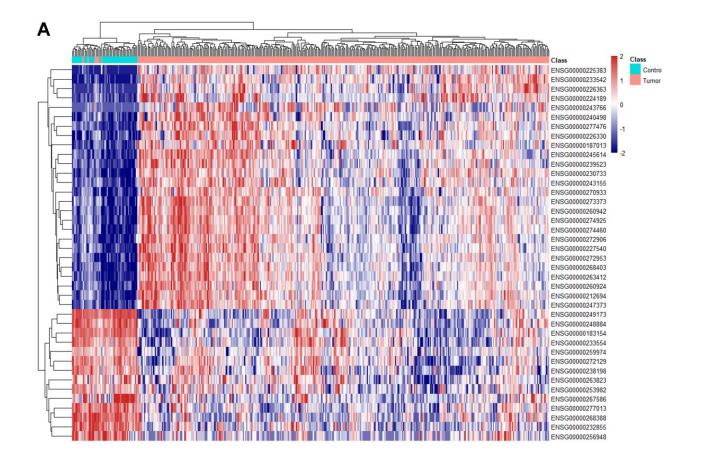
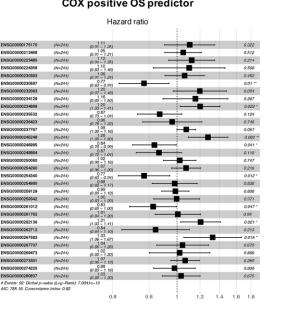
SUPPLEMENTARY FIGURES



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

COX positive OS predictor

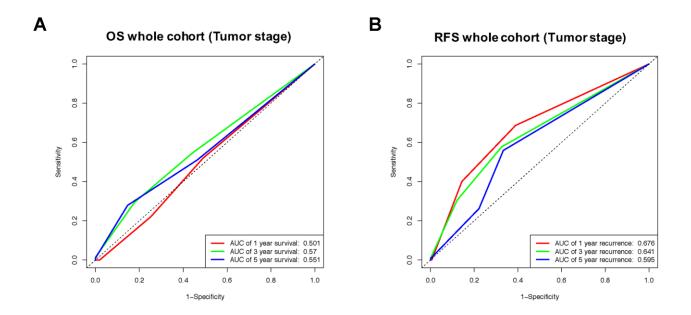




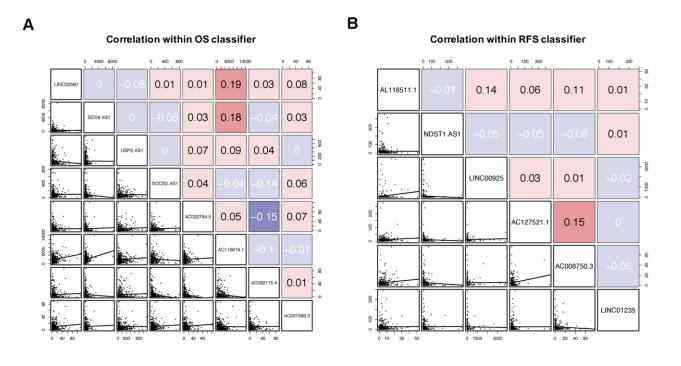
Hazard ratio							
ENSG00000213468	(N=207)	1.09 (0.95 - 1.24)	F				0.216
ENSG00000223393	(N=207)	(1.17 – 1.69)				_	0.003 **
ENSG00000224292	(N=207)	(0.88 - 1.44)		-			0.359
ENSG00000254333	(N=207)	(1.03 - 1.32)			-		0.018 *
ENSG00000255571	(N=207)	0.88 (0.78 - 0.98)					0.023 *
ENSG00000257543	(N=207)	1.24 (0.91 – 1.69)	-	-			0.178
ENSG00000259605	(N=207)	1.17 (0.86 - 1.59)		-		_	0.315
ENSG00000262712	(N=207)	1.09 (0.87 – 1.36)			-		0.47
ENSG00000262823	(N=207)	(0.65 - 0.94)					0.008 **
ENSG00000264548	(N=207)	1.01 (0.78 – 1.31)		•	-		0.951
ENSG00000267905	(N=207)	1.19 (1.02 - 1.39)					0.025 *
ENSG00000268201	(N=207)	1.22 (0.96 - 1.56)	,	-	_	-	0.102
ENSG00000268388	(N=207)	0.86 (0.73 - 1.02)		-			0.09
ENSG00000270547	(N=207)	1.20 (1.06 - 1.36)			-		0.005 **
ENSG00000275426	(N=207)	1.08 (0.85 - 1.38)		-			0.507
ENSG00000277142	(N=207)	(0.90 - 1.36)	-		-		0.327
ENSG00000277715	(N=207)	0.97 (0.74 - 1.26)					0.799
# Events: 88; Global p-value (Log-Rank): 2.5491e-12 AIC: 761.75; Concordance Index: 0.79 0.8 1.2 1.4 1.6						1.6	1.8

COX positive RFS predictor

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



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.



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