

# Predicting Associations of miRNAs and Candidate Gastric Cancer Genes for Nanomedicine

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**Table S1.** The list of candidate gastric cancer genes.

Gene	PMID	Gene	PMID	Gene	PMID
<i>ACE</i>	18059164	<i>HIF1A</i>	26339797	<i>PDCD4</i>	27021515
<i>AQP3</i>	26768614	<i>HPSE</i>	31257534	<i>PGC</i>	25549793
<i>ARID1A</i>	24744582	<i>IGF1</i>	29731870	<i>PIK3CA</i>	26543351
<i>ATM</i>	24841718	<i>IGF2</i>	24451943	<i>POU5F1</i>	30628031
<i>AURKA</i>	31871591	<i>IGFBP3</i>	24451943	<i>PRKAA1</i>	30253744
<i>BRCA1</i>	25266802	<i>IL10</i>	26088449	<i>PTEN</i>	26753960
<i>CASP10</i>	31611962	<i>IRF1</i>	27866197	<i>SFRP1</i>	23943784
<i>CCND1</i>	31982864	<i>JAK2</i>	25055044	<i>SIRT1</i>	24107295
<i>CDH1</i>	19168852	<i>JUN</i>	22002117	<i>SMAD2</i>	31773690
<i>CDH17</i>	24465527	<i>KRAS</i>	31217166	<i>SMAD4</i>	28440445
<i>CDKN1A</i>	28571676	<i>LEP</i>	33061532	<i>SP1</i>	24613927
<i>CDX2</i>	29113265	<i>LGALS3</i>	24971481	<i>STAT3</i>	32545648
<i>CEACAM5</i>	26374829	<i>MACC1</i>	26919111	<i>TBC1D9</i>	29137307
<i>CLDN18</i>	24073219	<i>MAPK1</i>	29550487	<i>TERT</i>	28423629
<i>CREB1</i>	25825983	<i>MDM2</i>	32023766	<i>TGFBI</i>	25118995
<i>DNMT1</i>	25595591	<i>MMP2</i>	24072772	<i>THBS1</i>	26075074
<i>E2F1</i>	32376557	<i>MTHFR</i>	25998065	<i>TIMP2</i>	24440352
<i>EGFR</i>	27997901	<i>MUC1</i>	24810688	<i>TIMP3</i>	27383203
<i>EPHB2</i>	32226496	<i>MUC6</i>	24816253	<i>TP53</i>	27323394
<i>ERBB3</i>	30621788	<i>NFKB1</i>	26801246	<i>TYMS</i>	28056823
<i>EZH2</i>	30952377	<i>ODC1</i>	28096401	<i>VEGFC</i>	29393383
<i>FGFR2</i>	26516773	<i>OGG1</i>	21822670	<i>XRCC1</i>	26768611
<i>FLT1</i>	24398900	<i>PARP1</i>	26540566	<i>ZEB1</i>	22466758

**Table S2:** The characteristics of the miRNA interactions with 5'UTR mRNAs of gastric cancer candidate genes

Gene; NX	miRNA	Start of site, nt	$\Delta G$ , kJ/mole	$\Delta G/\Delta G_m$ , %	Length, nt
<i>AURKA</i> ; 4.3	miR-5095	420	-108	93	21
	miR-619-5p	426	-119	98	22
<i>DNMT1</i> ; 9.0	ID02052.5p-miR	137	-134	90	24
<i>EGFR</i> ; 7.8	ID02457.3p-miR	89	-132	95	22
<i>EZH2</i> ; 2.7	ID02761.3p-miR	120	-138	93	24
<i>FGFR2</i> ; 9.3	ID03047.3p-miR	48	-132	89	24
<i>HIF1A</i> ; 16.0	miR-6789-5p	54	-132	90	24
<i>JUN</i> ; 47.0	ID02008.5p-miR	269	-123	91	22
<i>KRAS</i> ; 23.6	ID01310.3p-miR	17, 29	-121, -123	92,94	22
	ID03332.3p-miR	37	-132	89	24
<i>LGALS3</i> ; 36.9	ID00329.3p-miR	21	-125	91	22
<i>MMP2</i> ; 20.5	ID00278.3p-miR	110	-123	89	23
	ID03345.5p-miR	124	-127	90	24
<i>NFKB1</i> ; 14.6	ID02064.5p-miR	128	-132	91	23
<i>POU5F1</i> ; 6.3	miR-1273a	181	-119	90	25

	miR-1273g-3p	203	-113	96	21
	miR-1273d	237	-119	87	25
<i>PTEN</i> ; 17.8	ID01310.3p-miR	531	-119	90	22
	ID02761.3p-miR	533	-132	89	24
	ID03037.3p-miR	536	-121	90	22
<i>SFRP1</i> ; 11.0	ID01641.3p-miR	111	-132	89	24
<i>SMAD2</i> ; 26.3	ID01492.3p-miR	16	-129	100	23
<i>TGFB1</i> ; 12.8	ID00457.3p-miR	209	-129	95	22
	ID02064.5p-miR	211	-132	91	23
<i>THBS1</i> ; 46.5	miR-328-5p	84	-123	89	23
	miR-6786-5p	88	-119	93	21
	ID01652.3p-miR	113	-129	92	23
<i>TIMP2</i> ; 24.2	ID01520.3p-miR	60	-123	92	21
	ID00252.5p-miR	61	-134	90	24
	ID02668.5p-miR	219	-127	88	24
	ID00961.3p-miR	239	-132	93	23
	ID00049.5p-miR	269	-136	90	24
	ID00417.3p-miR	278	-123	94	21
	ID01293.5p-miR	281	-127	94	22
<i>TIMP3</i> ; 22.9	ID02903.3p-miR	1102	-121	90	22
<i>TYMS</i> ; 4.2	ID00252.5p-miR	87	-132	89	24

**Table S3: The characteristics of the miRNA interactions with CDS mRNAs of gastric cancer candidate genes**

Gene; NX	miRNA	Start of site, nt	$\Delta G$ , kJ/mole	$\Delta G/\Delta G_m$ , %	Length, nt
<i>ACE</i> ; 1.9	ID00522.5p-miR	62	-125	89	23
	ID02294.5p-miR	64	-132	90	24
<i>ARID1A</i> ; 19.5	ID01473.3p-miR	1093	-125	89	23
	ID03167.3p-miR	1399	-123	91	23
	ID01508.5p-miR	1459	-129	90	23
<i>CDX2</i> ; 0.1	ID01895.5p-miR	416	-138	93	24
	ID00522.5p-miR	419	-125	89	23
	ID02052.5p-miR	608	-136	91	24
	ID01041.5p-miR	609	-129	88	24
	miR-3960	613	-117	93	20
<i>EPHB2</i> ; 2.3	miR-4253	1089	-102	100	18
<i>IGFBP3</i> ; 8.3	ID02982.3p-miR	435	-123	100	21
<i>MUC1</i> ; 105.0	ID00645.5p-miR	507	-110	93	20
	miR-6752-5p	510	-119	90	22
<i>MUC6</i> ; 76.6	miR-6815-3p	1218	-104	91	21
	ID02841.5p-miR	1238	-108	93	20
	miR-939-5p	1330	-121	88	24
<i>OGG1</i> ; 10.8	ID00920.5p-miR	882	-134	94	24
<i>PARP1</i> ; 15.9	ID01616.3p-miR	1275	-119	90	23
<i>PGC</i> ; 963.7	ID01303.5p-miR	715	-115	92	20
<i>SIRT1</i> ; 13.2	miR-4767	236	-134	94	23
	ID01560.3p-miR	264	-123	89	23
	ID03332.3p-miR	280, 287	-132, 138	89, 93	24
	ID00278.3p-miR	294	-123	89	23
	ID00811.3p-miR	300	-125	88	24

**Table S4: The characteristics of the miRNA interactions with 3'UTR mRNAs of gastric cancer candidate genes**

<b>Gene; NX</b>	<b>miRNA</b>	<b>Start of site, nt</b>	<b><math>\Delta G</math>, kJ/mole</b>	<b><math>\Delta G/\Delta G_m</math>, %</b>	<b>Length, nt</b>
<i>AQP3</i> ; 3.9	miR-466	1255	-106	91	23
	ID00436.3p-miR	1255	-104	89	23
	ID01030.3p-miR	1259, 1269	-108	89	23
<i>BRCA1</i> ; 5.1	miR-5095	6406	-106	91	21
	miR-619-5p	6412	-119	98	22
	miR-5096	6486	-110	98	21
	miR-5585-3p	6554	-110	95	22
<i>CASP10</i> ; 8.7	miR-1273h-5p	2234	-106	91	21
	miR-1285-3p	2357	-106	91	22
	miR-1273g-3p	2589	-108	93	21
	miR-1273d	2623	-119	87	25
	miR-1273h-5p	2623	-117	100	21
	miR-619-5p	3247	-113	93	22
	miR-5585-3p	3389	-108	93	22
<i>CCND1</i> ; 19.2	miR-574-5p	2593+2597 (3)	-108+-113	89+93	23
	ID00470.5p-miR	2595, 2597	-108	89	23
<i>CDH1</i> ; 21.6	miR-1273c	3251	-110	91	22
	miR-1273g-3p	3271	-108	93	21
	miR-1273h-5p	3305	-113	96	21
<i>CDH17</i> ; 0.3	miR-1273a	2773	-119	90	25
	miR-1273g-3p	2795	-110	95	21
	miR-1273d	2829	-121	89	25
<i>CDKN1A</i> ; 25.2	miR-4433-3p	1601	-106	91	21
<i>CEACAM5</i> ; 20.1	miR-5585-3p	2441	-108	93	22
	miR-5095	3229	-115	98	21
	miR-619-5p	3235	-119	98	22
	miR-5585-3p	3378	-113	96	22
<i>CLDN18</i> ; 126.9	miR-5095	1852	-106	91	21
	miR-619-5p	1858	-115	95	22
	miR-1273h-3p	2053	-113	90	22
<i>CREB1</i> ; 13.3	miR-5095	2791	-110	95	21
	miR-619-5p	2797	-119	98	22
	miR-5096	2871	-106	94	21
	miR-619-5p	2932	-110	91	22
	miR-5585-3p	2939	-108	93	22
<i>ERBB3</i> ; 32.9	miR-619-5p	4950	-117	96	22
	miR-619-5p	5104	-121	100	22
<i>HPSE</i> ; 2.4	miR-1273g-3p	2081	-106	91	21
	miR-1273g-3p	2376	-108	93	21
	miR-5095	2759	-106	91	21
	miR-619-5p	2765	-110	91	22
	miR-5096	2839	-110	98	21
<i>IL10</i> ; 2.0	miR-5095	1210	-115	98	21
	miR-619-5p	1216	-119	98	22
	miR-5096	1290	-106	94	21
<i>IRF1</i> ; 17.5	miR-5095	2229	-110	95	21
	miR-619-5p	2235	-115	95	22
	miR-619-5p	2523	-110	91	22
	miR-5096	2597	-110	98	21
	miR-5095	2653	-110	95	21

	miR-619-5p	2659	-119	98	22
	miR-5585-3p	2800	-110	95	22
<i>KRAS</i> ; 23.6	ID03224.5p-miR	3163	-121	92	23
	miR-1273g-3p	3176	-108	93	21
	miR-1273f	3209	-104	100	19
<i>LEP</i> ; 0.2	miR-5095	3094	-110	95	21
	miR-619-5p	3100	-119	98	22
	miR-5096	3172	-104	92	21
	miR-5585-3p	3240	-108	93	22
<i>MACC1</i> ; 5.0	ID01030.3p-miR	2962, 2976	-108	89	23
	ID01727.5p-miR	2963÷2981 (3)	-104	89	23
	miR-466	2966÷2990 (4)	-104÷-106	89÷91	23
	ID01030.3p-miR	3949÷3965 (8)	-108÷-110	89÷91	23
	miR-466	3951÷3967 (9)	-106÷-108	91÷93	23
	ID00436.3p-miR	3953÷3967 (8)	-104÷-106	89÷91	23
	miR-619-5p	4856	-117	96	22
	miR-1273f	5717	-102	98	19
	miR-1273d	5718	-123	91	25
<i>MDM2</i> ; 9.8	miR-1273g-3p	2117	-113	96	21
	miR-1273g-3p	2486	-106	91	21
	miR-1273e	2521	-108	93	22
	miR-1273g-3p	6739	-113	96	21
<i>MTHFR</i> ; 13.6	miR-5095	6855	-110	95	21
	miR-619-5p	6861	-115	95	22
	miR-5585-3p	7003	-110	95	22
<i>MUC6</i> ; 76.6	ID01401.3p-miR	7895	-108	91	21
<i>PDCD4</i> ; 27.6	miR-5095	3215	-106	91	21
	miR-619-5p	3221	-121	100	22
	miR-619-5p	3355	-110	91	22
<i>PRKAA1</i> ; 22.1	miR-1273g-3p	2260	-110	95	21
	miR-1273f	2293	-102	98	19
	miR-1273d	2294	-121	89	25
	ID01404.5p-miR	2297	-113	91	23
	miR-1273e	2303	-106	91	22
<i>SMAD4</i> ; 19.3	ID01838.5p-miR	4291	-113	90	24
	miR-1273g-3p	4312	-110	95	21
	ID01656.3p-miR	4342	-115	89	23
	miR-1273d	4346	-119	87	25
	ID01404.5p-miR	4349	-115	93	23
	ID02732.3p-miR	7721	-123	91	23
	miR-574-5p	7740÷7756 (8)	-108÷-113	89÷93	23
	ID00470.5p-miR	7744÷7752 (5)	-108	89	23
	ID00106.5p-miR	7825	-106	91	22
	miR-574-5p	7830	-108	89	23
<i>STAT3</i> ; 29.4	miR-5095	3125	-106	91	21
	miR-619-5p	3131	-119	98	22
	miR-5585-3p	3268	-110	95	22
<i>TGFB1</i> ; 12.8	miR-6089	2060, 2065	-132, -136	89, 91	24
	ID03306.3p-miR	2060	-123	94	21
	ID01382.3p-miR	2062	-113	93	20
	ID03208.5p-miR	2066	-125	88	24
	miR-4651	2087	-113	95	20
	ID00978.5p-miR	2089	-119	90	22
	ID00296.3p-miR	2093	-140	89	25

	miR-1183	4361	-132	90	27
<i>TIMP2</i> ; 24.2	ID01941.5p-miR	1427	-117	89	24
<i>TIMP3</i> ; 22.9	miR-1224-5p	3268	-104	96	19
<i>TP53</i> ; 12.0	ID00548.3p-miR	1393	-115	89	23
	ID02379.3p-miR	1397	-119	89	24
	miR-1273c	2297	-110	91	22
	miR-1285-3p	2301	-110	95	22
	miR-1273g-3p	2317	-106	91	21
	miR-1273h-5p	2351	-106	91	21
	ID01838.5p-miR	2460	-110	88	24
	ID00785.5p-miR	2520	-113	90	23







<i>ATM</i> , miR-1273a, 11054, -119, 90 5'-GACAGAGUCUUGCUCUCUACCC-3'       3'-UUCUUUCUCAGAAACAGCGGG-5'	<i>ATM</i> , miR-1273c, 11056, -104, 86 5'-GACAGAGUCUUGCUCUCUACCC-3'       3'-CUGUCCAGAGCAAAACAGCGG-5'
<i>ATM</i> , miR-1273e, 11119, -108, 93 5'-UCUGCCUCCUGGUCAAGCAA-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'	<i>ATM</i> , miR-1273f, 11109, -89, 86 5'-CACUGAACCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'
<i>ATM</i> , miR-1273g-3p, 11076, -113, 96 5'-CCAGGGCGGAGUCAGUGGC-3'       3'-GAGUCCGACCUACGUCACCA-5'	<i>CASP10</i> , miR-1273d, 2623, -119, 87 5'-ACUGAGCCUCCUCCUCCAGUUC-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'
<i>CASP10</i> , miR-1273f, 2622, -89, 86 5'-CACUGAGCCUUGACUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'	<i>CASP10</i> , miR-1273g-3p, 2589, -108, 93 5'-CCUGGCGUGAGUCAGUGGU-3'       3'-GAGUCCGACCUACGUCACCA-5'
<i>CASP10</i> , miR-1273h-5p, 2234, -106, 91 5'-ACUGUAGUCUCCAGUCCUCCAG-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>CASP10</i> , miR-1273h-5p, 2623, -117, 100 5'-ACUGAGCCUUGACUCCUCCAG-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'
<i>CDH1</i> , miR-1273g-3p, 3271, -108, 93 5'-CCAGGCGGAGUCAGUGGU-3'       3'-GAGUCCGACCUACGUCACCA-5'	<i>CDH1</i> , miR-1273h-5p, 3305, -113, 96 5'-ACUGAGCCUUGACUCCUCCAG-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'
<i>CDH1</i> , miR-1273c, 3251, -110, 91 5'-GACAGGUCUCAUUCUUCGCCC-3'       3'-CUGUCCAGAGCAAAACAGCGG-5'	<i>CDH17</i> , miR-1273a, 2773, -119, 90 5'-GAGGUGAGUCUUGUCUUGCGCC-3'       3'-UUCUUUCAGAAACAGCGGG-5'
<i>CDH17</i> , miR-1273d, 2829, -121, 89 5'-ACUGCAACUCCUCCUCCUGGUUC-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>CDH17</i> , miR-1273f, 2828, -100, 96 5'-GACUGCAACUCCUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'
<i>CDH17</i> , miR-1273g-3p, 2795, -110, 95 5'-CCAGGCGGAGUACAGUGGU-3'       3'-GAGUCCGACCUACGUCACCA-5'	<i>HPSE</i> , miR-1273c, 2356, -104, 86 5'-GACAGGUAUCAUUCUUGUCC-3'       3'-CUGUCCAGAGCAAAACAGCGG-5'
<i>HPSE</i> , miR-1273g-3p, 2081, -106, 91 5'-CCAGGCGGAGUCCAUUGGU-3'       3'-GAGUCCGACCUACGUCACCA-5'	<i>HPSE</i> , miR-1273g-3p, 2376, -108, 93 5'-CCAGGCGUAGUGGAGUAGUGGU-3'       3'-GAGUCCGACCUACGUCACCA-5'
<i>KRAS</i> , miR-1273e, 3219, -102, 87 5'-DCAUCUCCAGGUCAAGCGA-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'	<i>KRAS</i> , miR-1273f, 3209, -104, 100 5'-CACUGAACCCUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'
<i>KRAS</i> , miR-1273g-3p, 3176, -108, 93 5'-CCAGGCGGAAUGCAGUGGC-3'       3'-GAGUCCGACCUACGUCACCA-5'	<i>KRAS</i> , miR-1273h-5p, 3210, -100, 85 5'-ACUGCAACUCCUCCUCCAG-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'
<i>MACC1</i> , miR-1273d, 5718, -123, 91 5'-ACUGCAACUCCUCCUCCUGGUUC-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>MACC1</i> , miR-1273e, 5727, -102, 87 5'-DCAUCUCCAGGUCAAGCGA-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'
<i>MACC1</i> , miR-1273f, 5717, -10, 98 5'-CACUGCAACUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'	<i>MACC1</i> , miR-1273g-3p, 5684, -102, 87 5'-CCAGGCGGAGUCCGUGGUU-3'       3'-GAGUCCGACCUACGUCACCA-5'
<i>MACC1</i> , miR-1273g-5p, 5714, -104, 87 5'-ACUCACUGCAACUCCUCCUCC-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>MDM2</i> , miR-1273a, 2795, -113, 85 5'-GACAGAGUCUUGCUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'
<i>MDM2</i> , miR-1273c, 3215, -104, 86 5'-GACAGGUCUCCUCCUCCUCC-3'       3'-CUGUCCAGAGCAAAACAGCGG-5'	<i>MDM2</i> , miR-1273e, 2521, -108, 93 5'-UCCGCUCCCGGUAACAGCCA-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'
<i>MDM2</i> , miR-1273e, 2860, -104, 89 5'-UCUGCCUCCUCCUCCUCCUCC-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'	<i>MDM2</i> , miR-1273f, 2850, -91, 88 5'-CACUGCAACUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'
<i>MDM2</i> , miR-1273f, 6772, -96, 92 5'-CACUGCAACUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'	<i>MDM2</i> , miR-1273g-3p, 2117, -113, 96 5'-CCAGGCGGAGUCCUCCUCCAG-3'       3'-GAGUCCGACCUACGUCACCA-5'
<i>MDM2</i> , miR-1273g-3p, 2486, -106, 91 5'-CCAGGCGGAGUCCUCCUCCAG-3'       3'-GAGUCCGACCUACGUCACCA-5'	<i>MDM2</i> , miR-1273g-3p, 6739, -113, 96 5'-CUCAGGCGUAGUCCAGUGGU-3'       3'-GAGUCCGACCUACGUCACCA-5'
<i>PRKAA1</i> , miR-1273d, 2294, -121, 89 5'-ACUGCAACUCCUCCUCCUCCUCC-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>PRKAA1</i> , miR-1273e, 2303, -106, 91 5'-UCCACUCCCGGUAACAGUGA-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'
<i>PRKAA1</i> , miR-1273f, 2293, -102, 98 5'-CACUGCAACUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'	<i>PRKAA1</i> , miR-1273g-3p, 2260, -110, 95 5'-CCAGGCGUAGUCCUCCUCCAG-3'       3'-GAGUCCGACCUACGUCACCA-5'
<i>PRKAA1</i> , miR-1273g-5p, 2290, -102, 86 5'-GUCACUGCAACUCCUCCUCC-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>PRKAA1</i> , miR-1273h-5p, 2294, -102, 87 5'-ACUGCAACUCCUCCUCCCG-3'       3'-GUGACGUUGGAGUAGAGG-5'
<i>SGCB</i> , miR-1273a, 3312, -113, 85 5'-GACAGAGUCUUGCUCUCUACCC-3'       3'-UUCUUUCUCAGAAACAGCGGG-5'	<i>SGCB</i> , miR-1273c, 3314, -110, 91 5'-GACAGAGUCUUGCUCUCUACCC-3'       3'-CUGUCCAGAGCAAAACAGCGG-5'
<i>SGCB</i> , miR-1273e, 3383, -100, 85 5'-UCUGCCUCCAGGUCAAGCGA-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'	<i>SGCB</i> , miR-1273f, 3373, -96, 92 5'-CACUGCAACUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'
<i>SGCB</i> , miR-1273g-3p, 3333, -106, 91 5'-CCAGGCGGAGUCCUCCUCCAG-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>SGCB</i> , miR-1273h-5p, 3374, -102, 87 5'-ACUGCAACUCCUCCUCCUCCAG-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'
<i>TP53</i> , miR-1273a, 2295, -113, 85 5'-GACAGGUCUCCUCCUCCUCCUCC-3'       3'-UUCUUUCUCAGAAACAGCGGG-5'	<i>TP53</i> , miR-1273c, 2297, -110, 91 5'-GACUGGUCUCCUCCUCCUCCUCC-3'       3'-CUGUCCAGAGCAAAACAGCGG-5'
<i>TP53</i> , miR-1273g-3p, 2317, -106, 91 5'-CCAGGCGGAGUCCUCCUCCAG-3'       3'-GAGUCCGACCUACGUCACCA-5'	<i>TP53</i> , miR-1273g-5p, 2347, -102, 86 5'-GCUACUGAGCCUCCUCCUCC-3'       3'-UGAAGGACGUCCAGUUGGUGG-5'
<i>POU5F1</i> , miR-1273a, 181*, -119, 90 5'-GACAGAGUCUUGCUCUCUACCC-3'       3'-UUCUUUCUCAGAAACAGCGGG-5'	<i>POU5F1</i> , miR-1273c, 183*, -104, 86 5'-GACAGAGUCUUGCUCUCUACCC-3'       3'-CUGUCCAGAGCAAAACAGCGG-5'
<i>POU5F1</i> , miR-1273d, 237*, -119, 87 5'-ACUGCAACUCCUCCUCCUCCUCC-3'       3'-UGACGUCGAGUUGGAGUACCAAG-5'	<i>POU5F1</i> , miR-1273e, 246*, -104, 89 5'-UCCGCUCCCGGUAACAGUGA-3'       3'-AGGUGAAGGACCAAGUUCGUU-5'
<i>POU5F1</i> , miR-1273f, 236*, -100, 96 5'-CACUGCAACUCCUCCUCCUCC-3'       3'-GUGACGUUGGAGUAGAGG-5'	<i>POU5F1</i> , miR-1273g-3p, 203*, -113, 96 5'-CCAGGCGGAGUCCUCCUCCAG-3'       3'-GAGUCCGACCUACGUCACCA-5'

Note. The top line contains sequentially: gene; miRNA; the beginning of the binding site; nt; AG, kJ/mole; AG/AGm,%. \* - the miRNA binding site is located in the 5'UTR. The top line of the diagram is the nucleotide sequence of the miRNA binding site; the bottom line is the nucleotide sequence of the mRNA. Non-canonical pairs are in bold.

Figure S9: The schemes of miR-1273 family interaction in the 3'UTR of mRNA of candidate gastric cancer genes





<p><i>CCND1</i>, miR-574-5p, 2595, -113, 93  5'-ACACACACACACACACACACA-3'                      3'-UGUGUGAGUGUGUGUGAGU-5'</p>	<p><i>CCND1</i>, ID00470.5p-miR, 2595, -108, 89  5'-ACACACAC<b>ACACACACACACA</b>-3'  3'-UGUGUGUG<b>CGUAUGUGUGCAUGU</b>-5'</p>
<p><i>IGF1</i>, miR-574-5p, 4042, -113, 93  5'-ACACACACACACACACACACA-3'                      3'-UGUGUGAGUGUGUGUGAGU-5'</p>	<p><i>IGF1</i>, ID00470.5p-miR, 4042, -108, 89  5'-ACACACAC<b>ACACACACACACA</b>-3'  3'-UGUGUGUG<b>CGUAUGUGUGCAUGU</b>-5'</p>
<p><i>IGF2</i>, miR-574-5p; 2299; -106; 88  5'-ACACACGCACACACA<b>UGCACACA</b>-3'                      3'-UGUGUGAGUGUGUGUG<b>UGUGAGU</b>-5'</p>	<p><i>IGF2</i>, ID00470.5p-miR; 2297; -113; 93  5'-ACACACACGCACACACA<b>UGCACA</b>-3'  3'-UGUGUGUG<b>CGUAUGUGUGCAUGU</b>-5'</p>
<p><i>IGF2</i>, miR-574-5p; 2343; -106; 88  5'-ACACACGCACACACA<b>UGCACACA</b>-3'                      3'-UGUGUGAGUGUGUGUG<b>UGUGAGU</b>-5'</p>	<p><i>IGF2</i>, ID00470.5p-miR; 2341; -113; 93  5'-ACACACACGCACACACA<b>UGCACA</b>-3'  3'-UGUGUGUG<b>CGUAUGUGUGCAUGU</b>-5'</p>
<p><i>IGF2</i>, miR-574-5p; 2522; -108; 89  5'-ACACA<b>UGCACACACAGCACACA</b> - 3'                          3'-UGUGUG<b>AGUGUGUGU</b>-GUGUGAGU - 5'</p>	<p><i>IGF2</i>, ID00470.5p-miR; 2520; -108; 89  5'-ACACACA<b>UGCACACACAGCACACA</b>-3'                                      3'-UGUGUGUG<b>CGUAUGUGU</b>-GCAUGU-5'</p>
<p><i>IGF2</i>, miR-574-5p; 2835; -104; 86  5'-ACACACA<b>UGCAGCACACACGCA</b>-3'                      3'-UGUGUGA<b>GUGUGUGUGAGU</b>-5'</p>	<p><i>IGF2</i>, ID00470.5p-miR; 2837; -110; 91  5'-ACACA<b>UGCAGCACACACGCA</b>-3'  3'-UGUGUG<b>UGCGUAUGUGUGCAUGU</b>-5'</p>
<p><i>SMAD4</i>, miR-574-5p, 7744, -113, 93  5'-ACACACACACACACACACA-3'                      3'-UGUGUGAGUGUGUGUGAGU-5'</p>	<p><i>SMAD4</i>, ID00470.5p-miR, 7744, -108, 89  5'-ACACACAC<b>ACACACACACA</b>- 3'  3'-UGUGUGUG<b>CGUAUGUGUGCAUGU</b>-5'</p>
<p><i>XRCC1</i>, miR-574-5p, 2035, -113, 93  5'-ACACACACACACACACACA-3'                      3'-UGUGUGAGUGUGUGUGAGU-5'</p>	<p><i>XRCC1</i>, ID00470.5p-miR, 2035, -108, 89  5'-ACACACAC<b>ACACACACACA</b>-3'  3'-UGUGUGUG<b>CGUAUGUGUGCAUGU</b>-5'</p>
<p><i>ZEB1</i>, miR-574-5p, 3587, -113, 93  5'-ACACACACACACACACACA-3'                      3'-UGUGUGAGUGUGUGUGAGU-5'</p>	<p><i>ZEB1</i>, ID00470.5p-miR, 3587, -108, 89  5'-ACACACAC<b>ACACACACACA</b>-3'  3'-UGUGUGUG<b>CGUAUGUGUGCAUGU</b>-5'</p>
<p>Note. The top line contains sequentially: gene; miRNA; the beginning of the binding site, nt; <math>\Delta G</math>, kJ/mole; <math>\Delta G/\Delta G_m</math>,%. * - the miRNA binding site is located in the 5'UTR. The top line of the diagram is the nucleotide sequence of the miRNA binding site; the bottom line is the nucleotide sequence of the miRNA. Non-canonical pairs are in bold.</p>	

**Figure S11:** The schemes of interaction of miR-574-5p and ID00470.5p-miR in the 3'UTR of mRNA of candidate gastric cancer genes