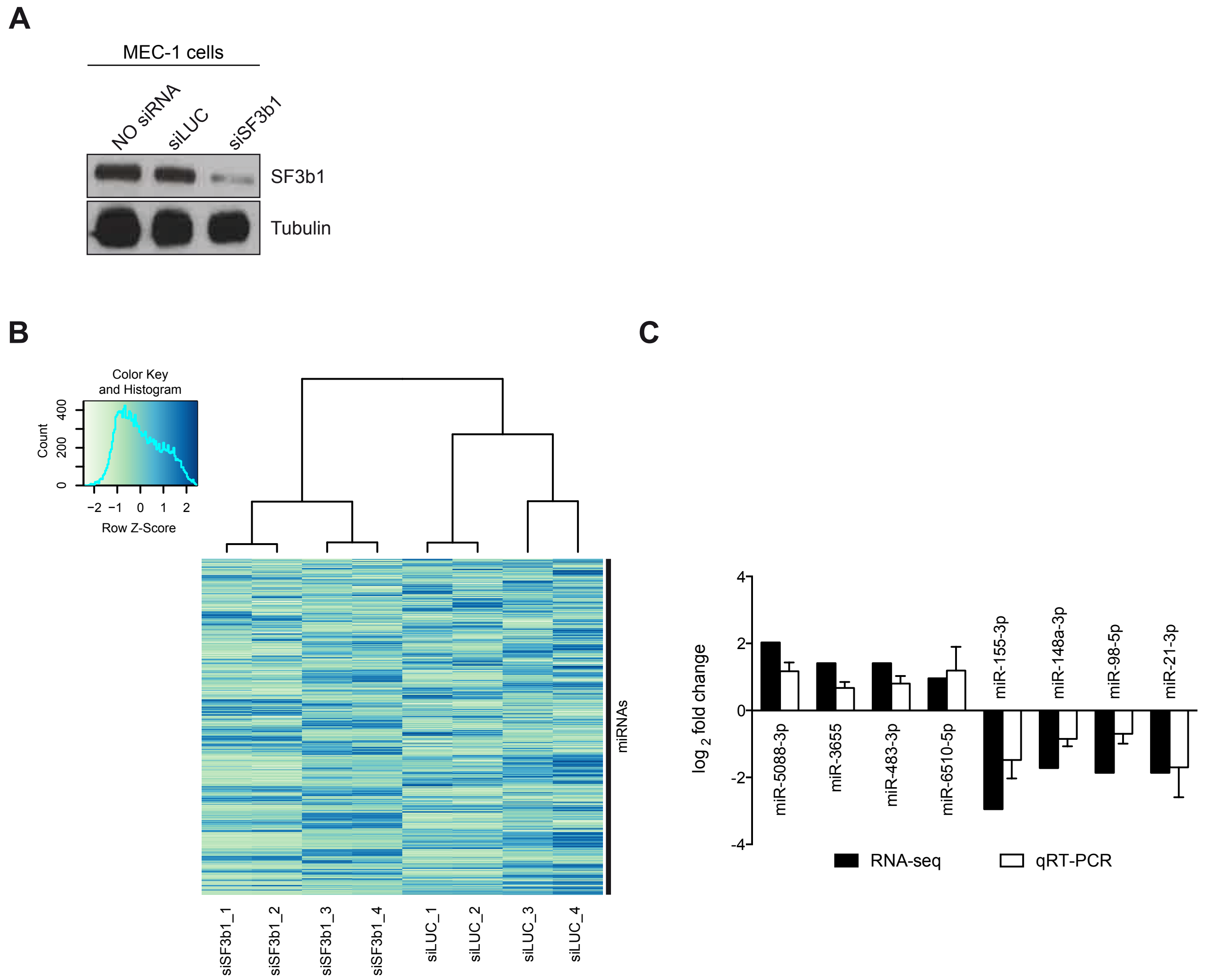

Supplemental Figure S2. miRNA expression profiles and small RNA-seq validation between SF3b1-depleted and control-treated MEC-1 cells.

(A) Western blot analysis of SF3b1 and Tubulin proteins from untreated (NO siRNA), control-treated (siLUC) and SF3b1 siRNA-treated MEC-1 cells (siSF3b1). Uncropped images of blots are shown in Supplementary Figure 7.

(B) Hierarchical clustering and heat map of individual miRNA expression from four SF3b1 siRNA-treated (siSF3b1_1-4) and four control-treated (siLUC_1-4) samples. Each column represents an individual sample. All miRNAs analyzed are plotted on Y-axis. Cluster of control-treated and SF3b1-depleted samples are shown by hierarchical tree on the X-axis. Colors represent miRNAs expression levels: the dark blue indicates high level of miRNA expression and the light blue shows low.

(C) Comparison of expression changes (expressed as $\log_2$fold change) detected by small RNA-seq (black columns) and TaqMan qRT-PCR analysis (white columns) for eight differently expressed miRNAs. qRT-PCR data are normalized to RNU6B. Error bars show SD (three independent experiments). Fold changes of the qRT-PCR are consistent with the fold changes of small RNA-seq data.