

CORRECTION

Open Access

Author Correction: Discovery of new genetic loci for male sexual orientation in Han population

Shao-Hua Hu, Hai-mei Li, Hao Yu, Yan Liu, Chen-Xing Liu, Xian-bo Zuo, Jing Lu, Jia-Jun Jiang, Cai-Xi Xi, Bo-Chao Huang, Hu-Ji Xu, Jian-Bo Hu, Jian-Bo Lai, Man-Li Huang, Jian-Ning Liu, Dan-Ge Xu, Xi-Chao Guo, Wei Wu, Xin Wu, Lei Jiang, Meng Li, Guang-Ping Zhang, Jin-Wen Huang, Ning Wei, Wen Lv, Jin-Feng Duan, Hong-Li Qi, Chan-Chan Hu, Jing-Kai Chen, Wei-Hua Zhou, Wei-Juan Xu, Chen-Feng Liu, Hai-Yong Liang, Jing Du, Shu-Fa Zheng, Qiao-Ling Lu, Lin Zheng, Xiao-Wei Hu, Feng-Xiang Chen, Peng Chen, Biao Zhu, Li-Jun Xu, Zhi-Min Ni, Ye-Zhen Fang, Zuo-Kai Yang, Xin-Ren Shan, En-de Zheng, Fan Zhang, Qing-qing Zhou, Yi Rao, Dick Swaab, Wei-Hua Yue and Yi Xu 

Correction to: *Cell Discovery* (2021) 7:103
<https://doi.org/10.1038/s41421-021-00341-7>,
Published online 31 October 2021

In the initial published version of this article¹, we missed some errors while proofreading the manuscript for the publication. The statistical values in Abstract and Results sections were inconsistent with those in Table 1. Upon careful examination of our original data, the second sentence in Abstract section should be “Here, we performed a two-stage genome-wide association study (GWAS) with a total sample of 1478 homosexual males and 3313 heterosexual males in Han Chinese populations and identified two genetic loci (rs17320865, Xq27.3, *FMR1NB*, $P_{meta} = 7.61 \times 10^{-9}$, OR = 1.31; rs7259428, 19q12, *ZNF536*, P_{meta}

$= 8.20 \times 10^{-15}$, OR = 0.65) showing consistent association with male sexual orientation.” On page 2, the second column, the lines 28–35 should be “All four SNPs showed consistent association in the independent validation samples, and two SNPs reached a genome-wide significance level ($P < 5 \times 10^{-8}$) after meta-analysis, including SNP rs7259428 on chromosome 19q12 (located in *ZNF536*, $P = 8.20 \times 10^{-15}$, OR = 0.65; Fig. 1e and Table 1) and rs17320865 on chromosome Xq27.3 (located in *FMR1NB*, $P = 7.61 \times 10^{-9}$, OR = 1.31; Fig. 1d and Table 1).” In Table 1, the gene symbol ‘*ZNF356*’ should be ‘*ZNF536*’. The corrected version of the Table 1 is displayed below.

Published online: 30 November 2021



Table 1 Evidence of an association of the four SNPs in a two-stage GWAS in Han Chinese population.

| SNP | CHR | BP | A1/A2 | Gene | Discovery stage (521 homosexual and 1270 heterosexual men) | | | Replication stage (957 homosexual and 2043 heterosexual men) | | | Meta-analysis (1478 homosexual and 3313 heterosexual men) | | |
|------------|-----|-----------|-------|--------|--|------|-------------------------|--|------|-------------------------|---|-------------------------|------------------------|
| | | | | | OR | SE | P | OR | SE | P | OR | P | P _{Het} |
| rs17320865 | X | 147085464 | A/T | FMR1NB | 1.39 | 0.07 | 9.77 × 10 ⁻⁶ | 1.26 | 0.06 | 8.81 × 10 ⁻⁴ | 1.31 | 7.61 × 10 ⁹ | 0.30 |
| rs7259428 | 19 | 31104579 | G/A | ZNF536 | 0.67 | 0.09 | 3.87 × 10 ⁻⁶ | 0.64 | 0.07 | 1.13 × 10 ⁻⁶ | 0.65 | 8.20 × 10 ¹⁵ | 0.69 |
| rs12039940 | 1 | 181952711 | C/T | ZNF648 | 1.57 | 0.10 | 9.22 × 10 ⁻⁶ | 1.01 | 0.04 | 8.72 × 10 ⁻¹ | 1.07 | 6.28 × 10 ² | 1.0 × 10 ⁻⁴ |
| rs7500300 | 16 | 5932886 | C/T | RBF0X1 | 1.45 | 0.08 | 5.28 × 10 ⁻⁶ | 1.11 | 0.05 | 6.84 × 10 ⁻² | 1.19 | 3.08 × 10 ⁻⁵ | 5.2 × 10 ⁻³ |

CHR chromosome, OR odds ratio, ORs were calculated according to the minor allele, A1/A2 minor/major allele, P_{Het} p values of heterogeneity test.

References

1. Hu, S. H. et al. Discovery of new genetic loci for male sexual orientation in Han population. *Cell Discov* **7**, 103, <https://doi.org/10.1038/s41421-021-00341-7> (2021).