1.R

The number of significantly differentially expressed genes of a curable oligometastatic state in colorectal liver metastasis.

2.R

Network characteristics of nodes. Compare the average shortest path and degree between nodes and nodes in the network.

3.R

The gene module is constructed by random walk algorithm. The inclusion relation of each module is calculated and the similarity of each module is calculated.

4.R

Random 1000 times, compare the degree, average shortest path and inclusion relationship between random results and real results.

5.R

The gene with inclusion relationship was deleted and the gene module was constructed by random walk.

6.R

The gene modules are clustered by Markov clustering algorithm, and the clustering results are displayed.

7.R

The cluster function and miRNA enrichment were analyzed

8.R

Remove the batch effect of TCGA download data

9.R

The differentially expressed miRNAs in primary and less metastatic (OM) cases were calculated

10.R

Three miRNAs with significant differences were enriched by KEGG and GO.

11.R

For miRNA validation, 17 and 3 miRNAs were used to construct random forest classifiers, and ROC curves were drawn.

12.R

Hierarchical clustering of clinical stage 3 and 4 patients was performed by three significantly different miRNAs.

13.R

Objective to study the relationship between the target genes of three miRNAs with significant differences and immune genes.

14.cys

The distribution of target genes of the three miRNAs with significant differences was plotted by Cytoscape.