

Author Correction: Discovery of 42 genome-wide significant loci associated with dyslexia

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 Check for updates

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In the version of this article originally published, a paragraph was omitted in the Methods section, reading “**Genomic control.** Top SNPs are reported from the more conservative GWAS results adjusted for genomic control (Fig. 1, Extended Data Figs. 1–4, and Supplementary Tables 1, 2, 9 and 10), whereas downstream analyses (including gene-set analysis, enrichment and heritability partitioning, genetic correlations, polygenic prediction, candidate gene replication) are based on GWAS results without genomic control.” The paragraph has now been included in the HTML and PDF versions of the article.

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