

## Supplementary materials

**Table S1** Correlations between DPP10-AS1 and clinical characteristics in 94 patients with lung cancer

Characteristics	<i>n</i>	DPP10-AS1		$\chi^2$ test	<i>P</i> value
		levelst	Low		
Total cases	94	47	47		
Gender					
Male	46	27	19	2.725	0.0988
Female	48	20	28		
Age (years)					
≤ 55	34	14	20	0.9570	0.3279
> 55	60	31	29		
Serum CYFRA21-1					
≤ 3.3	50	32	18	6.033	0.0140*
> 3.3	46	17	27		
Tumor number					
Single	72	39	33	2.136	0.1438
Multiple	22	8	14		
Tumor size (cm)					
≤ 5	64	38	26	7.050	0.0079**
> 5	30	9	21		
TNM stage					
I/II	65	35	30	4.191	0.0406*
III	29	9	20		
Microvascular invasion					
Present	36	17	19	0.5626	0.4532
Absent	58	32	26		
Smoking history					
Yes	44	18	26	1.607	0.2049
No	50	27	23		

\*Median expression level was used as a cutoff. Low expression of DPP10-AS1 in 94 patients was defined as a value below the 50th percentile, and high expression was defined as a value above the 50th percentile. *P* values were determined with Pearson's chi-square test. \**P* < 0.05, \*\**P* < 0.01.

**Table S2** Univariate and multivariate analysis of clinicopathological variables for RFS rates in 94 patients with lung cancer

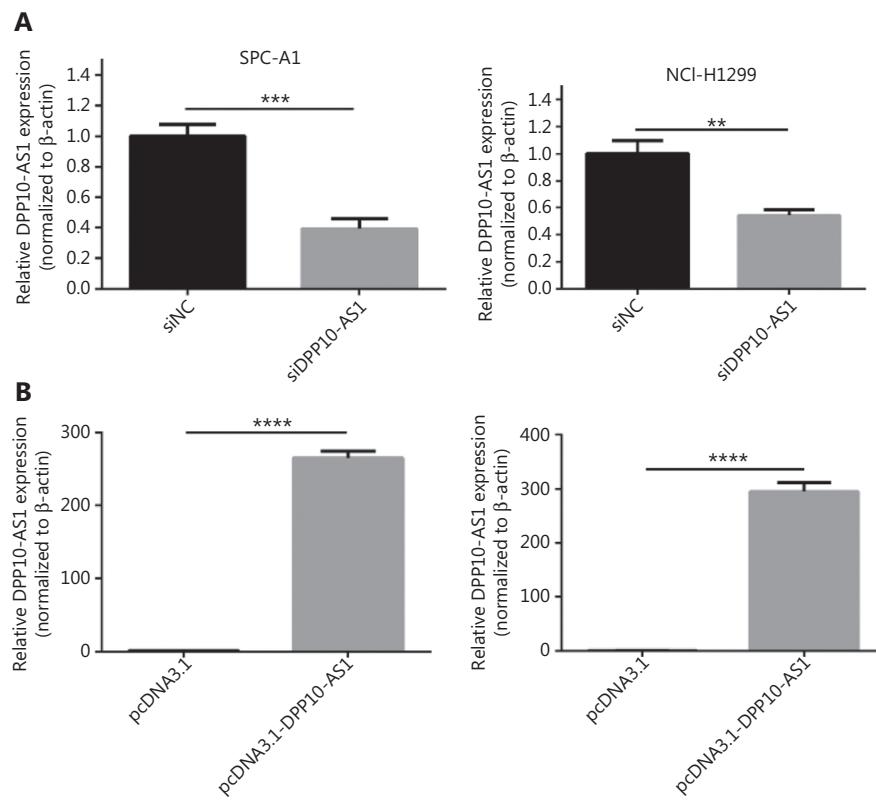
Variables	Univariate analysis			Multivariate analysis		
	P value	HR	95%CI	P value	HR	95%CI
Gender (male vs. female)	0.324	1.036	0.575–1.686			
Age (> 55 vs. ≤ 55 years)	0.431	1.231	0.787–2.325			
Serum CYFR1 (> 3.3 vs. ≤ 3.3 ng/mL)	0.336	0.957	0.794–3.240			
Smoking history (yes vs. no)	0.759	1.325	0.885–3.945			
Tumor number (single vs. multiple)	0.576	1.695	0.759–5.621			
Microvascular invasion (present vs. absent)	0.042	2.168	1.285–4.326			
TNM stage (I/II vs. III)	0.036	0.413	0.226–0.894			
Tumor size (> 5 cm vs. ≤ 5 cm)	0.021	2.186	1.273–4.536	0.032	2.304	1.219–3.947
DPP10-AS1 expression (higher vs. lower)	0.009	2.84	1.363–5.975	0.012	2.446	1.116–5.823

RFS, recurrence-free survival; HR, hazard ratio; CI, confidence interval.

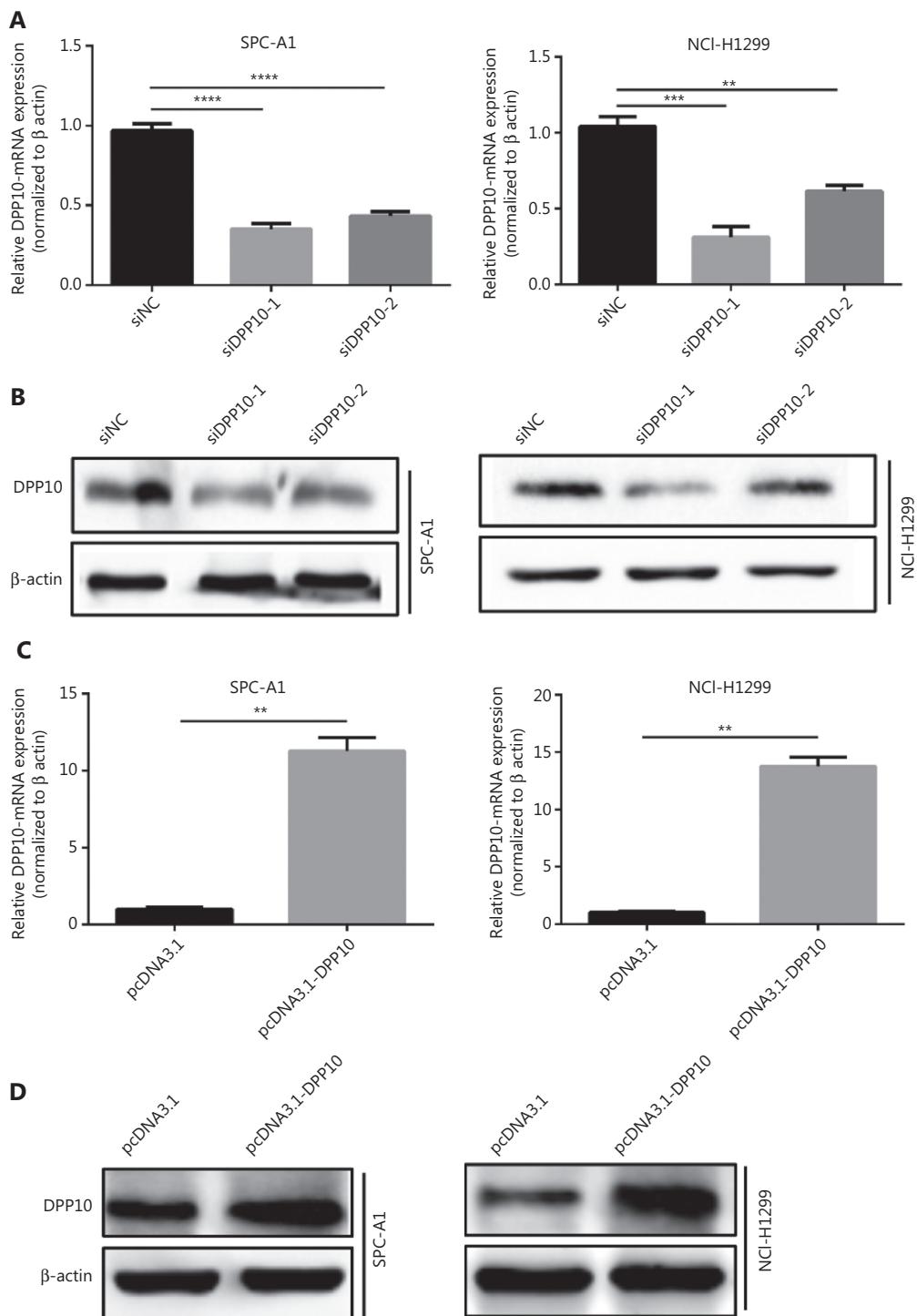
**Table S3** Univariate and multivariate analysis of clinicopathological variables for OS rates in 94 patients with lung cancer

Variables	Univariate analysis			Multivariate analysis		
	P value	HR	95%CI	P value	HR	95%CI
Gender (male vs. female)	0.527	1.196	0.687–2.080			
Age (> 55 vs. ≤ 55 years)	0.921	1.001	0.976–1.028			
Serum CYFR1 (> 3.3 vs. ≤ 3.3 ng/mL)	0.405	0.759	0.398–1.450			
Smoking history (yes vs. no)	0.302	1.526	0.684–3.405			
Microvascular invasion (present vs. absent)	0.546	1.156	0.789–2.123			
Tumor number (single vs. multiple)	0.865	1.191	0.159–8.932			
Tumor size (> 5 cm vs. ≤ 5 cm)	0.008	3.382	1.374–8.330	0.652	1.304	0.411–4.145
TNM stage (I/II vs. III)	<0.001	0.313	0.114–0.899	0.037	3.166	1.070–9.369
DPP10-AS1 expression (higher vs. lower)	0.019	2.55	1.167–5.572	0.016	2.765	1.212–6.307

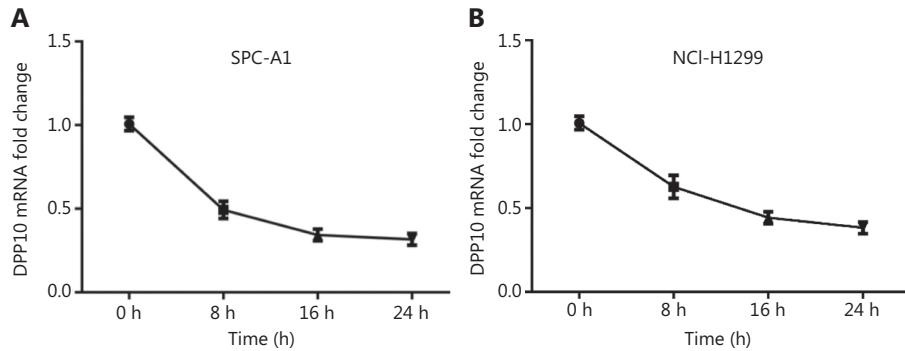
OS, overall survival; HR, hazard ratio; CI, confidence interval.



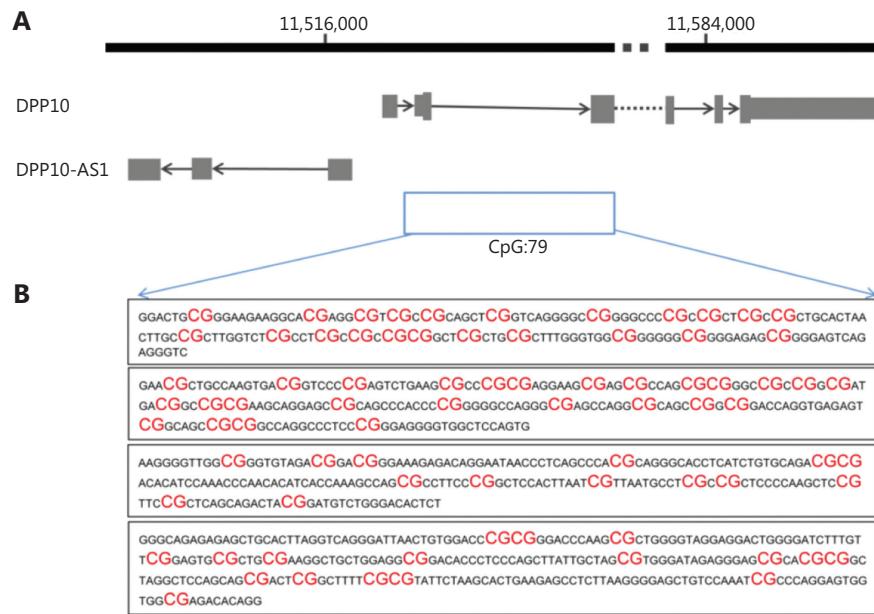
**Figure S1** Knockdown and overexpression of DPP10-AS1 in lung cancer cells. (A) qRT-PCR analysis of DPP10-AS1 in SPC-A1 and NCI-H1299 lung cancer cells transfected with control siRNA (siNC) or DPP10-AS1 siRNA (siDPP10-AS1). (B) qRT-PCR analysis of DPP10-AS1 in SPC-A1 and NCI-H1299 lung cancer cells transfected with empty vector (pcDNA3.1) or DPP10-AS1 overexpression plasmid (pcDNA3.1-DPP10-AS1). Data are shown as mean ± SD from 3 independent experiments. \*\*P < 0.01, \*\*\*P < 0.001, \*\*\*\*P < 0.0001.



**Figure S2** Knockdown and overexpression of DPP10 in lung cancer cells. (A) qRT-PCR analysis of DPP10 mRNA levels in SPC-A1 and NCI-H1299 lung cancer cells transfected with control siRNA (siNC) or DPP10 mRNA siRNA (siDPP10-1 or siDPP10-2). (B) Western blot analysis of DPP10 protein in SPC-A1 and NCI-H1299 lung cancer cells transfected with control siRNA (siNC) or DPP10 mRNA siRNA (siDPP10-1 or siDPP10-2). (C) qRT-PCR analysis of DPP10 mRNA levels in SPC-A1 and NCI-H1299 lung cancer cells transfected with empty vector (pcDNA3.1) or DPP10-AS1 overexpression plasmid (pcDNA3.1-DPP10-AS1). (D) Western blot analysis of DPP10 protein in SPC-A1 and NCI-H1299 lung cancer cells transfected with empty vector (pcDNA3.1) or DPP10-AS1 overexpression plasmid (pcDNA3.1-DPP10-AS1). Data are shown as mean ± SD from 3 independent experiments. \*\*P < 0.01, \*\*\*P < 0.001, \*\*\*\*P < 0.0001.



**Figure S3** Effect of actinomycin D on DPP10 mRNA stability. (A) SPC-A1 cells; (B) NCI-H1299 cells.



**Figure S4** DNA methylation analysis of DPP10 and DPP10-AS1 genes. (A) Predicted CpG islands (gray boxes) located in 5'-flanking regions of DPP10-AS1 and DPP10 genes (black boxes). Dotted lines indicate the positions of DNA methylation analysis in this study. (B) The sites of DNA methylation (CpG sites in red) in the sequences of the DPP10 and DPP10-AS1 promoter regions.