In May 2020 the authors of the research article "The genetic architecture of the human cerebral cortex" found a formatting error in one of the phenotype files that was used to perform genome-wide association (GWAS) analyses within the UK Biobank cohort. We immediately informed the journal and requested that an erratum be published and corrected. At this time, we also updated the publicly available GWAS summary statistics for this work and contacted those who had downloaded the summary statistics and advised them to download the corrected summary statistics. The error only affected the regional cortical thickness imaging phenotypes in this cohort. The error occurred when the file was sorted by participant ID and resulted in the randomisation of IDs within this file, the corresponding author takes full responsibility for this error and apologises that this was not found prior to the publication of the manuscript. This meant that in the GWAS meta-analyses for the regional cortical thickness imaging phenotypes the GWAS results from this cohort contributed random noise rather than true signal. None of the other 59 cohorts contributing to the meta-analysis were affected; the average cortical thickness was not affected by this error nor were the total or regional cortical surface area phenotypes.

The detection and correction of this error increased the power of the meta-analyses for the regional cortical thickness imaging phenotypes. Due to the genome-wide nature of these meta-analyses these corrections resulted in corrections to the beta, standard-errors and p-values for all loci for these traits. As GWAS downstream analyses take the meta-analytic results as input this further resulted in increased power for and led to corresponding changes to the results of the downstream analyses for the regional thickness traits. An additional 69 significant loci influencing the regional thickness traits were identified (Table S1 and S5; Figure 1B and 4B, and the summary figure panel B). The bioinformatic information provided for these loci (Table S11) was updated, an additional 220 genes were mapped to the regional thickness loci (Table S12), and additional putatively casual variants were noted (Table S13). An additional 68 genes were identified as enriched (Table S6). The results of the SNP heritability (Table S7; Figure 3B), polygenic scores (Table S8), and genetic correlation analyses (Tables S14-S17; Figure 3B) were updated and the new results were estimated with greater precision. Throughout the text the number of loci and corresponding test statistics and significance values have been updated. In addition, it was discovered that in Table S5 the columns labelled 95% confidence intervals incorrectly contained 99% confidence intervals; this error has been corrected.

As the focus of the results and the discussion within the paper was on the average cortical thickness and total cortical surface area phenotypes these corrections do not change the main findings, biological interpretations, or conclusions of the paper. In the sections of the paper that discuss the results of the regional cortical thickness phenotypes that impact has been to increase the power of these analyses which has resulted in the detection of additional loci. The manuscript text, figures and supplementary materials and summary statistics have been corrected. In addition to clarify these changes and a version of the manuscript with highlighted changes can be viewed at (http://enigma.ini.usc.edu/downloads/ENIGMA3_Erratum/).