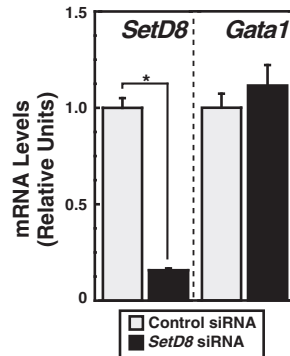


# Supporting Information

DeVilbiss et al. 10.1073/pnas.1302771110



**Fig. S1.** Murine erythroleukemia (MEL) cells were transfected with histone lysine methyltransferase (SetD8) siRNA or control siRNA. *SetD8* and erythroid transcription factor (GATA-1) mRNA levels were quantified by RT-PCR ( $n = 3$ , mean  $\pm$  SE) \* $P < 0.0001$ .

GATA-1-Repressed	
Gene Name	ChIP-Seq Peaks
<i>Vim</i>	+
<i>Limd2</i>	+
<i>Clec10a</i>	+
<i>Myo1g</i>	+
<i>Kank3</i>	+
<i>Rgs19</i>	+
<i>Apoc1</i>	+
<i>Serpib2</i>	-
<i>Arap3</i>	+
<i>Acaa2</i>	+
<i>Tie6</i>	+
<i>Cyba</i>	-
<i>Lgals9</i>	+
<i>Inf2</i>	+
<i>Dbp</i>	+
<i>Flot1</i>	+
<i>Glipr1</i>	+
<i>chr9:96664617-96683617</i>	+
<i>Slc22a18</i>	+
<i>Rec8</i>	+
<i>Bst2</i>	+
<i>Alox5ap</i>	+
<i>Ephx2</i>	+
<i>Nr2f6</i>	-
<i>Tnfrsf18</i>	+
<i>Sla</i>	+
<i>Snx21</i>	+
<i>Cpped1</i>	+
<i>Tbc1d10c</i>	-

**Fig. S2.** GATA-1 occupancy at GATA-1/SetD8-corepressed genes in MEL cells. -, no GATA-1 peaks; +, GATA-1 occupancy in the gene body, promoter, or the surrounding chromatin.