

Figure S1. Disease-free survival, progression-free survival and overall survival curves of lung squamous cell carcinoma with high and low expression of (A) C1SD1, (B) FANCD2, (C) FDFT1, (D) GPX4, (E) HSPB1, (F) NCOA4, (G) NFE2L2, (H) RPL8, (I) SLC1A5, (J) SLC7A11 and (K) TFRC from TCGA dataset.

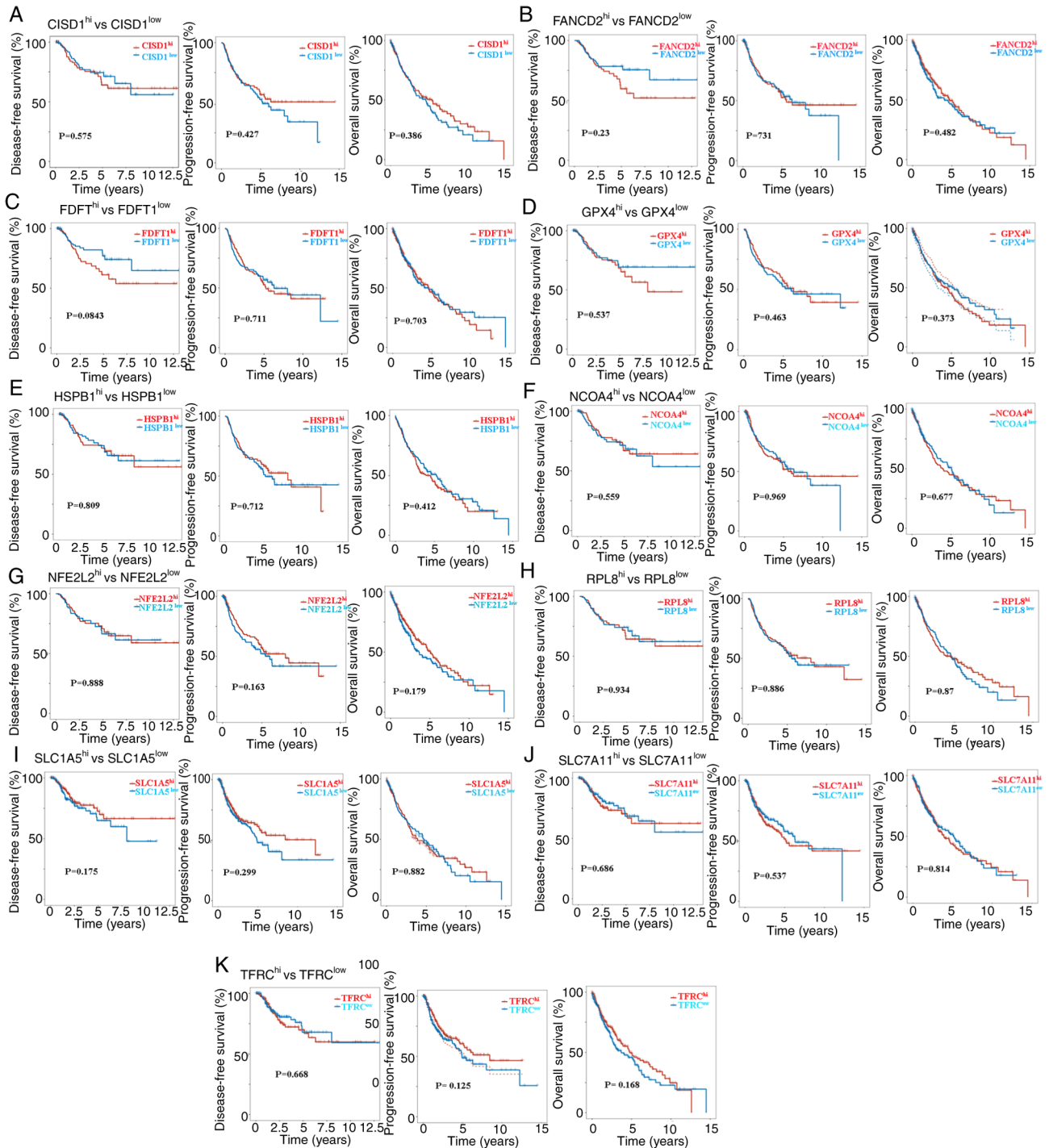


Figure S2. (A) mRNA expression of HSPA5 in lung adenocarcinoma and normal tissues from TCGA dataset. (B) Disease-free survival, (C) progression-free survival and (D) overall survival curves of lung adenocarcinoma with high and low expression of HSPA5 from TCGA dataset. *** $P < 0.001$. HSPA5, heat shock protein A5; HSPA5^{hi}, high expression of HSPA5.

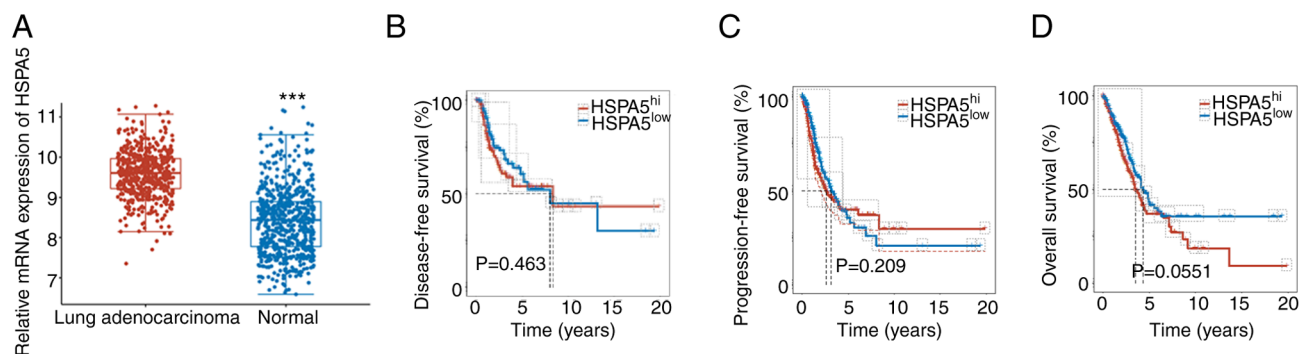


Figure S3. Hazard ratios and P-values of factors influencing OS according to (A) univariate and (B) multivariate Cox regression, including HSPA5, p-TNM stage, age, sex and smoking from the TCGA dataset. (C) Nomogram predicting the 1-, 3- and 5-year OS of patients with lung squamous cell carcinoma from TCGA dataset. (D) Calibration curve for the OS nomogram in the discovery group from TCGA dataset. The dashed diagonal line represents an ideal nomogram, whereas the red, orange and blue-gray lines represent the 1-, 3- and 5-year nomograms, respectively. OS, overall survival; HSPA5, heat shock protein A5; p-TNM, pathological tumor-node-metastasis.

