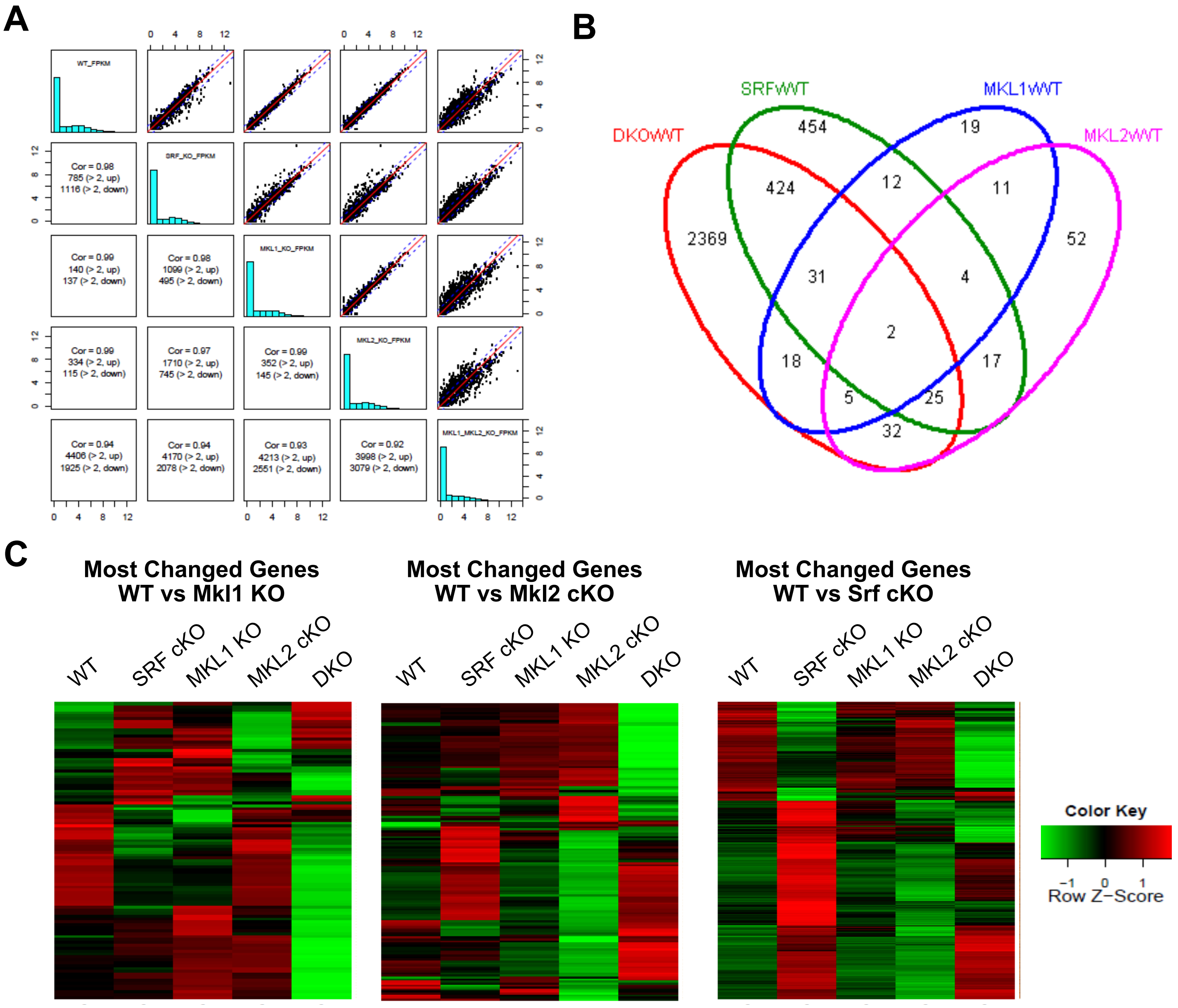

Figure S1: RNA sequencing analysis of megakaryocytes

(A) The diagonal boxes (light blue) show histograms of individual sample FPKM (fragments per kilobase of transcript per million fragments mapped). The lower left boxes show correlation coefficients of pairwise sample comparisons and the number of genes with >2 fold changes. The upper right boxes show pairwise plots of $\log_2$(FPKM) for 2000 randomly chosen genes. (FDR filter was not applied for any of these analyses). (B) 4-way Venn Diagram showing comparisons of Mkl1 KO, Mkl2 Pf4-cKO, DKO, and Srf-Pf4-cKO with WT megakaryocyte gene expression data. (C) Heat maps displaying the differential gene expression patterns between the indicated genotypes.

SUPPLEMENTARY FIGURE 1

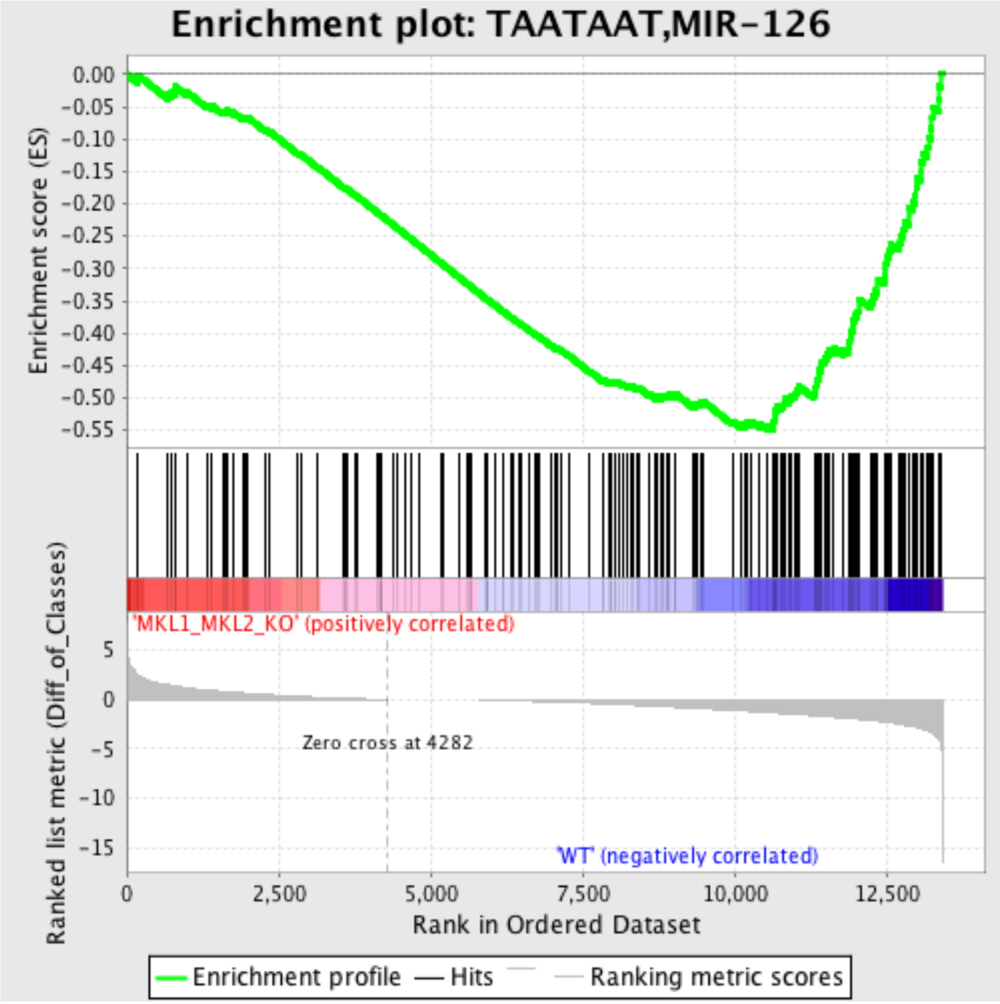

Figure S2: Gene Set Enrichment Analysis

Gene set enrichment analysis was performed by comparing the log2 FPKM WT and DKO RNA sequencing data for enrichment with the TAATAAT,MIR-126 gene set (MSigDB C3 genes that are predicted to have miR-126 3'UTR binding). Default parameters were used except that permutation was performed based on Gene Sets using the difference of classes as the metric for ranking genes. The normalized enrichment score (NES) = -1.7 showed significant enrichment of the MIR-126 gene set, as did the false discovery rate adjusted q value < .001, which gives the estimated probability that the normalized enrichment score represents a false positive finding. In the figure, ES (upper plot, Y axis) is the enrichment score for the gene set; that is, the degree to which this gene set is overrepresented at the top or bottom of the ranked list of genes in the expression dataset. High deflection of the ES from 0 at the beginning or end but not the middle of the ranked list shows strong enrichment of the gene set in the data comparison. The black bars represent positions of genes in the gene set along the ranked gene list, and the bottom panel shows the log2 difference of WT and DKO FPKM.

SUPPLEMENTARY FIGURE 2