Supplementary Table 1 LINC01767 and characteristics in HCC

Characteristics	Low expression of LINC01767	High expression of LINC01767	*P* value
n	187	187	
Gender, *n* (%)			0.224
Female	55 (14.7%)	66 (17.6%)	
Male	132 (35.3%)	121 (32.4%)	
Age, *n* (%)			0.234
≤ 60	94 (25.2%)	83 (22.3%)	
> 60	92 (24.7%)	104 (27.9%)	
Race, *n* (%)			0.827
Asian	78 (21.5%)	82 (22.7%)	
Black or African American	9 (2.5%)	8 (2.2%)	
White	96 (26.5%)	89 (24.6%)	
BMI, *n* (%)			0.299
≤ 25	93 (27.6%)	84 (24.9%)	
> 25	75 (22.3%)	85 (25.2%)	
Histological type, *n* (%)			0.112
Fibrolamellar carcinoma	3 (0.8%)	0 (0%)	
Hepatocellular carcinoma	179 (47.9%)	185 (49.5%)	
Hepatocholangiocarcinoma (mixed)	5 (1.3%)	2 (0.5%)	
AFP (ng/mL), *n* (%)			0.038[a]
≤ 400	111 (39.6%)	104 (37.1%)	
> 400	24 (8.6%)	41 (14.6%)	
Prothrombin time, *n* (%)			0.586
≤ 4	98 (33%)	110 (37%)	
> 4	45 (15.2%)	44 (14.8%)	
Histologic grade, *n* (%)			0.554
G1	25 (6.8%)	30 (8.1%)	
G2	95 (25.7%)	83 (22.5%)	

G3	58 (15.7%)	66 (17.9%)	
G4	5 (1.4%)	7 (1.9%)	
Child-Pugh grade, *n* (%)			0.494
A	106 (44%)	113 (46.9%)	
B	8 (3.3%)	13 (5.4%)	
C	0 (0%)	1 (0.4%)	
Fibrosis ishak score, *n* (%)			0.279
0	31 (14.4%)	44 (20.5%)	
1/2	16 (7.4%)	15 (7%)	
3/4	12 (5.6%)	16 (7.4%)	
5	7 (3.3%)	2 (0.9%)	
6	36 (16.7%)	36 (16.7%)	
Tumor status, *n* (%)			0.126
Tumor free	109 (30.7%)	93 (26.2%)	
With tumor	70 (19.7%)	83 (23.4%)	
Residual tumor, *n* (%)			0.110
R0	160 (46.4%)	167 (48.4%)	
R1	12 (3.5%)	5 (1.4%)	
R2	0 (0%)	1 (0.3%)	
Adjacent hepatic tissue inflammation, *n* (%)			0.148
None	51 (21.5%)	67 (28.3%)	
Mild	55 (23.2%)	46 (19.4%)	
Severe	11 (4.6%)	7 (3%)	
Albumin(g/dL), *n* (%)			0.926
< 3.5	33 (11%)	36 (12%)	
≥ 3.5	109 (36.3%)	122 (40.7%)	
Vascular invasion, *n* (%)			0.526
No	100 (31.4%)	108 (34%)	
Yes	57 (17.9%)	53 (16.7%)	
Pathologic T stage, *n* (%)			0.781

T1	87 (23.5%)	96 (25.9%)	
T2	51 (13.7%)	44 (11.9%)	
T3	41 (11.1%)	39 (10.5%)	
T4	7 (1.9%)	6 (1.6%)	
Pathologic N stage, *n* (%)			0.670
N0	131 (50.8%)	123 (47.7%)	
N1	3 (1.2%)	1 (0.4%)	
Pathologic M stage, *n* (%)			0.583
M0	138 (50.7%)	130 (47.8%)	
M1	1 (0.4%)	3 (1.1%)	
Pathologic stage, *n* (%)			0.778
Stage I	81 (23.1%)	92 (26.3%)	
Stage II	46 (13.1%)	41 (11.7%)	
Stage IV	2 (0.6%)	3 (0.9%)	

Supplementary Table 2 Cox regression based on Proportional Risk Assumption (PH)

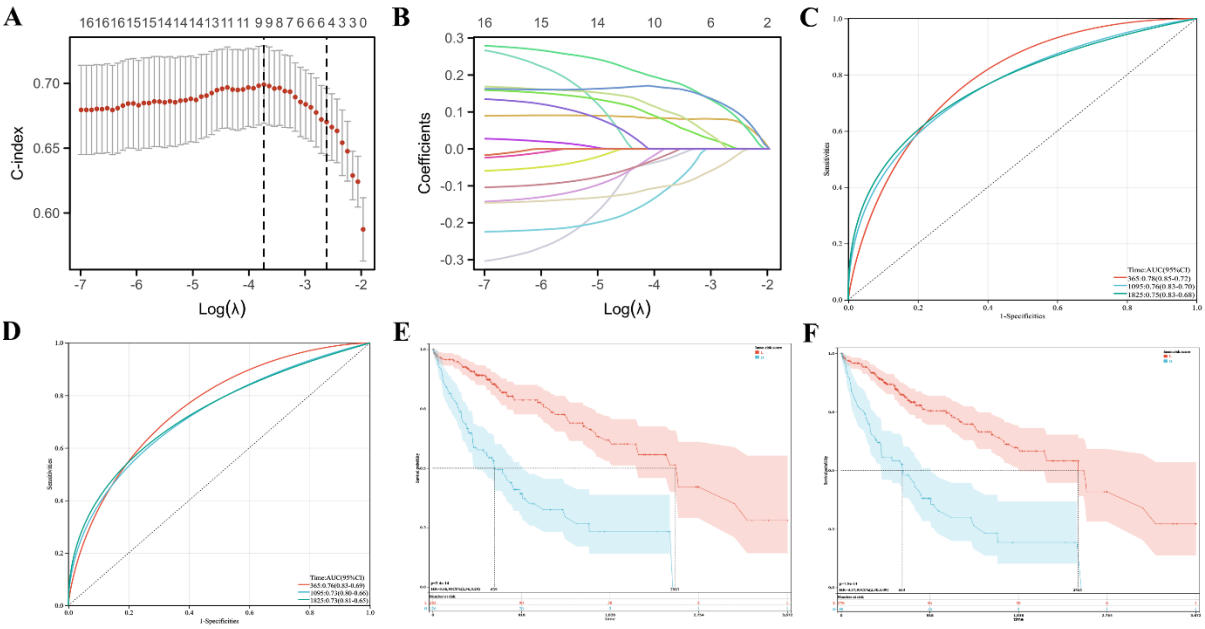
Variables	Statistics (chi-square values)	Degree of freedom (df)	*P* value
Pathologic T stage	6.2148	3	0.1016
Pathologic N stage	2.2945	1	0.1298
Pathologic M stage	6.5735	1	0.0104
BMI	0.60183	1	0.4379
Residual tumor	3.0755	2	0.2149
Vascular invasion	0.14608	1	0.7023
LINC01767	0.13681	1	0.7115
GLOBAL	13.704	10	0.1869

Cox regression is applied on the premise that the independent variables are required to meet the proportional risk hypothesis (P > 0.05), that is, the risk of the independent variables does not change over time, and if they are not met, Cox regression is not suitable for testing. Only multivariate models and included variables are tested for the PH hypothesis here,Note: (1) The result of the direct PH hypothesis for a single variable is different from the PH hypothesis for this variable in the model; (2) The results of the PH hypothesis of the same variable in the same data are different in the Cox model, and if the global (GLOBAL) satisfies p > 0.05, it can be considered that the multi-factor model satisfies the proportional risk hypothesis

Supplementary Table 3 The variance inflation factor in lasso model of LINC01767

Variables	Type	VIF
Pathologic T stage	ordinal variable	
T1		Reference
T2		1.5339
T3		1.3263
T4		3.2979
Pathologic N stage	ordinal variable	
N0		Reference
N1		1.0624
Pathologic M stage	ordinal variable	
M0		Reference
M1		4.627
BMI	ordinal variable	
≤ 25		Reference
> 25		1.1418
Residual tumor	ordinal variable	
R0		Reference
R1		1.0625
R2		2.8656
Vascular invasion	ordinal variable	
No		Reference
Yes		1.5348
LINC01767	ordinal variable	
Low		Reference
High		1.1133

It is generally believed that when 0 < VIF < 10, there is no multicollinearity (Supplement: it is also believed that there is multicollinearity when VIF > 4). When 10 or less 2 VIF is based < 100, stronger multicollinearity was indicated; When VIF ≥ 100 or NaN occurs, serious multicollinearity was identified.



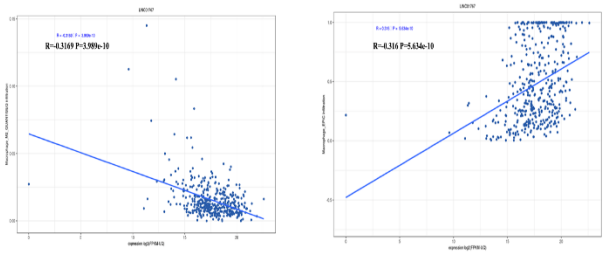
Supplementary Figure 1 Lasso penalized cox regression analysis was performed with LINC01767 related genes and 9 genes were finally identified in the model. A and B: The lasso cox regression of the LINC01767 related genes; C: The ROC curve was calculated to test the performance of lasso model, the result showed that the 9-genes model; D: 5-gene model to predict the overall survival of liver cancer patients; E: The K-M plot based on the 9-genes lasso cox; F: The K-M plot based on the 5-genes lasso cox.

A

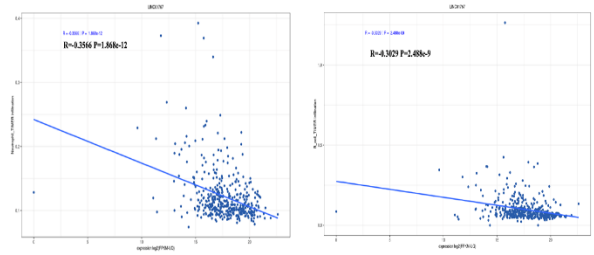
lncRNA is : ENSG00000223956
Cancer is :LIHC
P value : p_value<0.05
R value : R> -0.5

Cancer	LncRNA ID	Symbol	Immune cell	Immune data source	P value	R value
LIHC	ENSG00000223956	LINC01767	B cell	TIMER	2.488e-09	-0.3029
LIHC	ENSG00000223956	LINC01767	T cell CD4+	TIMER	1.152e-09	-0.3105
LIHC	ENSG00000223956	LINC01767	Neutrophil	TIMER	1.868e-12	-0.3566
LIHC	ENSG00000223956	LINC01767	Myeloid dendritic cell	TIMER	5.546e-10	-0.3161
LIHC	ENSG00000223956	LINC01767	Macrophage M2	QUANTISEQ	3.989e-10	-0.3169
LIHC	ENSG00000223956	LINC01767	uncharacterized cell	QUANTISEQ	0.000e+00	0.416
LIHC	ENSG00000223956	LINC01767	Endothelial cell	MCPCOUNTER	6.709e-11	-0.3319
LIHC	ENSG00000223956	LINC01767	Cancer associated fibroblast	MCPCOUNTER	5.364e-11	-0.3335
LIHC	ENSG00000223956	LINC01767	Cancer associated fibroblast	EPIC	7.844e-17	-0.4002
LIHC	ENSG00000223956	LINC01767	Macrophage	EPIC	5.634e-10	0.316

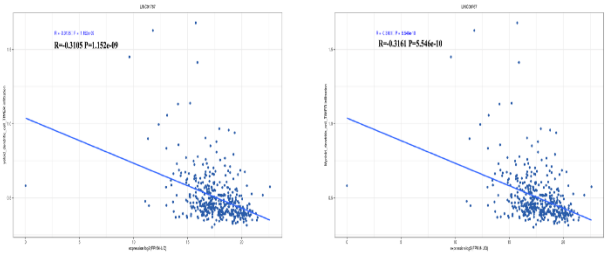
B



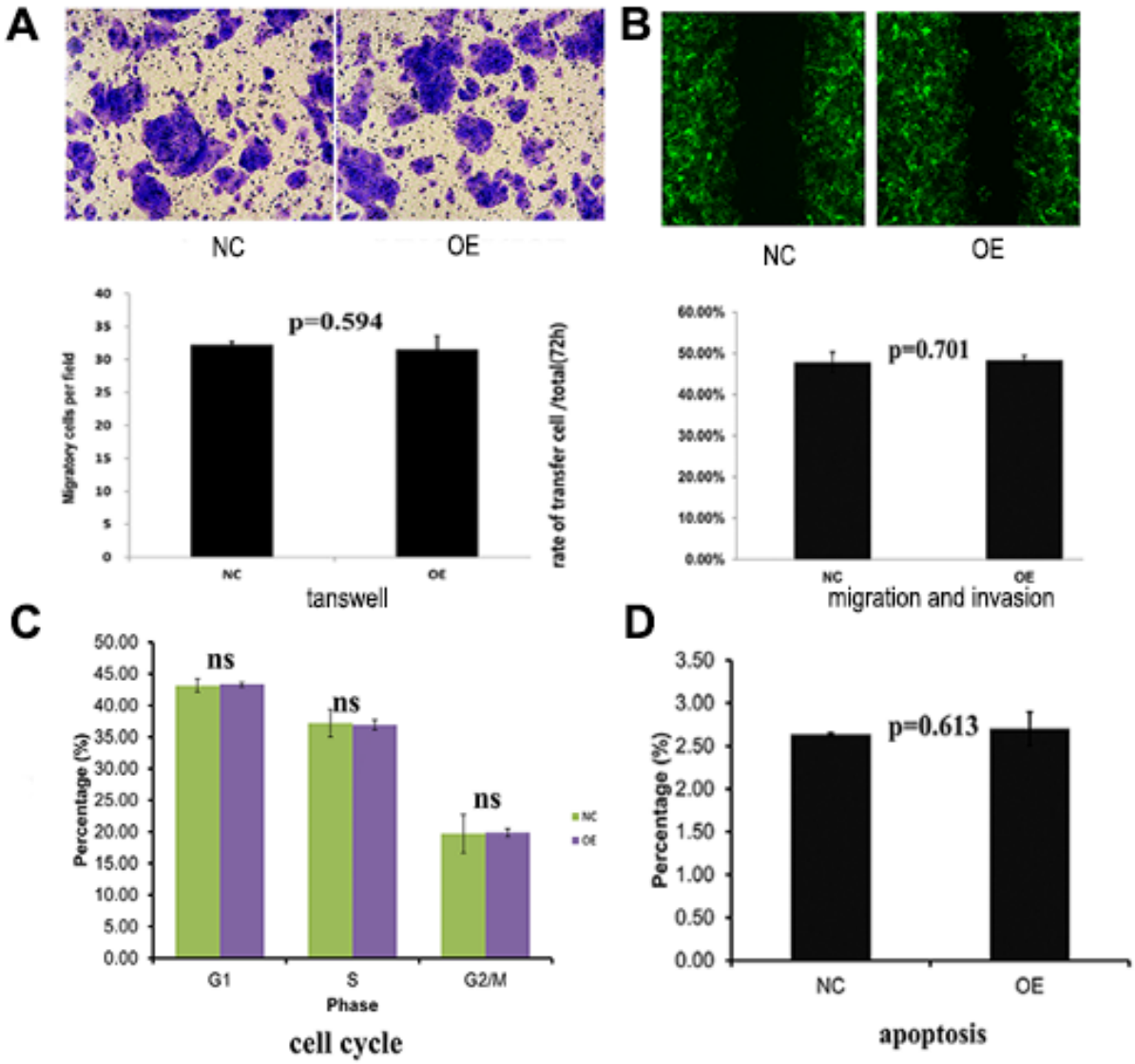
C



D



Supplementary Figure 2 LINC01767 in immune cells of liver cancer based on ImmReg (hrbmu.edu.cn), using the $R > 0.5$, $P < 0.05$. A: The results showed the LINC01767 was correlated with the immune microenvironment; B: Macrophage M2 cell and positively correlated with Macrophage, C: Negatively correlated with the Neutrophil and B cell; D: CD4+cell, Myeloid dendritic.



Supplementary Figure 3 INC01767 have no significant influence on the cell migration/invasion/cell cycle or apoptosis in Huh7 cell.