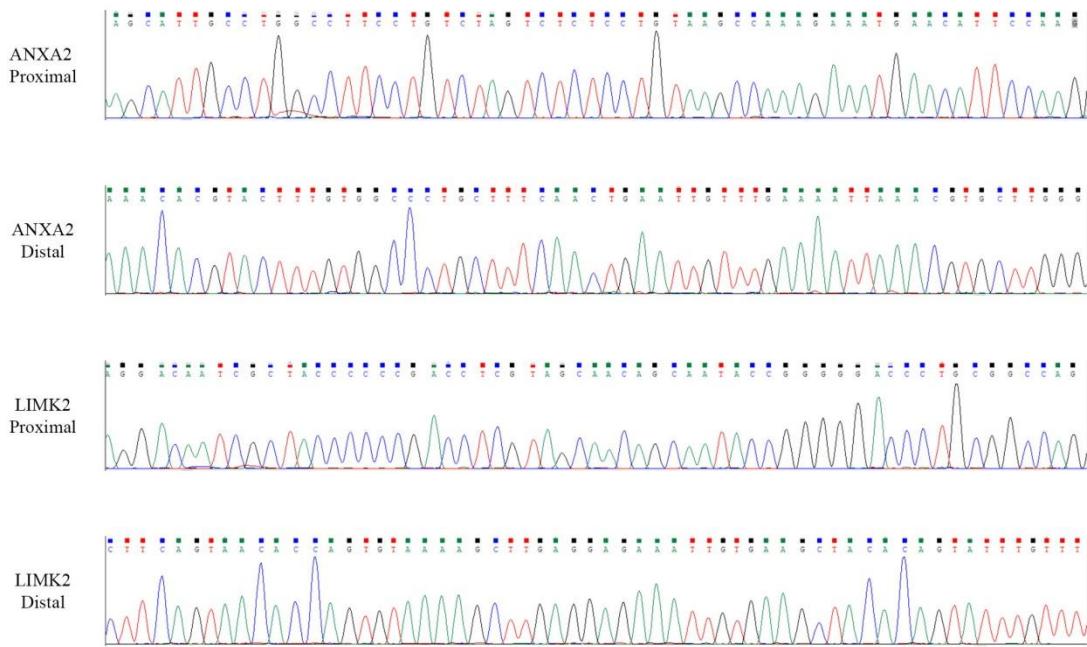
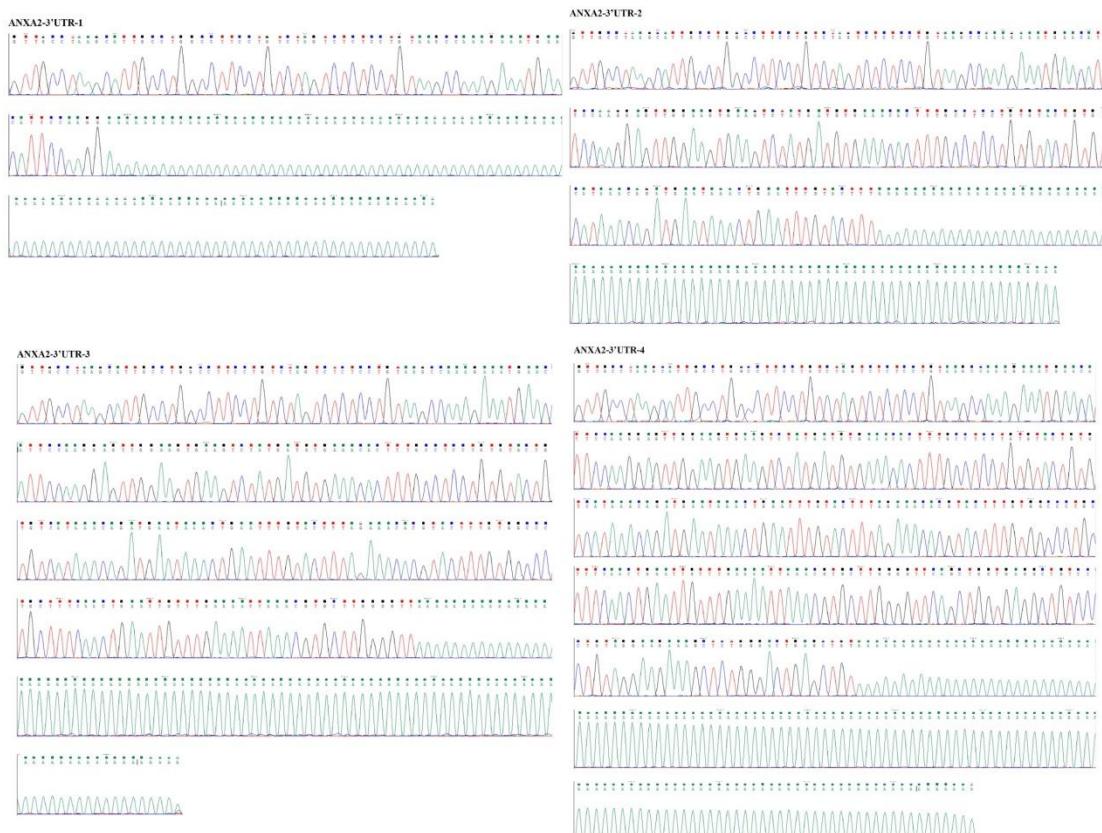


## Supplemental Figure 1



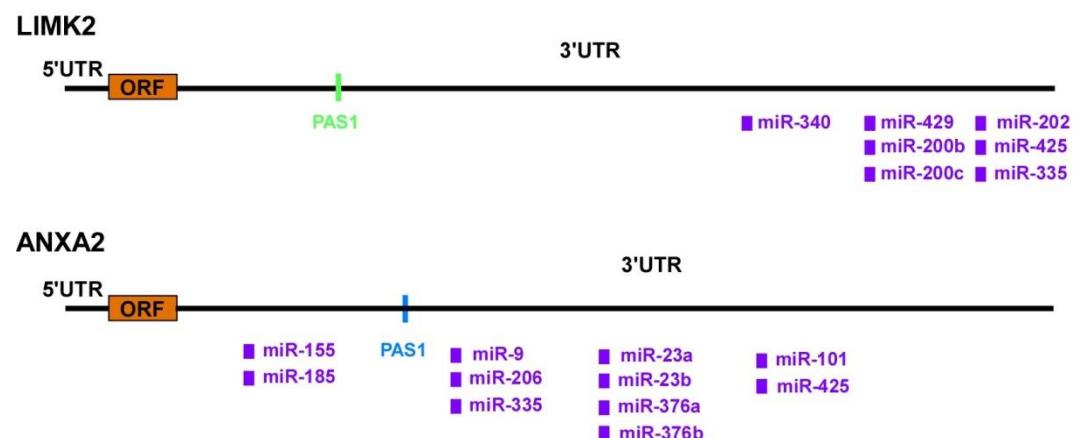
## Supplemental Figure 2



Supplemental Figure 3



Supplemental Figure 4



Supplemental table 1. Primers sequences.

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
<b>mRNA real-time qPCR for figure 1D and 1F</b>		
NUDT21	TGCATTGGTAACTGGTGGAGAC	TGGGTCCATATCCTGGTGCATT
GAPDH	TCAAGAAGGTGGTGAAGCAG	CGTCAAAGGTGGAGGAGTG
<b>Cloning Primers for figure 4D</b>		
NUDT21-3'UTR-wt	CCGCTCGAGATT CCT GCGCA	AAATATGC GGCC GCT TCT CTTTC AA
NUDT21-3'UTR-mu	CTT GCC AGATGGGACTACTTAA GGAA	TTC CTT AAG TAGTCCC ATCTGGC AAG
<b>PCR for figure 5B</b>		
CDK7 proximal	CAT GTGGGCT GTTGGCT GTAT	CACT GTT CCT CAG TTGGT GTGC
CDK7 distal	TTGGGCACACCAACTGAGGAA	GCC GTA ATT CGAGCACATGGGA
CCBL2 proximal	TGACACACTCTGCATCAGCGA	TGTTCTCTCCCACATA CCTGGGA
CCBL2 distal	ACTCCACATAACCCACTTGGC	TTGTTCTCTCCCACATA CCTGGGA
PTPN18 proximal	CAC ACC CTGCTAGACTTCTGGA	GTC CCT ATT CAG CC ACTT CCTCCT
PTPN18 distal	AAGTCTAACGCCAGTT CCTGC	TCCAGGCCACTGTTCCATT
ENSA proximal	CAAGAAGAAGAGAACCCCTGCG G	CGAAGAACCTCCTTAGCTCAA
ENSA distal	CAAGAAGAAGAGAACCCCTGCG GA	TTTGGCCTTAGCTTGCCTCT
UXS1 proximal	ACGTGTTGCAGAGACCATGTG	AAGTTGCTGACTACTGCCA
UXS1	TCAGTTCTCTCCGAAGCCCA	TGGCGAGTCCGTCCTTCTTT

distal		
ANXA2 proximal	ACACATCTGGTGAATTCCGCA	TTCCTCTTCACTCCAGCGTCA
ANXA2 distal	TTGCCTTCGCCTACCAGAGAA	AGCGTCATACTGAGCAGGTGT
EPB41L1 proximal	AAACCACGCCGAGACACAAG	CCGGTGGATGAGTTGCTGTT
EPB41L1 distal	GCGTTCTTCCAGCAAACCGTA	CTTGTGTCTCGCGTGGTTT
MTHFSD proximal	AGTGCTCGCTTCTCGTCCTT	TCCCACCACAACTAAATCCACGA
MTHFSD distal	TGGTTCCAACACCACGACTGA	GTAGCCTTCTCCCTTCCCGATT
GATA3 proximal	AAATGAACGGACAGAACCGGC	TTGGCATTCCCTCCAGAGTG
GATA3 distal	AAATGAACGGACAGAACCGGC	TGTGGTTGTGGTGGTCTGACA
LIMK2 proximal	CGAACACTGGACTTTGGCCT	TCTAGGTTGAGGTGCTCCGT
LIMK2 distal	ACTGTCAACGAAACCTGGCAC	ACCTTGCAGCTCATACAGGCA
MTHFD2 proximal	ATGGCTGCGACTTCTCTAATGT C	ACTTCCTGCTTGATCTGCTGGG
MTHFD2 distal	GCTGCGACTTCTCTAATGTCTG C	TTCTGCCAACCAACCAGGATCACA
MPPE1 proximal	GCCTGTGCTCAAAGCCATGTT	ACGCTCTCTCCATCTGCCATT
MPPE1	AGCTGTTGTCTTGCTGTGCT	AACGCTCTCTCCATCTGCCATT

distal		
DNASE1L1 proximal	TTCTTGTTGGGCTTGTGCC	CCCACTTGTCTCCACTCCTGA
DNASE1L1 distal	CAGCCTCACTGTTCTGTTGCTG	TCTAGGCACAAGCCCCAACCAA
TFIP11 proximal	ACCTGGGTTGGAAGTCGATGT	TAGGCAATGTTCTCCGTGCT
TFIP11 distal	TGACGAGCGGGAGAACTTGA	AGTTGACTGGCGCAGAGTAGT

Gene	
<b>3'-RACE for figure 5C</b>	
ANXA2	GTTGCCTAAGCATTGCCTGG
LIMK2	GGCTCCCATAAGGACAATCGC

Supplementary Table 2. Correlation between NUDT21 expression and clinicopathological features.

Feature	No.	NUDT21 expression		<i>P</i>
		Low	High	
Sex		0.233		
Male	121	67	54	
Female	75	48	27	
Age (y)		0.995		
≤60	92	54	38	
>60	104	61	43	

Tumor grade				<b>0.014</b>
Low	117	77	40	
High	79	38	41	
Tumor size				<b>0.024</b>
<3cm	143	77	66	
≥3cm	53	38	15	
T classification				<b>0.016</b>
Ta,T1	130	68	62	
T2-T4	66	47	19	
Total NO. of patients	196	115	81	

Supplementary Table 3. Multivariate analysis of overall survival (OS) and Recurrent-free survival (RFS) in patients with bladder cancer

Prognostic variables	OS		RFS	
	Hazard ratio (95% CI)	P	Hazard ratio (95% CI)	P
Sex (M vs F)	1.035 (0.547-1.957)	0.916	1.097 (0.695-1.732)	0.691
Age (>60 vs ≤60)	1.058 (0.584-1.916)	0.853	1.163 (0.778-1.738)	0.461
Tumor grade (High vs Low)	1.774 (0.941-3.344)	0.076	1.100 (0.699-1.733)	0.680
Tumor size (≥3cm vs <3cm)	1.758 (0.839-3.680)	0.135	1.685 (1.043-2.723)	<b>0.033</b>
T classification (T2-4 vs T1,Ta)	1.819 (1.015-3.262)	<b>0.045</b>	1.117 (0.721-1.733)	0.620
NUDT21 (High vs Low)	0.430 (0.224-0.826)	<b>0.011</b>	0.535 (0.352-0.815)	<b>0.004</b>