Supplemental Data

De-regulated microRNAs in pediatric cancer stem cells target pathways involved in cell proliferation, cell cycle and development

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Table S1.	Cell cycle and cell proliferation related genes in the cancers.	(\checkmark indicates the gene is in the
	gene set named in the column header).	

	CHRONIC Myeloid Leukemia	GLIOMA	MELANOMA	PANCREATIC CANCER	PROSTATE CANCER	SMALL CELL LUNG CANCER
CDKN1A	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark	
CDKN1B	\checkmark			\checkmark	\checkmark	\checkmark
E2F1	\checkmark		\checkmark	\checkmark	\checkmark	
RB1	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark	
PTEN		\checkmark	\checkmark		\checkmark	\checkmark

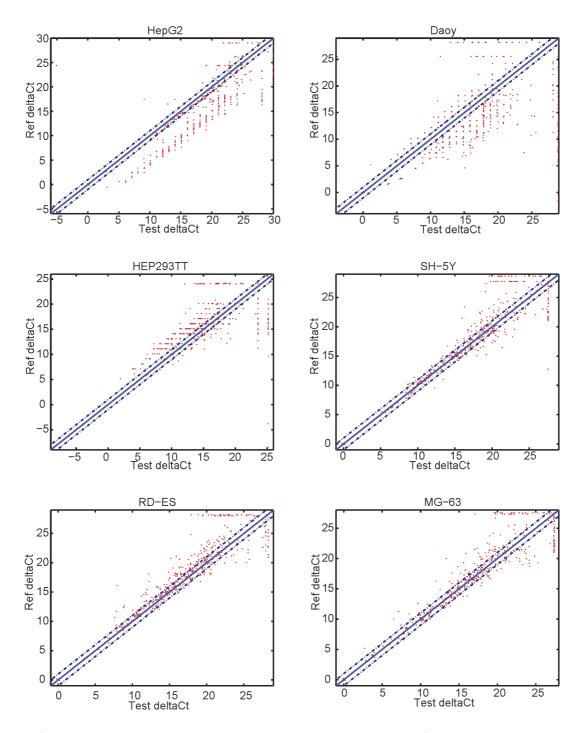


Figure S1. The scatter plots of raw ΔCt of 6 cell lines between test (enriched CSC miRNAs) and reference (non-enriched counterpart) samples before normalization.

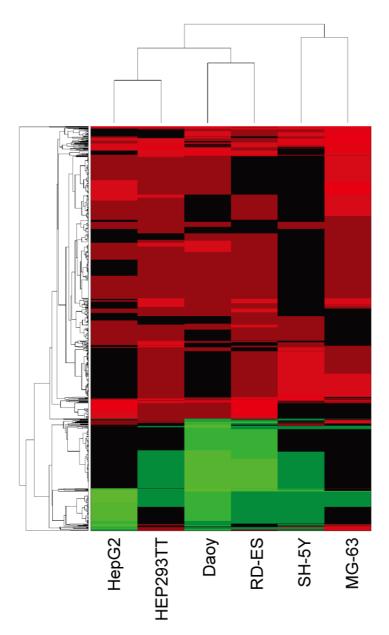


Figure S2. The heatmap of 865 putative microRNA target genes. 630 of 865 putative microRNA target genes were up-regulated and 235 were down regulated. The 863 target genes' value were computed by $\mathbf{B}\Delta x_j$ (see Eq. 2, Materials and Methods Section for details).

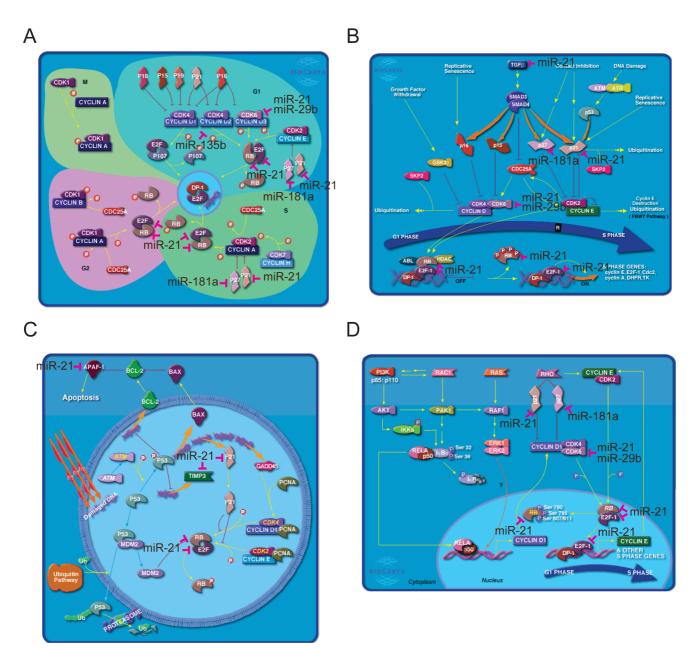


Figure S3-1. The CSC associated Biocarta pathways regulated by miRNAs identified in Figure 1B. A) CELLCYCLE, 2) G1, 3) P53, and 4) RACCYCD pathway.

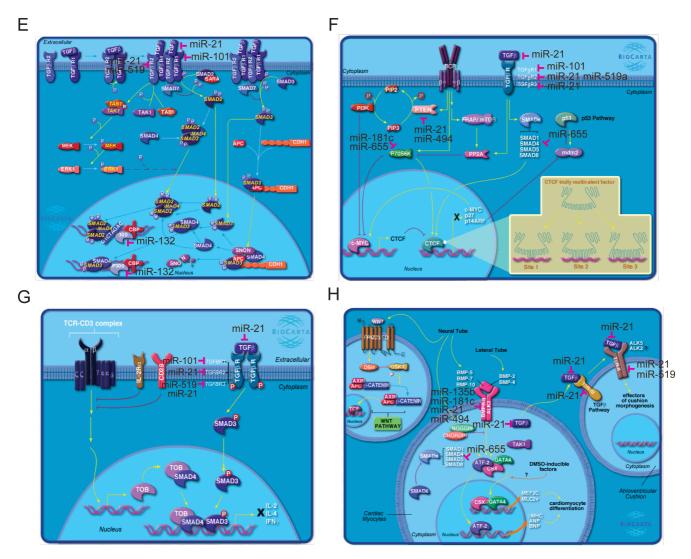


Figure S3-2. The CSC associated Biocarta pathways regulated by miRNAs identified in Figure 1B. E) CTCF, F) TOB1, G) ALK, and H) PTEN pathway.