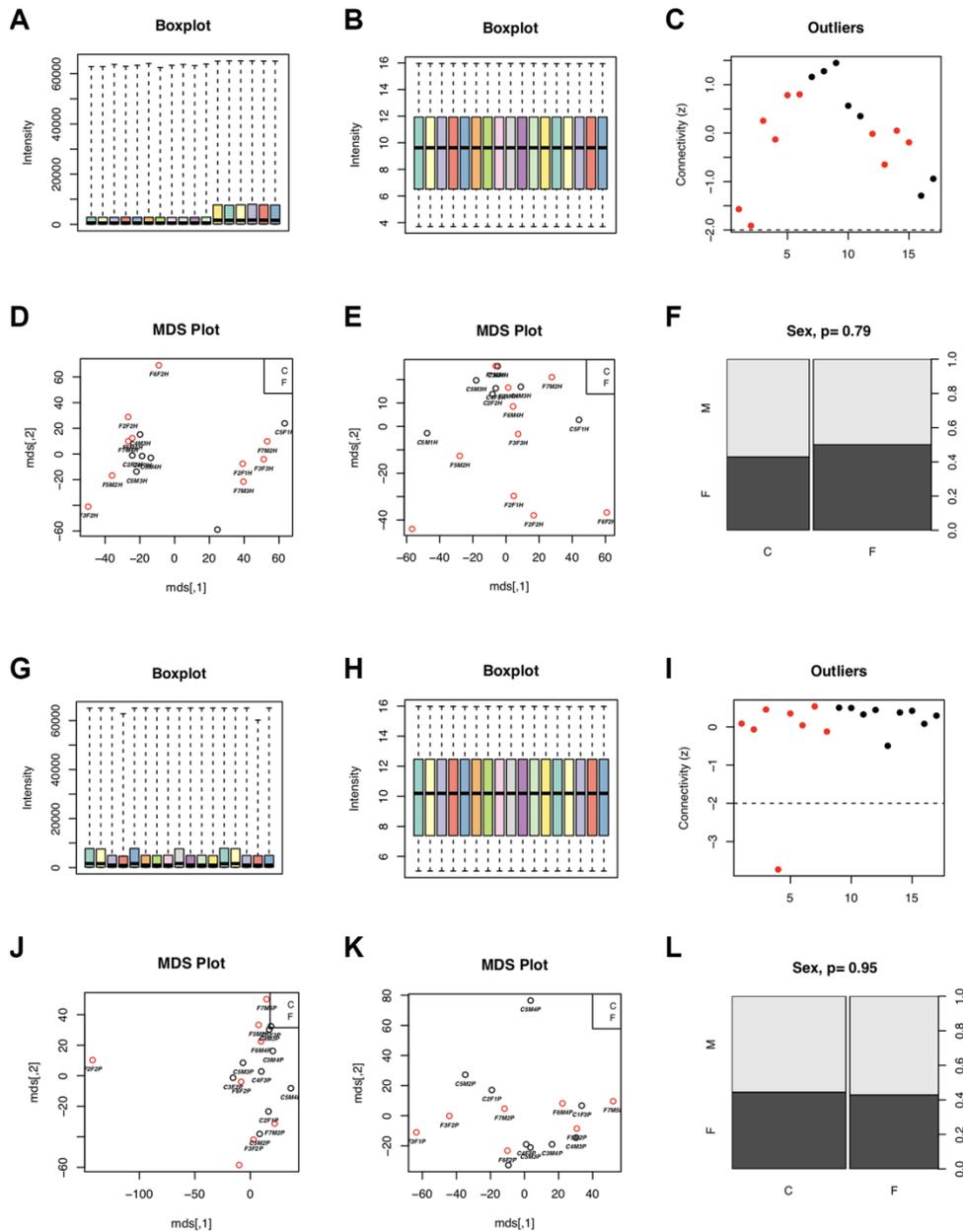
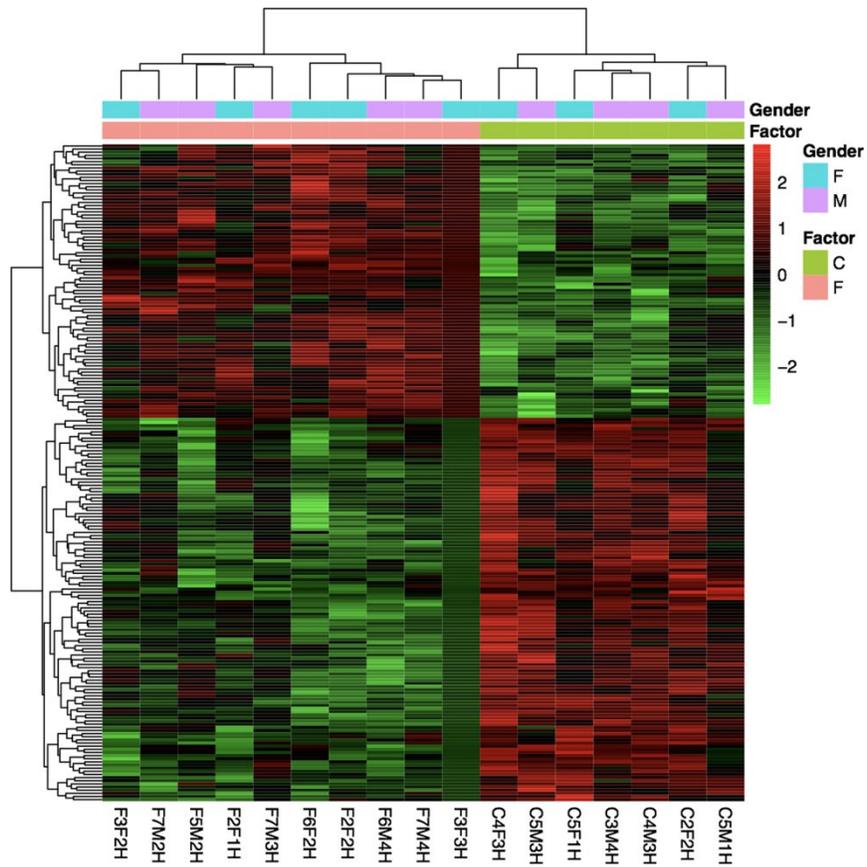


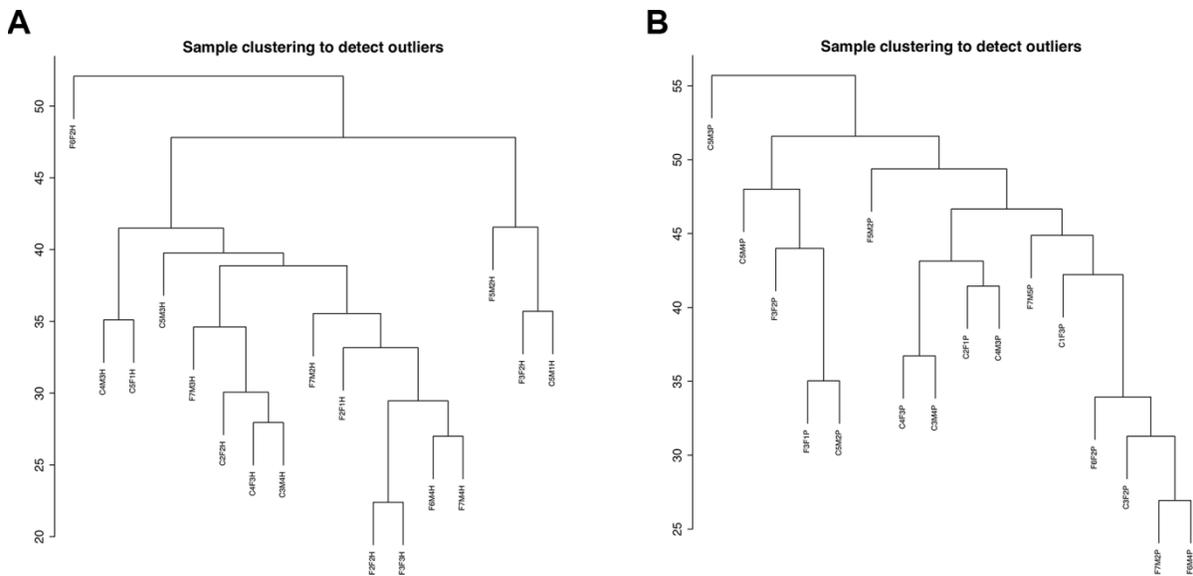
**SUPPLEMENTARY FIGURES**



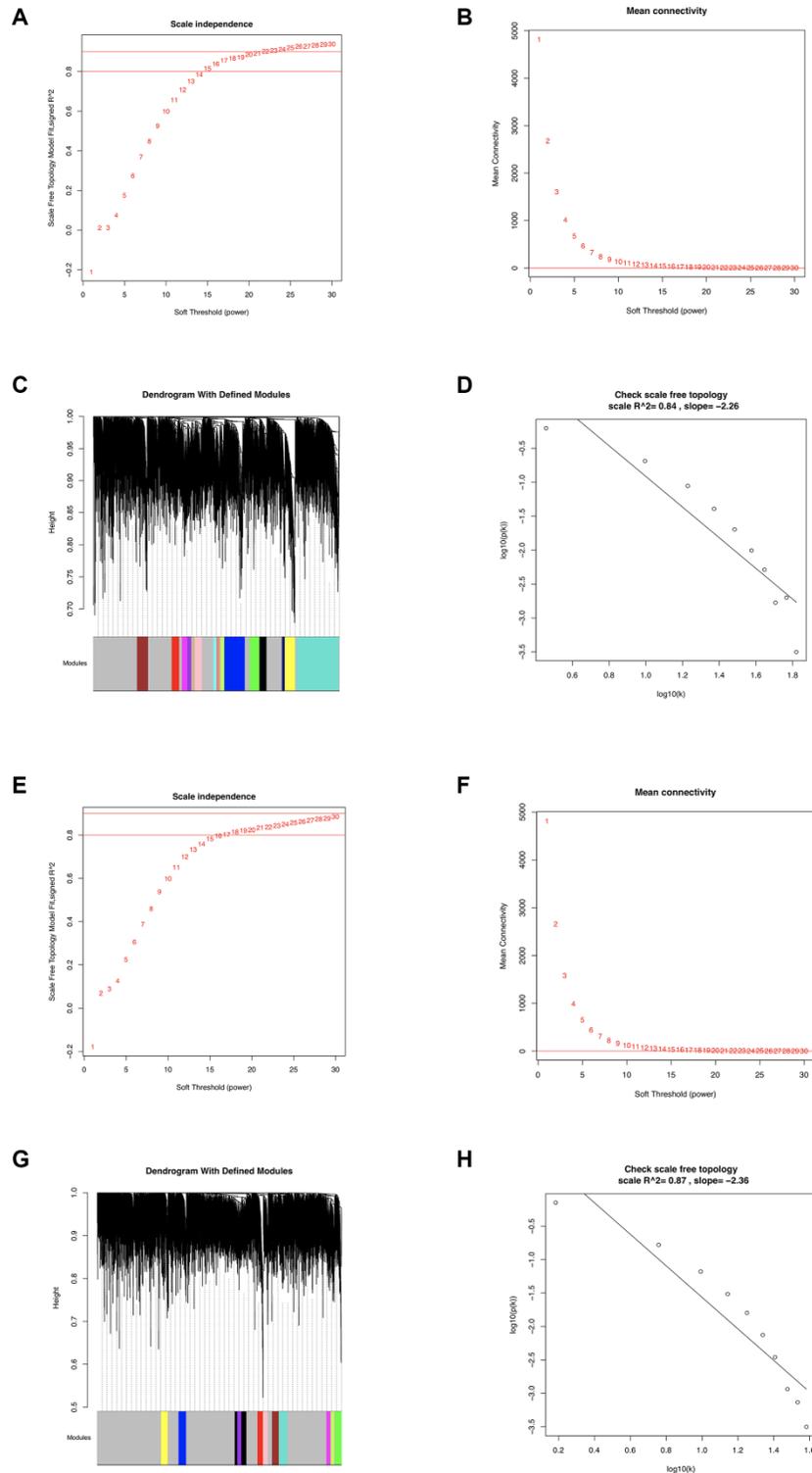
**Supplementary Figure 1. Quality control and data preprocessing.** (A, B) Pre- and post-normalization of expression profiles in hippocampus; (C) Detection of outlier based on standardized network connectivity z-scores in hippocampus; (D, E) Pre- and post-processing of batch effect in hippocampus; (F) Gender distribution for hippocampus samples between two groups treated with different prenatal nutritional status; (G, H) Pre- and post-normalization of expression profiles in prefrontal cortex. (I) Detection of outlier based on standardized network connectivity z-scores in prefrontal cortex. (J, K) Pre- and post-processing of batch effect in prefrontal cortex. (L) Gender distribution for prefrontal cortex samples between two groups treated with different prenatal nutritional status.



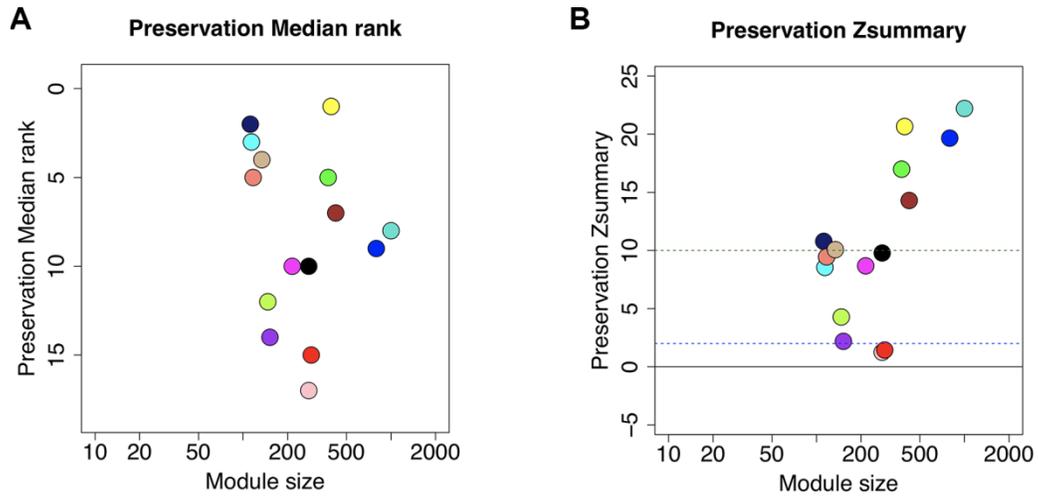
Supplementary Figure 2. Heatmap of 209 differentially expressed gene in hippocampus (Factor: C, control offspring; F, famine offspring, Gender: M, Male; F, Female).



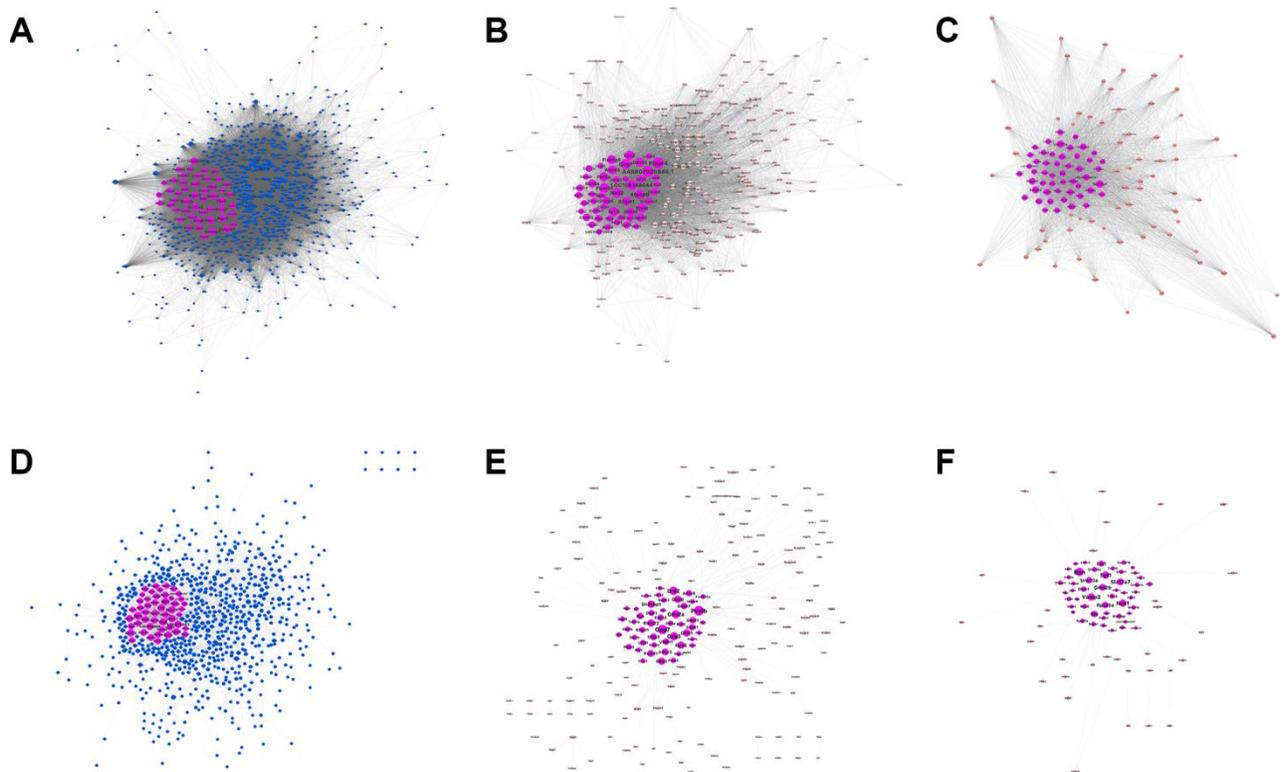
Supplementary Figure 3. Sample clustering analysis for detecting outliers in the hippocampus (A) and prefrontal cortex (B).



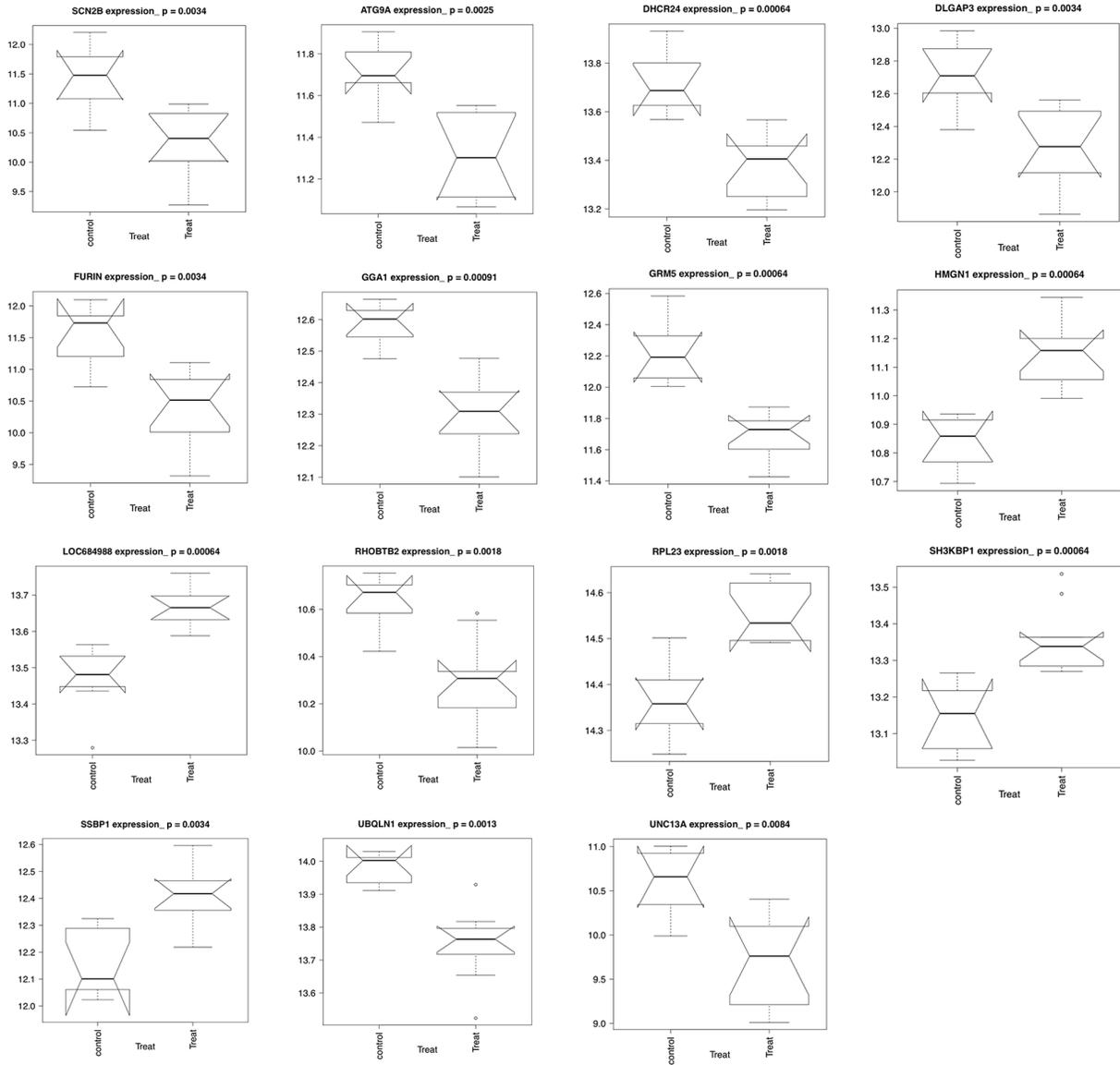
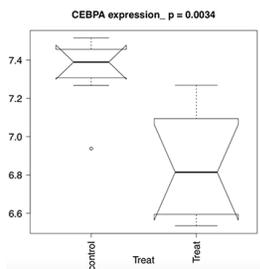
**Supplementary Figure 4. Parameter selection for construction of weighted gene co-expression network in hippocampus and prefrontal cortex.** (A) Selection of the scale-free fit index based on different soft-threshold powers ( $\beta$ ) in hippocampus ( $\beta$  15 was determined); (B) Selection of the mean connectivity of different soft-threshold powers in hippocampus; (C) Dendrogram of 9553 expressed genes clustered based on a dissimilarity measure (1-TOM) in hippocampus; (D) Check of scale-free topology with soft-threshold power  $\beta$  equaling 15 in hippocampus; (E) Selection of the scale-free fit index based on different soft-threshold powers ( $\beta$ ) in prefrontal cortex ( $\beta$  17 was determined); (F) Selection of the mean connectivity of different soft-threshold powers in prefrontal cortex; (G) Dendrogram of 9553 expressed genes clustered based on a dissimilarity measure (1-TOM) in prefrontal cortex; (H) Check of scale-free topology with soft-threshold power  $\beta$  equaling 17 in prefrontal cortex.



**Supplementary Figure 5. Module preservation analysis between hippocampus and prefrontal cortex.** The Y-axis represents preserved values and the X-axis represents module size. (A) median Rank test; and (B) Z summary statistics test.



**Supplementary Figure 6. Co-expression (A–C) and PPI networks (D–F) for the corresponding blue, pink, and salmon modules.**

**A****B**

**Supplementary Figure 7.** Differentially expressed hub genes (A), and transcription factors (B) between two groups related to prenatal nutritional status in the interesting modules.