

Author Correction: Sparse whole-genome sequencing identifies two loci for major depressive disorder

<https://doi.org/10.1038/s41586-023-06276-1>

Published online: 11 August 2023

Correction to: *Nature* <https://doi.org/10.1038/nature14659>

Published online 15 July 2015

 Check for updates

CONVERGE consortium*

We are updating the section on data availability for this article. The genotype and whole genome sequence data used in this publication were made publicly available at the time of publication through the GigaDB database at <http://gigadb.org/dataset/100155>. The whole genome sequence data files were subsequently withdrawn from GigaDB following a change in data sharing regulations in China. Variant calls and GWAS summary statistics remain publicly available as laid out in the updated “Additional information” section below. The original Letter has not been corrected.

Additional information

Variant calls are available at the European Nucleotide Archive (ENA) under accession code PRJNA289433. In addition, GWAS summary statistics and variant calls are available from figshare (<https://doi.org/10.6084/m9.figshare.3840339> and <https://doi.org/10.6084/m9.figshare.3840696>). Raw whole-genome sequencing data cannot be shared due to restrictions on data sharing and privacy concerns.

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