

CORRECTION

Open Access



# Correction to: Genome-wide association study reveals 14 new SNPs and confirms two structural variants highly associated with the horned/polled phenotype in goats

Jiazhong Guo<sup>1</sup>, Rui Jiang<sup>1</sup>, Ayi Mao<sup>1</sup>, George E. Liu<sup>2</sup>, Siyuan Zhan<sup>1</sup>, Li Li<sup>1</sup>, Tao Zhong<sup>1</sup>, Linjie Wang<sup>1</sup>, Jiaxue Cao<sup>1</sup>, Yu Chen<sup>3</sup>, Guojun Zhang<sup>3</sup> and Hongping Zhang<sup>1\*</sup>

**Correction to: BMC Genomics 22, 769 (2021)**  
<https://doi.org/10.1186/s12864-021-08089-w>

Following publication of the original article [1], the authors noted several typographical errors [corrections in boldface]:

1. The second sentence of the first paragraph of the Results should read: “A total of **14,112,599** single nucleotide polymorphisms (SNPs) (**14,047,290** biallelic and **65,309** multiallelic) and **1,303,926** short insertions and deletions (Indels) were identified across the goat autosomal genome.”
2. The last sentence of the first paragraph of the ‘Short-read alignment and variant calling annotation’ should read: “The **ARS1** goat assembly was generated from a horned adult male San Clemente goat.”
3. The second-to-last sentence of the last paragraph of the ‘Methods’ section should read: “We then used the combination of the 1822-bp and **369-bp** fragments

to classify horned, polled, and PIS-affected goats, in 333 sampled goats from four Chinese goat breeds (i.e., JT:  $n = 150$  [86 horned, 60 polled, and 4 PIS-affected], CB:  $n = 23$ , TC:  $n = 42$ , and NJ:  $n = 118$  [54 male, 64 female]).”

The authors apologize for any inconvenience that these errors may have caused.

The original article [1] has been updated.

#### Author details

<sup>1</sup>College of Animal Science and Technology, Sichuan Agricultural University, Chengdu 611130, China. <sup>2</sup>Animal Genomics and Improvement Laboratory, BARC, Agricultural Research Service, USDA, Beltsville, MD 20705, USA. <sup>3</sup>Nanjing Yellow Goat Scientific Research Institute, Bazhong 635600, China.

Published online: 10 February 2022

#### Reference

1. Guo J, Jiang R, Mao A, et al. Genome-wide association study reveals 14 new SNPs and confirms two structural variants highly associated with the horned/polled phenotype in goats. *BMC Genomics*. 2021;22:769. <https://doi.org/10.1186/s12864-021-08089-w>.

The original article can be found online at <https://doi.org/10.1186/s12864-021-08089-w>.

\*Correspondence: [zhp@sicau.edu.cn](mailto:zhp@sicau.edu.cn)

<sup>1</sup> College of Animal Science and Technology, Sichuan Agricultural University, Chengdu 611130, China

Full list of author information is available at the end of the article



© The Author(s) 2022. **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.