

Table 1 The prognostic value of individual COL4As according to GSE62254

Gene	HR	95% CI	P
COL4A1	2.17	1.51-3.11	< 0.001
COL4A2	2.78	1.93-3.99	< 0.001
COL4A3	2.34	1.63-3.37	< 0.001
COL4A4	2.3	1.6-3.31	< 0.001
COL4A5	2.52	1.7-3.72	< 0.001
COL4A6	2.32	1.47-3.66	< 0.001

Table 2 The prognostic value of COL4As expression with different genders according to GSE62254

	Gender	Cases	HR	95% CI	P-value
COL4A1	Female	98	3.43	1.84-6.4	<0.001
	male	185	1.94	1.24-3.04	<0.01
COL4A2	Female	98	3.64	1.95-6.8	<0.001
	male	185	2.39	1.52-3.76	<0.001
COL4A3	Female	98	3.16	1.68-5.94	<0.001
	male	185	2.03	1.3-3.18	<0.01
COL4A4	Female	98	3.88	2.08-7.22	<0.001
	male	185	1.86	1.14-3.01	<0.05
COL4A5	Female	98	3.46	1.73-6.92	<0.001
	male	185	2.32	1.46-3.7	<0.001
COL4A6	Female	98	2.86	1.46-5.61	<0.01
	male	185	1.98	1.18-3.32	<0.01

Table 3 The prognostic value of COL4As expression with different stages according to GSE62254

	Stage	Cases	HR	95% CI	P-value
COL4A1	I	28	1.3	0.12-1.56	0.08
	II	91	2.09	0.71-6.19	0.17
	III	88	1.67	0.88-3.17	0.11
	IV	74	2.3	1.34-3.94	<0.001
COL4A2	I	28	5.38	0.49-5.93	0.12
	II	91	2.03	0.79-5.2	0.13
	III	88	2.21	1.16-4.21	<0.05
	IV	74	3.75	1.75-8	<0.05
COL4A3	I	28	0.33	0.03-3.6	0.34
	II	91	1.83	0.79-4.24	0.15
	III	88	1.89	1-3.55	<0.05
	IV	74	2.41	1.37-4.22	<0.05
COL4A4	I	28	5.38	0.49-5.93	0.12
	II	91	0.56	0.23-1.33	0.18
	III	88	2.08	1.11-3.91	<0.05
	IV	74	1.99	1.16-3.41	<0.05
COL4A5	I	28	2.36	1.26-3.65	<0.001
	II	91	4.55	1.78-11.64	<0.001
	III	88	1.98	1.06-3.73	<0.05
	IV	74	1.93	1.07-3.49	<0.05
COL4A6	I	28	4.21	1.36-6.32	<0.05
	II	91	2.86	0.97-8.45	<0.001
	III	88	1.42	0.76-2.67	0.27
	IV	74	1.6	0.91-2.84	0.1

Table 4 The prognostic value of COL4As expression with different lauren classifications according to GSE62254

Gene	Lauren classification	Cases	HR	95% CI	P
	Intestinal	141	2.2	1.21-4	<0.01
COL4A1	Diffuse	135	2.46	1.45-4.18	<0.001
	Mixed	7	-		
	Intestinal	141	2	1.11-3.61	<0.05
COL4A2	Diffuse	135	2.92	1.81-4.71	<0.001
	Mixed	7	-		
	Intestinal	141	2.19	1.2-3.97	<0.01
COL4A3	Diffuse	135	2.4	1.47-3.92	<0.001
	Mixed	7	-		
	Intestinal	141	2	1.09-3.65	<0.05
COL4A4	Diffuse	135	2.41	1.49-3.91	<0.001
	Mixed	7	-		
	Intestinal	141	1.84	1.03-3.31	<0.05
COL4A5	Diffuse	135	2.52	1.44-4.41	<0.001
	Mixed	7	-		
	Intestinal	141	2.06	1.08-3.94	<0.05
COL4A6	Diffuse	135	1.84	1.13-2.99	<0.05
	Mixed	7	-		

Table 5 The prognostic estimation of CpG sites in the COL4As

CpG site	Gene	Group	CpG Island	HR	CI	P
cg0005079 2	COL4A 1	Body	Open_Sea	0.62	0.442- 0.869	0.005 6
cg0209957 2	COL4A 1	Body	Open_Sea	0.64 5	0.458-0.91	0.013
cg0273049 2	COL4A 1	Body	Open_Sea	0.66 7	0.481- 0.924	0.015
cg0823425 6	COL4A 1	Body	Open_Sea	0.69 1	0.501- 0.953	0.024
cg1052730 0	COL4A 1	Body	Open_Sea	0.64 5	0.457- 0.911	0.013
cg0298875 5	COL4A 1	Body	Island	0.54 8	0.363- 0.826	0.004 1
cg0329624 8	COL4A 1	Body	Island	0.55	0.395- 0.765	0.000 38
cg0526541 4	COL4A 1	Body	N_Shelf	0.62 7	0.447-0.88	0.007
cg1643678 2	COL4A 1	Body	N_Shore	0.60 4	0.437- 0.836	0.002 3
cg0665972 7	COL4A 2	TSS1500;1stEx on;5'UTR	Island	0.51 6	0.328- 0.811	0.004 1
cg0986313 8	COL4A 4	3'UTR	Open_Sea	0.67 2	0.446- 1.015	0.049
cg0506492 5	COL4A 6	TSS1500;1stEx on;5'UTR	Open_Sea	0.62 2	0.451- 0.859	0.003 9
cg1273716 0	COL4A 6	TSS1500;1stEx on;5'UTR	Open_Sea	0.55 5	0.394- 0.782	0.000 76
cg2427547 5	COL4A 6	Body	Open_Sea	0.64 8	0.467- 0.899	0.009 4

Table 6 The Kinase, miRNA and transcription factor-target networks of COL4A1 in stomach cancer

Enriched Category	Gene Set	Leading Edge Number	P Value
Transcription Factor Target	V\$SRF_01	21	0.00
	V\$HLF_01	67	0.00
	V\$RREB1_01	50	0.00
	V\$NF1_Q6_01	86	0.00
	V\$VDR_Q3	53	0.00
	AACTTT_UNKNOWN	625	0.00
	V\$OCT1_Q6	82	0.00
	V\$OCT1_04	83	0.00
	V\$LYF1_01	77	0.00
	V\$CEBP_Q2_01	87	0.00
	V\$FOX_Q2	80	0.00
	V\$CART1_01	65	0.00
	YTATTTTNR_V\$MEF2_02	219	0.00
	TTCYNRGAA_V\$STAT5B_01	93	0.00
	V\$GATA4_Q3	72	0.00
	V\$MMEF2_Q6	91	0.00
	GKCGCNNNNNNNTGAYG_UNKNOWN	27	0.00
	V\$PPARG_01	18	0.00
	GGAANCGGAANY_UNKNOWN	42	0.00
	KTGGYRSGAA_UNKNOWN	33	0.00
	GCCNNNWTAAR_UNKNOWN	54	0.00
	YTAATTAA_V\$LHX3_01	46	0.00
	V\$HFH3_01	50	0.00
	V\$CEBPB_02	72	0.00
	YGCANTGCR_UNKNOWN	44	0.00
	ACCTGTTG_UNKNOWN	65	0.00
	CCTNTMAGA_UNKNOWN	25	0.01
RNTCANNRNNYNATTW_UNKNOWN	25	0.02	
miRNA Target	ACTTTAT,MIR-142-5P	81	0.00
	CTACCTC,LET-7A,LET-7B,LET-7C,LET-7D,LET-7E,LET-7F,MIR-98,LET-7G,LET-7I	94	0.00
	GCACTTT,MIR-17-5P,MIR-20A,MIR-106A,MIR-106B,MIR-20B,MIR-519D	197	0.00
	GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367	102	0.00
	CAGTGTT,MIR-141,MIR-200A	87	0.00
	CTACTGT,MIR-199A	50	0.01
	AAAGACA,MIR-511	40	0.01
	CTTTGCA,MIR-527	88	0.01
	ATGTAGC,MIR-221,MIR-222	42	0.01

	ATGAAGG,MIR-205	44	0.01
	AAGCAAT,MIR-137	65	0.02
	CCCAGAG,MIR-326	54	0.02
	GTGCAAA,MIR-507	47	0.03
	ACTGTAG,MIR-139	33	0.03
	GGTGTGT,MIR-329	38	0.04
	ATGCTGG,MIR-338	25	0.04
	AGGGCCA,MIR-328	25	0.04
	ACTGCAG,MIR-17-3P	27	0.05
	ATGTCAC,MIR-489	22	0.05
Kinase Target	Kinase_ATR	34	0.00
	Kinase_PRKACA	105	0.00
	Kinase_SRC	68	0.00
	Kinase_AURKB	46	0.00
	Kinase_FYN	34	0.00
	Kinase_PRKG1	14	0.00
	Kinase_PRKCA	68	0.00
	Kinase_NEK2	4	0.01
	Kinase_PIK3CB	1	0.02
	Kinase_PKMYT1	3	0.02
	Kinase_RPS6KA4	11	0.03
	Kinase_WEE1	4	0.04
	Kinase_MKNK1	4	0.05

Table 7 The Kinase, miRNA and transcription factor-target networks of COL4A2 in stomach cancer

Enriched Category	Gene Set	Leading Edge Number	P Value
Transcription Factor Target	V\$SRF_01	19	0.00
	V\$SRF_C	93	0.00
	CCAWWNAAGG_V\$SRF_Q4	36	0.00
	YNTTTNNNANGCARM_UNK		
	NOWN	30	0.00
	V\$RP58_01	87	0.00
	V\$SRF_Q5_01	93	0.00
	V\$SRF_Q6	93	0.00
	V\$SRF_Q4	95	0.00
	V\$STAT5B_01	75	0.00
	V\$TTF1_Q6	68	0.00
	V\$OCT1_01	84	0.00
	CAGCTG_V\$AP4_Q5	510	0.00
	CATTGTYY_V\$SOX9_B1	121	0.00
	V\$LMO2COM_02	89	0.00
	V\$FREAC4_01	47	0.00
	TGGNNNNNNKCCAR_UNKN		
	OWN	116	0.00
	V\$LHX3_01	74	0.00
	CTGCAGY_UNKNOWN	275	0.00
	V\$OCT1_05	79	0.00
	V\$S8_01	71	0.00
	V\$AFP1_Q6	78	0.00
	V\$NKX62_Q2	83	0.00
	TMTCGCGANR_UNKNOWN	62	0.00
	GGAANCGGAANY_UNKNOWN		
	N	43	0.00
GKCGCNNNNNNNTGAYG_U			
NKNOWN	31	0.00	
CGGAARNGGCNG_UNKNOWN			
N	17	0.00	
GCGSCMNTTT_UNKNOWN	30	0.00	
V\$GABP_B	102	0.00	
V\$FXR_Q3	33	0.00	
YAATNRNNNYNATT_UNKNO			
WN	34	0.00	
RNTCANNRNNNYNATTW_UN			
KNOWN	26	0.01	
miRNA Target	AAGCCAT,MIR-135A,MIR-135B	113	0.00
	ACACTGG,MIR-199A,MIR-199B	39	0.00
	AGGAAGC,MIR-516-3P	27	0.00
	ATGTACA,MIR-493	98	0.00

	CAGTATT,MIR-200B,MIR-200C,MIR-429	134	0.00
	GTGCCAA,MIR-96	109	0.00
	TGCACTG,MIR-148A,MIR-152,MIR-148B	65	0.00
	TGTGTGA,MIR-377	45	0.00
	ATATGCA,MIR-448	57	0.00
	CCCAGAG,MIR-326	51	0.00
	GTATTAT,MIR-369-3P	60	0.00
	CCAGGGG,MIR-331	32	0.00
	GACAATC,MIR-219	52	0.00
	GCACCTT,MIR-18A,MIR-18B	45	0.00
	GTTATAT,MIR-410	37	0.00
	ACATATC,MIR-190	23	0.02
	CTAGGAA,MIR-384	15	0.02
	AGGGCCA,MIR-328	24	0.02
	AATGGAG,MIR-136	20	0.02
	GGGACCA,MIR-133A,MIR-133B	68	0.02
	GGGGCCC,MIR-296	26	0.02
	GTGTGAG,MIR-342	16	0.04
Kinase Target	Kinase_ATR	31	0.00
	Kinase_PLK3	10	0.00
	Kinase_MKNK1	4	0.00
	Kinase_AURKB	31	0.00
	Kinase_PKMYT1	3	0.00
	Kinase_NEK1	3	0.00
	Kinase_PLK1	35	0.00
	Kinase_PRKG1	10	0.00
	Kinase_CDK5	25	0.00
	Kinase_PRKACG	29	0.00
	Kinase_PRKX	24	0.00
	Kinase_PAK2	4	0.00
	Kinase_CSNK1G2	3	0.01
	Kinase_FYN	36	0.01
	Kinase_CSNK1G1	3	0.01
	Kinase_CSNK1A1L	3	0.01
	Kinase_WEE1	4	0.01
	Kinase_PAK3	1	0.01
	Kinase_PAK5	1	0.01
	Kinase_NEK2	5	0.01
	Kinase_PAK6	2	0.02
	Kinase_BUB1	4	0.02
	Kinase_ROCK1	11	0.02
	Kinase_PDGFRB	10	0.02
	Kinase_HCK	15	0.02
	Kinase_ADRBK1	8	0.03
	Kinase_CDC7	3	0.03

Table 8 The Kinase, miRNA and transcription factor-target networks of COL4A3 in stomach cancer

Enriched Category	Gene Set	Leading Edge Number	P Value
Transcription Factor Target	V\$PAX5_02	6	0.00
	V\$MEF2_Q6_01	89	0.00
	V\$OCT1_03	88	0.00
	V\$TCF11_01	87	0.00
	V\$HFH3_01	72	0.00
	V\$NKX62_Q2	79	0.00
	V\$PBX1_01	99	0.00
	TAAWWATAG_V\$RSRFC4_Q2	51	0.00
	V\$MEF2_03	111	0.00
	V\$CREBP1_01	75	0.00
	V\$HFH4_01	68	0.00
	V\$CDX2_Q5	86	0.00
	V\$GATA1_02	95	0.00
	V\$S8_01	83	0.00
	TGCCAAR_V\$NF1_Q6	241	0.00
	V\$OCT1_B	92	0.00
	V\$GATA3_01	78	0.00
	V\$FREAC2_01	71	0.00
	V\$GF11_01	86	0.00
	YTAATTAA_V\$LHX3_01	49	0.00
	V\$RSRFC4_Q2	70	0.00
	V\$OCT1_01	95	0.00
	YKACATTT_UNKNOWN	81	0.00
	V\$POU3F2_01	37	0.00
	V\$CEBP_Q2	72	0.00
	GKCGCNNNNNNTGAYG_UNKNOWN	23	0.00
	KRCTCNNNNMANAGC_UNKNOWN	35	0.00
	GGAANCGGAANY_UNKNOWN	49	0.00
	KTGGYRSGAA_UNKNOWN	16	0.00
	V\$E2F_01	18	0.00
	CGGAARNGGCNG_UNKNOWN	13	0.00
	MCAATNNNNNGCG_UNKNOWN	20	0.00
	miRNA Target	ACATATC,MIR-190	23
TGCAAAC,MIR-452		38	0.00
ATACTGT,MIR-144		71	0.00
TTGCCAA,MIR-182		113	0.00
ATGTAGC,MIR-221,MIR-222		65	0.00

	GTTATAT,MIR-410	36	0.00	
	TATTATA,MIR-374	110	0.00	
	CATGTAA,MIR-496	75	0.00	
	TAATAAT,MIR-126	93	0.00	
	ATGTACA,MIR-493	109	0.00	
	CTTTGTA,MIR-524	134	0.00	
	TAGCTTT,MIR-9	82	0.00	
	AAGCAAT,MIR-137	95	0.00	
	ATAGGAA,MIR-202	43	0.00	
	AAAGGAT,MIR-501	36	0.00	
	GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367	121	0.00	
	ATGCTGC,MIR-103,MIR-107	78	0.00	
	CATTTCA,MIR-203	99	0.00	
	ATCTTGC,MIR-31	28	0.00	
	ATGCTGG,MIR-338	44	0.00	
	TCTGATC,MIR-383	8	0.01	
	CTAGGAA,MIR-384	27	0.01	
	CTCTAGA,MIR-526C,MIR-518F,MIR-526A	10	0.01	
	ACCAATC,MIR-509	24	0.02	
	GCAAGAC,MIR-431	18	0.02	
Kinase Target				0.061
	Kinase_PLK3	11	0.00	831
				0.079
	Kinase_CHEK2	11	0.00	579
				0.080
	Kinase_ATR	27	0.00	724
				0.109
	Kinase_WEE1	5	0.00	06
				0.124
	Kinase_PKMYT1	3	0.00	91
	Kinase_AURKB	33	0.00	0.19
				0.269
	Kinase_PRKACG	28	0.00	68
				0.286
	Kinase_PRKX	29	0.00	8
				0.288
	Kinase_PRKG1	12	0.00	83
				0.300
	Kinase_PRKACB	29	0.00	65
				0.125
	Kinase_CDK8	1	0.01	04
				0.095
	Kinase_PKN2	4	0.01	323
				0.095
	Kinase_NEK2	5	0.01	495
				0.295
	Kinase_BTK	5	0.01	9

Kinase_PIK3CD	2	0.02	59	0.234
Kinase_MKMK2	3	0.02	708	0.097
Kinase_DAPK3	4	0.02	81	0.240
Kinase_LYN	20	0.02	15	0.331
Kinase_MAP2K7	1	0.02	06	0.308
Kinase_RPS6KA4	14	0.02	27	0.144
Kinase_MARK3	1	0.02	16	0.231
Kinase_CSNK1G3	3	0.02	04	0.284
Kinase_GRK5	3	0.02	68	0.290
Kinase_LMTK2	1	0.02	01	0.154
Kinase_NEK1	3	0.02	42	0.176
Kinase_MYLK2	2	0.02	51	0.214
Kinase_PDGFRB	7	0.03	92	0.277
Kinase_TEC	4	0.03	28	0.280
Kinase_CSNK1G1	4	0.03	48	0.329
Kinase_BUB1	4	0.03	163	0.097
Kinase_HCK	12	0.03	12	0.322
Kinase_SRPK1	1	0.04	11	0.285
Kinase_ADRBK1	8	0.04	51	0.315
Kinase_MAPKAPK5	2	0.04	96	0.156
Kinase_TTK	7	0.05	7	0.268

Table 9 The Kinase, miRNA and transcription factor-target networks of COL4A4 in stomach cancer

Enriched Category	Gene Set	Leading Edge Number	P Value
Transcription Factor Target	KRCTCNNNNMANAGC_UNKNOWN	31	0.00
	GKCGCNNNNNNNTGAYG_UNKNO		
	WN	23	0.00
	V\$OCT1_05	83	0.00
	CTGRYYNATT_UNKNOWN	27	0.00
	V\$MEF2_Q6_01	95	0.00
	V\$OCT1_02	81	0.00
	V\$NCX_01	58	0.00
	V\$AP3_Q6	84	0.00
	YKACATTT_UNKNOWN	81	0.00
	V\$NKX61_01	87	0.00
	V\$RSRFC4_01	84	0.00
	RAAGNYNNCTTY_UNKNOWN	58	0.00
	V\$OCT1_Q6	73	0.00
	V\$PITX2_Q2	78	0.00
	V\$SRF_Q4	91	0.00
	V\$SRY_02	79	0.00
	V\$EVII_05	51	0.00
	V\$NKX62_Q2	65	0.00
	V\$PAX4_04	78	0.00
	WGTTNNNNNAAA_UNKNOWN	194	0.00
	V\$FOXO4_02	101	0.00
	V\$RSRFC4_Q2	81	0.00
	RNTCANNRNNYNATTW_UNKNOW		
	N	27	0.00
	V\$HFH4_01	68	0.00
	CAGNYGKNAAA_UNKNOWN	25	0.00
GGAANCGGAANY_UNKNOWN	45	0.00	
KTGGYRSGAA_UNKNOWN	19	0.00	
MCAATNNNNNGCG_UNKNOWN	21	0.00	
CCGNMNTNACG_UNKNOWN	11	0.00	
YWATTWNNRGCT_UNKNOWN	24	0.00	
V\$EVII_01	7	0.02	
miRNA Target	ACATATC,MIR-190	25	0.00
	TATTATA,MIR-374	95	0.00
	AAGCACT,MIR-520F	73	0.00
	ATACCTC,MIR-202	72	0.00
	TGAATGT,MIR-181A,MIR-181B,MIR-181C,MIR-181D	157	0.00
	TCCAGAG,MIR-518C	49	0.00
	GCAAAA,MIR-129	70	0.00
	ATGCTGC,MIR-103,MIR-107	71	0.00
	TGGTGCT,MIR-29A,MIR-29B,MIR-	170	0.00

	29C		
	AAAGGAT,MIR-501	33	0.00
	TAGCTTT,MIR-9	68	0.00
	AAGCACA,MIR-218	124	0.00
	GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367	121	0.00
	TAATAAT,MIR-126	78	0.00
	AAGCCAT,MIR-135A,MIR-135B	121	0.00
	CTTGTAT,MIR-381	66	0.00
	GTATTAT,MIR-369-3P	86	0.00
	GTTATAT,MIR-410	37	0.00
	TTGCCAA,MIR-182	87	0.00
	TTGCACT,MIR-130A,MIR-301,MIR-130B	145	0.00
	GCACTTT,MIR-17-5P,MIR-20A,MIR-106A,MIR-106B,MIR-20B,MIR-519D	212	0.00
	CAATGCA,MIR-33	27	0.00
	AATGGAG,MIR-136	36	0.00
	AGTTCTC,MIR-146A,MIR-146B	24	0.01
	TCGATGG,MIR-213	1	0.03
Kinase Target	Kinase_PLK1	34	0.00
	Kinase_ATR	24	0.00
	Kinase_AURKB	39	0.00
	Kinase_PLK3	9	0.00
	Kinase_MKNK2	3	0.00
	Kinase_PKMYT1	3	0.00
	Kinase_PRKACG	29	0.00
	Kinase_FYN	28	0.00
	Kinase_PRKX	30	0.00
	Kinase_PRKACB	30	0.00
	Kinase_CDK5	25	0.00
	Kinase_MYLK2	2	0.00
	Kinase_BUB1	4	0.01
	Kinase_MKNK1	4	0.01
	Kinase_MARK3	1	0.01
	Kinase_NEK1	3	0.01
	Kinase_WEE1	4	0.02
	Kinase_TEC	4	0.02
	Kinase_PDGFRB	7	0.02
	Kinase_LYN	23	0.02
	Kinase_BTK	5	0.02
	Kinase_CDK8	1	0.02
	Kinase_GRK5	3	0.02
	Kinase_STK38	1	0.02
	Kinase_NEK2	5	0.03
	Kinase_CSNK1G2	3	0.03
	Kinase_CHEK2	12	0.03
	Kinase_CSNK1G1	4	0.04
	Kinase_FGR	8	0.05

Kinase_LMTK2	1	0.05
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Table 10 The Kinase, miRNA and transcription factor-target networks of COL4A5 in stomach cancer

Enriched Category	Gene Set	Leading Edge Number	P Value
Transcription Factor Target	CCAWWNAAGG_V\$SRF_Q4	34	0.00
	V\$FREAC7_01	64	0.00
	V\$HMEF2_Q6	55	0.00
	V\$TAL1BETAE47_01	89	0.00
	CAGNYGKNAAA_UNKNOWN	24	0.00
	CTGRYYNATT_UNKNOWN	25	0.00
	V\$OCT1_03	100	0.00
	YWATTWNNRGCT_UNKNOWN	29	0.00
	V\$OCT1_02	72	0.00
	V\$HFH4_01	72	0.00
	V\$OCT1_04	72	0.00
	AAAYWAACM_V\$HFH4_01	99	0.00
	AAAYRNCTG_UNKNOWN	116	0.00
	V\$FOXO4_02	108	0.00
	V\$HNF3_Q6	69	0.00
	V\$RP58_01	94	0.00
	V\$DBP_Q6	81	0.00
	V\$FOXJ2_02	85	0.00
	V\$GATA1_04	74	0.00
	V\$EVI1_04	76	0.00
	V\$RSRFC4_01	90	0.00
	V\$FOXJ2_01	61	0.00
	V\$MEF2_01	53	0.00
	KTGGYRSGAA_UNKNOWN	15	0.00
	GKCGCNNNNNNNTGAYG_UNKNOWN	24	0.00
	V\$E2F_Q3	69	0.00
	KRCTCNNNNMANAGC_UNKNOWN	22	0.00
	RRCCGTTA_UNKNOWN	18	0.00
	GGAANCGGAANY_UNKNOWN	36	0.00
	V\$MYOGNF1_01	16	0.00
	V\$SRF_01	23	0.00

miRNA Target	ACCAATC,MIR-509	25	0.00	
	GCAAAAA,MIR-129	61	0.00	
	ATGTACA,MIR-493	117	0.00	
	ATGTTTC,MIR-494	70	0.00	
	AGGAGTG,MIR-483	19	0.00	
	CTTGTAT,MIR-381	63	0.00	
	AAAGGAT,MIR-501	32	0.00	
	GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367	113	0.00	
	ACACTGG,MIR-199A,MIR-199B	52	0.00	
	TAATAAT,MIR-126	81	0.00	
	GTATTAT,MIR-369-3P	84	0.00	
	ACATATC,MIR-190	24	0.00	
	TCTCTCC,MIR-185	45	0.00	
	CATTTCA,MIR-203	102	0.00	
	CTACTGT,MIR-199A	69	0.00	
	CAGTATT,MIR-200B,MIR-200C,MIR-429	157	0.00	
	ATATGCA,MIR-448	96	0.00	
	GCTTGAA,MIR-498	38	0.00	
	AATGGAG,MIR-136	38	0.00	
	CAGCACT,MIR-512-3P	64	0.00	
	CAATGCA,MIR-33	36	0.00	
	GTGTCAA,MIR-514	23	0.00	
	TCCCCAC,MIR-491	17	0.00	
	GTACAGG,MIR-486	21	0.01	
	GGTAACC,MIR-409-5P	15	0.02	
	Kinase Target	Kinase_ATR	28	0.00
		Kinase_PLK1	29	0.00
		Kinase_AURKB	35	0.00
		Kinase_PLK3	9	0.00
		Kinase_CHEK1	41	0.00
		Kinase_RPS6KA4	10	0.00
		Kinase_CDC7	3	0.00
		Kinase_BUB1	3	0.00
Kinase_WEE1		5	0.00	
Kinase_PKMYT1		3	0.00	
Kinase_PRKACG		26	0.00	
Kinase_PRKX		27	0.00	
Kinase_FYN		17	0.00	
Kinase_PRKACB		27	0.00	
Kinase_NEK1		3	0.01	
Kinase_PKN2		4	0.01	
Kinase_DAPK3		4	0.01	
Kinase_PLK4		2	0.01	
Kinase_PTK2B		3	0.01	
Kinase_NEK2		5	0.02	
Kinase_UHMK1		1	0.02	
Kinase_ADRBK1	9	0.02		

Kinase_CHEK2	11	0.02
Kinase_PRKG1	12	0.02
Kinase_CAMKK2	3	0.02
Kinase_GRK5	3	0.02
Kinase_MAP2K7	1	0.03
Kinase_SRPK1	1	0.03
Kinase_PRKDC	13	0.03
Kinase_RPS6KA6	2	0.04
Kinase_MARK2	9	0.04
Kinase_PDGFRB	5	0.04
Kinase_NTRK1	5	0.04
Kinase_PHKG1	1	0.05
Kinase_PHKG2	1	0.05

Table 11 The Kinase, miRNA and transcription factor-target networks of COL4A6 in stomach cancer

Enriched Category	Gene Set	Leading Edge Number	P Value
	V\$SRF_C	78	0.00
	V\$SRF_01	17	0.00
	V\$SRF_Q5_01	78	0.00
	V\$SRF_Q6	82	0.00
	CCAWWNAAGG_V\$SRF_Q4	30	0.00
	V\$COMP1_01	36	0.00
	V\$SRF_Q4	68	0.00
	V\$E2F_Q4	72	0.00
	V\$E2F_Q6	85	0.00
	V\$E2F1_Q4_01	68	0.00
	SGCGSSAAA_V\$E2F1DP2_01	65	0.00
	V\$POU6F1_01	79	0.00
	V\$MEF2_02	87	0.00
	CTGRYYNATT_UNKNOWN	26	0.00
	V\$MEF2_Q6_01	92	0.00
	V\$RSRFC4_Q2	72	0.00
	V\$HMEF2_Q6	56	0.00
	CAGNYGKNAAA_UNKNOWN	28	0.00
	WWTAAGGC_UNKNOWN	45	0.00
Transcription Factor Target	V\$RP58_01	75	0.00
	V\$MEF2_01	54	0.00
	V\$FOXJ2_02	71	0.00
	V\$EN1_01	43	0.00
	V\$GATA_Q6	64	0.00
	V\$HNF3_Q6	72	0.00
	V\$FOXD3_01	64	0.00
	AAANWWTGC_UNKNOWN	81	0.00
	V\$E2F1_Q6_01	66	0.00
	KRCTCNNNNMANAGC_UNKNOWN	33	0.00
	KTGGYRSGAA_UNKNOWN	21	0.00
	V\$ELK1_02	87	0.00
	GKCGCNNNNNNNTGAYG_UNKNOWN	24	0.00
	V\$E2F_01	24	0.00
	GGAANCGGAANY_UNKNOWN	43	0.00
	AACYNNNNTTCCS_UNKNOWN	18	0.00
	TMTCGCGANR_UNKNOWN	34	0.00
	GCGSCMNTTT_UNKNOWN	16	0.05
miRNA Target	ACATATC,MIR-190	22	0.00
	AGGAGTG,MIR-483	19	0.00

	CTAGGAA,MIR-384	22	0.00
	GACAATC,MIR-219	61	0.00
	GCTTGAA,MIR-498	39	0.00
	ATGTAGC,MIR-221,MIR-222	58	0.00
	TGCAAAC,MIR-452	43	0.00
	TGTGTGA,MIR-377	57	0.00
	ATGTACA,MIR-493	100	0.00
	ATGCTGC,MIR-103,MIR-107	84	0.00
	TATTATA,MIR-374	100	0.00
	GTATTAT,MIR-369-3P	61	0.00
	CAATGCA,MIR-33	26	0.00
	AAGCCAT,MIR-135A,MIR-135B	84	0.00
	ATATGCA,MIR-448	71	0.00
	GCAAAAA,MIR-129	61	0.00
	TGAATGT,MIR-181A,MIR-181B,MIR-181C,MIR-181D	122	0.00
	GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367	98	0.00
	AAAGGAT,MIR-501	34	0.00
	CAGCACT,MIR-512-3P	61	0.00
	GCTCTTG,MIR-335	28	0.00
	AAACCAC,MIR-140	24	0.00
	GTGTCAA,MIR-514	23	0.00
	TCCCCAC,MIR-491	17	0.00
	ACCAATC,MIR-509	24	0.01
	Kinase_ATR	29	0.00
	Kinase_PLK3	9	0.00
	Kinase_PLK1	33	0.00
	Kinase_AURKB	36	0.00
	Kinase_CHEK1	39	0.00
	Kinase_ATM	38	0.00
	Kinase_CHEK2	12	0.00
	Kinase_WEE1	5	0.00
	Kinase_PRKACG	26	0.00
	Kinase_NEK1	3	0.00
	Kinase_PKMYT1	3	0.00
Kinase Target	Kinase_CDC7	3	0.00
	Kinase_PRKACB	27	0.00
	Kinase_FYN	16	0.00
	Kinase_PRKX	27	0.00
	Kinase_PRKG1	9	0.00
	Kinase_MAP2K1	3	0.01
	Kinase_DAPK3	4	0.01
	Kinase_ADRBK1	8	0.02
	Kinase_NEK2	4	0.02
	Kinase_BUB1	4	0.02
	Kinase_PHKG1	1	0.02
	Kinase_PHKG2	1	0.02
	Kinase_CDK5	17	0.02

Kinase_RPS6KA4	14	0.02
Kinase_NTRK1	5	0.02
Kinase_MARK3	1	0.03
Kinase_PLK4	2	0.03
Kinase_CAMKK2	3	0.03
Kinase_MARK2	7	0.03
Kinase_MKMK1	4	0.04
Kinase_MAP2K7	1	0.05
Kinase_TNK2	1	0.05
Kinase_ROCK1	12	0.05
