

CORRECTION

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# Correction to: Genome evolution of SARS-CoV-2 and its virological characteristics



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**Correction to: *Inflamm Regener* 40, 17 (2020)**  
<https://doi.org/10.1186/s41232-020-00126-7>

After publication of the original article [1] the authors spotted an error in the last sentence of the 1st paragraph of “Phylogeny of SARS-CoV-2” in the Main text. This sentence originally stated:

- In addition, the genus *Betacoronavirus* is reported to be divided into four lineages (subgenera): Lineage A (subgenus *Embecovirus*), Lineage B (subgenus *Sarbecovirus*), Lineage C (subgenus *Merbecovirus*), and Lineage D (subgenus *Nobecovirus*) [7, 8].

However, Bat Hp-betaCoV belong to *Hibecovirus*. Therefore, the corrected sentence reads as followed:

- In addition, the genus *Betacoronavirus* is reported to be divided into five subgenera: *Sarbecovirus*, *Hibecovirus*, *Nobecovirus*, *Merbecovirus*, and *Embecovirus* [7, 8].

This error also affected Figure 1. The incorrect (Fig. 1) and correct (Fig. 2) version of figure 1 are shown in this correction article. The original article has been updated to rectify the above errors.

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## Reference

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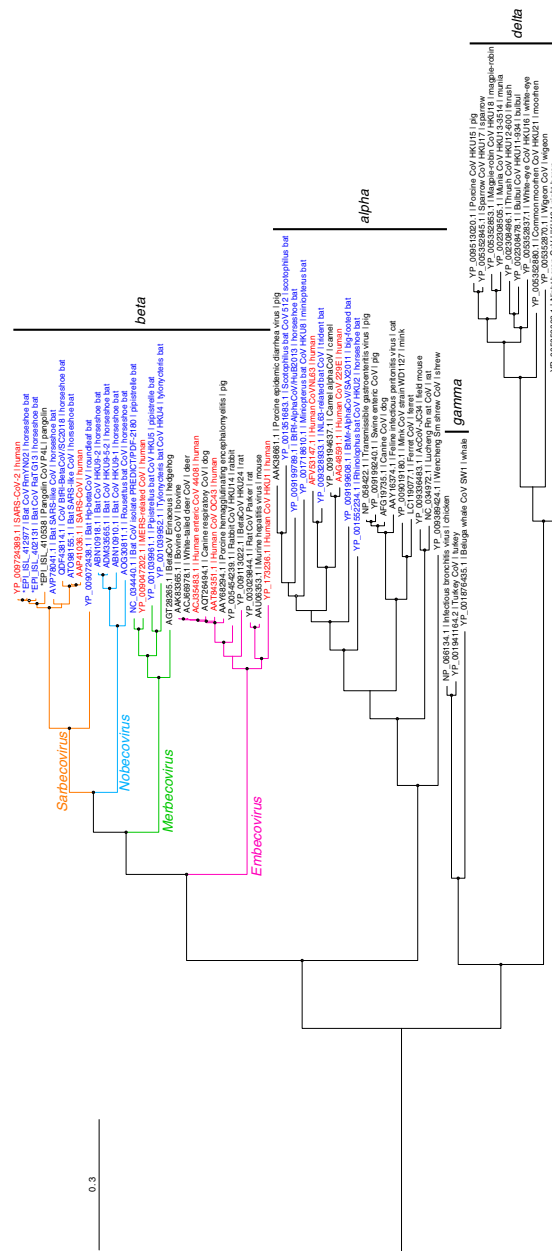
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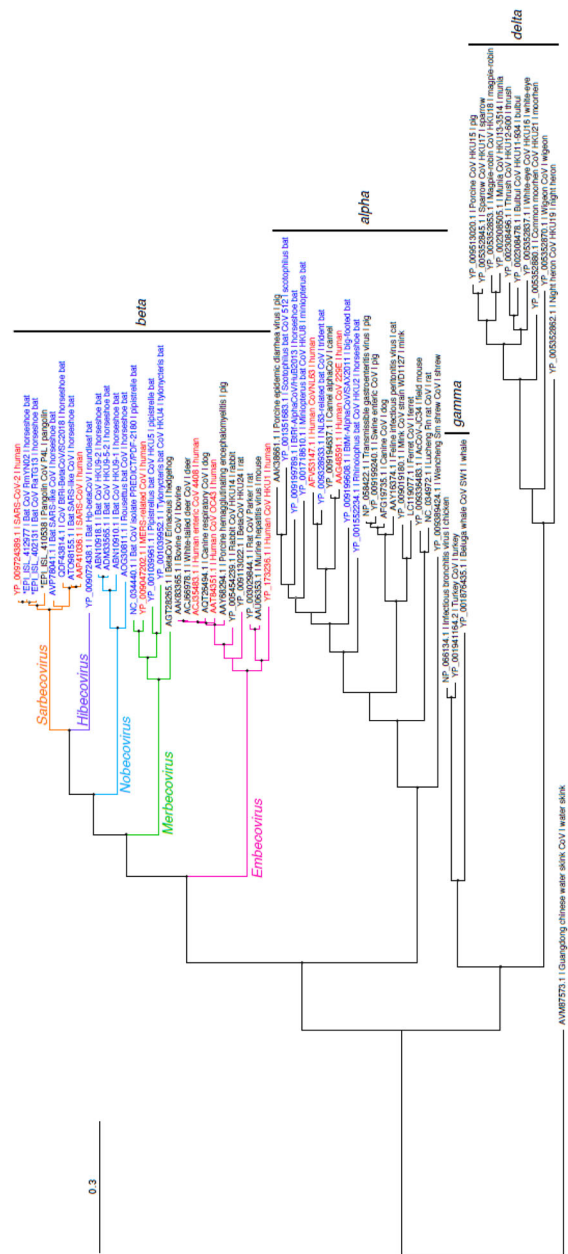
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**Fig. 1** The incorrect version of figure 1 as originally published



**Fig. 2** The correct version of figure 1