






Author Correction: GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk

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Correction to: *Nature Communications* <https://doi.org/10.1038/s41467-017-01490-8>, published online 17 November 2017.

We have been alerted¹ that in our recent Article² the calculations used to transform the heritability from the observed scale to the liability scale did not take into account the individuals in category 2 of the baldness scale, who were removed in our original analysis. This led to an overestimation of the heritability on the liability scale, which should have been 0.62 instead of 0.94. Moreover, in the Title and in the Abstract, we report that we can explain 38% of the risk, while in fact that is the proportion of heritability explained by the loci we discovered. These errors do not substantially change the paper or its conclusions apart from the statement MBP is therefore probably one of the most heritable complex traits. Genome-wide significant associations and pathway analyses are not affected in any way and male-pattern baldness remains less genetically complex than other complex traits. We wish to thank Yap et al. for bringing this to our attention.

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References

1. Yap C. X. et al. Correspondence: mis-estimation of heritability and prediction accuracy of male-pattern baldness. *Nat Commun.* 2018; <https://doi.org/10.1038/s41467-018-04807-3>
2. Pirastu, N., Joshi, P. K. & de Vries, P. S. et al. GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. *Nat. Commun.* **8**, 1584 (2017).

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