

CORRECTION

Open Access



Correction: Near complete genome sequences from Southern Vietnam revealed local features of genetic diversity and intergenerational changes in SARS-CoV-2 variants in 2020–2021

Anna S. Gladkikh¹, Thang M. Cao², Ekaterina O. Klyuchnikova^{1*}, Manh H. Dao², Alena A. Sharova¹, Vasilina D. Melnichenko¹, Margarita R. Popova¹, Tatiana V. Arbuzova¹, Valeriya A. Sbarzaglia¹, Nadezhda A. Tsyganova¹, Edward Ramsay¹ and Vladimir G. Dedkov^{1,3}

Correction: BMC Infect Dis 23, 806 (2023)
<https://doi.org/10.1186/s12879-023-08814-8>

In the original publication of this article [1] Figs. 4 and 5 were swapped. The incorrect and correct information is shown in this correction article, the original article has been updated.

The original article can be found online at <https://doi.org/10.1186/s12879-023-08814-8>.

*Correspondence:

Ekaterina O. Klyuchnikova
ekaterina.ibg@gmail.com

¹ Saint Petersburg Pasteur Institute, 14 Mira Street, Saint, Petersburg 197101, Russia

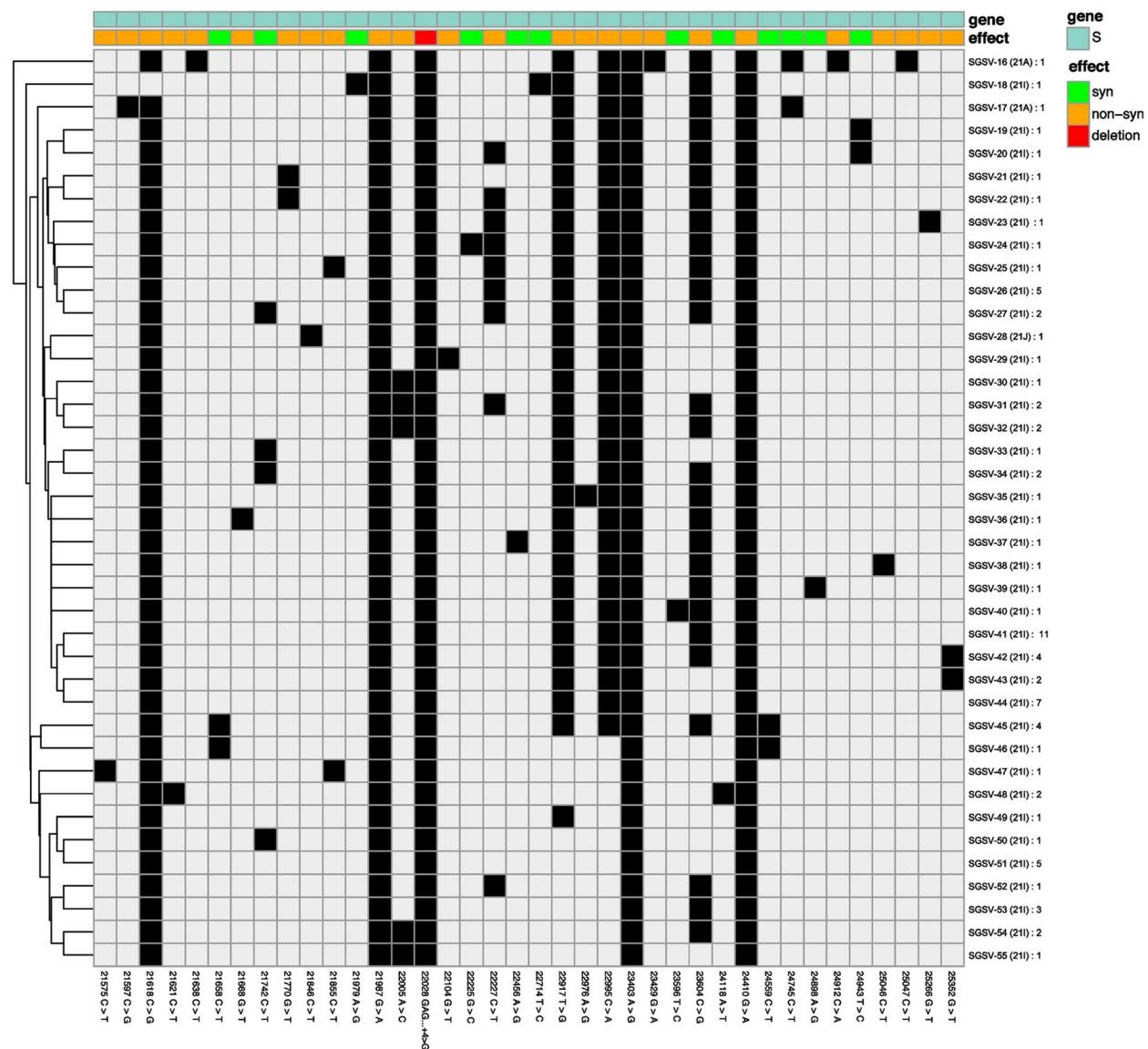
² Pasteur Institute in Ho Chi Minh City, Ho Chi Minh City, Vietnam

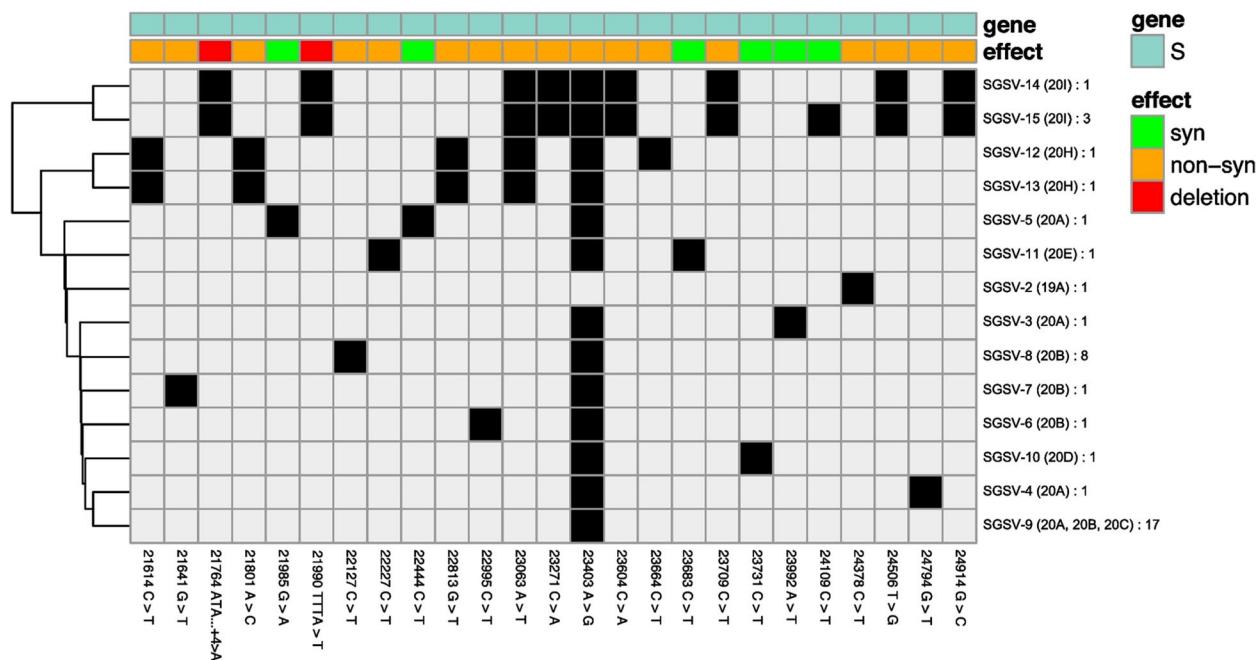
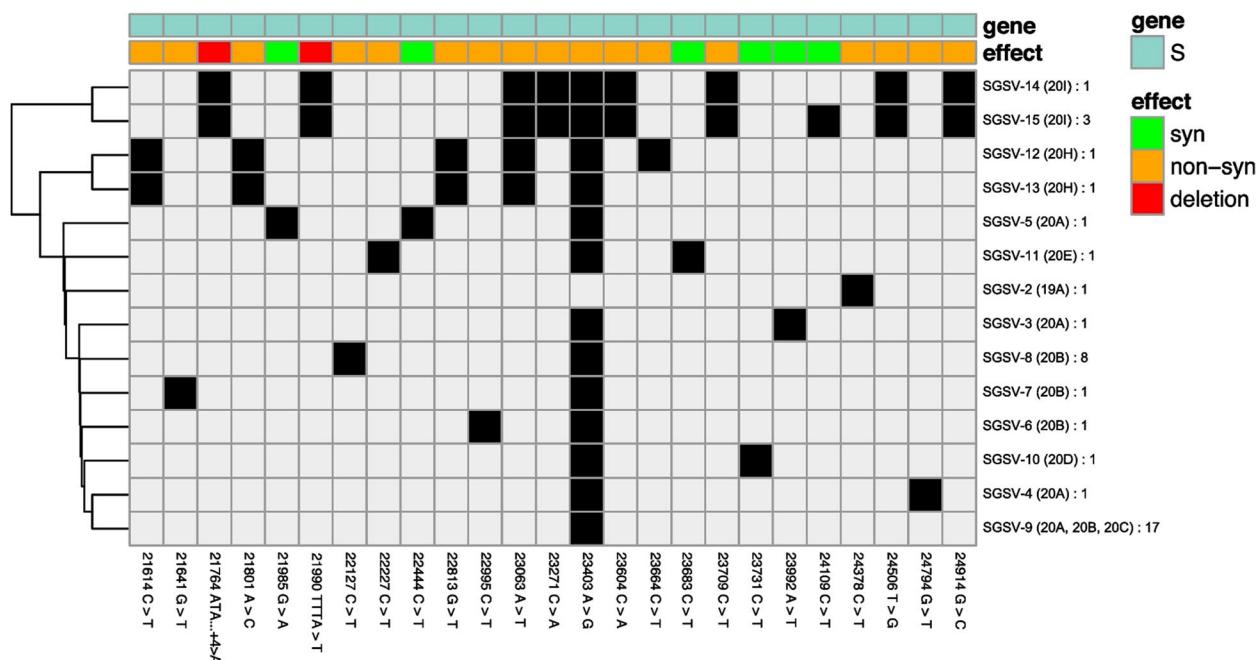
³ Martsinovsky Institute of Medical Parasitology, Tropical and Vector Borne Diseases, Sechenov First Moscow State Medical University, Moscow, Russia



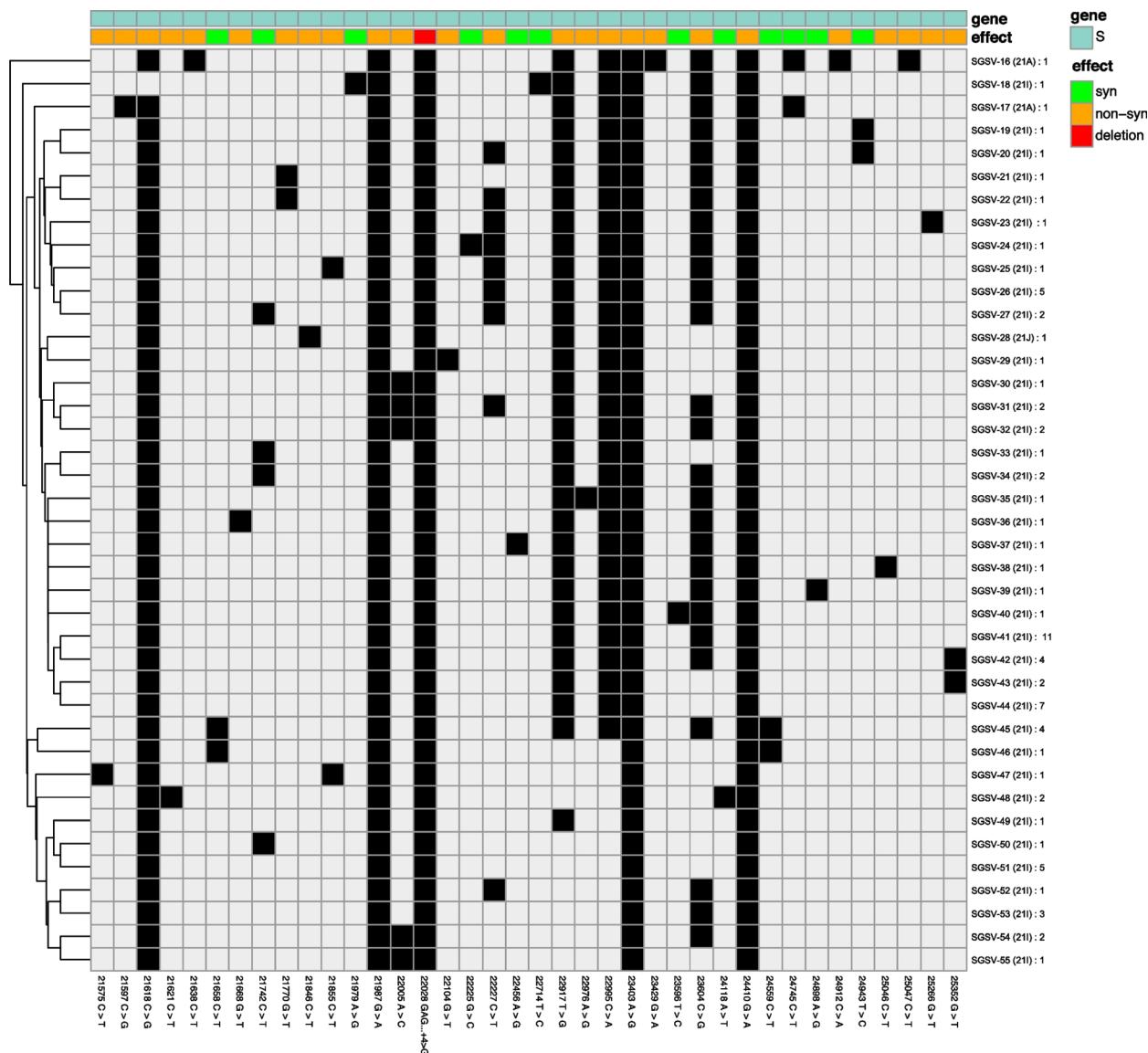
© The Author(s) 2023. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

Incorrect Figure 4



Incorrect Figure 5**Correct Figure 4**

Correct Figure 5



Published online: 21 December 2023

Reference

- Gladkikh AS, et al. Near complete genome sequences from Southern Vietnam revealed local features of genetic diversity and intergenerational changes in SARS-CoV-2 variants in 2020–2021. BMC Infect Dis. 2023;23:806. <https://doi.org/10.1186/s12879-023-08814-8>.