

Figure S1. RBM14 gene expression level in different clinical trait subgroups was analyzed by UALCAN using TCGA LUAD dataset. **p <0.01, ***p <0.001.

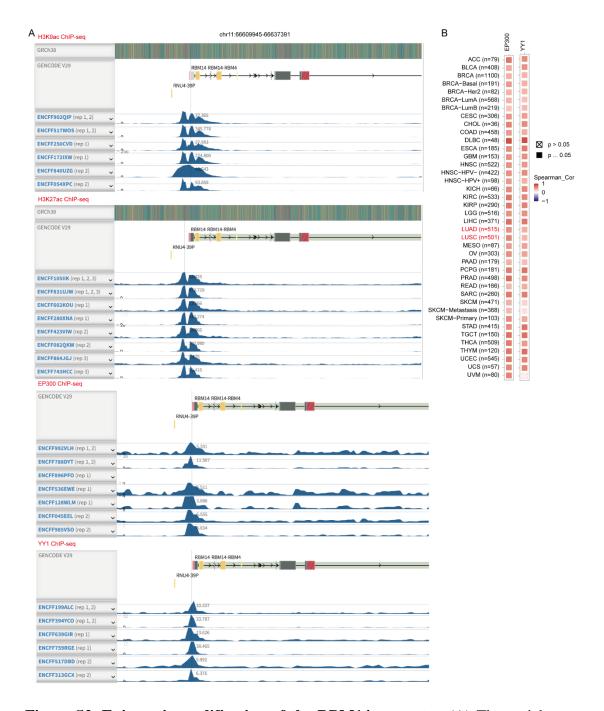


Figure S2. Epigenetic modification of the RBM14 promoter. (A) The enrichment of H3K9ac, H3K27ac, EP300, and YY1 in RBM14 promoter was evaluated by using ChIP-seq data of A549 cells in ENCODE database. (B) Correlation analysis of RBM14 expression with EP300 and YY1 expression was visualized by TIMER using TCGA dataset.

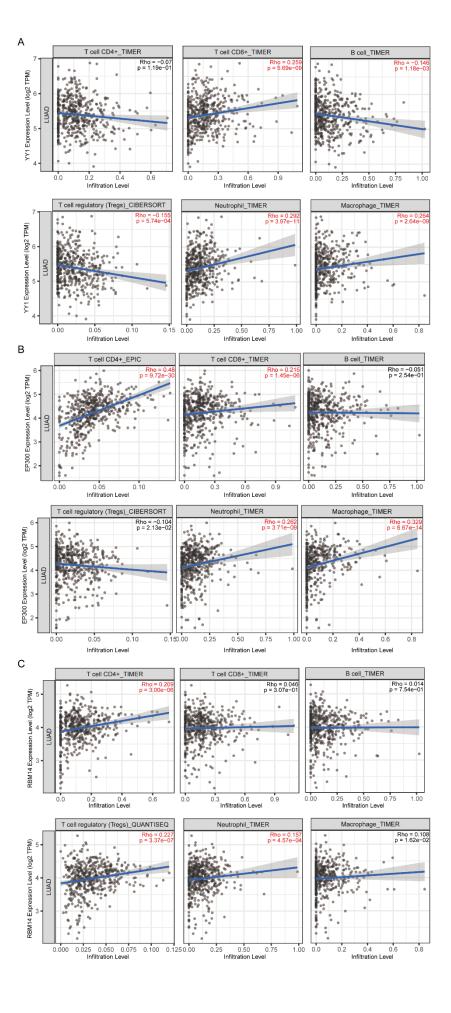


Figure S3. Correlation of YY1-RBM14 axis with immune infiltration in LUAD.

(A) Correlation analysis of YY1 expression with the level of immune cell infiltration in LUAD was visualized by TIMER. (B) Correlation analysis of EP300 expression with the level of immune cell infiltration in LUAD was visualized by TIMER. (C) Correlation analysis of RBM14 expression with the level of immune cell infiltration in LUAD was visualized by TIMER.

$\begin{tabular}{ll} \textbf{Supplementary Table S1} The clinical information of lung adenocarcinoma samples in TCAG \end{tabular}$

Parameters		Size
Age	<60	102
	>60	181
Gender	Male	238
	Female	276
Race	Caucasian	387
	African-American	51
	Asian	8
Individual cancer	Stage1/2	402
stage	Stage3/4	113
	Non smoker	75
Smoking habit	Smoker	118
	Reformed smoker	303
Nodal Metastasis	No	331
status	Yes	172

$\begin{array}{c} \textbf{Supplementary Table S2} \ \textbf{The clinical information of lung adenocarcinoma samples in} \\ \textbf{CPTAC} \end{array}$

Parameters		Size	
Age		<60	48
		>60	63
Gender		Male	73
	Female	38	
		Caucasian	34
Race		African-American	1
		Asian	1
Individual	cancer	Stage1/2	89
stage		Stage3/4	31