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	all unbalanced structural aberrations that result in loss or gain of					
loss or gain	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

			Cox proportional hazards model									
EFS			os			Relapse incidence						
HR	CI	P	HR	CI	P	HR	CI	Р				
1	reference		1	reference		1	reference					
0.68	(0.37-1.25)	0.214	0.75	(0.37-1.51)	0.425	0.56	(0.32 - 0.99)	0.046*				
2.12	(1.08-4.18)	0.029*	3.02	(1.44-6.34)	0.003+	2.24	(1.08-4.64)	0.029*				
0.91	(0.44-1.89)	0.794	0.90	(0.40-1.99)	0.785	0.68	(0.32-1.44)	0.314				
1	reference		1	reference		1	reference					
1.32	(0.78-2.23)	0.292	1.38	(0.74-2.57)	0.310	1.67	(1.01-2.76)	0.045*				
1.39	(0.94-2.06)	0.102	1.41	(0.88-2.26)	0.148	1.08	(0.77-1.51)	0.650				
1	reference		1	reference		1	reference					
0.47	(0.33-0.69)	0.000†	0.48	(0.31-0.75)	0.001†	0.75	(0.53-1.06)	0.106				
		-										
1	reference		1	reference		1	reference					
1.68	(1.13-2.50)	0.011*	1.92	(1.18-3.12)	0.008†	1.21	(0.89-1.64)	0.220				
1.45	(0.92-2.29)	0.110	1.61	(0.93-2.81)	0.090	1.22	(0.86-1.73)	0.272				
	1 0.68 2.12 0.91 1 1.32 1.39 1 0.47	HR CI 1 reference 0.68 (0.37-1.25) 2.12 (1.08-4.18) 0.91 (0.44-1.89) 1 reference 1.32 (0.78-2.23) 1.39 (0.94-2.06) 1 reference 0.47 (0.33-0.69) 1 reference 1.68 (1.13-2.50)	HR CI P 1 reference 0.68 (0.37-1.25) 0.214 2.12 (1.08-4.18) 0.029* 0.91 (0.44-1.89) 0.794 1 reference 1.32 (0.78-2.23) 0.292 1.39 (0.94-2.06) 0.102 1 reference 0.47 (0.33-0.69) 0.000† 1 reference 1.68 (1.13-2.50) 0.011*	HR CI P HR 1 reference 1 0.75 0.68 (0.37-1.25) 0.214 0.75 2.12 (1.08-4.18) 0.029* 3.02 0.91 (0.44-1.89) 0.794 0.90 1 reference 1 1.32 1.32 (0.78-2.23) 0.292 1.38 1.39 (0.94-2.06) 0.102 1.41 1 reference 1 0.000† 0.48 1 reference 1 0.001* 1.92	HR CI P HR CI 1 reference 1 reference 0.68 (0.37-1.25) 0.214 0.75 (0.37-1.51) 2.12 (1.08-4.18) 0.029* 3.02 (1.44-6.34) 0.91 (0.44-1.89) 0.794 0.90 (0.40-1.99) 1 reference 1 reference 1.32 (0.78-2.23) 0.292 1.38 (0.74-2.57) 1.39 (0.94-2.06) 0.102 1.41 (0.88-2.26) 1 reference 1 reference 0.47 (0.33-0.69) 0.000† 0.48 (0.31-0.75) 1 reference 1 reference 1.68 (1.13-2.50) 0.011* 1.92 (1.18-3.12)	HR CI P HR CI P 1 reference 1 reference 0.37-1.51) 0.425 2.12 (1.08-4.18) 0.029* 3.02 (1.44-6.34) 0.003† 0.91 (0.44-1.89) 0.794 0.90 (0.40-1.99) 0.785 1 reference 1 reference 1.32 (0.78-2.23) 0.292 1.38 (0.74-2.57) 0.310 1.39 (0.94-2.06) 0.102 1.41 (0.88-2.26) 0.148 1 reference 0.47 (0.33-0.69) 0.000† 0.48 (0.31-0.75) 0.001† 1 reference 1 reference 1.92 (1.18-3.12) 0.008†	HR CI P HR CI P HR 1 reference 0.68 (0.37-1.25) 0.214 0.75 (0.37-1.51) 0.425 0.56 2.12 (1.08-4.18) 0.029* 3.02 (1.44-6.34) 0.003† 2.24 0.91 (0.44-1.89) 0.794 0.90 (0.40-1.99) 0.785 0.68 1 reference 1.32 (0.78-2.23) 0.292 1.38 (0.74-2.57) 0.310 1.67 1.39 (0.94-2.06) 0.102 1.41 (0.88-2.26) 0.148 1.08 1 reference 0.47 1 reference 0.33-0.69) 1 reference 0.48 1 0.001† 0.75 1 reference 0.47 1 1 reference 0.48 1 0.001† 0.75	HR CI P HR CI P HR CI 1 reference 1 reference 1 reference 0.68 (0.37-1.25) 0.214 0.75 (0.37-1.51) 0.425 0.56 (0.32-0.99) 2.12 (1.08-4.18) 0.029* 3.02 (1.44-6.34) 0.003† 2.24 (1.08-4.64) 0.91 (0.44-1.89) 0.794 0.90 (0.40-1.99) 0.785 0.68 (0.32-1.44) 1 reference 1 reference 1 reference 1.32 (0.78-2.23) 0.292 1.38 (0.74-2.57) 0.310 1.67 (1.01-2.76) 1.39 (0.94-2.06) 0.102 1.41 (0.88-2.26) 0.148 1.08 (0.77-1.51) 1 reference 1 reference 1 reference 0.47 (0.33-0.69) 0.000† 0.48 (0.31-0.75) 0.001† 0.75 (0.53-1.06) 1 reference 1 <t< td=""></t<>				

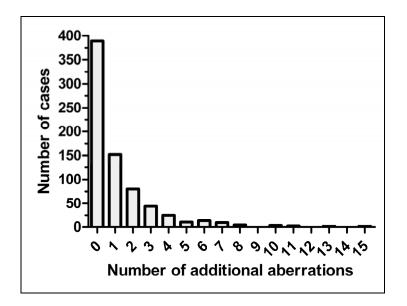
Note: Results of 3 independent analyses.

Abbreviations: EFS indicates event-free survival; OS, overall survival HR, hazard ratio; CI, 95% confidence interval.

* Values significant at *P*<0.05 level.

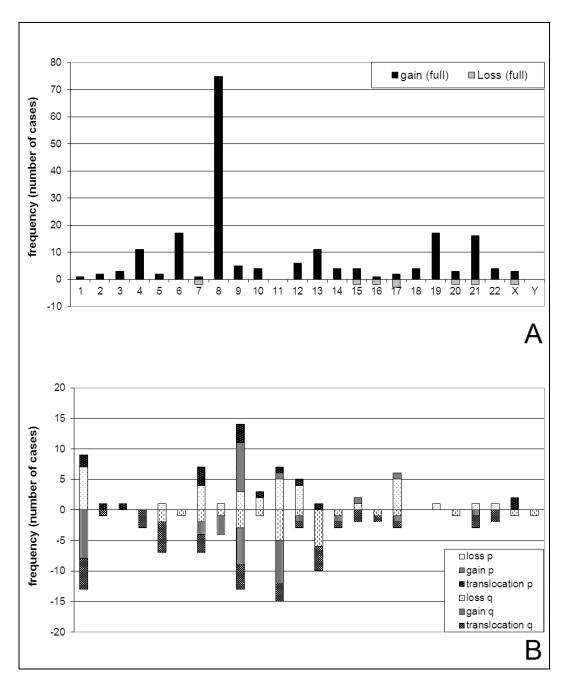
† Values significant at *P*<0.01 level.

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.