Supplementary Materials

Supplementary materials included Supplementary Figures 1-3 and Table S1-3.

Supplementary figure 1. Statistical analysis of cleaned reads from the control and treatment group.

Supplementary figure 2. Volcano plot of the differentially expressed mRNAs, lncRNAs and miRNAs.

Supplementary figure 3. KEGG enrichment analyais of ceRNA network.

Supplementary Table S1. The list of significantly differential expressed RNAs in HepG2 cells treated with Dox.

Supplementary Table S2. The list of ceRNA pairs of ceRNA network.

Supplementary Table S3. A ceRNA network that consists of 54 miRNAs, 173 lncRNAs and 494 mRNAs with experimentally confirmed p53 binding sites.

A

Control
Mapped(85.05%)
Unmapped(14.95%)

Treatment
Mapped(83.29%)
Unmapped(16.71%)

B

Control
Multiple mapped(4.63%)
Uniquely mapped(80.42%)

Treatment
Multiple mapped(3.28%)
Uniquely mapped(80.01%)

C

Control
Antisense(0.7%)
LincRNA(0.8%)
Other(7.9%)
Processed_transcript(4.2%)
Protein_coding(77%)
Pseudogene(0.2%)
Retained_intron(9.2%)

Treatment
Antisense(0.9%)
LincRNA(1%)
Other(7.5%)
Processed_transcript(4.2%)
Protein_coding(76.4%)
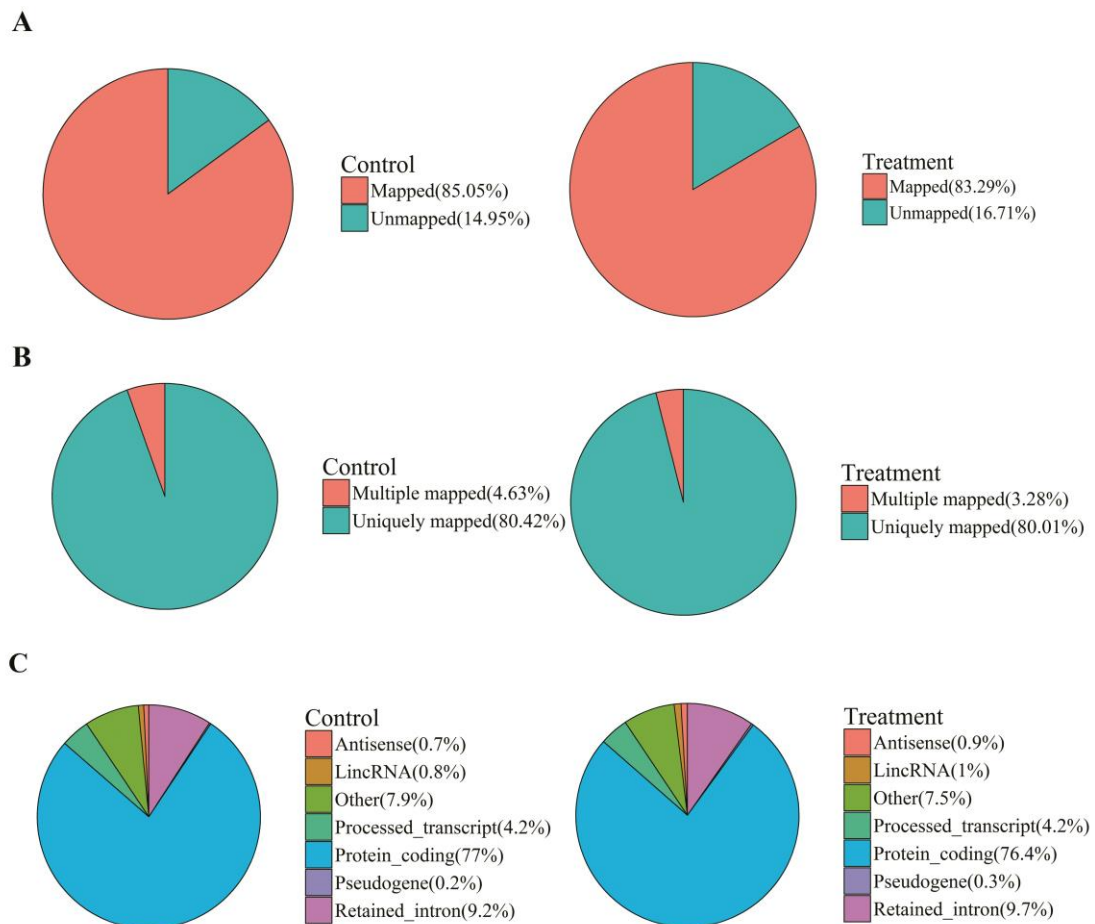Pseudogene(0.3%)
Retained_intron(9.7%)

Figure S1. Statistical analysis of cleaned reads from the control and treatment group. A: The percentage of the clean reads in the control and treatment group mapped to the human reference genome. B: The proportion of mapped reads of uniquely mapped and multiple mapped. C: The proportion of aligned reads assigned to known RNA categories.
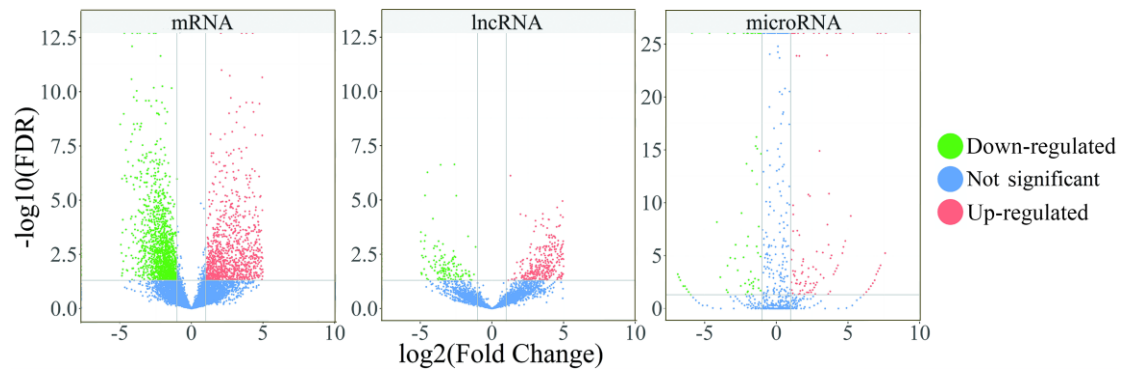
Figure S2. Volcano plot of the differentially expressed mRNAs (left), lncRNAs (middle) and miRNAs (right). In detail, mRNA or lncRNA with a –log10(q-*value*) >1.301 and the absolute value of log2(Fold Change) > 1 was considered as significant differentially expressed RNAs.
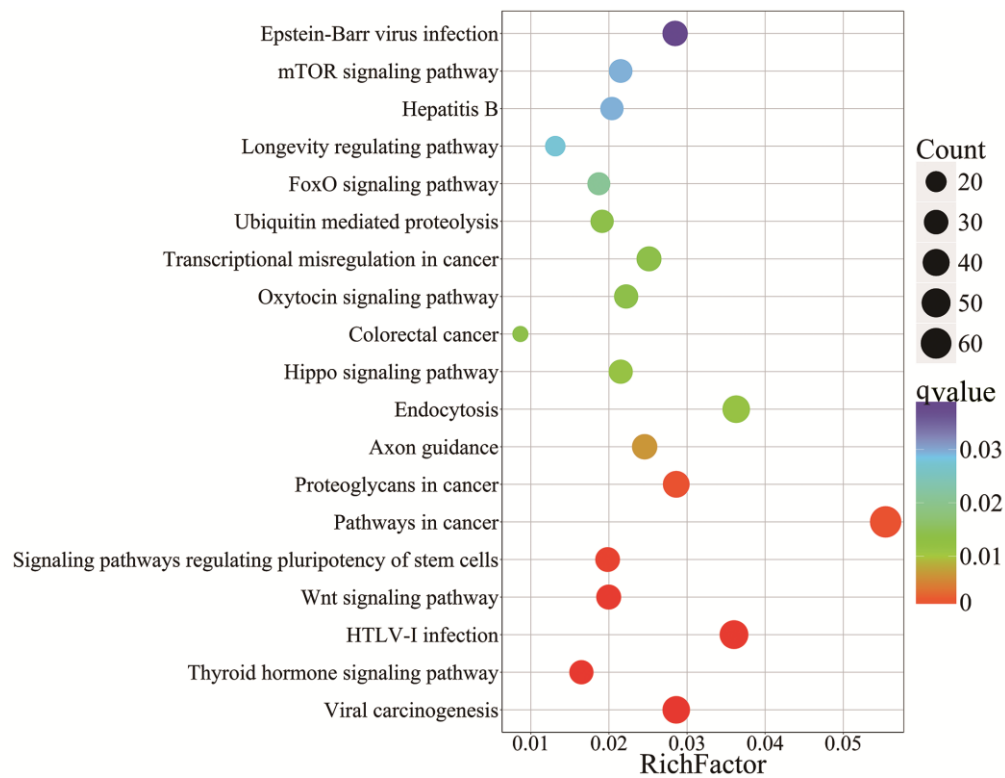

Figure S3. KEGG annotation results of mRNA from ceRNA network. The size of the dots represents the number of RNAs that enriched in corresponding pathways. The color indicates the significant level of the enriched pathways.