

CORRECTION

# Correction: Methylation Profiles Reveal Distinct Subgroup of Hepatocellular Carcinoma Patients with Poor Prognosis

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In [Table 1](#), there are errors in the AFP row. The number of patients (n) with AFP levels <100ng/ml should be 36, and the n with AFP >100ng/ml should be 15. Please view the corrected [Table 1](#) here.



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**Table 1. Clinicopathological data for 59 HCC patients.**

Parameters	Available Data	Variables	n	%
Age at diagnosis (Median = 65, range 35–85)	59	≥65 years old	31	53
		<65 years old	28	47
Gender	59	Male	53	90
		Female	6	10
HBV status	59	Postive	36	61
		Negative	23	39
Tumor size	59	≥5 cm	33	56
		<5 cm	26	44
Differentiation (Edmonson)	59	I	5	8.5
		II	23	39
		III	26	44
		IV	5	8.5
TNM staging	58	1	32	55
		2	16	28
		3	10	17
Cirrhosis	58	Absent	37	64
		Present	21	36
Tumor multifocality	55	Absent	45	82
		Present	10	18
Tumor encapsulation	53	Absent	35	66
		Present	18	34
AFP level	51	>100ng/ml	15	71
		<100ng/ml	36	29

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## Reference

1. Mah W-C, Thurnherr T, Chow PKH, Chung AYW, Ooi LLPJ, Toh HC, et al. (2014) Methylation Profiles Reveal Distinct Subgroup of Hepatocellular Carcinoma Patients with Poor Prognosis. PLoS ONE 9(8): e104158. doi:[10.1371/journal.pone.0104158](https://doi.org/10.1371/journal.pone.0104158) PMID: [25093504](https://pubmed.ncbi.nlm.nih.gov/25093504/)