

Supplemental Table 1. Primer sequences for real-time qPCR.

Gene	Forward Primer	Reverse Primer
Sat1	5'-CAGTGGAGCGCCAGAACATAGAA-3'	5'-CCTGTGCCCTCAAGGAG-3'
Ucp1	5'-AGGCTTCCAGTACCATTTAGGT-3'	5'-CTGAGTGAGGCAAAGCTGATT-3'
Cidea	5'-TGACATTATGGGATTGCAGAC-3'	5'-GGCCAGTTGTGATGACTAAGAC-3'
Pgc1a	5'-TATGGAGTGACATAGAGTGTGCT-3'	5'-CCACTTCAATCCACCCAGAAAG-3'
Pgc1b	5'-TCCTGTAAAAGCCCCGGAGTAT-3'	5'-GCTCTGGTAGGGGCAGTGA-3'
Cox7a1	5'-GCTCTGGTCCGGTCTTTAGC-3'	5'-GTACTGGGAGGTCATTGTCGG-3'
Cox8b	5'-TGTGGGGATCTCAGCCATAGT-3'	5'-AGTGGGCTAAGACCCATCCTG-3'
Pparg	5'-TCCTGTAAAAGCCCCGGAGTAT-3'	5'-GCTCTGGTAGGGGCAGTGA-3'
Acox1	5'-CAGGAAGAGCAAGGAAGTGG -3'	5'-CCTTCTGGCTGATCCCATA-3'
Cpt1	5'-CCAGGCTACAGTGGGACATT-3'	5'-GAACATTGCCATGTCCTTGT-3'
Cd36	5'-AACTTGTGGCCTTGCACCT-3'	5'-GCAGAATCAAGGGAGAGCAC -3'
LPL	5'-GCCAGCAACATTATCCAGT-3'	5'-GGTCAGACTTCCTGCTACGC-3'
Acc1	5'-TGTACAAGCAGTGTGGGCTGGCT-3'	5'-CCACATGGCCTGGCTTGGAGGG-3'
Fas	5'-GCTGCGGAAACTTCAGGAAAT-3'	5'-AGAGACGTGTCACTCCTGGACTT-3'
Pdk4	AAGATGCTCTTGCAGGACAGTAT	5'-GAAGGTGTGAAGGAACGTACA-3'
Cd14	5'-CTCTGTCCTTAAAGCGGCTTAC-3'	5'-GTTGCGGAGGTTCAAGATGTT-3'
Tnf-a	5'-ACCCTGGTATGAGCCATATAC-3'	5'-ACACCCATTCCCTCACAGAG-3'
Ccl8	5'-TCTACGCAGTGCTTCTTGCC-3'	5'-AAGGGGGATCTTCAGCTTAGTA-3'
Foxp3	5'-CCCATCCCCAGGAGTCTT-3'	5'-ACCATGACTAGGGCACTGTA-3'
Cxcr6	5'-GAGTCAGCTCTGTACGATGGG-3'	5'-TCCTGAACTTAGGAAGCGTT-3'
Cxcr3	5'-TACCTGAGGTTAGTGAACGTCA-3'	5'-CGCTCTCGTTTCCCCATAATC-3'
IL-1 β	5'-ATGAGAGCATCCAGCTTCAA-3'	5'-TGAAGGAAAAGAAGGTGCTC-3'
IL-10	5'-CCCATTCCCTCGTCACGATCTC-3'	5'-TCAGACTGGTTGGGATAGGTT-3'
IL-6	5'-GAGGATACCACTCCAACAGACC-3'	5'-AAGTGCATCATCGTTGTTCATACA-3'
Mcp-1	5'-GCATCTGCCCTAACGGCTTCA-3'	5'-TGCTGAGGTGGTTGGAA-3'
ODC	5'-GACGAGTTGACTGCCACATC-3'	5'-CGCAACATAGAACGCATCCTT-3'
Apaox	5'-CTTCGGTGGTGTAGTGGAGC-3'	5'-TCCGATAATTCTTCTCCCCCAG-3'
Nrf2	5'-ATGATGGACTGGAGTTGCC-3'	5'-TCCTGTTCTCTGGAGTTG-3'
Tbp	5'-CCCTATCACTCCTGCCACAC-3'	5'-ACGAAGTGCAATGGTCTTAGG-3'

Supplemental Table 2. Significantly reduced clusters in adipose tissue of SAT1-aKO mice by DAVID analysis

Cluster	Term	Enrichment Score	Count	%	PValue	List Total	Fold Enrichment	FDR
Annotation Cluster 1	Immunity	5.17	35	5.6	1.89E-09	592	3.34	2.55E-06
Annotation Cluster 2	Mitochondrion	5	61	9.8	1.37E-08	592	2.21	1.86E-05
Annotation Cluster 3	Nucleotide-binding	3.33	76	12.3	1.50E-05	592	1.66	0.0202324
Annotation Cluster 4	Ribonucleoprotein	2.98	25	4.0	2.08E-06	592	3.11	0.0028139
Annotation Cluster 5	Disulfide bond	2.88	146	23.5	9.96E-13	592	1.79	1.35E-09
Annotation Cluster 6	RNA-binding	2.51	39	6.3	5.31E-07	592	2.49	7.17E-04

Supplemental Table 3. Top 10 biological processes over-represented in reduced genes from adipose tissue of SAT1-aKO mice by Panther GO biological process analysis

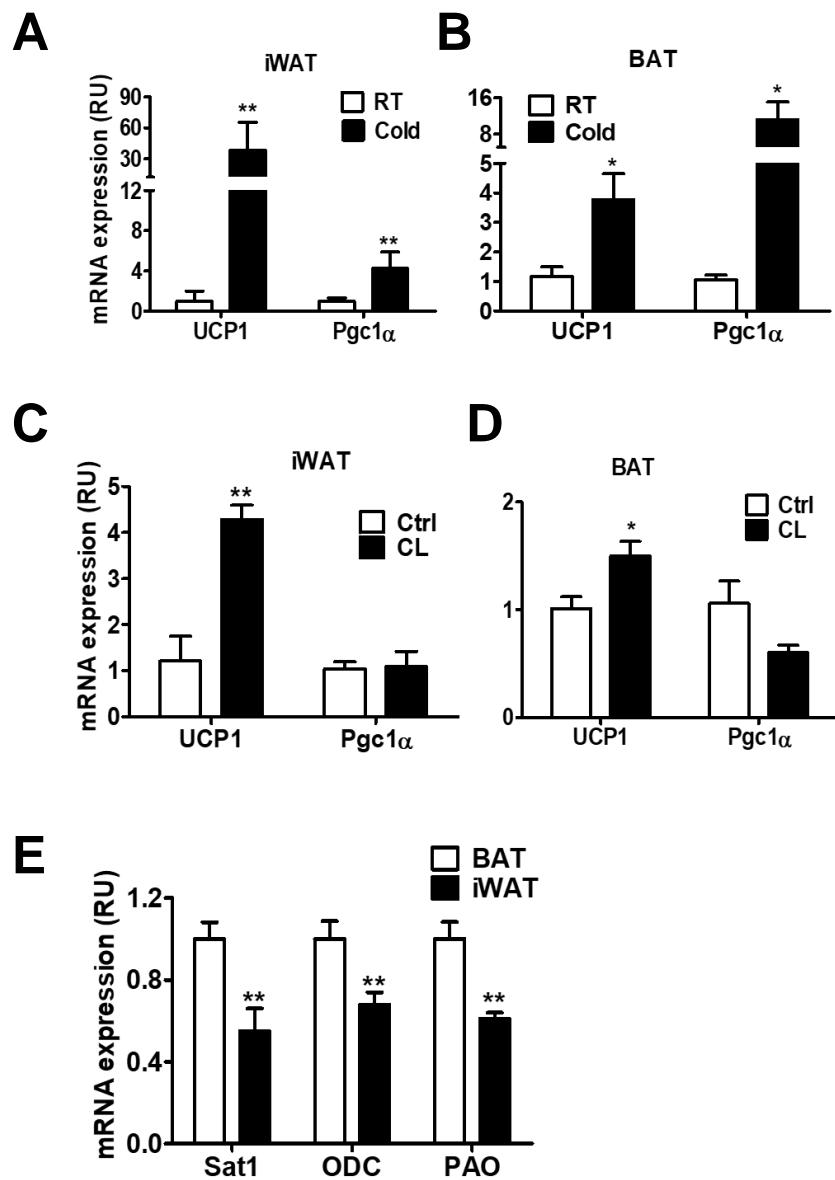
GO biological process complete	Fold Enrichment	Raw P-value	FDR
immune system process (GO:0002376)	2.39	8.37E-20	1.29E-15
regulation of immune system process (GO:0002682)	2.61	4.85E-16	3.73E-12
positive regulation of biological process (GO:0048518)	1.61	1.06E-15	5.41E-12
positive regulation of cellular process (GO:0048522)	1.64	8.55E-15	3.28E-11
immune response (GO:0006955)	2.6	1.81E-14	5.55E-11
sensory perception of chemical stimulus (GO:0007606)	0.05	3.55E-14	9.10E-11
cellular process (GO:0009987)	1.23	1.03E-13	1.98E-10
cellular response to chemical stimulus (GO:0070887)	2.09	9.28E-14	2.04E-10
response to organic substance (GO:0010033)	2	1.45E-13	2.48E-10
cellular response to organic substance (GO:0071310)	2.22	3.27E-13	5.03E-10

Supplemental Table 4. Significantly increased clusters in adipose tissue of SAT1-aKO mice by DAVID analysis

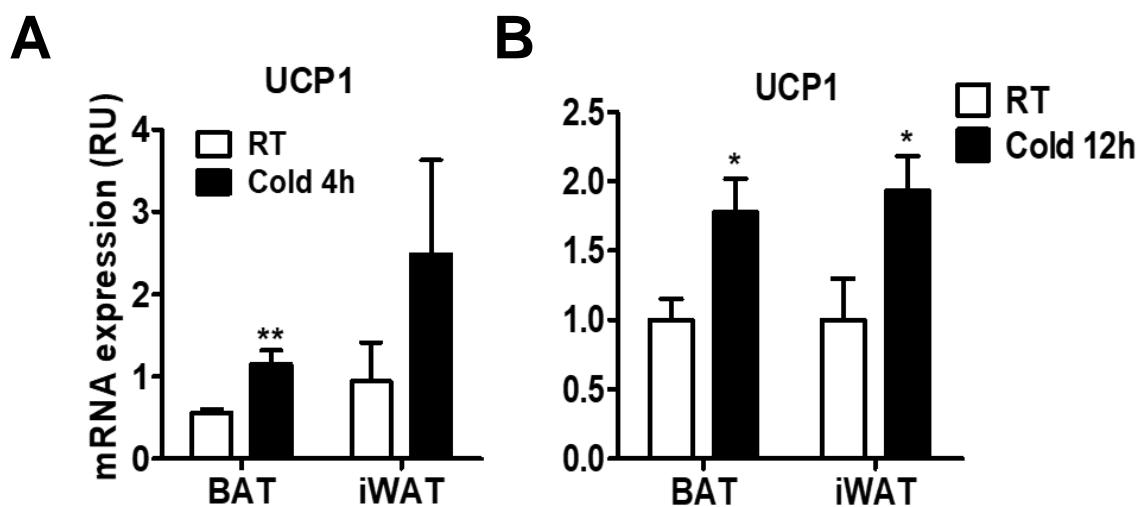
Cluster	Term	Enrichment Score	Count	%	PValue	List Total	Fold Enrichment	FDR
Annotation Cluster 1	Membrane	7.25	426	46.3	6.86E-09	896	1.24	9.37E-06
Annotation Cluster 2	Glycoprotein	7.24	251	27.3	7.57E-18	896	1.67	1.03E-14
Annotation Cluster 3	Endoplasmic reticulum	5.11	72	7.8	1.14E-06	896	1.83	0.00156506
Annotation Cluster 4	Metal-binding	3.52	185	20.1	2.75E-06	896	1.38	0.00375275
Annotation Cluster 5	Lysosome	3.23	19	2.1	8.97E-07	896	4.01	0.00116877

Supplemental Table 5. Reduced immunity-related genes in inguinal white adipose tissue of SAT1-aKO mice

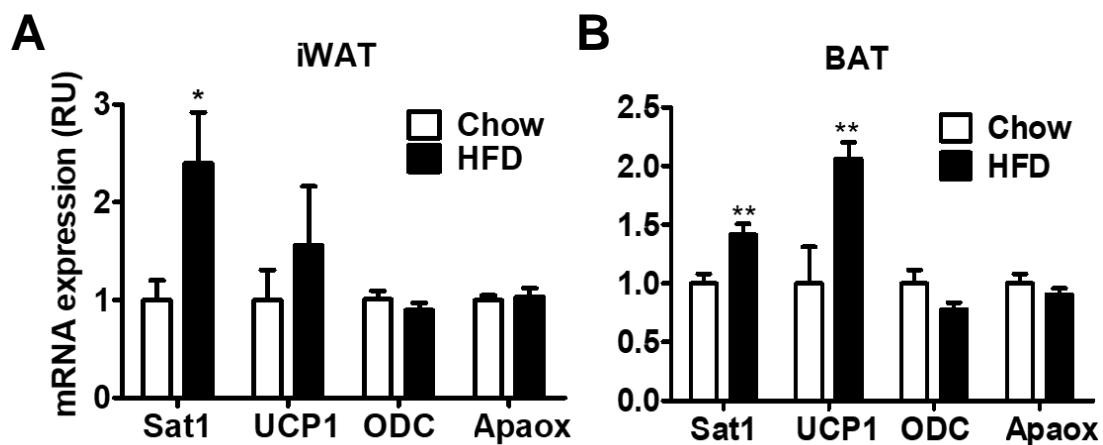
Gene ID	Description	log2FC	pvalue
Chemokines and cytokines			
Ccl21a	chemokine (C-C motif) ligand 21A (serine) [Source:MGI Symbol;Acc:MGId:1349183]	-0.48	0.0372
Ccl22	chemokine (C-C motif) ligand 22 [Source:MGI Symbol;Acc:MGId:1306779]	-0.46	0.0503
Ccl5	chemokine (C-C motif) ligand 5 [Source:MGI Symbol;Acc:MGId:98262]	-0.61	0.0084
Ccl8	chemokine (C-C motif) ligand 8 [Source:MGI Symbol;Acc:MGId:101878]	-0.63	0.0088
Cxcl13	chemokine (C-X-C motif) ligand 13 [Source:MGI Symbol;Acc:MGId:1888499]	-0.41	0.0330
Cxcl14	chemokine (C-X-C motif) ligand 14 [Source:MGI Symbol;Acc:MGId:1888514]	-0.44	0.0242
Cxcl16	chemokine (C-X-C motif) ligand 16 [Source:MGI Symbol;Acc:MGId:1932682]	-0.45	0.0337
Tnf	tumor necrosis factor [Source:MGI Symbol;Acc:MGId:104798]	-0.5	0.03599
Receptors			
Ccr10	chemokine (C-C motif) receptor 10 [Source:MGI Symbol;Acc:MGId:1096320]	-0.56	0.0188
Ccr7	chemokine (C-C motif) receptor 7 [Source:MGI Symbol;Acc:MGId:103011]	-0.52	0.0250
Cx3cr1	chemokine (C-X3-C motif) receptor 1 [Source:MGI Symbol;Acc:MGId:1333815]	-0.64	0.0074
Cxcr3	chemokine (C-X-C motif) receptor 3 [Source:MGI Symbol;Acc:MGId:1277207]	-0.63	0.0052
Cxcr4	chemokine (C-X-C motif) receptor 4 [Source:MGI Symbol;Acc:MGId:109563]	-0.48	0.0296
Cxcr6	chemokine (C-X-C motif) receptor 6 [Source:MGI Symbol;Acc:MGId:1934582]	-0.72	0.0016
Il12rb1	interleukin 12 receptor, beta 1 [Source:MGI Symbol;Acc:MGId:104579]	-0.47	0.0397
Il1r2	interleukin 1 receptor, type II [Source:MGI Symbol;Acc:MGId:96546]	-0.47	0.0491
Ifnlr1	interferon lambda receptor 1 [Source:MGI Symbol;Acc:MGId:2429859]	-0.47	0.0495
Il12rb1	interleukin 12 receptor, beta 1 [Source:MGI Symbol;Acc:MGId:104579]	-0.47	0.0397
Il1r2	interleukin 1 receptor, type II [Source:MGI Symbol;Acc:MGId:96546]	-0.47	0.0491
Il12rb2	interleukin 12 receptor, beta 2 [Source:MGI Symbol;Acc:MGId:1270861]	-0.51	0.0307
Il2rg	interleukin 2 receptor, gamma chain [Source:MGI Symbol;Acc:MGId:96551]	-0.51	0.0288
Il7r	interleukin 7 receptor [Source:MGI Symbol;Acc:MGId:96562]	-0.49	0.0385
Il12rb1	interleukin 12 receptor, beta 1 [Source:MGI Symbol;Acc:MGId:104579]	-0.47	0.0397
Il1r2	interleukin 1 receptor, type II [Source:MGI Symbol;Acc:MGId:96546]	-0.47	0.0491
Il10ra	interleukin 10 receptor, alpha [Source:MGI Symbol;Acc:MGId:96538]	-0.41	0.0478
Il20rb	interleukin 20 receptor beta [Source:MGI Symbol;Acc:MGId:2143266]	-0.4	0.0178
Il20rb	interleukin 20 receptor beta [Source:MGI Symbol;Acc:MGId:2143266]	-0.4	0.0178
Il2ra	interleukin 2 receptor, alpha chain [Source:MGI Symbol;Acc:MGId:96549]	-0.39	0.0499
Il17ra	interleukin 17 receptor A [Source:MGI Symbol;Acc:MGId:107399]	-0.32	0.0500
Ifnlr1	interferon lambda receptor 1 [Source:MGI Symbol;Acc:MGId:2429859]	-0.47	0.0495
Cluster of differentiation (CD)			
Cd14	CD14 antigen [Source:MGI Symbol;Acc:MGId:88318]	-0.79	0.0001
Cd209e	CD209e antigen [Source:MGI Symbol;Acc:MGId:2157948]	-0.46	0.0473
Cd244	CD244 natural killer cell receptor 2B4 [Source:MGI Symbol;Acc:MGId:109294]	-0.59	0.0124
Cd300e	CD300E molecule [Source:MGI Symbol;Acc:MGId:2387602]	-0.58	0.0045
Cd300ld	CD300 molecule like family member d [Source:MGI Symbol;Acc:MGId:2442358]	-0.34	0.0520
Cd300lf	CD300 molecule like family member F [Source:MGI Symbol;Acc:MGId:2442359]	-1.01	0.0000
Cd38	CD38 antigen [Source:MGI Symbol;Acc:MGId:107474]	-0.39	0.0426
Cd3d	CD3 antigen, delta polypeptide [Source:MGI Symbol;Acc:MGId:88331]	-0.48	0.0340
Cd3e	CD3 antigen, epsilon polypeptide [Source:MGI Symbol;Acc:MGId:88332]	-0.46	0.0469
Cd3g	CD3 antigen, gamma polypeptide [Source:MGI Symbol;Acc:MGId:88333]	-0.46	0.0521
Cd4	CD4 antigen [Source:MGI Symbol;Acc:MGId:88335]	-0.52	0.0276
Cd5	CD5 antigen [Source:MGI Symbol;Acc:MGId:88340]	-0.47	0.0505
Cd53	CD53 antigen [Source:MGI Symbol;Acc:MGId:88341]	-0.46	0.0312
Cd7	CD7 antigen [Source:MGI Symbol;Acc:MGId:88344]	-0.62	0.0077
Cd74	CD74 antigen [Source:MGI Symbol;Acc:MGId:96534]	-0.44	0.0512
Cd83	CD83 antigen [Source:MGI Symbol;Acc:MGId:1328316]	-0.66	0.0032
Cd96	CD96 antigen [Source:MGI Symbol;Acc:MGId:1934368]	-0.51	0.0321
Transcription factors			
Foxp3	forkhead box P3 [Source:MGI Symbol;Acc:MGId:1891436]	-0.77	0.0009
Gata3	GATA binding protein 3 [Source:MGI Symbol;Acc:MGId:95663]	-0.62	0.0079
Others			
Ticam1	toll-like receptor adaptor molecule 1 [Source:MGI Symbol;Acc:MGId:2147032]	-0.41	0.0157
Ifit1	interferon-induced protein with tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGId:103011]	-0.47	0.0116
Ly9	lymphocyte antigen 9 [Source:MGI Symbol;Acc:MGId:96885]	-0.47	0.0424
Ifit1	interferon-induced protein with tetratricopeptide repeats 1 [Source:MGI Symbol;Acc:MGId:103011]	-0.47	0.0116
Tnfsf11	tumor necrosis factor (ligand) superfamily, member 11 [Source:MGI Symbol;Acc:MGId:104798]	-0.51	0.03155
Ticam1	toll-like receptor adaptor molecule 1 [Source:MGI Symbol;Acc:MGId:2147032]	-0.41	0.01568



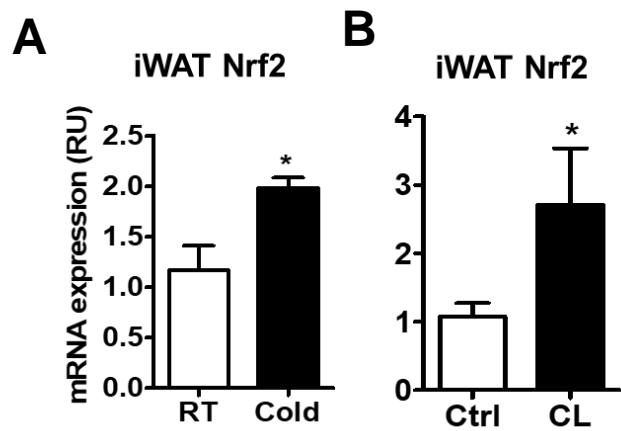
Supplementary Fig. 1. (A-D) UCP1 and Pgc-1 α mRNA levels in inguinal (iWAT) and brown (BAT) adipose tissue of cold-challenged (A-B) and CL-316,243-treated mice (C-D). (E) Relative mRNA expression of SAT1, ODC and APAOX in iWAT and BAT of wide type mice at room temperature. n=5-10 per group, * p<0.05, ** p<0.01 vs controls (Ctrl).



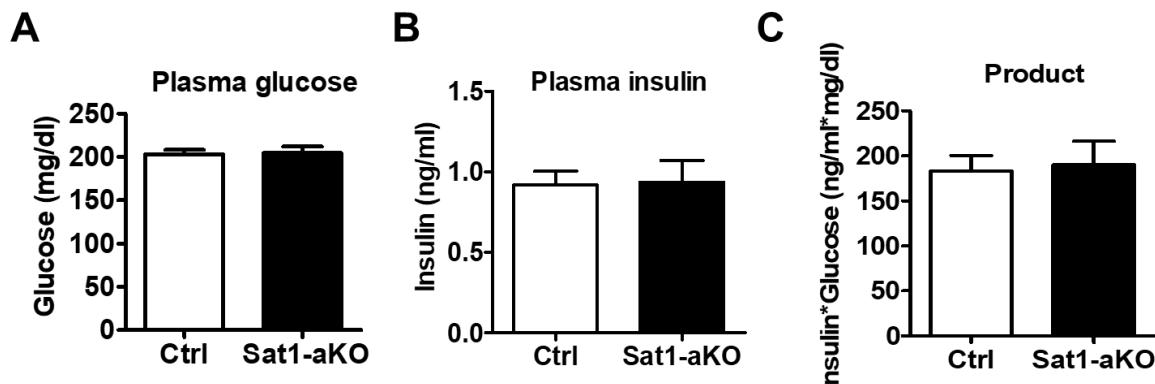
Supplementary Fig. 2. UCP1 mRNA levels in inguinal (iWAT) (A) and brown (BAT) (B) adipose tissue of mice challenged with cold (5°C) acutely for 4 hrs or 12 hrs. n=5-6 per group, *p<0.05, **p<0.01 vs controls (Ctrl).



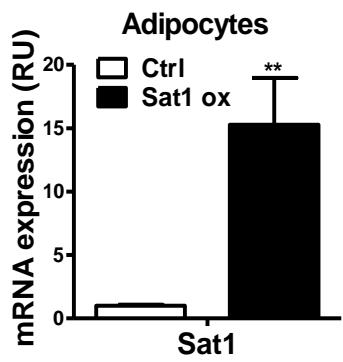
Supplementary Fig. 3. mRNA expression of SAT1, UCP1, ODC and APAOX in inguinal (iWAT) (A) and brown (BAT) (B) adipose tissue of mice fed a high fat diet (HFD) for 1 week. n=5 per group, *p<0.05, ** p<0.01 vs chow diet.



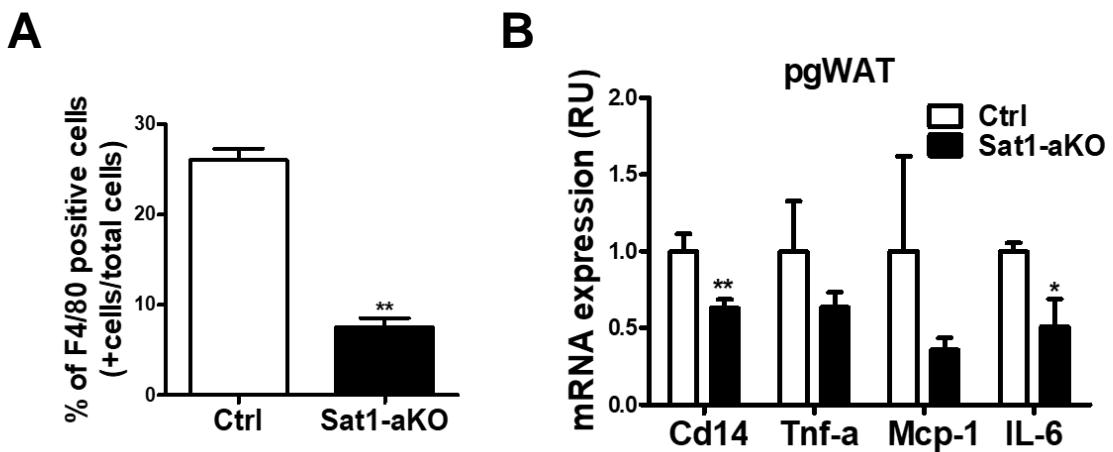
Supplementary Fig. 4. Nuclear factor (erythroid-derived 2)-like 2 (Nrf2) expression in iWAT of cold (A) and CL-316,243 (B) treated mice. n=5 per group, * $p<0.05$ vs room temperature (RT) or control vector (Ctrl).



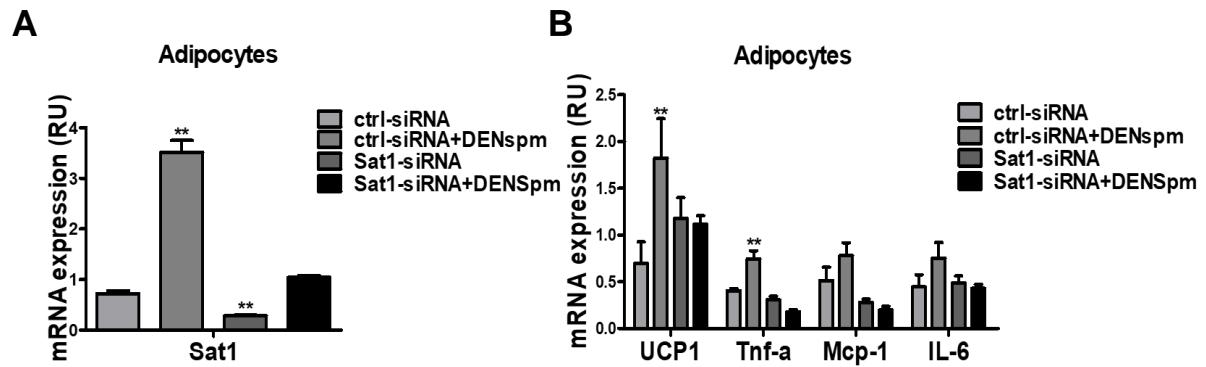
Supplementary Fig. 5. Plasma glucose (A), insulin (B) and insulin x glucose product (C) in control and SAT1-aKO mice fed a HFD for 30 weeks. n=9-15 per group.



Supplementary Fig. 6. SAT1 levels in adipocytes with lentiviral SAT1 overexpression. n=6 per group, **p<0.01 vs controls (Ctrl).



Supplementary Fig. 7. (A) Percent of F4/80-positive macrophages in stromal vascular fraction cells in adipose tissue sections of cold-challenged SAT1-aKO and control mice. (B) Inflammation-related gene expression (Cd14, Tnf- α , Mcp-1, IL-6) in perigonadal white adipose tissue (pgWAT) of cold-challenged SAT1-aKO and control mice. n=4-6 per group, *p<0.05, **p<0.01 vs Controls (Ctrl).



Supplementary Fig. 8. (A) Expression of SAT1 and (B) expression of UCP1 and inflammation-related genes in DENspm-treated adipocytes with or without SAT1 siRNA knockdown. n=4-6 per group, *p<0.05, **p<0.01 vs controls (Ctrl-siRNA).