Supplementary Fig. S7. TGFβ3-induced ETV4/SMAD2/CARM1 complex epigenetically upregulates SQOR expression. (**a**) ChIP assay analysis of enrichment of SMAD2, SMAD3 and SMAD4 on the *SQOR* promoter in the indicated cells. (**b-c**) The relative luciferase activity of *SQOR* promoter (**b**), the *SQOR* mRNA level (**c**-upper) and IB analysis of expression of SQOR, SMAD2, SMAD3 and SMAD4 (**c**-bottom) in the RT4/TGFβ3 or MI-PDBC#1 cells transfected with the indicated siRNAs. (**d**) The relative luciferase activity of *SQOR* promoter (left) and *SQOR* mRNA level (right) in the indicated cells transduced with SMAD2, SMAD3 and SMAD4, respectively. *GAPDH* served as a loading control. (**e**) Co-IP/IB analysis showing the expression of ETV4/CARM1 and immunoprecipitated flag-SMAD2 (left), SMAD2/CARM1 and immunoprecipitated myc-ETV4 (middle), and SMAD2/ETV4 and immunoprecipitated HA-CARM1 (right) in the indicated cells treated with TGFβ3. (**f**) ChIP analysis of enrichment of p-SMAD2, ETV4 and CARM1 on the *SQOR* promoter in the cells that transduced with individual siRNAs that targeted SMAD2, ETV4 and CARM1, respectively. (**g**) Co-IP assays analysis of the interaction of SMAD2-S2D or SMAD2-S3A with ETV4 and CARM1 in the indicated cells using anti- Flag antibody. (**h**) ChIP assay analysis of CARM1 and ETV4 enrichment on the *SQOR* promoter in the indicated cells. (**i**) IB analysis of expression of SQOR, p-SMAD2, SMAD2, ETV4 and CARM1 in indicated cells. GAPDH serve as a loading control. (**j**) Real-time PCR analysis of the mRNA expression of *SQOR* in the indicated cells. *GAPDH* serve as a loading control. (**k**) IB analysis of expression of SQOR, ETV4, and CARM1 in the indicated cells. GAPDH serve as a loading control. (**l**) Co-IP assays were performed using anti- H3 or anti-H3R17me2a antibodies in the indicated cells. (**m**) ChIP assay analysis of H2BK120ub and H3K4me3 enrichment on the *SQOR* promoter in the indicated cells. $^{***}P < 0.001$ for vs. control, $^{\#\#\#}P < 0.001$ for vs. TGFβ3/scr group. (**n**) ChIP analysis of occupancy of RNAPII, CTD S2-phosphorylation, PAF1, and H3R17me2a at distal and proximal promoter and encoding regions of *SQOR* gene. Each error bar in a, b, d, f, h and j represents the mean ± SD of three independent experiments. Statistical analysis was performed using one-way ANOVA with Dunnett's multiple comparison tests for (d, f, h and j), Two-way ANOVA with Šídák's multiple comparisons test for (j and k). $^{***}P < 0.001$; ns, not significant.

Supplementary Fig. S7