



Figure S2. Co-representation network.

Edge files generated by WGCNA software were imported into Cytoscape to construct this network selected according to the actual requirements. According to the weight value of connectivity between all genes in the Module, firstly screen the relationship with sufficient strength, and then calculate the degree of connectivity. The top 5 genes were separated according to the degree of connectivity to construct the network map.

Note: A showed genes with black-weight Greater than 0.45 (node degree 5); B showed genes with brown-weight Greater than 0.66 (node degree 5)