

Figure S1. Flowchart of the research techniques and methods used in the present study. DEG, differentially expressed genes; KEGG, Kyoto Encyclopedia of Genes and Genomes; LUAD, lung adenocarcinoma; ROC, receiver operating characteristic; TCGA, The Cancer Genome Atlas.

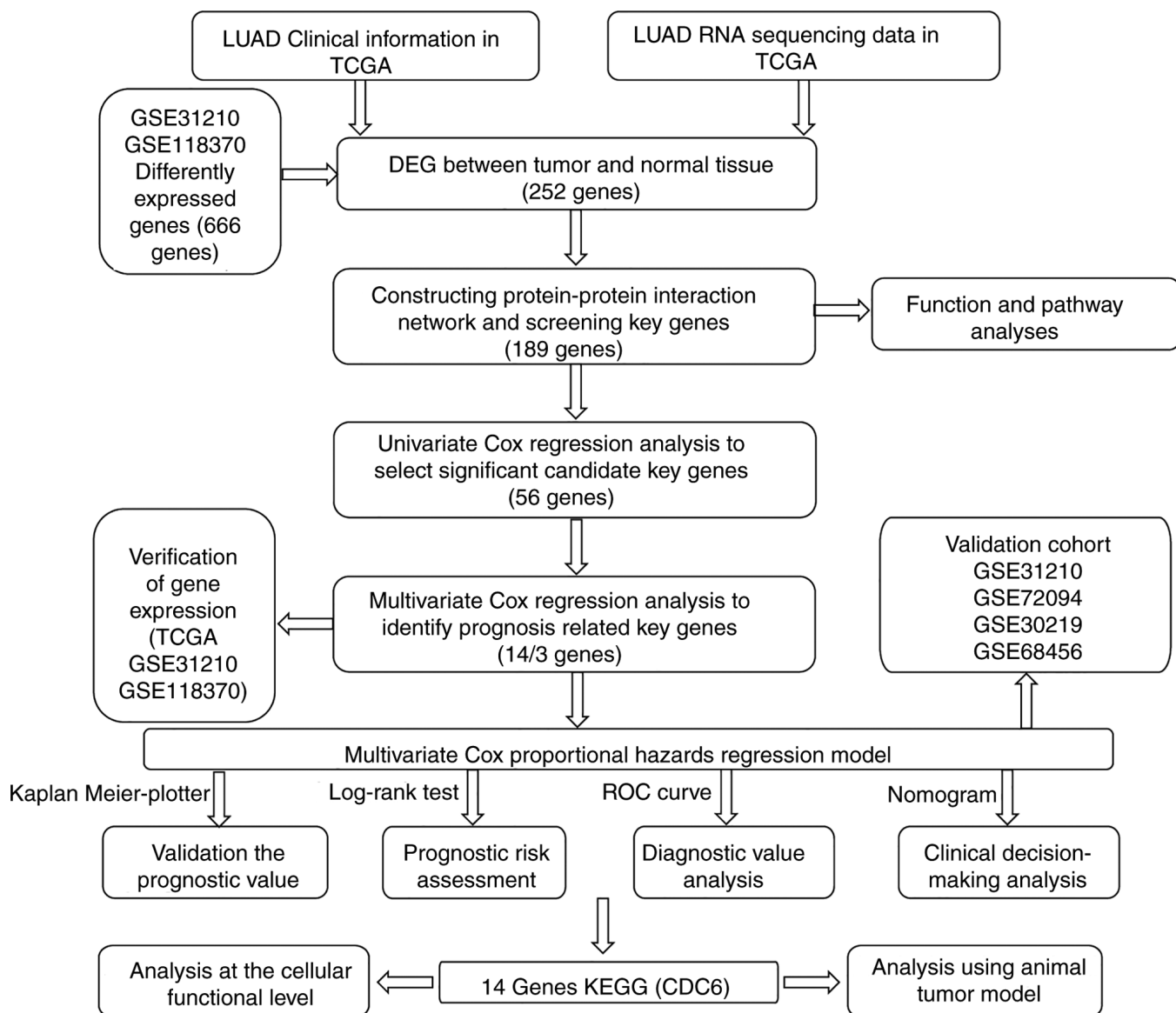


Figure S2. Expression of 14 genes in patients with LUAD based on TCGA and GEO datasets. (A) Heatmap showing expression of 14 LUAD genes in TCGA dataset. (B) Heatmap showing expression of 14 LUAD genes in the GSE118370 and GSE31210 datasets. GEO, Gene Expression Omnibus; N, normal tissue; T, tumor tissue; TCGA, The Cancer Genome Atlas.

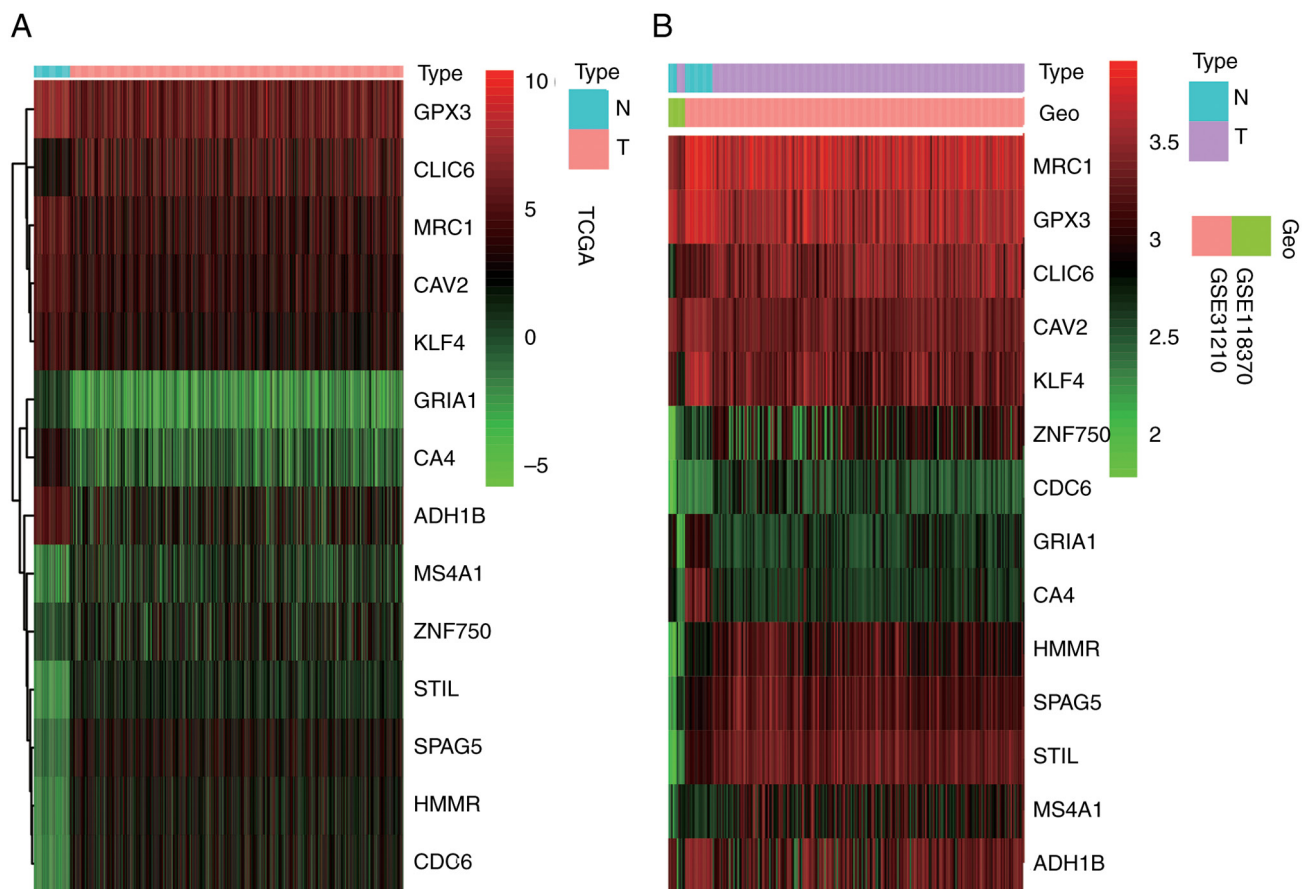


Figure S3. Gene expression heatmaps and patient survival status in high and low risk groups of the 14 and 3-gene models. (A) Gene expression heatmaps and patient survival status in high and low risk groups of TCGA dataset. Gene expression heatmaps and patient survival status in high and low risk groups of the (B) GSE72094, (C) GSE30219, (D) GSE31210 and (E) GSE68456 Gene Expression Omnibus datasets. TCGA, The Cancer Genome Atlas.

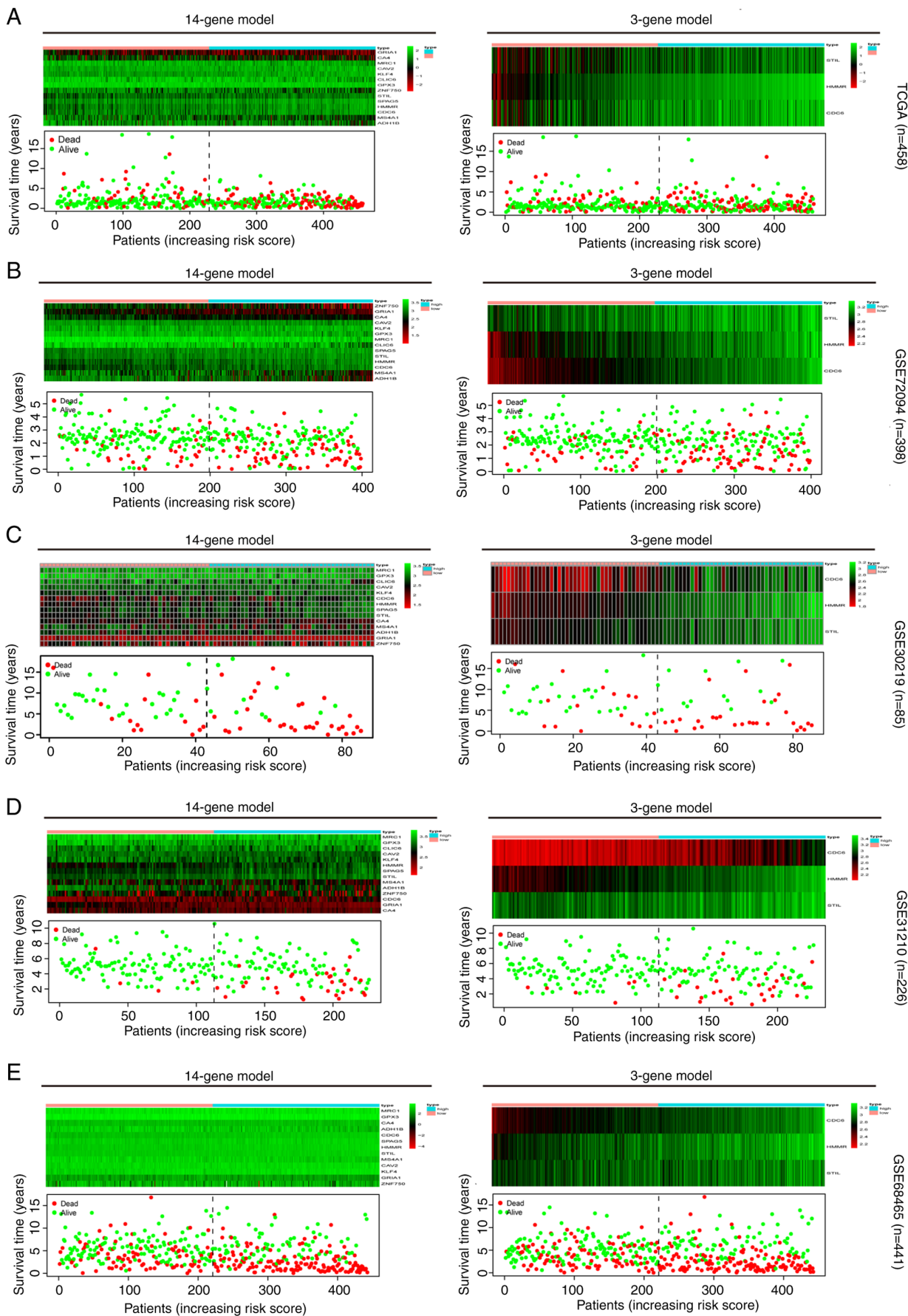


Figure S4. Analysis of the wound healing, migration and invasion *in vitro* results and animal weight. Bar chart analyses of the (A) wound healing, (B) cell migration and (C) cell invasion results. (D) Line chart of the mouse weight changes in the tumor model. n=3; *P<0.05 and **P<0.01. nc, negative control; ns, not significant; si(RNA), small interfering (RNA).

