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## **Author Correction: Automated Gleason grading of prostate cancer tissue microarrays via deep learning**

Arvaniti, Eirini; Fricker, Kim S; Moret, Michael; Rupp, Niels; Hermanns, Thomas; Fankhauser, Christian; Wey, Norbert; Wild, Peter J; Rüschoff, Jan H; Claassen, Manfred

Abstract: A correction to this article has been published and is linked from the HTML and PDF versions of this paper. The error has not been fixed in the paper.

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# SCIENTIFIC REPORTS

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## Author Correction: Automated Gleason grading of prostate cancer tissue microarrays via deep learning

Eirini Arvaniti<sup>1,5</sup>, Kim S. Fricker<sup>2</sup>, Michael Moret<sup>1</sup>, Niels Rupp<sup>2</sup>, Thomas Hermanns<sup>3</sup>, Christian Fankhauser<sup>3</sup>, Norbert Wey<sup>2</sup>, Peter J. Wild<sup>2,4</sup>, Jan H. Rüschoff<sup>2</sup> & Manfred Claassen<sup>1,5</sup>

Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-018-30535-1>, published online 13 August 2018

This Article contains an error in the Discussion section.

“The low-risk and intermediate-risk groups defined by the model’s predictions were more significantly separated compared to the first study where deep learning-based predictions are used for survival analysis in a prostate cancer cohort.”

should read:

“The low-risk and intermediate-risk groups defined by the model’s predictions were more significantly separated compared to the corresponding groups defined by either pathologist’s annotations. To our knowledge, this is the first study where deep learning-based predictions are used for survival analysis in a prostate cancer cohort.”



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