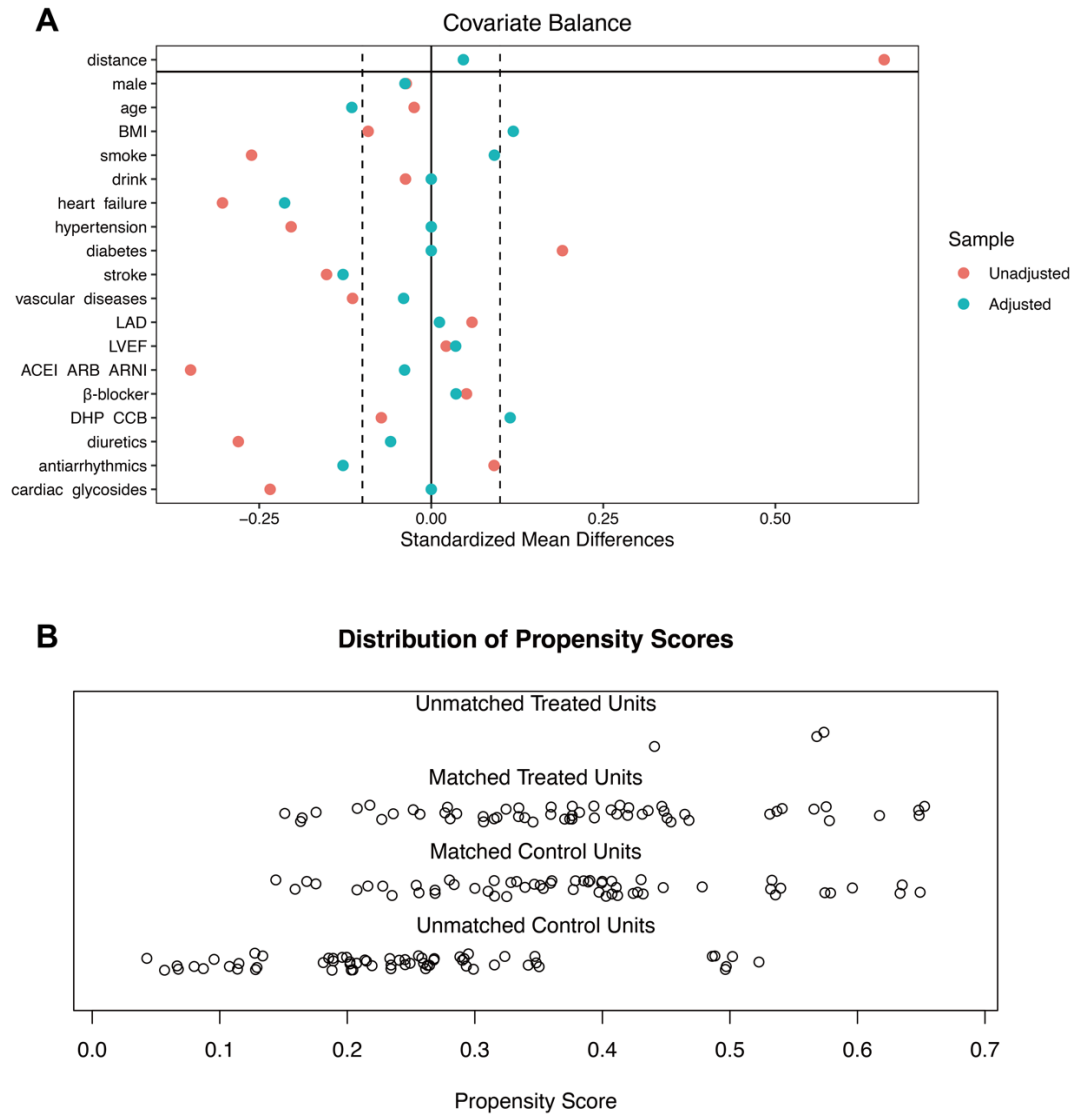
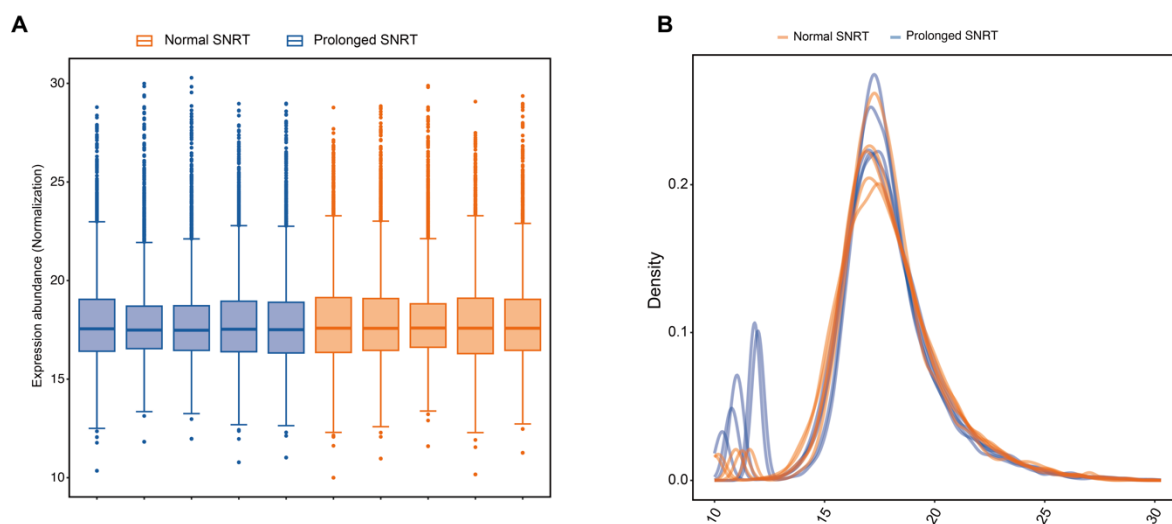
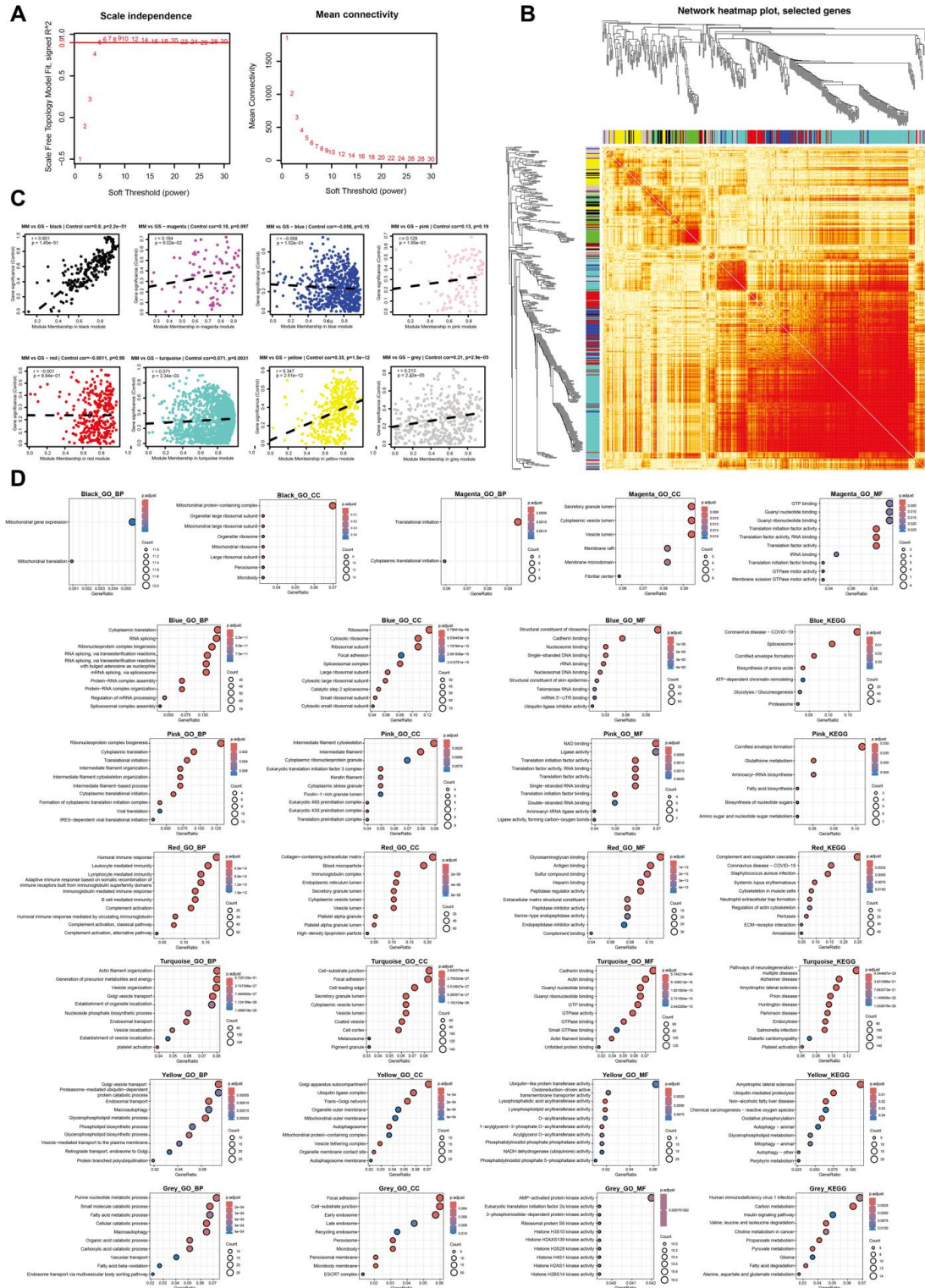




Supplementary Figure 1. Covariate balance for propensity score matching (PSM). (A) Covariate balance plot displaying standardized mean differences of baseline variables before and after matching. After PSM, all covariates achieved adequate balance (standardized mean difference < 0.1). (B) Distribution of propensity scores in experimental and control groups, showing substantial overlap between matched treated and matched control units, indicating successful matching. Data are expressed as mean $\pm$ SD.



Supplementary Figure 2. Quality control of proteomic data. (A) Boxplot showing normalized protein expression levels across all samples, confirming uniform data distribution and no batch effects. (B) Density plot of normalized protein abundance illustrating consistent overall distribution between experimental and control groups.



Supplementary Figure 3. Supplementary analyses of the weighted protein co-expression network. (A) Selection of the soft-thresholding power for WGCNA network construction. The scale-free topology fit index (R^2) and mean connectivity were assessed at different powers, and a power of 5 was chosen to approximate scale-free topology. (B) Weighted network heatmap illustrating the topological overlap among representative proteins. Warmer colors

indicate stronger co-expression similarity, confirming the network's robustness and modular structure. (C) Scatterplots showing the relationships between module membership (MM) and gene significance (GS) for all modules except the brown and green ones. Each point represents a protein. Positive correlations suggest that highly connected proteins within these modules are also associated with the SND phenotype (control vs. prolonged SNRT). (D) Functional enrichment analyses for modules other than brown and green, including Gene Ontology (GO) and KEGG pathway analyses. Dot plots display the top enriched biological processes (BP), cellular components (CC), molecular functions (MF), and KEGG pathways for each module. The x-axis indicates gene ratio, dot size reflects the number of enriched proteins, and color represents adjusted p-values.