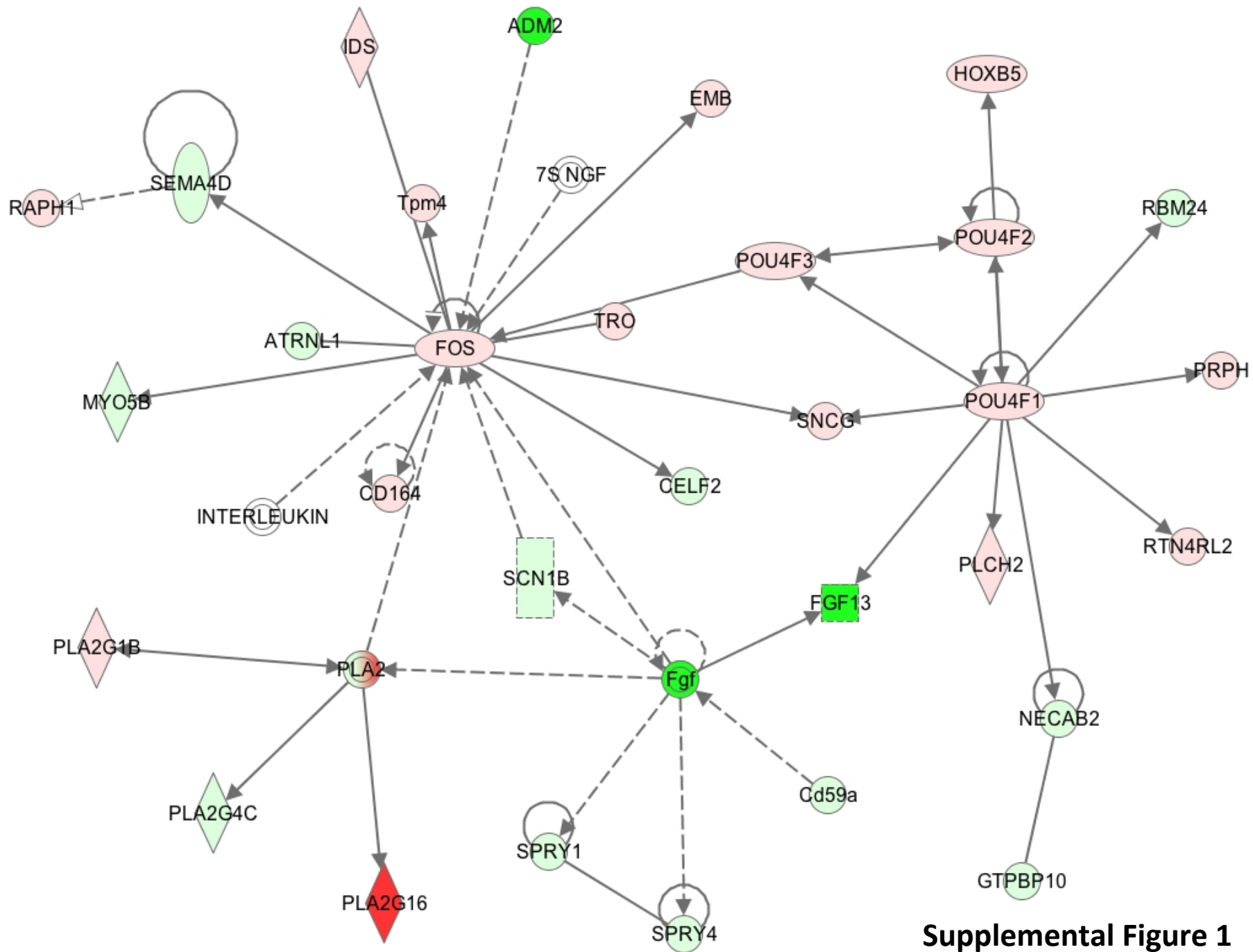
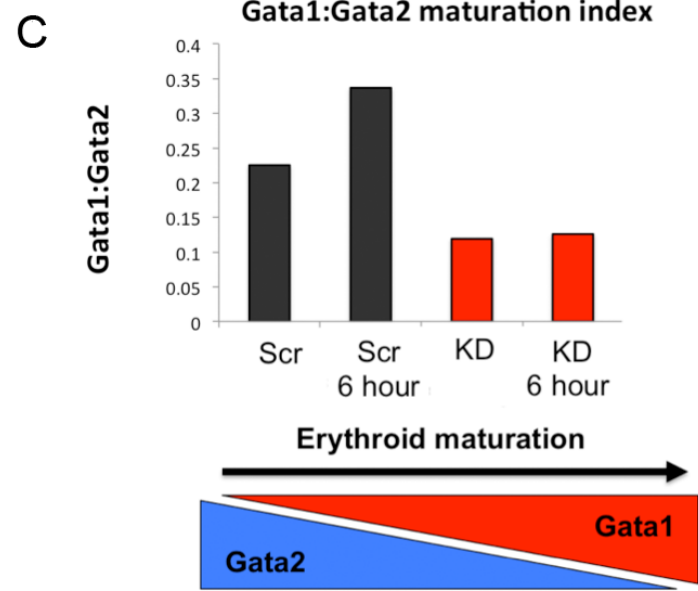
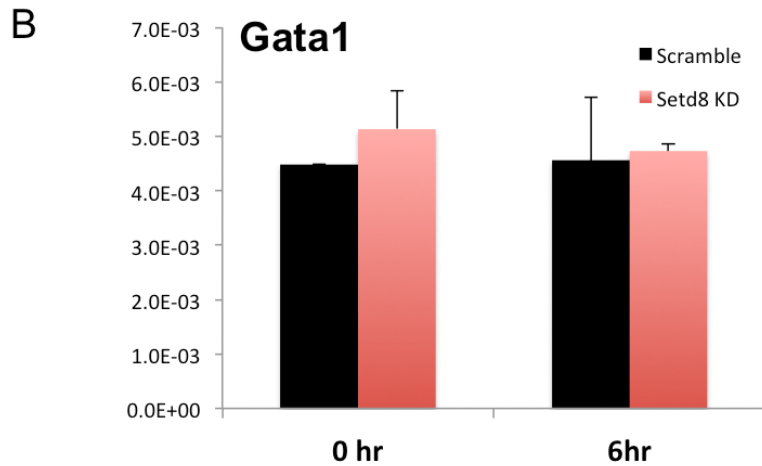
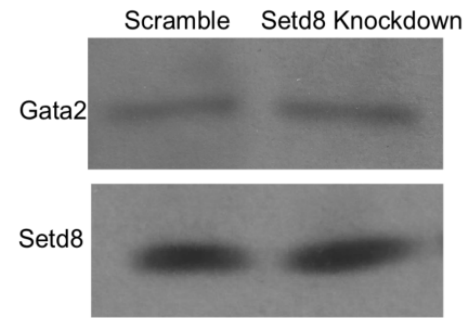
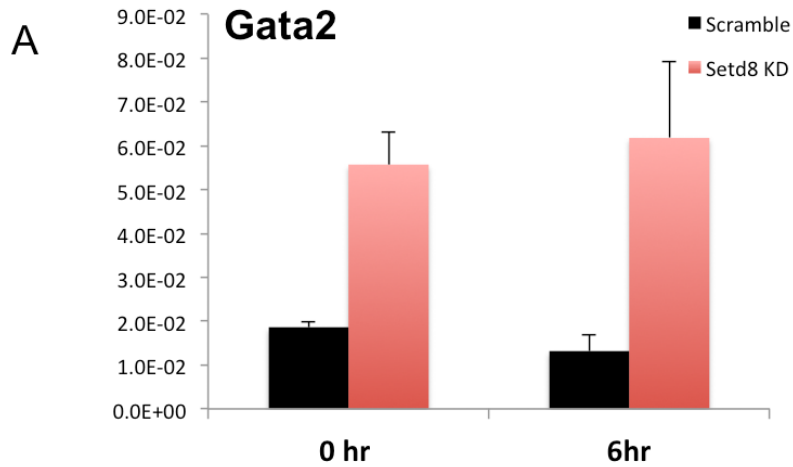


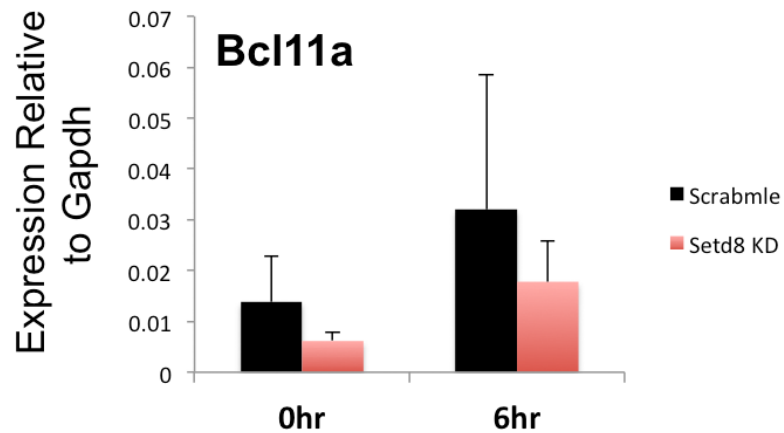
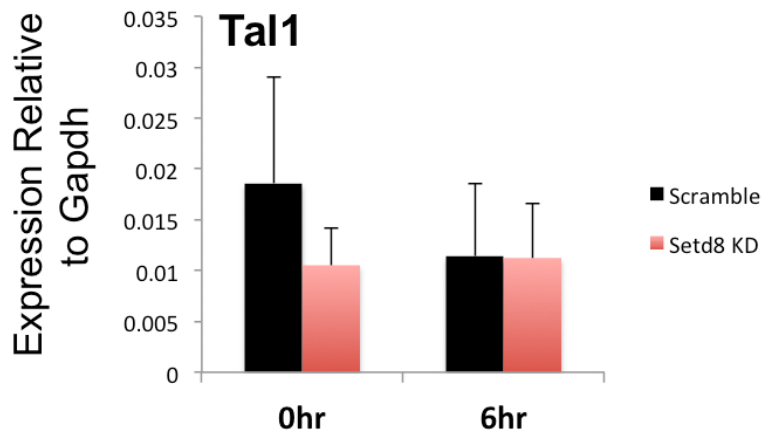
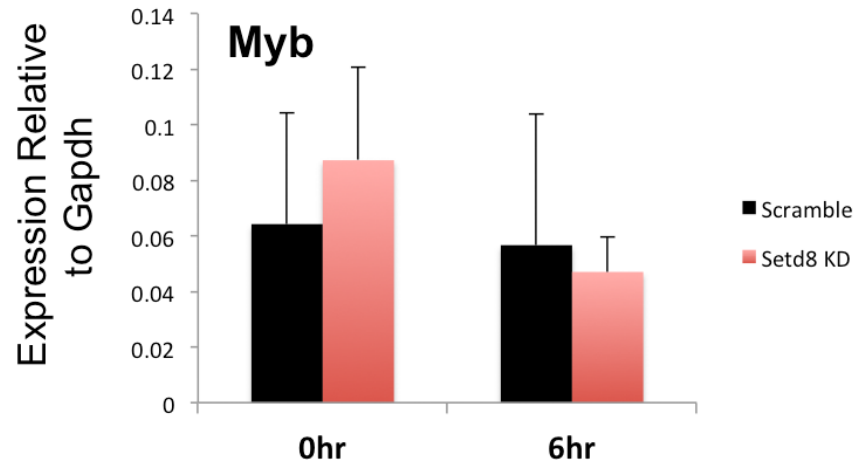
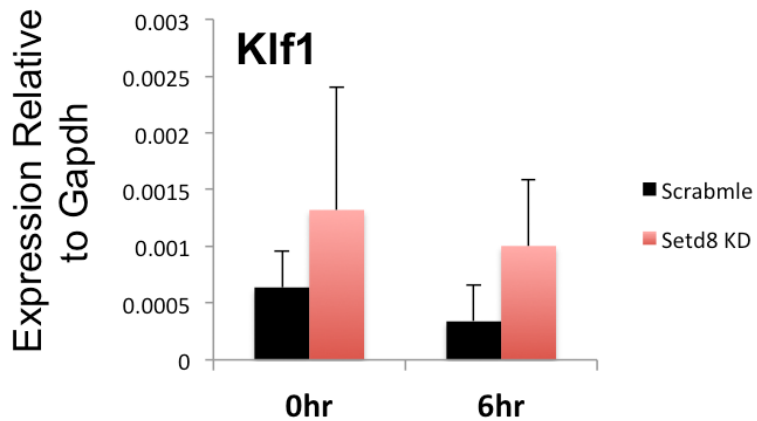
Supplemental Figures



Supplemental Figure 1



Supplemental Figures 2A, 2B, and 2C



Supplemental Figure Legends

Supplemental Figure 1. IPA analyses of differentially regulated genes in proliferating cells. Ingenuity Pathway Analyses (IPA) of the differentially expressed genes in self-renewing cells identified Cell Morphology, Cellular Function and Maintenance, and Cellular Growth and Proliferation as the top network (score 44, focus molecules 31).

Supplemental Figure 2. Validation of RNA-seq results. Supplemental Figure 2A. Quantitative PCR and western blot confirms that the expression of Gata2 is increased in Setd8 knockdown cells compared to control. Supplemental Figure 2B. Quantitative PCR confirms that the expression of Gata1 is unchanged. Supplemental Figure 2C. Quantitative PCR confirms altered Gata1:Gata2 ratio following Setd8 knockdown. Supplemental Figure 2D. Quantitative PCR confirms that there are no significant differences in the expression of Klf1, Tal1, Myb, or Bcl11a following Setd8 knockdown in either self-renewing or maturing cells. Data represent the mean and SEM of a minimum of three independent experiments.

Supplemental Table 1. Primers used for quantitative PCR.

Supplemental Table 2. Genes differentially expressed following Setd8 knockdown in self-renewing cells.

Supplemental Table 3. Genes differentially expressed following Setd8 knockdown in maturing cells.