



## Correction: Single-cell RNA sequencing reveals the lineage of malignant epithelial cells and upregulation of TAGLN2 promotes peritoneal metastasis in gastric cancer

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In this article the caption to Fig. 4E was incorrectly given as “E Representative pairs of low-power (left, solid line) and high-power (right, dotted line) photomicrographs of FFPE tissues that were subjected to TAGLN2 staining are shown.” and should have read “E Representative pairs of low-power (up, solid line) and high-power (down, dotted

line) photomicrographs of FFPE tissues that were subjected to TAGLN2 staining are shown.”

In Fig. 5H, the representative image of the invasion assays about the HGC27-TAGLN2 overexpression group was mistakenly uploaded. The authors apologize for any confusion this may have caused. The correct Fig. 5 is given below. The images have been replaced with the correct images from the raw data. The corrections do not have any effect on the conclusions of the paper.

The original article has been corrected.

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The original article can be found online at <https://doi.org/10.1007/s12094-023-03194-6>.

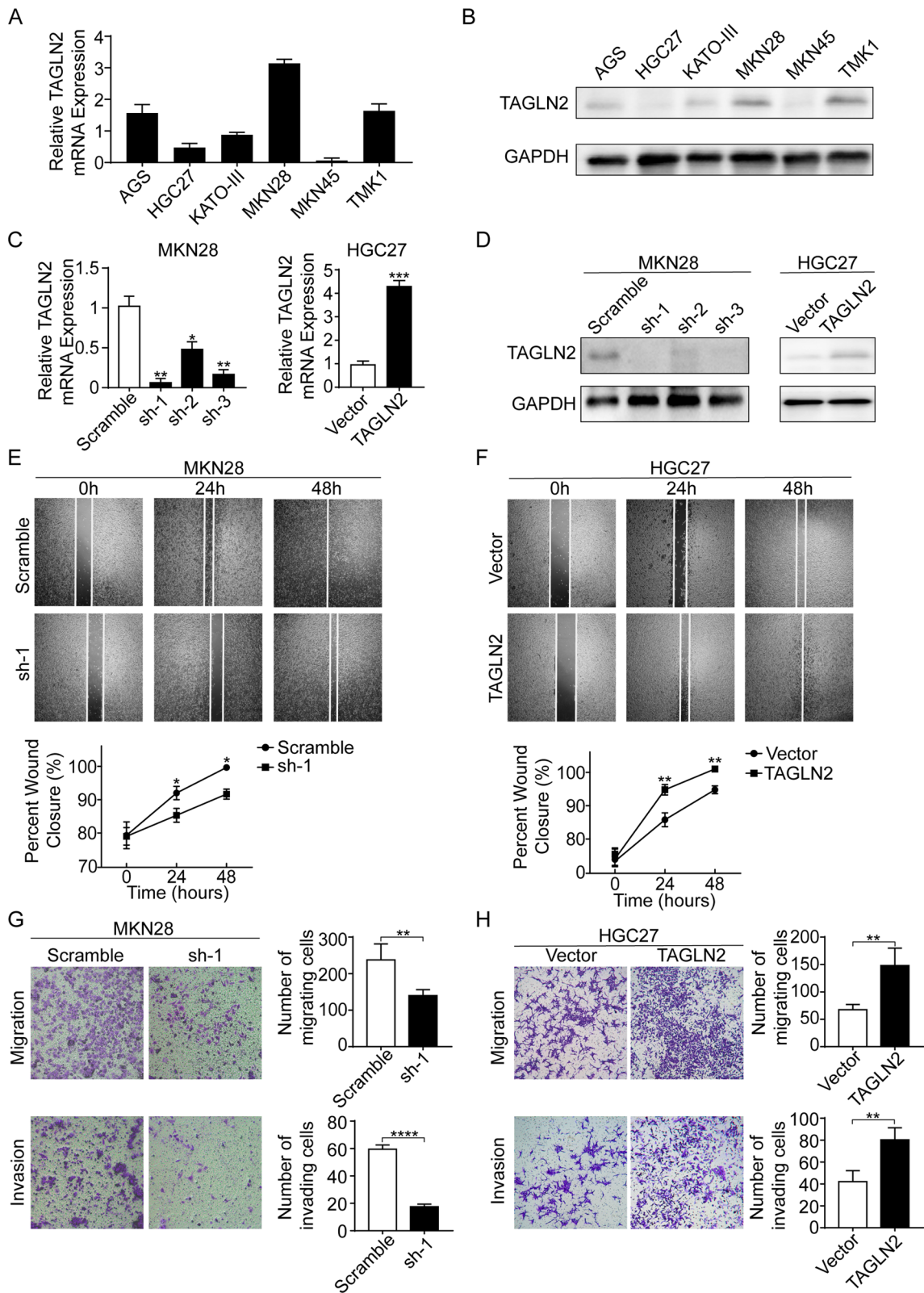
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◀**Fig. 5** TAGLN2 promotes GC cell lines migration and invasion. **A** and **B** The relative mRNA expression and protein expression of TAGLN2 were examined in GC cell lines. **C** and **D** MKN28 and HGC27 cells transfected with TAGLN2 silencing or overexpression vectors, respectively, were verified by qPCR and western blotting. GAPDH was used as an internal control. MKN28 sh1 was selected for the experiments. **E–H** The effects of TAGLN2 depletion or overexpression on the wound healing (**E** and **F**), migration and invasion (**G** and **H**) abilities of the indicated cell lines. Original magnification:  $\times 100$ . The data are presented as the mean  $\pm$  SD of three independent experiments. \* $P < 0.05$ , \*\* $P < 0.01$  and \*\*\*\* $P < 0.0001$

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