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Corrigendum

Corrigendum to 'Silencing of circular RNA HIPK2 in neural stem cells enhances functional recovery following ischaemic stroke' [EBioMedicine 52 (2020) 102660]

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The authors have recently noticed that the published version of this article contained errors in Figs. 1e and 7e. These errors were inadvertently caused during the assembly of the western blot images due to our negligence. The corrected Figs. 1 and 7 are given below. This correction has not changed the description, interpretation, or the original conclusions of the manuscript. The authors apologize for any inconvenience caused.

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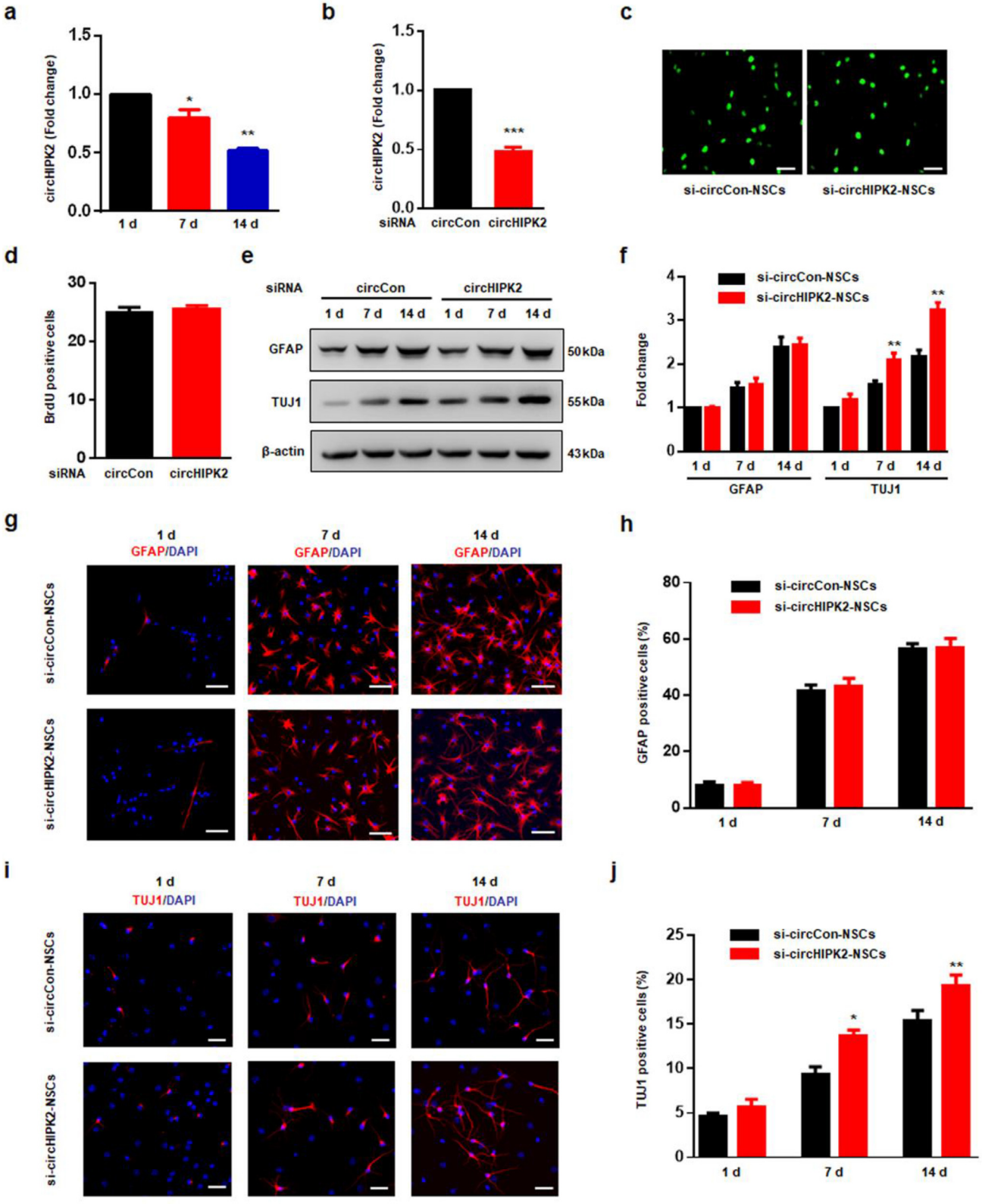

Fig. 1. circHIPK2 is involved in the differentiation of NSCs. (a) qPCR analysis of circHIPK2 expression in NSCs cultured for 1, 7, and 14 d in differentiation medium. All data were presented as mean ± SEM of 3 independent experiments. $^{*}P < 0.05$, $^{**}P < 0.01$ vs the 1 d one-way ANOVA followed by Holm-Sidak *post hoc* multiple comparison test. (b) qPCR confirmed that circHIPK2 siRNA lentivirus-transducted NSCs successfully decreased circHIPK2 expression. All data were presented as mean ± SEM of 3 independent experiments. $^{***}P < 0.001$ vs the circCon siRNA group using Student's *t*-test. (c-d) Representative image of BrdU immunostaining (c) and quantification of BrdU immunofluorescence-positive cell numbers (d). All data were presented as mean ± SEM of 3 independent experiments. (e-f) Western blot analysis showing GFAP (astrocyte marker) and TUJ1 (neuronal marker) protein expression in the si-circCon-NSC group and in the si-circHIPK2-NSC group. All data were presented as mean ± SEM of 3 independent experiments. $^{**}P < 0.01$ vs the si-circCon-NSCs using two-way ANOVA followed by Holm-Sidak *post hoc* multiple comparison test. (g–j) Representative immunostaining of GFAP^{+} (g) or TUJ1^{+} (i) cells from differentiated NSCs with si-circHIPK2 lentivirus transduction. Scale bar = 50 μm. Quantification of GFAP^{+} (h) or TUJ1^{+} (j) cell numbers using ImageJ software. Timescale indicates days after NSC differentiation. All data were presented as mean ± SEM of 3 independent experiments. $^{*}P < 0.05$, $^{**}P < 0.01$ vs the si-circCon-NSC group cultured in differentiation medium for 7 and 14 d using two-way ANOVA followed by Holm-Sidak *post hoc* multiple comparison test.

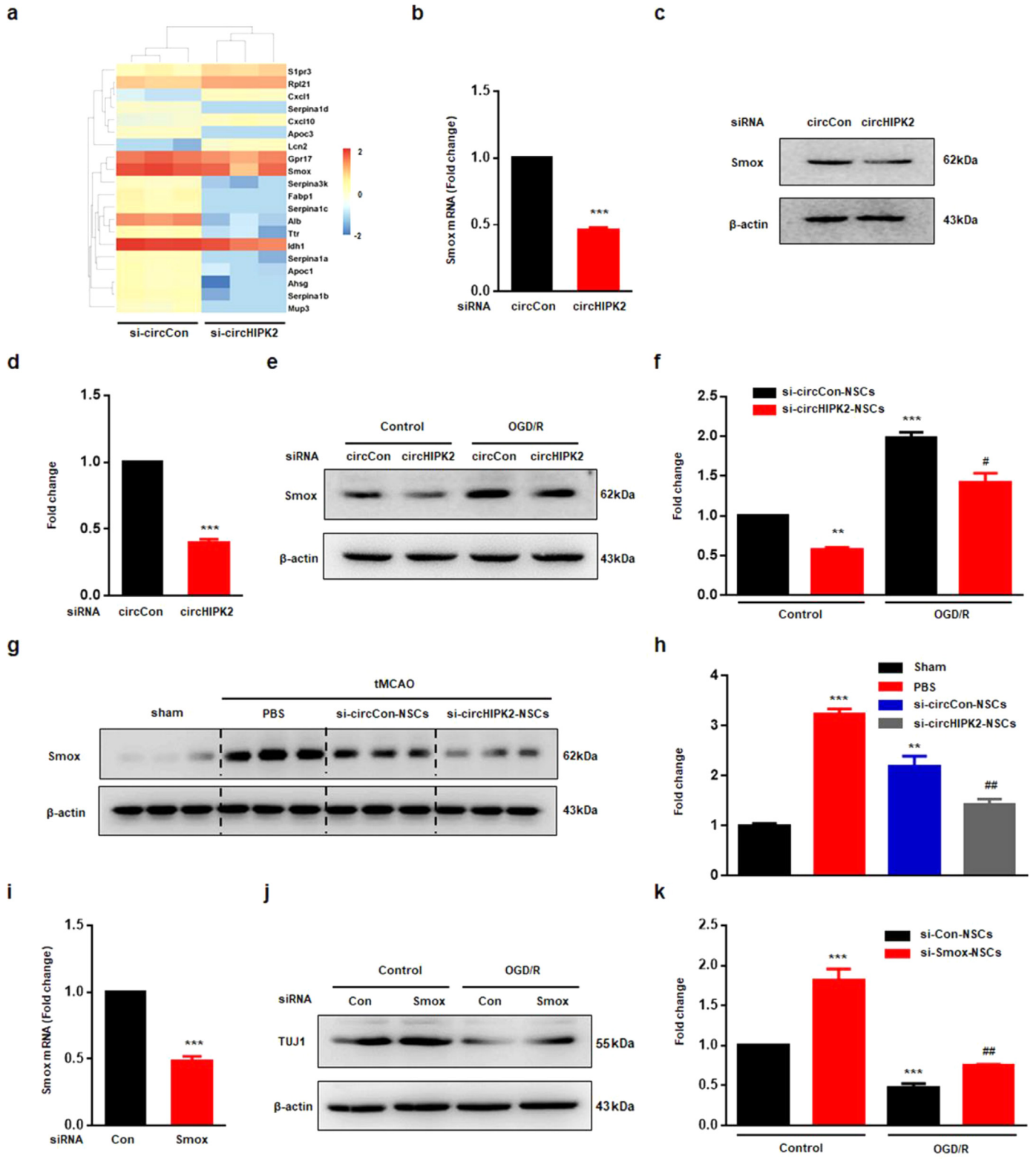

Fig. 7. Silencing of circHIPK2 promotes NSC differentiation via Smox. (a) Heatmap assessing the variations in mRNA expression between the si-circCon-NSC group and the si-circHIPK2-NSC group. $n = 3$ per group. $^{*}P < 0.05$ vs the si-circCon-NSC group. (b) The level of Smox mRNA in circHIPK2 siRNA transduced NSCs analysed by qPCR. All data were presented as mean ± SEM of 3 independent experiments. $^{***}P < 0.001$ vs the circCon siRNA group using Student's *t*-test. (c-d) Western blot analysis of Smox expression in circHIPK2 siRNA transduced NSCs. All data were presented as mean ± SEM of 3 independent experiments. $^{***}P < 0.001$ vs the circCon siRNA group using Student's *t*-test. (e-f) circHIPK2 siRNA attenuated the expression of OGD/R-induced Smox expression in NSCs, as determined by western blot analysis. NSCs were treated with OGD for 2 h and reperfused for 6 h. All data were presented as mean ± SEM of 3 independent experiments. $^{**}P < 0.01$, $^{***}P < 0.001$ vs the control si-circCon group; $^{\#}P < 0.05$ vs the OGD/R-treated si-circCon group using two-way ANOVA followed by Holm-Sidak *post hoc* multiple-comparison tests. (g-h) Western blot analysis of Smox expression in tMCAO mice injected with si-circCon-NSCs and si-circHIPK2-NSCs. $n = 6$ per group. $^{**}P < 0.01$, $^{***}P < 0.001$ vs the sham group; $^{\#\#}P < 0.01$ vs the si-circCon-NSC group using two-way ANOVA followed by Holm-Sidak *post hoc* multiple-comparison tests. (i) qPCR analysis of Smox mRNA in the si-Con-NSC group and si-Smox-NSC group. All data were presented as mean ± SEM of 3 independent experiments. $^{***}P < 0.001$ vs the si-Con-NSC group. (j-k) Smox siRNA attenuated the expression of OGD/R-induced TUJ1 in NSCs determined by western blot. All data were presented as mean ± SEM of 3 independent experiments. $^{***}P < 0.001$ vs the si-Con-NSC group; $^{\#\#}P < 0.01$ vs the OGD/R si-Con group using two-way ANOVA followed by Holm-Sidak *post hoc* multiple-comparison tests.