| NKRD65 | (N=508) | 1.06 (0.90 – 1.26) | ⊢ | 0.47 |
|---------------|------------------------|-----------------------|---------------------------------------|-----------------|
| CASZ1 | (N=508) | 0.98 (0.76 - 1.26) | | 0.86 |
| QCC | (N=508) | (0.61 - 1.33) | | 0.58 |
| CRL6 | (N=508) | (0.65 - 1.10) | - | 0.20 |
| (LHDC9 | (N=508) | 1.01 (0.82 - 1.24) | F 1 | 0.92 |
| NTS7 | (N=508) | (0.78 - 1.60) | • | 0.53 |
| (CNK1 | (N=508) | 1.08 (0.92 - 1.27) | ⊢ | 0.32 |
| P53I3 | (N=508) | 0.98 (0.77 - 1.23) | • # • | 0.83 |
| STAP1 | (N=508) | 0.94 (0.78 - 1.13) | · · · · · · · · · · · · · · · · · · · | 0.48 |
| IPSE | (N=508) | (0.97 - 1.46) | | 0.09 |
| FAP2A | (N=508) | (0.88 - 1.18) | | 0.81 |
| / IYO6 | (N=508) | (0.53 - 0.94) | | 0.01 |
| DDX56 | (N=508) | 1.08 (0.62 - 1.89) | | 0.78 |
| CT6A | (N=508) | 0.85 (0.54 - 1.33) | | 0.46 |
| GPR37 | (N=508) | 1.11 (0.98 – 1.26) | | 0.09 |
| ITUS1 | (N=508) | 0.78 (0.62 - 0.97) | | 0.02 |
| ITRA4 | (N=508) | 0.90 (0.73 - 1.11) | | 0.32 |
| SQLE | (N=508) | 1.24 (1.00 - 1.54) | | 0.05 |
| -GR4 | (N=508) | 1.11 (0.90 - 1.37) | ⊢ ∎(| 0.31 |
| KRT18 | (N=508) | 1.13 (0.88 - 1.44) | • • • • • • • • • • • • • • • • • • • | 0.33 |
| АВРС3 | (N=508) | 1.39 (1.05 - 1.83) | · | - 0.02 |
| FNB2 | (N=508) | 1.21 (1.02 - 1.43) | | 0.02 |
| VD | (N=508) | 0.92 (0.72 - 1.18) | | 0.53 |
| IGRN | (N=508) | 1.31 (0.94 – 1.82) | | 0.11 |
| IS3ST2 | (N=508) | 1.02 (0.86 - 1.20) | · | 0.83 |
| CD68 | (N=508) | 0.66 (0.42 - 1.04) | | 0.07 |
| RRC37A3 | (N=508) | 1.46 (1.10 - 1.93) | · | — — 0.00 |
| NF750 | (N=508) | 0.97 (0.86 - 1.09) | | 0.59 |
| RAB27B | (N=508) | 1.09 (0.94 - 1.27) | ⊢ | 0.27 |
| NF77 | (N=508) | 0.71 (0.48 - 1.04) | i | 0.07 |
| CAMSAP3 | (N=508) | 0.68 (0.50 - 0.90) | | 0.00 |
| PTPRH | (N=508) | 1.15 (1.01 - 1.31) | | 0.04 |
| RIM28 | (N=508) | 1.37 (0.88 - 2.14) | | 0.16 |
| EBPB | (N=508) | 1.36 (1.01 - 1.83) | | — 0 .04 |
| | ıl p−value (Log−Rank): | | | |

Hazard ratio(95%CI)

Figure S1 Prognostic-related genes incorporated into the IRRS formula. Forest plot illustrating the 34 genes selected and incorporated into the risk score formula after the LASSO regression analysis. *, P<0.05; **, P<0.01.

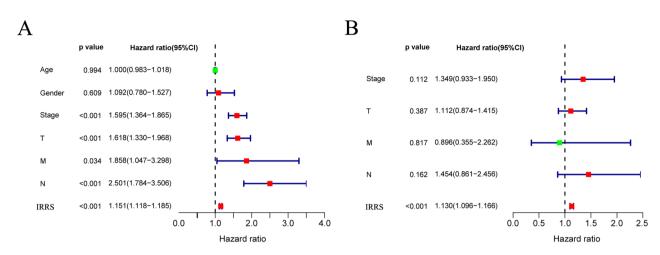


Figure S2 The IRRS independently predicted OS in patients with LUAD. (A) Univariate Cox regression analysis revealed that clinical stage, T stage, N stage, M stage, and IRRS were independent predictors for OS in LUAD. (B) Multivariate regression analysis revealed that the IRRS was an independent predictor for overall OS in patients with LUAD.