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EDITED AND REVIEWED BY
Ahmed A. Al-Karmalawy,
University of Mashreq, Iraq

*CORRESPONDENCE
Jian-Hong Li,
✉ gracelee100@163.com

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Correction: Investigation of the mechanism of Xiaoyin Jiedu Yin in the treatment of psoriasis based on bioinformatics, machine learning

Ru-Nan Fang¹, Yang Zhou², Yang Shen¹, Yuan Sun¹ and
Jian-Hong Li^{1*}

¹Department of Dermatology, Dongzhimen Hospital, Beijing University of Chinese Medicine, Beijing, China, ²Department of Endocrinology, Guang'anmen Hospital, Beijing University of Chinese Medicine, Beijing, China

KEYWORDS

psoriasis, bioinformatics, network pharmacology, Xiaoyin Jiedu Yin, machine learning, single-cell RNA sequencing

A Correction on

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by Fang R-N, Zhou Y, Shen Y, Sun Y and Li J-H (2025). *Front. Chem.* 13:1623449. doi: 10.3389/fchem.2025.1623449

There was a mistake in **Figure 6B** as published. The β -Tubulin bands were indentified as target protein, and the AKR1B10 bands were identified as internal control. The β -Tubulin bands should serve as the internal control, while the AKR1B10 bands represent the target protein. The corrected figure appears below.

The original article has been updated

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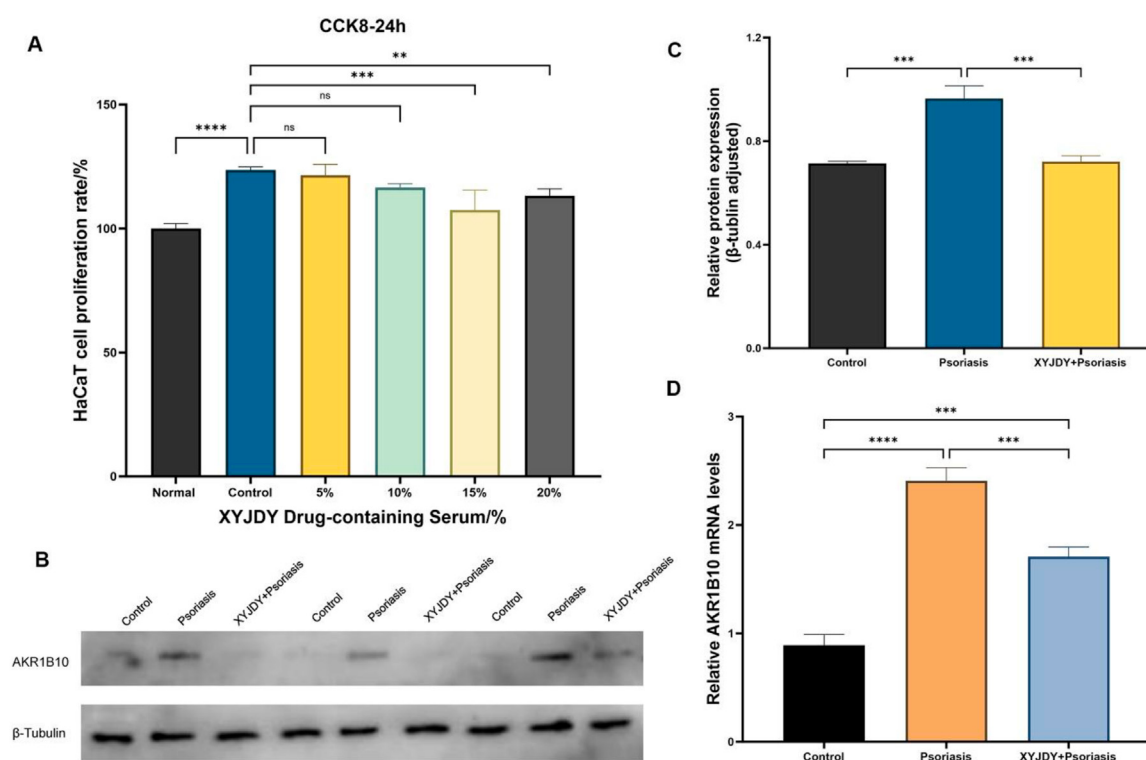


FIGURE 6

(A) CCK-8 Detection of cell proliferation rate in a psoriasis-like inflammation model of HaCaT cells after 24 h of intervention with XYJDY drug-containing serum; (B) Western blot analysis of AKR1B10 expression in HaCaT cells induced by IL-17A in different treatments; (C) Western blot detection of AKR1B10 expression in each group (n = 3/group); (D) RT-qPCR analysis to detect the expression of AKR1B10 mRNAs in each group (n = 3/group); ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$.