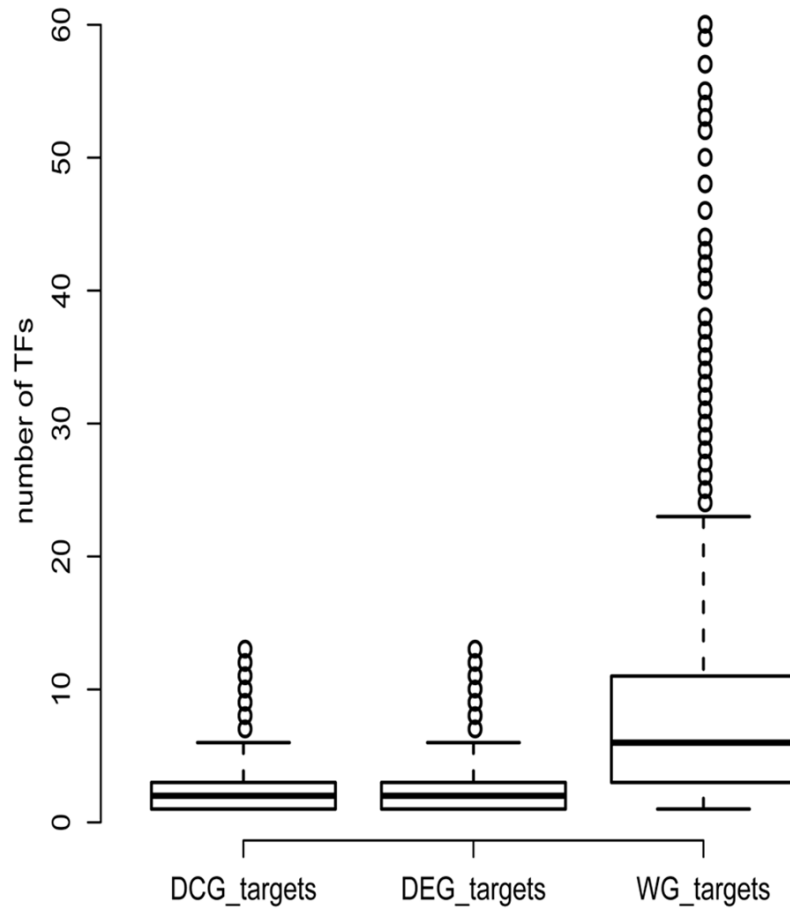**Figure S1.** The distribution of number of TFs for DCG targets, DEG targets and WG targets in the candidate TF-target relationships. The horizontal axis represents each group of targets and the vertical axis represents the number of TFs.

Table S1. The enrichment *p* values of cancer genes and drug targets in four groups of targets

Group	Interest genes		Common group				Differential group		
Normal vs. adenoma	Cancer genes		Common	Non Common	Total		Differential	Non Differential	Total
		Known cancer gene	4	343	347	Known cancer gene	33	314	347
		Other genes	128	12183	12311	Other genes	737	11574	12311
		Total	132	12526	12658	Total	770	11888	12658
		p-value			0.785	*p*-value			0.012
	Drug targets		Common	Non Common	Total		Differential	Non Differential	Total
		Drug targets	26	1628	1654	Drug targets	134	1520	1654
		Other genes	106	10898	11004	Other genes	636	10368	11004
		Total	132	12526	12658	Total	770	11888	12658
		p-value			0.027	*p*-value			0.0003
Adenoma vs. carcinoma	Cancer genes		Common	Non Common	Total		Differential	Non Differential	Total
		Known cancer gene	6	341	347	Known cancer gene	32	315	347
		Other genes	139	12172	12311	Other genes	749	11562	12311
		Total	145	12513	12658	Total	781	11877	12658
		p-value			0.297	*p*-value			0.023
	Drug targets		Common	Non Common	Total		Differential	Non Differential	Total
		Drug targets	25	1629	1654	Drug targets	148	1506	1654
		Other genes	120	10884	11004	Other genes	633	10371	11004
		Total	145	12513	12658	Total	781	11877	12658
		p-value			0.137	*p*-value			1.67E-06

Table S2. Top 4% genes of normal vs. adenoma DRG list and top 6% genes of adenoma vs. carcinoma DRG list

Normal vs. Adenoma		Adenoma vs. Carcinoma			
Genes	DR_rank	Genes	DR_rank	Genes	DR_rank
LIMS1	1	**ESRRG**	1	**HEPH**	37
FOSB	2	**LIMS1**	2	**PTK7**	38
MRPL36	3	IRF2	3	SYNPO	39
GATA3	4	RGS3	4	ACSL5	40
RGS3	5	FOSB	5	ETFB	41
TRIB1	6	**CEBPB**	6	**MMP7**	42
GATA6	7	TRIB1	7	**CTSA**	43
SOX9	8	**AHR**	8	PPP1R1B	44
HEPH	9	**POU2F1**	9	**E2F3**	45
RIC8B	10	**TGIF1**	10	STAM	46
AHR	11	FOSL1	11	**CCND2**	47
MGAM	12	**ID1**	12	**PBX3**	48
GIF	13	**GSTP1**	13	ABR	49
MME	14	CITED1	14	**ITM2C**	50
RARA	15	**EYA1**	15	**GATA6**	51
CEBPB	16	ERBB3	16	**DDIT3**	52
TGIF1	17	**IRF1**	17	CRLS1	53
POU2F1	18	ELF1	18	ITGB1BP2	54
FABP2	19	**IL10**	19	GK	55
RGS5	20	PFN1	20	**CDX1**	56
TM4SF20	21	**STAT5A**	21		
CITED1	22	**PRKACB**	22		
SYNPO	23	ZMYND8	23		
DDIT3	24	CYP8B1	24		
ZNF609	25	**SOX9**	25		
EYA1	26	**ID3**	26		
STAM	27	DMKN	27		
PDGFRB	28	**SERPINA1**	28		
MYO15B	29	NAV2	29		
ID1	30	**GATA3**	30		
DMKN	31	MRPL36	31		
IRF1	32	SOX5	32		
PRKACB	33	**GKN1**	33		
PFN1	34	STAT2	34		
ACSL5	35	GABRA5	35		
MYL9	36	ISG15	36		

The genes are sorted by the DR values. Genes in bold refer to GC-related genes.

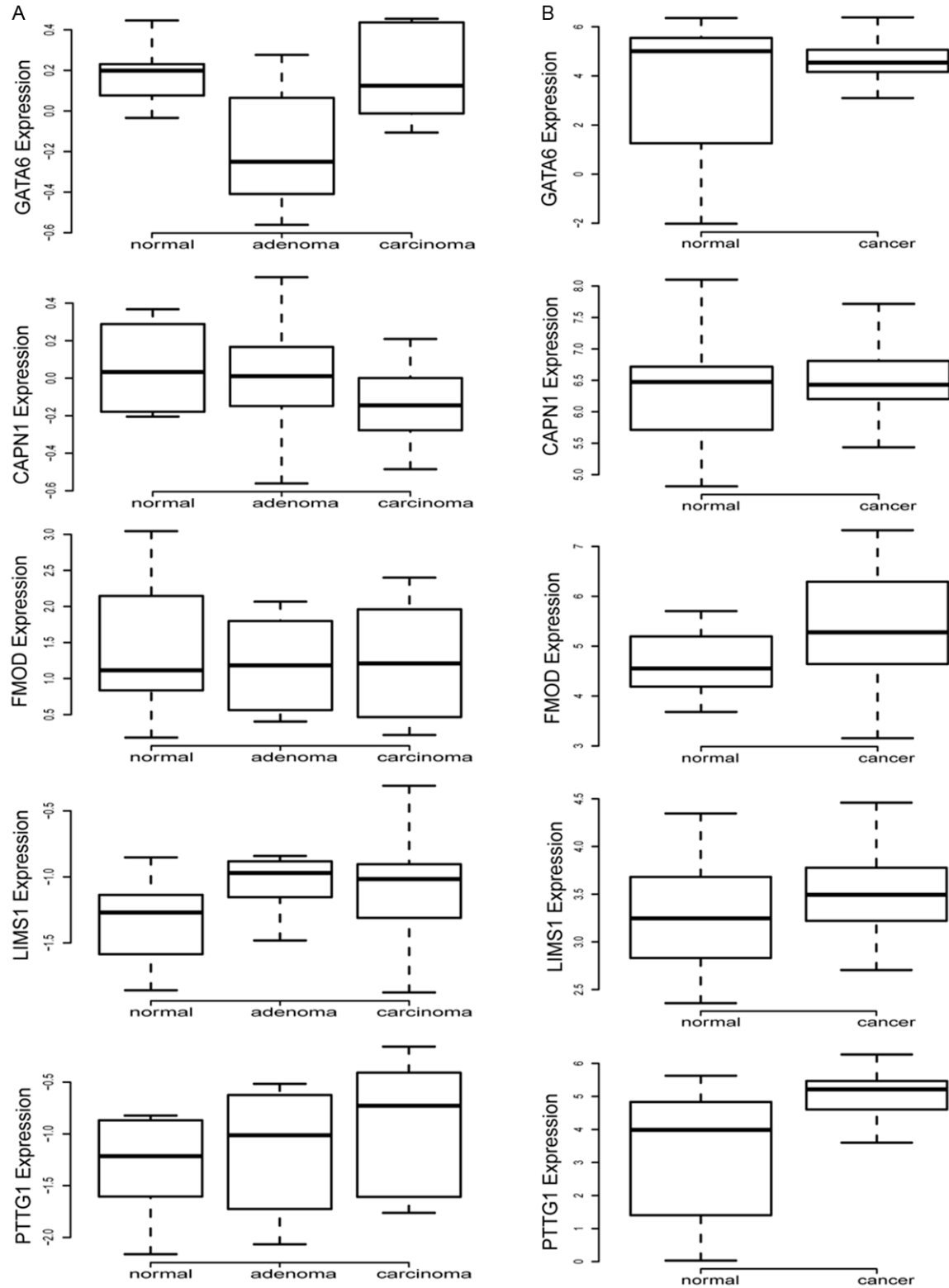# Differential regulation network analysis in gastric carcinogenesis

A

B

Figure S2. The expression level of GATA6, CAPN1, FMOD, LIMS1 and PTTG1 in GSE24375 (A) and TCGA (B) data sets. (A) The log2 transformed expression level of GATA6, CAPN1, FMOD, LIMS1 and PTTG1 in normal, adenoma and carcinoma samples of GSE24375 dataset. (B) The log2 transformed expression level of GATA6, CAPN1, FMOD, LIMS1 and PTTG1 in normal and carcinoma samples of TCGA dataset.

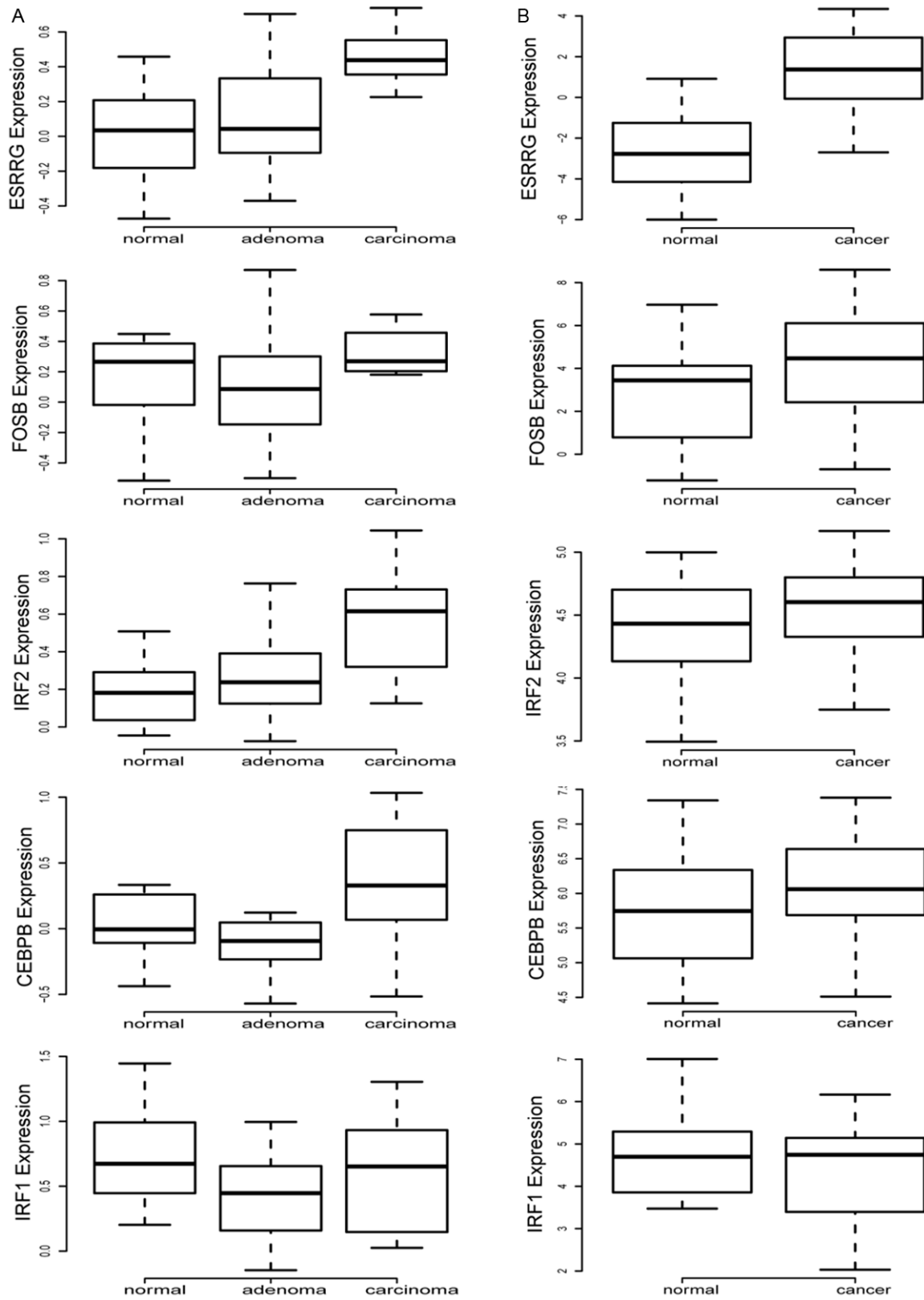# Differential regulation network analysis in gastric carcinogenesis

Figure S3. The expression level of ESRRG, FOSB, IRF2, CEBPB and IRF1 in GSE24375 (A) and TCGA (B) data sets. (A) The expression level of ESRRG, FOSB, IRF2, CEBPB and IRF1 in normal, adenoma and carcinoma samples of GSE24375 dataset. (B) The expression level of ESRRG, FOSB, IRF2, CEBPB and IRF1 in normal and carcinoma samples of TCGA dataset.