

Figure S1: Heat map of differentially expressed gene samples between lung adenocarcinoma and normal tissues.

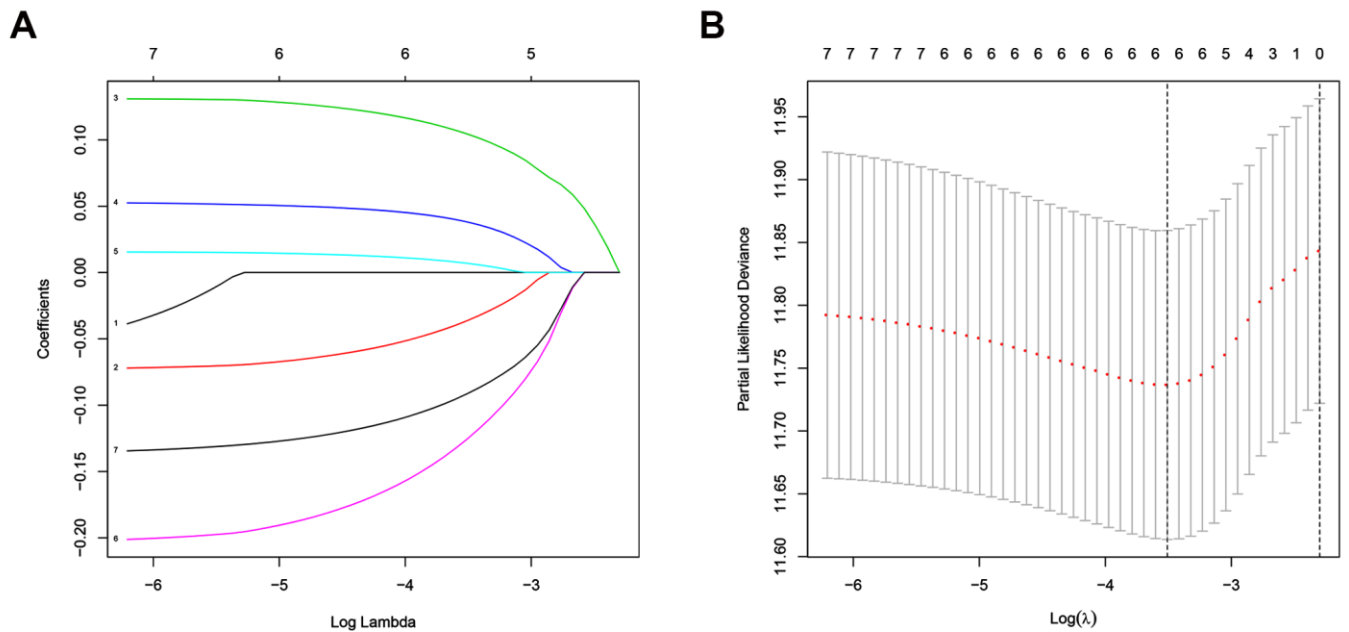


Figure S2: Gene selection using the least absolute shrinkage and selection operator model. (A) 10-fold cross-validation for the coefficients of 7 GPX4-related DEGs in the LASSO model. (B) X-tile analysis of the 6 selected GPX4-related prognostic DEGs.

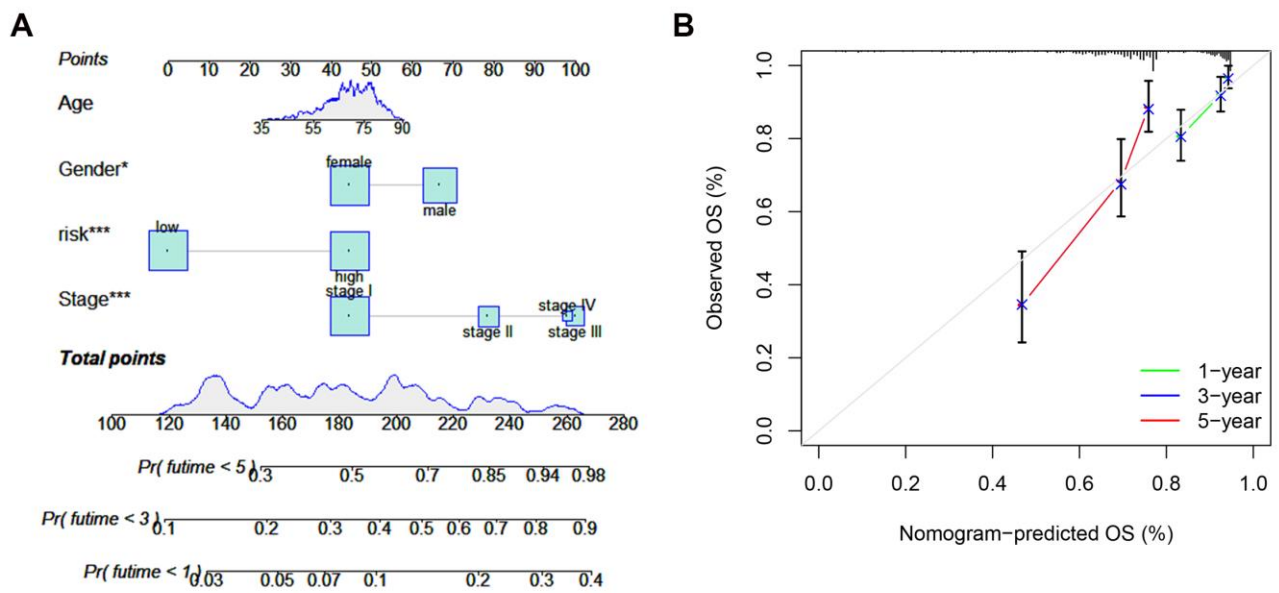


Figure S3: Validation of nomogram based on GSE72094 dataset. (A) The nomogram plot. (B) The nomogram calibration curves in the years 1, 3, 5.

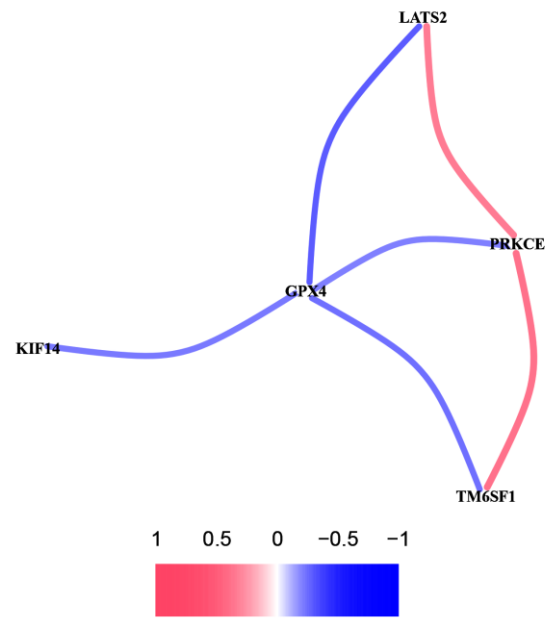


Figure S4: Connection network for four GPX4-related prognostic genes and GPX4.