

Supplementary

Table S1 Clinicopathological characteristics of ESCA patients from TCGA database

Variables	Subgroup	Patients (n=161), n (%)
Age (years)	≤60	83 (51.6)
	>60	78 (48.4)
Gender	Male	138 (85.7)
	Female	23 (14.3)
Grade	1	16 (9.9)
	2	66 (41.0)
	3	43 (26.7)
	G	36 (22.4)
Stage	I	16 (9.9)
	II	68 (42.2)
	III	49 (30.4)
	IV	8 (5.0)
	Unknown	20 (12.4)
Tumor status	Tumor free	61 (37.9)
	With tumor	34 (21.1)
	Unknown	66 (41.0)
Vital status	Dead	64 (39.8)
	Alive	97 (60.2)

ESCA, esophageal cancer; TCGA, The Cancer Genome Atlas.

Table S2 Multivariate Cox proportional hazard model analyses results of ESCA patients

Variables	Group	b	SE	Wald	P	HR	HR 95% CI
<i>AC005515.1</i>	Low-expression	0*					
	High-expression	1.6	0.72	4.96	0.03	4.94	1.21–20.13
Age (years)		−0.03	0.03	1.04	0.31	0.97	0.92–1.03
Gender	Female	0*					
	Male	0.6	1.22	0.24	0.62	1.82	0.17–19.88
Tumor status	With tumor	0*					
	Tumor free	−2.2	0.89	6.17	0.01	0.11	0.02–0.63
Stage	Early-stage	0*					
	Late-stage	1.06	0.72	2.22	0.14	2.90	0.71–11.78
Grade				12.27	0.01		
	1	−0.63	1.28	0.24	0.62	0.53	0.04–6.53
	2	−1.23	1.39	0.78	0.38	0.29	0.02–4.47
	3	2.84	1.39	4.18	0.04	17.11	1.13–259.97

*, control group. Early-stage = stage I + stage II; late-stage = stage III + stage IV. ESCA, esophageal cancer; HR, hazard ratio; CI, confidence interval.

Table S3 Validation of *AC005515.1* prognostic and co-expression genes in pan-cancer*

eRNA	Co-expression genes	KIRP	LGG	MESO	OV	SKCM	THCA	UVM
<i>AC005515.1</i>	<i>CCL8</i>	0.33	0.18	0.54	0.55	0.64	0.38	0.58
<i>AC005515.1</i>	<i>CD274</i>	0.22	0.39	0.34	0.57	0.71	0.56	0.51
<i>AC005515.1</i>	<i>CD300A</i>	0.15	0.34	0.30	0.29	0.53	0.59	0.71
<i>AC005515.1</i>	<i>CD80</i>	0.35	0.45	0.41	0.44	0.64	0.57	0.46
<i>AC005515.1</i>	<i>CD86</i>	0.15	0.31	0.40	0.41	0.65	0.67	0.67
<i>AC005515.1</i>	<i>CTLA4</i>	0.37	0.38	0.42	0.45	0.39	0.74	0.72
<i>AC005515.1</i>	<i>FOXP3</i>	0.37	0.08	0.39	0.40	0.57	0.64	0.50
<i>AC005515.1</i>	<i>HAVCR2</i>	0.11	0.33	0.35	0.37	0.66	0.66	0.70
<i>AC005515.1</i>	<i>IDO1</i>	0.32	0.56	0.66	0.66	0.78	0.62	0.82
<i>AC005515.1</i>	<i>IL2RA</i>	0.23	0.37	0.10	0.28	0.53	0.58	0.55
<i>AC005515.1</i>	<i>IL4I1</i>	0.23	0.46	0.55	0.36	0.67	0.68	0.70
<i>AC005515.1</i>	<i>LAG3</i>	0.45	0.21	0.71	0.50	0.79	0.72	0.80
<i>AC005515.1</i>	<i>LILRB4</i>	0.11	0.28	0.37	0.37	0.63	0.63	0.58
<i>AC005515.1</i>	<i>MNDA</i>	0.24	0.28	0.20	0.39	0.62	0.64	0.61
<i>AC005515.1</i>	<i>TIGIT</i>	0.46	0.25	0.53	0.43	0.76	0.76	0.82

*, *AC005515.1* with co-expressed genes in all tumors above Spearman correlation P value <0.001. eRNA, enhancer RNA; KIRP, kidney renal papillary cell carcinoma; LGG, brain lower grade glioma; MESO, mesothelioma; OV, ovarian serous cystadenocarcinoma; SKCM, skin cutaneous melanoma; THCA, thyroid carcinoma; UVM, uveal melanoma.