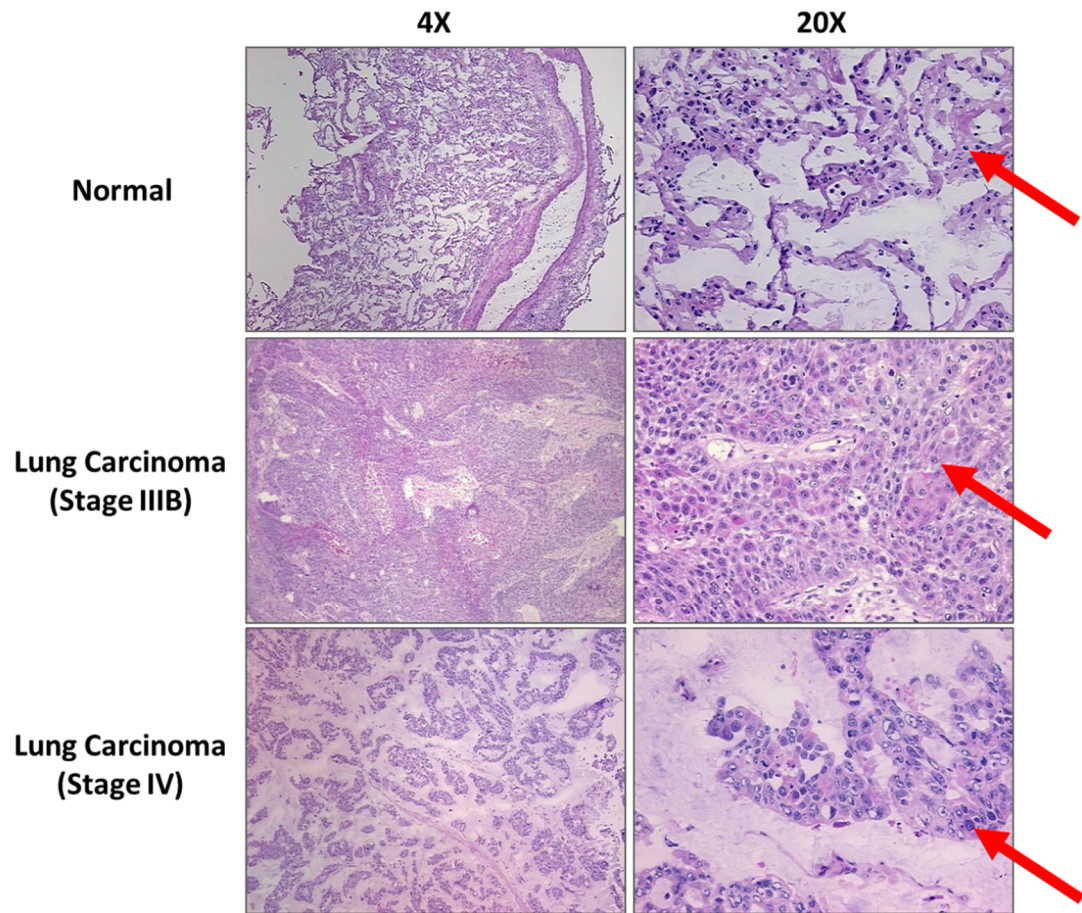
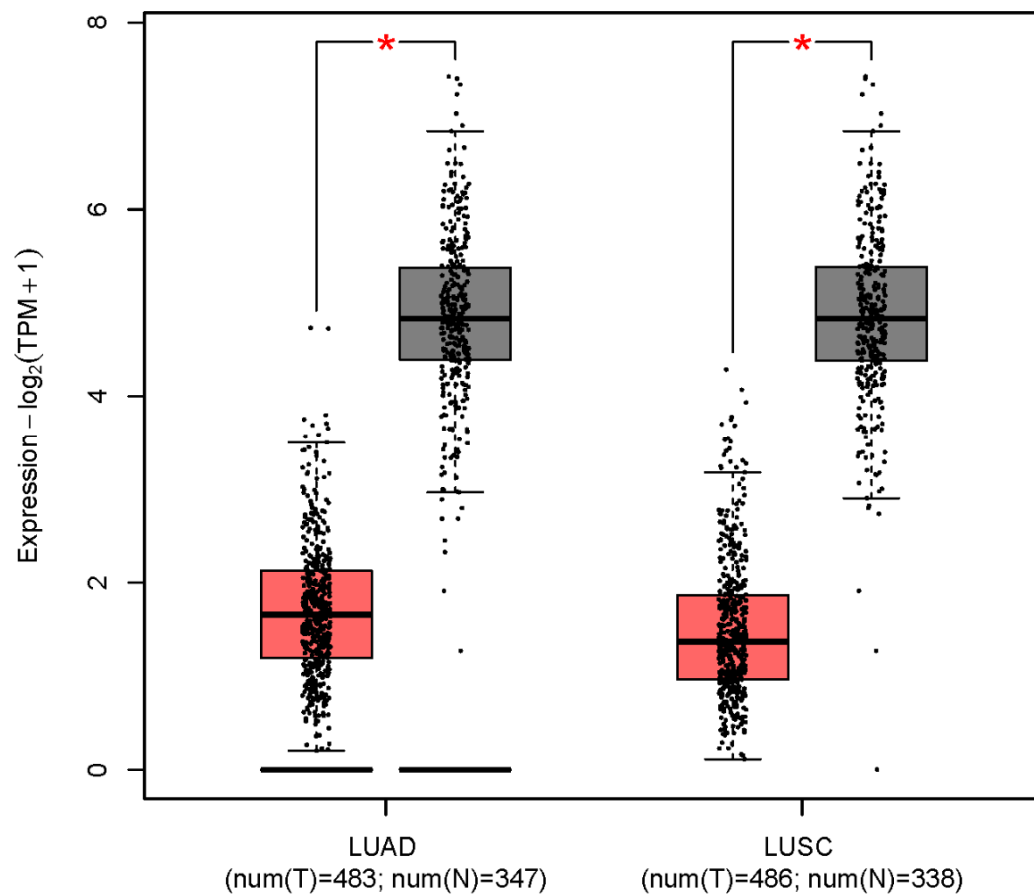


Characteristics	No. of patients	Relative FOXF1 expression (Mean $\pm$ SEM)	P-value
<b>Gender</b>			0.1655
Male	24	0.070 $\pm$ 0.031	
Female	17	0.025 $\pm$ 0.005	
<b>Age (y)</b>			0.4031
$\leq 65$	20	0.036 $\pm$ 0.006	
$> 65$	21	0.066 $\pm$ 0.035	
<b>Histopathology</b>			0.1457
Adenocarcinoma	22	0.058 $\pm$ 0.034	
Squamous cell carcinoma	13	0.053 $\pm$ 0.010	
Large cell carcinoma	6	0.024 $\pm$ 0.005	
<b>Histologic grade</b>			0.3753
Well differentiated (G1)	3	0.018 $\pm$ 0.006	
Moderately differentiated (G2)	13	0.034 $\pm$ 0.009	
Poorly differentiated (G3)	18	0.073 $\pm$ 0.041	
Unknown	7	0.044 $\pm$ 0.013	
<b>Primary Tumor (T-stage)</b>			0.8337
T1	9	0.043 $\pm$ 0.013	
T2	17	0.030 $\pm$ 0.005	
T3	7	0.144 $\pm$ 0.103	
T4	6	0.027 $\pm$ 0.007	
Tx	2	0.018 $\pm$ 0.001	
<b>Regional Lymph Nodes (N-stage)</b>			0.4063
N0	20	0.076 $\pm$ 0.037	
N1	10	0.024 $\pm$ 0.006	
N2	7	0.039 $\pm$ 0.009	
N3	1	0.019	
Nx	3	0.020 $\pm$ 0.003	
<b>Overall stage</b>			0.9648
I	11	0.038 $\pm$ 0.010	
II	13	0.089 $\pm$ 0.056	
III	14	0.031 $\pm$ 0.006	
IV	3	0.033 $\pm$ 0.008	

**Supplementary Table 1.** Patient demographic and clinicopathological characteristics.



**Supplementary Figure 1.** Representative lung tissue sections (H&E stain) of normal lung and lung carcinoma (Stage III and IV). Images are captured at 4X and 20X magnification. The data are provided from Origene company (<https://www.origene.com/catalog/tissues/tissuescan/hlrt105/tissuescan-lung-cancer-cdna-array-v>)



**Supplementary Figure 2.** *In silico* analysis of FOXF1 expression profiles from The Cancer Genome Atlas (TCGA) and genotype-tissue expression (GTEx) projects using GEPIA2 online platform (<http://gepia2.cancer-pku.cn/#index>). The FOXF1 expression of lung adenocarcinoma (LUAD) and lung squamous cell carcinoma (LUSC) are represented as box plot, and *p-value* cutoff is set at 0.05.