AMENDMENTS

Author Correction: The copy number variation landscape of congenital anomalies of the kidney and urinary tract

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Correction to: *Nature Genetics* https://doi.org/10.1038/s41588-018-0281-y, published online 21 December 2018.

In the version of this article initially published, affiliation 38 incorrectly read "ICNU-Nephrology and Urology Department, Barcelona, Spain"; "Renal Division, Hospital Clinic, IDIBAPS, University of Barcelona, Barcelona, Spain" is the correct affiliation. The error has been corrected in the HTML and PDF versions of the article.

Author Correction: Repurposing large health insurance claims data to estimate genetic and environmental contributions in 560 phenotypes

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Correction to: *Nature Genetics* https://doi.org/10.1038/s41588-018-0313-7, published online 14 January 2019.

In the version of Fig. 4b initially published, there was a calculation error in the estimates of shared environmental variance (c^2) for MaTCH functional domains. For all MaTCH functional domains except the 'all traits' functional domain, the estimate of c^2 was calculated with monozygotic twin correlation (r_{MZ}) and dizygotic twin correlation (r_{DZ}) for each functional domain provided by the MaTCH website (http://match.ctglab.nl/). The c^2 value should have been estimated as $c^2 = 2r_{DZ} - r_{MZ}$ but, owing to a coding error, was erroneously estimated as $c^2 = 2r_{DZ} - r_{DZ}$. The c^2 estimate for the 'all traits' functional domain was correct in the version of the article initially published, and therefore no conclusions are affected; however, the contribution of c^2 among MaTCH functional domains is decreased. The authors thank G. Gibson and M. Nordborg for pointing out the error.

To correct this error, Fig. 4 has been revised to include corrected c^2 estimates in the data in panel b as well as to include the numbers of phenotypes in both the CaTCH and MaTCH functional domains in the y axes of panels a and b. The number of phenotypes for each MaTCH functional domain in Fig. 4 is based on the number of phenotypes for which h^2 and c^2 were estimated with twin correlation (r_{MZ} and r_{DZ}) taken from the MaTCH website. The total numbers of phenotypes within each MaTCH functional domain where h^2/c^2 were estimated with either twin correlation or variance component models (ACE) and can be found in Supplementary Table 1. The legend of Fig. 4 has been revised to include descriptions of the red and blue values and a description of the numbers of phenotypes in the y axes in panels a and b. In the Results section, the description of Fig. 4b reading "For c^2, the 95% CI from CaTCH estimates overlapped with the 95% CI from the MaTCH estimates for only the infection domain (Fig. 4b)" has been changed to "For c^2, the 95% CI from CaTCH estimates overlapped with the 95% CI from the MaTCH estimates for 11 out of 21 functional domains, namely cardiovascular, dermatological, endocrine, gastrointestinal, hematological, immunological, infection, metabolic, psychiatric, reproduction, and skeletal functional domains (Fig. 4b)."