

Erratum

Genome-wide target interactome profiling reveals a novel *EEF1A1* epigenetic pathway for oncogenic lncRNA *MALAT1* in breast cancer: Am J Cancer Res. 2019; 9(4): 714-729

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Received April 27, 2026; Accepted May 10, 2026; Epub September 25, 2026; Published September 30, 2026

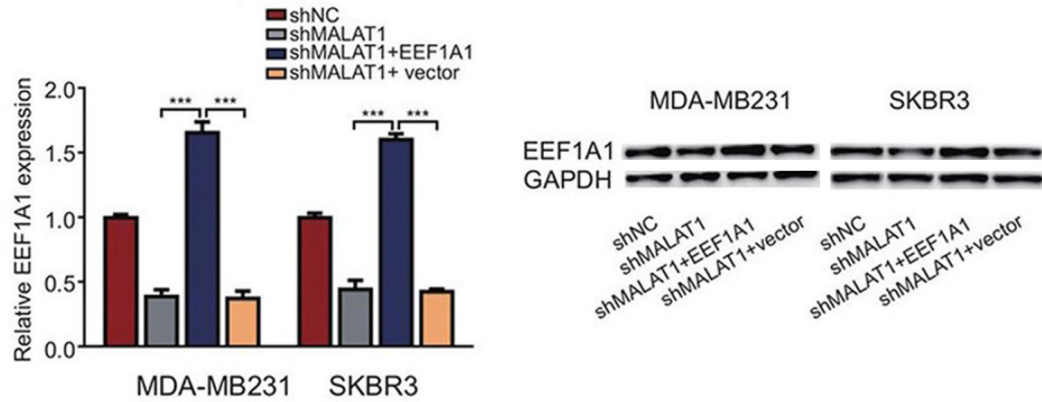
In the previous erratum, there was an error in **Figure 7C**. We have now repeated the assay and would like to publish a correction with the new data. This correction does not affect the interpretation and conclusions of the study. We sincerely apologize for this oversight and any confusion that may have caused. The corrected **Figure 7** is shown as follows.

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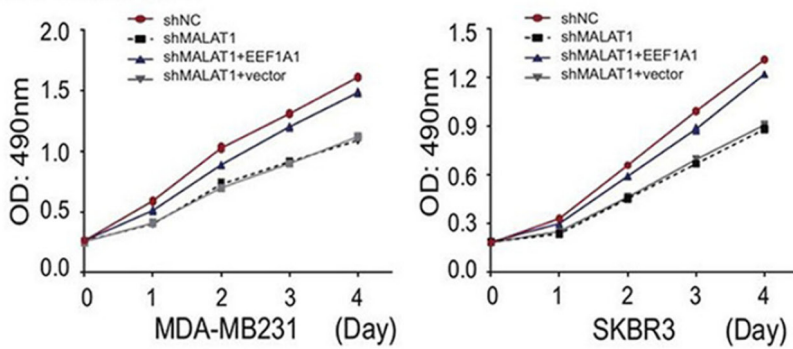
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MALAT1 epigenetically targets *EEF1A1*

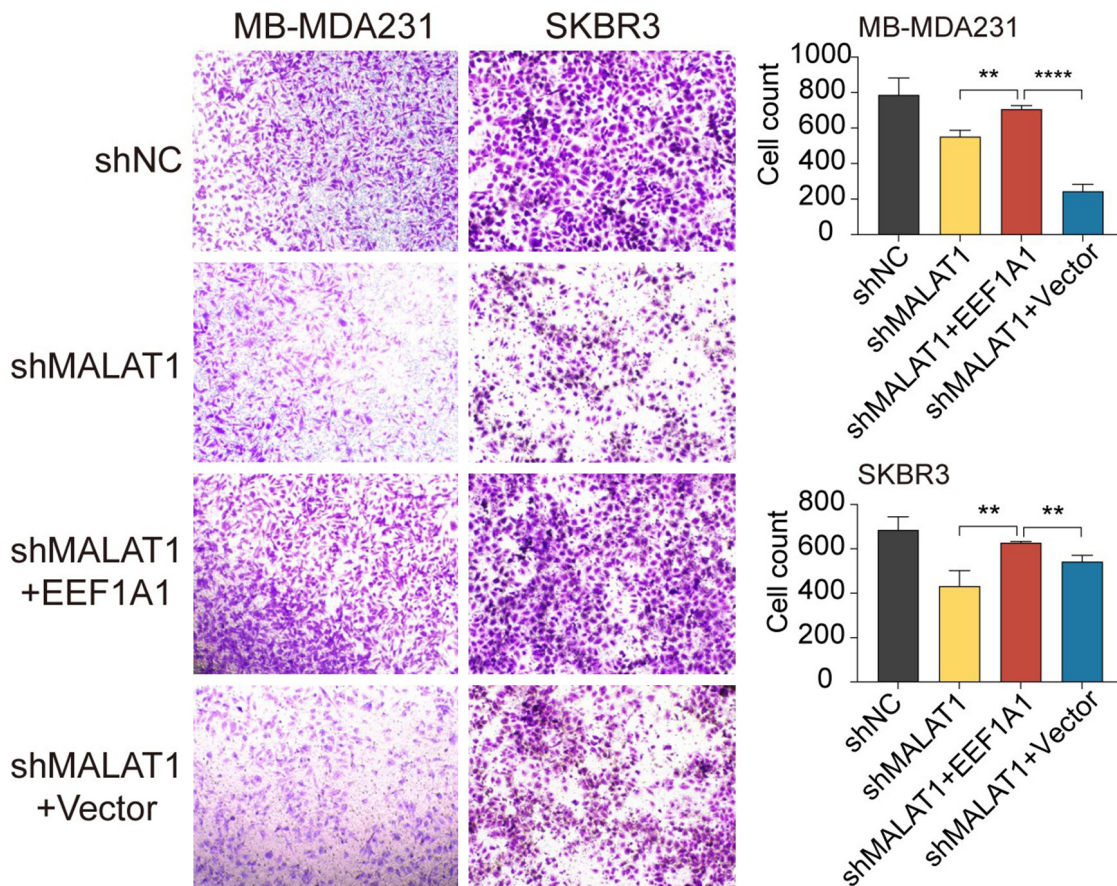
A EEF1A1 over-expression



B Cell Proliferation



C Cell invasion



MALAT1 epigenetically targets *EEF1A1*

Figure 7. *EEF1A1* rescues the effect induced by *MALAT1* knockdown. A. Overexpression of *EEF1A1* in breast cancer cells. The expression of *EEF1A1* was quantitated by Q-PCR. shNC: random shRNA control; shMALAT1: Cells that were transfected with *MALAT1* shRNA-1. β -Actin was used as an internal control. *** $P < 0.001$ as compared with the control groups. Overexpression of *EEF1A1* in breast cancer cells was measured by Western blot. B. Cell growth viability as measured by CCK-8 assay. C. Cell invasion as examined by Transwell assay. shNC: random shRNA control; shMALAT1: Cells that were transfected with *MALAT1* shRNA-2; shMALAT1+*EEF1A1*: *MALAT1* shRNA-knockdown cells were rescued by the *EEF1A1*-overexpression vector; shMALAT1+Vector: *MALAT1* shRNA-knockdown cells were transduced by the vector control lentivirus. The experiment was repeated for three times, and representative pictures are shown. Cell count of the invaded cells was analyzed by Image J software. The quantitation was shown as mean $\pm$ SD, ** $P < 0.01$, **** $P < 0.0001$ as compared with the control groups.