

Table SI. The inclusion and exclusion criteria for the selection of patients with bladder cancer in the present study.	
Inclusion criteria	Exclusion criteria
Complete clinical data of patients available.	Have a history of other systemic malignancies.
The patient did not have other bladder diseases, such as cystitis glandularis.	Those who have recently received radiotherapy, chemotherapy or immunosuppressive therapy.
The patient has no other serious systemic diseases, such as coagulation disorders, severe malnutrition, rheumatic immune system diseases and other systemic diseases.	Patients with incomplete or uncooperative clinical data.
Post-operative pathological examination confirmed bladder cancer.	

Table SII. Sequences of primers for transfection.

Name		Sequence
METTL3 siRNA	Sense	5'-AAUGUACGAGGCUUUAUAGAA-3'
	Antisense	5'-CUAUAAGCCUCGUACAUUGG-3'
METTL3 siRNA-NC	Sense	5'-UACUUUAAACUACUAUGACUU-3'
	Antisense	5'-GUCAUAGUAGUUUAAAGUAGA-3'
YTHDF2 siRNA	Sense	5'-UGAAUUACUCCUUGUUAGCGA-3'
	Antisense	5'-GCUAACAAGGAGUAAUUCAUU-3'
YTHDF2 siRNA-NC	Sense	5'-AUAUUCUAGGAAAAGCAUCAC 3'
	Antisense	5'-GAUGCUUUUCCUAGAUUAUUC-3'
METTL3 shRNA	Sense	5'-GGCAATAATTAGTAGTCAA-3'
	Antisense	5'-TTGACTACTAATTATTGCC-3'
METTL3 shRNA-NC	Sense	5'-AGAACAGGCTAGTCCTCAA-3'
	Antisense	5'-TTGAGGACTAGCCTGTTCT-3'

METTL3, methyltransferase-like 3.

Table SIII. Sequences of primers used for RT-qPCR.

Name	Sequence
METTL3	Forward: 5'-TTGTCTCCAACCTTCCGTAGT-3'
	Reverse: 5'-CCAGATCAGAGAGGTGGTGTAG-3'
RRAS	Forward: 5'-GACCCCACTATTGAGGACTCC-3'
	Reverse: 5'-CGGTCGTTAATGGCGAACAC-3'
GAPDH	Forward: 5'-GGAGCGAGATCCCTCCAAAAT-3'
	Reverse: 5'-GGCTGTTGTCATACTTCTCATGG-3'

METTL3, methyltransferase-like 3; RRA, RAS related; GAPDH, glyceraldehyde 3-phosphate dehydrogenase.

Table SIV. The potential genes that were highly correlation with METTL3 in breast cancer.						
Positive correlation	Pearson's correlation coefficient	Negative correlation	Pearson's correlation coefficient			
RAB2B	0.7	LDLRAD2	-0.37			
ACIN1	0.67	RRAS	-0.36			
PNN	0.66	GUK1	-0.35			
SFRS14	0.65	TNFSF12-TNFSF13	-0.35			
PPP1R3E	0.65	CEBPB	-0.34			
METT11D1	0.63	FAM38A	-0.33			
LOC646471	0.63	S100A10	-0.32			
CHD8	0.61	PSMB10	-0.31			
PARP2	0.61	IL3RA	-0.31			
APEX1	0.61	ANXA2	-0.31			

METTL3, methyltransferase-like 3; RAB2B, member RAS oncogene family; ACIN1, apoptotic chromatin condensation inducer 1; PNN, pinin, desmosome associated protein; SFRS14, SURP and G-patch domain containing 2; PPP1R3E, protein phosphatase 1 regulatory subunit 3E; METT11D1, methyltransferase like 17; LOC646471, uncharacterized LOC646471; CHD8, chromodomain helicase DNA binding protein 8; PARP2, poly(ADP-ribose) polymerase 2; APEX1, apurinic/aprimidinic endodeoxyribonuclease 1; LDLRAD2, low density lipoprotein receptor class A domain containing 2; RRAS, RAS related; GUK1, guanylate kinase 1; TNFSF12-TNFSF13, TNFSF12-TNFSF13 readthrough; CEBPB, CCAAT enhancer binding protein beta; FAM38A, piezo type mechanosensitive ion channel component 1; S100A10, S100 calcium binding protein A10; PSMB10, proteasome 20S subunit beta 10; IL3RA, interleukin 3 receptor subunit alpha; ANXA2, annexin A2.