

Figure S1 Single cell clustering, WGCNA soft thresholding, and correlation analysis of CS1RS genes. (A) t SNE plot colored by various cell clusters. (B) Determination of the optimal soft threshold in WGCNA analysis. (C) Correlation among the three CS1RS genes (SMS, PSMD1, YBX1). t-SNE, t-distributed Stochastic Neighbor Embedding; WGCNA, weighted gene co-expression network analysis; CS1RS, CS1-related signature; SMS, spermine synthase; PSMD1, proteasome 26S subunit, non-ATPase 1; YBX1, Y-box binding protein 1.

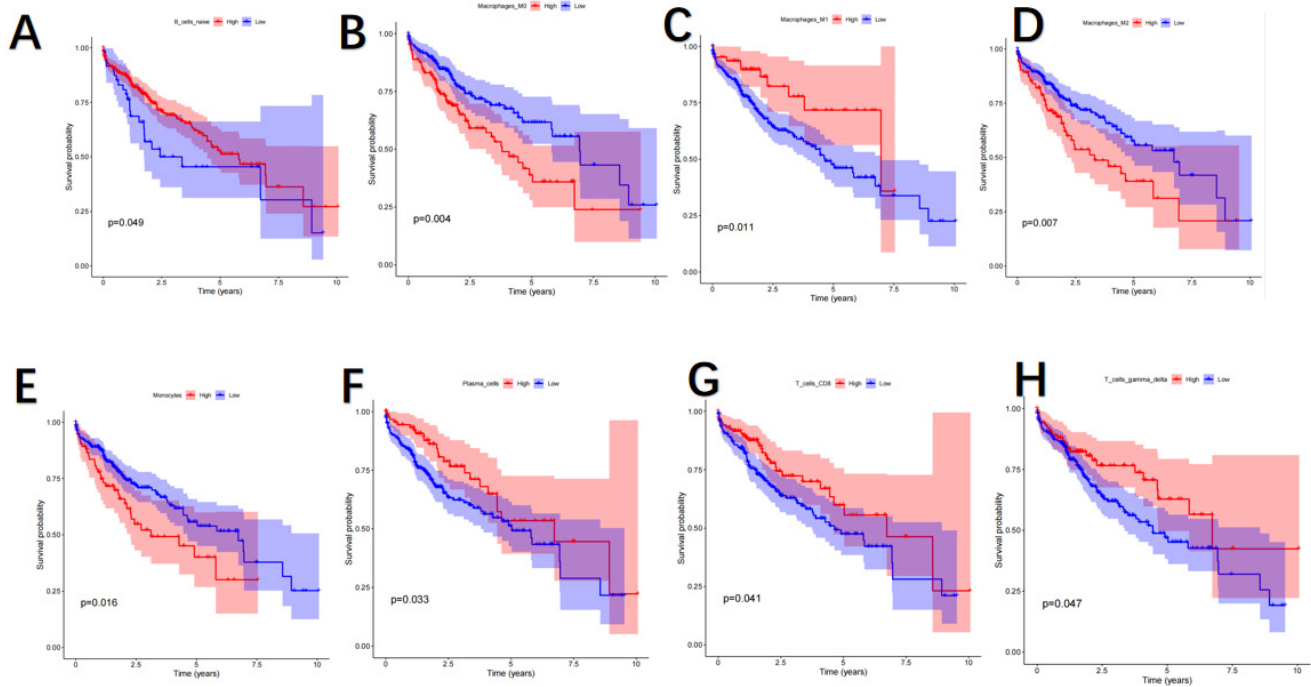


Figure S2 Correlation between tumor microenvironment (TME)-infiltrating immune cell types and prognosis of hepatocellular carcinoma (HCC). (A) Kaplan-Meier curve for naïve B cells; (B) Kaplan Meier curve for M0 macrophages; (C) Kaplan-Meier curve for M1 macrophages; (D) Kaplan-Meier curve for M2 macrophages; (E) Kaplan-Meier curve for monocytes; (F) Kaplan Meier curve for plasma cells; (G) Kaplan-Meier curve for CD8+ T cells; (H) Kaplan Meier curve for gamma delta T cells. TME, tumor microenvironment; HCC, hepatocellular carcinoma; CD8, cluster of differentiation 8.

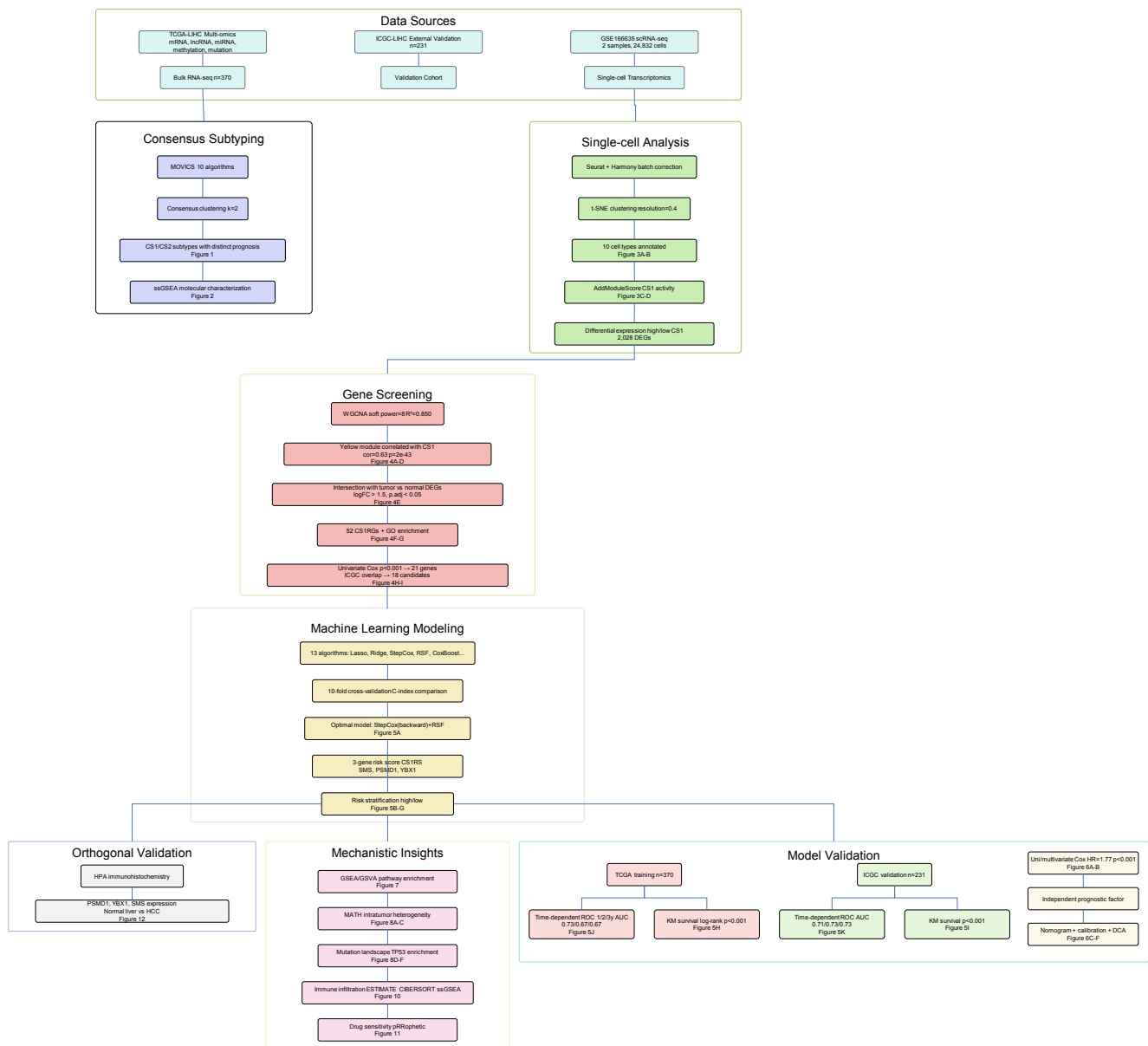


Figure S3 Study workflow diagram for multi-omics integration, machine learning model construction, and validation. The diagram outlines the overall analytical pipeline, including data collection, consensus subtyping, single-cell analysis, gene screening, machine learning modeling, model validation, mechanistic exploration, and orthogonal protein validation. TCGA-LIHC, The Cancer Genome Atlas-Liver Hepatocellular Carcinoma; ICGC, International Cancer Genome Consortium; scRNA-seq, single-cell RNA sequencing; CS1/CS2, consensus subtype 1/2; ssGSEA, single-sample gene set enrichment analysis; t-SNE, t-distributed Stochastic Neighbor Embedding; WGCNA, weighted gene co-expression network analysis; cor, correlation; DEGs, differentially expressed genes; logFC, log fold change; p.adj, adjusted P value; CS1RGs, CS1-related genes; GO, Gene Ontology; RSF, random survival forest; CS1RS, CS1-related signature; SMS, spermine synthase; PSMD1, proteasome 26S subunit, non-ATPase 1; YBX1, Y-box binding protein 1; OS, overall survival; ROC, receiver operating characteristic; AUC, area under the curve; HR, hazard ratio; CI, confidence interval; DCA, decision curve analysis; GSEA, gene set enrichment analysis; GSVA, gene set variation analysis; MATH, Mutant Allele Tumor Heterogeneity; TP53, tumor protein p53; ESTIMATE, Estimation of Stromal and Immune cells in Malignant Tumour tissues using Expression data; CIBERSORT, Cell-type Identification By Estimating Relative Subsets Of RNA Transcripts; HPA, Human Protein Atlas; HCC, hepatocellular carcinoma.