

Figure S1 lncRNA-miRNA-mRNA regulatory network of gastric cancer. LncRNAs are represented by diamonds, miRNAs are represented by triangles, and mRNA are represented by circles; the connections represent the regulatory relationship between the two RNAs; red represents the upregulation, and blue represents downregulation.

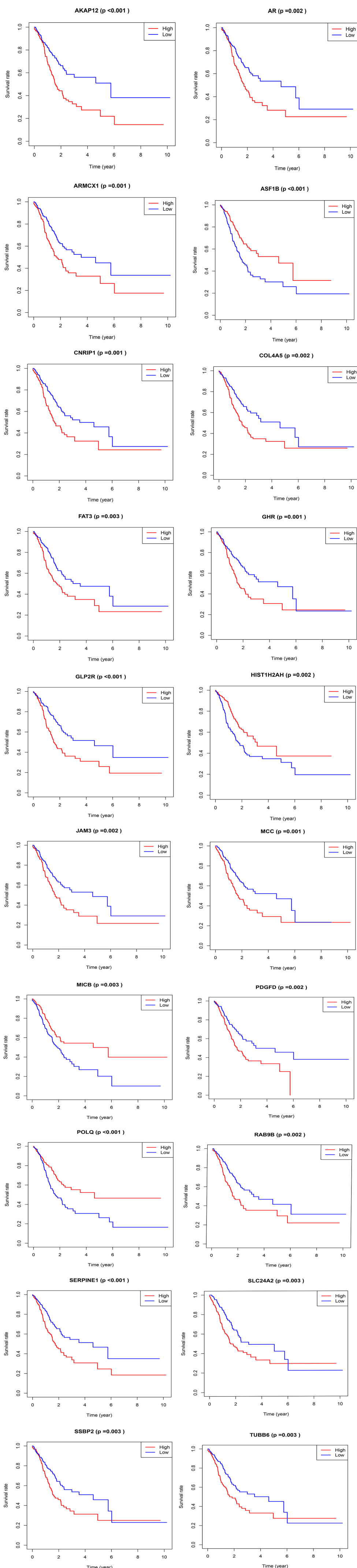


Figure S2 Survival analysis of the lncRNA ADAMTS9-AS2 regulatory network target genes. Vertical axis: overall survival. Horizontal axis: total survival time. $P < 0.05$ was considered statistically significant.

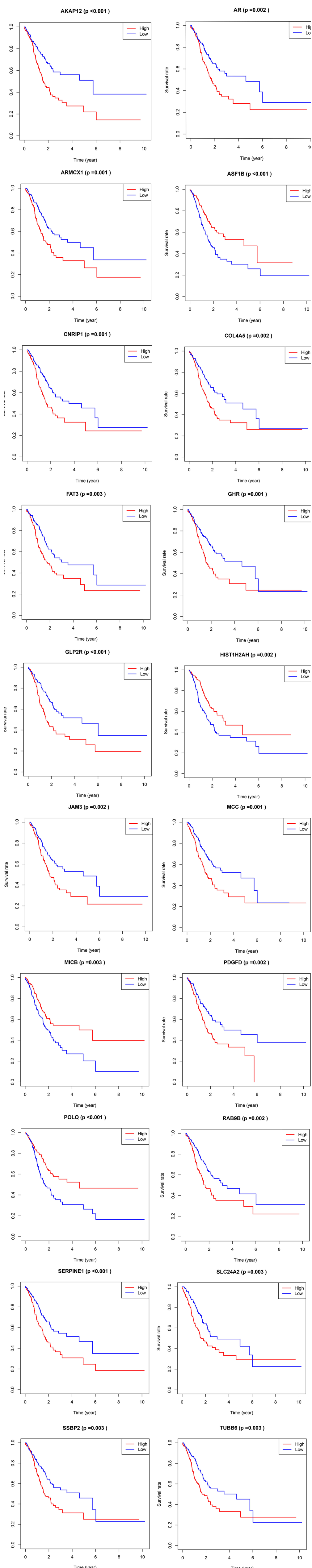


Figure S3 Survival analysis of lncRNA PVT1 regulatory network target genes. Vertical axis: overall survival. Horizontal axis: total survival time. P<0.05 was considered statistically significant.

Table S1 gene list of lncRNA-miRNA-mRNA regulatory network in TCGA gastric cancer dataset (lncRNA top100, mRNA top100, according to logFC)

Gene category	Gene symbol	logFC	P value	FDR
LncRNA	LINC00392	7.10	8.74E-07	8.03E-06
	ERVMER61-1	6.16	1.64E-07	1.87E-06
	HOTAIR	5.51	1.32E-19	1.62E-17
	AL139002.1	5.50	3.60E-07	3.71E-06
	LINC00355	5.16	2.18E-09	4.13E-08
	AL513123.1	4.87	1.26E-12	4.85E-11
	DSCR4-IT1	4.77	1.12E-05	7.48E-05
	HULC	4.69	1.47E-07	1.70E-06
	C10orf126	4.56	7.92E-07	7.37E-06
	AP002478.1	4.42	4.03E-15	2.47E-13
	POU6F2-AS2	4.40	1.46E-06	1.25E-05
	LINC00454	4.32	2.36E-05	1.41E-04
	AC061975.6	4.18	7.07E-05	3.60E-04
	LINC00326	3.88	0.000139	6.48E-04
	C7orf69	3.84	6.19E-13	2.56E-11
	LINC00200	3.73	0.000354	1.45E-03
	LINC00393	3.72	4.83E-05	2.59E-04
	NOVA1-AS1	3.70	8.78E-06	6.05E-05
	NKX2-1-AS1	3.47	0.002207	6.75E-03
	AC026320.1	3.46	0.000811	2.93E-03
	LINC00460	3.26	2.84E-09	5.25E-08
	LINC00052	3.24	4.28E-05	2.35E-04
	AP000525.1	3.16	7.25E-12	2.38E-10
	BOK-AS1	3.13	8.79E-05	0.000435
	DLX6-AS1	3.10	1.29E-07	1.52E-06
	UCA1	3.06	5.39E-07	5.25E-06
	LINC00534	3.04	1.19E-05	7.89E-05
	HOTTIP	3.01	6.66E-08	8.57E-07
	AC087269.1	3.01	8.26E-10	1.72E-08
	LINC00221	3.00	0.001243	0.004188
	C8orf31	2.97	4.92E-12	1.68E-10
	FREM2-AS1	2.96	0.000553	0.00211
	MYB-AS1	2.95	1.47E-09	2.91E-08
	LINC00524	2.80	4.51E-05	0.000246
	IGF2-AS	2.79	2.45E-05	0.000146
	AP002992.1	2.77	2.43E-05	0.000145
	NAALADL2-AS2	2.75	1.19E-05	7.89E-05
	C15orf54	2.73	6.81E-09	1.13E-07

TCGA, The Cancer Genome Atlas.

