

Correction for: miR-150-5p suppresses tumor progression by targeting VEGFA in colorectal cancer

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Original article: *Aging (Albany NY)* 2018; 10: pp 3421–3437

PMID: [30476901](https://pubmed.ncbi.nlm.nih.gov/30476901/)

PMCID: [PMC6286841](https://pubmed.ncbi.nlm.nih.gov/PMC6286841/)

doi: [10.18632/aging.101656](https://doi.org/10.18632/aging.101656)

This article has been corrected: The authors replaced panel D of Figure 7, where the images of HCT116/siVEGFA-1 and HCT116/siVEGFA-2 were identical, because the image HCT116/siVEGFA-1 was accidentally used twice. The correct image of HCT116/siVEGFA-2 from the original set of experiments was used for new panel 7D, which is provided below.

The authors replaced panel B of Supplementary Figure 1, where the images of HCT8/agomiR-NC (0 h) group and agomiR-150-5p+vector (24h) group were used instead of the images of HCT8/agomiR-150-5p group (0, 24h). The correct images of HCT8/agomiR-150-5p group (0, 24h) from the original set of experiments were used for new panel S1B. Additionally, authors added 0 and 24h marks to the panel S1B, which is provided below.

Authors deeply apologize for these errors and testify that these alterations do not affect the results or conclusions of this work.

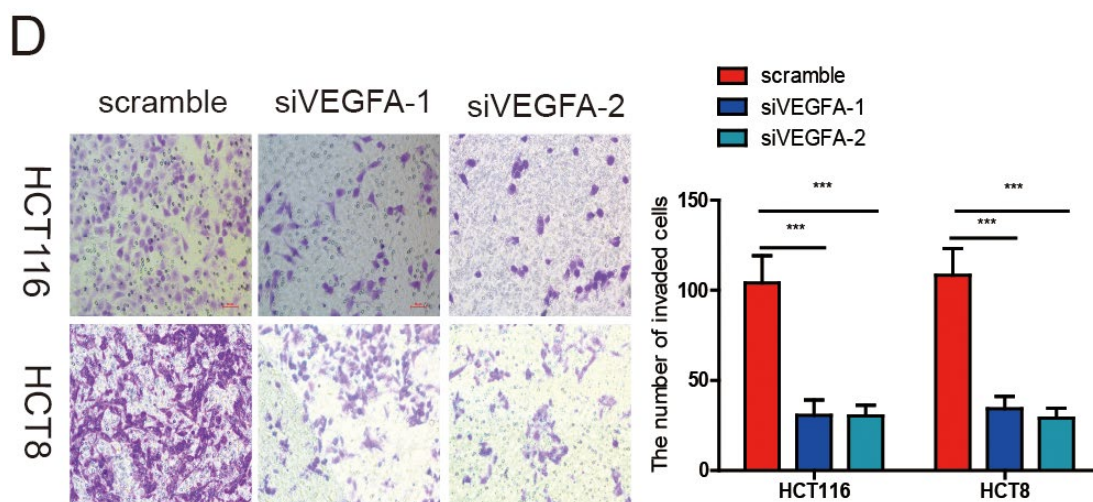
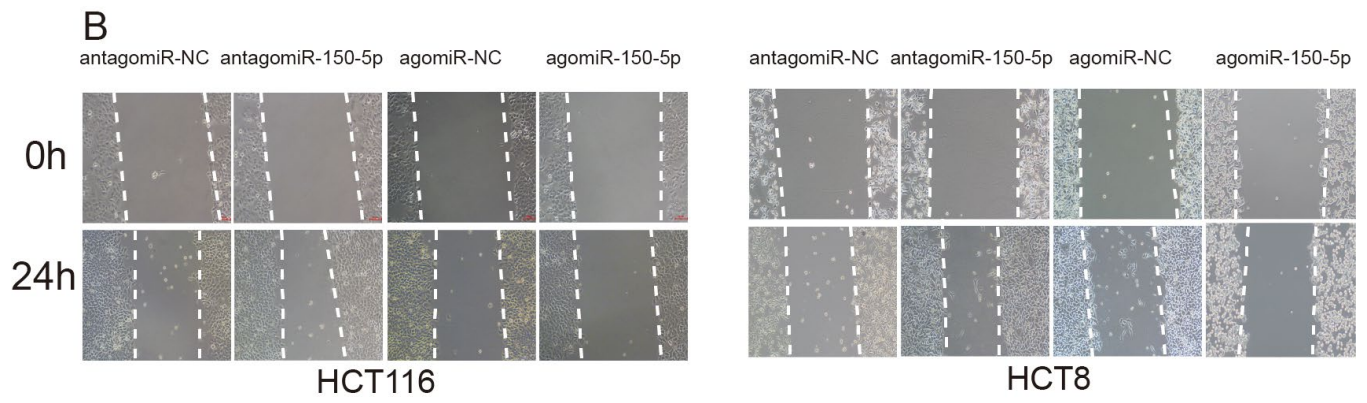


Figure 7. VEGFA knockdown significantly inhibited CRC progression. (A) VEGFA expression was downregulated in HCT116 and HCT8 cells transfected with siVEGFA-1 or siVEGFA-2. (B-E) VEGFA knockdown inhibited CRC cell proliferation (B), migration (C), invasion (D) and HUVECs tube formation (E). Data are shown as the mean±SD of three independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supplementary Figure S1. (A-D) Representative images of colony formation (A), wound healing (B, $\times 40$), transwell (C, $\times 200$) and tube formation (D, $\times 100$) in antagomiR-NC group, antagomiR-150-5p group, agomiR-NC group and agomiR-150-5p group.