

## Description of Additional Supplementary Files

### Supplementary Data-12:

**Supplementary Data 1 • SD1. Brain folding map nomenclature.** List of the 62 sulcal regions under investigation, including abbreviated name and full name.

**Supplementary Data 2 • SD2. List of UK Biobank measurements.** List of imaging-derived phenotypes in the UK Biobank used in t-SNE clustering analysis.

**Supplementary Data 3 • SD3. GWAS associations.** All genome-wide significant associations, replicated at  $p < 0.05$ , across specific brain regions.

**Supplementary Data 4 • SD4. Brain folding map nomenclature.** All genome-wide significant associations, replicated at  $p < 0.05$ , averaged across hemispheres.

**Supplementary Data 5 • SD5. GWAS associations summary.** Summary of number of significant associations per sulcal shape parameter/hemisphere.

**Supplementary Data 6 • SD6. Multi-trait colocalization results.** Results of multi-trait colocalization analysis, for loci associated with  $>1$  sulcal measure.

**Supplementary Data 7 • SD7. Overlapping brain imaging GWAS loci.** List of genetic associations from the present study that overlap with previously reported brain imaging GWAS associations.

**Supplementary Data 8 • SD8. Coding proxy associations.** GWAS associations in linkage disequilibrium (LD;  $r^2 > 0.8$ ) with coding variants or splice site proxies.

**Supplementary Data 9 • SD9. Burden analysis results.** List of rare variant burden association results at  $p < 2.7 \times 10^{-6}$ .

**Supplementary Data 10 • SD10. Expression quantitative trait loci (eQTL) colocalization results.** Results of eQTL colocalization analysis at  $PP4 > 0.5$ .

**Supplementary Data 11 • SD11. GWAS Catalog overlap.** List of associations overlapping with genetic associations reported in the NHGRI-EBI GWAS Catalog ([ebi.ac.uk/gwas/](http://ebi.ac.uk/gwas/)).

**Supplementary Data 12 • SD12. Neurocognitive correlations.** Genetic correlations between measures of sulcal morphometry and neurocognitive phenotypes, at  $p < 0.05$ .