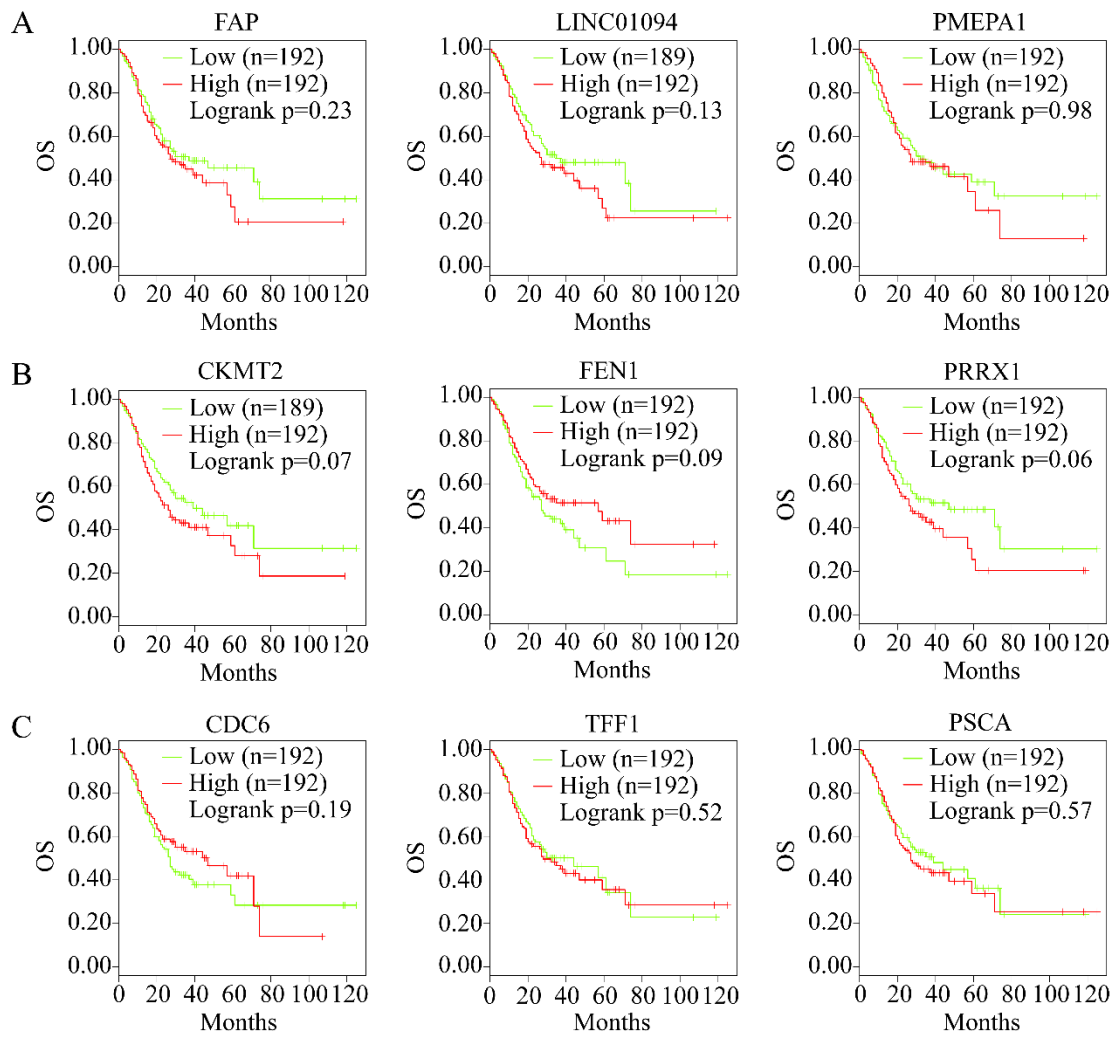
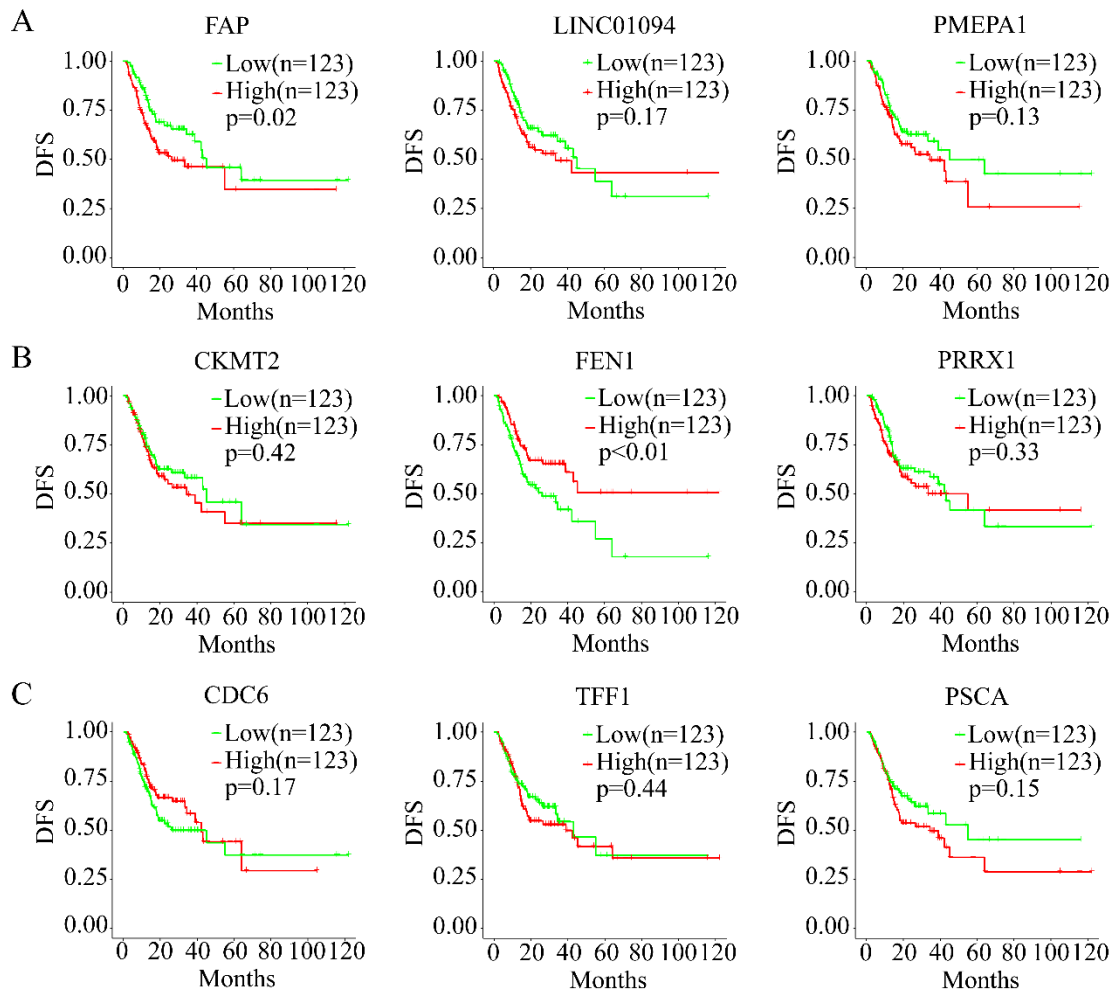


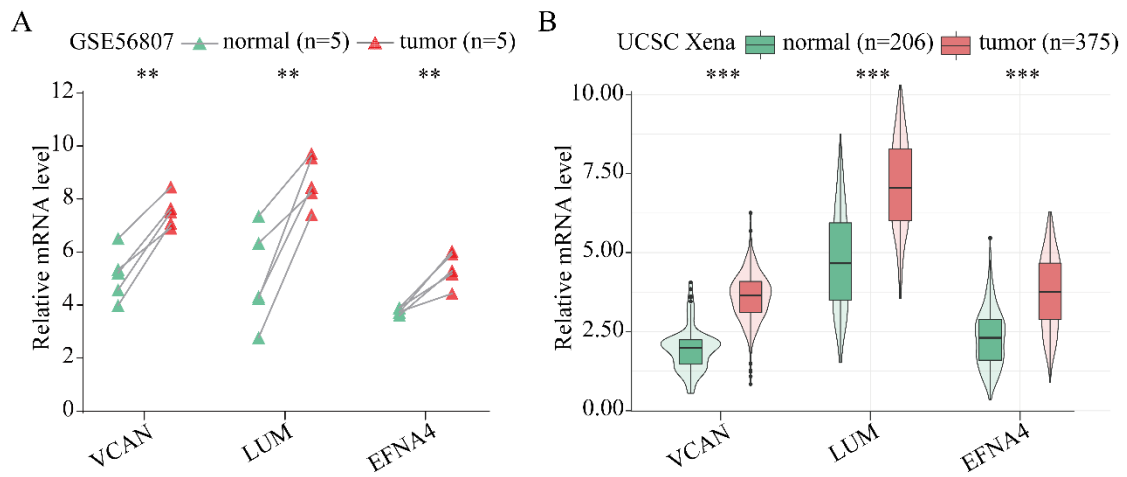
**Figure S1.** The expression of the 10 hub genes in GC (ONCOMINE). The numbers of datasets with 13 statistically significant mRNA upregulation (red) or downregulation (blue) of the 10 hub genes are shown. The upper label of the horizontal axis indicates the name of the hub genes; the lower label of the horizontal axis indicates the total number of datasets and the number of datasets with  $|FC| > 2$  and  $P\text{-value} < 0.05$ .



**Figure S2.** OS analysis of FAP, LINC01094, PMEPA1, CKMT2, FEN1, PRRX1, CDC6, TFF1, PSCA.



**Figure S3.** DFS analysis of FAP, LINC01094, PMEPA1, CKMT2, FEN1, PRRX1, CDC6, TFF1, PSCA.



**Figure S4.** The expression of the three genes in GC and normal gastric tissues datasets. (A) The expression of the three genes in GSE56807 dataset with paired 5 GC and 5 normal gastric tissues samples. (B) The expression of the three genes in the integrated 206 normal gastric tissues samples and 375 GC tissues samples from UCSC Xena database. Expression values of genes are log<sub>2</sub>-transformed. \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ .

**Table S1** | Sequence Information

Name	Sequence
LUM-F	CTCGGCTTTGAGTTCTTACC
LUM-R	CTTGCAGCAGACAGACACC
VCAN-F	ATTACGGGTGGCTGTCGG
VCAN-R	TCTGCTATCAGGGGGAGGG
EFNA4-F	CTCGGCTTTGAGTTCTTACC
EFNA4-R	CTTGCAGCAGACAGACACC
GAPDH-F	GAACGGGAAGCTCACTGG
GAPDH-R	GCCTGCTTCACCACCTTCT
CDC6-F	CTGTTACCATCAACTTCTGAG
CDC6-R	CTGTTACCATCAACTTCTGAG
CDC20-F	AATGTGTGGCCTAGTGCTCC
CDC20-R	AGCACACATTCCAGATGCGA
BUB1B-F	TGAGGCAGCAATCTGTGAG
BUB1B-R	GAATCCACGATCCCTATGA
TOP2A-F	CTAGTTAATGCTGCGGACAAC
TOP2A-R	CATTTGACCACCTGTCACCT
CDK1-F	CGGTTGACATCTGGAGTATAGG
CDK1-R	GCCACACTTCGTTGTTAGGA
AURKA-F	AAAGAGCAAGCAGCCCCTGC
AURKA-R	GAATCAACCCGTGATATTCTT
CCNA2-F	TGGAAAGCAAACAGTAAACAGCC
CCNA2-R	GGGCATCTTCACGCTCTATTT
CCNB1-F	CTTGCAGTAAATGATGTGGATG
CCNB1-R	GTGACTTCCCGACCCAGTAG
MAD2L1-F	GTTCTTCTCATTTCGGCATCAACA
MAD2L1-R	GAGTCCGTATTTCTGCACTCG
KIF11-F	GAACAATCATTAGCAGCAGAA
KIF11-R	TCAGTATAGACACCACAGTTG

**Table S2** | The mRNA levels of 10 hub genes in different types of GC tissues and normal tissues at transcriptome level (ONCOMINE)

Genes	Type	Fold change	P-value	t-Test	Preferences
CCNB1	Gastric Mixed Adenocarcinoma	2.41	1.12E-4	4.43	(1)
CDK1	Gastric Intestinal Type Adenocarcinoma	2.54	7.42E-13	9.47	(2)
MAD2L1	Gastric Mixed Adenocarcinoma vs. Normal	3.77	7.12E-6	6.39	(1)
	Gastric Intestinal Type Adenocarcinoma	2.59	3.28E-5	4.67	(3)
AURKA	Gastric Intestinal Type Adenocarcinoma	3.07	1.78E-5	4.86	(3)
BUB1B	Gastric Intestinal Type Adenocarcinoma	3.56	1.80E-11	8.31	(4)
CCNA2	Gastric Intestinal Type Adenocarcinoma	4.07	1.08E-5	5.06	(3)
	Gastric Mixed Adenocarcinoma	2.06	6.20E-4	3.85	(1)
CDC6	Gastric Intestinal Type Adenocarcinoma	6.92	2.79E-6	5.41	(3)
TOP2A	Gastric Intestinal Type Adenocarcinoma	5.65	3.19E-7	6.06	(3)
	Gastric Mixed Adenocarcinoma	3.90	3.08E-5	5.49	(4)
CDC20	Gastric Intestinal Type Adenocarcinoma	3.06	6.73E-5	4.58	(3)
KIF11	Gastric Intestinal Type Adenocarcinoma	2.04	0.02E-1	3.25	(3)

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3. Förster S, Gretschel S, Jöns T, et al. THBS4, a novel stromal molecule of diffuse-type gastric adenocarcinomas, identified by transcriptome-wide expression profiling. *Mod Pathol.* 2011;24(10):1390-403.
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