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Correction to: Construction of a competitive endogenous RNA network and analysis of potential regulatory axis targets in glioblastoma

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Following the publication of the original article [1], we were notified of an error in Fig. 7. The corrected Fig. 7 can be found below.

The online version of the original article can be found at https://doi.org/10.1186/s12935-021-01789-z.

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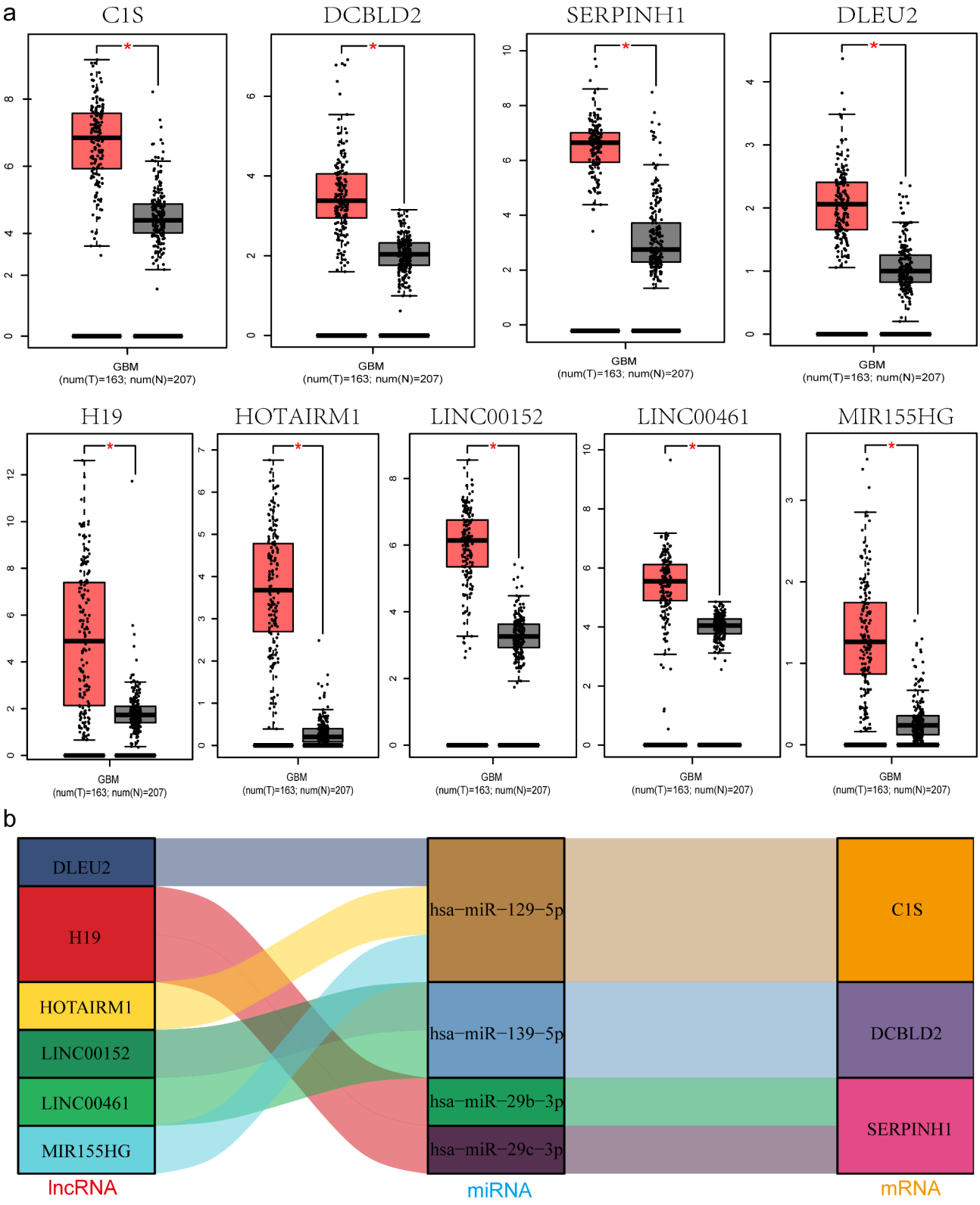

Fig. 7 Expression of genes and construction of the GBM lncRNA-miRNA-mRNA network. **a** Expression of nine key genes, including 6 lncRNAs and 3 mRNAs, in GBM and normal tissue samples from the GEPIA databases (*$p < 0.05$). **b** Ji mulberry figure revealing four pairs of ceRNA networks: H19/miR-29b-3p/SERPINH1, H19/miR-29c-3p/SERPINH1, LINC00152 LINC00461/miR-139-5p/DCBLD2, and MIR155HG HOTAIRM1 DLEU2/ miR-129-5p/C1S. GBM glioblastoma, GEPIA Gene Expression Profiling Interactive Analysis

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1. Yu K, Yang H, Lv QL, Wang LC, Tan ZL, Zhang Z, Ji YL, Lin QX, Chen JJ, He W, Chen Z, Shen XL. Construction of a competitive endogenous RNA network and analysis of potential regulatory axis targets in glioblastoma. Cancer Cell Int. 2021;21:102. https://doi.org/10.1186/s12935-021-01789-z

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