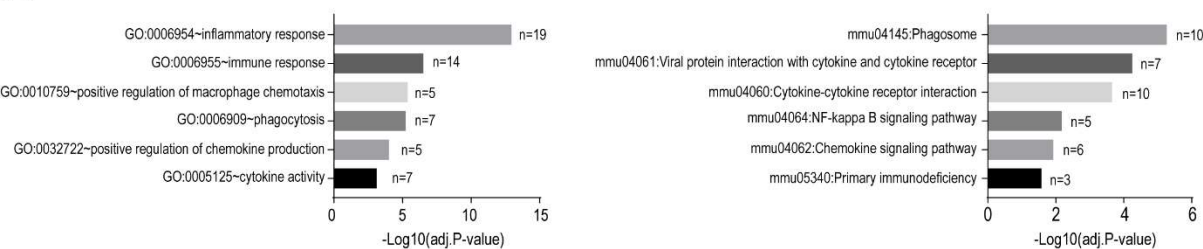


Supplementary Figures and Figure Legends

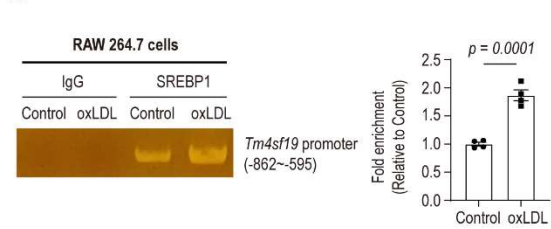
A



B

Target Sequences	Motif	Transcription ID	Best Match	Score
GGGTTTCTCT	GGGAAATCC	MA0105.1	NFKB1 (Mus musculus)	0.801
GGAATGTTT	GGGAAATCC	MA0105.1	NFKB1 (Homo sapiens)	0.817
Mus musculus: CTCACTCCAC Homo sapiens: ATCACCTGAT	TCACCCCA	MA0595.1	SREBF1	0.954 0.894
Mus musculus: GTGGGGTGAG Homo sapiens: TTGCAGTGAG	TGGGGTGA	MA0596.1	SREBF2	0.964 0.851

C



D

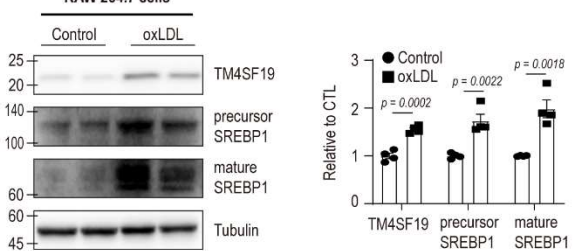


Figure S1. Characterization of obesity-induced upregulation of *Tm4sf19* in adipose tissue macrophages.

A. Gene ontology (GO) enrichment analysis and KEGG pathway analysis of the top 100 genes upregulated by obesity from each dataset.

B. Conserved sequences of NFKB1, SREBF1, and SREBF2 binding sites in the promoter of mouse *Tm4sf19* and human *TM4SF19*. Scores described the similarity values of the transcription factor binding sites.

C. Chromatin immunoprecipitation (ChIP) enrichment analysis of recruitment of SREBP1 to *Tm4sf19* promoter in RAW264.7 cells treated with oxLDL (100 µg/ml for 24 hours) by PCR and q-PCR. PCR amplification was carried out with DNA fragments immunoprecipitated by anti-SREBP1 antibody and negative control IgG (n = 4 biologically independent replicates).

D. Immunoblot analysis of TM4SF19 and SREBP1 protein levels in RAW264.7 cells after oxLDL treatment (100 µg/ml) for 24 hours.

Source data are provided as a Source Data file.

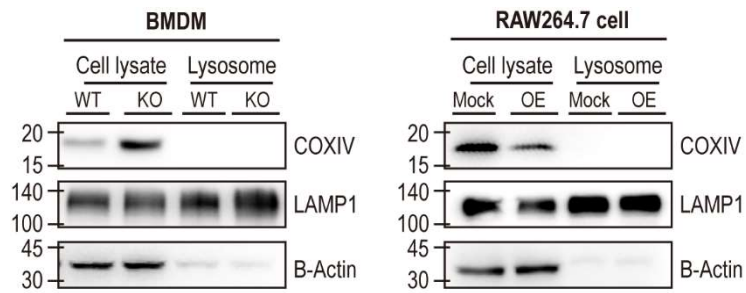


Figure S2. Immunoblot analysis of lysosome fraction from TM4SF19 overexpressing RAW264.7 cells and TM4SF19 KO BMDMs.

Immunoblot analysis confirmed the purity of lysosomal fraction obtained from BMDM of WT and TM4SF19 KO mice, and TM4SF19 overexpressing RAW 246.7 cells used for Figure 2E. LAMP1 was used as a lysosomal marker and β -actin was used as a cytosol marker. (n = 3 biologically independent replicates).

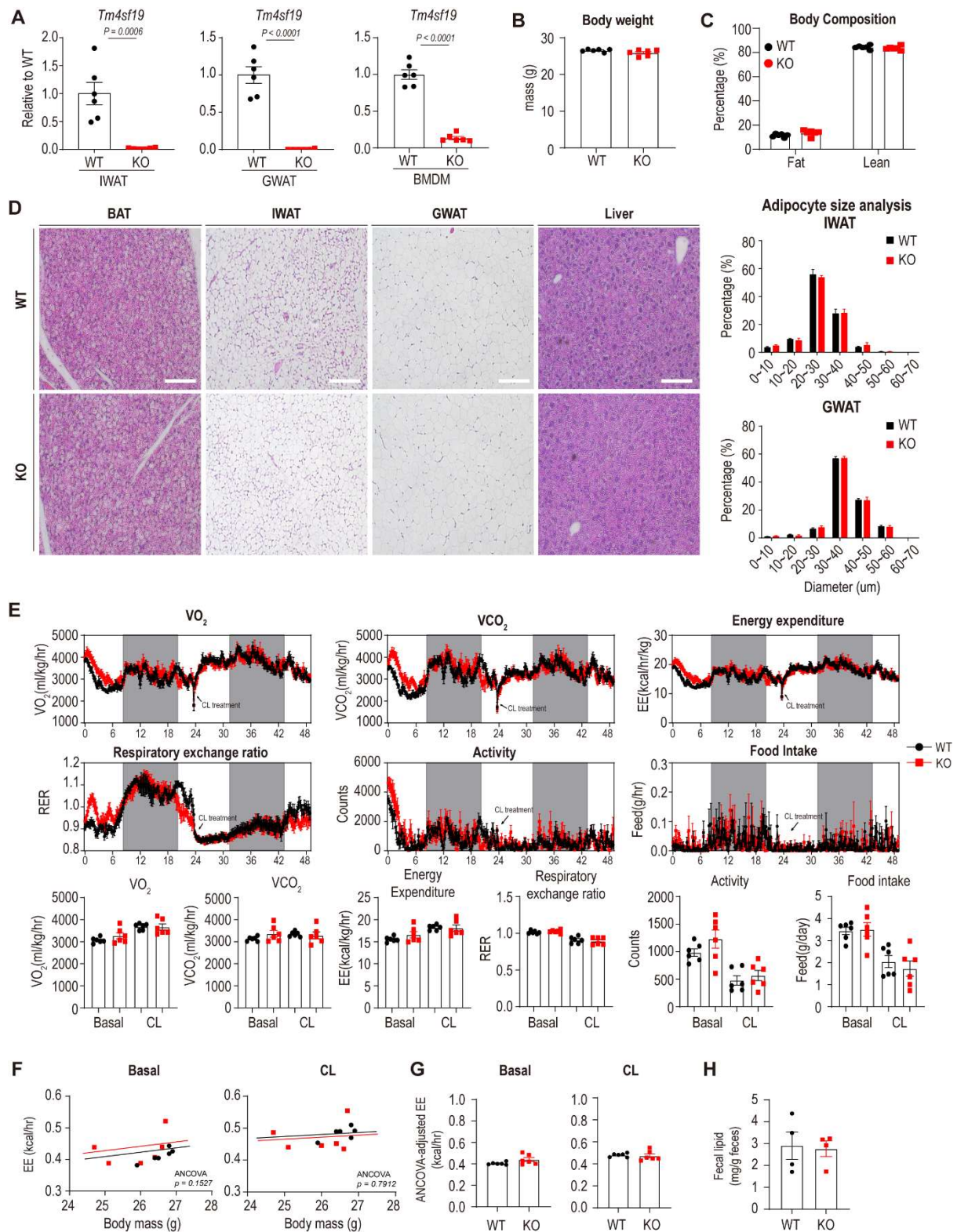


Figure S3. Metabolic phenotype analysis in WT and TM4SF19 KO mice under chow diet feeding.

A. *Tm4sf19* mRNA expression levels in IWAT, GWAT, and bone-marrow-derived macrophages (BMDM) of wild-type (WT) and TM4SF19 KO mice fed a normal chow diet (NCD) (n = 6

biologically independent replicates).

B. Body weight monitoring of WT and TM4SF19 KO mice for 10 weeks (n = 10 mice).

C. Body composition analysis of WT and TM4SF19 KO mice (n = 9 mice).

D. Representative hematoxylin and eosin (H&E) stained image of paraffin sections of BAT, IWAT, GWAT, and liver, along with quantification of lipid droplet sizes in IWAT and GWAT from WT and TM4SF19 KO mice (n = 6 mice). Scale bar = 50 μ m

E. Indirect calorimetry analysis of WT and TM4SF19 KO mice before and after CL 316,243 treatment (1mg/kg, i.p.) (n = 6 mice). The points of CL treatment are indicated by the arrows in the graph.

F. Regression plots of energy expenditure against body mass and ANCOVA test using body mass as a covariate. (n = 6 mice).

G. ANCOVA -adjusted energy expenditure (EE) (predicted at the mean body mass (26.2 g)). (n = 6 mice).

H. Lipid content in feces of WT and TM4SF19 KO mice (n = 4 mice).

Source data are provided as a Source Data file.

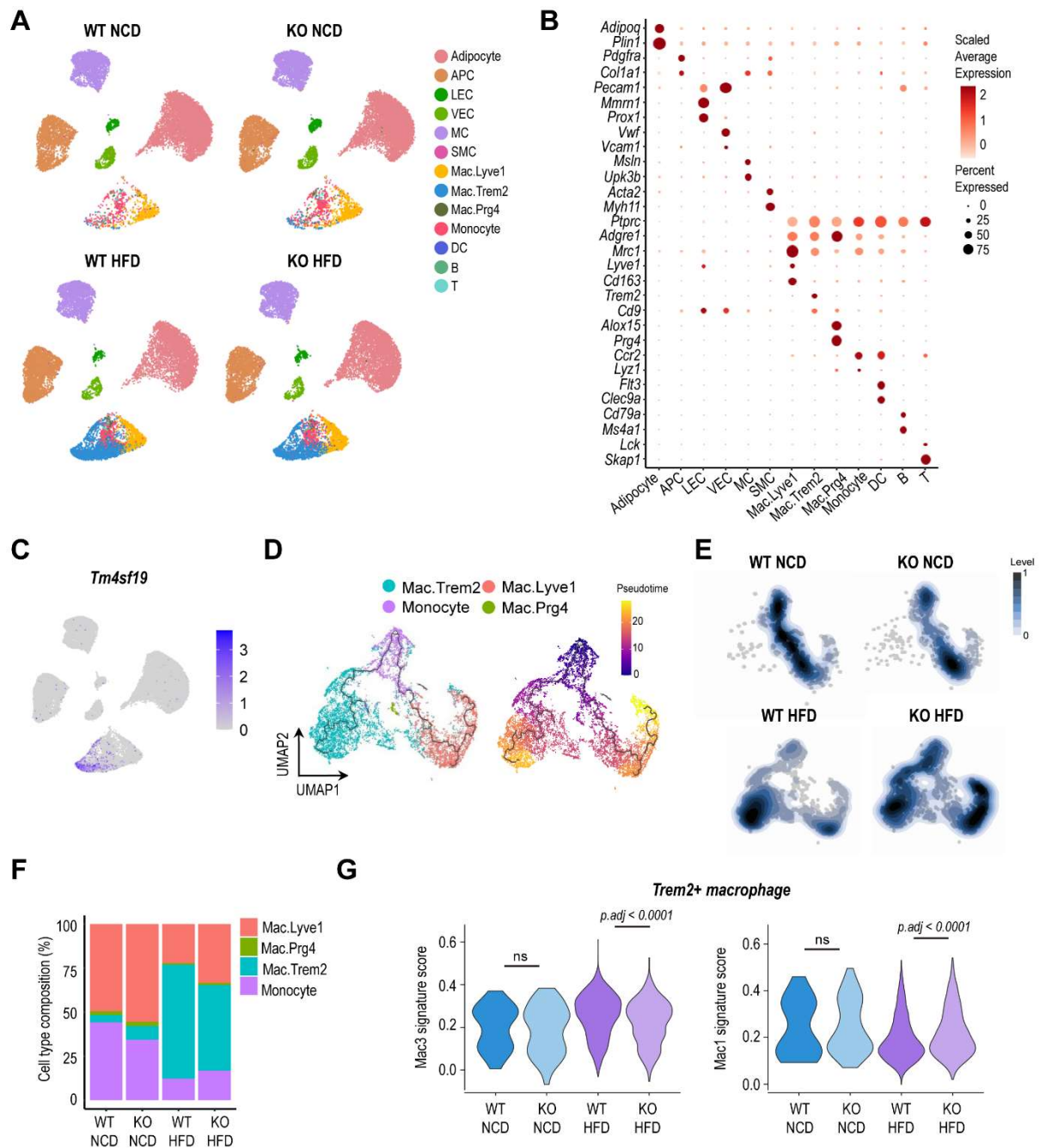


Figure S4. Characterization of cell types in mouse GWAT and trajectory analysis of monocytes/macrophages.

A. UMAP plots isolated from GWAT of NCD and HFD-fed WT and TM4SF19 KO mice.

B. Dot plot showing the marker gene expression to define the cell types.

C. *Tm4sf19* gene expression on UMAP plot. The density of purple colors presents the expression levels of *Tm4sf19* in GWAT.

D. UMAP plot showing the differentiation paths from monocyte to macrophages constructed using Monocle3. Cells were colored by cell types (left) and pseudotime (right). The line on the UMAP plot shows a differentiation trajectory.

E. UMAP plots split by condition (WT NCD, TM4SF19 KO NCD, WT HFD, TM4SF19 KO

HFD). The color indicates the density of cells in each condition.

F. Cell type compositions of monocyte and macrophage population in each condition (WT NCD, TM4SF19 KO NCD, WT HFD, TM4SF19 KO HFD).

G. Mac3 and Mac1 signature scores of *Trem2*⁺ macrophage in each condition (WT NCD, TM4SF19 KO NCD, WT HFD, TM4SF19 KO HFD).

Source data are provided as a Source Data file.

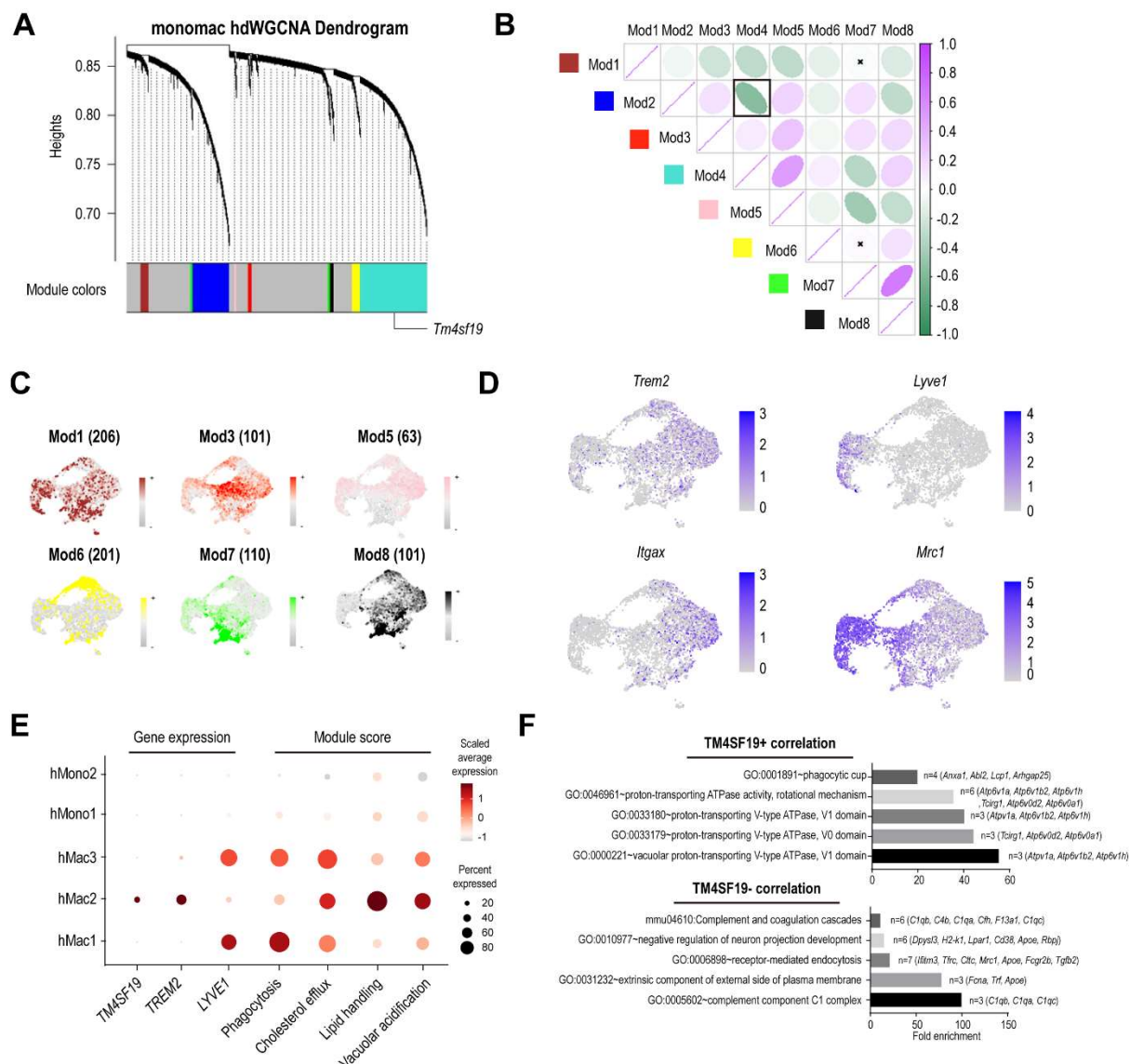


Figure S5. Molecular characterization of adipose tissue macrophage subtypes by snRNA-seq analysis.

A. WGCNA dendrogram showing co-expression modules from the network analysis of monocyte and macrophage population from WT HFD condition. Each leaf represents a gene, and each color indicates a co-expression gene module. Genes expressed over 5% of cells were used for analysis.

B. Correlation between each module from A. *Tm4sf19* gene is included in Mod4.

C. UMAP plot showing module eigengenes (MEs) score. The number indicates the number of genes in each module in the WT HFD mice.

D. *Trem2*, *Lyve1*, *Itgax*, *Mrc1* gene expression on UMAP plot. The density of purple colors presents the expression levels of each gene in GWAT of WT HFD.

E. Dot plot showing specific gene expression and module scores in human macrophage and monocyte population (GSE176171).

F. Gene ontology enrichment analysis of different gene expressions of TM4SF19 positive/negative correlation genes in monocyte/macrophage clusters in WT HFD groups.

Source data are provided as a Source Data file.

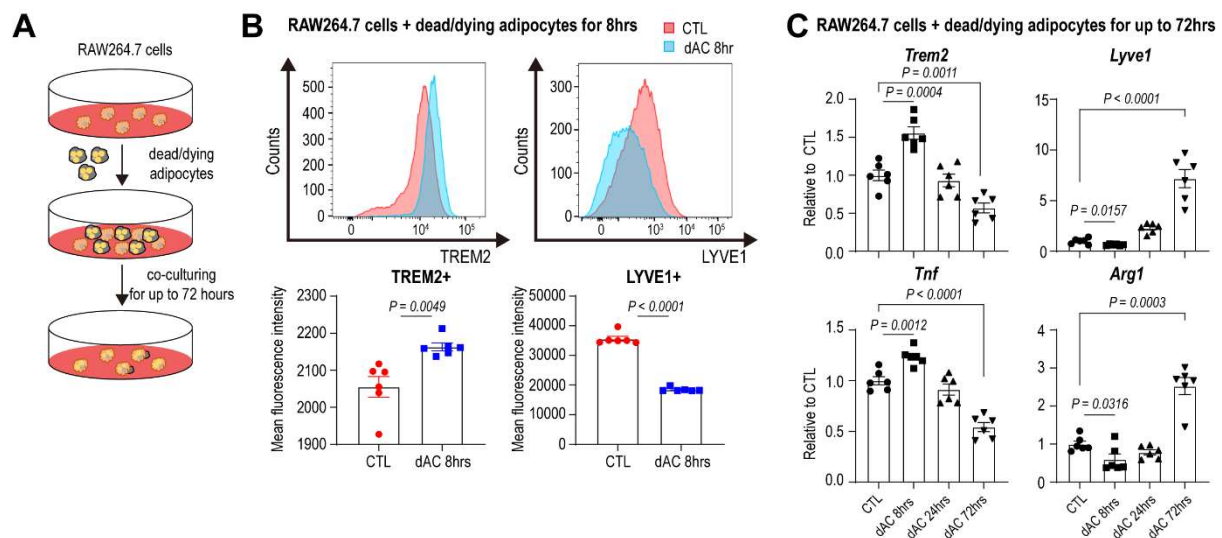


Figure S6. Molecular characterization of macrophages by single-cell analysis and macrophage/adipocyte co-cultures

A. Schematic diagram of RAW264.7 cells co-cultured with dead/dying adipocytes.

B. Histogram of TREM2+ and LYVE1+ macrophages in RAW264.7 cells co-cultured with dead/dying adipocytes for 8 hours (n = 6 biologically independent replicates).

C. qPCR analysis of *Trem2*, *Lyve1*, *Tnf*, and *Arg1* gene expression levels in RAW264.7 cells co-cultured with dead/dying adipocytes for up to 72 hours (n = 6 biologically independent replicates).

Source data are provided as a Source Data file.

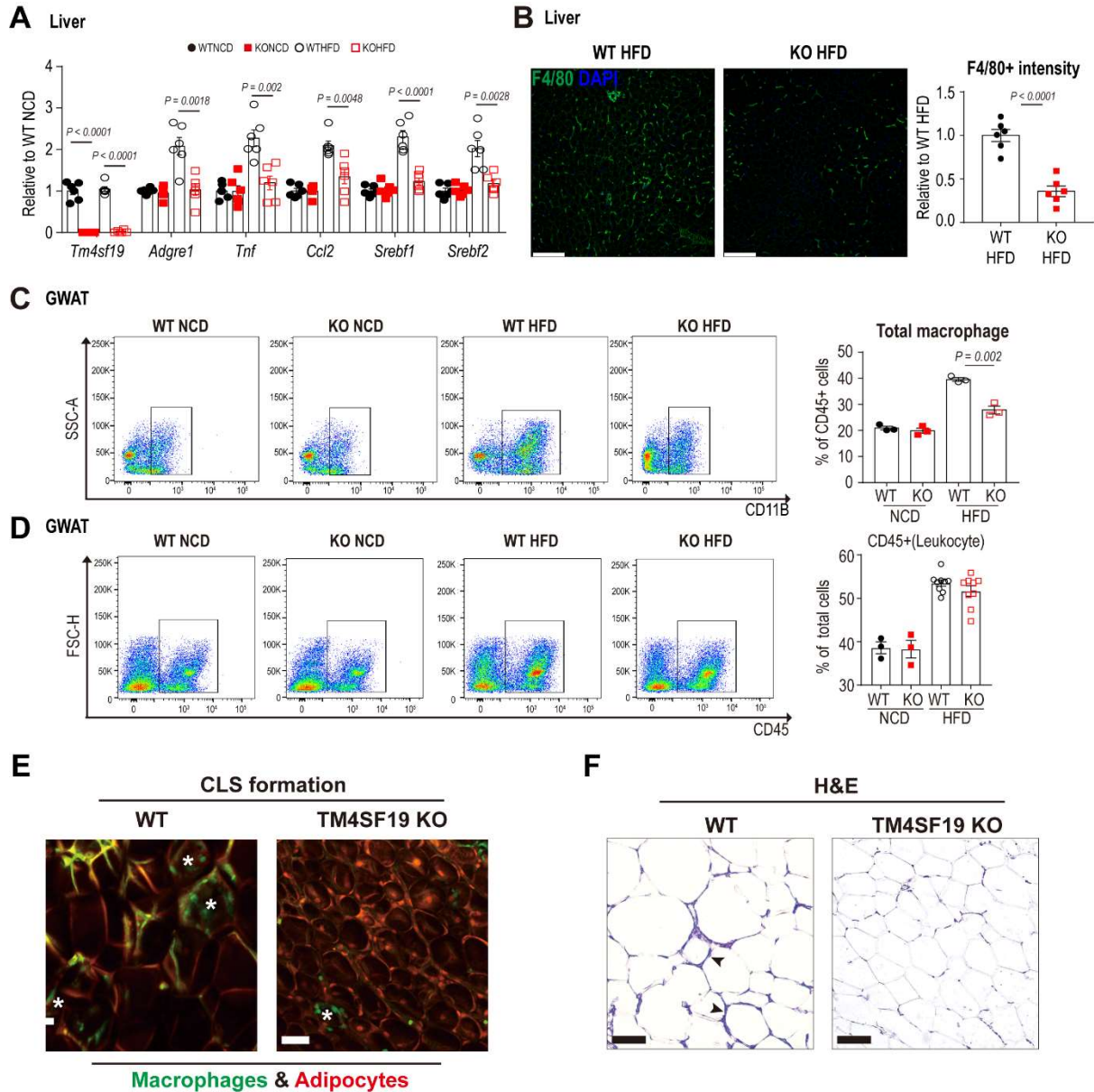


Figure S7. Effects of TM4SF19 KO on HFD-induced macrophage recruitment in liver and adipose tissue

A. mRNA expression levels of genes involved in inflammatory response and lipogenesis in liver of WT and TM4SF19 KO HFD mice (n = 6 mice).

B. Immunofluorescence staining of F4/80 in paraffin sections from liver of WT and TM4SF19 KO HFD mice (n = 6). Scale bar = 50 μ m

C-D. Representative flow profiles of CD11b (C) and CD45 (D) expression levels from GWAT of WT and TM4SF19 KO mice fed NCD or HFD for 12 weeks (n = 3, 9 mice).

E. Representative fluorescent images of CX3CR1-GFP expression (visualized monocytes/macrophages) and Pdgfra-Cre/Td-tomato expression (visualized PDGFRA⁺ cell-derived progeny (adipocytes and PDGFRA⁺ cells)) in GWAT of WT and TM4SF19 KO mice.

F. Representative hematoxylin and eosin (H&E) stained images of paraffin sections of GWAT of WT and TM4SF19 KO mice. White asterisks (E) and black arrows (F) indicated the crown-like structures (CLS). Scale bars = 50 μ m.

Source data are provided as a Source Data file.

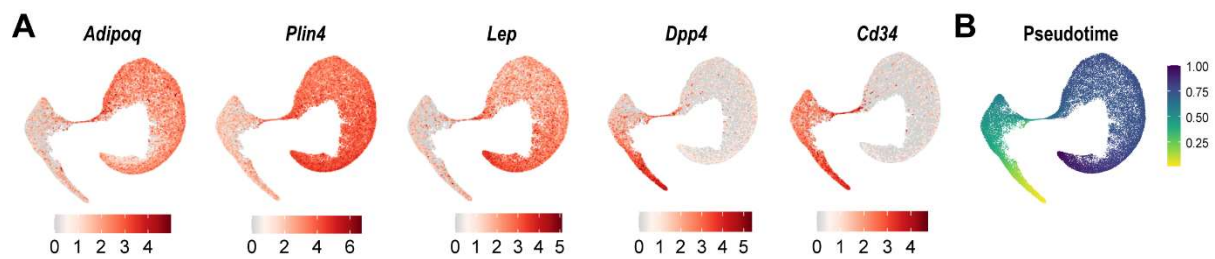


Figure S8. Trajectory analysis of APC/Adipocyte populations

A. *Adipoq*, *Plin4*, *Lep*, *Dpp4*, and *Cd34* gene expression in APCs and Adipocyte populations.
 B. Pseudotime showing differentiation trajectory of APCs to adipocytes.

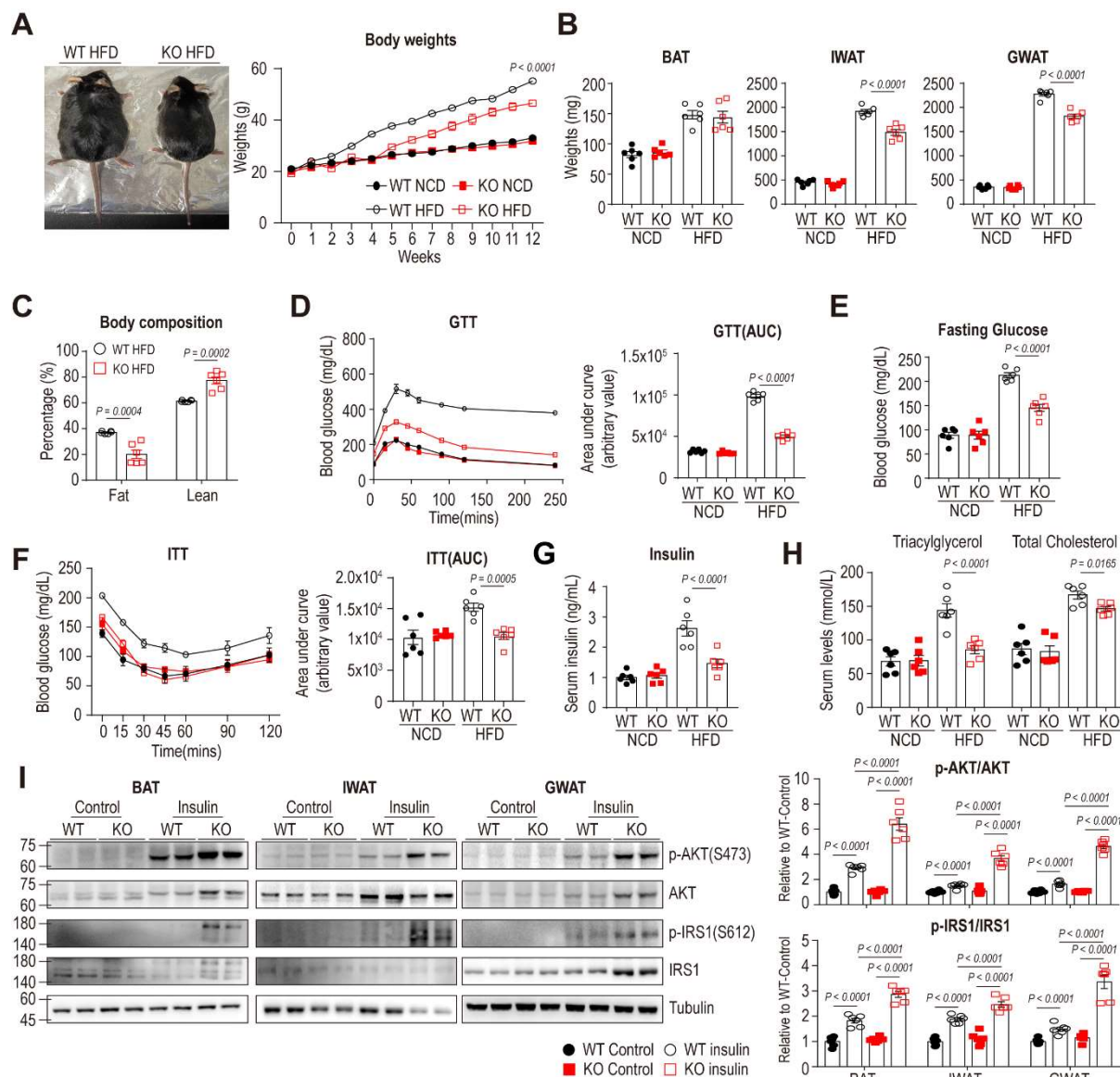


Figure S9. TM4SF19 KO protects mice from obesity-induced metabolic dysfunction.

A. Representative images of wild-type (WT) and TM4SF19 KO mice after 12 weeks of high-fat diet (HFD) feeding, and mouse weight monitoring of WT and TM4SF19 KO mice fed a normal chow diet (NCD) or HFD for 12 weeks ($n = 6$ mice).

B-F. Adipose tissue mass (B), body composition (C), glucose tolerance test (GTT) (D), fasting glucose levels (E), and insulin tolerance test (ITT) (F) of WT and TM4SF19 KO mice after 12 weeks of NCD and HFD feeding ($n = 6$ mice).

G. Serum insulin levels of WT and TM4SF19 KO mice after 12 weeks NCD and HFD feeding ($n = 6$).

H. Serum triacylglycerol and total cholesterol of WT and TM4SF19 KO mice after 12 weeks of NCD and HFD feeding ($n = 6$ mice).

I. Immunoblot analysis of p-AKT, AKT, p-IRS1, and IRS1 protein expression levels of WT and TM4SF19 KO mice after 12 weeks of HFD feeding. Tissues were collected 10 min after insulin treatment (0.75IU/kg) ($n = 6$ mice).

Source data are provided as a Source Data file.

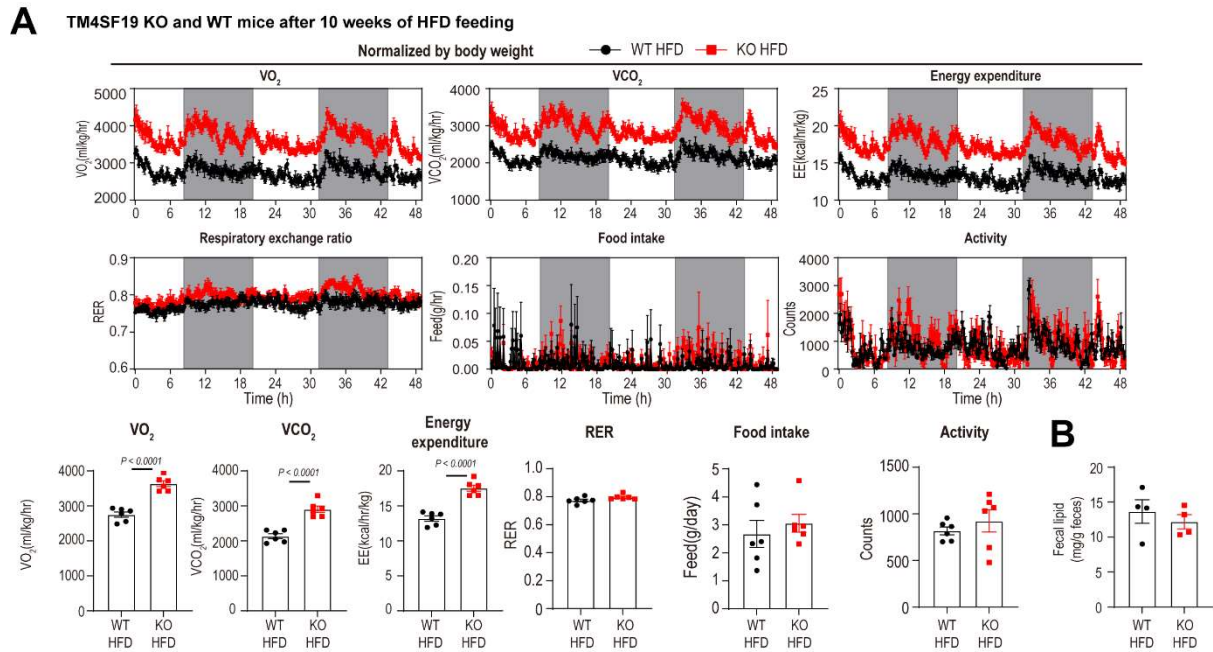


Figure S10. Indirect calorimetry analysis of HFD-fed TM4SF19 KO and WT mice.

A. Indirect calorimetry analysis of WT and TM4SF19 KO mice after 10 weeks of HFD feeding (n = 6 mice). VO_2 , VCO_2 , and energy expenditure normalized by body weight.

B. Lipid content in feces of WT and TM4SF19 KO mice after 10 weeks of HFD feeding (n = 4 mice).

Source data are provided as a Source Data file.

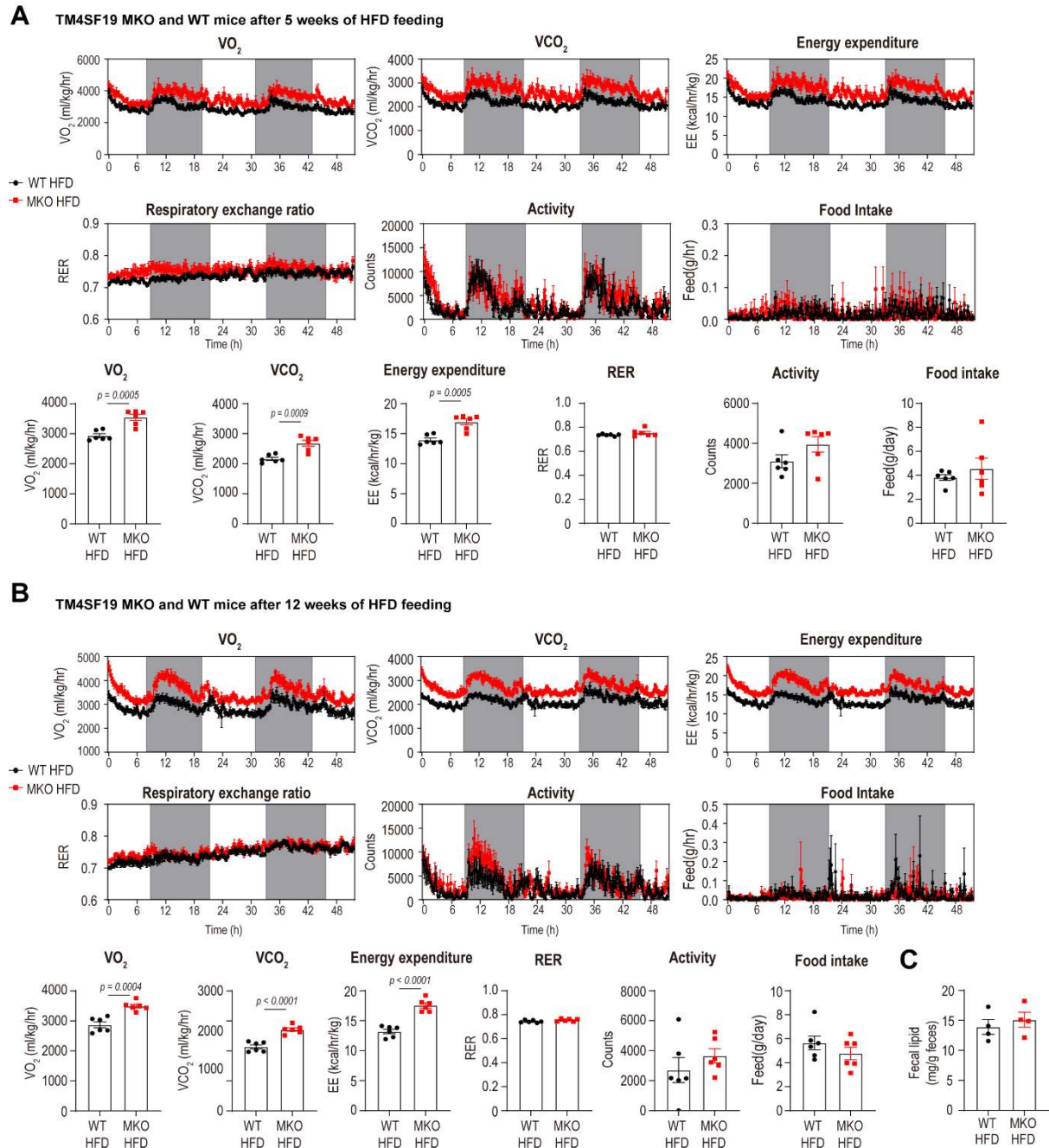


Figure S11. Indirect calorimetry analysis of TM4SF19 MKO and WT mice.

A-B. Indirect calorimetry analysis of WT and macrophage-specific TM4SF19 MKO mice after 5 weeks (A) and 12 weeks (B) of HFD feeding ($n = 6$ mice). VO_2 , VCO_2 , and energy expenditure were normalized by body weight ($n = 6$ mice).

B. Lipid content in feces of WT and TM4SF19 MKO mice after 12 weeks of HFD feeding ($n = 4$ mice).

Source data are provided as a Source Data file.

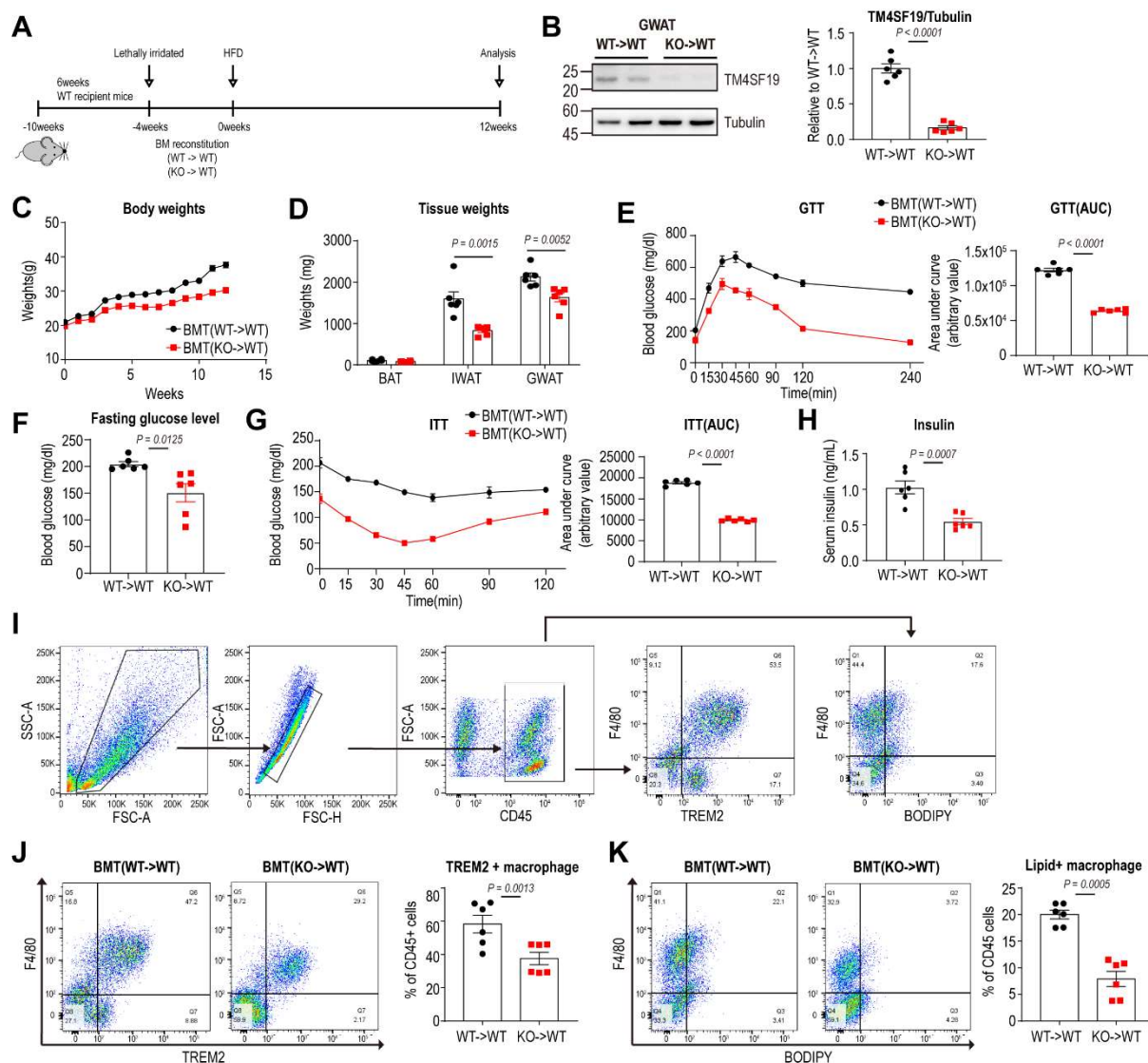


Figure S12. Bone marrow transplantation of TM4SF19 KO cells reduced adiposity and improved obesity-related metabolic dysfunction.

A. Experimental strategy of bone marrow transplantation (BMT) of TM4SF19 KO cells. After bone marrow (BM) reconstitution, HFD feeding was begun for 12 weeks.

B. Immunoblot analysis of TM4SF19 protein in GWAT of BMT KO mice after HFD feeding (n = 6 mice).

(C-D) Body weights monitoring (C) and adipose tissue weights (D) of BMT KO mice after HFD feeding (n = 6 mice).

(E-G) Glucose tolerance test (GTT) (E), fasting glucose levels (F) and insulin tolerance test (ITT) (G) of BMT KO mice after 12 weeks of HFD feeding (n = 6 mice).

H. Serum insulin levels of BMT WT and KO mice after HFD feeding (n = 6 mice).

(I-K). Representative flow profiles of the gating strategy (I), TREM2 positive macrophages (J) and lipid-associated macrophages (K) from GWAT of BMT WT and KO mice fed a HFD for 12 weeks (n = 6 mice).

Source data are provided as a Source Data file.

Supplementary Table S1. Top 100 upregulated genes from different publicly available transcriptomic analyses related to Figure. 1.

GSE150102 Top 100 upregulated genes		
Gene.symbol	LogFC	adj.P.Val
<i>Gpr50</i>	7.890476556	0.001007
<i>Slc5a7</i>	7.141463377	0.000254
<i>Tm4sf19</i>	6.978878633	0.000216
<i>Tph2</i>	6.900754589	0.000121
<i>Itgad</i>	6.892271013	0.001814
<i>Mstn</i>	6.506231466	0.000014
<i>Cck</i>	6.440078236	0.000375
<i>Trdn</i>	6.401707161	0.000125
<i>S100a7l2</i>	6.084438949	0.001061
<i>Atp6v0d2</i>	5.989930696	0.000192
<i>Olr1</i>	5.938936996	0.000168
<i>Wif1</i>	5.919110142	0.000931
<i>Lipf</i>	5.812053067	0.000301
<i>Vsig8</i>	5.777637934	0.000354
<i>Rgs1</i>	5.67091904	0.000266
<i>Gpnmb</i>	5.667433221	0.000085
<i>Eef1a2</i>	5.622523292	0.000041
<i>Otop1</i>	5.61908277	0.000087
<i>Pex5l</i>	5.566735059	0.000041
<i>Gdf3</i>	5.482301852	0.000696
<i>Mmp12</i>	5.458365177	0.000285
<i>Ubd</i>	5.422495296	0.000723
<i>Heph1l</i>	5.346107514	0.001476
<i>Grid1</i>	5.305010534	0.000316
<i>Il1rn</i>	5.224092193	0.000117
<i>Serpinb9b</i>	5.18116133	0.000422
<i>Gm5150</i>	5.114769885	0.000907
<i>Myh15</i>	5.110145099	0.041507
<i>Dppa3</i>	5.049513422	0.000230
<i>Hmga2</i>	5.046214068	0.009796
<i>Serpinb1c</i>	5.034865355	0.001767
<i>Lipn</i>	5.034706329	0.000041
<i>Dsg1a</i>	4.847153531	0.006625

<i>Dsg1b</i>	4.834303364	0.000721
<i>Spp1</i>	4.715826833	0.012169
<i>Tfr2</i>	4.696939778	0.000040
<i>Siglec15</i>	4.671861703	0.002069
<i>Npy</i>	4.629758461	0.000157
<i>Xirp2</i>	4.600211522	0.000013
<i>Ppp1r3a</i>	4.591795883	0.001103
<i>Brinp2</i>	4.591011408	0.000339
<i>Adam8</i>	4.525814818	0.000203
<i>Ltf</i>	4.455184488	0.045771
<i>St18</i>	4.43578045	0.001942
<i>Dlgap2</i>	4.373301168	0.000069
<i>F7</i>	4.347670427	0.000071
<i>Pvalb</i>	4.341038627	0.000403
<i>Il7r</i>	4.33908119	0.000230
<i>Gzme</i>	4.336507219	0.000021
<i>Slc37a2</i>	4.315773452	0.000173
<i>Npas4</i>	4.267222561	0.000085
<i>Sncb</i>	4.186794065	0.001144
<i>Fgf13</i>	4.176235694	0.000318
<i>Itgax</i>	4.163303609	0.000175
<i>Apoc4</i>	4.111802467	0.004131
<i>Areg</i>	4.096051051	0.003092
<i>Hapln4</i>	4.086582287	0.001291
<i>Nptx1</i>	4.08111701	0.005071
<i>SI00a8</i>	4.078727216	0.000187
<i>Ear1</i>	4.067183446	0.000462
<i>Rhov</i>	4.05157647	0.039607
<i>Chil3</i>	4.030903099	0.000771
<i>Plppr4</i>	4.027572067	0.000036
<i>Mrc2</i>	4.026833459	0.000014
<i>Mmp3</i>	4.026159053	0.000216
<i>Dnmt3l</i>	3.970974616	0.000358
<i>Coll0a1</i>	3.959037251	0.000173
<i>Mmp8</i>	3.943842765	0.000627
<i>Fosl1</i>	3.931283441	0.000514
<i>Nxf7</i>	3.912193139	0.000813
<i>Clec4d</i>	3.90088119	0.000576

<i>Trem2</i>	3.89713253	0.000441
<i>Slc15a5</i>	3.888149863	0.001008
<i>Acox1</i>	3.876354686	0.000625
<i>Cngb3</i>	3.864682202	0.002768
<i>Ptprn</i>	3.841263973	0.003865
<i>Ceacam19</i>	3.836246697	0.001004
<i>Arl14epl</i>	3.830183902	0.017945
<i>Oit3</i>	3.828538741	0.002343
<i>Tlr13</i>	3.790451969	0.000274
<i>Ina</i>	3.749649729	0.001713
<i>Ereg</i>	3.742668918	0.002979
<i>Ankdd1a</i>	3.72638737	0.002219
<i>Mmp13</i>	3.682757317	0.000613
<i>H2bc7</i>	3.663369797	0.000129
<i>Slc15a3</i>	3.635776038	0.000413
<i>Car12</i>	3.635765918	0.000352
<i>Fbxo40</i>	3.635224043	0.000230
<i>Cdkn1a</i>	3.630344167	0.000042
<i>Gdf15</i>	3.628152951	0.002276
<i>Tnip3</i>	3.626565868	0.000383
<i>Olfir1388</i>	3.603100238	0.007750
<i>Dppa2</i>	3.601949713	0.000037
<i>Cyp2b9</i>	3.577586218	0.026157
<i>Ccl3</i>	3.566283775	0.001007
<i>Fitm1</i>	3.562296488	0.026499
<i>Pla2g4e</i>	3.559056842	0.001712
<i>Sirpb1c</i>	3.527554229	0.000216
<i>Igsf21</i>	3.521337949	0.000230
<i>Oxtr</i>	3.500335459	0.000089

GSE59034 Top 100 upregulated genes

Gene.symbol	LogFC	adj.P.Val
<i>EGFL6</i>	3.15	0.0001700
<i>SPPI</i>	2.77	0.0000124
<i>TDRD6</i>	2.62	0.0000070
<i>TM4SF19</i>	2.38	0.0000258

<i>MMP9</i>	2.16	0.0000124
<i>MSR1</i>	2.14	0.0000195
<i>CHI3L1</i>	1.97	0.0003350
<i>MSC</i>	1.94	0.0000036
<i>STMN2</i>	1.92	0.0005790
<i>C3AR1</i>	1.79	0.0000587
<i>FCGR1CP</i>	1.76	0.0000124
<i>IFI30</i>	1.75	0.0000173
<i>IL1RN</i>	1.73	0.0000934
<i>ABCC3</i>	1.7	0.0000043
<i>FPR3</i>	1.68	0.0000930
<i>TNC</i>	1.68	0.0000037
<i>CD163</i>	1.67	0.0000266
<i>MS4A6E</i>	1.65	0.0000454
<i>/FCGR1B</i>	1.63	0.0000032
<i>SELE</i>	1.61	0.0001650
<i>FCGR1A</i>	1.61	0.0000033
<i>IGHD</i>	1.57	0.0071500
<i>Clorf204</i>	1.56	0.0000064
<i>ALCAM</i>	1.55	0.0000589
<i>VSIG4</i>	1.55	0.0000401
<i>LCPI</i>	1.55	0.0000070
<i>AQP9</i>	1.54	0.0004760
<i>LBP</i>	1.54	0.0000169
<i>IGSF6</i>	1.53	0.0000359
<i>CCL18</i>	1.51	0.0030100
<i>MRC1</i>	1.51	0.0001090
<i>MRC1</i>	1.51	0.0001090
<i>FCGR2A</i>	1.51	0.0000206
<i>HP</i>	1.5	0.0013100
<i>JCHAIN</i>	1.49	0.0045200
<i>ITGB2</i>	1.48	0.0000165
<i>CCR1</i>	1.47	0.0000065
<i>ACP5</i>	1.46	0.0000286
<i>HLA-DRB1</i>	1.45	0.0597000
<i>DHRS9</i>	1.45	0.0000128
<i>NCKAP1L</i>	1.44	0.0000527
<i>SLCO2B1</i>	1.44	0.0000384

<i>CD180</i>	1.44	0.0000061
<i>CHIT1</i>	1.43	0.0015800
<i>KYNU</i>	1.43	0.0000046
<i>NPL</i>	1.41	0.0000051
<i>RGS1</i>	1.4	0.0007380
<i>CYBB</i>	1.38	0.0000620
<i>GPR183</i>	1.38	0.0000511
<i>TFEC</i>	1.38	0.0000069
<i>ITGAX</i>	1.37	0.0000699
<i>C1orf162</i>	1.37	0.0000154
<i>VNN1</i>	1.36	0.0000046
<i>IGLJ3</i>	1.35	0.0142000
<i>DCSTAMP</i>	1.34	0.0001440
<i>UCHL1</i>	1.34	0.0000431
<i>ST14</i>	1.34	0.0000155
<i>PLEK</i>	1.34	0.0000118
<i>IL6</i>	1.33	0.0005110
<i>CD84</i>	1.33	0.0000725
<i>MS4A14</i>	1.3	0.0004570
<i>FCER1G</i>	1.3	0.0000905
<i>CD53</i>	1.3	0.0000339
<i>RNASE6</i>	1.3	0.0000098
<i>MS4A4A</i>	1.29	0.0004000
<i>FCGBP</i>	1.29	0.0000203
<i>MMP7</i>	1.28	0.0005690
<i>TREM2</i>	1.27	0.0003490
<i>C1QB</i>	1.27	0.0002510
<i>CD209</i>	1.27	0.0000294
<i>NCEH1</i>	1.26	0.0000260
<i>CXorf21</i>	1.26	0.0000228
<i>ALPL</i>	1.26	0.0000086
<i>TIGAR</i>	1.26	0.0000013
<i>LYZ</i>	1.25	0.0005640
<i>AOAH</i>	1.25	0.0001310
<i>PRG4</i>	1.24	0.0005440
<i>CCL2</i>	1.24	0.0003540
<i>KRR1</i>	1.24	0.0000186
<i>FCGR2C</i>	1.23	0.0001430

<i>IL18</i>	1.23	0.0000239
<i>HLA-DRB5</i>	1.22	0.0110000
<i>C1QC</i>	1.22	0.0007500
<i>MXRA5</i>	1.22	0.0001680
<i>IGHG1</i>	1.21	0.0183000
<i>FCGR2B</i>	1.21	0.0001250
<i>CTSS</i>	1.21	0.0001230
<i>CP</i>	1.2	0.0009980
<i>CCL19</i>	1.2	0.0000896
<i>C14orf99</i>	1.19	0.0088500
<i>CD52</i>	1.19	0.0003810
<i>F13A1</i>	1.19	0.0002830
<i>MILR1</i>	1.19	0.0001070
<i>DOCK2</i>	1.19	0.0000509
<i>CXCL16</i>	1.19	0.0000215
<i>NCF2</i>	1.18	0.0000743
<i>CECRI</i>	1.18	0.0000434
<i>P2RX6</i>	1.18	0.0000036
<i>PTPRC</i>	1.17	0.0001710
<i>CD28</i>	1.17	0.0000111

GSE182930 Top 100 upregulated genes

Gene.symbol	LogFC	adj.P.Val
<i>Spp1</i>	6.625957971	0.0133000
<i>Sfrp5</i>	6.458689959	0.0014000
<i>Cxcl2</i>	5.248440106	0.0436000
<i>Atp6v0d2</i>	4.765768962	0.0130000
<i>Il1rn</i>	4.726162268	0.0010500
<i>Thbs1</i>	4.692036743	0.0019700
<i>GpnmB</i>	4.479968789	0.0114000
<i>S100a8</i>	4.422122606	0.0320000
<i>F7</i>	4.329044855	0.0021200
<i>Adam8</i>	4.32237103	0.0030500
<i>Timp1</i>	4.304811014	0.0071100
<i>Mmp12</i>	4.164477499	0.0259000
<i>Ubd</i>	4.027556352	0.0016200

<i>Rgs1</i>	3.933677541	0.0047100
<i>Ccl3</i>	3.790841493	0.0273000
<i>Dhrs9</i>	3.735028861	0.0054100
<i>Gp49a</i>	3.729441998	0.0013400
<i>Lilr4b</i>	3.729441998	0.0013400
<i>Pla2g7</i>	3.727345821	0.0010500
<i>Baspl1</i>	3.701524387	0.0010300
<i>Cdkl4</i>	3.66701496	0.0018700
<i>Clec4d</i>	3.644742763	0.0133000
<i>Tm4sf19</i>	3.63519044	0.0306000
<i>Thbs2</i>	3.633779725	0.0020500
<i>Slc5a7</i>	3.612987003	0.0365000
<i>Slc15a3</i>	3.604827237	0.0010300
<i>Il7r</i>	3.583291662	0.0069300
<i>Saa3</i>	3.563811565	0.0248000
<i>Lilrb4a</i>	3.549166814	0.0012500
<i>Lilrb4</i>	3.549166814	0.0012500
<i>Gm5150</i>	3.527920772	0.0025500
<i>Ccl9</i>	3.492332903	0.0012500
<i>Lox</i>	3.490037951	0.0068500
<i>Slc37a2</i>	3.469916882	0.0037400
<i>C5ar1</i>	3.454855718	0.0010500
<i>Tlr13</i>	3.442756315	0.0010300
<i>Ccl2</i>	3.432576539	0.0056500
<i>Ctss</i>	3.423687091	0.0010500
<i>Cd300lb</i>	3.417782188	0.0026800
<i>Ccr1</i>	3.387900059	0.0148000
<i>Cd44</i>	3.371281564	0.0010300
<i>Nceh1</i>	3.35337968	0.0038400
<i>Trem2</i>	3.320080192	0.0047600
<i>Cd200r1</i>	3.274735649	0.0029700
<i>Ccl4</i>	3.273540608	0.0391000
<i>Cd300a</i>	3.262257043	0.0020500
<i>Atf3</i>	3.262216889	0.0054100
<i>Cd300c2</i>	3.252913382	0.0013200
<i>Cd84</i>	3.240886299	0.0026000
<i>C3ar1</i>	3.231954638	0.0010300
<i>Pvalb</i>	3.189841599	0.0209000

<i>Lgmn</i>	3.18561272	0.0012500
<i>Ms4a6d</i>	3.184870593	0.0079000
<i>Ccl6</i>	3.178552165	0.0026600
<i>Peg3</i>	3.17323718	0.0021200
<i>Itgax</i>	3.172549319	0.0156000
<i>Soat1</i>	3.17017966	0.0020400
<i>Pdk4</i>	3.154163256	0.0027400
<i>Hk3</i>	3.152299148	0.0014600
<i>Cd300ld</i>	3.122031172	0.0015600
<i>Sfrp4</i>	3.103470306	0.0112000
<i>Bmp3</i>	3.102888781	0.0012500
<i>Csf3r</i>	3.101793076	0.0357000
<i>Cd72</i>	3.099539309	0.0012500
<i>Mmp3</i>	3.093383905	0.0018700
<i>Lgals3</i>	3.084939719	0.0056000
<i>Bst1</i>	3.072922016	0.0111000
<i>Ccl7</i>	3.07032996	0.0392000
<i>Mpeg1</i>	3.070166992	0.0022200
<i>Dpep2</i>	3.069268603	0.0024800
<i>Cd68</i>	3.068781206	0.0024000
<i>Bcl2a1b</i>	3.061579979	0.0010300
<i>Tfpi2</i>	3.054772239	0.0012500
<i>Plek</i>	3.052010885	0.0036500
<i>Ccr5</i>	3.046208034	0.0030800
<i>Peg10</i>	3.042379901	0.0099100
<i>Crtac1</i>	3.027525842	0.0016200
<i>Msr1</i>	3.023822418	0.0045900
<i>Adgre1</i>	3.023677678	0.0027300
<i>Arl11</i>	3.011574958	0.0043000
<i>Pik3r5</i>	2.99801592	0.0012500
<i>Pik3ap1</i>	2.983902685	0.0026300
<i>F10</i>	2.975985606	0.0036200
<i>Arhgap25</i>	2.975953864	0.0122000
<i>Lcp1</i>	2.974516853	0.0022500
<i>Vnn1</i>	2.970512459	0.0036200
<i>Tlr1</i>	2.964651212	0.0032500
<i>Cd53</i>	2.960755403	0.0013100
<i>Adss1</i>	2.957567127	0.0016200

<i>Adssl1</i>	2.957567127	0.0016200
<i>Dock8</i>	2.940010922	0.0042000
<i>Slc11a1</i>	2.916787163	0.0016200
<i>Gpr35</i>	2.913936377	0.0061100
<i>Hspb7</i>	2.912618016	0.0032600
<i>Fcgr1</i>	2.906637542	0.0107000
<i>Itgb2</i>	2.905744252	0.0027800
<i>Myo1f</i>	2.899386047	0.0037800
<i>Rab7b</i>	2.897457259	0.0019300
<i>Pirb</i>	2.895900874	0.0013100
<i>Lilrb3</i>	2.895900874	0.0013100

Supplementary Table S2 Population characteristics of human subcutaneous adipose tissue, related to Figure 5.

Variable	
Age, y	9 ~ 79
Male, n (%)	62.5
Female, n (%)	37.5
BMI, kg/m ²	19.11 ~ 32.38
Height, m	138.6 ~ 178
Weight, kg	40.8 ~ 91.2

Supplementary Table S3 Primers used for genotyping and qPCR

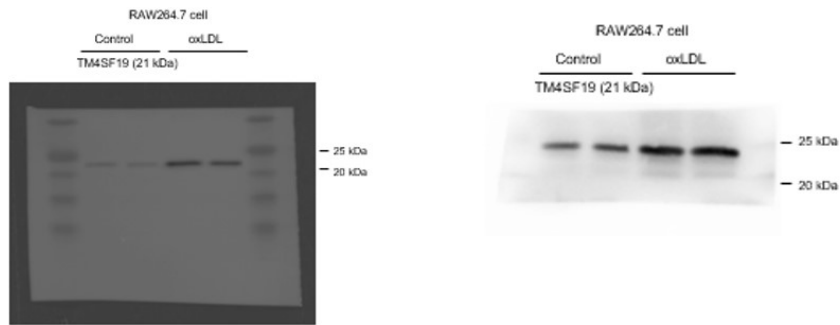
Genotyping primers		
Name	Forward primer	Reverse primer
<i>Tm4sf19</i> (C57BL/6N-Tm4sf19em1c yagen)	1. TTAGAGGAAGTCCTTGAG ACCCC 2. ATCTGTATGACCGTTCAC TTGGA	AACATGTGGCCAACCTTT ATGAGA
<i>Tm4sf19</i> (C57BL/6JSmoc-Tm4sf19em1Smoc)	AGGGCAAAGAAGGAAGTGG CTAAT	CAGGAAGGGGGCAGACA AGGAGT
<i>Csf1r-CreER</i> (FVB-Tg (Csf1r-cre/Esr1*)1Jwp/J))	CTTCCAAAGCATGGTCCAGT	TGAACCAGCTCCCTATCT GC
qPCR primers		
Transcript	Forward primer	Reverse primer
<i>Tm4sf19</i>	CTTGCCATCACAAACAGGAT GC	GAAAGAGGAGCGCGATG TTG
<i>TM4SF19</i>	GGATGTCACCTACCTGTTGA GG	ACTGAAGCAGCCGTATCT CCAG
<i>Ccl2</i>	CTGGATCGGAACCAAATGA G	AAGGCATCACAGTCCGA GTC
<i>Adgre1</i>	GTGACTCACCTTGTGGTCCT	CAGACACTCATCAACATC TGCG
<i>Rgs1</i>	AATGCAGTGGTCTCAGTCTC TGG	ATAGTCCTCACAAGCCAA CCAGA
<i>Msr1</i>	GCTCACTTTGGACAAGGTAC TG	GCTTAGTACTCCCCACTG GTT
<i>Srebf1</i>	CGACTACATCCGCTTCTTGC AG	CCTCCATAGACACATCTG TGCC
<i>Srebf2</i>	AGAAAGAGCGGTGGAGTCC TTG	GAACTGCTGGAGAATGG TGAGG
<i>Tnf</i>	GGTGCCTATGTCTCAGCCTC TT	GCCATAGAACTGATGAG AGGGAG
<i>IRS1</i>	AGTCTGTCTCCAGTAGCAC CA	ACTGGAGCCATACTCATC CGAG
<i>INSR</i>	GCAACATCACCCACTACCTG GT	GAATGGTGGAGACCAGG TCCTC
<i>PDE3B</i>	TCCTGGCTTACAGCAGATCC AC	GGCAGCCATAACTCTCAT CAGG
<i>LEP</i>	GCTGTGCCCATCCAAAAAGT CC	CCCAGGAATGAAGTCCA AACCG
<i>FASN</i>	TTCTACGGCTCCACGCTCTT CC	GAAGAGTCTTCGTCAGCC AGGA

<i>PDE4D</i>	GGACACTTTGGAGGACAATC GTG	CCTTTTCCGTGTCTGACT CACC
<i>NF-κB</i>	GCAGCACTACTTCTTGACCA CC	TCTGCTCCTGAGCATTGA CGTC
<i>Lyve1</i>	TGGTGTTACTCCTCGCCT CT	TTCTGCGCTGACTCTA CCTG

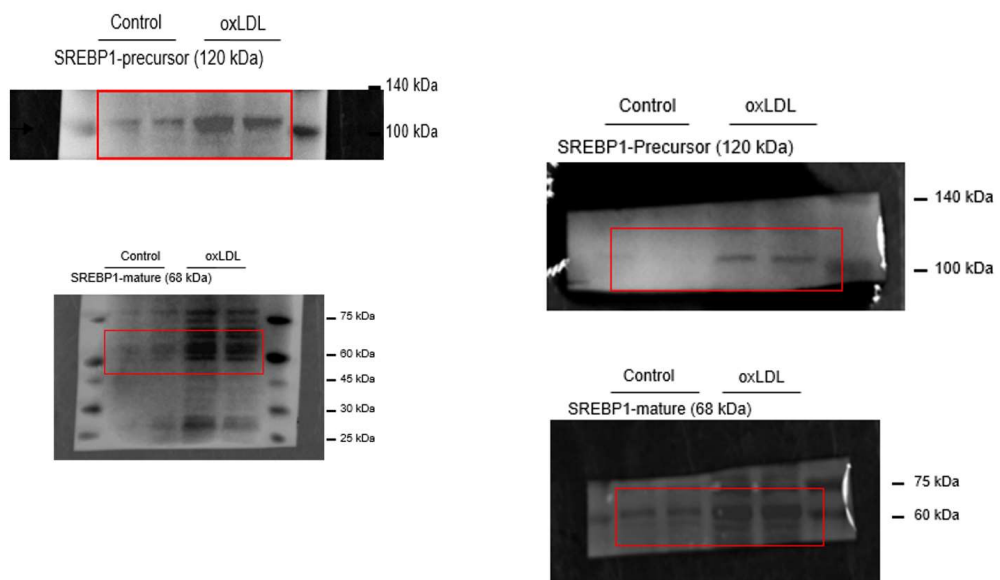
Uncropped western blot images used for supplementary figures

Figure S1D

TM4SF19



SREBP1



Tubulin

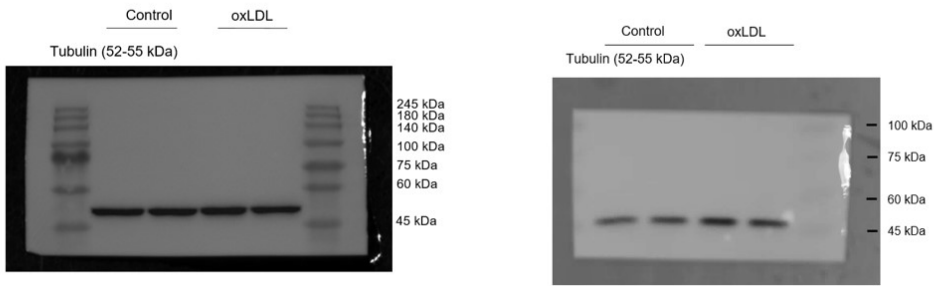


Figure S2 BMDM

Figure S2 BMDM

COXIV

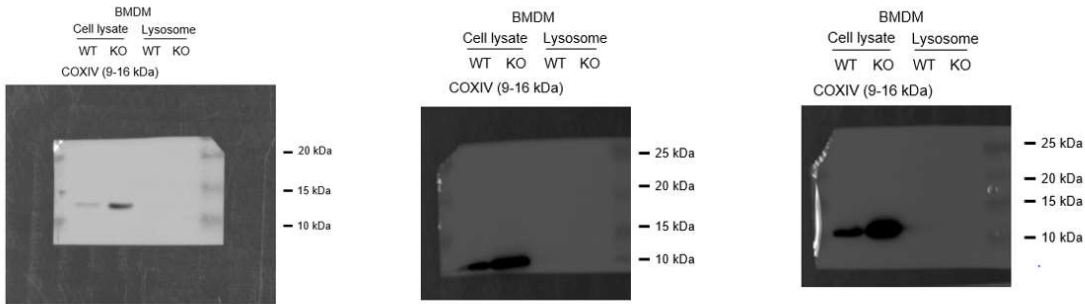


Figure S2 BMDM

LAMP1

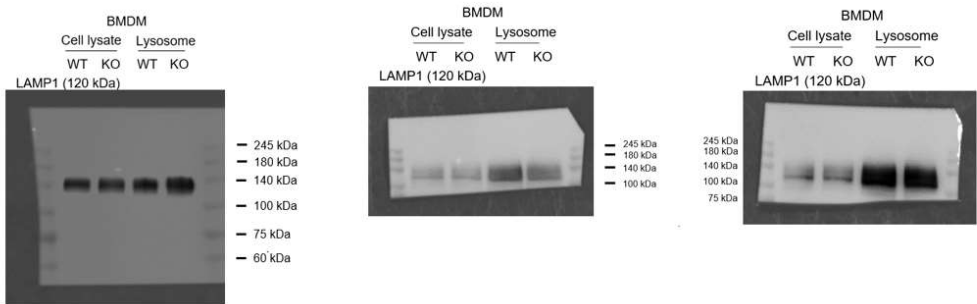


Figure S2 RAW264.7 cell

Figure S2 RAW264.7 cell

COXIV

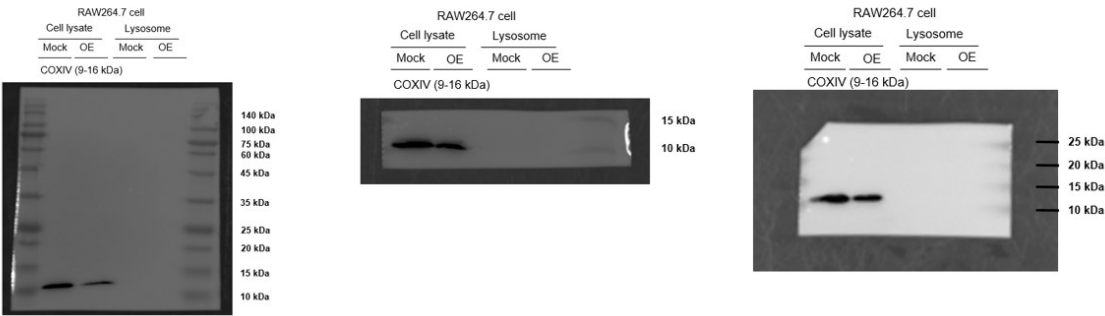


Figure S2 RAW264.7 cell

LAMP1

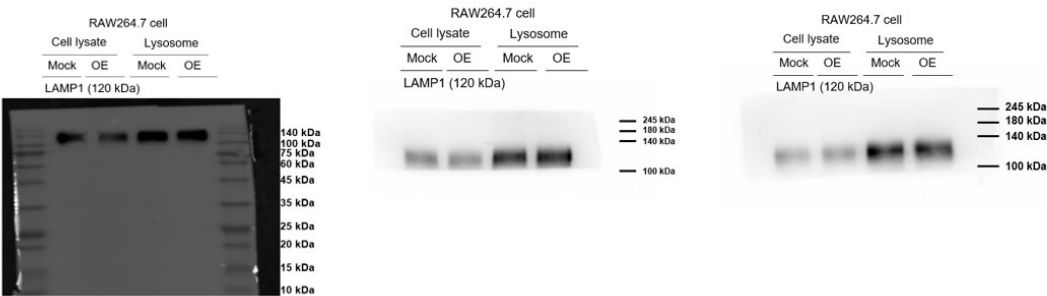


Figure S2 BMDM

B-Actin

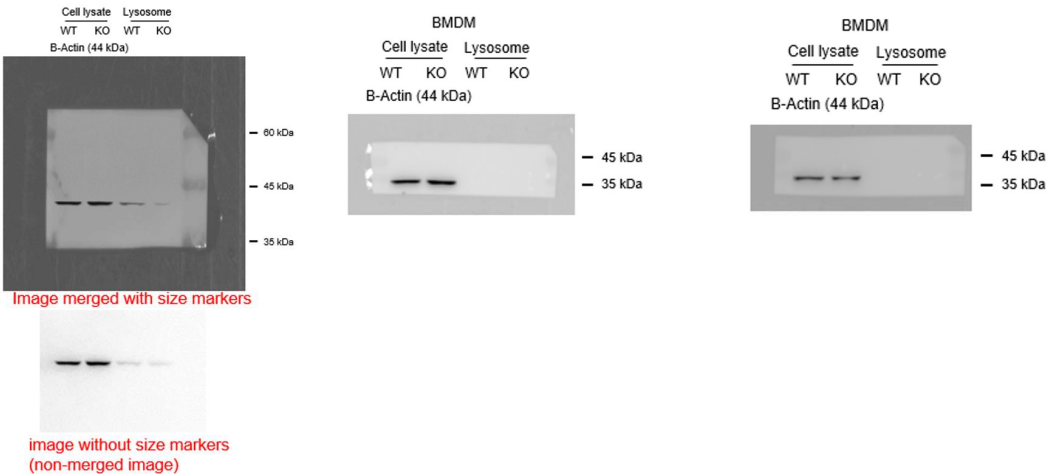


Figure S9I BAT

Figure S9I BAT

P-AKT

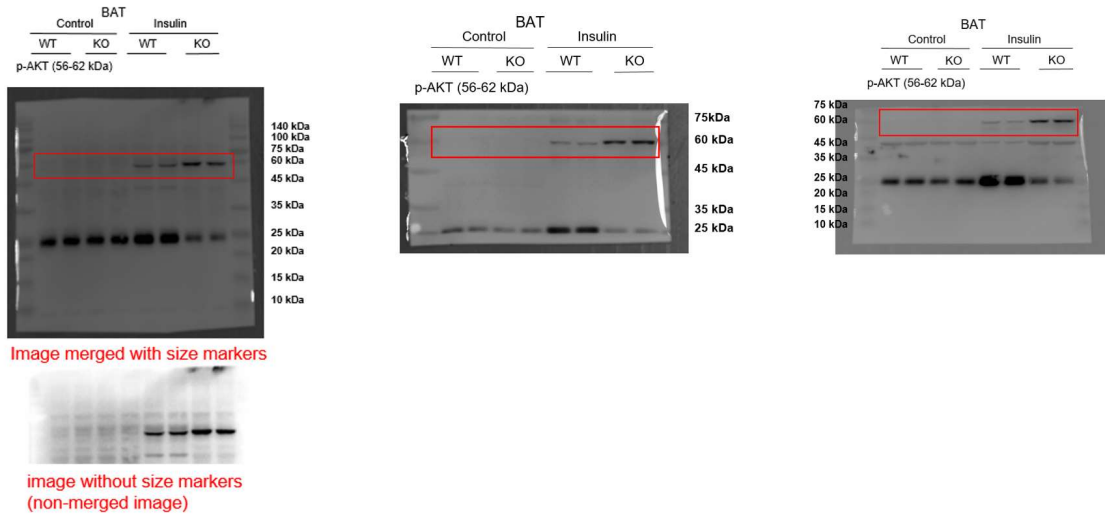


Figure S9I BAT

AKT

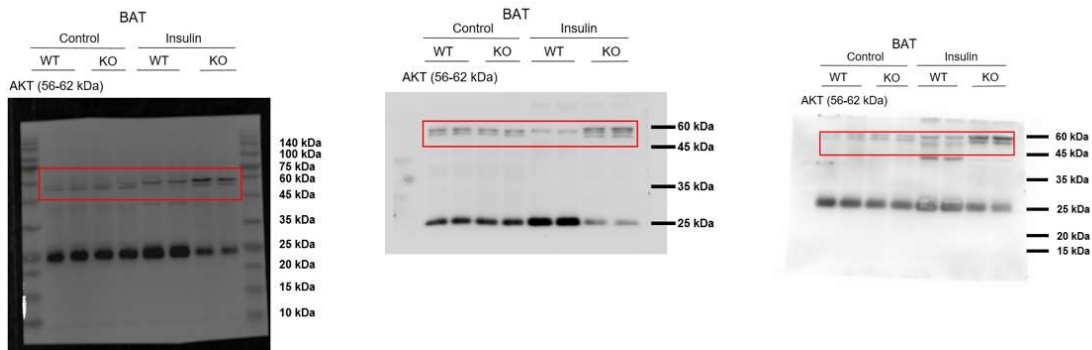


Figure S9I BAT

P-IRS1

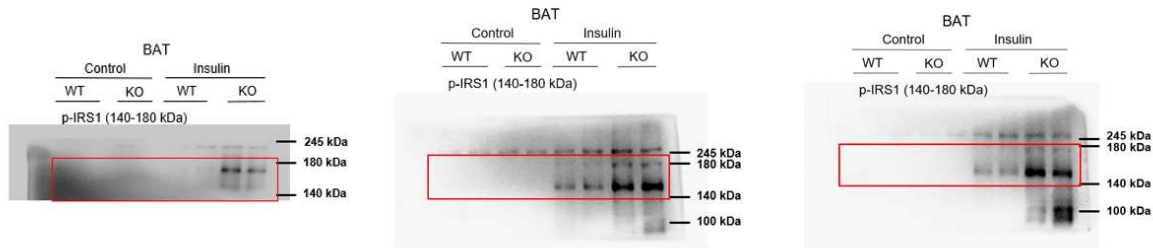


Figure S9I BAT

IRS1

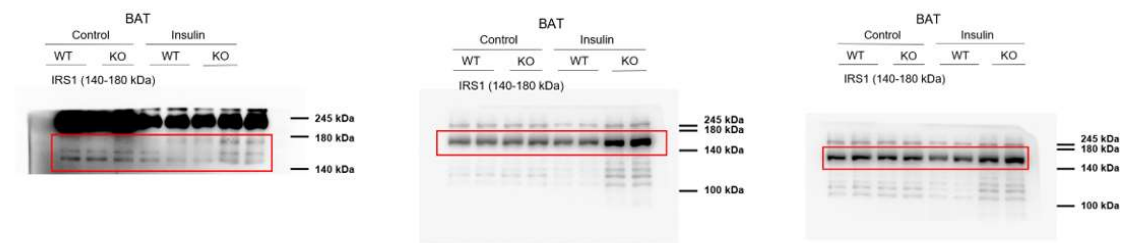


Figure S9I BAT

Tubulin

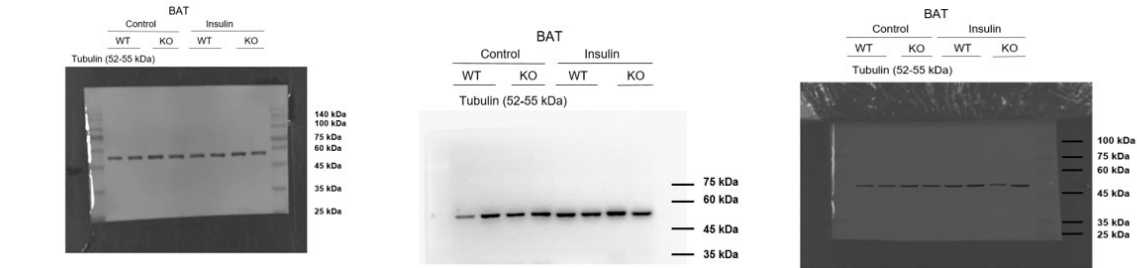


Figure S9I IWAT

Figure S9I IWAT

P-AKT

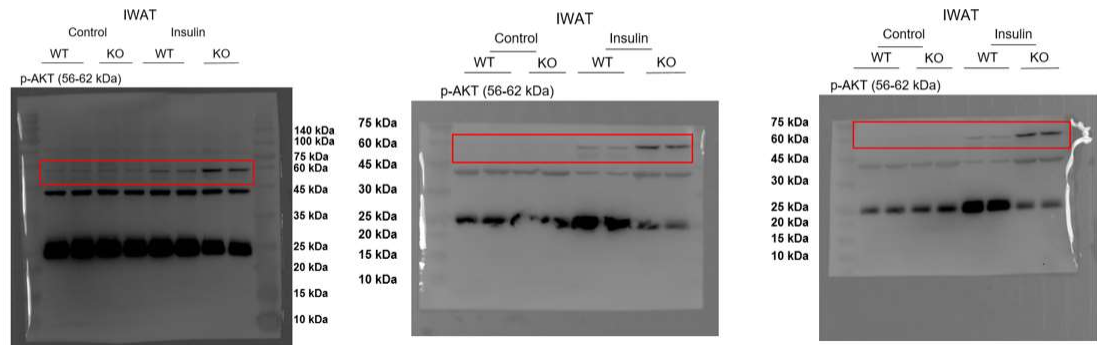


Figure S9I IWAT

AKT

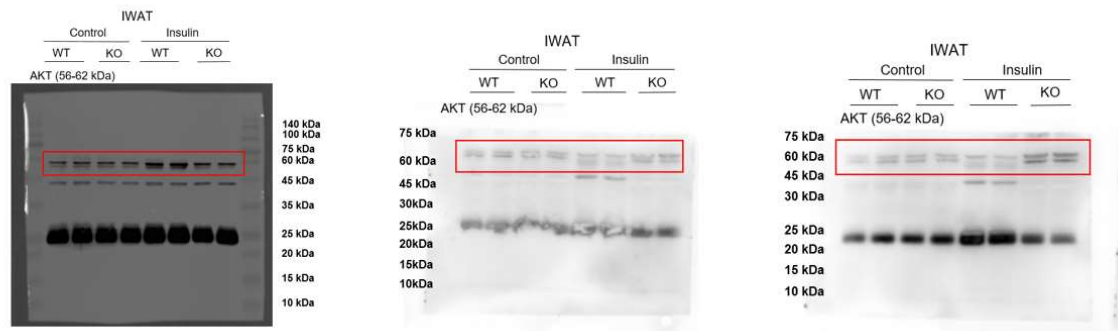


Figure S9I IWAT

P-IRS1

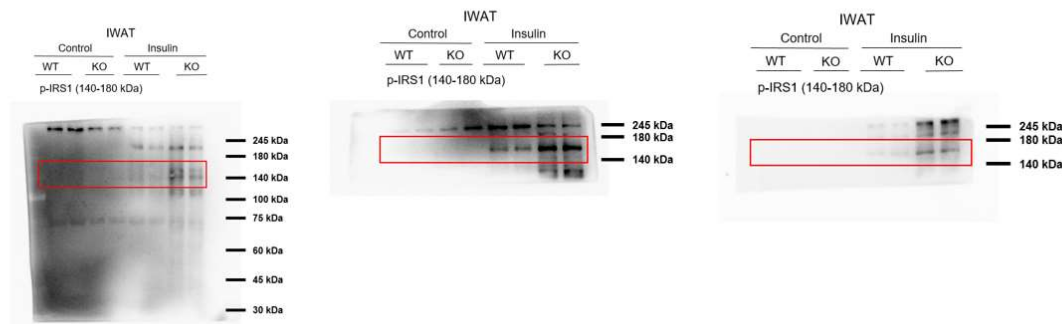


Figure S9I IWAT

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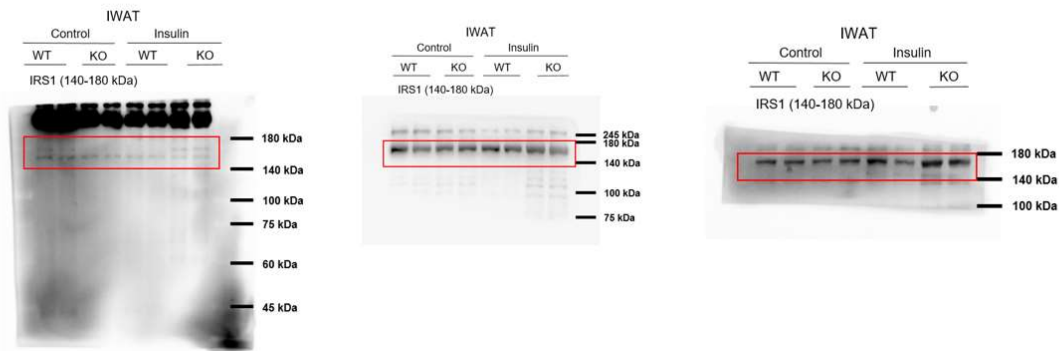


Figure S9I IWAT

Tubulin

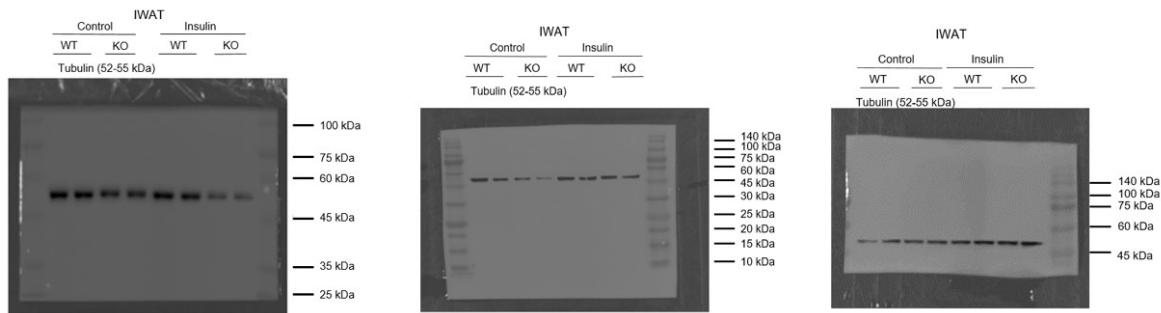


Figure S9I GWAT

Figure S9I GWAT

P-AKT

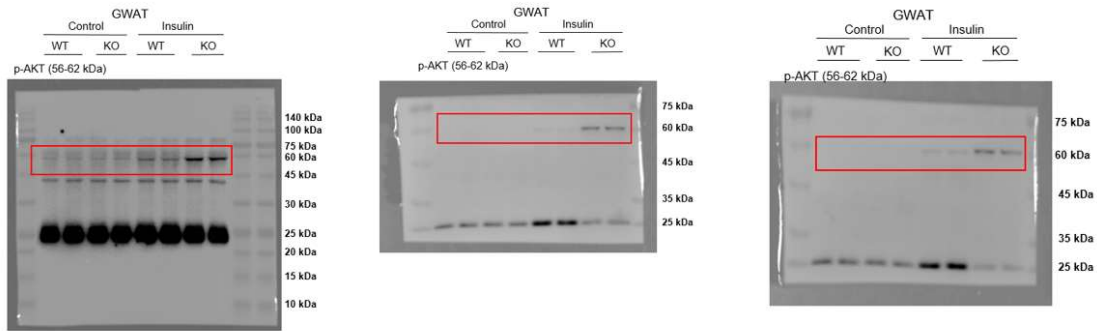


Figure S9I GWAT

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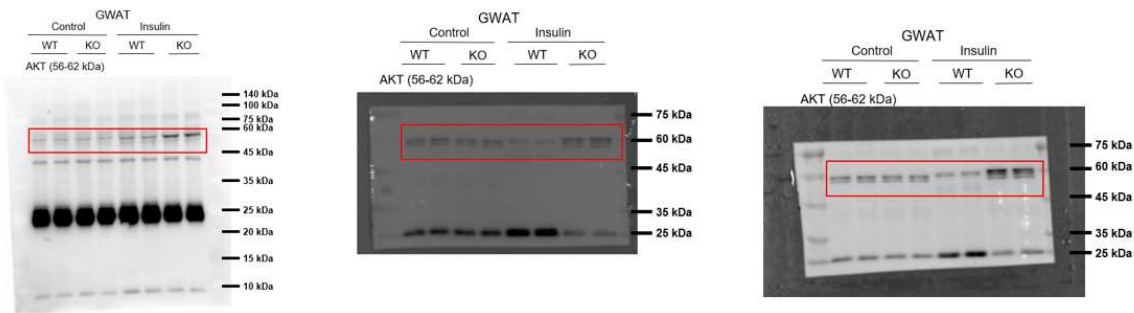


Figure S9I GWAT

P-IRS1

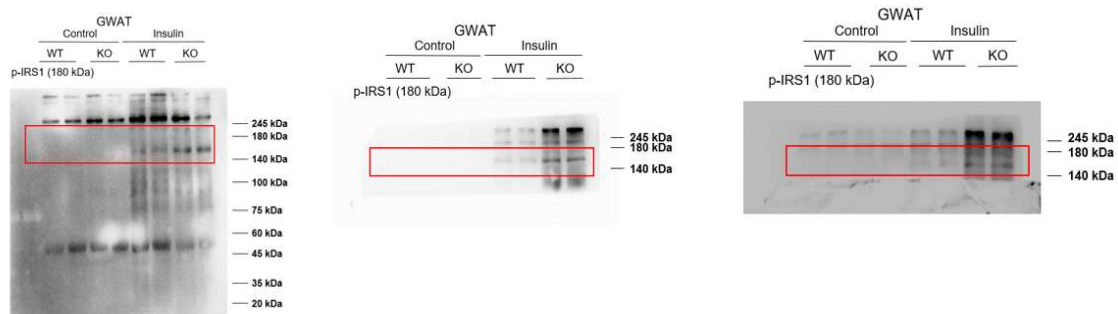


Figure S9I GWAT

IRS1

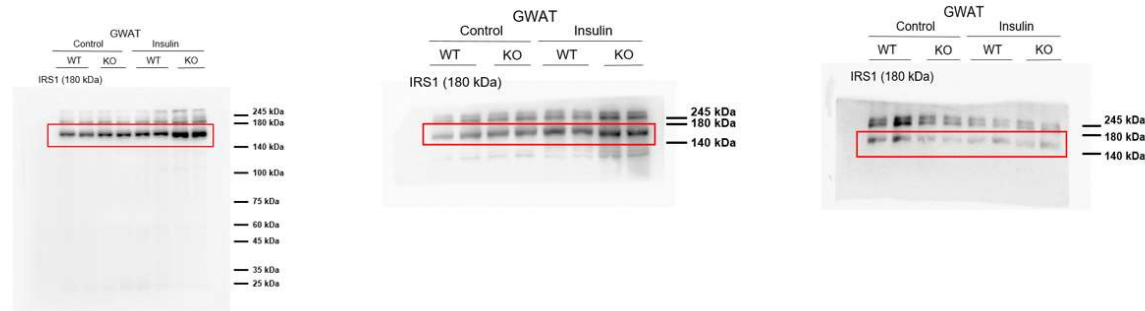


Figure S9I GWAT

Tubulin

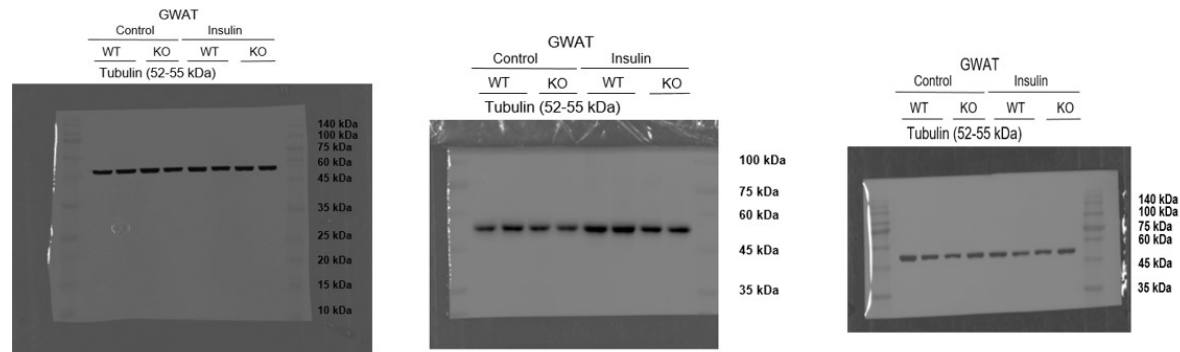
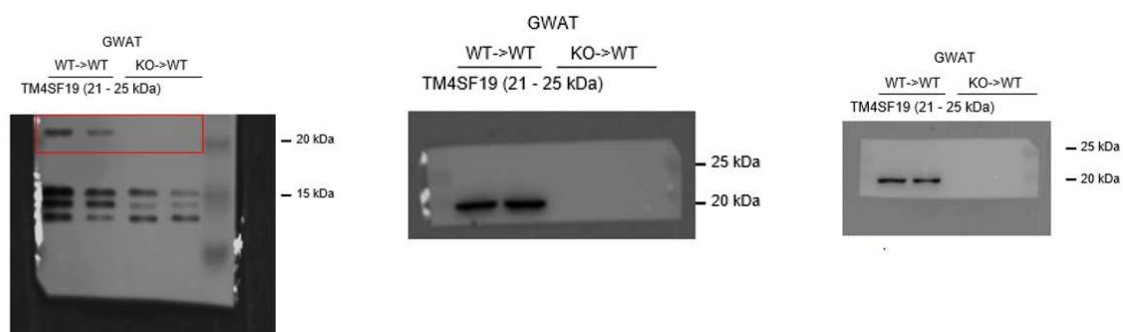


Figure S12B

TM4SF19



Tubulin

