

Supplementary Materials

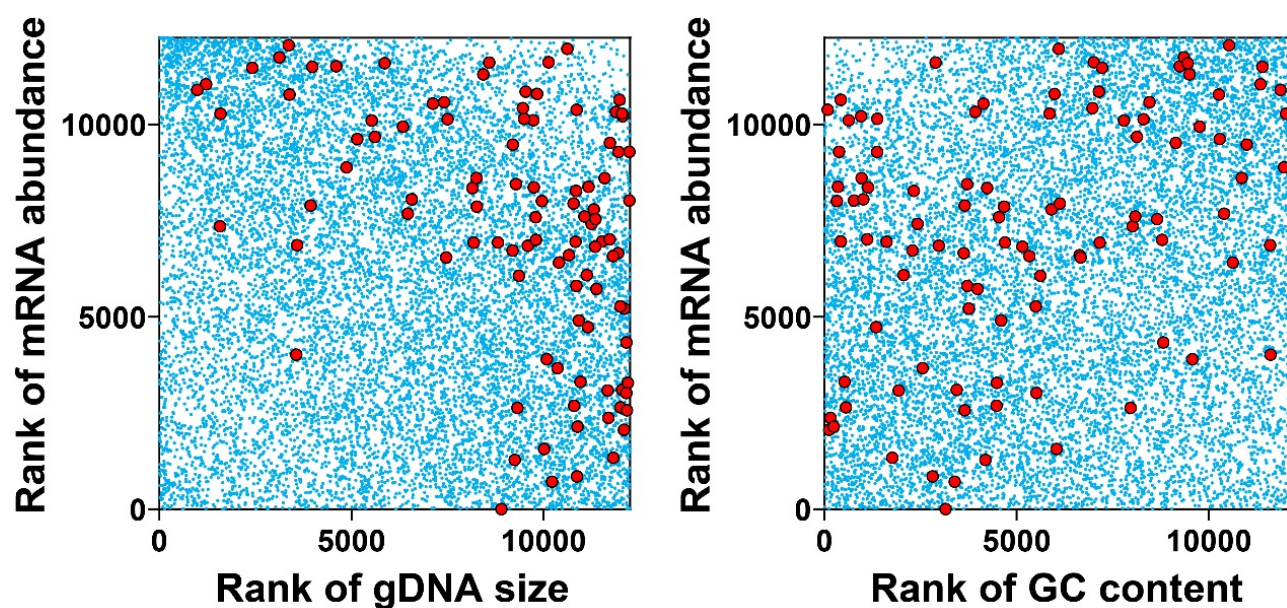


Fig. S1 Distribution of hcASDs in gene rank matrices. Genes in the whole genome are ranked by gDNA size, GC content (horizontal axis), and mRNA abundance level (vertical axis) and plotted in matrices (blue dots, single genes; red dots, hcASD genes). Values of both horizontal and vertical axes are ranks (orders) of the 12,250 genes under 3 different gene ranking conditions.

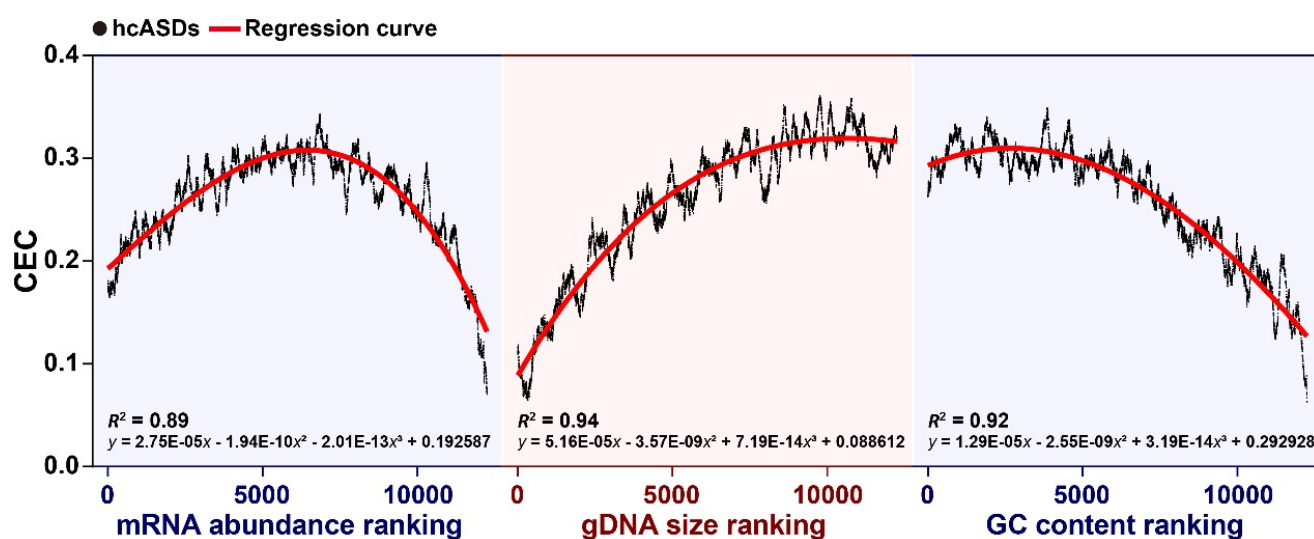


Fig. S2 Fitting (regression) of CEC distribution curves under three different gene ranking conditions.

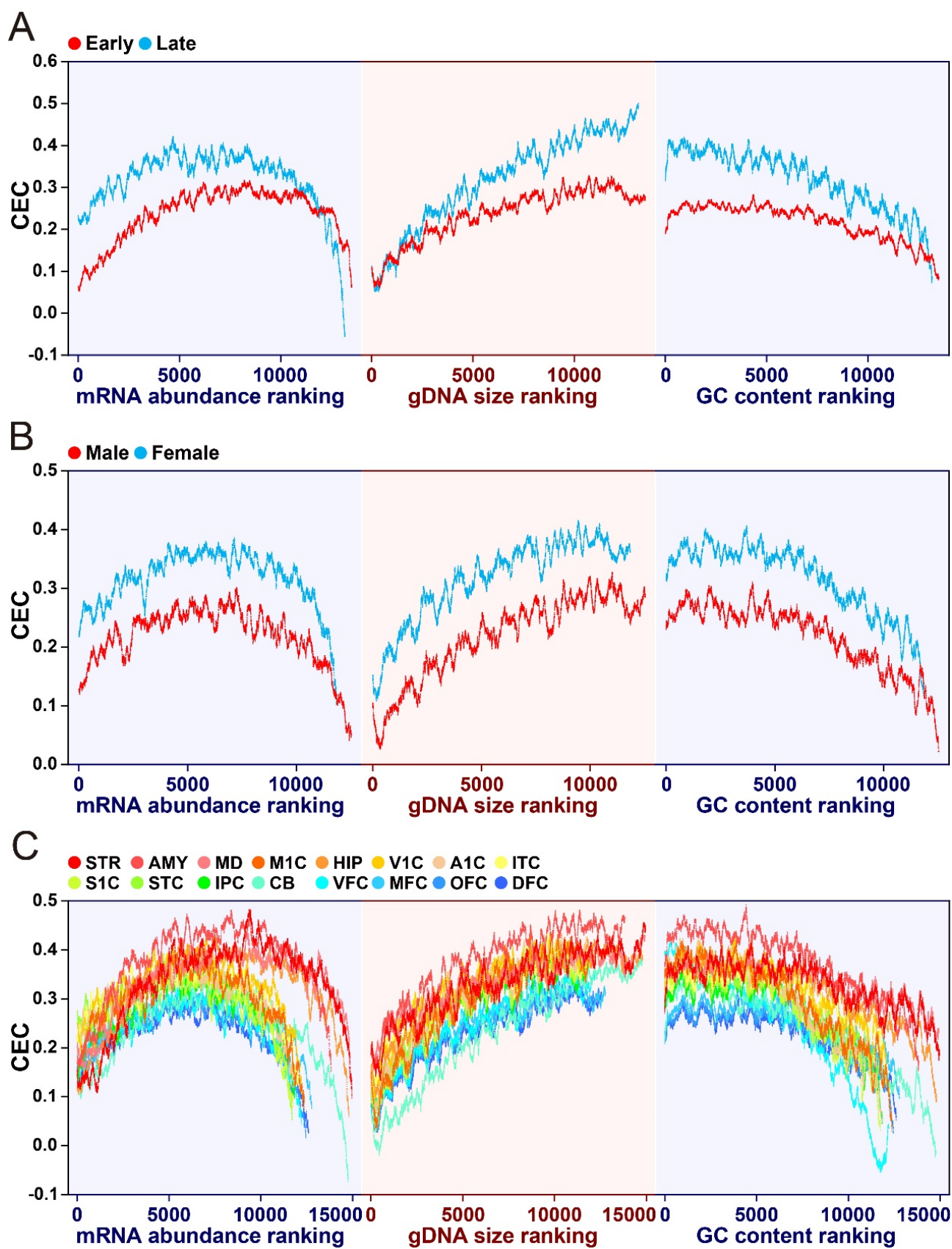


Fig. S3 CEC distribution curves for different developmental stages, sex, and brain regions.

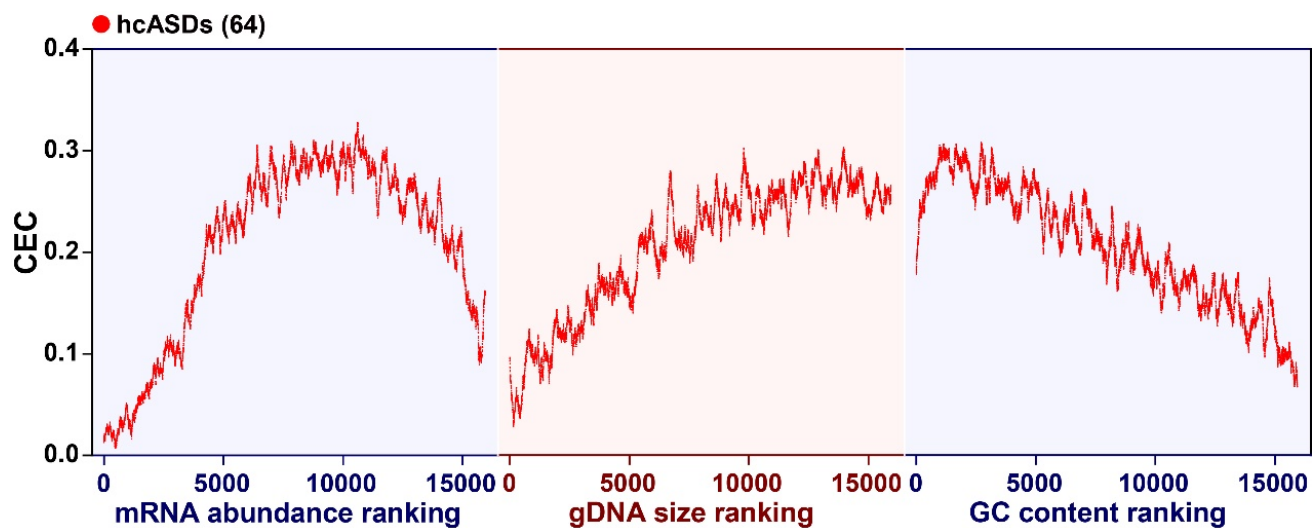


Fig. S4 Genome-wide distribution of CECs of each gene with the hcASD (64) gene set under three different gene ranking conditions.

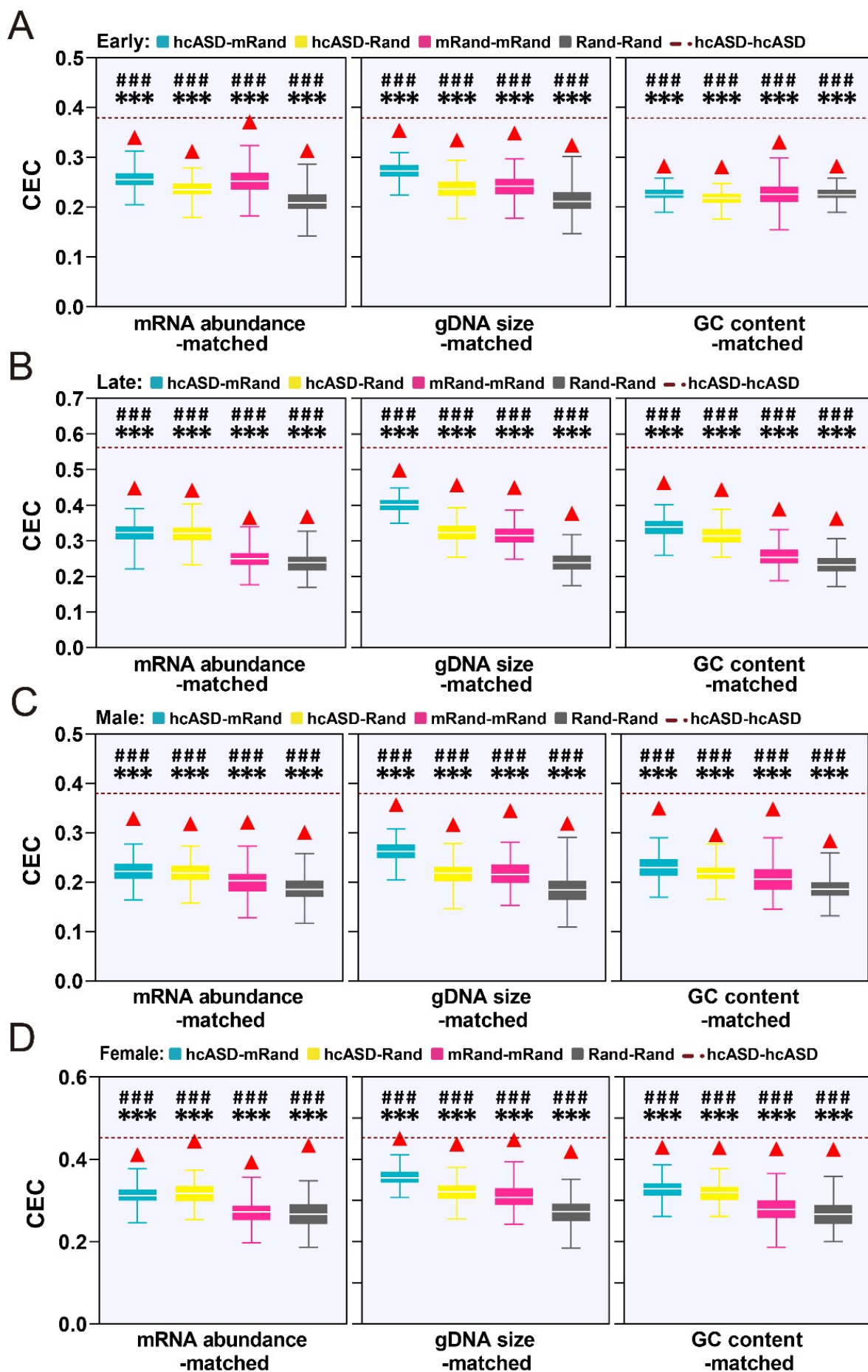


Fig. S5 Co-expression of hcASDs in the brain at different developmental stages and sex. **A, B** Data from early (**A**; PCW8 to 2Y) and late (**B**; 3Y–40Y) developmental stages. **C, D** Data from male (**C**) and female (**D**) brain tissue.

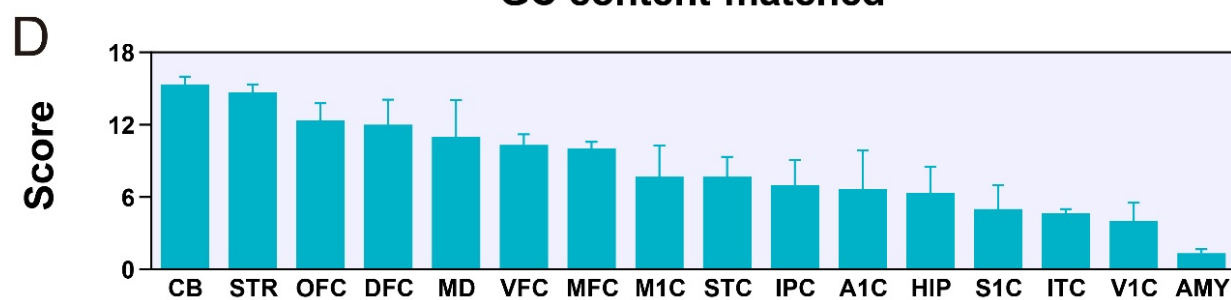
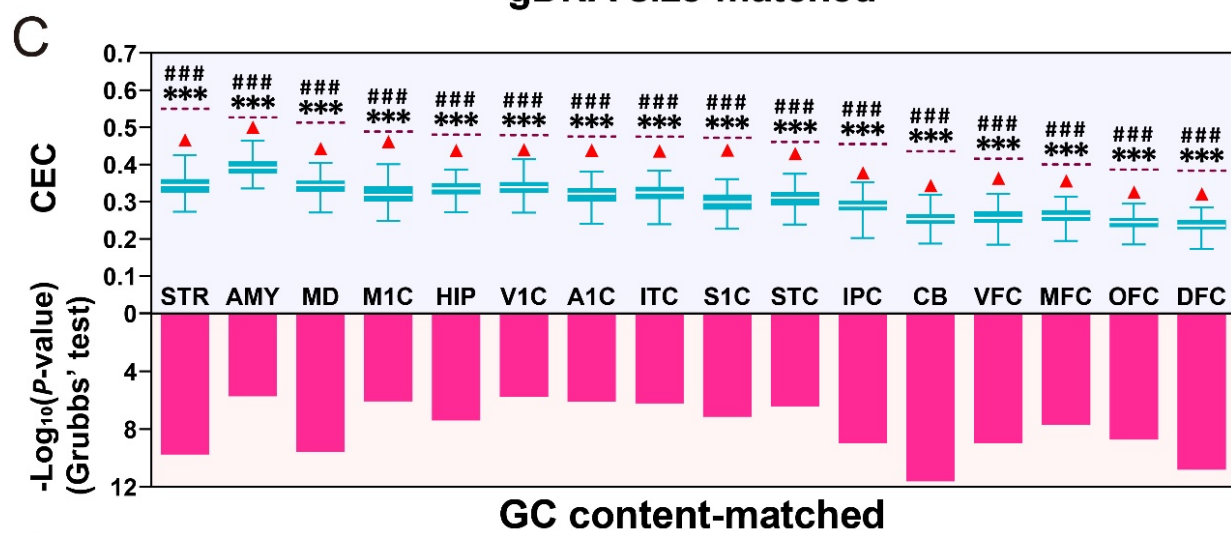
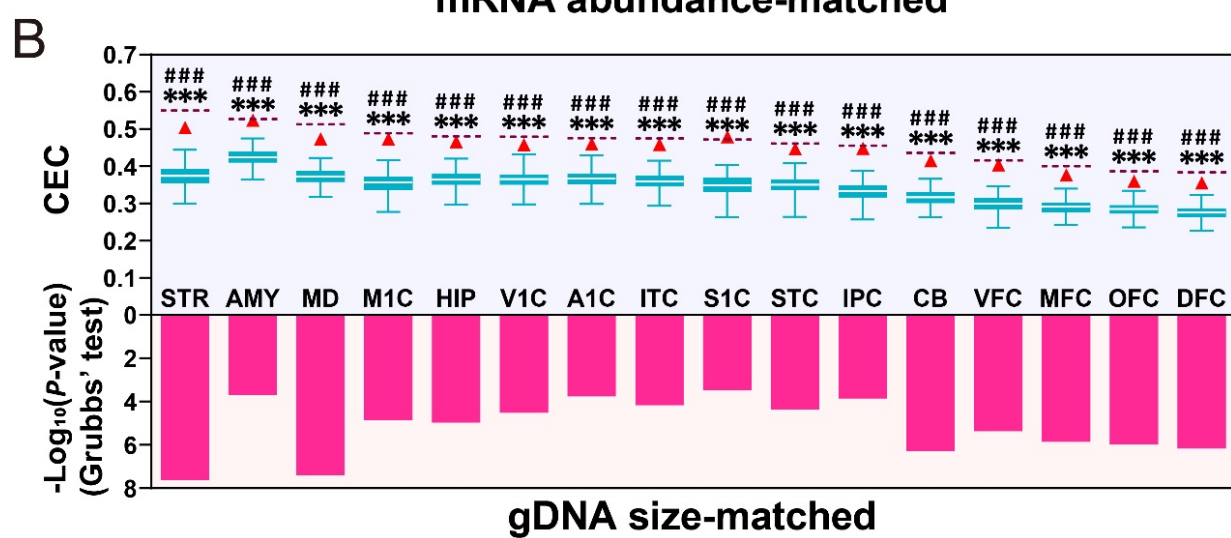
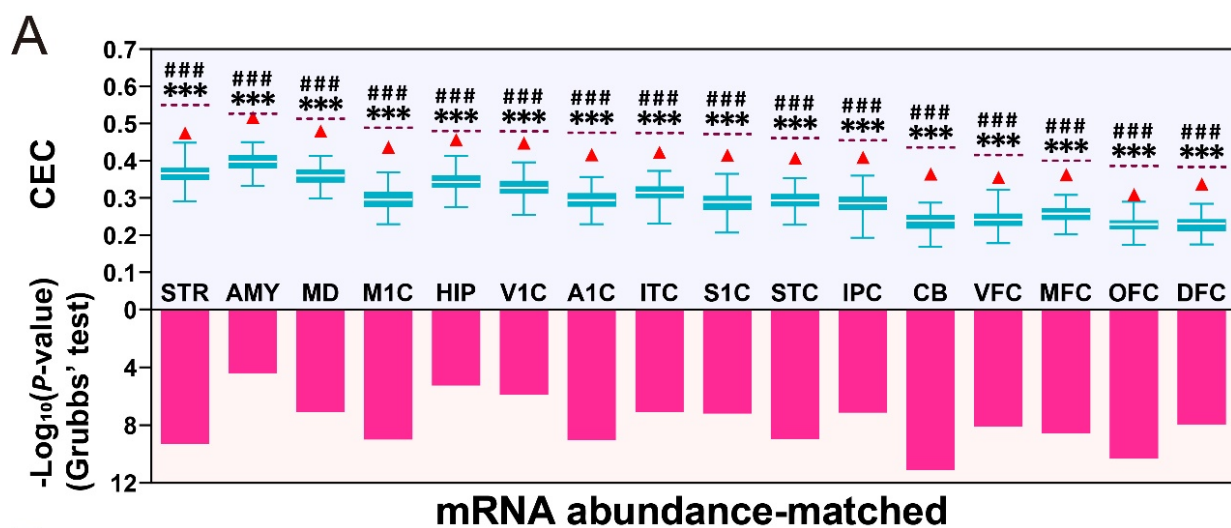


Fig. S6 Co-expression of hcASDs in different brain regions. **A–C** Box plots showing the range of CECs of hcASD–mRNA and in different brain regions. **D** Significant scores of co-expression of hcASDs in different brain regions. Score = $N - R$ where N is the number of regions and R is the integrated ranking (average of 3 conditions) of $-\log_{10}(P\text{-value})$ in Grubbs' test under four different ranking conditions.

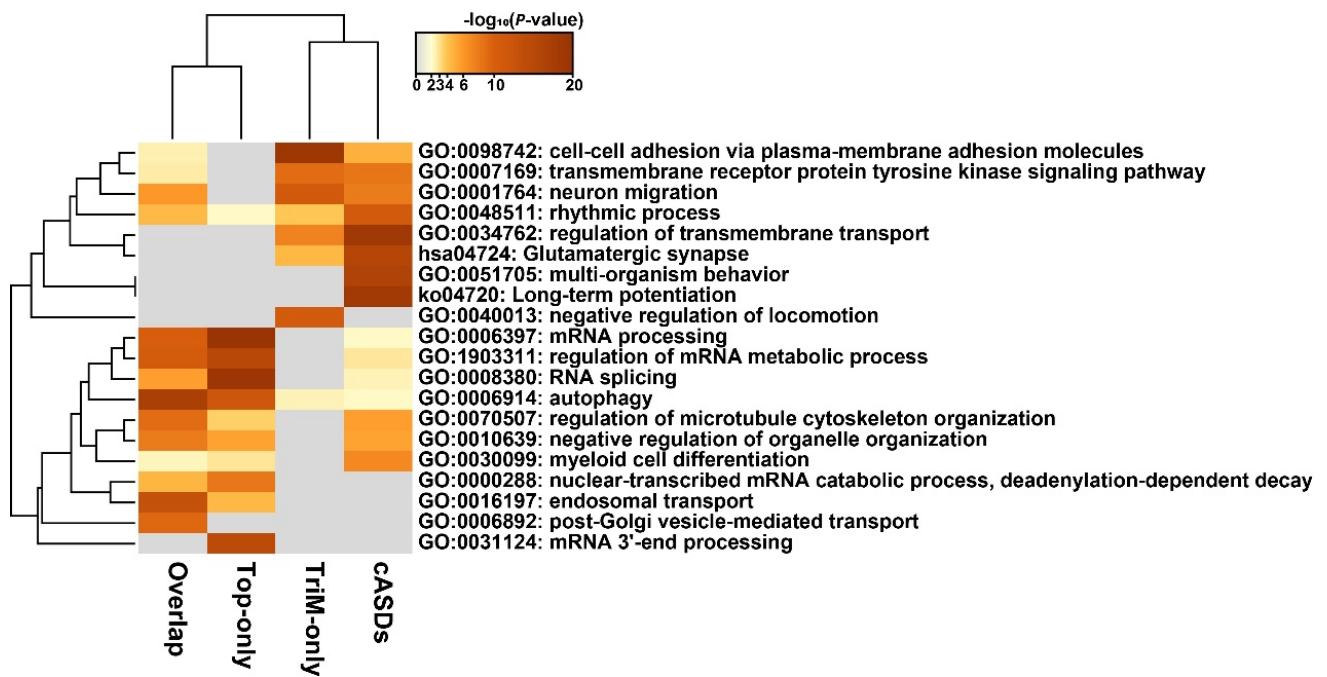


Fig. S7 Cluster analysis of $-\log_{10}(P\text{-value})$ in GO analysis of TriM-only, Top-only, Overlapped, and combined ASD gene sets (cASDs). $-\log_{10}(P\text{-value})$ values (0–20) are color-coded and shown in the heatmap. Boxes were colored according to their P -values. Gray boxes indicate a lack of enrichment for a specific GO term.