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Correction: Serum levels of perand polyfluoroalkylated substances and methylation of DNA from peripheral blood

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A Correction on

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In the published article, there was an error in [Figure 3] as published. [Only the two panels corresponding to PFOS (3B) were displayed, while those related to Figure PFOA (3A) were missing]. The corrected [Figure 3] and its caption [ORIGINAL Caption] appear below.

The original article has been updated.

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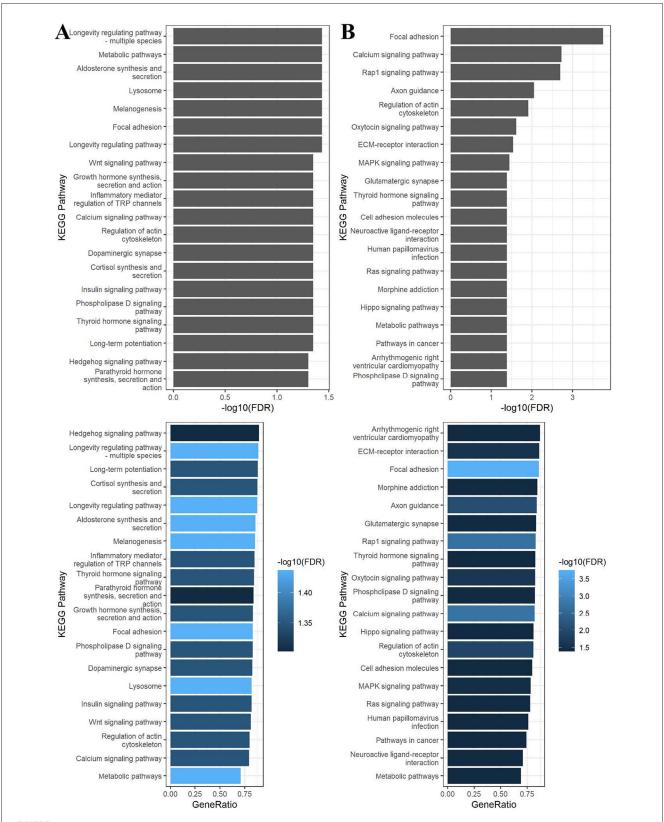


FIGURE 3
Bar charts for KEGG enrichment analysis of differentially methylated CpG sites associated with **(A)** PFOA and **(B)** PFOS at threshold unadjusted p-value <0.01 in the epigenome-wide association analyses. Pathways were considered significant when the FDR < 0.05. The terms of the KEGG pathways are depicted on the y-axis. On the top figure, the x-axis is the $-\log 10$ FDR of the tests of the gene set enrichment in each pathway. On the bottom figure, the x-axis is the ratio between the number of differentially methylated genes and the number of genes in the KEGG term. The different colors represent the $-\log 10$ FDR.

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