RESEARCH ARTICLE

The Wnt-target gene Dlk-1 is regulated by the Prmt5-associated factor Copr5 during adipogenic conversion

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ABSTRACT

Protein arginine methyl transferase 5 (Prmt5) regulates various differentiation processes, including adipogenesis. Here, we investigated adipogenic conversion in cells and mice in which Copr5, a Prmt5- and histone-binding protein, was genetically invalidated. Compared to control littermates, the retroperitoneal white adipose tissue (WAT) of Copr5 KO mice was slightly but significantly reduced between 8 and 16 week/old and contained fewer and larger adipocytes. Moreover, the adipogenic conversion of Copr5 KO embryoid bodies (EB) and of primary embryo fibroblasts (Mefs) was markedly delayed. Differential transcriptomic analysis identified Copr5 as a negative regulator of the Dlk-1 gene, a Wnt target gene involved in the control of adipocyte progenitors cell fate. Dlk-1 expression was upregulated in Copr5 KO Mefs and the Vascular Stromal Fraction (VSF) of Copr5 KO WAT. Chromatin immunoprecipitation (ChiP) show that the ablation of Copr5 has impaired both the recruitment of Prmt5 and β-catenin at the Dlk-1 promoter. Overall, our data suggest that Copr5 is involved in the transcriptional control exerted by the Wnt pathway on early steps of adipogenesis.

KEY WORDS: β-catenin, Copr5, Dlk-1, Prmt5, Adipocyte, Differentiation

INTRODUCTION

Adipose tissue has various regulatory functions in the metabolism of animals and acts both as a fat reservoir and an endocrine/paracrine/autocrine organ that can expand throughout the entire lifespan. This functional plasticity can lead to pre-adipocyte hyperplasia and adipocyte hypertrophy. Fat tissue includes many different cellular components, including preadipocytes, multipotent stem cells (MSC) and mature adipocytes (Zeve et al., 2009).

Adipogenesis is a multi-step process during which the increase in adipocyte number is triggered by various extra- and intra-cellular signalling factors that induce MSC conversion into preadipocytes (Tang and Lane, 2012). This commitment is restricted to the adipocyte lineage upon activation of a transcriptional programme in which key factors of adipocyte differentiation like C/Ebpz and Pparγ are induced (MacDougald and Lane, 1995; Rosen and MacDougald, 2006; Tontonoz and Spiegelman, 2008). Among sensors of external signals to trigger adipocyte differentiation during embryonic development and adult life, the Wnt signalling pathway is crucial for progenitor fate determination and acts through Dlk-1 that regulates negatively preadipocyte proliferation (Moon et al., 2002; Mortensen et al., 2012; Smas and Sul, 1993).

In association with protein complexes involved in different phases of transcription, Protein arginine methyl transferase 5 (Prmt5) was implicated in myogenic, adipogenic and glial cell differentiation (Dacwag et al., 2009; Huang et al., 2011; LeBlanc et al., 2012; Paul et al., 2012). Consistently with this biological function, we reported previously that the depletion of the Prmt5- and histone-associated protein Copr5 delays the myogenic conversion (Paul et al., 2012), suggesting that Copr5 elicits a fine tuning of Prmt5 functions related to cell differentiation.

In this work, we generated mice in which Copr5 was genetically invalidated and show that adipogenic conversion was delayed in vitro both in EBs and Mefs derived from these mice compared to control cells. In addition, the retroperitoneal WAT of Copr5 KO (KO) mice was slightly reduced and contained larger adipocytes compared to control mice. Finally, we show that the expression of Dlk-1 was upregulated in KO cells and coincides with an altered recruitment of Prmt5 and β-catenin to the Dlk-1 promoter. Altogether, our data highlight unsuspected functions of Copr5 in the modulation of adipogenic differentiation, notably through an impact on the Wnt/β-catenin-dependent regulation of the Dlk-1 promoter.

RESULTS AND DISCUSSION

Adipogenesis is impaired in Copr5 KO cells

We generated a mouse model in which the Copr5 gene was genetically invalidated by homologous recombination (supplementary material Fig. S1). In contrast to Prmt5 KO mice, which is early embryonic-lethal due to loss of pluripotent cells (Tee et al., 2010), Copr5 KO mice were viable and ES cells could be derived from KO blastocysts, indicating that the Copr5-independent functions of Prmt5 are not essential for mouse development. However, when tested for their capacity to differentiate in vitro into adipocytes (Dani et al., 1997), lipid droplets were observed mostly in WT EBs cultures at D21 (Fig. 1A). Moreover, the mRNA level of Myf5, which was used as a read-out of differentiation, confirmed that mesodermic lineage differentiation was already delayed at D4 in KO compared to WT EBs (Fig. 1B). O Red Oil staining and mRNA analysis showed that adipogenic conversion was also very ineffective in KO compared to WT Mefs (Fig. 1C,D), as well as in Copr5 shRNA-treated F-442A preadipocyte cell line (supplementary material Fig. S2D,E).
KO cells, 34 were bona fide Wnt/b-catenin target genes, including Kron20, Klf4 and Klf5 (Birsoy et al., 2011; Chen et al., 2005). As expected, the mRNA level of these factors was downregulated in KO Mefs (supplementary material Fig. S2B). Surprisingly, a transient ectopic re-expression of Copr5 in KO cells failed to rescue their capacity to differentiate (supplementary material Fig. S2C). These results suggest that Copr5 deficiency had impacted on very early and irreversible events required for the adipogenic conversion of Mefs.

Fig. 1. Adipogenic conversion is delayed in Copr5 KO cells. (A) Phase contrast micrographs of EB generated from WT and KO ES cells at D0 (third day of treatment with 10−6 M retinoic acid) and at D4 and D21 after induction of EB adipogenic differentiation with insulin and triiodothyronin (T3). (B) RNA was extracted at D0 and D4 from WT and KO EB and used in RT-qPCR analysis to assess the expression profile of the indicated markers. Normalisation was done with S26 RNA and values are expressed in arbitrary units (a.u.). (C) O Red Oil staining of post-confluent (D0) and differentiating (D7) WT and KO Mefs. Differentiation was induced at D0 in the presence of insulin and rosiglitazone. (D) mRNA expression in differentiating WT and KO Mefs was monitored by RT-qPCR and is shown at D0 and D7. Normalisation was done with S26 RNA. Values are expressed as the fold change compared to control and are the mean ± s.e.m. of three independent experiments.

Altogether, these data indicate that Copr5 is required for an efficient adipogenic conversion of cells in culture. Although the mRNA level of Copr5 did not vary significantly during fat tissue development (supplementary material Fig. S2A) (Birsoy et al., 2011), it was induced at the early time points of the adipogenic conversion of WT Mefs, preceding those of transiently-expressed players involved in the initiation of adipocyte differentiation, including Kron20, Klf4 and Klf5 (Birsoy et al., 2011; Chen et al., 2005). As expected, the mRNA level of these factors was downregulated in KO Mefs (supplementary material Fig. S2B). Surprisingly, a transient ectopic re-expression of Copr5 in KO cells failed to rescue their capacity to differentiate (supplementary material Fig. S2C). These results suggest that Copr5 deficiency had impacted on very early and irreversible events required for the adipogenic conversion of Mefs.

Copr5 controls the expression of Dlk-1 gene, a key regulator of preadipocyte differentiation

To unravel the molecular mechanisms that could explain the poor capacity of KO Mefs to undergo an adipogenic conversion, we compared their transcriptome profile with that of WT Mefs (supplementary material Table S1). Notably, among the 538 genes that were significantly deregulated (Zr>2;Zpval>0.05) in KO cells, 34 were bona fide Wnt/b-catenin target genes (p=4.67×10−12, Fisher’s test) (supplementary material Fig. S3A–C). Biochemical fractionation showed that KO Mefs contained higher amounts of the activated form of b-catenin in their nucleus than WT cells (supplementary material Fig. S3D), a difference that was lessened upon treatment with either LiCl or C59, two chemicals known to activate and inhibit the Wnt pathway, respectively (supplementary material Fig. S3D). Consistently, reporter assays confirmed that TCF/b-catenin transcriptional activity was increased in KO cells (supplementary material Fig. S3E). Within this list, we noticed the presence of Dlk-1, a gene encoding a key regulator of adipose tissue homeostasis in vivo whose expression in WAT is linked to inhibition of adipocyte differentiation (Moon et al., 2002; Mortensen et al., 2012; Smas and Sul, 1993). Interestingly, Dlk-1 is one of the few non-conventional target genes of the Wnt pathway that were reported to be directly repressed by the TCF/b-catenin complex (Blauwkamp et al., 2008; Weng et al., 2009). Analysis of Dlk-1 expression confirmed its sensitivity to LiCl in WT Mefs and its upregulation in KO Mefs (Fig. 2A–C), suggesting that this gene was derepressed in KO cells, despite their high levels of activated b-catenin. Based on our previous reports showing that Copr5/Prmt5 complex could be involved in transcriptional repression (Lacroix et al., 2008), we hypothesised it could be involved in the repression of the Dlk1 promoter. Consistently, ChIP performed in Mefs during the early phase of their adipogenic conversion showed that Prmt5 was present on the Dlk1 promoter in WT but not KO Mefs (Fig. 2D). Similarly, the association of b-catenin on the two TCF binding sites (TCFbs 1 and 2) present on this promoter was significantly reduced in KO Mefs (Fig. 2E), suggesting that Copr5/Prmt5 is required for b-catenin recruitment and TCF-mediated transcriptional repression of Dlk-1. Of note, we failed to detect a direct protein-protein interaction between Copr5/Prmt5 and b-catenin in vitro (data not shown). Interestingly, we found that the recruitment of Brg-1, a chromatin remodeler that can be recruited by b-catenin to TCF target gene promoters and able to interact with Prmt5 (Curtis and Griffin, 2012; de la Serna et al., 2001; Griffin et al., 2011), decreased slightly in KO compared to WT cells (supplementary material Fig. S4). To which extent proteins that are able to antagonise b-catenin/TCF activity might be responsible of this reduced binding of b-catenin at the Dlk1 promoter in KO cells still remains. We next assessed whether a shRNA-mediated depletion of Dlk1 could restore the capacity of these cells to differentiate. Because they differentiated poorly once infected with shRNAs, we used Copr5-depleted F442A cells. Although a reduction of Dlk-1 level was obtained in these cells, this...
repression complex on this promoter.

Catenin binding and formation of a functional TCF-associated recruitment on the Dlk-1 gene expression in Mefs and suggest that Copr5/Prmt5 exclusively on Dlk-1 cellularity in containing VSF of the WAT and modification of the adipocyte cellularity in adult mice for the adipocyte number, a phenotype also encountered in transgenic findings in ES cells and Mefs, and consistent with a reduction in dependent metabolic axis (data not shown). In agreement with our mice, ruling out major alteration of the glucose and insulin-glucone and insulin tolerance tests were similar in both types of adipocytes but of larger size than WT tissue (Fig. 3B). Of note, weeks of age (Fig. 3A, right panel) and that it contained fewer but reproducibly decreased in KO compared to controls at 16 A more in depth analysis revealed that its mass was moderately, E.F., data not shown), excepted in retroperitoneal adipose tissue. Analysis did not reveal significant morphological changes (C.P., similar mean body weight (Fig. 3A, left panel). Histological analysis did not reveal significant morphological changes (C.P., E.F., data not shown), excepted in retroperitoneal adipose tissue. Knockout and WT male mice were indistinguishable with a similar mean body weight (Fig. 3A, left panel). Histological analysis did not reveal significant morphological changes (C.P., E.F., data not shown), excepted in retroperitoneal adipose tissue. A more in depth analysis revealed that its mass was moderately, but reproducibly decreased in KO compared to controls at 16 weeks of age (Fig. 3A, right panel) and that it contained fewer adipocytes but of larger size than WT tissue (Fig. 3B). Of note, glucose and insulin tolerance tests were similar in both types of mice, ruling out major alteration of the glucose and insulin-dependent metabolic axis (data not shown). In agreement with our findings in ES cells and Mefs, and consistent with a reduction in the adipocyte number, a phenotype also encountered in transgenic mice for Dlk-1 (Lee et al., 2003), the mRNA levels of aP2, Lpl, C/Ebpa, C/Ebpb and Ppary were downregulated, whereas that of Dlk-1 was upregulated in KO WAT, supporting a role of Copr5 in controlling adipogenesis in vivo (Fig. 3C). Hence, we hypothesised that the large adipocytes detected in KO mice could reflect an adaptive response to a reduced proliferation/differentiation of KO preadipocytes. Consistently, the proliferation index of the VSF, a main source of progenitor cells, was lower in KO compared to WT mice (Fig. 3D) and associated with a strong upregulation of Dlk-1 expression, whereas no difference was noted in mature adipocytes (Ad), as expected (Fig. 3E). In addition, we found that the Dlk-1 membrane-bound isoform (Dlk-1) which exerts a negative effect on preadipocyte proliferation (Mortensen et al., 2012), was increased in WAT (Fig. 3F).

Altogether, our data suggest a model depicted in Fig. 4 in which modification of the adipocyte cellularity observed in KO WAT is a consequence of Dlk-1 upregulation, leading consequently to a low pool of precursor cells that is able to differentiate into adipocytes. This impaired adipocyte differentiation resulted, at least in part, from a reduced recruitment of Prmt5, Brg1 and β-catenin to the Dlk-1 promoter in Copr5 KO mice.

Further studies are now required to understand whether Prmt5/Copr5 complex participates in the transcriptional regulation of other β-catenin-regulated genes that are deregulated in KO Mefs. It will be also interesting to explore whether this complex controls Dlk-1 expression in the other few adult tissue/glands/neurons that maintain an expression of Dlk-1, and whether a deregulation of its expression generated subtle and yet unidentified phenotypes in these organs.

Fig. 2. Dlk-1 upregulation in Copr5 KO Mefs is related to impaired recruitment of Prmt5 to the Dlk-1 promoter. (A) Expression of indicated mRNAs in Mefs was monitored by RT-qPCR after treatment of the cells with LiCl (10 mM) for 24 h. Results are expressed in arbitrary units (a.u.). (B) Expression of Dlk-1 mRNA in WT and KO Mefs was monitored by RT-qPCR at D0 and D7 of differentiation. Normalisation and expression was done as in Fig. 1D. (C) Western Blot detection of WT and KO Mef whole cell extracts treated as in (A) using an anti-Dlk-1 antibody is shown. (D) Prmt5 recruitment to A and B regions of the Dlk-1 promoter was analysed by ChIP at D0 and D7. Values are expressed as the percentage of immunoprecipitated (ip) chromatin relative to input and are the mean±s.e.m. of triplicates. No antibody (noAb) was used as negative control. (E) Immunoprecipitation was performed as in (D) to assess the recruitment of activated β-catenin (β-cat) to three regions of the Dlk-1 promoter: two of them encompass the TCF binding sites 1 and 2 (TCFb1 and TCFb2), the third one is B, as in (D). (F) Expression of Dlk-1 mRNA in shCopr5 F442A-treated cells was monitored by RT-qPCR upon inactivation of Dlk-1 using shRNA (shDlk1) encoding retroviral particles. A scramble shRNA (shScr) was used as control. Normalisation and expression were performed as in (B). (G) Oil Red Oil staining at D6 of shCopr5 F442A-treated cells infected as in (F). *: non specific band.
MATERIALS AND METHODS

Cell culture conditions
Adipogenic differentiation was induced in post-confluent cells upon addition of a differentiation cocktail (50 nM insulin, 0.5 mM IBMX, 1 mM dexamethasone and 10^{-6} M rosiglitazone) to the medium. ES cells and EBs were cultivated as described previously (Dani et al., 1997).

Mice and animal care
Animal experiments were approved by the Ethics Committee of the Languedoc-Roussillon Region (France).

Vascular stromal fraction (VSF) isolation
Adipose tissue was dissected, washed in PBS with a 2% penicillin/streptomycin/gentamycin mixture, minced, and incubated in DMEM supplemented with 10 mg/ml BSA, 0.35% type II collagenase (SIGMA) at 37°C with shaking for 30 min. Cell suspensions were obtained after filtration through 100 μm cell strainers, centrifuged. The remaining pellet was resuspended, filtered through 40 μm cell strainers and centrifuged to recover the VSF.

Flow cytometry
In vivo labelling was performed by intraperitoneal injection of either BrdU at a concentration of 50 μg BrdU/g body weight or PBS included as negative controls in 7-week-old animals that were sacrificed seven days later for VSF isolation. VSF was processed using the BrdU FITC kit, as recommended by BD Pharmingen.

Determination of the adipocyte size
Sections of paraffin-embedded adipose tissue were stained with haematoxylin/eosin. Quantification was performed from images within a 500 μm measurement frame using ImageJ. Three independent measurements were performed in both WT and KO mice (n=3).

RNA isolation, cDNA synthesis and RT-qPCR amplification
RNA isolation and RT-qPCR were performed as described (Paul et al., 2012). The sequence of the oligonucleotides is listed in supplementary material Table S2.

Fig. 3. Modification of adipocyte cellularity in adipose tissue of Copr5 KO mice. (A) Histograms showing the total (left panel) and retroperitoneal fat (right panel) weights in WT and KO mice at 8 and 16 weeks of age (n=5). *p<0.1 Student’s t test; ns, not significant. (B) Histogram showing the size distribution of adipocytes from WT and KO mice. Measurements were performed on equivalent frames using the ImageJ software. Data are representative of three independent mice. A digitalised image of WAT sections from WT and KO mice stained with haematoxylin/eosin is presented. Scale bar: 125 μm. (C) RNA from adipose tissue of WT and KO mice was used to assess by RT-qPCR the expression profile of different adipogenic markers, as indicated. Result expressed in arbitrary units (a.u.) were normalised to S26 RNA and is the mean±s.d. of three independent mice. (D) Histogram from FACS analysis showing the percentage of BrdU incorporation in SVF cells one week after peritoneal injection of the marker in WT and KO mice (n=4). (E) RNA from VSF and mature adipocytes (Ad) isolated from 8 week/old KO and WT mice was extracted and assessed as in (C) to analyse Dlk-1 expression. (F) Western blot of WAT protein extracts from WT and KO mice using anti-Dlk-1 membrane isoform and anti-Tubulin antibodies is shown. In C, the box-plot representation shows the median value of mRNA expression (bold line), the lower and upper limits of each box representing the first and third quartiles, respectively. Whiskers represent the limits of extreme measurements (n=3). For A,D,E, values are expressed as a mean±s.e.m. (n=5, n=4 and n=4, respectively).

Fig. 4. Schematic diagram recapitulating the transcriptional regulation on the Dlk-1 promoter. See Results and Discussion for explanations.
Chromatin immunoprecipitation
Anti-Prmt5 and β-catenin (S33/37/41) antibodies (Euromedex and Cell Signaling, respectively) were used for ChIP, as described (Paul et al., 2012). Sequence of the oligonucleotides is listed in supplementary material Table S2.

Western blot
Anti-Prmt5 (Millipore), β-catenin (Cell Signaling), Histone H3 (Millipore), -Dlk-1 (Abcam) and -Tubulin antibodies were used.

Microarray analysis
Microarray analysis was performed using total RNA isolated from either Copr5 KO or WT Mefs from male embryos (n = 3), hybridised onto a GeneChip® Mouse Gene 2.0 ST Array and analysed for differentially expressed genes (KFB, Germany) that were considered significant when the Z ratio and the adjusted Zp value was >2 and 0.05, respectively.

Acknowledgements
We would like to thank specially C. Chavey for insulin tolerance tests, C. Pescia-Begon for ES cell isolation and the RHEM facility for tissue sections. We are grateful to all members of the cell culture lab. This work was realised with the institutional support of the French CNRS.

Competing interests
The authors declare no competing or financial interests.

Author contributions
CP and EF performed the experiments. EF conceived and designed the experiments. All participated in data analysis. EF and CS wrote the manuscript.

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References


Fig. S1. Targeting strategy and validation of the Copr5 allele. (A) Diagram of the mouse Copr5 gene. Copr5 gene was targeted by homologous recombination and a Cre-loxP strategy. Embryonic stem cells were generated in which exons E2 to E4 of Copr5 were flanked by two loxP sites. To obtain Copr5 floxed/floxed (Copr5 KO) mice, loxed exons were deleted by breeding wild type/flox (WT/f) mice carrying the recombined allele with CMV-Cre mice, which led to the generation of a heterozygous null allele. Then, we performed Copr5 WT/floxed crosses and obtained Copr5 KO mice. Of note, deletion of E2 to E4 is expected to produce a shorter mRNA that, if stable, would give rise to a Copr5 protein truncated at amino acid 23. Consequently, the Prmt5 binding domain localised previously between amino acids 160 and 184 (full length Copr5 protein consists of 184 amino acids) is absent in KO mice, thereby eliminating Copr5-mediated Prmt5 functions, as published in Lacroix et al., 2008.

The positions of the LoxP (black triangles) and FRT (white triangles) sites surrounding exons 2 to 4 and the neo marker are shown, respectively. Black arrows indicate the positions of the primers used for genotyping by PCR. (B) Southern Blot Neo: 5’ and 3’ arm validation. Four different digests were used to validate correct homologous recombination event. Two digests validate the 5’ insertion, two other digests validate the 3’ insertion, as indicated. (C) Southern Blot with external 5’ and 3’ probes. Two different digests were used to validate 5’ and 3’ arm, as indicated. From (B) and (C), correctly targeted clone 43 was injected into C57BL6/J blastocysts. (D) Beside genotyping identification by PCR using Lf, Er, Ef and Er primers (not shown), analysis of Copr5 mRNA level in different tissues from WT and Copr5 KO mice confirmed that mice were invalidated for Copr5.
Fig. S2. Impaired adipogenic conversion in Copr5-depleted cells. (A) Expression level of Copr5 mRNA during development in fat tissue was extracted from previously published Illumina data (Birsoy et al., 2011). (B) Expression level of very early adipogenic markers was assessed in WT, Copr5 KO Mefs and Copr5 KO Mefs overexpressing a human form of Copr5 (hCopr5) and monitored by RT-qPCR at early time point of differentiation. Values were normalised to S26 RNA expression. Values expressed in arbitrary units (a.u.) are the mean ± s.e.m. of three independent experiments. (C) As a cue of perturbation of adipocyte conversion, plates seeded in parallel with the three different populations of Mefs in (B) were visualised after O Red Oil staining at day 6 (D6) of differentiation. (D) Phase contrast micrographs of post-confluent (D0) and differentiated (D7) F442A cells transduced with LUC (shLuc) or Copr5 (shCopr5) shRNAs. Cells were induced to differentiate into adipocytes by addition of 50 nM insulin and 10⁻⁶ M rosiglitazone at D0. Differentiation was visualised after O Red Oil staining. (E) Expression of mRNA in F442A cells transduced as in (D) was monitored by RT-qPCR and is shown at D0 and D7 of differentiation. Values normalised to S26 RNA expression and expressed as fold change compared to control are the mean ± s.e.m. of three independent experiments.
**Fig. S3. β-catenin signaling pathway is activated in KO Mefs.** (A) Processes involved in KO Mefs are shown. (B) The most relevant network identified with Metacore analysis is shown. The list of significantly deregulated genes obtained from comparative transcriptome analysis between WT and KO Mefs was used for generation of biological networks using Analyze Network algorithm with default settings. This is a variant of the shortest path algorithm with main parameters of 1. relative enrichment with the data, and 2. relative saturation of network with canonical pathways. This network is built on the fly and unique for these data. The network is prioritised based on the number of fragments of canonical pathway of the network. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; downregulated with blue circles. (C) Sublist of deregulated genes in KO Mefs that are Wnt/β-catenin target genes. (D) Western blot analysis using indicated antibodies was performed on cytoplasmic and nuclear extracts of WT and KO Mefs. Cells were either untreated or treated for 24 h with lithium (LiCl 10 mM) which stabilises β-catenin, or treated with C59 (10 μg/ml) (Abcam), an inhibitor of the Wnt pathway that prevents Wnt secretion. (E) WT and KO Mefs were transfected with CMV-β-gal and Luciferase reporters driven by either four synthetic wild type (TOPLuc) or mutated (FOPLuc) TCF binding sites in the presence or the absence of a plasmid encoding for a stabilised form of β-catenin (β-catS33Y). Results normalised to β-galactosidase activity are expressed as relative luciferase activity (RLU) and show that high level of activated β-catenin was present in KO cells.

**Fig. S4. Brg1 recruitment to the Dlk-1 promoter is slightly impaired in KO Mefs.** Brg1 recruitment to TCFbs1, TCFbs2 and B regions of the Dlk-1 promoter in WT and KO Mefs was analysed by ChIP. Values are expressed as the percentage of immunoprecipitated (ip) chromatin relative to input and are the mean±s.e.m. of triplicates. No antibody (noAb) was used as negative control. The recruitment of Brg1 at TCFbs1 but not TCFbs2 in WT cells decreased slightly in KO cells, whereas that observed at region B was Copr5/Prmt5-independent and might be allotted for activation.
Table S1: See supplementary webpage

Table S2. Oligonucleotides used for RT-qPCR and ChIP PCR

Oligonucleotides used for RT-qPCR

Pparγ: 5′fCGGGGTAGTCACCATAACA, 5′rCTTTTTGCCATTGCCACAGA;
C/Ebpa: 5′fGCTGTATTGGTAGAATCT, 5′rTGATCTCCTGTGTAACCA;
C/Ebpβ: 5′fAGTCGGTGCGACACGACG, 5′rACTCCAGCACCTCTGTTGC;
C/EBPβ: 5′fTTCTCTGACAGGTGGGAGT, 5′rGCTGCCAGAGGTGGCAGT;
ap2: 5′fAACACCGAGATTTCTTCA, 5′rAGTCACGCGCTTTCAATAACACA;
Fas: 5′fTGCTCCAGCTGCAGGC, 5′rGCCGGGTAGCTCTGGGTGA;
Atgl: 5′fGAGCCCCGGGAGTGGGAACGTA, 5′rAAAGGTTGTTGCGGAGTAGGG;
Lpl: 5′fACCAAGCTGTTGGGAATGTGTG, 5′rCCAGCTGGATCAGAACCAGTAT;
Gata6: 5′fGAGCTCGGTGCTACCAAGAGG, 5′rACGAAAGCCTTGGAGATG;
Myf5: 5′fACAGACGCTTTGCACAGAC, 5′rAGCAATCCAAGCTGGACAG;
Dlk-1: 5′fGAATAGACGTTCGGGCTTG, 5′rAGGGAGAACATTGATCAG

Oligonucleotides used for ChIP PCR

Dlk-1 TCFbs1 5′f TGGAGATTTAATCTAGCTG, 5′r GCAGCCAACTTGGAGTGTGTC;
Dlk-1 TCFbs2 5′f CATTTAGCGGTGACCATATTGG, 5′r GCGCCGAACCCAAATTCAG;
Dlk-1 region B (-381/-37) 5′f-GCGCGGGACTCCAGCCCTAAGT, 5′r-GCGGTGCAGGGCTGGCTCCGG,
Dlk-1 region A (-263/-213) 5′f-CTCTGAAACTCCTACTACACTCAAA, 5′r-CTCTGAGAAGAAGATGGGATTT