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ERRATUM

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Erratum to: Genetic alterations of m^{6}A regulators predict poorer survival in acute myeloid leukemia

Chau-To Kwok[1,2,3], Amy D. Marshall[1,3], John E. J. Rasko[1,3,4] and Justin J. L. Wong[1,2,3*]

Erratum

The original article [1] contained an error whereby the formatting of Table 1 was not presented correctly; this error has now been corrected.

Furthermore, the error was mistakenly carried forward by the production team handling this article, and thus was not the fault of the authors.

Author details
[1]Gene & Stem Cell Therapy Program, Centenary Institute, University of Sydney, Camperdown 2050, Australia. [2]Gene Regulation in Cancer Laboratory, Centenary Institute, University of Sydney, Camperdown 2050, Australia. [3]Sydney Medical School, University of Sydney, Camperdown, NSW 2006, Australia. [4]Cell and Molecular Therapies, Royal Prince Alfred Hospital, Camperdown 2050, Australia.

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1. Kwok, et al. Genetic alterations of m^{6}A regulators predict poorer survival in acute myeloid leukemia. J Hematol Oncol. 2017;10:39.

* Correspondence: j.wong@centenary.org.au
[1]Gene & Stem Cell Therapy Program, Centenary Institute, University of Sydney, Camperdown 2050, Australia
[2]Gene Regulation in Cancer Laboratory, Centenary Institute, University of Sydney, Camperdown 2050, Australia

Table 1 Clinical and molecular characteristics of TCGA AML patients according to the mutation and/or copy number variation status of genes encoding m^6A regulatory enzymes

	Mutation and/or CNV			CNV only[a]			Mutation		
	Yes ($n = 23$)	No ($n = 168$)	*P*	Yes ($n = 18$)	No ($n = 168$)	*P*	Yes ($n = 5$)	No ($n = 186$)	*P*
Age			0.083			0.193			0.205
Median (range)	65 (18–81)	57 (21–88)		62.5 (18–81)	57 (21–88)		65 (45–76)	57.5 (18–88)	
Sex, no. (%)			0.123			0.321			0.376
Male	16 (8.4)	87 (45.5)		12 (6.5)	87 (46.8)		4 (2.1)	99 (51.8)	
Female	7 (3.7)	81 (42.4)		6 (3.2)	81 (43.5)		1 (0.5)	87 (45.5)	
BM blast			0.072			**0.038**			0.915
Median % (range)	60 (30–97)	73 (30–100)		54 (30–97)	73 (30–100)		75 (33–90)	72 (30–100)	
WBC, $\times 10^3/mm^3$			0.084			**0.047**			0.889
Median (range)	5.4 (0.7–202.7)	17.5 (0.4–298.4)		5.2 (2.3–101.3)	17.45 (0.4–298.4)		14.5 (2.3–101.3)	15.6 (0.4–298.4)	
Cytogenetic risk, no. (%)			**<0.0001**			**<0.0001**			0.483
Favorable	0 (0)	37 (19.4)		0 (0)	37 (19.9)		0 (0)	37 (19.4)	
Intermediate	4 (2.1)	105 (55)		1 (0.5)	105 (56.5)		3 (1.6)	106 (55.5)	
Unfavorable	19 (9.9)	21 (11)		17 (9.1)	21 (11.3)		2 (1)	38 (19.9)	
Missing data	0 (0)	5 (2.6)		0 (0)	5 (2.6)		0 (0)	5 (2.6)	
Mutation, no./total no. (%)									
FLT3	1/23 (4.3)	53/168 (31.5)	**0.005**	0/18 (0)	53/168 (31.5)	**0.002**	1/5 (20)	53/186 (28.4)	1.000
NPM1	1/23 (4.3)	51/168 (30)	**0.006**	0/18 (0)	51/168 (30.3)	**0.004**	1/5 (20)	51/186 (27.4)	1.000
DNMT3A	4/23 (17.4)	43/168 (25.6)	0.453	2/18 (11.1)	43/168 (25.6)	0.249	2/5 (40)	45/186 (24.2)	0.598
IDH1 or *IDH2*	1/23 (4.3)	34/168 (20.2)	0.084	0/18 (0)	34/168 (20.2)	**0.048**	1/5 (20)	34/186 (18.3)	1.000
NRAS or *KRAS*	3/23 (13)	20/168 (11.9)	0.744	3/18 (16.7)	20/168 (11.9)	0.471	0/5 (0)	23/186 (12.4)	1.000
RUNX1	2/23 (8.7)	17/168 (10.1)	1.000	0/18 (0)	17/168 (10.1)	0.380	2/5 (40)	17/186 (9.1)	0.078
TET2	1/23 (4.3)	15/168 (8.9)	0.698	1/18(5.6)	15/168 (8.9)	1.000	0/5 (0)	16/186 (8.6)	1.000
TP53	15/23 (65.2)	1/168 (0.6)	**<0.0001**	13/18 (72.2)	1/168 (0.6)	**<0.0001**	2/5 (40)	14/186 (7.5)	0.057
CEBPA	2/23 (8.7)	10/168 (6.0)	0.641	2/18 (11.1)	10/168 (6.0)	0.327	0/5 (0)	12/186 (6.5)	1.000
WT1	0/23 (0)	12/168 (7.1)	0.366	0/18 (0)	12/168 (7.1)	0.610	0/5 (0)	12/186 (6.5)	1.000
PTPN11	2/23 (8.7)	6/168 (3.6)	0.248	2/18 (11.1)	6/168 (3.6)	0.175	0/5 (0)	8/186 (4.3)	1.000
KIT	1/23 (4.3)	6/168 (3.6)	0.599	0/18 (20)	6/168 (3.6)	1.000	1/5 (20)	6/186 (3.2)	0.172

Significant *P* values are in bold
CNV copy number variation, *BM* bone marrow, *WBC* white blood cell
[a]Excluding samples with m^6A regulatory gene mutations