**Adipocyte-specific tribbles pseudokinase 1 regulates plasma adiponectin and plasma lipids in mice**

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**ABSTRACT**

Objective: Multiple genome-wide association studies (GWAS) have identified SNPs in the 8q24 locus near TRIB1 that are significantly associated with plasma lipids, and other markers of cardiometabolic health, and prior studies have revealed the roles of hepatic and myeloid TRIB1 in plasma lipid regulation and atherosclerosis. The same 8q24 SNPs are additionally associated with plasma adiponectin levels in humans, implicating TRIB1 in adipocyte biology. Here, we hypothesize that TRIB1 in adipose tissue regulates plasma adiponectin, lipids, and metabolic health.

Methods: We investigate the metabolic phenotype of adipocyte-specific Trib1 knockout mice (Trib1_ASKO) fed on chow and high-fat diet (HFD). Through secretomics of adipose tissue explants and RNA-seq of adipocytes and livers from these mice, we further investigate the mechanism of TRIB1 in adipose tissue.

Results: Trib1_ASKO mice have an improved metabolic phenotype with increased plasma adiponectin levels, improved glucose tolerance, and decreased plasma lipids. Trib1_ASKO adipocytes have increased adiponectin production and secretion independent of the known TRIB1 function of regulating proteasomal degradation. RNA-seq analysis of adipocytes and livers from Trib1_ASKO mice indicates that alterations in adipocyte function underlie the observed plasma lipid changes. Adipocyte tissue explant secretomics further reveals that Trib1_ASKO adipose tissue has decreased ANGPTL4 production, and we demonstrate an accompanying increase in the lipoprotein lipase (LPL) activity that likely underlies the triglyceride phenotype.

Conclusions: This study shows that adipocyte Trib1 regulates multiple aspects of metabolic health, confirming previously observed genetic associations in humans and shedding light on the further mechanisms by which TRIB1 regulates plasma lipids and metabolic health.

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Keywords Adipose; Metabolic syndrome; Lipoproteins; GWAS; Tribbles; Pseudokinases

1. INTRODUCTION

Genome-wide association studies (GWAS) have repeatedly identified SNPs in the 8q24 locus associated with multiple traits related to cardiometabolic disease, including plasma triglyceride (TG) [1,2], HDL-cholesterol (HDL-C), total cholesterol (TC), LDL-cholesterol (LDL-C) [1–6], coronary artery disease (CAD) [6,7], circulating liver transaminases (ALTs/ASTs) [8], and most recently with HbA1c levels [9]. These SNPs lie ~40 kb downstream of the TRIB1 gene, which codes for the Tribbles pseudokinase 1 [10], implicating TRIB1 in numerous facets of metabolism. As a pseudokinase, TRIB1 lacks the ability to phosphorylate target proteins. Rather, TRIB1 is best known as a scaffolding protein that facilitates protein–protein interactions leading to the post-translational modification (phosphorylation or ubiquitination) of the target proteins [11]. Subsequent in vivo studies confirmed the role of hepatic TRIB1 in these metabolic phenotypes, as liver-specific overexpression of Trib1 in mice decreases plasma cholesterol and TGs [12], whereas hepatic deletion of Trib1 increases plasma cholesterol and TGs and also increases hepatic steatosis due to elevated de novo lipogenesis [13]. Furthermore, myeloid-specific Trib1 knockout mice have reduced foam cell formation and atherosclerotic burden [14], implicating myeloid TRIB1 in CAD pathogenesis. These studies highlight the importance of tissue-specific gene functions and raise the question of how much Trib1 function in other tissues contributes to the GWAS associations.

In addition to the traits listed above, the TRIB1 GWAS SNPs are also associated with plasma adiponectin levels in humans, with the effect allele associated with a 3% increase in circulating adiponectin [15] (Figure S1). Adiponectin (ADIPOQ) is an adipokine secreted exclusively from the adipose tissue, implicating TRIB1 in adipose tissue biology. Adiponectin acts predominantly as an insulin-sensitizing agent through signaling to the liver and skeletal muscle [16], while further studies...
have linked adiponectin with hepatic fat content [17], decreased plasma TG [18], increased HDL-C [18], decreased NAFLD [19], and decreased risk of CAD [20]. Thus, adiponectin has a beneficial effect on various markers of metabolic health, indicating a therapeutic benefit of increasing circulating adiponectin levels [21]. Adipose tissue is increasingly recognized as a critical regulator of metabolic homeostasis and health, chiefly due to its function in storing TGs through lipoprotein lipase (LPL)-mediated uptake from TG-rich lipoproteins during the states of excess energy [22], and the subsequent release of the stored TGs during the states of energy depletion [23]. Dysfunctional adipose tissue, such as in lipodystrophy and obesity, is marked by impaired ability to store lipids, decreased insulin sensitivity and glucose uptake, adipose tissue inflammation, and altered adipokine secretion, which can together precipitate systemic insulin resistance, dyslipidemia, and metabolic disease [24,25].

Given the genetic evidence linking TRIB1 with multiple features of cardiometabolic disease and to adipocyte biology, and the important roles of adiponectin and adipose tissue in cardiometabolic health, we hypothesized that TRIB1 in adipose tissue may be contributing to the myriad human genetic associations between the 8q24 locus and cardiometabolic traits. Here, we report the first adipocyte-specific Trib1 knockout mouse and show that these mice have an overall improved metabolic phenotype with increased plasma adiponectin levels, decreased plasma TG and cholesterol levels, and improved glucose tolerance. Further mechanistic studies reveal that TRIB1 regulates plasma adiponectin through increased adiponectin production and secretion and TRIB1 modulates plasma TG clearance through the regulation of adipose tissue-specific LPL activity.

2. MATERIALS AND METHODS

2.1. Animals

The previously reported Trib1_fl/fl mice [13] and Rosa26.Trib1 (Trib1-RosaSTOP-/ and Trib1-RosaSTOP/fl) transgenic mice [14] were bred in-house. Trib1_fl/fl mice were crossed with Adipoq-Cre mice (Jackson Labs stock #010803) to generate Trib1_fl/fl, Adipoq-Cre + mice (Trib1 adipocyte-specific knockout (Trib1_ASKO)) and Trib1_fl/fl, Adipoq-Cre - mice (control Trib1_fl/fl). The mice were bred in a manner such that all Trib1_fl/fl and Trib1_ASKO mice were true littermates. The Trib1_ASKO mice were crossed with Ldlr KO mice (Jackson Labs stock #002207) to generate Trib1_fl/fl, Adipoq-Cre +; Ldlr KO mice and Trib1_fl/fl, Adipoq-Cre -; Ldlr KO mice.

Adipose tissue-specific Trib1 overexpressing transgenic mice were generated by crossing Rosa26 Trib1 mice with Adipoq-Cre mice (Jackson Labs stock #028020). All mice were on the C57BL/6J background. For experiments with less than 8 mice per group (N < 8 mice/group), the experiment was repeated in three independent animal cohorts. The mice were fed ad-libitum on a chow diet unless otherwise noted. All experiments were performed when the mice were 8–12 weeks old unless stated otherwise. For fasting/refeeding experiments, the mice were euthanized at 5 pm (fed), at 9 am the next day after 16-h fast (fasted), and after 3-h refeeding (refed). The mice were fasted for 4 h prior to collecting plasma samples, unless stated otherwise. Blood was collected retro-orbitally and fasting at 10,000 rpm for 7 min. Fasting cholesterol and TGs were measured via plate assay using the TC and Infinity triglyceride reagents (Fisher Scientific PI78444). The lysate was clarified via centrifugation at 12,000 × g for 15 min at 4 °C. Approximately 30 μg protein was loaded onto 10% bis-tris SDS-PAGE gel and transferred onto a nitrocellulose membrane. The membrane was blocked in 5% milk or BSA (for phospho-protein analysis) and incubated in the appropriate primary antibody overnight (see supplementary methods). Protein was detected using a secondary HRP-linked antibody and Luminata Classic Western HRP Substrate (Millipore WBLUC0020). To reprobe membranes, the membranes were incubated in stripping buffer (Fisher Scientific PI21059) for 15 min before reblocking. All western blots were repeated a minimum of three times, with the representative results shown.

2.2. FPLC analysis of pooled plasma

Pooled plasma (200 μl) from gender- and genotype-matched mice was loaded onto a Superose 6 column (GE Healthcare) calibrated with elution buffer (0.15 M NaCl, 1 mM EDTA). The lipoproteins were eluted in a total of 20 ml elution buffer in 0.5 ml fractions at a rate of 0.3 ml/min. The cholesterol and TG content of each fraction was determined by plate assay using the TC and Infinity triglyceride reagents.

2.3. Western blot analysis

Tissues or cells were lysed and homogenized in RIPA buffer supplemented with 1x Halt Protease and Phosphatase inhibitor (Fisher Scientific PI78444). The lysate was clarified via centrifugation at 12,000 × g for 15 min at 4 °C. Approximately 30 μg protein was loaded onto 10% bis-tris SDS-PAGE gel and transferred onto a nitrocellulose membrane. The membrane was blocked in 5% milk or BSA (for phospho-protein analysis) and incubated in the appropriate primary antibody overnight (see supplementary methods). Protein was detected using a secondary HRP-linked antibody and Luminata Classic Western HRP Substrate (Millipore WBLUC0020). Gene expression data were normalized to Gapdh and presented as fold change relative to the Trib1_fl/fl control group (exceptions indicated in the figure legend).

2.5. Microscopy

For adipose tissue histology, scWAT samples (<4 mm thick) from Trib1_fl/fl and Trib1_ASKO mice were fixed in 4% PFA for 24 h. The tissues were then embedded in paraffin, sectioned at 7 μm, and H&E stained. For each mouse, 4 sections at 70 μm intervals were imaged on a Nikon Eclipse Ti microscope with the 40x objective and analyzed using the Adiposoft ImageJ plugin (parameters: minimum diameter = 10 μm, maximum diameter = 100 μm). For Oil Red O staining, the cells were fixed in 4% PFA for 15 min and then placed in 0.3% w/v Oil Red O in 60% isopropanol for 30 min. The cells were washed 5X in distilled H2O and then imaged with the 20x objective.

2.6. RNA-seq of adipocytes and hepatocytes

Eight-to 12-week-old male mice were euthanized and perfused with PBS after a 4-h fast. scWAT from individual mice were harvested, minced, and then placed in 6 ml digestion media (0.14 U/ml Liberase TM, 50 U/ml DNAase I, 20 mg/ml BSA in DMEM) for 1 h at 37 °C, with shaking at 250 rpm. The tissue prep was then filtered through a 100 μm cell strainer and spun at 300 × g for 10 min. The floating adipocyte fraction was collected in 1 ml Qiazol, and RNA was isolated using the RNeasy Lipid Tissue Mini Kit (Qiagen). Livers from the same
mice were harvested and homogenized in TRIzol, and RNA was isolated before chloroform extraction. RNA quality was assessed via BioAnalyzer before being submitted to the core for bulk, paired-end RNA-sequencing (NextSeq 500). Reads were aligned using STAR and featurecounts, and differential expression analysis was performed using the DESeq2 package. Differentially expressed genes (padj < 0.050) were ranked by the signal-to-noise ratio of DESeq2-normalized counts and analyzed by gene set enrichment analysis (GSEA) using the Gene Ontology gene sets (c5.go.v7.2.symbols.gmt) from MSigDB, with gene set size ≤ 200 and 1000 permutations of the gene sets to determine the enrichment score. Cytoscape enrichment plots were constructed from the GSEA results using FDR < 0.01, and a combined coefficient > 0.375 with combined constant 0.5 as described in [27]. Nodes were clustered using the MCL clustering algorithm in the Autoannotate Cytoscape App. Annotations of the clusters were manually curated.

2.7. SVF generation and differentiation
Subcutaneous inguinal fat pads from 3 to 5 mice of the same gender and genotype were combined and minced in digestion buffer (L-15 Leibovitz media, 0.15% BSA, 1% Pen/Strep, 10 U/mL DNase, 480 U/mL Hyaluronidase, 0.14 U/mL Liberase TM). Tissue was allowed to dissociate in digestion buffer for 1 h at 37 °C, with shaking at 250 rpm. The tissue prep was then filtered through a 100 µm cell strainer and spun at 300 × g, 4 °C, for 10 min. The pellet was washed, saved in 10 mL culture medium (DMEM, 10% FBS, 1% Pen/Strep, 2 mM L-Glut), and then resuspended in 5 mL culture medium supplemented with 1 µg/mL insulin before seeding. The media were changed every 2–3 days until the cells were > 95% confluent. Differentiation was initiated with a cocktail including 10% FBS, 1% Pen/Strep, 5 µg/mL insulin, 1 µM Rosiglitazone, 1 µM Dexamethasone, and 250 µM IBMX in DMEM/F12. After 48 h, the cells were maintained in DMEM/F12 supplemented with only 10% FBS, 1% Pen/Strep, 5 µg/mL insulin, and 1 µM Rosiglitazone. The experiments were started after day 7 of differentiation.

2.8. Global quantitative proteomics of explant secretomics
The mice were euthanized and perfused with PBS before the dissection of subcutaneous adipose tissue fat pads. Then, 50 mg of tissue was placed into 1 mL of warm, serum-free DMEM in a 12-well plate and pinned down with a transwell insert. The media were collected after 6 h, and proteins were precipitated using methanol. The precipitated proteins were identified and quantified by data-independent acquisition (DIA)-based proteomics as described in the supplementary methods.

2.9. Cloning and lentiviral production
Lentiviral constructs for tetracycline-inducible expression of proteins (mTrib1 and eGFP) in adipocytes for overexpression experiments were cloned by first introducing a 3xFlagHA tag at the C-terminal end of each protein. The fusion proteins were then cloned into the pEN-TTMCS entry vector to introduce a tight TRE promoter and subsequently cloned into the pSLIK-neo lentiviral plasmid via Gateway cloning. mTrib1 and eGFP were also cloned into the pLentiCMVPuroDEST lentiviral vector for constitutive overexpression under the CMV promoter.

To produce the virus, 5 × 10^6 293T cells were seeded in T75 flasks and transfected with 2 µg MD2G, 3 µg Pax2, and 5 µg lentiviral construct with 30 µL Fugene 6 (Promega) the following day. The media were changed the day after transfection, and the viral supernatant was collected and pooled after 24 h and 48 h. The supernatant was filtered through a 0.45 µm filter, aliquoted, and stored at − 80 °C until use.

2.10. Adipocyte cell culture
3T3-L1 cells were purchased from ATCC and cultured in DMEM supplemented with 10% FBS, 1 mM sodium pyruvate, and 1% Pen/Strep. The cells were tested for mycoplasma every three months. To differentiate the 3T3-L1 cells to adipocytes, the cells were induced with growth media supplemented with 1 µM dexamethasone, 0.5 mM IBMX, and 1 µg/mL insulin for 48 h and then maintained in growth media supplemented with only 1 µg/mL insulin. Stable doxycycline-inducible 3T3-L1 cells were generated by transducing the cells with lentivirus at an MOI ~ 100, followed by selection with 1.5 µg/mL puromycin. Conditioned media were collected in OptiMEM I reduced serum media.

2.11. Fluorescent LPL assay
The LPL activity assay was adapted from Basu et al. [28]. Briefly, adipose tissue was minced in 5 µL x mg tissue weight volume in tissue incubation buffer (PBS, 2 mg/mL FA-free BSA, 5 U/mL heparin), incubated for 1 h in a 37 °C shaker, and centrifuged at 3,000 rpm for 15 min at 4 °C. The clarified supernatant was placed in fresh tubes and diluted 1:10 in tissue incubation buffer. Then, 4 µL of lysate was placed in duplicate in a black-walled 96-well plate, and 100 µL reaction buffer (0.15 M NaCl, 20 mM Tris–HCl pH 8.0, 0.0125% Zwittergent, 1.5% FA-free BSA, 0.62 µM EnzChek (Invitrogen E33955)) was added to each well. The reaction was allowed to incubate for 20 min at 37 °C, and was then read at an excitation of 485 and emission of 515. A blank RFU value was subtracted from all the experimental RFU values, and the resulting values were reported.

2.12. Statistics
GraphPad Prism 8 was used to graph data and to perform parametric 2-tailed Student’s t-tests for comparison between the two groups, and 1- and 2-way ANOVA analyses with multiple corrections were performed for comparison between multiple groups using either Sidak’s or Tukey’s method as indicated in the figure legends.

2.13. Study approval
All in vivo studies described were approved by the Institutional Animal Care and Use Committee at Columbia University and Helmholtz Centre Munich prior to commencement.

3. RESULTS

3.1. Adipocyte-specific Trib1 knockout does not alter body weight
We generated Trib1_ASKO mice by crossing previously described Trib1-floxed (Trib1_fl/f1) C57BL/6 mice [13] with transgenic mice expressing Cre recombinase under the adipocyte-specific Adipog promoter. Efficient Trib1 deletion in the adipose tissue of Trib1_ASKO mice was confirmed by qPCR in subcutaneous white adipose tissue (scWAT) (Figure 1A), gonadal white adipose tissue (gWAT), and brown adipose tissue (BAT) (Figure 1B), and we did not detect any compensatory changes in Trib2 or Trib3 expression in scWAT (Figure 1A). Trib1 message was unchanged in other tissues, including the livers (Figure 1B) of Trib1_ASKO mice, confirming the specificity of the model. Chow-fed Trib1_ASKO mice had a similar overall body weight and fat pad mass to Trib1_fl/f1 mice (Figure 1C,D), and there was no difference in the adipocyte morphology or size as measured by H&E staining and subsequent morphometric analysis (Figure 1E). Similar results were observed in mice fed a 45% kcal HFD for 12 weeks (Figure 1F,G).
A previous study reported that Trib1 haploinsufficiency in mice impairs the upregulation of inflammatory genes in adipose tissue in response to proinflammatory stimuli such as LPS, TNF-α, and HFD feeding [29]. Given the known contribution of adipose tissue inflammation to metabolic disease [30], we checked whether Trib1_ASKO mice had decreased inflammatory markers in adipose tissue. We measured the inflammatory gene expression in adipose tissue under both chow-fed and HFD-fed conditions and observed no difference between the groups in either diet setting (Figure S2a-c). To investigate the inflammatory response in vitro, we treated adipocytes differentiated from the stromal vascular fraction (SVF) from the scWAT of Trib1_/fl/fl and Trib1_ASKO mice with TNF-α. Similarly, we did not observe any changes in the transcriptional response to TNF-α treatment in SVF-derived adipocytes from Trib1_ASKO mice compared with Trib1_/fl/fl controls (Figure S2d). These data suggest that the phenotypes we observe in our mice are not due to changes in adipose tissue inflammation.

3.2. Trib1_ASKO mice have increased plasma adiponectin

Given the association in humans between SNPs near TRIB1 and plasma adiponectin, we first sought to determine whether Trib1_ASKO mice had altered circulating adiponectin levels. We found that both male and female Trib1_ASKO mice on chow diet have significantly increased plasma adiponectin levels compared with their wild-type counterparts, with Trib1_ASKO males demonstrating a 40% increase (9.92 ng/mL vs. 14.3 ng/mL, p = 0.014) and females demonstrating a 20–30% increase (14.4 ng/mL vs. 17.5 ng/mL, p = 0.027) (Figure 2A). We also specifically assayed the levels of the high-molecular weight (HMW) form of adiponectin and found this to be increased in Trib1_ASKO mice as well (Figure 2B). The increase in plasma adiponectin was not accompanied by detectable changes in the adiponectin message levels in the scWAT or gWAT (Figure 2C), suggesting a posttranscriptional role of TRIB1 in plasma adiponectin regulation. To determine whether Trib1_ASKO mice had global alterations in adipokine secretion, we investigated the levels of resistin and

Figure 1: Adipocyte-specific knockout of Trib1 does not result in defects in adiposity. A, Taqman qPCR for Trib1, Trib2, and Trib3 in scWAT from 8 to 10-week-old Trib1_/fl/fl and ASKO mice (n = 5). B, Taqman qPCR for Trib1 from gWAT (n = 5), BAT (n = 4), and livers (n = 6) from Trib1_/fl/fl and Trib1_ASKO mice. C,D, Body weight (g) and adipose tissue depot masses (D) in chow-fed Trib1_/fl/fl and ASKO mice (n = 6). E, Representative H&E stain of scWAT from Trib1_/fl/fl and ASKO mice and quantification of cell size by Adiposoft (n = 4 mice). Bar = 100 μm. F,G, Body weight (F) and adipose tissue depot masses (G) in 12-week-old HFD-fed Trib1_/fl/fl and ASKO mice (n = 8). All gene expression data are depicted as the mean ± s.e.m. All other data are depicted as the mean ± s.d. Significance in all panels is determined by Student’s t test (*p < 0.05, **p < 0.01).
leptin, two well-studied adipokines in mice. We found that resistin levels were also increased in Trib1_ASKO mice (Figure 2D), while plasma levels of leptin were not significantly changed (Figure 2E), demonstrating that Trib1 regulates the secretion of specific adipokines and not global adipokine secretion. Despite increased adiponectin levels, glucose tolerance was not significantly changed in 8–12-week-old chow-fed mice (Figure 2F–J), and SVF-derived adipocytes did not demonstrate increased insulin signaling upon insulin stimulation (Figure S3a). HFD-fed Trib1_ASKO mice maintained increased adiponectin levels (Figure 2F) as well as a trend of increased resistin (Figure 2G) compared with wild-type mice. In contrast with chow-fed mice, HFD-fed Trib1_ASKO mice also had significantly improved glucose tolerance (Figure 2H–J) and decreased fasting plasma insulin levels (Figure S3b) compared with HFD-fed wild-type mice, consistent with improved insulin sensitivity that may be expected in the setting of increased plasma adiponectin levels [16]. Finally, we observed that overnight fasting drastically reduces Trib1 expression in scWAT, and this reduction is reversed by refeeding of fasted mice (Figure S3c,d). To test whether adipocyte-specific Trib1 overexpression would result in the opposite phenotype, we inserted Trib1 in the Rosa26 locus under the control of the CAG promoter followed by a floxed Stop codon and crossed this mouse with Adipoq-Cre mice. Adipoq-Cre + mice had 6-fold and 3-fold increased Trib1 expression in gWAT and scWAT (Figure S4a), respectively. We did not observe significant changes in plasma adiponectin in transgenic mice compared with controls (Figure S4b). However, glucose tolerance was significantly impaired in 8-week-old HFD-fed transgenic mice (Figure S4c,d). In addition, transgenic mice had unaltered plasma cholesterol levels but a modest, significant increase in plasma triglycerides (Figure S4e,f). Thus, adipocyte-specific knockout and overexpression mouse models confirm the role of adipocyte TRIB1 as a regulator of glucose and lipid homeostasis in vivo.

3.3. TRIB1 in adipocytes negatively regulates adiponectin secretion through a proteasome-independent mechanism

Since plasma adiponectin levels were increased in Trib1_ASKO mice, we hypothesized that Trib1 deficiency in adipocytes promotes increased adiponectin secretion. To test this hypothesis, we investigated adiponectin protein expression and secretion in SVF-derived adipocytes from the scWAT of Trib1_f/f and Trib1_ASKO mice. Indeed, consistent with the lack of an adiposity phenotype in the adult mice, SVF-derived adipocytes from Trib1_f/f and ASKO mice differentiated similarly, as assessed by cellular morphology and lipid accumulation (Figure S5a,b). Importantly, Trib1 expression in adipocytes derived from ASKO mice was lower relative to adipocytes derived from Trib1_f/f mice (Figure S5c), demonstrating that Adipoq-Cre is efficiently expressed in the in vitro setting upon differentiation. As the Adipoq-Cre Transgene is only active after adipogenesis has begun, we do not believe that this model can address any potential role for Trib1 in adipogenesis. Consistent with the observations in whole adipose tissue, adiponectin mRNA expression was unchanged in SVF-derived adipocytes (Figure 3A). However, adiponectin was increased in the conditioned media from adipocytes derived from Trib1_ASKO SVF compared with Trib1_f/f SVF (Figure 3B), confirming increased adiponectin secretion. This was also accompanied by a clear increase in intracellular
adiponectin protein levels (Figure 3C), suggesting that increased secretion is in part due to increased cellular adiponectin protein levels, despite the lack of a transcriptional change.

We next investigated whether \textbf{Trib1} overexpression in adipocytes would also have an effect on adiponectin secretion and intracellular protein. We generated a doxycycline-inducible 3xFlagHA-tagged \textbf{Trib1} overexpression 3T3-L1 stable cell line that was able to overexpress \textbf{Trib1} >500-fold over wild-type values (Figure 3D). We found that \textbf{TRIB1} protein was barely detectable in these cells via Western blot unless the cells were first treated with the proteasome inhibitor MG132 for 4 h, which increased the expression of \textbf{TRIB1} protein (Figure 3D).

**Figure 3**: Adipocyte-specific knockout of \textbf{Trib1} results in increased adiponectin secretion. A. Taqman qPCR for \textbf{Trib1} and \textbf{Adipoq} in SVF-derived adipocytes (n = 4). Conditioned media was generated by culturing SVF-derived adipocytes in OptiMEM reduced-serum media for 4 h. C. Western blot analysis of adiponectin (ADIPQ) in SVF-derived adipocytes. A Western blot of tubulin is shown as a loading control. D. Taqman qPCR for \textbf{Trib1} in pSilk-neo-TTMCs_eGFP-3xFlagHA and pSilk-neo-TTMCs_mTrib1-3xFlagHA stable 3T3-L1 adipocytes at D14 of differentiation treated with doxycycline (1 \mu g/mL) for 48 h (n = 3). Gene expression is expressed relative to the GFP stable cells. E. Western blot for Flag-tagged protein overexpression in pSilk-neo-TTMCs_eGFP-3xFlagHA and pSilk-neo-TTMCs_mTrib1-3xFlagHA stable D14 3T3-L1 adipocytes induced with 1 \mu g/mL Dox for 48 h and treated with or without 30 \mu M MG132 for 5 h. F. Western blot of CEBP\textalpha in scWAT from Trib1\_fl/\_fl and Trib1\_ASKO mice. A Western blot of tubulin is shown as a loading control. G. qPCR for Cebpa gene expression in scWAT from Trib1\_fl/\_fl and Trib1\_ASKO mice (n = 5). H. ADIPOQ and C/EBP\textalpha protein levels were measured by Western blot in Trib1\_fl/\_fl and Trib1\_ASKO adipocytes (n = 3). Data on gene expression are presented as the mean ± s.e.m. All other data are presented as the mean ± s.d. The significance in (I) was determined by 2-way ANOVA (Tukey’s multiple correction). The significance in all other panels was determined by Student’s t test (*p < 0.05, **p < 0.01, ****p < 0.0001).
MG132, indicating that TRIB1 is unstable and undergoes rapid proteasomal degradation in 3T3-L1 cells (Figure 3E). To avoid differences in the cell-line differentiation capacity caused by selection, we further employed lentiviral delivery of Trib1 and eGFP expressed under the CMV promoter in mature 3T3-L1 adipocytes to assess the effects of Trib1 overexpression in culture. Despite >60-fold overexpression of Trib1 via this method, we did not observe any changes in adiponectin secretion or protein levels compared with the GFP control (Figure S6). This is similar to our transgenic mouse data, in which the overexpression of Trib1 did not alter the adiponectin levels in vivo. Thus, we demonstrate here that TRIB1 protein is highly unstable in adipocytes due to rapid proteasomal degradation.

To better understand the molecular function of TRIB1 in adipose tissue and how it may be regulating adiponectin, we next investigated the previously reported functions of TRIB1 described in other models [13,31]. As a pseudokinase, TRIB1 lacks catalytic phosphorylation activity and is instead understood to function as a scaffolding protein that mediates the interactions between its binding partners [11]. In this

Figure 4: Trib1_ASKO mice have decreased plasma cholesterol and triglycerides. A,B, Plasma triglyceride (A) and total cholesterol (B) levels in 8–10-week-old, 4-h-fasted chow-fed male Trib1_fl/fl and Trib1_ASKO mice (n = 8). C, Plasma cholesterol FPLC profiles of pooled plasma (n = 4) from 4-h-fasted chow-fed male Trib1_fl/fl and Trib1_ASKO mice. D,E, Plasma triglyceride (D) and total cholesterol (E) levels in 4-h-fasted male Trib1_fl/fl; Ldr KO and Trib1_ASKO; Ldr KO mice (n = 9). H, Cholesterol FPLC profile of pooled plasma (n = 3) from 4-h-fasted chow-fed male Trib1_fl/fl; AdipoQ_Cre -/-. Data are presented as mean ± s.d. The significance in all the panels are determined by Student’s t test (*p < 0.05, **p < 0.01, ***p < 0.001).
regard, TRIB1 is best known for its role in the proteasomal degradation of the transcription factor C/EBPα via mediating its ubiquitination by the COP1 E3 ubiquitin ligase [31]. In keeping with that function, we found that C/EBPα protein levels were increased in the adipose tissue of Trib1_ASKO mice (Figure 3F) without observable changes in the Cebpa message levels (Figure 3G). Although C/EBPα is a known transcriptional regulator of adiponectin expression [32], we did not observe a consistent increase in adiponectin expression in either tissue or SVF-derived adipocytes (Figures 2C, 3A), suggesting TRIB1 regulates adiponectin through a mechanism independent of C/EBPα-mediated transcription.

Given TRIB1’s role in mediating the ubiquitination of proteins for proteasomal degradation, we further asked whether the proteasome was important in TRIB1’s regulation of C/EBPα and adiponectin. We treated Trib1_AS KO and Trib1_fl/fl SVF-derived adipocytes with MG132 to determine whether proteasomal inhibition would increase C/EBPα and adiponectin protein levels in the control cells but not the KO cells, abrogating the difference in the protein levels between the two. We found that proteasomal inhibition increased C/EBPα protein levels in Trib1_fl/fl adipocytes to levels similar to those observed in Trib1_ASKO adipocytes (Figure 3H), consistent with the known function of TRIB1 regulating C/EBPα degradation. However, MG132 treatment did not affect adiponectin secretion (Figure 3I) or protein levels (Figure 3H) in the control cells, which indicates that adiponectin levels are not subject to proteasomal regulation, ruling this out as the mechanism through which TRIB1 controls adiponectin levels.

3.4. Adipocyte-specific Trib1 knockout mice have decreased plasma lipids

Since the SNPs in the 8q24 locus significantly associate with both plasma adiponectin and plasma lipids (LDL-C, HDL-C, and TG), we next asked whether adipocyte Trib1 contributes to plasma lipid regulation. We found that Chow-fed Trib1_ASKO mice exhibit decreased plasma TG (>-28%) and TC (15%) levels compared with their wild-type counterparts (Figure 4A,B), demonstrating the role of adipocyte Trib1 in plasma lipid regulation. Given that the majority of cholesterol circulates in the HDL fraction in chow-fed C57BL/J mice, FPLC fractionation revealed that the reduced cholesterol in TRIB1_ASKO mice was reflected in the HDL fraction (Figure 4C). We note that the phenotype of decreased plasma lipids is the opposite direction of effect of the liver-specific knockout of Trib1, which results in increased plasma lipids [13], demonstrating opposing tissue-specific roles for TRIB1 in regulating plasma lipids. When placed on HFD for 12 weeks, Trib1_ASKO mice no longer exhibited a change in plasma TG compared with Trib1_fl/fl littermates (Figure 4D). However, Trib1_ASKO mice continued to demonstrate decreased cholesterol levels compared with Trib1_fl/fl mice (Figure 4E).

3.5. RNA-sequencing of adipocytes and hepatocytes reveals a primary role for adipose tissue in altered plasma lipid metabolism in Trib1_ASKO mice

To understand the mechanism by which adipocyte-specific Trib1 regulates plasma lipids, we sequenced RNA from adipocytes isolated from the scWAT of Trib1_fl/fl and Trib1_ASKO mice. Differential expression analysis revealed over 2000 genes that were differentially expressed at a greater than 2-fold change (Figure 5A), emphasizing a widespread role of TRIB1 in adipose tissue. We considered the possibility that altered hepatic metabolism could explain the phenotypes observed in Trib1_ASKO mice, given that the liver is a major regulator of lipoprotein metabolism and that adipokines such as adiponectin can signal to the liver [17]. However, RNA-seq of livers from the same mice revealed very few differentially expressed genes, none of which were major lipid regulators (Figure 5B, Table S1). Thus, we concluded that adipocyte TRIB1 is regulating plasma lipids through direct regulation by adipose tissue itself.

We next ranked differentially expressed genes by signal-to-noise ratio in expression and performed GSEA (Figure 5C). Notably, GSEA highlighted a striking enrichment of the mitochondrial genes among the upregulated genes, including genes coding for proteins in the electron transport chain, mitochondrial ribosomes, and the mitochondrial membrane, suggesting a potential role for mitochondria in the phenotypes we observed. Furthermore, multiple gene sets involved in lipid metabolism were upregulated, pointing toward the role of adipocyte-specific Trib1 in the regulation of lipids through lipid breakdown and metabolism (Dataset S1).

3.6. LPL activity is increased in Trib1_ASKO adipose tissue

Given the importance of adipocytes in TG storage, we next sought to identify the physiological mechanism whereby adipocyte-specific knockout of Trib1 results in reduced plasma TG levels. One mechanism through which adipose tissue contributes to plasma TGs is through the lipolysis of TGs in the lipid droplet and their release as free fatty acids into the bloodstream; subsequently, free fatty acids can be repackaged as TGs and secreted by the liver in the form of VLDL [33]. To assess the effect of Trib1 deletion in adipose tissue, we first measured plasma nonesterified free fatty acids (NEFA) and glycerol, markers of lipolysis, after stimulating lipolysis by fasting mice overnight for 16 h. We found that NEFA and glycerol levels were comparable between Trib1_ASKO and Trib1_fl/fl mice after prolonged fasting (Figure S7a,b), indicating that loss of adipocyte Trib1 does not impact lipolysis rates under stimulation. We also assessed the protein levels of adipose triglyceride lipase (ATGL), the rate-limiting enzyme of triglyceride lipolysis, and the activation of hormone sensitive lipase (HSL), a key lipolytic driver in adipose tissue that is activated by the phosphorylation of key residues [23]. We were unable to detect any differences in the abundance of ATGL or phospho-HSL in subcutaneous adipose tissue from Trib1_ASKO and Trib1_fl/fl mice (Figure S7c–e). Consistent with these observations, when we treated the mice with poloxamer 407 to inhibit peripheral lipolysis [34], we did not observe a difference in the accumulation of plasma triglycerides, indicating no change in hepatic triglyceride production in Trib1_ASKO mice (Figure S7f), indicating that the adipose tissue does not provide significantly different amounts of fatty acids to the liver.

Given the observed changes in plasma adipokine secretion and the importance of adipocyte endocrine functions, we next performed unbiased secretomics experiments to identify differentially secreted proteins from Trib1_ASKO adipose tissue. We incubated scWAT explant tissue from Trib1_fl/fl and Trib1_ASKO mice for 6 h in serum-free media and then identified and quantified the proteins in the
conditioned media via data independent acquisition (DIA) (Dataset S2). Consistent with our earlier findings of increased plasma adiponectin and resistin (Figure 2A,D), an increase in adiponectin (>50%) and resistin was found in the conditioned media from the ASKO tissue (Figure 6A), thus validating our secretomics data. Interestingly, we observed significantly decreased ANGPTL4 secretion from Trib1_ASKO scWAT explants (Figure 6A). ANGPTL4 is an inhibitor of LPL, which binds to the endothelium in capillaries and hydrolyzes TGs in circulating lipoproteins to free fatty acids, allowing for their uptake and clearance into tissues, including adipose tissue [35,36]. In addition to changes in secretion, Angptl4 expression was decreased and Lpl expression was increased significantly in our RNA-seq dataset. The expression of Lmf1, which codes for the lipase maturation factor and is important for the proper folding and secretion of LPL [37], was also notably increased in ASKO adipocytes (Figure 6B). Overall, these suggest increased LPL activity in ASKO adipose tissue. We next measured LPL activity in adipose tissue extracts from Trib1_fl/fl and Trib1_ASKO mice via the cleavage of a fluorescent lipid substrate and found that adipose tissue extracts from both scWAT and gWAT from Trib1_ASKO mice demonstrated increased lipase activity (Figure 6C,D), likely contributing to increased TG clearance in Trib1_ASKO mice. As BAT LPL activity is also a critical regulator of metabolism, we measured both LPL activity and Lpl and Angptl4 gene expression in Trib1_fl/fl and Trib1_ASKO BAT. We observed no changes in LPL activity between mouse groups nor did we observe changes in the gene expression of most key BAT genes (Figure S8a,b).

4. DISCUSSION

GWAS have identified SNPs near the TRIB1 gene that are significantly associated with plasma lipids, liver enzymes, plasma adiponectin, HbA1c, and CAD [1—6,8,9,15]. Previous studies focusing on hepatic and myeloid TRIB1 have shown various tissue-specific beneficial and detrimental roles of TRIB1 in plasma lipid regulation and CAD as well as in hepatic lipogenesis [12—14]. Here, we report the first adipocyte-specific deletion of Trib1 in mice and provide the first in vivo validation of the association between Trib1 and adiponectin. In addition, Trib1_ASKO mice exhibit a beneficial metabolic profile that includes

Figure 5: Trib1_ASKO adipocytes have widespread transcriptional changes in mitochondrial and lipid metabolism pathways. A, Volcano plot of DESeq2 analysis of RNA-seq data from adipocytes isolated from scWAT from Trib1_fl/fl and Trib1_ASKO mice (n = 4). B, Volcano plot of DESeq2 analysis of RNA-seq data from hepatocytes from Trib1_fl/fl and Trib1_ASKO mice (n = 4). C, Cytoscape enrichment plot of gene set enrichment analysis (GSEA) of differentially expressed adipocyte genes (padj < 0.05). Enrichment analysis and clustering were performed as described in the Methods section. Clusters upregulated in the Trib1_ASKO samples are shown in red, and clusters upregulated in the Trib1_fl/fl samples are shown in blue. Dashed blue outlines indicate larger clusters that were further subclustered manually to facilitate interpretation. NES = normalized enrichment score.

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Glucose tolerance compared with Trib1_\text{fl/fl} HFD-fed ASKO mice have reduced plasma insulin and improved [21]. Thus, mechanisms that increase endogenous adiponectin may be challenging due to the complex multimeric structure of adiponectin [41,42]. We found that adiponectin has therapeutic potential in the treatment of metabolic disease.

Plasma adiponectin levels are associated with improved metabolic health in both humans [16,18] and mice [38,39], and although studies using recombinant adiponectin in mice have been promising [40], they are challenging due to the complex multimeric structure of adiponectin [21]. Thus, mechanisms that increase endogenous adiponectin may be a more viable approach. Here, we show that inhibiting TRIB1 in adipocytes results in a robust increase (up to 40%) in circulating adiponectin, improved glucose tolerance, reduced plasma TGs and cholesterol observed in Trib1_\text{ASKO} mice is contrary to the finding in previously reported liver-specific knockout mice, which exhibited increased plasma TC and TG [13]. These in vivo findings demonstrate that a reduction of adipocyte TRIB1 has therapeutic potential in the treatment of metabolic disease.

Figure 6: Trib1_\text{ASKO} mice exhibit increased adipose tissue lipoprotein lipase activity. A, DIA secretomics data of conditioned media from Trib1_\text{ASKO} vs. Trib1_\text{fl/fl} scWAT explants (n = 3). Differential secretion was determined by Spectronaut analysis, and the results were filtered for secreted proteins (Uniprot keywords). Size and color of datapoints are for facilitating visualization. B, DESSeq2 results for Lpl, Angptl4, and Lmf1 from RNA-seq of Trib1_\text{fl/fl} and Trib1_\text{ASKO} adipocytes. C, D. Lpl activity in scWAT (C) and gWAT (D) from Trib1_\text{fl/fl} and Trib1_\text{ASKO} mice (n = 5). Data are presented as mean ± s.d. Significance in C,D is determined by Student’s t test (*p < 0.05).

The 8q24 SNPs are associated most strongly with plasma TG in humans [1,2,10]. White adipose tissue is a major contributor to plasma TG regulation due to its ability to clear circulating TGs through LPL or to output FFAs through lipolysis. While chow-fed ASKO mice did not demonstrate changes in the markers of lipolysis, adipose explant secretomics and gene expression profiling revealed increased LPL and decreased ANGPTL4 production in their adipose tissue, and this was accompanied by increased adipose tissue LPL activity in Trib1_\text{ASKO} mice. Trib1_\text{ASKO} mice also exhibit decreased plasma TG levels, consistent with observations in humans where loss-of-function variants in endogenous inhibitors of LPL such as ANGPTL4, ANGPTL3, and APOC3 are found to be associated with reduced plasma TGs as well as with reduced CAD [43–45]. ANGPTL4 has additionally been found to be positively associated with other markers of the metabolic syndrome (MetS), including BMI, fasting glucose, and insulin levels [46]. Thus, in addition to regulating plasma TGs, increased LPL activity and decreased ANGPTL4 production may regulate several aspects of metabolic health in ASKO mice.

We also found that Trib1_\text{ASKO} mice exhibit decreased plasma TC and LDL-C levels. There is precedent that the observed increase in LPL activity in the Trib1_\text{ASKO} mice drives the decrease in plasma cholesterol, as multiple studies using transgenic Lpl animal models [47–49] or Angptl4 knockout or transgenic mice [50,51] demonstrate that increased LPL activity protects from diet-induced hypercholesterolemia and decreases plasma LDL-C levels. Mechanistically, lipolysis-mediated reductions of TGs in VLDL particles have been proposed to facilitate enhanced clearance of the resulting remnant particles via receptors such as the LDLR [52,53]. While further studies are needed to determine whether increased LPL activity is responsible for the reduced plasma lipids in Trib1_\text{ASKO} mice, regulation of LPL activity by adipocyte-specific TRIB1 is a novel finding that deepens our understanding of the mechanisms by which TRIB1 can contribute to dyslipidemia as suggested by GWAS. These findings also raise the question that through which tissue Trib1 predominantly affects plasma lipid metabolism. This could be tested in animal models through the deletion of Trib1 in both hepatocytes and adipocytes in the same animal. However, to answer this question in humans, the understanding of which tissue the GWAS SNPs are functionally relevant in is required, a critical knowledge gap in the field that warrants further attention.

Given the established role of LPL in hydrolyzing circulating triglycerides and allowing for their clearance from circulation into nearby tissues [54], increased LPL activity would be expected to drive increased uptake of plasma TGs into adipocytes in Trib1_\text{ASKO} mice. Interestingly, previously reported adipocyte-specific LPL transgenic mice do not display changes in adiposity [49,55], indicating that there are compensatory mechanisms to maintain body weight. Similarly, we did not observe changes in body weight or adiposity in Trib1_\text{ASKO} mice despite increased LPL activity. GSEA of our RNA-seq data revealed the
upregulation of genes encoding mitochondrial components, suggestive of increased mitochondrial activity. Notably, the expression of the mitochondrial protein, Ucp1, was unchanged in Trib1_ASKO based on our RNA-seq data, implying that no WAT browning is occurring. A resulting increase in energy expenditure could potentially explain the lack of an adipocyte size phenotype in Trib1_ASKO mice despite increased adipose tissue LPL activity and presumed fatty acid uptake.

Given that adiponectin has many well-studied roles in regulating cardiometabolic traits, including lipid metabolism and coronary artery disease [18,20], an important outstanding question is whether increased adiponectin also contributes to, and perhaps drive, the lipid phenotypes observed in the Trib1_ASKO mice. Experimental evidence indicate that adiponectin plays a role in TG metabolism, as plasma adiponectin correlates with decreased plasma Tgs and large VLDL levels and with increased HDL-C in humans [56]. Additionally, adiponectin transgenic mice with 3-fold increased plasma adiponectin levels have increased LPL expression and activity in adipose tissue as well as increased TG clearance [38]. Thus, although the adiponectin phenotype in Trib1_ASKO mice is mild (~20–40% increase) compared with transgenic mouse models, it is possible that the increased adipose tissue LPL activity we observe in Trib1_ASKO mice is secondary to the increased adiponectin levels. The role of adiponectin in plasma cholesterol regulation is less clear. One previous report using transgenic mice with 10-fold increased adiponectin levels found decreased cholesterol in those mice [57]. In humans, epidemiological studies looking at associations between adiponectin and plasma LDL-cholesterol are conflicting or inconclusive [18]. Further studies are required to determine whether the adiponectin phenotype is required for the observed changes in Trib1_ASKO plasma lipids.

TRIB1 is one of three mammalian homologs of the Tribbles pseudokinase, which was first discovered in Drosophila [11]. These proteins bear homology to serine/threonine kinases, but lack the key catalytic residues that render them unable to catalyze phosphorylation. Instead, they are best understood to function as scaffold proteins that bring other proteins into proximity with each other to mediate signaling events [11]. One of the best understood molecular functions for TRIB1 is its role in mediating the ubiquitination and degradation of the transcription factor C/EBPα by bringing it into proximity of the COP1 E3 ubiquitin ligase. Tribbles-mediated regulation of C/EBPα protein levels has been shown to be an important function in several models, including as a causal mechanism for the hepatic lipogenesis phenotype in Trib1 liver-specific knockout mice [13], for myeloid cell proliferation in the context of leukemia [31], and in oogenesis in drosophila [58]. We report here that Trib1_ASKO adipocytes also exhibit increased C/EBPα protein levels in the absence of any change in gene expression, and that C/EBPα protein levels are normalized between control and Trib1_ASKO SVF-derived adipocytes under conditions of proteasomal inhibition. Thus, it appears that adipocyte Trib1α also regulates C/EBPα through proteasomal degradation. Given the important role of C/EBPα in metabolism and adipocyte differentiation [59], we consider its potential role in the phenotype of the Trib1_ASKO mice. Notably, C/EBPα regulates genes involved in lipid metabolism in adipose tissue and is a known transcriptional regulator of Lpl [60,61]. Polymorphisms in C/EBPα have also been found to be associated with plasma TG levels in humans [61]. It is thus possible that increased C/EBPα protein levels in Trib1_ASKO adipose may contribute to the plasma lipid phenotype. C/EBPα is also a known transcriptional regulator of adiponectin [32]. While we have not observed an increase in Adipoq gene expression via repeated qPCR measurements in whole adipose tissue, we note that Adipoq expression was modestly increased in Trib1_ASKO adipocytes in our RNA-seq dataset (padj = 0.011, fold change = 1.33). This raises the possibility that increased protein levels of C/EBPα (or a different unknown transcription factor) is driving a small increase in Adipoq gene expression that qPCR is not sensitive enough to reliably measure. However, while MG132 treatment of SVF-derived adipocytes increases C/EBPα protein levels, it actually decreases the secretion of adiponectin in wild-type SVF-derived adipocytes (Figure S3). Thus, while TRIB1 certainly appears to regulate C/EBPα in adipose tissue, we propose that this is a separate mechanism from the one governing the Trib1 regulation of adiponectin. One possibility, given the increase in intracellular adiponectin in the absence of increased mRNA or decreased protein degradation, is that Trib1 is regulating the translation of adiponectin, a hypothesis we are currently pursuing among others.

Although C/EBPα is a critical regulator of adipocyte differentiation, we did not observe any differences in adiposity or adipose tissue morphology in Trib1_ASKO mice despite the perturbed C/EBPα protein levels. This could be a result of the Adipoq promoter-driven Cre, which is induced late in the process of adipocyte differentiation, thus making our mouse model a post-differentiation knockout of adipocyte TRIB1. A previous report showed that Trib1 overexpression can inhibit the differentiation of 3T3-L1 cells [62], providing a precedent for the role of Trib1 in adipogenesis. Further studies utilizing a different Cre transgene would be required to determine whether Trib1 plays a similar role in regulating adipogenesis in vivo.

5. CONCLUSIONS

In summary, homeostatic control by adipose tissue is crucial to metabolic health, and our study provides evidence that TRIB1 is an important regulator of major adipocyte functions, including the secretion of adiponectin and plasma lipid regulation through LPL. Overall, our studies show that adipocyte-specific Trib1 is a negative regulator of adiponectin secretion and this appears to be independent of the known function of TRIB1 in promoting proteasomal degradation of C/EBPα. Furthermore, we show that adipocyte-specific Trib1 regulates plasma lipids in a direction opposite to that of the previously studied liver-specific knockout model and the regulation of TG clearance via adipose tissue LPL in part explains the decreased plasma TG levels in ASKO mice. In contrast to the findings reported for hepatic Trib1, these data suggest a therapeutically beneficial effect of reduced adipocyte TRIB1 activity in improving multiple aspects of metabolic health and underscore the continued importance of further studies on TRIB1 and the 8q24 GWAS locus.

AUTHOR CONTRIBUTIONS

R.C.B conceived the project, designed the experiments, supervised the analyses, and edited the manuscript. E.E.H. performed the majority of the experiments and data analysis, wrote the first draft of the manuscript, and edited the subsequent versions. G.I.O helped establish the mouse colony, assisted with SVF isolation, and performed the related molecular biology experiments (i.e. cloning, western blots). R.L. performed western blotting for lipolysis proteins and ELISA analysis. C.X. performed the DESeq2 analysis of the RNA-seq data. A.H. performed the initial FPLC analysis and assisted with all FPLC analyses. K.Y.H performed Western blotting in stable 3T3-L1s and also measured plasma lipids and gene expression in the transgenic mice. C.V.M performed SVF isolation and qPCR work related to the resubmission. R.L. performed the DESeq2 analysis of the RNA-seq data. A.H. performed the initial FPLC analysis and assisted with all FPLC analyses. K.Y.H performed Western blotting in stable 3T3-L1s and also measured plasma lipids and gene expression in the transgenic mice. C.V.M performed SVF isolation and qPCR work related to the resubmission. R.L. performed Western blotting in stable 3T3-L1s and also measured plasma lipids and gene expression in the transgenic mice. C.V.M performed SVF isolation and qPCR work related to the resubmission. R.L. performed Western blotting in stable 3T3-L1s and also measured plasma lipids and gene expression in the transgenic mice. C.V.M performed SVF isolation and qPCR work related to the resubmission. R.L. performed Western blotting in stable 3T3-L1s and also measured plasma lipids and gene expression in the transgenic mice. C.V.M performed SVF isolation and qPCR work related to the resubmission.
A.G. designed the transgenic Trib1 mouse and oversaw all the experimental procedures. S.H. and N.S.P. developed the transgenic Trib1 mouse line, while R.A.K executed the phenotyping of the Trib1 transgenic mice. R.K.S. performed and analyzed the secretomics MS experiment. All the authors read and approved the manuscript.

DATA AVAILABILITY STATEMENT

RNA-seq data will be available from GEO (GSE168596) prior to publication. The full list of the identified proteins and differentially secreted proteins from DIA secretomics (Figure 6A) are available in Dataset S2. Other data that support the findings of this study are available from the corresponding author upon reasonable request.

ACKNOWLEDGMENTS

These studies were funded by R01HL141745 (R.C.B) from the National Heart, Lung, and Blood Institute (NHLB), Scientific Development Grant 16DSG1180039 (R.C.B) from the American Heart Association, AMPro funding ZT-0026 (S.H.) from the European Union’s Horizon 2020 Marie Skłodowska-Curie Innovative Training Network, TRAIN (project no. 721532) (A.G., N.S.P, S.H, and R.A.K.). In addition, E.E.H. was supported by a Predoctoral F30 NRSA (F30HL146676-01A1) from the NHLB, and K.Y.H. was supported by an institutional T32 (T32DK007326-41A1) from the NIDDK. A.G and R.A.K were supported with predoctoral funds by the International Helmholtz Research School for Diabetes (Graduate Students call 41A1) from the NIDDK, and A.G and R.A.K were supported with predoctoral funds by the European Union’s Horizon 2020 Marie Skłodowska-Curie Innovative Training Network, TRAIN (project no. 721532) (A.G., N.S.P, S.H, and R.A.K.).

CONFLICT OF INTEREST

The authors declare no conflict of interest.

APPENDIX A. SUPPLEMENTARY DATA

Supplementary data to this article can be found online at https://doi.org/10.1016/j.molmet.2021.101412.

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