Supplementary information

Figure S1. Network topological characteristics in regulatory network consisting of 67 FFLs in OVC. The in-degree (A), out-degree (B), path length (C), and closeness centrality (D) are plotted against to the number of nodes, neighbours, or frequency.

Table S1. List of 799 miRNAs, 524 human TFs, and 1257 ovarian cancer (OVC) related genes.

Table S2. List of 67 coherent feed-forward loops detected in the TCGA serous ovarian cancer samples.

Table S3. List of 32 coherent feed-forward loops involved in cell differentiation in the serous ovarian cancer.

Table S4. Pathway annotations of 47 protein-coding genes in the ovarian cancer regulatory network with FFLs. The functional annotation and statistical enrichment results were obtained from the IPA pathway analysis tool.

Table S5. Summary of the 17 datasets having more than 67 FFLs from randomization analyses.