

# A retrospective analysis of gene fusions and treatment outcomes in pediatric acute megakaryoblastic leukemia without Down syndrome

## Authors

---

Kyogo Suzuki,<sup>1</sup> Asahito Hama,<sup>1</sup> Yusuke Okuno,<sup>2</sup> Yinyan Xu,<sup>1</sup> Atsushi Narita,<sup>1</sup> Nao Yoshida,<sup>3</sup> Hideki Muramatsu,<sup>1</sup> Nobuhiro Nishio,<sup>4</sup> Koji Kato,<sup>3</sup> Seiji Kojima,<sup>1</sup> Keon Hee Yoo<sup>5#</sup> and Yoshiyuki Takahashi<sup>1#</sup>

<sup>1</sup>Department of Pediatrics, Nagoya University Graduate School of Medicine, Aichi, Japan; <sup>2</sup>Department of Virology, Nagoya City University Graduate School of Medical Sciences, Aichi, Japan; <sup>3</sup>Department of Hematology and Oncology, Children's Medical Center, Japanese Red Cross Aichi Medical Center Nagoya First Hospital, Aichi, Japan; <sup>4</sup>Department of Advanced Medicine, Nagoya University Hospital, Aichi, Japan and <sup>5</sup>Department of Pediatrics, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, South Korea

*#KHY and YT contributed equally as senior authors.*

Correspondence:

Y. TAKAHASHI - [ytakaha@med.nagoya-u.ac.jp](mailto:ytakaha@med.nagoya-u.ac.jp)

K.H. YOO - [hema2170@skku.edu](mailto:hema2170@skku.edu)

<https://doi.org/10.3324/haematol.2023.283760>

## **Supplementary Material**

**Supplementary Tables** pp. 2–3

**Table S1.** Primer sets for reverse transcription-polymerase chain reaction.

**Table S2.** Key clinical information of the patients.

## Supplementary Tables

**Table S1. Primer sets for reverse transcription-polymerase chain reaction.**

Target	Forward (F) / Reverse (R)	Primer sequences (from 5' to 3')
<i>KMT2A</i> <sup>†</sup>	F	CGTCGAGGAAAAGAGTGA
:: <i>MLLT3</i>	R	ATGTTTCCAGGTAACCTCTGTAGT
:: <i>MLLT10</i>	R	CTGGAAATTGCATTTGAA
:: <i>MLLT1</i>	R	TACCCCGACTCCTCTACTT
:: <i>ELL</i>	R	CCCATGACTGGAGACATACT
<i>CBFA2T3::GLIS2</i>	F1	CATCTGGAGGAAGGCTGA
	R1	CGGTTGTGGATCTTCAGGT
	F2	TCGGGAAAGGCAGTCCTGGTAGA
	R2	CACAGAACAGTTCCGTTCGTCGG
<i>NUP98::KDM5A</i>	F1	AGGGCCTCTGGTACAG
	R1	TAGCTTCCGTTCCGTTCT
	F2	GTAAACCAGCACCTGGGACTCTTG
	R2	GCCCCCTGCTTCTTGACAGTTAT
<i>RBM15::MRTFA</i>	F1	CAAAGACAAGGAAAACACCGG
	R1	TCCAAAATGTGCATCCTGACC
	F2	ATGCCTTCCCACCTTGTGAG
	R2	CGCTCCAAGCTCCTCTCTG
<i>FUS::ERG</i>	F	CAGAGCTCCCAATCGTCTTACGG
	R	CAGGAGCTCCAGGAGGAACCTGC
<i>MN1::FLI1</i>	F	CGGCCTGGGCATCATGTCTAAC
	R	ACTGATCGTTGTGCCCTCCA
<i>GATA2::HOXA2</i>	F	TGACGGAGAGCATGAAGATGGAAAG
	R	GAAGGGGGACGGACAGTTCTTCTT
<i>NIPBL::HOXB9</i>	F	CCATGCACAGTAGTCCTGCATCTCC
	R	TAGAACCCGGGCTTGCGCTGACA
<i>C8orf76::HOXA11AS</i>	F	CTCTGCGAGCCGCAGTGGTTT
	R	GCGCCGGCCTCTCAAGAAATG

<sup>†</sup>The *KMT2A* forward primer was shared between every reaction for *KMT2A* rearrangements.

**Table S2. Key clinical information of the patients.**

	Total, n = 30	
<i>Age at diagnosis, median, years</i>	1.3	(IQR, 0.3–1.8)
<i>Sex, n</i>		
Male	14	(47%)
Female	16	(53%)
<i>WBC count, median, × 10<sup>9</sup> /L</i>	12.7	(IQR, 6.0–18.7)
<i>Blast count in blood, median, × 10<sup>9</sup> /L</i>	1.3	(IQR, 0.3–4.4)
<i>Hemoglobin, median, g/L</i>	82	(IQR, 68–88)
<i>Platelet count, median, × 10<sup>9</sup> /L</i>	37.5	(IQR, 20.8–61.3)
<i>Serum LDH, median, IU/L</i>	1,513	(IQR, 577–3,153)
<i>Hepatomegaly, n</i>	21	(70%)
<i>Splenomegaly, n</i>	16	(53%)
<i>Hematopoietic cell transplantation, n</i>	18	(60%)
<i>Follow-up period, median, months</i>	91	(IQR, 12–145)
<i>Status at the final follow-up, n</i>		
Alive	20	(67%)
Dead	10	(33%)

Abbreviations; IQR, interquartile range; LDH, lactate dehydrogenase; WBC, white blood cell.