

**Supplementary Figure S1. DLC1-correlated immune and stromal infiltration landscape.** The supplementary figure summarizes pan-cancer correlations between DLC1 expression and immune or stromal infiltration estimates across tumor types using complementary deconvolution approaches. The displayed cell categories include major lymphoid, myeloid, macrophage, dendritic, mast-cell, progenitor and endothelial-related populations. These analyses were used to provide broad tumor-microenvironment context for the HCC-focused study.

**Supplementary Figure S2. DLC1-correlated immune infiltration, immune checkpoint, TMB and MSI features.** (A,B) Pan-cancer correlations between DLC1 expression and immune-cell infiltration estimates calculated using QUANTISEQ and TIMER. (C) Correlations between DLC1 expression and immune checkpoint genes across cancer types. (D,E) Correlations between DLC1 expression and tumor mutational burden and microsatellite instability. These analyses provide immune-context information for the HCC-focused study and were not interpreted as the central mechanism of the present work.

**Supplementary Figure S3. Global UMAP clustering of GSE149614 before fibroblast-stellate extraction.** The supplementary figure shows the overall UMAP representation and cluster structure of the single-cell dataset before extraction and downstream analysis of fibroblast-stellate cells. This plot was used as the global single-cell overview rather than as a fibroblast-stellate reclustering result.

**Supplementary Figure S4. Marker-gene support for fibroblast-stellate substate annotation.** The dot plot shows representative marker-gene expression across fibroblast-stellate substates, including perivascular myofibroblast, activated-matrix fibroblast, transitional fibroblast, C7-SFRP4-stromal, CXCL12-RBP1-stellate, FABP4-CYGB-stellate and PI16-IGF1-quiescent fibroblast states. These marker patterns support the assignment of fibroblast-stellate substates and the interpretation of C1-like and C3-like programs.

**Supplementary Figure S5. Spatial module maps across seven GSE238264 samples.** The multipage supplementary PDF shows H&E images and spot-level spatial distributions of DLC1 expression, C1-like score, C3-like score, MIF ligand score, CD74/CXCR4 receptor score and ECM-integrin context score across HCC1R, HCC2R, HCC3R, HCC4R, HCC5NR, HCC6NR and HCC7NR. These maps provide sample-level spatial context for the C1/C3 proximity and matrix-context analysis.