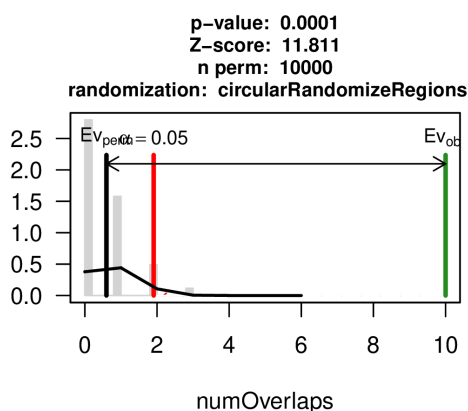


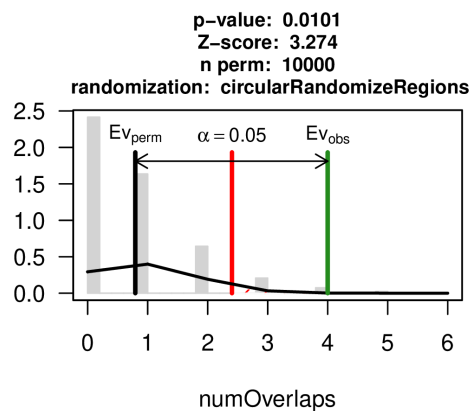
Supplementary Figures

Figure S1: **Enrichment analyses.** Permutation tests were applied to determine enrichment of enhancers/promoters within human positively-selected regions (n=314, from [8]; overlap = 10 prom; 4 enh), schizophrenia genomic loci (n=108, from [20]; overlap = 2 prom; 3 enh), and autism risk variants (n=58, [21], retrieved from [22]; no overlap).

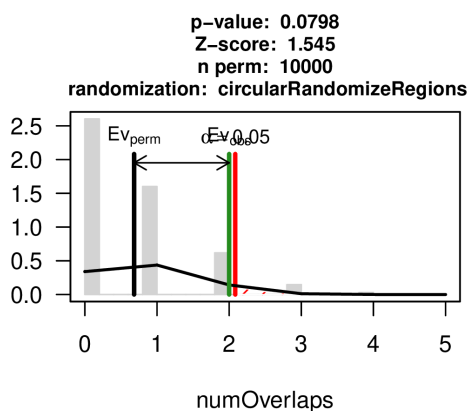
Promoters in human positively-selected regions



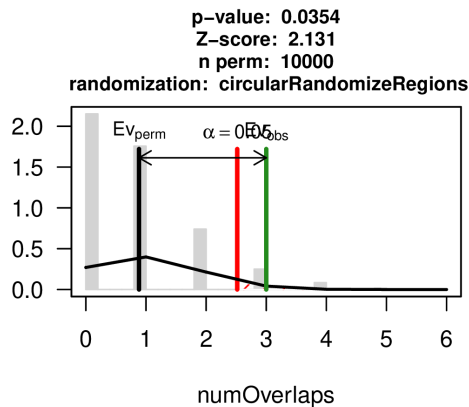
Enhancers in human positively-selected regions



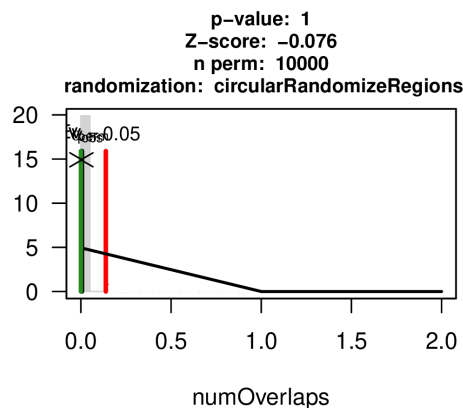
Promoters in schizophrenia genomic loci



Enhancers in schizophrenia genomic loci



Promoters with autism risk variants



Enhancers with autism risk variants

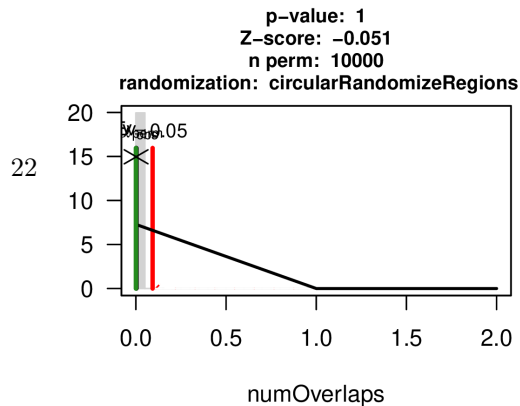


Figure S2: **Clustering results obtained in the original study.** [57] generated and analysed the single-cell transcriptomic data used in this study (5 to 20 post-conception weeks human prenatal brain). They reported two clustering results (A and B) after using different methodologies. Note in B the presence of the three clusters for intermediate progenitor cells and the two clusters of radial glial cells, as in our analysis. Images are reproduced with copyright permission from *Science*.

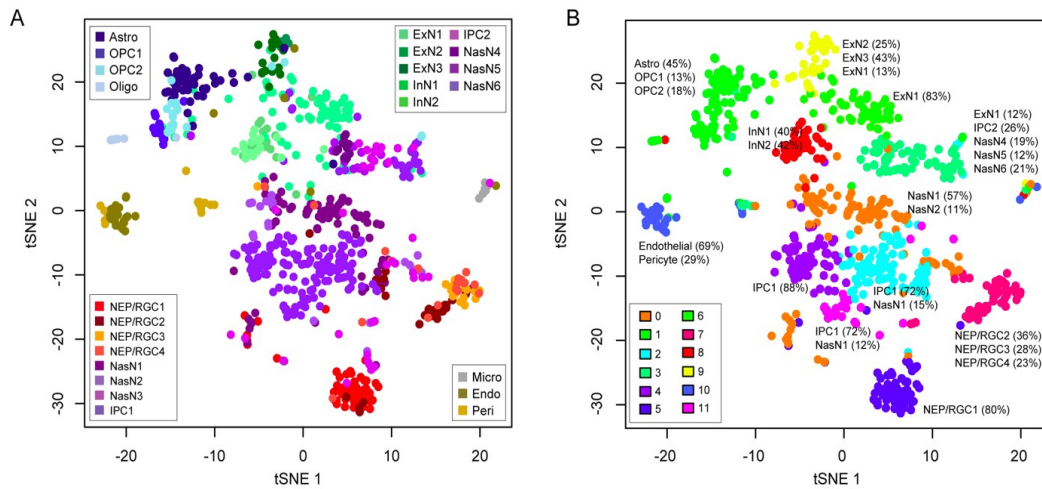


Figure S3: **Co-expression network analysis - Radial glial cells gene modules.** We used the two identified radial glial cell clusters for co-expression analyses. The dendrogram shows genes grouped in different modules (y-axis: distance metrics between clusters) that were assigned a color code (x-axis). A total of 32 modules were detected for RGC-1 sub-population and 26 modules for RGC-cluster 2.

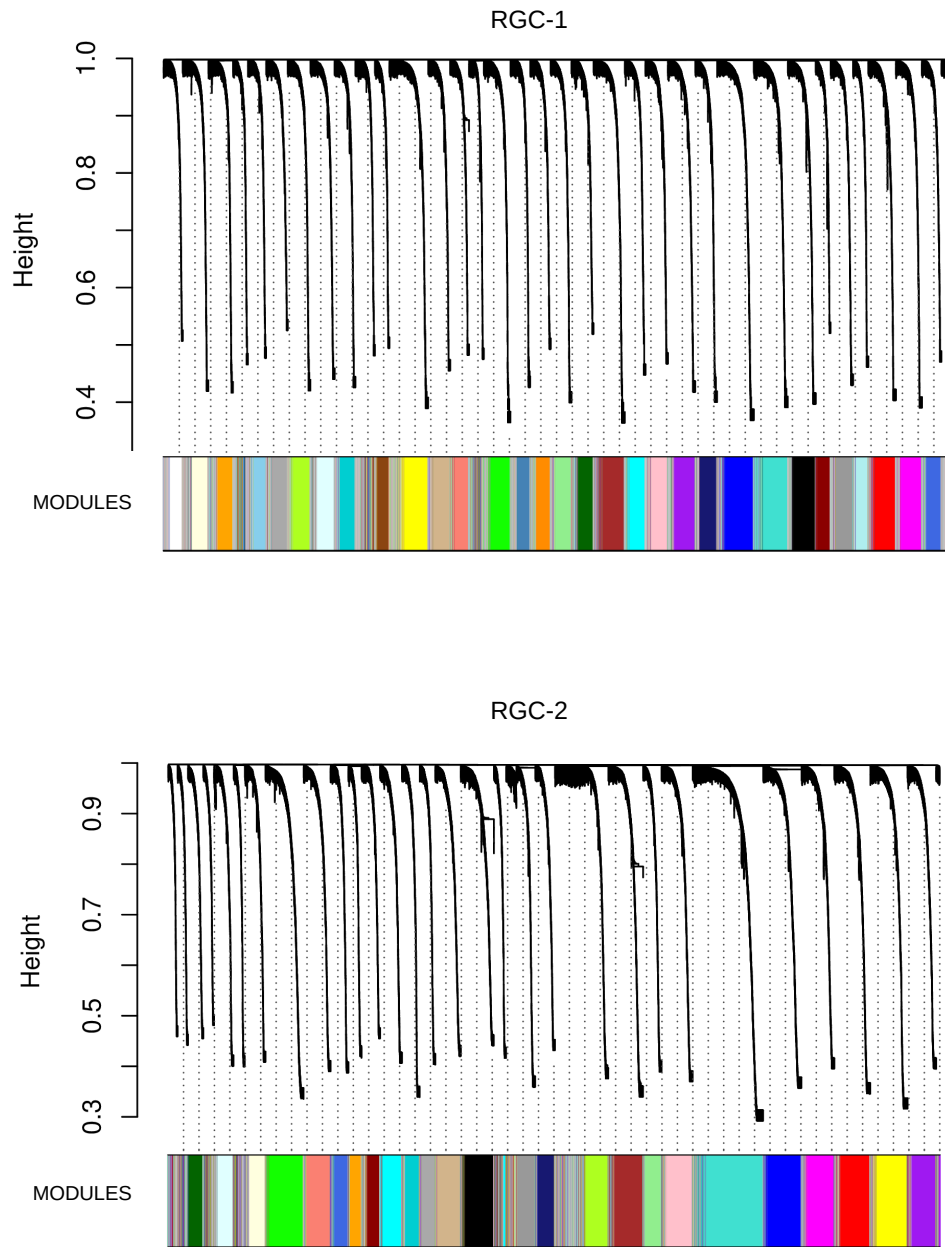


Figure S4: **Co-expression network analysis - Intermediate progenitor cells gene modules.** Two intermediate progenitor cell clusters (IPC-cluster 1 and IPC-cluster 2) were used for co-expression analyses. A total of 9 modules were detected for IPC-cluster 1 and 23 modules for IPC-cluster 2 (y-axis: distance metrics between clusters; x-axis: color code)

