

Table S1 GO terms and KEGG pathway analyses for the candidate high expressed DE-mRNAs in BC

Group	ID	Description	Gene ratio	adj.P value	Gene ID
BP	GO:0000082	G1/S transition of mitotic cell cycle	13/143	6.42E-04	BID, CCNE1, CDC25A, CDKN3, RCC1, ARID3A, EIF4EBP1, MCM4, SKP2, TYMS, KIF14, TRIM71, E2F7
BP	GO:0044843	Cell cycle G1/S phase transition	13/143	6.80E-04	BID, CCNE1, CDC25A, CDKN3, RCC1, ARID3A, EIF4EBP1, MCM4, SKP2, TYMS, KIF14, TRIM71, E2F7
BP	GO:0048596	Embryonic camera-type eye morphogenesis	4/143	3.89E-02	PAX2, SOX11, TBX2, FZD5
BP	GO:0021846	Cell proliferation in forebrain	4/143	3.95E-02	KIF1A, WNT7A, KIF14, ARX
KEGG	hsa04110	Cell cycle	6/59	4.19E-02	CCNE1, CDC25A, E2F2, MCM4, SKP2, TTK

Through GO terms analysis for the 151 candidate high expressed mRNAs targeted by the hub down-regulated solasonine-related DE-miRNAs in BC, four remarkably enriched BP were obtained (adj.P value ≤ 0.05); through KEGG pathway enrichment analysis, one remarkably enriched pathways was obtained (adj.P value ≤ 0.05). GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; DE-mRNAs, differentially expressed messenger RNAs; BC, bladder xarcinoma; adj.P value, adjusted P value; BP, biological process.

Table S2 KEGG pathway analyses for the top three significant modules in the PPI network

Group	ID	Description	Gene ratio	adj.P value	Gene ID
Module 1					
KEGG	hsa04350	TGF-beta signaling pathway	2/2	1.61E-03	THBS1, THSD4
KEGG	hsa05219	Bladder cancer	1/2	4.94E-02	THBS1
KEGG	hsa05144	Malaria	1/2	4.94E-02	THBS1
KEGG	hsa04115	p53 signaling pathway	1/2	5.20E-02	THBS1
KEGG	hsa04512	ECM-receptor interaction	1/2	5.20E-02	THBS1
Module 2					
KEGG	hsa04380	Osteoclast differentiation	7/12	8.85E-09	FOS, FOSB, JUNB, JUND, NFATC1, NFATC2, FOSL1
KEGG	hsa05166	Human T-cell leukemia virus 1 infection	7/12	1.94E-07	EGR1, EGR2, FOS, NFATC1, NFATC2, SRF, FOSL1
KEGG	hsa05161	Hepatitis B	5/12	4.03E-05	EGR2, EGR3, FOS, NFATC1, NFATC2
KEGG	hsa04657	IL-17 signaling pathway	4/12	1.11E-04	FOS, FOSB, JUND, FOSL1
KEGG	hsa04625	C-type lectin receptor signaling pathway	4/12	1.19E-04	EGR2, EGR3, NFATC1, NFATC2
KEGG	hsa04928	Parathyroid hormone synthesis, secretion and action	4/12	1.19E-04	EGR1, FOS, JUND, MEF2D
KEGG	hsa04022	cGMP-PKG signaling pathway	4/12	6.14E-04	MEF2D, NFATC1, NFATC2, SRF
KEGG	hsa04662	B cell receptor signaling pathway	3/12	1.45E-03	FOS, NFATC1, NFATC2
KEGG	hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	3/12	1.64E-03	FOS, NFATC1, NFATC2
KEGG	hsa04658	Th1 and Th2 cell differentiation	3/12	1.64E-03	FOS, NFATC1, NFATC2
KEGG	hsa04660	T cell receptor signaling pathway	3/12	2.13E-03	FOS, NFATC1, NFATC2
KEGG	hsa04659	Th17 cell differentiation	3/12	2.13E-03	FOS, NFATC1, NFATC2
KEGG	hsa04010	MAPK signaling pathway	4/12	2.91E-03	FOS, JUND, NFATC1, SRF
KEGG	hsa05135	Yersinia infection	3/12	3.76E-03	FOS, NFATC1, NFATC2
KEGG	hsa04921	Oxytocin signaling pathway	3/12	4.92E-03	FOS, NFATC1, NFATC2
KEGG	hsa04310	Wnt signaling pathway	3/12	5.15E-03	NFATC1, NFATC2, FOSL1
KEGG	hsa05167	Kaposi sarcoma-associated herpesvirus infection	3/12	8.30E-03	FOS, NFATC1, NFATC2
KEGG	hsa05203	Viral carcinogenesis	3/12	9.18E-03	EGR2, EGR3, SRF
KEGG	hsa05170	Human immunodeficiency virus 1 infection	3/12	9.71E-03	FOS, NFATC1, NFATC2
KEGG	hsa05031	Amphetamine addiction	2/12	1.26E-02	FOS, FOSB
KEGG	hsa04933	AGE-RAGE signaling pathway in diabetic complications	2/12	2.46E-02	EGR1, NFATC1
KEGG	hsa04668	TNF signaling pathway	2/12	2.92E-02	FOS, JUNB
KEGG	hsa04935	Growth hormone synthesis, secretion and action	2/12	3.14E-02	FOS, JUNB
KEGG	hsa04650	Natural killer cell mediated cytotoxicity	2/12	3.62E-02	NFATC1, NFATC2
KEGG	hsa04371	Apelin signaling pathway	2/12	3.78E-02	EGR1, MEF2D
KEGG	hsa04218	Cellular senescence	2/12	4.64E-02	NFATC1, NFATC2
Module 3					
KEGG	hsa04110	Cell cycle	3/5	5.53E-04	CCNA2, MCM4, TTK

After module analysis for the PPI network of the candidate mRNAs, the top three significant modules were identified. Through KEGG pathway enrichment analysis, 5, 26, and 1 remarkably enriched KEGG pathways for the top three modules were obtained, respectively (adj.P value ≤ 0.05). KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein-protein interaction; adj.P value, adjusted P value; mRNAs, messenger RNAs.