Corrigendum: transcriptome analysis showed a differential signature between invas...

Health & Medicine

A Corrigendum on

Transcriptome Analysis Showed a Differential Signature Between Invasive and Non-invasive Corticotrophinomas

by de Araújo, L. J. T., Lerario, A. M., de Castro, M., Martins, C. S., Bronstein, M. D., Machado, M. C., et al. (2017). Front. Endocrinol. 8: 55. doi: 10.3389/fendo. 2017. 00055

In the original article, there was an error. We stated that *USP8* genetic abnormalities were not identified in DNA from tumor samples analyzed by microarray technology.

A correction has been made toAbstract, Paragraph Number 1, Lines 18–19.

Somatic mutations in *USP8* were also investigated and mutations were identified in six cases.

A correction has been made toResults, Paragraph Number 1.

Before microarray analysis, we performed the screening for mutations in *USP8* in our patients, and somatic variants were found in patients #2 and #5 (p. Ser718Pro), #4 (p. Ser718Cys), patients #3 and #6 (p. Pro720Arg), and #9 (p. Pro720Gln). Both mutations were found in heterozygosis and have been previously described (17, 18).

A correction has been made toDiscussion, Paragraph Number 1.

In the microarray study cohort, we identified six *USP8* mutations in 12 samples (50%). In the patients included in the validation study, we could

identify somatic *USP8* mutations in 5 (non-invasive corticotrophinomas) out of 18 patients (27. 7%). According to Reincke et al. (17) and Perez-Rivas et al. (18), these mutations occur in ≈36% of patients with CD. Interestingly, the presence of *USP8* mutations did not interfere in the transcriptome expression analysis results comparing invasive vs. non-invasive tumors and in its validation study.

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.