Figure S1. Screening consistent genes and functional analysis.
A. The distributions of RRA scores via integrative analysis of 9 GEO datasets. Venn distribution shows that a total of 710 consistent deregulated genes are collected through GEO and TCGA datasets.
B. A scatter plot shows the expression distributions of all the relevant genes in TCGA dataset.
C. Significantly enriched GO terms based on up-regulated screened genes. BP indicates biological process, CC indicates cellular component, and MF indicates molecular function.
D. Significantly enriched GO terms based on down-regulated screened genes.
Figure S2. Contributed cell cycle pathway by analyzing primarily screened 710 genes.
Figure S3. Functional analysis of the screened 31 hub genes.
A. All of these 31 genes are detected certain roles in activating and inhibiting pathways.
B. The correlations of these 31 hub genes with drug sensitivity.
C. The expression correlations between paired genes.
D. The binding sites between different RNAs.

Table S1. The gene expression data in LUAD used in the study.

| Datasets   | Tumor | Normal | Total | Platforms | PMID number        |
|------------|-------|--------|-------|-----------|--------------------|
| GSE31210   | 226   | 20     | 246   | GPL570    | PMID: 23028479     |
| GSE118370  | 6     | 6      | 12    | GPL570    | PMID: 30545439     |
| GSE75037   | 83    | 83     | 166   | GPL6884   | PMID: 27354471     |
| GSE32863   | 58    | 58     | 116   | GPL6884   | PMID: 22613842     |
| GSE85716   | 6     | 6      | 12    | GPL19612  | PMID: 29127420     |
| GSE85841   | 8     | 8      | 16    | GPL20115  | PMID: 28178989     |
| GSE63459   | 33    | 32     | 65    | GPL6883   | PMID: 26134223     |
| GSE130779  | 8     | 8      | 16    | GPL20115  | PMID: 32869486     |
| GSE148036  | 5     | 5      | 10    | GPL21290  | PMID: 33097805     |
| TCGA-LUAD  | 483   | 59     | 542   | IlluminaHiSeq |                |
| Total      | 916   | 285    | 1201  |           |