MEIS2 Is an Oncogenic Partner in AML1-ETO-Positive AML

Highlights

- **MEIS2** is aberrantly expressed in **AML1-ETO** AML
- Co-expression of **MEIS2** with **AML1-ETO** induces AML in a murine model
- **MEIS2** strongly binds to **AML1-ETO**
- **MEIS2** increases **YES1** expression by impairing **AML1-ETO** DNA binding

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In Brief

**AML1-ETO** is the most frequent fusion gene in human acute myeloid leukemia, but it is difficult to target therapeutically. Vegi et al. find that the homeobox gene **MEIS2** is an oncogenic partner in **AML1-ETO**-positive AML. **MEIS2** alters the DNA binding properties of **AML1-ETO**, resulting in reduced transcriptional repression of **YES1**, which is thus a possible therapeutic target.

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MEIS2 Is an Oncogenic Partner in AML1-ETO-Positive AML

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SUMMARY

Homeobox genes are known to be key factors in leukemogenesis. Although the TALE family homeodomain factor Meis1 has been linked to malignancy, a role for MEIS2 is less clear. Here, we demonstrate that MEIS2 is expressed at high levels in patients with AML1-ETO-positive acute myeloid leukemia and that growth of AML1-ETO-positive leukemia depends on MEIS2 expression. In mice, MEIS2 collaborates with AML1-ETO to induce acute myeloid leukemia. MEIS2 binds strongly to the Runt domain of AML1-ETO, indicating a direct interaction between these transcription factors. High expression of MEIS2 impairs repressive DNA binding of AML1-ETO, inducing increased expression of genes such as the druggable proto-oncogene YES1. Collectively, these data describe a pivotal role for MEIS2 in AML1-ETO-induced leukemia.

INTRODUCTION

Aberrant expression of clustered homeobox genes, or HOX genes, is a molecular hallmark of acute myeloid leukemia (AML), and many experimental studies have proven that dysregulated expression of this highly conserved family of transcription factors is a key factor in leukemia development (Alharbi et al., 2013; Argiropoulos et al., 2007; Jung et al., 2015; McGonigle et al., 2008; Spencer et al., 2015). Besides HOX genes, non-clustered homeobox genes, such as the ParaHox gene CDX2, have been shown to play an essential role in leukemogenesis (Faber et al., 2013; Lengerke and Daley, 2012; Rawat et al., 2012), as have members of the three-amino-acid-loop extension (TALE) superfamily, MEIS1 and PBX1 (Argiropoulos et al., 2007). The TALE superfamily is characterized by three highly conserved additional residues, proline-tyrosine-proline, in the first loop region of the homeodomain (Birglin, 1997). So far, three functional Meis genes have been identified (Meis1, Meis2, and Meis3). MEIS1 and MEIS2 show 82% homology at the amino acid level. Homology is particularly high within the homeodomain and in a second conserved domain, the homothorax homology domain (Hth) (Moens and Selleni, 2006). There is a rich body of evidence arguing that Meis1 plays a pivotal role in normal and malignant hematopoiesis. Murine transplantation models clearly showed that Meis1 collaborates with native Hox genes such as Hoxa9 and HoxA10 and multiple NUP98-HOX fusion genes in inducing AML (Kroon et al., 1998; Pineault et al., 2003; Thorsteinsdottir et al., 2001). Furthermore, MEIS1 and multiple HOX genes are aberrantly expressed in a variety of human AML genotypes such as NPM1 mutated cytogenetically normal (CN)-AML or AML with complex karyotype (Kawagoe et al., 1999; Rawat et al., 2008). Interestingly, to date, MEIS1 is the only MEIS family member to be implicated in normal or leukemic hematopoiesis. In this report, we characterize MEIS2 as a potent oncogene in AML1-ETO (AE)-positive AML.

RESULTS

The Homeobox Gene MEIS2 Is Aberrantly Expressed in Patients with AE-Positive AML

Because there are few reports on the expression and function of MEIS2 in AML, expression of this gene was evaluated in a large cohort of patients with AML and normal CD34+ bone marrow (BM) cells by real-time qPCR (Table S1). Strikingly, MEIS2 expression in AE-positive AML was significantly higher than in PML–RARα and inv(16) positive cases (n = 11) (p < 0.0001) (Figure 1A). There was also high expression in CN-AML, independent of the NPM1 mutational status, an AML genotype
Previously associated with elevated homeobox gene expression in contrast to AE-positive AML (n = 10). Importantly, the majority AE-positive AML cases showed significantly on average 22.3-fold-higher MEIS2 transcript levels (p < 0.005) compared to normal human CD34+ BM samples (Figure 1A). Furthermore, MEIS2 was highly expressed in CD34+/CD38- leukemic stem cell (LSC) candidates isolated from AE-positive cases (n = 3), whereas no expression of this gene was detectable in four of five samples of the corresponding normal counterpart (Figure 1B). Importantly, MEIS2 protein expression could be validated in representative (8:21)-positive patients at levels comparable to normal human cord blood cells (Figure S1A).

In summary, these data indicate that AE-positive AML is characterized by aberrant expression of MEIS2 in all leukemic compartments, including the most primitive CD34+/CD38- compartment associated with LSC activity.

MEIS2 Collaborates with AE in Inducing AML

To test whether aberrant expression of MEIS2 is of any functional relevance in human AML, the impact of small hairpin RNA (shRNA)-mediated MEIS2 depletion in the AE-positive cell lines SKNO-1 or Kasumi-1 was analyzed. Knockdown of MEIS2 by three independent shRNA constructs in vitro resulted in a significant reduction in proliferation and colony formation that was reflected in a statistically significant increase in the proportion of cells in G0/G1phase and also an increase in cells expressing the differentiation maker CD11b in SKNO-1 cells (Figures 2A–2C and S1B–S1E). The functional relevance of MEIS2 expression was confirmed in a primary AE sample that showed 38% reduction in cell viability after small interfering RNA (siRNA)-mediated suppression of MEIS2 expression in comparison to the scrambled control (Figure 2D).

To further validate collaboration of MEIS2 with AE, we tested expression of Meis2 in normal murine hematopoiesis and mimicked co-expression of Meis2 with the AE fusion gene in human AML by retrovirally engineered co-expression of MEIS2 and AE in murine progenitor cells. In line with our findings in normal human BM, Meis2 expression was low in hematopoietic stem cells and absent in most samples of more differentiated hematopoietic cells (Figure S2A). AE collaborated significantly with MEIS2 as reflected in the colony forming unit-spleen (CFU-S) assay, increasing the median colony number on the spleen by 2.3-fold (p < 0.05) 12 days post-transplant compared to mice transplanted with cells carrying AE alone (Figure S2B). Mice transplanted with BM cells expressing constitutively AE, MEIS2, or GFP did not develop any disease up to 500 days post-transplantation. In contrast, mice injected with only 3.1% ± 2.3% transduced BM cells co-expressing both the AE fusion and MEIS2 developed AML 171 days after transplantation (n = 7), with an average engraftment of 92.4% ± 0.01% SEM and significant shortening of survival compared to the GFP control mice, indicating collaboration of both genes in vivo. Leukemias generated by AE and MEIS2 were transplantable and induced disease after a short latency of 33 days in secondary recipients (n = 11) (Figure 3A). Examination of the peripheral blood (PB) of diseased mice showed hyperleukocytosis, accumulations of blasts, splenomegaly, and severe multi-organ infiltration with leukemic blasts, which were highly positive for Mac1, Gr1, and c-Kit (Figures 3B, S2C, and S2D; Tables S2 and S3). According to the Bethesda criteria for hematological neoplasms, all mice in the AE/MEIS2 arm died of AML with maturation (Figure 3C). In contrast to the observed synergy in leukemogenic activity between MEIS2 and AE, MEIS2 overexpression did not shorten disease latency when combined with the more potent AML1-ETO9a (AE9a) gene, previously shown on its own to be able to cause AML within 175 days (Yan et al., 2006) (Figures S2E–S2G). This was in line with results from the CFU-S assay, which did not show any differences in splenic colony formation between AE9a/MEIS2 and AE9a alone (Figure S2H). Of note, overexpression of AE9a was observed to enhance endogenous Meis2 expression 6.2-fold (±1.60 SEM) in murine BM progenitor cells, a level of induction substantially higher than that seen with AE alone (3.05-fold ±0.48 SEM) (Figure S2I). Importantly, there were no recurrent retroviral integration sites in both AE/MEIS2- and AE9a- or AE9a/MEIS2-positive leukemias enlisted...
in the retroviral tagged cancer genes database (RTCGD) (data not shown).

To characterize genes and pathways differentially expressed by overexpression of MEIS2 and AE-positive cells, we performed microarray analyses 48 hr after successful gene transduction in 5-fluorouracil (5-FU)-mobilized murine progenitor cells. In comparison to the GFP control, MEIS2 with AE induced upregulation of 75 probesets corresponding to 23 genes and downregulation of 159 probesets corresponding to 122 genes. In contrast to the upregulated genes, the vast majority of downregulated genes did not overlap between AE/MEIS2 and AE alone (Figures S3A and S3B; Table S4). When these differentially expressed genes between AE/MEIS2 and GFP were analyzed in the Kyoto Encyclopedia of Genes and Genomes (KEGG)-based pathway analysis, “cytokine-cytokine receptor interaction,” “transcriptional misregulation in cancer,” and “pathways in cancer” scored among the top-five ranking categories. In a direct comparison between AE and AE/MEIS2 BM, out of 195 differentially regulated probesets referring to 145 genes, 29 probesets (12 genes) were upregulated and 166 probesets (80 genes) were downregulated (Table S4). Interestingly, Hoxa genes such as Hoxa5, Hoxa7, Hoxa9, and Hoxa10 were downregulated in AE and AE/MEIS2 compared to the empty vector. This was further validated by qRT-PCR, indicating that the leukemogenicity of AE/MEIS2 does not depend on upregulation of oncogenic Hoxa genes (Figures S3C and S3D). Gene set enrichment analysis (GSEA) analysis for oncogenic signature (MsigDB version 5.0) showed enrichment for gene sets such as “JAK2” and “PTEN” in AE/MEIS2 versus AE alone (Figure S3E; Table S4). Consistent with the finding that MEIS2 did not increase leukemogenicity of AE9a, RNA-seq of leukemic BM showed a close overlap in gene expression between AE9a and AE9a/MEIS2, indicating that adding of MEIS2 to the leukemogenic truncated AE9a does not induce gross changes in the molecular phenotype of AE9a-positive leukemias (Figures S3F and S3G).

Taken together, these data indicate that MEIS2 functionally collaborates with AE in AML.

**MEIS2 Binds to AE**

To understand the mechanism of AE-MEIS2 collaboration, we first sought to identify domains of the fusion gene that may be critical for collaboration between AE and MEIS2 using the CFU-S assay as readout for growth-promoting activity (Figures S4A and S4B). Only the inactivating point mutation in the Runt
domain, not deletion of the NHR1 or C-terminal stretch, reduced collaboration between MEIS2 and the fusion gene, indicating that DNA binding properties are crucial for AE-MEIS2 leukemicogenic collaboration. There was a trend that MEIS2 could further enhance CFU-S activity of the C-terminally truncated D540 AE construct that contains the TAF/NHR1 domain and lacks the zinc-finger domains, previously shown to have similar activity as the wild-type AE (Westendorf et al., 1998) (Figure S4C). To test for a possible direct interaction between AE and MEIS2, co-immunoprecipitation (coIP) assays along with various other mutants of MEIS2 (Figure S4D) were performed in HEK293 cells. Surprisingly, strong binding of MEIS2 to the Runt domain of AE could be documented (Figures 4A and 4B). Additional experiments showed that AE9a is also able to strongly bind to MEIS2 (Figure S4E) and that the N-terminal region (amino acids [aa] D1–68 or 69–470) of MEIS2 is critical for binding to the Runt domain of AE and AE9a (Figures 4C, 4D, S4E, and S4F). The binding of MEIS2 to AE was validated in a human leukemic background by performing immunoprecipitation for ETO and western blotting for MEIS2 in the AE-positive human cell line (Figures S4H–S4J). Collectively, these data provide evidence that MEIS2 is able to directly interact with the most frequent fusion gene in AML and that binding to AE is critical for its full collaborative activity in the CFU-S assay.

MEIS2 Alters Target Gene Binding of AE

To analyze whether MEIS2 expression levels impact AE DNA binding properties, chromatin immunoprecipitation (ChIP) sequencing was performed in the human AE-positive Kasumi cell line after shRNA-mediated MEIS2 knockdown (shMEIS2-44) compared to the scrambled control, using an AE fusion-specific antibody (Martens et al., 2012). Successful enrichment for AE target genes by the antibody used was first validated by ChIP qPCR for known specific binding partners of AE such as SPI1, OGG1, FUT7, and NFE2, each of which showed substantial enrichment (showing an up to 18-fold) (Figures S5A and S5B). In addition, motif analyses of the AE binding sites in the ChIP-seq revealed enrichment for both the RUNX1 and ETS1 target sites as previously reported (Martens et al., 2012) in both experimental arms, comprising between 35% and 42% of all target regions, as well as the presence of weaker motifs with 44.32% and 65.8% for scrambled (SCR) and shMEIS2, respectively (Figures S5C–S5F; Table S5). As we observed increased binding of AE to RUNX1 after MEIS2 knockdown, changes in expression of RUNX1 were tested in the t(8;21)-positive cell lines SKNO-1 and Kasumi after MEIS2 depletion: however, knockdown induced no major change of RUNX1 expression in both cell lines (n = 3) (data not shown).
At a cutoff of \( \geq 10 \)-fold with a FDR rate threshold of 0.001 and a FDR effective Poisson threshold of 0, a total of 13,003 high-confidence DNA binding regions for AE with or without expression of shMEIS2 were detectable. Of note, knockdown of MEIS2 increased the number of AE binding sites compared to the control by >2-fold. In addition, knockdown of the MEIS2 gene induced >7,900 unique AE binding sites, indicating gross changes in the DNA binding behavior of the fusion gene after MEIS2 depletion (Figure 5A). When we focused on the promoter regions (defined as binding regions 1 kb upstream and 100 bp downstream of the transcription start site), AE still bound to significantly more DNA sites after MEIS2 knockdown, with >1,100 unique binding sites compared to the control (Figure 5B; Table S4). The higher number of AE DNA binding sites after MEIS2 depletion was a consistent characteristic throughout the differentially annotated DNA regions (Figure 5C). Among those genes that showed substantial increase of AE binding after MEIS2 knockdown were IGFBP7, mir-4442, OGG1, RUNX1, and WT1. A smaller proportion of genes showed decreased AE binding after MEIS2 depletion, such as mir-145, NDUFA4, and KRAS (Figure S6A). Other genes did not meet the above-mentioned criteria for AE binding in the scrambled control but met the requirements with a >10-fold increase in AE binding, such as ASLX2, FLT3, CREB1, GSK3a, and HMGA1 (Table S6). Of note, expression of MEIS2 decreased after AE shRNA-mediated knockdown in SKNO-1 cells, although there was no documented binding of AE to the MEIS2 promoter (Figures S6B and S6C).

Thus, these data demonstrated that high MEIS2 expression is associated with a reduction of AE binding to DNA targets and, vice versa, that knockdown of MEIS2 increases AE binding sites. Furthermore, the data show that AE binds to a distinct and unique set of DNA sites in human AML cells when MEIS2 is highly expressed.
High Expression of MEIS2 Is Associated with Loss of AE Binding to the YES1 Promoter Region and Increased YES1 Expression

To correlate AE target gene binding with expression levels, RNA-seq was performed in parallel to ChIP sequencing (ChIP-seq) for the same samples in duplicates. Genes were considered as differentially expressed when the difference in FPKM (fragments per kilobase per millions reads) was significant at a p value of 0.05, with a false discovery rate (FDR) of 0.05. First, differentially expressed genes were analyzed independent of AE target binding: 868 genes were differentially expressed between Kasumi cells transduced with the MEIS2 shRNA versus scrambled control (Table S4). KEGG analysis showed changes in the expression of genes belonging to the categories ribosomes, lysosomes, and adherence junction (Tables S4 and S7). Of note, MEIS2 knockdown induced major differences in gene expression, with an up to 2.25 log2 fold change for upregulated genes (n = 365) and up to 9 log2 fold for downregulated genes (n = 123 genes) compared to the SCR control (Table S4).

As a second step, we correlated differentially expressed genes with AE DNA binding. Among the genes with changes in expression and AE binding, there were two categories. The first showed an increase in expression accompanied by an enhanced AE binding to their promoter region (e.g., MPO, KIT, NUCB2, and CD34 MYOG1). The second group showed decreased expression level parallel to increased AE binding (e.g., YES1, BCL2L1, HMGA1, IGFBP2, and TXNIP) after MEIS2 knockdown (Table S8). We validated these findings for selected genes and found a significant (p < 0.05) positive correlation between expression levels determined by RNA-seq and qRT-PCR (Figure S6D). There was no decrease in the expression of the targetable receptor tyrosine kinases c-Kit and FLT3 after MEIS2 knockdown as validated by qRT-PCR. In contrast, knockdown of MEIS2 induced a substantial decrease in expression of the Src kinase YES1 accompanied by increased AE promoter binding of this gene (Figure 6A). This finding thus provided an intriguing gene whose expression was strongly dependent on MEIS2 overexpression and whose effects were potentially druggable. Of note, knockdown of YES1 resulted in an up to 78% reduction in proliferation and 95% reduction in clonogenic growth in Kasumi cells (Figures 6B–6D), indicating that YES1 expression is relevant for the cell growth of this AE-positive AML cell line. This was in line with the observation that knockdown of Yes1 in primary leukemic murine AE9a/MEIS2 cells impaired primary clonogenic growth by, on average, 70.5% (sh84) and 71.14% (sh152) and re-plating by 93.98% and 69.13% for the two
shRNAs, respectively (Figures S6F–S6H). Indeed, all AML genotypes, including the AE-positive AML subtype showed YES1 expression as previously indicated in The Cancer Genome Atlas (TCGA) database (Network, 2013) (Figure S6E). Next, we tested the efficacy of pharmacological YES1 inhibition. So far, there are no selective YES1 inhibitors available. One of the most potent YES1 inhibitors is dasatinib, which also impairs other kinases such as c-Src, Fyn, and Lyn (BMS-354825) (Patel et al., 2013). The AE-positive Kasumi cell line, expressing high levels of MEIS2, is also positive for YES1 expression and showed complete loss of phosphorylation of the kinase after dasatinib treatment. With a half maximal inhibitory concentration (IC50) value of 6.8 μM, dasatinib was highly efficient in impairing Kasumi cell growth in vitro (Figures 6E and 6F). Although it has to be taken into account that dasatinib is a multikinase inhibitor known to target several other kinases such as Lyn, PDGFR, KIT, Lck, Fyn, and c-Src, these data at least suggest that YES1 is an attractive target in AE-positive AML.

All together, these data point to a regulatory network, in which high MEIS2 expression collaborates with AE in inducing leukemia, involving at least in part MEIS2’s ability to strongly bind to AE and thereby grossly change binding of AE to its target genes on a global scale. This results in loss of repression of proto-oncogenes, exemplified by an increase in the expression of the YES1 kinase in AML cells, thereby opening avenues to link a leukemogenic liaison between transcription factors to a druggable target.

**DISCUSSION**

AML characterized by the translocation t(8;21) counts for 15% of all human AML cases and is characterized by expression of the most frequent fusion gene detectable in patients with this disease. So far, the AE-positive AML genotype was not associated with deregulated homeobox gene expression (Andreeff et al., 2008; Lo et al., 2012). In this report, we now provide evidence that TALE homeobox genes are involved in AE leukemogenesis and that they can directly interact with the fusion gene. We initiated the study quantifying the expression of the TALE homeobox gene MEIS2 in a larger AML patient cohort and could readily demonstrate that MEIS2 is aberrantly highly expressed not only in virtually all AE-positive AML samples compared to normal CD34+ hematopoiesis but also in comparison to other core binding factor (CBF) leukemias. The mechanism behind this observation is unclear. Despite the gross differences in MEIS2 expression between AE AML samples and normal CD34+ BM cells, both populations did not show any major methylation differences at the CpG regions of the MEIS2 promoter as determined by MassARRAY technology, indicating that expression of this gene is not regulated by...
methylation, at least of these CpG islands (data not shown). Interestingly, published microarray data documented a significantly increased expression of MEIS2 after retrovirally induced overexpression of AE in human CD34+ cord blood cells compared to the control (expression atlas EMBL-EBI; Krejci et al., 2008), in line with our own data showing the same observation for murine progenitor cells, whereas in the human setting, a reduction of MEIS2 expression after knockdown of AE was only observed in the t(8;21)-positive SKNO-1 cell line and not in Kasumi cells (data not shown). The mechanism of this is not clear, as we did not see any major binding of AE to the MEIS2 region, as also described by Ptasinska et al. (Ptasinska et al., 2012).

Functional relevance of high MEIS2 expression in collaboration with AE could be clearly demonstrated by knockdown in human AML cells and in the BM transplantation assay, in which only MEIS2, in collaboration with AE, induced leukemia in contrast to MEIS2 or AE alone, as shown by us and several other groups (de Guzman et al., 2002; Fenske et al., 2004; Licht, 2001; Schessl et al., 2005). However, in our model, the latency time until development of AML was long, with a median time of 171 days until disease post-transplant. The long latency suggests that MEIS2 in concert with the human full-length AE fusion gene needs additional partners. To test how this homeobox gene might functionally interconnect with AE, we analyzed binding between the two proteins and surprisingly found strong binding between MEIS2 and AE. Interaction between endogenous MEIS2 and AE could be re-confirmed in the human AML SKNO-1 cell line. These results thus implicate a previously unrecognized direct interaction between AE and MEIS2 in human AML. An important question is whether direct binding to AE is relevant for the collaboration between MEIS2 and AE. To address this, we generated a mutant that lost binding to AE. Importantly, this construct showed reduced hematopoietic activity compared to the full-length protein. MEIS2 was also highly expressed in AML cases with NPM1 mutation or normal karyotype with an NPM1 wild-type protein. Indeed, we could demonstrate that AE changes MEIS2 co-expression, in line with published data demonstrating crosstalk between the most frequent fusion gene in AML and the MEIS2 homeobox gene, identifying MEIS2 as a potent collaborative leukemogenic partner that affects DNA binding of the most frequent fusion gene in human AML.

EXPERIMENTAL PROCEDURES

Patient Samples, Cell Lines, and Mouse Experiments

Mononuclear cells isolated from diagnostic BM or PB with AML leukemias from 92 adult patients were analyzed (n = 70 for t(8;21), n = 11 for PML-RARα, n = 11 for inv(16), and n = 5 for NPM-WT and NPM+). CD34+ from bone marrow mononuclear cells (BM MCs; Lonza) (n = 13) from healthy individuals were taken as controls. Cytochemistry and cytogenetics (Table S1) were performed in all cases as described. Cases were classified according to the French-American-British criteria and World Health Organization classification (Bennett et al., 1976; Harris et al., 1999). The study was approved by the ethics committees of all participating institutions, and informed consent was obtained from all patients before they entered the study in accordance with the Declaration of Helsinki (http://www.wma.net/en/30publications/10policies/b3/index.html). The t(8;21)-positive AML cell lines Kasumi-1 (all DMSZ) and SKNO-1 (kindly provided by Michael Lucibbert, Freiburg, Germany) were used for expression analysis. Kasumi-1 and OCI-AML3 were cultured in RPMI 1640 with 20% fetal bovine serum (FBS) and 1% penicillin-streptomycin.
using Klenow and T4 PNK. A 3\'-end repair was performed using the precipitated DNA of the second exon of the myoglobin gene or the promoter of the Illumina sequencing adapters using trimm galore (Martin, 2011), high-quality RNA-seq was performed using libraries prepared by TruSeq RNA Sample Preparation Kit version 2. Chromatin was harvested as described previously (Denissov et al., 2007). ChIP-Seq and Peak Detection were performed as described previously (Salat et al., 2008; Wacker et al., 2011). Protein concentrations were determined using the Bradford assay method (Bio-Rad). Details regarding cold and western blot can be found in Supplemental Experimental Procedures.

ChiP-Seq and Peak Detection
Chromatin was harvested as described previously (Denissov et al., 2007). ChiP was analyzed by qPCR or ChiP-seq as previously described (Martens et al., 2012). Primers for qPCR used were as follows:

- SP1: forward, 5’-GGGTAAGAGCCCTGTGACG-3’; reverse, 5’-CAGATG CACGTGGCTGATAC-3’
- FUT7: forward, 5’-TGAAACCAACCCCTGAGTGTC-3’; reverse, 5’-TCAGT GACATGAATGAGAGC-3’
- NFE2: forward, 5’-GTGTAGAGCATACTTGAGG-3’; reverse, 5’-ACGATA CGAGAAAACACG-3’
- OGG1: forward, 5’-CCACCGTTATATGATCAAGC-3’; reverse, 5’-CAACCA CGGCTCATTTAC-3’
- VAV1: forward, 5’-AGAAGGCTTGGAGGCTAGG-3’; reverse, 5’-CTGTTA CCAAGGGCTTTGGT-3’
- H2B: forward, 5’-TGCTACGATCTTATATAAACGG-3’; reverse, 5’-AT AAAGGCCCAACGGAAAGG-3’
- MYOD: forward, 5’-AAGGTGAGAGCAGCTGGACCTG-3’; reverse, 5’-TG GCACCATGTGCTTATAGTGC-3’.

Relative occupancy was calculated as fold over background, for which the second exon of the myoglobin gene or the promoter of the H2B gene was used. Illumina sequencing was done as previously described (Martens et al., 2010). Briefly, end repair was performed using the precipitated DNA of ~30 million cells using Klenow and T4 PKM. A 3’ protruding A base was generated using T4 polynu-merase, and adapters were ligated. The DNA was loaded on gel and a band corresponding to ~300 bp (ChiP fragment + adapter) was excised. The DNA was used for qPCR, and used for cluster generation on the Illumina genome analyzer. Fastq files were quality controlled and adaptor trimmed using trimm galore (Martin, 2011), and sequences with phred score of 20 or higher were considered for downstream analysis. Sequences were then aligned to the human genome version hg19 using bowtie2 (Barbie et al., 2009). Peak calling and annotation was done using CisGenome (Ji et al., 2008) and HOMER v3.12 (http://homer.salk.edu/homer/ngs/peaks.html).

RNA-Seq and Analysis
RNA-Seq was performed using libraries prepared by TruSeq RNA Sample Preparation Kit version 2. The samples were run on HiSeq2000. After trimming Illumina sequencing adapters using trimm galore (Martin, 2011), high-quality raw Fastq files (phred score of 20 or higher) were aligned using tophat and respective RefSeq files (the human hg19 assembly and the murine mm10 genome version). Differential expression analysis was performed using CUFFlinks (Trapnell et al., 2009, 2010) and R packages (Team, 2013).

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SUPPLEMENTAL INFORMATION
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