Check for updates

Correction: Identification of hub genes within the CCL18 signaling pathway in hepatocellular carcinoma through bioinformatics analysis

Jinlei Mao†, Yuhang Tao†, Keke Wang, Hanru Sun, Manqi Zhang, Liang Jin* and Yi Pan*

State Key Laboratory of Natural Medicines, Jiangsu Key Laboratory of Druggability of Biopharmaceuticals, School of Life Science and Technology, China Pharmaceutical University, Nanjing, Jiangsu, China

A Correction on

Identification of hub genes within the CCL18 signaling pathway in hepatocellular carcinoma through bioinformatics analysis

By Mao J, Tao Y, Wang K, Sun H, Zhang M, Jin L and Pan Y (2024). *Front. Oncol.* 14:1371990. doi: 10.3389/fonc.2024.1371990

In the published article, there were errors in Figure 6. Due to carelessness during the preparation of the Figures 6E and F, the images labeled "CCR3" in the row for "Migration, LM3, MHCC-97H", images labeled "LDHA" in the row for "Migration, LM3, MHCC-97H", images labeled "CCR3","LDHA" in the row for "Invasion, LM3", images labeled "CCR3","LDHA" in the row for "Invasion, MHCC-97H" and images labeled"Vector","CDC25C" in the row for "Invasion, MHCC-97H" show overlapping fields of view. We replaced images with the correct ones. The corrected Figure 6 and its caption appear below.

The original version of this article has been updated.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.
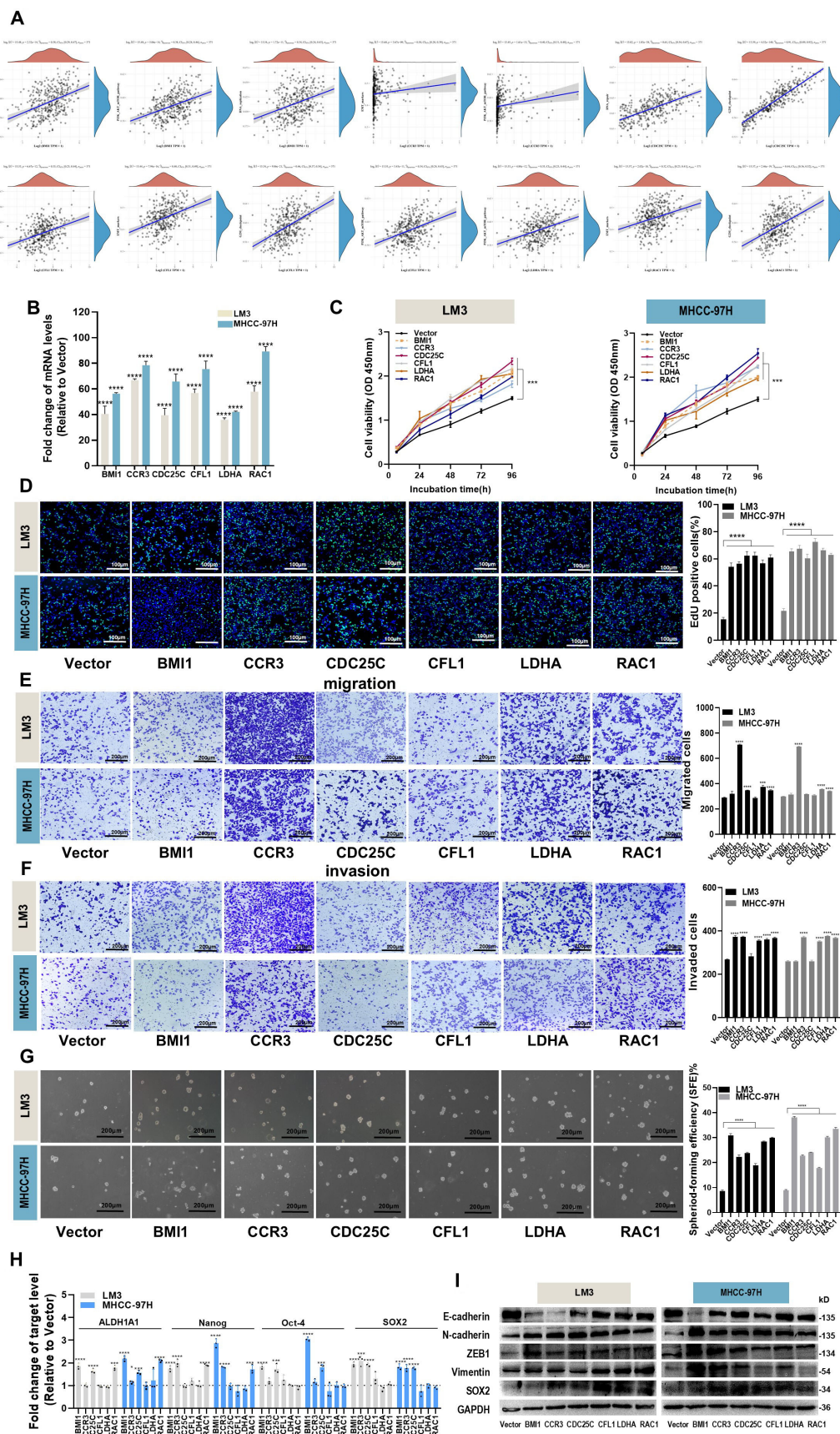
FIGURE 6 (Continued)

FIGURE 6 (Continued)

Effects of hub genes on proliferation, migration, invasion and stemness properties in HCC cells. **(A)** The correlations between six hub genes and pathway score were analyzed using Spearman. The abscissa represents the distribution of gene expression, and the ordinate represents the distribution of pathway score. The density curve on the right represents the trend in the distribution of pathway immune score, while the upper density curve represents the trend in the distribution of gene expression. The value on the top represents the correlation p value, correlation coefficient and correlation calculation method. **(B)** The overexpression efficiency of BMI1, CCR3, CDC25C, CFL1, LDHA and RAC1 overexpression plasmid was assessed by RT-qPCR. **(C, D)** Proliferation of LM3 and MHCC-97H cells after transfection with BMI1, CCR3, CDC25C, CFL1, LDHA and RAC1 overexpression plasmid for 48h was examined by CCK-8 assays **(C)** and EdU assays (**(D),** Scale bar:100 μm). **(E, F)** Migration **(E)** and invasion **(F)** of LM3 and MHCC-97H cells after transfection with BMI1, CCR3, CDC25C, CFL1, LDHA and RAC1 overexpression plasmid for 48h were detected by Transwell assays. Scale bar:200 μm. **(G)** Sphere-formation abilities of LM3 and MHCC-97H cells were observed after transfection with BMI1, CCR3, CDC25C, CFL1, LDHA, and RAC1 overexpression plasmids for 48h. Scale bar: 200 μm. **(H)** The expression of stemness-related genes in LM3 and MHCC-97H cells was analyzed after transfection with BMI1, CCR3, CDC25C, CFL1, LDHA, and RAC1 overexpression plasmids for 48h. **(I)** The protein levels of EMT-related genes in LM3 and MHCC-97H cells were measured after