Genes & Diseases (2023) 10, 627–629

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Corrigendum to "The development of a sensitive fluorescent protein-based transcript reporter for high throughput screening of negative modulators of lncRNAs" [Genes & Diseases 5 (2018) 62–74]

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DOI of original article: https://doi.org/10.1016/j.gendis.2018.02.001.
Peer review under responsibility of Chongqing Medical University.

https://doi.org/10.1016/j.gendis.2023.02.004

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The authors regret having an image assembly error in Figure 5Ca, in which the image for the "0h dBiFP-AdRFP" group was erroneously duplicated with an overlapping image from the "36h BiFP dBIFP-AdR-simH19" group.

We confirm the error is restricted to the image assembly, and the underlying data and conclusions are correct and unchanged.

The authors would like to apologize for any inconvenience caused.

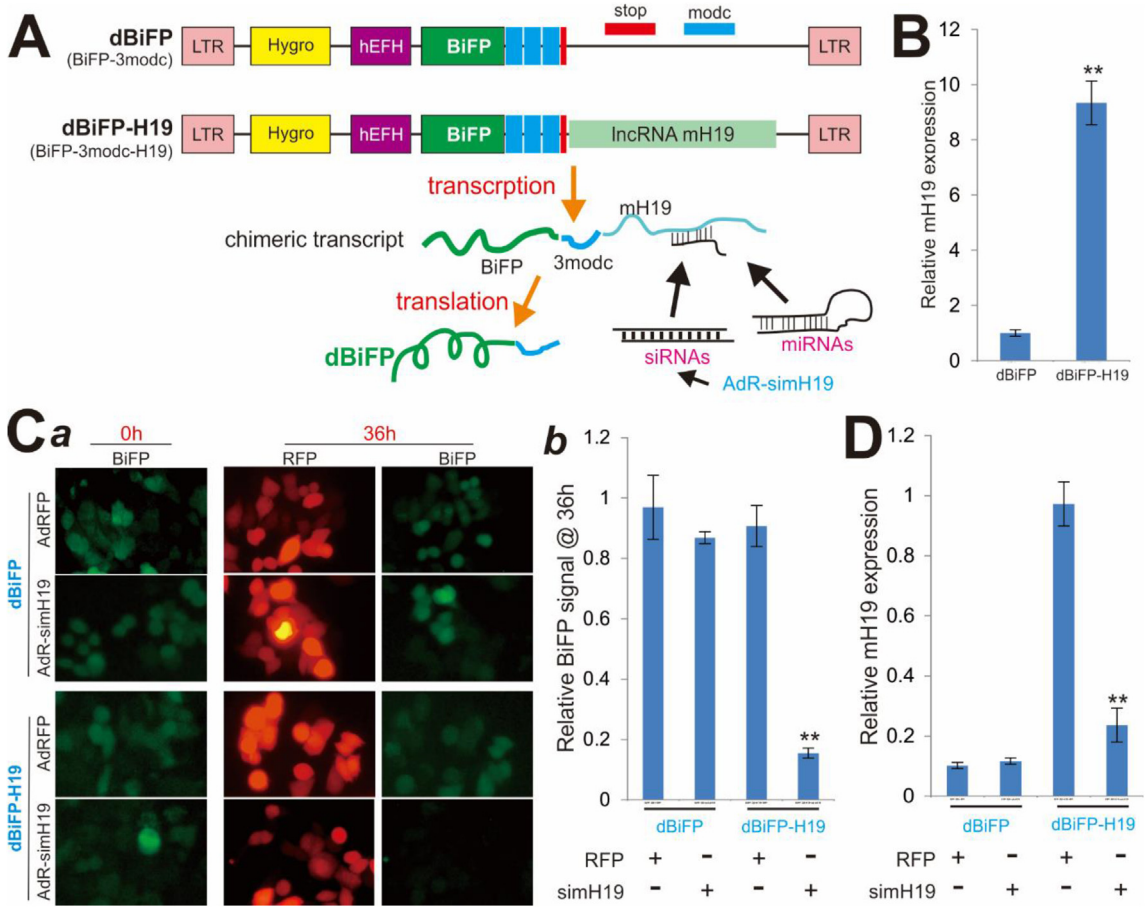

Figure 5 The highly degradable dBiFP as a sensitive transcription reporter of lncRNA H19. **(A)**Schematic representation of the construction of dBiFP-H19 transcriptional reporter. Mouse lncRNA H19 (mH19) was cloned into the downstream of the stop codon of the dBiFP coding region. It is expected a chimeric transcript of dBiFP-mH19 will be generated, which will be further translated into the highly degradable protein dBiFP. Targeting mH19 by siRNAs, miRNAs, naturally occurring or synthetic modulatory RNAs, or

small molecule compounds may lead to a decrease in the chimeric transcript and thus the decrease in BiFP signal. As a proof-of-principle experiment, we use an adenoviral vector expressing mH19-specific siRNAs, AdR-simH19 to knockdown mH19 transcript. **(B)** Generation of a stable dBiFP-H19 reporter line from HCT116 cells. TqPCR analysis indicates the high expression of mouse H19 in the dBiFP-H19 HCT116 stable line ($p < 0.01$ compared with that of the control line dBiFP). **(C)** H19-specific siRNAs effectively down-regulate dBiFP expression in dBiFP-H19 cells. Subconfluent dBiFP and dBiFP-H19 cells were infected with AdR-simH19 or AdRFP. Fluorescence signals were recorded at 0h and 36h after infection **(a)**. The BiFP fluorescence signal was quantitatively analyzed **(b)**. "**", $P < 0.01$ compared the AdR-simH19 infection with that of AdRFP infection. **(D)** TqPCR analysis of mouse H19 in dBiFP-H19 cells upon AdR-simH19 silencing. Subconfluent dBiFP and dBiFP-H19 cells were infected with AdR-simH19 or AdRFP for 36h. Total RNA was isolated and subjected to RT-PCR analysis. TqPCR assay was done in triplicate. "**" $P < 0.01$ when compared the expression level of AdR-simH19 infection with that of AdRFP infection