

ERRATUM

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Erratum to: An integrative genomics approach for identifying novel functional consequences of *PBRM1* truncated mutations in clear cell renal cell carcinoma (ccRCC)

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Erratum

Following publication of the original article [1] it was brought to our attention that there were three errors in the “Results” section of the article’s abstract. Please see below for the two sentences in which these errors occur:

1. We identified 613 differentially expressed genes (128 up-regulated and 485 down-regulated genes using cutoff $|\log_2FC| < 1$ and $p < 0.05$) in *PBRM1* mutated group versus “pan-negative” group.

2. In addition, we identified 1405 differentially methylated CpG sites (targeting 1308 genes, $|\log_2FC| < 1$, $p < 0.01$) and 185 significantly altered microRNAs ($|\log_2FC| < 1$, $p < 0.05$) associated with truncated *PBRM1* mutations.

In both sentences the present expression in the article is “ $|\log_2FC| < 1$ ”. However, this is incorrect, as the cutoff should be “ $|\log_2FC| > 1$ ”.

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1. Wang Y, et al. An integrative genomics approach for identifying novel functional consequences of *PBRM1* truncated mutations in clear cell renal cell carcinoma (ccRCC). *BMC Genomics*. 2016;17 Suppl 7:515.

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