

Supplementary Material

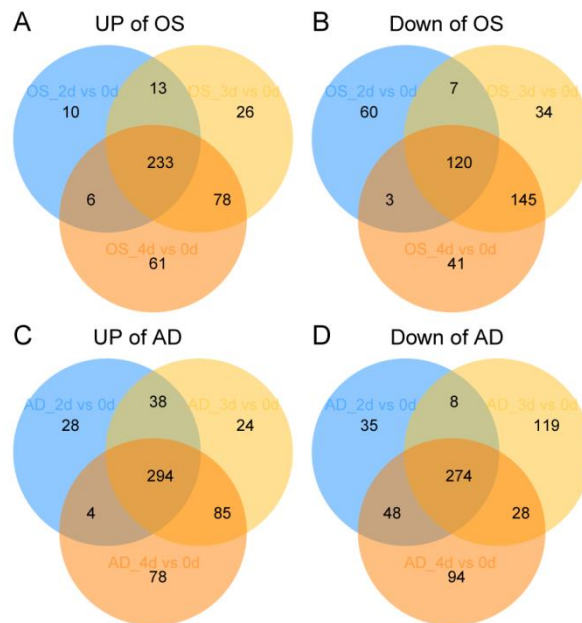


Figure S1. Common up-and downregulations in each time points of OS and AD. (A): up of OS (B): down of OS (C): up of OS (D): down of AD.

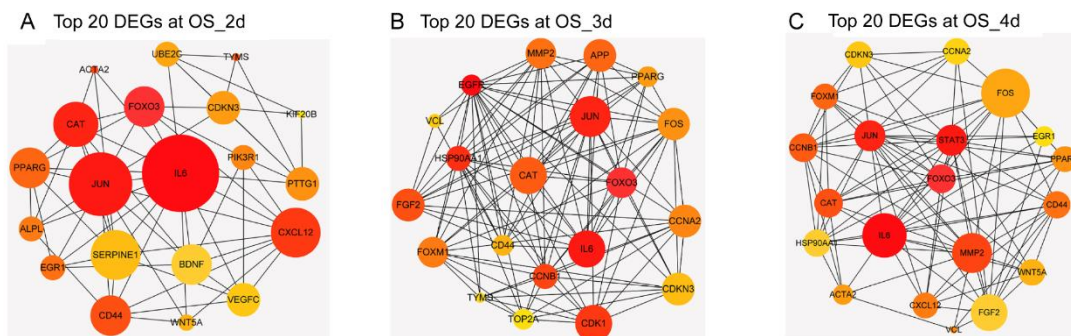


Figure S1S2. Key genes analysis in the OS. (A-C) Network representation of the protein-protein interactions (PPI) between the top 20 genes of the DEGs in different time points in the OS by the Stress mode using cytoHubba app in the cytoscape. The node's colors donated the clustering coefficient, and the brighter the color, the higher the clustering, which meant stronger interaction (rang from red (high) to yellow (low)), while the size of each node represented node degree distribution. (A) 2d vs 0d; (B) 3d vs 0d; (C) 4d vs 0d.

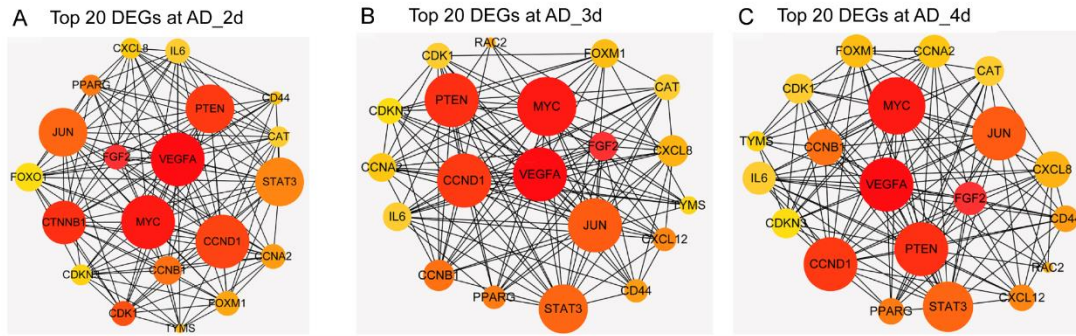


Figure S2S3. Key genes analysis in the AD. (A-C) Network representation of the protein-protein interactions (PPI) between the top 20 genes of the DEGs in different time points in the AD by the Stress mode using cytoHubba app in the cytoscape. The node's colors donated the clustering coefficient, and the brighter the color, the higher the clustering, which meant stronger interaction (rang from red (high) to yellow (low)), while the size of each node represented node degree distribution. (A) 2d vs 0d; (B) 3d vs 0d; (C) 4d vs 0d.