

Corrigendum to 'single-cell transcriptomics of blood reveals a natural killer cell subset depletion in tuberculosis'

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Yi Cai,^a Youchao Dai,^{a,b} Yejun Wang,^a Qianting Yang,^c Jiubiao Guo,^a Cailing Wei,^c Weixin Chen,^c Huanping Huang,^a Jialou Zhu,^a Chi Zhang,^d Weidong Zheng,^d Zhihua Wen,^e Haiying Liu,^f Mingxia Zhang,^c Shaojun Xing,^a Qi Jin,^f Carl G Feng,^{a,g} and Xinchun Chen^{a,*}

^aGuangdong Key Laboratory of Regional Immunity and Diseases, Department of Pathogen Biology, Shenzhen University School of Medicine, Shenzhen 518000, China

^bResearch Institute of Infectious Diseases, Guangzhou Eighth People's Hospital, Guangzhou Medical University, Guangzhou 510000, China

^cGuangdong Key Lab for Diagnosis and Treatment of Emerging Infectious Diseases, Shenzhen Third People's Hospital, Southern University of Science and Technology, Shenzhen 518000, China

^dShenzhen University General Hospital, Shenzhen University School of Medicine, Shenzhen, China

^eYuebei Second People's Hospital, Shaoguan 512000, China

^fThe MOH Key Laboratory of Systems Biology of Pathogens, Institute of Pathogen Biology, and Centre for Tuberculosis, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100176, China

^gDepartment of Infectious Diseases and Immunology, Sydney Medical School, the University of Sydney, Sydney, NSW 2006, Australia

The authors regret that there was an error in [Figure 5](#) of this article. Specifically, for [Figure 5g](#), the X axis label of "After" and "Before" were reversed. The level of CD3-CD7+GZMB+ increased after initiation of treatment in TB patients. The corrected figures are shown below.

These corrections have not changed the description, interpretation, or the conclusions of the manuscript in the originally published version. The authors apologize for any inconvenience caused.

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*Corresponding author.

E-mail address: chenxinchun@szu.edu.cn (X. Chen).

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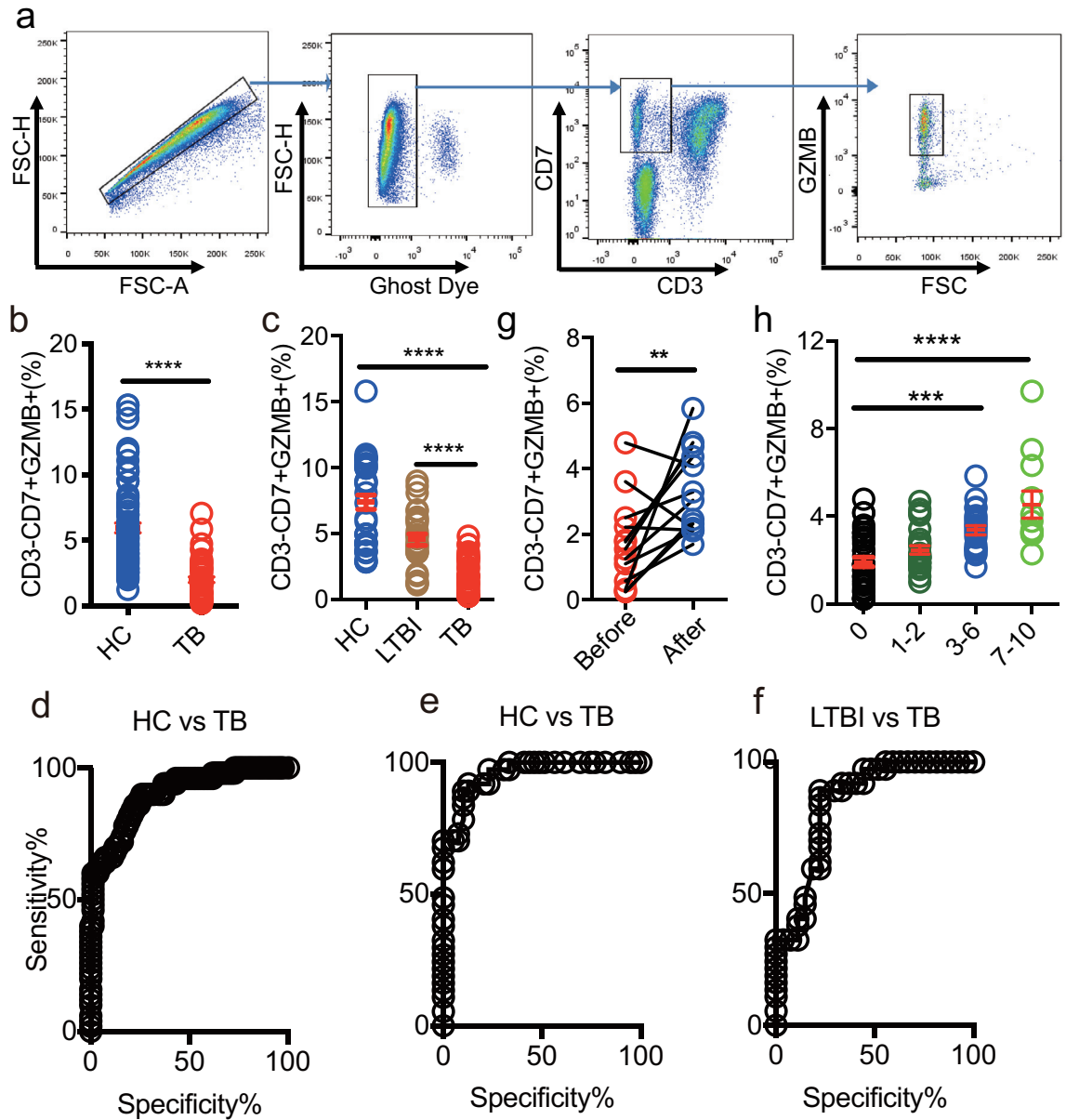


Figure 5. Flow cytometry analysis of CD3-CD7+GZMB+ subsets in HC, LTBI and TB. (a) Gating strategy of CD3-CD7+GZMB+ by flow cytometry. (b) The frequency of CD3-CD7+GZMB+ in HC and TB in the second cohort (HC=81, TB=50). (c) The frequency of CD3-CD7+GZMB+ in HC, LTBI and TB in the third cohort (HC=39, LTBI=27, and TB=37). (d–f) ROC curve for CD3-CD7+GZMB+ to separate TB from HC (d), or LTBI (f). AUC=0.93 (d), AUC=0.96 (e), AUC=0.85 (f). AUC, area under curve. (g–h) The frequency of CD3-CD7+GZMB+ is increased after anti-TB treatment in TB patients. (g) follow-up TB patients ($n = 11$); (h) TB patients received anti-TB treatment from 1 to 10 months ($n = 73$). A one-way ANOVA Newman-Keuls multiple comparison test was used to compare the differences among multiple groups. An unpaired t -test was used to analyze the differences between two groups. An paired t -test was used to analyze the differences in the follow-up patients. The data represent the means \pm SEM. ** $P < 0.001$, *** $P < 0.001$, **** $P < 0.0001$.