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BCL11B-activated pediatric acute myeloid leukemia: a high-risk disease with frequent induction failure

Valeria Ceolin[1,2], Harm van Tinteren[1], David T. Teachey[3], Hiroto Inaba[4], Jeffery M. Klco[4], Soheil Meshinchi[5], Andishe Attarbaschi[6,7], Anthony V Moorman[8], Daisuke Tomizawa[9], Elena Varotto[10], Daniel Cheuk[11], Lindsey Montefiori[4], Danika Di Giacomo[4,12], Franca Fagioli[2], Hélène Lapillonne[13], C. Michel Zwaan[1,14#], Bianca F. Goemans[1#]

# BFG and CMZ contributed equally as last authors

[1]Princess Máxima Center for Pediatric Oncology, Utrecht, Netherlands
[2]Regina Margherita Children's Hospital, Turin, Italy
[3]Children's Hospital of Philadelphia, Philadelphia, PA, USA
[4]St. Jude Children's Research Hospital, Memphis, TN, United States of America
[5]Fred Hutchinson Cancer Center, Seattle, WA, United States of America
[6]Medical University of Vienna, Austria
[7]St. Anna Children's Cancer Research Institute, Vienna, Austria
[8]Faculty of Medical Sciences, Newcastle University, Newcastle, United Kingdom
[9]National Center for Child Health and Development, Tokyo, Japan
[10]Maternal and Child Health Department, University of Padova and Padova University Hospital, Padova, Italy
[11]The University of Hong Kong and Hong Kong Children's Hospital, and Hong Kong Pediatric Hematology & Oncology Study Group
[12]University of Perugia, Perugia, Italy
[13]Sorbonne University, APHP, Trousseau hospital, Paris, France
[14]Erasmus MC-Sophia Children's Hospital, Rotterdam, Netherlands

Corresponding author
C. Michel Zwaan, MD, PhD
Princess Máxima Center for Pediatric Oncology
Heidelberglaan 25, 3584CS, Utrecht, The Netherlands
E-mail: c.m.zwaan-2@prinsesmaximacentrum.nl
Telephone: +31889725206

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Authorship Contributions

Study conception and design: BF Goemans, CM Zwaan, H Lapillonne, V Ceolin

Data collection and patient management: DT Teachey, I Hiroto, JM Klco, S Meshinchi, A Attarbaschi, AV Moorman, D Tomizawa, E Varotto, D Cheuk, L Montefiori, D Di Giacomo, BF Goemans, V Ceolin

Data analysis and interpretation: V Ceolin, H Tinteren, BF Goemans, CM Zwaan

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as well as agreed to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of this work were appropriately investigated and resolved.

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OpenAI's ChatGPT (GPT-6, proprietary commercial software) was used to assist with English-language editing, sentence restructuring, and refinement of manuscript clarity. The authors critically reviewed and verified the AI-assisted text and take full responsibility for the accuracy, originality, and integrity of the final manuscript. AI was not used to generate or modify primary research data.

Data-sharing statement

The data supporting the findings of this study are not publicly available due to patient confidentiality and privacy restrictions.

To the Editor,

Immature acute leukemias, including AML (M0/M1), early T-cell precursor ALL (ETP-ALL), and T/myeloid mixed-phenotype acute leukemia (T/M MPAL), may harbor structural variants (SVs) activating *BCL11B* at 14q32.[1, 2] These include rearrangements juxtaposing regulatory elements to *BCL11B* and *BCL11B* enhancer tandem amplification (BETA), involving a ~2.5-kb noncoding region 730 kb downstream (Supplementary Figure 1). These alterations induce elevated, allele-specific *BCL11B* expression (ASE), defining *BCL11B*-activated (*BCL11B*-a) leukemia in children and adults.[3-6] Although biologically distinct, outcomes may vary by lineage and treatment, and remain poorly defined in AML. We investigated the clinical, molecular, and treatment characteristics and outcomes of pediatric and young adult patients with *BCL11B* SVs, focusing on AML.

We retrospectively analyzed patients aged 0–25 years diagnosed with T/B-ALL, MPAL, or AML harboring *BCL11B* SVs between January 2000 and December 2023, identified through the International BFM Study Group and Ponte di Legno ALL Working Group. SVs were detected by cytogenetics, fluorescence in situ hybridization, whole-genome/exome sequencing (WGS/WES), or RNA sequencing.[4, 5, 7] Participating centers provided clinical and outcome data and obtained required local approvals; the study was approved by the Institutional Review Board of the Princess Máxima Center (PMCLAB2023.449). Overall survival (OS) was measured from diagnosis to death, and event-free survival (EFS) to induction failure (IF) (day 0), relapse, or death. Patients without the respective endpoint were censored at last follow-up. OS and EFS were estimated using the Kaplan–Meier method for groups of at least five patients. Forty-six patients with *BCL11B*-a leukemia were identified, including 15 with AML (4 FAB M0; 6 FAB M1; 2 FAB M2; 1 FAB M4; 2 unknown), 8 with T/M MPAL, 23 with T-ALL (17 ETP). This includes 19 previously unpublished cases (Supplementary Table 2). While previous reports focused on molecular characterization, we aimed to characterize the clinical features

and treatment outcomes of these patients. The median age at diagnosis was 12.5 years (range, 2–23.5 years), and 28 patients (61%) were male; median white blood cell count was 37 400/μL (range 800 –520 000) (Table 1). Immunophenotypic data were available for 28 patients. All but one expressed immature markers, and 26 expressed CD13 and/or CD33. CD2 and CD7 were frequently expressed, including in AML, whereas mature T-lineage markers were largely absent, consistent with an immature differentiation state (Supplementary Table 1). These findings emphasize the close biological relationship between *BCL11B*-a leukemias classified into different diagnostic categories and the potential limitations of assigning treatment solely according to immunophenotypic lineage.

BCL11B SVs were identified in 44 of 46 patients, while 2 cases, both with AML, showed *BCL11B* ASE without an identifiable translocation or amplification (Table 1 and Supplementary Table 2). As WGS was not performed in one patient, an underlying cryptic structural or mutational variant cannot be excluded, while epigenetic mechanisms cannot be excluded in both. The rearrangement of *BCL11B* to the intergenic region upstream of *ARID1B* was the most frequent alteration (n=18), predominantly observed in T-ALL, whereas *ZEB2*-*BCL11B* rearrangement (n=10) was enriched in AML and MPAL. Nine patients (19.6%) harbored BETA. Age varied significantly across the 3 most frequent *BCL11B* SVs (Kruskal–Wallis p=0.004), with a lower median age in *ZEB2* cases (4.5 years [range, 2–17]) compared with *ARID1B* (14 years [5.9–23.5]) and BETA (14.2 years [8–19]). *FLT3* mutations were identified in 30 of 42 evaluable patients (71%), including 20 *FLT3*-ITD and 10 tyrosine kinase domain mutations. *WT1* and *RUNX1* mutations were detected in 48% and 36% of cases, respectively. Despite the high frequency of cooperating genetic alterations, none of these abnormalities was significantly associated with EFS or OS in our cohort. The molecular landscape therefore did not identify a clear prognostic marker that could explain the markedly different clinical behavior observed across diagnostic categories, as described below.

Outcome data were available for 43 patients. Among 23 patients with T-ALL, 21 (91%) achieved complete remission (CR), only one relapsed, and 5-year EFS and OS were 78% and 83%, respectively. Among 7 patients with MPAL, 3 initially failed induction but subsequently achieved CR; 6 underwent stem cell transplantation (SCT) in 1st CR, and 5-year EFS and OS were 57% and 71%, respectively. In contrast, patients with AML showed striking resistance to conventional induction therapy. Among the 13 of 15 patients with AML for whom outcome data were available, 8 (62%) failed to respond to the 1st induction course, and 4 (31%) remained refractory after a 2nd induction course and were classified as IF. All 4 patients were then treated with a non-protocol treatment plan using AML-based regimens, 3 patients were salvaged with SCT in 1st CR. Four out of 13 patients relapsed, 1/4 received SCT in 2nd CR. The 5-year EFS was 9% (95% CI, 1.5–59), whereas the 5-year OS was 66% (95% CI, 43–100) (Figure 2). The 5-year cumulative probabilities of relapsed/refractory disease and treatment-related mortality were 75.4% and 15.4%, respectively.

To evaluate outcome according to treatment backbone rather than diagnostic classification, we next analyzed all patients who received AML-directed therapy. Among the 43 patients with available outcome data, 19 (13 AML and 6 MPAL) received AML-based therapy. Overall, 11/19 (58%) were non-responders after the 1st induction course and 4/19 (21%) remained refractory after the 2nd induction course. Five-year EFS and OS were 24% (95% CI, 10–55) and 67% (95% CI, 48–93), respectively (Figure 3).

AML diagnosis was the only variable significantly associated with inferior EFS in univariate analysis (HR, 6.76; 95% CI, 2.29–19.9; P<0.001). No multivariable analysis was performed because of the limited cohort size.

In this study, we describe the largest multicenter published cohort of pediatric and young adult patients with *BCL11B* SVs and report the molecular and clinical characteristics of these 46 patients. Among participating centers, *BCL11B* SVs were identified in approximately 0.5–1%

of screened patients, although differences in patient selection and screening methods preclude a precise estimate of population-based incidence. Thus, under-recognition remains possible, particularly as this alteration is not routinely investigated at diagnosis. We confirmed that different genomic alterations deregulating *BCL11B* in hematopoietic progenitor cells may result in different types of immature acute leukemia. The preferential association of *ARID1B-BCL11B* rearrangements with T-ALL and of *ZEB2-BCL11B* with AML/MPAL suggests that the genomic context of *BCL11B* activation may contribute to phenotypic heterogeneity. Mechanistically, ectopic *BCL11B* activation in hematopoietic progenitors has been shown to induce T-lineage programs while maintaining an immature progenitor state. [1, 4]

Our findings identify *BCL11B*-activated AML as a high-risk subgroup characterized by a high rate of IF and poor EFS. This indicates that conventional frontline treatment is frequently insufficient to achieve durable disease control and suggests marked resistance to conventional genotoxic chemotherapy. These findings are consistent with a recent report of pediatric AML with *BCL11B* SVs, in which high measurable residual disease levels after 1st induction and a 4-year OS below 60% were reported.[8] Together, these data provide a rationale for investigating alternative treatment strategies. Whether the poorer outcome of *BCL11B*-a AML reflects intrinsically more aggressive biology associated with the AML phenotype or, alternatively, lower sensitivity to AML-directed therapy remains unclear. In our cohort, treatment and phenotype were strongly associated, with all AML patients receiving AML-directed therapy and all T-ALL patients receiving ALL-directed therapy, precluding separation of these effects. Moreover, none of the refractory AML patients received lymphoid-directed salvage therapy. Given the shared molecular features of *BCL11B*-a leukemias across diagnostic categories, the hypothesis that treatment strategies guided by underlying biology rather than lineage assignment alone may be considered. ALL initial therapy may be the first choice for all *BCL11B*-a leukemia patients, adapting therapy and performing SCT in CR1 in patients with a

poor initial response, as is recommended for children with MPAL. [9, 10] In patients with an AML phenotype, SCT in 1st CR may improve their chance of cure.

The molecular features of *BCL11B*-a leukemia also provide a rationale for targeted therapeutic approaches. Activating *FLT3* mutations are frequent in *BCL11B*-a leukemia, and *ex vivo* drug profiling has shown sensitivity to FLT3 and JAK/STAT pathway inhibitors,[5] providing a rationale for molecularly targeted approaches. Moreover, recent preclinical studies demonstrated activity of combined venetoclax and gilteritinib in *FLT3*-mutant BCL11B-a leukemia,[11] supporting further investigation of simultaneous targeting of *FLT3* signaling and BCL-2 dependence.

This study is limited by its retrospective nature, the relatively small cohort size, incomplete immunophenotypic data, and the heterogeneity of treatment approaches, precluding definitive conclusions regarding optimal therapy. Nevertheless, our findings support the clinical relevance of identifying *BCL11B* activation and highlight the need for prospective studies evaluating lineage- and molecularly informed treatment strategies in this rare leukemia subgroup.

Moving forward, diagnosis of *BCL11B*-a leukemia remains challenging, as conventional karyotyping, fusion calling, and panel sequencing may miss 14q32 rearrangements or focal enhancer amplifications. WGS/WES, targeted FISH, or RNA-seq may improve detection of *BCL11B* SVs, while allele-specific expression (ASE) analysis may provide additional evidence of activation, with deep total RNA-seq potentially identifying informative intronic reads. Importantly, the characteristic immunophenotypic profile of *BCL11B*-a leukemia, including immature features and aberrant lineage marker expression, may help prioritize cases for confirmatory molecular testing when comprehensive genomic profiling is unavailable.

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Table 1. Patient characteristics

	Total (n=46)	AML (n=15)	MPAL (n=8)	T-ALL (n=23)
Male, *n* (%)	28 (61)	8 (53)	4 (50)	16 (70)
Median age at diagnosis, years (range)	12.5 (2-23.5)	10.5 (2-23.5)	6.5 (2-17)	14 (8-21)
WBCs >100 000/µL at diagnosis, *n* (%)	12 (28)	3 (23)	5 (63)	4 (18)
(unknown[#])	(3)	(2)	-	(1)
CNS 2 or 3 at diagnosis, *n* (%)	10 (26)	3 (27)	2 (33)	5 (22)
(unknown[#])	(7)	(4)	(2)	(1)
Classified as High Risk*, *n* (%)	20 (45)	6 (46)	7 (88)	7 (30)
(unknown[#])	(2)	(2)	-	-
Treatment				
• AML therapy, *n* (%)	22 (48)	15 (100)	7 (88)	-
• ALL therapy, *n* (%)	24 (52)	-	1 (12)	23 (100)
BCL11B SVs				
• t(6;14)(q25;q32), *n*	18	3	2	13
• t(2;14)(q22;q32) , *n*	10	5	4	1
• BETA, *n*	9	1	1	7
• t(21;14)(q22;q32), *n*	2	2	0	0
• t(7;14)(q21;q32), *n*	2	1	1	0
• ASE, *n*	2	2	0	0
• t(12;14)(p13;q32), *n*	1	1	0	0
• t(22;14), *n*	1	0	0	1
• t(17;14), *n*	1	0	0	1
FLT3 mutation, *n* (%)	30 (71)	10 (83)	1 (14)	19 (76)
(unknown[#])	(4)	(3)	(1)	-
• ITD, *n*	20	4	1	15
WT1 mutation, *n* (%)	20 (48)	8 (53)	2 (25)	10 (53)
(unknown[#])	(4)	-	-	(4)
RUNX1 mutation, *n* (%)	13 (36)	6 (43)	3 (38)	4 (29)
(unknown[#])	(10)	(1)	-	(9)

ALL=acute lymphoblastic leukemia; AML=acute myeloid leukemia; ASE= allele-specific expression; BETA= BCL11B enhancer tandem amplification; CNS=central nervous system; ITD=internal tandem duplication; MPAL=mixed phenotype acute leukemia; SVs=structural variants; WBCs=white blood cells

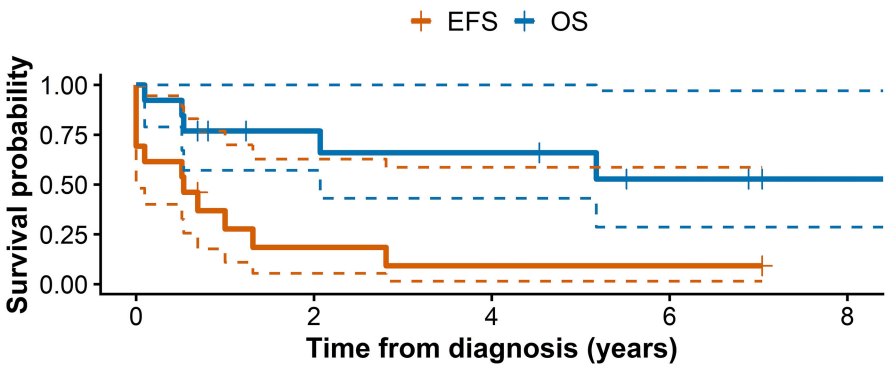
[#] unknown data were omitted from proportion calculations

* Reason for high risk:
- Response to treatment, n=11
- Genetic characteristics, n=7
- Hyperleukocytosis, n=1
- FAB M0, n=1

Figure 1. Event free survival and overall survival of the entire cohort, according to diagnosis (A, AML; B, ALL; C, MPAL)

Figure 2. Event free survival and overall survival of the entire cohort, according to treatment received (AML protocol; ALL protocol)

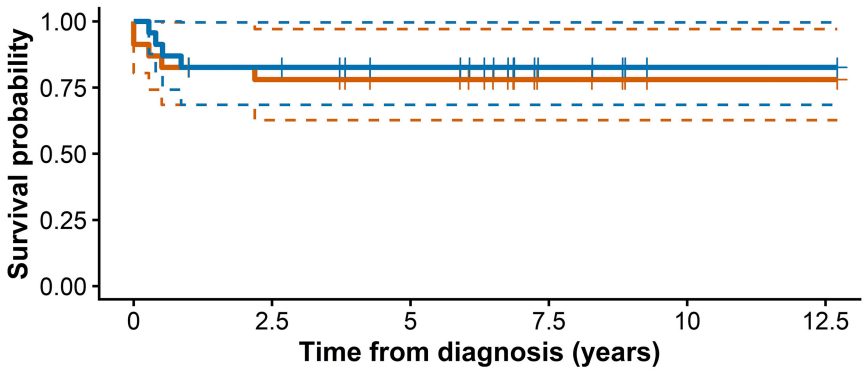
A. AML



Number at risk

EFS	13	2	1	1	0
OS	13	7	6	3	1

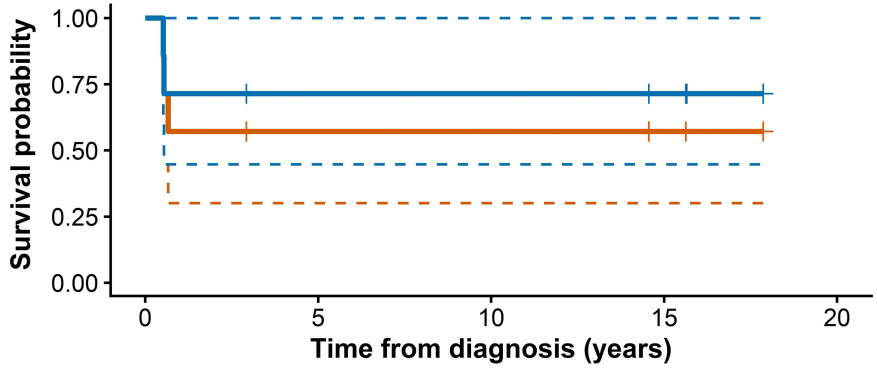
B. ALL



Number at risk

EFS	23	17	14	5	1	1
OS	23	18	14	5	1	1

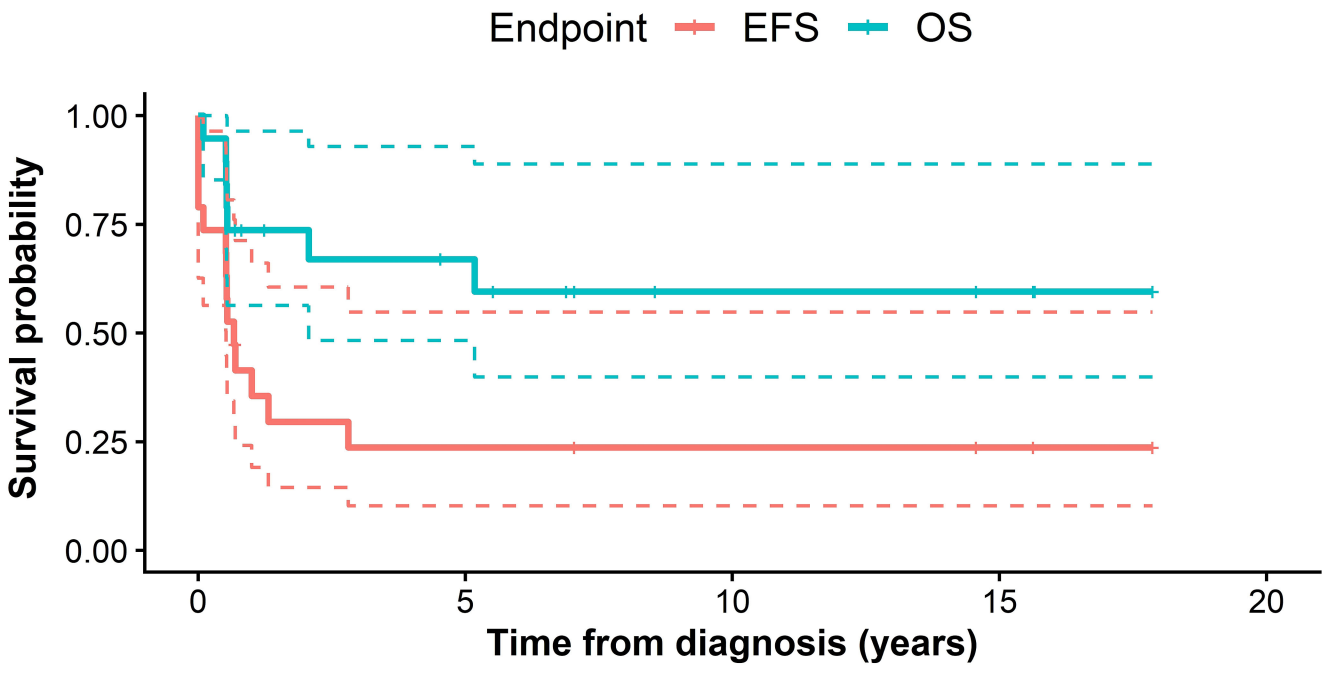
C. MPAL



Number at risk

EFS	7	3	3	2	0
OS	7	4	4	3	0

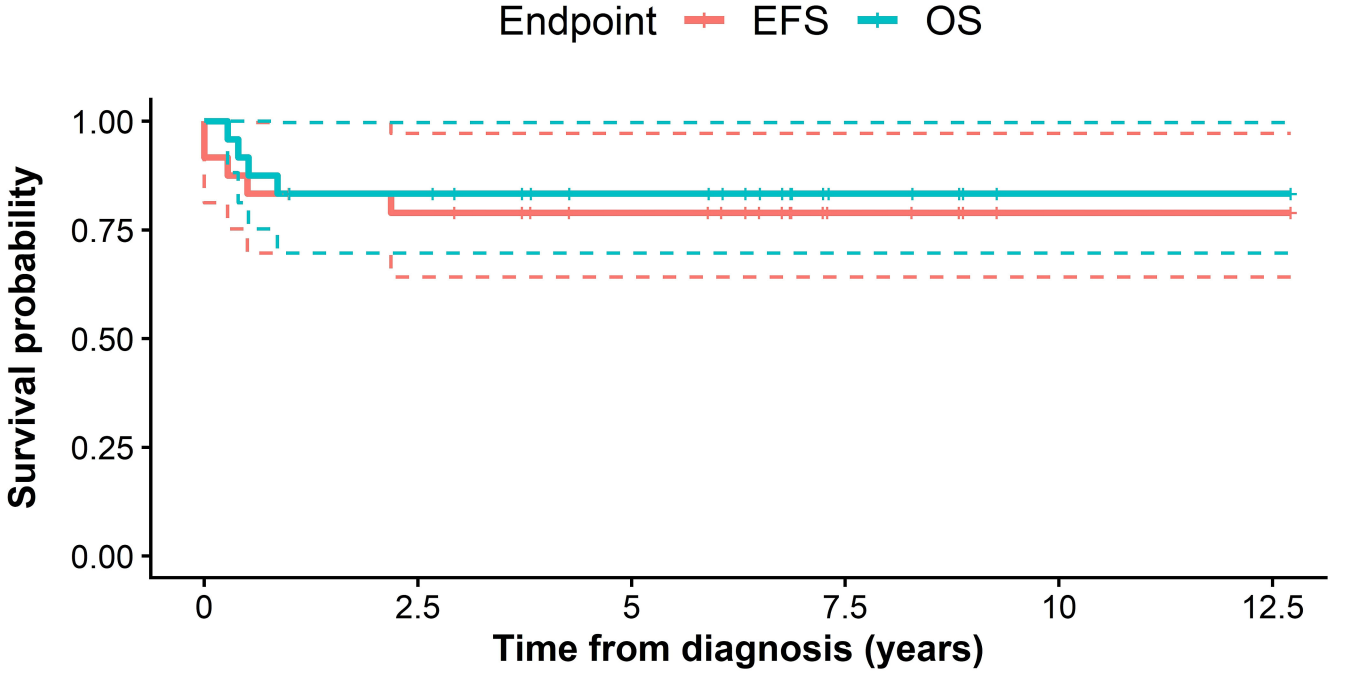
AML protocol



Number at risk

EFS	19	4	3	2	0
OS	19	9	4	3	0

ALL protocol

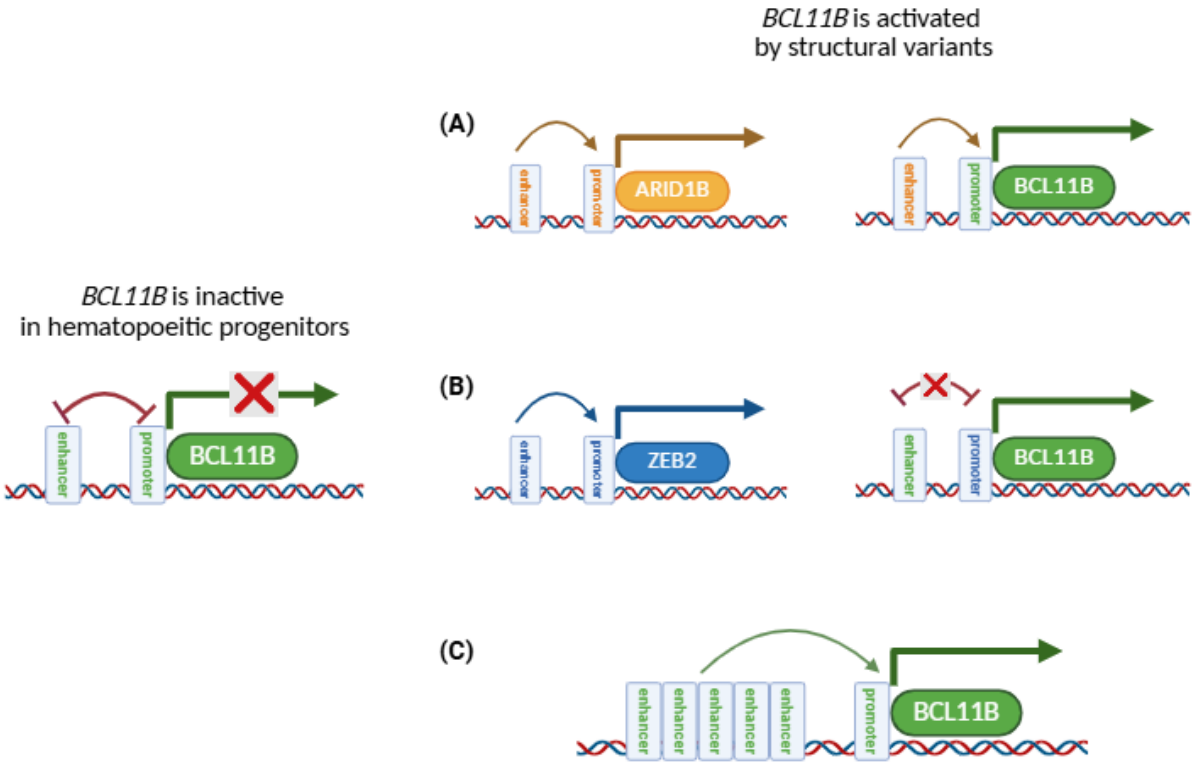


Number at risk

EFS	24	18	14	5	1	1
OS	24	19	14	5	1	1

Supplementary Figure 1. Mechanisms of *BCL11B* activation by structural variants.

(A) Enhancer hijacking: the enhancer of an active gene in hematopoietic stem cells (e.g. *ARID1B*) translocates near the *BCL11B* promoter, activating the gene transcription (B) Promoter translocation: the promoter of an active gene in hematopoietic stem cells (e.g. *ZEB2*) translocates near the gene *BCL11B*, activating its transcription (C) *BCL11B* Enhancer Tandem Amplification (BETA): a tandem amplification event of a short non-coding region located downstream of BCL11 acts as a potent enhancer capable of activating *BCL11B*. Created using Biorender®, adapted by Umeda et al. Haematologica 2025.



Supplementary Table 1. Immunophenotype profile of 28 *BCL11B* SVs cases

Case	Diagnosis	CD1a	CD2	sCD3	cCD3	CD5	CD7	CD8	CD13	CD33	CD34	CD117	MPO	HLA-DR	TCR
1	AML	NR	pos	NR	NR	NR	pos	NR	pos	NR	pos	pos	pos	pos	NR
7	AML	NR	pos	NR	NR	NR	pos	NR	pos	NR	pos	pos	NR	pos	NR
8	AML	NR	pos	NR	NR	NR	pos	NR	pos	NR	NR	NR	NR	pos	NR
10	AML	NR	pos	neg	neg	NR	neg	neg	pos	neg	pos	pos	pos	pos	NR
12	AML	NR	pos	neg	neg	NR	pos	neg	pos	neg	pos	pos	pos	pos	NR
13	AML	NR	NR	NR	NR	NR	NR	NR	pos	pos	pos	NR	pos	pos	NR
15	AML	NR	neg	neg	neg	NR	dim	NR	pos	weak	pos	pos	NR	dim	NR
22	AML	NR	NR	NR	NR	NR	NR	NR	pos	neg	pos	pos	NR	pos	NR
23	AML	NR	NR	NR	NR	NR	NR	NR	pos	neg	pos	pos	NR	pos	NR
24	AML	NR	NR	NR	NR	NR	NR	NR	pos	neg	pos	pos	NR	pos	NR
25	AML	NR	NR	NR	NR	NR	NR	NR	pos	neg	pos	pos	NR	pos	NR
26	AML	NR	NR	NR	NR	NR	NR	NR	pos	neg	pos	pos	NR	pos	NR
27	AML	NR	NR	NR	NR	NR	NR	NR	pos	neg	pos	pos	NR	pos	NR
2	MPAL	NR	pos	NR	pos	NR	pos	NR	pos	pos	pos	pos	pos	pos	pos
3	MPAL	NR	pos	NR	pos	NR	pos	NR	pos	pos	pos	pos	NR	pos	pos
4	MPAL	NR	pos	NR	NR	pos	pos	NR	pos	NR	pos	pos	pos	pos	NR
5	MPAL	NR	pos	NR	pos	NR	pos	NR	pos	NR	pos	pos	pos	pos	NR
6	MPAL	NR	pos	NR	pos	pos	pos	NR	pos	pos	NR	pos	pos	pos	NR
9	MPAL	neg	pos	neg	pos	weak	pos	neg	pos	neg	pos	pos	pos	pos	NR
11	MPAL	neg	pos	neg	pos	weak	pos	neg	pos	neg	pos	pos	pos	pos	NR
14	MPAL	neg	pos	neg	pos	neg	pos	neg	pos	pos	pos	pos	pos	pos	neg
16	T-ALL	neg	pos	neg	pos	neg	pos	neg	weak	NR	neg	neg	neg	pos	NR
47	T-ALL	neg	neg	weak	pos	pos	pos	neg	pos	NR	NR	pos	pos	weak	NR
17	T-ALL (ETP)	weak	pos	pos	pos	pos	pos	neg	neg	NR	neg	neg	neg	neg	NR
21	T-ALL (ETP)	pos	pos	neg	pos	pos	pos	pos	neg	neg	pos	pos	neg	neg	NR
35	T-ALL (ETP)	weak	pos	neg	pos	neg	pos	neg	pos	NR	NR	pos	pos	pos	NR
44	T-ALL (ETP)	neg	pos	neg	pos	weak	pos	neg	pos	NR	NR	pos	pos	pos	neg
18	T-ALL (ETP)	NR	pos	pos	pos	weak	pos	neg	pos	neg	weak	NR	NR	pos	NR

ALL=acute lymphoblastic leukemia; AML=acute myeloid leukemia; ETP= early T-cell precursor; MPAL= mixed-phenotype acute leukemia; neg=negative; NR =not reported; pos=positive

Supplementary Table 2. Molecular details of *BCL11B* structural variants cases, grouped by diagnosis (ALL, green; AML, orange; MPAL, blue) and by fusion partner.

Case	Diagnosis	BCL11B SVs	Detected by	Karyotype	Enhancer hijacking / fusion partner	[Ref]#
34	T-ALL	t(6;14)(q25;q32)	WGS		ARID1B	[1]
16	T-ALL	t(6;14)(q25;q32)	FISH	46,XY[8].nuc ish 14q32(3'BCL11Bx2,5'BCL11Bx3)[64/100]	ARID1B	-
18	T-ALL	t(6;14)(q25;q32)	Karyotype*, FISH	46,XY,t(6;14)(q25;q32),del(12)(p11p13)[9]	ARID1B	-
17	T-ALL (ETP)	t(6;14)(q25;q32)	FISH	47,XY,+Y[20]. ish t(6;14;21)(BCL11B5'-,3'-; BCL11B5'+,3'+;BCL11B5'+,BCL11B3'-)[13]	ARID1B	-
31	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
36	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
37	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
38	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
43	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
44	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
45	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
46	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
47	T-ALL (ETP)	t(6;14)(q25;q32)	WGS	-	ARID1B	[1]
29	T-ALL	BETA	WGS	-	BETA	[1]
42	T-ALL	BETA	WGS	-	BETA	[1]
28	T-ALL (ETP)	BETA	WGS	-	BETA	[1]
33	T-ALL (ETP)	BETA	WGS	-	BETA	[1]
35	T-ALL (ETP)	BETA	WGS	-	BETA	[1]
41	T-ALL (ETP)	BETA	WGS	-	BETA	[1]
48	T-ALL (ETP)	BETA	WGS	-	BETA	[1]
30	T-ALL (ETP)	t(22;14)	WGS	-	GRK3	[1]
40	T-ALL	t(17;14)	WGS	-	NME	[1]
21	T-ALL (ETP)	t(2;14)(q22;q32)	Karyotype*, RNA-seq	46,XY, t(2;14)(q21;q32)	ZEB2	-
24	AML	t(6;14)(q25;q32)	WGS/TCS	47,XY,+4,t(15;21)(q22;q22)[11]	ARID1B	-
25	AML	t(6;14)(q25;q32)	WGS/TCS	46,XX,add(9)(p13),+21[16]	ARID1B	-
27	AML	t(6;14)(q25;q32)	WGS	46,XY,add(14)(q32)[18]	ARID1B	-
23	AML	BETA	WGS/TCS	46,XY[20]	BETA	-
26	AML	t(7;14)(q21;q32)	WGS	46,XX,del(7)(q22)[15]	CDK6	-
22	AML	t(12;14)(p13;q32)	WGS/TCS	46,XX,inv(2)(p13q22)mat[25]	ETV6	-
1	AML	t(21;14)(q22;q32)	WGS, RNA-seq	46,XY	RUNX1	[2] ; [3]
20	AML	t(21;14)(q22;q32)	RNA-seq	46,XY,?add(1)(q2?),-21,+mar,inc[cp5]	RUNX1	-
10	AML	t(2;14)(q22;q32)	Karyotype*, RNA-seq	46,XX,t(2;14)(q22;q3?2)[18]	ZEB2	-
12	AML	t(2;14)(q22;q32)	Karyotype*, RNA-seq	46,X,add(X)(p21),add(1)(p33),t(2;14)(q1?3;q32),der(10)t(1;10)(p33;q2?2),add(13)(p10),add(19)(q13)[18]	ZEB2	-
13	AML	t(2;14)(q22;q32)	Karyotype*	46,XX,inv(12)(p13q13),add(19)(p13)[8]/46,idem,t(2;14)(p11.2;q32)[5]	ZEB2	-
15	AML	t(2;14)(q22;q32)	Karyotype*, RNA-seq	48~50,XY,t(2;14)(q22.3;q32.2),+4,+4,+14,+21,+mar,inc[cp15]	ZEB2	-
19	AML	t(2;14)(q22;q32)	Karyotype*, FISH, RNA-seq	47,XXY?c,t(2;14)(q22;q32)[12]	ZEB2	-
7	AML	ASE	RNA-seq, WGS	47,XX,r(1)(p36.3q42),+4[13]	?	[3]
8	AML	ASE	RNA-seq	46,XY,del(16)(q21q24)[12]	?	[3]
2	MPAL	t(6;14)(q25;q32)	WGS	46,XY,inv(7)(p24q11.2)[20]	ARID1B	[2]
14	MPAL	t(6;14)(q25;q32)	Karyotype*	46,XX,t(6;14)(q25;q32)[17]	ARID1B	-
3	MPAL	BETA	WGS	46,XY[20]	BETA	[2]
4	MPAL	t(7;14)(q21;q32)	Karyotype*, WGS, RNA-seq	46,XY,t(7;14)(q21;q32.1)[30]	CDK6	[2]
5	MPAL	t(2;14)(q22;q32)	WGS, RNA-seq	46,xx,?t(2;6;14)(q13;q25;q22),del(6)(p21),del(6)(q13),add(19)(p13.1),add(21)(q22)[20]	ZEB2	[2]
6	MPAL	t(2;14)(q22;q32)	Karyotype*, WGS, RNA-seq	46,XX,der(2)?inv(2)(p11.2q13)t(2;14)(14qter->14q32.1::2p?->2qter),der(14)t(2;14)(14pter->14q32.1:: 2q13->2p12->2pter)[19]	ZEB2	[2]
9	MPAL	t(2;14)(q22;q32)	Karyotype*, RNA-seq	46,XX,t(2;14;21)(q22;q32;q22)[19]	ZEB2	-
11	MPAL	t(2;14)(q22;q32)	Karyotype*, RNA-seq	46,XY,t(2;14)(q2?2;q?32),del(6)(q?16q2?4),-13,der(16)t(13;16)(?;q11),+mar[?der(13)][17]/46,XY[4]. ish t(2;14)(IGH+;IGH-)[4]	ZEB2	-

if the case was previously published. [1] Pölönen et al.. Nature 2024. [2] Montefiori et l. Cancer Discov 2021. [3] Umeda et al. Nat Genet. 2024.

AML=acute myeloid leukemia; ASE= allele-specific expression; BETA= BCL11B enhancer tandem amplification; ETP=early T-cell precursor acute lymphoblastic leukemia; FISH= fluorescence in situ hybridization; ID=identification; MPAL= mixed-phenotype acute leukemia; Ref=reference; RNA-seq=RNA sequencing; T-ALL=T-cells acute lymphoblastic leukemia; WGS=whole genome sequence