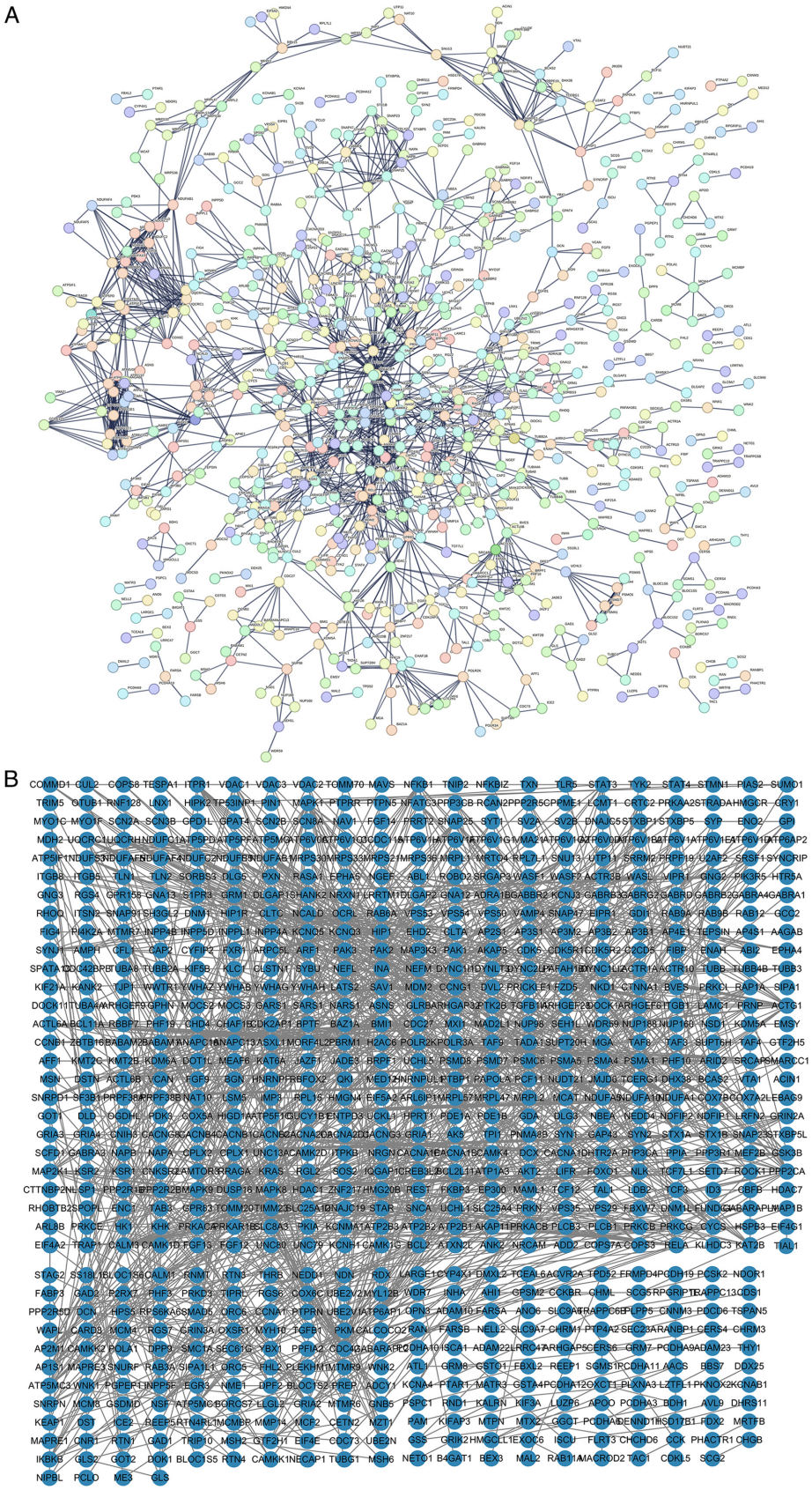Figure S1. Identification of hub genes in AD through integrated PPI network and multi-algorithm topological analysis. (A) The initial PPI network was constructed using the STRING database with 1,714 candidate genes that showed significant associations with AD. The network displays all protein-protein interactions meeting a medium confidence threshold (>0.9). (B) Optimized visualization of the PPI network after analysis in Cytoscape using the cytoHubba plugin. The top 200 genes from each of four distinct topological algorithms (Degree, MNC, MCC and Stress) were identified. The intersection of these four gene sets yielded 108 common key genes. AD, Alzheimer's disease; PPI, protein-protein interaction; MNC, Maximal Clique Centrality; MCC, Maximal Clique Centrality.