



Figure S1 Validation analysis of prognostic genes. (A-C) Kaplan-Meier curve of OS in patients with in LUSC based on the expression levels of the screened apoptosis prognostic-associated genes. (D-F) Correlation of apoptosis prognostic-associated genes.

Table S1 Gene list of differentially expressed apoptosis-related genes

Gene	conMean	treatMean	logFC	P value	FDR
<i>AIFM3</i>	0.270773	0.700559	1.371425	6.69E-08	1.10E-07
<i>ANKH</i>	4.639122	9.392967	1.017729	9.89E-07	1.53E-06
<i>ATF3</i>	54.70707	17.50801	-1.64371	1.91E-14	4.64E-14
<i>BCL2L10</i>	0.045896	1.73876	5.243544	6.85E-28	8.78E-27
<i>BID</i>	6.35349	15.31675	1.269489	3.17E-23	1.36E-22
<i>BIK</i>	1.830894	14.68505	3.003728	1.49E-27	1.62E-26
<i>BIRC3</i>	15.72846	7.547526	-1.0593	1.27E-14	3.15E-14
<i>BMP2</i>	23.95174	5.34826	-2.16299	1.43E-25	7.76E-25
<i>BRCA1</i>	0.713776	3.135381	2.135097	1.34E-28	2.69E-27
<i>BTG2</i>	142.7783	56.20679	-1.34496	7.94E-20	2.67E-19
<i>CASP2</i>	4.215971	9.014885	1.096444	1.32E-25	7.69E-25
<i>CASP3</i>	8.595004	18.14378	1.077905	1.14E-25	7.33E-25
<i>CAV1</i>	337.4961	40.01923	-3.07611	4.43E-31	2.08E-29
<i>CCNA1</i>	1.065788	5.686832	2.415704	0.010996	0.01314
<i>CD69</i>	12.63208	3.051671	-2.04942	6.73E-24	3.06E-23
<i>CDK2</i>	4.647218	10.33843	1.153578	5.67E-26	3.92E-25
<i>CFLAR</i>	12.04202	4.650073	-1.37275	5.65E-28	7.97E-27
<i>CLU</i>	91.8612	44.61314	-1.04199	1.92E-17	5.88E-17
<i>DAP3</i>	14.15325	29.59325	1.064134	8.87E-30	2.50E-28
<i>DCN</i>	100.0508	41.5101	-1.2692	1.10E-20	4.10E-20
<i>DDIT3</i>	6.445955	15.33592	1.250448	3.84E-16	1.06E-15
<i>DIABLO</i>	0.103024	0.220453	1.097496	1.31E-16	3.84E-16
<i>DPYD</i>	11.93815	4.864436	-1.29524	4.47E-25	2.25E-24
<i>EGR3</i>	7.441904	2.605934	-1.51387	2.67E-08	4.42E-08
<i>ENO2</i>	10.06642	27.91277	1.471374	1.38E-15	3.67E-15
<i>FDXR</i>	3.970727	9.511052	1.260202	1.85E-18	5.92E-18
<i>GADD45B</i>	115.6195	20.36706	-2.50508	8.80E-27	6.89E-26
<i>GNA15</i>	9.529412	19.55855	1.037341	3.93E-12	8.41E-12
<i>GPX3</i>	351.7765	36.11748	-3.28389	1.63E-31	1.15E-29
<i>GSR</i>	18.16806	51.13136	1.492804	4.48E-11	8.90E-11
<i>H1-0</i>	56.29045	170.4876	1.598705	8.17E-25	3.84E-24
<i>HGF</i>	3.35189	0.814742	-2.04056	5.68E-27	5.00E-26
<i>HMGB2</i>	20.46248	57.22352	1.483627	1.35E-25	7.69E-25
<i>HMOX1</i>	82.43122	38.63852	-1.09315	1.94E-11	3.96E-11
<i>HSPB1</i>	159.7064	726.5315	2.185603	3.38E-25	1.77E-24
<i>IL6</i>	41.90234	6.273794	-2.73962	2.79E-11	5.62E-11
<i>JUN</i>	124.6739	60.62578	-1.04016	1.73E-13	4.07E-13
<i>LEF1</i>	1.362673	4.48433	1.718453	1.64E-16	4.71E-16
<i>NEDD9</i>	39.26205	9.685224	-2.01928	1.32E-29	3.10E-28
<i>PAK1</i>	6.642692	25.20642	1.923951	1.62E-30	5.70E-29
<i>PLAT</i>	7.680957	22.88883	1.575286	0.000201	0.000259
<i>PLCB2</i>	6.824408	2.669019	-1.35439	1.20E-22	4.97E-22
<i>PLPPR4</i>	1.526761	0.570044	-1.42133	3.70E-16	1.04E-15
<i>PMAIP1</i>	3.319633	17.83038	2.425242	4.74E-27	4.46E-26
<i>PRF1</i>	18.64637	6.339824	-1.55638	1.58E-20	5.55E-20
<i>RARA</i>	17.49067	6.605723	-1.4048	4.52E-28	7.38E-27
<i>RHOB</i>	244.8673	79.7188	-1.61901	1.36E-25	7.69E-25
<i>SMAD7</i>	13.62529	4.953945	-1.45964	1.16E-27	1.36E-26
<i>SPTAN1</i>	29.06338	14.43624	-1.00951	2.66E-23	1.17E-22
<i>TGFB2</i>	4.242182	2.116273	-1.00328	5.82E-17	1.74E-16
<i>TGFBR3</i>	11.33088	3.034507	-1.90073	4.38E-27	4.41E-26
<i>TIMP2</i>	77.319	38.02221	-1.02398	8.83E-19	2.89E-18
<i>TIMP3</i>	374.9014	80.91822	-2.21197	4.71E-28	7.38E-27
<i>TOP2A</i>	1.693839	35.42218	4.386284	1.52E-31	1.15E-29
<i>TXNIP</i>	380.003	111.6687	-1.76679	4.69E-25	2.28E-24
<i>VDAC2</i>	17.54686	38.48762	1.133182	6.40E-27	5.31E-26

FC, fold change; FDR, false discovery rate.

Table S2 Top 10 GO and KEGG analysis results based on differentially expressed ARGs with the smallest P values

Category	Term	P value	FDR
BP	apoptotic process	1.03E-27	1.78E-24
BP	positive regulation of apoptotic process	3.95E-22	3.40E-19
BP	negative regulation of apoptotic process	3.85E-18	2.21E-15
BP	regulation of apoptotic process	5.71E-14	2.46E-11
BP	execution phase of apoptosis	1.13E-12	3.91E-10
BP	apoptotic signaling pathway	2.34E-11	5.78E-09
BP	extrinsic apoptotic signaling pathway in absence of ligand	2.35E-11	5.78E-09
BP	activation of cysteine-type endopeptidase activity involved in apoptotic process	1.28E-09	2.76E-07
BP	positive regulation of intrinsic apoptotic signaling pathway	1.83E-09	3.50E-07
BP	release of cytochrome c from mitochondria	2.54E-09	4.38E-07
CC	cytosol	1.46E-12	3.95E-10
CC	macromolecular complex	2.18E-10	2.27E-08
CC	Bcl-2 family protein complex	2.52E-10	2.27E-08
CC	mitochondrion	6.01E-08	4.06E-06
CC	mitochondrial outer membrane	1.80E-07	9.69E-06
CC	membrane raft	1.35E-06	6.08E-05
CC	cytoplasm	2.24E-06	8.65E-05
CC	cell cortex	3.95E-06	1.33E-04
CC	perinuclear region of cytoplasm	1.94E-05	5.81E-04
CC	nucleus	4.96E-05	0.001266352
MF	cysteine-type endopeptidase activity involved in execution phase of apoptosis	1.54E-07	1.62E-05
MF	protein binding	2.22E-07	1.62E-05
MF	identical protein binding	2.52E-07	1.62E-05
MF	cysteine-type endopeptidase activity involved in apoptotic signaling pathway	2.56E-07	1.62E-05
MF	cysteine-type endopeptidase activity involved in apoptotic process	2.56E-07	1.62E-05
MF	death receptor binding	2.16E-06	1.14E-04
MF	macromolecular complex binding	7.83E-06	3.53E-04
MF	protein kinase binding	1.27E-05	5.01E-04
MF	protein heterodimerization activity	1.63E-05	5.33E-04
MF	ubiquitin protein ligase binding	1.69E-05	5.33E-04
KEGG_PATHWAY	Apoptosis	2.94E-21	3.70E-19
KEGG_PATHWAY	Pathways in cancer	6.28E-14	3.96E-12
KEGG_PATHWAY	Lipid and atherosclerosis	2.59E-11	1.09E-09
KEGG_PATHWAY	Platinum drug resistance	4.88E-10	1.54E-08
KEGG_PATHWAY	Apoptosis - multiple species	1.84E-09	4.64E-08
KEGG_PATHWAY	NOD-like receptor signaling pathway	1.80E-08	3.79E-07
KEGG_PATHWAY	MAPK signaling pathway	2.90E-08	5.22E-07
KEGG_PATHWAY	Chagas disease	2.14E-07	3.38E-06
KEGG_PATHWAY	Pathogenic Escherichia coli infection	3.24E-07	4.54E-06
KEGG_PATHWAY	Proteoglycans in cancer	5.13E-07	5.45E-06

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; ARG, apoptosis-related genes; BP, biological processes; CC, cellular component; MF, molecular function; NOD, nucleotide-binding oligomerization domain; MAPK, mitogen-activated protein kinase; FDR, false discovery rate.