Table S1. Prognostic factors in patients with gastric cancer by univariate analysis.

Parameter	n	*P* value	Hazard Ratio	95% Confidence Interval
Gender				
Male	62	0.479	1.224	0.700 - 2.141
Female	28			
Age				
< 60	31	0.328	0.751	0.423 - 1.333
≥ 60	59			
Location				
Cardia	12	0.061		
Fundus/body of stomach	15	0.032	0.310	0.106 - 0.906
Antrum	55	0.246	0.582	0.233 - 1.454
Diffuse	8	0.015	0.373	0.169 - 0.825
Tumor size				
< 5cm	30	0.014*	0.456	0.244 - 0.852
≥ 5cm	60			
Invasion depth				
Without Infiltration into serous layer	11	0.047*	0.307	0.096 - 0.986
Infiltration into serous layer	79			
Lymph node metastasis				
negative	25	0.000*	0.169	0.067 - 0.426
positive	65			
Lymphatic and/or vascular invasion				
negative	72	0.238	0.687	0.368 - 1.283
positive	18			
AJCC stage				
I / II	25	0.001*	0.259	0.117 - 0.575
III/IV	65			
POU2F2 expression				
Negative	31	0.000*	0.129	0.055 – 0.304
Positive	59			

Table S2. Multivariate analysis using the Cox proportional hazards model.

Parameter	n	*P* value	Hazard Ratio	95% Confidence Interval
Location				
Cardia	12	0.440		
Fundus/body of stomach	15	0.112	0.401	0.130 - 1.236
Antrum	55	0.387	0.660	0.258 - 1.691
Diffuse	8	0.202	0.585	0.257 - 1.333
Tumor size				
< 5cm	30	0.102	0.551	0.270 - 1.125
≥ 5cm	60			
Invasion depth				
Without Infiltration into serous layer	11	0.943	1.049	0.283 - 3.885
Infiltration into serous layer	79			
Lymph node metastasis				
negative	25	0.819	0.823	0.156 - 4.340
positive	65			
AJCC stage				
I / II	25	0.015*	0.349	0.149 - 0.816
III/IV	65			
POU2F2 expression				
Negative	31	0.023*	0.167	0.036 – 0.780
Positive	59			

Table S3. Sequence of primers used in the study.

Gene		Primer Sequence (5'-3')
GAPDH	Forward primer	ATAGCACAGCCTGGATAGCAACGTAC
	Reverse primer	CACCTTCTACAATGAGCTGCGTGTG
POU2F2	Forward primer	GCCGGAGCGGTCGAGTTCTG
	Reverse primer	GTACAGCTCGTCCAGGCCGC
ROBO1 promoter	Forward primer	GACTTCAAATTAATATATATTAAGA
	Reverse primer	TTCCATCAATGACAATGGCGTCA
POU2F2 promoter	Forward primer	GCTGAAATGGGAGCGCCGCAGC
	Reverse primer	CTGAGGATCAGAGAGGTGAGCAGTA

Table S4. Interference targets of each gene involved in the study.

Gene Symbol	NO.	Target Seq
POU2F2 NM_002698	POU2F2- shRNA1	TCAACGATGCAGAGACTAT
	POU2F2- shRNA2	TACCGACACCAAATCTATT
	POU2F2- shRNA3	ACACAGACACCGAAAGAAA
	POU2F2- shRNA4	GTACAAAGATCAAGGCTGA
ROBO1 NM_002941	ROBO1- shRNA1	GGCATATTTGGAAGTTACA
	ROBO1- shRNA2	AGACAAAGAGAACAAGCAA
	ROBO1- shRNA3	CACCAGCAAGGATGTATTT
	ROBO1- shRNA4	CCACCATTTCATGGAAGAA
IKK-β AF080158.1	IKK-β- shRNA	AAAGTGTCAGCTGTATCCT