

CORRECTION

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Correction to: *ARNTL* hypermethylation promotes tumorigenesis and inhibits cisplatin sensitivity by activating *CDK5* transcription in nasopharyngeal carcinoma

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Correction to: *J Exp Clin Cancer Res* 38, 11 (2019)
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Following publication of the original article [1], the authors identified some minor errors in Supplemental Figs. 1 and 4, specifically:

- Fig. S1b: incorrect sample size listed; correct sample size is 25
- Fig. S4b: incorrect image used for SUNE1-ARNTL (24h); correct image is now used

The authors provided the journal with their original data. The corrected figures are given here. The corrections do not have any effect on the final conclusions of the paper. The original article has been corrected.

The original article can be found online at <https://doi.org/10.1186/s13046-018-0997-7>.

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Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s13046-021-02238-5>.

Additional file 2: Fig. S1. *ARNTL* methylation levels in the GSE52068 and GSE62366 nasopharyngeal carcinoma datasets.

Additional file 5: Fig. S4. Overexpression of *ARNTL* had no impact on nasopharyngeal carcinoma cells invasion and migration. **(A)** Images of Transwell invasion (left) and migration (right) assay with *ARNTL*-overexpression or Vector-overexpression SUNE1 and HONE1 cells. **(B)** Images of wound healing assay with *ARNTL*-overexpression or Vector-overexpression SUNE1 and HONE1 cells.

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Reference

1. Peng H, Zhang J, Zhang PP, et al. *ARNTL* hypermethylation promotes tumorigenesis and inhibits cisplatin sensitivity by activating *CDK5* transcription in nasopharyngeal carcinoma. *J Exp Clin Cancer Res*. 2019;38:11. <https://doi.org/10.1186/s13046-018-0997-7>.



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