

CORRECTION

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Correction to: Long non-coding RNA HUMT hypomethylation promotes lymphangiogenesis and metastasis via activating FOXC1 transcription in triple-negative breast cancer

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The original article [1] contains an error in Fig. 5b whereby two panels have been mistakenly duplicated. The correct version of Fig. 5b can be viewed ahead alongside the rest of Fig. 5.

The original article can be found online at <https://doi.org/10.1186/s13045-020-00852-y>.

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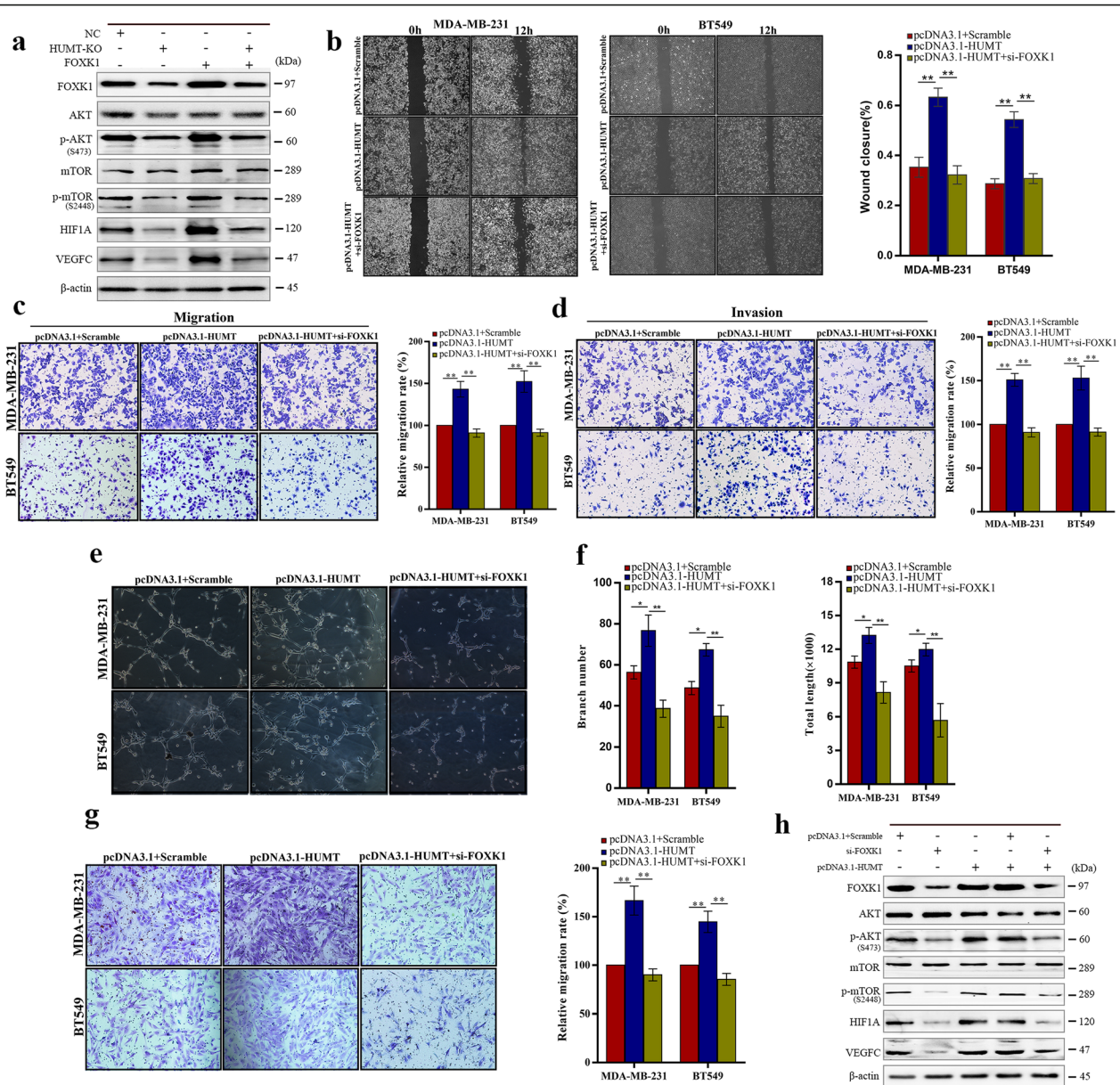


Fig. 5 HUME exerted its function by regulating the FOXK1 expression and downstream signaling. **a** Western blot analysis of the corresponding signaling in HUMT-KO- and FOXK1-overexpressed MDA-MB-231 cells. **b-d** Representative graphs and quantification of wound healing assay, Transwell migration, and invasion assay in the MDA-MB-231 and BT549 cells cotransfected with HUME overexpression vector or empty vector together with si-FOXK1 or scrambled control. **e** Representative pictures of tube formation assay in HLECs cultured in medium supernatant of the abovementioned cells. **f** Quantitative analysis of the branch number and total tube length in tube formation assay. **g** Representative graphs and quantification of Transwell migration assay in HLECs cultured in medium supernatant of the abovementioned cells. **h** Western blot analysis of the corresponding signaling in MDA-MB-231 and BT549 cotransfected with HUME overexpression vector or empty vector together with si-FOXK1 or scrambled control. Data were shown as mean \pm SD; * $P < 0.05$; ** $P < 0.01$