Table S1 Clinicopathological characteristics of bladder cancer patients from TCGA database

Characteristics	Groups	Training cohort (N=277)		Validation cohort (N=116)		P value
		No.	%	No.	%	
Gender	Male	206	74.4	85	73.3	0.90
	Female	71	25.6	31	26.7	
Age at Diagnosis	<50	18	6.5	4	3.4	0.13
	50-70	146	52.7	45	38.8	
	>70	113	40.8	53	45.7	
Fustat	0	172	62.1	69	59.5	0.65
	1	105	37.9	47	40.5	
Pathologic T	Tx-T1	3	1.1	2	1.7	0.36
	T2-T4	256	92.4	102	88.0	
	Unknown	18	6.5	12	10.3	
Pathologic N	Nx	25	9.0	11	9.5	0.65
	N0	163	58.8	64	55.2	
	N1	29	10.5	15	12.9	
	N2	54	19.5	21	18.1	
	N3	3	1.1	4	3.4	
	Unknown	3	1.1	1	0.9	
Pathologic M	Mx	140	50.5	54	46.6	0.44
	M0	131	47.3	56	48.3	
	M1	5	1.8	5	4.3	
	Unknown	1	0.4	1	0.9	
Pathologic Stage	I	1	0.4	1	0.9	0.66
	II	89	32.1	34	29.3	
	III	98	35.4	38	32.8	
	IV	87	31.4	43	37.1	
	Unknown	2	0.7	0	0	
Pathologic Grade	High	264	95.3	108	93.1	0.66
	Low	11	4.0	7	6.0	
	Unknown	2	0.7	1	0.9	

Table S2 KEGG analysis of genes in candidate module

KEGG	-logP
WNT signaling pathway	2.14
MAPK signaling pathway	1.99
Leukocyte transendothelial migration	1.90
TGF-beta signaling pathway	1.86
Chemokine signaling pathway	1.70
Cytokine receptor interaction	1.63
JAK-STAT signaling pathway	1.51
Toll-like receptor signaling pathway	1.45
T cell receptor signaling pathway	1.42
B cell receptor signaling pathway	1.24

Table S3 GO analysis of genes in candidate module

Items	Name	-logP
GO		
BP	Positive regulation of epithelial to mesenchymal transition	2.31
	Cell cell adhesion via plasma membrane adhesion molecules	2.25
	Epithelial to mesenchymal transition	2.17
	Regulation of wnt signaling pathway	2.10
	Response to transforming growth factor beta	2.04
CC	Cell cell adherens junction	2.34
	Cell cell junction	2.11
	Protein complex involved in cell adhesion	1.93
	Autophagosome	1.58
	MHC protein complex	0.54
MF	Cytokine binding	2.03
	Notch binding	2.00
	wnt protein binding	1.64
	Chemokine receptor binding	1.56
	Cytokine receptor activity	1.55