Diet and temperature interactively impact brown adipose tissue gene regulation controlled by DNA methylation

Tobias Hagemann[1,*], Anne Hoffmann[1,*], Kerstin Rohde-Zimmermann[1,*], Helen Broghammer[1], Lucas Massier[1,2], Peter Kovacs[3], Michael Stumvoll[1,3], Matthias Blüher[1,3], John T. Heiker[1,3,*, §] & Juliane Weiner[1,3,*, §]

[1]Helmholtz Institute for Metabolic, Obesity and Vascular Research (HI-MAG) of the Helmholtz Zentrum München at the University of Leipzig and University Hospital Leipzig, Leipzig, Germany
[2]Department of Medicine H7, Karolinska Institute, Stockholm, Sweden
[3]Leipzig University Medical Center, Divisions of Endocrinology and Nephrology, University of Leipzig, Leipzig, Germany

*These authors contribute equally

[§]**Corresponding authors:**
Juliane Weiner
[2]Leipzig University Medical Center, Divisions of Endocrinology and Nephrology, University of Leipzig, Leipzig, Germany,
Liebigstr. 21, D-04103 Leipzig, Germany
Email: Juliane.Weiner@medizin.uni-leipzig.de
Phone: +49-341-97 20919

John T. Heiker
Helmholtz Institute for Metabolic, Obesity and Vascular Research (HI-MAG)
Helmholtz Zentrum München at the University of Leipzig and University Hospital Leipzig
Philipp-Rosenthal-Straße 27, D-04103 Leipzig, Germany
Email: John.Heiker@helmholtz-munich.de
Phone: +49-341-97 22909

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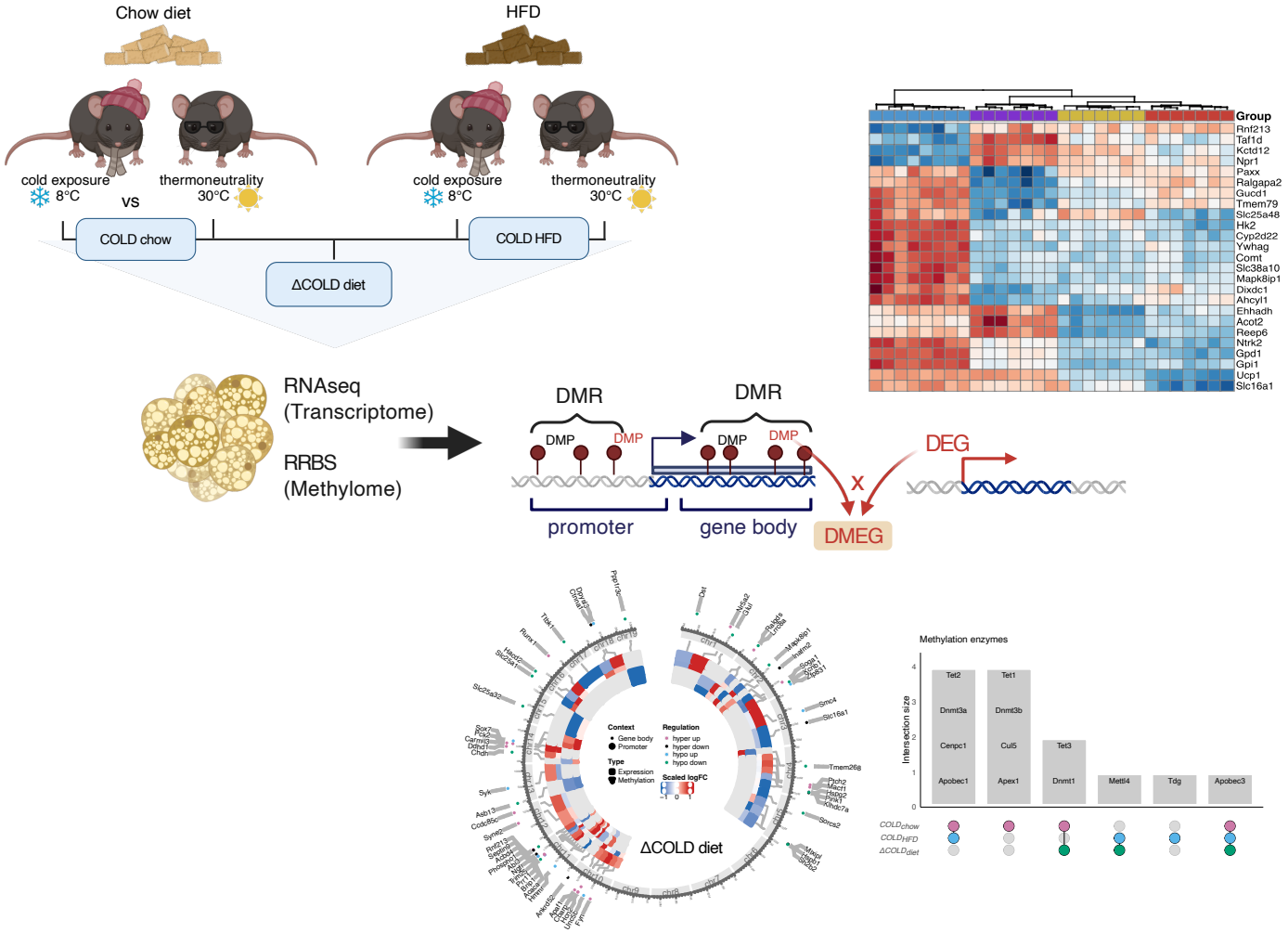
Abbreviations: Aza: 5'aza-2'-deoxycytidine (Aza), BAT: Brown adipose tissue, BH: Bonferroni-Holm, DEG: differentially expressed gene, DGE: differential gene expression, DMEG: Differentially methylated and expressed gene, DMP: differentially methylated positions, DMR: differentially methylated regions, eWAT: epididymal white adipose tissue, FC: fold change, FDR: false discovery rate, HFD: high-fat diet, imBA: immortalized brown adipocytes, iWAT: white adipose tissue, PCA: principal component analysis, qPCR: quantitative real-time-PCR, RNAseq: RNA sequencing, RRBS: reduced representation bisulfite sequencing, SAM: S-adenosylmethionine, SVF: stromal vascular fraction, VST: variance stabilization transformation

Abstract

Controlling brown adipose tissue (BAT) plasticity in adulthood holds promising potential for effective new obesity therapies by targeting the mechanisms of adaptive thermogenesis. Recent studies have shown that BAT development and function are under epigenetic control, with DNA methylation linked to the regulation of key thermogenic and metabolic genes. Here we sought to understand how diet and cold exposure interactively shape BAT gene regulation controlled by DNA methylation. Mice (N = 8 per group) were housed under cold exposure (8°C) or thermoneutrality (30°C) and fed either chow or high-fat diet (HFD). BAT was isolated for transcriptome (RNAseq) and methylome (RRBS) analyses. We identified differentially methylated and expressed genes (DMEGs) by comparing the effects of cold exposure under chow and high-fat diet, as well as by analyzing the interaction between temperature and diet. Functional pathway enrichment and EpiFactors Database screening were used to assess epigenetic regulators, and candidate gene expression was validated by modulating DNA-methylation in vitro.

We identified ~1,360 differentially expressed genes (DEGs) uniquely affected by the diet-temperature interaction with most downregulated in HFD-fed mice, indicating that obesity limits the transcriptional response of BAT to cold. 65 DMEGs (4% of DEGs) were largely diet-specific in response to cold exposure, suggesting that DNA methylation contributes to a selective layer of gene regulation during BAT adaptation to distinct metabolic states. In HFD-fed mice, DMEGs were enriched in pathways related to mitochondrial dysfunction, altered lipid metabolism, neuroendocrine signaling, and compensatory stress responses, contrasting the adaptive thermogenic profile observed in chow-fed controls. Differentially expressed genes of epigenetic regulators such as *Tet2*, *Dnmt3a* and *Apobec1* showed diet- and cold-dependent regulation, indicating impaired methylation flexibility under obesogenic conditions. Using cell culture experiments, we confirmed the regulation of gene expression of candidate genes, validating the functional link between DNA methylation and thermogenic gene regulation. This is the first study to demonstrate an epigenetic response to cold exposure that differs by dietary condition, particularly in obesity. Our findings highlight a coordinated transcriptional and epigenetic remodeling of BAT, shaped by both environmental and metabolic signals. These insights may inform targeted epigenetic or nutritional strategies to restore BAT function and would further strengthen our understanding of how these might be used as therapeutic basis to improve metabolic health in obesity.

Graphical abstract



Mice were housed under cold exposure or thermoneutrality and fed either chow or high-fat diet (HFD). RNA sequencing (RNAseq) and reduced representation bisulfite sequencing (RRBS) was performed on brown adipose tissue (BAT) which provide the fundament for the identification of differentially methylated positions (DMP) and regions (DMR) as well as differentially expressed genes (DEG) in three models: $COLD_{chow}$, comparing 8° vs 30°C mice on chow diet; $COLD_{HFD}$, comparing 8° vs 30°C mice on HFD diet and $\Delta COLD_{diet}$, comparing $COLD_{chow}$ vs $COLD_{HFD}$. Differentially methylated and expressed genes (DMEGs; circos plot shows a representative example) were identified for all comparisons based on those DMPs which correlated significantly with differentially expressed genes (DEGs; the heatmap shows a representative example). DMEGs were taken forward for pathways enrichment analyses and to identify differentially regulated epigenetic regulators using the EpiFactors Database. The figure was created with BioRender.

1. Introduction

Brown adipose tissue (BAT) is a specialized fat tissue that is rich in mitochondria and promotes non-shivering thermogenesis by expressing the *uncoupling protein 1 (UCP1).* Unlike white adipose tissue, it burns calories to produce heat and therefore plays a key role in energy regulation and controlling metabolic health. Increasing energy expenditure by BAT activation is an intriguing therapeutic approach to combat the overwhelming obesity pandemic, either alone or to complement the current pharmacotherapy that mainly addresses energy intake based on the incretin-mimetic poly-agonist class of drugs [1]. With this in mind it is not surprising that a lot of research was conducted to understand the molecular underpinnings of BAT regulation specifically addressing environmental cues. Cold exposure is the most powerful inducer of BAT activation leading to the upregulation of thermogenic gene program and adrenergic receptor-mediated activation of lipolysis and metabolism. BAT activation also occurs post-prandially, especially after acute overfeeding, to trigger diet-induced thermogenesis [2,3]. However, this compensatory component of energy-expenditure is impaired during chronic overfeeding, a phenomenon that was termed adaptive thermogenesis, and is believed to further drive weight gain and obesity [2,4,5].

In any case the mechanistical switch enabling the high plasticity of BAT changing from passive thermoneutral to active thermogenic states may be regulated by epigenetic mechanisms that are affected by, e.g. temperature and diet [6]. Indeed, studies have shown changes in DNA methylation for key BAT regulatory genes such as *Ucp1, PR domain containing 16* (*Prdm16*) or *PPARG coactivator 1 alpha* (*Ppargc1a*) , altering their expression level and impacting BAT function [7,8]. Moreover, during the development of precursor cells into major brown adipocytes, DNA methylation patterns change and lineage commitment towards a thermogenic adipocyte is epigenetically controlled [8]. The major relevance of the ambient temperature in this context has just recently been implied, as cold exposure of parents at conception is related to increased brown adipogenesis and thermogenesis along with reduced obesity risk in the offspring [9]. Mechanistically, sperm DNA methylation is altered in response to cold exposure which leads to adaptations in BAT activity of the offspring [10,11]. In addition, DNA methylation in key genes of thermogenesis and fatty acid oxidation, such as *acetyl-CoA acyltransferase 2* (*Acaa2*) and *acyl-CoA synthetase long chain family member 1* (*Acsl1*), is increased in BAT of offsprings from mice fed a high fat diet [12]. These studies strongly imply the relevance of cold, diet and obesity on the transgenerational modulation of BAT function. However, these environmental cues, either alone or in combination, also trigger and control BAT plasticity during adulthood. Rats with a blockade in afferent vagal nerve signaling that triggered by high-fat diet showed a reduced BAT activation after cold exposure [13]. The relevance of diet for regulating DNA methylation in later life comes with nutritional compounds such as folate or methionine as critical components of the one-carbon metabolism, which are classically enriched in vegetable-rich diets but diminished in high fat diets.

However, the interaction of especially cold exposure and high fat diet on BAT's epigenetic machinery is less understood. In this study, we aimed to address DNA methylation alterations in response to temperature and diet, and link this to changes in gene expression of BAT in mice on a

genome-wide level. We explored the interactive impact of diet and cold exposure on the epigenetic regulation of BAT gene expression. Using a stringent bioinformatic workflow we focused on differentially methylated and expressed genes (DMEGs) by taking forward only candidates whose differential methylation signal correlates to the gene expression level in order to provide only top functional relevant candidates. Providing a profound overview over the impact of DNA methylation on genes expression affected by cold and diet is of strong relevance to understand adult BAT plasticity and adaptive thermogenesis and provides the fundament for new obesity treatment strategies.

2. Material and methods

2.1. Animal studies

Male C57BL/6NTac mice (Taconic Bioscience, Lille Skensved, Denmark) were housed in pathogen-free facilities at 23°C on a 12h light/dark cycle at the Sächsische Inkubator für Klinische Translation (SIKT), Leipzig. Starting from five weeks of age, mice were either fed a standard chow diet (EV153, 3.3% from fat, Ssniff, Soest, Germany) or a high fat diet (HFD, E15742, 60 kJ% from fat, Ssniff) with ad libitum access to food and water. At 11 (chow) or 22 (HFD) weeks of age, mice were adapted to single housing in rodent climate chambers (MKKL1200, Flohr Instruments, Netherlands) for 5 days, before randomization into four groups (each N = 8 mice) and housed either at thermoneutrality (30°C) or in the cold (8°C) for 7 days. After a 4-hour fasting period, body weight and rectal temperature were measured. BAT and tail surface temperatures were measured by thermal imaging (VarioCAM®, InfraTec, Dresden, Germany). Mice were sacrificed and tissue samples of intrascapular brown adipose tissue (BAT) were collected, snap frozen in liquid nitrogen and stored at -80°C before further analyses. All animal experiments were approved by the local authorities of the Free State of Saxony, Germany (Landesdirektion Leipzig: TVV51/20), as recommended by the responsible local animal ethics review board.

2.2. RNA sequencing of brown adipose tissue

RNA from BAT was isolated using RNeasy Lipid Tissue Mini kit (Qiagen, Hilden, Germany) as specified by the manufacturer. RNA sequencing (RNAseq) was performed by the core unit DNA-Technologien, Medical Faculty Leipzig. 50ng of total RNA were depleted of ribosomal RNA using the NEBNext rRNA Depletion Kit v2 (NEB, USA) according to the manufacturer's instructions. Depleted RNA was transcribed using SuperScript IV reverse transcriptase (ThermoFisher Scientific, USA) for 2h at 55°C. After second strand synthesis (TargetAmp kit, EPICENTRE, USA), the DNA was fragmented using the Illumina Tagment DNA TDE1 Enzyme and Buffer Kits, which fragments DNA and inserts partial sequencing adapter sequences. Final PCR amplification of the libraries was done using KAPA HiFi HotStart Library Amplification Kit with unique dual indexing by IDT for Illumina Nextera DNA Unique Dual Indexes Sets. The barcoded libraries were purified and quantified using Qubit Fluorometric Quantification (ThermoFisher Scientific, USA). Size distribution of the library DNA was analyzed using the FragmentAnalyzer (Agilent,

USA). Sequencing of 2x150 bp was performed with NovaSeq sequencer (Illumina, USA) according to the manufacturer's instructions, with a read depth of 20 million reads per sample.

2.3. Reduced representation bisulfite sequencing in brown adipose tissue

Genomic DNA from BAT samples were isolated using the DNeasy blood and tissue kit according to the manufacturer's instructions (Qiagen, Hilden, Germany). Reduced representation bisulfite sequencing (RRBS) library preparation was performed on 100 ng DNA using the Zymo-Seq RRBS Library Kit (Zymo Research, Freiburg, Germany) by the core unit DNA-Technologien, Medical Faculty Leipzig. Briefly, DNA was digested with 20U/µl MspI for 4h followed by RRBS adapter ligation using 400U/µl T4 DNA ligase and gap filling with 2U/µl Taq DNA polymerase and 10mM 5-methylcytosine dNTP Mix. Bisulfite conversion was performed with lightning conversion reagent, and the final samples were amplified using 5µM of the unique dual index Primer Set (indexes 1-12) supplied by the manufacturer. Quality control was performed on the Bioanalyzer (Illumina, USA) prior paired-end sequencing on the NovaSeq6000 platform (Illumina, USA) were 20 million reads per sample were obtained.

2.4. RNAseq data preprocessing

Raw RNAseq reads where quality-filtered and adapter-trimmed using Trimmomatic (v0.39) [14], discarding reads shorter than 36 bp. Afterwards, reads were aligned to GRCm38.p6 reference assembly using STAR (v2.7.8a) [15], allowing for a maximum of 50 multi-mapped reads. Gene counts were quantified with featureCounts from the subread software package (v2.0.1) [16] with multimappings counted by fractions.

2.5. Differential gene expression analysis

Transcripts without gene annotation and genes with a total count sum <10 were removed resulting in 18k genes for subsequent gene expression analysis. Variance stabilization transformation (VST) was applied to the filtered gene count matrix using the R package DESeq2 (v1.42.1) [17]. A principal component analysis (PCA) was conducted to verify clustering of diet (HFD, chow) and temperature (8°C, 30°C) groups within the gene expression signals. Three samples were identified as outliers which did not cluster in their respective group according to the first two principal components and were subsequently removed from the analysis. This resulted in group sizes of 7-8 mice reflecting all diet-temperature combinations ($N_{total} = 29$; $N_{HFD_30°C} = 7$; $N_{HFD_8°C} = 7$; $N_{chow_30°C} = 7$; $N_{chow_8°C} = 8$). Afterwards, differential gene expression (DGE) analysis was performed with DESeq2. Three comparisons were conducted: chow-fed mice at 8°C versus those at 30°C ($COLD_{chow}$), HFD-fed mice at 8°C versus those at 30°C ($COLD_{HFD}$), and an interaction model comparing $COLD_{HFD}$ versus $COLD_{chow}$ contrasts ($\Delta COLD_{diet}$). DEGs with a false discovery rate (FDR) < 0.05 were considered statistically significant. DEG lists from each contrast where subsequently matched with entries in the EpiFactors Database (v2.0, https://epifactors.autosome.org, accessed on 10.09.2024) to investigate diet-specific methylation regulators.

209 2.6. RBBS data processing

210 Raw RRBS reads from N = 29 mice ($N_{HFD_30°C}$ = 7; $N_{HFD_8°C}$ = 7; $N_{chow_30°C}$ = 7; $N_{chow_8°C}$ = 8) were
211 processed with the nextflow (v 23.04.3) [18] pipeline nf-core/methylseq (v2.4.0) [19] using the
212 parameters *--genome GRCm38 --non_directional --rrbs --skip_deduplication* and --
213 *cytosine_report*. In brief, quality filtering and adapter trimming of raw RRBS fastq files was
214 conducted with trimgalore (v0.6.7) [20] before running sequence alignments with Bismark
215 (v0.24.0) [21]. Afterwards, methylation signals are called with the Bismark methylation extractor
216 script including the build-in *coverage2cytosine* module for a genome-wide cytosine methylation
217 report which served as input for downstream analysis. Sex chromosomes were excluded.

218 2.7. Differential methylation analysis

219 To identify differentially methylated positions (DMPs) and differentially methylated regions
220 (DMRs), differential methylation analysis was conducted for $COLD_{chow}$, $COLD_{HFD}$, and
221 $\Delta COLD_{diet}$, utilizing beta values and the R packages limma (v3.54.0) [22] and RnBeads (v2.16.0)
222 [23] with parameters filtering.low.coverage.masking = TRUE, filtering.high.coverage.outliers =
223 TRUE and filtering.snp = "any". Based on their chromosomal position and respective annotation,
224 individual methylations can be contextualized within gene bodies or promoter regions (1500 bases
225 upstream and 500 bases downstream of the transcription start site), both of which were considered
226 in our analysis.

227 2.8. Integration of methylation and transcriptome data

228 After differential analysis of individual omics data, both gene expression and methylation signals
229 were combined to find biological associative effects between transcriptomics and epigenomics.
230 The R package biomaRt (v2.58.2) [24] was used to gather gene loci information for differentially
231 expressed genes (DEGs) and DMRs in gene and promotor context. Beta methylation values were
232 transformed to M-values using RnBeads. For each DEG, the corresponding DMR was selected
233 based on the alignment of gene IDs. M-values of all significantly DMPs overlapping with the DMR
234 were considered using the bedR (v1.0.7) [25] and the GenomicRanges (v1.54.1) [26] R packages.
235 Pearson correlation was then applied to find associations between DEG expression values and M-
236 values of each intersecting DMP using the multtest.cor function from RVAideMemoire (v0.9-83-
237 7) [27]. All DMPs with significant absolute Pearson correlations >0.5 between expression and
238 methylation signal ($p < 0.05$ without adjustment for multiple testing) were defined as differentially
239 methylated and expressed genes (DMEGs). If a DMEG is associated to both promoter and gene
240 body region, it was assigned to the DMR with the highest significance. This step was parallelized
241 with the foreach package (v1.5.2) [28]. The final list of DMEGs is comprised of genes with
242 significantly regulated expression signal (absolute $\log_2$ fold change (FC) >0.5) and methylation
243 signal (absolute $\log_2$ FC >1). Since several DMRs or DMPs can be differentially methylated within
244 a gene, several DMEGs were generated for such genes.

245 Subsequently, functional analysis of DMEGs was done with the use of QIAGEN Ingenuity
246 Pathway Analysis software (QIAGEN Inc., https://digitalinsights.qiagen.com/IPA, Winter Release
247 Q4 2024) [29] covering the catalog for disease and bio functions and canonical pathways. The
248 database query was limited within the IPA software to relationships with adipose tissue or
249 adipocytes in mice that are experimentally observed. Enrichments are reported with p after
250 Bonferroni-Holm (BH) adjustment and activation z-scores. Enrichments with BH corrected $p < 0.05$
251 are considered significant.

252 2.9. In vitro validation experiments

253 2.9.1. Immortalized and primary brown adipocytes

254 Immortalized (imBA [30]) and primary brown adipocytes were cultured and differentiated as
255 previously described [31]. At day 10, cells were harvested and subjected to further analyses.

256 2.9.2. In vitro manipulation of cellular DNA methylation levels

257 To analyze the effect of DNA methylation status on gene expression in imBA and primary brown
258 adipocytes, pre-adipocytes were treated with indicated concentrations of 5'aza-2'-deoxycytidine
259 (Aza) for 48h and subsequently differentiated [31]. Differentiated adipocytes at day 6 were treated
260 with indicated concentrations of S-adenosylmethionine (SAM, New England Biolabs) for 48h.
261 Differentiated adipocytes were harvested and subjected to further analysis.

262 2.9.3. Quantitative real-time-PCR (qPCR)

263 RNA from imBA and human primary SAT cells was isolated using RNeasy Lipid Tissue Mini kit.
264 qPCR was performed using the LightCycler System LC480 and LightCycler-DNA Master SYBR
265 Green I Kit (Roche, Mannheim, Germany). Adipocyte gene expression of candidate genes was
266 calculated by ΔΔCT method and normalized to *Nono* or *36b4* levels as indicated. Primer sequences
267 are listed in (Suppl. Table 1).

268 2.10. Statistical analysis

269 Analyses were performed under R version 4.3.2, except for mouse phenotyping data that was
270 analyzed using GraphPad Prism 10 (GraphPad, San Diego, CA, USA). Statistical tests are stated
271 in the figure legends. If not stated otherwise, adj. $p < 0.05$ were considered statistically significant.

272

3. Results

3.1. Phenotyping of chow and high fat diet-fed mice held at thermoneutrality or exposed to cold

Groups of 8 mice per diet were held at thermoneutrality (30°C) or in the cold (8°C) for 7 days (Figure 1A). Before the temperature challenge, mice were held at 23°C with HFD-fed mice presenting significantly higher body weights than chow fed mice (48.2 g vs 28.3 g, Figure 1B). In the cold, mice on chow diet maintained a steady body weight, while mice on HFD lost about 10% body weight (Figure 1B, C). All mice in the cold showed a significant drop in body temperature during the first days, but this loss in temperature was significantly higher in mice on HFD (-0.5°C vs -2°C after d1, Figure 1D). After 7 days, mice on chow diet recovered their body temperature to normal levels, while mice on HFD still had significantly lower temperatures (-1°C) (Figure 1D, E). Under thermoneutrality, mice on HFD had significantly higher BAT surface temperatures, consistent with increased diet-induced thermogenesis, but BAT surface temperatures were not different after cold exposure (Figure 1F, G). Extended phenotyping data is presented in Suppl. Figure 1.

3.2. Obesity impairs core transcriptome remodeling of BAT in response to cold

Gene expression data was used from all mice samples that also had methylation signal data available. After removal of outliers, N = 29 samples ($N_{HFD_30°C}$ = 7; $N_{HFD_8°C}$ = 7; $N_{chow_30°C}$ = 7; $N_{chow_8°C}$ = 8) remained for subsequent differential gene expression and methylation analysis. Analysis of VST normalized RNAseq expression counts shows clear clustering of all diet (chow, HFD)- and temperature (8°C, 30°C)-specific subgroups in the principal component analysis (Figure 2A), providing a solid basis for subsequent differential gene expression analysis. Moreover, temperature groups are separated by principal component 1 describing 33% of variance while diet groups are rather distinguished by principal component 2 covering 16,8% of total variance demonstrating an overall stronger impact of temperature compared to diet on overall gene expression patterns. Mice on HFD are older compared to chow fed mice. The age gap of 11 weeks could potentially interfere and explain a variance in the principal component analyses which was not addressed here.

To dissect BAT's physiological response to cold normal-weight control mice, we compared chow-fed mice held in the cold (8°C) with mice held at thermoneutrality (30°C) for one week. We will refer to this condition pair as $COLD_{chow}$. Additionally, to assess the effects of obesity on cold-induced BAT activation, we compared HFD-induced obese mice held in the cold (8°C) with mice held at thermoneutrality (30°C) for one week. This comparison will be referred to as $COLD_{HFD}$. Differential gene expression analysis (FDR <0.05) resulted in 7,089 DEGs for the $COLD_{chow}$ (Suppl. Figure 2A, B; Suppl. Table 2) and 5,249 DEGs for the $COLD_{HFD}$ (Suppl. Figure 2C, D; Suppl. Table 3) condition pairs. Reflecting the dominating effect of temperature on BAT activity, the majority of the significant DEGs overlap between the $COLD_{chow}$ and $COLD_{HFD}$ conditions are regulated similarly (N = 3,786; $COLD_{chow}$: 53%; $COLD_{HFD}$: 72%). Furthermore, 45% and 26% are

310 specifically regulated in $COLD_{chow}$ and $COLD_{HFD}$, respectively, while a total of 92 DEGs are
311 contrarily regulated (Suppl. Figure 4A).

312 To benchmark our $COLD_{chow}$ results with previously published data, we overlapped our DEGs with
313 those reported by Taylor et al. (2024) [32], who performed a comparable study in chow-fed male
314 mice exposed to severe cold (8 °C) versus thermoneutrality (28 °C) (Suppl. Figure 3; Suppl. Table
315 2). We found that 80% of our upregulated and 52% of our downregulated genes overlapped with
316 their DEGs, demonstrating a strong concordance across both directions in these independent
317 analyses.

318 Additionally, to investigate how diet affects BAT activation in response to cold exposure, we
319 employed an interaction model ($\Delta COLD_{diet}$) that compares the difference between both $COLD_{HFD}$
320 and $COLD_{chow}$ contrasts, rather than relying solely on simple group comparisons. This approach
321 enabled us to assess the combined and potentially synergistic or antagonistic effects of diet and
322 environment on BAT function [33]. Although an age gap of 11 weeks is indicated, mice on chow
323 or HFD are in a comparable age-range regarding BAT function and diet-independent body weight
324 development [34–37]. In total, we observed 1,364 genes (FDR <0.05) which are differentially
325 expressed between $COLD_{HFD}$ and $COLD_{chow}$ (Figure 2B, C; Suppl. Table 4). Since the most
326 significant DEGs are downregulated in the $COLD_{HFD}$ condition compared to $COLD_{chow}$, this
327 highlights a potential mechanism by which obesity may impair thermogenic capacity and energy
328 expenditure, suggesting that a high-fat diet disrupts the normal activation of BAT in response to
329 cold exposure.

330 3.3. Associations of gene expression and methylation signals underscore the influence of diet on
331 gene regulatory mechanisms

332 To explore the associative effects between transcriptomics and epigenomics, we correlated all
333 expression signals of DEGs with significant DMPs found within the DMRs of the corresponding
334 genes. This approach allowed us to define a set of differentially methylated and expressed genes
335 (DMEGs), using specific criteria: a Pearson correlation coefficient greater than ± 0.5, DEGs with
336 a $\log_2$ FC greater than ± 0.5 (adj. P <0.05), and DMPs with a $\log_2$ FC greater than ± 1 (p <0.05).
337 Importantly, we set a higher threshold for DMPs and focused on DMEGs located in both the
338 promoter and gene body regions, ensuring that our analysis captures the most relevant regulatory
339 elements influencing gene expression. To verify our findings, we analyzed the effect of DNA-
340 demethylation (using Aza) or hypermethylation (using SAM) on the expression of selected genes
341 in mouse adipocytes *in vitro* (Suppl. Figure 5). The observed effects of DNA methylation and the
342 manipulation on gene expression were in line with the results of our analysis correlating gene
343 expression and methylation and confirmed epigenetic control of gene expression in adipocytes.

344 In the $COLD_{chow}$ control comparison, we identified a total of 3,142 DMEGs among 21% (N =
345 1,524) of all DEGs. The data showed a balanced distribution of DMEGs, with 55% located within
346 gene bodies and 45% found in promoter regions (Figure 3A; Suppl. Table 5), indicating that
347 methylation can affect gene regulation through various mechanisms, such as promoter accessibility

348 or splice site manipulation. As illustrated in Figure 3B, DMEGs within the top 100 DMRs (ranked
349 by absolute $\log_2$ FC) are predominantly found in promoter regions and show distinctly higher
350 prevalence on chromosome 11.

351 To investigate which cell types might drive DNA methylation changes in BAT, we overlapped
352 DMEGs from the $COLD_{chow}$ condition with cell-type-specific marker genes derived from single-
353 cell RNAseq (scRNAseq) of BAT from male mice exposed to cold (5 °C) versus thermoneutrality
354 (30 °C) [38]. This analysis revealed that DMEGs were distributed across multiple cell types, with
355 the highest proportions in vascular smooth muscle cells (VSM, 43%), adipocytes (35%),
356 endothelial cells (EC, 31.8%), and stromal populations, including *Pdgfra*$^+$ adipocyte progenitor
357 cells (APCs, 28.1%) and pericytes (20.9%). In contrast, immune cells contributed more modestly,
358 with macrophages at 18.2%, NK cells at 9.3%, and T cell subsets (CD4$^+$, CD8$^+$, Treg) ranging from
359 5–9%. Across nearly all cell types, most DMEGs belonged to the hypo up category - genes
360 exhibiting hypomethylation accompanied by increased expression. This pattern was particularly
361 pronounced in adipocytes (26.4%) and vascular populations, including VSM (21.6%) and EC
362 (11.9%). Hyper up DMEGs were most notable in adipocytes (10%), whereas hypo down DMEGs
363 were enriched in vascular and stromal populations, including VSM (15%), EC (14.9%), *Pdgfra*$^+$
364 APCs (13.6%), and to a lesser extent in adipocytes (2.8%). Conversely, the fractions of hyper down
365 DMEGs were relatively small, ranging from 1-6% depending on the cell type (Figure 3C; Suppl.
366 Table 5).

367 Additionally, we detected 1,886 DMEGs from 19% (N = 1001) of all DGEs in the $COLD_{HFD}$
368 condition. Similar to the $COLD_{chow}$ condition, 60% of the DMEGs are located within gene bodies
369 and 40% in promoter regions (Figure 4A; Suppl. Table 6); however, the most highly regulated
370 DMEGs do not exhibit significant enrichment in the promoter regions (Figure 4B).

371 Although we previously observed that the majority of significant DEGs overlapping between the
372 $COLD_{chow}$ and $COLD_{HFD}$ conditions are regulated in a similar direction (Suppl. Figure 5), we
373 identified a contrasting pattern among the DMEGs. The gene expression of DMEGs shows
374 consistent regulatory patterns, with only 245 ($COLD_{chow}$: 16%; $COLD_{HFD}$: 24%) genes being
375 upregulated and 159 ($COLD_{chow}$: 10%; $COLD_{HFD}$: 16%) genes being downregulated in both
376 conditions (Suppl. Figure 4B; Suppl. Figure 6). In contrast, 73% and 60% are specifically regulated
377 in the $COLD_{chow}$ and $COLD_{HFD}$ conditions, respectively, while only one gene (*guanylyl cyclase*
378 *domain containing 1* (*Gucd1*)) is regulated in the opposite direction (Suppl. Figure 4B; Suppl.
379 Figure 7). This suggests that the response to temperature conditions is strongly dependent on the
380 specific environment and that methylation changes may be purposefully employed to adapt to
381 different metabolic or physiological demands.

382 Our previous findings revealed pronounced differences in the regulatory patterns of DMEGs
383 between the $COLD_{chow}$ and $COLD_{HFD}$ conditions by emphasizing the direction of regulation. To
384 further elucidate the nuances of diet-specific regulation, we utilized the $\Delta COLD_{diet}$ contrast to
385 detect more subtle differences in regulatory effects including regulation strength, directly

386 identifying diet-related differences in DMEGs associated with BAT activation induced by cold
387 exposure (Figure 5; Suppl. Table 7). For the $\Delta COLD_{diet}$ contrast, we detected 65 DMEGs from only
388 4% (N = 56) of all DEGs. Interestingly, these are primarily enriched in the gene bodies (69%),
389 suggesting that the regulation of these genes may be more influenced by post-transcriptional
390 mechanisms in response to cold exposure.

391 3.4. Adaptive divergence in thermogenic signaling reflects metabolic stress in obese BAT

392 For further characterization of the reported DMEGs, pathway enrichment analysis was performed
393 using the IPA software. The DMEGs were categorized into four groups: those exhibiting similar
394 regulation in both $COLD_{chow}$ and $COLD_{HFD}$ condition pairs, and those that are uniquely regulated
395 in each individual condition ($\Delta COLD_{diet,}$ $COLD_{chow}$, and $COLD_{HFD}$). Querying the catalog for
396 significant (BH-adjusted $p < 0.05$) canonical pathways (Figure 6; Suppl. Table 8) shows similar
397 activation of pathways with respect to lipid metabolism except for ketolysis which is only
398 significantly activated in the $COLD_{HFD}$ condition. Cell signaling and energy expenditure seem to
399 be activated or inhibited more differentially between $COLD_{chow}$ and $COLD_{HFD}$ condition pairs. For
400 example, the process of white adipose tissue browning is significantly inhibited in $COLD_{HFD}$ but
401 shows (unsignificant) activation in $COLD_{chow}$. Additionally, type II diabetes mellitus signaling is
402 significantly activated under $COLD_{HFD}$ considerations but tends to be (insignificantly) inhibited
403 under $COLD_{chow}$.

404 3.5. Diet and cold exposure shape epigenetic regulation in BAT

405 To gain deeper insights into the epigenetic mechanisms that regulate BAT activation and
406 thermogenesis under different dietary conditions, we matched DEGs from each condition pair with
407 the EpiFactors database (v2.0, https://epifactors.autosome.org, accessed on 10.09.2024), with the
408 analysis being restricted to DNA-methylation-related factors, while histone-modifying enzymes,
409 chromatin remodelers and RNA-based epigenetic regulators were omitted. As summarized in
410 Figure 7, we identified eleven differentially expressed methylation regulators for the $COLD_{chow}$,
411 seven for $COLD_{HFD}$, and four for $\Delta COLD_{diet}$ condition pairs. Notably, five regulators were found
412 to be common to both the $COLD_{chow}$ and $COLD_{HFD}$ conditions including *Tet2* (*ten-eleven*
413 *translocation methylase 2*), *Dnmt3* (*DNA methyltransferase 3*), *Cenpc1* (*centromere protein C*),
414 *Apobec1* (*apolipoprotein B mRNA editing enzyme catalytic subunit 1*) which are all downregulated
415 in $COLD_{chow}$ *and* $COLD_{HFD}$. This overlap indicates a conserved epigenetic mechanism that is
416 essential for the physiological response to cold exposure, regardless of diet. However, the majority
417 of methylation enzymes exhibited unique regulation within each condition pair, highlighting the
418 nuanced regulation of epigenetic mechanisms based on dietary composition. For instance, *Tet3* and
419 *Dnmt1* were differently regulated within the $\Delta COLD_{diet}$ and $COLD_{chow}$ conditions, while *Mettl4*
420 (*methyltransferase-like protein 4*) and *Apobec3b* showed differential regulation within the
421 $\Delta COLD_{diet}$ contrast.

422

4. Discussion

We aimed to explore how environmental factors and DNA methylation may influence BAT function. To investigate potential links between DNA methylation and gene expression, we integrated RNA-seq data with RRBS methylation profiles to identify genes with coordinated changes in expression and methylation (DMEGs) under different dietary and thermal conditions. This approach provides insights into BAT plasticity and adaptive thermogenesis, contributing to a foundational understanding that could inform future obesity-related research and interventions.

Consistent with BAT's physiological adaptation to cold, our data show that cold exposure robustly increases BAT activity regardless of diet, evidenced by strong transcriptomic responses with 7,089 DEGs in chow-fed and 5,249 DEGs in HFD-fed mice. A substantial overlap (~3,780 genes) between both dietary groups suggests a conserved "core" thermogenic program that remains inducible under obesogenic conditions. Notably, *Ucp1*, a central mediator of non-shivering thermogenesis, and *Letmd1* (*leucine zipper-EF-hand-containing transmembrane protein domain containing 1*), which is essential for mitochondrial integrity and cold response, were among the top upregulated genes across both diets. Their consistent induction under cold exposure, aligns with previous reports of diet-insensitive thermogenic regulators [39,40]. Beside this shared response, ~1,360 genes were differentially expressed between the cold-exposed groups ($\Delta COLD_{diet}$), with most downregulated in diet-induced obese mice, consistent with a high-fat diet impairing thermoregulatory capacity driven by mitochondrial dysfunction, inflammation, and insulin resistance [41,42]. This functional attenuation under high-fat diet conditions is also reflected among the most strongly regulated DGEs. Downregulation of *Hk2* (*hexokinase 2*), a key glycolytic enzyme, has been linked to reduced glucose uptake [43]. Similarly, reduced *Gpd1* (*glycerol-3-phosphate dehydrogenase 1*) expression, part of the glycerol-3-phosphate shuttle, may reflect compromised lipid metabolism. *Ucp1* stayed cold-inducible in all diets but was lower in HFD-fed mice, showing that thermogenic response is maintained but reduced under metabolic stress. This aligns with reports of reduced BAT activity in obesity despite retained gene expression [39]. Our results of $COLD_{chow}$ are in line with those of Taylor et al. (2024) [32], who performed a comparable study in chow-fed mice exposed to severe cold (8°C) versus thermoneutrality (28°C). The strong overlap of DEGs highlights the reproducibility of cold-induced BAT transcriptional responses across independent studies and supports the generalizability of our findings.

To identify epigenetically regulated genes, we correlated methylation changes (M-values of DMPs overlapping DMRs) with gene expression levels to define DMEGs. While these correlations suggest potential regulatory links, they do not establish causality, as gene expression is also influenced by other epigenetic modifications and transcription factors [32,44,45]. More comprehensive approaches integrating histone modifications, proteomics, or single-cell epigenomics could further elucidate the complex regulation within heterogeneous BAT cell populations [46]. Compared to generalized linear models with distributional assumptions [47,48], our site-specific correlation approach offers higher sensitivity for detecting local methylation-expression relationships, though it may miss broader regulatory patterns and is more sensitive to

462 noise. Our thresholds for defining significant DMEGs were set at |log FC| >0.5 for expression
463 changes and |log FC| >1 for methylation differences; correlations were considered significant if |r|
464 >0.5 and p <0.05. These cutoffs balance sensitivity and specificity but also limit detection power
465 given our sample size. When DMEGs overlapped promoter and gene body regions, assignment
466 was based on the strongest correlation, which enhances interpretability but may introduce bias due
467 to regional variability or technical factors.

468 By analyzing DMEGs, ~3,100 DMEGs (21% of DGEs) were identified in $COLD_{chow}$, with a
469 roughly equal distribution between promoter and gene body methylation. In contrast, HFD-fed
470 mice exhibited only ~1,900 DMEGs (19% of DEGs), with a higher proportion of gene body
471 methylation. As gene body methylation is often linked to transcript fine-tuning rather than
472 activation, this may reflect constrained thermogenic adaptability under obesogenic conditions [49].
473 Notably, DMEGs were largely condition-specific despite substantial overlap in DEGs, highlighting
474 that diet and cold exposure interact to shape BAT-specific regulatory states, rather than acting
475 independently. These condition-specific methylation-expression relationships suggest that DNA
476 methylation may play an active role in modulating transcriptional plasticity and energy
477 metabolism, enabling BAT to adapt epigenetically to distinct environmental challenges.

478 To gain further insight into the cellular context of these DNA methylation changes, we mapped
479 DMEGs of the $COLD_{chow}$ condition onto cell-type-specific markers derived from male mice
480 scRNAseq data of cold-exposed BAT [38]. This analysis revealed that the majority of DMEGs
481 belonged to the hypo up category, particularly in adipocytes, vascular cells, and *Pdgfra*$^{+}$ adipocyte
482 progenitors, suggesting coordinated activation of thermogenic programs and vascular remodeling.
483 Hypo down DMEGs were enriched in vascular and stromal populations, indicating selective
484 repression of pathways supporting tissue structure and function. Hyper up DMEGs were primarily
485 observed in adipocytes, whereas hyper down DMEGs were rare (1–6%), implying that DNA
486 methylation mediated silencing plays a limited role in the cold response. The observed cell type-
487 specific DMEG distributions are consistent with prior evidence of increased intercellular signaling
488 among adipocytes, vascular, stromal, and immune cells under cold conditions in chow-fed mice,
489 suggesting an epigenetic basis for the transcriptional remodeling in BAT [38].

490 Pathway enrichment analysis further supports this adaptive divergence of DMEGs and highlighting
491 the diet-dependent rewiring of thermogenic signaling. Cold exposure activated distinct lipid
492 metabolic pathways (triacylglycerol, phosphatidylglycerol, and CDP−diacylglycerol biosynthesis)
493 in both dietary groups, however, ketolysis was selectively enriched in HFD-fed mice. In line with
494 previous findings that HFD suppresses ketone body utilization for lipogenesis in BAT via
495 downregulation of *acetoacetyl-CoA synthetase* (*Aacs*) [50], our DGE analysis show that *Aacs* was
496 significantly upregulated by cold in both dietary groups, but this response was markedly stronger
497 in chow-fed mice ($\log_2$ FC: 1.77) than in HFD-fed mice ($\log_2$ FC: 0.74), with a negative interaction
498 effect ($\Delta COLD_{diet}$ l $\log_2$ FC: –0.81). These results indicate that cold-induced ketone body recycling
499 remains inducible but is dampened under HFD, potentially limiting metabolic flexibility and
500 compensatory lipid synthesis in insulin-resistant BAT. Consistently, only $COLD_{HFD}$ showed

activation of the Type II Diabetes Mellitus signaling pathway under cold stress, reflecting a diabetogenic transcriptional environment marked by insulin resistance and impaired glucose homeostasis [51]. This suggests that cold exposure does not fully overcome metabolic dysfunction in BAT during obesity, potentially limiting its systemic metabolic benefits.

Further, cold-exposed HFD mice uniquely activated Sirtuin signaling, potentially a compensatory response to mitochondrial stress, while suppressing pathways related to mitochondrial dysfunction and white adipose tissue browning, indicating a shift from efficient thermogenesis to cellular maintenance [52]. Further, a selective activation of neuroendocrine pathways (e.g., corticotropin-releasing hormone and orexin signaling) may reflect rewiring of central and peripheral regulatory mechanisms to compensate for reduced intrinsic thermogenic capacity [53]. Concurrent suppression of nitric oxide and neuronal nitric oxide synthase (nNOS) signaling, crucial for vascular perfusion and mitochondrial function, points to impaired BAT structural and vascular adaptation under HFD.

We identified several epigenetic regulators differentially expressed in response to cold and diet. Core factors such as *Tet2*, *Dnmt3*, *Cenpc1*, and *Apobec1* responded similarly under both diets, suggesting a foundational epigenetic program supporting cold-induced chromatin remodeling and transcriptomic flexibility. In contrast to white adipose tissue, where *Mettl4* is upregulated under obesogenic conditions [54], we observed its downregulation in BAT only in $COLD_{HFD}$. Given that Mettl4-mediated N6-adenine methylation has been implicated in adipocyte differentiation and lipid production [55], it is conceivable that high-fat diets constrain the differentiation and functional capacity of BAT through epigenetic mechanisms. Conversely, cold exposure decreased *Tet3* and *Dnmt1* expression under chow but not HFD. As Tet3 and Dnmt1 regulate adipocyte expansion and mitochondrial function as well as chromatin architecture, respectively, their cold-induced downregulation may favor thermogenesis by limiting hypertrophy and enhancing mitochondrial and epigenetic adaptability [56–58]. *Dnmt1* deletion in BAT has no metabolic impact under standard diets [59], but may gain relevance under thermogenic or obesogenic stress. A previous study demonstrated the downregulation of *Dnmt1*, *Dnmt3a,* and *Dnmt3b* in BAT upon cold exposure under chow diet conditions, linking reduced DNA methylation to enhanced thermogenic activation [60]. Our findings confirm this pattern under chow conditions but reveal a lack of regulation under HFD, supporting the notion that epigenetic flexibility is impaired in obesogenic environments. *Apobec3*, a cytidine deaminase implicated in RNA and potentially DNA editing [61], was downregulated by cold under both diets, though significantly more under chow. This pattern may reflect its role in facilitating transcriptomic remodeling during thermogenic activation that may be blunted under HFD. Therefore, BAT activation appears to be governed by a conserved core of methylation regulators responsive to cold, while additional, context-specific pathways are modulated by the dietary environment. This dual mechanism supports a model in which a stable epigenetic framework is dynamically adjusted to accommodate metabolic demands, thereby fine-tuning the thermogenic capacity of BAT.

539 By conducting in vitro methylation analyses, we confirmed the epigenetic transcription control of
540 certain DMEGs and important BAT regulatory genes such as *Bmp8b* or *Cpne5* pointing towards a
541 valid impact of the DNA methylation on BAT function. By using Aza and SAM, we cannot rule
542 out the possibility that other epigenetic mechanisms than DNA methylation led to these
543 observations as especially SAM serves as methyldonor for various processes [62]. In any case, our
544 results strongly support the highly dynamic control of BAT by epigenetic alterations.

545 **4.1. Limitations**

546 A limitation arises from age differences between diet groups (11 weeks chow vs. 22 weeks HFD).
547 First, the difference in bodyweight between chow and HFD mice may have partially arisen from
548 the age gap, as there is still a slow increase in body weight beyond adulthood at 12 weeks of age
549 [37]. However, male chow fed mice at 22 weeks of age would reach approximately 30g bodyweight
550 which still is significantly different from mice on HFD at the same age. Second, although BAT
551 function declines with age, mice used in this study are of a comparable age-range related to BAT
552 function. Studies show that mice aged between 12 weeks and six months present a stable metabolic
553 active BAT, with stable mitochondrial content and thermogenic potential before these factors start
554 to decline and lipid accumulation increases [34–36]. Although we cannot bioinformatically address
555 this issue in our comparative analyses, we believe that age is not a main driving factor of the here
556 observed effects as we addressed a comparable age range regarding bodyweight and cold
557 adaptation of BAT. Anyway, regardless of BAT function, global DNA methylation reduces with
558 age while specifically promoter regions tend to get hypermethylated with age [63]. While we
559 cannot address the age factor in our analyses due to group specific age differences, we expect a
560 limited impact of age on our results based on comparing mice in a suitable age range meaning only
561 "young adult mice" [64]. A further limitation is the use of only male mice, which may limit
562 generalizability to females. However, given the known sex-specific differences in adipose biology,
563 BAT activity, and epigenetic regulation, addressing only males is beneficial regarding the
564 addressed methodology. Future studies should include female mice to assess potential sex-by-diet
565 or sex-by-temperature interactions. Small sample sizes (7-8 per group) limit statistical power to
566 detect subtle effects. In addition, RRBS data provides only partial genome coverage, primarily
567 focusing on CpG-rich regions, potentially overlooking important regulatory areas outside these
568 regions. In contrast, whole-genome bisulfite sequencing could provide more comprehensive
569 methylation profiling.

570 **5. Conclusions**

571 In conclusion, this study provides the first evidence that cold-induced DNA methylation
572 remodeling in BAT is strongly shaped by dietary context, particularly under obesogenic conditions.
573 Our integrative analysis reveals that, while cold exposure activates a conserved thermogenic
574 transcriptional program, high-fat diet attenuates epigenetic flexibility and restricts full BAT
575 activation. These findings underscore that environmental temperature and dietary intake interact to
576 regulate BAT function via interconnected transcriptional and epigenetic mechanisms. Importantly,

577 we identify both core and context-specific regulators that mediate this response, offering potential
578 molecular targets for future therapies. By demonstrating that obesity alters the epigenetic landscape
579 of cold adaptation, our study opens new avenues for nutritional or epigenetic interventions aimed
580 at restoring BAT plasticity and enhancing thermogenic capacity in metabolic disease.

581 **Data Availability**

582 Raw RNAseq and RRBS data have been deposited in the Sequence Read Archive (SRA,
583 https://www.ncbi.nlm.nih.gov/sra/) [65] under the BioProject number PRJNA1294891.

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589 **Author contributions**

590 Conceptualization: TH, AH, KRZ, JTH, and JW; Methodology: AH, TH, KRZ, and JW;
591 Investigation: KRZ, HB, and JW; Validation: KRZ, HB, and JW; Formal analysis: TH; Data
592 curation: TH and AH; Writing – original draft: TH, AH, KRZ, JW, and JTH; Writing – review &
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602 **Conflict of interest**

603 MB received honoraria as a consultant and speaker from Amgen, AstraZeneca, Bayer, Boehringer-
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Figures

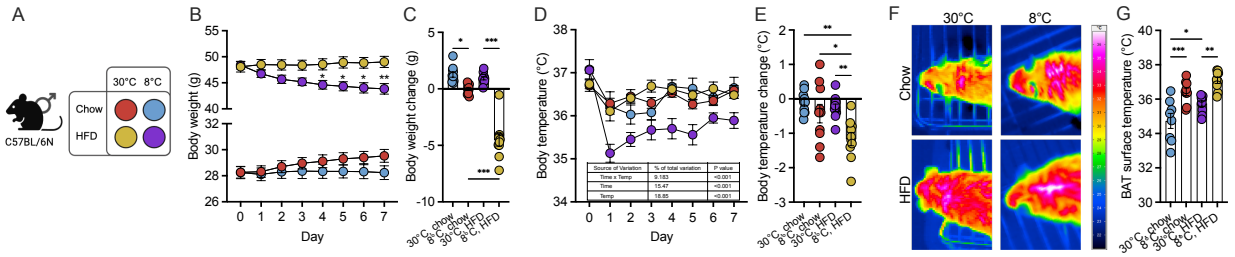


Figure 1: Phenotyping of chow and HFD-fed mice housed at 30°C or 8°C. (A) Schematic overview and corresponding color code of the cohort mouse groups stratified by dietary (chow, HFD) and environmental (thermoneutrality vs cold) conditions. (B) Body weight development and (C) body weight change in chow and HFD-fed mice housed at thermoneutrality (30°C) or in the cold (8°C) for 7 days. Body temperature (D) and temperature change (E) in chow and HFD-fed mice housed at thermoneutrality (30°C) or in the cold (8°C) for 7 days. (F) Thermal images from brown adipose tissue (BAT) and (G) BAT surface temperature in chow and HFD-fed mice housed at thermoneutrality (30°C) or in the cold (8°C) for 7 days. N = 7-8 per condition. (B, D) Statistical significance was evaluated by two-way ANOVA with uncorrected Fischer's LSD, (E) Šídák's post-hoc test, (C, G) or one-way ANOVA with Tukey's post-hoc test. $p < 0.05$ (*), $p < 0.01$ (**), $p < 0.001$ (***). Scale bar: 100 µm.

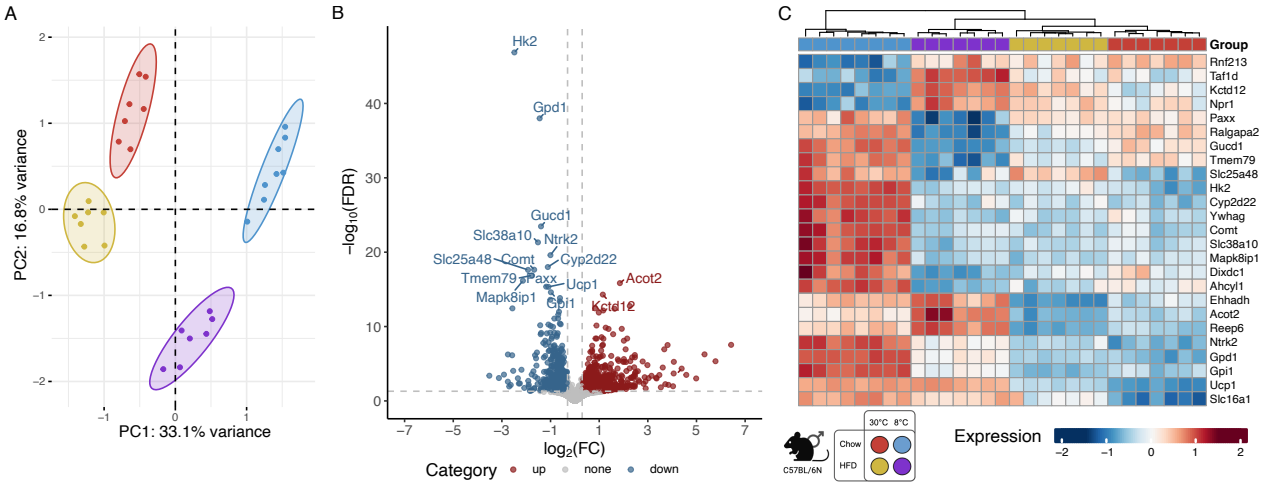
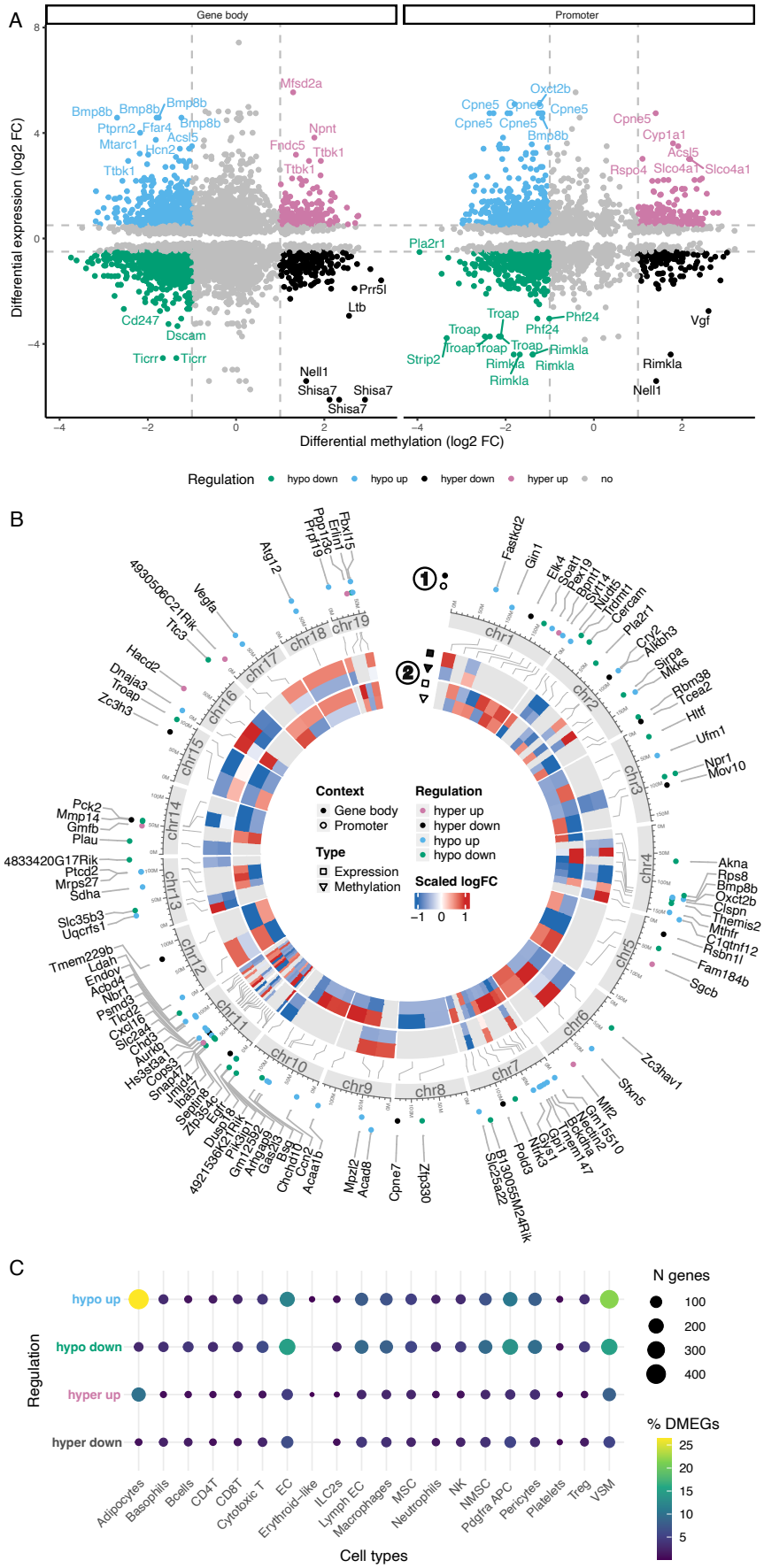
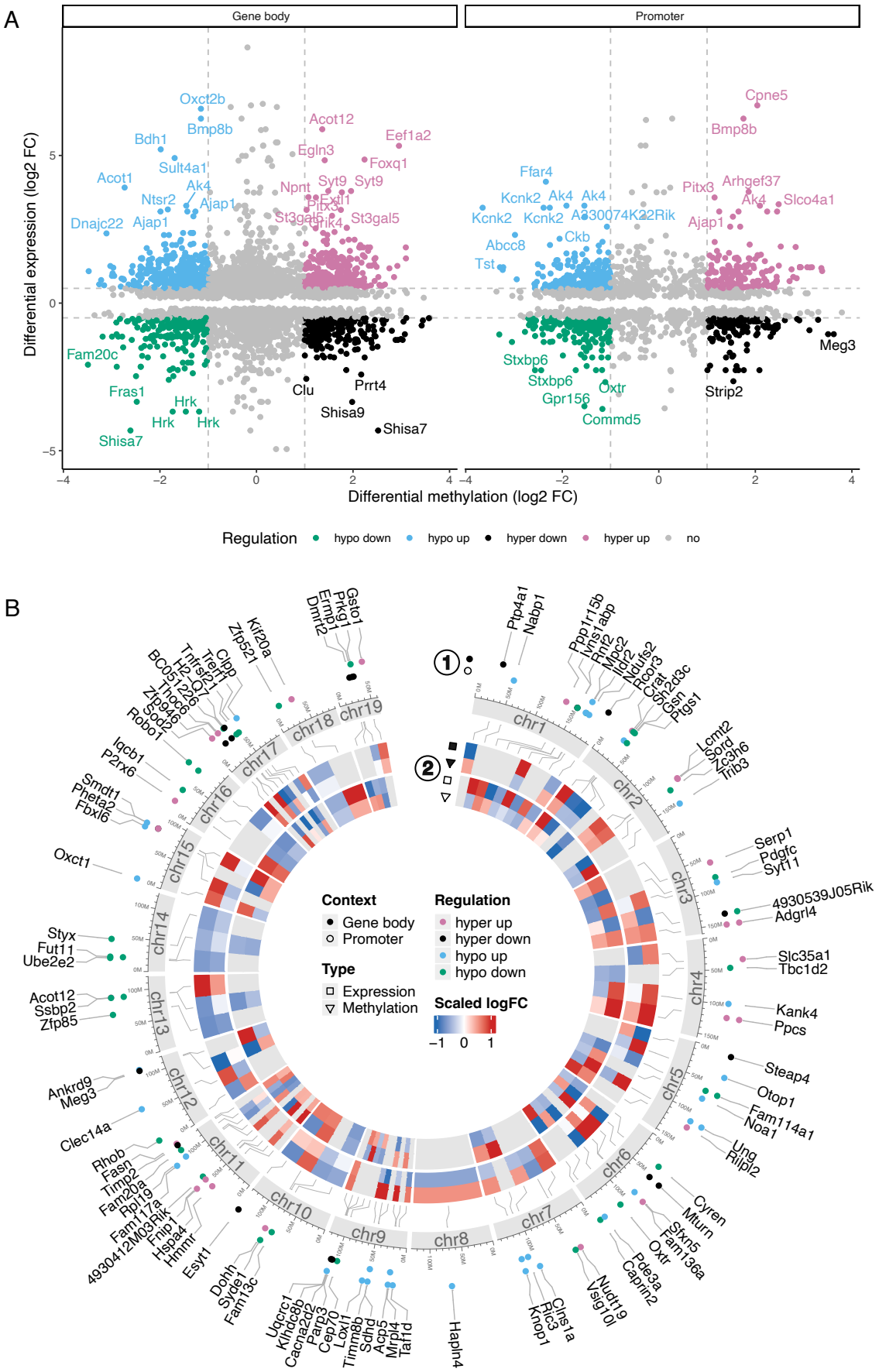


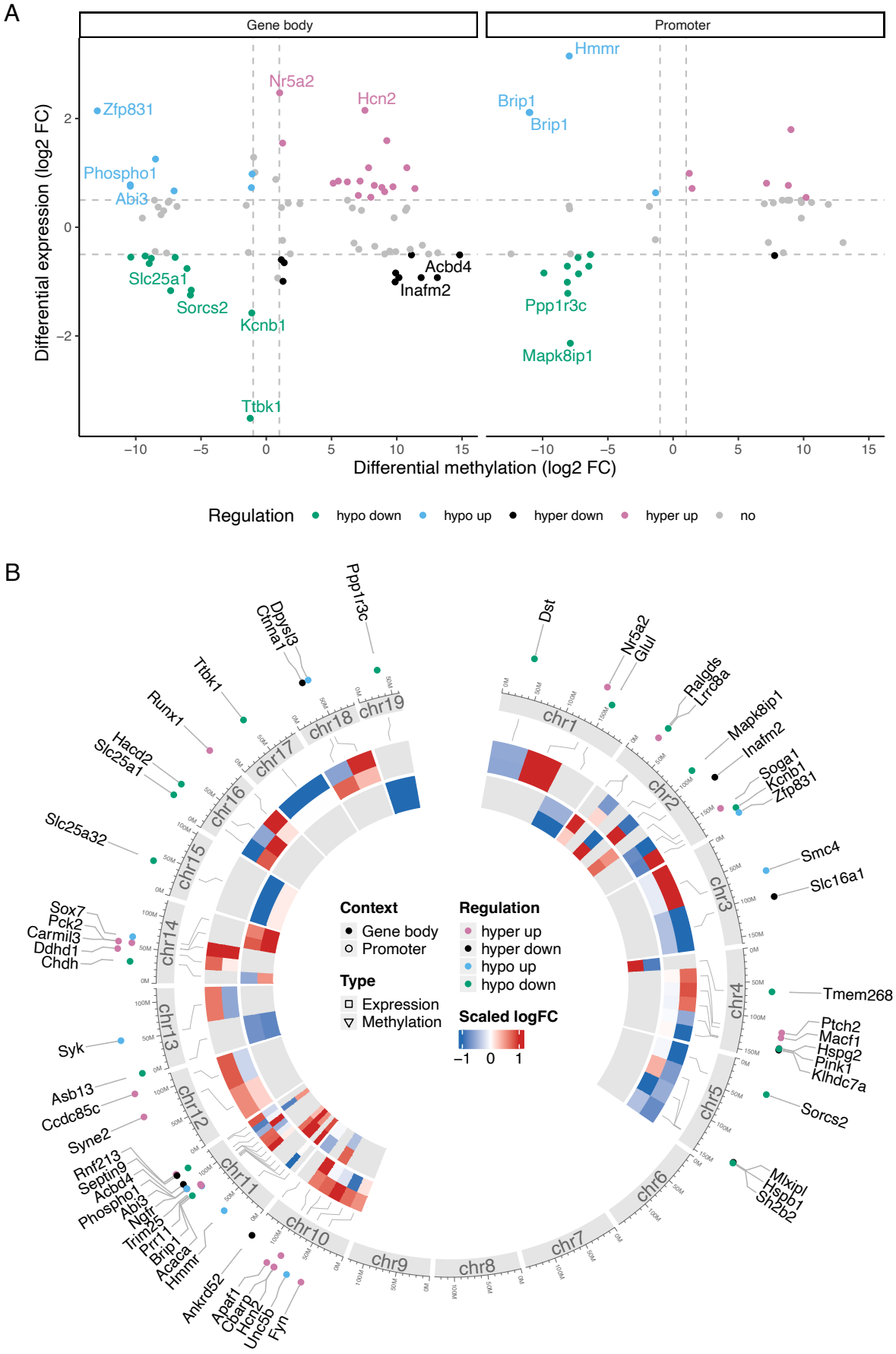
Figure 2: RNA sequencing-based gene expression data revealse distinct clusters of treatment groups. (A) Principal component analysis separates temperature and diet. All considered subgroups reveal distinct expression profiles and cluster according to the first two principal components. (B) Volcano plot highlights most significantly (false discovery rate (FDR) <0.05) regulated genes under $\Delta COLD_{diet}$ condition. (C) Heatmap of expression values shows that the subgroups can be clearly separated by the top significant regulated genes. Abbreviations: HFD: high fat diet; PC: principal component.


A
Gene body
Promoter
Differential expression (log2 FC)
Differential methylation (log2 FC)
Regulation
hypo down
hypo up
hyper down
hyper up
no
B
Context
Gene body
Promoter
Type
Expression
Methylation
Regulation
hyper up
hyper down
hypo up
hypo down
Scaled logFC
C
N genes
% DMEGs
Regulation
hypo up
hypo down
hyper up
hyper down
Adipocytes
Basophils
Bcells
CD4T
CD8T
Cytotoxic T
EC
Erythroid-like
ILC2s
Lymph EC
Macrophages
MSC
Neutrophils
NK
NMSC
Pdgfra APC
Pericytes
Platelets
Treg
VSM
Cell types

804 **Figure 3: Multi-layered insights into DMEGs under *$COLD_{chow}$* condition.** (A) The scatter plot
805 displays the $\log_2$ fold changes (FC) in gene expression and DNA methylation signals for all
806 differentially methylated and expressed genes (DMEGs) in both gene body and promoter contexts
807 under the *$COLD_{chow}$* condition. Colors indicate the direction of regulation. DMEGs with absolute
808 $\log_2$ FC >0.5 in expression and >1 in methylation signals are highlighted as significant, while
809 DMEGs in the 5% and 95% quantile of both differentially methylated position (DMP) and
810 differentially expressed gene (DEG) $\log_2$ FC signals are labeled. (B) The circos visualization
811 illustrates the DMEGs covering the top 100 significant differentially methylated regions (DMRs;
812 ranked by $\log_2$ FC). This plot integrates multiple layers of information from outer to inner ring: Dot
813 colors indicate the direction of regulation, while dot positions denote whether the DMR of the
814 DMEG is located in the gene body or promoter context (1); a stylized ideogram of chromosomes
815 provides a genomic reference frame; and a heatmap displays scaled log2 FC for both gene
816 expression and DNA methylation signals in gene body and promoter contexts for each DMEG (2).
817 (C) Overview of assigned cell types to the DMEGs, categorized as hypo up, hypo down, hyper up,
818 and hyper down. The color scale reflects the percentage of DMEGs, and the size of the dots reflects
819 the absolute number of DMEGs.


A
Gene body
Promoter
Differential expression (log2 FC)
Differential methylation (log2 FC)
Oxct2b
Bmp8b
Bdh1
Sult4a1
Acot1
Ak4
Ntsr2
Ajap1
Dnajc22
Ajap1
Acot12
Eef1a2
Egln3
Foxq1
Npnt
Syt9
Syt9
Pitx3
Fxtl1
St3gal5
St3gal5
Hrk4
Fam20c
Fras1
Hrk
Hrk
Hrk
Shisa7
Clu
Prrt4
Shisa9
Shisa7
Cpne5
Bmp8b
Ffar4
Kcnk2
Ak4
Ak4
Kcnk2
Kcnk2
A330074K22Rik
Pitx3
Arhgef37
Ak4
Slco4a1
Ajap1
Abcc8
Ckb
Tst
Stxbp6
Stxbp6
Gpr156
Oxtr
Commd5
Meg3
Strip2
Regulation
hypo down
hypo up
hyper down
hyper up
no
B
Context
Gene body
Promoter
Type
Expression
Methylation
Regulation
hyper up
hyper down
hypo up
hypo down
Scaled logFC
−1
0
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
Gsto1
Prkg1
Ermp1
Dmrt2
Kif20a
Zfp521
Clpp
Trefh1
Tnfrsf21
Hs3st1
BC051226
Tnfrsf9
Zfp446
Tnfrsf9
Sod3
Robo1
Iqcb1
P2rx6
Smdt1
Pheta2
Fbxl6
Oxct1
Styx
Fut11
Ube2e2
Acot12
Ssbp2
Ztp85
Ankrd9
Meg3
Clec14a
Rhob
Fasn
Timp2
Fam20a
Rpl19
Fam117a
4930412M03Rik
Fnip1
Hspa4
Hmmr
Esyt1
Dohh
Syde1
Fam13c
Uqcrc1
Klhdc8b
Cacna2d2
Parp3
Cep70
Loxl1
Timm8b
Sdhd
Acp5
Mrpl4
Taf1d
Hapln4
Clns1a
Ric3
Knop1
Nudt19
Vsig10l
Pde3a
Caprin2
Oxtr
Fam136a
Stxn5
Mturn
Cyren
Ung
Ripl2
Noa1
Fam114a1
Otop1
Steap4
Kank4
Ppcs
Slc35a1
Tbc1d2
4930539J05Rik
Adgrl4
Serp1
Pdgfc
Syt11
Lcmt2
Sord
Zc3h6
Trib3
Ptp4a1
Nabp1
Ppp1r15b
Vns1abp
Rnf2
Mpc2
Igf2
Ndufs2
Rcor3
Cyrat
Sh2d3c
Gsn
Ptgs1
1
2

821 **Figure 4: Multi-layered insights into DMEGs under *$COLD_{HFD}$* condition.** (A) The scatter plot
822 displays the $\log_2$ FC in gene expression and DNA methylation signals for all DMEGs in both gene
823 body and promoter contexts under the *$COLD_{HFD}$* condition. Colors indicate the direction of
824 regulation. DMEGs with absolute $\log_2$ FC >0.5 in expression and >1 in methylation signal are
825 highlighted as significant, while DMEGs in the 5% and 95% quantile of both DMP and DEG $\log_2$
826 FC signals are labeled. (B) The circos visualization illustrates the DMEGs covering the top 100
827 most significant DMRs (ranked by $\log_2$ FC). This plot integrates multiple layers of information
828 from outer to inner ring: Dot colors indicate the direction of regulation, while dot positions denote
829 whether the DMR of the DMEG is located in the gene body or promoter context (1); a stylized
830 ideogram of chromosomes provides a genomic reference frame; and a heatmap displays scaled $\log_2$
831 FC for both gene expression and DNA methylation signals in gene body and promoter contexts for
832 each DMEG (2).


A
Gene body
Promoter
Differential expression (log2 FC)
Differential methylation (log2 FC)
Zfp831
Phospho1
Abi3
Nr5a2
Hcn2
Slc25a1
Sorcs2
Kcnb1
Ttbk1
Acbd4
Inafm2
Hmmr
Brip1
Brip1
Ppp1r3c
Mapk8ip1
Regulation
hypo down
hypo up
hyper down
hyper up
no
B
Ppp1r3c
Dpysl3
Ctnna1
Ttbk1
Runx1
Hacd2
Slc25a1
Slc25a32
Sox7
Pck2
Carmil3
Ddhd1
Chdh
Syk
Asb13
Ccdc85c
Syne2
Rnf213
Septin9
Acbd4
Phospho1
Abi3
Ngfr
Trim25
Prr11
Brip1
Acaca
Hmmr
Ankrd52
Apaf1
Coarp
Hcn2
Unc5b
Fyn
Dst
Nr5a2
Glul
Ralgds
Lrrc8a
Mapk8ip1
Inafm2
Soga1
Kcnb1
Zfp831
Smc4
Slc16a1
Tmem268
Ptch2
Macf1
Hspg2
Pink1
Klhdc7a
Sorcs2
Mlxipl
Hspb1
Sh2b2
Context
Gene body
Promoter
Type
Expression
Methylation
Regulation
hyper up
hyper down
hypo up
hypo down
Scaled logFC
−1
0
1

833

834 **Figure 5: Multi-layered insights into DMEGs under *ΔCOLD*$_{diet}$ condition.** (A) The scatter plot
835 displays the $\log_2$ FC in gene expression and DNA methylation signals for all DMEGs in both gene
836 body and promoter contexts under the *ΔCOLD*$_{diet}$ condition. Colors indicate the direction of
837 regulation. DMEGs with absolute $\log_2$ FC >0.5 in expression and >1 in methylation signals are
838 highlighted as significant, while DMEGs in the 5% and 95% quantile of both DMP and DEG $\log_2$
839 FC signals are labeled. (B) The circos visualization illustrates all detected DMEGs in their
840 respective DMRs. This plot integrates multiple layers of information from outer to inner ring: Dot
841 colors indicate the direction of regulation, while dot positions denote whether the DMR of the
842 DMEG is located in the gene body or promoter context (1); a stylized ideogram of chromosomes
843 provides a genomic reference frame; and a heatmap displays scaled $\log_2$ FC for both gene
844 expression and DNA methylation signals in gene body and promoter contexts for each DMEG (2).

845

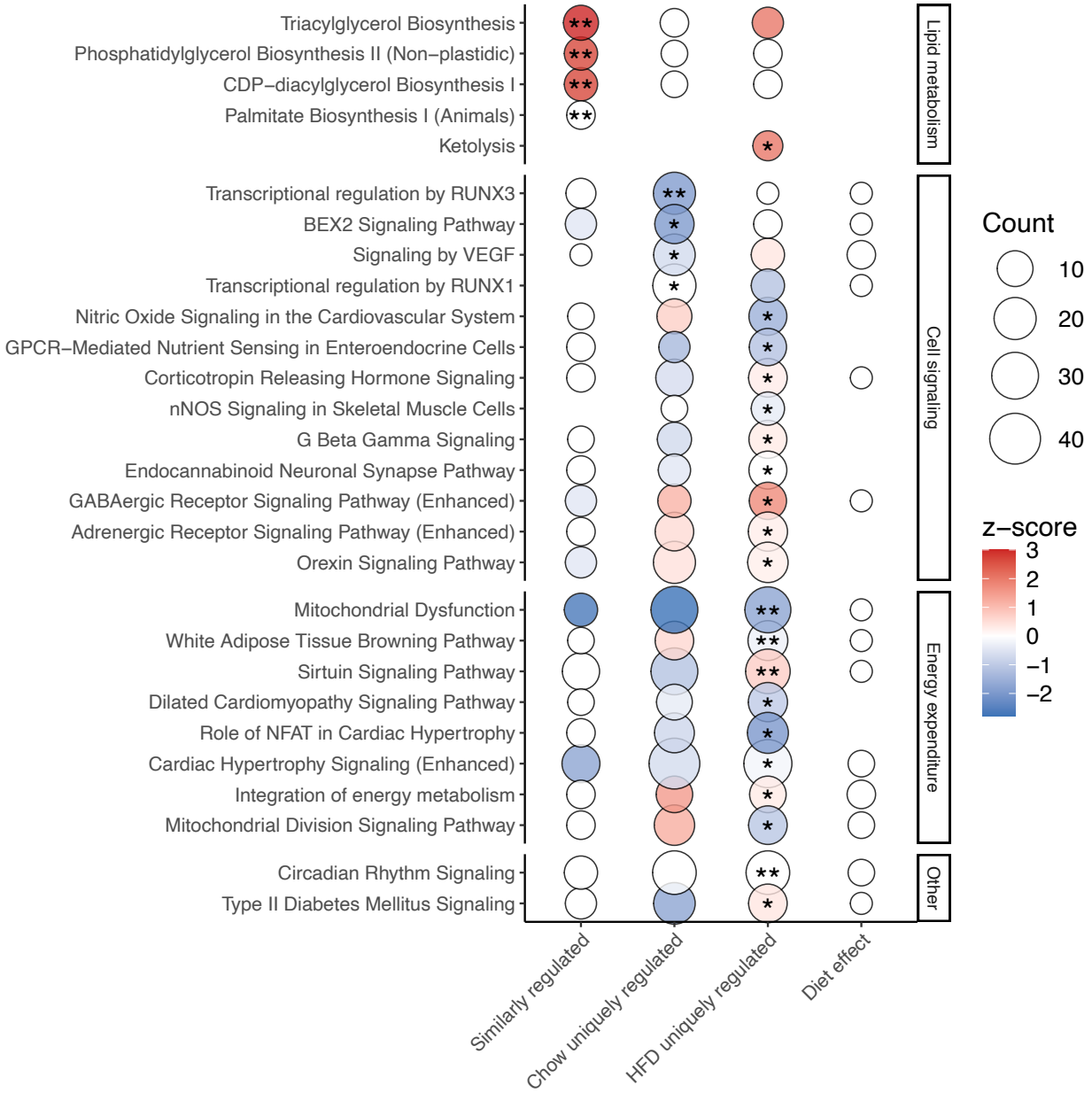


Figure 6: Pathway enrichment analysis of DMEGs for canonical pathways, diseases, and biological functions. Ingenuity Pathway Analysis (IPA) with enrichments of DMEGs were categorized into four groups: those exhibiting similar regulation in both $COLD_{chow}$ and $COLD_{HFD}$ condition pairs, and those that are uniquely regulated in each individual condition ($\Delta COLD_{diet}$, $COLD_{chow}$, and $COLD_{HFD}$). Top ten statistically significant enrichments are shown for canonical pathways. More then ten enrichments are listed in case of p ties. Circle sizes reflect the number of genes in each enrichment while the color highlights the activation z-score. Significance levels for p after adjustment for multiple testing with Bonferroni-Holm are indicated as $p < 0.05$ (*), $p < 0.01$ (**).

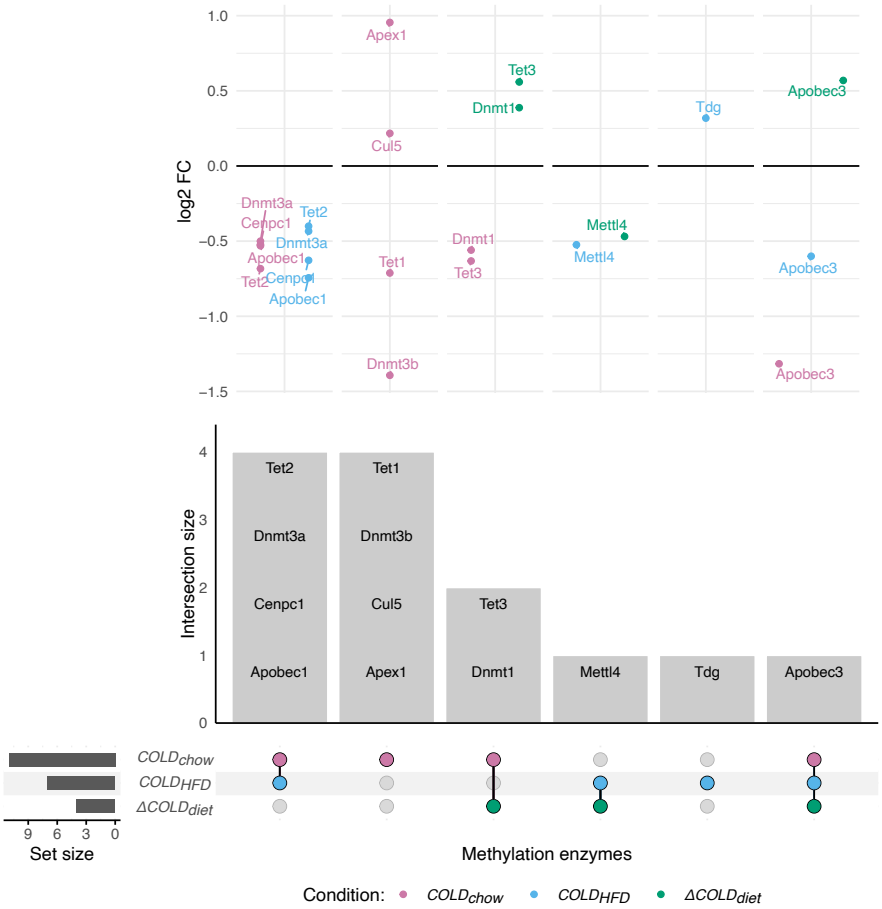
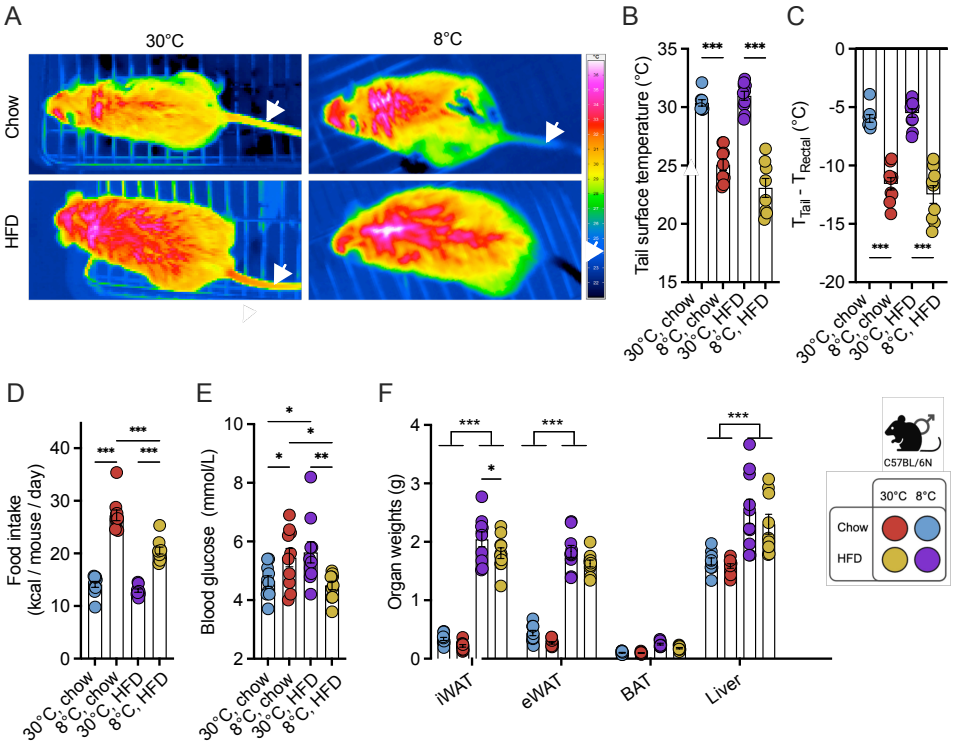
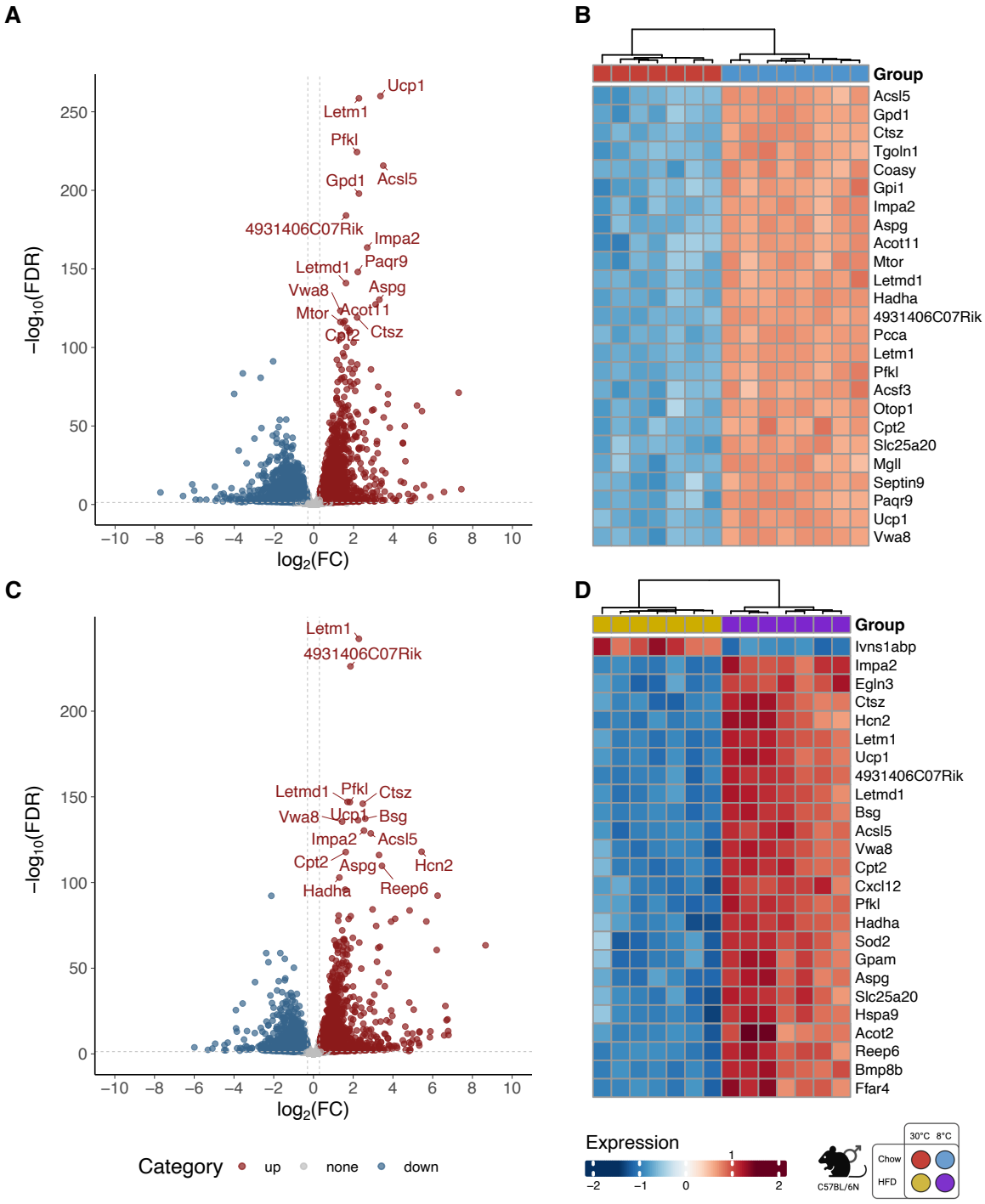


Figure 7: Overlap of methylation regulators in cold-induced BAT activation across dietary conditions. Upset plot displays the overlap of differentially expressed methylation regulators detected for the $COLD_{chow}$, $COLD_{HFD}$, and $\Delta COLD_{diet}$ condition pairs. The scatterplot shows log2 FC values for each differentially expressed methylation regulator of the respective intersect in each condition highlighted by coloring.

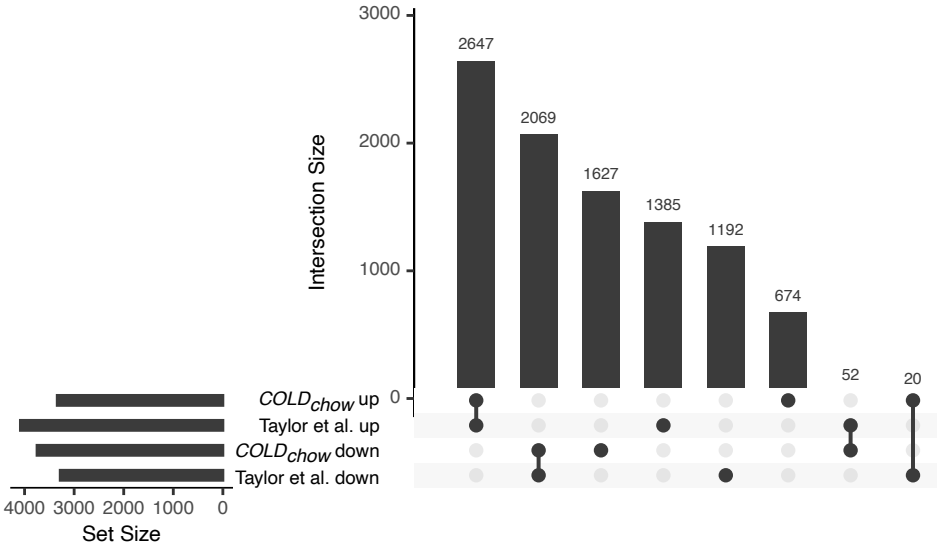
Supplementary Figures



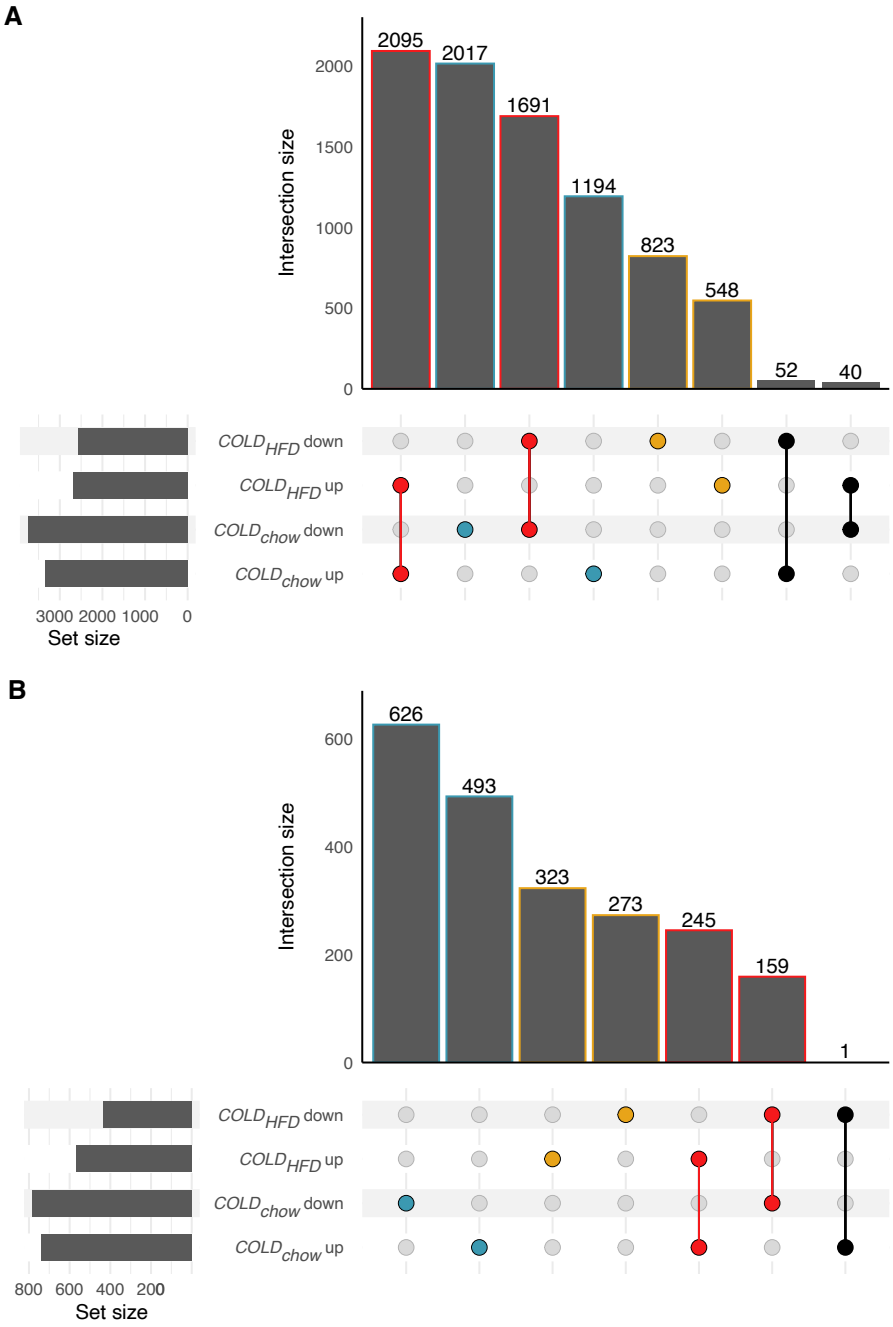
Suppl. Figure 1: Extended phenotyping of chow and HFD-fed mice housed at 30°C or 8°C. Overview thermal images from brown adipose tissue (BAT) (A), tail surface temperature (B) and heat loss (Ttail – Trectal; (C) in chow and HFD-fed mice housed at thermoneutrality (30°C) or in the cold (8°C) for 7 days. Average daily calory intake (D), final fasted blood glucose (E) and absolute organ weights (F) of inguinal white adipose tissue (iWAT), epididymal white adipose tissue (eWAT), BAT and liver of chow and HFD-fed mice housed at thermoneutrality (30°C) or in the cold (8°C) for 7 days. N = 7-8 per condition. Statistical significance was evaluated one-way ANOVA with Tukey's post-hoc test (B-D) or uncorrected Fischer's LDS (E) or two-way ANOVA with uncorrected Fischer's LDS (F). $p < 0.05$ (*), $p < 0.01$ (**), $p < 0.001$ (***).



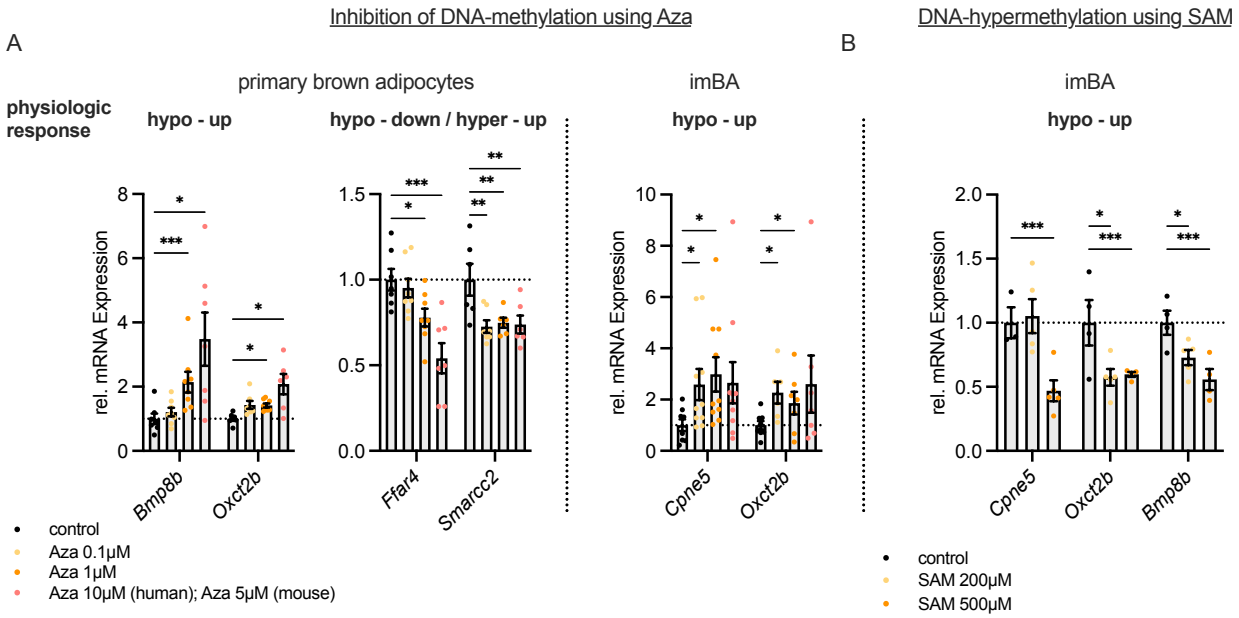
Suppl. Figure 2: Differential gene expression in response to cold exposure in chow diet and HFD-fed mice. Summary of differential gene expression signals for cold-induced BAT activation in (A, B) normal-weight control mice (*COLD*$_{chow}$) and (C, D) high fat diet (HFD)-induced obese mice (*COLD*$_{HFD}$). Volcano plots (A, C) and heatmaps (B, D) display differentially expressed genes (DGEs) based on $\log_2$ fold change (FC) and false discovery rate (FDR) signals and show clustering of the top 25 DGEs, respectively.



Suppl. Figure 3: Overlap of DEGs in the *$COLD_{chow}$* condition with published data. Upset plots show the intersection of DEGs from the *$COLD_{chow}$* condition and DEGs reported by Tayler et al. (2024) [60] for chow-fed male mice (8°C vs 28°C), categorized by positive (up) and negative (down) regulation. DEGs with adj. P >0.05 were compared. Set size indicates the total number of DEGs.

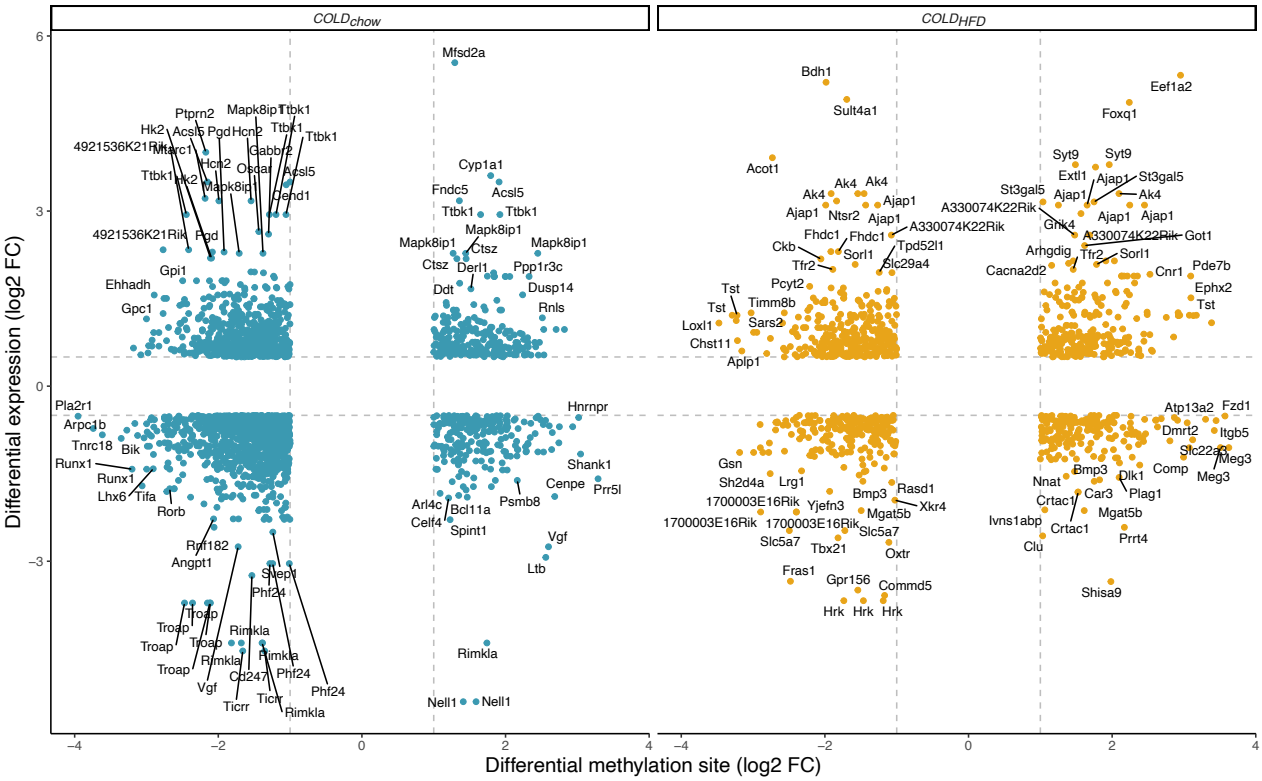


Suppl. Figure 4: Overlap of DEGs and DMEGs between the *COLD$_{chow}$* and *COLD$_{HFD}$* conditions. Upset plots display the overlap of (A) DEGs and (B) differentially methylated and expressed genes (DMEGs) for the *COLD$_{chow}$* and *COLD$_{HFD}$* condition pairs, categorized by positive (up) and negative (down) regulation. Significant DEGs or DMEGs that show the same and contrary regulatory direction in both conditions are highlighted in red and black respectively. Those significant only in the *COLD$_{chow}$* condition are shown in blue, while those significant only in the *COLD$_{HFD}$* condition are marked in yellow. Genes are counted uniquely, even though multiple DMEGs may be associated with the same gene. Set size indicates the total number of DEGs or DMEGs.



Suppl. Figure 5: In vitro validation of DNA methylation affecting expression of candidate genes. (A) Inhibition of DNA methylation using indicated concentrations of Aza in mouse immortalized (imBA, left) and primary brown adipocytes (right). Gene expression was analyzed by qPCR, N = 6-10 per condition. (B) Induction of DNA hypermethylation using indicated concentrations of SAM in mouse imBA. Gene expression was analyzed by qPCR, n = 3-5 per condition. Statistical significance was evaluated by two-way ANOVA with uncorrected Fischer's LSD. $p < 0.05$ (*), $p < 0.01$ (**), $p < 0.001$ (***).

Suppl. Figure 6: Overlapping DMEGs between *COLD$_{chow}$* and *COLD$_{HFD}$*. The scatter plot displays the $\log_2$ FC in gene expression and DNA methylation signals for all DMEGs which overlap in both *COLD$_{chow}$* and *COLD$_{HFD}$* condition. Colors correspond to highlights in Suppl. Figure 3. DMEGs with absolute $\log_2$ FC >0.5 in expression and >1 in methylation signals are shown, while DMEGs in the 5% and 95% quantile of both DMP and DEG $\log_2$ FC signals are labeled.



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929 **Suppl. Figure 7: DMEGs that are specifically regulated within each condition.** The scatter plot
930 displays the $\log_2$ FC in gene expression and DNA methylation signals for all DMEGs which are
931 specifically regulated in both $COLD_{chow}$ and $COLD_{HFD}$ conditions. Colors correspond to highlights
932 in Suppl. Figure 3. DMEGs with absolute $\log_2$ FC >0.5 in expression and >1 in methylation signals
933 are shown, while DMEGs in the 5% and 95% quantile of both DMP and DEG $\log_2$ FC signals are
934 labeled.

935 **Supplementary Table legends**

936 **Suppl. Table 1:** Overview of primers used for PCR.

937 **Suppl. Table 2:** Overview of significant (FDR <0.05) DEGs for the $COLD_{chow}$ contrast. DEGs that
938 overlap with Tayler et al. (2024) [60] (chow-fed mice, 8°C vs 28°C) are listed.

939 **Suppl. Table 3:** Overview of significant (FDR <0.05) DEGs for the $COLD_{HFD}$ contrast.

940 **Suppl. Table 4:** Overview of significant (FDR <0.05) DEGs for the $\Delta COLD_{diet}$ condition.

941 **Suppl. Table 5:** Overview of DMEGs in the $COLD_{chow}$ contrast with absolute expression $\log_2$ FC
942 >0.5 and absolute methylation $\log_2$ FC >1, including the cell type assignment derived from single-
943 cell RNAseq data obtained from [38].

944 **Suppl. Table 6:** Overview of DMEGs in the $COLD_{HFD}$ contrast with absolute expression $\log_2$ FC
945 >0.5 and absolute methylation $\log_2$ FC >1.

946 **Suppl. Table 7:** Overview of DMEGs in the $\Delta COLD_{diet}$ contrast with absolute expression $\log_2$ FC
947 >0.5 and absolute methylation $\log_2$ FC >1.

948 **Suppl. Table 8:** Significant IPA enrichment (before p adjustment) for canonical pathways
949 categorized by four groups: those exhibiting similar regulation in both $COLD_{HFD}$ and $COLD_{chow}$
950 condition pairs, and those that are uniquely regulated in each individual condition ($\Delta COLD_{diet}$,
951 $COLD_{chow}$, and $COLD_{HFD}$.)