Table S1 Survival analysis for lncRNAs

				HR	95%CI	P-value
TCGA	OS	LUAD	LINC00174	0.74	0.55-0.99	0.044
	RFS	LUAD	LOC644656	1.66	1.08-2.55	0.02
		LUSC	MEG3	0.6	0.36-0.99	0.042
			LINC00863	0.5	0.27-0.93	0.025
			LINC00174	0.49	0.29-0.82	0.0062
			WDFY3-AS2	0.52	0.31-0.87	0.011
Chip	OS	LUAD	210794_s_at (MEG3)	0.66	0.53-0.84	6.4E-04
			1558290_a_at (PVT1)	1.54	1.2-1.97	6.4E-04
			1562953_s_at (WDFY3-AS2)	0.51	0.4-0.64	1.6E-08
		LUSC	1558290_a_at (PVT1)	1.61	1.17-2.22	0.0033
		All	210794_s_at (MEG3)	0.81	0.71-0.92	9.7E-04
			1558290_a_at (PVT1)	1.58	1.34-1.87	3.3E-08
			1562953_s_at (WDFY3-AS2)	0.54	0.46-0.65	9.6E-13
	FPS	LUAD	228889_at (ARHGAP5-AS1)	1.44	1.04-1.98	0.027
			210794_s_at (MEG3)	0.68	0.49-0.95	0.024
			1558290_a_at (PVT1)	1.69	1.21-2.36	0.0016
			1562953_s_at (WDFY3-AS2)	0.52	0.37-0.71	4.9E-05
		LUSC	228889_at (ARHGAP5-AS1)	1.88	1.12-3.18	0.016
			1558290_a_at (PVT1)	1.83	1.02-3.31	0.04
		All	228889_at (ARHGAP5-AS1)	1.55	1.17-2.05	1.9E-03
			1558290_a_at (PVT1)	1.73	1.32-2.26	6.1E-05
			1562953_s_at (WDFY3-AS2)	0.64	0.48-0.85	1.9E-03
	PFS	LUAD	210794_s_at (MEG3)	0.59	0.35-0.99	0.042
			1558290_a_at (PVT1)	1.72	1.02-2.9	0.038
		All	1558290_a_at (PVT1)	1.76	1.13-2.72	0.011

OS, overall survival; RFS, recurrence-free survival; FPS, first progression survival; PPS, post progression survival; HR, hazard ratio; CIs, confidence intervals; LUAD, lung adenocarcinoma; LUSC, and squamous cell carcinomas; TCGA, The Cancer Genome Atlas.