Table S1. Definitions used in ACAs classification

Aberration	• Count 1 for each aberration separated from the rest of the karyotype by a comma, regardless of the complexity • Count each aberration only once (in multiple clones) • Constitutional abnormality: count 0, if uncertain count 1 • Clonal tetraploidy or triploidy: count 1
ACAs cases	all cases harboring 2 or more aberrations
Complex karyotype	all cases harboring 3 or more aberrations
Numerical ACAs	loss or gain of a complete chromosome. Cases also harboring a marker chromosome were excluded for numerical losses
Structural ACAs	all aberrations that include breakpoints within the chromosomes
Partial chromosomal loss or gain	all unbalanced structural aberrations that result in loss or gain of chromosomal material, not being a complete chromosome
Balanced translocation	exchange of material from one chromosome to another and vice versa without loss of material (as observed by conventional karyotyping)
Balanced karyotype	karyotype of a patient which contains two complete copies of all autosomes and complete copies of sex chromosomes, without additional material (2n)

Abbreviations: ACAs indicates additional cytogenetic aberrations

Table S2. Multivariate survival analysis of the t(9;11)(p22;q23) subgroup by using the Cox proportional hazards model

	\EFS\			\OS\			\Relapse incidence\		
	HR	CI	*P*	HR	CI	*P*	HR	CI	*P*
Trisomy									
no trisomy	1	reference		1	reference		1	reference	
8	0.68	(0.37-1.25)	0.214	0.75	(0.37-1.51)	0.425	0.56	(0.32-0.99)	0.046*
19	2.12	(1.08-4.18)	0.029*	3.02	(1.44-6.34)	0.003†	2.24	(1.08-4.64)	0.029*
21	0.91	(0.44-1.89)	0.794	0.90	(0.40-1.99)	0.785	0.68	(0.32-1.44)	0.314
Type									
no ACAs	1	reference		1	reference		1	reference	
numerical	1.32	(0.78-2.23)	0.292	1.38	(0.74-2.57)	0.310	1.67	(1.01-2.76)	0.045*
structural	1.39	(0.94-2.06)	0.102	1.41	(0.88-2.26)	0.148	1.08	(0.77-1.51)	0.650
FAB									
non **M5**	1	reference		1	reference		1	reference	
M5	0.47	(0.33-0.69)	0.000†	0.48	(0.31-0.75)	0.001†	0.75	(0.53-1.06)	0.106
Age									
2-9 yr	1	reference		1	reference		1	reference	
<2 yr	1.68	(1.13-2.50)	0.011*	1.92	(1.18-3.12)	0.008†	1.21	(0.89-1.64)	0.220
≥10 yr	1.45	(0.92-2.29)	0.110	1.61	(0.93-2.81)	0.090	1.22	(0.86-1.73)	0.272

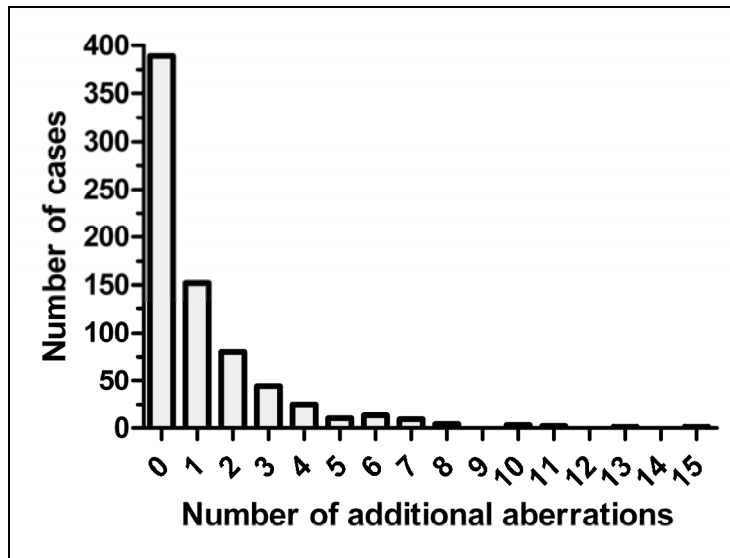**Cox proportional hazards model**

Note: Results of 3 independent analyses.
Abbreviations: EFS indicates event-free survival; OS, overall survival HR, hazard ratio; CI, 95% confidence interval.
* Values significant at *P*<0.05 level.
† Values significant at *P*<0.01 level.

Figure S1. Histogram showing number of additional aberrations found in 733 cases

Note: Number of additional aberrations are on the X-axis, number of cases are on the Y-axis. All aberrations additional to a balanced 11q23/*MLL*-rearrangement are included in the total number of additional aberrations.

Figure S2. Frequency (number of cases) of numerical ACAs (A) and structural ACAs (B) in the t(9;11)(p22;q23) subgroup
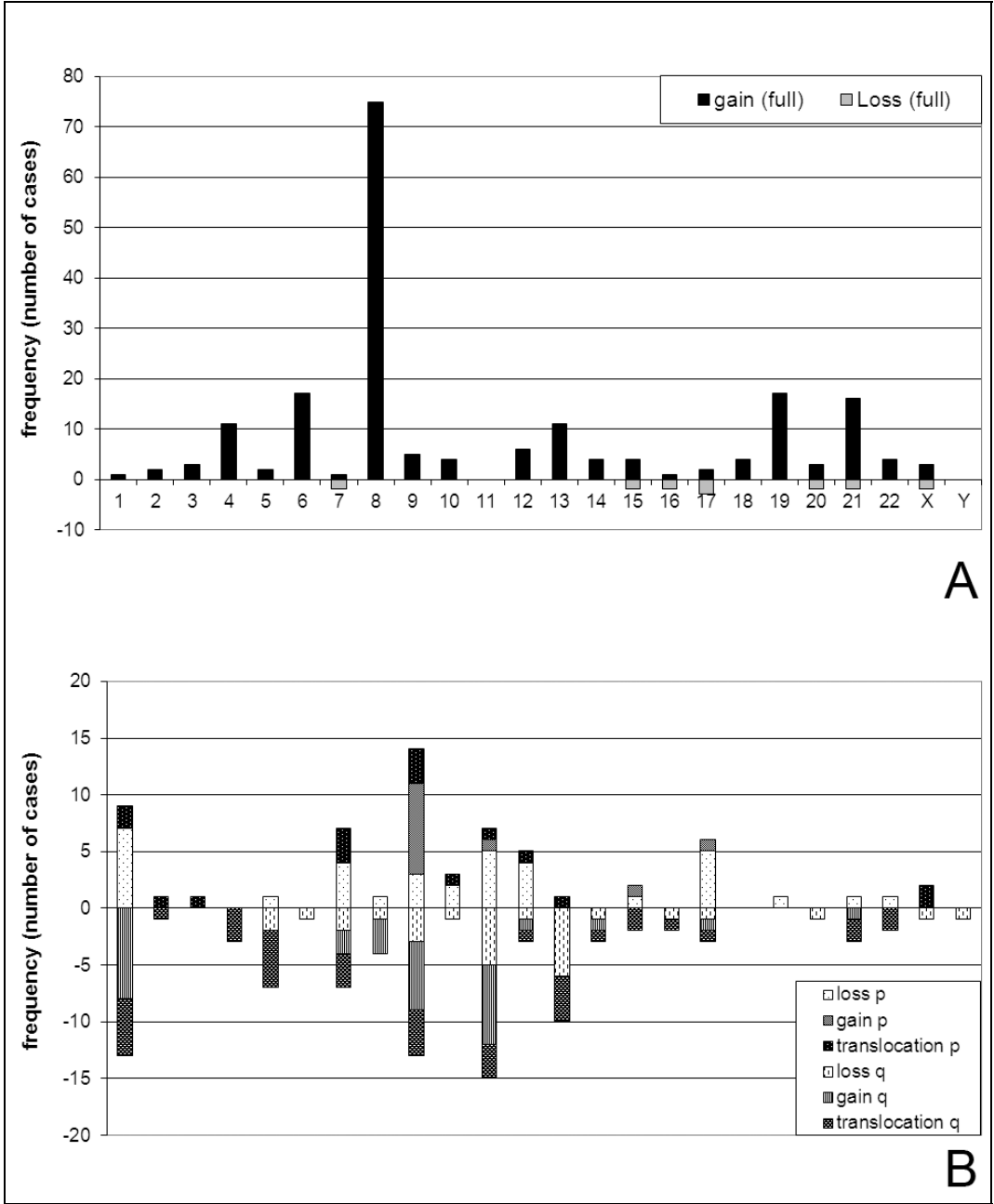
Note: In figure 3A gains are shown on the positive Y-axis, losses are shown on the negative Y-axis. Chromosomes are on the X-axis; figure 3B, the short arms (p) of the chromosomes are shown on the positive Y-axis, the long arms (q) on the negative Y-axis. Lightest shades are used for losses, medium shaded colors are used for gains, darkest shaded colors for translocation breakpoints. Chromosomes are on the X-axis. Balanced 11q23 translocations are not included in the figure.