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Supplemental Information

Activation of IRF1 in Human Adipocytes Leads to Phenotypes Associ-

ated with Metabolic Disease

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Figure S1, Adipocyte identity validation. Related to Figure 1.

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Days of Differentiation

Figure S2, IRF1 overexpression. Related to Figure 2 & 3.

















Figure S3, In vivo IRF1 expression. Related to Figure 4.



Supplemental Figure Legends

Figure S1. A) ASC-adipocytes were co-stained with BoDIPY (green), DAPI (blue), and anti-C/EBPα (red) to assess differentiation efficiency. An Image J binary mask was used to count stained foci. B) RT-qPCR was used to quantify expression of adipogenic genes during a timecourse of ASC-adipocyte differentiation. "Day 0" represents undifferentiated ASCs. C) Venn diagram of genes higher expressed in primary adipocytes versus ASC-adipocytes overlapping with genes higher expressed in obese versus lean individuals.

Figure S2. Error bars represent +/- standard deviation of biological triplicates and statistically significant p-values are denoted by an asterisk (≤ 0.05 , ≤ 0.005). A) RT-qPCR was used to test expression of the inducible IRF1 transgene in ASC-adipocytes, in both the presence and absence of doxycycline (+/- DOX). ASC-adipocyte transfection with a DOXinducible GFP transgene serves as a negative control. B) ChIP/gPCR was performed for IRF1 in rtTA control cells without IRF1 expression at putative binding sites (H3K4me1 bound IRF1 motif) (PARP14, IFIT3, ISG15). OAS3 and ZNF74 represent a negative control site where IRF1 is not predicted to bind. Signals are expressed as percentage of total chromatin input. C) A multiplex ELISA assay was utilized to measure adipokines and cytokines in secreted into culture media from adipocytes expressing IRF1. D) Expression of IL6, IL8 and MCP-1 in obese and lean individuals' adipocytes from the GEO dataset, related to figure 3A. E) Glycerol release into the media in response to forskolin (FSK) activated lipolysis was measured in IRF1- and rtTA-adipocytes. Two separate biological triplicates were averaged and plotted. Replication of and related to figure 3B. F) A plot of abundance ratio against number of double bonds for each total of carbon atoms for triglycerides in IRF-adipocytes vs. control (rtTA).

Figure S3. A) RT-qPCR was used to assay for doxycycline (DOX)-inducible expression of hIRF1 in 3T3-F442A cells. B) rtTA only or IRF1-expressing 3T3-F442A cells from were injected into 6-week old nude mice. 6 weeks post-injection, exogenous fat explants (EXP) and control autologous white adipose tissue (WAT) were harvested and stained with hemotoxylin and eosin (H&E). C) Autologous WAT and skin (positive control for macrophage localization) were harvested, probed with anti-F4/80 (green) to assess macrophage infiltration, α -PLIN1 (red) to verify adipocyte identity, and stained with DAPI. Negligible numbers of macrophages are observed in control WAT.

Supplemental experimental procedures

Primer List

Expression Analysis

hMCP-1 exp For #1 hMCP-1 exp Rev #1 mf4/80 exp For #1mf4/80 exp Rev #1 mMHCI F mMHCI R mMHCII F mMHCII R Viral IRF1 qPCR 1 For pDL38R (LentiViral 3'UTR) Rev ADIPOQ For ADIPOQ Rev FABP4 For FABP4 Rev PPARG2 For PPARG2 Rev Lep For Lep Rev PLIN1 For PLIN1 Rev CIDEC For CIDEC Rev HPRT For HPRT Rev

CAG CCA GAT GCA ATC AAT GCC TGG AAT CCT GAA CCC ACT TCT TTG TAC GTG CAA CTC AGG ACT GAT CCC AGA GTG TTG ATG CAA GTGATCTCTGGCTGTGAAGT GTCTCCACAAGCTCCATGTC CAACCGTGACTATTCCTTCC CCACAGTCTCTGTCAGCTC TCT GAA GAA CAT GGA TGC CAC C AGCAGCGTATCCACATAG GATGAAGTCCTGTCTTGGAAGG CAGCACTTAGAGATGGAGTTGG TCATGAAAGGCGTCACTTCC GCTTGCTAAATCAGGGAAAACA GCAGGAGATCTACAAGGACTTG CCCTCAGAATAGTGCAACTGG AAGGTTTGGTGTGTGGAGATG CTCCTGTCTCTTCTTTCTCTGC CCCCCTGAAAAGATTGCTTCT GGAACGCTGATGCTGTTTCTG AAGTCCCTTAGCCTTCTCTACC CCTTCCTCACGCTTCGATCC TGACACTGGCAAAACAATGCA GGTCCTTTTCACCAGCAAGCT

ChIP-qPCR

IFIT3 Prom ChIP-1 For IFIT3 Prom ChIP-1 Rev PARP 14 ChIP-1 For PARP 14 ChIP-1 Rev ISG15 ChIP For ISG15 ChIP Rev IRS-1 ChIP For IRS-1 ChIP Rev CTG AGG CAG GAG AAT CAC TT TGA CTG TTG CTC TTT GAC CT GAT CTC TCT GCC TCC ACT CT GAT ATC AGG GGA TAG CCT TG CGC TTT GTG ACC AGA CCT CAC T ATT TTG AAG GCA TGG CCG G TTTCTCCACCCGCCGAGATG CAGCGATTCCCGAGGCAAAT