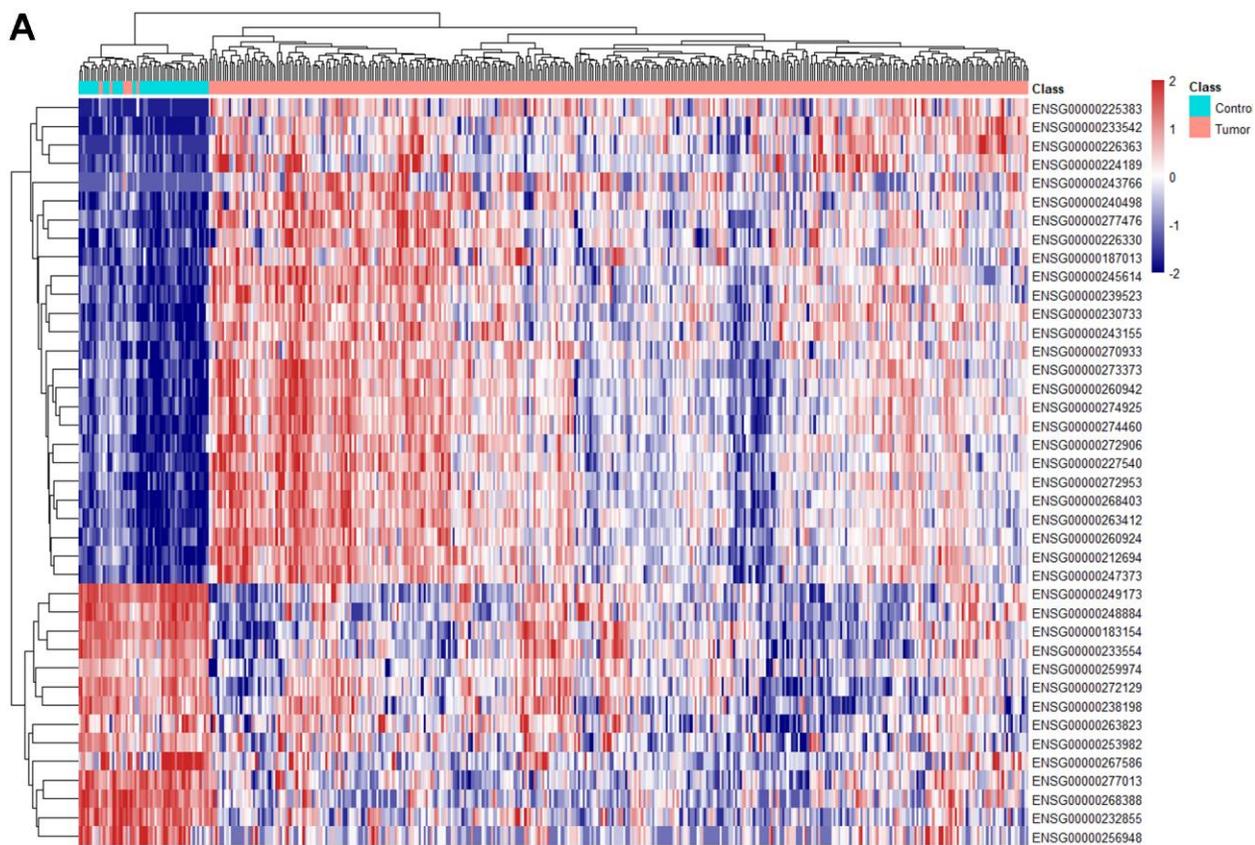
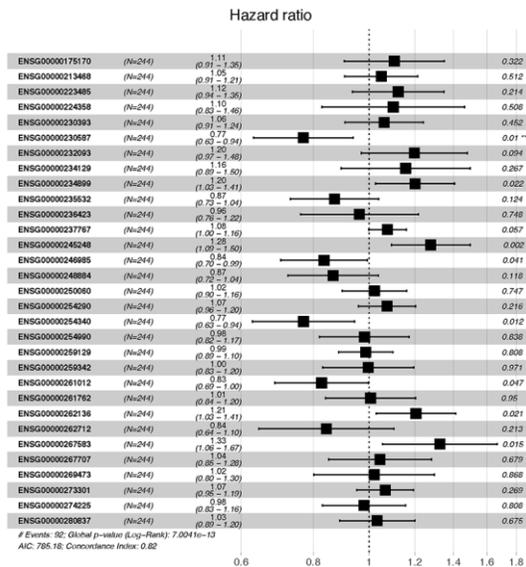
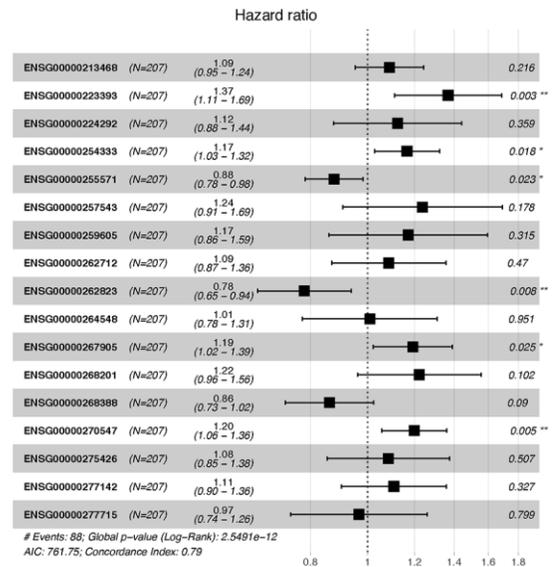


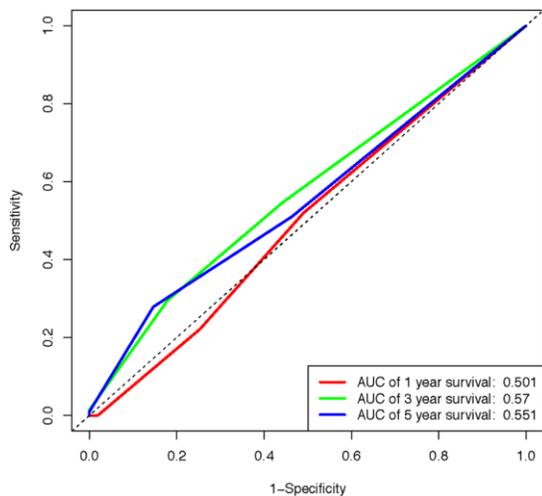
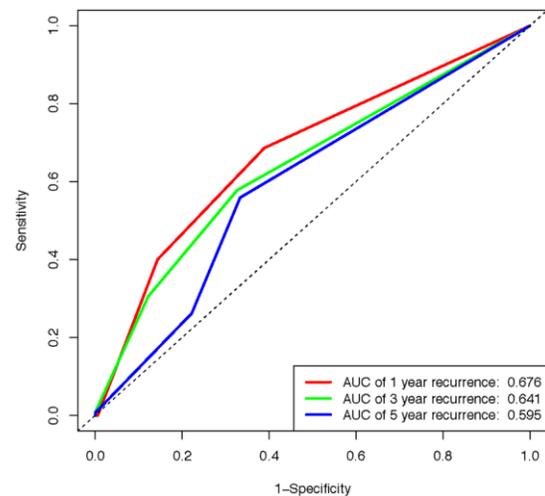
## SUPPLEMENTARY FIGURES



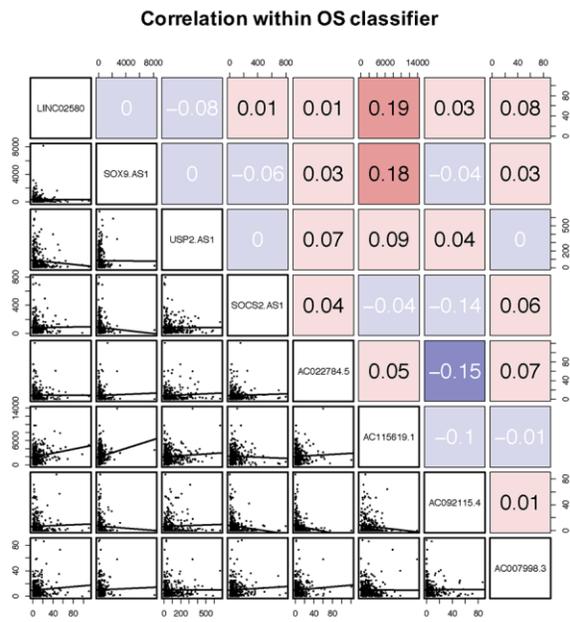
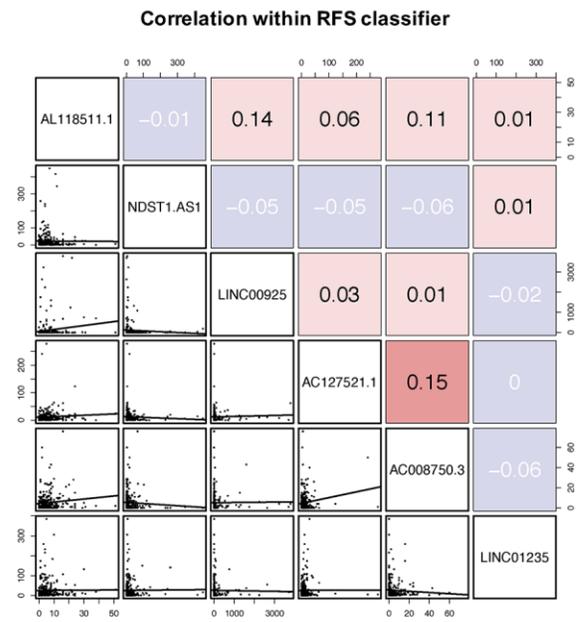
**Supplementary Figure 1. Heatmap of differentially expressed lncRNAs in TCGA-LIHC cohort. (A)** Heatmap showing 20 most up-regulate lncRNAs and 20 most down-regulated lncRNAs in TCGA-LIHC cohort (control tissue vs. tumor) by adjust p value.

**A****COX positive OS predictor****B****COX positive RFS predictor**

**Supplementary Figure 2. COX regression analysis indicating candidate lncRNAs for prognostic signature. (A) COX regression analysis selecting prognostic candidate from LASSO-positive lncRNAs in OS cohort. (B) COX regression analysis selecting prognostic candidate from LASSO-positive lncRNAs in RFS cohort.**

**A****OS whole cohort (Tumor stage)****B****RFS whole cohort (Tumor stage)**

**Supplementary Figure 3. The time-dependent ROC curve evaluating the efficiency of tumor stage as prognostic indicator. (A) The ROC curves showing tumor stage for OS prognosis assessment. (B) The ROC curves showing tumor stage for RFS prognosis assessment.**

**A****B**

**Supplementary Figure 4. Expressional correlation of member lncRNAs in lncRNA-based classifiers. (A)** Correlation of 8 lncRNAs consisting OS prognosis signature. **(B)** Correlation of 6 lncRNAs consisting RFS prognosis signature.