Supplementary Figures

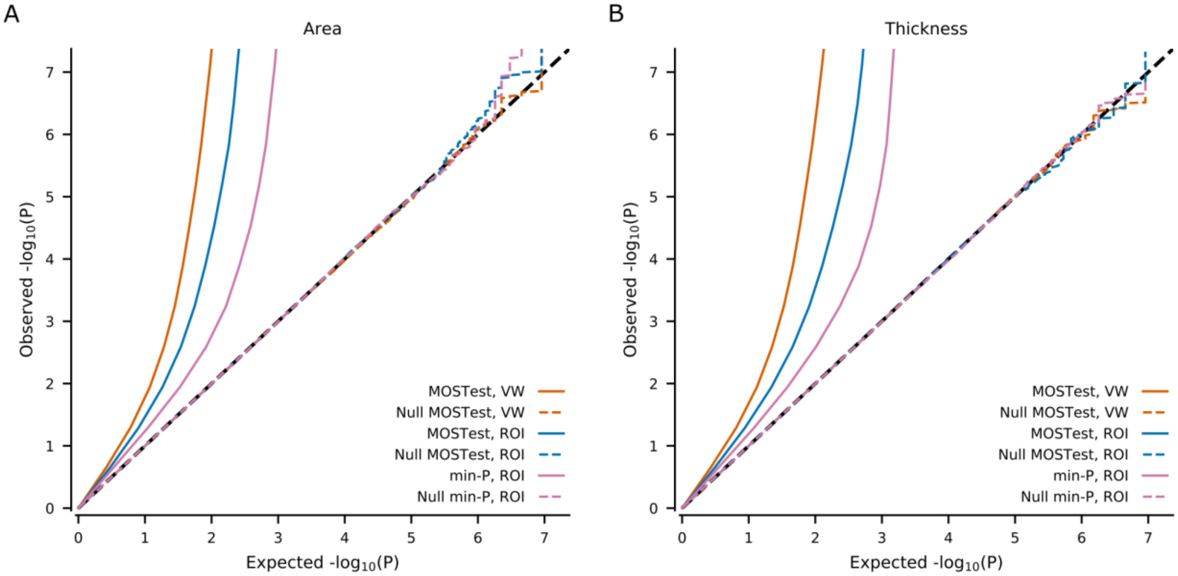

Figure S1: Q-Q plots.

Q-Q plots show association p-values for MOSTest VW, MOSTest ROI and min-P ROI for area (A) and thickness (B). P-values obtained with original (non-permuted) genotypes are shown with solid lines and p-values obtained with null (permuted) genotypes are shown with dashed lines. VW = vertex-wise. ROI = region of interest. QQ plots of p-values generated under null hypothesis (permuted genotypes) follow expected null line (black dashed line), indicating that null distribution is well-calibrated.

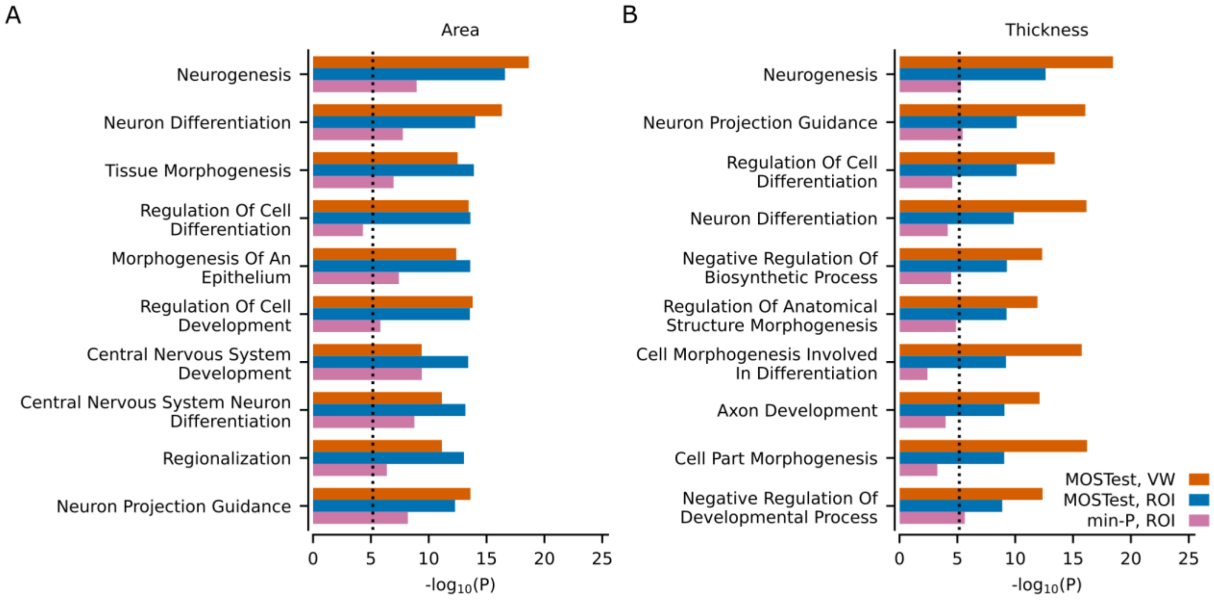

Figure S2: Gene-set analyses with MAGMA prioritized based on MOSTest ROI results.

Results from the gene-set analysis based on multivariate GWAS on area and thickness. Ten most significant Gene Ontology sets (N=7,343) in the MOSTest ROI analysis are listed on the y-axis for (A) Area (B) Thickness. Corresponding uncorrected -log10(p-values) are shown on the x-axis. P-values were obtained using MAGMA analysis as implemented in FUMA. Vertical dotted line shows Bonferroni correction threshold (p=0.05/7343). VW = vertex-wise. ROI = region of interest.

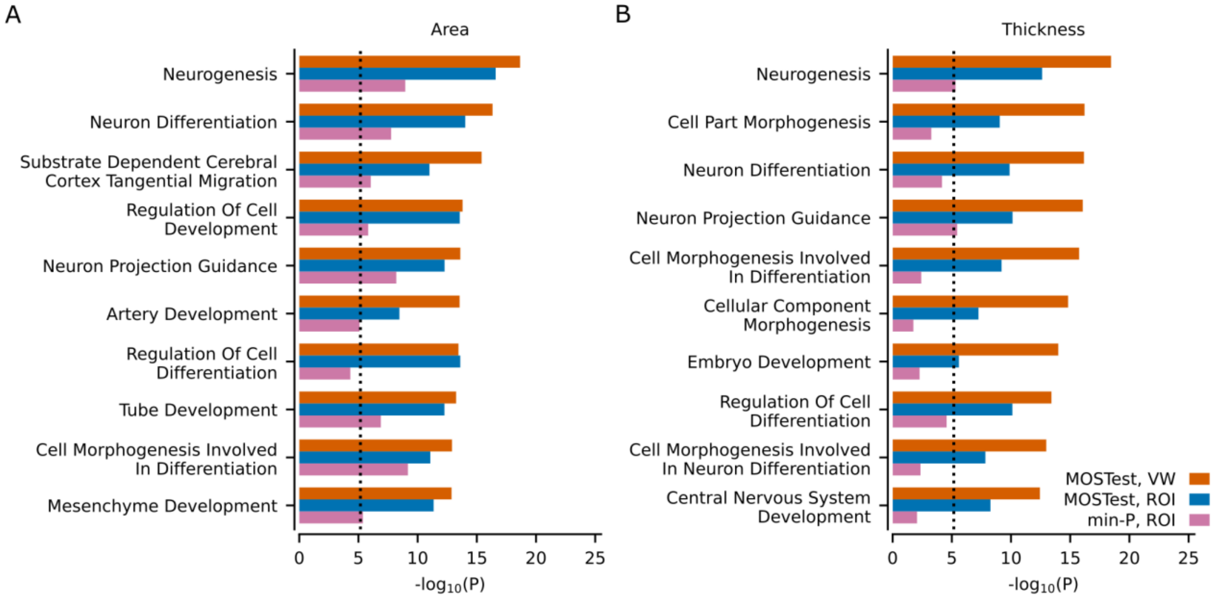

Figure S3: Gene-set analyses with MAGMA prioritized based on min-P ROI results.

Results from the gene-set analysis based on multivariate GWAS on area and thickness. Ten most significant Gene Ontology sets (N=7343) in the min-P ROI analysis are listed on the y-axis for (A) Area, (B) Thickness. Corresponding uncorrected -log10(p-values) are shown on the x-axis. P-values were obtained using MAGMA analysis as implemented in FUMA. Vertical dotted line shows Bonferroni correction threshold (p=0.05/7343). VW = vertex-wise. ROI = region of interest.

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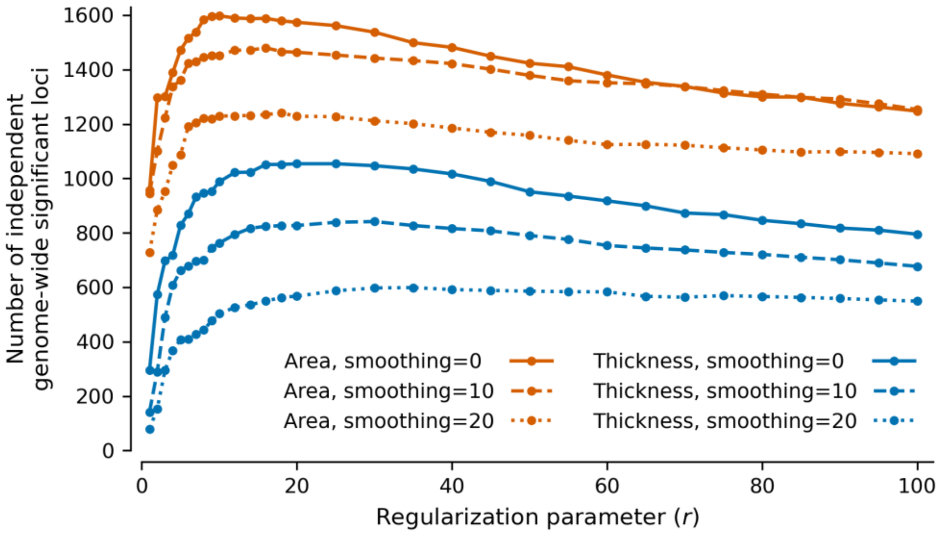

Figure S4: **Effect of regularization parameter on loci yield.**

Number of genome-wide significant loci (ENIGMA-based locus definition) identified for cortical area and thickness applying MOSTest with different regularization parameters (r=1,2,3, …, 100) to vertex-wise measures (ico3 downsampling) with various degrees of smoothing (FWHM=0, 10, 20). Smoothing was performed before downsampling to ico3. Regularization parameter r=N, where N is a number of analyzed vertices, corresponds to unregularized version.

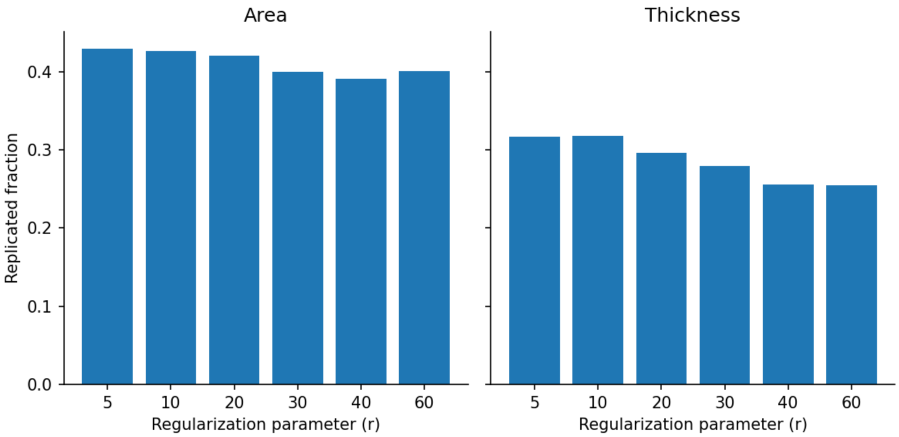

Figure S5. MOSTest replication rates with different regularization parameters.
For each of six tested regularization parameters (r=5,10,20,30,40,60) MOSTest analyses were conducted separately for cortical area and thickness in discovery (UK Biobank, N=35,657) and replication (ABCD, N=8,060) cohorts. For each regularization parameter the fraction of replicated loci was estimated using replication criterion described in the Methods section.