

Supplementary Material

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Supplementary Tables

Supplementary Table S1. Distribution of *KMT2A* fusion-based groups stratified by I-BFM-SG affiliated study group/country

Fusion-based group	AIEOP		BFM		BSPHO		CCLG		COG		CPH		DCOG		Greece		HKPHOSG		INS		JPLSG		LAME		NOPHO		SEHOP		St. Jude		Total
	2005-2011	2005-2011	2005-2016	2005-2016	2010-2016	2010-2016	2005-2016	2005-2016	2006-2016	2006-2016	2006-2016	2006-2016	2005-2016	2005-2016	2007-2014	2007-2014	2010-2013	2010-2013	2005-2016	2005-2016	2007-2010	2007-2010	2005-2015	2005-2015	2010-2016	2010-2016	2008-2016	2008-2016	2005-2016	2005-2016	
9p22/ <i>KMT2A</i> :: <i>MLLT3</i>	20	45.5	90	58.1	7	35	34	43.6	189	38.7	17	53.1	15	29.4	3	60	4	57.1	4	40	39	56.5	54	40.6	26	50.0	11	57.9	31	33.3	544
10p12/ <i>KMT2A</i> :: <i>MLLT10</i>	7	15.9	32	20.6	5	25	12	15.4	84	17.2	9	28.1	14	27.5	1	20	0	0	1	10	8	11.6	18	13.5	9	17.3	2	10.5	16	17.2	218
6q27/ <i>KMT2A</i> :: <i>AFDN</i>	6	13.6	9	5.8	1	5	8	10.3	39	8.0	1	3.1	2	3.9	0	0	0	0	2	20	3	4.3	8	6.0	3	5.8	1	5.3	9	9.7	92
19p13	2	4.5	5	3.2	1	5	8	10.3	0	0	0	0	2	3.9	0	0	0	0	0	0	1	1.4	0	0	4	7.7	0	0	0	0	23
19p13.1/ <i>KMT2A</i> :: <i>ELL</i>	0	0	1	0.6	1	5	5	6.4	36	7.4	2	6.3	1	2.0	0	0	1	14.3	0	0	8	11.6	5	6.4	0	0	0	0	9	9.7	75
19p13.3/ <i>KMT2A</i> :: <i>MLLT1</i>	0	0	2	1.3	1	5	3	3.8	27	5.5	1	3.1	3	5.9	0	0	0	0	0	4	5.8	7	5.3	0	0	0	0	8	8.6	56	
1q21/ <i>KMT2A</i> :: <i>MLLT11</i>	1	2.3	5	3.2	2	10	1	1.3	11	2.3	0	0	0	0	0	0	0	0	0	0	0	6	4.5	1	1.9	0	0	1	1.1	28	
10p11.2/ <i>KMT2A</i> :: <i>AB11</i>	2	4.5	0	0	0	0	2	2.6	15	3.1	0	0	0	0	0	0	1	14.3	0	0	0	0	2	1.5	0	0	0	0	2	2.2	24
Xq24/ <i>KMT2A</i> :: <i>SEPT6</i>	3	6.8	0	0	0	0	1	1.3	11	2.3	0	0	2	3.9	0	0	0	0	0	0	0	5	3.8	0	0	0	0	0	0	0	22
17q21	1	2.3	0	0	0	0	1	1.3	2	0.4	0	0	2	3.9	1	20	0	0	1	10	1	1.4	1	0.8	0	0	1	5.3	0	0	13
4q21/ <i>KMT2A</i> :: <i>AFF1</i>	0	0	5	3.2	1	5	0	0	3	0.6	0	0	1	2.0	0	0	0	0	0	0	0	1	0.8	1	1.9	0	0	0	0	0	12
1p32/ <i>KMT2A</i> :: <i>EPS15</i>	0	0	1	0.6	0	0	0	0	5	1.0	0	0	1	2.0	0	0	0	0	0	0	0	3	2.3	1	1.9	1	5.3	1	1.1	13	
17q12	0	0	0	0	0	0	0	0	6	1.2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1.9	1	5.3	2	2.2	10	
Other	2	4.5	3	1.9	1	5	3	3.8	60	12.3	2	6.3	8	15.7	0	0	1	14.3	2	20	5	7.2	17	12.8	6	11.5	2	10.5	14	15.1	126
Total	44	100	155	100	20	100	78	100	488	100	32	100	51	100	5	100	7	100	10	100	69	100	133	100	52	100	19	100	93	100	1,256

9p22/*KMT2A*::*MLLT3* refers to t(9;11)(p22;q23), 10p12/*KMT2A*::*MLLT10* to t(10;11)(p12;q23), 6q27/*KMT2A*::*AFDN* to t(6;11)(q27;q23), 19p13 to t(11;19)(q23;p13)-without ascertained sub-band, 19p13.1/*KMT2A*::*ELL* to t(11;19)(q23;p13.1), 19p13.3/*KMT2A*::*MLLT1* to t(11;19)(q23;p13.3), 1q21/*KMT2A*::*MLLT11* to t(1;11)(q21;q23), 10p11.2/*KMT2A*::*AB11* to t(10;11)(p11.2;q23), Xq24/*KMT2A*::*SEPT6* to t(X;11)(q24;q23), 17q21 to t(11;17)(q23;q21), 4q21/*KMT2A*::*AFF1* to t(4;11)(q21;q23), 1p32/*KMT2A*::*EPS15* to t(1;11)(p32;q23), and 17q12 to t(11;17)(q23;q12). Ten centers affiliated with the CCLG (i.e., Leeds, Bristol, Marsden, Nottingham, Sheffield, Southampton, Edinburgh, Liverpool, Manchester, Newcastle) and one center from Greece participated (i.e., Aghia Sophia Children's hospital (T.A.O.)).

AIEOP, Associazione Italiana Ematologia Oncologia Pediatrica (Italy); BFM, Berlin-Frankfurt-Münster (Germany and Austria); BSPHO, Belgian Society of Pediatric Hematology Oncology (Belgium); CCLG, Children's Cancer and Leukaemia Group (United Kingdom); COG, Children's Oncology Group (United States); CPH, Czech Pediatric Hematology (Czech Republic); DCOG, Dutch Childhood Oncology Group (the Netherlands); HKPHOSG, Hong Kong Pediatric Hematology and Oncology Study Group (Hong Kong); I-BFM-SG, International Berlin-Frankfurt-Münster study group; INS, Israel National Study (Israel); JPLSG, Japanese Pediatric Leukemia/Lymphoma Study Group (Japan); LAME, Leucémie Aiguë Myéloblastique Enfant (France); No., number of patients; NOPHO, Nordic Society for Pediatric Hematology and Oncology (Scandinavia); SEHOP, Spanish Society of Pediatric Hematology and Oncology (Spain); St. Jude, St. Jude Children's Research Hospital (United States); T.A.O., The Department of Pediatric Hematology and Oncology.

Supplementary Table S2. Clinical characteristics and outcome of children with *KMT2A*-rearranged acute myeloid leukemia with and without complete karyotypes

Characteristic	Incomplete karyotype	Complete karyotype	P
No. (%)	56 (4.5)	1,200 (95.5)	
Sex, No. (%) (n = 1,235)			0.80
Male	27 (50)	611 (51.7)	
Female	27 (50)	570 (48.3)	
Age at diagnosis, years. (n = 1,256)			
Median (IQR)	2.1 (0.9-10.2)	2.5 (1.0-9.9)	0.54
WBC count, x10 ⁹ /L. (n = 1,186)			
Median (IQR)	14.6 (4.8-86.7)	21.5 (5.8-87.8)	0.62
CNS involvement, No. (%) (n = 722)			
Negative	31 (83.8)	543 (79.3)	0.51
Positive	6 (16.2)	142 (20.7)	
FAB-type, No. (%) (n = 866)			0.94
FAB-M0	1 (2.0)	17 (2.1)	
FAB-M1	3 (5.9)	30 (3.7)	
FAB-M2	2 (3.9)	17 (2.1)	
FAB-M4	6 (11.8)	115 (14.1)	
FAB-M5	35 (68.6)	584 (71.7)	
FAB-M7	2 (3.9)	29 (3.6)	
FAB unspecified	2 (3.9)	23 (2.8)	
Fusion-based group, No. (%) (n = 1,256)			0.18
9p22/ <i>KMT2A</i> :: <i>MLL3</i>	28 (50)	516 (43)	
10p12/ <i>KMT2A</i> :: <i>MLL10</i>	8 (14.3)	210 (17.5)	
6q27/ <i>KMT2A</i> :: <i>AFDN</i>	3 (5.4)	89 (7.4)	
19p13	0 (0)	23 (1.9)	
19p13.1/ <i>KMT2A</i> :: <i>ELL</i>	3 (5.4)	72 (6)	
19p13.3/ <i>KMT2A</i> :: <i>MLL1</i>	1 (1.8)	55 (4.6)	
1q21/ <i>KMT2A</i> :: <i>MLL11</i>	0 (0)	28 (2.3)	
10p11.2/ <i>KMT2A</i> :: <i>ABII</i>	0 (0)	24 (2)	
Xq24/ <i>KMT2A</i> :: <i>SEPT6</i>	0 (0)	22 (1.8)	
17q21	2 (3.6)	11 (0.9)	
4q21/ <i>KMT2A</i> :: <i>AFF1</i>	0 (0)	12 (1)	
1p32/ <i>KMT2A</i> :: <i>EPS15</i>	0 (0)	13 (1.1)	
17q12	0 (0)	10 (0.8)	
Other	11 (19.6)	115 (9.6)	
Clinical outcome			
5-year pEFS (95% CI)	42.1 (26.8-57.4)	44.8 (41.9-47.7)	0.52
5-year pCIR (95% CI)	48.6 (32.3-63.1)	44.7 (41.5-47.8)	0.89
5-year pOS (95% CI)	58.9 (45-72.8)	62.7 (59.8-65.6)	0.82

9p22/*KMT2A*::*MLL3* refers to t(9;11)(p22;q23), 10p12/*KMT2A*::*MLL10* to t(10;11)(p12;q23), 6q27/*KMT2A*::*AFDN* to t(6;11)(q27;q23), 19p13 to t(11;19)(q23;p13)-without ascertained sub-band, 19p13.1/*KMT2A*::*ELL* to t(11;19)(q23;p13.1), 19p13.3/*KMT2A*::*MLL1* to t(11;19)(q23;p13.3), 1q21/*KMT2A*::*MLL11* to t(1;11)(q21;q23), 10p11.2/*KMT2A*::*ABII* to t(10;11)(p11.2;q23), Xq24/*KMT2A*::*SEPT6* to t(X;11)(q24;q23), 17q21 to t(11;17)(q23;q21), 4q21/*KMT2A*::*AFF1* to t(4;11)(q21;q23), 1p32/*KMT2A*::*EPS15* to t(1;11)(p32;q23), and 17q12 to t(11;17)(q23;q12).

CI, confidence interval; CNS, central nervous system; FAB, French-American-British; IQR, interquartile range; No., number of patients; pCIR, probability of cumulative incidence of relapse; pEFS, probability of event-free survival; pOS, probability of overall survival; WBC, white blood cell count.

Supplementary Table S3. Frequency distribution of numerical additional cytogenetic aberrations in the total cohort and stratified by *KMT2A* fusion-based group

Trisomy	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
1	15	10 (66.7)	-	-	-	3 (20)	-	-	-	-	-	-	-	1 (6.7)	1 (6.7)
2	4	2 (50)	1 (25)	-	-	-	-	-	-	1 (25)	-	-	-	-	-
3	16	10 (62.5)	3 (18.8)	1 (6.3)	-	-	-	-	-	-	-	-	-	-	2 (12.5)
4	25	8 (32)	6 (24)	8 (32)	-	-	1 (4)	-	-	-	-	-	-	-	2 (8)
5	6	3 (50)	2 (33.3)	1 (16.7)	-	-	-	-	-	-	-	-	-	-	-
6*	65	31 (47.7)	13 (20)	3 (4.6)	1 (1.5)	-	4 (6.2)	1 (1.5)	-	1 (1.5)	3 (4.6)	1 (1.5)	-	1 (1.5)	6 (9.2)
7	10	5 (50)	1 (10)	3 (30)	-	-	-	-	-	-	-	-	1 (10)	-	-
8*	210	119 (56.7)	22 (10.5)	8 (3.8)	9 (4.3)	18 (8.6)	13 (6.2)	2 (1.0)	1 (0.5)	1 (0.5)	1 (0.5)	2 (1.0)	2 (1.0)	1 (0.5)	11 (5.2)
9	18	10 (55.6)	1 (5.6)	2 (11.1)	-	1 (5.6)	2 (11.1)	-	-	-	-	1 (5.6)	1 (5.6)	-	-
10	6	3 (50)	1 (16.7)	1 (16.7)	-	1 (16.7)	-	-	-	-	-	-	-	-	-
11	4	4 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
12	14	6 (42.9)	4 (28.6)	1 (7.1)	-	-	1 (7.1)	-	-	-	2 (14.3)	-	-	-	-
13	18	4 (22.2)	2 (11.1)	3 (16.7)	2 (11.1)	2 (11.1)	2 (11.1)	-	-	1 (5.6)	1 (5.6)	1 (5.6)	-	-	-
14	12	9 (75)	1 (8.3)	-	-	-	-	-	-	-	-	-	-	-	2 (16.7)
15	7	4 (57.1)	2 (28.6)	-	-	-	1 (14.3)	-	-	-	-	-	-	-	-
16	13	7 (53.8)	4 (30.8)	1 (7.7)	-	-	-	-	-	-	-	-	-	-	1 (7.7)
17	10	6 (60)	1 (10)	-	-	-	2 (20)	-	-	-	-	-	-	-	1 (10)
18	23	11 (47.8)	4 (17.4)	2 (8.7)	-	1 (4.3)	1 (4.3)	-	-	-	1 (4.3)	-	1 (4.3)	-	2 (8.7)
19*	79	43 (54.4)	7 (8.9)	11 (13.9)	-	-	3 (3.8)	1 (1.3)	1 (1.3)	2 (2.5)	1 (1.3)	1 (1.3)	-	1 (1.3)	8 (10.1)
20*	26	13 (50)	5 (19.2)	3 (11.5)	1 (3.8)	-	2 (7.7)	-	-	-	-	-	-	-	2 (7.7)
21*	51	24 (47.1)	12 (23.5)	10 (19.6)	1 (2.0)	-	1 (2.0)	1 (2.0)	-	-	-	-	-	-	2 (3.9)
22*	27	16 (59.3)	4 (14.8)	1 (3.7)	-	-	1 (3.7)	-	-	-	1 (3.7)	2 (7.4)	-	-	2 (7.4)
X	15	5 (33.3)	2 (13.3)	2 (13.3)	2 (13.3)	-	-	-	-	-	1 (6.7)	1 (6.7)	1 (6.7)	-	1 (6.7)
Y	3	1 (33.3)	-	1 (33.3)	-	1 (33.3)	-	-	-	-	-	-	-	-	-

Highlighted in green are the recurring numerical ACAs (i.e., occurring in at least 10 patients). 9p22 refers to *KMT2A::MLLT3/t(9;11)(p22;q23)*, 10p12 to *KMT2A::MLLT10/t(10;11)(p12;q23)*, 6q27 to *KMT2A::AFDN/t(6;11)(q27;q23)*, 19p13 to *t(11;19)(q23;p13)*-without ascertained sub-band, 19p13.1 to *KMT2A::ELL/t(11;19)(q23;p13.1)*, 19p13.3 to *KMT2A::MLLT1/t(11;19)(q23;p13.3)*, 1q21 to *KMT2A::MLLT11/t(1;11)(q21;q23)*, 10p11.2 to *KMT2A::AB11/t(10;11)(p11.2;q23)*, Xq24 to *KMT2A::SEPT6/t(X;11)(q24;q23)*, 17q21 to *t(11;17)(q23;q21)*, 4q21 to *KMT2A::AFF1/t(4;11)(q21;q23)*, 1p32 to *KMT2A::EPS15/t(1;11)(p32;q23)*, and 17q12 to *t(11;17)(q23;q12)*.

No., number of patients.

*Two additional copies of chromosome 6 ($n = 3$ patients), two additional copies of chromosome 8 ($n = 12$ patients), three additional copies of chromosome 8 ($n = 1$ patient), two additional copies of chromosome 19 ($n = 1$ patient), two additional copies of chromosome 20 ($n = 1$ patient), two additional copies of chromosome 21 ($n = 7$ patients), three additional copies of chromosome 21 ($n = 4$ patients), and two additional copies of chromosome 22 ($n = 1$ patient).

Supplementary Table S3. Continued

Monosomy	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
1	2	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-	1 (50)
4	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
5	3	2 (66.7)	-	-	-	-	-	-	-	-	-	1 (33.3)	-	-	-
6	2	-	-	-	-	2 (100)	-	-	-	-	-	-	-	-	-
7	13	6 (46.2)	4 (30.8)	-	-	-	1 (7.7)	-	-	-	1 (7.7)	-	-	-	1 (7.7)
8	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
9	5	-	2 (40)	-	-	1 (20)	-	-	-	-	-	-	-	-	2 (40)
10	13	2 (15.4)	4 (30.8)	1 (7.7)	-	-	-	-	-	-	-	-	-	-	6 (46.2)
11	6	1 (16.7)	3 (50)	-	-	-	-	-	-	-	-	-	-	-	2 (33.3)
12	3	-	-	-	-	-	-	-	-	1 (33.3)	-	-	-	-	2 (66.7)
13	7	2 (28.6)	-	1 (14.3)	-	-	-	-	-	-	-	1 (14.3)	-	-	3 (42.9)
14	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
15	2	1 (50)	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-
16	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
17	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
18	2	1 (50)	-	-	-	1 (50)	-	-	-	-	-	-	-	-	-
19	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
21	2	-	-	1 (50)	-	-	1 (50)	-	-	-	-	-	-	-	-
X	6	3 (50)	1 (16.7)	-	-	1 (16.7)	-	-	-	-	-	-	-	-	1 (16.7)
Y	9	1 (11.1)	2 (22.2)	-	-	2 (22.2)	-	-	1 (11.1)	-	1 (11.1)	-	-	-	2 (22.2)

Supplementary Table S4. Frequency distribution of structural additional cytogenetic aberrations in the total cohort and stratified by *KMT2A* fusion-based group

Structural aberration	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
add(1p)	14	8 (57.1)	3 (21.4)	-	-	-	-	-	-	-	-	1 (7.1)	-	-	2 (14.3)
add(1q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
add(2p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
add(2q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
add(3p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
add(3q)	3	-	2 (66.7)	-	-	-	-	-	1 (33.3)	-	-	-	-	-	-
add(4p)	2	1 (50)	-	-	-	-	-	1 (50)	-	-	-	-	-	-	-
add(4q)	2	-	1 (50)	1 (50)	-	-	-	-	-	-	-	-	-	-	-
add(5p)	1	-	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-
add(5q)	3	1 (33.3)	-	-	-	-	-	-	-	-	-	-	-	-	2 (66.7)
add(6q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
add(7p)	3	2 (66.7)	-	-	-	-	-	-	-	-	-	-	-	-	1 (33.3)
add(7q)	4	-	2 (50)	-	-	-	-	-	-	-	-	-	-	1 (25)	1 (25)
add(8p)	6	-	3 (50)	1 (16.7)	-	-	1 (16.7)	-	1 (16.7)	-	-	-	-	-	-
add(8q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
add(9q)	3	1 (33.3)	1 (33.3)	-	-	-	-	1 (33.3)	-	-	-	-	-	-	-
add(10p)	2	1 (50)	-	-	-	-	1 (50)	-	-	-	-	-	-	-	-
add(10q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
add(11p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
add(11q)	3	-	1 (33.3)	-	-	-	1 (33.3)	-	-	-	-	-	-	-	1 (33.3)
add(12p)	13	1 (7.7)	2 (15.4)	4 (30.8)	-	1 (7.7)	-	-	-	-	-	-	1 (7.7)	1 (7.7)	3 (23.1)
add(13p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
add(13q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
add(14q)	4	1 (25)	-	1 (25)	-	-	-	-	-	-	-	-	-	-	2 (50)
add(15q)	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
add(16p)	2	-	2 (100)	-	-	-	-	-	-	-	-	-	-	-	-
add(16q)	4	2 (50)	2 (50)	-	-	-	-	-	-	-	-	-	-	-	-
add(17p)	4	2 (50)	2 (50)	-	-	-	-	-	-	-	-	-	-	-	-
add(17q)	2	-	-	1 (50)	-	1 (50)	-	-	-	-	-	-	-	-	-
add(18p)	1	-	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-
add(18q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
add(19p)	1	-	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-
add(20p)	3	1 (33.3)	-	1 (33.3)	-	-	-	-	-	-	-	-	-	-	1 (33.3)
add(20q)	4	1 (25)	3 (75)	-	-	-	-	-	-	-	-	-	-	-	-
add(22q)	4	1 (25)	3 (75)	-	-	-	-	-	-	-	-	-	-	-	-
add(Xq)	2	-	-	-	-	-	-	1 (50)	-	-	-	-	-	-	1 (50)
del(1p)*	10	4 (40)	3 (30)	-	-	1 (10)	-	-	-	-	-	-	1 (10)	-	1 (10)
del(1q)	3	-	-	-	-	1 (33.3)	-	-	-	-	-	2 (66.7)	-	-	-
del(2q)	2	1 (50)	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-
del(3p)	3	1 (33.3)	1 (33.3)	-	-	-	-	-	-	-	-	-	-	-	1 (33.3)
del(3q)	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
del(4p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-

Structural aberration	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
del(4q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
del(4?)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
del(5q)	5	2 (40)	-	1 (20)	-	1 (20)	-	-	-	-	-	1 (20)	-	-	-
del(6p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
del(6q)	2	2 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
del(7p)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
del(7q)	5	1 (20)	1 (20)	-	-	1 (20)	1 (20)	-	-	-	-	-	-	-	1 (20)
del(8p)*	2	-	-	-	2 (100)	-	-	-	-	-	-	-	-	-	-
del(9p)*	5	2 (40)	-	-	-	1 (20)	1 (20)	-	-	-	-	-	-	-	1 (20)
del(9q)*	16	6 (37.5)	2 (12.5)	1 (6.3)	-	2 (12.5)	-	-	2 (12.5)	-	-	-	1 (6.3)	-	2 (12.5)
del(10p)	3	-	1 (33.3)	-	-	-	-	-	-	-	-	1 (33.3)	-	-	1 (33.3)
del(10q)	2	-	1 (50)	-	-	1 (50)	-	-	-	-	-	-	-	-	-
del(11p)	3	1 (33.3)	-	1 (33.3)	-	-	-	1 (33.3)	-	-	-	-	-	-	-
del(11q)	7	2 (28.6)	2 (28.6)	-	-	-	-	-	-	1 (14.3)	-	1 (14.3)	-	-	1 (14.3)
del(12p)	9	2 (22.2)	3 (33.3)	2 (22.2)	-	-	-	-	-	-	-	-	-	-	2 (22.2)
del(12q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
del(13q)	10	6 (60)	2 (20)	-	-	-	1 (10)	-	-	-	-	-	-	-	1 (10)
del(14q)	4	1 (25)	-	1 (25)	-	-	-	-	-	-	-	-	-	-	2 (50)
del(15q)	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
del(16q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
del(17p)	2	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (100)
del(17q)	3	1 (33.3)	-	-	-	-	-	-	1 (33.3)	-	-	1 (33.3)	-	-	-
del(18p)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
del(18q)	2	1 (50)	-	-	-	-	-	-	-	-	-	1 (50)	-	-	-
del(19p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
del(20q)	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
del(21q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
del(22q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
del(Xq)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(1p)	3	2 (66.7)	1 (33.3)	-	-	-	-	-	-	-	-	-	-	-	-
der(1q)	2	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-	1 (50)
der(1pq)	4	4 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(2p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
der(2q)	4	2 (50)	1 (25)	-	-	-	-	-	-	-	1 (25)	-	-	-	-
der(3p)	3	2 (66.7)	-	-	-	-	-	-	-	-	-	-	-	-	1 (33.3)
der(3q)	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
der(3pq)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(4p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(4q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(4pq)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
der(5q)*	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(6p)	4	3 (75)	-	-	-	-	-	-	-	-	-	-	-	-	1 (25)
der(6q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
der(6?)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-

Structural aberration	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
der(7p)	2	2 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(7q)	7	3 (42.9)	2 (28.6)	-	2 (28.6)	-	-	-	-	-	-	-	-	-	-
der(7pq)	1	-	-	-	-	-	-	-	-	-	-	1 (100)	-	-	-
der(8p)	2	1 (50)	-	-	-	-	-	-	1 (50)	-	-	-	-	-	-
der(8q)	2	2 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(9p)	4	-	1 (25)	-	-	-	-	-	-	-	-	-	-	-	3 (75)
der(9q)	4	2 (50)	1 (25)	-	-	-	1 (25)	-	-	-	-	-	-	-	-
der(9?)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(10)	4	1 (25)	1 (25)	-	-	-	-	-	-	1 (25)	-	1 (25)	-	-	-
der(10q)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
der(11p)	2	1 (50)	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-
der(11q) [*]	7	2 (28.6)	1 (14.3)	-	1 (14.3)	-	-	-	1 (14.3)	-	-	-	-	-	2 (28.6)
der(12p)	5	2 (40)	-	-	-	-	-	-	3 (60)	-	-	-	-	-	-
der(12q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(13p) [*]	2	-	-	-	-	-	-	-	1 (50)	-	-	1 (50)	-	-	-
der(13q)	3	1 (33.3)	1 (33.3)	-	-	-	-	-	-	-	-	-	-	-	1 (33.3)
der(14p)	2	-	-	-	-	-	1 (50)	-	1 (50)	-	-	-	-	-	-
der(14q)	2	1 (50)	-	-	-	-	-	-	-	-	-	-	1 (50)	-	-
der(15p)	3	-	2 (66.7)	-	-	-	-	-	-	-	-	-	-	-	1 (33.3)
der(15q)	3	2 (66.7)	-	-	-	-	-	-	-	-	-	-	-	-	1 (33.3)
der(16q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(17p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(17q)	2	-	-	1 (50)	-	-	-	-	-	-	-	-	-	-	1 (50)
der(17?)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(18p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(18q)	3	-	1 (33.3)	-	-	-	1 (33.3)	-	-	-	-	1 (33.3)	-	-	-
der(19p)	2	1 (50)	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-
der(19?)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
der(20q)	4	2 (50)	1 (25)	-	-	-	-	-	-	-	-	-	-	-	1 (25)
der(21p)	2	2 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(21q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(22q) [*]	3	-	2 (66.7)	-	-	-	-	-	-	-	-	1 (33.3)	-	-	-
der(Xp)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(Xq)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(Yq)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
der(1;5)(q;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(1;13)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(1;15)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
der(1;18)(q;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
der(1;22)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	1 (100)	-
der(8;12)(q;q)	2	-	1 (50)	-	-	-	-	-	1 (50)	-	-	-	-	-	-
der(12;19)(q;p)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
der(X;1)(q;q)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
i(1q)	4	3 (75)	-	-	-	-	-	-	-	-	-	-	-	-	1 (25)

Structural aberration	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
i(6p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
i(8q)	9	5 (55.6)	2 (22.2)	-	-	-	-	-	1 (11.1)	-	-	-	-	-	1 (11.1)
i(9q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
i(10q)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
i(12q)	2	1 (50)	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-
i(17q)	3	3 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
i(Xq)	2	2 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
ins(3;14)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
ins(17;11)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
ins(20;11)(p;q)	1	-	-	-	-	-	-	-	-	1 (100)	-	-	-	-	-
dup(1q)	4	2 (50)	1 (25)	-	-	-	-	-	-	-	-	-	-	-	1 (25)
dup(1)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
dup(5q)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
dup(7p)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
dic(1;8)(p;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
dic(1;11)(p;q)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
dic(1;15)(p;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
dic(2;9)(q;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
dic(7;10)(p;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
dic(7;13)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
dic(8?)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
dic(8;9)(p;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
dic(8;12)(p;p)	3	-	2 (66.7)	-	-	-	1 (33.3)	-	-	-	-	-	-	-	-
dic(12;14)(p;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)	-
dic(12;17)(p;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
idic(7p)	1	-	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-
inv(1)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
inv(3q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
inv(8q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
inv(8)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
inv(10)(p;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
inv(12)(p;q)	1	-	-	-	-	-	-	-	-	1 (100)	-	-	-	-	-
inv(14q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
inv(17)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
inv(X)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
r(7)(p;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
r(12)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
trp(1q)	1	-	-	-	-	-	-	-	1 (100)	-	-	-	-	-	-
+del(1p)	2	-	1 (50)	-	-	1 (50)	-	-	-	-	-	-	-	-	-
+del(9q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+del(12p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(1p)	3	-	-	-	-	1 (33.3)	1 (33.3)	-	-	-	-	-	-	-	1 (33.3)
+der(1?)	1	-	-	-	-	-	-	-	-	-	-	1 (100)	-	-	-
+der(1;2)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-

Structural aberration	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
+der(1;5)(q;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(1;5)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
+der(1;13)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
+der(1;16)(q;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(4q)	3	1 (33.3)	-	-	-	-	-	-	-	-	-	2 (66.7)	-	-	-
+der(5q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(6q)	10	-	-	10 (100)	-	-	-	-	-	-	-	-	-	-	-
+der(8p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
+der(8q)*	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
+der(8pq)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(9p)	17	17 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(10p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
+der(10?)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
+der(11p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(11q)	2	2 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(17q)	1	-	-	-	-	-	-	-	-	-	1 (100)	-	-	-	-
+der(18p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+der(19p)*	12	1 (8.3)	-	-	3 (25)	2 (16.7)	6 (50)	-	-	-	-	-	-	-	-
+der(19q)	1	-	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-
+der(20p)*	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
+i(1q)	2	-	-	-	1 (50)	-	1 (50)	-	-	-	-	-	-	-	-
+i(5p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
+i(8q)*	5	2 (40)	1 (20)	-	-	-	-	-	-	-	-	-	1 (20)	1 (20)	-
+ins(8q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
+ider(9p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
+ider(19p)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
+idic(1p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
+r(?)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
+neo(13q)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
t(1;3)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(1;4)(q;p)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
t(1;4)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(1;5)(p;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(1;6)(p;q)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
t(1;7)(q;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(1;7)(q;q)	1	-	-	-	-	-	-	-	-	-	-	-	1 (100)	-	-
t(1;10)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(1;11)(q;q)	2	1 (50)	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-
t(1;11)(q;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(1;12)(p;q)	1	-	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-
t(1;14)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(1;19)(p;p)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
t(2;9)(q;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(2;14)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-

Structural aberration	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
t(3;4)(p;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(3;4)(q;q)	1	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-	-
t(3;5)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(3;9)(q;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(3;10)(p;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(3;20)(p;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(4;5)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(4;9)(q;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(4;11)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(5;7)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(5;7)(q;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(5;9)(q;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(5;11)(q;q)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
t(5;13)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(5;17)(p;p)	1	-	-	-	-	-	-	-	-	-	-	-	1 (100)	-	-
t(5;18)(q;p)	1	-	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-
t(6;12)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(6;12)(q;p)	1	-	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-
t(6;12;9)(q;q;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(6;16)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(6;17)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(6;22)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(7;10)(q;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(7;10)(q;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
t(7;11)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(7;12)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(7;16)(p;p)	1	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)	-
t(7;17)(p;q)	1	-	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-
t(7;20)(q;q)	1	-	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-
t(7;20)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(8;9)(p;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(8;10)(q;p)	2	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(8;15)(p;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(8;18)(p;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(9;10)(p;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(9;11)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(9;13)(q;q)	2	-	-	-	2 (100)	-	-	-	-	-	-	-	-	-	-
t(9;14)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(9;17)(p;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(10;12)(q;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(10;15)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(11;14)(q;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(11;14)(q;q)	2	1 (50)	1 (50)	-	-	-	-	-	-	-	-	-	-	-	-
t(11;20)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-

Structural aberration	Total	9p22 No. (%)	10p12 No. (%)	6q27 No. (%)	19p13 No. (%)	19p13.1 No. (%)	19p13.3 No. (%)	1q21 No. (%)	10p11.2 No. (%)	Xq24 No. (%)	17q21 No. (%)	4q21 No. (%)	1p32 No. (%)	17q12 No. (%)	Other No. (%)
t(12;14)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(12;17)(q;q)	2	-	1 (50)	-	-	-	-	-	-	-	-	-	-	-	1 (50)
t(12;18)(q;p)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(12;19)(q;q)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
t(13;16;17)(q;p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(13;17)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(14;14)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(14;21)(p;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(15;16)(q;p)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(15;19)(q;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(15;22)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(X;2)(q;q)	1	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-	-
t(X;4)(q;q)	1	-	1 (100)	-	-	-	-	-	-	-	-	-	-	-	-
t(X;5)(p;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)
t(X;16)(q;q)	1	-	-	-	-	-	1 (100)	-	-	-	-	-	-	-	-
t(Y;20)(q;q)	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (100)

Highlighted in green are the recurring structural ACAs (i.e., occurring in at least 10 patients). 9p22 refers to *KMT2A::MLLT3*/t(9;11)(p22;q23), 10p12 to *KMT2A::MLLT10*/t(10;11)(p12;q23), 6q27 to *KMT2A::AFDN*/t(6;11)(q27;q23), 19p13 to t(11;19)(q23;p13)-without ascertained sub-band, 19p13.1 to *KMT2A::ELL*/t(11;19)(q23;p13.1), 19p13.3 to *KMT2A::MLLT1*/t(11;19)(q23;p13.3), 1q21 to *KMT2A::MLLT11*/t(1;11)(q21;q23), 10p11.2 to *KMT2A::AB11*/t(10;11)(p11.2;q23), Xq24 to *KMT2A::SEPT6*/t(X;11)(q24;q23), 17q21 to t(11;17)(q23;q21), 4q21 to *KMT2A::AFF1*/t(4;11)(q21;q23), 1p32 to *KMT2A::EPS15*/t(1;11)(p32;q23), and 17q12 to t(11;17)(q23;q12).

No., number of patients.

*One patient had both del(1p) and del(1q), one patient had two copies of del(8p), one patient had two copies of del(8q), one patient had both del(9p) and del(9q), one patient had two copies of der(5q), one patient had two copies of der(11q), one patient had two copies of der(13p), one patient had two copies of der(22q), one patient had two additional copies of der(8q), one patient had two additional copies of der(19q), one patient had two additional copies of der(20p), and two patients had two additional copies of i(8q).

Supplementary Table S5. Univariable Cox regression analyses of event-free survival, cumulative incidence of relapse, and overall survival in childhood *KMT2A*-rearranged acute myeloid leukemia

	pEFS				pCIR				pOS			
	No.	HR	95% CI	P	No.	HR	95% CI	P	No.	HR	95% CI	P
Age at diagnosis, years												
≤10	901	1.0			784	1.0			916	1.0		
>10	298	1.2	1.0-1.4	0.03	273	1.3	1.0-1.6	0.02	301	1.6	1.3-2.0	<0.01
WBC count, x10 ⁹ /L												
≤100	900	1.0			814	1.0			911	1.0		
>100	257	1.3	1.1-1.5	0.01	203	1.1	0.9-1.4	0.39	263	1.4	1.1-1.7	<0.01
CNS involvement												
No	571	1.0			527	1.0			572	1.0		
Yes	147	1.3	1.0-1.6	0.09	121	1.0	0.7-1.4	0.87	147	1.3	0.9-1.7	0.17
Fusion-based group												
9p22/ <i>KMT2A</i> :: <i>MLLT3</i>	512	1.0			459	1.0			522	1.0		
Xq24/ <i>KMT2A</i> :: <i>SEPT6</i>	21	0.4	0.2-1.1	0.07	21	0.5	0.2-1.3	0.15	21	0.3	0.1-1.2	0.08
1p32/ <i>KMT2A</i> :: <i>EPS15</i>	12	0.5	0.2-1.6	0.24	10	0.2	0-1.7	0.15	13	0.2	0.0-1.7	0.15
17q21	12	0.7	0.3-1.9	0.52	11	0.2	0-1.8	0.16	13	1.1	0.4-2.8	0.93
17q12	10	1.0	0.4-2.7	0.99	9	1.1	0.4-3.5	0.86	10	1.7	0.6-4.5	0.32
1q21/ <i>KMT2A</i> :: <i>MLLT11</i>	27	1.0	0.6-1.8	0.94	22	0.7	0.3-1.6	0.37	27	0.9	0.4-1.9	0.73
19p13.1/ <i>KMT2A</i> :: <i>ELL</i>	71	1.3	0.9-1.8	0.15	61	1.2	0.8-1.9	0.30	72	1.1	0.7-1.7	0.73
19p13	20	1.4	0.8-2.4	0.32	19	1.3	0.6-2.6	0.48	20	1.4	0.7-2.9	0.34
19p13.3/ <i>KMT2A</i> :: <i>MLLT1</i>	55	1.6	1.1-2.3	0.01	50	1.8	1.2-2.7	<0.01	55	1.6	1.1-2.5	0.03
10p12/ <i>KMT2A</i> :: <i>MLLT10</i>	212	1.7	1.4-2.1	<0.01	186	1.9	1.5-2.4	<0.01	214	1.7	1.3-2.2	<0.01
4q21/ <i>KMT2A</i> :: <i>AFF1</i>	12	2.7	1.4-5.2	<0.01	6	1.5	0.5-4.6	0.51	12	4.4	2.2-8.6	<0.01
6q27/ <i>KMT2A</i> :: <i>AFDN</i>	89	2.0	1.5-2.7	<0.01	77	2.3	1.7-3.1	<0.01	90	2.2	1.6-3.0	<0.01
10p11.2/ <i>KMT2A</i> :: <i>ABII</i>	24	2.5	1.6-4.1	<0.01	22	3.5	2.1-5.9	<0.01	24	1.9	1.0-3.5	0.04
Other	122	1.5	1.1-1.9	<0.01	104	1.6	1.1-2.1	<0.01	124	1.4	1.0-2.0	0.04
ACA												
No	614	1.0			549	1.0			621	1.0		
Yes	540	1.2	1.0-1.4	0.03	464	1.1	0.9-1.4	0.20	544	1.5	1.2-1.8	<0.01
ACA type												
No ACA	614	1.0			549	1.0			621	1.0		
Structural	155	1.5	1.2-1.8	<0.01	133	1.5	1.2-2.0	<0.01	155	1.6	1.2-2.1	<0.01
Numerical	205	0.9	0.7-1.1	0.25	183	0.8	0.6-1.0	0.06	207	1.1	0.9-1.5	0.36
Both	180	1.4	1.1-1.7	<0.01	148	1.3	1.0-1.7	0.03	182	1.9	1.4-2.4	<0.01
Recurring ACAs*	Yes/No				Yes/No				Yes/No			
Monosomy 7	13/527	0.9	0.4-1.9	0.81	11/453	0.5	0.2-1.7	0.29	13/531	1.1	0.5-2.5	0.81
Monosomy 10	13/527	2.4	1.3-4.3	<0.01	10/454	3.1	1.5-6.3	<0.01	13/531	2.9	1.5-5.5	<0.01
Trisomy 1	13/527	1.7	0.9-3.2	0.10	10/454	1.9	0.9-4	0.10	13/531	2.7	1.4-5.0	<0.01
Trisomy 3	16/524	1.5	0.8-2.7	0.19	10/454	1.1	0.4-2.6	0.91	16/528	1.6	0.8-3.2	0.15
Trisomy 4	23/517	2.1	1.3-3.3	<0.01	17/447	2.3	1.3-4.1	<0.01	23/521	1.9	1.1-3.2	0.02
Trisomy 6	61/479	1.5	1.1-2.1	0.01	47/417	1.6	1.1-2.4	0.02	61/483	1.5	1.0-2.2	0.04
Trisomy 7	9/531	1.6	0.7-3.7	0.24	4/460	0.4	0.1-3.2	0.42	9/535	1.1	0.4-3.0	0.81

Trisomy 8	198/342	0.7	0.6-0.9	<0.01	172/292	0.7	0.5-0.9	<0.01	200/344	0.7	0.5-0.9	0.01
Trisomy 9	17/523	1.0	0.5-1.9	0.96	15/449	1.0	0.5-2.1	0.98	17/527	0.9	0.4-1.9	0.82
Trisomy 12	14/526	2.1	1.1-3.8	0.02	11/453	2.6	1.3-5.3	<0.01	14/530	2.0	1.0-4.0	0.04
Trisomy 13	17/523	1.4	0.8-2.5	0.30	12/452	1.2	0.5-2.6	0.70	17/527	1.5	0.8-3.0	0.21
Trisomy 14	11/529	1.4	0.7-2.8	0.34	10/454	1.9	0.9-4.0	0.10	11/533	1.2	0.5-3.0	0.66
Trisomy 16	12/528	2.8	1.5-5.1	<0.01	9/455	3.8	1.9-7.8	<0.01	12/532	2.0	0.9-4.2	0.08
Trisomy 17	8/532	2.2	1.1-4.7	0.04	6/458	2.7	1.1-6.6	0.03	8/536	2.4	1.1-5.4	0.03
Trisomy 18	21/519	1.4	0.8-2.4	0.28	17/447	1.7	0.9-3.2	0.11	21/523	1.6	0.9-3.0	0.12
Trisomy 19	78/462	1.1	0.8-1.5	0.41	65/399	1.2	0.8-1.7	0.30	78/466	1.2	0.8-1.7	0.34
Trisomy 20	24/516	1.3	0.8-2.2	0.24	21/443	1.6	0.9-2.7	0.13	24/520	1.3	0.7-2.3	0.38
Trisomy 21	47/493	1.3	0.9-1.9	0.17	40/424	1.3	0.8-2.1	0.21	47/497	1.5	1.0-2.3	0.06
Trisomy 22	24/516	1.4	0.9-2.3	0.17	19/445	1.5	0.9-2.7	0.15	24/520	1.4	0.8-2.5	0.20
Trisomy X	13/527	2.6	1.4-4.8	<0.01	7/457	2.3	0.9-5.5	0.07	13/531	2.1	1.1-4.3	0.04
add(1p)	13/527	1.3	0.7-2.6	0.40	10/454	1.3	0.6-3.0	0.49	13/531	1.2	0.5-2.7	0.66
add(12p)	13/527	2.4	1.4-4.3	<0.01	9/455	2.4	1.1-5.1	0.02	13/531	1.5	0.7-3.2	0.29
del(1p)	10/530	0.7	0.2-1.7	0.39	8/456	0.5	0.1-1.9	0.29	10/534	0.7	0.2-2.1	0.51
del(9q)	16/524	2.0	1.2-3.5	0.01	14/450	2.6	1.4-5	<0.01	16/528	2.5	1.4-4.5	<0.01
del(13q)	9/531	1.1	0.4-2.5	0.92	9/455	1.6	0.7-3.9	0.31	9/535	0.5	0.1-2.0	0.32
+der(6q)	10/530	1.8	0.9-3.6	0.11	8/456	1.8	0.7-4.3	0.21	10/534	1.6	0.7-3.7	0.23
+der(9p)	16/524	0.9	0.5-1.8	0.84	13/451	0.9	0.4-2	0.79	16/528	1.1	0.5-2.2	0.90
+der(19p)	10/530	1.0	0.4-2.2	0.95	8/456	0.5	0.1-1.9	0.28	10/534	0.9	0.3-2.4	0.80

Values in bold indicate statistical significance. 9p22/*KMT2A::MLLT3* refers to t(9;11)(p22;q23), 10p12/*KMT2A::MLLT10* to t(10;11)(p12;q23), 6q27/*KMT2A::AFDN* to t(6;11)(q27;q23), 19p13 to t(11;19)(q23;p13)-without ascertained sub-band, 19p13.1/*KMT2A::ELL* to t(11;19)(q23;p13.1), 19p13.3/*KMT2A::MLLT1* to t(11;19)(q23;p13.3), 1q21/*KMT2A::MLLT11* to t(1;11)(q21;q23), 10p11.2/*KMT2A::ABII* to t(10;11)(p11.2;q23), Xq24/*KMT2A::SEPT6* to t(X;11)(q24;q23), 17q21 to t(11;17)(q23;q21), 4q21/*KMT2A::AFF1* to t(4;11)(q21;q23), 1p32/*KMT2A::EPS15* to t(1;11)(p32;q23), and 17q12 to t(11;17)(q23;q12).

ACA, additional cytogenetic aberrations; CI, confidence interval; CNS, central nervous system; HR, hazard ratio; No., number of patients; pCIR, probabilities of cumulative incidence of relapse; pEFS, probabilities of event-free survival; pOS, probabilities of overall survival; WBC, white blood cell count.

*Patients with specific ACAs are compared with patients with other ACAs.

Supplementary Table S6. Presence and type of additional cytogenetic aberrations by clinical characteristics

	No.	ACAs		P	Type of ACA			P
		Absent No. (%)	Present No. (%)		Numerical No. (%)	Structural No. (%)	Both* No. (%)	
Sex, No. (%)								
Male	611	324 (53.0)	287 (47.0)	0.87	110 (38.3)	82 (28.6)	95 (33.1)	0.90
Female	570	305 (53.5)	265 (46.5)		97 (36.6)	76 (28.7)	92 (34.7)	
Age at diagnosis, years								
Median (IQR)	1,200	2.3 (0.8-9.9)	3.0 (1.1-10.0)	0.06	3.9 (1.3-12.1)	1.9 (1.0-8.4)	2.6 (1.1-9.2)	0.01
WBC count, x 10 ⁹ /L								
Median (IQR)	1,134	35.8 (7.0-110.0)	13.7 (5.0-54.6)	<0.01	13.4 (4.9-60.9)	19.7 (5.5-54.3)	12.3 (5.0-51.9)	0.39
CNS involvement, No. (%)								
Negative	543	282 (51.9)	261 (48.1)	0.91	113 (43.3)	72 (27.6)	76 (29.1)	0.57
Positive	142	73 (51.4)	69 (48.6)		25 (36.2)	21 (30.4)	23 (33.3)	
FAB-type, No. (%)				<0.01				0.23
FAB-M0	17	4 (23.5)	13 (76.5)		3 (23.1)	5 (38.5)	5 (38.5)	
FAB-M1	30	18 (60.0)	12 (40)		5 (41.7)	4 (33.3)	3 (25)	
FAB-M2	17	12 (70.6)	5 (29.4)		3 (60)	2 (40)	0 (0)	
FAB-M4	115	81 (70.4)	34 (29.6)		16 (47.1)	7 (20.6)	11 (32.4)	
FAB-M5	584	308 (52.7)	276 (47.3)		108 (39.1)	87 (31.5)	81 (29.3)	
FAB-M7	29	2 (6.9)	27 (93.1)		15 (55.6)	1 (3.7)	11 (40.7)	
FAB unspecified	23	11 (47.8)	12 (52.2)		4 (33.3)	3 (25)	5 (41.7)	

Values in bold indicate statistical significance.

ACA, additional cytogenetic aberration; CNS, central nervous system; FAB, French-American-British; IQR, interquartile range; No., number of patients; WBC, white blood cell count.

*Including patients who had separate numerical and structural aberrations, as well as patients with gain of a chromosome with a structural aberration (e.g., +der(9p), +i(8q)).

Supplementary Table S7. Survival estimates of children with *KMT2A*-rearranged acute myeloid leukemia

	5-year pEFS				5-year pCIR				5-year pOS			
	No.	%	95% CI	<i>P</i>	No.	%	95% CI	<i>P</i>	No.	%	95% CI	<i>P</i>
ACA				0.03				0.25				<0.01
No	614	47.4	43.3-51.5		549	43.2	38.9-47.4		621	67.9	64.2-71.6	
Yes	540	41.8	37.5-46.1		464	46.5	41.7-51.1		544	56.8	52.5-61.1	
ACA type				<0.01				<0.01				<0.01
Structural	155	33.7	25.9-41.5		133	57.0	47.5-65.4		155	53.9	47.7-62.1	
Numerical	205	52.0	44.9-59.1		183	34.5	27.5-41.6		207	64.0	57.1-70.9	
Both	180	37.3	30.1-44.6		148	51.7	43.2-59.6		182	50.8	43.0-58.6	
9p22/<i>KMT2A</i>::<i>MLL3</i> group												
FAB-type				<0.01				<0.01				<0.01
Non-M5	81	37.9	26.9-48.9		70	48.6	35.9-60.1		84	52.3	42.0-63.5	
M5	298	65.9	60.2-71.6		274	24.5	19.4-29.9		305	80.3	75.6-85.0	
Trisomy 6*				<0.01				0.02				<0.01
No	208	55.1	48.2-62.0		188	35.1	28.1-42.1		208	68.4	61.7-75.1	
Yes	27	19.4	2.0-36.8		19	72.4	37.1-90.0		27	39.8	19.6-60.0	
FAB-type – Trisomy 6				<0.01				<0.01				<0.01
FAB-M5/No trisomy 6	273	68.3	62.6-74.0		253	23.4	18.3-29.0		278	82.1	77.4-86.8	
FAB-M5/Trisomy 6	11	29.1 [†]	0-59.9		7	54.3 [†]	5.2-88.1		11	47.7	13.2-82.2	
Non-FAB-M5/No trisomy 6	66	39.1	26.8-51.5		55	43.5	29.5-56.6		66	55.6	43.1-68.1	
Non-FAB-M5/Trisomy 6	10	26.7	0-56.1		10	73.3	24.8-93.3		10	32.0	0-65.3	
Flow-MRD at EO12				0.02				0.39				<0.01
Negative	198	54.2	47.1-61.3		191	40.3	33.3-47.4		198	73.6	67.3-79.9	
Positive	17	35.3	12.6-58.0		12	50.0	19.2-74.8		17	47.1	23.4-70.8	
FAB-type – Flow-MRD at EO12												
FAB-M5/MRD-negative	85	67.2	57.0-77.4	0.21	82	28.4	18.2-38.6	0.60	85	82.7	74.5-90.9	0.05
FAB-M5/MRD-positive	10	50.0	19.0-81.0		8	37.5	4.0-71.0		10	60.0	29.6-90.4	
Non-FAB-M5/MRD-negative	30	45.8	27.6-64.0	0.08	28	40.9	22.3-59.5	0.54	30	66.0	48.8-83.3	0.44
Non-FAB-M5/MRD-positive	4	25.0	0-67.5		2	50.0	0-100		4	50.0	1.0-99.0	

Values in bold indicate statistical significance. 9p22/*KMT2A*::*MLL3* refers to t(9;11)(p22;q23). In analyses concerning the 9p22/*KMT2A*::*MLL3* group, two-sided *P*-values ≤ 0.05 were considered statistically significant.

ACA, additional cytogenetic aberrations; CI, confidence interval; EO12, end of induction 2; flow-MRD, flow cytometry-based measurable residual disease; No., number of patients; pCIR, probabilities of cumulative incidence of relapse; pEFS, probabilities of event-free survival; pOS, probabilities of overall survival.

*Patients with trisomy 6 are compared with patients with other ACAs.

[†]For patients with FAB-M5 morphology and trisomy 6, the 3-year pEFS and pCIR are shown because these estimates could not be extrapolated to 5 years.

Supplementary Table S8. Univariable and multivariable Cox regression analyses of event-free survival, cumulative incidence of relapse, and overall survival in children with 9p22/*KMT2A::MLLT3* acute myeloid leukemia

Univariable analyses	pEFS				pCIR				pOS			
	No.	HR	95% CI	P	No.	HR	95% CI	P	No.	HR	95% CI	P
Age at diagnosis, years												
≤10	396	1.0			353	1.0			405	1.0		
>10	116	0.9	0.7-1.2	0.52	106	0.9	0.6-1.3	0.41	117	1.3	0.9-1.9	0.16
WBC count, x10 ⁹ /L												
≤100	394	1.0			365	1.0			401	1.0		
>100	104	1.4	1.0-1.9	0.05	81	1.1	0.7-1.6	0.76	107	1.4	0.9-2.0	0.10
CNS involvement												
No	274	1.0			253	1.0			274	1.0		
Yes	54	1.2	0.8-1.9	0.37	49	1.1	0.6-2.0	0.70	54	0.6	0.3-1.2	0.17
FAB-type												
Non-M5	81	1.0			70	1.0			84	1.0		
M5	298	0.4	0.3-0.6	<0.01	274	0.4	0.3-0.6	<0.01	305	0.4	0.3-0.6	<0.01
ACA												
No	258	1.0			233	1.0			263	1.0		
Yes	235	1.2	0.9-1.6	0.13	207	1.2	0.9-1.6	0.32	235	1.6	1.1-2.2	<0.01
ACA type												
No ACA	258	1.0			233	1.0			263	1.0		
Structural	52	1.4	0.9-2.2	0.09	47	1.5	1.0-2.5	0.08	52	1.5	0.9-2.6	0.15
Numerical	107	1.0	0.7-1.4	0.88	96	0.8	0.5-1.3	0.37	107	1.3	0.8-2.0	0.29
Both	76	1.5	1.0-2.1	0.03	64	1.5	1.0-2.3	0.06	76	2.1	1.4-3.2	<0.01
Recurring ACAs [†]												
Trisomy 1	9	2.7	1.3-5.8	0.01	6	2.9	1.1-7.9	0.03	9	4.8	2.2-10.5	<0.01
Trisomy 3	10	2.0	0.9-4.3	0.08	6	1.5	0.5-4.6	0.51	10	1.8	0.7-4.4	0.22
Trisomy 6	27	2.2	1.3-3.6	<0.01	19	2.2	1.2-3.9	0.01	27	2.4	1.4-4.2	<0.01
Trisomy 8	114	0.6	0.4-0.9	<0.01	102	0.7	0.5-1.0	0.08	114	0.6	0.4-0.9	0.02
Trisomy 9	9	1.1	0.5-2.8	0.80	9	1.8	0.7-4.3	0.21	9	0.9	0.3-2.7	0.79
Trisomy 18	9	1.4	0.6-3.4	0.47	8	1.9	0.7-5.2	0.20	9	1.5	0.5-4.0	0.46
Trisomy 19	42	1.6	1.0-2.4	0.04	35	1.8	1.1-2.9	0.02	42	1.8	1.1-2.9	0.03
Trisomy 20	12	1.8	0.9-3.6	0.12	10	2.3	1.0-5.2	0.04	12	1.4	0.5-3.3	0.52
Trisomy 21	21	1.7	1.0-2.9	0.08	17	1.7	0.9-3.4	0.11	21	1.7	0.9-3.3	0.11
Trisomy 22	13	1.8	0.9-3.5	0.10	11	2.3	1.1-5.0	0.03	13	1.8	0.9-4.0	0.12
+der(9p)	16	1.2	0.6-2.4	0.61	13	1.2	0.5-2.7	0.71	16	1.4	0.6-2.9	0.44
Flow-MRD at EO12												
Negative	198	1.0			191	1.0			198	1.0		
Positive	17	2.1	1.1-3.9	0.02	12	1.4	0.6-3.3	0.40	17	2.8	1.4-5.7	<0.01
Multivariable analyses including ACAs	pEFS				pCIR				pOS			
	No.	HR	95% CI	P	No.	HR	95% CI	P	No.	HR	95% CI	P
WBC count, x10 ⁹ /L												
≤100	*	*			NA	NA			NA	NA		

>100	*	*	*	*	NA	NA	NA	NA	NA	NA	NA	NA
FAB-type												
Non-M5	76	1.0			65	1.0			76	1.0		
M5	284	0.5	0.4-0.7	<0.01	260	0.5	0.3-0.8	<0.01	289	0.4	0.3-0.7	<0.01
Recurring ACAs	Yes/No				Yes/No				Yes/No			
Trisomy 1	*	*	*	*	*	*	*	*	4/361	3.7	0.9-15.1	0.07
Trisomy 3	*	*	*	*	NA	NA	NA	NA	NA	NA	NA	NA
Trisomy 6	21/339	2.2	1.2-4.0	<0.01	17/308	2.7	1.3-5.3	<0.01	21/344	2.3	1.2-4.4	0.01
Trisomy 8	93/267	0.7	0.4-1.0	0.07	86/239	0.6	0.4-1.1	0.08	*	*	*	*
Trisomy 19	*	*	*	*	*	*	*	*	*	*	*	*
Trisomy 20	NA	NA	NA	NA	*	*	*	*	NA	NA	NA	NA
Trisomy 21	*	*	*	*	NA	NA	NA	NA	NA	NA	NA	NA
Trisomy 22	NA	NA	NA	NA	*	*	*	*	NA	NA	NA	NA
Multivariable analyses including the combination FAB-M5/Trisomy 6	pEFS				pCIR				pOS			
	No.	HR	95% CI	P	No.	HR	95% CI	P	No.	HR	95% CI	P
WBC count, x10 ⁹ /L												
≤100	*	*			NA	NA			NA	NA		
>100	*	*	*	*	NA	NA	NA	NA	NA	NA	NA	NA
FAB-type – Trisomy 6												
FAB-M5/No trisomy 6	273	1.0			253	1.0			278	1.0		
FAB-M5/Trisomy 6	11	3.9	1.9-8.2	<0.01	7	3.3	1.2-9.3	0.02	11	4.3	1.9-10.2	<0.01
Non-FAB-M5/No trisomy 6	66	2.3	1.6-3.3	<0.01	55	2.1	1.3-3.4	<0.01	66	2.8	1.8-4.5	<0.01
Non-FAB-M5/Trisomy 6	10	3.1	1.4-6.9	<0.01	10	5.0	2.2-11.2	<0.01	10	4.1	1.7-9.6	<0.01
Recurring ACAs	Yes/No				Yes/No				Yes/No			
Trisomy 1	*	*	*	*	*	*	*	*	4/361	3.7	0.9-15.2	0.07
Trisomy 3	*	*	*	*	NA	NA	NA	NA	NA	NA	NA	NA
Trisomy 8	93/267	0.7	0.4-1.0	0.08	86/239	0.6	0.4-1.1	0.09	*	*	*	*
Trisomy 19	*	*	*	*	*	*	*	*	*	*	*	*
Trisomy 20	NA	NA	NA	NA	*	*	*	*	NA	NA	NA	NA
Trisomy 21	*	*	*	*	NA	NA	NA	NA	NA	NA	NA	NA
Trisomy 22	NA	NA	NA	NA	*	*	*	*	NA	NA	NA	NA
Multivariable analyses including flow-MRD at EO12	pEFS				pCIR				pOS			
	No.	HR	95% CI	P	No.	HR	95% CI	P	No.	HR	95% CI	P
WBC count, x10 ⁹ /L												
≤100	100	1.0			NA	NA			NA	NA		
>100	25	0.5	0.2-1.1	0.07	NA	NA	NA	NA	NA	NA	NA	NA
FAB-type												
Non-M5	33	1.0			65	1.0			34	1.0		
M5	92	0.5	0.3-0.9	0.02	260	0.5	0.3-0.8	<0.01	95	0.5	0.2-1.1	0.07
Flow-MRD at EO12												
Negative	112	1.0			NA	NA			115	1.0		
Positive	13	2.4	1.1-5.5	0.04	NA	NA	NA	NA	14	2.5	1.0-6.0	0.05

Owing to the absence of flow-MRD at EO12 data in 60% of patients with 9p22/*KMT2A::MLL3*, it was not feasible to assess its prognostic significance in both the context of FAB-type and recurring ACAs. Consequently, we proceeded to conduct multivariable Cox regression analyses, considering either FAB-type and recurring ACAs, or FAB-

type and flow-MRD at EO12. Values in bold indicate statistical significance. ACA type was excluded from multivariable analyses as the recurring ACAs and the ACA type variables are related. 9p22/*KMT2A::MLLT3* refers to t(9;11)(p22;q23). Variables with *P*-values < 0.10 in univariable Cox regression analyses entered multivariable Cox regression models. Variables in the multivariable models with *P*-values > 0.15 were omitted from the final multivariable models by stepwise backward elimination. Two-sided *P*-values ≤ 0.05 were considered statistically significant.

ACA, additional cytogenetic aberrations; CI, confidence interval; EO12, end of induction 2; flow-MRD, flow cytometry-based measurable residual disease; FAB, French-American-British; HR, hazard ratio; NA, not applied (not significant variables in univariable Cox regression analyses); No., number of patients; pCIR, probabilities of cumulative incidence of relapse; pEFS, probabilities of event-free survival; pOS, probabilities of overall survival; WBC, white blood cell count.

*Omitted from the final multivariable model of EFS/CIR/OS due to a *P*-value > 0.15 in stepwise backward elimination.

†Patients with specific ACAs are compared with patients with other ACAs.

Supplementary Table S9. Overview of recurrent additional cytogenetic aberrations that were independently associated with survival over time in childhood *KMT2A*-rearranged acute myeloid leukemia

Recurrent ACAs	Coenen et al. 2011				Van Weelderen et al. 2024			
	5-year pEFS		5-year pOS		5-year pEFS		5-year pOS	
	No.	%	No.	%	No.	%	No.	%
Monosomy 10	NA	NA	NA	NA	13	15	13	21 [†]
Trisomy 1	NA	NA	NA	NA	NA	NA	13	14 [†]
Trisomy 4	NA	NA	NA	NA	23	16	23	37
Trisomy 6	NA	NA	NA	NA	61	29 [†]	61	47 [†]
Trisomy 8	130	53*	130	61*	198	51	200	65
Trisomy 12	NA	NA	NA	NA	14	21	14	32
Trisomy 16	NA	NA	NA	NA	12	8 [†]	NA	NA
Trisomy 17	NA	NA	NA	NA	8	13 [‡]	8	25
Trisomy 19	37	17 [†]	37	24 [†]	NA	NA	NA	NA
Trisomy 21	35	19	35	28	NA	NA	NA	NA
Trisomy X	NA	NA	NA	NA	13	15	13	39 [†]
Add(12p)	NA	NA	NA	NA	13	15 ^{†,‡}	NA	NA
Del(9q)	NA	NA	NA	NA	16	15	16	31 ^{†,‡}

This table exclusively includes recurrent additional cytogenetic aberrations that were subjected to multivariable Cox regression analysis in the respective studies. Notably, in the study by Coenen et al. (Blood, 2009), *P*-values were considered significant if ≤ 0.05 , while in the present study, *P*-values were considered significant if ≤ 0.01 . ACA, additional cytogenetic aberration; NA, not applicable; No. number of patients; pEFS, probability of event-free survival; pOS, probability of overall survival.

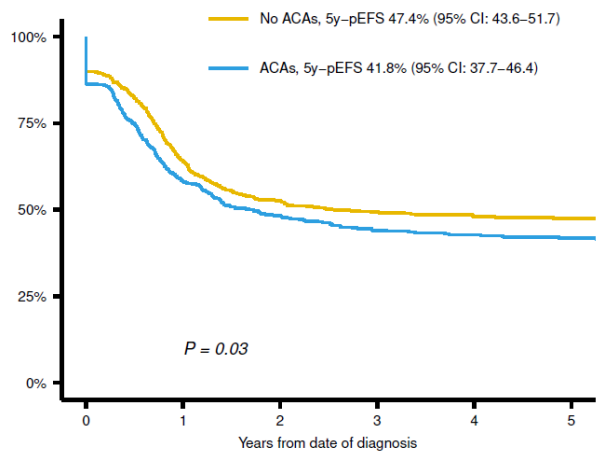
*Independently associated with superior EFS/OS.

[†]Independently associated with inferior EFS/OS.

[‡]For patients with trisomy 17 and add(12p), the 3-year pEFS are shown, and for patients with del(9q), the 3-year pOS is shown because these estimates could not be extrapolated to 5 years.

Supplementary Figures

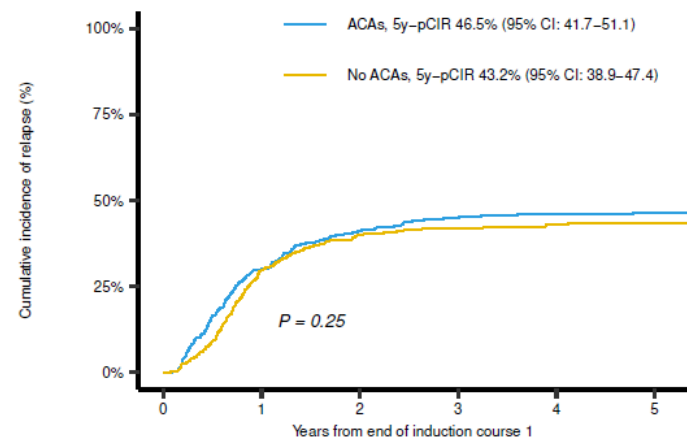
A



Number at risk (number censored)

614 (0)	391 (3)	310 (15)	259 (47)	200 (100)	150 (148)
540 (0)	310 (5)	232 (31)	187 (57)	148 (91)	111 (125)

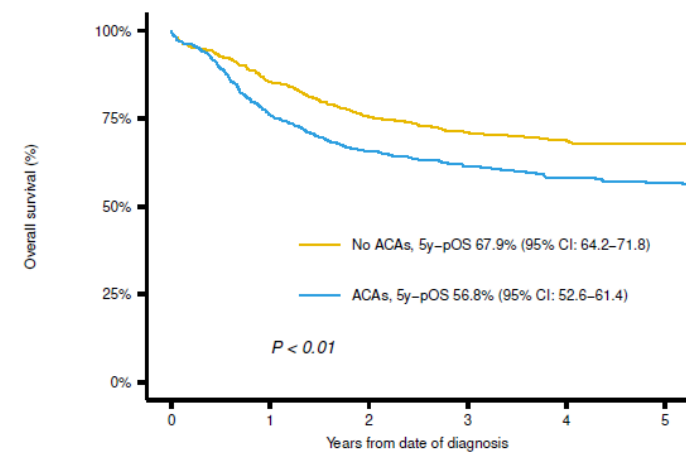
B



Number at risk (number censored)

549 (0)	372 (15)	298 (33)	251 (71)	192 (127)	151 (166)
464 (0)	306 (20)	226 (50)	187 (74)	143 (114)	108 (148)

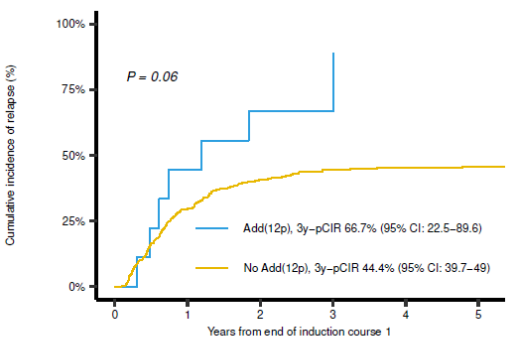
C



Number at risk (number censored)

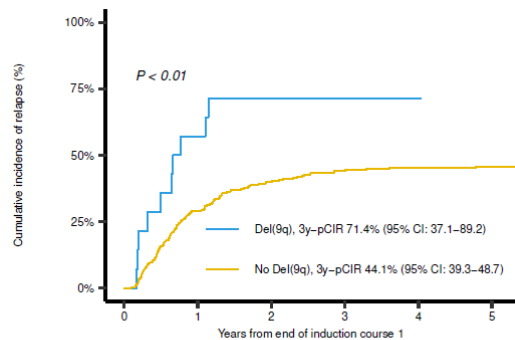
621 (0)	528 (4)	448 (22)	378 (67)	292 (142)	226 (205)
544 (0)	410 (5)	325 (35)	276 (64)	213 (114)	159 (163)

Supplementary Figure S1. Kaplan-Meier estimates of (A) event-free survival, (B) cumulative incidence of relapse, and (C) overall survival of children with *KMT2A*-rearranged acute myeloid leukemia with and without additional cytogenetic aberrations. ACA, additional cytogenetic aberration; pCIR, probability of cumulative incidence of relapse; pEFS, probability of event-free survival; pOS, probability of overall survival.

A

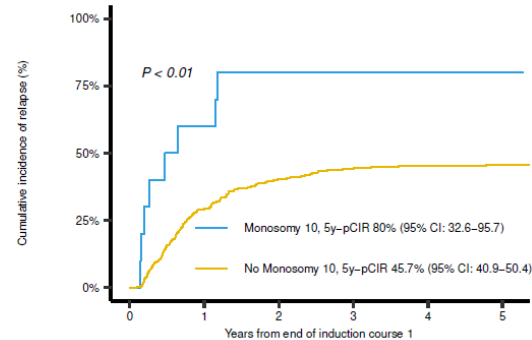
Number at risk (number censored)

455 (0)	302 (19)	224 (49)	186 (72)	143 (112)	108 (146)
9 (0)	4 (1)	2 (1)	1 (2)	0 (2)	0 (2)

B

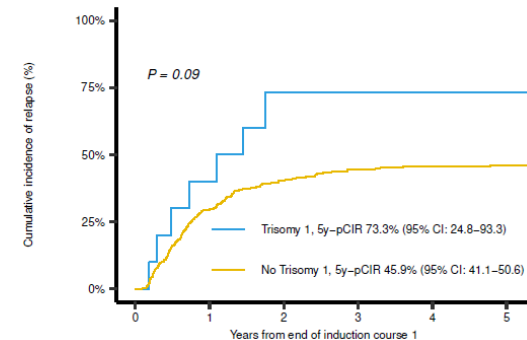
Number at risk (number censored)

450 (0)	301 (19)	223 (49)	185 (72)	142 (111)	108 (144)
14 (0)	5 (1)	3 (1)	2 (2)	1 (3)	0 (4)

C

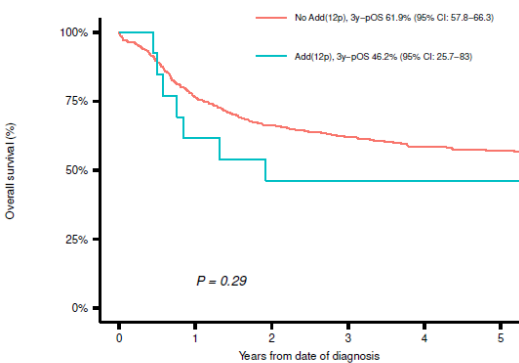
Number at risk (number censored)

454 (0)	302 (20)	224 (50)	185 (74)	141 (114)	107 (147)
10 (0)	4 (0)	2 (0)	2 (0)	2 (0)	1 (1)

D

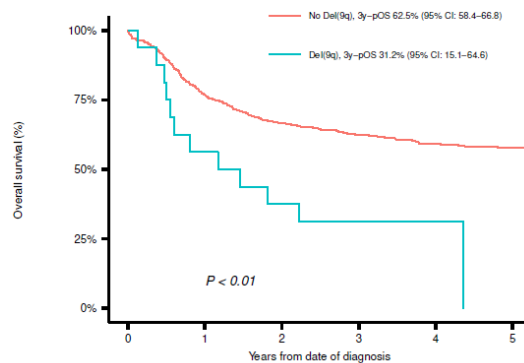
Number at risk (number censored)

454 (0)	300 (20)	224 (49)	185 (73)	142 (112)	107 (146)
10 (0)	6 (0)	2 (1)	2 (1)	1 (2)	1 (2)

E

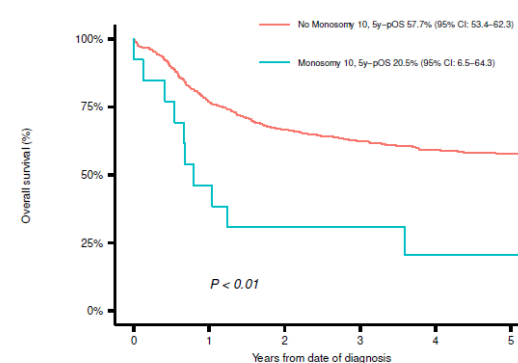
Number at risk (number censored)

531 (0)	402 (5)	319 (35)	271 (63)	209 (112)	158 (158)
13 (0)	8 (0)	6 (0)	5 (1)	4 (2)	1 (5)

F

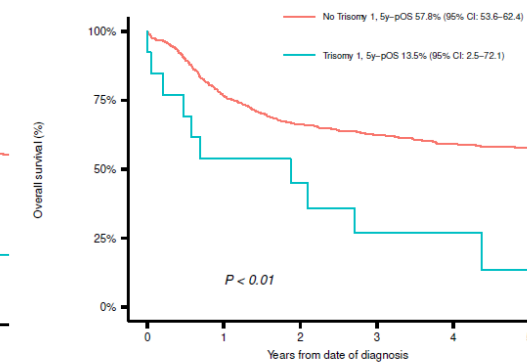
Number at risk (number censored)

528 (0)	401 (5)	319 (35)	272 (63)	210 (112)	159 (159)
16 (0)	9 (0)	6 (0)	4 (1)	3 (2)	0 (4)

G

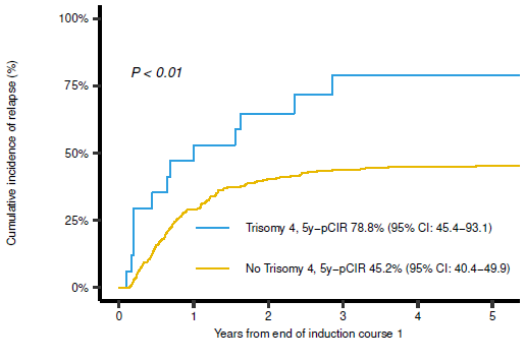
Number at risk (number censored)

531 (0)	404 (5)	321 (35)	272 (64)	211 (113)	158 (161)
13 (0)	6 (0)	4 (0)	4 (0)	2 (1)	1 (2)

H

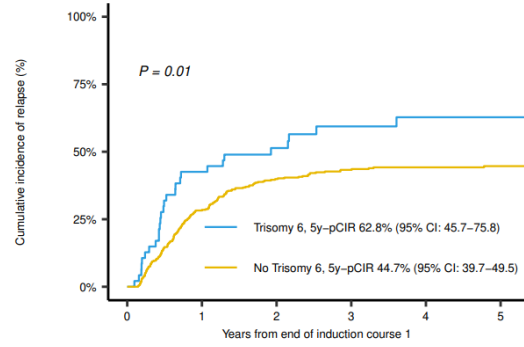
Number at risk (number censored)

531 (0)	403 (5)	320 (34)	273 (63)	210 (113)	158 (161)
13 (0)	7 (0)	5 (1)	3 (1)	3 (1)	1 (2)

I

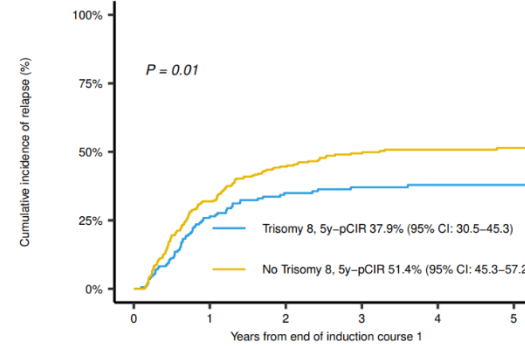
Number at risk (number censored)

447 (0)	298 (20)	221 (49)	184 (73)	140 (113)	107 (145)
17 (0)	8 (0)	5 (1)	3 (1)	3 (1)	1 (3)

J

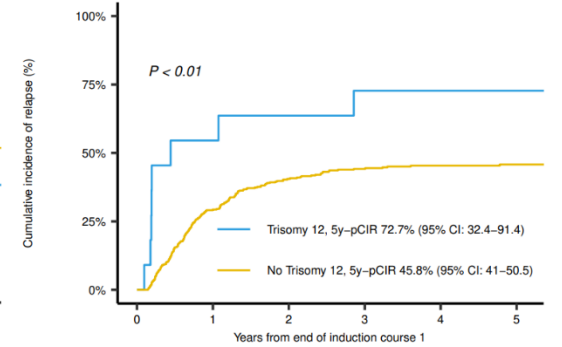
Number at risk (number censored)

417 (0)	279 (20)	206 (47)	173 (68)	133 (105)	101 (136)
47 (0)	27 (0)	20 (3)	14 (6)	10 (9)	7 (12)

K

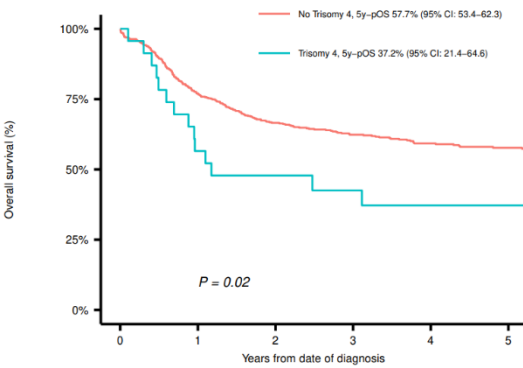
Number at risk (number censored)

292 (0)	186 (13)	133 (30)	108 (43)	84 (64)	59 (88)
172 (0)	120 (7)	93 (20)	79 (31)	59 (50)	49 (60)

L

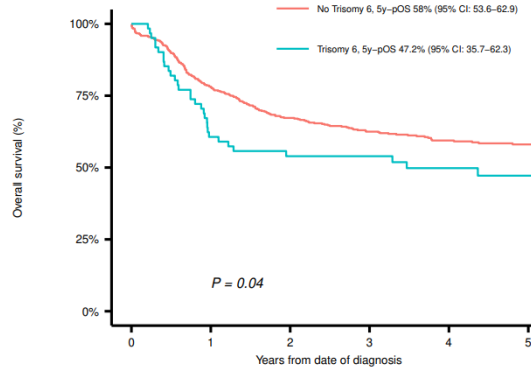
Number at risk (number censored)

453 (0)	301 (20)	222 (50)	184 (74)	142 (112)	107 (146)
11 (0)	5 (0)	4 (0)	3 (0)	1 (2)	1 (2)

M

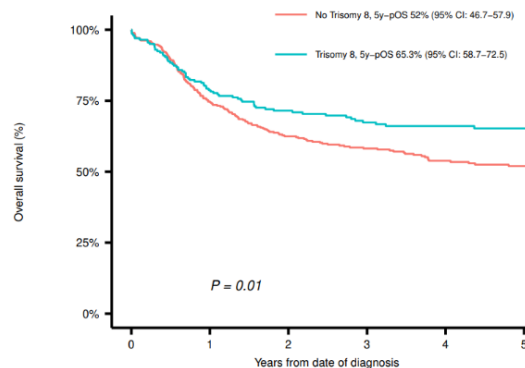
Number at risk (number censored)

521 (0)	397 (5)	315 (34)	268 (62)	208 (110)	156 (157)
23 (0)	13 (0)	10 (1)	8 (2)	5 (4)	3 (6)

N

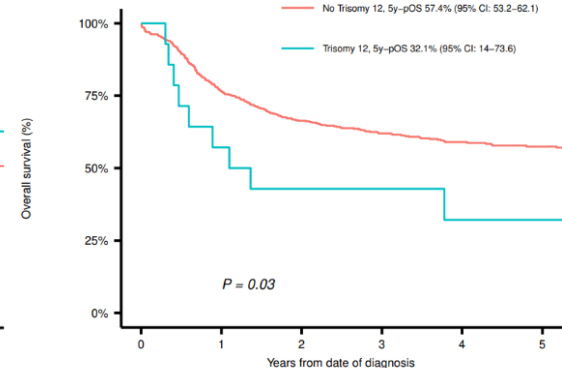
Number at risk (number censored)

483 (0)	373 (5)	295 (32)	249 (58)	191 (105)	145 (147)
61 (0)	37 (0)	30 (3)	27 (6)	22 (9)	14 (16)

O

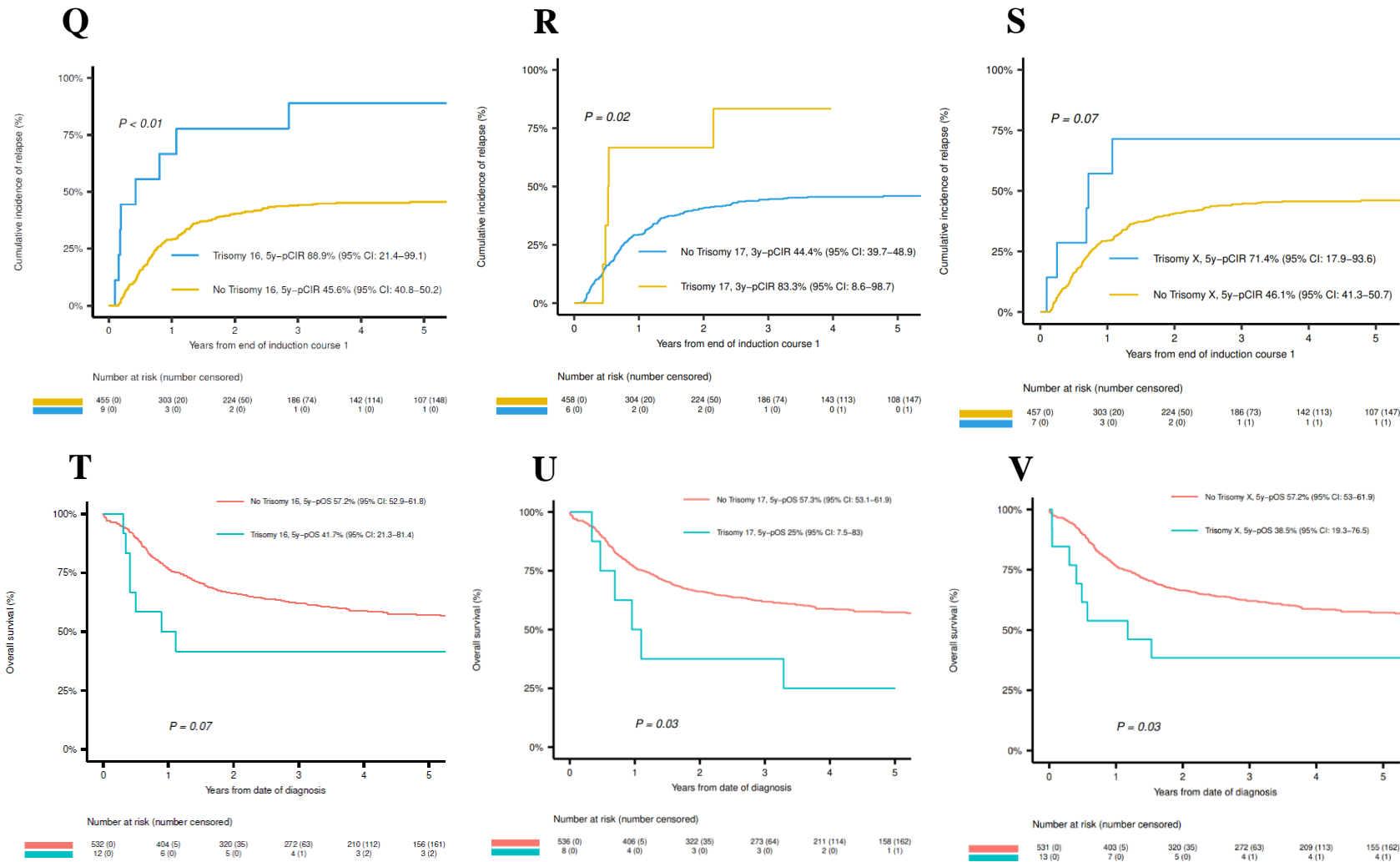
Number at risk (number censored)

344 (0)	255 (2)	196 (20)	167 (36)	126 (66)	93 (95)
200 (0)	155 (3)	129 (15)	109 (28)	87 (48)	66 (68)

P

Number at risk (number censored)

530 (0)	402 (5)	319 (35)	270 (64)	211 (111)	157 (160)
14 (0)	8 (0)	6 (0)	6 (0)	2 (3)	2 (3)



Supplementary Figure S2. Kaplan-Meier estimates of (A/B/C/D/I/J/K/L/Q/R/S) cumulative incidence of relapse and (E/F/G/H/M/N/O/P/T/U/V) overall survival of children with *KMT2A*-rearranged acute myeloid leukemia and with and without (A, E) add(12p), (B, F) del(9q), (C, G) monosomy 10, (D, H) trisomy 1, (I, M) trisomy 4, (J, N) trisomy 6, (K, O) trisomy 8, (L, P) trisomy 12, (Q, T) trisomy 16, (R, U) trisomy 17, and (S, V) trisomy X. Patients with a specific ACA are compared with patients with other ACAs. CI, confidence interval; pCIR, probability of cumulative incidence of relapse; pOS, probability of overall survival.