

Table S1. Primers used in the study.

Gene	Sequences	Applications
TMBIM6	F: 5'-TCATATAACCCCGTCAACGC-3'	MeRIP -qPCR
	R: 5'-CAAATCCAGCAAGAAGTCCC-3'	
ATAD3A	F: 5'-TTTCCGTCACCCGTTTGC-3'	MeRIP -qPCR
	R: 5'-ATTCAGGGCGTCCTTGGC-3'	
CASP9	F: 5'-GGTCGCTAATGCTGTTTCGGT-3'	MeRIP -qPCR
	R: 5'-GTGCAAGATAAGGCAGGGTGAG-3'	
MAP3K6	F: 5'-GTGCTTCCCCAGCGTAGG-3'	MeRIP -qPCR
	R: 5'-TCCGTGTACTCATAATCAAACCTCC-3'	
CPNE5	F: 5'-CCCCTCCTCAATTTCTTGG-3'	MeRIP -qPCR
	R: 5'-GTACCCCTCTTTCACCCGT-3'	
HMG20A	F: 5'-CCTTCCCCCTCCTTAGTGA-3'	MeRIP -qPCR
	R: 5'-TCTGTGAATAGCCACCGCA-3'	
RBM15	F: 5'-GGCTGCCTGAGGAGAGTGGAG-3'	qRT-PCR
	R: 5'-CGGCTACTGCTCAATTCTGGACTG-3'	
TMBIM6	F: 5'-GCACGGACTCTGGAACCATGAAC-3'	qRT-PCR
	R: 5'-GCAGCCGCCACAAACATACAAAG-3'	
ATAD3A	F: 5'-ATCAATGAGATGGTCCACTTCG-3'	qRT-PCR
	R: 5'-CCGGCTTAAGAACATACTTGTC-3'	
CASP9	F: 5'-GACCAGAGATTCGCAAACCAGAGG-3'	qRT-PCR
	R: 5'-AAGAGCACCGACATCACCAAATCC-3'	

MAP3K6	F: 5'-CTCTACAGCGGCTGAATGAG-3' R: 5'-TGAATCCACATTCAGTTCCTGT-3'	qRT-PCR
CPNE5	F: 5'-AAAGACATGTTTTCCAAGTCCG-3' R: 5'-ACGTCGTATAGATCAAAACGGA-3'	qRT-PCR
HMG20A	F: 5'-GGAGAGTAATGATCTGGCTACC-3' R: 5'-ACAAATTCTGGATTGTTGGTGG-3'	qRT-PCR
IGF2BP3	F: 5'-GAGGCGCTTTCAGGTAAAATAG-3' R: 5'-AATGAGGCGGGATATTCGTAT-3'	qRT-PCR
GAPDH	F: 5'-TGAACGGGAAGCTCACTGG-3' R: 5'-TCCACCACCCTGTTGCTGTA-3'	qRT-PCR
TMBIM6-2222	F: 5' TTCAGTGTGAGAGGATCGAGC 3' R: 5' CTGAGGCCACTGTGTCAAAC 3'	MeRIP -qPCR
CPNE5-1572	F: 5' CCATGAAGCTGATGGGTTTG 3' R: 5' ATGGCCTACGGTCCATGATTA 3'	MeRIP -qPCR

Abbreviation: ATAD3A: ATPase family AAA domain containing 3A; CASP9: caspase 9; CPNE5: copine 5; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; HMG20A: high mobility group 20A; IGF2BP3: insulin like growth factor 2 mRNA binding protein 3; MAP3K6: mitogen-activated protein kinase kinase kinase 6; RBM15: RNA binding motif protein 15; TMBIM6: transmembrane BAX inhibitor motif containing 6

Table S2. The top 6 mRNAs with differential m6A methylation modifications were screened out.

Gene	Foldchange(log2-Scaled)	<i>P</i> -value(paired t-test)
TMBIM6	0.649519554	0.033421116
ATAD3A	0.626995376	0.049728946
CASP9	0.667971081	0.033006025
MAP3K6	0.617107056	0.000669577
CPNE5	0.614209974	0.020752312
HMG20A	0.736722214	0.029893781

Abbreviation: ATAD3A: ATPase family AAA domain containing 3A; CASP9: caspase 9; CPNE5: copine 5; HMG20A: high mobility group 20A; MAP3K6: mitogen-activated protein kinase kinase kinase 6; TMBIM6: transmembrane BAX inhibitor motif containing 6;

Figure S1

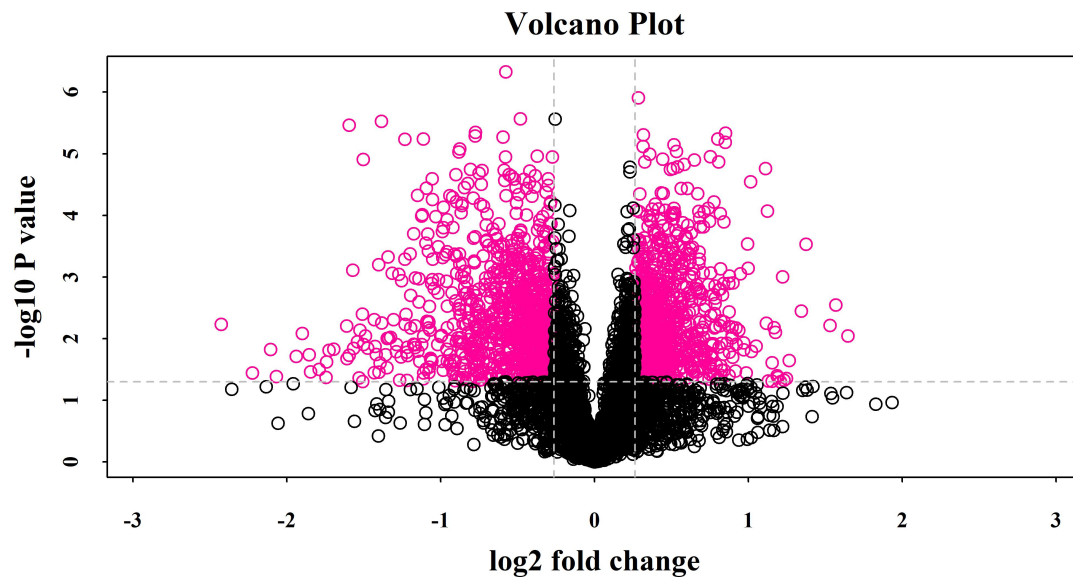


Figure S1. Volcano plot showing significantly differentially expressed proteins in 5 pairs of LSCC tissues and adjacent nontumor tissue. The pink circles on both sides represent 1826 significantly differentially proteins, the absolute fold change is ≥ 1.2 , and the p -value is < 0.05 .

Figure S2

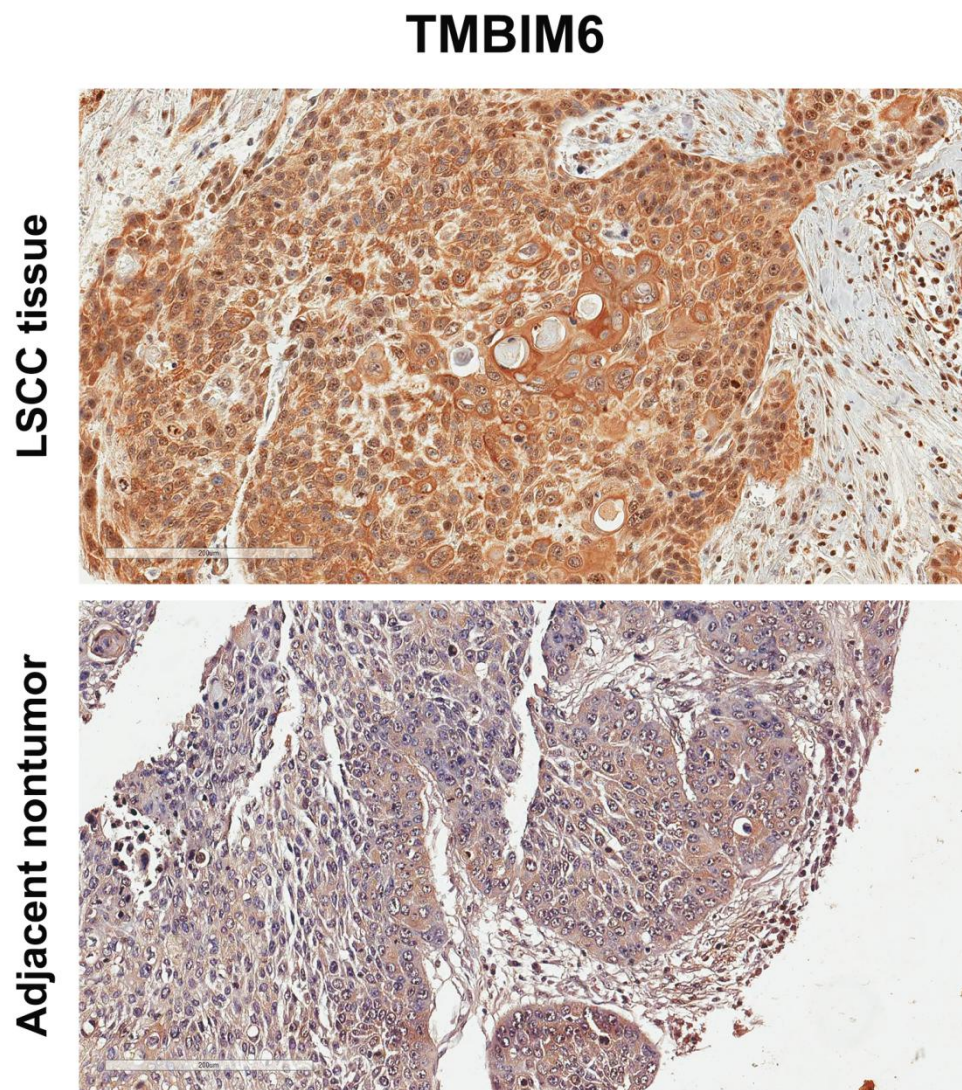


Figure S2. IHC was performed to investigate the expression of TMBIM6 in 122 pairs of LSCC samples.

Figure S3

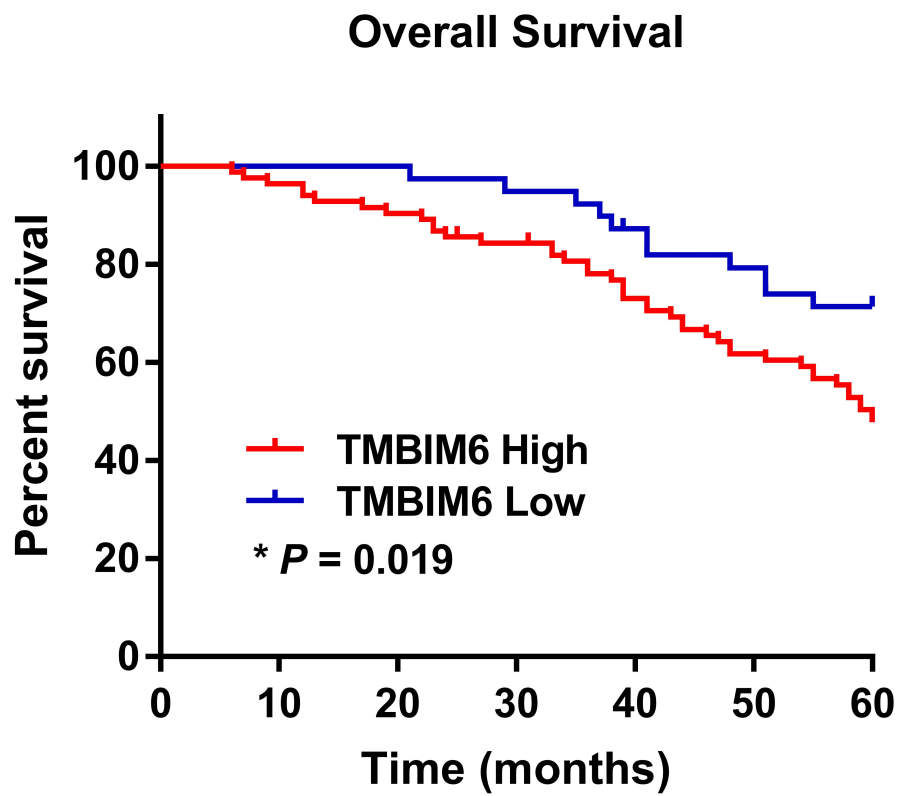


Figure S3. Kaplan-Meier survival analysis suggested that patients with high TMBIM6 expression in LSCC had a worse prognosis.

Figure S4

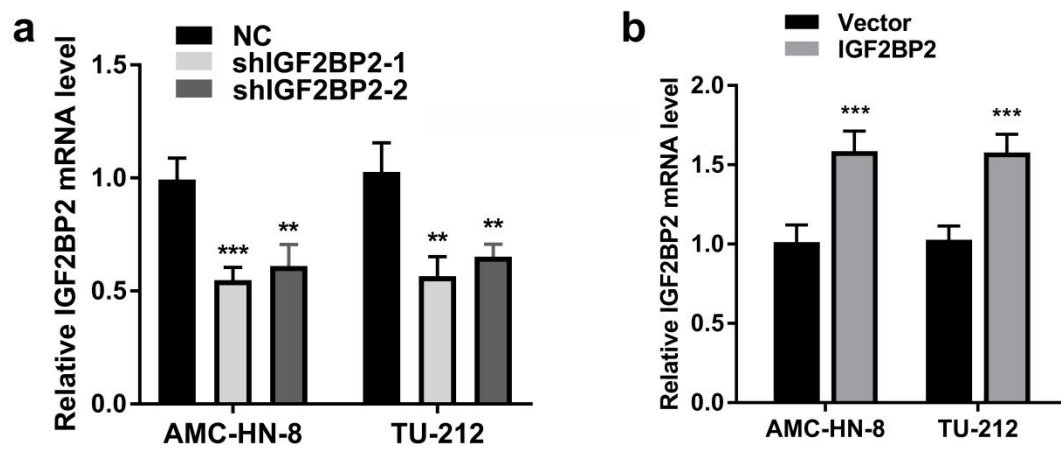


Figure S4. **a** The expression efficiency of IGF2BP2 after knocked down the IGF2BP2 in LSCC cells. **b** The efficiency of IGF2BP2 expression after IGF2BP2 overexpressed in LSCC cells.

Figure S5

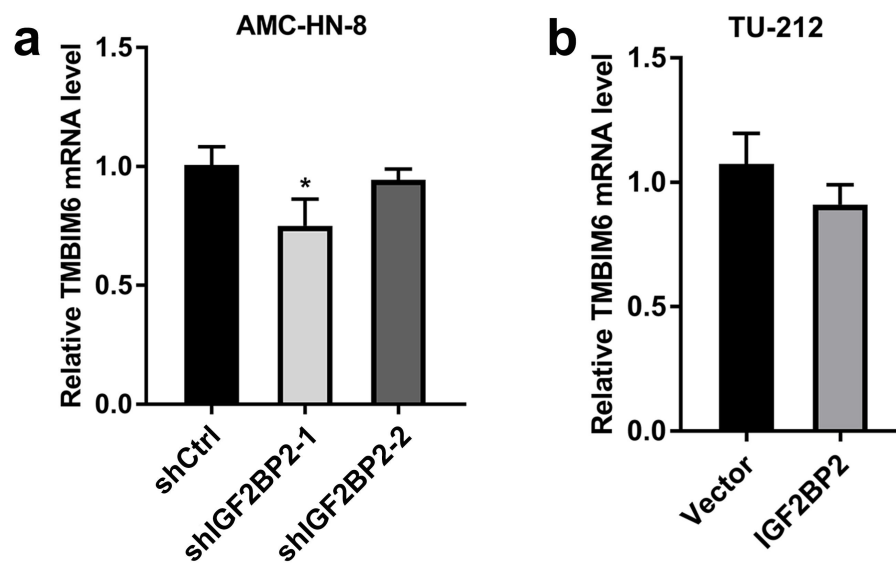


Figure S5. a, b qRT-PCR results of TMBIM6 expression after ablation or overexpression of IGF2BP2 in LSCC cells.

Figure S6

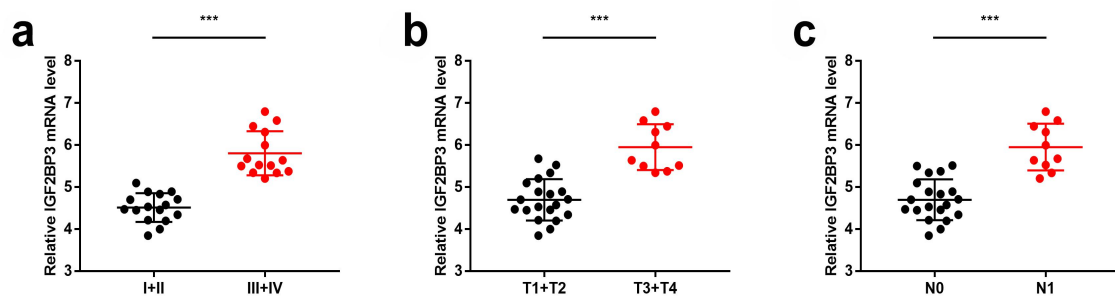


Figure S6. a-c The relationship between the expression level of IGF2BP3 and clinicopathological characteristics in LSCC patients.

Figure S7

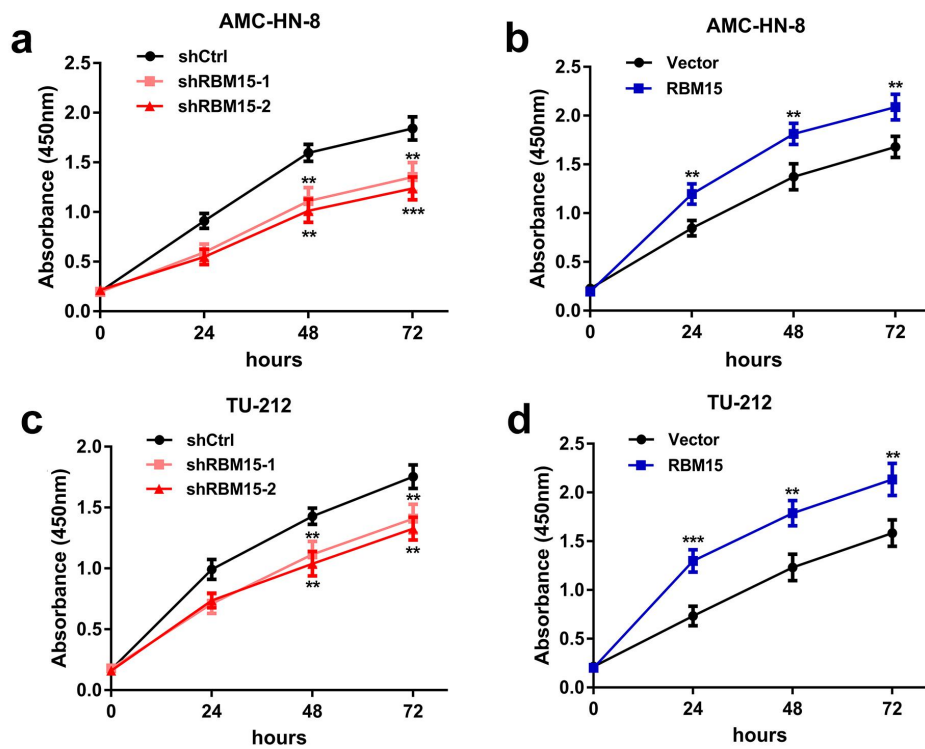


Figure S7. a-d CCK-8 assays were conducted to examine the cell proliferation ability in LSCC cells after transfection with shCtrl and/or shRBM15 and/or RBM15 vectors.