Table 1. *Primer sequences for different ALL chimeric transcripts.*

Translocation	Target	Primer sequence	5' to 3' position
t(12;21): ETV6-RUNX1	ETV6	CTCTGTCTCCCCGCCTGAA	984–1002
	RUNX1	CGGCTCGTGCTGGCAT	557–542
t(1;19): TCF3-PBX1	TCF3	CCAGCCTCATGCACAACCA	1436–1454
	PBX1	GGGCTCCTCGGATACTCAAAA	409–389
t(4;11): KMT2A-AF4	KMT2A	CCCAAGTATCCCTGTAAAACAAAAA	4050–4074
	AF4	GAAAGGAAACTTGGATGGCTCA	1581–1560
t(9;22): BCR-ABL1	BCR (p190)	CGCAAGACCGGGCAGAT	1818–1834
	BCR (p210)	TCCGCTGACCATCAATAAGG	3281–3300
	ABL	GGTTGTGCTTCACACCATTC	484–503



Supplementary Figure 1. Comparison of amplification performance at 40 and 35 PCR cycles using no-template controls (NTC) and positive controls (PC). *Amplification plots and corresponding melt-curve profiles are shown for both NTC and PC reactions under two cycling conditions (40 cycles, top panel; 35 cycles, bottom panel).* ***At 40 cycles,*** *the NTC displayed no amplification curve but produced a weak nonspecific melt signal, which corresponded to a faint band on the gel. In contrast, the PC generated strong amplification with a sharp melt peak at the expected Tm and a clearly defined amplicon band.* ***At 35 cycles,*** *the NTC showed no detectable amplification, no melt peak, and no visible gel band, indicating elimination of nonspecific background. The PC remained robust, exhibiting consistent amplification, a distinct melt peak, and a correctly sized band under both cycling conditions.*