

Figure S1. The 68 dysregulated lncRNAs along with 236 overlapping target mRNAs were used to establish a ceRNA network by Cytoscape 3.6.1 tool. The yellow arrowheads indicate miRNAs. The circles represent mRNAs, hexagons represent lncRNAs, red indicates upregulation, and blue indicates downregulation. ceRNA, competing endogenous RNA; lncRNA, long non-coding RNA; mRNA, messenger RNA; miRNA, microRNA.

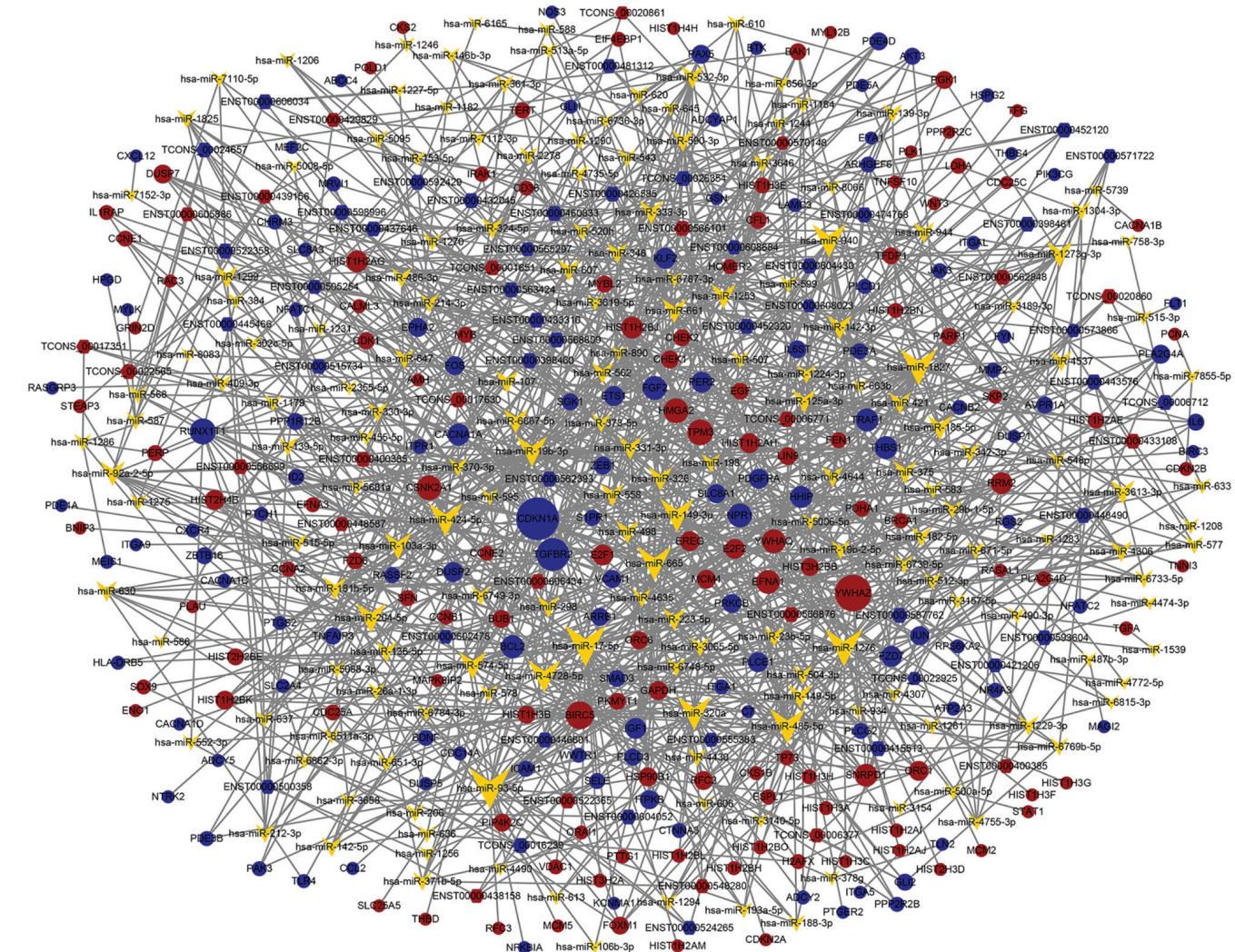


Table SI. Data statistics of patients with BC.

Variables	No. of patients (%)
Sex	
Male	56 (87.5)
Female	8 (12.5)
Age	
<60	16 (25)
≥60	48 (75)
Smoking history	
Lifelong non-smoker	28 (43.7)
Smoker	36 (56.3)
Tumor size	
<3 cm	32 (50)
≥3 cm	32 (50)
Number of tumors	
Solitary	30 (46.9)
Multiple	34 (53.1)
Pathological stage	
pTa-pT1	31 (48.4)
pT2-T4	33 (51.6)
Histologic grade	
Low	25 (39.1)
High	39 (60.9)
Lymphatic metastasis	
Yes	26 (40.6)
No	38 (59.4)

BC, bladder cancer.

Table SII. Predicted ceRNAs for lncRNAs.

lncRNAs	No. of sponge miRNAs	No. of target genes
All DE-lncRNAs	180	236
Selected four DE-lncRNAs	19	93

ceRNAs, competing endogenous RNA; lncRNA, long non-coding RNA; DE, differentially expressed.

Table SIII. Relative expression of 4 lncRNAs and 2 mRNAs screened in 64 pairs of BC tissues and normal tissues.

lncRNA/mRNA	Expression level		
	Control	BC	P-value
ENST00000433108	1.150±0.695	4.351±14.868	0.0765
ENST00000398461	0.952±0.386	0.416±0.737	<0.0001 <sup>a</sup>
ENST00000524265	1.038±0.356	0.497±0.862	<0.0001 <sup>a</sup>
ENST00000598996	0.987±0.340	0.363±0.578	<0.0001 <sup>a</sup>
CDK1	1.088±0.522	8.727±11.317	<0.0001 <sup>a</sup>
CCNB1	1.029±0.407	5.992±8.155	<0.0001 <sup>a</sup>

<sup>a</sup>P<0.0001 vs. the control group; Student's t-test (two-tailed). lncRNA, long non-coding RNA; mRNA, messenger RNA; BC, bladder cancer.