



Fig S1. The distribution of hepatic CSC markers and the expression of CSC-miRNAs in HCC cohorts.

(A) Relative levels of five different hepatic CSC biomarkers in Cohort 2. For each biomarker, red and green dots referred to HCC patients with the top 25% expression levels (CSC⁺ HCCs), and patients with the bottom 25% levels (CSC⁻ HCCs), respectively. (B) Hierarchical clustering analysis using the positive or negative status for five different CSC biomarkers of each patient in two HCC cohorts. (C) Expression levels of miR-181a-5p, miR-181b-5p, and miR-181c-5p in five

groups of CSC⁺ HCCs and CSC⁻ HCCs from HCC Cohort 1. Unpaired t-test was used. (D) Gene surrogates of miR-192-5p identified by Pearson's correlation between miR-192-5p and 13,100 genes in 176 HCC cases from Cohort 1. (E) The signaling pathways revealed by Ingenuity Pathway Analysis using genes significantly correlated with miR-192-5p from Fig S1D. Enriched signaling pathways with $p < 0.01$ were showed.