

Table SI. Clinical characteristics of patients with colorectal cancer.

Characteristic	Number of patients (%)
Age, years	
<60	9 (50.0)
≥60	9 (50.0)
Sex	
Male	10 (55.6)
Female	8 (44.4)
Tumor location	
Left colon	3 (16.7)
Right colon	4 (22.2)
Rectum	11 (61.1)
TNM stage	
I-III	15 (83.3)
IV	3 (16.7)
Lymph node metastasis	
Yes	6 (33.3)
No	12 (66.7)
Histological differentiation	
Poor	4 (22.2)
Moderate	14 (77.8)

Table SII. circSODs in circBank.

CircBank ID	Gene	CircBase ID	Position	Strand	Length, bp
hsa_circSOD1_001	SOD1	hsa_circ_0061417	chr21:33031934-33038831	+	387
hsa_circSOD1_002	SOD1	hsa_circ_0115795	chr21:33040814-33040946	+	132
hsa_circSOD2_001	SOD2	hsa_circ_0004662	chr6:160103505-160109274	-	462
hsa_circSOD2_002	SOD2	hsa_circ_0078541	chr6:160105885-160106065	-	180
hsa_circSOD2_003	SOD2	hsa_circ_0005472	chr6:160103505-160106065	-	345

circSOD, circular RNA generated by superoxide dismutase; +, forward strand; -, reverse strand.

Table SIII. Primers for amplification of circRNAs and genes.

Gene	Forward primer, 5'→3'	Reverse primer, 5'→3'
circ_0004662	CGATCGTTATGCTGAGAGAT	CGTTAGGGCTGAGGTTTGTC
circ_0078541	GGGTTGGCTTGGTTTCAATA	TTCCAGCAACTCCCCTGTT
SOD2	AACCTCACATCAACGCGCA	AGGTTGTTACGTAGGCCG
hnRNPM	CTCTTAATGGACGCTGAAGGAAA	CGCTCAGACTATGCTTGTTTAGG
U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT
18s rRNA	CAGCCACCCGAGATTGAGCA	TAGTAGCGACGGGCGGTGTG

circ, circular; SOD, superoxide dismutase; hnRNPM, heterogeneous nuclear ribonucleoprotein.

Table SIV. Target siRNA or shRNA sequences of circ_0004662 and hnRNPM.

Name of genes	Forward, 5'→3'	Reverse, 5'→3'
siRNA-NC	UUCUCCGAACGUGUCACGUTT	ACGUGACACGUUCGGAGAATT
circ_0004662-shRNA#1	TATGCTGAGAGATGTTACATCAAG AGTGTAACATCTCTCAGCATA	/
circ_0004662-shRNA#2	CGATCGTTATGCTGAGAGATCAAG AGTCTCTCAGCATAACGATCG	/
circ_0004662-shRNA#3	TCGTTATGCTGAGAGATGTTCAAG AGACATCTCTCAGCATAACGA	/
siRNA-hnRNPM#1	GCACAGUAUUUGUAGCAAATT	UUUGCUACAAAUACUGUGCTT
siRNA-hnRNPM#2	GAGGAGAGAUCAUUGCAAATT	UUUGCAAUGAUCUCUCCUCTT
siRNA-hnRNPM#3	GGAAGAUGC UAAAGGACAATT	UUGUCCUUUAGCAUCUUCCTT

circ, circular; si, smallinterfering; NC, negative control; sh, short hairpin; hnRNPM, heterogeneous nuclear ribonucleoprotein.

Table SV. Ribosomal proteins that may bind circular RNA.

Hit no.	Gene	Protein score	Protein Mass/Da	Protein Matches	Significant matches	Sequences	Significant sequences	Protein cover	protein π	emPAI
127	RPL29	44	17798	1	1	1	1	10.1	11.7	0.2
185	RPL35A	28	12587	1	1	1	1	9.1	11.1	0.3
206	MRPL16	25	28488	1	1	1	1	4.0	10.1	0.1
208	RPL26L1	25	17246	2	1	2	1	11.0	10.6	0.2
211	RPL36	25	12303	1	1	1	1	9.5	11.6	0.3
216	RPL34	23	13513	1	1	1	1	6.0	11.5	0.3
227	RPL13A	21	23619	2	1	2	1	5.9	10.9	0.1
230	RPL32	19	15964	1	1	1	1	7.4	11.3	0.2

emPAI, exponentially modified protein abundance index; RPL, large ribosomal subunit protein; MRPL, Mitochondrial Ribosomal Protein.

Table SVI. Proteins binding circ_0004662.

Number	Gene	Protein score	Protein mass, Da	Protein matches	Significant prot matches	Proteinsequences	Significant prot sequences	Protein cover	Protein π	emPAI
1	EEF1A1P5	87	50495	3	3	3	3	5.8	9.1	0.2
2	HNRNPM	78	77749	3	2	3	2	4.4	8.8	0.1
3	SRSF8	57	32382	2	1	2	1	5.0	11.7	0.1
4	KPLCE	42	28557	2	2	2	2	3.6	8.4	0.3
5	PKM	42	58470	3	2	3	2	6.2	8.0	0.1
6	H1-4	41	21852	1	1	1	1	4.6	11.0	0.2
7	PIMREG	40	27634	1	1	1	1	2.8	10.2	0.1
8	FOXF2	38	46591	1	1	1	1	2.0	9.2	0.1
9	FOXC1	36	57096	2	2	2	2	3.6	8.7	0.1
10	LCN1	31	19409	1	1	1	1	4.5	5.4	0.2
11	PGK1	30	44985	2	1	2	1	3.6	8.3	0.1
12	TRA2B	29	33760	1	1	1	1	3.5	11.3	0.1
13	S100A9	28	13291	2	1	2	1	18.4	5.7	0.3
14	SUB1	28	14386	1	1	1	1	4.7	9.6	0.2
15	SLBP	26	31551	1	1	1	1	5.2	7.1	0.1
16	HNRNPC	26	33707	2	1	2	1	8.2	5.0	0.1
17	SNX20	26	36668	1	1	1	1	2.2	8.9	0.1
18	MRPL16	25	28488	1	1	1	1	4.0	10.1	0.1
19	CTSV	25	37818	2	1	2	1	11.0	9.0	0.1
20	OR6F1	19	34509	1	1	1	1	3.6	8.9	0.1

emPAI, exponentially modified protein abundance index.