



Supplementary Materials

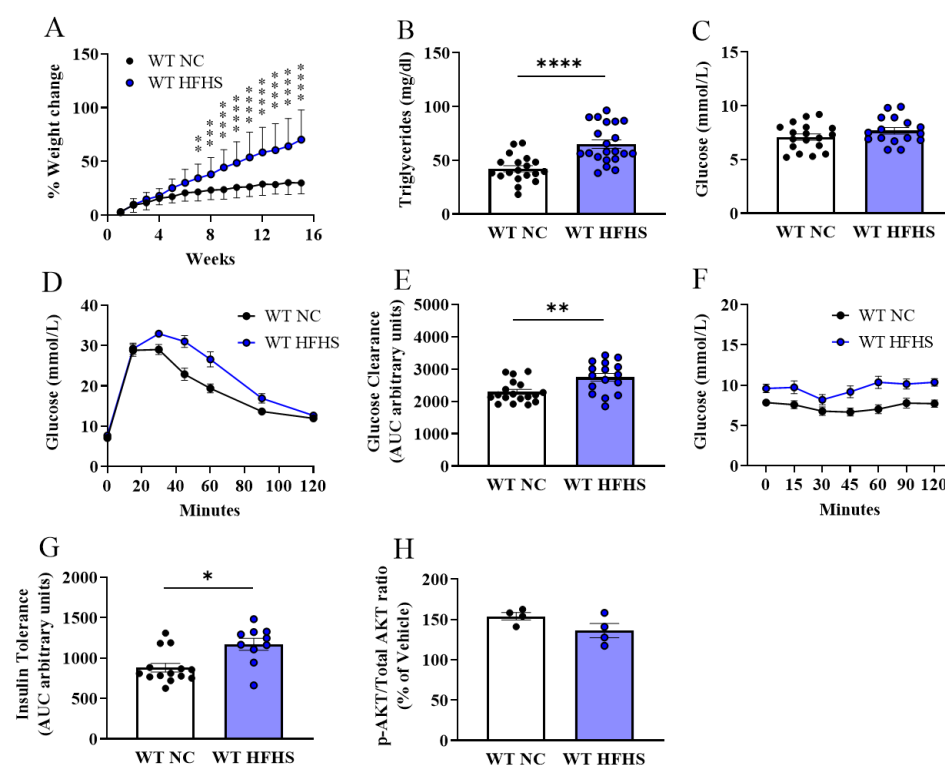


Figure S1. Weight gain and metabolic parameters of WT mice under obesogenic stress. A. Percentage weight change at endpoint from baseline. B. Plasma triglyceride levels. C. Fasting plasma glucose levels. D-E. Area under the curve analysis of IP-glucose tolerance test. F-G. Area under the curve analysis of IP-insulin tolerance test. H. Phosphorylated AKT/Total AKT ratio displayed as a percentage of vehicle control in insulin-stimulated adipose tissue. For statistical analysis, 2-way ANOVA was performed in A; Mann-Whitney test was performed in E and G; unpaired t-test was performed on B, C and H. Normality was assessed using the Shapiro-Wilk test. All values are represented as means with error bars representing SEM. * $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$.

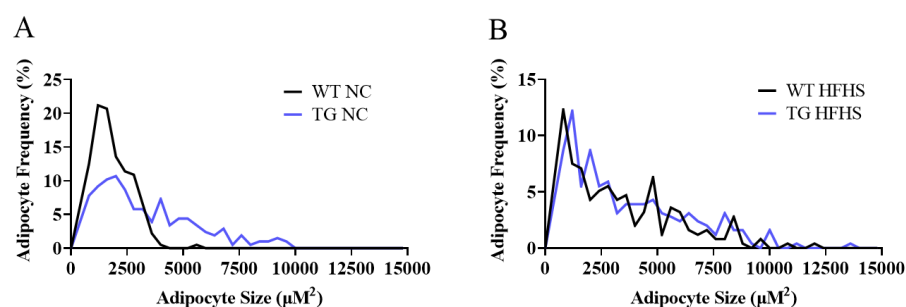


Figure S2. Adipocyte size frequency histogram. A. Frequency histogram of adipocytes by area (μm^2) in WT vs AdipoQ-mCAT TG mice under physiological diet conditions. B. Frequency histogram of adipocytes by area (μm^2) in WT vs AdipoQ-mCAT mice under obesogenic stress.

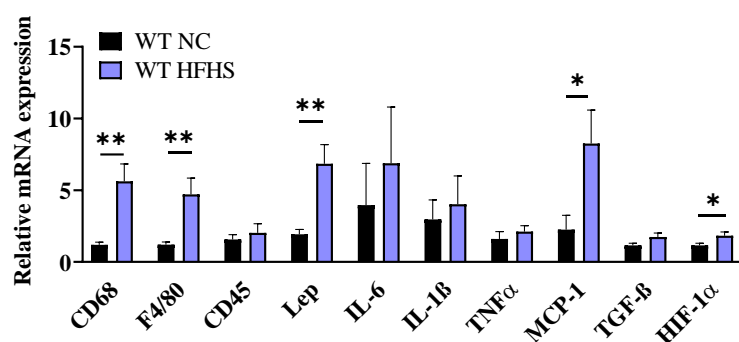


Figure S3. Gene expression analysis of white adipose tissue of WT mice under obesogenic stress. A. Quantitative PCR analysis of gene expression in white adipose tissue of WT mice fed NC diet versus HFHS diet ($n = 9,10$ per group). For statistical analysis, unpaired t-tests or Mann-Whitney tests were performed. Normality was assessed using the Shapiro-Wilk test. All values are represented as means with error bars representing SEM. * $p < 0.05$, ** $p < 0.01$.

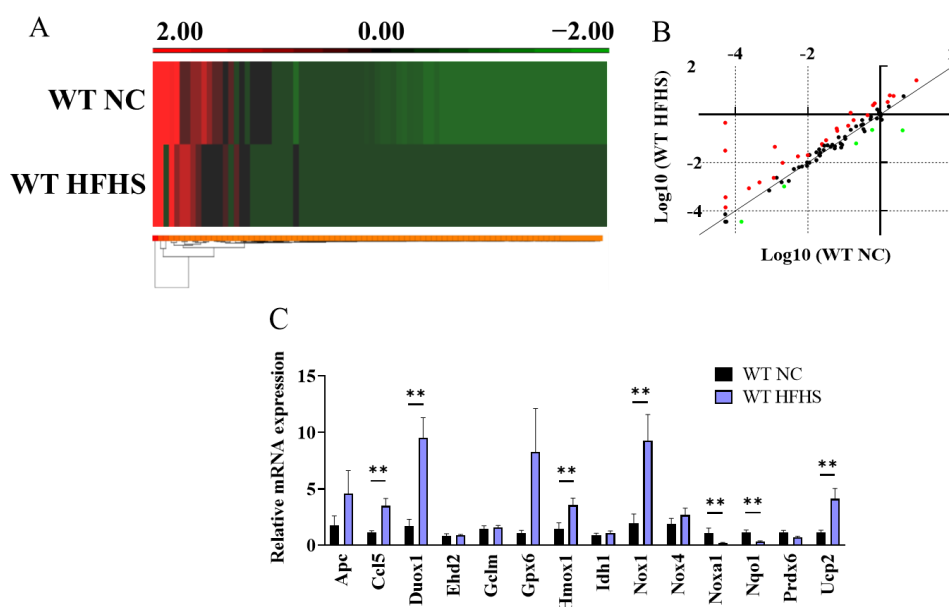


Figure S4. Analysis of oxidative stress genes in adipose tissue of WT mice under conditions of obesogenic stress. A. Gene expression heat map comparing oxidative stress genes in adipose tissue of WT mice after 16 weeks of HFHS diet compared to NC diet. B. Scatterplot representing differentially expressed genes in an oxidative stress qPCR panel. Red: Genes over-expressed 2-fold or more in WT HFHS vs WT NC mice; Green: Genes under-expressed 2-fold or more in WT HFHS vs WT NC mice. C. Differentially expressed genes were validated in adipose tissue using qPCR ($n = 6-9$ per group). Normality was determined using Shapiro-Wilk test in B-D. Unpaired t-tests or Mann-Whitney tests were performed in C. All values are represented as means with error bars representing SEM. ** $p < 0.01$.

Table S1. Pre-designed qPCR primers.

Primer Name	Catalogue Number	Manufacturer
Mouse IL6	M_Il6_1	Sigma-Aldrich KicqStart Primers
Mouse IL1B	M_Il1b_1	Sigma-Aldrich KicqStart Primers
Mouse LEP	M_Lep_1	Sigma-Aldrich KicqStart Primers
Mouse MCP-1	M_Ccl2_1	Sigma-Aldrich KicqStart Primers
Mouse HIF1a	M_Hif1a_1	Sigma-Aldrich KicqStart Primers
Mouse Duox1	M_Duox1_1	Sigma-Aldrich KicqStart Primers
Mouse Gpx5	M_Gpx5_1	Sigma-Aldrich KicqStart Primers

Mouse Noxa1	M_Noxa1_1	Sigma-Aldrich KicqStart Primers
Mouse Nqo1	M_Nqo1_1	Sigma-Aldrich KicqStart Primers
Mouse Prdx6	M_Prdx6_1	Sigma-Aldrich KicqStart Primers
Human Catalase	Hs00156308_m1	Thermo Fisher Taqman Assay
Mouse GAPDH	4326317	Thermo Fisher Taqman Assay

Table S2. qPCR primer sequences.

Primer Name	Forward Primer 5' -> 3'	Reverse Primer 5' -> 3'
Mouse CD68	AGGACCGCTTATAGCCCAAG	GGATGGCAGGAGAGTAACGG
Mouse F4/80	GTGACTCACCTTGTGGTCCT	CAGACACTCATCAACATCTGCG
Mouse CD45	AGAAGTCTTTGTCACAGGGCA	AAGAAGGGCATTCTCTGTTGTG
Mouse TGFB1	ACTGGAGTTGTACGGCAGTG	GGGGCTGATCCCGTTGATT
Mouse TNFA	CCCACGTCGTAGCAAACCA	ACAAGGTACAACCCATCGGC
Mouse PPIA	CATTCTGGACCCAAAACG	GGCAAATGCTGGACCAAAC
Mouse Ccl5	ATATGGCTCGGACACCACTC	CTTCGAGTGACAAACACGACTG
Mouse Gclm	ACAATGACCCGAAAGAAGTGC	GAGCTGGAGTTAAGAGCCCC
Mouse Gpx6	GTCACGGTTTTGGGCTTTCC	GCCTGGACGCACATACTTGA
Mouse Hmox1	GCCCCACCAAGTTCAAACAG	GCTCCTCAAACAGCTCAATGT
Mouse Nox1	GTTTCTCTCCCGAAGGACCTCT	GGCCAAGGCAGTCCCAAGAA
Mouse Nox4	CCAAATGTTGGGCGATTGTGT	AGGATGAGGCTGCAGTTGAG
Mouse Apc	CCCTATGTACGCCTTCCTGC	CTACCCTTGGACCTGCCAGA
Mouse Ehd2	TCGTTGTGGACCCAGAGAAG	GGCGCACATAAACCTGTTG
Mouse Idh1	TTCCGAGCGAAGGTTGTGG	TTTACTTCAATAACCCGGCTCAC
Mouse Ucp2	CCTCCCTTGCCACTTCACTT	GGAAGGCATGAACCCCTTGTA
Mouse Hsp90ab1	AGATTCCAATAACCGACGCC	TGCTCTTTGCTCTCACCAGT
Mouse GAPDH	TACGGGTGCACGTAGCTCA	AATACGGCCAAATCCGTTTAC

Table S3. Differentially expressed (>2-fold) oxidative stress genes in adipose tissue of AdipoQ-mCAT mice versus Wild-type.

Gene Symbol	Refseq ID	Gene Name	Fold Regulation (vs Wild-type)
<i>Alb</i>	NM_009654	Albumin	-79.35
<i>Aox1</i>	NM_009676	Aldehyde oxidase 1	2.78
<i>Apc</i>	NM_007462	Adenomatosis polyposis coli	2.25
<i>Ccl5</i>	NM_013653	Chemokine (C-C motif) ligand 5	3.37
<i>Duox1</i>	NM_001099297	Dual oxidase 1	3.36
<i>Ehd2</i>	NM_153068	EH-domain containing 2	2.13
<i>Gclm</i>	NM_008129	Glutamate-cysteine ligase, modifier subunit	2.03
<i>Gpx5</i>	NM_010343	Glutathione peroxidase 5	37222.98
<i>Gpx6</i>	NM_145451	Glutathione peroxidase 6	241.36
<i>Hmox1</i>	NM_010442	Heme oxygenase (decycling) 1	-2.84
<i>Hspa1a</i>	NM_010479	Heat shock protein 1A	3.41
<i>Idh1</i>	NM_010497	Isocitrate dehydrogenase 1 (NADP+), soluble	4354.68
<i>Ift172</i>	NM_026298	Intraflagellar transport 172 homolog (Chlamydomonas)	708.21
<i>Mb</i>	NM_013593	Myoglobin	3.17
<i>Mpo</i>	NM_010824	Myeloperoxidase	3.87
<i>Ncf2</i>	NM_010877	Neutrophil cytosolic factor 2	3.41
<i>Nox1</i>	NM_172203	NADPH oxidase 1	4.68
<i>Noxa1</i>	NM_172204	NADPH oxidase activator 1	2.57

<i>Nqo1</i>	NM_008706	NAD(P)H dehydrogenase, quinone 1	5.85
<i>Prdx6</i>	NM_007453	Peroxiredoxin 6	2.22
<i>Prnp</i>	NM_011170	Prion protein	2.31
<i>Ptgs1</i>	NM_008969	Prostaglandin-endoperoxide synthase 1	2.89
<i>Ptgs2</i>	NM_011198	Prostaglandin-endoperoxide synthase 2	319.82
<i>Srxn1</i>	NM_029688	Sulfiredoxin 1 homolog (S. cerevisiae)	−2.84
<i>Ucp2</i>	NM_011671	Uncoupling protein 2 (mitochondrial, proton carrier)	2.72
<i>Vim</i>	NM_011701	Vimentin	2.72

Table S4. Differentially expressed (>2-fold) oxidative stress genes in adipose tissue of Wild-type mice fed NC vs HFHS diet.

Gene Symbol	Refseq ID	Gene Name	Fold Regulation (vs Wild-type NC)
<i>Alb</i>	NM_009654	Albumin	−18.87
<i>Aox1</i>	NM_009676	Aldehyde oxidase 1	2.43
<i>Ccl5</i>	NM_013653	Chemokine (C-C motif) ligand 5	3.41
<i>Ctsb</i>	NM_007798	Cathepsin B	4.08
<i>Cyba</i>	NM_007806	Cytochrome b-245, alpha polypeptide	4.14
<i>Cygb</i>	NM_030206	Cytoglobin	2.13
<i>Duox1</i>	NM_001099297	Dual oxidase 1	3.28
<i>Ehd2</i>	NM_153068	EH-domain containing 2	3.18
<i>Epx</i>	NM_007946	Eosinophil peroxidase	−4.21
<i>Gpx1</i>	NM_008160	Glutathione peroxidase 1	2.04
<i>Gpx7</i>	NM_024198	Glutathione peroxidase 7	2.06
<i>Gstp1</i>	NM_013541	Glutathione S-transferase, pi 1	−2.64
<i>Idh1</i>	NM_010497	Isocitrate dehydrogenase 1 (NADP+), soluble	8689.38
<i>Ift172</i>	NM_026298	Intraflagellar transport 172 homolog (Chlamydomonas)	604.75
<i>Mpo</i>	NM_010824	Myeloperoxidase	6.84
<i>Ncf2</i>	NM_010877	Neutrophil cytosolic factor 2	2.68
<i>Ngb</i>	NM_022414	Neuroglobin	−2.17
<i>Nox1</i>	NM_172203	NADPH oxidase 1	2.64
<i>Nox4</i>	NM_001285833	NADPH oxidase 4	4.86
<i>Prnp</i>	NM_011170	Prion protein	2.61
<i>Ptgs2</i>	NM_011198	Prostaglandin-endoperoxide synthase 2	37.03
<i>Recql4</i>	NM_058214	RecQ protein-like 4	3.65
<i>Scd1</i>	NM_009127	Stearoyl-Coenzyme A desaturase 1	2.62
<i>Serpinb1b</i>	NM_173052	Serine (or cysteine) peptidase inhibitor, clade B, member 1b	2.05
<i>Sod3</i>	NM_011435	Superoxide dismutase 3, extracellular	2.09
<i>Srxn1</i>	NM_029688	Sulfiredoxin 1 homolog (S. cerevisiae)	−3.43
<i>Ucp2</i>	NM_011671	Uncoupling protein 2 (mitochondrial, proton carrier)	7.72
<i>Vim</i>	NM_011701	Vimentin	3.85

Table S5. Differentially expressed (>2-fold) oxidative stress genes in adipose tissue of AdipoQ-mCAT HFHS mice versus Wild-type HFHS.

Gene Symbol	Refseq ID	Gene Name	Fold Regulation (vs Wild-type)
<i>Ccl5</i>	NM_013653	Chemokine (C-C motif) ligand 5	3.55

<i>Il19</i>	NM_001009940	Interleukin 19	2.01
<i>Lpo</i>	NM_080420	Lactoperoxidase	2.05
<i>Mb</i>	NM_013593	Myoglobin	140.79
<i>Mpo</i>	NM_010824	Myeloperoxidase	2.73
<i>Ucp3</i>	NM_009464	Uncoupling protein 3 (mitochondrial, proton carrier)	2.03
<i>Alb</i>	NM_009654	Albumin	−7.39
<i>Ngb</i>	NM_022414	Neuroglobin	−2.53
<i>Ptgs2</i>	NM_011198	Prostaglandin-endoperoxide synthase 2	−12.67
