

Correction

Correction for: High expression of CCNB1 driven by ncRNAs is associated with a poor prognosis and tumor immune infiltration in breast cancer

Hongtao Fu¹, Kun Li², Shui Wang¹, Yuming Li³

¹Department of Breast Surgery, Jiangsu Province Hospital, The First Hospital Affiliated Hospital with Nanjing Medical University, Nanjing 210029, China

²Department of Emergency, Changsha Central Hospital, The Affiliated Changsha Central Hospital of Hengyang Medical School, University of South China, Changsha 410004, China

³Department of Traditional Chinese Medicine and Western Medicine, Hunan Cancer Hospital, The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, Changsha 410006, China

Correspondence to: Yuming Li; **email:** liyuming@hnca.org.cn

Keywords: biomarker, bioinformatics analysis

Original article: [Aging \(Albany NY\) 2022; 14: pp 6780–6795](#)

PMID: [36040381](#)

PMCID: [PMC9467392](#)

doi: [10.18632/aging.204253](#)

This article has been corrected: The authors corrected the order of the affiliations and correct order is listed below:

Hongtao Fu^{1,2}, Kun Li³, Shui Wang², Yuming Li¹

¹Department of Traditional Chinese Medicine and Western Medicine, Hunan Cancer Hospital, The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University, Changsha 410006, China

²Department of Breast Surgery, Jiangsu Province Hospital, The First Hospital Affiliated Hospital with Nanjing Medical University, Nanjing 210029, China

³Department of Emergency, Changsha Central Hospital, The Affiliated Changsha Central Hospital of Hengyang Medical School, University of South China, Changsha 410004, China