

SCIENTIFIC REPORTS

OPEN **Corrigendum: Identification of a 5-Methylcytosine Site that may Regulate C/EBP β Binding and Determine Tissue-Specific Expression of the *BPI* Gene in Piglets**

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In this Article the Authors incorrectly stated that they had developed a novel method termed bisulfite amplicon sequencing (BSAS). The method was reported by Masser *et al.* (reference 18 in the Article). Thus the following sentence (which appears verbatim in ref. 18):

“By combining the benefits of bisulfite conversion, targeted amplification, tagmentation-based library construction, and NGS, we have developed a novel method termed bisulfite amplicon sequencing (BSAS) for targeted digital high accuracy quantitation of DNA methylation¹⁸”

should read:

“In a previous study, Masser *et al.* developed a method termed bisulfite amplicon sequencing (BSAS) for targeted digital high accuracy quantitation of DNA methylation by combining the benefits of bisulfite conversion, targeted amplification, tagmentation-based library construction, and NGS¹⁸”

The following sections in “Materials and Methods” failed to appropriately cite the protocols followed:

“DNA bisulfite conversion and bisulfite specific PCR.”

should read:

“DNA bisulfite conversion and bisulfite specific PCR¹³”

“NGS library preparation and sequencing.”

should read:

“NGS library preparation and sequencing¹⁸”

“Real-time PCR analysis.”

should read:

“Real-time PCR analysis¹³”

An additional reference is listed below as reference 1 and should appear in the text as below:

“NGS data analysis and digital methylation quantitation”.

should read:

“NGS data analysis and digital methylation quantitation¹”.

The Authors apologize for these errors.

References:

1. Pei, L. *et al.* Genome-wide DNA methylation analysis reveals novel epigenetic changes in chronic lymphocytic leukemia. *Epigenetics* **7**, 567–578 (2012).



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