

Author Correction

Correction for Köndgen et al., “A robust, scalable, and cost-efficient approach to whole genome sequencing of RSV directly from clinical samples”

Sophie Köndgen, Djin-Ye Oh, Andrea Thürmer, Somayyeh Sedaghatjoo, Livia V. Patrono, Sébastien Calvignac-Spencer, Barbara Biere, Thorsten Wolff, Ralf Dürrwald, Stephan Fuchs, Janine Reiche

Volume 62, no. 3, e011111-23, 2024, <https://doi.org/10.1128/jcm.01111-23>. Page 7: Figure 2 should appear as shown in this correction. In Fig. 2A, the total number of genotype GA2.3.5 was mislabeled; 56 samples were sequenced instead of the indicated 55. In Fig. 2B, bar lengths have been adjusted to reflect the timespans as originally provided by Goya et al. (*Influenza Other Respir Viruses* 14:274–285, 2020, <https://doi.org/10.1111/irv.12715>): the correct circulation periods are 1999–2013 for genotype GA3.0.4, 1999–2010 for GA2.3.2, and 2004–2015 for GB5.0.2.

This correction does not alter the overall results or conclusions of the paper.

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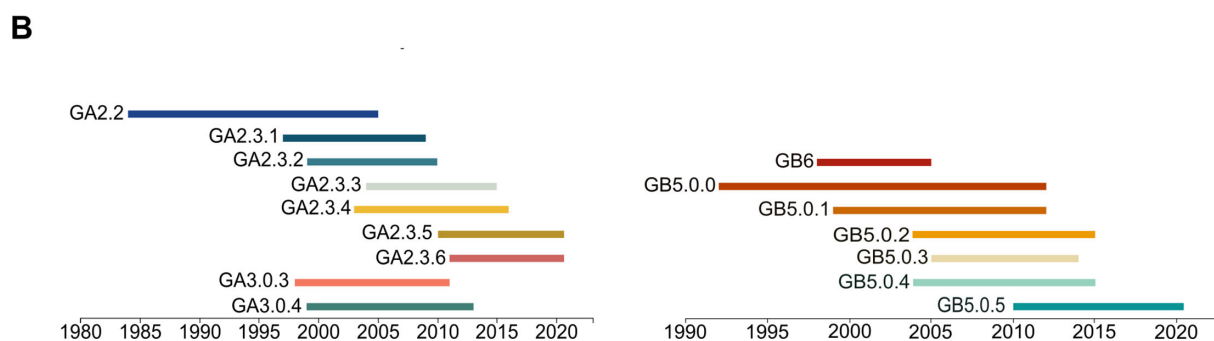
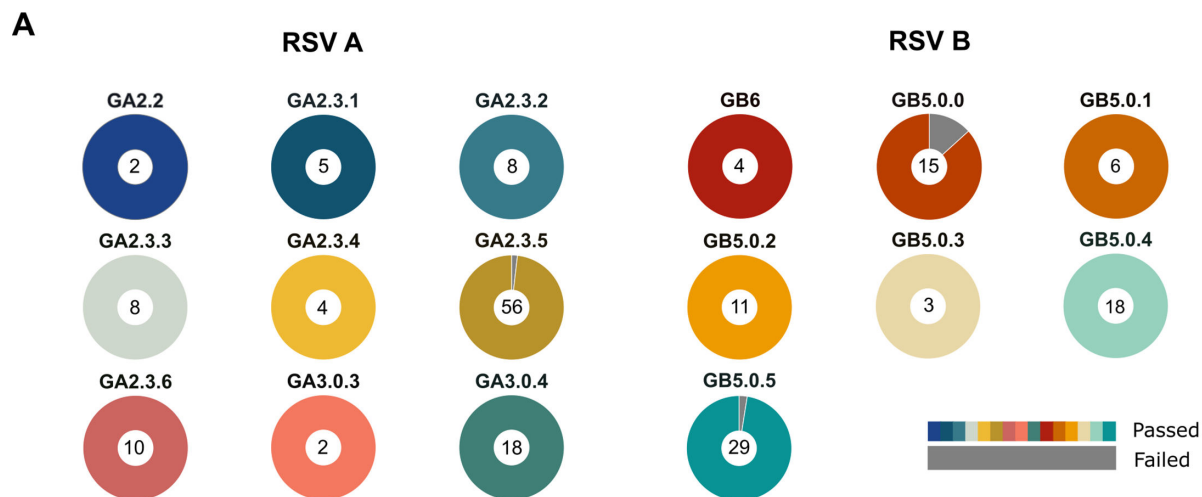


FIG 2

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