

CORRECTION

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# Correction: Long-term environmental metal exposure is associated with hypomethylation of CpG sites in *NFKB1* and other genes related to oncogenesis

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**Correction to: *Clinical Epigenetics* (2023) 15:126**  
<https://doi.org/10.1186/s13148-023-01536-3>

Following publication of the original article [1], the author noticed that the descriptions of Figs. 2 and 3 are

placed incorrectly in the textual part instead of figure captions.

This has now been corrected with this erratum.  
The original article has been corrected.

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The original article can be found online at <https://doi.org/10.1186/s13148-023-01536-3>.

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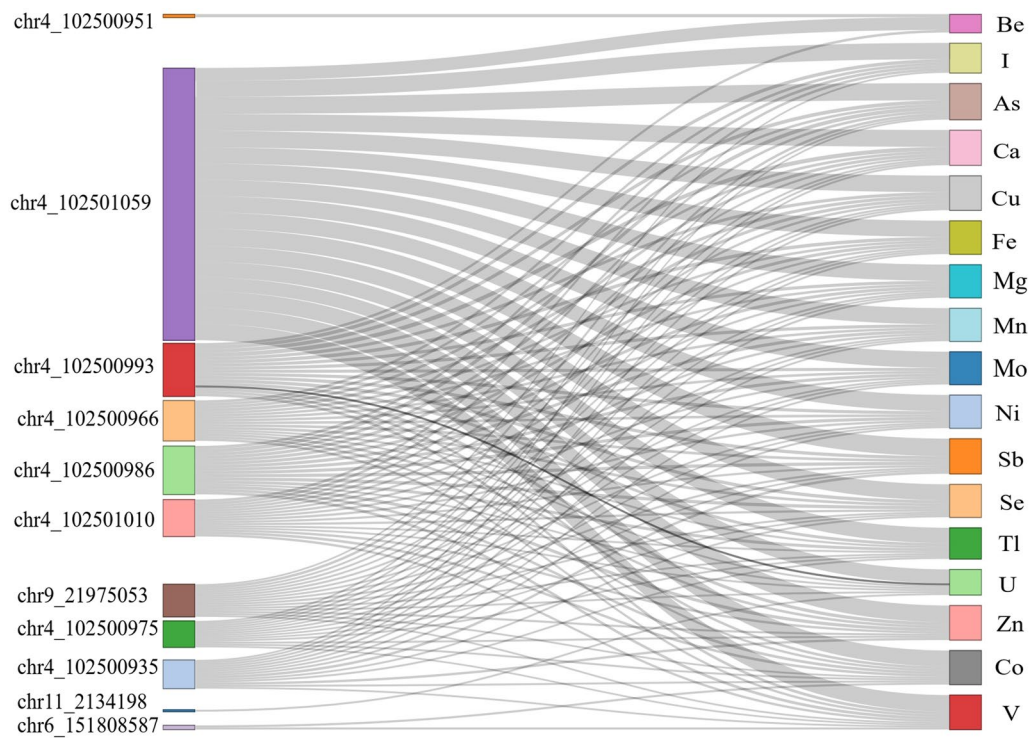
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**Fig. 2** Differentially methylated positions in association with the plasma levels of chemical elements. Sankey diagram visualizes the association between methylation status of differentially methylated CpGs and plasma concentrations of chemical elements. The x-axis represents differentially methylated CpGs and chemical elements. The nodes on y-axis represent the positions of CpGs differentially methylated in association with chemical elements, number of later is proportional to the size of each node and width of each arc



**Fig. 3** CpGs associated with plasma levels of chemical elements. Sankey diagram visualizes the association between methylation status of CpGs (right) and plasma concentrations of chemical elements (left)

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**Reference**

- Stepanyan A, Petrackova A, Hakobyan S, Savara J, Davitavyan S, Kriegova E, Arakelyan A. Long-term environmental metal exposure is associated with hypomethylation of CpG sites in *NFKB1* and other genes related to oncogenesis. *Clin Epigenet.* 2023;15:126. <https://doi.org/10.1186/s13148-023-01536-3>