



Corrigendum: Identification of Diverse Bat Alphacoronaviruses and Betacoronaviruses in China Provides New Insights Into the Evolution and Origin of Coronavirus-Related Diseases

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A Corrigendum on

Identification of Diverse Bat Alphacoronaviruses and Betacoronaviruses in China Provides New Insights Into the Evolution and Origin of Coronavirus-Related Diseases

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In the original article, there was a mistake in **Table 1** as published. All instances of “*Rhinolophus affinis*” in **Table 1** should be corrected into “*Rhinolophus sinicus*.” The corrected **Table 1** appears below.

In the original article, there was an error. All instances of “*Rhinolophus affinis*” or “*R. affinis*” in the text should be corrected into “*Rhinolophus sinicus*” or “*R. sinicus*.”

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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TABLE 1 | Coronavirus distribution in different bat species and locations.

Province	Species	Pool code for NGS	Collection date [year.month]	Virus detection rate (pos. /indiv. [%])	Sequencing reads related to CoV	Virus
Sichuan	<i>Rhinolophus</i> spp.	55	2016.08	2/22 [9.1%]	1598	BtRI-BetaCoV/SC2018
Yunnan	<i>Rhinolophus sinicus</i>	57	2016.09	2/39 [5.1%]	84818	BtRs-BetaCoV/YN2018A
	<i>Rhinolophus sinicus</i>	60	2016.09	4/40 [10%]	884839	BtRs-BetaCoV/YN2018B BtRs-AlphaCoV/YN2018
	<i>Rhinolophus sinicus</i>	61	2016.09	2/46 [4.3%]	37997	BtRs-BetaCoV/YN2018C
	<i>Rhinolophus sinicus</i>	62	2016.09	4/51 [7.8%]	11131	BtRs-BetaCoV/YN2018D
Guangxi	<i>Scotophilus kuhlii</i>	3	2017.05	2/27 [7.4%]	5609	BtSk-AlphaCoV/GX2018A
	<i>Scotophilus kuhlii</i>	4	2017.05	1/39 [2.6%]	4381	BtSk-AlphaCoV/GX2018D
	<i>Cynopterus sphinx</i>	11	2017.05	2/30 [6.7%]	6138	BtCs-BetaCoV/GX2018
	<i>Scotophilus kuhlii</i>	12	2017.05	1/41 [2.4%]	4353	BtSk-AlphaCoV/GX2018B
	<i>Scotophilus kuhlii</i>	13	2017.05	2/43 [4.7%]	37	BtSk-AlphaCoV/GX2018C