Table S1. Number of the Differentially Expressed Genes of Each In Vitro Model and Their Enriched Gene Ontology Categories, Related to Figure 1

Upregulated genes

in vitro model	# Upregulated genes	Top GO of upregulated genes	# gene in GO[a]	p-value*
TNFα	1307	immune response	111	9.8E-29
		defense response	75	6.4E-10
Dex	547	response to peptide hormone stimulus	16	1.8E-04
		positive regulation of programmed cell death	24	1.0E-03
High Ins	719	sterol biosynthetic process	19	1.2E-15
		lipid biosynthetic process	46	5.6E-14
Hypoxia	786	transcription	143	4.5E-14
		glycolysis	16	5.3E-08
Cotreatment	3065	immune response	153	1.6E-20
		translation	115	5.1E-19

Downregulated genes

in vitro model	# Downregulated genes	Top GO of downregulated genes	# gene in GO[a]	p-value*
TNFα	1388	fatty acid metabolic process	39	1.5E-06
		negative regulation of biosynthetic process	64	1.1E-05
Dex	486	NA		
High Ins	924	translation	40	3.6E-05
		transcription	122	1.8E-03
Hypoxia	1158	oxidation reduction	81	8.4E-08
		fatty acid metabolic process	36	1.1E-07
Cotreatment	2974	oxidation reduction	183	3.1E-15
		coenzyme metabolic process	56	2.0E-9

Only the top two categories were shown.

a: It represents the number of upregulated or downregulated genes which are included in the particular GO category.

*P-values were calculated by Fisher-Exact tests assessing the significance of over-representation. Multiple hypothesis testings were corrected by Benjamini-Hochberg correction.

Table S2. Diet-Induced Obese Mouse Adipose Tissue Expression Data Sets Used in This Study, Related to Figures 2 and 3

DIO mouse dataset	High-fat diet*	Duration of high-fat feeding	Method	Accession No.
WAT1	60%	12 weeks	Microarray	GSE14363
WAT2	30%	24 weeks	Microarray	GSM498652
WAT3	45%	13 weeks	Microarray	GSE28440

* indicate the percent of calories from fat

Table S3. Adipogenesis Data Sets Used in This Study, Related to Figures 2 and 3

Adipogenesis dataset	Abbreviation	Method	Accession No.
3T3-L1 preadipocyte differentiation in vitro	Adipogenesis1	Microarray	GSE20696
3T3-L1 preadipocyte differentiation in vitro	Adipogenesis2	Microarray	GSE14004
Primary preadipocyte differentiated in vitro	Adipogenesis3	RNA-Seq	GSE29899

Table S4. Results from Gene Set Enrichment Analysis Based on Genome-wide Data and the 1,319 Adipogenesis-Related Genes, Related to Figure 3

See Excel file

Table S5. DNA Sequence Motif Analysis of Regions that Gain DNase Hypersensitivity after the Different Insulin Resistance Treatments, Related to Figure 4

TNFα		
Motif	P-value	CV error
Bach,FRA1	**6.6E-135**	**0.28**
CREB	**3.4E-109**	**0.37**
NF-kappaB	**2.6E-102**	**0.33**
C/EBP	**3.0E-102**	**0.37**
Tax/CREB	3.0E-93	0.40
Nrf-2	**8.2E-86**	**0.33**
RORA	7.8E-67	0.41
TEF-1	1.8E-55	0.41
Ik-1	4.7E-46	0.40
DEAF1	2.1E-31	0.42

Hypoxia		
Motif	P-value	CV error
Bach	**3.9E-210**	**0.28**
Nrf-2	**4.7E-111**	**0.33**
Tax/CREB	**4.1E-84**	**0.36**
RORA	**8.6E-70**	**0.38**
CREB	**1.5E-59**	**0.37**
PPARG	2.5E-42	0.45
Myc	4.9E-38	0.42
Arnt/Hif	1.7E-33	0.42
ER	5.3E-24	0.41
Pax	7.0E-24	0.43

Dexamethasone		
Motif	P-value	CV error
GR	**9.81E-186**	**0.33**
Arnt/Hif	**7.46E-109**	**0.39**
Bach	**8.16E-104**	**0.37**
Nrf-2	8.56E-54	0.41
Myc	**9.06E-40**	**0.38**
VDR:RXR	4.35E-37	0.41
C/EBP	1.23E-32	0.40
CREB	1.72E-28	0.43
TEF	4.44E-28	0.40
NF-1	1.66E-24	0.45

High Insulin		

Motif	P-value	CV error
E2F	5.7E-24	0.44
NF-1	4.5E-22	0.42
AP-2alpha	3.1E-14	0.46
Zfx	1.8E-12	0.46
Whn, AhR	2.2E-10	0.45
Arnt/Hif	2.9E-10	0.45
MIZF	1.4E-08	0.44
CNOT3	4.8E-08	0.46
PEA3	4.9E-08	0.47
Olf-1	2.0E-07	0.46

Motifs highlighted in bold are those with a cross-validation error (CV error) < 0.4.

Table S6. DNA Sequence Motif Analysis of Regions that Lose DNase Hypersensitivity after the Different Insulin Resistance Treatments, Related to Figure 4

TNFα		
Motif	P-value	CV error
MyoD,TCF3	2.3E-95	0.40
NF-1	**3.6E-90**	**0.39**
Arnt/Hif	1.9E-69	0.43
E2F	2.4E-52	0.40
Myc	5.7E-41	0.43
Tal-1	**5.7E-31**	**0.39**
TGIF	3.6E-27	0.44
AP-4	2.1E-26	0.45
XBP-1	6.4E-25	0.44
PPAR	1.1E-22	0.44

Hypoxia		
Motif	P-value	CV error
XBP1	1.9E-29	0.43
Myc	8.7E-28	0.41
NRF1	6.1E-20	0.42
MyoD,TCF3	5.7E-15	0.42
AP-4	6.0E-14	0.43
AhR, Arnt, HIF-1	7.9E-11	0.43
TCF3	1.1E-08	0.44
TTF1	1.0E-07	0.44
MTF1	4.8E-06	0.45
P53	1.3E-05	0.46

Dexamethasone		
Motif	P-value	CV error
NF-1	1.2E-75	0.42
MyoD,TCF3	2.9E-46	0.41
HEN1	2.7E-24	0.43
Elk-1	1.0E-20	0.45
Tal-1	3.6E-20	0.42
Nanog	2.8E-19	0.45
AP-4	5.6E-18	0.44
AP-2alphaA	4.2E-17	0.46
E2F	1.8E-16	0.43
Ikzf1	3.1E-15	0.45

High Insulin		
Motif	P-value	CV error
Nrf-2	**4.2E-79**	**0.37**
E2F	6.1E-65	0.42
Myc	3.7E-48	0.40
Arnt/Hif	**1.9E-45**	**0.38**
RORA	1.2E-44	0.40
Bach	**3.8E-43**	**0.34**
Tax/CREB	3.4E-40	0.41
XBP-1	8.2E-35	0.40
C/EBP	1.1E-33	0.41
ATF6	1.6E-32	0.42

Motifs highlighted in bold are those with a cross-validation error (CV error) < 0.4.

Table S7. DNA Sequence Motif Analysis of Enriched Regions Identified from p65 ChIP-Seq Experiment, Related to Figure 4

Motif Name	P value	CV error
NF-kappaB	**2.94E-164**	**0.27**
C/EBP	**8.06E-53**	**0.37**
PARP	8.26E-43	0.43
TEF-1	3.50E-27	0.43
RBP-Jkappa	2.42E-19	0.44
GABP	2.92E-19	0.42
E2F	1.34E-18	0.41
Olf-1	1.79E-18	0.43
Helios A	8.32E-16	0.42
MAF	5.53E-15	0.45
HSF	7.14E-14	0.45
MIZF	2.09E-13	0.42
STAT	1.82E-11	0.44
EBF	2.24E-10	0.43

Motifs highlighted in bold are those with a cross-validation error (CV error) < 0.4.

Table S8. Primers Used in the Current Study, Related to Figures 1, 3, and 5

qPCR primers

Adipoq	TGGAATGACAGGAGCTGAAGG
	GCGAATGGGTACATTGGGAAC
Fasn	GGAGGTGGTGATAGCCGGTAT
	TGGGTAATCCATAGAGCCCAG
Pparg	TCGCTGATGCACTGCCTATG
	GAGAGGTCCACAGAGCTGATT
Glut4	GTGACTGGAACACTGGTCCTA
	CCAGCCACGTTGCATTGTAG
Glut1	CAGTTCGGCTATAACACTGGTG
	GCCCCCGACAGAGAAGATG
Cebpa	CCCACTCAGCTTACAACAGG
	GCTGGCGACATACAGTACAC
Cebpb	ACACGTGTAACTGTCAGCCG
	GCTCGAAACGGAAAAGGTTC
Rps27	CCTTCATCCCTCTCCAGAAGA
	CCGTGGTGATTTTATAGCATCTC
Ccl2	TTAAAAACCTGGATCGGAACCAA
	GCATTAGCTTCAGATTTACGGGT
Ccl5	GCTGCTTTGCCTACCTCTCC
	TCGAGTGACAAACACGACTGC
Ccl9	GCTGCTTTGCCTACCTCTCC
	TCGAGTGACAAACACGACTGC
Tnf	CCCTCACACTCAGATCATCTTCT
	GCTACGACGTGGGCTACAG
Il6	TAGTCCTTCCTACCCCAATTTCC
	TTGGTCCTTAGCCACTCCTTC
Mmp2	CAAGTTCCCCGGCGATGTC
	TTCTGGTCAAGGTCACCTGTC

ChIP-PCR primers

Lcn2	GCGGGGTAGTCCATCCTTTACCA
	CCCTGTGCCTGCCAGAATCCAA
Socs3	AGAAACATAAAACTCCCGTCT
	CCCCATAAGCACAGATCAGC
Irf2	TCTGCCCACCTCTTACCAC
	CCAATGCCCCATGAGTCG
Glut1	ACAGCCCGTCATTGCAAG
	CCTACTGTGCCCGTCCA

Il15	ATCGCCTCAAAGCTTGGTC
	CGGCCAATAACATTGAGTCAC
Alb	CAATGAAATGCGAGGTAAGTATGG
	TCTTTAACCAATAACTGTAGATCATTA