

Supplementary Figure legends

Figure S1 (A) qRT-PCR analysis was used to verify the results of RNA-seq by investigating the expression of 15 genes (random selected) in gastric cancer and paratumor tissues. **(B)** Correlation of qRT-PCR detection and the indicated genes from RNA-Seq in gastric cancer. **(C)** ZFP64 mRNA expression in 408 gastric cancer specimens and 211 normal specimens from TCGA database.

Figure S2 (A) The indicated GC cell lines were treated with nab-paclitaxel for 72 hours, and the dose-response curves were shown according to different concentration. **(B)** Apoptosis rate of different groups. **(C)** qRT-PCR analysis of indicated genes in ZFP64-overexpressive HGC-27 cells and control cells. **(D)** Correlation of qRT-PCR detection and the indicated genes from RNA-Seq in ZFP64-overexpressive HGC-27 cells.

Figure S3 (A-D) ZFP64 and vector-transfected HGC27 and MGC-803 cells were treated with 5-Fu, Cisplatin, Oxaliplatin or Irinotecan for 72h. Cell viability was quantified by CCK8 assay and IC50 values were calculated. Data represent means $\pm$ SEM. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.005$.

Figure S4 (A-B) Pie graphs showing the distribution of chromatin occupancy peak location. **(C)** Luciferase reporter assay revealed the luciferase activity of wild and mutant GAL1 promoter by up-regulation of ZFP64. Data represent means $\pm$ SEM. **** $P < 0.001$, ns, nonsignificant.

Figure S5 (A) ZFP64 mRNA expression in subcutaneous xenograft tumors. **(B)** Representative images of orthotopic tumor model. Data represent means $\pm$ SEM. *** $P < 0.005$

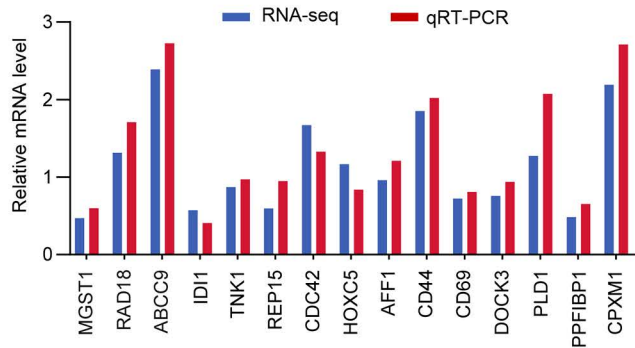
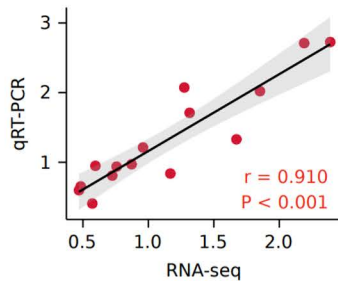
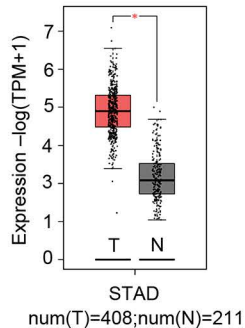
A**B****C**

Figure S1

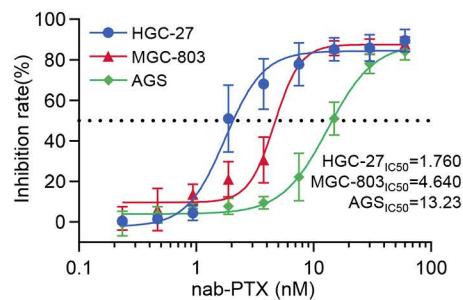
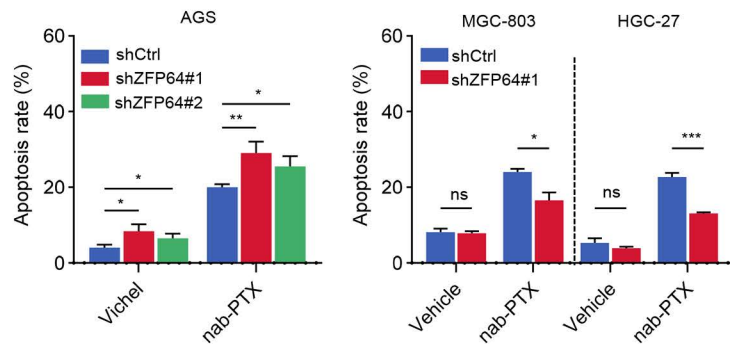
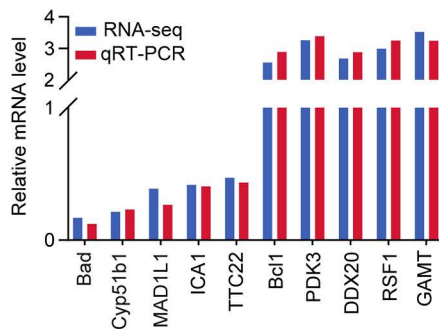
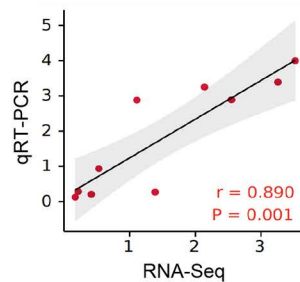
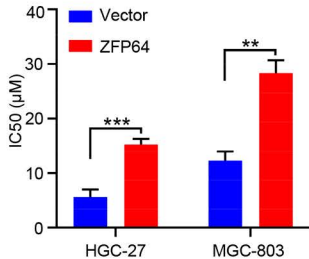
A**B****C****D**

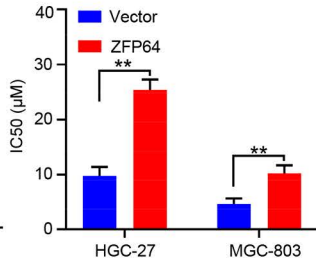
Figure S2

A

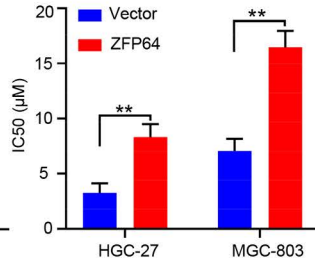
5-FU

**B**

Cisplatin

**C**

Oxaliplatin

**D**

Irinotecan

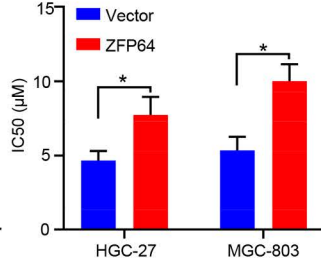


Figure S3

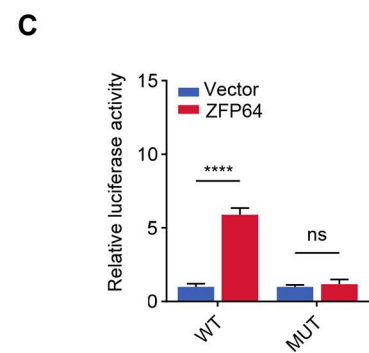
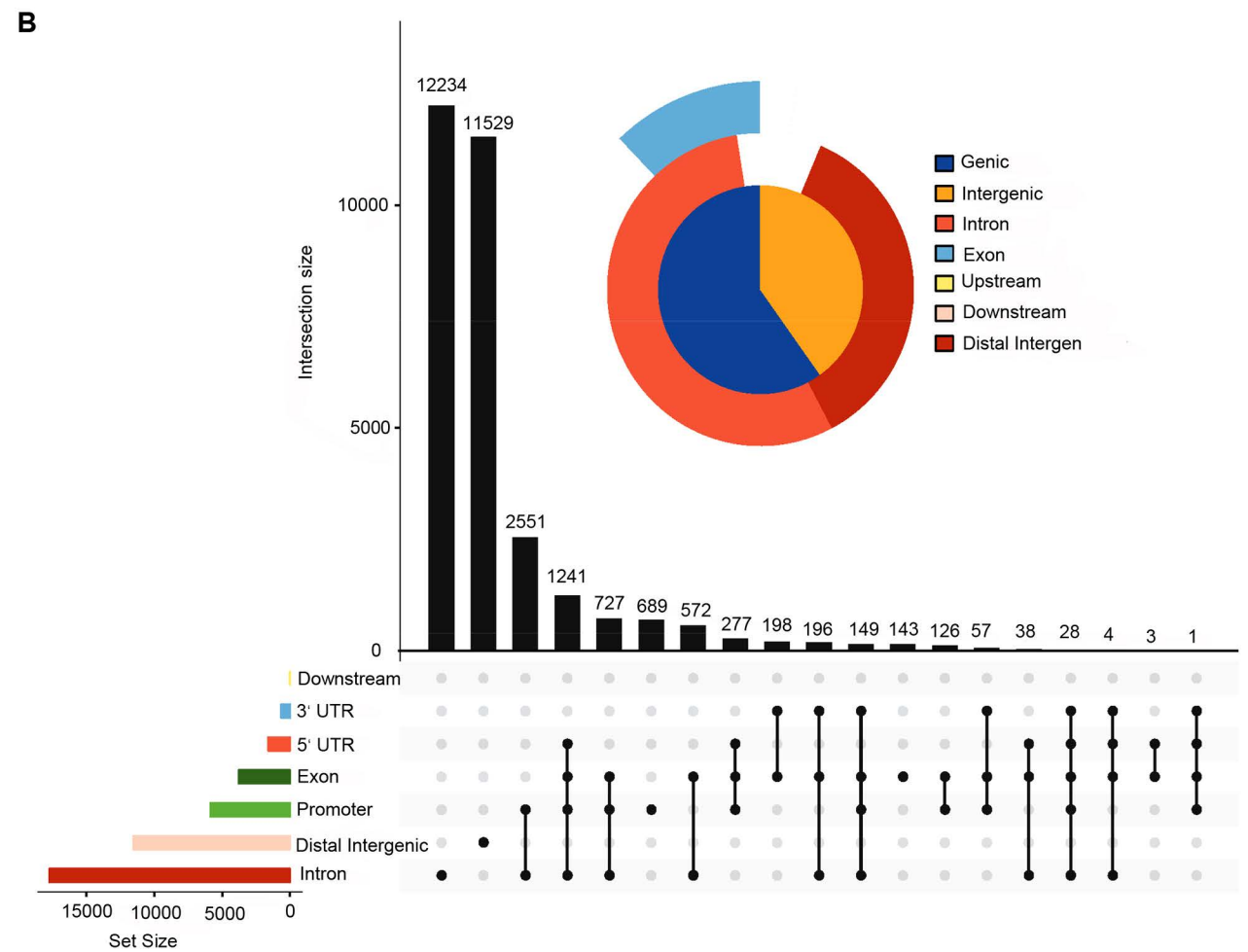
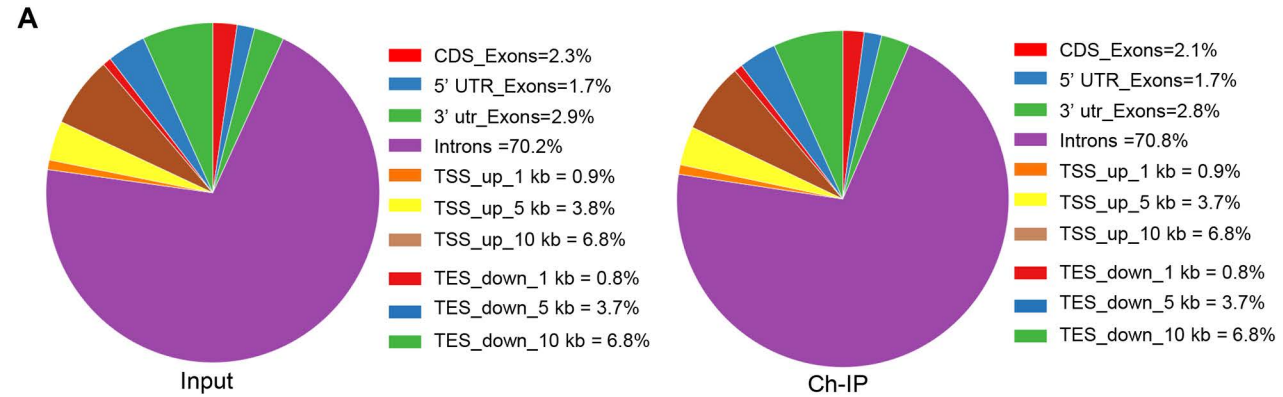


Figure S4

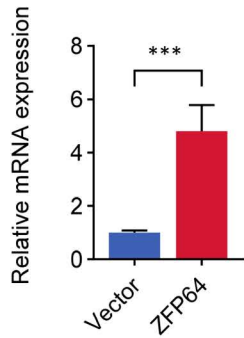
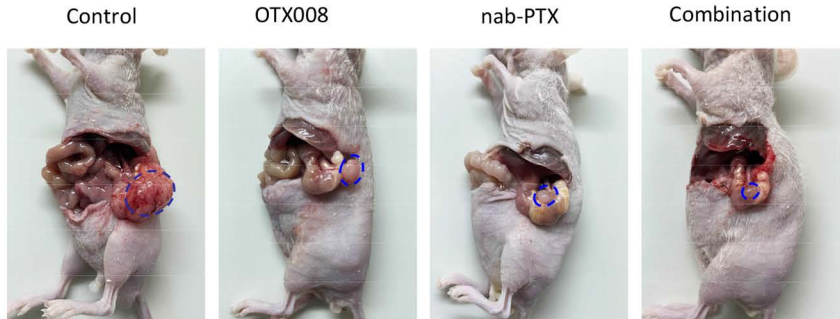
A**B**

Figure S5

Table S1. List of primary antibodies used in the study.

Antibody	Applications	Company
ZFP64	IP, WB	Abcam (ab117787)
ZFP64	IF, IHC	Abcam (ab204610)
Galectin 1	F, IHC, WB	Abcam (ab138513)
Vimentin	F, IF, IHC, WB	Abcam (ab8978)
E-Cadherin	F, IHC, WB	Abcam (ab231303)
ERK1/2	WB, IHC, IF, F	CST (4696)
p-ERK1/2	WB, IF, IHC, IP	CST (4370)
ALDH1A1	WB, IP, IHC, IF, ELISA	Proteintech (15910-1-AP)
LGR6	WB, IHC, F, ELISA	Proteintech (17658-1-AP)
AKT	WB, IP, IHC, IF, F, ChIP	CST (4685)
p-AKT	WB, IP, IF, IHC	CST (4060)
CD8	WB, IHC, IF	Abcam (ab93278)
CD44	WB, IP, IF, F	CST (5640)
CD44	F	eBioscience (17-0441-83)
IgG	WB, IHC, IP, CHIP, F	Abcam (ab172730)
GAPDH	WB, IP, IF	Proteintech (60004-1-Ig)

Abbreviations: WB, western blot; IHC, immunohistochemistry; IF, immunofluorescence; IP, immunoprecipitation; ELISA, enzyme-linked immunosorbent assay; FCA, flow cytometric analysis; CHIP, Chromatin Immunoprecipitation.

Table S2. Primers of genes used in the study.

Genes	Forward Sequence (5' -> 3')	Reverse Sequence (5' -> 3')
ZFP64	AGGTTGCCAATTCAAGACTGC	CACCGCATGTGAGTTTTTCAGC
GAL-1	CTGTGCCTGCACTTCAACC	CATCTGGCAGCTTGACGGT
MGST1	ATTGGCCTCCTGTATTCCTTGA	GTGCTCCGACAAATAGTCTGAAG
RAD18	GAGCCGGATCTGAAAAATAACCG	GCTGGTGACTCTAAAGCAAACCTG
ABCC9	TTACATTCGCTCTCCTGTTTGTG	GGTGGAGGTGCCTTGATTCC
IDI1	AACACTAACCACCTCGACAAGC	AGACACTAAAAGCTCGATGCAA
TNK1	TGAAAAGGCTACGTTCTGGGC	ACCCTCTGGGATCAGACACTT
REP15	AAGAAAAGGGAGTTGATGAGTGG	TTCTGGATTGGAAAGGTCACAAG
HOXC5	CTAAGAGCAGTGGGGAGATCA	GTCATCCACGGGTAAATCTGTG
CDC42	GTCATCCACGGGTAAATCTGTG	CCATCGGAATATGTACCGACTG
CD69	ATTGTCCAGGCCAATACACATT	CCTCTCTACCTGCGTATCGTTTT
AFF1	GCCAAGTCTCCATGCCAAAAG	CTTGTGATGACTAGAGCCGAAC
CD44	CTGCCGCTTTGCAGGTGTA	CATTGTGGGCAAGGTGCTATT
DOCK3	ACAAGAATGGGCAAGTTTGTGG	TCATCACATGGCGTAGTTTGTAG
PLD1	CCCAGCGATCCCAAGATACAA	GACAGCCGGAGAGATACGTCT
PPFIBP1	ACAAGTGTTCCTGGAAGAGTTCC	CACAGTTGGGTATCAACAGTGG
CPXM1	GGCGATCTATATGATGGAGCCT	CCTGTGTGATAACACCCGAGAA
Bad	CCCAGAGTTTGAGCCGAGTG	CCCATCCCTTCGTGCTCCT
CYP51A1	GAAACGCAGACAGTCTCAAGA	ACGCCCATCCTTGTATGTAGC

ICA1	CTTCGATCCCAAGGTTTCCAA	TCGACACAAAGGATTCGTAAGG
TTC22	GCAGTTGAACTTCGAGCCG	TCCTCCAGGTAGAATGCGAAA
Bcl1	GCTGCGAAGTGGAACCATC	CCTCCTTCTGCACACATTTGAA
PDK3	CGCTCTCCATCAAACAATTCCT	CCACTGAAGGGCGGTAAAGTA
DDX20	GCTGCGGGCTCGATTTAATTG	GTCCAAAGCTATGGTGGAGAAC
RSF1	GGATGCCGATACTATGCGTCT	GCCAACTCGTTTCGATTTCTGA
GAMT	CGCCCATTGATGAGCATTGG	GGCCTTTCAAGGGGATGACC
MAD1L1	TGGACTGGATATTTCTACCTCGG	CCTCACGCTCGTAGTTCCTG
LGR6	TGGGGAACCCTCTGCTACAG	CAGGTACTGGAATGCCGATCT
ALDH1A1	GCACGCCAGACTTACCTGTC	CCTCCTCAGTTGCAGGATTAAAG
GAPDH	CTGGGCTACACTGAGCACC	AAGTGGTCGTTGAGGGCAATG

Table S3. The correlation between ZFP64 and clinicopathologic features in 420 GC Patients.

Variable	Number of Patients		p-value*
	ZFP64 ^{low}	ZFP64 ^{high}	
	(N=240)	(N=180)	
Age			
<55	89	58	0.352
≥55	151	122	
Gender			
Female	112	67	0.058
Male	128	113	
Lauren's type			
Intestinal type	124	99	0.553
Non-intestinal type	116	81	
Lymph node metastasis			
Negative	87	24	P<0.001
Positive	153	156	
pTNM stage			
I-III	122	45	P<0.001
IV	188	135	
Cancer thrombus in vessel			
Negative	163	88	P<0.001
Positive	77	92	

Note: A Chi-square test was used for comparing groups between low and high ZFP64 expression.

* $P < 0.05$ was regarded as statistically significant.