ERRATUM

Correction to: Population-wide sampling of retrotransposon insertion polymorphisms using deep sequencing and efficient detection

Qichao Yu [1,2], Wei Zhang [1,2], Xiaolong Zhang[2], Yongli Zeng[2], Yeming Wang [2], Yanhui Wang[2], Liqin Xu [2], Xiaoyun Huang [2], Nannan Li [2], Xinlan Zhou [2], Jie Lu [3], Xiaosen Guo [2], Guibo Li [2,4], Yong Hou [2,4], Shiping Liu [2,5] and Bo Li [2,6]

[1]BGI Education Center, UCAS: Building 11, Beishan Industrial Zone, Yantian District, Shenzhen, 518083, China; [2]BGI-Shenzhen: Building 11, Beishan Industrial Zone, Yantian District, Shenzhen, 518083, China; [3]BGI College: Building 11, Beishan Industrial Zone, Yantian District, Shenzhen, 518083, China; [4]Department of Biology, University of Copenhagen: Noregade 10, Copenhagen 1165, Denmark; [5]School of Biology and Biological Engineering, SCUT: Postdoctoral Apartment Building, South China University of Technology, Wushan RD., TianHe District, Guangzhou, 510640, China and [6]BGI-Forensics: Building 11, Beishan Industrial Zone, Yantian District, Shenzhen, 518083, China

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In the original version of the article "Population-wide sampling of retrotransposon insertion polymorphisms using deep sequencing and efficient detection," by Qichao Yu et al. [1], the author names for reference 16 (Tellier LC) [2] and 50 [3] were incorrect.

Furthermore, the protocol DOIs for reference 52 [4] and 53 [5] were incorrect and did not resolve. The names and DOIs have been corrected, and the authors apologize for the error.

References

1. Yu Q, Zhang W, Zhang X et al. Population-wide sampling of retrotransposon insertion polymorphisms using deep sequencing and efficient detection. GigaScience 2017;**6**(9):1–7.

2. Lan T, Lin H, Tellier LC et al. Deep whole-genome sequencing of 90 Han Chinese genomes. Gigascience 2017;**6**(9):1–7.

3. Lan T, Lin H, Zhu W et al. Deep whole-genome sequencing of 90 Han Chinese genomes. GigaScience 2017;**6**(9):1–7.

4. Lin H. SNP INDEL calling. Protocols.io. 2017 dx.doi.org/10.17504/protocols.io.grkbv4w.

5. Yu Q, Zhang W, Zhang X et al. Simulating reads for detection of transportable element insertions. Protocols.io. 2017. dx.doi.org/10.17504/protocols.io.imrcc56.