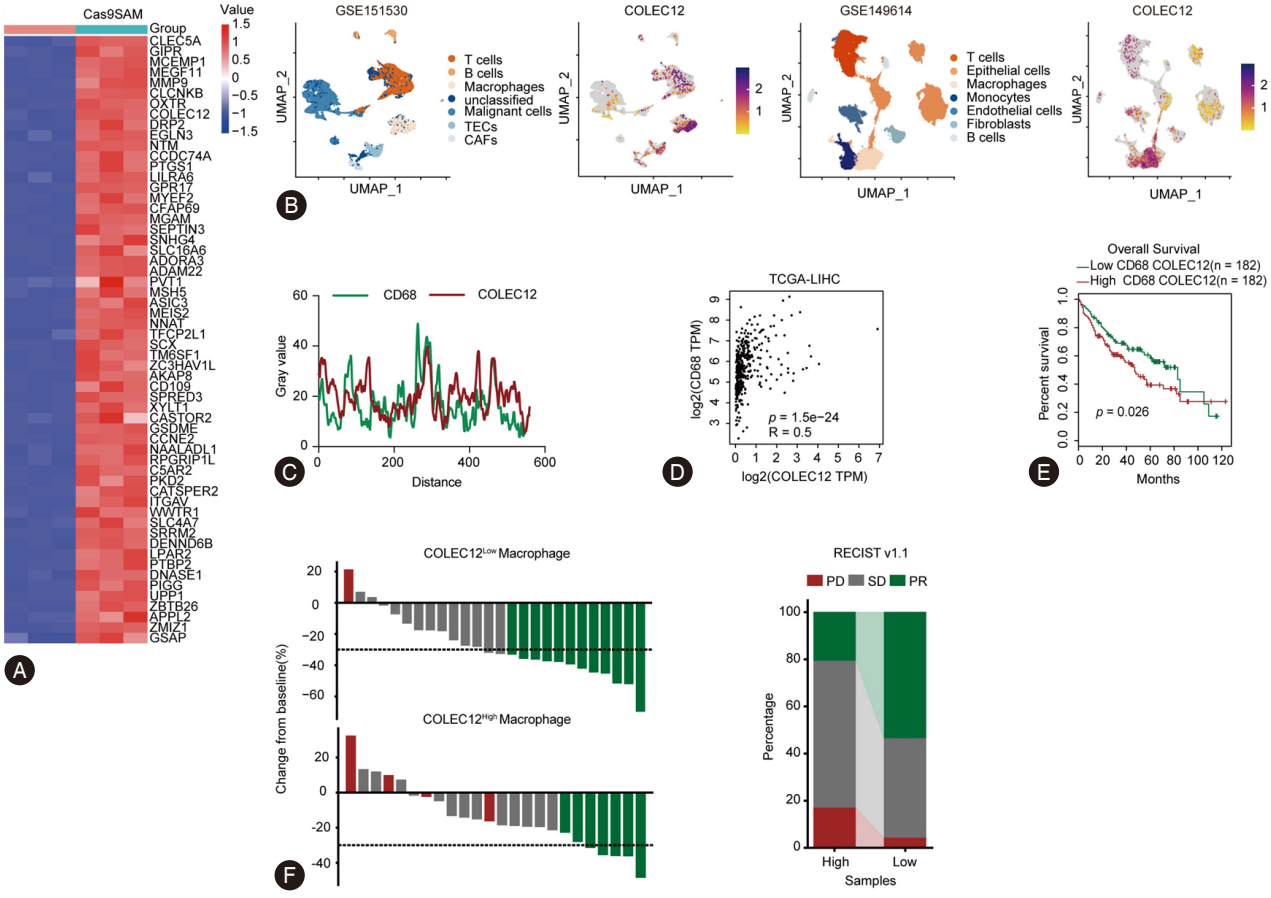

Supplementary Figure 1. COLEC12^{high} TAMs promote lenvatinib resistance in HCC. (A) Heatmap showing the qPCR validation of 58 sgRNAs targeting genes in THP-1 cells after CRISPR/dCas9-mediated transcriptional activation (n=3). (B) Left: UMAP projection of integrated single-cell RNA-seq datasets from HCC patients (GSE151530 and GSE149614), annotated by cell type. Right: Feature plot showing expression of COLEC12 across cell clusters, with color intensity representing normalized expression levels. (C) Spatial co-localization of COLEC12 and CD68 signals based on gray value distribution profiles across tumor regions. (D) Correlation analysis of COLEC12 and CD68 mRNA expression levels in the TCGA-LIHC cohort. (E) Kaplan-Meier survival curve based on the level of macrophages COLEC12 in the TCGA-LIHC dataset. (F) Waterfall plot (left) showing the percentage change in tumor size from baseline for patients with COLEC12^{high} (bottom) macrophage infiltration, as classified by RECIST v1.1 criteria. Bar chart (right) illustrating the distribution of lenvatinib treatment response (PR, SD, PD) in COLEC12^{high} and COLEC12^{low} macrophage groups. Data are presented as mean±standard error of the mean. Statistical significance was assessed using Student's t-test. Survival data were analyzed by the log-rank test. COLEC12, Collectin Subfamily Member 12; TAMs, tumor-associated macrophages. Source data are provided as a Source Data file.

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