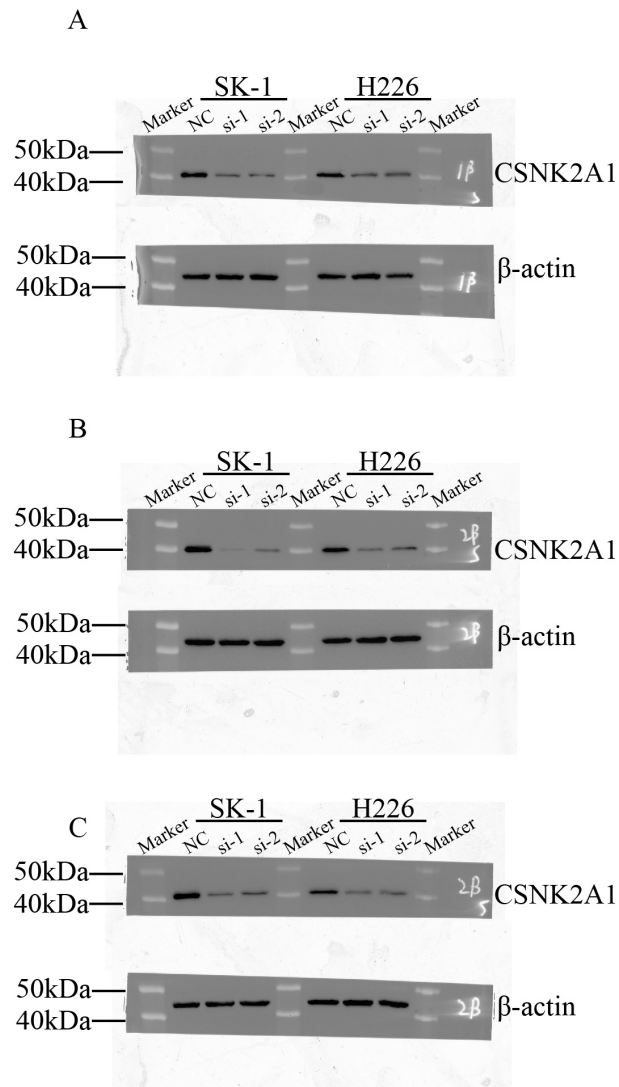
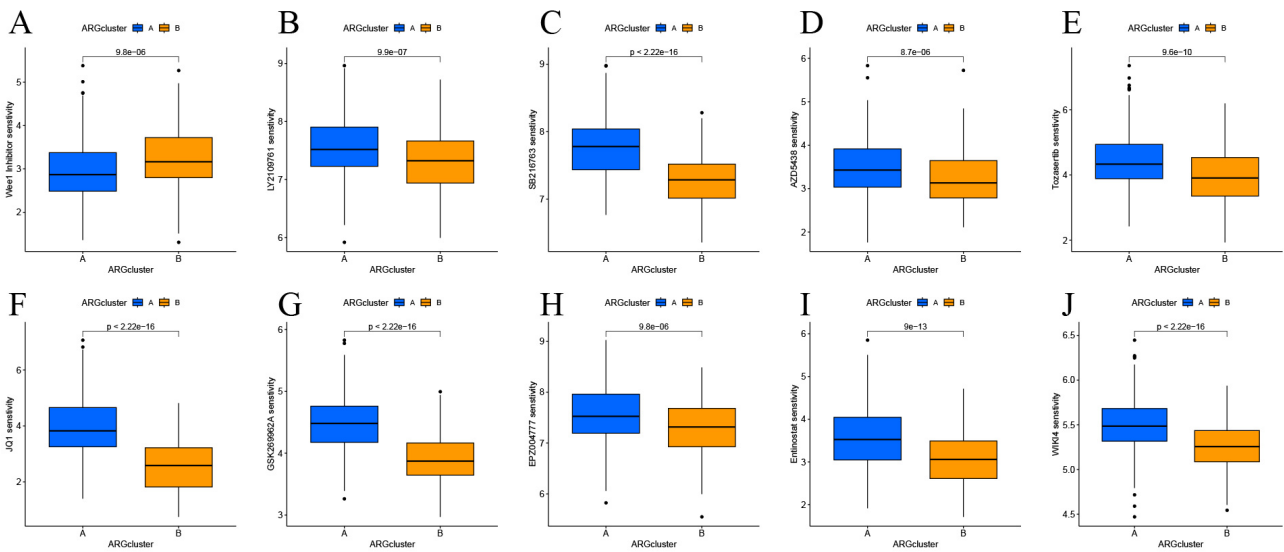


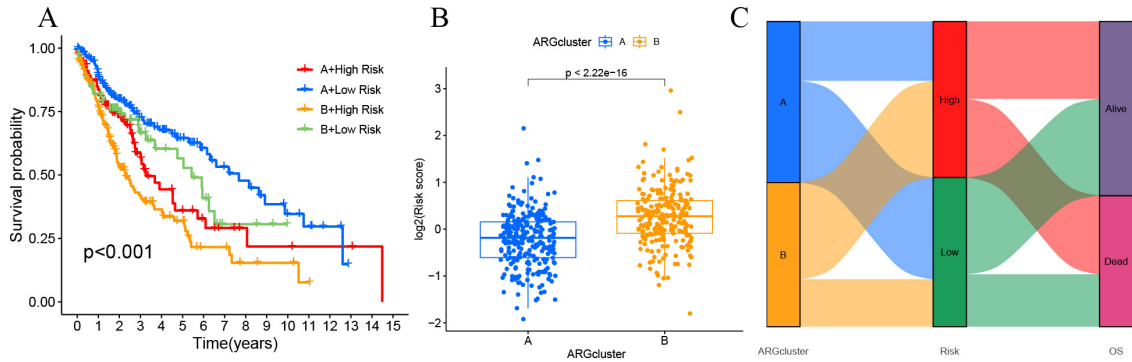
**Figure S1** Expression and prognostic analysis of CSNK2A1 in LUSC. (A-F) Kaplan-Meier survival curves of risk model genes. (G) Differential expression analysis of CSNK2A1 between LUSC tumor tissues and adjacent normal tissues. LUSC, lung squamous cell carcinoma.



**Figure S2** Original Western blot images for H226 and SK-1 cell lines and other replicates. (A-C) The images for the three repeated Western blot experiments. The H226 in the main text corresponds to (C), and SK-1 corresponds to (A). NC, negative control; si, small interfering RNA.



**Figure S3** Drug sensitivity prediction of consensus clusters. (A-J) OncoPredict-derived drug sensitivity landscapes of consensus clusters.



**Figure S4** Interplay between consensus clustering and prognostic risk stratification in LUSC. (A) Kaplan-Meier survival analysis of integrated subgroups. (B) Risk score distribution across clusters, demonstrating significantly elevated scores in Cluster B. (C) Mortality incidence stratification. ARG, anoikis-related gene; LUSC, lung squamous cell carcinoma; OS, overall survival.