

Supplementary material

Identification of Function Genes regulating Gastric Cancer progression using Integrated Bioinformatics Analysis

Supplementary Table 1 All 251 commonly differentially expressed genes (DEGs) were detected from three profile datasets, including 187 down-regulated genes and 64 up-regulated genes in the Gastric cancer tissues and normal gastric tissues.

DEGs	Genes Name
Up-regulated	<i>IGF2BP3 CCNB1 LOC100129518///SOD2 COL1A1 BIRC5 ADAMTS2 KLHL7 KIF14 MAD2L1 BICD1 SPP1 FAM72A///FAM72D///FAM72B///FAM72C NDC80 CCNA2 NUF2 UBE2T TEAD4 ECT2 CDH3 MTFR2 PRC1 LRP8 CEP55 CEMIP DDIAS S100A2 WISP1 AJUBA CLDN1 APOC1 NEK2 ESM1 PLAU DEPDC1B HMGB3 CXCL8 IL13RA2 HOXA10 KIF2C CDCA7 BUB1 TRIP13 DUXAP10 LOC101928195///LOC100996643///MTHFD1L TMEM158 ASPM INHBA ATAD2 KNL1 STIL UBE2C ULBP2 TOP2A WDR72 DTL MEST KIF20A COL10A1 PMEPA1 HOXC6 CTHRC1 CDKN3 LINC01296///DUXAP10 CENPF</i>
Down-regulated	<i>BTG2 ATP5F1 PDE1C MAOA ZNF385B PWP2 ALAD ACADL PIR-FIGF///FIGF ZBTB20 HDHD2 NTN4 SERP1 SYNJ2BP-COX16///SYNJ2BP PPID SCNN1B KLHDC2 ADCYAP1R1 UBE2QL1 FAM13A ADHFE1 SLC25A4 LOC100506870///LOC283140 MYOC GIF SYNE1 GNG7 VSTM2A ZSCAN31 PRDM5 EFCC1 STAM2 TLE4 SH3GL2 CKMT2 BBIP1 KCNJ16 SLC26A7 ADAMTSL1 KIAA2022 PCBP1- AS1 FAHD2CP SLC16A7 FMO4 PGRMC2 ATP4 ACD36 FGD4 MAL AQP4 ESRRG LYRM5 CPA2 ABCA8 EFCAB14 DBT SLC1A2</i>

TPCN2 TCEB3 USP53 ARRDC4 TMEM100 CREBL2 SPINK2
 CNTN3 PRDM11 ETNPPL RGS5 LOC101927263 PACRG RCCD1
 UBL3 CYB5R1 LINC01105 ADGRL3 ATP4B TMEM116 SMIM14
 6-Mar ZNF626 LOC728730 ENPP6 CIRBP ECHDC2 GPX3
 KCNMB2 THSD4 HDC MTERF2 SAR1B TRIM50 FAM214A MITF
 TRIM74//TRIM73 RNF14 CLTA IGH KL BDH2 APOBEC2 DGKD
 RPS6KA6 MFSD4A ALDH6A1 PHYKPL NEDD4L PDGFD KIT
 GCNT2 MIR29C//MIR29B2 SIK2 DMXL1 CWH43
 PGA4//PGA3//PGA5 PDK4 GFRA2 TRIP11 HACD1 GPR155
 NR3C2 MUT UMAD1 OPCML LOC100505501 PLIN5 RNASE1
 MYZAP SMIM5 PLPP3 ACACB GRIA4 BAALC RPRM CYFIP2
 FBXL13 SPC24 YIF1B RGMB SMDT1 FBP2 FAM150B CADM2
 LINC00849//SLC25A16 MAGI3 CHGA WIPF3 TOM1L2 VAPA
 RAB11B-AS1 ADH7 ASPA PDILT C14orf159 TXNL1 LINC00982
 CCKBR ADRB2 GRIA3 NTRK3 SLC7A8 SCARA5 ACADSB
 CPEB2 SLC2A12 LIFR STX12 FNDC5 PCAT18 HADH 2-Mar
 GSTA3 SIDT2 CHIA ZEB2 METTL7A KCNE2 RAB27A TAPT1
 LOC101926959 SIGLEC11 LOC101929219//C1orf186 DNER GAB1
 C21orf58 KAT6B DYX1C1-CCPG1//CCPG1

Supplementary Table 2 Gene ontology analysis of differentially expressed genes in GC

Expres sion	Category	Term	Co un t	%	p- Valu e	FDR
UP-	GOTERM_B	GO:0051301~cell division	14	14.	1.2E-	1.74
	P_DIRECT			2	10	E-07
regula ted	GOTERM_B	GO:0007067~mitotic	11	11.	9.7E-	1.4 E-
	P_DIRECT	nuclear division		16	09	05
	GOTERM_B	GO:0007062~sister	8	8.1	5.5E-	7.93
	P_DIRECT	chromatid cohesion			08	E-05

GOTERM_B	GO:0007059~chromosome	5	5	8.3E-	0.119
P_DIRECT	segregation			05	83
GOTERM_B	GO:0007080~mitotic	4	4	2.7E-	0.384
P_DIRECT	metaphase plate congression			04	43
GOTERM_B	GO:0000910~cytokinesis	4	4	5.8 E-	0.831
P_DIRECT				04	662
GOTERM_C	GO:0030496~midbody	9	9.1	6.26E-	7.16
C_DIRECT			3	09	E-06
GOTERM_C	GO:0000777~condensed	8	8.1	9.6 E-	1.10E
C_DIRECT	chromosome kinetochore		2	09	-05
GOTERM_C	GO:0000776~kinetochore	6	6.0	5.35E-	0.006
C_DIRECT			9	06	12
GOTERM_C	GO:0000775~chromosome	5	5.0	3.00E-	0.034
C_DIRECT	, centromeric region		7	05	353
GOTERM_C	GO:0000942~condensed	3	3.0	5.74E-	0.065
C_DIRECT	nuclear chromosome outer kinetochore		4	05	715
GOTERM_C	GO:0000922~spindle pole	5	5.0	3.75E-	0.428
C_DIRECT			7	05	069
GOTERM_M	GO:0042802~identical	10	10.	6.46E-	0.747
F_DIRECT	protein binding		15	04	165
GOTERM_M	GO:0005515~protein	41	41.	0.001	1.596
F_DIRECT	binding		60	39	840
GOTERM_M	GO:0016887~ATPase	4	4.0	0.022	22.56
F_DIRECT	activity		6	18	086
GOTERM_M	GO:0004842~ubiquitin-	5	5.0	0,028	22.92
F_DIRECT	protein transferase activity		7	01	955
GOTERM_M	GO:0003777~microtubule	3	3.0	0.030	28.10
F_DIRECT	motor activity		4	28	169

Down	GOTERM_B	GO:0034220~ion	8	3.0	0.002	3.701
-	P_DIRECT	transmembrane transport	4	43		22
regula	GOTERM_B	GO:0006635~fatty acid	4	1.5	0.006	9.731
ted	P_DIRECT	beta-oxidation	2	57		282
	GOTERM_B	GO:0009083~branched-	3	1.1	0.011	16.64
	P_DIRECT	chain amino acid catabolic process	4	65		097
	GOTERM_B	GO:0030318~melanocyte	3	1.1	0.012	18.22
	P_DIRECT	differentiation	4	87		66
	GOTERM_B	GO:0008152~metabolic	6	2.2	0.015	21.83
	P_DIRECT	process	8	74		896
	GOTERM_B	GO:0032762~mast cell	2	0.7	0.017	23.75
	P_DIRECT	cytokine production	6	31		48
	GOTERM_C	GO:0005759~mitochondri	12	4.5	1.14E-	0.139
	C_DIRECT	al matrix	6	04		087
	GOTERM_C	GO:0005739~mitochondri	22	8.3	0.004	5.251
	C_DIRECT	on	6	42		997
	GOTERM_C	GO:0005887~integral	22	8.3	0.008	10.12
	C_DIRECT	component of plasma membrane	6	73		515
	GOTERM_C	GO:0043235~receptor	5	1.9	0.023	24.90
	C_DIRECT	complex		25		296
	GOTERM_C	GO:0005886~plasma	47	17.	0.024	26.00
	C_DIRECT	membrane	9	44		801
	GOTERM_C	GO:0070062~extracellular	34	12.	0.031	32.1
	C_DIRECT	exosome	9	32		178
	GOTERM_M	GO:0015459~potassium	4	0.4	0.004	6.175
	F_DIRECT	channel regulator activity	7	676		478
	GOTERM_M	GO:0005496~steroid	3	2.1	0.021	25.87
	F_DIRECT	binding	7	778		697
	GOTERM_M	GO:0008900~hydrogen:po	2	2.5	0.025	29.32

F_DIRECT	tassium-exchanging ATPase activity	2	2	705	
GOTERM_M	GO:0000062~fatty-acyl-	3	2.6	0.026	30.64
F_DIRECT	CoA binding	5	548	53	
GOTERM_M	GO:0004971~AMPA	4	3	0.033	37.04
F_DIRECT	glutamate receptor activity			459	963

Supplementary Table 3 The prognostic information of the 26 key candidate genes

Category	Genes
Genes with significantly worse survival (P < 0.05)	<i>ASPM ATAD2 BIRC5 BUB1 CASC5 CCNA2 CCNB1 CDKN3 CENPF CEP55 DEPDC1B DTL ECT2 KIF14 MAD2L1 NDC80 NEK2 NUF2 PRC1 STIL TOP2A TRIP13 UBE2C UBE2T</i>
Genes with significantly worse survival (P > 0.05)	<i>RAB6KIFL KIF2C</i>

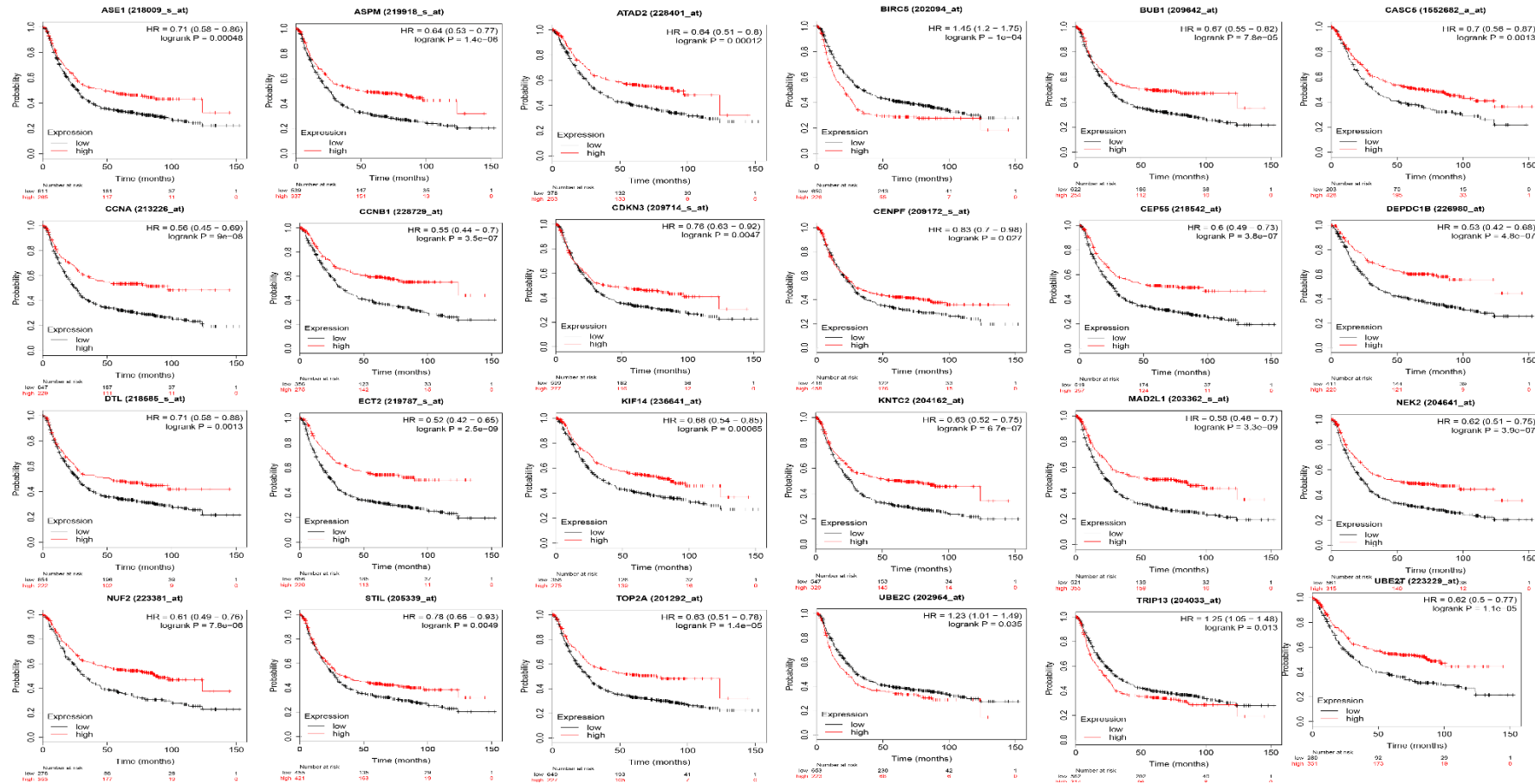
Supplementary Table 4 Validation of 22 genes via GEPIA

Category	Genes
Genes with high expressed in GC (P < 0.05)	<i>ASPM ATAD BUB1 BIRC5 CCNA2 CCBB1 CDKN3 CENPF CEP55 DEPDC1B DTL ECT2 KIF14 MAD2L1 NDC80 NEK2 NUF2 STIL TOP2A TRIP13 UBE2C UBE2T</i>
Genes without high expressed in OC (P > 0.05)	<i>CASC5 PRC1 5</i>

Supplementary Table 5 Pathway Enrichment Analysis of Common Genes
Function in Gastric Cancer

Pathway ID	Name	Count	%	p-value	Genes
hsa04914	Progesterone-mediated oocyte maturation	4	6,67	0.001636	<i>CCNB1, MAD2L1, BUB1, CCNA2</i>
hsa04110	Cell cycle	4	6.67	0.0044859	<i>CCNB1, MAD2L1, BUB1, CCNA2</i>
hsa04114	Oocyte meiosis	3	5	0.0369046	<i>CCNB1, MAD2L1, BUB1</i>
hsa05161	Hepatitis B	3	5	0.0597128	<i>CCNA2, CXCL8, BIRC5</i>
hsa04390	Hippo signaling pathway	3	5	0.0641468	<i>TEAD4, BIRC5, AJUBA</i>
hsa05202	Transcriptional misregulation in cancer	3	5	0.0765009	<i>HOXA10, CXCL8, PLAU</i>

Supplementary Figure 1 The prognostic information of the 24 core genes. Kaplan meier plotter online tools were used to identify the prognostic information of the 26 core genes and 24 of 26 genes had a significantly worse survival rate ($P < 0.05$).



Supplementary Figure 2 Significantly expressed 24 genes in GC cancer patients compared to healthy people.

