

Figure S1 Networks of each group.

The yellow, red, green and pink networks are from the vehicle, JA, UA, JU groups, respectively. Networks of each group are absolute scale-free networks, and the node degree follows a power-law distribution. Purple nodes represent the differentially expressed genes obtained from experiment.

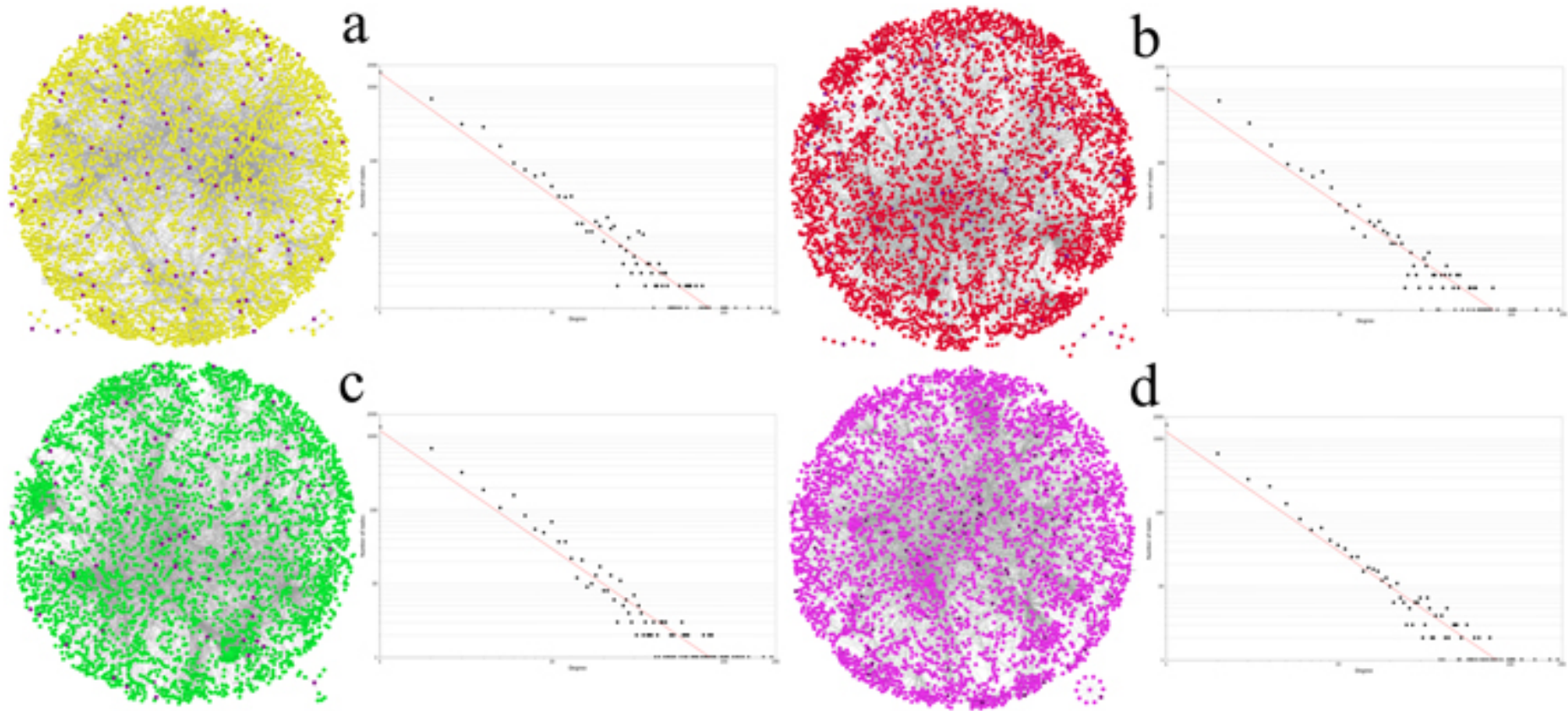


Figure S2 Modules of each group.

The yellow, red, green and pink modules are identified by MCODE from the networks of the vehicle, JA, UA, JU groups, respectively. Purple nodes represent the differentially expressed genes obtained from experiment

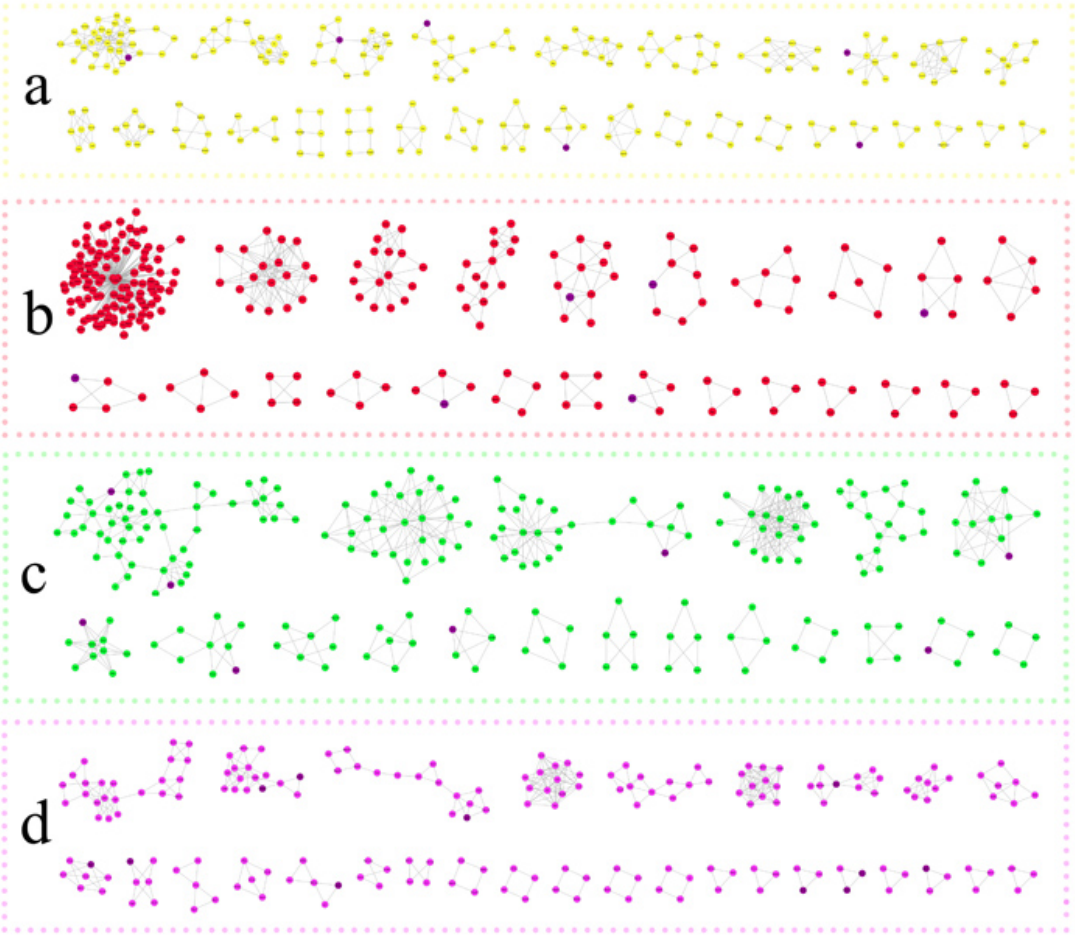


Figure S3 Comparison of the GO classification (biological processes) between the monotherapy groups and the drug combination group.

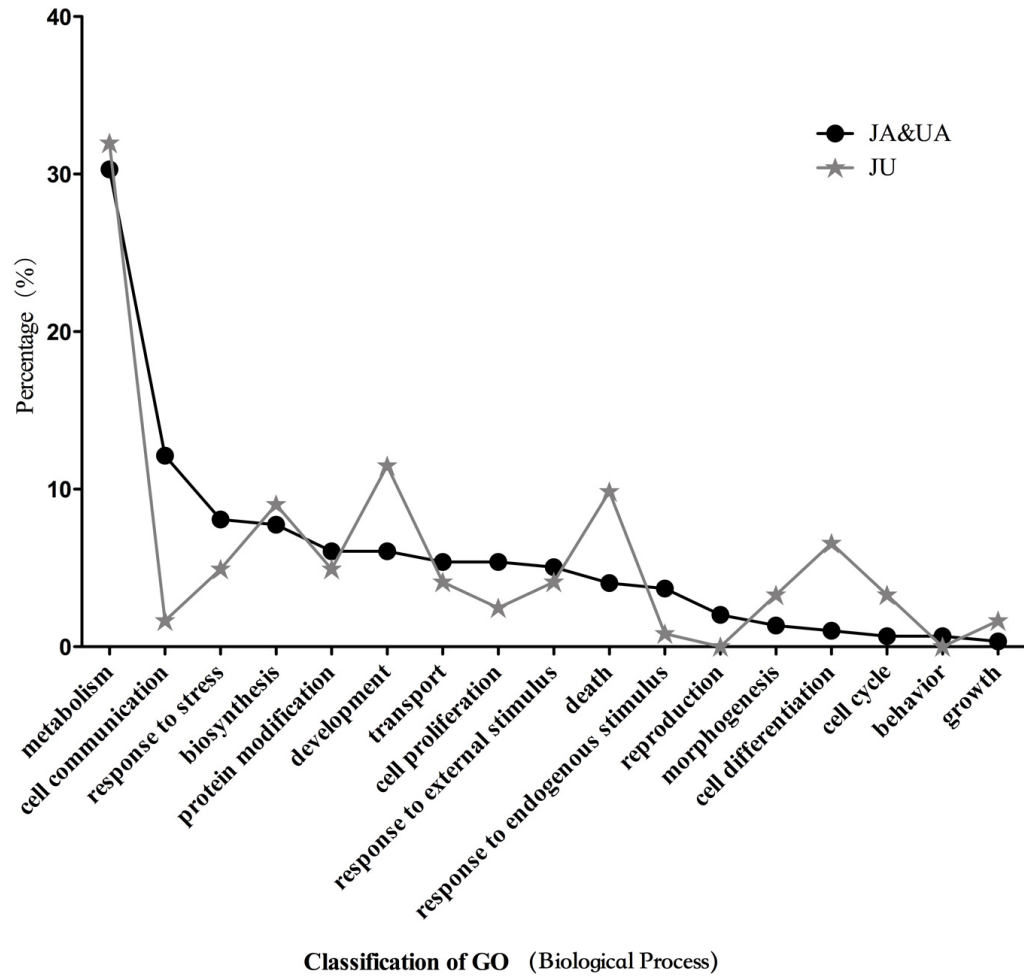


Figure S4 The distribution of eigenvalue set in each module.

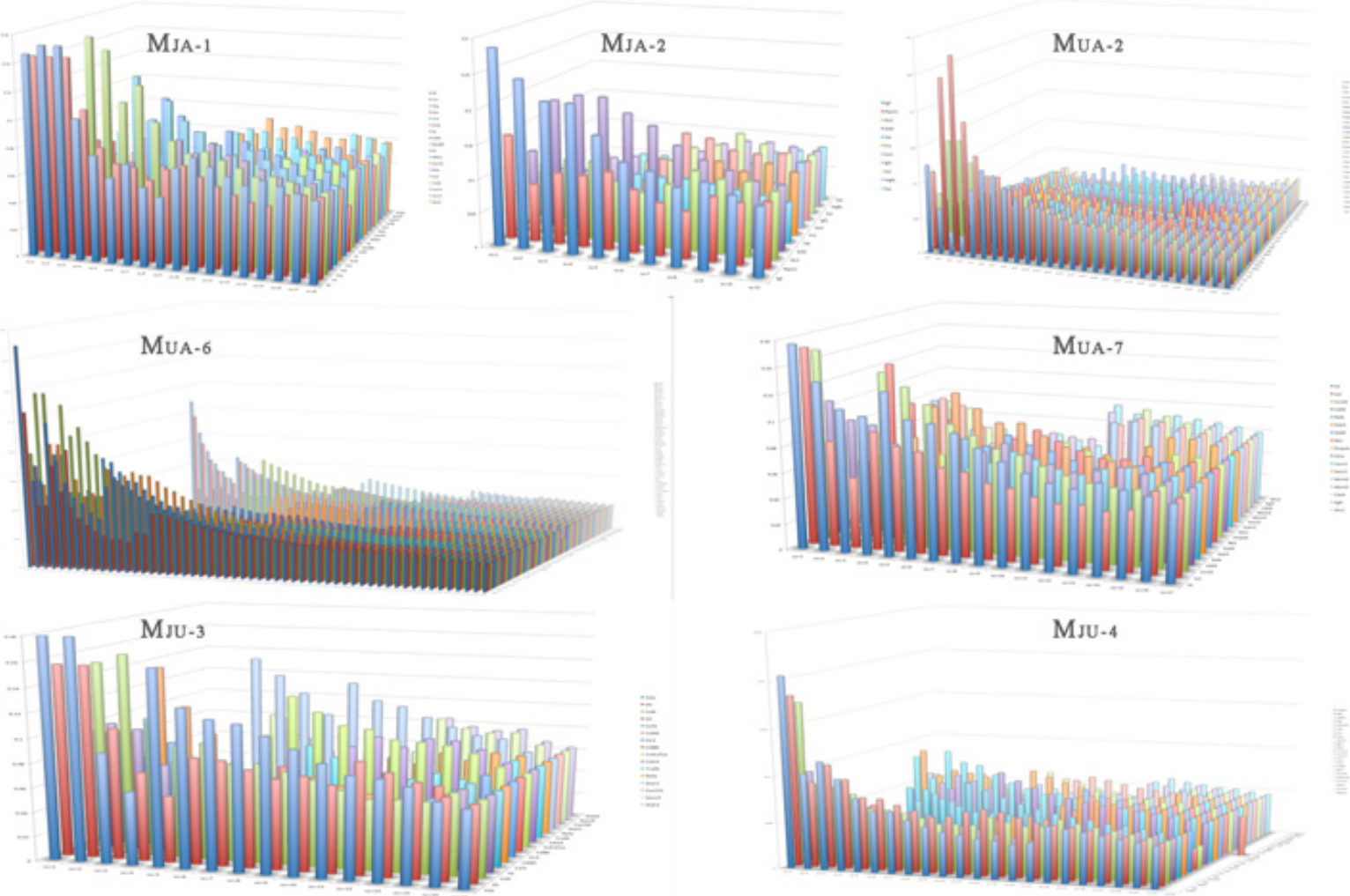


Figure S5 Biological verification by Western blotting.

A. Validation of CYCLIN expression levels between different groups by Western blotting analysis. *P < 0.05 versus sham. ##P < 0.01 versus vehicle (n=3). B. Validation of IL1RA expression levels between different groups by Western blotting analysis, #P < 0.01 versus sham, *P < 0.05 versus vehicle, **P < 0.01 versus vehicle (n=3).

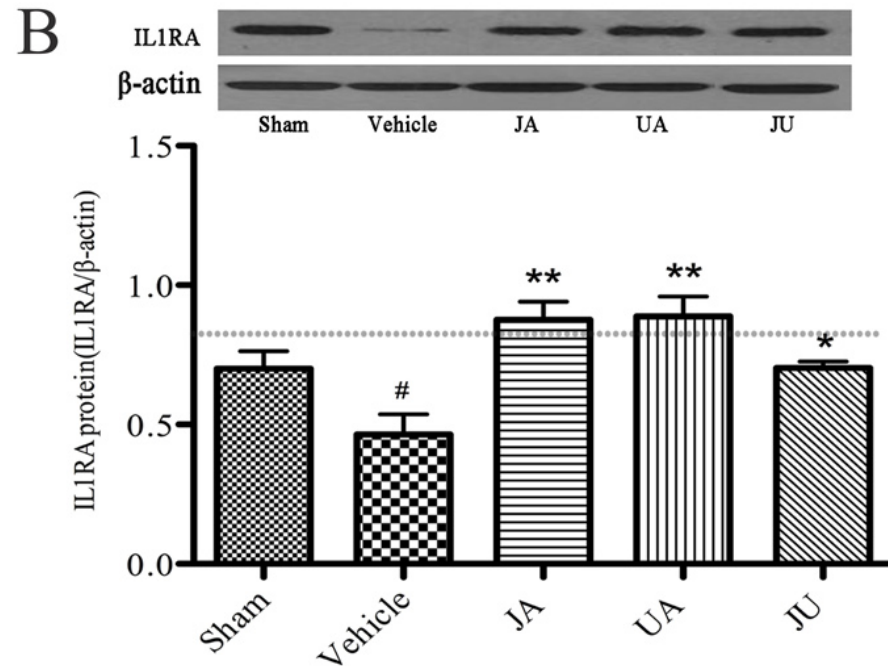
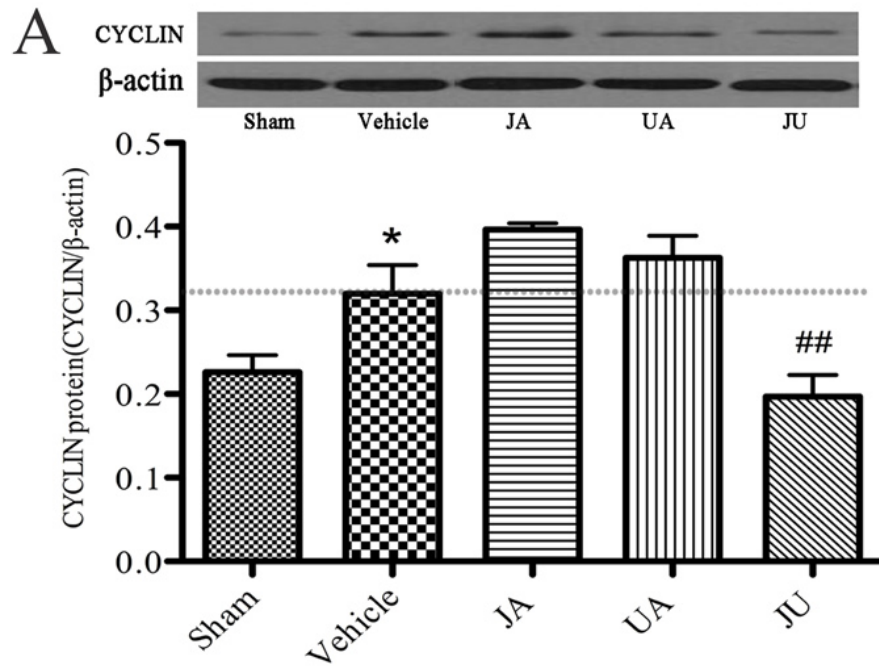


Figure S6 Pathways in cancer from KEGG database.

The nodes labeled with red star are the overlapping nodes between core modules and pathways in cancer.

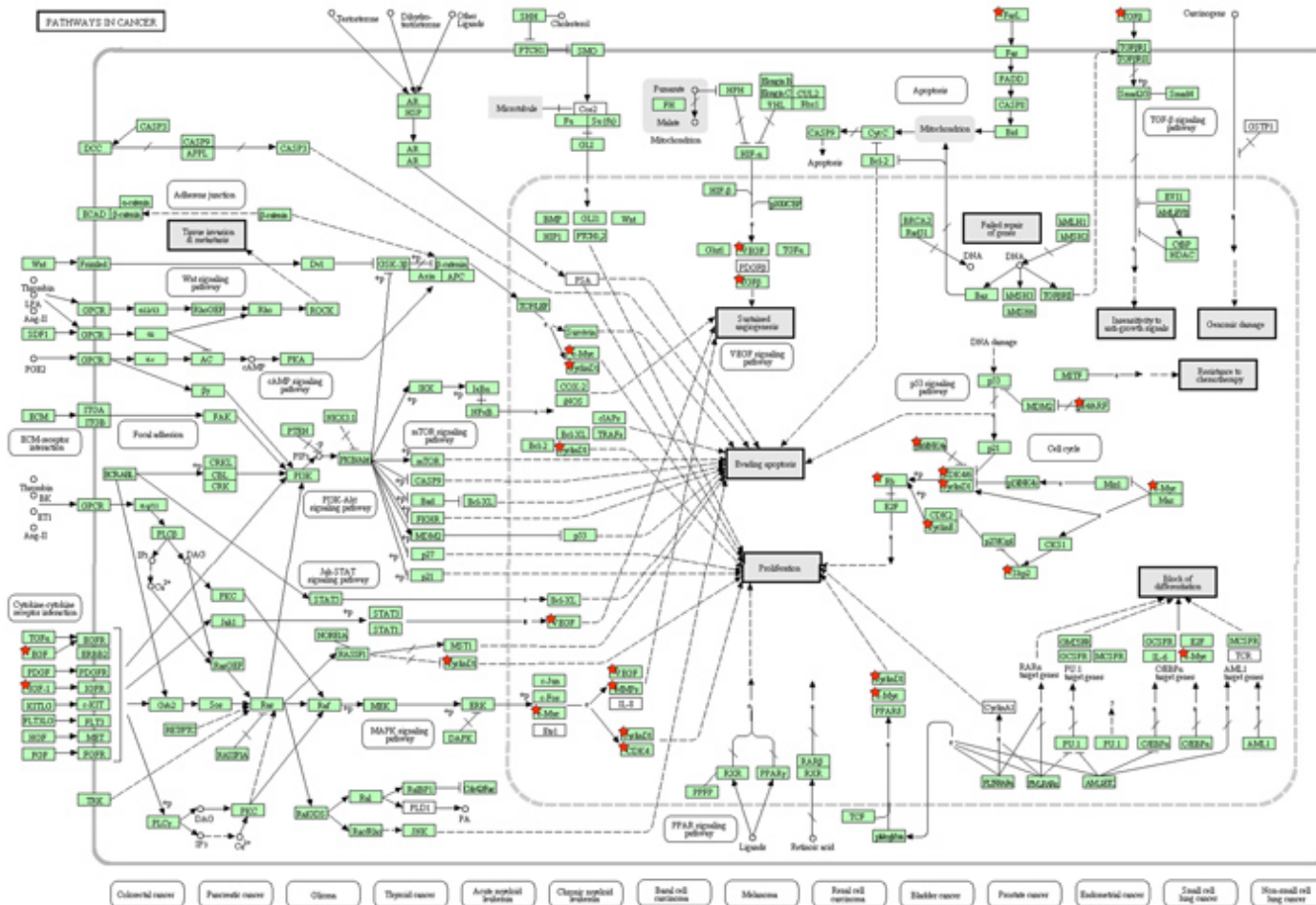


Figure S7 Pathway convergence based on the PMDs in the JU group.

