Supplementary Materials

Contents

Figure Legend

Figure S1: Fluorescent images of the cell transfection efficiency. A,B. Bright field and fluorescent images of AGS cells. C,D. Bright field and fluorescent images of HGC-27 cells. E,F. Bright field and fluorescent images of MKN-45 cells.

Figure S1

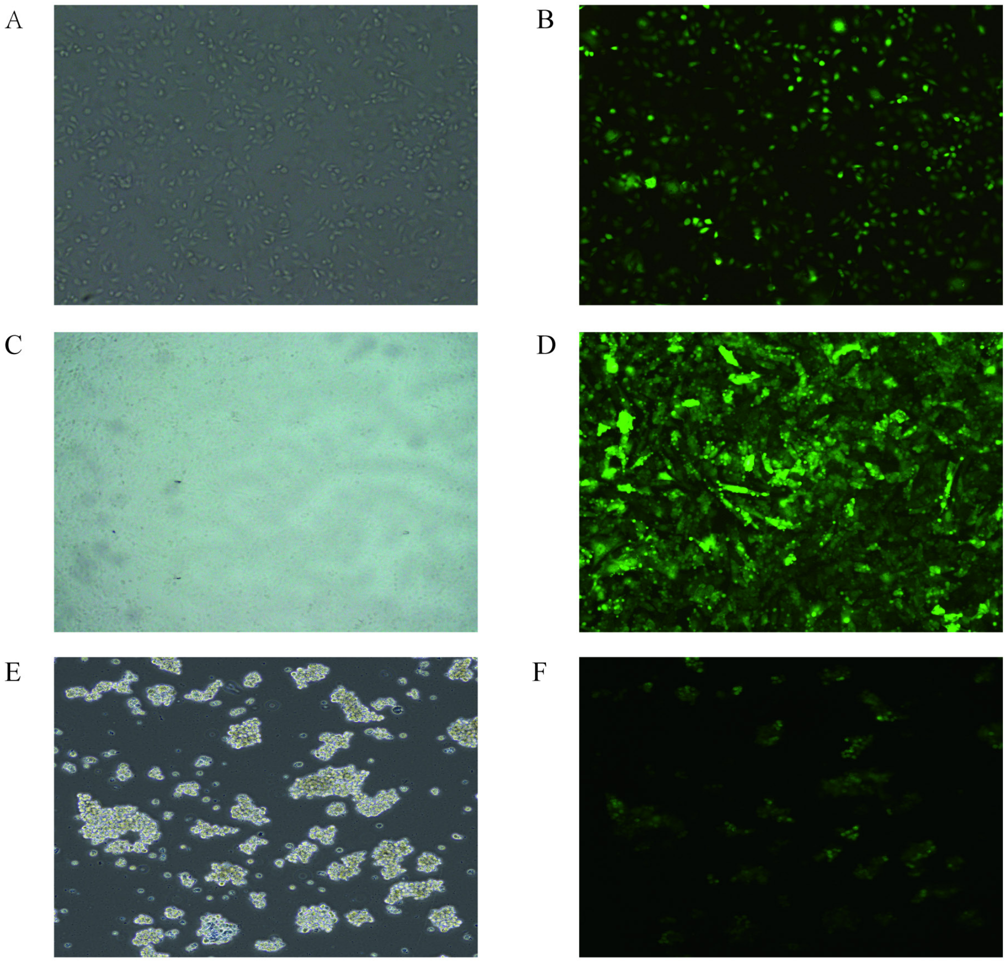

Table S1. Primers of candidate circRNAs for qRT-PCR

Names	Primiers
hsa_circ_0001483F	AGCACGACAAGAAGGAGGTT
hsa_circ_0001483R	AGTGATACCCGTCTCTGCAA
hsa_circ_0001610F	ATGACTCCAACCCAGAACCG
hsa_circ_0001610R	CACGGTCAACATGGCGGTAT
hsa_circ_0001614F	ATCCCAGAAAGTTGCTGATAGGA
hsa_circ_0001614R	TTCCAAACCGGGGAAACAAAC
hsa_circ_0001685F	AGTGGAAGTGTCACCCTAAAAA
hsa_circ_0001685R	AGGTCTATTTCTTCTGCTCCAGT
hsa_circ_0012126F	TCCACCCTCAACCCATCTTCC
hsa_circ_0012126R	CGCAGACTCCACAGAAGAGGT
hsa_circ_0000365F	CTTCTTGGGAGACGGTCCAC
hsa_circ_0000365R	GCCACGGCGATAAGGAAAAT
hsa_circ_0000149F	AAGCCAAGAACGGTGAAAAGG
hsa_circ_0000149R	GCGAGCTCTTGACCTTGAAT
hsa_circ_0002557F	CCCCAACACCTTCAGGAAAAC
hsa_circ_0002557R	CGGCCTCTGCTCTATTTCTCC
hsa_circ_0000504F	GGCGAAGCGGATGGAATACA
hsa_circ_0000504R	CTTGTCGTGCCACAGTCGAT
hsa_circ_0001324F	TAGCTGATTGGTGGGCTGTT
hsa_circ_0001324R	TCGTTTTCCAACCCCTTCTCC

hsa_circ_1051F	GAAACCTGTGGAGCAGAAAGC
hsa_circ_1051R	GCGCAAAATCCCAGCCATAAG
hsa_circ_1355F	TATGGCTCCAGAAGGAAACGA
hsa_circ_1355R	GTATCTGATGACCGACGTCCC

Table S2. Sequence information of these 39 candidate miRNAs

Name	Sequence-forward	Sequence-reverse
hsa-mir-662	5' UCCCACGUUGUGGCCCAGCAG 3'	5' GCUGGGCCACAACGUGGGAUU 3'
hsa-mir-198	5' GGUCCAGAGGGGAGAUAGGUUC 3'	5' ACCUAUCUCCCCUCUGGACCUU 3'
hsa-let-7a	5' UGAGGUAGUAGGUUGUAUAGUU 3'	5' CUAUACAACCUACUACCUCAUU 3'
hsa-mir-320a	5' AAAAGCUGGGUUGAGAGGGCGA 3'	5' GCCCUCUCAACCCAGCUUUUUU 3'
hsa-mir-365	5' UAAUGCCCCUAAAAAUCCUUAU 3'	5' AAGGAUUUUUAGGGGCAUUAUU 3'
hsa-mir-126-5p	5' CAUUAUUACUUUUGGUACGCG 3'	5' CGUACCAAAAGUAAUAAUGUU 3'
hsa-mir-520a-5p	5' CUCCAGAGGGAAGUACUUUCU 3'	5' AAAGUACUUCCCUCUGGAGUU 3'
hsa-mir-525-5p	5' CUCCAGAGGGAUGCACUUUCU 3'	5' AAAGUGCAUCCCUCUGGAGUU 3'
hsa-mir-939	5' UGGGGAGCUGAGGCUCUGGGGGUG 3'	5' CCCCCAGAGCCUCAGCUCCCCAUU 3'
hsa-mir-185	5' UGGAGAGAAAGGCAGUUCCUGA 3'	5' AGGAACUGCCUUUCUCUCCAUU 3'

hsa-mir-98	5' UGAGGUAGUAAGUUGUAUUGUU 3'	5' CAAUACAACUUACUACCUCAUU 3'
hsa-let-7b	5' UGAGGUAGUAGGUUGUGUGGUU 3'	5' CCACACAACCUACUACCUCAUU 3'
hsa-let-7c	5' UGAGGUAGUAGGUUGUAUGGUU 3'	5' CCAUACAACCUACUACCUCAUU 3'
hsa-let-7d	5' AGAGGUAGUAGGUUGCAUAGUU 3'	5' CUAUGCAACCUACUACCUCUUU 3'
hsa-mir-363-5p	5' CGGGUGGAUCACGAUGCAAUUU 3'	5' AUUGCAUCGUGAUCCACCCGUU 3'
hsa-mir-518f-5p	5' CUCUAGAGGGAAGCACUUUCUC 3'	5' GAAAGUGCUUCCCUCUAGAGUU 3'
hsa-let-7e	5' UGAGGUAGGAGGUUGUAUAGUU 3'	5' CUAUACAACCUCCUACCUCAUU 3'
hsa-let-7f	5' UGAGGUAGUAGAUUGUAUAGUU 3'	5' CUAUACAAUCUACUACCUCAUU 3'
hsa-let-7g	5' UGAGGUAGUAGUUUGUACAGUU 3'	5' CUGUACAAACUACUACCUCAUU 3'
hsa-let-7i	5' UGAGGUAGUAGUUUGUGCUGUU 3'	5' CAGCACAAACUACUACCUCAUU 3'
hsa-mir-10b-3p	5' ACAGAUUCGAUUCUAGGGGAAU 3'	5' UCCCCUAGAAUCGAAUCUGUUU 3'
hsa-mir-135b-3p	5' AUGUAGGGCUAAAAGCCAUGGG 3'	5' CAUGGCUUUUAGCCCUACAUUU 3'
hsa-mir-1827	5' UGAGGCAGUAGAUUGAAU 3'	5' UCAAUCUACUGCCUCAUU 3'

hsa-mir-335	5' UCAAGAGCAAUAACGAAAAAUGU 3'	5' AUUUUUCGUUAUUGCUCUUGAUU 3'
hsa-mir-4283	5' UGGGGCUCAGCGAGUUU 3'	5' ACUCGCUGAGCCCCAUU 3'
hsa-mir-4795-3p	5' AUAUUAUUAGCCACUUCUGGAU 3'	5' CCAGAAGUGGCUAAUAAUAUUU 3'
hsa-mir-493-3p	5' UGAAGGUCUACUGUGUGCCAGG 3'	5' UGGCACACAGUAGACCUUCAUU 3'
hsa-mir-518d-5p	5' CUCUAGAGGGAAGCACUUUCUG 3'	5' GAAAGUGCUUCCCUCUAGAGUU 3'
hsa-mir-518e-5p	5' CUCUAGAGGGAAGCGCUUUCUG 3'	5' GAAAGCGCUUCCCUCUAGAGUU 3'
hsa-mir-526a	5' CUCUAGAGGGAAGCACUUUCUG 3'	5' GAAAGUGCUUCCCUCUAGAGUU 3'
hsa-mir-526c	5' CUCUAGAGGGAAGCGCUUUCUG 3'	5' GAAAGCGCUUCCCUCUAGAGUU 3'
hsa-mir-532	5' CAUGCCUUGAGUGUAGGACCGU 3'	5' GGUCCUACACUCAAGGCAUGUU 3'
hsa-mir-539	5' GGAGAAAUUAUCCUUGGUGUGU 3'	5' ACACCAAGGAUAAUUUCUCCUU 3'
hsa-mir-583	5' CAAAGAGGAAGGUCCCAUUAC 3'	5' AAUGGGACCUUCCUCUUUGUU 3'
hsa-mir-601	5' UGGUCUAGGAUUGUUGGAGGAG 3'	5' CCUCCAACAAUCCUAGACCAUU 3'
hsa-mir-627	5' GUGAGUCUCUAAGAAAAGAGGA 3'	5' CUCUUUUCUUAGAGACUCACUU 3'

hsa-mir-759	5' GCAGAGUGCAAACAAUUUUGAC 3'	5' CAAAAUUGUUUGCACUCUGCUU 3'
hsa-mir-875-3p	5' CCUGGAAACACUGAGGUUGUG 3'	5' CAACCUCAGUGUUUCCAGGUU 3'
hsa-mir-885-3p	5' AGGCAGCGGGGUGUAGUGGAUA 3'	5' UCCACUACACCCCGCUGCCUUU 3'
hsa-miR-16 (endogenous reference control)	5' UAGCAGCACGUAAAUAUUGGCG 3'	5' CCAAUAUUUACGUGCUGCUAUU 3'

Table S3. The screening of miRNAs by transfecting mimics

miRNAs	The average of luc/renilla	The standard deviation	The average of every miRNA/The average of no miRNA group
No RNA	2.131834816	0.018534865	1.00

hsa-miR-662	1.04341438	0.128299676	0.49
hsa-miR-365	1.138878923	0.071279693	0.53
hsa-let-7f	1.663178636	0.051399805	0.78
hsa-miR-98	1.676506245	0.082009321	0.79
hsa-miR-525-5p	1.696141786	0.117231313	0.80
hsa-miR-520a-5p	1.723876161	0.17534501	0.81
hsa-let-7i	1.803890037	0.242644251	0.85
hsa-miR-126-5p	1.819700798	0.222913827	0.85
hsa-let-7c	1.898091117	0.127006131	0.89
hsa-let-7b	1.949973736	0.19906586	0.91
hsa-miR-939	1.978972968	0.112297242	0.93
hsa-let-7a	2.050810576	0.117018488	0.96
hsa-miR-320a	2.067392733	0.269203011	0.97

hsa-let-7g	2.101607236	0.049195764	0.99
hsa-miR-518f-5p	2.116382415	0.063327551	0.99
hsa-let-7e	2.167361007	0.178667206	1.02
hsa-miR-198	2.287032242	0.115654225	1.07
hsa-miR-363-5p	2.408342415	0.112103244	1.13
hsa-miR-185	2.424203146	0.308621272	1.14
hsa-miR-4795-3p	2.521273286	0.211477306	1.18
hsa-miR-526a	3.019809922	0.209309968	1.42
hsa-miR-518e-5p	3.110414738	0.131294206	1.46
hsa-miR-885-3p	3.114338933	0.243632844	1.46
hsa-miR-518d-5p	3.142133001	0.178387804	1.47
hsa-miR-627	3.248331916	0.148712329	1.52
hsa-miR-601	3.331457544	0.085947965	1.56

hsa-miR-4283	3.377654344	0.052081429	1.58
hsa-miR-1827	3.392767189	0.16056333	1.59
hsa-miR-875-3p	3.415138075	0.255779662	1.60
hsa-miR-493-3p	3.466340021	0.128688117	1.63
hsa-miR-135b-3p	3.469067325	0.102132528	1.63
hsa-miR-10b-3p	3.608660244	0.142712445	1.69
hsa-miR-759	3.617386342	0.235793117	1.70
hsa-miR-583	3.678820932	0.085209955	1.73
hsa-miR-539	3.693944749	0.28324481	1.73
hsa-miR-532	3.872661435	0.219379495	1.82
hsa-let-7d	3.912028155	0.164350754	1.84
hsa-miR-526c	4.033709788	0.046227977	1.89
hsa-miR-335	4.530819415	0.166705744	2.13

hsa-miR-16	3.03281007	0.17715557	1.42

Table S4. The screening of miRNAs by using miRNA overexpression plasmids

miRNAs	The average of luc/renilla	The standard deviation	The average of every miRNA/The average of no miRNA group
No miRNA	0.307449181	0.017530277	1.00
hsa-miR-365	0.246686788	0.00267131	0.80
hsa-miR-520a	0.24710689	0.002081163	0.80
hsa-let-7f	0.254508583	0.006503693	0.83

hsa-let-7c	0.256151125	0.009799912	0.83
hsa-miR-98	0.26191731	0.004995316	0.85
hsa-miR-525	0.272758824	0.010348326	0.89
hsa-miR-662	0.27506534	0.009631735	0.89
hsa-miR-126	0.276722642	0.004809872	0.90
hsa-let-7i	0.282080068	0.0057359	0.92

Table S5. Correlation between hsa-let-7c, hsa_circ_0001483 and hsa_circ_0001324 and environment factors

	N	Age		Gender		Smoking		Alcohol Drinking		Family History		Peritumoral Inflammatory Cells		Lymphatic metastasis	
GC		r	*P*	r	*P*	r	*P*	r	*P*	r	*P*	r	*P*	r	*P*
hsa-let-7c		0.002	0.990	0.023	0.903	0.136	0.474	0.139	0.464	0.07	0.714	0.319	0.092	0.009	0.964

hsa_circ_0001483	66	-0.077	0.538	-0.164	0.189	0.135	0.278	0.096	0.442	0.094	0.453	0.195	0.120	**-0.249**	**0.044**
hsa_circ_0001324	66	**-0.350**	**0.004**	0.013	0.916	0.039	0.756	0.038	0.76	0.020	0.874	0.095	0.454	-0.120	0.336

Note: The correlation analysis was performed by Spearman's correlation coefficient for the skewed ditribution data. GC, gastric cancer; r, Spearman's correlation coefficient.

Table S6. Clinicopathological parameters of patients and univariate analysis of overall survival

		All GC	Death	MST^{a}	
Factors		n (%)	n (%)	(M)	*P*-value
Cases		66	26		
Gender					0.897
	Male	42(63.64)	17(65.38)	18.8^{b}	
	Female	24(36.36)	9(24.62)	18.8^{b}	

Age					0.116
	⩾60	38(57.58)	18(69.23)	17.6[b]	
	<60	28(42.42)	8(30.77)	20.5[b]	
Smoking					0.658
	Ever Smoker	16(24.24)	7(26.92)	17.8[b]	
	Never Smoker	50(75.76)	19(73.08)	19.2[b]	
Drinking					**0.034**
	Ever Drinker	9(13.64)	6(23.08)	10.0	
	Never Drinker	57(86.36)	20(76.92)	19.5[b]	
Family History					0.995
	Yes	15(22.73)	6(23.08)	19.0[b]	
	No	51(77.27)	20(76.92)	18.8[b]	
Location					**0.029**

	Body	20(30.77)	11(42.31)	18.0	
	Angle	11(16.92)	1(3.85)	23.1[b]	
	Antrum	23(35.38)	7(26.92)	20.0[b]	
	Entire	11(16.92)	7(26.92)	10.0	
Macroscopic Type					0.087
	Protruded Type	3(4.55)	1(3.85)	22.0[b]	
	Ulcerative Type	13(19.70)	2(7.69)	21.6[b]	
	Ulcerative Infiltrative Type	32(48.48)	12(46.15)	19.2[b]	
	Diffuse Infiltrative Type	18(27.27)	11(42.31)	10.0	
Histological Type					0.159
	Papillary Adenocarcinoma (I)	0	0	NA	
	Well Differentiated Type (II)	1(1.56)	0	NA	
	Moderately Differentiated Type (III)	8(12.50)	2(7.69)	NA	

	Poorly Differentiated Type (IV)	39(60.94)	19(73.08)	NA	
	Mucinous Adenocarcinoma (V)	6(9.38)	0	NA	
	Signet-ring Cell Cinoma (VI)	10(15.63)	5(19.23)	NA	
Lauren Classification					
	Intestinal	55(85.94)	24(92.31)	23.2[b]	0.183
	Diffuse	9(14.06)	2(7.69)	17.9[b]	
TNM stage					**0.001**
	I	7(10.61)	0	NA	
	II	23(34.85)	5(19.23)	NA	
	III	36(54.55)	21(90.77)	NA	
	IV	0	0	NA	
					<0.001
	Ⅰ+Ⅱ	30(45.45)	5(19.23)	22.4[b]	

	III+IV	36(56.06)	21(80.77)	13.0	
Peritumoral Inflammatory Cells					0.211
	+	18(27.69)	9(34.62)	18.0	
	++	26(40.00)	7(26.92)	20.6[b]	
	+++	21(32.31)	10(38.46)	18.3[b]	
Lymphovascular invasion					0.067
	+	42(63.64)	20(76.92)	17.6[b]	
	-	24(36.36)	6(23.08)	21.0[b]	
Ganglion Invasion					0.071
	+	53(81.54)	24(92.31)	17.8[b]	
	-	12(32.31)	2(7.69)	22.8[b]	
Lymphatic metastasis					**0.001**
	+	45(68.18)	24(92.31)	18.0	

	-	21(31.82)	2(7.69)	23.4[b]	
Depth of Invasion					
	Mucous Layer (pT1)	2(3.03)	0	NA	0.088
	Submucosal Layer (pT2)	5(7.58)	0	NA	
	Muscular Layer (pT3)	7(10.61)	1(3.85)	NA	
	Subserosa Layer (pT4)	1(1.52)	0	NA	
	Serosal Layer or Invasion Adjacent Organs(pT5)	51(77.27)	25(96.15)	NA	
					0.018
	pT1+pT2	7(10.61)	0	NA	
	pT3+pT4	8(12.12)	1(3.85)	NA	
	pT5	51(77.27)	25(96.15)	NA	
Growth Pattern					0.107
	Massive or Nested	11(16.67)	2(7.69)	23.0[b]	

Diffuse Infiltrative or Infiltralive	55(83.33)	24(92.31)	18.0[b]

Note: a, MST, median survival time (months); b, mean survival time was provided when MST could not be calculated; GC, gastric cancer; NA, not avaliable.

Table S7. Univariate and multivariate cox proportional hazard analysis for the association of circRNAs and GC in tumor and normal tissues

		All GC	Death	MST[a]	Univariate		Multivariate[c]	
Variables		n	n (%)	(M)	P-value	Hazard ratio (95% CI)	P-value	Hazard ratio (95% CI)
has_circ_1324	Low	33	15(57.69)	18.0[b]	0.328	1(ref)	0.070	1(ref)
	High	33	11(42.30)	19.6[b]		0.67(0.31-1.48)		0.48(0.21-1.06)
has_circ_1483	Low	33	10(38.46)	20.0[b]	0.164	1(ref)		1(ref)
	High	33	16(61.54)	17.6[b]		0.56(0.25-1.23)	0.081	0.42(0.16-1.11)

Note: GC, gastric cancer; HR, hazard rate; CI, confidence interval; a, MST, median survival time (months); b, mean survival time was provided when MST could not be

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calculated; c, Multivariate survival analysis was carried out by adding the clinicopathological parameters with $P<0.05$. NA: not available.