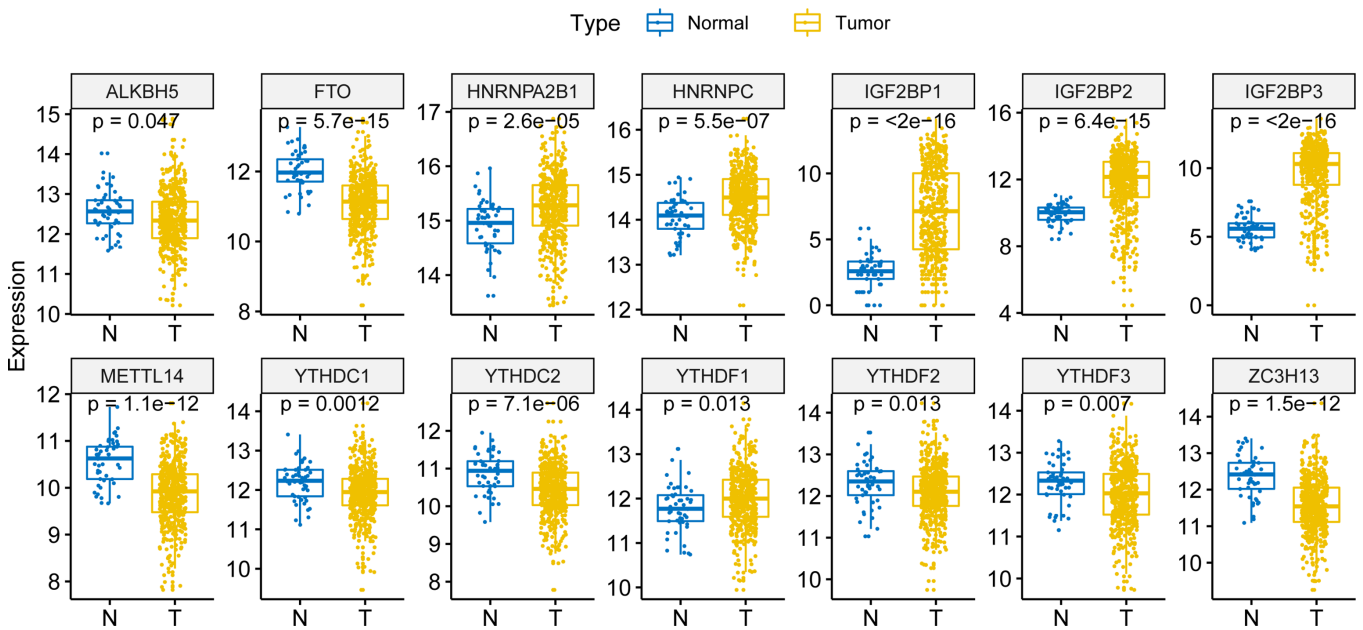


**Figure S1** Survival analysis of differential expression m6A regulators. Two of 14 m6A regulators on differential expression were identified to be correlation with OS by Kaplan-Meier plot ( $P < 0.05$ ). (A) *FTO* gene ( $P = 0.041$ ); (B) *KIAA1429* gene ( $P = 0.034$ ); cutoff:  $P < 0.05$ . m6A, N6-methyladenosine; OS, overall survival.

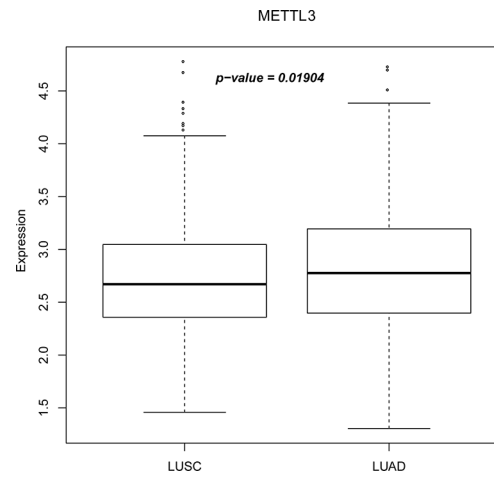


**Figure S2** The differential expression levels of 14 m6A RNA methylation regulators between LUSC samples and normal control samples from TCGA-LUSC database ( $P < 0.05$ ). *ALKBH5*, *METTL14*, *YTHDC1*, *YTHDC2*, *YTHDF2*, *YTHDF3*, *ZC3H13* and *FTO* were low expressed in LUSC, *HNRNPA2B1*, *HNRNPC*, *IGF2BP1*, *IGF2BP2*, *IGF2BP3* and *ALKBH5* were high expressed. m6A, N6-methyladenosine; LUSC, lung squamous cell carcinoma; TCGA, The Cancer Genome Atlas.

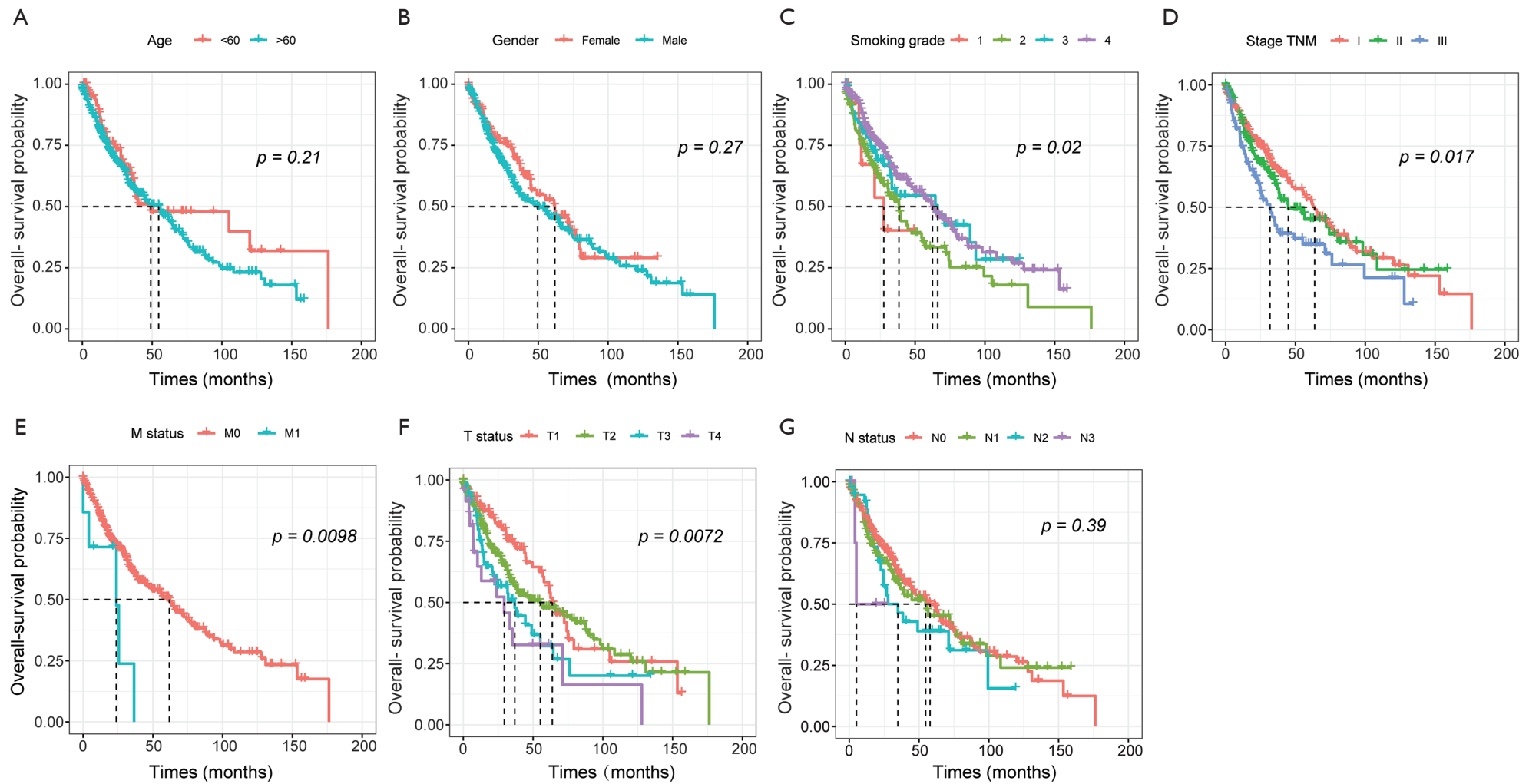
**Table S1** The profile of somatic mutations on LUSC

Sample	<i>FMR1</i>	<i>FTO</i>	<i>HNRNPA2B1</i>	<i>HNRNPC</i>	<i>IGF2BP1</i>	<i>IGF2BP2</i>	<i>METTL14</i>	<i>METTL3</i>	<i>RBM15</i>	<i>RBMX</i>	<i>KIAA1429</i>	<i>WTAP</i>	<i>YTHDC1</i>	<i>YTHDC2</i>	<i>YTHDF1</i>	<i>YTHDF2</i>	<i>YTHDF3</i>	<i>ZC3H13</i>
TCGA-66-2785	P334S										E1664Q							
TCGA-85-6561	R180L																	
TCGA-66-2786	R454P																	
TCGA-66-2789	V621E																	
TCGA-43-2578	V67=																	
TCGA-66-2766		E253Q																
TCGA-18-3407		Q398L																
TCGA-22-5485		S318I								F138S								
TCGA-22-5473			E92Q															
TCGA-33-4566			G237V				D29Y											I327V
TCGA-66-2759				G264W														
TCGA-63-5131				K176N														K821I
TCGA-18-3421					E445*													
TCGA-60-2726					N570K													
TCGA-66-2787					S389I													
TCGA-18-3417						E347K												
TCGA-66-2727						R177Q												
TCGA-37-5819						V111M												
TCGA-85-6560							R21M											
TCGA-60-2708								L172Qfs*10										
TCGA-66-2767									G126R									
TCGA-66-2734									G8V, G8*									
TCGA-34-2600									P300H, M40I									
TCGA-37-3783									R164T									
TCGA-18-4721										I753M								
TCGA-21-1070										K1388*								
TCGA-46-3769										V544L								
TCGA-34-5236										X1547_splice								
TCGA-66-2744											E86K							
TCGA-22-4595											X3_splice							
TCGA-33-6737												D313H						
TCGA-22-4591												R719Q						
TCGA-56-6545													D475Y					
TCGA-18-3419													D820G					
TCGA-66-2763													G18E					
TCGA-66-2756													L1105F					
TCGA-66-2788														R327L				
TCGA-60-2725																R574P		
TCGA-22-1012																		D494G
TCGA-33-4538																		F464L
TCGA-66-2791																		P267L
TCGA-60-2715																		R458Q

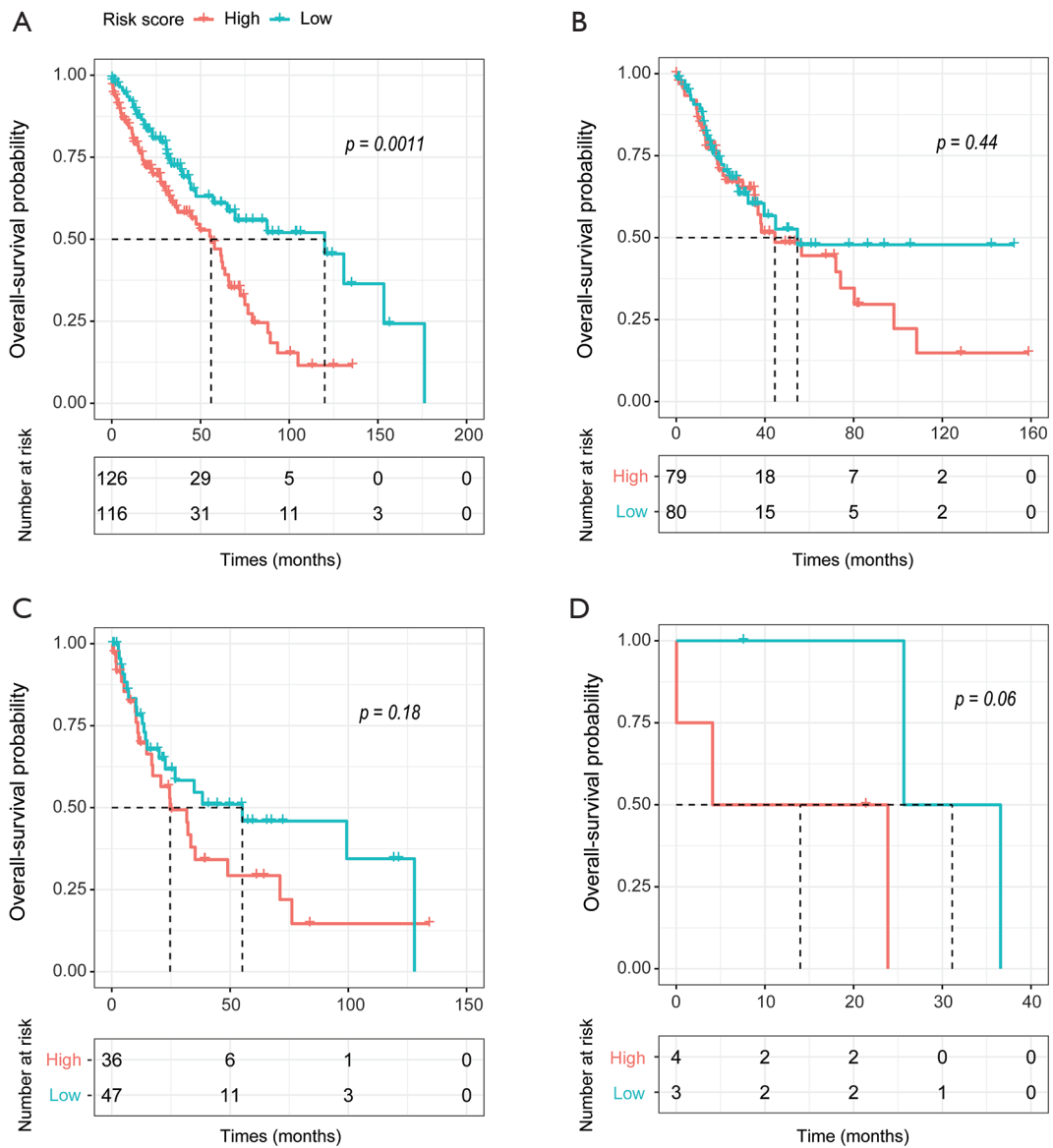
\*, stop code (nonsense mutation). LUSC, lung squamous cell carcinoma; TCGA, The Cancer Genome Atlas.



**Figure S3** Comparing METTL3 differential expression between LUSC and LUAD. The expression in LUAD was higher than in LUSC by Wilcox test ( $P=0.01904$ ). Y-axis for METTL3 expression. LUSC, lung squamous cell carcinoma; LUAD, lung adenocarcinoma.



**Figure S4** Association to clinical characteristics with OS. Kaplan-Meier plot showed clinical features including smoking grade, stage TNM, M status, T status N status were associated with OS ( $P<0.05$ ). (A) Age ( $P=0.21$ ); (B) gender ( $P=0.27$ ); (C) smoking grade ( $P=0.02$ ); (D) stage TNM ( $P=0.017$ ); (E) M status ( $P=0.00098$ ); (F) T status ( $P=0.0072$ ); (G) N status ( $P=0.39$ ). OS, overall survival; TNM, tumor node metastasis.



**Figure S5** Survival analysis for TNM stage based on risk score. Kaplan-Meier plot illustrates the results in LUSC. (A) Risk score in patients with stage I ( $P=0.0011$ ); (B) stage II ( $P=0.44$ ); (C) stage III ( $P=0.18$ ); (D) stage IV ( $P=0.06$ ). TNM, tumor node metastasis; LUSC, lung squamous cell carcinoma.

**Table S2** Comparing percentage of TNM stages with one previously reported

Patients (n=504)	Alive	Dead	Total	Percentage (%)	Percentage previously reported
Stage I				48.6	
Patients	143	102	245		
Patients (>5 years)	31	21	52	21.22	70%
Stage II				32.3	
Patients	97	66	163		
Patients (>5 years)	13	5	18	11.04	
Stage III				16.9	
Patients	40	45	85		
Patients (>5 years)	9	4	13	15.29	
Stage IV				1.4	
Patients	2	5	7		
Patients (>5 years)	0	0	0	0	2%

TNM, tumor, node and metastasis.