Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1

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Supplemental Figures

Supplemental Figure S1: Identification of GATA1-bound enhancers during of differentiation of HSCs. (A) Genome browser images showing the profiles of GATA1 binding and H3K4me1 in HSCs and CD36+ cells. The four DNase I hypersensitive sites (HS) in the LCR of the beta-globin domain are indicated at the bottom. (B) Percentage of genes activated during differentiation of HSCs (Y-axis) correlates with the number of distal GATA1 binding sites with ±20kb of TSSs. The p-values are calculated by chi-square test.

Supplemental Figure S2: Scatter plots of BRG1 tag densities and GATA1 binding levels at GATA1 binding sites. The GATA1 binding sites are grouped into four quartiles based on the nucleosome tag densities calculated from the MNase-Seq data (A) or based on the nucleosome occupancy predictions from (Kaplan et al. 2009) (B). I to IV denote the lowest to the highest.

Supplemental Figure S3: Nucleosome re-organization during differentiation from HSCs to CD36$^+$ sells surrounding GATA1 binding sites is independent of GATA1 binding. (**A**) Nucleosome profiles in HSCs surrounding the distal GATA1 binding sites that are identified in CD36$^+$ cells and are not associated with BRG1 binding. The sites are grouped into four quarters according to the level of GATA1 binding in CD36$^+$ cells (I to IV denote low to high). The profiles are organized such that the nearest nucleosome is upstream of the GATA1 site. **(B)**. Nucleosome profiles in CD36$^+$ cells surrounding the same sites as in (**A**).

Supplemental Figure S4: Of all the GATA1 binding sites that have the nucleosome shift away over 10 bps from HSCs to the CD36$^+$ cells, what percentages (y-axis) show the nucleosome shift back over 10 bps by BRG1 knockdown in the CD36$^+$ cells? The GATA1 binding sites are sorted into four quartiles (~200 sites per group) based on the BRG1 binding levels in CD36$^+$ cells (I to IV denote the lowest to the highest). Genomic sites randomly chosen are included as control. Only sites that are predicted at linkers and show nucleosomes within ±200 bps for HSCs and CD36$^+$ cells (control and BRG1 knock-down) are included for analysis.

Supplementary Figure S5: Motif analysis for TAL1 binding sites in HSCs. (A) Sequence logo of the motifs derived from top 200 HSC-specific TAL1 binding sites by MEME (E-value < 0.01). The # of motif occurrence, E-values, and potential associated TFs are shown within each logo. (B) The top 200 constitutive TAL1 binding sites are included for comparison. (C) Gene expression levels for SPI1, *FLI1*, *ERG* and *RUNX1* between HSCs and the CD36$^+$ cells. Microarray gene expression data is from (Cui et al. 2009).

Supplementary Figure S6: Nucleosome profile changes at constitutive TAL1 binding sites. Two sets of constitutive TAL binding sites are included, namely BRG1-dependent (left panel; #471) and BRG1-independent (right panel; #68). See main text for the definition of “BRG1-independent” and “BRG1-depedent” TAL1 binding site.

Supplementary Figure S7: Nucleosome profiles changes at “BRG1-independent” TAL1 binding sites that are enriched with BRG1 binding. See main text for the definition of “BRG1-independent” TAL1 binding sites.

Figure S1

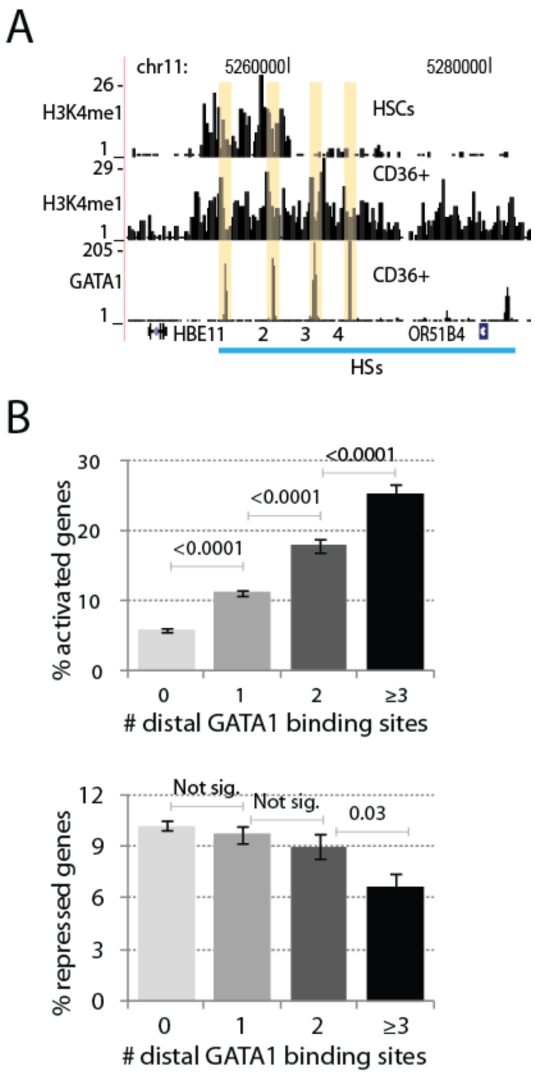

A
chr11:
5260000
5280000
26
H3K4me1
1
HSCs
29
H3K4me1
1
CD36+
205
GATA1
1
CD36+
HBE11
2
3
4
OR51B4
HSs
B
30
20
10
0
% activated genes
<0.0001
<0.0001
<0.0001
0
1
2
≥3
distal GATA1 binding sites
12
9
6
3
0
% repressed genes
Not sig.
Not sig.
0.03
0
1
2
≥3
distal GATA1 binding sites

Figure S2

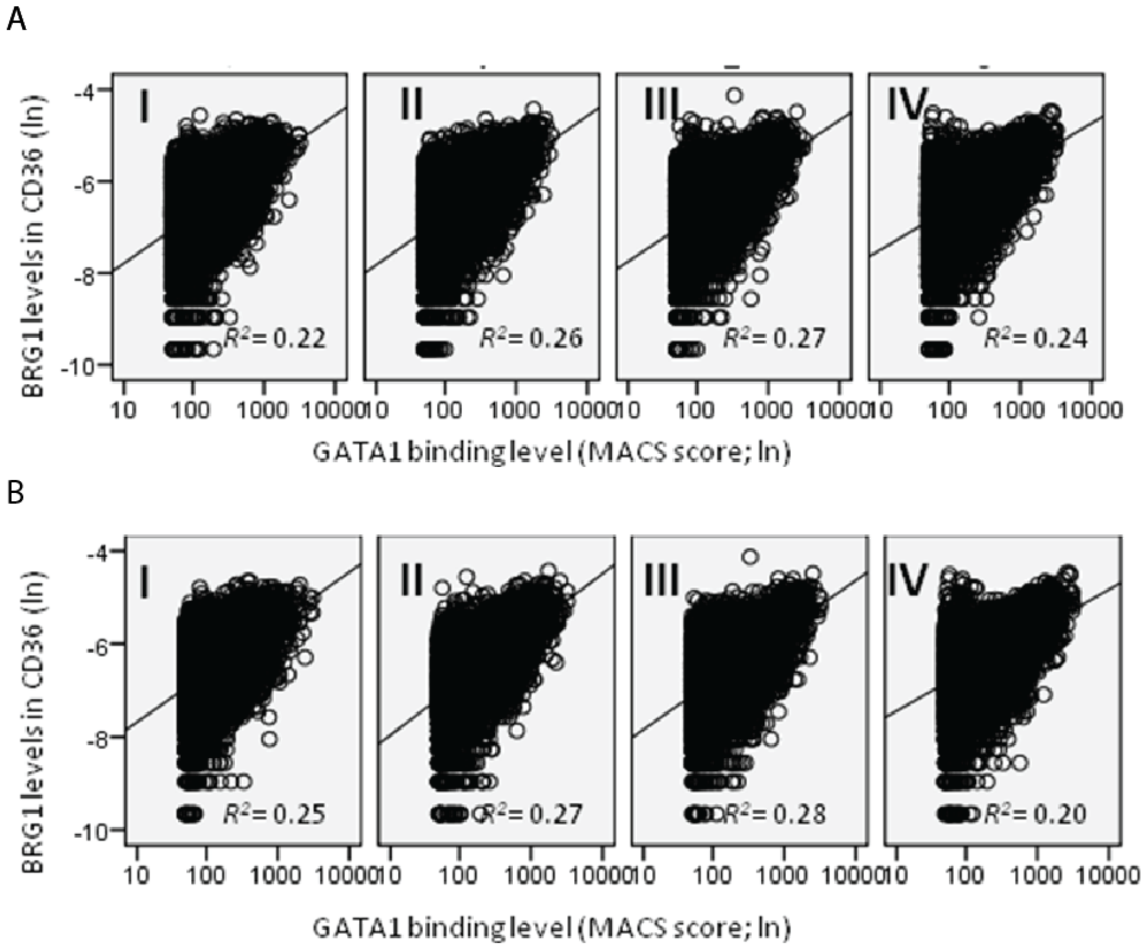
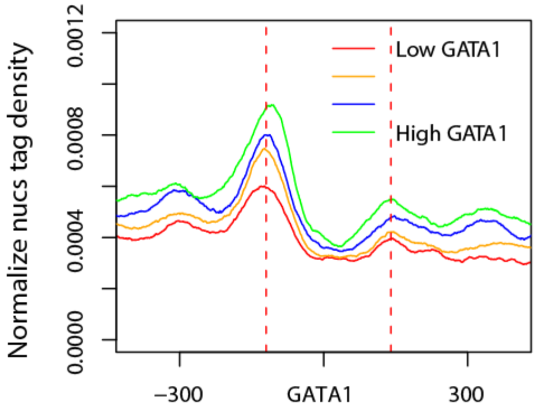

A
B
I
II
III
IV
R^2= 0.22
R^2= 0.26
R^2= 0.27
R^2= 0.24
R^2= 0.25
R^2= 0.27
R^2= 0.28
R^2= 0.20
BRG1 levels in CD36 (ln)
-4
-6
-8
-10
10
100
1000
10000
GATA1 binding level (MACS score; ln)

Figure S3

A) HSCs



B) CD36

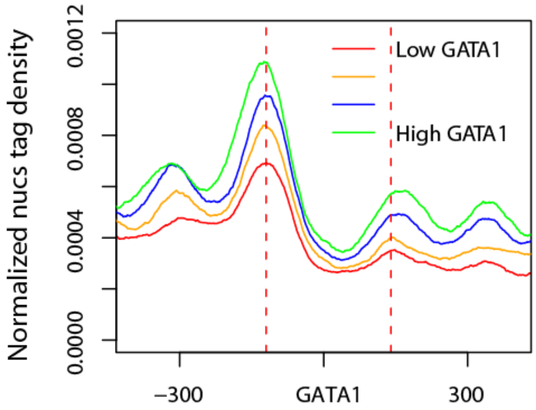


Figure S4

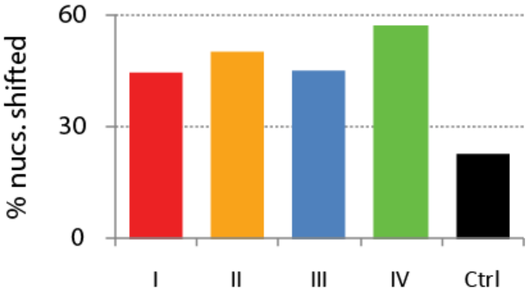
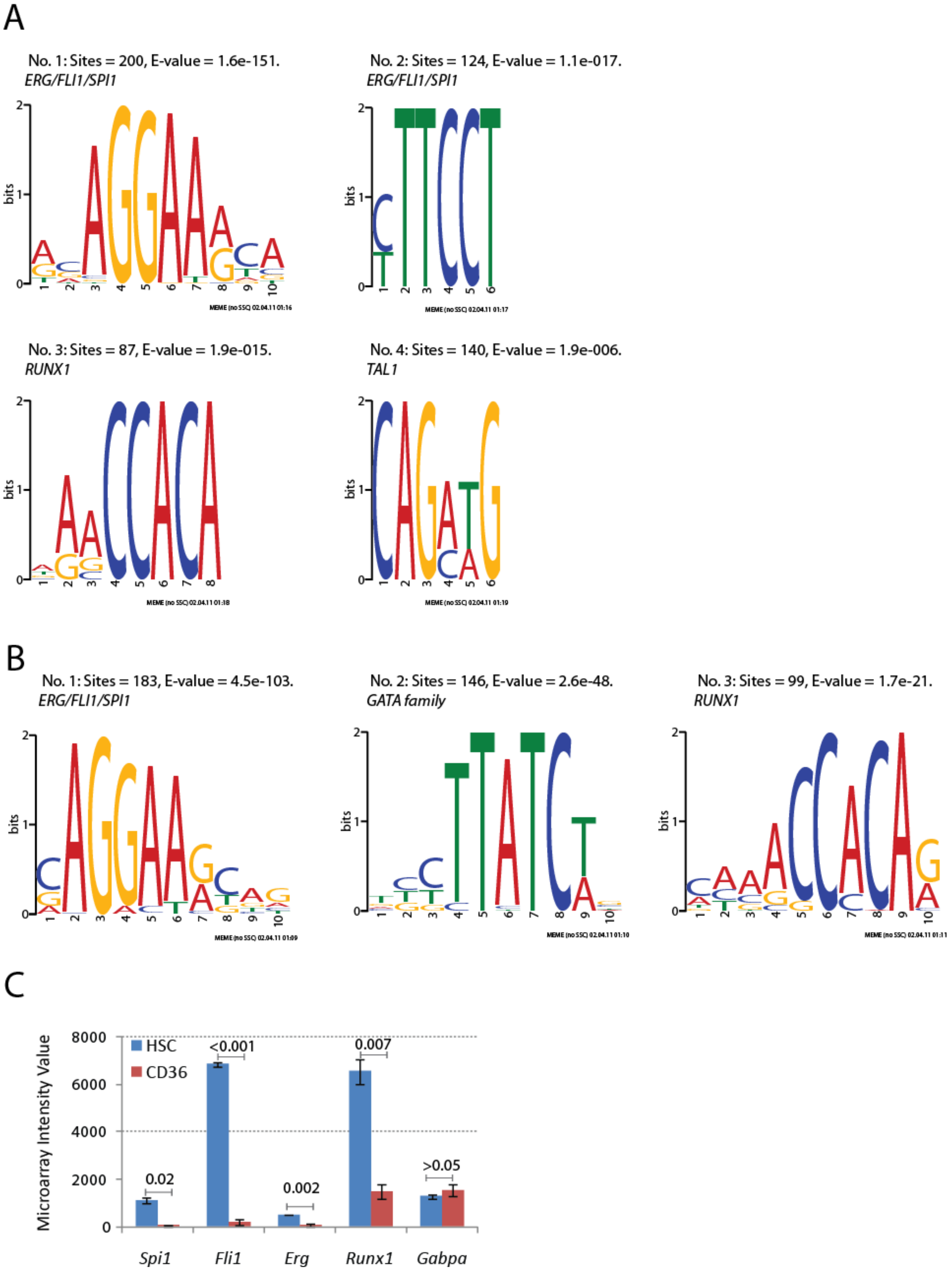


Figure S5



No. 1: Sites = 200, E-value = 1.6e-151.
ERG/FLI1/SPI1

No. 2: Sites = 124, E-value = 1.1e-017.
ERG/FLI1/SPI1

No. 3: Sites = 87, E-value = 1.9e-015.
RUNX1

No. 4: Sites = 140, E-value = 1.9e-006.
TAL1

No. 1: Sites = 183, E-value = 4.5e-103.
ERG/FLI1/SPI1

No. 2: Sites = 146, E-value = 2.6e-48.
GATA family

No. 3: Sites = 99, E-value = 1.7e-21.
RUNX1

Figure S6

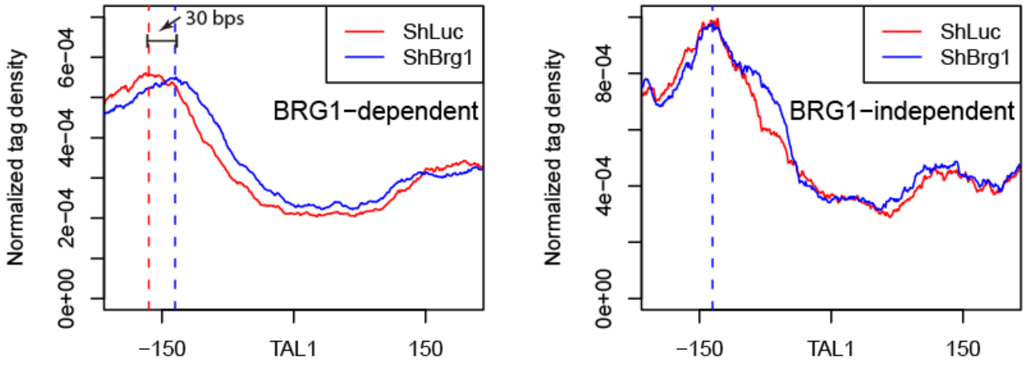
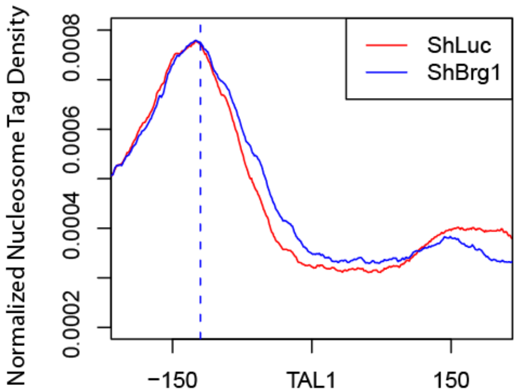

30 bps
ShLuc
ShBrg1
BRG1−dependent
Normalized tag density
0e+00
2e−04
4e−04
6e−04
−150
TAL1
150
ShLuc
ShBrg1
BRG1−independent
Normalized tag density
0e+00
4e−04
8e−04
−150
TAL1
150

Figure S7



References:

Cui, K., Zang, C., Roh, T.Y., Schones, D.E., Childs, R.W., Peng, W., and Zhao, K. 2009. Chromatin signatures in multipotent human hematopoietic stem cells indicate the fate of bivalent genes during differentiation. *Cell Stem Cell* **4**(1): 80-93.

Kaplan, N., Moore, I.K., Fondufe-Mittendorf, Y., Gossett, A.J., Tillo, D., Field, Y., LeProust, E.M., Hughes, T.R., Lieb, J.D., Widom, J. et al. 2009. The DNA-encoded nucleosome organization of a eukaryotic genome. *Nature* **458**(7236): 362-366.