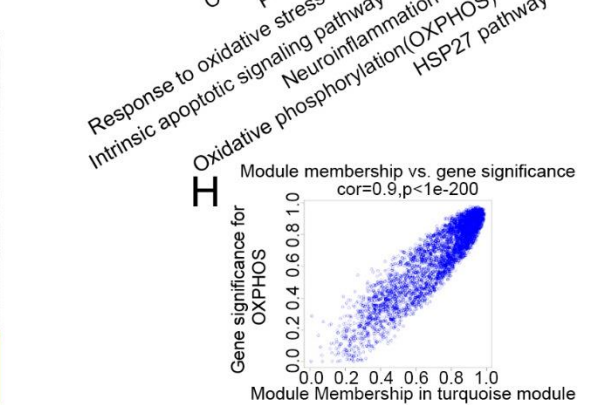
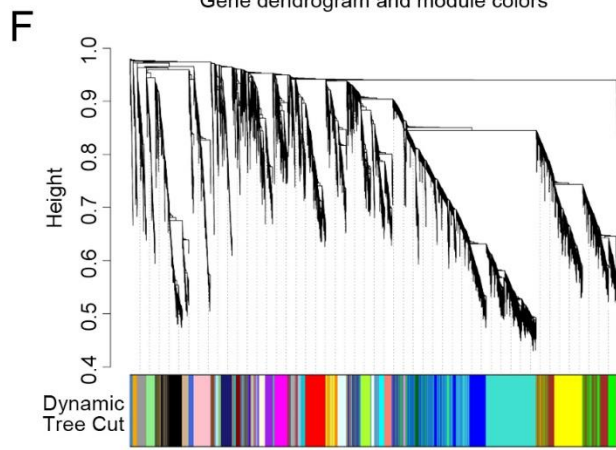
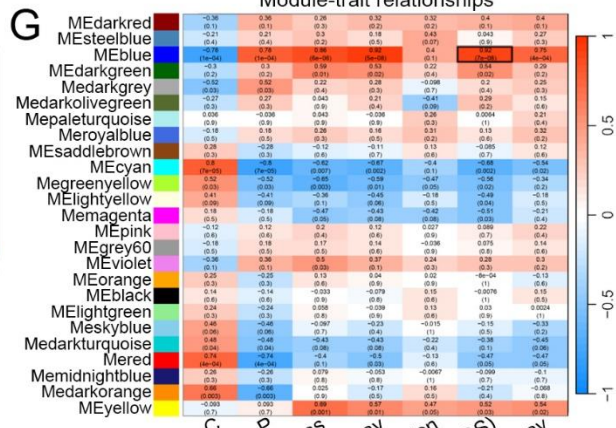
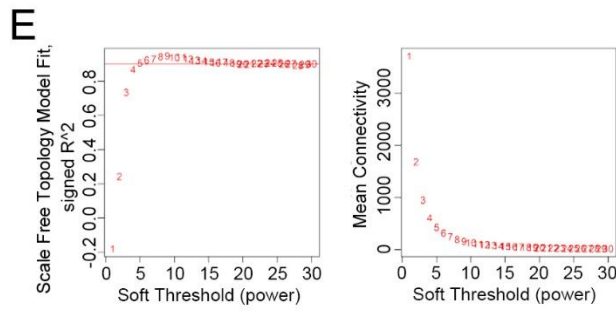
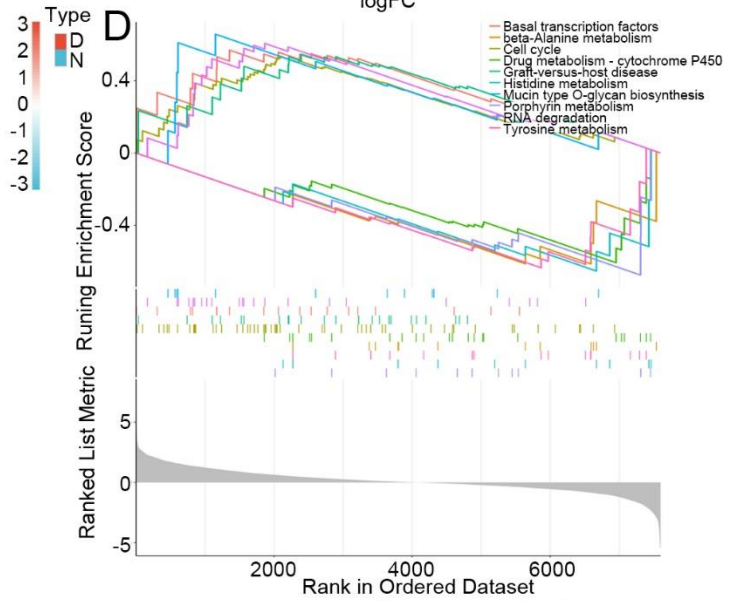
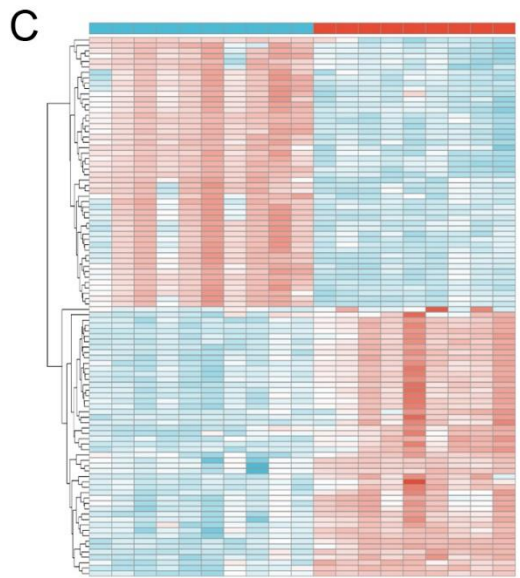
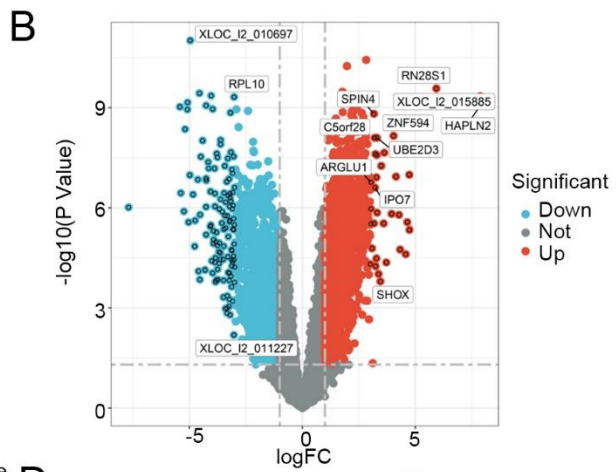
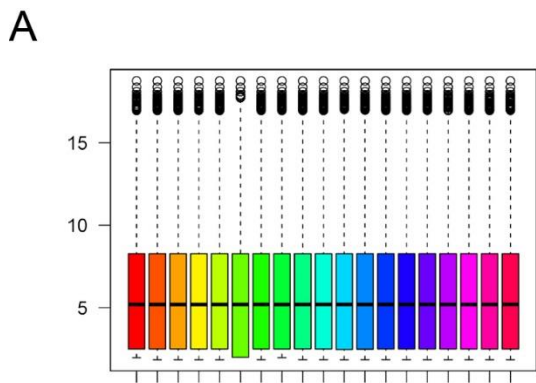
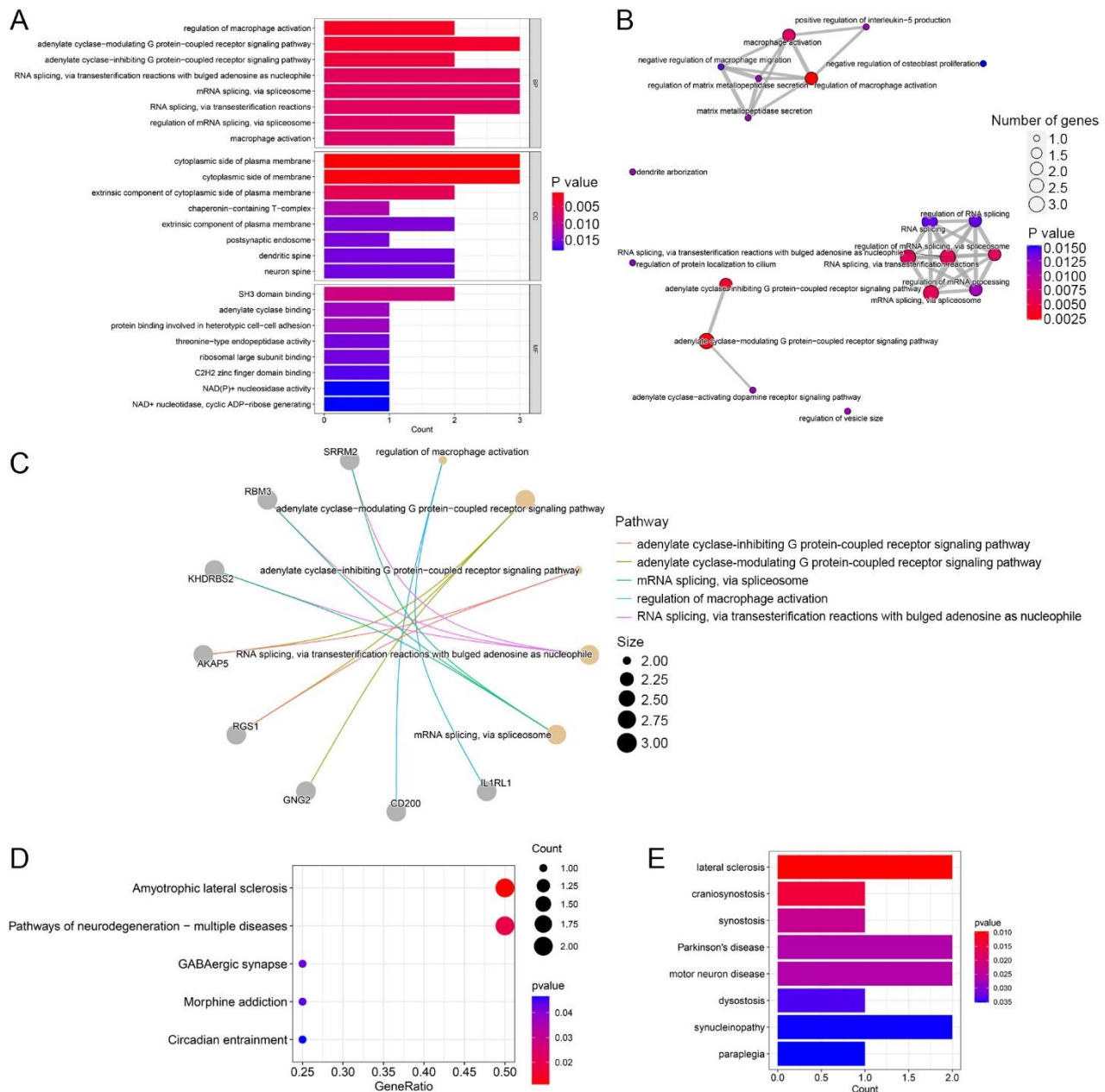


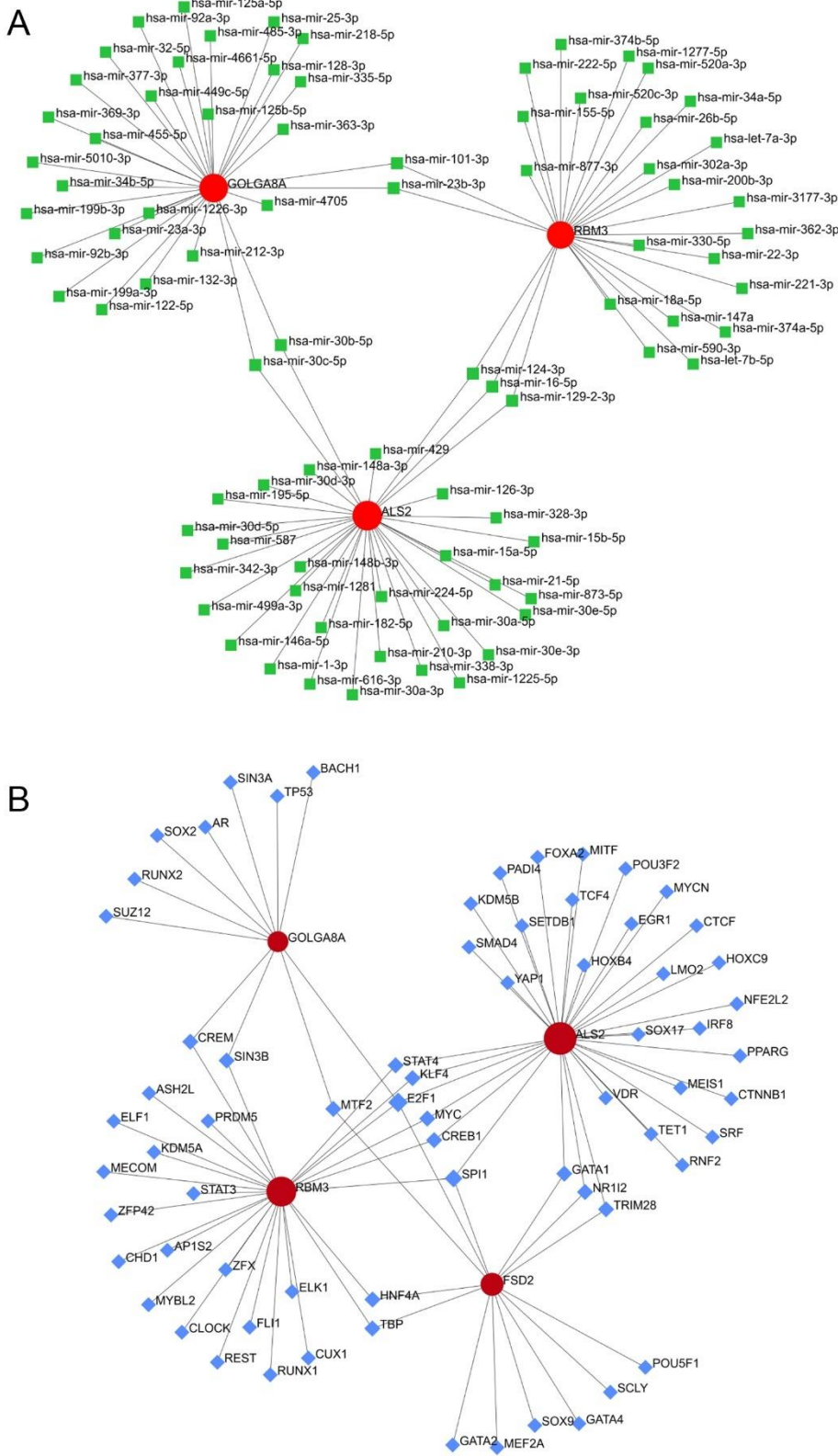
Supplementary Figure S1. Identification of DEGs in blood samples and results of WGCNA. **A** – Blood samples displayed after standardization. **B** – Volcano plot showing the expression characteristics of DEGs, where red represents gene upregulation in the AD group, and blue represents gene upregulation in the normal control group. **C** – Heat map showing expression of the top 50 DEGs in the blood samples. **D** – GSEA (gene set enrichment analysis) of DEGs. **E** – The left panel shows the scale-free fit index (scale independence, y -axis) as a function of soft threshold power (x -axis); the right panel shows the average connectivity (degree, y -axis) as a function of soft threshold power (x -axis). **F** – AD module clustering dendrogram based on a dissimilarity measure (1-TOM). The colored squares below the dendrogram represent the module assignment identified by dynamic tree cutting. **G** – Feature-module correlations. Each column corresponds to a clinical feature, whereas individual rows in the heat map correspond to an ME. Individual cells contain the corresponding p -value and correlation coefficient. **H** – Scatter plot of OXPHOS pathway correlation with genes in the blue module



Supplementary Figure S2. Enrichment analysis of function and disease of potential target genes. **A** – Bar plot showing the top 8 enriched results of target genes from 3 aspects of BP, CC, and MF. **B** – Net plot showing the connection of all the pathways from the 3 aspects of BP, CC, and MF. **C** – Circle chart showing the pathways and target genes from the aspect of BP. **D** – Bubble plot showing the top 5 enriched KEGG pathways of target genes. **E** – Bar plot showing the most enriched results of target genes from disease



Supplementary Figure S3. Regulatory network of potential biomarker markers. **A** – The miRNA–potential biomarker network, where the red nodes symbolize potential biomarkers, the green nodes symbolize microRNA (miRNA). **B** – The TF–potential biomarker network, where the red nodes symbolize potential biomarkers, the blue nodes symbolize transcription factors (TFs)



Supplementary Figure S4. Results of immune cell infiltration of AD blood samples. **A** – Relative percentage of 22 immune cells in each AD blood sample. **B** – Box plot for immune cell infiltration analysis in AD blood. Red represents the AD group and blue represents the control group. ns: not significant, * $p < 0.05$; ** $p < 0.01$

