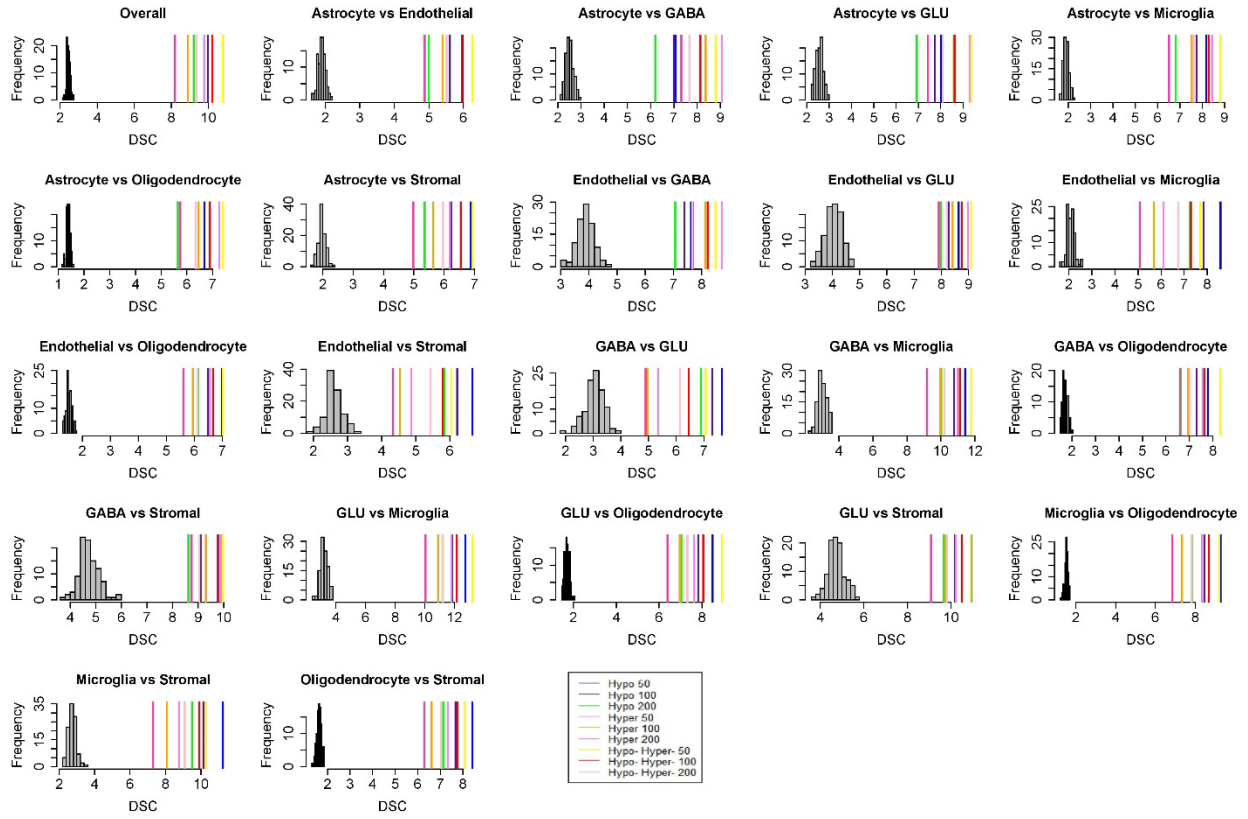


Supplementary Materials

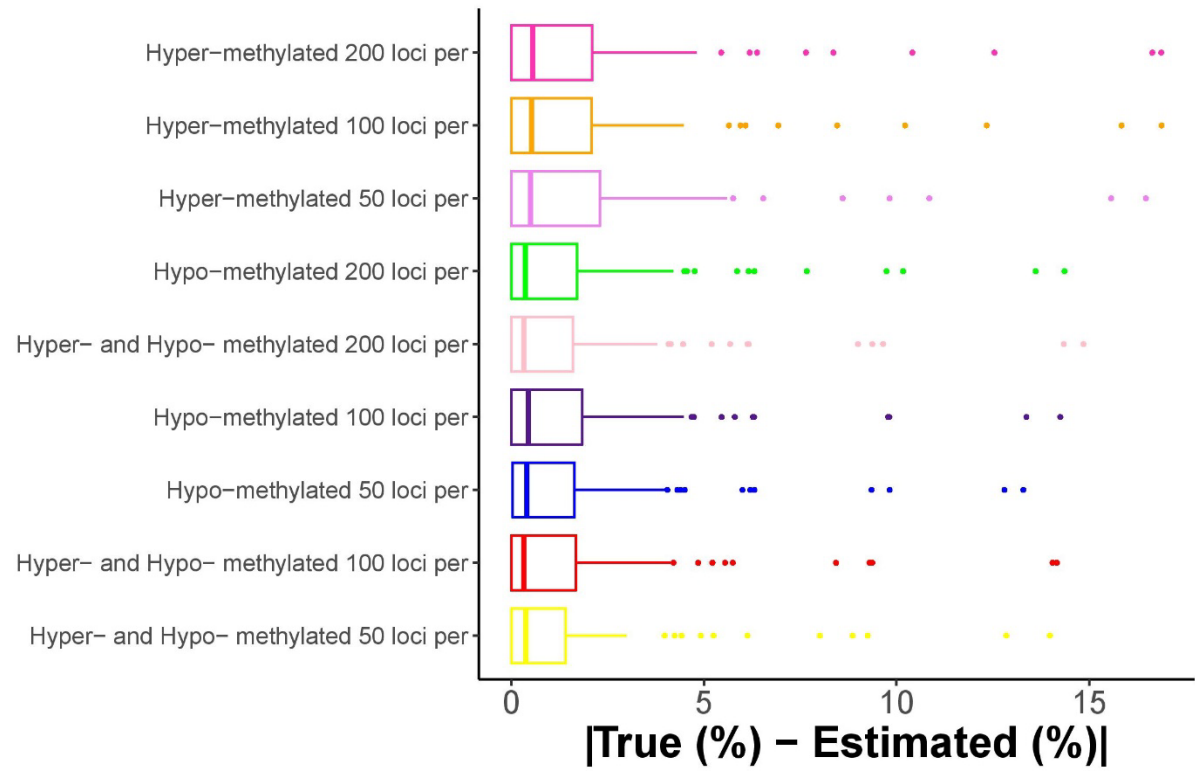
Hierarchical deconvolution for extensive cell type resolution in the human brain using DNA methylation

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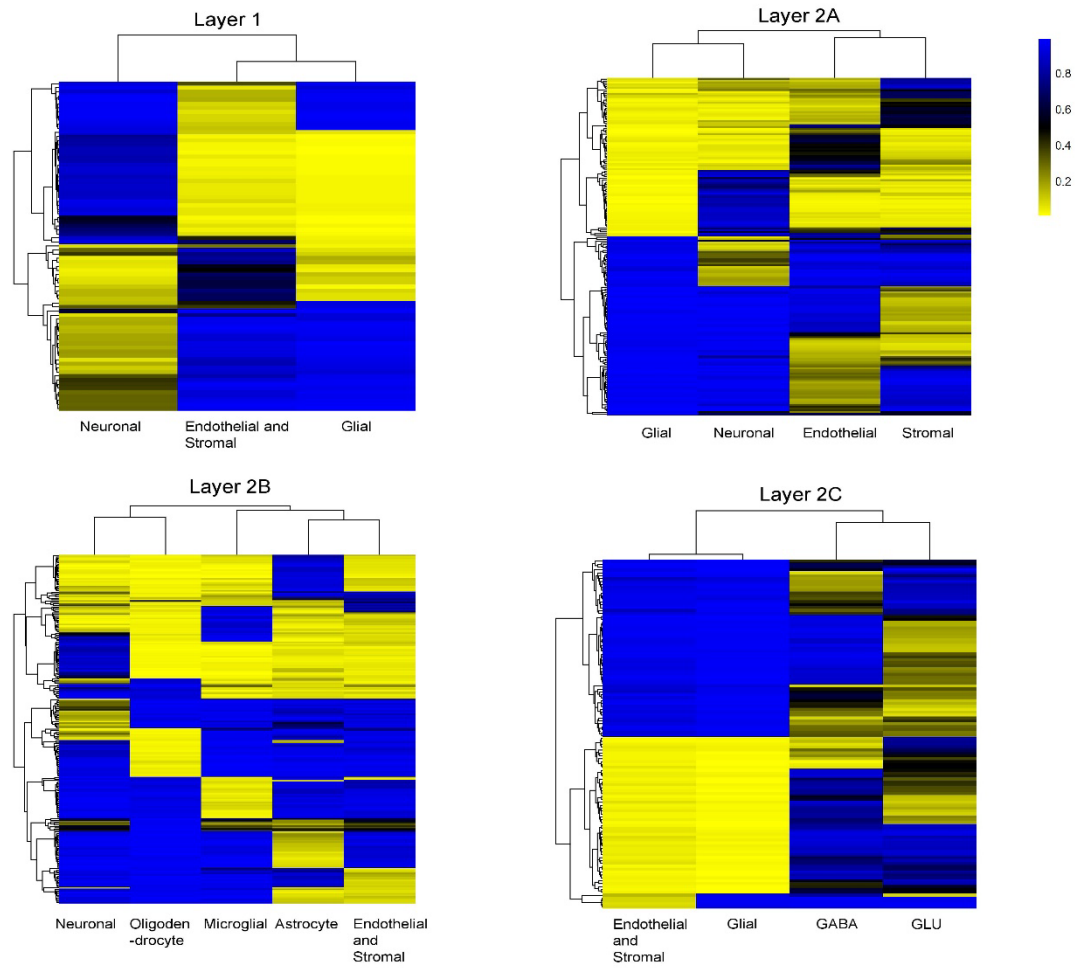
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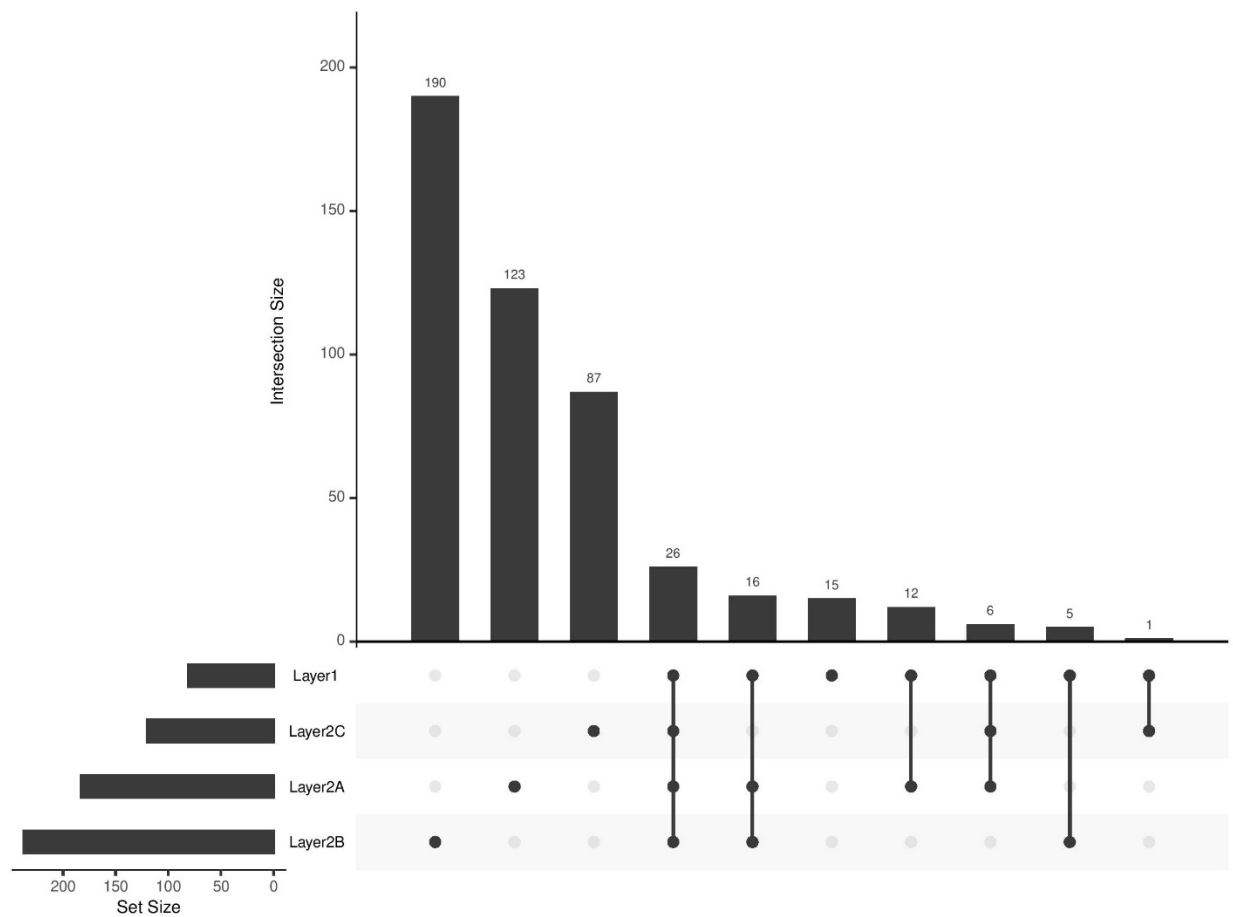
Supplementary Figure 1. Dispersion separability criterion between brain cell types across the tested libraries.



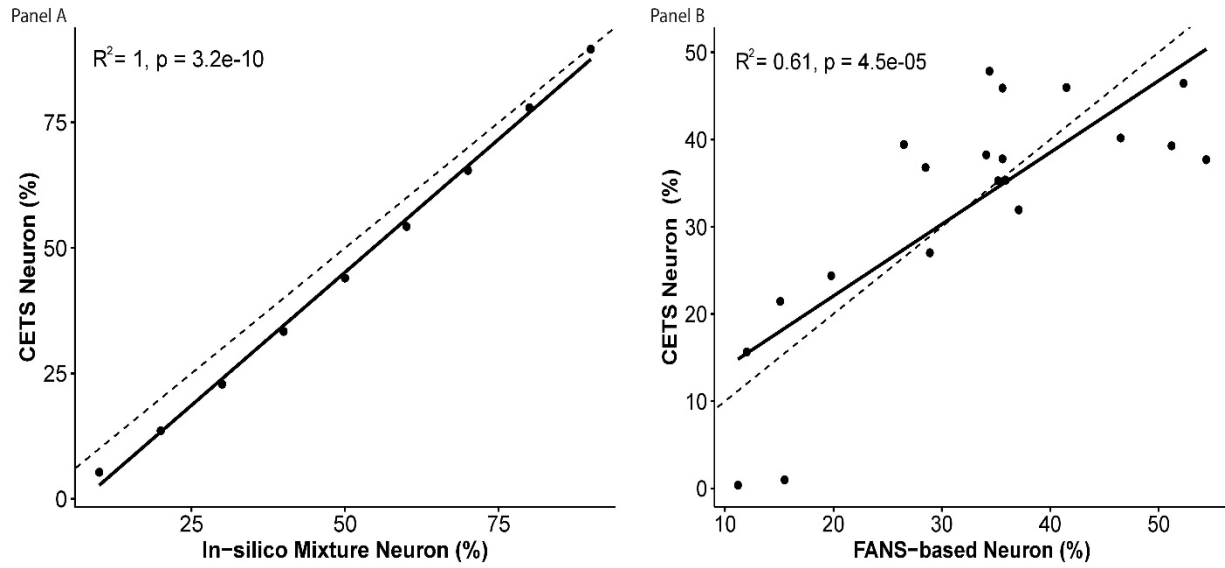
Supplementary Figure 2. Absolute difference values between predicted and true cell proportions in the discovery data sets across the tested libraries.



Supplementary Figure 3. Heatmaps of the methylation status of the HiBED CpGs across the layers in the deconvolution hierarchy.



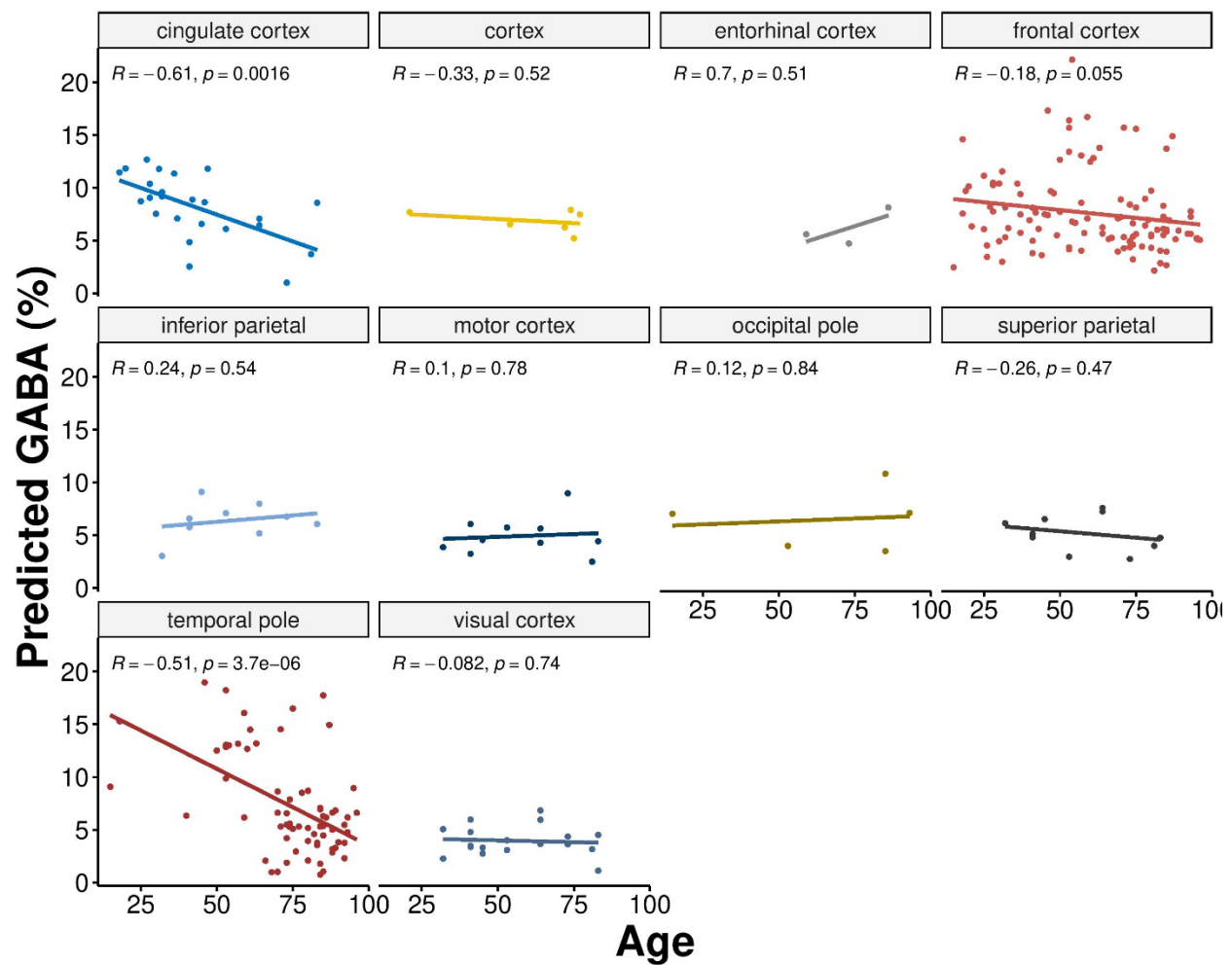
Supplementary Figure 4. The number of overlapping CpGs across the four libraries in HiBED.



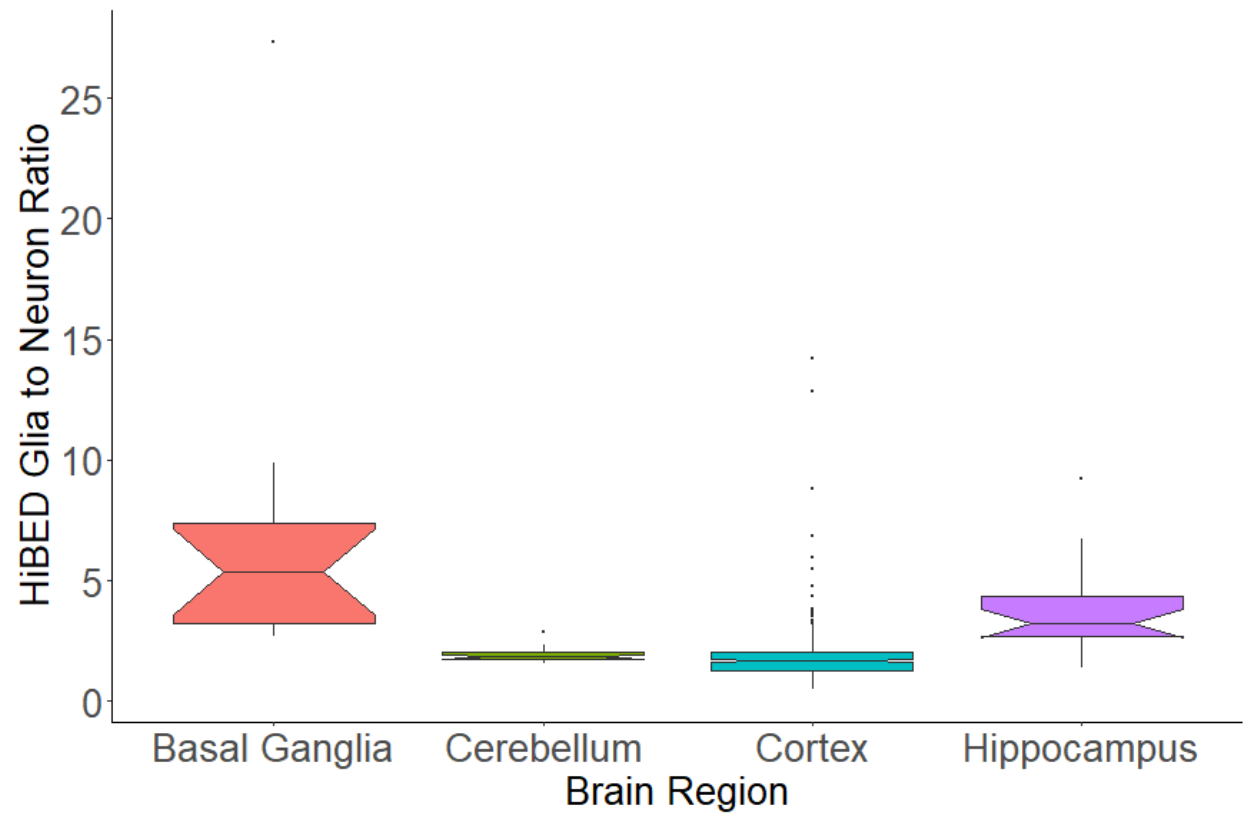
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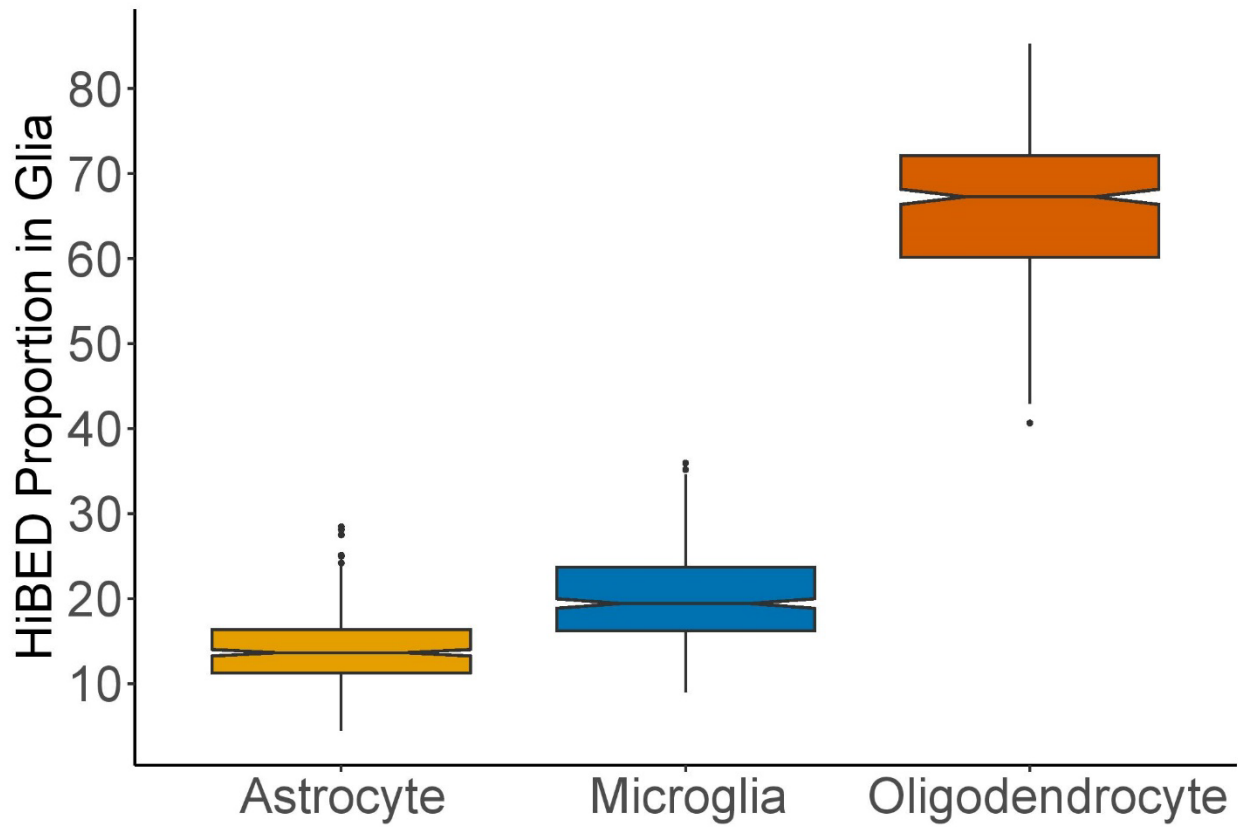
Supplementary Figure 6. Stacked bar plots of HiBED deconvolved cell proportions in four brain regions.



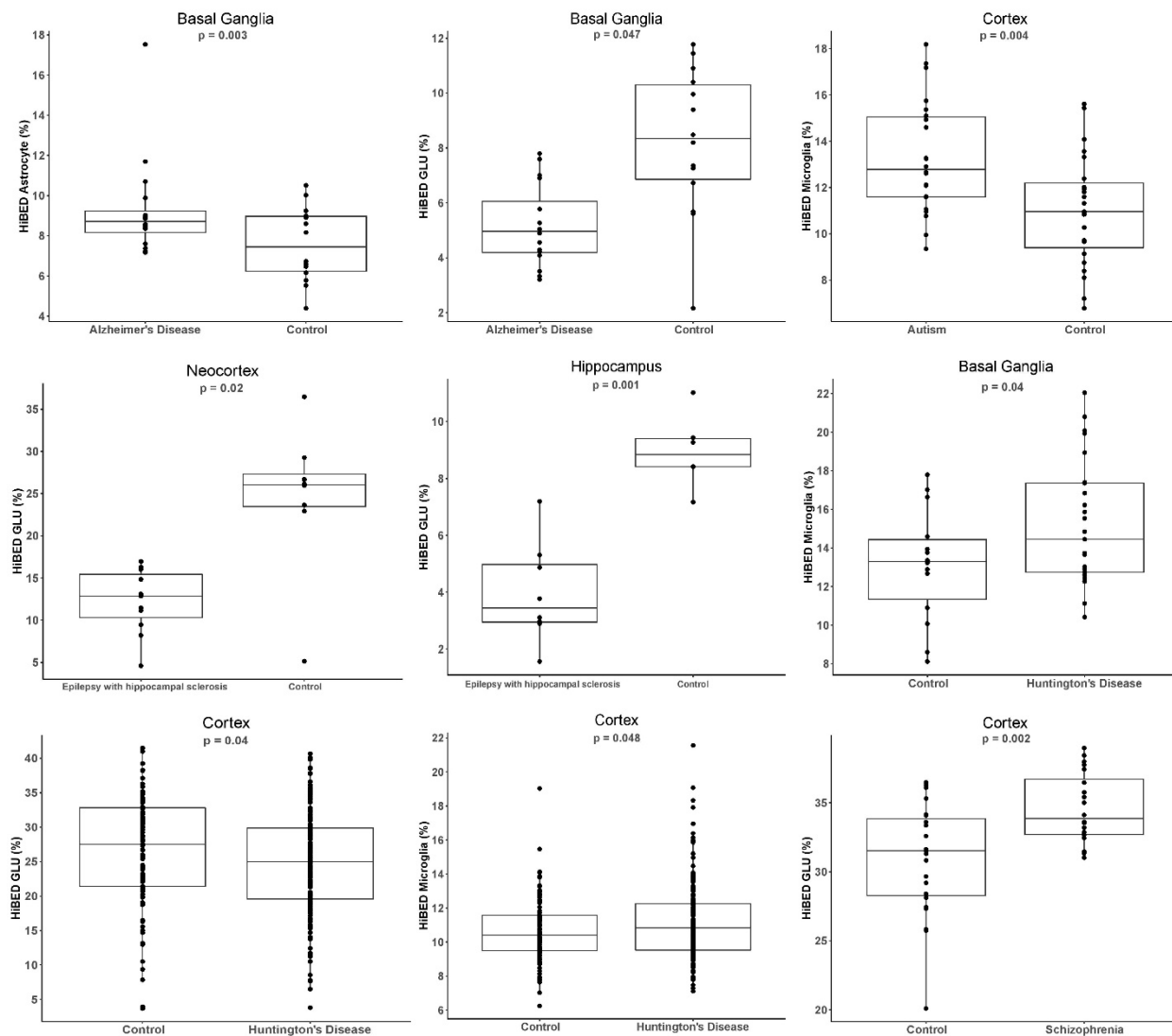
Supplementary Figure 7. Aging effect on HiBED-predicted GABA proportion in cortical subregions in males.



Supplementary Figure 8. HiBED-predicted glia-to-neuron ratio in four brain regions.



Supplementary Figure 9. HiBED-predicted glial cell composition in the human cortex.



Supplementary Figure 10. Comparisons of HiBED-predicted cell proportions between diseased and normal controls in Alzheimer's disease, autism, Huntington's disease, epilepsy, and schizophrenia across different brain regions.