

Figure S1. Batch effects in the GSE122697, GSE146114 and GSE63514 datasets. (A) Raw gene expression box plots before batch correction. (B) PCA before batch correction. (C) Box plots after batch correction. (D) PCA plot of the corrected datasets. PCA, Principal component analysis.

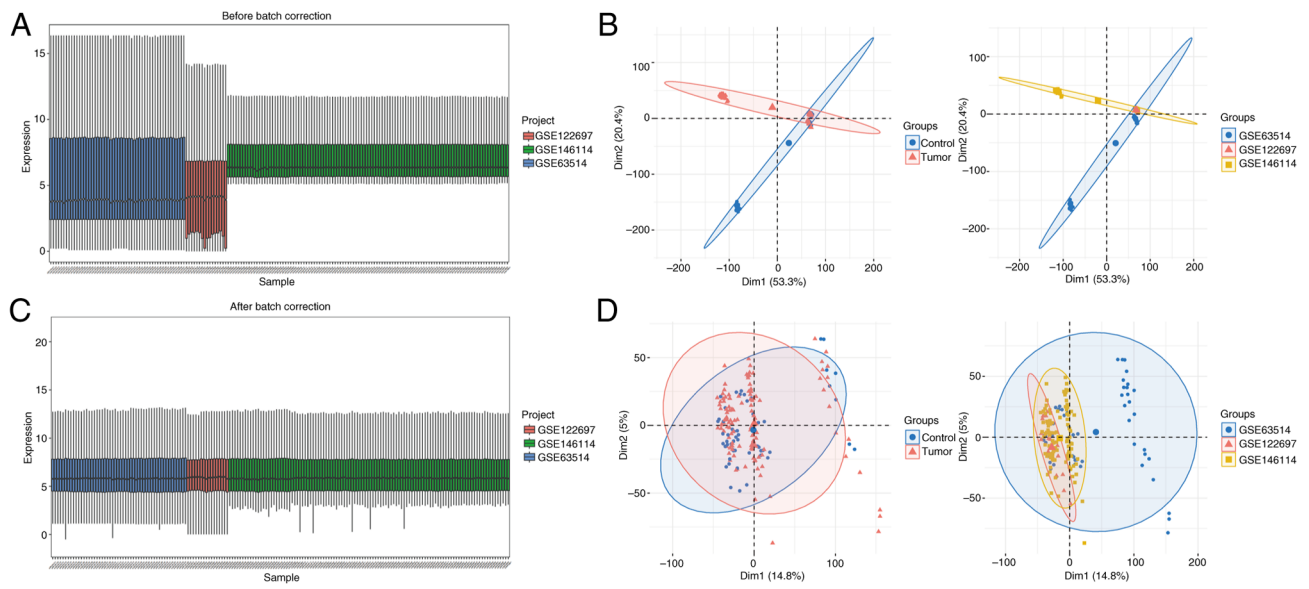


Figure S2. Multidimensional prognostic and immune-related analysis of LAGs prediction models. (A) Kaplan-Meier survival analysis of prognostic genes associated with the LAGs risk model, including PFKM, HDGF, HMG1, TKT and PGK1. Univariate and multivariate Cox regression analyses of (B) DSS and (C) PFI and clinical characteristics of LAGs in The Cancer Genome Atlas-cervical squamous cell carcinoma patient cohort. (D) Kaplan-Meier survival analysis assessing the prognostic significance of KRAS signaling downregulation (KRAS_SIGNALING_DN). (E) Cellular communication network analysis based on single-cell transcriptomic data. (F) Correlation analysis between tumor microenvironment immune-infiltrating cells and genes in the LAGs predictive model. Survival analysis of various TME immune-infiltrating cell types about patient prognosis, including (G) M0 and (K) M1 macrophages, (H) resting mast cells, (J) CD8⁺ T cells, (I) γ - Δ T cells and (L) regulatory T cells. PFKM, phosphofructokinase, muscle type; HDGF, hepatoma-derived growth factor; HMG1, high-mobility group nucleosome-binding protein 1; TKT, transketolase; PGK1, phosphoglycerate kinase 1; DSS, disease-specific survival; PFI, progression-free interval; LAGs, lactylation-associated genes; HR, hazard ratio; T, tumor stage; N, lymph node stage.

