Table S1 The 38 prognostic ARGs

Gene	HR(95% CI)	P value
CAV1	1.123 (1.014–1.244)	0.026
BIRC5	1.226 (1.103–1.363)	<0.001
KL	0.763 (0.634–0.919)	0.004
SLC2A1	1.246 (1.130–1.374)	<0.001
ZEB2	0.839 (0.714–0.986)	0.033
PAK1	1.273 (1.024–1.582)	0.030
PHLDA2	1.154 (1.029–1.294)	0.014
TIMP1	1.250 (1.064–1.467)	0.007
PIK3R1	0.834 (0.699–0.995)	0.043
PDGFB	1.264 (1.091–1.465)	0.002
PPARG	1.135 (1.011–1.273)	0.031
E2F1	1.132 (1.005–1.275)	0.041
VTN	1.139 (1.001–1.297)	0.048
HGF	0.788 (0.677–0.919)	0.002
TWIST1	1.130 (1.016–1.257)	0.025
CEMIP	1.105 (1.014–1.203)	0.023
ITGB4	1.203 (1.093–1.323)	<0.001
ANGPTL4	1.177 (1.087–1.275)	<0.001
PLK1	1.378 (1.219–1.557)	<0.001
CDC25C	1.379 (1.196–1.590)	<0.001
SESN1	0.809 (0.657–0.996)	0.046
TUBB3	1.257 (1.017–1.552)	0.034
UBE2C	1.171 (1.068–1.283)	<0.001
DAPK2	0.717 (0.601–0.855)	<0.001
ITGA8	0.848 (0.747–0.962)	0.011
ITPRIP	1.261 (1.048–1.516)	0.014
PBK	1.253 (1.127–1.394)	<0.001
HMGA1	1.317 (1.170–1.484)	<0.001
BUB1	1.225 (1.087–1.381)	<0.001
CDKN3	1.308 (1.163–1.472)	<0.001
MAD2L1	1.274 (1.123–1.446)	<0.001
CDK1	1.273 (1.130–1.434)	<0.001
PLK4	1.244 (1.075–1.439)	0.003
LAMA3	1.161 (1.062–1.269)	0.001
SFN	1.197 (1.056–1.356)	0.005
HMCN1	0.875 (0.768–0.996)	0.043
SLCO1B3	1.179 (1.072–1.297)	<0.001
LMO3	0.890 (0.822–0.964)	0.004
EDAR	1.208 (1.037–1.408)	0.015

Table S2 The 120 prognostic ERGs

Gene	HR(95% CI)	P value
CAV1	1.123 (1.014–1.244)	0.026
BIRC5	1.226 (1.103–1.363)	<0.001
KL	0.763 (0.634–0.919)	0.004
SLC2A1	1.246 (1.130–1.374)	<0.001
ZEB2	0.839 (0.714–0.986)	0.033
PAK1	1.273 (1.024–1.582)	0.030
PHLDA2	1.154 (1.029–1.294)	0.014
TIMP1	1.250 (1.064–1.467)	0.007
PIK3R1	0.834 (0.699–0.995)	0.043
PDGFB	1.264 (1.091–1.465)	0.002
PPARG	1.135 (1.011–1.273)	0.031
E2F1	1.132 (1.005–1.275)	0.041
VTN	1.139 (1.001–1.297)	0.048
HGF	0.788 (0.677–0.919)	0.002
TWIST1	1.130 (1.016–1.257)	0.025
CEMIP	1.105 (1.014–1.203)	0.023
ITGB4	1.203 (1.093–1.323)	<0.001
ANGPTL4	1.177 (1.087–1.275)	<0.001
AGER	0.920 (0.859–0.986)	0.018
PRKCE	0.767 (0.620–0.949)	0.014
GOLM1	1.301 (1.121–1.508)	<0.001
ERG	0.826 (0.689–0.990)	0.038
UHRF1	1.279 (1.122–1.458)	<0.001
TCF21	0.855 (0.735–0.995)	0.044
LGR4	1.214 (1.065–1.384)	0.004
TNS1	0.867 (0.763–0.986)	0.029
FERMT1	1.223 (1.083–1.380)	0.001
MYBL2	1.151 (1.057–1.255)	0.001
TRAP1	1.283 (1.017–1.618)	0.036
NME1	1.249 (1.043–1.497)	0.016
FOXM1	1.260 (1.134–1.399)	<0.001
SLIT3	0.860 (0.758–0.976)	0.019
TERT	1.250 (1.006–1.552)	0.044
GJB2	1.164 (1.078–1.258)	<0.001
CCNA2	1.286 (1.148–1.440)	<0.001

Table S2 *(continued)*

Table S2 *(continued)*

Gene	HR(95% CI)	P value
KLF4	1.177 (1.051–1.318)	0.005
GAPDH	1.590 (1.347–1.877)	<0.001
TIMELESS	1.242 (1.069–1.443)	0.005
GREM1	1.091 (1.002–1.189)	0.046
LMNB1	1.272 (1.106–1.464)	<0.001
TLR4	0.851 (0.729–0.993)	0.041
MAP3K3	0.797 (0.652–0.976)	0.028
AURKA	1.259 (1.112–1.426)	<0.001
ECT2	1.356 (1.186–1.550)	<0.001
SFTPC	0.952 (0.918–0.987)	0.007
KAT2B	0.812 (0.681–0.969)	0.021
GPC3	0.889 (0.811–0.975)	0.013
ARRB1	0.791 (0.671–0.932)	0.005
TACC3	1.369 (1.178–1.590)	<0.001
NTRK3	0.408 (0.208–0.800)	0.009
PKP3	1.432 (1.200–1.710)	<0.001
BOP1	1.279 (1.092–1.499)	0.002
MMP1	1.095 (1.028–1.166)	0.005
ENO1	1.420 (1.153–1.749)	<0.001
TPBG	1.245 (1.076–1.441)	0.003
SMAD9	0.807 (0.694–0.939)	0.006
PEBP4	0.930 (0.873–0.990)	0.023
FGFR2	0.868 (0.771–0.978)	0.020
RDX	1.272 (1.067–1.516)	0.007
GATA1	0.605 (0.387–0.946)	0.027
NDRG2	0.843 (0.733–0.970)	0.017
GPI	1.532 (1.262–1.861)	<0.001
NES	1.159 (1.019–1.319)	0.024
FBP1	0.845 (0.746–0.956)	0.008
CCND2	0.860 (0.748–0.989)	0.035
KCNN4	1.110 (1.017–1.212)	0.020
CA9	1.066 (1.006–1.130)	0.031
FHL2	1.146 (1.024–1.283)	0.018
GMNN	1.200 (1.016–1.418)	0.032

Table S2 *(continued)*

Table S2 *(continued)*

Gene	HR(95% CI)	P value
MTHFD2	1.255 (1.069–1.473)	0.006
SIX1	0.904 (0.820–0.996)	0.040
ADAM12	1.139 (1.027–1.264)	0.014
EPB41L5	0.819 (0.692–0.968)	0.019
EPHB2	1.166 (1.034–1.315)	0.012
IGFBP3	1.139 (1.025–1.265)	0.016
KRT8	1.423 (1.224–1.654)	<0.001
IL11	1.254 (1.094–1.439)	0.001
ETV1	0.886 (0.788–0.996)	0.042
KRT18	1.453 (1.246–1.693)	<0.001
CIP2A	1.193 (1.045–1.363)	0.009
EGLN3	1.155 (1.059–1.260)	0.001
TYMS	1.330 (1.137–1.555)	<0.001
TWIST2	1.269 (1.095–1.471)	0.002
EFNB2	1.248 (1.087–1.433)	0.002
LHX2	1.215 (1.042–1.418)	0.013
BRCA1	1.185 (1.024–1.370)	0.022
JUNB	1.204 (1.029–1.409)	0.020
PTX3	1.168 (1.035–1.318)	0.012
IRF8	0.819 (0.719–0.934)	0.003
CYP4Z1	0.783 (0.624–0.982)	0.035
POSTN	1.118 (1.010–1.237)	0.032
LYPD3	1.223 (1.136–1.318)	<0.001
CFTR	0.835 (0.754–0.926)	<0.001
TNFAIP8L2	0.870 (0.757–0.998)	0.047
SIM2	1.251 (1.061–1.475)	0.008
LOXL2	1.293 (1.159–1.442)	<0.001
ID1	1.159 (1.051–1.279)	0.003
HOXB9	1.075 (1.008–1.145)	0.027
S100P	1.077 (1.028–1.129)	0.002
HMGA2	1.156 (1.064–1.257)	<0.001
SPOCK1	1.161 (1.065–1.265)	<0.001
KLK6	1.113 (1.035–1.197)	0.004
ROS1	0.923 (0.853–0.998)	0.044

Table S2 *(continued)*

Table S2 *(continued)*

Gene	HR(95% CI)	P value
HOXA10	1.186 (1.061–1.326)	0.003
PRRX2	1.096 (1.003–1.198)	0.043
MUC16	1.100 (1.007–1.203)	0.035
ISG15	1.132 (1.032–1.242)	0.009
HOXB7	1.146 (1.048–1.254)	0.003
ELF5	0.822 (0.741–0.913)	<0.001
CXCL5	1.077 (1.002–1.156)	0.043
SALL1	1.140 (1.012–1.284)	0.031
CDX2	1.282 (1.129–1.456)	<0.001
PFN2	1.115 (1.001–1.243)	0.049
HOXA13	1.438 (1.210–1.710)	<0.001
F2	1.236 (1.108–1.379)	<0.001
CDKL2	0.833 (0.748–0.926)	<0.001
MUC2	1.230 (1.083–1.396)	0.001
SERPINB4	1.095 (1.005–1.194)	0.039
CCL20	1.126 (1.051–1.206)	<0.001
KRT17	1.096 (1.031–1.166)	0.003

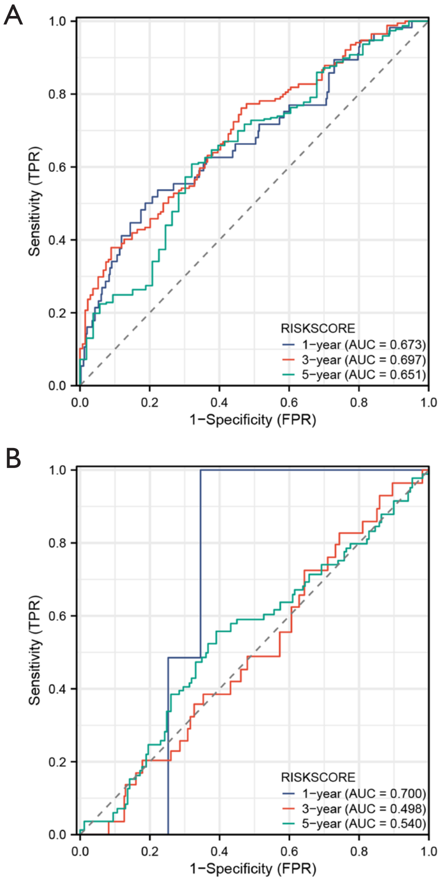

Figure S1 Validation of the prognostic risk model using ROC analysis. (A) ROC curves of a risk score for predicting the 1-/3-/5-year survival in the TCGA cohort. (B) ROC curves of risk score for predicting the 1-/3-/5-year survival in the GSE68465.

Table S3 LUAD cell lines (nTPM) in the HPA database

Gene	H1975	PC9	H1650	H1299	A459	H292	HCC827	H920	H1435	H647
SLC2A1	64.5	94.1	96.0	20.0	42.9	94.6	154.0	177.5	1599.6	176.7
BIRC5	73.4	85.5	104.0	118.1	129.9	52.1	86.3	61.0	129.7	49.1
ANGPTL4	34.4	0.7	40.5	23.0	25.3	3.7	15.4	14.9	0.9	0.2
PIK3R1	4.0	2.0	6.8	8.5	8.7	6.2	8.4	9.3	8.7	5.9
KL	0	0.3	0	0	0	0	0	0	0	0