



Fig S3. Expression analysis of mature and precursor of miR-192-5p in HCC patients with different levels of multiple stem cell-related biomarkers, and miRNA sequence alignment analysis.

(A-D) For each stem cell-related biomarker, HCC patients with the top 25% expression levels were named positive cases (“+”), and patients with the bottom 25% levels were referred to negative cases (“-”). (A) In Cohort 1 with miRNA array data, expression levels of mature miR-192-5p were compared between “+” and “-” groups for each biomarker, respectively. Un-paired t-test was used. (B) In Cohort 2 with miRNA sequencing data, expression levels of mir-192 precursor were compared between “+” and “-” groups for each biomarker, respectively. Non-

parametric test was used. (C) In Cohort 1, expression levels of mature miR-192-5p were compared among CD133⁺ALDH1A1⁺, CD133⁺ALDH1A1⁻, CD133⁻ALDH1A1⁻, and CD133⁻ALDH1A1⁺ HCCs. (D) In Cohort 2, expression levels of mature miR-192-5p were compared among CD133⁺ALDH1A1⁺, CD133⁺ALDH1A1⁻, CD133⁻ALDH1A1⁻, and CD133⁻ALDH1A1⁺ HCCs. (E) Sequence alignment of mature miR-192-5p among different species. The blue color represents the conserved base among different species. The red bases refer to seed sequence of mature miRNA. (F) Sequence alignment analysis of precursor mir-192. The sequence of mature miR-192-5p is underlined and the star represents the conserved base among different species. All data are collected from miRBase Sequence Database.