Erratum to: Genomic breakpoint-specific monitoring of measurable residual disease in pediatric non-standard risk acute myeloid leukemia

Margarita Maurer-Granofszky,[1,2*] Stefan Köhrer,[1,2*] Susanna Fischer,[1,2] Angela Schumich,[1] Karin Nebral,[1,2] Patrizia Larghero,[3] Claus Meyer,[3] Astrid Mecklenbräuker,[1,2] Nora Mühlegger,[1] Rolf Marschalek,[3] Oskar A. Haas,[1] Renate Panzer-Grümayer[1] and Michael N. Dworzak[1,2,4]

[1]St. Anna Children's Cancer Research Institute (CCRI), Vienna, Austria; [2]Labdia Labordiagnostik, Vienna, Austria; [3]Institute of Pharmaceutical Biology/Diagnostic Center of Acute Leukemia (DCAL), Goethe University, Frankfurt/Main, Germany and [4]St. Anna Children's Hospital, Department of Pediatrics, Medical University of Vienna, Vienna, Austria

**MMG and SK contributed equally as first authors.*

Correspondence: N. Dworzak_Michael
dworzak@stanna.at

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In the article pre-published online and in the March 2024 issue of *Haematologica*,[1] we have to correct that:

- Since the percentage minimal residual disease for patient 8 was 0.0100 at the first induction timepoint (day 28), the polymerase chain reaction minimal residual disease result should be "positive" instead of "negative" (Page 5, Table 1, P8, Column 6). In the main text on Page 5 the sentence "Three of these samples were positive by gDNA-PCR but below the threshold of 0.1% (Table 1)" should be replaced by "All of these samples were positive by gDNA-PCR but below the threshold of 0.1% (Table 1)."
- In Table 2, the numbers in column 3 (PCR^{pos}/FCM^{pos}) apply to column 4 (PCR^{neg}/FCM^{neg}) and *vice versa*.
- No threshold was applied for the results shown in Figure 5, as described correctly in the main text (Page 8). Figure 5 itself contained an error, stating that a cut-off of 0.1% was used.

The corrected Table 1, Table 2 and Figure 5 are shown below.

The authors apologize for the errors and state that these do not change any scientific conclusions or interpretations of the data.

Table 1. Summary of cases with discrepant MRD votes between gDNA-PCR and FCM-MRD.

gDNA-PCR^{neg}/FCM-MRD^{pos}									
Patient	Timepoint	FAB subtype	Genetic subtype	PCR			FCM		
				MRD, %	MRD result	Cut-off ≥0.1%	MRD, %	MRD result	Cut-off ≥0.1%
P8	d15	M5	*KMT2A::MLLT3*	<0.01	pos not quantified	negative	0.1800	positive	positive
	Ind1 (d28)	-	-	0.0100	positive	negative	0.5000	positive	positive
P24	Ind2	M7	*NUP98::KDM5A*	0.0900	positive	negative	0.1040	positive	positive
P35	Ind1 (d21)	M5	*KMT2A::MLLT10*	0.0700	positive	negative	0.2300	positive	positive

Continued on following page.

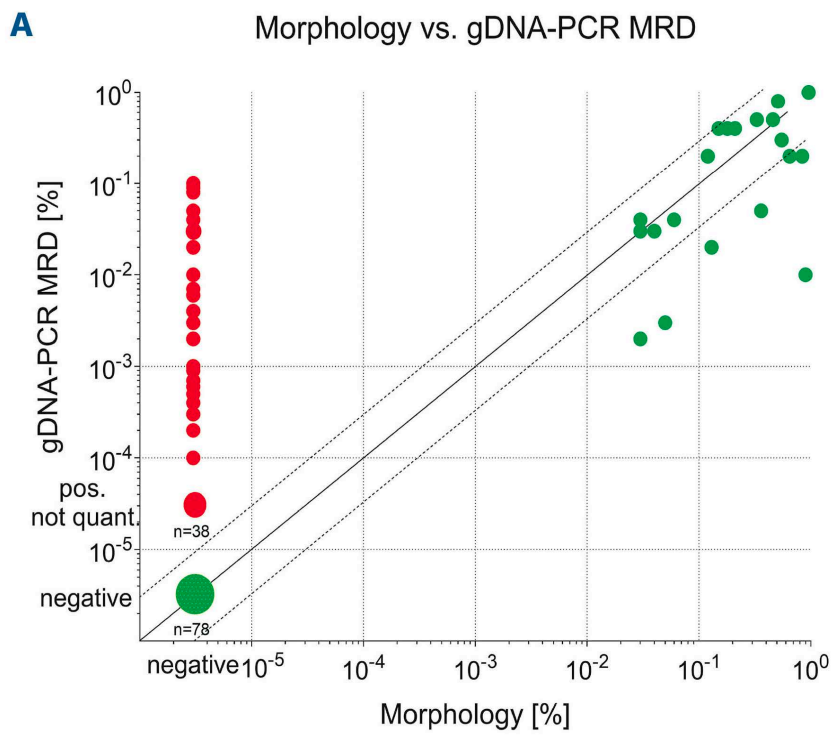
gDNA-PCR^{pos}/FCM-MRD^{neg}									
Patient	Timepoint	FAB subtype	Genetic subtype	PCR			FCM		
				MRD, %	MRD result	Cut-off ≥0.1%	MRD, %	MRD result	Cut-off ≥0.1%
P2	FUP	M7	*KMT2A::MLLT3*	0.6000	positive	positive	0.0200	ambiguous	negative
P5	d15	M5	*KMT2A::MLLT3*	3.0000	positive	positive	0.0010	negative	negative
P9	d15	M5a	*KMT2A::MLLT3*	0.2000	positive	positive	0.0010	negative	negative
P12	Ind1 (d28)	M5a	*KMT2A::MLLT10*	0.1000	positive	positive	0.0010	negative	negative
P13	Ind1 (d28)	M5	*KMT2A::MLLT10*	0.3000	positive	positive	1.1400	ambiguous	negative
P15	Ind1 (d28)	M5a	*KMT2A::MLLT1*	0.3000	positive	positive	0.0500	positive	negative
P23	Ind1 (d28)	M2	*KMT2A::ELL*	0.7000	positive	positive	0.0900	positive	negative
P25	Ind1 (d21)	M5b	*KMT2A::MLLT3*	0.2000	positive	positive	0.0010	negative	negative
	Ind1 (d28)	-	-	0.1000	positive	positive	0.0010	negative	negative
P31	Con2	M7	*KMT2A::MLLT4*	0.4000	positive	positive	0.0900	positive	negative
P32	FUP	M2	*NUP98::NSD1*	0.3000	positive	positive	0.0800	ambiguous	negative
P36	Ind1 (d21)	M4	*NUP98::NSD1*	1.0000	positive	positive	0.0500	ambiguous	negative
	Ind2	-	-	0.1000	positive	positive	0.0010	negative	negative
	Con1	-	-	0.4000	positive	positive	0.0010	negative	negative

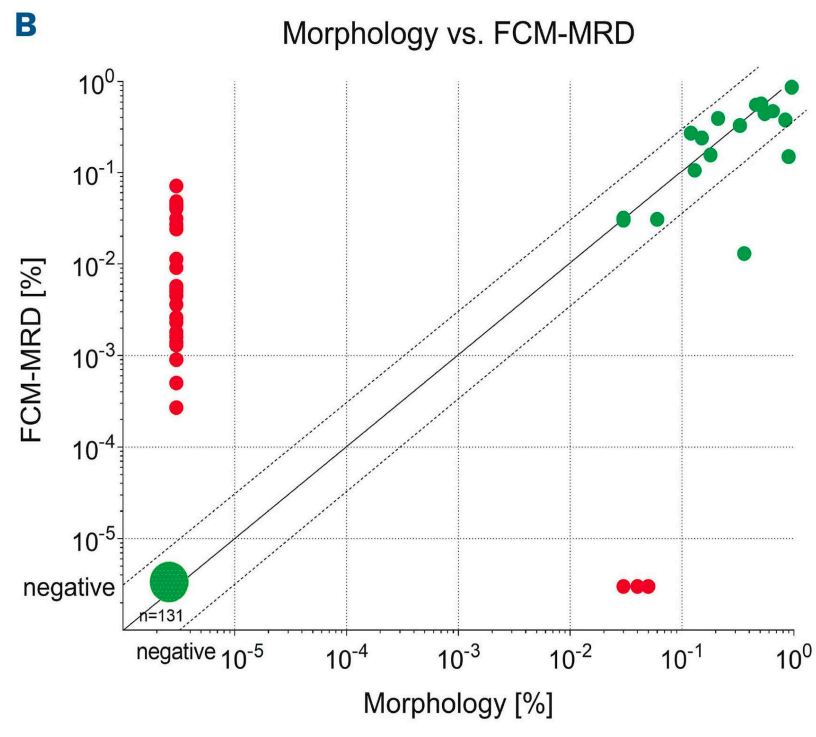
MRD: measurable residual disease; gDNA: genomic DNA; PCR: polymerase chain reaction; FCM: flow cytometry; FAB: French-American-British; d: day; FUP: follow-up; Ind: induction; Con: consolidation.

Table 2. Concordance of gDNA-PCR MRD and FCM-MRD data based on genetic subtype. A threshold of ≥0.1% was used to define positivity.

Genetic subtype	Total N of samples	PCR^{pos}/FCM^{pos} N	PCR^{neg}/FCM^{neg} N	PCR^{pos}/FCM^{neg} N	PCR^{neg}/FCM^{pos} N	Concordance %
All	183	40	125	14	4	90.2
KMT2A::MLLT3	63	9	47	5	2	88.9
KMT2A::MLLT10	37	3	31	2	1	91.9
NUP98::NSD1	17	1	12	4	0	76.5
KMT2A::MLLT1	11	2	8	1	0	90.9
DDX3X::MLLT10	11	6	5	0	0	100.0
KMT2A::CREBBP	9	3	6	0	0	100.0
NUP98::KMD5A	8	7	0	0	1	87.5
KMT2A::ELL	7	2	4	1	0	85.7
CBFA2T3::GLIS2	6	2	4	0	0	100.0
KMT2A-PTD	5	1	4	0	0	100.0
KMT2A::MLLT4	4	2	1	1	0	75.0
RUNX1::CBFA2T3	3	2	1	0	0	100.0
DEK::NUP214	2	0	2	0	0	100.0

gDNA: genomic DNA; PCR: polymerase chain reaction; MRD: measurable residual disease; FCM: flow cytometry; PTD: partial tandem duplication.





		gDNA-PCR-MRD		
		pos*	neg	Total
Morphology	pos*	20	0	20
	neg	79	78	157
	Total	99	78	177

* no cut-off; any positive=positive

		FCM-MRD		
		pos*	neg	Total
Morphology	pos*	17	3	20
	neg	26	131	157
	Total	43	134	177

* no cut-off; any positive=positive

Figure 5. Concordance of gDNA-PCR MRD and FCM-MRD with conventional morphological assessment. Each symbol represents one MRD estimate. Values that are MRD-positive or MRD-negative using both methodologies are considered concordant (green dots), whereas discordant samples are negative with one methodology but positive with another (red dots). In addition, dashed lines above/below the x=y line mark the range of variance according to Dworzak *et al.*,[35] i.e. between 3x larger or smaller till 1/3 of the x=y value. Statistics performed using GraphPad Prism. gDNA: genomic DNA; PCR: polymerase chain reaction; MRD: measurable residual disease; FCM: flow cytometry.

References

1. Maurer-Granofszky M, Köhrer S, Fischer S, et al. Genomic breakpoint-specific monitoring of measurable residual disease in pediatric non-standard risk acute myeloid leukemia. Haematologica. 2024;109(3):740-750.