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Supplemental Data

Short Article

Interferon-Regulatory Factors

Are Transcriptional Regulators of Adipogenesis

Jun Eguchi, Qing-Wu Yan, Dustin E. Schones, Michael Kamal, Chung-Hsin Hsu, Michael Q. Zhang, Gregory E. Crawford, and Evan D. Rosen

Supplemental Experimental Procedures

Identification of Conserved Islands

We identified murine regions of interest around the twenty-seven adipocyte-selective genes as follows. Our regions extended 50 kb upstream of each gene, or until the nearest exon from a neighboring gene was encountered. We also included the first intron, and in the small number of cases in which the first intron was small we also added the largest intron. These regions were mapped to the human genome and conserved islands were identified using a sliding window of 70 bp. Those windows for which at least 56 human bp (80% of 70bp) aligned to dog and either mouse or rat, and showing at least 80% identity against dog, and at least 73% identity for either mouse or rat were identified as conserved windows.

Next, adjacent conserved windows separated by no more than 30bp were merged into contiguous genomic regions; those regions extending over at least 80bp became the list of conserved islands. For five genes (*Retn, Adn, Adpn, Fasn, Pparg*) the percent identity had to be lowered to 70% (for dog and rodent) to obtain enough conserved islands. Each conserved human island was assigned corresponding location in the mouse genome through the underlying genomic alignments. Primers were devised to flank these regions and to generate amplicons of <250 bp; in cases where a conserved island was too large to be contained in one amplicon of <250 bp, we split the island into multiple primer sets (see Table S4).

DNase Hypersensitivity Analysis

3T3-L1 pre-adipocytes and adipocytes were harvested by scraping, suspended in PBS and centrifuged for 10 min at 4°C. Pellets were resuspended in TNM buffer (10 mM Tris-HCl [pH 7.5], 10 mM NaCl, 3 mM $MgCl_2$) at 5 x 10^6 cells/ml and incubated for 10 min on ice. The swollen cells were broken in a tight-fitting Dounce homogenizer (10 strokes with a B pestle). Intact nuclei were precipitated through a layer of 0.25 M sucrose in TNM buffer by centrifugation at 1,300 x *g* for 10 min, then resuspended in digestion buffer (15 mM Tris-HCl [pH 7.5], 15 mM NaCl, 3 mM $MgCl_2$, 60 mM KCl, 0.25 mM sucrose, 0.5 mM dithiothreitol, 1 mM phenylmethylsulfonyl fluoride) at 2 x 10^7 nuclei/ml. Nuclei were digested with various amounts of DNase I (0-20 U) at 37°C for 10 min. Samples were treated with proteinase K overnight at 50°C, followed by phenol:chloroform extraction and isopropranol precipitation. DNA pellets were dissolved in 10 mM Tris (pH 8.0), and the extent of DNase digestion was

determined by agarose gel electrophoresis. DNA was quantitated three independent times using PicoGreen dsDNA Quantitation Reagent (Invitrogen) and a fluorimeter (Molecular Devices).

Quantitative real-time PCR was used to identify valid DNase hypersensitive sites. Primer sets were designed to flank highly conserved sequences surrounding genes involved in adipocyte development. DHS originally identified from human CD4+ T cells, B cells, HeLa cells, and hepatocytes were mapped to the orthologous positions in the mouse genome (Crawford et al., 2006b). Primer sets designed around the orthologous DNase HS sites were shown to identify valid DNase HS sites in mouse CD4+ T cells, and were used as positive controls for this study (Crawford et al., 2006b). A negative control set of 96 primer sets were designed to flank random unique sequences in the mouse genome. Each primer set was used to amplify non-digested or DNase-digested nuclear DNA. A total of 9 ng of non-digested and DNase-digested DNA were pipetted into 384 well plates (Quadra 384, Tomtec), followed by the addition of primers and SYBR green PCR mix (Qiagen). All PCR reactions were performed in duplicate on a 7900 real-time PCR machine (Perkin Elmer) on two separate days. Dissociation curves were examined manually for each reaction, and any curve showing a reaction failure, multimers suggesting distinct amplification products, or any other form of aberrancy were discarded. Of 268 primer sets chosen to flank conserved islands, 38 resulted in failed reactions or aberrant dissociation curves in either Day 0 or Day 7 samples (14.1%). Fourteen of 96 (14.5%) random primers and 8 of 96 (8.3%) positive control regions were discarded for similar reasons. To determine which regions should be considered hypersensitive, we set a cut-off of a 5% false discovery rate (occurring at ΔC_T=1.0, i.e., 95% of random amplicons have a ΔC_T<1.0) for Day 7 samples. For Day 0 samples the threshold was also set to give a 5% false discovery rate, at ΔC_T= 0.2. A differentiation-dependent DHS was defined as a site that exceed the hypersensitivity threshold set for Day 7, but not the threshold set for Day 0.

Computational Analysis

The Discriminating Matrix Enumerator (DME) algorithm (Smith et al., 2005) was used for *de novo* motif discovery in the DHS. The DME algorithm enumerates motifs and chooses those that best distinguish between two sequence sets, referred to as foreground and background sets. In this case, the foreground set was composed of the sequences corresponding to the DHS and the background sets were obtained by randomly sampling in the regions surrounding the DHS.

The Matcompare (Schones et al., 2005) algorithm was used to annotate the discovered motifs. Motifs discovered with DME were compared to all vertebrate profiles in the TRANSFAC database (v9.3) (Matys et al., 2006) using the Kullback-Leibler divergence (KL div) as a scoring function. The TRANSFAC profile most similar to each DME profile and below a dissimilarity threshold (KL div <= 1.5) was chosen to annotate the DME profile and determine the likely transcription factor corresponding to the *de novo* discovered motif. The motifclass algorithm, which is part of the CREAD package (http://rulai.cshl.edu/cread), was used to measure how well each *de novo* discovered motif classified the foreground and background sequence sets.

For classification of the sequence sets, we define the sensitivity and specificity of a motif as

$$Sensitivity = \frac{n_{fg}}{N_{fg}} \quad \text{and} \quad Specificity = 1 - \frac{n_{bg}}{N_{bg}},$$

where N_{fg} (N_{bg}) is the number of sequences composing the foreground (background) set and n_{fg} (n_{bg}) is the number of sequences in the foreground (background) that contain the motif in

question. The statistic used to measure the ability of the motif to classify the sequence sets is the Error Rate (Smith et al., 2006), defined as

$$ErrorRate = 1 - \frac{Sensitivity + Specificity}{2}.$$

Putative IRF-REs were predicted using STORM (Schones et al., 2007). STORM scans through the input sequences with a position weight matrix (PWM) and reports sites scoring above a threshold. To obtain a scoring threshold for the IRF PWM, the following procedure was carried out. Promoter regions (-1000: +300 with respect to TSS) from human, mouse, rat, chicken and cattle were obtained from the Eukaryotic Promoter Database (EPD) (Perier et al., 2000) by selecting the 'Representative set of not closely related sequences' for each species. Each promoter in this set was scanned with the IRF PWM and the maximum score in each sequence was recorded. An extreme value distribution was fit to this set of scores and the score S corresponding to allowing 20% of the distribution to be greater than S was selected as a scoring threshold. This threshold was then used to scan the DHSS regions for putative IRF-REs.

Northern Blot Analyses

Total RNA was isolated from murine tissues with Trizol® reagent (Invitrogen). For Northern blot analysis, 20 μg total RNA was subjected to 2.2 M formaldehyde 1% agarose gel electrophoresis and capillary transferred to Hybond XL nylon membranes (Amersham Biosciences). Membranes were hybridized with [α-^{32}P] dCTP-radiolabeled mouse IRFs cDNAs.

Protein Extraction and Western Blot Analysis

Murine tissue lysates were prepared using RIPA buffer (Boston BioProducts) supplemented with Complete protease inhibitor cocktail (Roche). For Western blot analyses, 20 μg of protein of each sample was subjected to SDS-PAGE under reducing conditions, transferred, and blotted using the same anti-IRF4 antibody described above.

Supplemental References

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Smith, A.D., Sumazin, P., Xuan, Z., and Zhang, M.Q. (2006). DNA motifs in human and mouse proximal promoters predict tissue-specific expression. Proc. Natl. Acad. Sci. USA *103*, 6275–6280.

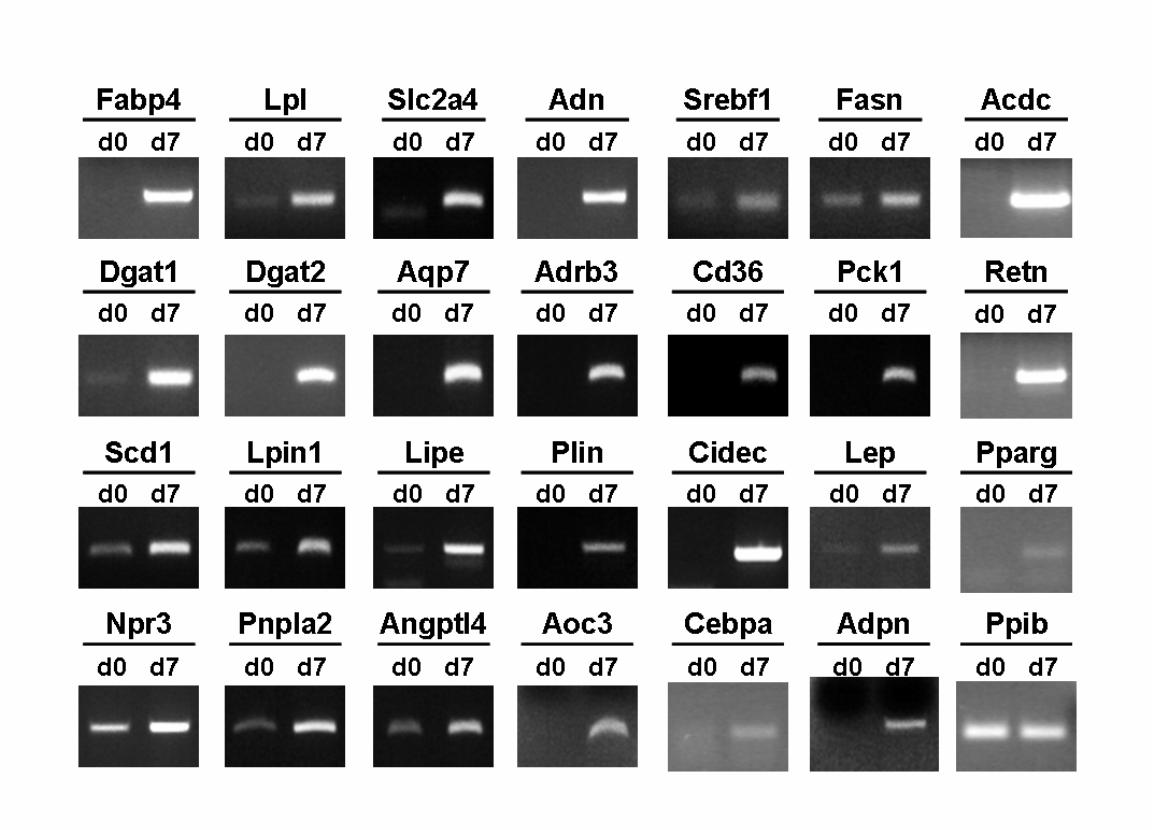

Figure S1. Gene Expression of Adipose-Selective Genes during 3T3-L1 Adipogenesis

All twenty-seven adipose-selective genes and the cyclophilin control (Ppib) were amplified from cDNA collected from 3T3-L1 pre-adipocytes (Day 0) and mature adipocytes (Day 7).

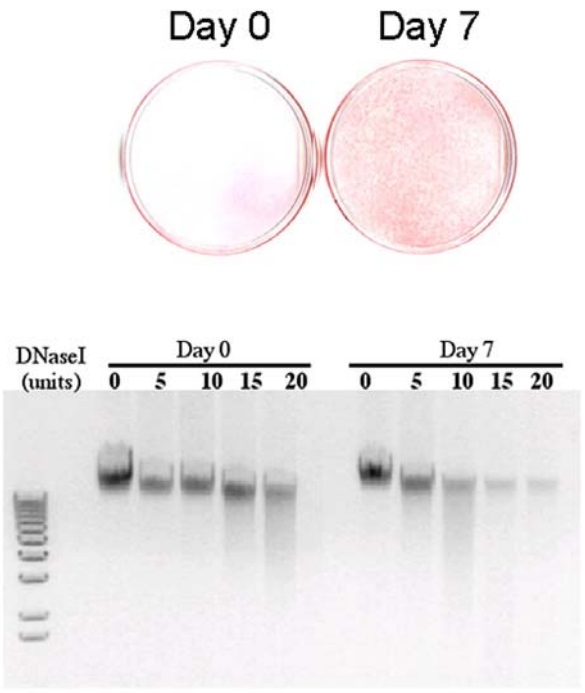

Figure S2. Differentiation of 3T3-L1 and Agarose Gel Analysis of the Purified Genomic DNA

Genomic DNA for DNase hypersensitivity analysis was harvested from 3T3-L1 pre-adipocytes and adipocytes. Oil red O staining shows excellent adipocyte conversion in harvested dishes (top). Nuclei from Day 0 and Day7 cells were treated with variable concentrations of DNase I as described in the methods. After proteinase K digestion and extraction, aliquots were run on agarose gels to determine the extent of digestion (bottom). We used 20U DNase from Day 0 and 10U DNase from Day 7 for subsequent experiments because of their similar degree of digestion.

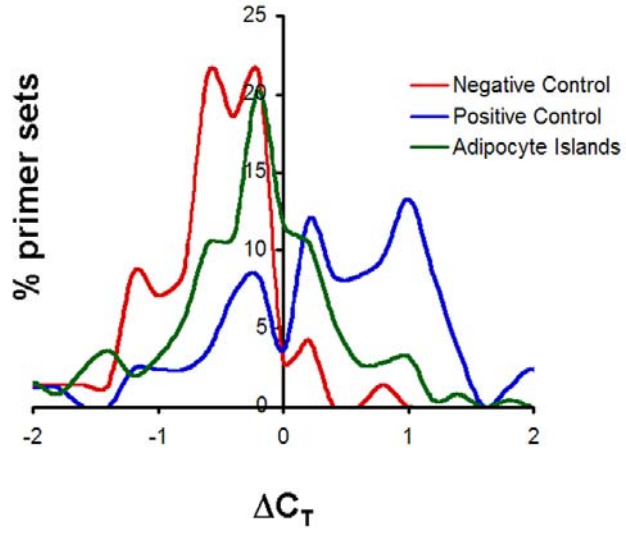

Figure S3. Results of DNase Hypersensitivity Analysis of Day 0 Samples

The X axis represents the difference in cycle threshold (ΔC_T) between DNase digested and undigested samples. The Y axis represents the percent of all primer sets that displayed any given ΔC_T. The red line describes results for random primer pairs, which serve as a negative control. The blue line describes results for primer pairs that amplify regions known to be hypersensitive in other cell types. The green line describes results using primer pairs derived from the adipocyte selective gene set.

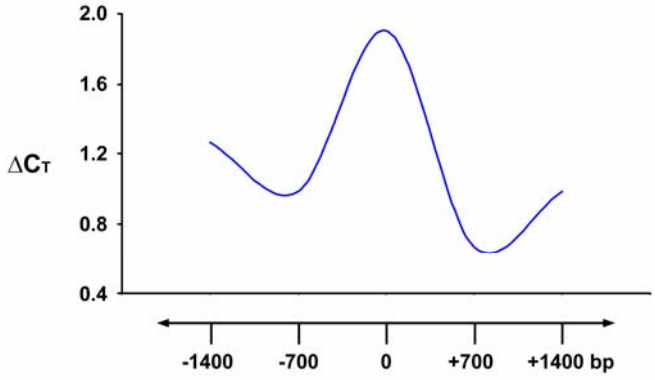

Figure S4. qPCR Analysis of the FABP4 I4 DHS

DNA from Day 7 adipocytes was subjected to qPCR with primers sets at increasing distance from the identified DHS. The difference between DNase-digested and undigested DNA (ΔC_T) is used a measure of hypersensitivity at the amplified locus.

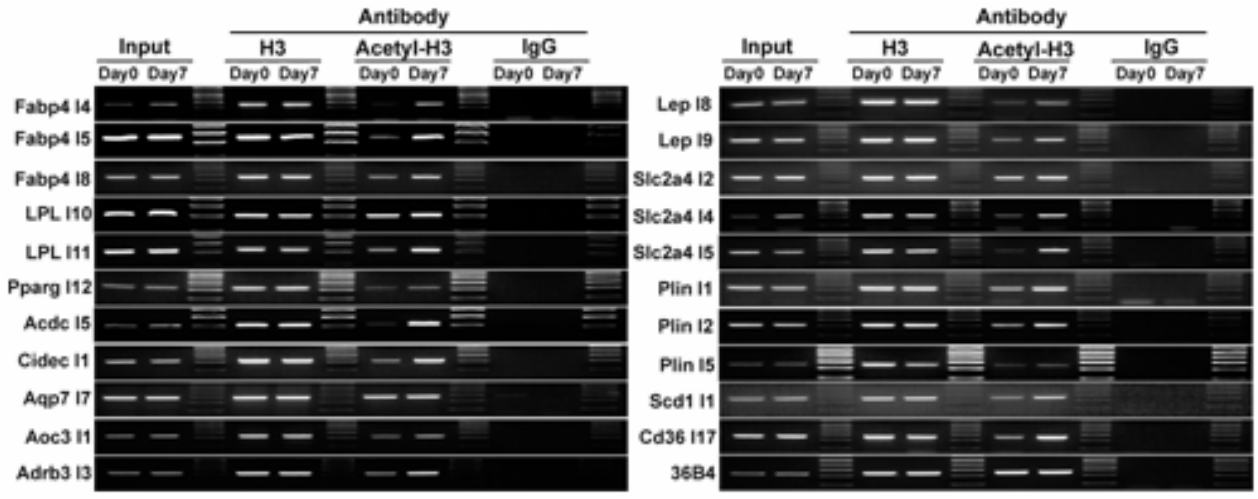

Figure S5. Differentiation-Dependent DHS Show Hyperacetylation of Histone 3 (H3) during Adipogenesis

The twenty-one differentiation-dependent DHS were studied using ChIP at Day 0 and Day 7. Fifteen of twenty-one differentiation-dependent DHS show enhanced acetyl-H3 at Day 7. The 36B4 promoter region was used as a positive control for the H3 acetylation.

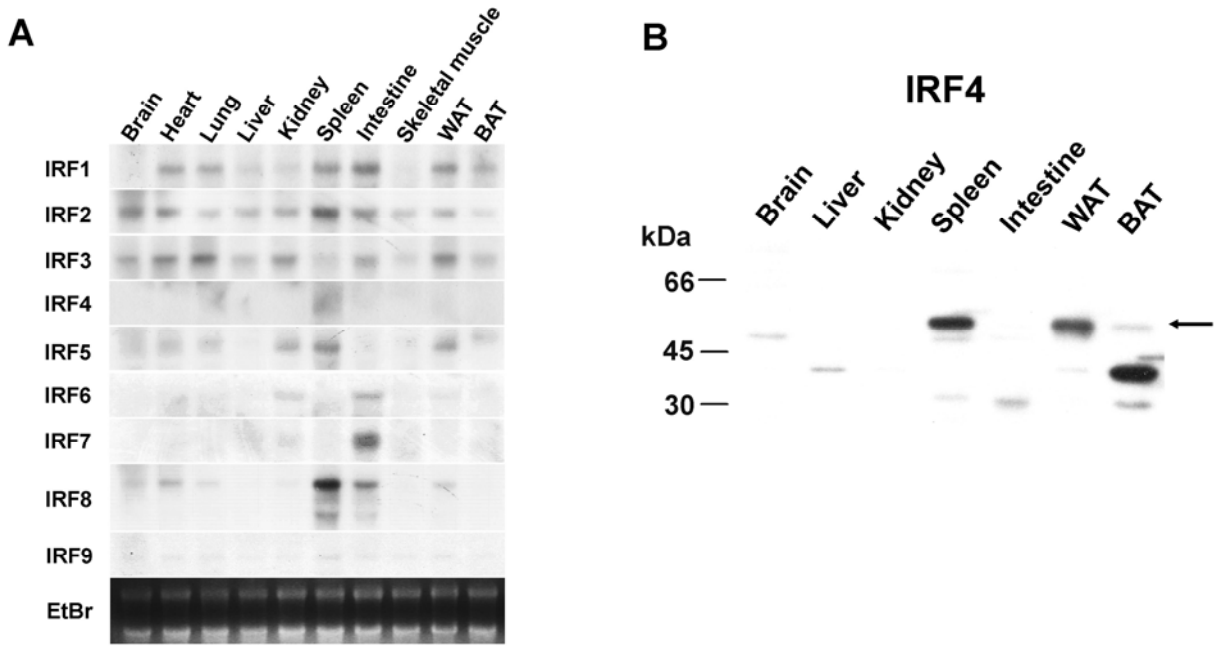

Figure 6. IRFs Are Expressed in Adipose Tissue

(A) Northern blots of murine tissues using probes specific for IRF1-9.
(B) Western blot analysis of IRF4 protein in various tissues.

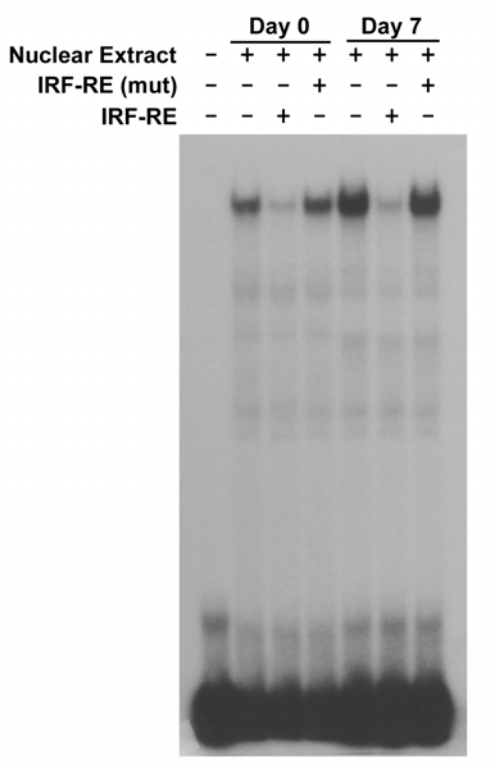

Figure S7. EMSA Showing Binding of Factors in Day 0 and Day 7 Nuclear Extract to the Putative IRF-RE in Pparg I8

The bound complex can be successfully competed (50X molar excess) with a consensus IRF-RE, but not with an IRF-RE that has key IRF recognition residues mutated (IRF-RE mut).

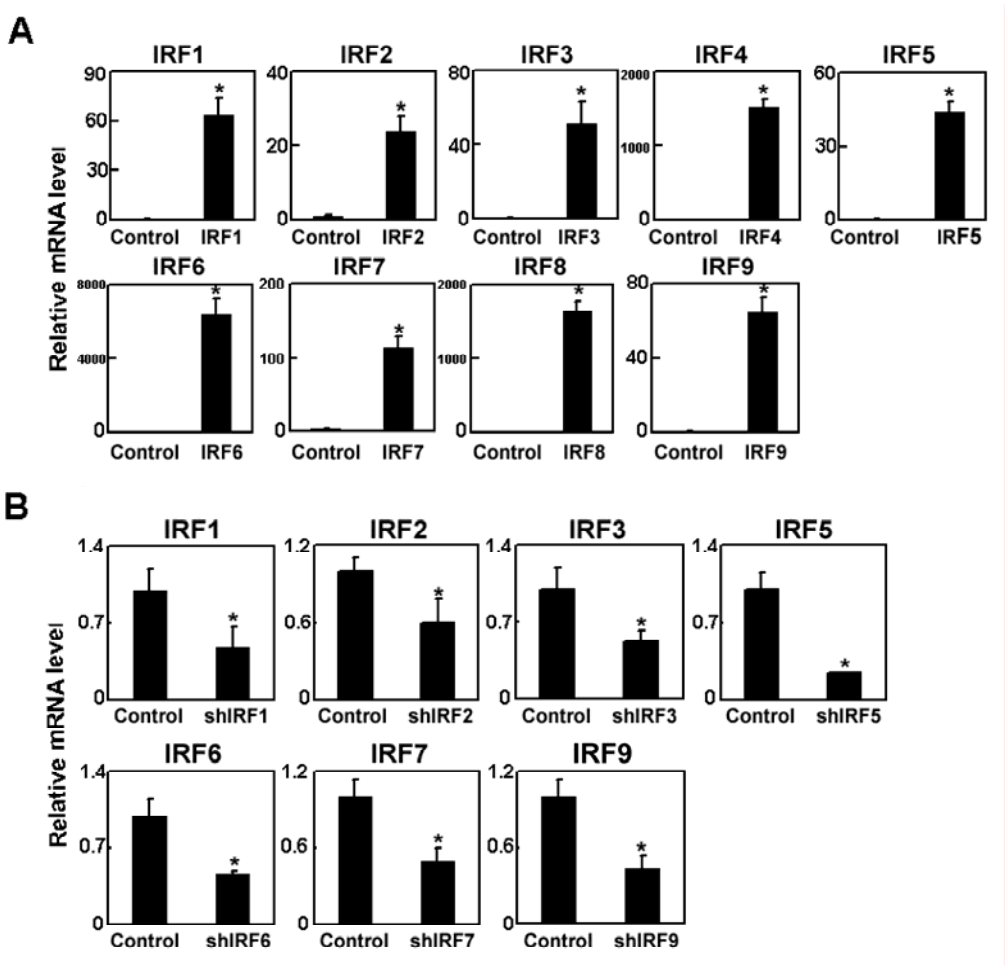

Figure S8.

(A) Level of IRF expression in virally transduced 3T3-L1 pre-adipocytes. Cells were transduced with retrovirus expressing an individual IRF isoform or control virus. Cells were selected, grown to confluence, and harvested for RNA and subsequent qPCR. Results reflect mean ± SD, n = 3, normalized to 36B4. Endogenous levels in control virus-infected cells are arbitrarily given a value of 1. *$p < 0.01$.

(B) Efficacy of isoform-specific IRF knockdown in 3T3-L1 pre-adipocytes. Cells were transduced with a lentivirus expressing a specific IRF shRNA or control virus. Cells were selected, grown to confluence, and harvested for RNA and subsequent qPCR. Results reflect mean ± SD, n = 3, normalized to 36B4. Endogenous levels in control virus-infected cells are arbitrarily given a value of 1. *$p < 0.05$.

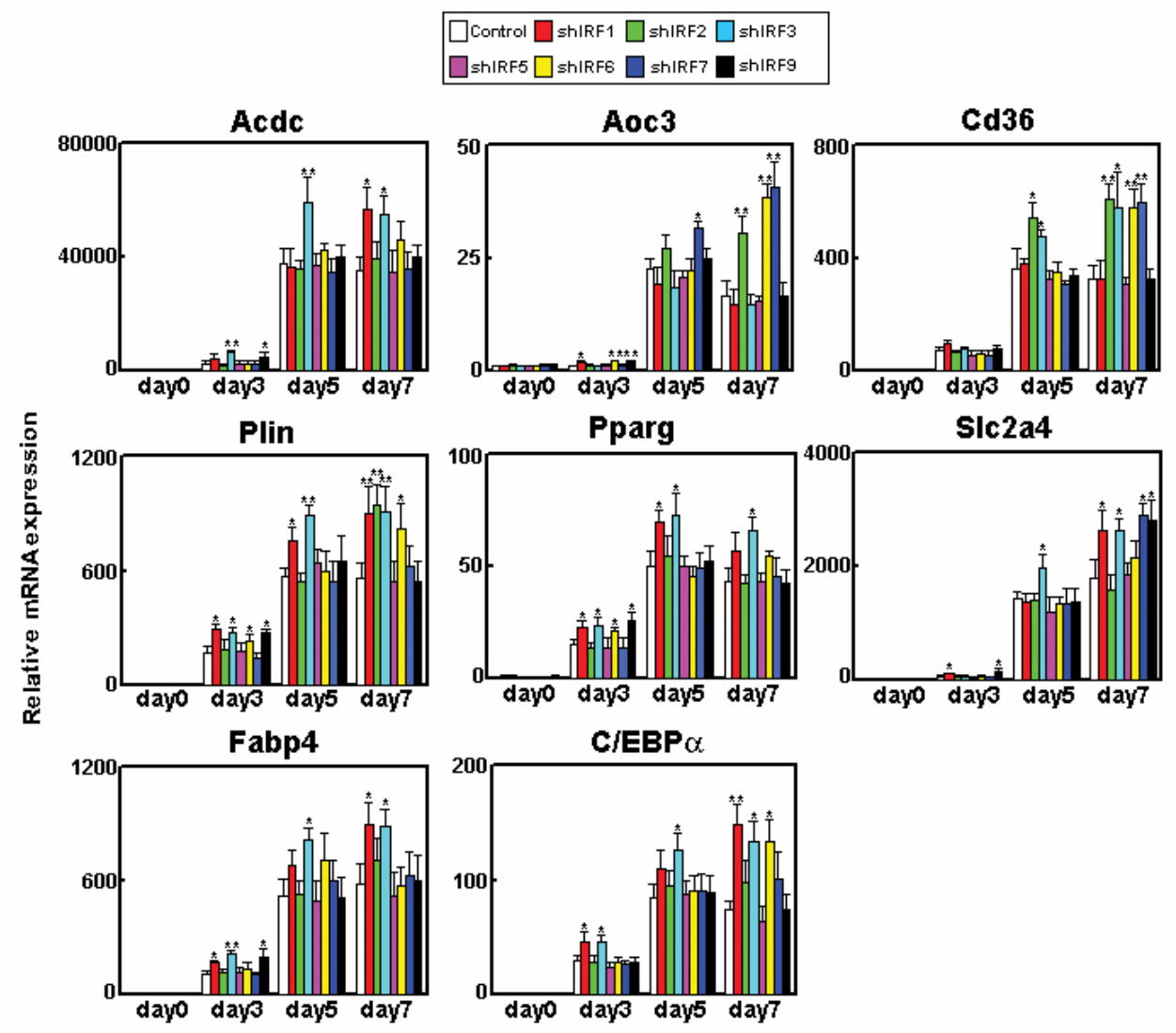

Figure S9. Adipocyte Gene Expression in 3T3-L1 Cells Undergoing Differentiation in the Presence of Isoform-Specific shRNAs

Cells from Figure S8B were differentiated with DMI, and RNA was harvested at Days 0, 3, 5, and 7 for qPCR. Mean ± SD, n = 3, normalized to 36B4. Endogenous levels in control virus-infected cells at Day 0 are arbitrarily given a value of 1. **p < 0.01.*p < 0.05.

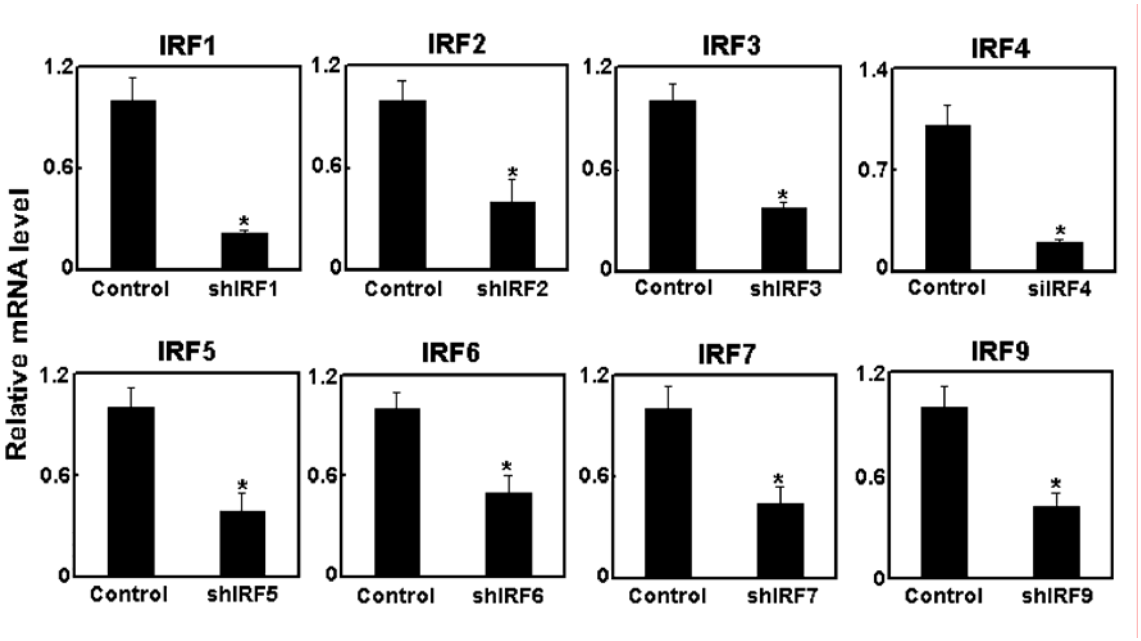

Figure S10. Efficacy of Isoform-Specific IRF Knockdown in Mature 3T3-L1 Adipocytes

Cells were transfected with a construct expressing a specific IRF shRNA or control vector. Forty-eight hours after transfection, cells were harvested for RNA and subsequent qPCR. Results reflect mean ± SD, n = 3, normalized to 36B4. *$p < 0.05$.

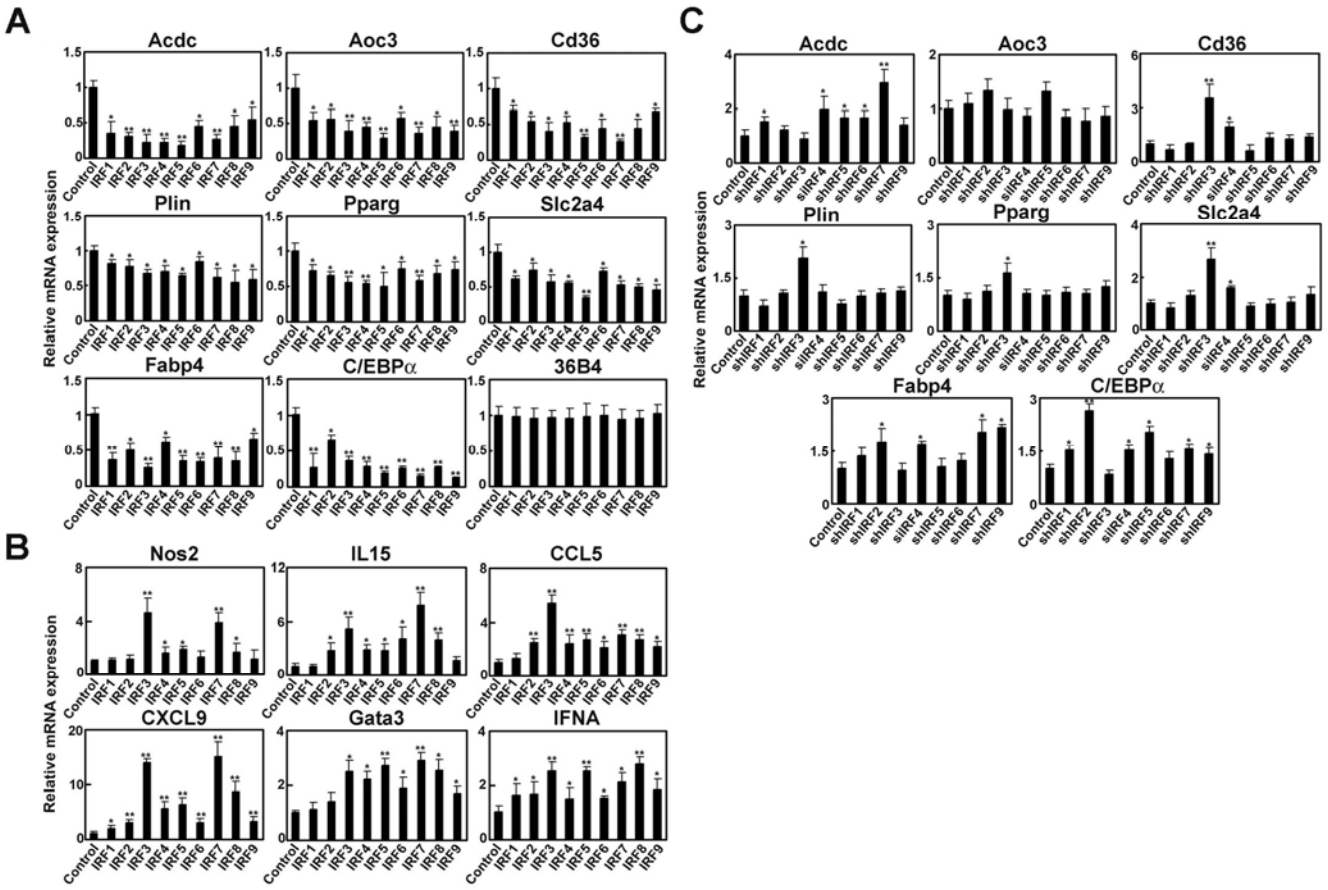

Figure S11. IRFs Regulate Adipocyte Gene Expression in Mature Adipocytes

(A and B) 3T3-L1 adipocytes were transfected with IRF expression plasmids or empty vector 5 days after the induction of differentiation. Total RNA was harvested 24 hours later for qPCR analysis. Data are expressed as fold induction relative to vector control. All samples are normalized to 36B4. Results are expressed as mean ± SD, n = 3, *p < 0.05, **p < 0.01 vs. vector control.

(C) 3T3-L1 adipocytes at Day 5 post-DMI were transfected with lentiviral plasmids expressing shRNAs directed against specific IRF isoforms, and total RNA was harvested 48 hours later. All samples are normalized to 36B4. Results are expressed as mean ± SD, n = 3, *p < 0.05, **p < 0.01 vs. vector control.

Table S1. Adipose-Selective Genes

Gene	TSS	Islands
Acdc	chr16:22990606	6
Adn	chr10:79787454	2
Adpn	chr15:84523445	3
Adrb3	chr8:26016986	6
Angptl4	chr17:32273399	6
Aoc3	chr11:101001729	4
Aqp7	chr4:41139373	15
Cd36	chr5:16198925	19
Cebpa	chr7:23536949	3
Cidec	chr6:113956001	3
Dgat1	chr15:76837471	7
Dgat2	chr7:86456164	15
Fabp4	chr3:10267743	17
Fasn	chr11:120495193	5
Lep	chr6:28912409	29
Lipe	chr7:14131862	7
Lpin1	chr12:16720814	6
Lpl	chr8:67906773	15
Npr3	chr15:11815300	22
Pck1	chr2:173216504	14
Plin	chr7:66811682	10
Pnpla2	chr7:129146181	3
Pparg	chr6:115748914	20
Retn	chr8:3618201	2
Scd1	chr19:43744211	13
Slc2a4	chr11:69560690	6
Srebf1	chr11:59833144	10

The twenty-seven murine adipose-selective genes chosen for this study are listed here, along with the number of conserved “islands” that were studied for each gene. Islands were at least 70 bp in length and 70% conserved, and were present in the proximal 50 kb upstream of the TSS or the first (or largest) intron. For *Pparg*, we used the more adipose-selective PPARγ2 promoter to define the TSS.

Table S2. Differentiation-dependent DHS

DHS	ΔC_T (D0)	ΔC_T (D7)	$\Delta\Delta C_T$	Distance from TSS (kb)
Cd36 I3	-1.85	1.66	3.51	-14.2
Pparg I8	-1.11	1.97	3.08	-10.5
Fabp4 I4	-1.65	1.26	2.91	-0.3
Plin I4	-1.41	1.39	2.80	-2.6
Adrb3 I3	-2.04	0.67	2.71	-1.5
Fabp4 I8	-1.43	1.06	2.49	-5.5
Pparg I9	-1.77	0.67	2.44	-10.0
Cd36 I7	-1.74	0.59	2.33	-11.4
Fabp4 I5	-1.63	0.53	2.16	-0.6
Lpl I10	-1.68	0.40	2.08	+0.2
Pparg I12	-1.26	0.78	2.04	-1.0
Aoc3 I1	-1.69	0.28	1.97	+2.2
Plin I5	-1.48	0.47	1.95	-2.8
Acdc I6	-1.55	0.29	1.84	-0.1
Lep I9	-1.03	0.68	1.71	-28.4
Plin I2	-1.12	0.47	1.59	-0.8
Acdc I5	-1.20	0.21	1.41	-0.4
Slc2a4 I4	-1.31	0.09	1.40	-0.2
Cd36 I17	-1.12	0.24	1.36	+3.2
Npr3 I5	-1.01	0.35	1.36	-8.8
Lep I8	-1.31	0.01	1.32	-29.0
Aqp7 I2	-1.26	0.02	1.28	-2.8
Cd36 I15	-1.16	0.10	1.26	-0.6
Lpl I11	-1.01	0.23	1.24	+1.3
Slc2a4 I5	-1.00	0.24	1.24	+0.7
Scd1 I1	-1.02	0.22	1.24	-39.1
Cidec I1	-1.14	0.07	1.21	+1.0
Plin I1	-1.08	0.13	1.21	-0.1
Cd36 I13	-1.20	0.01	1.21	-4.2
Scd1 I6	-1.12	0.05	1.17	-14.9
Aqp7 I7	-1.04	0.13	1.17	-28.1
Slc2a4 I2	-1.06	0.10	1.16	-0.8

Differentiation-dependent DHS in 3T3-L1 cells. For each DHS, the difference between DNase treated and untreated amplification (ΔC_T) is given for template collected from pre-adipocytes (D0) and mature adipocytes (D7). The DHS are ranked by the $\Delta\Delta C_T$, which is the difference between the ΔC_T at Day 0 and at Day 7, and thus provides a measure of the differentiation dependence of the hypersensitivity. Also given is the distance of the DHS from the TSS. A negative number means that the DHS is in the 5' flanking region while a positive number means that the DHS is intronic.

Table S3. IRF Binding Motifs Identified in Differentiation-Dependent DHS

DHS	Motif	Location	Strand
Slc2a4 I2	CCTTTCTTTCCA	chr11:69561327	+
Cd36 I3	CTTTCCTTTCCT	chr5:16213127	-
Cd36 I3	CTTTCCTTTCCT	chr5:16213132	-
Cd36 I3	CTTTCCTTTCCT	chr5:16213137	-
Pparg I9	CCTCCCTTTCCT	chr6:115800123	-
Plin I4	CCTCCCTTTCCT	chr7:66814192	-
Acdc I5	CCTCCCTTTCCC	chr16:22990252	-
Pparg I8	CTTCTCATTTCA	chr6:115799789	+
Aoc I1	CCCTCCTTTCCC	chr11:101003735	-

Nine potential IRF binding sites were identified by STORM in the adipocyte DHS. Note that three of these sites are within a single DHS (*Cd36 I3*).

Table S4. PCR Primers Used to Amplify Genes of Interest in This Study

Gene	Primer	Sequence
Acdc	Forward	GTTGCAAGCTCTCCTGTTCC
	Reverse	GCTTCTCCAGGCTCTCCTTT
Adn	Forward	CCTTGCAATACGAGGACAAAGA
	Reverse	CACACCCCAACCAGCCAC
Adpn	Forward	ACGGAGGAGTGAGCGACAAC
	Reverse	CGCCACCAAGGACAGACTCA
Adrb3	Forward	ATTGGCGCTGACTGGCCATT
	Reverse	CCTCGGCATCTGCCCCTACA
Angptl4	Forward	ACAGCATCACAGGGAACCGA
	Reverse	CCCACGGAGGTCATGGTCTT
Aoc3	Forward	TACATGCGGGATGTGACTGT
	Reverse	CAGGTTCTGTCCCTGGTGTT
Aqp7	Forward	TGTCGCTAGGCATGAACTCC
	Reverse	ACCTTCTGGTCTCTTGCTGT
Cd36	Forward	TCTGTTGGAACAGAGGATGA
	Reverse	TGGAACCAAACTGAGGAATG
Cebpa	Forward	TGTGCGAGCACGAGACGTC
	Reverse	AACTCGTCGTTGAAGGCGG
Cidec	Forward	GATCGATGTGGCCCGGGTAA
	Reverse	TAGCTGGAGGTGCCAAGCAG
Dgat1	Forward	GGAGACCGCGAGTTCTACAG
	Reverse	CTCATGGAAGAAGGCTGAGG
Dgat2	Forward	TCTCAGCCCTCCAAGACATC
	Reverse	GCCAGCCAGGTGAAGTAGAG
Fabp4	Forward	TTCGATGAAATCACCGCAGA
	Reverse	AGGGCCCCGCCATCT
Fasn	Forward	TTGCTGGCACTACAGAATGC
	Reverse	AACAGCCTCAGAGCGACAAT
Lep	Forward	CTGGAGAATCTCCGAGACCT
	Reverse	TCAGGGCTAACATCCAACTG
Lipe	Forward	CCGCTGACTTCCTGCAAGAG
	Reverse	CTGGGTCTATGGCGAATCGG
Lpin1	Forward	AGCTCAAGGCCCCATATCCC
	Reverse	GGTGACTGGTTGGCTGACCT
Lpl	Forward	GCCCAGCAACATTATCCAGT
	Reverse	GGTCAGACTTCCTGCTACGC
Npr3	Forward	CTGGTCTACAGCGACGACAA
	Reverse	CACCGCCAACATGATTCTCC
Pck1	Forward	ACGACCCCTTTGCCATGCGA
	Reverse	TAGCCGATGGGCGTGAGCTT
Plin	Forward	GATCGCCTCTGAACTGAAGG
	Reverse	CTTCTCGATGCTTCCCAGAG
Pnpla2	Forward	GGTGACCATCTGCCTTCCAG
	Reverse	TGCAGAAGAGACCCAGCAGT

Pparg	Forward	GCATGGTGCCTTCGCTGA
	Reverse	TGGCATCTCTGTGTCAACCATG
Ppib	Forward	GGTGGAGAGCACCAAGACAG
	Reverse	GCCGGAAGTCGACAATGATG
Retn	Forward	TCATTTCCCCTCCTTTTCCT
	Reverse	GGGCTGCTGTCCAGTCTATC
Scd1	Forward	CGCCCAAGCTGGAGTACGTC
	Reverse	GGGCCCATTCGTACACGTCA
Slc2a4	Forward	GATTCTGCTGCCCTTCTGTC
	Reverse	ATTGGACGCTCTCTCTCCAA
Srebf1	Forward	GCAGACCCTGGTGAGTGG
	Reverse	GTCGGTGGATGGGCAGTTT
Irf1	Forward	GCAAAACCAAGAGGAAGCTG
	Reverse	CAGAGAGACTGCTGCTGACG
Irf2	Forward	GTCACTAACCCGCCAGACAT
	Reverse	GCTCCTCTTCCTCCAGTGTG
Irf3	Forward	GGCTTGTGATGGTCAAGGTT
	Reverse	CATGTCCTCCACCAAGTCCT
Irf4	Forward	GCAGCTCACTTTGGATGACA
	Reverse	CCAAACGTCACAGGACATTG
Irf5	Forward	CAGGTGAACAGCTGCCAGTA
	Reverse	CTCATCCACCCCTTCAGTGT
Irf6	Forward	AGTGTGGCCCAAAACAGAAC
	Reverse	GGGTTGCTCACCGTCATAGT
Irf7	Forward	CCAGTTGATCCGCATAAGGT
	Reverse	GAGCCCAGCATTTTCTCTTG
Irf8	Forward	GATCGAACAGATCGACAGCA
	Reverse	GCTGGTTCAGCTTTGTCTCC
Irf9	Forward	GTCTGGAAGACTCGCCTACG
	Reverse	TGGTCCTCCCATTTTCCATA
36B4	Forward	GAGGAATCAGATGAGGATATGGGA
	Reverse	AAGCAGGCTGACTTGGTTGC
Ccl5	Forward	C C C T C A C C A T C A T C C T C A C T
	Reverse	C C T T C G A G T G A C A A A C A C G A
Cxcl9	Forward	A C C A A C A A G C A C C C T G A A T C
	Reverse	A A G G C G T G A T G A A T T T T G
Gata3	Forward	G T C A T C C C T G A G C C A C A T C T
	Reverse	G T A G A A G G G G T C G G A G G A A C
Ifna	Forward	TCTGATGCAGCAGGTGGG
	Reverse	AGGGCTCTCCAGACTTCTGCTCTG
Il15	Forward	T T G C A G T G C A T C T C C T T A C G
	Reverse	G T G C T T T G A A G A G C C A G A G G
Nos2	Forward	C C T G T G T T C C A C C A G G A G A T
	Reverse	CCCTGGCTAGTGCTTCAGAC

Table S5. PCR Primers Used to Amplify Genomic Islands in Hypersensitivity Studies

Island	Left Primer	Right Primer
Acdc I1	ACACACAGGACAGAATGTGGAC	ATTATGCCAATAATCCCCACAG
Acdc I2	TCGCTAAGCAAGTGTGTGTTTT	CCCATATAGGAACACTGCTGGT
Acdc I3	AAGCATGACTCTTAGGCTCTGTG	GGCGGACTCACATCTTATTTTT
Acdc I4	GTGAGTGGTGACTGCTAGTTGC	GCCCAGTGTCACAGAACACTTA
Acdc I5	CTGAACCACACAGCTTCACATT	CTCTACCAGAGCAAGAGATGGG
Acdc I6	TGGATTAAACCAGGTTCCCTAA	GCCAGCCGAGAATATAGAATTG
Adn I1	GAAGGCAGAATTCACAGGAAAT	CATGTGTCTGTCATGGTGTCTG
Adn I2	GTTCACATCATCTGTCCCAGAA	GTCCACTCACCACATACAGCC
Adpn I1	CAGGAAGTCCATAATAGGGTGC	GGTGAGTGTAATTGGGAATCGT
Adpn I2	CTGGGGCCTCTTTAACACTTTA	CACTCTCACTGCCCTTTACTCC
Adpn I3	ATCAAAGACCATTGGGAAACAG	TAATTTTGTGCCCTCTCTGTGA
Adrb3 I1	AGAGAGCCGTTTCTGTGAGG	CTCTTGTGACTATTGGACGCTG
Adrb3 I2	TGTCAAGACTGCTCCATGAGTT	TTAGGTTCTCTCTTCCCCTTCC
Adrb3 I3	CTTCTTGCTGGTCATCAGGGT	TTGAGTATGTCTTGGGGGAGAT
Adrb3 I4	CCTCACTATCACTTTTGGTGGC	CCACACTCACTATGATTGCCTC
Adrb3 I5	AAACTGTGCCAGCAATACCTCT	TTGTCCCAACCTATCCCTTAGA
Adrb3 I6 P1	CCATAGTCACAATCACAGCCAT	CACAGCTACGGAGAGATGAGTG
Adrb3 I6 P2	CGTATAGAAGCAGGAGGAGGTC	GAGTAGAGCCAGGCAGTGACTT
Adrb3 I6 P3	TCTCACCACTCATCTCTCCGTA	ACATTTGTTTGCAGAGTTTCCC
Angptl4 I1	CTCAGATTCTACTGTAGGCCCG	GCGTGGTTGACTTTACCTGAAT
Angptl4 I2	CCTGTCTGACAAGAAGACCCTT	CCTACTCTTCCTGTCTGCCTGT
Angptl4 I3	AGGCAGAGACAAAAGAGGACTG	GTTTCAGATTCCAGAGGTTTGC
Angptl4 I4	GGATCATAAGTGAAGAGGGTGC	AAAGAGGCTTCCCAAGATGAC
Angptl4 I5	ACATCACCCATCCAGAACCTAT	ATTCGTTCACCCTTCTTGACAT
Angptl4 I6	TAGCTCCCTTTCCCCTACTTTC	ATAGGTTCTGGATGGGTGATGT
Aoc3 I1	AGGTTGCTCACCAAACAAAGAT	TTGAACGGAGGCCTACATAAAC
Aoc3 I2	AGCCCATGGCATCTCTTTTT	CAAAACTTTCTGAGTCCTGCCT
Aoc3 I3 P1	GCAAGGCAGGACTCAGAAAGT	GAGAGGGAGAACCTGACATCC
Aoc3 I3 P2	TGTGAGAAGCTGCAGGACC	CTCTTCCATGACATACAGTGGC
Aoc3 I3	TCCATGGAAGAGCCAGTTTT	CAAGGAGCCTAGCACTCTCATC
Aoc3 I4	TGTCTTCCCTTAAGGTCACCAG	CTCAGGCTCTCATAGGCACAG
Aqp7 I1	AAAGAACATTAAGAAGGCACCG	GGTACCCCAGCTATTCTCTCCT
Aqp7 I10	TTTCAACATCGCAACTGTTTTC	TAGAAGAGAGCCTTGGTGGAAC
Aqp7 I11	GTTCCACCAAGGCTCTCTTCTA	TCAACACCTGTGGGATGAATAG
Aqp7 I12	CTCTTTACCCCTTGCTCTGAAA	CATAGGAGCTGGCTTTGATTCT
Aqp7 I13	CCACAGCTTGCTCATAGATTCA	CTTCCTTACTGCTCAGAGCCAC
Aqp7 I14	AGCGTTTCTATACTGGGTGGAG	AAGTAACACCAGCCAACCATCT
Aqp7 I15	CTGCTTGGTACACTGAAGGAAA	AAGTTCAGGCCACAGAACTAGG
Aqp7 I2	TGCAACTGAACTGTAGCTCTGC	GACTATGAGGCCCAGAATTCAC
Aqp7 I3	TTACTTCCTATATCCCCGAGGC	ATCTTGTCAGCTCTCCCAGGTA
Aqp7 I4	CACACACACACACACACACACT	AGGCTGAACAGGGAGTGAAGT
Aqp7 I5	AACACTTCTCTTCACCTCCTGG	TCAGCGTCTATGCTGAGAAATG
Aqp7 I6	GAGGGAGGGACAGAACCTAGTC	TCTGTTGAACTGTGCGTTTAGC

Aqp7 I7	TCCCTATGACTAGCATGCACAC	CTTCAGGGTCCTTCACAAAACT
Aqp7 I8	GGTAATGAGGGACAGACTCCTG	ACGGAACTACTTTCCGTGATGT
Aqp7 I9	GGGGAACATAAGACTGTCATGG	TAAGGGAGGTGGGTAGAGTGAA
Cd36 I1	CATGGAAAATAACCACTCAGCA	TAAACTCTTTGCACTGGAGGGT
Cd36 I10	TTTGTGGTGCTCCTTAACACTG	TACTTCCATCCTCTTTCCTCCA
Cd36 I11	TTGTAAAGCCAGGGGAGACATA	GTTTATTTCACTGTAAGGCGGG
Cd36 I12	GTGCACATTATAAAGAATGAACAGG	TATAATTTCCCATGTAATACACACTTG
Cd36 I13	ATTATACCCTTTACCCCGCAGT	ATCATGTGCTGTGTCAGATCCT
Cd36 I14	GCCATCTAGAGCTAGGTTTCCA	TGGCATGTACAGTGGAAGATGT
Cd36 I15	GTCCCAACAAAGCCTGAAAAT	GCATATCACCATCCTCTTGAAA
Cd36 I16	GCTCACAAGGGTCTATTTCTGG	CACTCCAGCATCTGGAATAACA
Cd36 I17	GATTGGGCAAAGTCTGAGGTAG	GGAGGAAAAGAGAATCCATGTG
Cd36 I18	TGGCCATCCATACTTATCTTCA	GTCCAAACAGTTCTCTGGTCCT
Cd36 I19	CCAAGAAATCAATCACAGGACA	TTCCACTCTGTCAAATATCAGCA
Cd36 I2	ATGATGCATGTCCTTCCCTAAT	GGATAAAAGCCTCAGAACCAGA
Cd36 I3	TGCAGTTGCAAGGTTACAGAGT	TCCTTTCCTTTCCTTTCCTTTC
Cd36 I4	ATTTGCAAGCACAAGTCTGGAT	TAAGTGGTGAGCAGCAGTGATT
Cd36 I5	TGAATGTTTACAGTGCTAAGTGCAT	TCACAATCTCAGGTAATTTCTACTTCA
Cd36 I6	CATACCATTTATTCTGGTTGCAT	GTCCTAGAGCAGTCTGTGGAGC
Cd36 I7	TAAATGATAATGCCCAGGAGGA	GTGGTCTTTTGTGGCTAGCTCT
Cd36 I8	AAAGTTCTGTGTGTGCCCTTCT	TATTGCTGTTCTTTCCTCCTGG
Cd36 I9	GTCCTAGATTTTTGGCCTTCCT	TAAAGGAGTCAAGGACCACAGG
Cebpa I1	GATGCCCGACCCTCTATAAAA	CTCTGGAGGTGACTGCTCATC
Cebpa I2	GGAGACGCAATGAAAAAGAAAG	TTGTGCGTCTTTTTCTCTGAAC
Cebpa I3	TGCTCACACCAGGTTGTTTATT	AAACTGTTAGGGAGGTCTGCTG
Cidec I1	AGCCTCACTCACTCCATTGTTT	CCCGTGGAGTTTCTGGACTAT
Cidec I2	GGCTTCCCTCCATTTTATTTCT	ACTCAGACCATAAGCCACATCC
Cidec I3	GTTAATTCCGCAATCGCTCTAC	CATTGTACAGAACTAAGGCCCC
Dgat1 I1	TCACTCACACCAACTATGGCTC	AAAAGGGCTTCAGTAGGATGGT
Dgat1 I2	GAAGAAAGGTCAAAGAGGCTGA	AACTCTGTAGAGCAGGCTGACC
Dgat1 I3	ACCAAAGCCATTTCACAAGACT	GGCCTACATAGGTCATGTCTCC
Dgat1 I4	CCATTCAGTAGACAAAACGCAC	GTAGCTCAGCCTATTGCAGCTC
Dgat1 I5	GCACACACACAACATCTTTTCA	GTGGCAAAGTCTGGTTCTCTTT
Dgat1 I7	CAAGGCCTGTTCTTCTTCACTT	CCTTCCTAAGCACAATAGCACC
Dgat2 I1	AGCTGGGAGAGGAAGGTAAAAC	ATAGCACACAGAGAGCATTTGG
Dgat2 I10	ACCTAGCCATTCAGCTGCTAAC	ATCTAAGGAGACTGGGATGCTG
Dgat2 I11	ACAGTGATGCAATGGTCTTTGA	GTCAAGAGCATGTGAGGTGGT
Dgat2 I12	GCCACTGGACTGAAACCTTATC	CCTCTAGAGCTGATGGTTCCAC
Dgat2 I13	AAATCTAGAAAGCAGAGGCACC	TCAAAGACCATTGCATCACTGT
Dgat2 I14	TGGAGTGGTGTTTAAGCAAAGA	GTCATTTGTCTTCCCTAGTGCC
Dgat2 I15	GCTAAGAGCAAGCTGTGGATTT	GGAAAGAAGGCTGTCCAGAGTA
Dgat2 I2	GGATTTGGGGATTTTTACAACA	ACAAGAAACTTCTGGTCCCAAG
Dgat2 I3	CTGTGCTGCTGCTCTTGTCTA	TAGAAGGGCAGATGAAAACTGG
Dgat2 I4	AGGGTGTTACCATTATGCAAGG	ACCACTGGTCTCATCTCTTGGT
Dgat2 I5	GAGCAGAAAAGAAAGGAGGTGA	GGACTACCACAGAGCATCATCA

Dgat2 I6	ATTTAAAAGCATTGACATGGGC	CTCCATCAGAGTGTTTCCACCT
Dgat2 I7	CTGAGGAGACAAACTAGGCCAC	TACCTCATAGACTGCAACCAGG
Dgat2 I8	GTACTATGAAGGTTGGGCCAGA	GGCTTTTCCCACTTTTGAGTC
Dgat2 I9	TACAAGTGACATGAGACCCCAG	CTCGTTCGTACCCTCTGTCATT
Fabp4 I1	ATTGAGGCAGTTTGACCATTTT	CAGACAATTCATTTCATGAGGG
Fabp4 I10	AGCTCCTGCTCTTTTCCCTACT	AACTGAGGGGTGTCTCACTGAC
Fabp4 I11	CTGACACTCCTACTGGAGAGGG	ACTATTGCTGATGCCATGTTGT
Fabp4 I12	GGGCTGGAGGCTTACTTAGATT	ATGAGAGGGACCATCTTTCATC
Fabp4 I13	TTATGCAGAGAACCTCCTGACA	GATTGATCAACCTTTAGCACCC
Fabp4 I14	TACTTCTAAAACGTGTGGCCCT	AAGATCATGGGAGACCACTGAC
Fabp4 I15	ACGGAGCTGTTTCTATCCCATA	ACGCTTTAGAAAAACAAGCTGC
Fabp4 I16	TGTGAGAACCGATGAGAAGAGA	ATCTTCACACTTCCAAGGCAAT
Fabp4 I17	TTCTCCTCCTTGGAATTTATTGA	TCCTTAGAAACCCCTGAAAGTG
Fabp4 I2	CCCTGCTTTCCTTCTGAATTAC	ACTGAAGTCATGATATTGCCCC
Fabp4 I3	TTTTAAGTAAAAGTTGCCCCCA	ACCCGCAAGAAAGAGTCTACAG
Fabp4 I4 P1	TTTTGTAAACCTTCGAGGAGGA	TAAGTCCAGTGATCATTGCCAG
Fabp4 I4 P2	CACTTTTAAAGATGCCCTGACC	AATCCATAAGGAATAATGGGGG
Fabp4 I4 P3	TGTTTTCCTCTGAGTCATGTTTTT	AAGAAGGTCAAATGTGTCCAAGA
Fabp4 I5	TGCAATAATGTGTTTAGTTCTTCTGA	AAACCAAACAAAGCCAAACAAC
Fabp4 I6	GGCTGAGGTCACATCTCAGAAT	CTAGAGTGGGGTCTGTTTCCTC
Fabp4 I7	GACTGAGAGTGCTTTGAAGGCT	GCTTCCACTTAATTCCTGATGG
Fabp4 I8	GATTGTTACAAGGCAAGGAAGG	GAATCAGGTAGCTGGAGAATCG
Fabp4 I9	TGTGTGCTAAGAGCTAGGCATC	CACAGTAAGGCAATACAGTGGG
Fasn I1	GAGGCCATAGGAAAGACAGAGA	CTGCCCAGGCTCTATCAAAG
Fasn I2	ACATTGGGGAGTGAGGAAACTA	AAAGGAAAAGGAGATGCAACAA
Fasn I5	GAAACCAATTGGACACCGAG	AGAGGGTGGGAGTCCGAG
Lep I1 P1	CAGTGGGGCTGACAGTCTTC	CGCCTGTGTATACTGAATGGTG
Lep I1 P2	GGGTTGGATTTCCATTATCATC	TGTCTTCATGGTTTCATTAGCC
Lep I1 P3	TTCATTTTATGGCTAATGAAACCA	GGCAACAAGTTGTCCCTTGTA
Lep I10	GAGACTAAGACTTGGAGGGGGT	CAGCATTTTTAACATTTTCGCA
Lep I11	GCATCTCTACAGGACCAAGACC	TGCCTATGACACACCTCAAAAC
Lep I12	AGGCTGAGGTTTAGCAAGACAG	TTAAACTGGCCATGATTGATTG
Lep I13	GGGGTGGGGGAAGTATAATAAA	TCTGGCTGTGGAAAAGCTAAAT
Lep I14	CTACCTATGGGAATGATCACGG	TTCCTGTCTTGTGGACACTCTG
Lep I15	AAACATTGTGGATGATGCTCAG	TCCCTGCCTTGTAAGGTCTCTA
Lep I16	TCAAAGGTATATGCCACCACAC	GAGACTTAAACAAAGGCCTCCC
Lep I17	AGCTTGCAACAAGCACTCAATA	GATGGTTGTGAGCTACCATGTG
Lep I18	CAGTTGACCTGTGCTTCCATAC	CACTTCTTTCTCCCTGTCTGCT
Lep I19	AAAGCACCTCAAAGTCTCCCTT	AGGTTAGCTCTCCAGGTCTCCT
Lep I2	TGTGGCTGTAACACAATGTCTG	AGAGTCAGATTGTAACGTGGGC
Lep I20	GGAGCCATTTGTGACAGTTTTT	GAGCTAGCCATCAACACTTCCT
Lep I21	TCCTCCCTTAGTACAGTGTGGG	TGAGATAAGGGCTGACTCCACT
Lep I22	TGTAACCAAGCTGCAGAAGAAA	TAGCTACTCGTGTGCTGGGTAA
Lep I23	GACTATGAGACTGGAGGATGCC	GCCTCCTGTCTGAGCCATATAC
Lep I24	AGAATGGAGCACTAGGTTGCTG	TGGATGGGGTGCTATTAGAAAG

Lep I25 P1	ATGGAACCAAACTTGAAAGGAG	AGGATGCTTCTTTAGCCAACAC
Lep I25 P2	TTGGTTCTTTCCTTTCTCAAGC	TTATTACAGCATCCCTGGCTCT
Lep I25 P3	AGTTCTTCTTGGTATCTGGGGG	GGTGCTCTGTAAAGGGAATTGT
Lep I26	TGATCAGAGTTGATGCAGGAGT	AAGTGCTGGCCACAGTATACAA
Lep I27	TGTGACCACTTCTTTCTGCAAC	TCCTTCCCGACCAAATTTACTA
Lep I28 P1	GCTCATCTTTCTGAGCCTCATT	TTCTGTTCTTCCTCATCTGGGT
Lep I28 P2	ATATTACCACCGATGGAGGACA	AGAAACAGGCCTAATGAGATGC
Lep I28 P3	GGAGAAGTTAGCTTTTCTGCCA	TTACTTAGAGCGCTGGGATTTC
Lep I29	GTCTGGGTCCATGATCTCTAGG	GAATGACACTTTTCAAGAGCCC
Lep I3	CACAGCTACCAAACTTCCACAG	CAGTGGAGAGAGACTCACATCG
Lep I4	CAGCTGTCTCCTTTGGATCTTT	CATGGTCACCCAGCAATACTAA
Lep I5	AGATCTTGAGAAACAAAAGCCC	GATGTCTTCCTGTCTCCAGGTG
Lep I6	TACAAGGCTGACTCATGACCAC	CAGACAGCAATACCCTCACTCA
Lep I7	TTCTTGGATTGTGTTCTTCCCT	CACACACAAACACACACACACA
Lep I8	CCCTGTAATTCCATAGTCCCAG	AGTTATCCATCCTCACAGGCTC
Lep I9	ACCCTGGGTGACAGATGACTTA	TCATTTGCCCTTCGATACTTCT
Lipe I1	CGAACACCTGCAAAGACATTAG	CTTTGGACTCCTGCATCTCAG
Lipe I2	GACAGTGTCTCCTCTCCCCTC	CAGCATGTGGTTCTCACTATCC
Lipe I3	CAGAAAGCTGTCCTCTCCTCTC	GCACATGTAAGAATAGCACCCA
Lipe I4	CCATTCAAGATTCCCTGAAGAC	AGGACTGGGTCATAGTTGGCTA
Lipe I5	CTCGTGGAAGTGGGTCAGTT	GGACTGGAAAGAATTGATGGAG
Lipe I6	CTTGGTAGCCGTTTGGAGAAG	TCATGAAGCAGAGCAGTAAGAA
Lipe I7	TATTCCCCAGAATCAAAGGAAA	CTGTCAAGAAGAAAATCGAGGC
Lpin1 I1	GAGGTGCCTGGACTGTTCTTAC	CAGTTGACTGTGGATAGCTTCG
Lpin1 I2	AGACTAGGCTTGCCTACAGTGG	AGCAGGTCATGGTTTGCTTATT
Lpin1 I3	CAGACTACACAGCCATCCTCAG	AAGGAGACAGAGCTCCAGACAC
Lpin1 I4	TGTCCACAGTGTCTTTGTACCC	TGACTCAGGCAGAGAGGTGATA
Lpin1 I5	AGCACTAATGCCTAGGGCTTCT	GTGTGTGGGGATTCTCTTCCTA
Lpin1 I6	CAGGAGATGGTCGCACTATACA	GTTATTTCCCCTCTTCCGACTT
Lpl I1	AAGAAGAAGAAGGAGGAGGAGG	TTGCCTTAGTGTCCCTTCCTAA
Lpl I10	CGGTAGGCAAACTGGAGTCTAA	GCACAGCTGTTTAAGTGACTGG
Lpl I11	CTCAGTCGTAAAAGAAGGCTGG	GTTCTGCCATGATGGATTCTCT
Lpl I12	GCAGGAAAGCAGAGAGCTAAAA	CAGTCTGTCAAAGGCACTGAAC
Lpl I13	GACAGGGTTTCTCTGTGTAGCC	AATCTGATTCTGCCCAACAAGT
Lpl I14	ACATAGTCTCGGTGGCAGGATA	TGTACACATACACAAGCAGGTCTC
Lpl I15	TTATCTCATTTGTTCATTTCCTGA	AAAGGAAAAATCGCTAAGTTGC
Lpl I2	AGAGGATGAAGTACCAACCTGC	TTAGTGTCCTGAGAAGTGCAGC
Lpl I3	CTCCTGTTTGTCATCTCCACAC	CACTTCTGAAACTCTGCTGACG
Lpl I4	TATTTGGGTACCGATTTCTCCA	ACTAAGCCATCTCCCTAGCCTT
Lpl I5	ACAAGAGAGAGCATGCATTGAA	TGCATCTCCAAACAGTGTTCTT
Lpl I6	AGCACATTACAGATAAGGGCGT	AAAAGTTCAGCGGAAAACACAT
Lpl I7	TGGAAAAGGATCCCTCACTCTA	TCCATGCCCAAACTTATACACA
Lpl I8	AAAGTTCCAGGTAGCAGTGCAG	GAAATGGCAGAGATACTCCAGG
Lpl I9	TCCCACTGAAAATCCAGGATAG	GGGACCTTAGGACACATATTGC
Npr3 I1	ATAAACCCTTCTTTCCTCCCCT	ACTTCAGAACCCACTACCTTGG

Npr3 I10	TATTACTACCCGGTATGCCCTG	AGGGTGCTAGCCATAACGTAAG
Npr3 I11	CCCTAAGCCTTCGCTGTAAGTA	ACAAATGTTTGCTCTCCCAAGT
Npr3 I12	GTCACGCAGCAAAGACATTTAC	CTATGACTTAACAGCAGCAGCC
Npr3 I13	TACACACACACTGCAAAAACGA	CTCTGCAAATGAATTTTCCTGC
Npr3 I14	CATTCTTACATCAGGGCTCCTC	TTAATCCTGGGGTTGGAGAAAG
Npr3 I15	TATATTCTCCCTCCCTTTGCAC	TATTTAAACCCCGGCTATGGAT
Npr3 I16	CGAGAAAGTGAACAGCAGCA	GAGGAATCTTCCTATCTTTTGGC
Npr3 I17	GGACCCGTGGGAAGGAAG	TCCACTGACCCTAGGTCTCTTT
Npr3 I18	CCCTGGCTCATAAAGGTAGAAG	GAGCTTTAGGCAGAGAAGACCA
Npr3 I19	CACTGATTACCACCAACAGAGC	TCACTTGTGCTTGTTAACGATGT
Npr3 I2	CACGATTCTCCTGAGATCCTTC	CTATATGGAATTCCTTTGGCCG
Npr3 I20	AACTGCAGATTGCTTAACTCCC	AGGGTCTGTTCTATCCTAGGGC
Npr3 I21	CATGCACACTAGAAAACACGGT	TACCTGCTTTATGAGATGCCCT
Npr3 I22	GCTATAAATTGCCTTACCACGC	GTCAGTCAGATCCTGGCTCTCT
Npr3 I3	TCTTCATTGCCCTTCATTCTTT	AGCAGGTGCTGTTAATATGGGT
Npr3 I4	GTCACAAACCACCCACACTCTA	CGAGACACTGATTTATTTGTGGA
Npr3 I5	TCTTTCTTTCCGGCAGTACATT	CATGACAACTGGATGAAGCAAT
Npr3 I7	GTAGCCTTCAAGGGCTTCTCTT	CCGCAGAGTTCTTTTTACTCCA
Npr3 I8	CGCTATTGAAGAAACGAGAGAAA	AAGCTCTGTGCTTTCAAGAGAA
Npr3 I9	CTGAAACTCGTGAAGTGAGGGT	GGTTTTTGGATATGTGTCAGGG
Pck1 I1	GATGCTATGGACTAAACTGCCC	ACAAGCTAATTGCTTCCTGAGC
Pck1 I10	AGCTGACAGTGCATTCGATTTA	TGCATAGTTACCACAAAAACCG
Pck1 I11	GAACTTCCAGAGAGAGGTCAGC	CTCCCTACATCGACAACAAGGT
Pck1 I12	ATGTCTCTGCCCCTTACTCTGA	GTCTTGAATGCCCAAGTGTCT
Pck1 I13	GGTAACACACCCCAGCTAACTC	AGGCTCTTGCCTTAATTGTCAG
Pck1 I14	CTCACTATGGCTGATAGAGGGG	CGCCCTCCTTGCTTTAAATACT
Pck1 I2	GCAATTAGCTTGTGGCTTCTGT	TTACATCTTTAACCCAGGCACC
Pck1 I3	GTTGAGCTAGCAGAACGGATG	TAAGCCCCATGACAAATACCTC
Pck1 I4	TTTGATGCACTTGAAAACATCC	TATCCAGTTGTGCCTGTGTCTC
Pck1 I5	TAACTTAAAAATGCCCAGGAGC	ATGAAGTGCTGTGCTCTGTGTT
Pck1 I6 P1	ATGGCTTTGAACAGACAGTGAC	TCAGTCTCTCCACAGCATTCAG
Pck1 I6 P2	GGGGAGGTAGAAGAGGAGTTTG	CCCTCTGTGTTGGCTTTTATTC
Pck1 I6 P3	TAAGTGTGTAATTGTGGGCTGC	CGTGTTTCCCAAACAAAGTACA
Pck1 I6 P4	GAATAAAAGCCAACACAGAGGG	AACACCTGCAAACCTTACCAAG
Pck1 I7 P1	GCGAAACAAAGGTTTCTAGCAT	TTCATCACTTGCTCTGAAGTGG
Pck1 I7 P2	AAAGGTTTCTAGCATGCAGTCC	ACCAAAATGAAGGAAGGAAAAA
Pck1 I7 P3	ACCACTTCAGAGCAAGTGATGA	GGGCAATTTACCATCTGAAAAG
Pck1 I8	CTAAAGTGGCTTGTTCAGGCTT	TGGGTAAGCACATCTTCCATAA
Pck1 I9 P1	GTAGTTTCAACCCCCTGTACGA	AGACAAACAGACGAATGTTCCA
Pck1 I9 P2	ACACGTGCCACCTAAAACTTTC	AGCCACTTTGAAAAAGAACAGG
Pck1 I9 P3	AATGTCACTTGTGGAACATTCG	ATTTAAATGAGAGCCTGGGTGA
Pck1 I9 P4	AAGTCACTCCCCGATGAAAGT	TTAACGATCAATTCTTTGTGGG
Pck1 I9 P5	ATCTACAAATGTCACCCAGGCT	GAGAAAGGGAGAGAACACATGC
Plin I1	ACTTACAGGGAGGTCTCCATCC	CTCCTATGTAACATTCGCCCTC
Plin I10	ATTTGTCCAGCAACACTAGGCT	GTGGAACAAACATTTGGTTTTG

Plin I2	GAAGGTCTCCTCCTCAGAAACA	CAGCTCTGAGAACCACCTCTTT
Plin I3	CTGGCTTTCAATGGACAGAAAT	CTATCCCTGTGTGGGTTTGAAT
Plin I4	CACACCCCAAATAAATGCATAA	CCAAAGGCTCAGACCAAGATTA
Plin I5	CTTTGGGCTGTAAGACAGCAG	TTTCACCCACATCCTAGAATCC
Plin I6	AGGCATTTGCTGGTATTTGTCT	CACACTTCACGGTTCAGTCTTC
Plin I7	CTTTCCTGTCCCTCTCAGTTGT	AGTTGATGGTTTCTGTCCCAGT
Plin I8	CTTGCTTGCTCCTAGCATTACC	TCCCAGCTCTGCTTAAGTTTTC
Plin I9	GAAAACTTAAGCAGAGCTGGGA	TCCTATGAGCAGAGGTAGGACC
Pnpla2 I1	GCTTGTGCTGCTTAAGGTTCTT	GAAACAAGTCCACAGTAAGCCC
Pnpla2 I2	CATTCTCTTGGTGCCCATGTA	AGAGTCACAGCAGTTTGTAGCG
Pnpla2 I3	CCCACTTAGATCTGGCCAAGTA	GCCACTTAAAGAAGAAGGCAGA
Pparg I1	ACCCAATGAGTTGCTTGTAGGT	TACCAAGCCCCTATACTGCCTA
Pparg I10	AGGCCATTGTGTTTTATCATGC	AGCCAGCATCACTACTGTCTGA
Pparg I11	CAACCTACTATGTTTGAATGCCA	GATTTGAATTTCTTTGATTGATTTG
Pparg I12	AGTTTGGCACAGCTAGGTTTTT	TGCAGTAGTATTCCAATGGTTGA
Pparg I13	GAACAGTGAATGTGTGGGTCAC	GGCTTATGGTCATCGAGCTTAT
Pparg I14	CTGTGTTTATTCCCACCTCTCC	CTTGTGAAGTGCTCATAGGCAG
Pparg I15	GCATGTTTGTTTTCCACATGTATT	TTCACCAAGTGTTCTGAAATGC
Pparg I16	AACCTCATGTTGGCTCTGATTT	ATTGCAGCATTTGTCATGTTTC
Pparg I17	GTCACACTGCATGTTTCCTTTC	TGGCCTGGAAAGTCTGTTTTAT
Pparg I18	GCCAAGTTTGAAGGTCAAAAAG	CATGAAAGAGCAAATGGACAAA
Pparg I19 P1	ACAGGACTCATGTCACCCATCT	TCCAGGAAAGCTGCTTCTTATT
Pparg I19 P2	TGTTCACGCAAATATTTTGTCC	TTTCCCTTTCTGTATTCTGGGA
Pparg I19 P3	AGCTTTCCTGGACCATCTCTAA	CCTTACTTTTCTAAGCAGGGGG
Pparg I2 P1	CTTGGCAGGACAGAGGAGATTA	AATCTTAAAAGGAGCCCACACA
Pparg I2 P2	GCCAGGACAAGAAACAATTAGG	TCGCAGATAAGCAATCACAAAT
Pparg I2 P3	TTGTGTGGGCTCCTTTTAAGAT	GCTCCATGGGAATTTAGATTTG
Pparg I2 P4	ATTTGTGATTGCTTATCTGCGA	TCATTTTTACCATGCTCTCTGG
Pparg I20	TCACCAATGCACACTCTTCTTT	TCCACGAGAAAACAAAGTTCCT
Pparg I3	TGATTTTATTATAAGGAGGGGCT	GTGGGTTGAAAGAATCCATAGG
Pparg I4	CTATGGATTCTTTCAACCCACC	TAATTGCAGCCATAACTTTCCC
Pparg I5	AAACATTTCACATGTAGCAGGC	TGTCTTGCTTGGGGTTTTAGTT
Pparg I6	GTGACCTTCCGTGTTAGGAGTC	CTCTCCTCCCTTGTACCTCTGA
Pparg I7	TGTATCTCCTGTTTTGGAAGCC	AAACACTAAAGGTTCACACGGG
Pparg I8 P1	TAAGTGCACAGTTCCCAAAATG	CAAAATCTTTATGGGGATCCAA
Pparg I8 P2	AGTACATGGGAGAAACAATGGG	CACATTGAAATGAGAAGTGGGA
Pparg I8 P3	ATCCCCATAAAGATTTTGGCTT	TTGAGCCTTAACTCAGTCCCTC
Pparg I9	TATCTGCAGAAACCTGGAAAGG	TCCACAGGGATTTTCAGTCTTT
Retn I1	CAAGACACTGGATCAGAAGCTG	TCAAGCCAATACTGACCCTACA
Retn I2	TTATCTCCAGACAACGTCCTGA	GTATTAGCTCCTGTCCCACAGC
Scd1 I1	ACAATGTATGCCAAATGTAGCG	AAGGATGTAAATGCTCTGGAGG
Scd1 I10	TCAGGAGCAGAGTGTGATCAAG	TGTGACTGTCCACACACAGAAG
Scd1 I11	ATTCCAGAGTAGACCTTGGAGG	GGATAAGGAGAAAAAGAGGGGA
Scd1 I12	CCGTTGGTGTAGGCGAGT	TTCCTTGGCTAGCTATCTCTGC
Scd1 I13	TCTTAACCTGTGTCTCACGCTC	CAACTTTCGTGCCTTTAGCTTT

Scd1 I2	AGGTTTGGATTCTGTACACCGT	GCCCCAAGACACTAACTGTAGG
Scd1 I3	AAGAGCTTCCATCCCTTTGTCT	AGAGTCATACAAGGCTGATCCC
Scd1 I4	TAATGAGATCTGACGCCCTCTT	ACTCACACAGACAGACGTCCAC
Scd1 I5	ATTGTAGGAAGTCCTAAGGGGG	TATGGTGCAAAGACAGAAATGG
Scd1 I6	TTTGACCTCTGTTTACCCGTCT	AGTACTGAGCCCTTTTCCTCCT
Scd1 I7	GTGAATGTAACTGTGGTGCGTT	AAAGAAGTTTGCCTCAGTGGTC
Scd1 I8	TGTTGACTGAGCTTCCTCTGTG	CTAGAAGGCCTCTCCTTCCCTA
Scd1 I9	CATGTAACCTCTGCTTCCACAG	CATGGGAGAATCACAGACTCCT
Slc2a4 I1	CTCTACACTGGTTCTTGGAGGG	AGCTCTCTCTCCACATTCTTCG
Slc2a4 I2	GAGATGATCCAAGGGACCAATA	GCTCAGGGACTTCAGGGAG
Slc2a4 I3	TATGTGTGTATGCCCCGAAGTA	AGGCATGGTCTCCAGATACACT
Slc2a4 I4	GATCTAGTGAGACCCGCTTGAG	CTTTGAAAACTCAGAAGCAGGC
Slc2a4 I5	CACAGTCTGTCTCCAAGAGGAA	ACACTCTGCCCACGACTCTATT
Slc2a4 I6	TAACAGTATCCCAGACAGTGCC	TACTTGGTCCCAGTTTAGGAGC
Srebf1 I1	TGGAAAAGCTCTCTTATCCTGG	GCCCCCTAGTGTTATGCTCACT
Srebf1 I10	AAGACTGAAGGCCATGAGAGC	CAGGTCACTACTGACTCTCCCA
Srebf1 I2	TAAACCGTTTGTTTGACACCCT	CTAATGTTGAGTGGGCATGAGA
Srebf1 I3	AGAGGCCCACCAATTTCC	GGGCCTGACAGGTGAAATC
Srebf1 I4	TTCTCCCGGTGCTCTGAAT	TAAAATGGTCCAGGCAAGTTCT
Srebf1 I5	ATCTCGGCCAGTGTCTGTTC	CAGGAGATTGCTAGAAACCAGG
Srebf1 I6	TGGTTTTCCCCAGTCAACTTAC	TCTGTGGAGCAGAGATTTGTGT
Srebf1 I7	TCTTGCATTGGAGACAGTCG	AATCTGCACTTTAGAAGCCCTG
Srebf1 I8	TAAGGAGTCGTGTGGGCTAACT	GGGTTCTTGTCCCTGTCTTATG
Srebf1 I9	TTTCTTTTACTGCTGCCTGATG	AAAGTCCTTAGAAGCTGGGTCC

Some islands were too large to be effectively amplified with a single set of primers; these regions were amplified by overlapping sets of primers designated P1, P2, P3, etc.

Table S6. C_T Values for Retrovirally Expressed IRF Isoforms in Day 0 3T3-L1 Preadipocytes

Isoform	C_T
IRF1	16.56
IRF2	17.62
IRF3	16.74
IRF4	17.26
IRF5	17.66
IRF6	16.69
IRF7	17.26
IRF8	17.95
IRF9	17.42