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EDITED AND REVIEWED BY
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SPECIALTY SECTION
This article was submitted to
Cancer Genetics,
a section of the journal
Frontiers in Oncology

RECEIVED 23 September 2022
ACCEPTED 23 September 2022
PUBLISHED 04 October 2022

CITATION
Mao W, Yu Q, Wang K, Ma Q, Zheng Y, Zhang G, Luo W, Wang N and Wang Y (2022) Corrigendum: Comprehensive analysis of the transcriptome-wide m6A methylome in lung adenocarcinoma by MeRIP sequencing. *Front. Oncol.* 12:103295. doi: 10.3389/fonc.2022.1032295

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Corrigendum: Comprehensive analysis of the transcriptome-wide m6A methylome in lung adenocarcinoma by MeRIP sequencing

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KEYWORDS

lung adenocarcinoma, m6A, MeRIP-seq, GPRIN1, prognosis

A corrigendum on

[Comprehensive analysis of the transcriptome-wide m6A methylome in lung adenocarcinoma by MeRIP sequencing](#)

by Mao W, Yu Q, Wang K, Ma Q, Zheng Y, Zhang G, Luo W, Wang N and Wang Y (2022). *Front. Oncol.* 12:791332. doi: 10.3389/fonc.2022.791332

In the published article, there was an error in [Figure 2B](#) as published. The corrected [Figure 2B](#) and its caption “GO function and KEGG pathway enrichment of differently methylated m6A genes. (A) The top 10 GO terms of genes with down-regulated m6A peaks. (B) The top 10 GO terms of genes with up-regulated m6A peaks. (C) The top 10 KEGG pathways of genes with down-regulated m6A peaks. (D) The top 10 KEGG pathways of genes with up-regulated m6A peaks.” appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

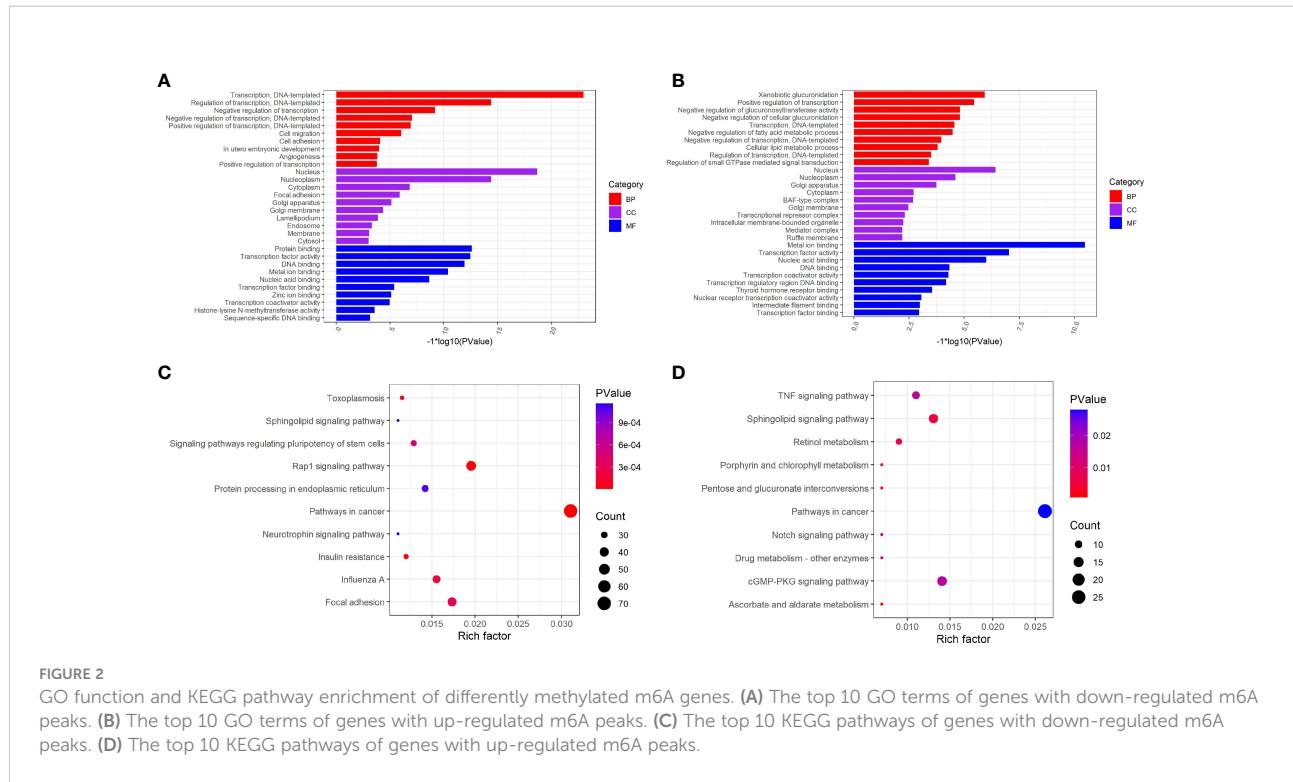


FIGURE 2

GO function and KEGG pathway enrichment of differently methylated m6A genes. **(A)** The top 10 GO terms of genes with down-regulated m6A peaks. **(B)** The top 10 GO terms of genes with up-regulated m6A peaks. **(C)** The top 10 KEGG pathways of genes with down-regulated m6A peaks. **(D)** The top 10 KEGG pathways of genes with up-regulated m6A peaks.

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