Table S4. Subclonal *BTG1* microdeletion occurrence within the cytogenetic subgroups.

	Number of Samples[a]	*BTG1* deletion in minor subclone (%)	No *BTG1* deletion (%)	P-value Chi-square
T-ALL	77	0 (0)	77 (100)	<0.001
BCP-ALL	89	16 (18.0)	73 (82.0)	
Cytogenetic subgroup				0.064
Hyperdiploid (>50chr)				0.030
Yes	19	0 (0)	19 (100)	
No	58	13 (22.4)	45 (77.6)	
ETV6-RUNX1				0.033
Yes	8	4 (50.0)	4 (50.0)	
No	33	5 (15.2)	28 (84.8)	
BCR-ABL1				1.000[d]
Yes	1	0 (0)	1 (100)	
No	59	10 (16.9)	49 (83.1)	
MLL rearranged				1.000[d]
Yes	1	0 (0)	1 (100)	
No	73	11 (15.1)	62 (84.9)	
Other subgroup[b]				0.452
Yes	23	5 (21.7)	18 (78.3)	
No	29	4 (13.8)	25 (86.2)	
Subgroup unknown[c]				0.845
Yes	37	7 (18.9)	30 (81.1)	
No	52	9 (17.3)	43 (82.7)	

All patients screened were *BTG1* deletion-negative as determined by MLPA. Subclonal *BTG1* deletion status was determined using the PCR-based detection of deletions III, V and VIII. [a]Because of missing values, numbers do not always add up to 89 BCP-ALL cases. Data was available for 77 cases on hyperdiploidy; 41 cases for *ETV6-RUNX1*; 60 cases for *BCR-ABL1;* 74 cases for *MLL*-rearrangement. [b]The other subgroup encompasses cases negative for *ETV6-RUNX1*, *MLL*, *BCR-ABL1* translocations and/or hyperdiploidy. This group does not contain any *E2A-PBX1* translocation cases. [c]Subgroup unknown includes all cases in which no data is available in one or more cytogenetic subgroups. [d]Fisher's exact test was used when sample groups were small.