

Table S1 Clinical characteristics of patients with LUSC in TCGA dataset

Patient characteristics	Entire series (%)
Gender	
Male	359/487 (73.7)
Female	128/487 (26.3)
Age (years)	
≥68	261/487 (53.6)
<68	226/487 (46.4)
Stage	
I	239/487 (49.2)
II	159/487 (32.6)
III	82/487 (16.8)
IV	7/487 (1.4)
Race	
Non-White	142/487 (29.1)
White	345/487 (70.9)
T stage	
T1	110/487 (22.6)
T2	286/487 (58.7)
T3	67/487 (13.8)
T4	24/487 (4.9)
N stage	
N0	310/487 (63.7)
N1	128/487 (26.3)
N2	38/487 (7.8)
N3	11/487 (2.2)
M stage	
M0	402/487 (82.5)
M1	85/487 (17.5)

LUSC, lung squamous cell carcinoma; TCGA, The Cancer Genome Atlas.

Table S2 Clinical characteristics of patients with LUSC treated with cisplatin

Patient characteristics	Entire series (%)	Cisplatin sensitive (%)	Cisplatin resistant (%)
Gender			
Male	47/70 (67.1)	32/50 (64.0)	15/20 (75.0)
Female	23/70 (32.8)	18/50 (36.0)	5/20 (25.0)
Age (years)			
≥68	36/70 (51.4)	25/50 (50.0)	11/20 (55.0)
<68	34/70 (48.6)	25/50 (50.0)	9/20 (45.0)
Stage			
I	37/70 (52.8)	24/50 (48.0)	13/20 (65.0)
II	23/70 (32.8)	19/50 (38.0)	4/20 (20.0)
III	8/70 (11.4)	7/50 (14.0)	1/20 (5.0)
IV	2/70 (2.85)	0/50 (0.0)	2/20 (10.0)
Race			
Non-White	22/70 (31.4)	13/50 (26.0)	9/20 (45.0)
White	48/70 (68.5)	37/50 (74.0)	11/20 (55.0)
T stage			
T1	15/70 (21.4)	11/50 (22.0)	4/20 (20.0)
T2	41/70 (58.6)	32/50 (64.0)	9/20 (45.0)
T3	8/70 (11.4)	4/50 (8.0)	4/20 (20.0)
T4	6/70 (8.6)	3/50 (6.0)	3/20 (15.0)
N stage			
N0	44/70 (62.8)	29/50 (58.0)	15/20 (75.0)
N1	18/70 (25.7)	13/50 (26.0)	5/20 (25.0)
N2	6/70 (8.6)	6/50 (12.0)	0/20 (0.0)
N3	2/70 (2.86)	2/50 (4.0)	0/20 (0.0)
M stage			
M0	57/70 (81.4)	41/50 (82.0)	16/20 (80.0)
M1	13/70 (18.6)	9/50 (18.0)	4/20 (20.0)

LUSC, lung squamous cell carcinoma.

Table S3 The HR and P values of genes using univariate Cox analysis

Gene	HR	P value
<i>GAB2</i>	1.2712	0.005
<i>BCAM</i>	1.2031	0.007
<i>RASD2</i>	1.2249	0.01
<i>HES6</i>	0.8094	0.02
<i>CD83</i>	1.2181	0.02
<i>LPCAT1</i>	1.1518	0.02
<i>SMPDL3B</i>	1.1797	0.02
<i>AZGP1</i>	1.1118	0.02
<i>VWA2</i>	1.2172	0.02
<i>CTTN</i>	1.2173	0.02
<i>ALDH3B1</i>	1.1340	0.03
<i>CSTA</i>	0.9157	0.04
<i>CPM</i>	1.1274	0.04
<i>TUBA1A</i>	1.1520	0.04
<i>hsa-miR-4746</i>	0.7359	<0.001
<i>hsa-miR-556</i>	0.7954	0.007
<i>hsa-miR-125a</i>	1.3560	0.009
<i>hsa-miR-627</i>	0.8016	0.01
<i>hsa-miR-4777</i>	1.2064	0.02
<i>hsa-let-7b</i>	1.2910	0.02

Table S3 (continued)

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Gene	HR	P value
<i>hsa-miR-570</i>	0.8553	0.04
<i>hsa-miR-10a</i>	1.2194	0.04
<i>hsa-miR-376a-1</i>	0.8613	0.04
<i>hsa-miR-4664</i>	1.1727	0.04
<i>hsa-miR-187</i>	0.9193	0.04
<i>hsa-miR-204</i>	0.9262	0.04
<i>VWA2 13197 AT</i>	8.001	0.005
<i>ZNF254 48840 ES</i>	0.0210	0.006
<i>TACC1 83470 ES</i>	0.3757	0.01
<i>OCIAD1 69238 AD</i>	0.2562	0.01
<i>ZNF675 48823 AT</i>	0.0036	0.01
<i>KIFC3 36607 AP</i>	29.6137	0.01
<i>VPS33B 32535 ES</i>	0.0004	0.02
<i>ZNF765 51717 AT</i>	0.0246	0.03
<i>SELP 8930 AT</i>	0.0326	0.03
<i>AIF1L 87921 ES</i>	63.2014	0.03
<i>USHBP1 48246 AA</i>	0.2129	0.03
<i>SELP 8929 AT</i>	7.5334	0.04
<i>PPP2R1A 51422 ES</i>	0.0033	0.04
<i>VEGFA 76346 ES</i>	0.0695	0.04

HR, hazard ratio.

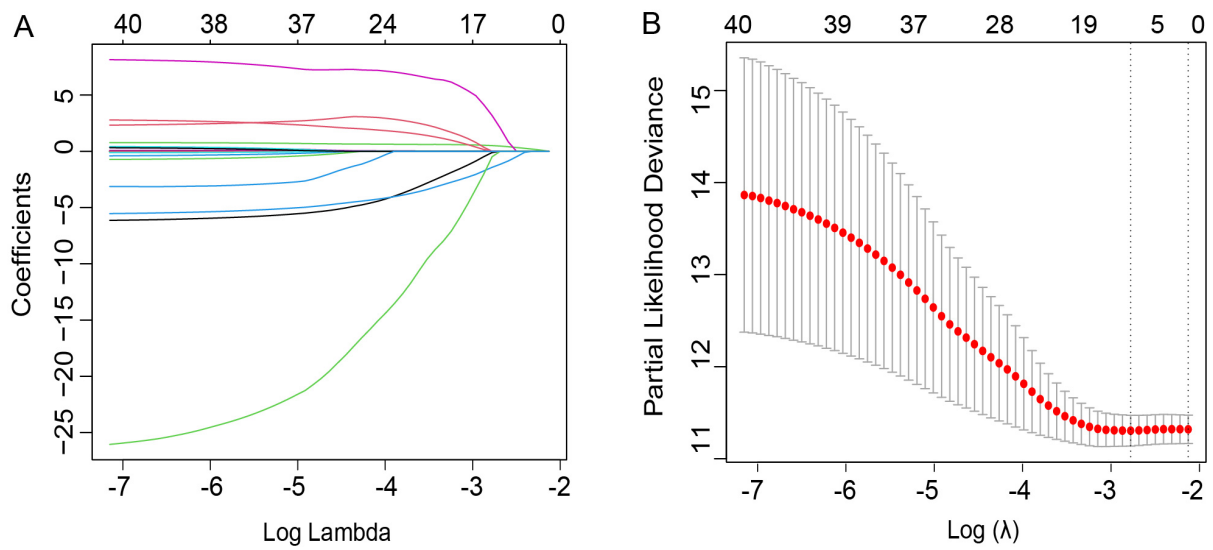


Figure S1 Survival-related AS events were selected using LASSO Cox regression. (A) LASSO coefficient profiles of the candidate survival-related AS events. (B) Dotted vertical lines are drawn at the optimal values according to the minimum criteria. AS, alternative splicing; LASSO, the least absolute shrinkage and selection operator.

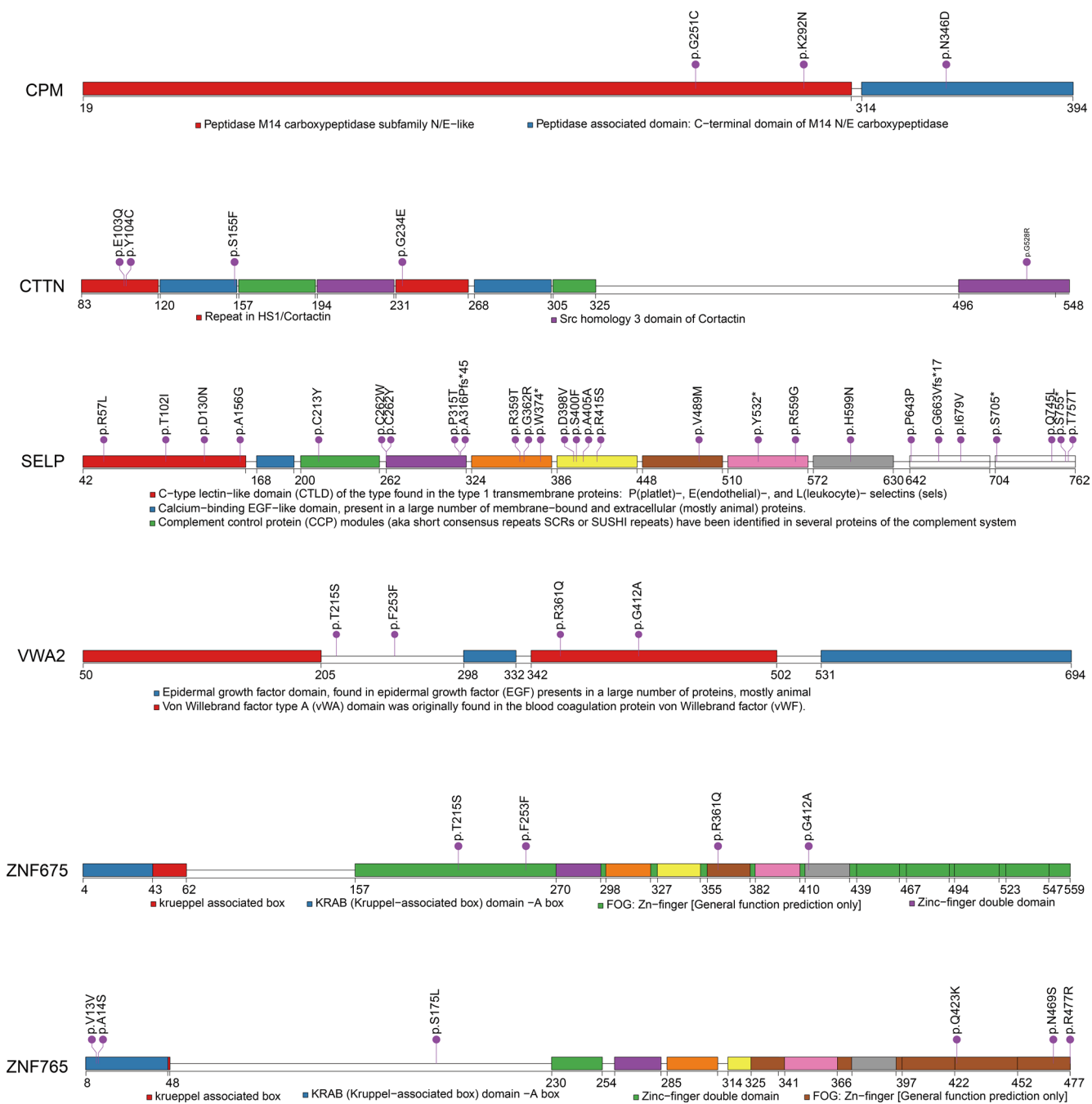


Figure S2 The mutation status of key genes identified. CPM, carboxypeptidase; CTTN, cortactin; SELP, selectin P; VWA2, von Willebrand factor A domain containing 2; ZNF675, zinc finger protein 675; ZNF765, zinc finger protein 765; SCR, short consensus repeats; SUSH1, a protein domain, also known as the complement control protein (CCP) module or short consistent repeat sequence (SCR); KRAB, Kruppel-associated box; FOG, friend of GATA protein 1.