

Table S1. Primer sequences

	sense	antisense
CDK1	5'- TAGAAAGTGAAGAGGAAGGGGTTC-3'	5'- TAGAAAGTGAAGAGGAAGGGGTTC-3'
YWHAZ	5'- CGTACTTGGCTGAGGTTGC-3'	5'- GTCTGATAGGATGTGTTGGTTGC-3'
SUM1	5'-CAGTGTGGTGCCTCCATCTC-3'	5'- TTAATATGCCTGCTCAGTTGTGTAG-3'
GAPDH	5'-CGGAGTCAACGGATTTGGTCGTAT-3'	5'-AGCCTTCTCCATGGTGGTGAAGAC-3'

Table S2. KEGG pathways showing gene enrichment. (up-regulation)

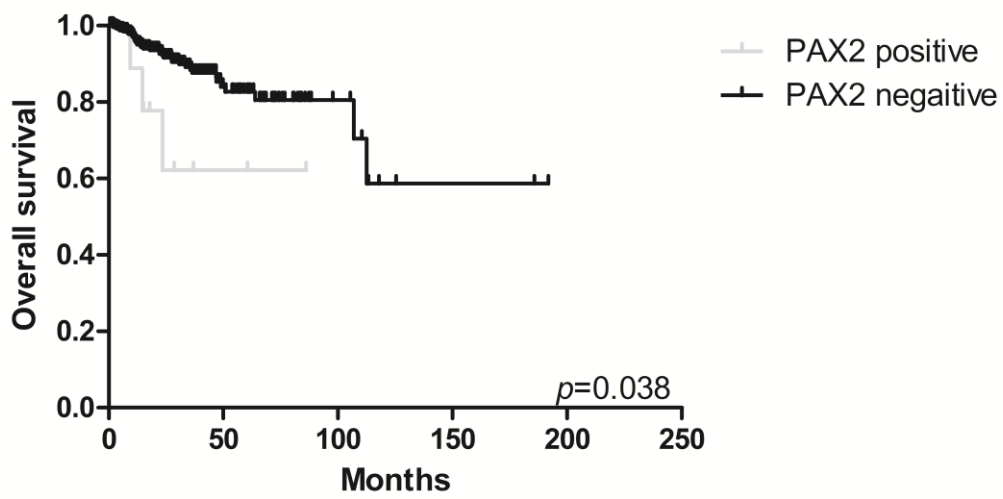
Pathway	Size (gene)	Genes contain pathway	Enrichment score	p-val
Fanconi anemia pathway	9	54	9.45860285	1.64E-06
Transcriptional misregulation in cancer	14	180	4.41401466	1.72E-05
Metabolic pathways	43	1189	2.0524134	6.02E-05
Cell cycle	9	124	4.11906898	0.0014662
Terpenoid backbone biosynthesis	4	21	10.8098318	0.0018035
RNA transport	10	165	3.43949194	0.0029472
Ubiquitin mediated proteolysis	9	138	3.70119242	0.0031883
Oocyte meiosis	8	112	4.05368693	0.0034142
Gap junction	7	89	4.46361033	0.0040544
Homologous recombination	4	28	8.10737387	0.0055955
PI3K-Akt signaling pathway	15	347	2.45323993	0.0057125
Pathogenic Escherichia coli infection	5	55	5.15923792	0.0112783
Pyrimidine metabolism	7	107	3.71272261	0.0117058
Viral carcinogenesis	10	207	2.74162401	0.0156985
mTOR signaling pathway	5	60	4.72930142	0.0164797
mRNA surveillance pathway	6	92	3.70119242	0.0232713
RIG-I-like receptor signaling pathway	5	71	3.99659275	0.0335668
Spliceosome	7	132	3.00955545	0.0364219

Synthesis and degradation of ketone bodies	2	9	12.6114705	0.0411321
Epstein-Barr virus infection	9	204	2.50374781	0.0426077
Systemic lupus erythematosus	7	138	2.87870521	0.0458028
Purine metabolism	8	173	2.62435224	0.0480624

Table S3. KEGG pathways showing gene enrichment. (down-regulation)

Pathway	Size(gene)	Genes pathway contain	Enrichment score	p-val
Olfactory transduction	24	408	8.5731874	6.55E-15
Chemokine signaling pathway	11	192	8.3499273	4.31E-07
Cytokine-cytokine receptor interaction	12	267	6.5503005	1.58E-06
Rheumatoid arthritis	6	94	9.3028204	0.0001948
Serotonergic synapse	6	114	7.6707466	0.0005692
Antigen processing and presentation	5	82	8.8868406	0.0010426
Tuberculosis	7	184	5.5446158	0.0011988
Natural killer cell mediated cytotoxicity	6	140	6.2461794	0.0017263
Autoimmune thyroid disease	4	56	10.410299	0.0024104
Toll-like receptor signaling pathway	5	108	6.747416	0.0036857
Cholinergic synapse	5	113	6.4488578	0.0045141
Arachidonic acid metabolism	4	67	8.7011454	0.0047418
Influenza A	6	179	4.88528	0.006189
Alcoholism	6	180	4.8581395	0.0063663
Asthma	3	34	12.859781	0.0065394

Metabolic pathways	18	1189	2.206388	0.0074125
Herpes simplex infection	6	188	4.6514102	0.0079267
PI3K-Akt signaling pathway	8	347	3.3600965	0.0116776
Neuroactive ligand-receptor interaction	7	275	3.709852	0.0122766
Hematopoietic cell lineage	4	88	6.6247357	0.0128947
GABAergic synapse	4	90	6.4775194	0.0139797
Graft-versus-host disease	3	45	9.7162791	0.0146695
Pancreatic secretion	4	96	6.0726744	0.0176033
Intestinal immune network for IgA production	3	51	8.5731874	0.0208883
Taste transduction	3	53	8.2496709	0.0232622
HIF-1 signaling pathway	4	106	5.4997806	0.0249616
Glutamatergic synapse	4	118	4.9404809	0.0361832
Toxoplasmosis	4	122	4.7784979	0.0405477
Cytosolic DNA-sensing pathway	3	66	6.6247357	0.0425738



Supplement figure. The overall survival of PAX2 positive patients and PAX2 negative patients in TCGA database.