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CORRECTION

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Correction to: Long non-coding RNA HUMT hypomethylation promotes lymphangiogenesis and metastasis via activating FOXK1 transcription in triple-negative breast cancer

Shaoquan Zheng[1,3†], Lu Yang[1,3†], Yutian Zou[1,3†], Jie-ying Liang[2,3†], Peng Liu[1,3], Guanfeng Gao[1,3], Anli Yang[1,3], Hailin Tang[1,3*] and Xiaoming Xie[1,3*]

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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.

Author details

[1]Department of Breast Oncology, Sun Yat-sen University Cancer Center, 651 East Dongfeng Road, Guangzhou 510060, China. [2]Department of Medical Oncology, Sun Yat-sen University Cancer Center, 651 East Dongfeng Road, Guangzhou 510060, China. [3]State Key Laboratory of Oncology in South China, Collaborative Innovation Center for Cancer Medicine, Sun Yat-sen University Cancer Center, 651 East Dongfeng Road, Guangzhou 510060, Guangdong, China.

Reference

1. Zheng S, et al. Long non-coding RNA HUMT hypomethylation promotes lymphangiogenesis and metastasis via activating FOXK1 transcription in triple-negative breast cancer. J Hematol Oncol. 2020;13:17 https://doi.org/10.1186/s13045-020-00852-y.

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* Correspondence: tanghl@sysucc.org.cn; xiexm@sysucc.org.cn
†Shaoquan Zheng, Lu Yang, Yutian Zou and Jie-ying Liang contributed equally to this work.
[1]Department of Breast Oncology, Sun Yat-sen University Cancer Center, 651 East Dongfeng Road, Guangzhou 510060, China
Full list of author information is available at the end of the article

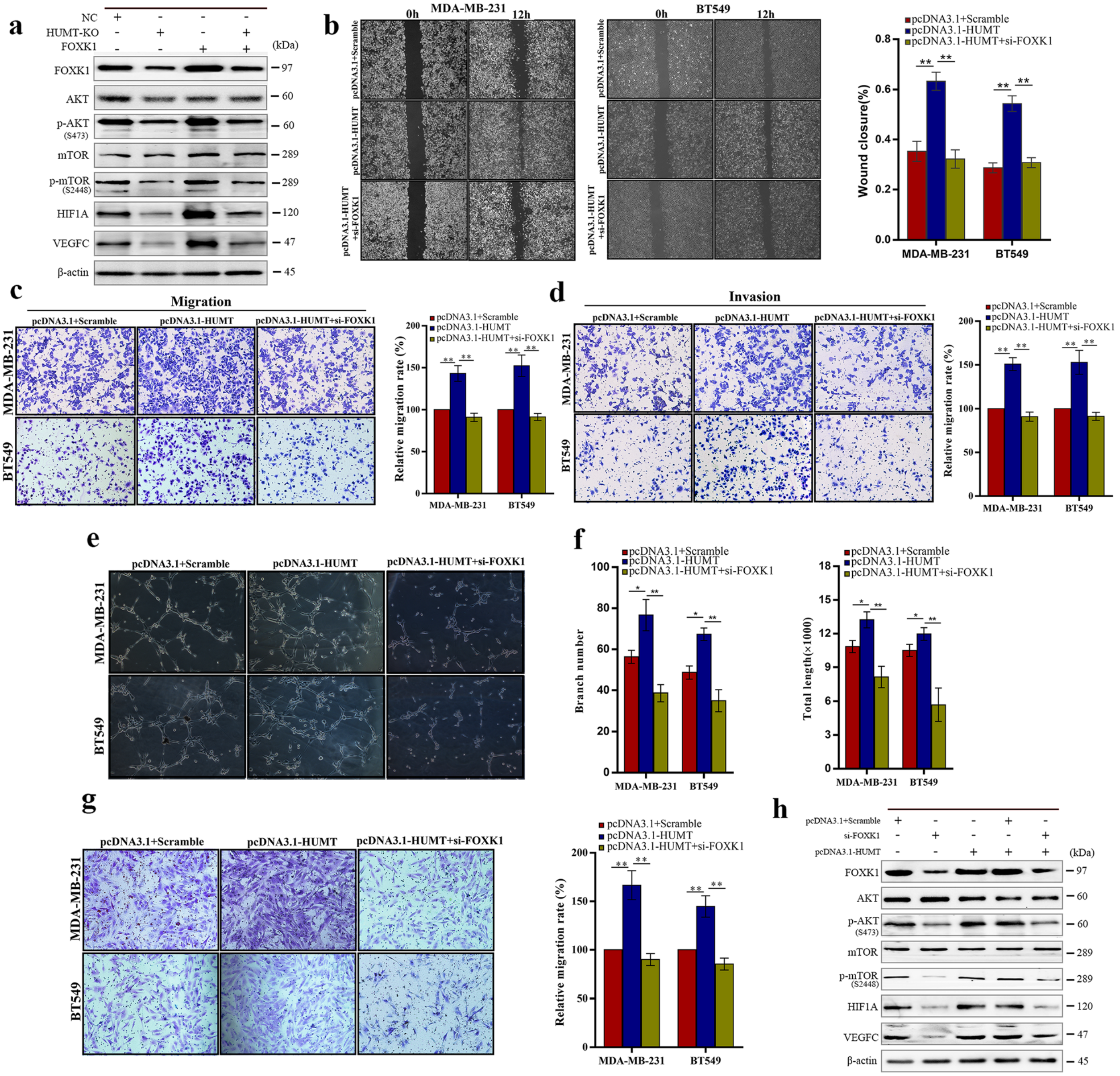

Fig. 5 HUMT exerted its function by regulating the FOXK1 expression and downstream signaling. **a** Western blot analysis of the corresponding signaling in HUMT-KO- and FOXK1-overexpressed MDA-MB-231 cells. **b**–**d** Representative graphs and quantification of wound healing assay, Transwell migration, and invasion assay in the MDA-MB-231 and BT549 cells cotransfected with HUMT 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 HUMT overexpression vector or empty vector together with si-FOXK1 or scrambled control. Data were shown as mean ± SD; *$P < 0.05$; **$P < 0.01$