Regulation of Early Adipose Commitment by Zfp521

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Abstract

While there has been significant progress in determining the transcriptional cascade involved in terminal adipocyte differentiation, less is known about early events leading to lineage commitment and cell fate choice. It has been recently discovered that zinc finger protein 423 (Zfp423) is an early actor in adipose determination. Here, we show that a close paralog of Zfp423, Zfp521, acts as a key regulator of adipose commitment and differentiation in vitro and in vivo. Zfp521 exerts its actions by binding to early B cell factor 1 (Ebf1), a transcription factor required for the generation of adipocyte progenitors, and inhibiting the expression of Zfp423. Overexpression of Zfp521 in cells greatly inhibits adipogenic potential, whereas RNAi-mediated knock-down or genetic ablation of Zfp521 enhances differentiation. In addition, Zfp521−/− embryos exhibit increased mass of interscapular brown adipose tissue and subcutaneous white adipocytes, a cell autonomous effect. Finally, Ebf1 participates in a negative feedback loop to repress Zfp521 as differentiation proceeds. Because Zfp521 is known to promote bone development, our results suggest that it acts as a critical switch in the commitment decision between the adipogenic and osteogenic lineages.

Introduction

Mesenchymal stem cells can differentiate into a variety of lineages, including fat, bone, muscle, and cartilage [1]. In particular, there has been emphasis placed on understanding how commitment is determined in cells that could become bone or fat, as these processes are considered relevant to the twin epidemics of obesity and osteoporosis. Numerous studies have shown an inverse relationship between bone and fat development, such that marrow adiposity increases with age [2], while the clinical use of proadipogenic PPARγ agonists increases fracture risk [3–6]. At the molecular level, reciprocal regulation between adipogenic and osteogenic regulatory factors has been noted. Activation of PPARγ inhibits the activity of the osteoblastogenic master regulator Runx2 [7], while the osteogenic transcription factor Mesp2 inhibits PPARγ and C/EBPα [8,9]. Other transcriptional components that exert opposing effects on adipogenesis and osteogenesis include Taz [10], ΔFosB [11], Rb [12], and Maf [13]. Together, these studies suggest that there is a molecular balance between these two lineages.

Late events in adipocyte terminal differentiation have been well-studied, and a transcriptional cascade has been identified that includes PPARγ, C/EBPα, and a burgeoning network of other factors [14]. Our understanding of early events in adipogenesis, however, is relatively underdeveloped. Notably, Zfp423 and Tcf7l1 have been recently proposed to facilitate early determination events in adipogenesis [15–17]. Zfp423 is a large and interesting molecule, containing 30 C2H2 Krüppel-like zinc fingers. In addition to promoting adipocyte lineage determination, Zfp423 also regulates development in the brain [18,19], exerting its actions in part through physical interactions with various binding partners, including RAR/RXR [20], Smads [15], and early B cell factor 1 (Ebf1) [21,22]. Originally described as a regulator of olfactory epithelial differentiation [23] and B-cell lymphopoiensis [24], Ebf1 is proadipogenic [25,26] and also appears to operate early in the commitment phase of differentiation [27]. Thus, Ebf1−/− mice are not only lipo dystrophic but actually lack adipocyte progenitor cells [27,28].

Zfp521, also known as Evi-3 in the mouse (ZNF521/EHZF in the human), is the only close paralog of Zfp423 in the mammalian genome; both factors contain he same array of 30 C2H2 Krüppel-like zinc fingers. Zfp521 is enriched in primitive cell types, such as neural precursor cells, immature ovarian cells, and CD34+...
Zfp521 Inhibits Adipogenesis In Vivo

We next sought to determine whether our findings could be replicated in vivo. Unfortunately, $Zfp521^{+/−}$ mice die shortly after birth, so we focused our analysis on the development of white and brown adipocytes in late stage embryos (embryonic day 18.5). $Zfp521^{+/−}$ embryos display an increased number of differentiating white adipocytes in the subdermal connective tissue when detected by the concordance of FABP4 immunostaining and cytoplasmic lipid droplets (Figures 2A, 2B). Remarkably, $Zfp521^{+/−}$ embryos display significantly enlarged brown adipose depots relative to wild-type littermates when assessed by histology (Figure 2C) and tissue weight (Figure 2D) without major gene expression changes (Figure S5A); liver weight, by contrast, is not different between the two genotypes. Together, these observations suggest that Zfp521 negatively regulates the embryonic development of white and brown adipose tissue.

To determine if these effects were cell autonomous, we took advantage of the ability of 3T3-F442A cells to develop into fat pads when implanted into nude mice [38] to create a competition-based assay for adipogenic potential in vivo. 3T3-F442A cells were transfused with retrovirus expressing either sh521 or a scrambled shRNA control (shScr), and the two cell types were then mixed together at a 1:1 ratio prior to implantation in nude mice; we reasoned that the hairpin conferring greater adipogenic potential should be overrepresented in the resulting fat pad. Hematoxylin–eosin (HE) staining and protein expression of C/EBPα and FABP4 from implants show that injected cells developed into adipose tissue (Figures S3B, S3C). The relative amount of each hairpin was determined using quantitative PCR (Q-PCR) to measure hairpin-specific sequences normalized to hairpin-independent sequences. By first determining the relative abundance of each hairpin in mixtures of input cells at fixed ratios, we established a baseline by which we could normalize results from the harvested tissue (Figure S3D). This analysis revealed that sh521 cells accounted for approximately 78% of the adipocytes in the fat pads, significantly greater than the 50% expected if Zfp521 knockdown had no effect (Figure 2E). We thus established that the effect of Zfp521 on adipogenesis is cell autonomous.

Zfp521 Is an Early Regulator of Adipogenesis

We next sought to determine whether Zfp521 was acting early, late, or perhaps at multiple time points in the differentiation process. As shown previously, Zfp521 sharply repressed lipid accumulation (Figure 1C). On the basis of its expression pattern, we predicted that Zfp521 would inhibit adipogenesis. This was indeed the case, as overexpression of Zfp521 in C3H10T1/2 cells (Figure 1D, 1E), 3T3-L1 cells (Figure S1D, S1E), and mouse embryonic fibroblasts (MEFs) (Figure S2F, S2G) blocked lipid accumulation and adipogenic gene expression, while shRNA-mediated knockdown of Zfp521 (sh521) had the opposite effect (Figures 1F, 1G, S1F, and S1G). This was not an off-target effect of the Zfp521 shRNA, as $Zfp521^{−/−}$ primary MEFs and stromal-vascular cells taken from the fat pads of $Zfp521^{−/−}$ mice also showed enhanced adipogenic potential compared to wild-type cells (Figures S1H–S1K). This effect was also true in human ASCs, indicating that the role of Zfp521 as an antiadipogenic factor is not confined to the rodent lineage (Figure S1L, S1M). Furthermore, overexpression of Zfp521 in C3H10T1/2 and MEFs pushed cells towards an osteoblastic fate, demonstrated by staining and gene expression patterns (Figure S2A S2D). Thus, the combined data from gain- and loss-of-function studies consistently demonstrate that Zfp521 acts as a repressor of adipogenesis and a promoter of osteogenesis in multiple systems in vitro.
Figure 1. Zfp521 is a suppressor of adipogenesis in vitro. (A) C3H10T1/2 cells were differentiated and RNA isolated at the indicated time points. Gene expression of Zfp521 and Pparg was measured by Q-PCR and normalized to cyclophilin. Data shown as mean of three biological replicates. (B) Protein lysates isolated during 3T3-L1 adipogenesis were subjected to western blotting with anti-Zfp521 antibody. (C, left) Zfp521 mRNA expression was measured in fractionated subcutaneous and epididymal fat tissue taken from wild-type mice (SV, stromal-vascular fraction; AD, adipocytes). (C, right) SV of epididymal fat tissue from Zfp423GFP transgenic mice was sorted with GFP antibody and plated. After washing away floating cells, Zfp521 mRNA expression was measured in GFP− and GFP+ cells. (D–G) C3H10T1/2 cells were retrovirally transduced with Zfp521, empty vector, shRNA specific for Zfp521 (sh521), or a scrambled hairpin (Scr). Overexpression and knock-down were confirmed by immunoblotting of Zfp521 prior to differentiation in the boxed insert. Cells were differentiated with DMI or DMI plus rosiglitazone (DMIR) and stained with oil red-O (D, F) and adipocyte markers were determined by Q-PCR (E, G) on day 8. Data presented as mean ± SD, n = 3, *p<0.05. doi:10.1371/journal.pbio.1001433.g001

Figure 2. Reduction of Zfp521 enhances adipogenic potential in vivo. (A) Sections of the subcutaneous region of e18.5 Zfp521+/− and Zfp521−/− embryos were stained with anti-FABP4 (red) and DAPI (blue). The magnified section shows representative FABP4+, lipid-filled adipocytes. (B) ~20–25 images per embryo were used to quantify the number of lipid-filled and FABP4-positive adipocytes. Zfp521−/−, n = 4 embryos; Zfp521+/−, n = 6 embryos; *p<0.05. (C, D) Representative histology (HE staining) of the interscapular BAT region from Zfp521−/− and Zfp521+/− e18.5 embryos (red arrowhead, interscapular BAT; white arrow, skeletal muscle) (C) and BAT and liver weight relative to total body weight (D). Data presented as mean ± SD, Zfp521−/− (n = 9); Zfp521+/− (n = 15), *p<0.05. (E) shZfp521 and scrambled hairpin (shScr) expressing F442A cells were mixed and injected into nude mice. Percentage contribution of shScr and sh521-expressing cells in fat pads determined using specific Q-PCR (see text for details). Data presented as mean ± SD, n = 11, *p<0.05. doi:10.1371/journal.pbio.1001433.g002

and adipocyte-specific gene expression in C3H10T1/2 cells; this effect was largely reversed by adding PPARγ or C/EBPα (Figures S3E, S3F). We also assessed whether knocking down Zfp521 in cells lacking PPARγ would allow adipogenesis to proceed. While viral delivery of shZfp521 promoted adipogenesis in cells that contain PPARγ (Pparγ+/−), cells lacking PPARγ entirely (Pparγ−/−) did not undergo differentiation (Figures S3G–S3K). Taken together, these data suggest that Zfp521 acts prior to PPARγ in the differentiation cascade.

Zfp521 Inhibits Preadipocyte Commitment Factor Zfp423

Because Zfp521 is a transcriptional regulator, we sought to identify downstream targets in preadipocytes using Affymetrix arrays. We performed these experiments in both gain-of-function and loss-of-function contexts to enhance our ability to identify bona fide targets of Zfp521, focusing on genes that showed coordinate regulation between Zfp521 overexpression and knockdown. There were 631 genes whose expression fell below 70% of baseline when Zfp521 was targeted by RNAi, while surprisingly few targets (five) increased by more than 1.5-fold when Zfp521 was overexpressed (Figure S4A). A total of three genes (Dusp1, Fos, and Serpin3a) showed coordinate regulation, demonstrating that they are bona fide positive targets of Zfp521. Conversely, there were 347 genes whose expression increased upon treatment with sh521, and 114 that were diminished by Zfp521 overexpression (Figure 3A); only seven of these genes were coordinately regulated. These seven genes include poorly annotated transcripts of uncertain function (e.g. 3830408D07Rik, some of which reside in a 1.3-MB cluster on the X chromosome (OTILOC434/LOC434865/LOC434864/LOC434863/LOC660284/LOC660260). Most of the others are also relatively unstudied, and include a sphingosine-1-phosphate receptor (Edg3), a per hexamer repeat gene (Phe5), and the cell structural and matrix genes synemin (Dm2) and fibromodulin (Fmod). The final gene on the list of those coordinately regulated by Zfp521 was, however, of particular interest to us: Zfp423, the most highly paralogous gene to Zfp21 and a factor recently shown to promote adipose lineage commitment [15]. Q-PCR analysis in preadipocytes confirmed that Zfp521 exerts strong repressive effects on Zfp423 expression (Figure 3B), and that reducing Zfp521 has the converse effect (Figure 3C).

Zfp521 Inhibits Ebf1 Transcriptional Activity through Physical Interaction

Zfp521 interacts with Ebf1 in the context of hematopoiesis [36]. Because we have previously shown that Ebf1 is a strong inducer of...
adipogenesis [25,26], we asked whether Zfp521 interacts with Ebf1 in preadipocytes, and whether this might underlie the anti-adipogenic actions of Zfp521. Zfp521 physically interacts with co-transfected Ebf1 in HeLa cells (Figure S4B), and this effect is also seen using co-immunoprecipitation of native proteins in 3T3-L1 preadipocytes (Figure 4A). Zfp521 inhibits the transcriptional activity of Ebf1 on the mouse mb-1 promoter region as well as the promoters of Sncg (a highly Ebf1-responsive gene in adipocytes; MJG and EDR, unpublished data) and Cebpa (Figure 4B–4D). Further, Zfp521 is recruited to the same location as Ebf1 on the Cebpa promoter [25] (Figure 4E). Ebf1 shows a slight ability to promote differentiation in immortalized Zfp521+/−/− MEFs, an effect dramatically enhanced in Zfp521+/−/− cells. Reinroduction of Zfp521 reversed the effect in both genotypes (Figure 4F, 4G). Zfp423 interacts with Ebf1 via its most C-terminal cluster of zinc fingers [32]. We therefore tested this in Zfp521 using a mutant allele missing zinc fingers 27–30 (Zfp521AZF27-30) (Figure S4D). Zfp521AZF27-30 is less able to interact with Ebf1 than wild-type Zfp521 in a co-immunoprecipitation assay (Figure S4E), and exhibits reduced ability to suppress Ebf1 transcriptional activity (Figure S4F). We also focused on the first 13 amino acids of Zfp521 (Figure S4D), which contain a motif conserved among other zinc finger transcriptional repressors like Fog-1 and Fog-2 that is required for Zfp521 to regulate erythropoiesis through physical interaction with GATA-1 and the nuclear remodeling and histone deacteylation (NuRD) complex [32]. In contrast to the AZF27-30 mutant, Zfp521Δ13aa is almost fully able to suppress Ebf1 activity on the Cebpa promoter (Figure S4F). Consistent with these results, wild-type Zfp521 and Zfp521Δ13aa, but not Zfp521AZF27-30, could fully repress adipogenesis in C3H10T1/2 cells (Figure 4H, 4I). Importantly, Ebf1 induces Zfp423 expression, an effect which can be blocked by WT Zfp521, but not Zfp521AZF27-30 (Figures 4J, 4K). This indicates that the effect of Zfp521 on Zfp423 expression is mediated via the interaction with Ebf1.

Given that Zfp521 and Zfp423 contain highly homologous Ebf1 binding domains, we speculated that Zfp521 might compete with Zfp423 for binding to Ebf1. Using coimmunoprecipitation assays, we confirmed that both Zfp521 and Zfp423 bind readily to Ebf1, but to our surprise, the addition of either Zfp521 or Zfp423 enhances binding of the other protein (Figure S5A), an effect seen even in the presence of a large excess of either protein. This suggested to us that Zfp521 and Zfp423 might heterodimerize, and this is indeed the case, even in the absence of Ebf1 (Figures S5B, S5C). The full significance of this interaction is still unclear, but it suggests that Ebf1 binds Zfp521 and Zfp423 simultaneously, with the heterodimer showing enhanced affinity for Ebf1 relative to Zfp521 or Zfp423 monomers or homodimers. We postulate that the downstream effect of Zfp binding to Ebf1 depends upon the content of Zfp521 in the dimer. Consistent with this idea, the Zfp521/Zfp423 ratio falls dramatically almost immediately upon the induction of differentiation, and becomes even more lopsided in favor of Zfp423 as adipogenesis proceeds (Figure S6).

Zfp521 and Ebf1 Negatively Regulate the Expression Each Other during Adipogenesis

In order to determine why Zfp521 levels decline during adipogenesis, we turned to our previously published genome-wide chromatin state maps generated from 3T3-L1 cells [39], which demonstrated a single strong H3K4me3 peak at the Zfp521 promoter that diminishes as differentiation proceeds (Figure 5A). H3K36me3, a mark of transcriptional elongation, also diminishes in a differentiation-dependent manner. Non-promoter H3K27 acetylation (H3K27Ac), which marks active regulatory sites, revealed a single cluster of peaks in the second intron of the Zfp521 gene, which was dramatically reduced in mature adipocytes, suggesting negative regulation at this locus. We have recently profiled Ebf1 binding sites in mature Li adipocytes and have found a cluster of peaks that precisely coincide with these enhancer sites (Figure 5A). Using ChIP-PCR, we could confirm Ebf1 binding to two of these peaks (Figure 5B). Zfp521 levels rise in 3T3-L1 cells after transduction of shEbf1 (Figure 5C), and are elevated in Ebf1−/− MEFs (Figure 5D). Furthermore, restoring Ebf1 levels in these cells represses Zfp521 (Figure 5E). These data indicate a role for Ebf1 as a negative regulator of Zfp521 gene expression.

Discussion

Here we have identified Zfp521 as a potent repressor of adipogenesis in vitro and in vivo. Zfp521 acts early in the cascade of terminal adipocyte differentiation. Our group previously showed that Ebf1 promotes adipogenesis by inducing the expression of PPARγ and C/EBPα [23] and a recent study showed that Ebf1 is required for early commitment of the adipose lineage [28]. Gupta et al. showed that Zfp423 acts as a preadipocyte commitment factor [15]. Zfp521 acts upstream, to inhibit the expression of Zfp423, and also inhibits the expression and function of Ebf1 through physical interaction. As differentiation proceeds, Ebf1 represses the expression of Zfp521 via direct binding to an intrinsic enhancer (see Figure 5F for a model). Therefore, our data suggest that Zfp521 participates in a feedback loop during adipose commitment and differentiation.

Interestingly, although the anti-adipogenic effects of Zfp521 were demonstrated in every model we tested, these actions were consistently most dramatic in C3H10T1/2 cells. C3H10T1/2 cells
are the most primitive in vitro model that we employed, with multi-lineage potential. This observation is consistent with reports that Zfp521 promotes bone and cartilage development in vivo [32]. In chondrocytes, Zfp521 acts downstream of parathyroid hormone-related peptide (PTHrP) to inhibit Runx2 and increasing cellular proliferation and subsequent growth plate thickness [32]. The published data on Zfp521 in bone development have been less clear, with discordance seen between in vitro (where Zfp521 inhibits osteogenesis) and in vivo (where overexpression of Zfp521 increases bone mass) studies [33], and it has been proposed that inhibition of Runx2 by Zfp521 may have differential effects on bone development depending upon timing [33]. Our own data support a role for Zfp521 as a pro-osteogenic factor in vitro (Figures S2A–D). The actions of Zfp521 on osteogenesis and adipogenesis place this factor among a group of transcription factors recently discovered to regulate the relative abundance of these two lineages. These factors, which include Rb, Maf, fosB, Taz, and Ebf1 [10–13,33], have been the subjects of intense inquiry given obvious links to two human diseases of great importance, osteoporosis and obesity.

How does Zfp521 inhibit adipogenesis? Our data point strongly to a mechanism involving the transcriptional repression of the proadipogenic factor Zfp423, although other targets are certainly possible. Relatively few genes were concordantly regulated by knockdown and overexpression of Zfp521 in preadipocytes, and most have no obvious link to adipocyte differentiation. An
Ebf1 mRNA expression was measured in confluent 3T3-L1 preadipocytes transduced with shScr or shEbf1. The three putative EBF-REs shown in (A). (C) Zfp521 mRNA expression precipitated DNA was amplified with Q-PCR using primers designed for a cluster of Ebf1 peaks highlighted in the red box contains three putative EBF-REs at four time-points during 3T3-L1 adipogenesis. A mutant allele of Zfp521 that cannot bind Ebf1 has inhibition of Ebf1 is a major mechanism by which Zfp521 inhibits remains to be proven. We show, however, that binding and inhibition of Ebf1 is a major mechanism by which Zfp521 inhibits adipogenesis. A mutant allele of Zfp521 that cannot bind Ebf1 has greatly reduced ability to repress differentiation. We posited that a simple competition could exist between Zfp423 and Zfp521 for Ebf1, given the high degree of similarity in their C-terminal zinc finger domains. In fact, this proved not to be the case, with Zfp521 and Zfp423 enhancing each other’s binding to Ebf1. Furthermore, Zfp521 and Zfp423 can bind directly to one another, suggesting that they form heterodimers that inhibit Ebf1 action. In this vein, we propose that Ebf1 action is contingent upon the relative amounts of Zfp521 and Zfp423 in the resulting complex, although this needs to be formally tested. Finally, this could explain the small amount of residual antiadipogenic activity seen with the Zfp521ZF27-30 mutant, which may bind to Zfp423 despite being unable to bind Ebf1. Zfp423 has Smad-binding properties, which have been implicated in its proadipogenic effects [15], and binding directly to Zfp521 could attenuate this activity. We have not investigated whether additional antiadipogenic actions of Zfp521 could be due to effects on the Smad pathway.

Our data thus add to our knowledge of early events in mesenchymal differentiation, and may be an exploitable angle in the battle to promote metabolic and skeletal health.

**Materials and Methods**

**Cell culture**

3T3-L1 preadipocytes were obtained from ATCC and maintained in DMEM with 10% calf serum. HeLa cells, 3T3-F442A cells, and MEFs were maintained in DMEM with 10% FBS. C3H10T1/2 cells were grown and differentiated in αMEM with 10% FBS. Primary Zfp521+/− and Zfp521+/−/− MEFs were generated and immortalized as described previously [41]. For adipose differentiation, cells were induced with a cocktail of dexamethasone (1 µM), insulin (5 µg/ml), and isobutyl methylxanthine (0.5 mM) (DMI) beginning 2 d after confluence was reached (day 0). For MEFs and C3H10T1/2 cells, rosiglitazone (Rosi, 100 nM) was added to the DMI cocktail (DMI). After 2 d, media was changed to DMEM/FBS plus insulin (5 µg/ml) for an additional 2 d and thereafter maintained until harvest in DMEM/FBS only. Human adipose derived stromal cells (hASCs) were obtained from Jeff Gimble and were maintained in MesenPro media (Invitrogen); cells were differentiated as described previously [42]. Primary MEFs were isolated on embryonic day 13.5 and differentiated with DMI plus Rosi. For osteoblastogenesis, confluent cells were fed with a-MEM media containing β-glycerophosphate (2 mM) and ascorbic acid (50 µg/ml) every other day.

**Plasmids**

Cebpα (−534/116) and Sncg (−2647/−1468) promoter constructs were generated by ligating PCR amplicons into pGL4 basic (Promega). 6-myc Ebf1 and 3×myc-1 reporter construct were obtained from M. Sigvardsson [43]. 2HA-Zfp521-pCMV, 3Flag-Zfp423-pBICEP, and 3Flag-Zfp521-pBICEP were subcloned at the SalI/BamHI sites. Oligonucleotides representing specific constructs and pSIREN-based knockdown constructs were cotransfected with gag-pol and VSV-G-expressing plasmids into 293T cells for 12 h along with 8 µg/ml Polybrene. For osteoblastogenesis, confluent cells were fed with a-MEM media containing β-glycerophosphate (2 mM) and ascorbic acid (50 µg/ml) every other day.

**Retrovirus Preparation and Infection**

Retroviral preparation and infection were performed as described previously [44]. Briefly, pMSCV-based overexpression constructs were ligated into pSiren-RetroQ (Clontech) at the BamHI/EcoRI sites. To construct WT-Zfp521-pMSCV and Zfp521ΔZF27-30-pMSCV, wild-type or zinc finger 1−26 regions were PCR amplified with primers containing flanking BamHI and SalI sites and subcloned into pMSCV at the BglII and XhoI sites.

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cells transduced with a virus carrying no antibiotic resistance cassette were all killed.

**RNA Extraction and Q-PCR**

Total RNA was extracted from cells or tissues using TRIzol reagent according to the manufacturer’s instructions. cDNA was reverse-transcribed from 2 µg of RNA by using the RETROscript first strand synthesis kit (Ambion). Q-PCR was performed with SYBR Green QPCR Master Mix (Applied Biosystems) using a 7900HT Fast-Real-Time PCR System (Applied Biosystems). The relative amount of mRNA normalized to cyclophilin B was calculated by using the delta-delta method [45].

**Western Blot Analysis**

Whole-cell protein lysates were prepared according to the manufacturer’s protocol using Triton-X lysis buffer and protease inhibitor cocktail. 20–30 µg of protein was resolved using 4–20% Tris-glycine gradient gels and transferred to PVDF membranes. After blocking with 5% non-fat dried milk in PBS-20% Tris-glycine, membranes were incubated with the appropriate antibodies overnight. The next day, protein A/G beads (Santa Cruz Biotechnology) were added and incubated for 1 h, washed with lysis buffer five times and PBS once. Beads were eluted with non-reducing SDS/PAGE loading buffer and subjected to SDS/PAGE and Western blotting. For ChIP-PCR, genomic DNA was extracted, and IP was performed according to the manufacturer’s protocol (Upstate Biotechnology). Cross-linking was performed as described in the manufacturer’s protocol. DNA was sheared using a sonic dismembrator model 100 (Fisher Scientific) at half maximum speed for 10 s. IP was performed using 2 µg of anti-Flag (Sigma), anti-Ebf1 (Abcam), or IgG (Sigma).

**Supporting Information**

All results are presented as means ± standard deviations. Statistical difference was determined using Student’s t test.

### Figure S1

Figure S1 (A, B) 3T3-L1 cells (A), 3T3-F442A cells (B), and human ASCs (C) were differentiated and RNA isolated at the indicated time points. Gene expression of Zfp521/ZNF521, Pparg/PPARG was measured by Q-PCR. Relative expression was normalized to cyclophilin. Data shown as mean of three biological replicates. (C, D) Retrovirally transduced 3T3-L1 cells expressing Zfp521, empty vector, shRNA specific forZfp521 (sh521) or a scrambled hairpin (Scr) were differentiated with DM or DMI and stained with oil red-O. Embryos were fixed with 4% paraformaldehyde. Tails were saved for genotyping and embryos were fixed with 4% paraformaldehyde. The next day embryos were washed with PBS, stored in 70% ethanol, and embedded in paraffin and sectioned for HE staining and immunostaining with FABP4 antibody. For secondary antibody, anti rabbit Alexa 647 (Invitrogen) was used along with the FX enhancer (Invitrogen) and Prolong Gold Anti-Fade Reagent with DAPI (Invitrogen) according to the manufacturer’s instructions. The number of adipocytes was measured by counting cells that were both lipid-filled and FABP4 positive. To detect Zfp521 mRNA expression in Zfp423-marked preadipocytes, epididymal fat tissue from Zfp423-grfp mice was fractionated and sorted as described in [16].

**Statistical Analyses**

Statistical analyses were performed using the Student’s t test.

**Reporters Assays**

Reporters were co-transfected with 6Mye-Ebf1, 3Flag-Zfp521-pBICEP, WT-Zip521-pMSCV, or Zip521AZF27-30-pMSCV to 3T3-L1 preadipocytes by using Lipofectamine 2000 or Amaxa nucleofactor (Lonza). Beta-galactosidase expression vector (50 ng) was cotransfected to normalize transfection efficiency. Statistics was performed using the Student’s t test.

**Implantation of 3T3-F442A Cells**

3T3-F442A cells were transduced with scrambled (Scr) or shZip521 expressing vectors. For transplantation, 10^6 shScr and shZip521 expressing cells were mixed together in 200 µl PBS and subcutaneously implanted (2×10^5 cells per site) to the sternum of 10–14 wk-old male nude mice (Crl:NU/Nu-nuBR, Taconic). An aliquot of the mixed cell population was saved at −80°C for quantification of input ratio. 10 wk after transplantation, fat pads were carefully dissected, and either fixed in buffered formalin or stored at −80°C for genomic DNA and protein isolation. For quantification of the relative abundance of Scr versus shZip521 cells from transplants, 50 ng of genomic DNA was used to amplify scrambled- , shZip521-specific, or common vector sequences (see Table S1).

**Assessment of Embryonic Development of Adipose Tissue**

Zfp521+/− male and female mice were mated on day 0 and males were removed early day 1. On embryonic day 18.5, pregnant females were euthanized and embryos were dissected. Body weight, liver, and interscapular brown adipose tissue weight of individual embryos was measured. Tails were saved for genotyping and embryos were fixed with 4% paraformaldehyde. The next day embryos were washed with PBS, stored in 70% ethanol, and embedded in paraffin and sectioned for HE staining and immunostaining with FABP4 antibody. For secondary antibody, anti rabbit Alexa 647 (Invitrogen) was used along with the FX enhancer (Invitrogen) and Prolong Gold Anti-Fade Reagent with DAPI (Invitrogen) according to the manufacturer’s instructions. The number of adipocytes was measured by counting cells that were both lipid-filled and FABP4 positive. To detect Zfp521 mRNA expression in Zfp423-marked preadipocytes, epididymal fat tissue from Zfp423-grfp mice was fractionated and sorted as described in [16].

**Animals**

Zfp521+/− mice were obtained from Soren Warming. Animal studies were performed in accordance with the Institutional Animal Care and Use Committee (IACUC) of the Beth Israel Deaconess Medical Center.

**Statistical Analyses**

All results are presented as means ± standard deviations. Statistical difference was determined using Student’s t test.
or empty vector were cultured in osteogenic media containing β-glycerophosphate and ascorbic acid. After 7 (10T1/2) or 18 (MEFs) d, cells were stained with alkaline phosphatase or Alizarin Red and osteogenic markers were measured by Q-PCR (Alp, Alkaline phosphatase; Osx, osterix; Ocn, Osteocalcin; Col1A1, Type I collagen; Bsp: Bone sialoprotein). (F) MEFS from (C, D) differentiated with DMR stained with oil red-O and adipocyte gene expression was measured by Q-PCR. (G) as indicated prior to differentiation with DMIR and staining with oil red-O and adipocyte gene expression was measured by Q-PCR. (H, I) Zfp521 mRNA was measured by Q-PCR prior to differentiation. (J) Zfp521+/− embryos were measured by Q-PCR. Data presented as mean ± SD, n = 4, *p<0.05. (B, C) shZip521 and shScr expressing F442A cells were mixed and injected into nude mice. Resulting fat pads were dissected and subjected to HE staining (B) and immunohostaining of C/EBP and FABP4 (n = 6) (C). (D) F442A cells expressing sh521 or shScr were mixed at the indicated ratios and subjected to genomic DNA isolation. 50 ng of genomic DNA was used as template for Q-PCR to detect variant and invariant hairpins. Relative fold ratio was determined by normalizing samples to the 1:1 mixture of cells 10 wk after transplantation. (E, F) C3H10T1/2 cells were transduced with pMSCV, PPARγ, or C/EBPα in the presence or absence of Zip521 as indicated prior to differentiation with DMR and staining with oil red-O and adipocyte gene expression was measured by Q-PCR. (G) Immortalized Pmyg+/− and Pmyg−/− MEFS were transduced with retrovirus bearing shScr or shZip521 and stained with oil red-O. (H, J) Zip521 mRNA was measured by Q-PCR prior to differentiation. (I, K) Cells from (H and J) were differentiated with DMR and adipocyte genes were measured by Q-PCR. Data presented as mean ± SD, n = 3, *p<0.05. (TIF)

Figure S3 (A) Adipocyte gene expression of BAT from Zip521+/− and Zip521−/− embryos were measured by Q-PCR. Data presented as mean ± SD, n = 4, *p<0.05. (B, C) shZip521 and shScr expressing F442A cells were mixed and injected into nude mice. Resulting fat pads were dissected and subjected to HE staining (B) and immunohostaining of C/EBP and FABP4 (n = 6) (C). (D) F442A cells expressing sh521 or shScr were mixed at the indicated ratios and subjected to genomic DNA isolation. 50 ng of genomic DNA was used as template for Q-PCR to detect variant and invariant hairpins. Relative fold ratio was determined by normalizing samples to the 1:1 mixture of cells 10 wk after transplantation. (E, F) C3H10T1/2 cells were transduced with pMSCV, PPARγ, or C/EBPα in the presence or absence of Zip521 as indicated prior to differentiation with DMR and staining with oil red-O and adipocyte gene expression was measured by Q-PCR. (G) Immortalized Pmyg+/− and Pmyg−/− MEFS were transduced with retrovirus bearing shScr or shZip521 and stained with oil red-O. (H, J) Zip521 mRNA was measured by Q-PCR prior to differentiation. (I, K) Cells from (H and J) were differentiated with DMR and adipocyte genes were measured by Q-PCR. Data presented as mean ± SD, n = 3, *p<0.05. (TIF)

Figure S4 (A) 3T3-L1 preadipocytes were transduced with retrovirus expressing sh521, shScr, Zip521, or empty vector. After puromycin selection, RNA was collected and submitted for analysis using Affymetrix arrays. The Venn diagram shows the number of genes down-regulated by sh521 (sh521/shScr<0.7-fold) and up-regulated by Zip521 (Zip521/pMSCV>1.5-fold). The heat map corresponds to genes in the intersecting set. (B) HeLa cells were transected with HA-Zip521, Myc-Ebf1, or empty vector as indicated. After 24 h, cells were harvested and immunoprecipitation was performed with anti-Myc beads. 10% input and the SDS eluate were subjected to Western blotting with antibodies against HA, Myc, WCL, whole cell lysate. (C) Immortalized 2f521+/− and 2f521−/− MEFS were transduced with a retrovirus expressing Flag-Ebf1; expression was measured by western blotting with anti-Flag prior to differentiation. (D) Schematic depicting the protein structure of WT Zip521, Zip521ΔZF27-30, and Zip521Δ13aa. Individual zinc fingers are depicted as black bars. (E) 3T3-L1 preadipocytes were transfected with Myc-Ebf1 and either Flag-Zip521WT or Flag-Zip521ΔZF27-30. 24 h after transfection, cells were harvested and immunoprecipitation was performed using anti-Myc beads. 10% input and the SDS eluate were subjected to Western blotting with antibodies against Zip521, Flag, or Myc. (F) 3T3-L1 preadipocytes were co-transfected with vectors expressing Zip521, Zip521ΔZF27-30, Zip521Δ13aa, Myc-Ebf1, and Cebpa-promoter. 24 h after transfection, luciferase activity was determined. Data presented as mean ± SD, n = 6, *p<0.05. (G) C3H10T1/2 cells were transduced with a retrovirus expressing Zip521 WT, Zip521ΔZF27-30, Zip521Δ13aa, or empty pMSCV vector. Protein expression of Zip521 was determined by immunoblotting. (TIF)

Figure S5 (A–C) 293T cells were transiently transfected with 2HA-Zip521 (521), 3Flag-Zip423 (423), and 6Myc-Ebf1 (Ebf1). After 48-h transfection, cell lysates were subjected to co-immunoprecipitation with α-Flag, α-HA, or α-Myc antibodies as indicated and 5% input were blotted with α-Flag, α-HA, or α-Myc antibodies. (TIF)

Figure S6 Gene expression was measured by Q-PCR before confluency (70%) and after adding DMR in C3H10T1/2 cells at indicated time points. (TIF)

Table S1 Primer sequences. (DOC)

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Author Contributions
The author(s) have made the following declarations about their contributions: Conceived and designed the experiments: SoK EDR RB. Contributed reagents/materials/analysis tools: RK MG JM. Performed the experiments: SoK RK MG JM. Analyzed the data: SoK RK EDR RB. Wrote the paper: EDR SoK.

References
1. Pittenger MF, Mackay AM, Beck SC, Jairak RL, Douglas R, et al. (1999) Multilineage potential of adult human mesenchymal stem cells. Science 284: 143–147.
2. N siftall ME, Gimble JM (2004) Controlling the balance between osteoblastogenesis and adipogenesis and the consequent therapeutic implications. Curr Opin Pharmacol 4: 290–294.
3. Dimitri P, Wales JK, Bishop N (2010) Fat and bone in children: differential effects of obesity on bone size and mass according to fracture history. J Bone Miner Res 25: 527–336.
4. Lazarenko OP, Rzonca SO, Swain FL, Suva LJ, Lecka-Czernik B (2006) Netoglitazone is a PPAR-gamma ligand with selective effects on bone and fat. Bone 38: 74–84.
5. Lazarenko OP, Rzonca SO, Hogue WR, Swain FL, Suva LJ, et al. (2007) Rosiglitazone induces decreases in bone mass and strength that are reminiscent of aged bone. Endocrinology 148: 2669–2680.
6. Schwartz AV, Schlueter DJ, Strotmeyer ES, Tylavsky FA, Feingold KR, et al. (2005) Diabetes and bone loss at the hip in older black and white adults. J Bone Miner Res 20: 596–603.
7. Khan E, Aboz-Mer Y (2000) Activation of peroxisome proliferator-activated receptor-gamma inhibits differentiation of preosteoblasts. J Lab Clin Med 142: 29–34.
8. Cheng SL, Shao JS, Charlton-Kachigian N, Loewy AP, Toderer DA (2003) MSX2 promotes osteogenesis and suppresses adipogenic differentiation of multipotent mesenchymal progenitors. J Biol Chem 278: 45969–45977.
9. Ichida F, Nishimura R, Hata K, Matsubara T, Ikeda F, et al. (2004) Reciprocal regulation of DeltaFosB transcription factor(s) increases bone formation and inhibits osteoblastogenesis. Nat Med 10: 1074–1078.
10. Hong JH, Hwang ES, McManus MT, Amsterdian A, Tian Y, et al. (2005) TAZ, a transcriptional modulator of mesenchymal stem cell differentiation. Science 309: 1074–1078.
11. Sabatacko G, Sims NA, Chen J, Aski K, Kelz MB, et al. (2000) Overexpression of DeltaFosB transcription factor(s) increases bone formation and inhibits osteoblastogenesis. Nat Med 6: 905–906.
12. Cale E, Quinto-Estades J, Danielson PS, Nendel S, Berman SD, et al. (2010) Rb regulates fate choice and lineage commitment in vivo. Nature 466: 1110–1114.
11. Nishikawa K, Nakashima T, Takeda S, Igoai M, Hamada M, et al. (2010) Maf promotes osteoblast differentiation in mice by mediating the age-related switch in mesenchymal cell differentiation. J Clin Invest 120: 3453–3465.

12. Cristancho AG, Lazar MA (2011). Forming functional fat: a growing understanding of adipocyte differentiation. Nat Rev Mol Cell Biol 11:722–734.

13. Gupta RK, Arany Z, Scale P, Mepani R, Ye L, et al. (2010) Transcriptional control of preadipocyte determination by Zfp423. Nature 464: 619–623.

14. Gupta RK, Mepani R, Klemmer S, Lo K, Khandekar MJ, et al. (2012) Zfp423 expression identifies committed preadipocytes and localizes to adipose endothelial and perivascular cells. Cell Metab 15: 230–239.

15. Cristancho AG, Schupp M, Leferova MI, Cao S, Cohen DM, et al. (2011) Represor transcription factor 7-like 1 promotes adipogenic competency in precursor cells. Proc Natl Acad Sci U S A 108: 16271–16276.

16. Alcaraz WA, Gold DA, Raponi E, Gent PM, Concepcion D, et al. (2006) Zfp423 controls proliferation and differentiation of neural precursors in cerebellar vermis formation. Proc Natl Acad Sci U S A 103: 19424–19429.

17. Cristancho AG, Lazar MA (2011). Forming functional fat: a growing understanding of adipocyte differentiation. Nat Rev Mol Cell Biol 11:722–734.

18. Huang S, Laoukili J, Epping MT, Koster J, Holzel M, et al. (2009) ZNF423 is critically required for retinoic acid-induced differentiation and is a marker of neuroblastoma outcome. Cancer Cell 15: 326–340.

19. Tsal KY, Reed RR (1998) Identification of DNA recognition sequences and protein interaction domains of the multiple-Zn-finger protein Roaz. Mol Cell Biol 18: 6447–6456.

20. Hata A, Soseue J, Laguna G, Montalvo E, Hemmati-Brivanlou A, et al. (2000) OAZ uses distinct DNA- and protein-binding zinc fingers in separate BMP-Smad and Off signaling pathways. Cell 100: 229–240.

21. Wang MM, Reed RR (1993) Molecular cloning of the olfactory neuronal transcription factor Olf1 by genetic selection in yeast. Nature 364: 121–126.

22. Hentges KE, Weiser KC, Schountz T, Woodward LS, Morse HC, et al. (2005) Zfp521 antagonizes Rax2, delays osteoblast differentiation in vivo, and promotes bone formation in vivo. Bone 44: 528–536.

23. Cristancho AG, Lazar MA (2011). Forming functional fat: a growing understanding of adipocyte differentiation. Nat Rev Mol Cell Biol 11:722–734.

24. Davis JA, Reed RR (1996) Role of Olf-1 and Pax-6 transcription factors in early B-cell development. Blood 106: 1995–2001.

25. Nishikawa K, Nakashima T, Takeda S, Isogai M, Hamada M, et al. (2010) Maf high expression in primitive human hematopoietic cells. Blood 103: 2062–2070.

26. Cristancho AG, Lazar MA (2011). Forming functional fat: a growing understanding of adipocyte differentiation. Nat Rev Mol Cell Biol 11:722–734.

27. Festa E, Fretz J, Berry R, Schmidt B, Rodeheller M, et al. (2011) Adipocyte lineage cells contribute to the skin stem cell niche to drive hair cycling. Cell 146: 761–771.

28. Fretz JA, Nelson T, Xi Y, Adams DJ, Rosen CJ, et al. (2010) Altered metabolism and lipodystrophy in the early B-cell factor 1-deficient mouse. Endocrinology 151: 1611–1621.

29. Bond HM, Mesuraca M, Carbone E, Bonelli P, Agosti V, et al. (2004) Early hematopoietic zinc finger protein (EHZF), the human homolog to mouse Ev3, is highly expressed in primitive human hematopoietic cells. Blood 103: 2002–2070.