

Table SI. Primers sequences used for reverse transcription-quantitative PCR

Gene name	Primer sequence (5'→3')
lncRNA 495810	F: CGTGGATTTGGGGATGGCTA
	R: CTGGACCACTATCACCCAAGC
PKM2	F: GCTGCCATCTACCACTTGC
	R: CCAGACTTGGTGAGGACGATT
Sense 495810	F: TAATACGACTCACTATAGGGAATTGATACCATTGAGATAA
	R: CTCTGGACCACTATCACCCA
Antisense 495810	F: AATTGATACCATTGAGATAA
	R: TAATACGACTCACTATAGGGCTCTGGACCACTATCACCCA
GAPDH	F: GCACCGTCAAGGCTGAGAAC
	R: TGGTGAAGAACGCCAGTGGGA

F, forward; R, reverse; lncRNA, long non-coding RNA; PKM2, pyruvate kinase isozyme M2.

Table SII. Clinical information of 68 cases of patients with colorectal cancer (cohort 1).

No.	Sex	Tumor size (cm)	Differentiation	TNM stage	Expression level of lncRNA 495810	Status
1	Female	3.5x2.5x1	Moderately	II	Low	0
2	Male	1.5x1.5x1	Moderately and poorly	II	Low	1
3	Male	2.5x2x1	Moderately and poorly	III	Low	1
4	Male	4.5x3.5x2	Moderately	II	Low	1
5	Female	7x5x3	Poorly	III	Low	1
6	Male	2.5x2x1	Moderately	II	Low	1
7	Female	4x3x3	Well	II	Low	0
8	Female	3.5x3.5x0.8	Moderately	II	Low	1
9	Male	4x2.5x0.8	Moderately	III	Low	0
10	Female	5x3x1	Moderately	II	Low	0
11	Female	7.5x3x3	Moderately	III	Low	0
12	Male	4x4x1	Moderately	I	Low	1
13	Male	4.5x4x1	Moderately and poorly	II	Low	0
14	Female	6.5x5x1.8	Moderately	II	Low	0
15	Male	3x3x0.5	Moderately	II	Low	0
16	Male	3x3x1	Well	I	Low	0
17	Male	3x2.5x1.5	Moderately and poorly	IV	Low	1
18	Female	5x4x1.5	Moderately	III	Low	0
19	Female	3x3x0.5	Moderately	I	Low	0
20	Female	5x4x1	Moderately	III	Low	1
21	Female	5x3.5x1	Moderately	II	Low	0
22	Male	10x9x6	Poorly	III	Low	1
23	Male	6.5x5x1	Moderately	II	Low	0
24	Female	2x2x0.7	Moderately	III	Low	1
25	Male	3x2x2	Moderately	II	Low	0
26	Male	7x7x1	Moderately	II	Low	0
27	Female	3.5x3x1	Moderately	III	Low	1
28	Male	5x3.5x3	Moderately	I	Low	0
29	Male	3.2x3x1	Moderately	II	Low	1
30	Female	2.4x1.5x1	Moderately	I	Low	0

31	Female	2.8x2x1	Moderately and poorly	III	Low	1
32	Female	4x2.5x0.6	Moderately	II	High	1
33	Female	8x6x1.5	Well	III	High	1
34	Male	3x2.5x0.5	Moderately	II	High	0
35	Male	4.5x1x1	Moderately	II	High	1
36	Female	3.5x2.5x2	Well	I	High	0
37	Male	9x6x1	Moderately and poorly	III	High	0
38	Male	7x5x4	Moderately	II	High	1
39	Female	4x3x1	Moderately	III	High	1
40	Female	5x4.5x1	Well	II	High	0
41	Male	3x3x1	Moderately	III	High	1
42	Female	3.5x2.5x0.8	Moderately	II	High	0
43	Male	4x3.5x1.5	Moderately	III	High	1
44	Male	6x3.5x0.6	Moderately	III	High	0
45	Male	10x6x1.5	Moderately	III	High	1
46	Male	7x5x1	Moderately	III	High	1
47	Male	5x2x1	Moderately	III	High	0
48	Female	4.5x3.5x0.3	Moderately and poorly	II	High	1
49	Female	7x4x1.5	Moderately	II	High	0
50	Female	4x3.5x1.5	Moderately	II	High	1
51	Male	3x2x0.6	Moderately	I	High	1
52	Male	8x8x2	Moderately	II	High	1
53	Male	10x8x5	Moderately	II	High	0
54	Male	7x4x1	Poorly	III	High	1
55	Female	2.5x2x0.5	Moderately	II	High	1
56	Female	13x7x1.5	Moderately and poorly	II	High	1
57	Female	7x3x2.5	Moderately	II	High	0
58	Female	7x6x2	Moderately and poorly	III	High	1
59	Male	3x3x1	Moderately	III	High	1
60	Female	7x4x1	Moderately	III	High	1
61	Male	3.5x3x1	Moderately	IV	High	1
62	Male	4x2x1	Moderately	II	High	1
63	Male	5x4x2.5	Moderately	II	High	1

64	Female	6x3.5x3.5	Moderately	III	High	0
65	Male	6x5x1	Moderately	II	High	1
66	Male	5x3.5x1	Moderately	III	High	1
67	Male	5x5x1	Moderately	II	High	1
68	Male	5x4x1	Moderately	II	High	1

lncRNA, long non-coding RNA.

Table SIII. The sequence (5'→3') of long non-coding RNA 495810.

>hg38_ENST00000495810.2 range=chr7:26195712-26201301 5'pad=0 3'pad=0 strand=- length=484 bp
GGGGCTCGTGGGGAGTGGGAGGAAGCTGGGGAGAAGATGAGTTGAGAGCAGTCCAGTGTGAGG GAAAGTGGGGATCCTGGGCCAACTTACCATTAAGAGGGTCCAGTCCTGTGACTGCTGTGAAGTA ACCAGGATTCCACATAGAGATGGGGCTCAAAGTCAGCCCAGGAGCAGCACTGTGGTCCCAGAAC TAATATTTGGCGACTCCAAGGCCAGGGATAAAAATGAAGAGATGGAGAGACAAGATTCCTGGC CTCTAATTGGCAGCACCCGTTGACTCTGCTCGTGACCAGACTCATGAACGCTTCATCCAAGGTTT CATGTCATCCGTGTGAGGAACCTCTCTGATTTGAGAAAATCTTTCTTAAATGGGCTTCTAGTTGT AAAGCCATTGTCTTTTATAGGAAATCATCAAATACCTTAAAGCTAGACACGCAATCAGCTGCATAA ATGACACACTCACTAAATCAATCCTTTATCAGG

Table SIV. The predicted result of RNA-Protein Interaction Prediction.

Input sequences	Protein: Pyruvate kinase isozyme M2 MSKPHSEAGTAFIQTTQLHAAMADTFLEHMCRLDIDSPPI TARNTGHICTIGPASRSVETLKEMIKSGMNVARLNFSHGTH EYHAETIKNVRTATESFASDPILYRPVAVALDTKGPEIRTG LIKSGSTAEEVELKKGATLKITLDNAYMEKCDENILWLDYK NICKVVEVGSKIYVDDGLISLQVKQKGADFLVTEVENGGG LGSKKGVNLPGAAVDLPVSEKDIQDLKFGVEQDVDMVF ASFIRKASDVHEVRKVLGEKGKNIISKIENHEGVRRFDEI LEASDGIMVARGDLGIEIPAEKVFLAQKMMIGRCNRAGKP VICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSG ETAKGDYPLEAVRMQHLLIAREAEAAIYHLQLFEELRRLAPI TSDPTEATAVGAVEASFKCCSGAIIVLTKSGRSAHQVARYR PRAPIIAVTRNPQTARQAHLYRGIFPVLCCKDPVQEAWAEDV DLRVNFAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTMR VVPVP
	RNA: 495810 GGGGCTCGTGGGGAGTGGGAGGAAGCTGGGGAGAAGATG AGTTGAGAGCAGTCCAGTGTGAGGGAAGTGGGGATCCTG GGCCAACTTACCATTAAGAGGGTCCAGTCCTGTGACTGCTG TGAAGTAACCAGGATTCCACATAGAGATGGGGCTCAAAGT CAGCCCAGGAGCAGCACTGTGGTCCCAGAACTAATATTTG GCGACTCCAAGGCCAGGGATAAAAATGAAGAGATGGAGA GACAAGATTTCTTGGCCTCTAATTGGCAGCACCCGTTGAC TCTGCTCGTGACCAGACTCATGAACGCTTCATCCAAGGTT TCATGTCATCCGTGTGAGGAACCTCTCTGATTTGAGAAAA TCTTTCTTAAAATGGGCTTCTAGTTGTAAAGCCATTGTCTT TTTAGGAAATCATCAAATACCTTAAAGCTAGACACGCAAT CAGCTGCATAAATGACACACTCACTAAATCAATCCTTTAT CAGG
Interaction probabilities	Prediction using RF classifier: 0.65
	Prediction using SVM classifier: 0.65