Correction to: Implication of connexin30 on the stemness of glioma: connexin30 reverses the malignant phenotype of glioma by modulating IGF-1R, CD133 and cMyc

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During the initial online submission, owing to an alignment error, Fig. 1 Cx30 panel b overlapped on Fig. 4 IGF-1R panel b; the correct Fig. 4 appears below.

The authors sincerely regret this error.

The original article can be found online at <https://doi.org/10.1007/s11060-017-2608-4>.

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Fig. 4 **A** IHC of Cx30, IGF-1R, pErk, pAkt, pmTOR, CD133 and cMyc in the control and experimental group of animals. **a** Control, **b** C6 cells-implanted rats, **c** Cx30-transfected C6 cells-implanted rats. **B** Quantitative analysis of **A**. The number of stained (positive) cells per 40 $\times$ field was averaged across five different fields for each sample. The hypothesis testing method included one-way ANOVA followed by LSD. A p value less than 0.05 was considered statistically significant. Scale bar 50 μ m. Compari-

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sons are made as group I versus group II and group II versus group III. **C** Western blot banding pattern of Cx30, IGF-1R, pErk, pAkt, pmTOR, CD133 and cMyc in control and experimental groups; β -actin served as internal control. **Lane 1** control; **lane 2** C6 cells-implanted rats; **lane 3** Cx30-transfected cells-implanted rats. **D** Densitometric results of **C**. All experiments were performed thrice, and the representative data were shown. Values were expressed as mean $\pm$ SD; p value < 0.05 considered significant