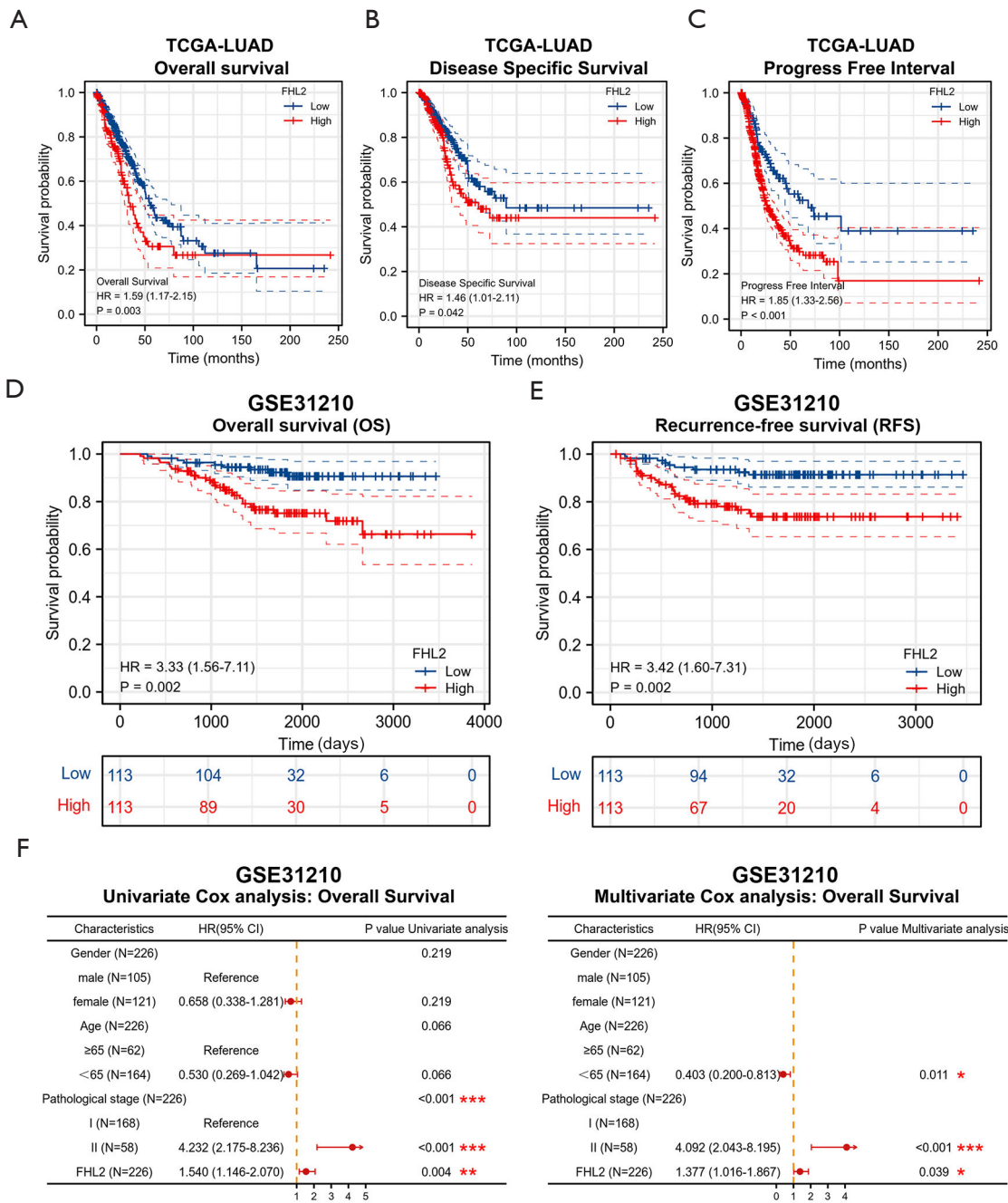**Figure S1** Correlation of FHL2 and mRNA modifications and immune microenvironment. (A) Association between FHL2 and m1A, m5C, and m6A methylation modification-related genes in pan-cancer. *, P<0.05. (B) Correlation between FHL2 and chemokines, receptors, MHC, immunoinhibitator and immunomodulators in pan-cancer. *, P<0.05. MHC, major histocompatibility complex.

Figure S2 Prognostic significance of FHL2 in lung adenocarcinoma. Kaplan-Meier survival curves for Overall survival (A), Disease Specific Survival (B), and Progress Free Interval (C) in patients with different FHL2 expression groups in lung adenocarcinoma using data from the The Cancer Genome Atlas (TCGA) database. Kaplan-Meier survival curves for Overall survival (D), and Recurrence-free survival (E) in patients with different expression groups of FHL2 in lung adenocarcinoma by using GSE31210. (F) Univariate cox regression analysis of FHL2 and other clinicopathological characteristics. (G) The forest plot presents the multivariate cox regression analysis of FHL2 combined with clinicopathological characteristics such as Gender, Age, and Pathological Stage. *, P<0.05; **, P<0.01; ***, P<0.001. Lung adenocarcinoma (LUAD)