

Figure S1. Venn diagrams exhibiting the overlap of DElncRNAs and DEMRNAs between two GEO datasets. (A) 30 overlapping DElncRNAs and (B) 505 overlapping DEMRNAs between the GSE55092 and GSE121248 datasets. DElncRNA, differentially expressed long non-coding RNA; DEMRNA, differentially expressed mRNA; GEO, Gene Expression Omnibus; HBV, hepatitis B virus; HCC, hepatocellular carcinoma; FC, fold change; FDR, false discovery rate.

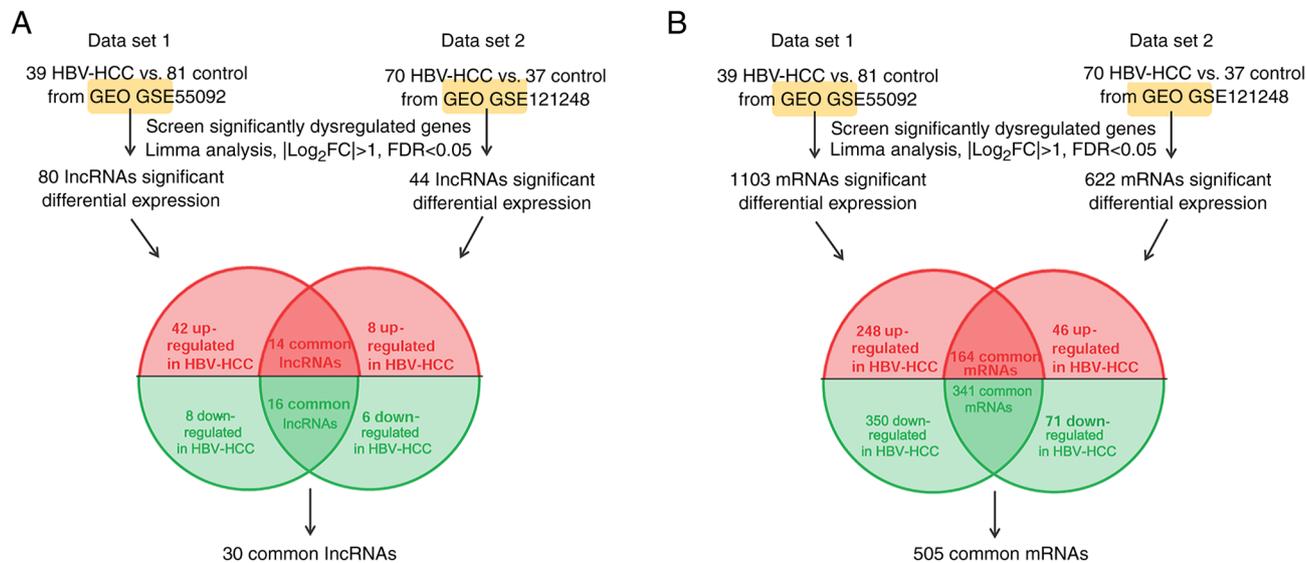


Figure S2. Identification of optimized lncRNA signatures. Three types of optimization algorithms, namely (A) recursive feature elimination, (B) LASSO and (C) random forest were respectively applied to screen optimized lncRNA signatures. lncRNA, long non-coding RNA; LASSO, least absolute shrinkage and selection operator.

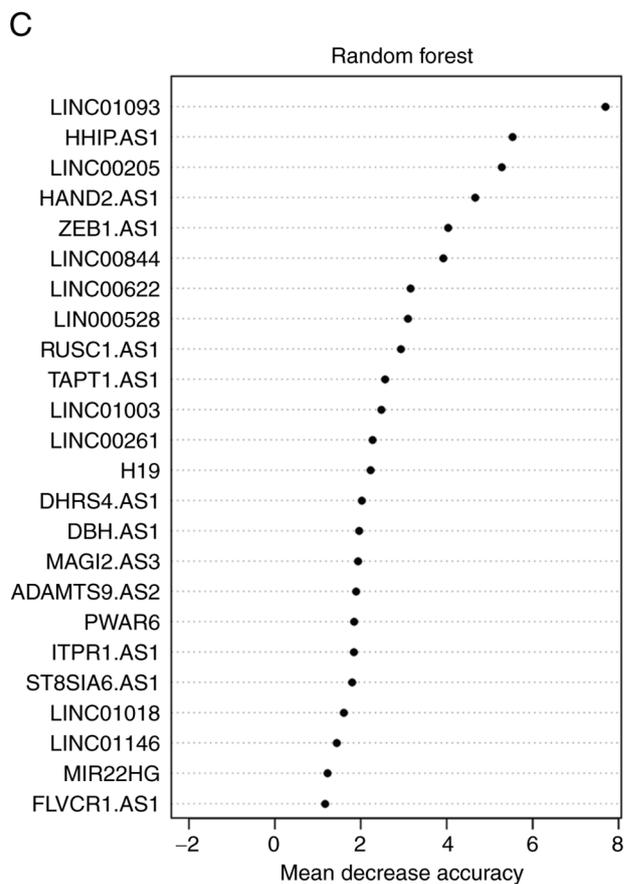
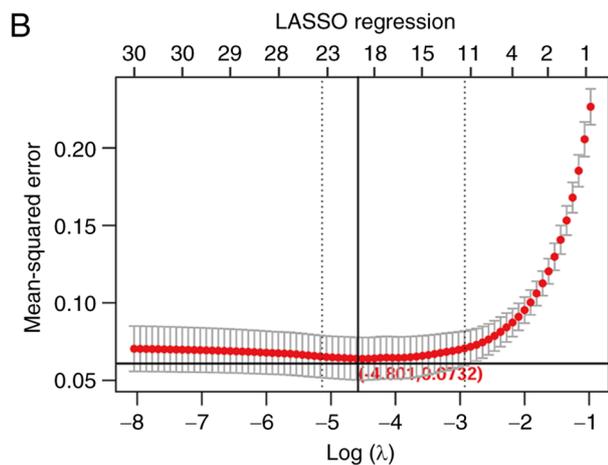
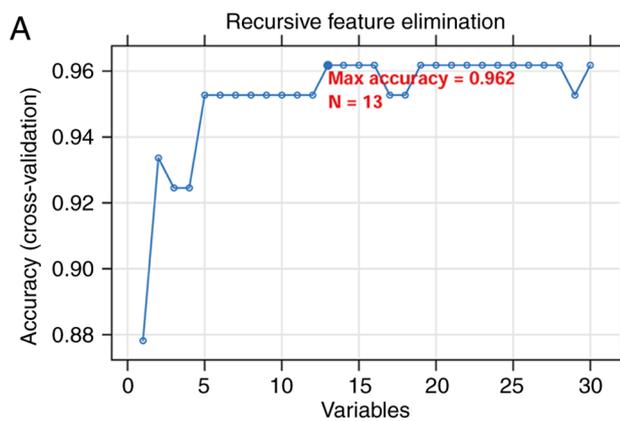


Figure S3. KEGG signaling pathways significantly associated with the regulated differentially expressed mRNAs in the competitive endogenous RNA network. The horizontal axis represents the number of genes, the vertical axis represents the KEGG term of the item, and the color represents significance, with red indicating higher significance. KEGG, Kyoto Encyclopedia of Genes and Genomes.

