Bone marrow adipose tissue does not express UCP1 during development or adrenergic-induced remodeling

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Adipocytes within the skeleton are collectively termed bone marrow adipose tissue (BMAT). BMAT contributes to peripheral and local metabolism, however, its capacity for cell-autonomous expression of uncoupling protein 1 (UCP1), a biomarker of beige and brown adipogenesis, remains unclear. To overcome this, *Ucp1-Cre* was used to drive diphtheria toxin expression in cells expressing UCP1 (*Ucp1cre+/DTA*). Despite loss of brown adipose tissue, BMAT volume was not reduced in *Ucp1cre+/DTA* mice. Comparably, in mTmG reporter mice (*Ucp1cre+/mTmG*), *Ucp1-Cre* expression was absent from BMAT in young (3-weeks) and mature (16-weeks) male and female mice. Further, β3-agonist stimulation failed to induce *Ucp1-Cre* expression in BMAT. This demonstrates that BMAT adipocytes are not UCP1-expressing beige/brown adipocytes. Thus, to identify novel and emerging roles for BMAT adipocytes in skeletal and whole-body homeostasis, we performed gene enrichment analysis of microarray data from adipose tissues of adult rabbits. Pathway analysis revealed genetic evidence for differences in BMAT including insulin resistance, decreased fatty acid metabolism, and enhanced contributions to local processes including bone mineral density through candidate genes such as osteopontin. In sum, this supports a paradigm by which BMAT adipocytes are a unique subpopulation that is specialized to support cells within the skeletal and hematopoietic niche.
function during both healthy and pathologic conditions is necessary to facilitate our understanding of BMAT’s relationship both to bone and to peripheral metabolism.

Extraskeletal adipocytes are grouped into functional classifications which range from brown or beige, to white and pink (reviewed in10). Even within a subclass, for example white adipose tissues (WAT), metabolic responsiveness can vary widely between depots reflecting diverse functions of adipocytes in both structural support and lipid partitioning (reviewed in9). In post-pubescent mice, BMAT adipocytes have been classified into two categories, regulated BMAT (rBMAT) and constitutive BMAT (cBMAT) (reviewed in10). Regulated BMAT adipocytes reside in diverse, multicellular niches which can include pericytes, hematopoietic cells and osteogenic cells11. These cells are capable of lipid droplet remodeling in response to β3-agonist stimulation, however, BMAT lipid droplet remodeling is modest and morphologically distinct from ‘beige-like’ remodeling traditionally observed in white adipose tissues2. Constitutive BMAT adipocytes reside in homologous cBMAT niches and are relatively resistant to adrenergic stimuli12.

Though bone marrow adipocytes generally resemble white adipocytes morphologically, whether BMAT adipocytes are ‘beige-like’ remains unclear. Fundamental characteristics of ‘beige’ adipocytes include their ability to remodel from a unilocular to multilocular morphology and their capacity for induced expression of uncoupling protein-1 (UCP1), a biomarker of thermogenesis13. UCP1 is a key brown/beige adipocyte protein that resides on the inner mitochondrial membrane where its presence allows energy released from fatty acids to be converted into heat14. In support of BMAT beiging, adipocytes in the proximal regions of the mouse skeleton (rBMAT) have been reported to express markers of brown fat, including Ucp1, at the level of RNA transcript15–17. In vivo, there is one report showing a multilocular appearing cell in the lumbar vertebrae of a developing mouse with immunohistochemical evidence that this cell expressed UCP1 protein18. Also in vivo, treatment of female C3H/HeJ mice with α3-adrenergic agonist CL316,243 has been shown to induce remodeling in a multilocular morphology, within a subpopulation of rBMAT adipocytes7. Finally, lineage tracing has provided anecdotal evidence that a subset of BMAT adipocytes have beiging potential. Specifically, BMAT adipocytes have been shown to express PdgfRα, a mediator of adipocyte progenitor commitment to a beige adipocyte19, following irradiation or rosiglitazone treatment (discussed in20).

Arguing against BMAT beiging includes a limitation in the above mentioned Ucp1 transcript studies. Ucp1 transcript was measured from RNA acquired from whole bone preparations which are highly heterogeneous and susceptible to contamination from extraskeletal adipocyte-containing soft tissues. In addition, the amount of Ucp1 transcript detected was significantly less than found in BAT (>10,000 fold)14,16. Second, the majority of brown adipocyte progenitors and a minority of beige progenitors express myogenic factor-5 (Myf5)21,22, however, lineage tracing has shown that BMAT progenitors do not express Myf5 (discussed in10). Finally, there is also preliminary in vivo evidence that UCP1 protein expression is absent in BMAT adipocytes. Specifically, a methionine-restricted diet was used to induce beiging of white adipocytes. This diet successfully resulted in increased UCP1 protein expression in inguinal white adipose tissue (a predominant site of beige adipocytes in rodents) but, unlike the findings of Nishino et al.,20 failed to induce UCP1 protein expression by IHC in BMAT adipocytes21,22. Thus, it is clear that significant controversy exists in the literature regarding this point.

To overcome this, we sought to track UCP1 expression in BMAT at the single cell level using multiple rodent models of development and adrenergic-stimulated remodeling. Our laboratory has previously observed BMAT adipocytes in adult mice containing multiple lipid droplets using 3D electron microscopy11, as well as modest lipid droplet remodeling in response to β3-agonist stimulation2, both are characteristics of beige adipocytes2,42 and of white adipocytes that are developing or undergoing stimulated lipolysis (reviewed in20). Until now, we had not definitively addressed whether BMAT adipocytes are truly beige-like adipocytes as defined by their capacity to express UCP1. Clarification of whether some BMAT adipocytes express UCP1 has important implications for our understanding of the role of BMAT in skeletal processes including hematopoiesis and bone turnover. Here, immunohistochemical studies were coupled with genetic ablation and lineage tracing of UCP1 expressing cells to determine whether any BMAT adipocyte population expressing UCP1 exists during development, in adulthood, or after systemic β3-adrenergic stimulation. In addition, to define novel pathways that separate BMAT and WAT, we performed serial gene enrichment and pathway analysis of microarrays from both white and bone marrow adipose tissues.

Results

Bone marrow adipocytes exist within a sinusoidal niche and are predominately unilocular. The lipid droplet morphology and localization of BMAT adipocytes in the developing limb was examined in male and female C57BL/6J mice. Adipocytes and vascular sinusoids were visualized using perilipin and endomucin immunohistochemistry, respectively. At 3-weeks of age, bone marrow adipocytes were nearly absent in the metaphyseal regions of the distal femur and the proximal metaphysis of the tibia. By contrast, prominent marrow adipocyte populations were noted in the distal tibia and in both the proximal tibia and distal femoral epiphyses. At 3-weeks of age, both unilocular and multilocular adipocytes were found on the exterior of the bone, near the periosteal surface (Fig. 1a). Multilocular adipocytes near the periosteum were largely observed in the proximal tibia-fibula junction and near the femoral neck. Within the bone marrow, it was observed that endomucin-positive endothelium forms a peri-sinusoidal niche for most, if not all, of the bone marrow adipocytes. The predominant morphology of the BMAT adipocytes was a single, large perilipin lipid droplet with an eccentric nucleus (Fig. 1a). The frequency of multilocular bone marrow adipocytes in 3-week-old mice (~5%) was found to be comparable across all regions of the femur and tibia (Fig. 1b). This finding remained constant even in postpubescent animals at 9-weeks of age (Fig. 1b).

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Immunostaining for UCP1 in BMAT is inconclusive. UCP1 protein expression was examined in BMAT and peripheral adipose tissues using immunohistochemistry. When calibrated using tissue from Ucp1−/− mice (Fig. 2a), immunostaining for UCP1 was positive in peripheral brown adipocytes of interscapular brown fat (BAT) and beige adipocytes within inguinal white adipose tissue (iWAT) (Fig. 2b). Cells with a morphology similar to beige adipocytes (multiple small lipid droplets associated with large lipid droplet) stained positive for UCP1. UCP1-positive adipocytes near the periosteal surface, most commonly seen in the femoral neck and proximal tibia-fibula junction. This finding indicates that whole bone RNA preparations are susceptible to contamination by UCP1-positive adipocytes near the periosteal surface. Within the bone, UCP1 staining was negative in tail BMAT regions (cBMAT). However, non-specific staining in BMAT regions rich in hematopoietic cells (rBMAT) made definitive conclusions on UCP1 expression in rBMAT challenging (Fig. 2b). Thus, we opted to move forward with the two genetic mouse models described below.
Genetic ablation of UCP1-expressing cells does not cause loss of BMAT at 4-weeks of age.

UCP1-Cre expressing mice were bred with mice carrying a floxed diphtheria toxin subunit A (DTA) gene, creating progeny (UCP1Cre−/DTA) (WT) and UCP1Cre+/DTA (male) mice. ROSA26 marks DTA (female) mice (Fig. 3a). Residual BAT in the remaining UCP1Cre+/DTA mice was ~10% of the WT average. Inguinal and gonadal fat pad masses were equivalent between male UCP1Cre+/DTA and control mice (Fig. 3b,c), however, female UCP1Cre+/DTA mice displayed reduced iWAT and gWAT tissue weights relative to their control littermates (~33% and ~46%, respectively). Total body weight and tibia length were normal in male UCP1Cre+/DTA mice, but reduced in female UCP1Cre+/DTA mice, reflecting an overall reduction in body size in female but not male UCP1Cre+/DTA mice.

Figure 3. Genetic ablation of UCP1-Cre expressing cells results in loss of BAT but not BMAT. (a–c) Tissue weights for UCP1Cre−/DTA (WT) and UCP1Cre+/DTA brown adipose tissue (BAT), inguinal white adipose tissue (iWAT), and gonadal white adipose tissue (gWAT). (d) UCP1Cre−/DTA and UCP1Cre+/DTA mouse total body weight (BW). (e) UCP1Cre−/DTA and UCP1Cre+/DTA tibia length measured by digital caliper. (f–h) UCP1Cre−/DTA and UCP1Cre+/DTA BAT, iWAT and gWAT tissue weights normalized to total body weight (BW). (i) Representative 3-D images of osmium stained bones to visualize UCP1Cre−/DTA (WT) and UCP1Cre+/DTA (UCP1) bone marrow (BMAT). Light grey is outline of bone. Dark grey is osmium-stained BMAT. Analysis and 3-D rendering of the µCT data sets were performed using Scanco software. (j–k) Regional analysis of osmium content in decalcified UCP1Cre−/DTA and UCP1Cre+/DTA tibias. (j) Proximal BMAT is osmium volume within the proximal epiphysis. (k) Distal BMAT is osmium volume from tibia-fibula junction to distal epiphysis. (l) Osmium content within the whole tibia bone marrow. Mean ± S.D. Two-tailed t-test, *P ≤ 0.05. Sample sizes: Male Cre− = 5–6, Male Cre+ = 4, Female Cre− = 7, Female Cre+ = 7. All ages were 4-weeks old.
Adipocytes within the developing skeleton express adiponectin, but not UCP1, by lineage tracing. Expression of UCP1 in BMAT was then assessed using lineage tracing. Ucp1-Cre reporter mice were crossed with mT/mG reporter mice to generate Ucp1Cre/+mTmGCre/+ mice. In the presence of Cre, recombination leads to excision of tomato (RFP) and expression of GFP. Thus, any cell having expressed Cre will change plasma membrane color from red to green. Adiponectin-Cre (Adipoq-Cre) mice were bred separately to mT/mG reporter mice (referred to as AdipoqCre/+mTmGCre/+ to serve as a positive control for this experiment. Confocal imaging of RFP and GFP in BAT, iWAT, cBMAT (tail) and rBMAT was completed in male and female mice aged 3-weeks and 16-weeks (Fig. 4).

Gene expression profiles in BMAT suggest enhanced roles in bone homeostasis and altered metabolism relative to WAT. To identify novel and emerging roles for BMAT adipocytes in both skeletal and whole-body homeostasis, we performed microarray analysis on white adipose tissues (inguinal and gonadal), liver, pancreas, spleen, lung, and intestine were negative for GFP expression in Ucp1Cre/+mTmGCre/+ mice at 3- and 16-weeks. However, there was notable Ucp1-Cre-mediated GFP expression in cells of the kidney collecting ducts. GFP expression in the kidneys of Ucp1Cre/+mTmGCre/+ mice was present regardless of age, sex or CL316,243 treatment (Fig. 5a, male and female, 3- and 16-weeks-old, with and without CL316,243, n = 34 total). By contrast, kidney, liver, pancreas, spleen, lung, and intestine were negative for Adipoq-Cre-mediated GFP expression in all conditions (AdipoqCre/+mTmGCre/+ male, 3-week, 16-week, +/- CL316,243, n = 30 total). However, widespread Adipoq-Cre-mediated GFP expression was observed in the stromal reticular cell network of the bone marrow, cells lining blood vessels within bone, and bone-lining cells of the femur and tibia in all AdipoqCre/+mTmGCre/+ mice regardless of age or treatment (Fig. 5b). As a control, neither the stromal reticular cell network of the bone marrow, vessel lining cells or bone lining cells expressed GFP in the Ucp1Cre/+mTmGCre/+ mice. Gonadal tissue was also assessed at 16-weeks of age and was negative regardless of sex or CL316,243 treatment (n = 19, Ucp1Cre/+mTmGCre/+; n = 18, AdipoqCre/+mTmGCre/+).

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Figure 4. Adipocytes within the developing skeleton express adiponectin, but not UCP1, by lineage tracing. (a) Representative images of Adipoq$^{Cre+/mTmG^+}$ and Ucp1$^{Cre+/mTmG^+}$ inguinal white adipose tissue (iWAT), constitutive bone marrow adipose tissue (cBMAT, caudal vertebrae), and regulated bone marrow adipose tissue (rBMAT, tibia). The presence of green (GFP-positive) cells indicates expression of Cre and conversion of the mTmG reporter. White boxes in images show inset for images to the right (GFP/RFP). Far right images (perilipin) demonstrate that the adipocytes in the GFP/RFP images are perilipin-positive. Images were acquired at 10X, scale bar is 50 µm or 25 µm for insets. (b–d) Quantification of Adipoq-Cre or Ucp1-Cre-mediated GFP expression in adipocytes relative to total number of adipocytes. White bars are the percent of adipocytes expressing GFP. Grey bars are the percent of adipocytes that do not express GFP (instead express RFP). Tissues collected from 3-week-old male and female mice (b) 16-week-old males (C) or females (d) treated with saline (−) or 0.3 mg/kg CL316,243 (CL) for 6-days. (b–d) Mean ± S.D. Sample sizes: (b) n = 5–6 (c) n = 3–5, (d) n = 3–7.
Figure 5. UCP1 and adiponectin mTmG reporter conversion occurs in non-adipocytes. (a) Representative images of kidneys from 16-week-old Ucp1\textsuperscript{Cre+}/mTmG\textsuperscript{+} and Adipoq\textsuperscript{Cre+}/mTmG\textsuperscript{+}. The presence of green (GFP-positive) cells in Ucp1\textsuperscript{Cre+}/mTmG\textsuperscript{+} images indicates expression of Cre and conversion of the mTmG reporter in kidney collecting ducts (non-adipocytes) of Ucp1\textsuperscript{Cre+}/mTmG\textsuperscript{+} mice. Numbered white boxes show inset for numbered images to the right. Dashed boxes in the bottom left (Adipoq\textsuperscript{Cre+}/mTmG\textsuperscript{+}) image show targeted expression of Adipoq-Cre in peri-renal adipocytes. Images were acquired at 10x then stitched together, scale bars are 1 mm and 200 \(\mu\)m. (b) Representative images of bone marrow from 16-week-old Ucp1\textsuperscript{Cre+}/mTmG\textsuperscript{+} and Adipoq\textsuperscript{Cre+}/mTmG\textsuperscript{+} mice. The presence of green (GFP-positive) cells in Adipoq\textsuperscript{Cre+}/mTmG\textsuperscript{+} images indicates expression of Cre and conversion of the mTmG reporter in bone lining cells (white arrowheads), cells along blood vessels, and cells along bone marrow reticular fibers of Adipoq\textsuperscript{Cre+}/mTmG\textsuperscript{+} mice. Numbered white boxes show inset for numbered images to the right. "B" indicates location of bone. "BV" indicates location of blood vessels. Images were acquired at 10X, scale bars are 50 \(\mu\)m and 25 \(\mu\)m.
involved in skeletal pathways related to decreased bone mineral density were enriched in BMAT. Of these, the osteopontin gene \( \text{Spp1} \) was among the most differentially expressed relative to WAT and had among the highest transcript levels detected (Fig. 6d). Thus, to validate our array and determine whether \( \text{Spp1} \) was differentially expressed in the BMAT adipocyte itself, we performed qPCR analysis of purified BMAT and iWAT adipocytes from rats. Comparable to rabbit whole tissues, we found that expression of \( \text{Spp1} \) transcript from rabbit whole tissues. 1-way-ANOVA with Tukey’s multiple comparisons test, \( *p < 0.05 \). (e) \( \text{Spp1} \) transcript from purified inguinal white adipose tissue (iWAT) and tail bone marrow adipocytes (BMAT) normalized to the geometric mean of reference genes \( \text{Tbp} \) and \( \text{Ppia} \). Two-tailed t-test. \( *p < 0.05 \). (f) Representative osteopontin immunohistochemistry of human bone and bone marrow. B = bone, Ad = bone marrow adipocytes, white arrows = osteopontin immunostaining in bone (pink), black arrows = osteopontin immunostaining in bone marrow (pink). Scale bar is 50 \( \mu \)m.

**Discussion**

In healthy individuals, BMAT can occupy up to 70% of the medullary cavity and accounts for ~8% of total body fat\[6\]. Despite the abundance of BMAT, its function remains unclear. The concept of BMAT functioning as an energy depot, similar to WAT adipocytes, seems relevant in areas of high hematopoietic activity and bone turnover, such as the proximal tibia and distal femur (rBMAT region), and is supported by recent publications. Electron
microscopy (EM) studies have shown BMAT adipocytes to interact with myeloid/granulocyte cells and erythroblast islands. The same EM study showed extensions of lipid droplet-filled cytoplasm from BMAT adipocytes adjacent to active osteoblasts. By contrast, regions of confluent constitutive BMAT adipocytes are selectively retained and often resist conventional lipid mobilization cues (reviewed in ). Our microarray study provides a novel list of 897 candidate genes that may underlie these functional relationships and differences in metabolic responsiveness (Fig. 6, Supplementary Table 1). Beyond this, in pathologic conditions, BMAT adipocytes have been shown to facilitate and fuel bone tumor progression (reviewed in ). Less clear is whether BMAT adipocytes also have ‘beige’-like properties, more specifically, whether these adipocytes express UCP1 and therefore have the capacity for thermogenesis. Several attempts have been made to determine whether BMAT adipocytes do indeed express UCP1, but collectively have yielded conflicting results. To overcome this, we sought to track UCP1 expression in BMAT at the single cell level using multiple rodent models.

Deciphering whether BMAT adipocytes express UCP1 is of importance because it informs the function of these cells. The capacity of BMAT adipocytes to undergo UCP1-mediated adaptive thermogenesis would have multiple advantages. First, positioning of thermogenic cells within stem cell niches may protect hematopoietic cells and therefore blood cell production from cold exposure in distal appendages. Second, the shunting of energy substrates toward adaptive thermogenesis has the benefit of lowering glucose and lipid load. Thus, clearance of lipids via adaptive thermogenesis may also protect hematopoietic and bone remodeling niches from lipotoxicity. As previously discussed, several lines of evidence both support and refute the existence of UCP1 expression in BMAT adipocytes. Briefly, Ucp1 transcript has been detected in whole bone RNA preparations, however, this type of tissue preparation is susceptible to contamination by adipocytes near the periosteal surface which we now show have the potential to express UCP1 (Fig. 2). Further, comparison of Ucp1 transcript amount in these bone preparations is ~10,000 fold less compared to BAT. It is also what we compared in a microarray transcript would result in UCP1 protein expression. One report did show putative UCP1 protein expression by IHC in comparable appearing, ‘multilocular’ BMAT adipocytes within the lumbar vertebrae of 3-week old mice. However, in this report, we show that immunostaining of bone marrow can easily provide false positive results, particularly in the absence of UCP1-KO tissue controls (Fig. 2). There are also reports that UCP1 protein is not expressed in BMAT, even after beiging induction by methionine-restriction.

In this study, three approaches were taken to specifically address whether BMAT adipocytes have the potential for UCP1 expression: 1) immunohistochemical detection of UCP1 protein in intact tissue, 2) Ucp1-Cre-driven and DTA-mediated cell ablation, and 3) Ucp1-Cre-mediated lineage tracing. Immunohistochemistry for UCP1 expression provided inconclusive results. Specifically, while cBAT adipocytes were clearly negative, non-specific DAB precipitation was present in hematopoietic-rich bone marrow of both control and UCP1-knockout mice making UCP1 expression in rBMAT cells difficult to assess. However, Ucp1-Cre driven cell ablation and lineage tracing provided compelling data that BMAT adipocytes, regardless of subregion, do not express UCP1. Ucp1-Cre driven expression of DTA resulted in loss of brown adipocytes and a subpopulation of iWAT adipocytes, but there was no detectable loss of BMAT adipocytes as assessed by 3-dimensional, regional analysis of BMAT in the proximal tibia, distal tibia and whole tibia. While these experiments cannot rule out the possibility of a loss of a Ucp-1 positive population that is replaced by a Ucp-1 negative BMAT population this possibility is not supported by our lineage tracing experiments. Lineage tracing using Ucp1-Cre and the mTmG reporter found that Ucp1-Cre successfully induced GFP expression in BAT and subpopulations of iWAT but did not induce GFP expression in BMAT of the femur, tibia or tail vertebrae regardless of age, sex, or induction by beiging factor CL316,243. A limitation of reporter models is that they rely on induction of the Ucp1-Cre. Cre recombinase models can have off-target expression or insufficient recombination. However, it is unlikely that these concerns would change the outcome of our study. First, there was no detectable difference in BMAT volume in the Ucp1-Cre/+DTA- Cre model nor GFP-positive BMAT in Ucp1Cre+/-mTmG+ mice, ruling out mis-expression in BMAT. Second, sufficient Ucp1-Cre-mediated recombination is supported by loss of peripheral brown and beige adipocytes in Ucp1Cre+/-DTA- mice, and conversion of the mTmG reporter in these adipocytes, as well as subpopulations of adipocytes near the periosteal surface in Ucp1Cre+/-mTmG+ mice. Further, conversion of the mTmG reporter by the Adipoq-Cre served as a positive control for the ability of BMAT adipocytes to support Cre-mediated recombination.

Lack of UCP1 expression despite a multilocular morphology could indicate that BMAT adipocytes transition from an early multilocular stage to a mature unilocular morphology; a physiologic transition similar to the fusion of immature lipid droplets in white adipocytes (reviewed in ). In this report, we show that the frequency of multilocular BMAT adipocytes is comparable across anatomical sites and is preserved between ages 3-weeks to 9-weeks old (~5%). Also, that this frequency is comparable to that reported for 12-week-old C3H/HeJ mice. Together, these findings indicate that ‘multilocularity’ is stable across age and mouse strain. If adipocytes transition through a multilocular stage, then it can be extrapolated that BMAT adipocyte turnover occurs at constant rate despite location or age. In addition, multilocularity could imply that these cells are undergoing simulated lipid droplet remodeling (lipolysis) and therefore have the ability to function as a local fuel reservoir. In support of this hypothesis, we recently demonstrated, using electron microscopy, that BMAT adipocytes directly interact with cells of the myeloid/granulocyte lineage, erythroblast islands, and active osteoblasts. Additionally, there are published reports showing BMAT provides fuel to cancer cells (reviewed in ) and that inflammatory arthritis is associated with BMAT depletion. As demonstrated by our microarray analysis and previous reports, the regulation of BMAT energy storage and partitioning is unique when compared to peripheral WAT. For example, pathway analysis indicated that BMAT likely has reduced quantity of glycogen relative to WAT, a finding that has previously been demonstrated by electron microscopy during BMAT adipogenesis. BMAT was also noted to be insulin resistant, which has recently been confirmed in both rodents and humans.

Lastly, lineage tracing studies have yielded mixed results regarding identification of a ‘beige’-like BMAT adipocyte. Specifically, BMAT adipocytes have been shown to express Pdgfrα, a mediator of adipocyte progenitor commitment to a beige adipocyte, following irradiation or rosiglitazone treatment (discussed in ). However,
myogenic factor-5 (Myf5), which is expressed in the majority of brown adipocyte progenitors and a minority of beige progenitors, was not detected in BMAT progenitors (discussed in [2]). In our study, lineage tracing clearly showed that BMAT adipocytes express the adipocyte marker adiponectin, but do not express the traditional beige cell marker Ucp1. However, Ucp1-Cre mediated conversion of the mTmG reporter did show Ucp1-Cre expression in cells of the kidney collecting ducts. Assessment of UCP1 expression in the mouse kidney has been evaluated by other labs. There is one report supporting UCP1 expression in mouse kidney, however, there are multiple reports indicating mammalian kidneys do not express UCP1. Thus, this is a point that warrants further clarification. Similarly, though Adipoq-Cre is not expressed in the stromal vascular fraction of adipose tissue or skin stromal cells, Adipoq-Cre/mTmG mice demonstrated prevalent Adipoq-Cre expression in bone lining cells, perivascular cells within bone, and cells within the reticular stromal network, a finding consistent with other reports. This continuity of expression between the stromal-reticular network and BMAT is also emphasized perivascular cells within bone, and cells within the reticular stromal network, a finding consistent with other reports. The continuity of expression between the stromal-reticular network and BMAT is also emphasized by other labs. There is one report supporting UCP1 expression in mouse kidney, however, there are multiple reports indicating mammalian kidneys do not express UCP1. Thus, this is a point that warrants further clarification.

Rats were housed at 22 °C on a 12-hour light/dark cycle and fed standard chow. Rabbit and rat studies were approved by the University of Michigan Committee on the Use and Care of Animals (Saint Louis, MO, USA). To generate Ucp1-Cre, ROSA26DTA/+ (Ucp1Cre/+DTA−) animals, heterozygous Ucp1-Cre+ males (Jackson Labs #024670) were bred to female diphtheria toxin subunit A (ROSA26DTA/DTA) homozygous mice (Jackson Labs #009669). Due to loss of brown adipose tissue and impaired thermoregulation, Ucp1-Cre−/DTA− animals do not survive when born at room temperature and thus were bred and housed at thermoneutrality (30 °C). Ucp1-Cre−/DTA− animals have a head tilt phenotype. Given there is no change in BMAT volume in Ucp1-Cre−/DTA− animals, this finding does not affect the conclusions of this paper. To generate Ucp1-Cre, ROSA26mTmG−/mTmG and Adipoq-Cre, ROSA26mTmG−/mTmG+ (Ucp1Cre−/mTmG− and AdipoqCre−/mTmG−) animals, heterozygous Ucp1-Cre−/mTmG− and Adipoq-Cre−/mTmG− males (Jackson Labs #024670 and #028020) were bred to homozygous mTmG (ROSA26mTmG−/mTmG−) female mice (Jackson Labs #007676). Ucp1Cre−/mTmG− or AdipoqCre−/mTmG− reporter animals have no deficiencies in thermoregulation and were thus bed and housed under standard conditions at 22 °C. All transgenic mice were maintained on an a C57BL/6J background (Jackson Labs #00664). All animals were housed in a vivarium with a 12-hour light/dark cycle and fed standard chow ad libitum (PicoLab 5053, LabDiet). Rabbit and rat studies were approved by the University of Michigan Committee on the Use and Care of Animals. Housing, monitoring, and euthanasia information for both the rabbits and rats included in this study has been previously reported. Briefly, male New Zealand White rabbits from Harlan Laboratories (Haslett, MI, USA) were euthanized at two ages, 13-weeks and 22-weeks, for tissue collection and analysis. Rabbit care was provided by the Unit for Laboratory Animal Medicine. Rabbits were housed at 22 °C on a 12-hour light/dark cycle and fed high-fiber diet (LabDiet: 5326 ad libitum (13-week old rabbits, body mass 2.70 ± 0.06 kg, n = 6) or a measured 100 g/day starting at 15-weeks of age (22-week old rabbits, body mass 3.17 ± 0.09 kg, n = 5). Sixteen-week-old male Sprague–Dawley rats were obtained from Charles River Laboratories (strain code: 400). Rats were housed at 22 °C on a 12-hour light/dark cycle and fed standard chow.

CL316,243 treatment regimen. Male and female Ucp1Cre−/mTmG− and AdipoqCre−/mTmG− reporter animals aged 15-weeks received six 0.03 mg/kg CL316,243 (Sigma) or saline injections over the course of eight days. On the ninth day, animals were perfused with 10% buffered formalin and tissues collected. 12-week-old C3H/HeJ mice received 5 μg CL316,243 injections daily for 3 days. After 72-hours, mice were euthanized and tissues collected.

Tissue collection (mouse). Following euthanasia, brown adipose tissue (BAT), inguinal white adipose tissue (iWAT), gonadal white adipose tissue (gWAT) and tibias were collected from Ucp1Cre−/DTA− animals. Tibia length was determined using a digital caliper. Tibias were post-fixed for 24-hours then decalcified in 14% EDTA, pH 7.4 for 3 weeks. Tissues from 3-week and 9-week-old C57BL/6J mice for paraffin embedding were post-fixed for 24-hours in 10% neutral buffered formalin (NBF) then stored in PBS. Prior to collection of Ucp1Cre−/mTmG−...
and Adipoq<sup>Cre<>/mTmG<sup> reporter tissues, mice were perfused with 10% NBF. Harvested tissues were then post-fixed for an additional 24-hours in 10% NBF. Paraffin embedding was performed by the WUSM Musculoskeletal Histology and Morphometry Core. All paraffin sections were 5 μm thick. Prior to embedding, bones were decalcified in 14% EDTA, pH 7.4 for 2-weeks.

**Biopsy specimens (human).** Human control biopsies from the iliac crest were included from the pathologic biobanks at Vejle Hospital in accordance with the approval by the Danish National Committee on Biomedical Research Ethics, journal no. S-20070121, as described previously<sup>33</sup>. The biopsies were diagnostic jamshidi biopsies obtained from patients formerly undergoing an examination for a hematological disorder, showing no skeletal disorders. The biopsies included in the study originated from patients not receiving any prior medications known to affect the bones and not declining use of their tissues for research in the National Tissue Application Register. The biopsies were blinded after inclusion (sex and age unknown).

**Paraffin immunohistochemistry.** Prior to hematoxylin/eosin or immunohistochemistry, sections were deparaffinized in xylene and hydrated in an ethanol gradient and distilled water.

Perilipin and endomucin immunohistochemistry (mouse) was performed as described previously<sup>34</sup>. Briefly, antigen retrieval was performed in 10 mM sodium citrate buffer (pH 6.0, 20-minutes, 90-95 °C) prior to permeabilization in 0.2% Triton-X in PBS and block in 10% donkey serum in TNT buffer (0.1 M Tris-HCL pH 7.4, 0.15 M sodium chloride, 0.05% Tween-20). Sections were co-stained with antibodies against endomucin (BioLegend, 1:500) and perilipin (1:400, Progen GP29) in TNT buffer containing 2.5% donkey serum overnight at 4 °C. Secondary antibodies (1:200 donkey anti guinea pig Cy3 and 1:200 donkey anti rat Alexa 488; Jackson ImmunoResearch) in TNT buffer were applied for 1-hour at room temperature. All washes between steps were performed in TNT buffer. Nuclei were counterstained with 1 μg/mL DAPI (Sigma). Slides were imaged on an Olympus FV1200 confocal microscope.

For UCP1 immunohistochemistry (mouse), tissue samples were permeabilized for 10-minutes and blocked for 1.5-hours with the buffer provided from Vectastain Elite ABC kit (Vector Laboratories). Primary antibody cocktail (1:2,000 UCP1, Abcam polyclonal ab10983) was made in TNT buffer containing 2% donkey serum and incubated overnight at 4 °C. Tissue sections were washed in TNT followed by quenching of endogenous peroxidases with 0.3% hydrogen peroxide in PBS for 30-minutes. Sections were washed 3x again in TNT prior to incubation with kit-provided secondary antibody (ImPRESS) for 30-minutes. After the secondary antibody, tissue samples were again washed 3x in TNT and 2x in PBS. Tissues were incubated with DAB substrate solution for 30-seconds for stain development, then washed in water. After a final wash, samples were stained with hematoxylin, dehydrated through a reverse ethanol gradient and mounted with Permount mounting media. Images were acquired using an upright DMRXAZ microscope (Leica) and a UC30 camera (Olympus).

For osteopontin (SPP1) immunohistochemistry (human), antigen retrieval was performed by heating samples in Tris/EDTA (pH 9.0) for overnight at 60 °C. Tissue sections were blocked for 20-minutes using 1% casein in using Nanozoomer 2.0-HT system. Paraffin sections were 5 μm thick. Prior to embedding, bones were decalcified in 14% EDTA, pH 7.4 for 2-weeks. Tissues were embedded in OCT mounting media and sectioned at 50 μm (tibia, iWAT, kidney) or 100 μm (tail) using a cryostat (Leica). Tissue sections were rinsed 3x in TNT and blocked for 1-hour with 10% donkey serum in TNT buffer (0.1 M Tris-HCL pH 7.4, 0.15 M sodium chloride, 0.05% Tween-20). Primary antibody cocktail (1:1,000 chicken anti-GFP; 1:500 rabbit anti-RFP; 1:1,000 guinea pig anti-perilipin; Abcam ab13970, ab62341 and Progen GP29, respectively) was made in TNT buffer containing 0.3% hydrogen peroxide in PBS for 30-minutes. Sections were washed 3x again in TNT prior to incubation with kit-provided secondary antibody (ImPRESS) for 30-minutes. After the secondary antibody, tissue samples were again washed 3x in TNT and 2x in PBS. Tissues were incubated with DAB substrate solution for 30-seconds for stain development, then washed in water. After a final wash, samples were stained with hematoxylin, dehydrated through a reverse ethanol gradient and mounted with Permucount mounting media. Images were acquired using an upright DMRXAZ microscope (Leica) and a UC30 camera (Olympus).

Quantification of multilocular bone marrow adipocyte frequency was performed on H&E stained tibia and femur sections from 3-week and 9-week-old C57BL/6J mice. As previously described<sup>3</sup>, BMAT adipocytes were considered multilocular if they contained three or more smaller lipid droplets associated with a large lipid droplet. All adipocytes within the epithysis (distal for femur, proximal for tibia), metaphysis (mid-diaphysis to growth plate for femur, growth plate to tibia-fibula junction for tibia), or distal tibia were counted. Two tissue sections per mouse were analyzed and the data averaged.

**Frozen immunohistochemistry.** Ucp1<sup>Cre<>/mTmG<sup> reporter animals were anesthetized with ketamine/xylazine cocktail (80 mg/kg and 5 mg/kg, respectively) perfused with 10% NBF prior to euthanasia. Harvested tissues were post-fixed for 24-hours in 10% NBF then washed in PBS. Bones were decalcified using 14% EDTA, pH 7.4 for 14-days. Tissues were embedded in OCT mounting media and sectioned at 50 μm (tibia, iWAT, kidney) or 100 μm (tail) using a cryostat (Leica). Tissue sections were rinsed 3x in TNT and blocked for 1-hour with 10% donkey serum in TNT buffer (0.1 M Tris-HCL pH 7.4, 0.15 M sodium chloride, 0.05% Tween-20). Primary antibody cocktail (1:1,000 chicken anti-GFP; 1:500 rabbit anti-RFP; 1:1,000 guinea pig anti-perilipin; Abcam ab13970, ab62341 and Progen GP29, respectively) was made in TNT buffer and incubated overnight at 4 °C. Secondary antibody cocktail (1:500 donkey anti-guinea pig Cy3 and 1:200 donkey anti chicken Alexa 488; Jackson ImmunoResearch) in TNT buffer was applied for 1-hour at room temperature. Chromogen staining was made with Liquid Permanent Red (DAKO). All washes between steps were performed in TNT buffer. Nuclei were counterstained with 1 μg/mL DAPI (Sigma). Slides were imaged using an upright DMRXAZ microscope (Leica) and a UC30 camera (Olympus).

Quantification of GFP/RFP positive adipocytes was performed in iWAT, gWAT, BAT and three regions of BMAT including tail vertebrae, femur, and proximal tibia (Fig. 4 and data not shown). All perilipin positive adipocytes in a full length, 50–100 μm section were assessed for each animal.

**Osmium staining and micro-computed-tomography (μCT).** Tibias from 4-week-old Ucp1<sup>Cre<>/DTA<sup>−/−</sup> and littermate controls were decalcified in 14% EDTA, pH 7.4 for 3-weeks then stained with osmium tetroxide and imaged as described previously<sup>35</sup>. Briefly, decalcified bones were incubated in a PBS solution containing 1% osmium tetroxide (Electron Microscopy Sciences) and 2.5% potassium dichromate (Sigma) for 48-hours.
Following thorough washing, osmium-stained bones were embedded in 2% agarose and scanned a 10μm voxel resolution using a Scanco μCT 40 (Scanco Medical AG). Analysis and 3-D rendering of the μCT data sets were performed using Scanco software, and a threshold of 400. Analysis regions included the tibia proximal epiphysis, distal tibia (tibia-fibula junction to distal epiphysis) and total medullary cavity.

**Microarray enrichment analysis (rabbit).** RNA was isolated from whole white adipose tissues (inguinal, iWAT; gonadal, gWAT) and bone marrow adipose tissues (distal tibia, dBMAT; radius/ulna, ruBMAT; proximal tibia, pBMAT) of rabbits as described previously. Briefly, rabbit tissues were frozen on dry ice, pulverized in liquid nitrogen with a mortar and pestle, and lysed in Stat60 reagent (Tel-Test Inc) by manual disruption with a needle and syringe. For microarray, purified rabbit RNA was digested on-column with DNase I and cleaned using the Qiagen RNeasy kit (Qiagen) as recommended by the manufacturer. Total RNA was then submitted to the microarray core at the University of Michigan. The samples were screened for quality and processed in the microarray facility using custom rabbit Affymetrix arrays and the IVT Express kit (Affymetrix). Samples that did not meet minimum RNA quality or concentration standards were excluded from microarray analysis. As a QC measure, the distribution of probe intensities and the 5' to 3' degradation profiles were checked to be consistent across samples. The core's statistician used RMA, from the Affy package of bioconductor, to fit log2 expression values to the data. Weighted, paired, linear models were then fit and contrast computed using the limma package. As before, P-values were adjusted using the Holm-Sidak method and 897 transcripts were retained for further identification of 1,657 transcripts that were statistically enriched in regions of high BMAT content (distal tibia BMAT and radius/ulna BMAT) were compared to a region of relatively decreased BMAT (proximal tibia BMAT). P-values were adjusted for multiple comparisons using the Holm-Sidak method with alpha set at 0.05, resulting in identification of 1,657 transcripts that were statistically enriched in regions of high BMAT. From there, expression of these transcripts in BMAT (all dBMAT and ruBMAT) was compared to all white adipose tissues (all gWAT and iWAT) to generate a list of genes with high probability of differential expression between BMAT and WAT. As before, P-values were adjusted using the Holm-Sidak method and 897 transcripts were retained for further pathway analysis (Fig. 6a, Supplemental Table 1). To ensure maximum compatibility with the Ingenuity Pathway Analysis software, rabbit gene identifiers were converted to their corresponding human homologues using the ‘BetterBunny’ algorithm. Homology-based human IDs were identified for 775 out of 897 genes which were then used for pathway analysis (Fig. 6a, Supplemental Table 1).

**Adipocyte purification and qPCR analysis (rat).** Cell isolation, RNA purification, and qPCR analysis was completed as previously described. Briefly, twelve 16-week-old male Sprague–Dawley rats were used to purify and isolate 6 BMAT adipocyte samples from caudal vertebrae (two animals pooled per sample) and 12 floated adipocyte preparations from inguinal WAT (one animal per sample) using a modified collagenase digestion protocol. Floated adipocytes were collected and lysed using Stat60 reagent (Ambion, Cambridge, MA, USA) to isolate total RNA. RNA was reverse-transcribed to cDNA (Applied Biosystems, Carlsbad, CA) and quantitative PCR was performed using qPCR BIO SyGreen mix, Hi-Rox, on an Applied Biosystems real-time PCR detection system. Gene expression was calculated based on a cDNA standard curve within each plate and normalized to the expression of the geometric mean of TATA-binding protein (Tbp) and cyclophilin A (Ppia) messenger RNA.

**Statistics.** Statistical analysis was performed using GraphPad Prism (GraphPad Software). Statistical tests are detailed in the corresponding figure legend. A p-value of <0.05 was considered statistically significant.

**Data availability** All data contained within this manuscript are available upon request.

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**Author contributions**

C.S.C., E.L.S., T.L.A., W.P.C. and O.A.M. conceived and planned the experiments. C.S.C., H.R., M.R.L., E.D.H., K.L.M., W.P.C., T.L.A. and E.L.S. performed the experiments. C.A.H., W.P.C., T.L.A. and O.A.M. provided critical feedback regarding the project and manuscript, and supplied the Cre recombinase mice. C.S.C. and E.L.S. co-wrote the manuscript. All authors revised and approved the manuscript.

**Competing interests**

The authors declare no competing interests.

**Additional information**

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