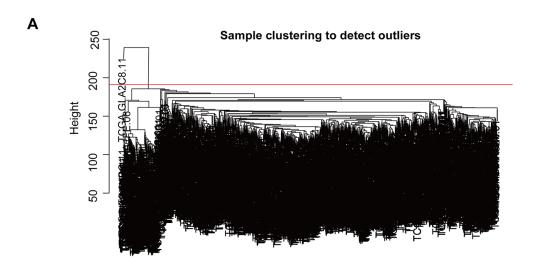
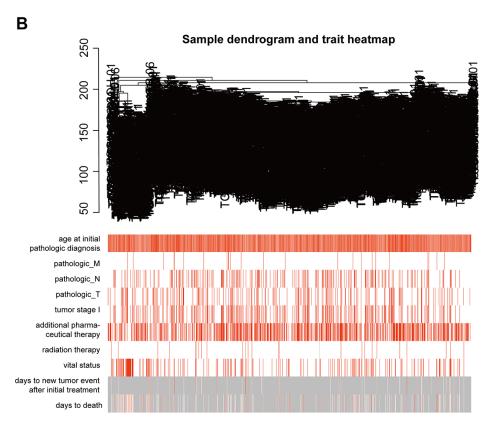
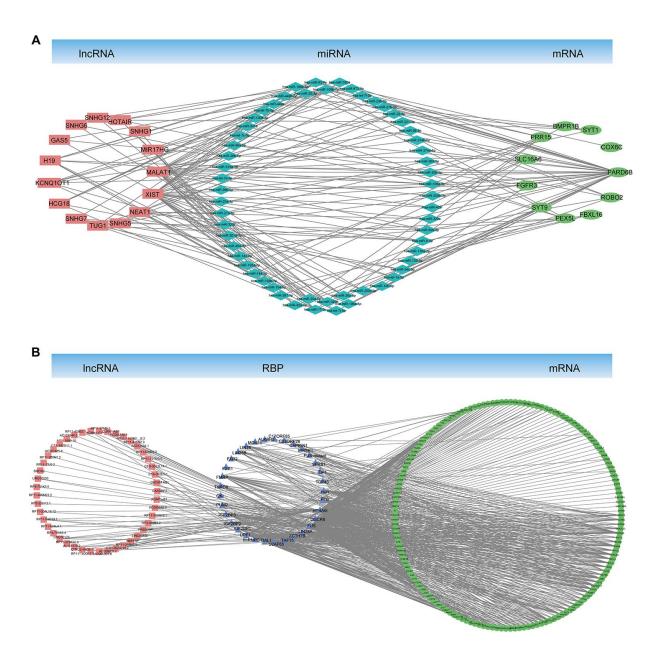
SUPPLEMENTARY FIGURES





Supplementary Figure 1. Sample cluster analysis. (A) Sample clustering to detect outliers based on RNA data (the red line (cut height = 200 cm) was used as the filter to remove outlier samples from the sample tree). (B) Sample dendrogram and clinical trait heatmap based on gene expression and clinical data. TNM = tumor, node, metastasis (classification).



Supplementary Figure 2. IncRNA-miRNA-mRNA ceRNA and IncRNA-RBP-mRNA networks. (A) IncRNA-miRNA-mRNA ceRNA network based on the co-expression Brown module. (B) IncRNA-RBP-mRNA network based on the co-expression Brown module.