

Author Correction: Parent-of-origin-specific signatures of *de novo* mutations

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Correction to: *Nature Genetics* <https://doi.org/10.1038/ng.3597>, published online 20 June 2016.

In the version of this article published, the *P* values for the enrichment of single mutation categories were inadvertently not corrected for multiple testing. After multiple-testing correction, only two of the six mutation categories mentioned are still statistically significant. To reflect this, the text “More specifically, paternally derived DNMs are enriched in transitions in A[.]G contexts, especially ACG>ATG and ATG>ACG (Bonferroni-corrected $P = 1.3 \times 10^{-2}$ and $P = 1 \times 10^{-3}$, respectively). Additionally, we observed overrepresentation of ATA>ACA mutations (Bonferroni-corrected $P = 4.28 \times 10^{-2}$) for DNMs of paternal origin. Among maternally derived DNMs, CCA>CTA, GCA>GTA and TCT>TGT mutations were significantly overrepresented (Bonferroni-corrected $P = 4 \times 10^{-4}$, $P = 5 \times 10^{-4}$, $P = 1 \times 10^{-3}$, respectively)” should read “More specifically, CCA>CTA and GCA>GTA mutations were significantly overenriched on the maternal allele (Bonferroni-corrected $P = 0.0192$ and $P = 0.048$, respectively).” Additionally, the last sentence to the legend for Fig. 3b should read “Green boxes highlight the mutation categories that differ significantly” instead of “Green boxes highlight the mutation categories that differ more than 1% of mutation load with a bootstrapping *P* value <0.05.” Corrected versions of Fig. 3b and Supplementary Table 25 appear with the Author Correction.

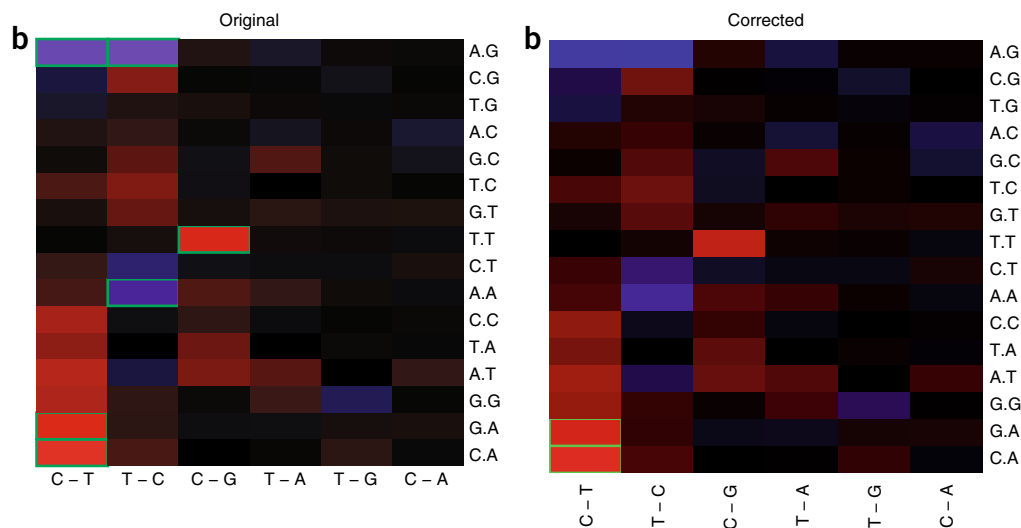


Fig. 3b | Original and corrected.

Additional information

Supplementary information is available for this paper at <https://doi.org/10.1038/s41588-018-0226-5>.

Published online: 5 October 2018

<https://doi.org/10.1038/s41588-018-0226-5>