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Frontiers Editorial Office,
Frontiers Media SA, Switzerland

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RECEIVED 16 April 2024

ACCEPTED 17 April 2024

PUBLISHED 22 April 2024

CITATION

She H, Tan L, Wang Y, Du Y, Zhou Y, Zhang J,
Du Y, Guo N, Wu Z, Li Q, Bao D, Mao Q,
Hu Y, Liu L and Li T (2024) Corrigendum:

Integrative single-cell RNA sequencing and
metabolomics decipher the imbalanced lipid-
metabolism in maladaptive immune
responses during sepsis.

Front. Immunol. 15:1418495.

doi: 10.3389/fimmu.2024.1418495

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Corrigendum: Integrative single-cell RNA sequencing and metabolomics decipher the imbalanced lipid-metabolism in maladaptive immune responses during sepsis

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KEYWORDS

sepsis, lipid-metabolism, machine learning algorithm, single-cell RNA sequencing, metabolomics

A Corrigendum on

Integrative single-cell RNA sequencing and metabolomics decipher the imbalanced lipid-metabolism in maladaptive immune responses during sepsis

By She H, Tan L, Wang Y, Du Y, Zhou Y, Zhang J, Du Y, Guo N, Wu Z, Li Q, Bao D, Mao Q, Hu Y, Liu L and Li T (2023). *Front. Immunol.* 14:1181697. doi: 10.3389/fimmu.2023.1181697

Missing Citation.

In the published article the reference Qiu X, Li J, Bonenfant J, Jaroszewski L, et al. Dynamic changes in human single-cell transcriptional signatures during fatal sepsis. *J Leukoc Biol.* 2021 Dec;110(6):1253-1268. PMID: 34558746. was not cited in the article. The citation has now been inserted in **Materials and methods section**; *Single cell RNA-seq analysis*, as followed:

“The scRNA-seq dataset GSE167363 [24] (included 5 sepsis patients and 2 healthy controls) was analyzed in this study”.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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