Supplementary Table 1. Clinical characteristics of patients under survey and mapping properties of their WT-seq and small RNA-seq datasets

Clinical characteristics					WT RNA-Seq			Small RNA		
Case No.	Sex	Age	Stage*	Histologics**	Total Reads (Millions)	Uniquely Mapped Reads (Millions)	Detected Genes*** (Thousands)	Total Reads (Millions)	Reads mapped to miRNAs (Millions)	Detected miRNAs****
1	M	83	I	Mixed	59.9	16.0	15.2	55.2	5.6	467
2	M	74	IV	Diffuse	60.0	21.5	15.1	30.4	6.3	429
3	M	63	III	Intestine	95.9	15.1	15.6	30.5	2.0	447
4	M	58	III	Intestine	70.7	28.2	15.4	NA	NA	NA
5	F	70	II	Diffuse	82.7	17.8	15.1	32.8	5.1	453
6	M	64	IV	Diffuse	81.7	27.0	15.9	NA	NA	NA
7	M	76	I	Diffuse	53.0	17.7	15.0	24.1	4.6	424
8	F	67	Normal#	Normal	67.1	9.8	15.4	22.4	2.6	435
9	M	61	I	Intestine	72.1	26.0	15.0	32.8	5.4	468
10	M	69	Normal	Normal	63.4	11.3	15.5	35.0	6.0	455
11	M	69	II	Diffuse	74.7	13.4	15.0	30.7	2.7	451
12	M	37	Normal	Normal	89.5	13.0	15.5	31.1	4.2	454
13	M	56	Normal	Normal	36.2	7.2	15.2	19.9	3.8	438
14	F	60	IV	Mixed	64.6	17.5	15.8	39.2	1.4	430
15	M	69	IV	Diffuse	59.0	10.6	15.5	39.3	6.0	462
16	M	52	II	unknown	53.2	10.8	15.5	43.9	1.6	431
17	F	32	Normal	Normal	68.8	10.9	15.6	21.6	5.5	438
18	F	73	III	Intestine	91.3	17.6	16.5	NA	NA	NA
19	F	66	I	Diffuse	59.7	14.0	14.8	37.3	4.3	465
20	M	66	II	Intestine	73.8	25.6	14.8	18.3	2.1	415
21	M	64	IV	Diffuse	59.0	13.3	15.6	NA	NA	NA
22	M	66	Normal	Normal	55.7	10.8	16.0	34.5	5.4	435
23	M	52	III	Diffuse	78.7	31.3	14.9	NA	NA	NA
24	M	47	III	Intestine	62.6	12.7	14.9	19.3	3.4	390
25	M	61	III	Intestine	73.7	15.4	14.7	36.0	3.7	418
26	M	64	I	Diffuse	96.0	26.2	16.4	30.4	7.1	462
27	M	55	III	Diffuse	80.7	20.8	16.0	182.4	25.4	464
28	M	72	III	Diffuse	89.3	26.5	17.2	19.7	4.6	421
29	M	unknown	IV	unknown	77.4	28.1	15.3	24.5	3.7	456
30	M	unknown	II	unknown	73.9	35.8	14.5	19.4	4.1	429

*AJCC stage; **Lauren's Classification; *** RPKM > 0.05; **** with mapped read; #Normal samples were collected from patients of different tumor stages; NA = not available.

Supplementary Table 2. List of differentially expressed genes related to gastric cancer

(A) List of 356 differentially expressed coding genes related to gastric cancer

Gene Symbol	Fold Change (I,II,III,IV vs. normal)	*P*-value (ANOVA)	Biological and Molecular Category
ABCC12	-9.13	3.05E-04	transporter
ABCC5	-2.76	1.71E-05	transporter
ABHD11	4.04	4.90E-04	enzyme
ACAD L	-23.86	2.28E-05	enzyme
ACER2	-4.84	1.43E-04	cell adhesion, motility and invasion
ADA	-3.61	9.75E-05	enzyme
ADAM28	-4.25	8.58E-04	cell adhesion, motility and invasion
ADAMTSL1	-4.62	5.43E-05	cell adhesion, motility and invasion
ADAMTSL3	-2.83	7.80E-04	cell adhesion, motility and invasion
ADH7	-173.66	1.36E-05	enzyme
ADHFE1	-9.01	2.62E-04	enzyme
ADRA1A	-8.71	3.23E-04	G-protein coupled receptor
AFAP1	1.84	8.68E-04	cell adhesion, motility and invasion
AGPAT5	1.60	8.39E-05	enzyme
AGXT2L1	-123.59	2.85E-04	enzyme
ALDH6A1	-2.99	4.76E-05	enzyme
ANGPTL3	-228.30	6.42E-06	growth factor
ANO7	-8.13	6.40E-07	transporter
AP2B1	1.60	8.36E-04	transporter
APLP1	-8.50	7.31E-04	transcriptional regulation
AQP4	-166.92	1.39E-05	transporter
ARHGAP20	-1.99	2.72E-04	signal transduction
ARHGAP28	-3.05	1.86E-04	signal transduction
ARHGEF12	1.34	5.31E-04	signal transduction
ARL4D	-3.91	4.87E-04	enzyme
ASB11	-337.90	4.60E-06	transcriptional regulation
ATP13A4	-8.05	3.97E-05	transporter
ATP13A5	-45.21	3.36E-05	transporter
ATP1B3	2.41	7.80E-04	transporter
ATP4A	-408.04	4.94E-06	transporter
ATP4B	-609.78	2.03E-05	transporter
ATP8A2	-7.18	7.90E-06	transporter
B3GAT1	-21.37	3.06E-07	enzyme
B4GALNT2	-77.22	8.11E-04	enzyme
BMP1	2.90	2.85E-04	peptidase
BRE	1.41	7.15E-04	signal transduction
C11Orf92	-10.74	8.02E-07	unknown
C12orf30	1.85	2.19E-04	unknown
C16Orf89	-57.61	2.59E-04	unknown

C1orf107	1.68	8.13E-04	differentiation
C20Orf194	-1.70	2.31E-04	unknown
C3Orf18	-2.26	8.88E-04	unknown
C3Orf57	-10.14	1.54E-04	lipid metabolism
C3Orf59	-1.10	6.89E-04	unknown
C5Orf38	-29.23	6.25E-04	unknown
C5Orf4	-3.18	6.32E-05	lipid metabolism
C6orf108	2.13	5.41E-04	metabolism
C6orf167	1.94	8.03E-04	protein binding
C8orf84	-10.07	7.14E-05	metabolism
C9orf3	1.78	4.31E-04	peptidase
CACNA2D2	-5.34	5.99E-05	ion channel
CALM2	1.53	6.69E-04	binding protein
CBFB	1.70	2.91E-04	transcriptional regulation
CBX3	2.57	7.27E-04	transcriptional regulation
CCDC150	4.10	6.87E-04	unknown
CCDC41	2.24	4.64E-04	unknown
CCDC6	1.68	3.84E-04	cytoskeleton
CCDC89	-3.33	3.42E-06	cytoskeleton
CCDC93	1.63	7.62E-04	unknown
CCKAR	-125.68	8.48E-04	G-protein coupled receptor
CCKBR	-60.34	7.84E-04	G-protein coupled receptor
CD3EAP	3.01	6.08E-04	transcriptional regulation
CDC123	1.85	7.02E-04	cell cycle
CDCA7	3.28	6.17E-04	cell cycle
CDK2	1.72	2.08E-04	kinase
CEBPZ	1.86	2.88E-04	transcriptional regulation
CELSR3	3.05	2.18E-04	G-protein coupled receptor
CGNL1	-3.30	5.63E-04	cell adhesion, motility and invasion
CHD1	1.56	8.78E-04	enzyme
CHEK1	2.65	7.92E-04	kinase
CHGA	-89.28	2.75E-05	unknown
CHGB	-15.62	6.74E-05	unknown
CHIA	-302.39	5.12E-04	enzyme
CKB	-10.69	5.10E-05	kinase
CKMT2	-30.92	3.68E-04	kinase
CLDN1	6.88	8.69E-04	cell adhesion, motility and invasion
CLDN15	2.65	6.68E-04	cell adhesion, motility and invasion
CLDN7	5.92	2.70E-05	cell adhesion, motility and invasion
CLIC6	-16.53	1.15E-04	ion channel
CNFN	76.53	3.29E-04	cell cycle
COL2A1	-41.18	4.93E-04	cell adhesion, motility and invasion
COL4A1	3.59	4.47E-04	cell adhesion, motility and invasion
COL6A3	3.28	3.71E-04	cell adhesion, motility and invasion

CORO1C	1.68	7.32E-04	signal transduction
CPEB3	-1.75	2.78E-04	unknown
CTSF	-3.44	1.34E-05	peptidase
CWH43	-133.53	1.34E-05	unknown
CYB5R1	-2.24	1.44E-06	enzyme
DBF4	3.23	3.31E-04	kinase
DCAF13	2.20	4.57E-04	protein binding
DCLRE1B	1.98	1.21E-04	cell cycle
DDX10	1.74	8.75E-04	enzyme
DGKD	-3.64	2.46E-06	kinase
DMRTA1	-10.65	4.70E-04	transcriptional regulation
DNER	-35.18	1.71E-04	receptor
DNTT	1.49	3.06E-04	enzyme
DTX3L	1.87	6.31E-04	protein binding
DUOX1	-8.88	7.84E-08	enzyme
DUOXA1	-9.20	2.12E-04	transporter
DUSP14	2.43	3.69E-04	phosphatase
DUSP19	-4.05	1.40E-05	phosphatase
E2F3	2.38	4.03E-04	transcriptional regulation
ECHDC3	-12.93	3.41E-04	enzyme
EEF1A2	-21.36	3.13E-05	translation regulator
ELK1	1.89	5.88E-04	transcriptional regulation
ELL2	-2.56	1.10E-05	transcriptional regulation
ENC1	2.57	1.27E-04	peptidase
ENDOD1	1.58	7.82E-04	enzyme
ENPEP	2.70	9.01E-04	peptidase
ENPP5	-8.94	5.64E-04	enzyme
EPCAM	3.28	4.97E-04	cell adhesion, motility and invasion
EPPK1	3.66	1.72E-04	protein binding
ESF1	2.35	1.73E-04	transcriptional regulation
ESRRG	-68.68	4.59E-08	receptor
ETV7	2.46	3.30E-04	transcriptional regulation
EZH2	2.51	3.98E-05	transcriptional regulation
FAM20A	-3.90	3.51E-04	unknown
FAM46C	-4.85	3.67E-04	unknown
FAM72B	46.71	6.82E-05	unknown
FBXL13	-6.24	2.55E-04	enzyme
FCGBP	-11.59	4.89E-07	protein binding
FGD6	2.95	3.32E-04	cell adhesion, motility and invasion
FKBP1A	1.57	7.65E-04	signal transduction
FLJ41603	-3.46	4.65E-04	signal transduction
FOXI2	10.84	9.36E-04	transcriptional regulation
FREM2	-3.08	1.15E-04	cell adhesion, motility and invasion
FUT9	-38.85	2.42E-06	enzyme

GALNT1	1.83	4.46E-04	enzyme
GBGT1	-3.05	9.97E-05	enzyme
GCNT4	-12.51	8.21E-06	enzyme
GHR	-3.82	1.02E-04	receptor
GHRL	-78.41	5.68E-06	growth factor
GIF	-278.81	2.64E-07	transporter
GKN1	-150.77	8.51E-07	transporter
GKN2	-187.09	7.65E-04	unknown
GLA	2.00	8.99E-04	enzyme
GLUL	-3.58	8.92E-05	enzyme
GPER	-18.74	3.23E-04	G-protein coupled receptor
GPN1	1.79	6.86E-04	transcriptional regulator
GPR137B	2.10	7.00E-05	unknown
GPR155	-8.12	5.12E-06	G-protein coupled receptor
GPR3	27.61	1.37E-04	G-protein coupled receptor
GPR44	-12.26	1.13E-04	G-protein coupled receptor
GPR98	-5.58	3.21E-04	G-protein coupled receptor
GPX3	-4.32	5.21E-06	glutamine metabolism
GRIA4	-27.50	1.19E-04	ion channel
GTF2F2	2.39	2.02E-04	transcriptional regulation
GTPBP4	1.77	9.32E-04	enzyme
HAUS2	1.81	3.60E-04	cell cycle
HDC	-12.38	1.17E-06	enzyme
HEATR1	1.90	5.02E-04	protein binding
HIPK1	1.28	4.09E-04	kinase
HPN	-11.96	6.82E-05	peptidase
HRH2	-9.22	7.20E-05	G-protein coupled receptor
HRK	10.46	7.79E-04	apoptosis
HSD17B4	1.05	8.22E-04	enzyme
HSP90AB1	2.02	5.23E-04	protein binding
IFT57	1.35	5.35E-04	apoptosis
IGJ	-28.01	2.06E-05	immune response
IL1RAPL1	-3.87	7.22E-04	receptor
ILDR1	5.22	2.23E-05	receptor
INTS10	1.38	7.37E-04	protein binding
ITGB1	1.96	4.06E-04	receptor
ITGB3BP	1.65	5.12E-04	apoptosis
KCNAB1	-2.84	3.77E-05	ion channel
KCNE2	-127.79	3.32E-04	ion channel
KCNJ15	-20.13	2.95E-04	ion channel
KCNJ16	-92.12	4.83E-07	ion channel
KCNT2	-2.30	7.08E-04	ion channel
KDM1B	2.17	9.44E-04	transcriptional regulation
KDSR	1.63	7.49E-04	enzyme

KIAA2022	-6.51	1.09E-04	nucleic acid metabolism
KLF15	-9.91	2.55E-04	transcriptional regulation
KLHL3	-1.90	2.48E-04	protein binding
KLHL7	1.56	3.38E-04	protein binding
KPNA3	1.85	5.85E-04	transporter
LCLAT1	2.31	5.41E-05	enzyme
LHFPL2	1.74	7.15E-04	enzyme
LIFR	-6.25	1.00E-05	receptor
LIMCH1	-1.76	6.21E-04	cell adhesion, motility and invasion
LIPF	-381.36	2.83E-07	enzyme
LPGAT1	2.32	5.75E-04	lipid metabolism
LRRCC1	1.84	8.95E-04	transporter
LTF	-36.60	2.14E-06	peptidase
LUZP1	1.69	2.96E-04	unknown
LUZP6	1.45	3.76E-04	unknown
MAK16	1.99	5.74E-04	unknown
MAMDC2	-6.91	2.14E-04	protein binding
MAPRE1	1.70	2.04E-04	cell cycle
MARVELD3	4.02	5.82E-04	unknown
MCM8	2.34	3.60E-04	enzyme
MEST	2.99	7.62E-04	peptidase
METTL7A	-4.88	3.57E-05	metabolism
MFSD4	-19.42	3.04E-05	transporter
MICALL1	-2.74	1.29E-04	ion binding
MIPEP	1.71	7.15E-04	peptidase
MKI67IP	2.17	2.99E-05	protein binding
MOCOS	2.35	3.09E-05	enzyme
MPZL1	1.67	5.79E-04	signal transduction
MTCH2	1.90	9.22E-04	transporter
MTPAP	1.59	1.26E-05	transcriptional regulation
MTPN	1.45	3.76E-04	transcriptional regulation
MTSS1	-2.45	7.80E-05	cell adhesion, motility and invasion
MYB	4.56	5.10E-05	transcriptional regulation
MYRIP	-19.75	8.40E-05	protein binding
NAMPT	1.75	5.45E-04	cytokine
NANP	2.29	3.17E-04	enzyme
NAT5	2.00	7.72E-05	enzyme
NCAM1	-6.08	4.54E-04	cell adhesion, motility and invasion
NEDD4	1.56	5.21E-04	enzyme
NFE2L3	3.56	5.25E-05	transcriptional regulation
NOD1	2.06	7.50E-04	apoptosis
NOP58	1.89	6.69E-04	enzyme
NR6A1	34.26	3.90E-04	ligand-dependent nuclear receptor
NTN4	-2.57	3.73E-04	protein binding

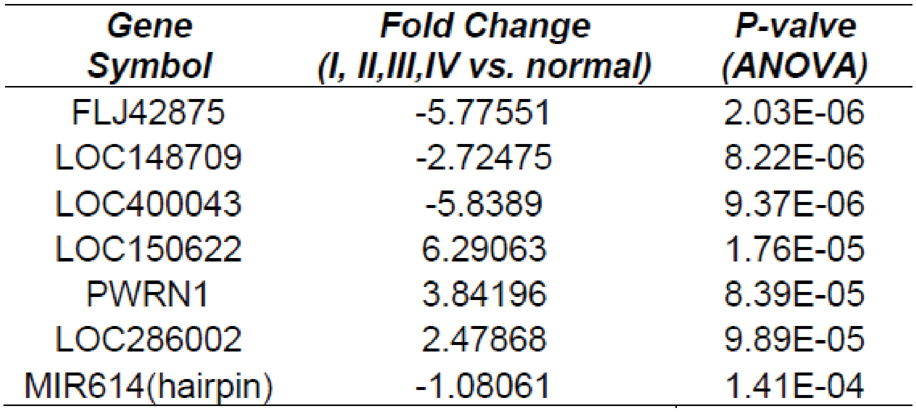
OXCT1	-2.68	4.15E-04	enzyme
PALB2	1.97	1.38E-04	protein binding
PARP14	2.24	4.61E-04	transcriptional regulation
PAWR	1.94	7.62E-04	transcriptional regulation
PAXIP1	1.81	6.89E-04	genome stability
PCDH7	-2.53	6.53E-05	cell adhesion, motility and invasion
PCDHAC2	-2.33	4.44E-04	cell adhesion, motility and invasion
PDILT	-214.19	1.33E-04	differentiation
PGA3	-339.60	3.13E-07	peptidase
PGA5	-593.80	8.06E-07	peptidase
PGC	-165.06	1.81E-07	peptidase
PGM2	1.86	3.65E-04	enzyme
PGM2L1	2.82	3.67E-04	enzyme
PHLDB2	-1.42	7.53E-04	unknown
PICALM	1.47	6.25E-04	transcriptional regulation
PINX1	1.68	4.01E-04	protein binding
PITPNB	1.61	7.59E-06	transporter
PKDCC	5.54	2.84E-06	kinase
PKHD1L1	-6.11	2.75E-04	receptor
PKNOX2	-4.44	8.17E-04	transcriptional regulation
PL-5283	1.62	9.65E-05	unknown
PLCXD3	-18.42	1.71E-04	lipid metabolism
PLEKHA1	2.09	2.24E-04	protein binding
PLEKHG1	2.19	8.05E-05	signal transduction
PLSCR1	2.06	8.79E-04	enzyme
PNO1	2.12	2.77E-04	unknown
PNPLA7	-4.38	7.77E-05	enzyme
POLB	1.54	4.64E-05	enzyme
POLR1C	2.14	1.44E-04	enzyme
PPA1	2.51	1.51E-04	enzyme
PPP1R3C	-4.75	1.52E-06	phosphatase
PRDM5	-2.43	7.33E-04	protein binding
PRICKLE2	-1.48	5.93E-05	ion binding
PRKAA2	-6.71	4.65E-06	kinase
PRKD1	-1.36	7.28E-04	kinase
PRKDC	2.16	1.46E-04	kinase
PRSS22	3.50	8.66E-04	peptidase
PSAPL1	-38.39	1.48E-04	lipid metabolism
PSCA	-69.71	1.84E-06	unknown
PTGER3	-6.07	5.87E-05	G-protein coupled receptor
PTPN12	2.25	2.79E-04	phosphatase
PTPRS	-3.05	8.34E-04	phosphatase
PUS7	2.78	9.28E-06	unknown
PVRL1	2.83	7.51E-04	cell adhesion, motility and invasion

QTRTD1	1.80	3.44E-04	unknown
RAB6B	-2.27	6.45E-04	enzyme
RAI14	2.30	3.58E-04	transcriptional regulation
RAP2A	2.24	4.71E-05	enzyme
RASAL2	2.56	1.18E-04	signal transduction
RBBP9	2.01	8.27E-04	cell cycle
RBL1	1.98	3.89E-05	cell cycle
RBPMS2	-3.56	1.62E-04	unknown
RCN1	3.19	3.21E-04	unknown
RELL1	-1.97	7.24E-04	unknown
REP15	-10.79	1.17E-05	unknown
RGPD2	13.66	4.32E-04	unknown
RHEB	1.65	6.66E-05	enzyme
RICH2	1.18	4.85E-04	unknown
RNASE1	-4.37	2.58E-04	enzyme
RNF148	2.99	9.51E-04	enzyme
RPF2	2.57	2.94E-04	protein binding
RSU1	1.45	1.94E-04	signal transduction
RTKN2	3.55	5.00E-05	signal transduction
SCGN	-20.60	1.94E-04	unknown
SCN2A	-1.81	1.36E-05	ion channel
SCN3A	-4.62	8.81E-04	ion channel
SCNN1G	-29.91	6.49E-04	ion channel
SCUBE2	-5.93	5.41E-04	unknown
SELI	1.76	2.35E-04	unknown
SERPINA4	-16.50	8.72E-06	cell adhesion, motility and invasion
SFRS13A	1.54	6.22E-04	binding
SH3GL2	-105.09	2.44E-05	enzyme
SIGLEC11	-12.17	6.76E-04	cell adhesion, motility and invasion
SLC16A7	-7.52	3.15E-06	transporter
SLC1A2	-15.27	1.40E-06	transporter
SLC26A5	-9.18	4.94E-05	transporter
SLC26A7	-14.88	1.23E-04	transporter
SLC26A9	-17.90	7.27E-06	transporter
SLC28A2	-41.28	1.23E-04	transporter
SLC5A5	-123.80	2.19E-04	transporter
SLC7A2	-1.81	3.15E-04	transporter
SLC9A4	-54.65	3.36E-06	transporter
SMC6	1.78	2.94E-04	DNA repair
SMG1	1.58	9.28E-04	kinase
SNX32	4.89	2.57E-04	protein binding
SNX5	1.65	1.78E-05	transporter
SOX2	-14.51	4.92E-04	transcriptional regulation
SPINK2	-188.53	2.73E-06	unknown

SRD5A1	2.24	2.27E-04	enzyme
SRPK1	2.30	1.26E-04	kinase
SST	-450.60	4.79E-05	signal transduction
STAM	1.04	6.12E-04	signal transduction
STX12	-1.71	1.36E-04	transporter
STX6	1.72	1.45E-04	transporter
SUGT1	1.66	8.62E-04	cell cycle
SULT2A1	-144.17	2.50E-04	enzyme
SVIL	2.26	7.12E-04	cell adhesion, motility and invasion
T PR	1.95	7.71E-04	protein binding
TASP1	-1.51	1.41E-04	peptidase
TBC1D14	-1.82	2.90E-04	signal transduction
TBC1D9	-21.85	4.77E-04	signal transduction
TFF1	-33.54	8.84E-04	growth factor
TFF2	1.70	8.73E-04	growth factor
TH1L	3.36	5.00E-05	transcriptional regulation
THY1	-10.23	1.40E-05	angiogenesis
TMED6	1.82	4.22E-04	transporter
TMEM202	-2.62	2.68E-04	unknown
TMEM37	2.24	6.02E-04	ion channel
TNFRSF10A	-5.64	6.63E-05	receptor
TPD52L1	1.94	7.13E-04	apoptosis
TPK1	1.75	9.07E-04	kinase
TRIM15	4.63	4.44E-04	protein binding
TRIM37	1.65	4.05E-04	unknown
TRIM50	-126.48	8.18E-04	protein binding
TRMT6	2.06	1.00E-04	transcriptional regulation
TSC22D3	-2.65	8.66E-04	transcriptional regulation
TTF2	1.96	2.04E-04	transcriptional regulation
TTLL7	-2.41	1.30E-04	differentiation
TTR	-26.58	2.93E-04	transporter
TUBB6	1.82	5.96E-04	cell adhesion, motility and invasion
UACA	2.03	4.39E-04	apoptosis
UBE2D1	1.89	6.25E-05	enzyme
UMPS	1.79	9.42E-04	enzyme
USP31	2.04	3.50E-05	peptidase
VSIG2	-11.40	1.61E-04	unknown
WASF3	-3.57	3.31E-04	protein binding
WDR43	2.07	1.92E-05	unknown
WIPF3	-5.20	1.07E-04	differentiation
XRN2	1.77	3.24E-04	enzyme
XYLT2	-4.02	4.44E-07	enzyme
YEATS2	1.86	5.47E-04	transcriptional regulation
YME1L1	1.49	4.07E-04	peptidase

ZFP1	1.21	6.82E-04	transcriptional regulation
ZNF280C	2.01	2.11E-04	transcriptional regulation
ZNF300	1.06	3.29E-04	transcriptional regulation
ZNF343	1.67	4.53E-04	transcriptional regulation
ZNF385B	-9.48	1.95E-04	unknown
ZNF536	-8.33	6.89E-04	transcriptional regulation
ZNF662	-2.66	9.39E-04	transcriptional regulation
ZNHIT6	1.75	4.34E-04	protein binding
ZNRF2	1.59	3.16E-04	unknown

(B) List of 7 differentially expressed long non-coding genes related to gastric cancer



Gene Symbol	***Fold Change (I, II,III,IV vs. normal)***	***P-valve (ANOVA)***
FLJ42875	-5.77551	2.03E-06
LOC148709	-2.72475	8.22E-06
LOC400043	-5.8389	9.37E-06
LOC150622	6.29063	1.76E-05
PWRN1	3.84196	8.39E-05
LOC286002	2.47868	9.89E-05
MIR614(hairpin)	-1.08061	1.41E-04

Supplementary Table 3. List of recurrent somatic mutation candidates in gastric cancer.

Chromosome	Position	Gene	Reference allele	Mutant allele	Mutation type
chr1	899383	KLHL17	C	T	NON_SYNONYMOUS_CODING
chr12	25398284	KRAS	C	T	NON_SYNONYMOUS_CODING
chr14	102900821	TECPR2	T	C	NON_SYNONYMOUS_CODING
chr16	66976553	CES2	T	C	NON_SYNONYMOUS_CODING
chr17	7578406	TP53	C	T	NON_SYNONYMOUS_CODING
chr17	7578406	TP53	C	T	NON_SYNONYMOUS_CODING
chr17	4713000	PLD2	G	A	NON_SYNONYMOUS_CODING
chr17	7577548	TP53	C	T	NON_SYNONYMOUS_CODING
chr17	7577539	TP53	G	A	NON_SYNONYMOUS_CODING
chr20	3028405	MRPS26	C	T	STOP_GAINED
chr3	172115078	FNDC3B	G	A	NON_SYNONYMOUS_CODING
chr3	45817323	SLC6A20	G	A	NON_SYNONYMOUS_CODING
chr6	33287277	DAXX	A	G	NON_SYNONYMOUS_CODING
chr9	118997676	PAPPA	A	G	NON_SYNONYMOUS_CODING

Supplementary Table 4. List of recurrent somatic mutation candidates in the COSMIC database.

Chromosome	Position	Gene	Reference allele	Mutant allele	Mutation type
chr12	9230420	A2M	T	G	Missense
chr17	79104885	AATK	T	C	Missense
chr17	76198669	AFMID	G	A	Missense
chr11	62294430	AHNAK	T	C	Missense
chr2	97817670	ANKRD36	A	G	Missense
chr11	108159732	ATM	C	T	Missense
chr1	169080710	ATP1B1	C	T	Missense
chr11	102248328	BIRC2	A	G	Missense
chr7	140481393	BRAF	T	G	Missense
chr6	121638666	C6orf170	G	A	Missense
chr1	1650797	CDC2L2	A	G	Missense
chr8	95158276	CDH17	G	A	Missense
chr16	55907868	CES5A	A	G	Missense
chr20	40084604	CHD6	T	C	Missense
chr13	111156500	COL4A2	C	T	Missense
chr19	1979811	CSNK1G2	A	G	Missense
chr6	348155	DUSP22	G	A	Missense
chr6	127635972	ECHDC1	T	A	Missense
chr17	37881332	ERBB2	G	A	Missense
chr1	46871457	FAAH	A	G	Missense
chr4	126408710	FAT4	A	G	Missense
chr6	146125581	FBXO30	C	T	Missense
chr5	180057711	FLT4	G	A	Nonsense
chr6	41557797	FOXP4	G	A	Missense
chr19	18497024	GDF15	G	C	Missense
chr16	74499607	GLG1	G	C	Nonsense
chr3	37370579	GOLGA4	C	T	Missense
chr13	94680032	GPC6	G	T	Missense
chr7	126173251	GRM8	G	A	Missense
chr4	89314721	HERC6	C	T	Missense
chr21	38309619	HLCS	C	A	Missense
chr15	77771649	HMG20A	G	A	Missense
chr5	35874575	IL7R	C	T	Missense
chr1	145536012	ITGA10	G	A	Missense
chr14	105615648	JAG2	C	T	Missense
chr4	55599321	KIT	A	T	Missense
chr12	25398284	KRAS	C	T	Missense
chr12	25378561	KRAS	G	A	Missense
chr1	27684715	MAP3K6	G	T	Missense
chr17	19285381	MAPK7	C	T	Missense
chr5	179707528	MAPK9	T	C	Missense
chr7	116340262	MET	A	G	Missense
chr16	58079165	MMP15	G	A	Missense
chr22	31330769	MORC2	G	A	Missense
chr7	100608884	MUC3B	G	A	Missense
chr11	1017069	MUC6	G	A	Missense
chr16	88724353	MVD	G	A	Nonsense
chr1	198201732	NEK7	A	C	Missense
chr16	47117173	NETO2	G	A	Nonsense

chr9	139399321	NOTCH1	G	T	Missense
chr1	120611964	NOTCH2	G	C	Missense
chr1	26303245	PAFAH2	C	T	Missense
chr14	24572812	PCK2	G	A	Missense
chr7	11076699	PHF14	T	C	Missense
chr4	527677	PIGG	T	C	Missense
chr19	282754	PPAP2C	C	T	Missense
chr22	22899234	PRAME	A	G	Missense
chr20	62191410	PRIC285	T	C	Missense
chr7	142460335	PRSS1	A	G	Missense
chr2	113950108	PSD4	C	T	Missense
chr11	244115	PSMD13	G	A	Missense
chr9	98239899	PTCH1	G	A	Missense
chr4	87690998	PTPN13	A	G	Missense
chr7	157874041	PTPRN2	C	T	Missense
chr2	1668790	PXDN	C	T	Missense
chr12	48142680	RAPGEF3	T	C	Missense
chr5	86668002	RASA1	G	A	Missense
chr21	36206763	RUNX1	C	T	Missense
chr6	166739646	SFT2D1	T	C	Missense
chr20	61596965	SLC17A9	A	G	Missense
chr17	18220202	SMCR8	A	G	Missense
chr17	1684605	SMYD4	G	T	Missense
chr2	220356957	SPEG	C	T	Nonsense
chr17	4391169	SPNS3	G	A	Missense
chr17	27011891	SUPT6H	A	G	Missense
chr6	152665261	SYNE1	C	A	Missense
chr12	11150054	TAS2R20	C	T	Missense
chr3	30732970	TGFBR2	G	A	Missense
chr6	138196841	TNFAIP3	G	A	Nonsense
chr7	47317781	TNS3	T	C	Missense
chr17	7579882	TP53	C	G	Missense
chr17	7578406	TP53	C	T	Missense
chr17	7577548	TP53	C	T	Missense
chr17	7577124	TP53	C	T	Missense
chr17	7577539	TP53	G	A	Missense
chr17	7578271	TP53	T	A	Missense
chr17	7577120	TP53	C	T	Missense
chr15	43720335	TP53BP1	G	A	Missense
chr15	74743861	UBL7	C	T	Missense
chr16	88665106	ZC3H18	C	T	Missense
chr5	833915	ZDHHC11	G	T	Missense
chr19	57328017	ZIM2	C	T	Missense

Supplementary Table 5. List of differentially expressed miRNAs related to gastric cancer

miRNA	*P*-Value	Fold Change
hsa-miR-551b	2.91E-06	-6.0
hsa-miR-204	1.01E-05	-21.4
hsa-miR-196b	4.05E-05	41.4
*hsa-miR-29c	9.15E-05	-3.9
hsa-miR-628-5p	1.15E-04	-1.8
hsa-miR-193b	1.82E-04	-2.8
hsa-miR-196a	2.14E-04	7.6
*hsa-miR-135b	3.31E-04	11.4
hsa-miR-548d-3p	8.49E-04	14.6
*hsa-miR-21	1.28E-03	1.7
hsa-miR-195	1.49E-03	-2.7
hsa-miR-145	2.14E-03	-1.7
hsa-miR-490	2.35E-03	-51.5
*hsa-miR-29b	2.52E-03	-2.1
*hsa-miR-93	2.59E-03	1.9
hsa-miR-1226	3.66E-03	2.1
hsa-miR-129-3p	3.92E-03	-10.0
hsa-miR-874	4.02E-03	-3.5
*hsa-miR-135a	5.42E-03	-4.6
hsa-miR-1	6.13E-03	-3.2
hsa-miR-193a-3p	7.46E-03	-2.1
hsa-miR-1973	8.78E-03	42.6
hsa-miR-20b	9.06E-03	-3.8
hsa-miR-140-3p	9.08E-03	-2.0
hsa-miR-1271	1.01E-02	-2.0
*hsa-miR-19a	1.08E-02	2.7

* Seven miRNAs identified in the present study of Asian gastric tumors consistent with the findings of Ueda et al. (2010) based on Japanese gastric tumors.