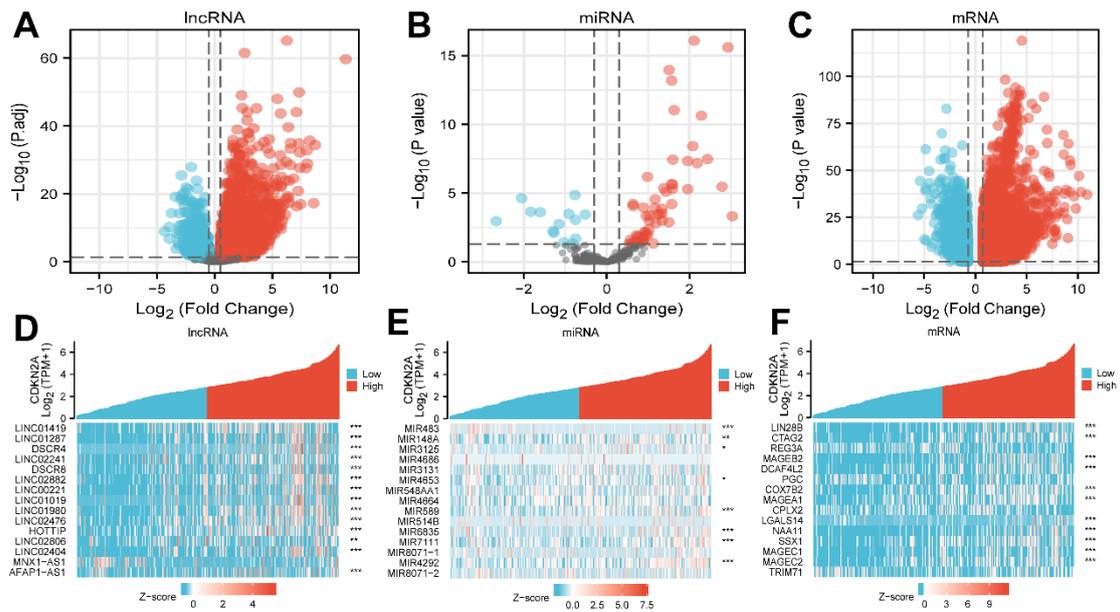


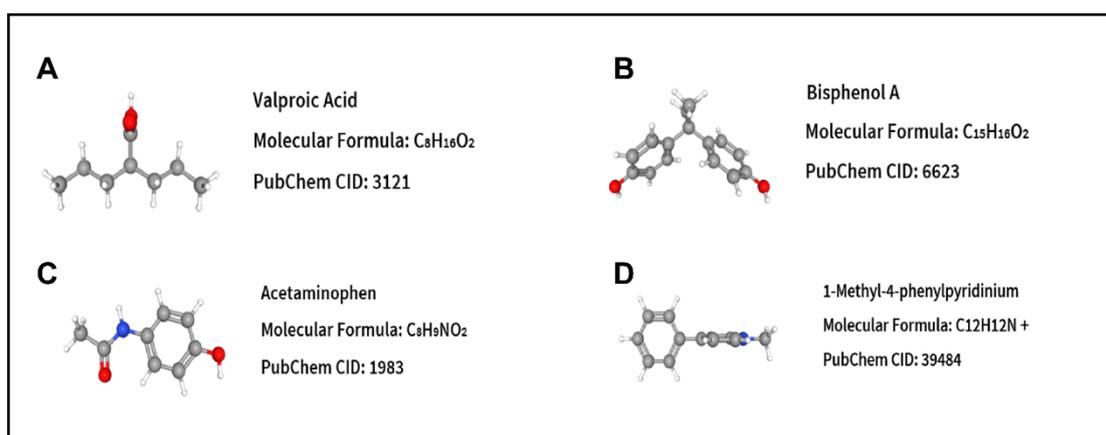
Supplementary Table 1 Baseline characteristics of the patients in the The Cancer Genome Atlas- Liver hepatocellular carcinoma cohort

characteristics	TCGA-LIHC cohort
Number of patients	374
Gender (%)	
Female	121(32.4)
Male	253(67.6)
Age (median, range)	61(16-90)
Tumor grade (%)	
G1+G2	233(62.3)
G3+G4	136(36.4)
Unknown	5(1.3)
Stage (%)	
I+II	260(69.5)
III+IV	90(24.1)
Unknown	24(6.4)
AFP (%)	
≤400ng/ml	215(57.5)
> 400ng/ml	65(17.4)
Unknown	94(25.1)
Vascular Invasion (%)	
Yes	110(29.4)
No	208(55.6)
Unknown	56(15.0)



Supplementary Figure 1 Volcano plots and heatmap plots of differentially expressed long non-coding RNAs, differentially expressed microRNAs, and differentially expressed messenger RNAs between the expression of hepatocellular carcinoma samples and normal samples.

A-C: The volcano plots describe (A) 4544 differentially expressed long non-coding RNAs ($|\log_2\text{fold change}| > 0.5$ and adjusted P value < 0.05), (B) 69 differentially expressed microRNAs ($|\log_2\text{fold change}| > 0.3$ and adjusted P value < 0.05), and (C) 6560 differentially expressed messenger RNAs ($|\log_2\text{fold change}| > 0.5$ and adjusted P value < 0.05). D-F: The horizontal axis of the heatmap indicates the samples, and the vertical axis of the heatmap indicates 15 significant differentially expressed genes.



Supplementary Figure 2 Prediction results of potential traditional Chinese medicine active components for the treatment of hepatocellular carcinoma based on growth arrest-specific 5.

(A–D) Prediction results of targeted traditional Chinese medicine active components.