



CORRECTION

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# Correction: Gene polymorphisms of molecules of the cGAS-STING signalling pathway are associated with AML in Chinese patients

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**Correction: *Holist Integ Oncol* 3, 15 (2024)**

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Following publication of the original article [1], the authors reported errors in Table 2, which have been corrected from:

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The original article can be found online at <https://doi.org/10.1007/s44178-024-00079-8>.

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**Table 2** Characteristics of AML patients and controls

Variable	control n (%)	case n (%)
Gender		
Male	106(34.9)	141(53.8)
Female	198(65.1)	121(46.2)
Age(years, median range)	40.5(20–88)	48.5(13–87)
< 60	281(92.4)	196(74.8)
≥ 60	23(7.6)	66(25.2)
WBC		
Median( $\times 10^9/L$ )	n.a	18.00(0.77–452.43)
< $100 \times 10^9/L$	n.a	212(80.9)
$\geq 100 \times 10^9/L$	n.a	50(19.1)
PLT		
Median( $\times 10^9/L$ )	n.a	39(2–235)
> $50 \times 10^9/L$	n.a	107(40.8)
$\leq 50 \times 10^9/L$	n.a	155(59.2)
HGB		
Median(g/L)	n.a	77(21–138)
> 60 g/L	n.a	219(83.6)
$\leq 60$ g/L	n.a	43(16.4)
Bone marrow blast		
Median(%)	n.a	77.5(21–98)
< 42%	n.a	31
$\geq 42\%$	n.a	131
Risk stratification		
Favourable	n.a	58
Intermediate	n.a	135
Adverse	n.a	67
Response		
CR	n.a	138
no CR	n.a	22

n.a Not applicable

To:

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< 60 g/L	n.a	43(16.4)
Bone marrow blast		
Median(%)	n.a	77.5(21–98)
< 42%	n.a	31
$\geq 42\%$	n.a	231
Risk stratification		
Favourable	n.a	58
Intermediate	n.a	135
Adverse	n.a	68
Response		
CR	n.a	138
no CR	n.a	22

n.a Not applicable

In Table 2, for the HGB, “> 60 g/L” has been replaced by “≥ 60 g/L”, and “≤ 60 g/L” replaced by “< 60 g/L”. For the Risk stratification, the patients in adverse group should have been “68” instead of “67”, and the description in Result 3.1 (Page 4) has been corrected accordingly. For the Bone marrow blast, the patients in ≥ 42% group should have been “231” instead of “131”. The other elements of the table and the interpretation of the results remain unchanged.

In addition, the author found an error in Fig. 1 legend, which has been corrected from: The overall survival of AML patients with TT, AA, and TA genotypes in IKKB rs3747811 under different models. a) codominant model, (b) dominant model, to: The overall survival of AML patients with TT, AA, and TA genotypes

in IKKB rs3747811 under different models. (a) dominant model, (b) codominant model.

The original article [1] has been corrected.

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#### Reference

1. Ma Y, Wang D, Feng L, et al. Gene polymorphisms of molecules of the cGAS-STING signalling pathway are associated with AML in Chinese patients. *Holist Integ Oncol.* 2024;3:15. <https://doi.org/10.1007/s44178-024-00079-8>.