

Supplementary Table 1 Association of *FUCA1* and *MMP-9* expression with clinicopathological characteristics in esophageal squamous cell carcinoma patients from The Cancer Genome Atlas (TCGA) database

Variable	FUCA1 expression		MMP-9 expression			
	Low expression (N = 66)	High expression (N = 10)	P	Low expression (N = 58)	High expression (N = 18)	P
Age (years, mean±SD)	57.67±10.35	62.90±12.88	0.15 3	58.29±10.40	58.56±12.21	0.929
Female (n, %)	12 (18.2%)	0 (0.0%)	0.14 2	12 (20.7%)	0 (0.0%)	0.035 ^a
T stage (n, %)						
T1-2	31 (47.0%)	2 (20.0%)	0.10	28 (48.3%)	5 (27.8%)	
T3-4	35 (53.0%)	8 (80.0%)	9	30 (51.7%)	13 (72.2%)	0.125
Lymphatic invasion (n, %)						
Negative (N0)	38 (57.6%)	6 (60.0%)	0.88	30 (51.7%)	14 (77.8%)	0.050 ^a

Positive (N+)	28 (45.4%)	4 (10.0%)	5	28 (48.3%)	4 (22.2%)	
TNM stage (n, %)						
I-II	49 (74.2%)	5 (50.0%)	0.11	40 (69.0%)	14 (77.8%)	0.471
III	17 (25.8%)	5 (50.0%)	5	18 (31.0%)	4 (22.2%)	
FUCA1 expression level (mean±SD)	—	—	—	1.46±0.21	1.47±0.18	0.692
High FUCA1 expression (n, %)	—	—	—	8 (13.8%)	2 (11.1%)	0.769
MMP-9 expression level (mean±SD)	1.59±0.60	1.62±0.49	0.88 7	—	—	—
High MMP-9 expression (n, %)	16 (24.2%)	2 (20.0%)	0.76 9	—	—	—

^aP<0.05. FUCA1: alpha-L-fucosidase-1; MMP-9: matrix metalloproteinase-9; SD: standard deviation.

Supplementary Table 2 Kaplan-Meier analysis and Cox multivariate regression analyses of overall survival in patients with esophageal squamous cell carcinoma from The Cancer Genome Atlas (TCGA) database

Negative (N0)	44	30.2%		0.483 (0.187-1.248)	0.133
Positive (N+)	32	14.8%	0.046 ^a	Reference	
TNM stage					
I-II	54	18.9%			
III	22	25.2%	0.236		
FUCA1					
expression					
Low	66	24.4%		0.264 (0.087-0.803)	0.019 ^a
High	10	0.0%	0.006 ^a	Reference	
MMP-9					
expression					
Low	58	22.9%			
High	18	34.9%	0.080		

^aP<0.05. No.: number; FUCA1: alpha-L-fucosidase-1; MMP-9: matrix metalloproteinase-9.