
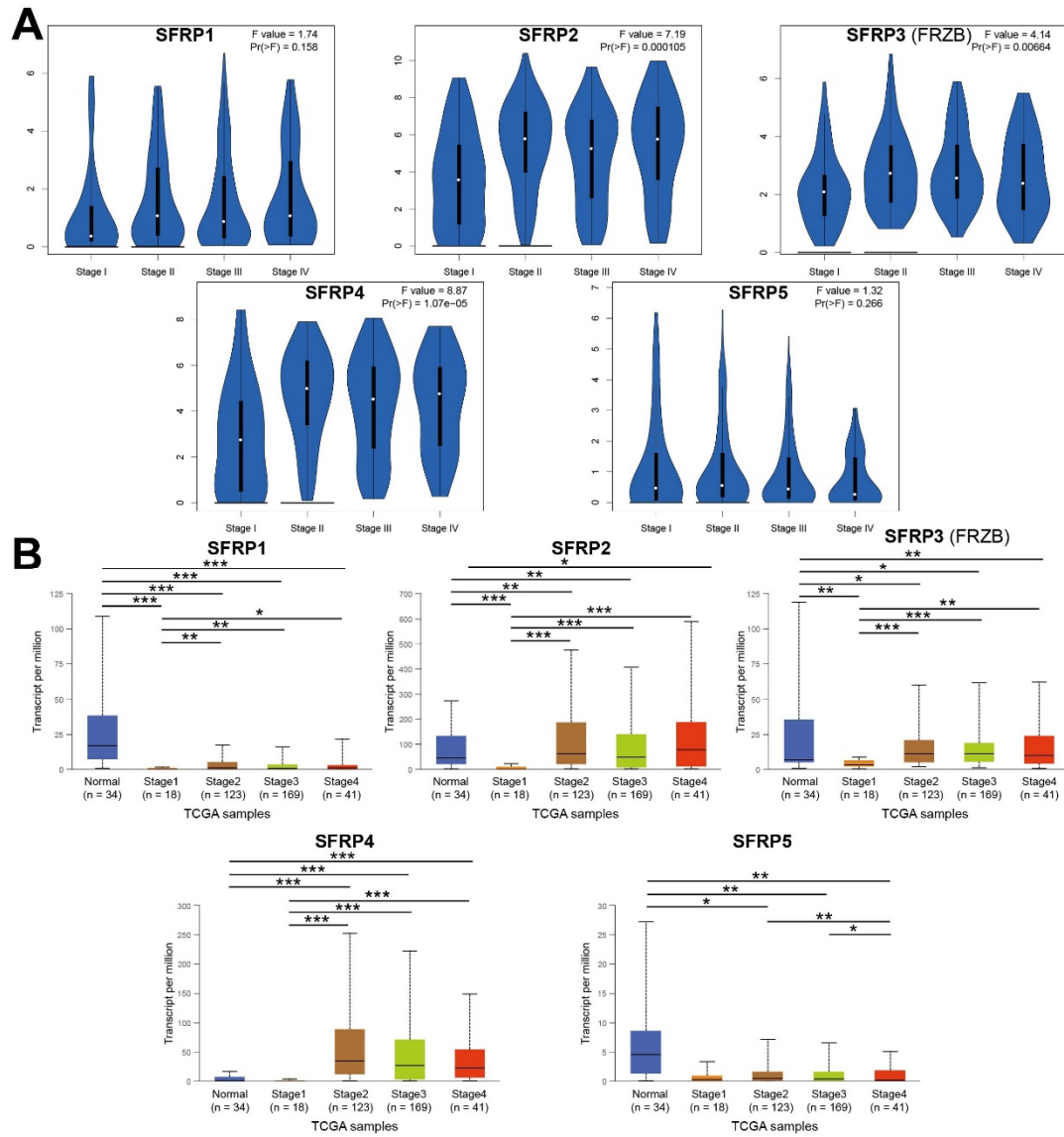


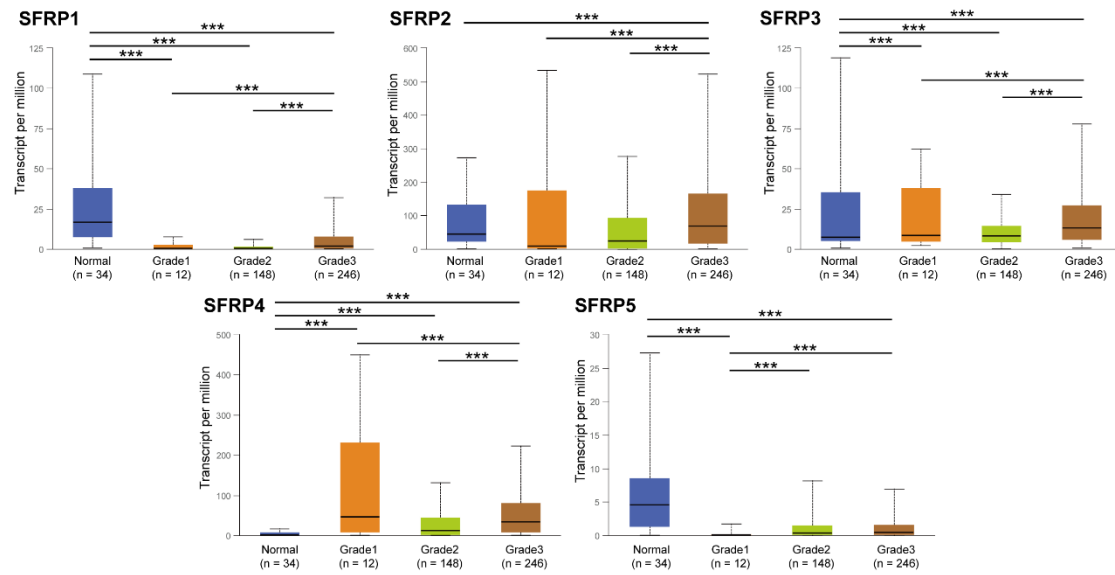
# Supplementary Materials

Analysis Type by Cancer		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal		Cancer vs. Normal	
		SFRP1		SFRP2		SFRP3 FRZB		SFRP4		SFRP5	
1 5 10 10 5 1  %											
Bladder Cancer		3		1				1			
Brain and CNS Cancer		3						5			
Breast Cancer		20		4 1		1 7		3			
Cervical Cancer								1			
Colorectal Cancer		17		4		9		9			
Esophageal Cancer		1				2		2			
Gastric Cancer		3		1				6			
Head and Neck Cancer		1				2					
Kidney Cancer		11				3		1			
Leukemia		1									
Liver Cancer						3		1			
Lung Cancer		2		1							
Lymphoma				2		2					
Melanoma		2				1					
Myeloma						2					
Other Cancer		1		4		1		1 1			
Ovarian Cancer		3		1		1		1			
Pancreatic Cancer				1				1		1	
Prostate Cancer		1 1						2			
Sarcoma		1 3				1					
Significant Unique Analyses		3 71		13 7		10 24		30 5			
Total Unique Analyses		428		310		441		424		339	

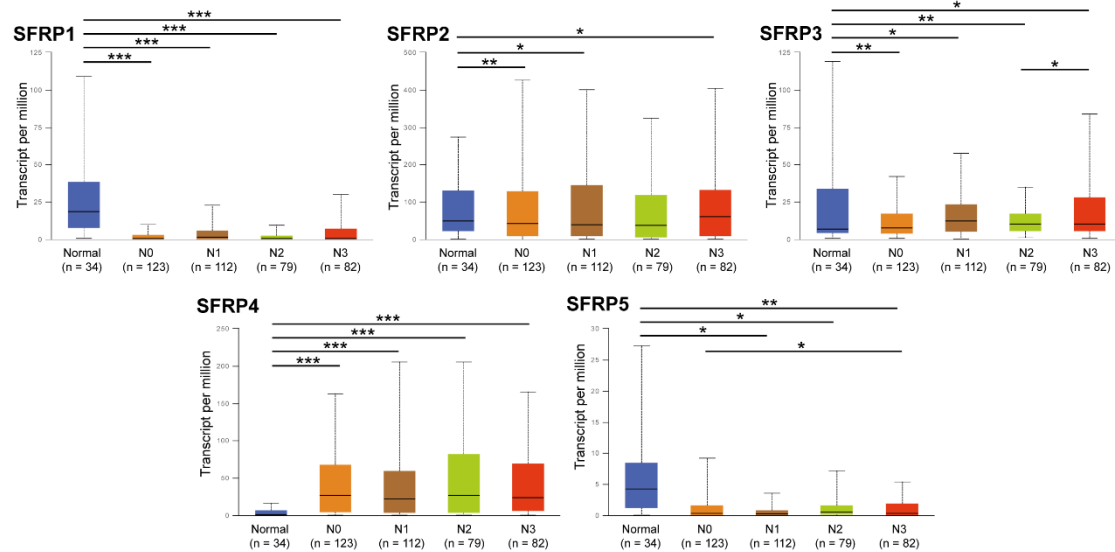
**Supplementary Figure S1.** The mRNA expression of *SFRPs* in different cancer types (Oncomine). Difference of transcriptional expression was compared by Students' *t*-test.



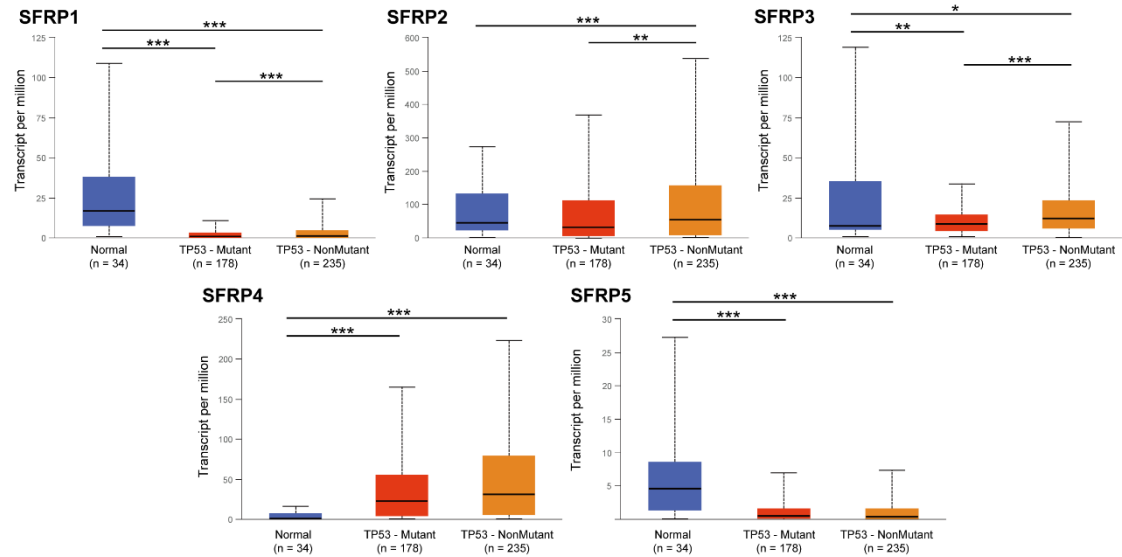
**Supplementary Figure S2.** Correlations between *SFRPs* expression and tumor stage in GC patients (A: GEPIA database, B: UALCAN database). One-way ANOVA was conducted for differential gene expression analysis using pathological stage as a variable and Log<sub>2</sub>(TPM + 1) transformed expression data were used for plotting in GEPIA.



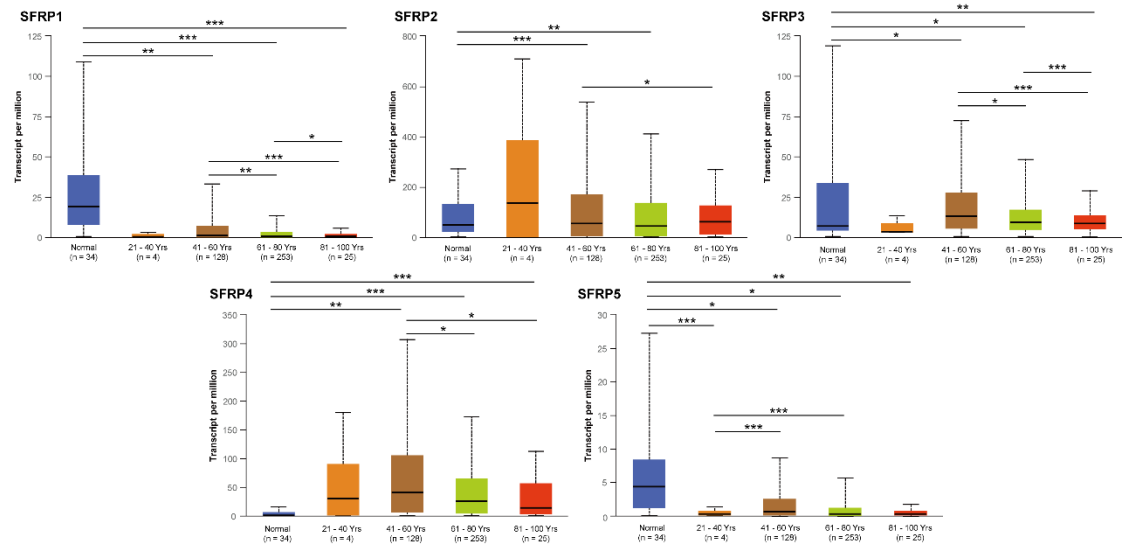
**Supplementary Figure S3.** The *SFRPs* expression in GC based on tumor grade (UALCAN database). The method for differential analysis is *t* test. \*:  $P < 0.05$ , \*\*:  $P < 0.01$ , \*\*\*:  $P < 0.001$ . Grade 1: well differentiated, Grade 2: moderately differentiated, Grade 3: poorly differentiated, Grade 4: undifferentiated.



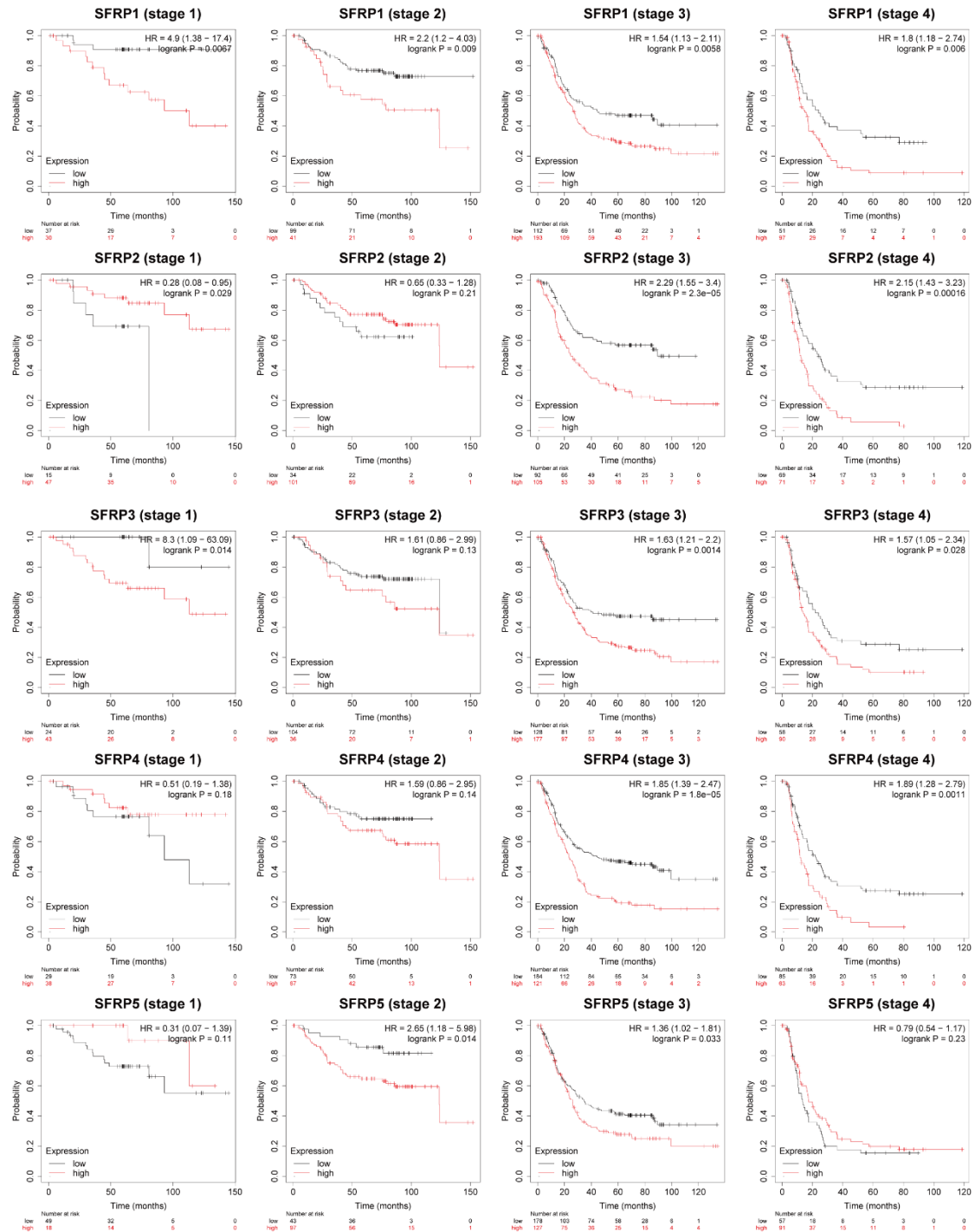
**Supplementary Figure S4.** The *SFRPs* expression in GC based on nodal metastasis status (UALCAN database). The method for differential analysis is *t* test. \*:  $P < 0.05$ , \*\*:  $P < 0.01$ , \*\*\*:  $P < 0.001$ . N0: no regional lymph node metastasis, N1: metastases in 1 to 3 axillary lymph nodes, N2: metastases in 4 to 9 axillary lymph nodes, N3: metastases in 10 or more axillary lymph nodes.



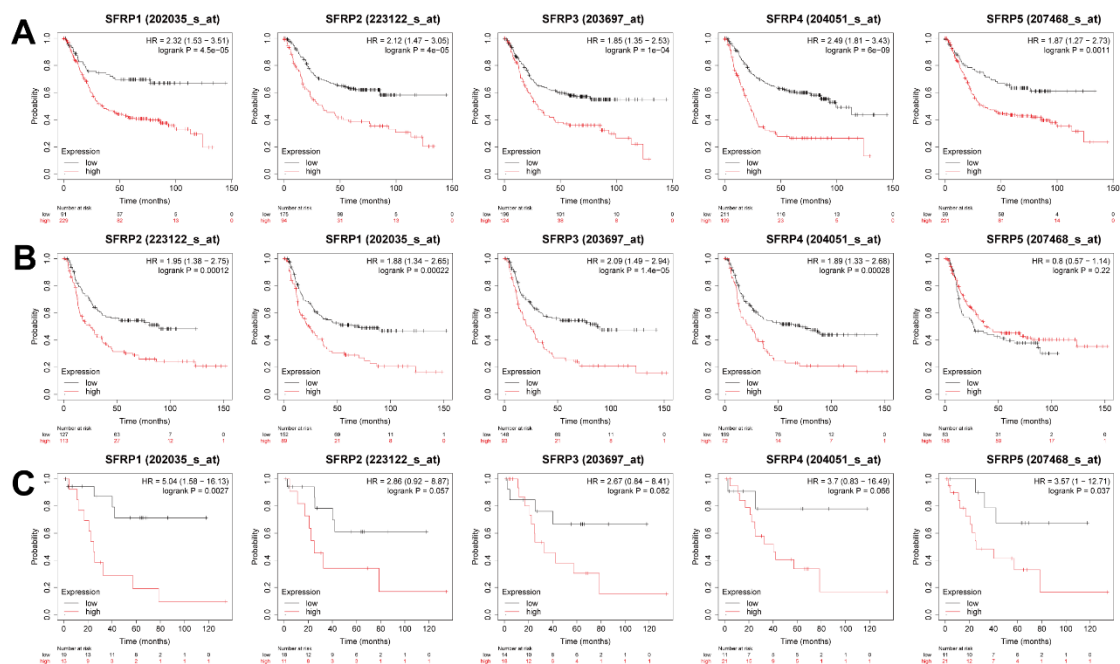
**Supplementary Figure S5.** The *SFRPs* expression in GC based on TP53 mutation status (UALCAN database). The method for differential analysis is *t* test. \*:  $P < 0.05$ , \*\*:  $P < 0.01$ , \*\*\*:  $P < 0.001$ .



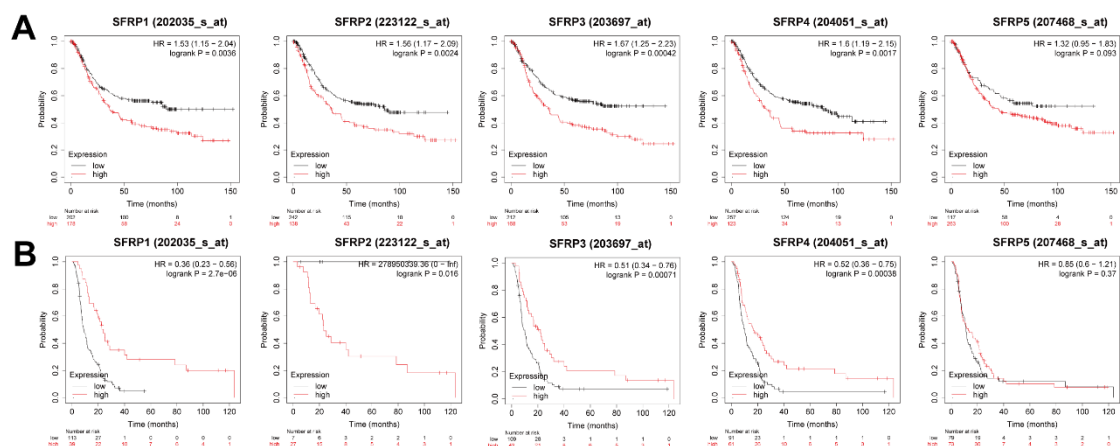
**Supplementary Figure S6.** The *SFRPs* expression in GC based on the ages of patients (UALCAN database). The method for differential analysis is *t* test. \*:  $P < 0.05$ , \*\*:  $P < 0.01$ , \*\*\*:  $P < 0.001$ . Yrs: years.



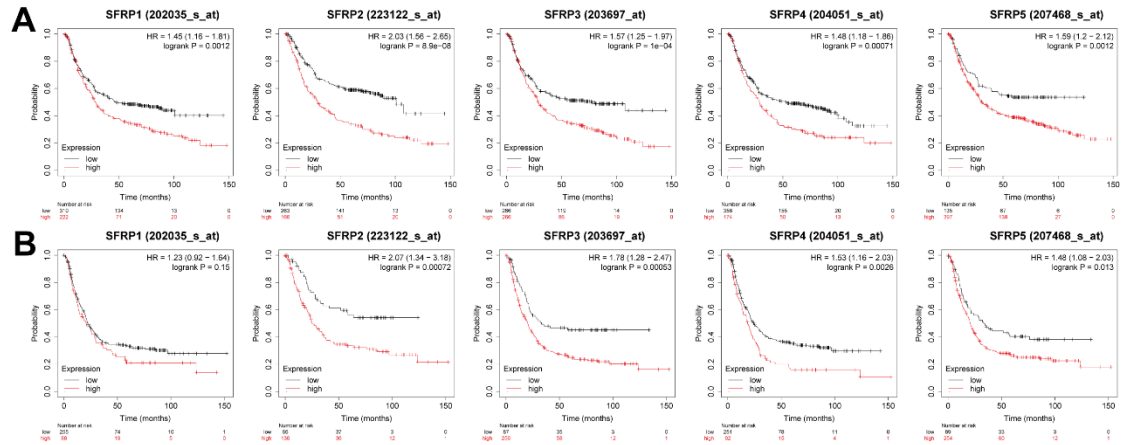
**Supplementary Figure S7.** The prognostic value of mRNA level of SFRPs in patients with different GC stages (Kaplan-Meier Plotter). The method for survival analysis is Log-rank test.



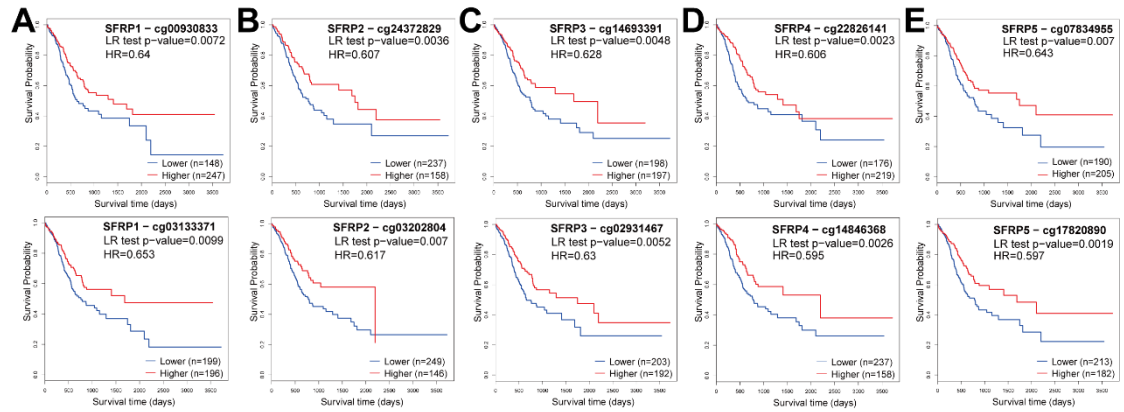
**Supplementary Figure S8.** The prognostic value of mRNA level of *SFRPs* in patients with different GC subtypes (Kaplan-Meier Plotter). A: intestinal type gastric carcinoma, B: diffuse type gastric carcinoma, C: mixed type gastric carcinoma. The method for survival analysis is Log-rank test.



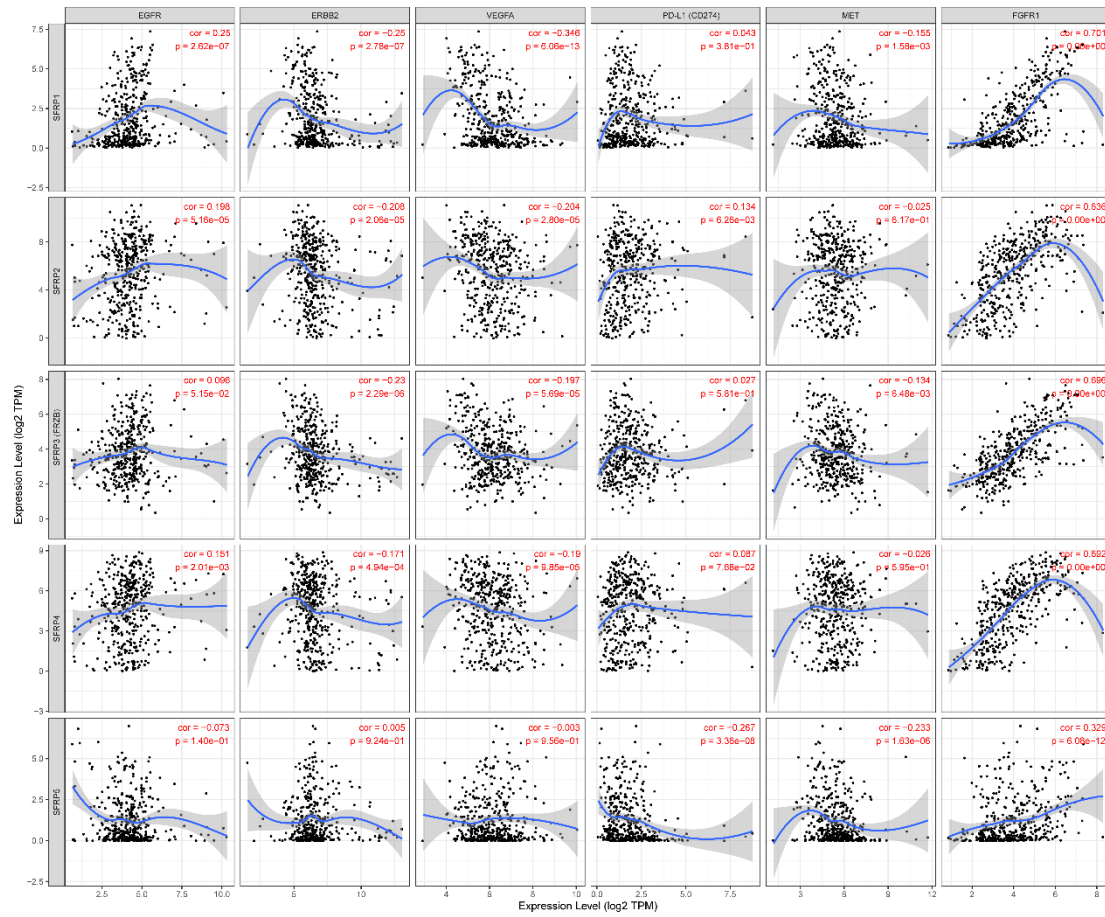
**Supplementary Figure S9.** The prognostic value of mRNA level of *SFRPs* in GC patients with different treatment (Kaplan-Meier Plotter). A: surgery alone, B: 5 FU based adjuvant therapy. The method for survival analysis is Log-rank test.



**Supplementary Figure S10.** The prognostic value of mRNA level of *SFRPs* in GC patients with different HER2 status (Kaplan-Meier Plotter). A: HER2 negative, B: HER2 positive. The method for survival analysis is Log-rank test.



**Supplementary Figure S11.** Kaplan-Meier curves of low and high *SFRPs* DNA promoter CpG sites in GC patients (A: *SFRP1*, B: *SFRP2*, C: *SFRP3*, D: *SFRP4*, E: *SFRP5*). The method for survival analysis is Log-rank test.



**Supplementary Figure S12.** Correlations between differentially expressed *SFRPs* and usual gene markers in GC (TIMER). Spearman's rho value was used for the analysis.