SUPPLEMENTAL MATERIALS & METHODS

Expression and reporter constructs

The human IL6 promoter construct and HA-GPS2 derivatives have been described previously (29, 36). We thank Dr. Marta Palmieri and Dr. Ronald Evans for providing the IL6 reporter plasmid and SMRT expression plasmid, respectively.

Western blot antibodies

GPS2: A rabbit polyclonal antiserum was raised against bacterially expressed and purified His-tagged human GPS2 N-terminus (aa 1-105) according to standard procedures (Agrisera AB, Sweden).

SMRT: rabbit polyclonal against human (LsBio LS-B1548)

NCOR: mouse monoclonal against human (LsBio LS-C108878) and rabbit polyclonal against human (LsBio LS-C118605)

Nuclear extracts

All nuclear extracts were performed using signosis nuclear extraction kit according to the manufacturer's instruction (signosis, SK-0001).

Western blot analysis of human adipocyte extracts

Samples for western blot analyses were diluted with water and reducing buffer (6 °— solution: 4.5 % sodium dodecyl sulfate (SDS), 15% β-mercaptoethanol, 0.018% bromophenol blue, and 36 % glycerol in 170 mM Tris-HCl pH 6.8) to a concentration of 20 µg of protein per 15 µl and heated at 70°C for 10 min. Samples were then processed using Invitrogen 4–12 % gradient gels and transferred to nitrocellulose membranes. The membranes were blocked

with LiCor blocking buffer (Lincoln, NE) for 1 h at room temperature, then probed with primary antisera diluted in 0.1% Tween LiCor blocking buffer. The membranes were washed twice for 10 min each in 0.1% Tween phosphate buffer solution (PBST) then probed with goat anti-mouse or goat anti-rabbit IR-Dye 670 or 800cw labeled secondary antisera in 0.1% Tween, 0.01 % SDS LiCor blocking buffer for 1 h at room temperature. Washes were repeated after secondary labeling, washing twice for 10 min in PBST, then placed in PBS. Membranes were imaged using a LiCor Odyssey scanner. Boxes were manually placed around each band of interest, which returned near-infrared fluorescent values of raw intensity with intra-lane background subtracted using Odyssey 3.0 analytical software (LiCor, Lincoln, NE).

Luciferase reporter assays in human adipocytes

For reporter assays, adipocytes were seeded in 24-well plates and transfected with indicated constructs. Luciferase and b-galactosidase activities were measured using luciferine, and ATP reagents (BioThema) and a galacto-Start Kit (Tropix) respectively, in a microplateluminometer (thermo Electron Corp). All transfections were performed using FuGENE 6 transfection reagent (Roche) according to the manufacturer's instructions.

Isolation of human (pre-) adipocytes from subcutaneous adipose tissue

Adipose tissue was digested for 30 min to 2 hours (depending on the tissue) by collagenase (ROCHE, USA). The digestion product was filtered and then centrifuged to separate the stromal vascular fraction (composed of endothelial cells, immune cells and adipocyte precursors) and the adipocyte fraction (containing only mature adipocytes). Isolated adipocytes were lysed for analysis or further cultured in DMEM/F12 culture medium supplemented with insulin (50 nM) for 2 days.

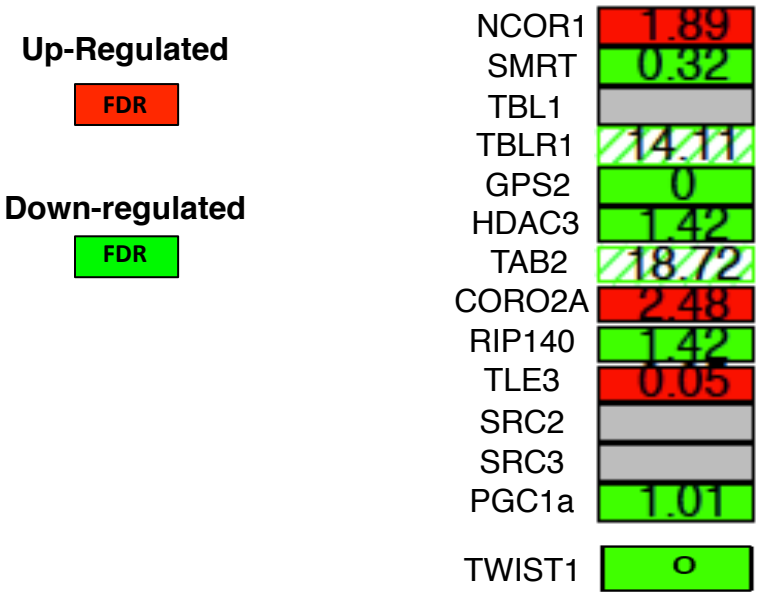
To isolate pre-adipocytes for analysis, the stromal vascular fraction was centrifuged. The cell pellet was resuspended in a buffer that allows the lysis of red blood cells (154 mM NH4CL, 5.7 mM K2PO4, and 0.1 mM EDTA, pH 7.0). After washing with PBS and filtration, the pellet was suspended in DMEM 10 % Foetal Bovine Serum (FBS) and used for cell culture at passage 2 to eliminate non-preadipocyte cell contamination.

RNA extraction and expression profiling by qPCR

RNA was extracted with the Mini RNAeasy kit (Qiagen, Courtabeauf, France) and assayed by lecture of the optical density at λ= 260nm (ND-1000, Nanaodrop, USA). Reverse transcription (RT) was made from an initial quantity of 500 ng of RNA to obtain cDNA. Real-time PCRs were conducted with 25 ng cDNA and both the sense and antisense oligonucleotides in a final volume of 20 µl using the SYBR green universal PCR mix (Applied Biosystems, Minneapolis, MN) monitored and assessed in a detection system instrument (Applied Biosystems). All values were normalized according to 18S expression.

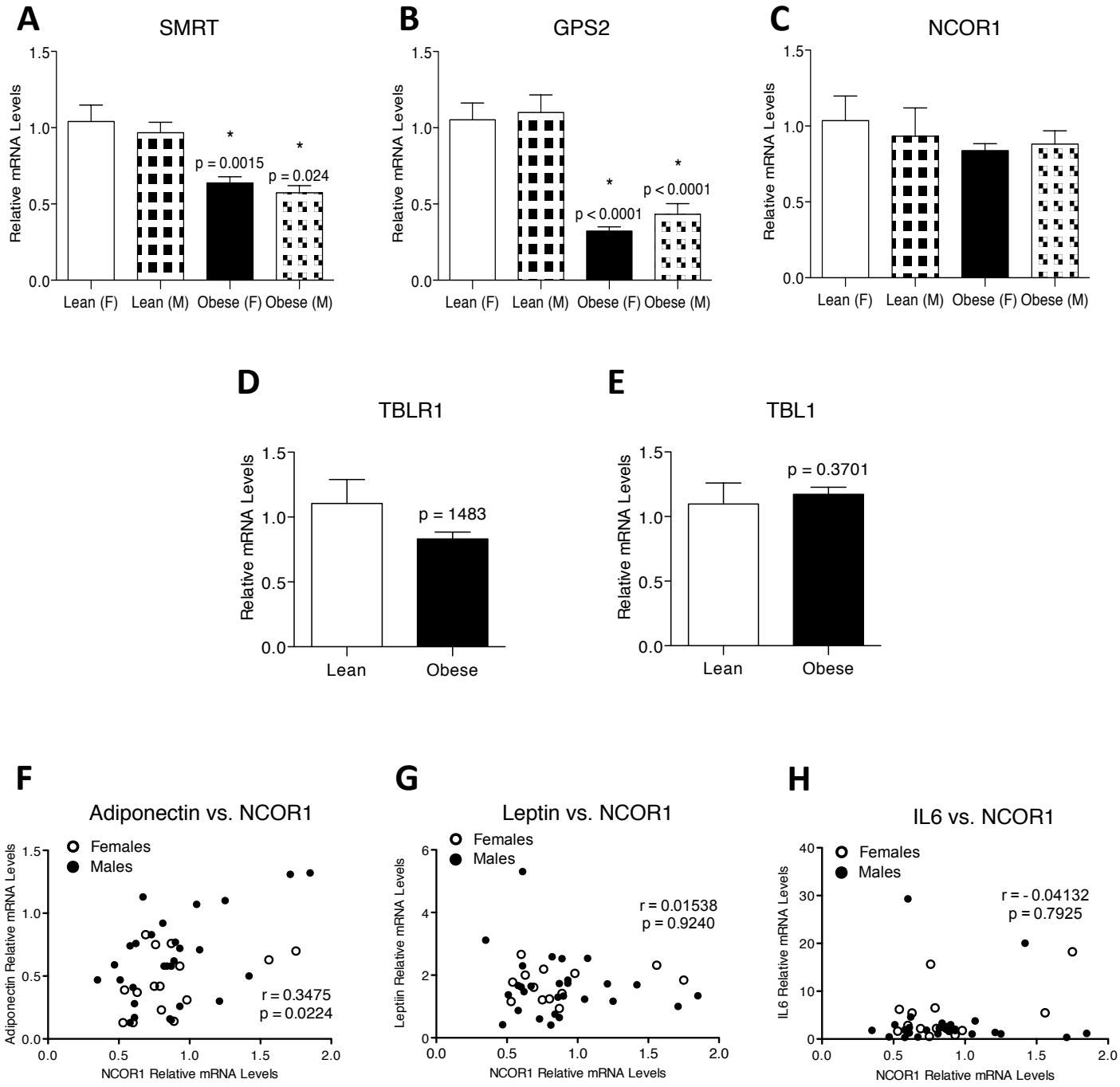
siRNA-mediated knockdown in pre-adipocytes

Adipocytes were transfected with 10 nM (10 ng) siRNAs using lipofectamine RNAi MAX (Invitrogen) according to the manufacturers instruction. After transfection, preadipocytes and adipocytes were incubated for 48 h in RPMI 1% FBS (preadipocytes) or DMEN/F12 (adipocytes). For ELISA and cytokine analysis via membrane array, medium was collected, while mRNA, protein and chromatin analysis was analysed from cell extracts.



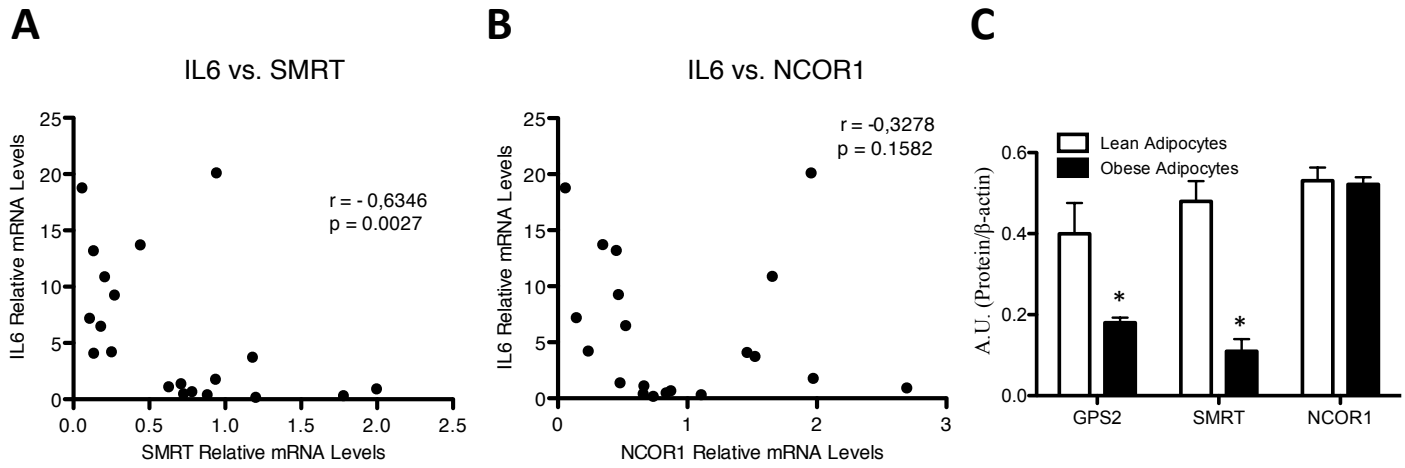
Supplemental Figure 1

Analysis of coregulator gene expression in subcutaneous adipose tissue of lean (n=10) and obese subjects (n=10) from our previously published microarray data (32). Up-regulated genes were marked in red whereas down-regulated genes in green. Values in the square represent the False Discovery Rate (FDR) in %. Genes were significantly regulated when FDR < 5 %.



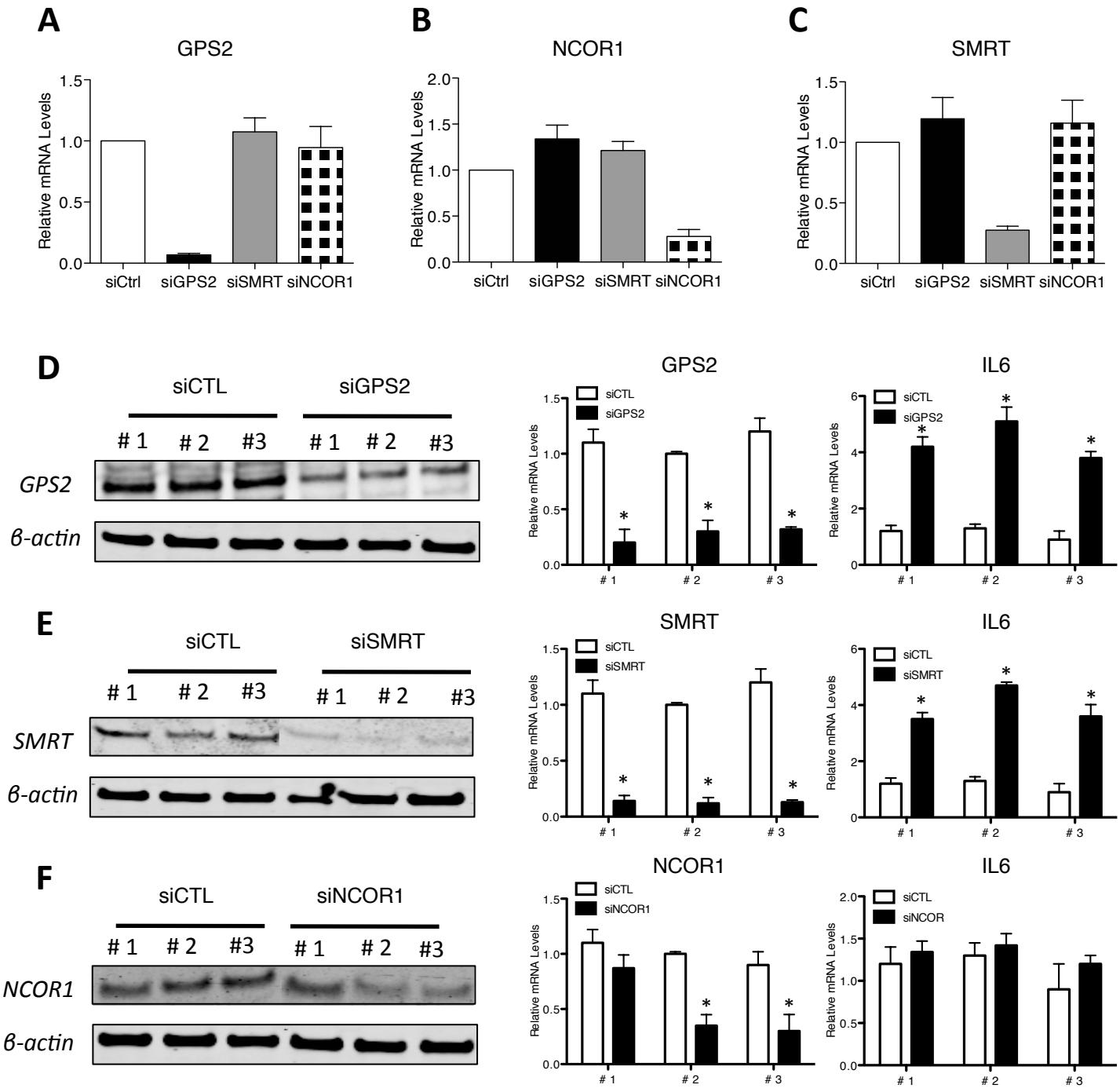
Supplemental Figure 2

(A - C) mRNA expression of corepressor complex subunits SMRT, GPS2, NCOR1 was analyzed by qPCR in subcutaneous adipose tissue of lean (female, n=10; male, n=4) and obese (female, n=20; male n=16) subjects. (D-E) mRNA expression of corepressor complex subunits TBL1 and TBLR1 was analyzed by qPCR in subcutaneous adipose tissue of female lean (n=14) and obese subjects (n=36). (F-H) Correlation between expression levels of NCOR1 versus ADIPOQ, LEP and IL6 in human subcutaneous adipose tissue of lean (n=10) and obese (n=36) subjects. Correlations were analyzed using Spearman statistical test. P-value *=p<0.05; r= Spearman coefficient.



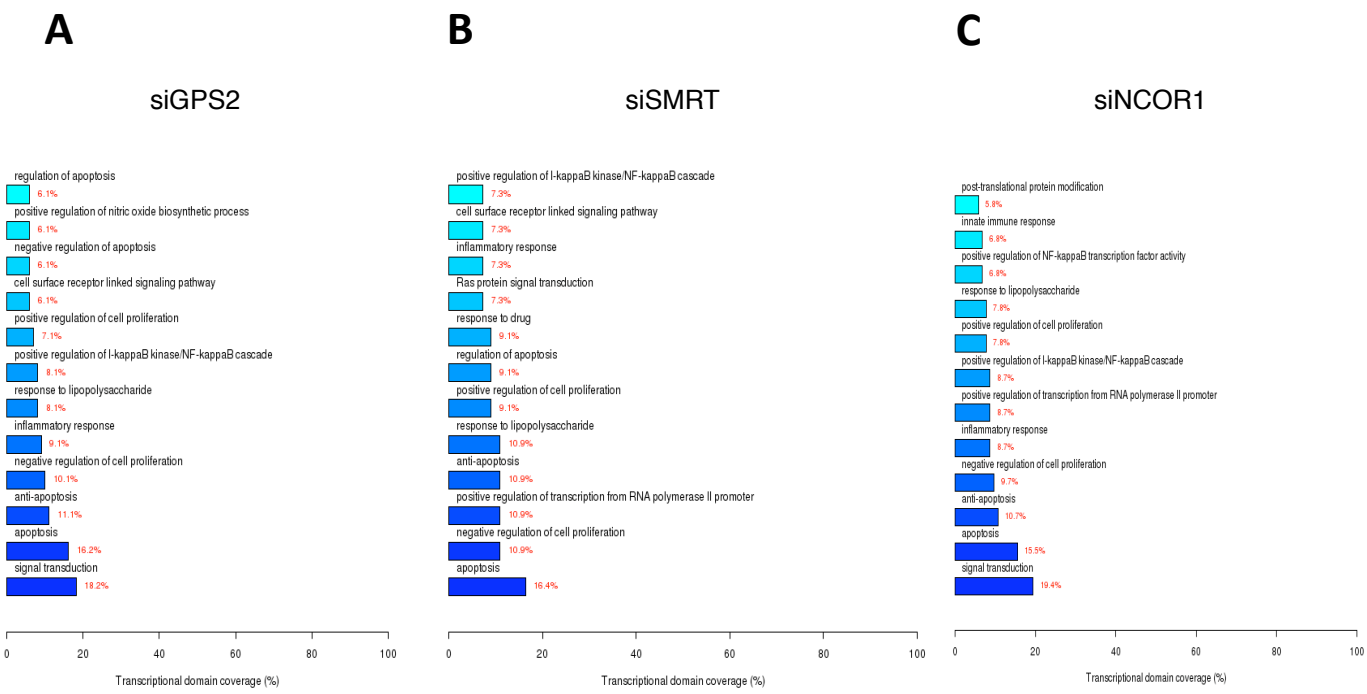
Supplemental Figure 3

(A) Significant negative correlation between expression levels of SMRT versus IL6 in human adipocytes isolated from subcutaneous adipose tissue of lean and obese subjects. (B) No significant correlation between expression levels of NCOR1 versus IL6 in human adipocytes isolated from subcutaneous adipose tissue of non-obese and obese subjects. Correlations were analyzed using Spearman statistical test. P-value *=p<0.05; r= Spearman coefficient. (C) Western blot quantification of GPS2, SMRT and NCOR1 protein levels in adipocytes from subcutaneous adipose tissue of non-obese and obese subjects (n=3) using the ODYSSEY CLx infrared detection imaging system (LI-COR Biosciences UK). β-Actin was used for normalization.



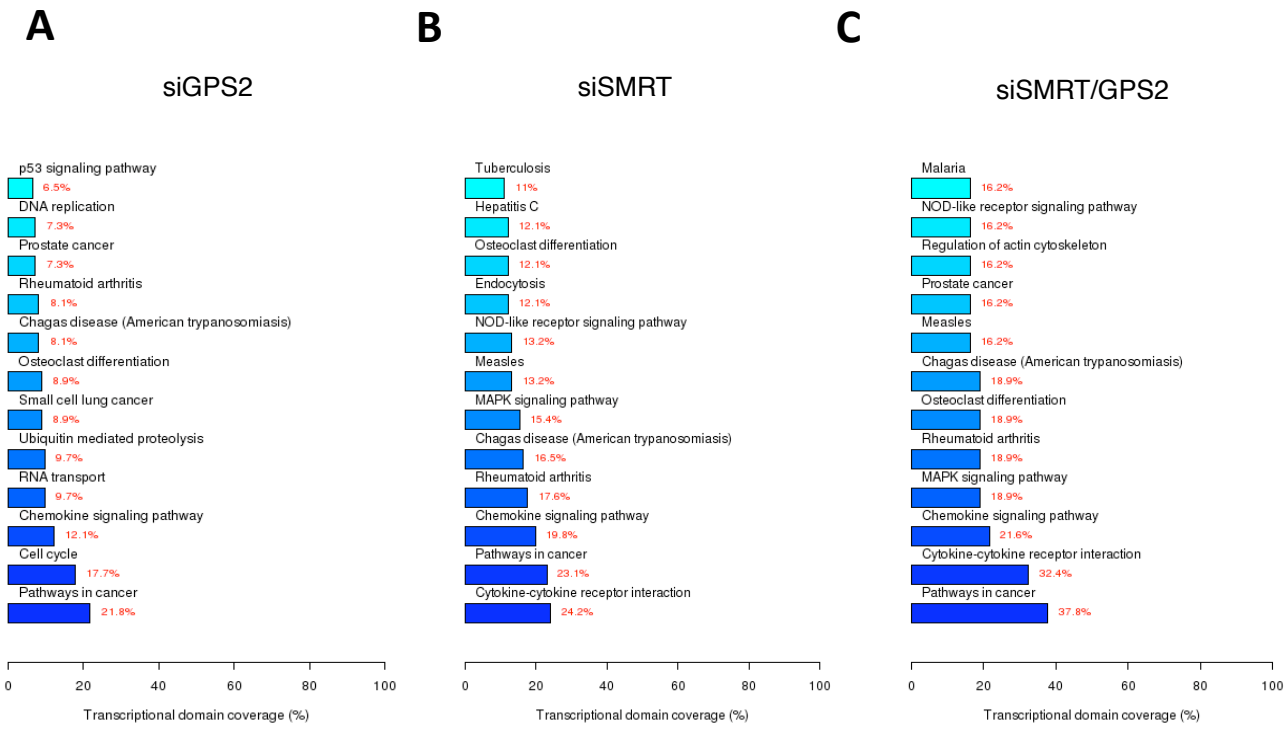
Supplemental Figure 4

Validation of the siRNA experiments. (A-C) Adipocytes were transfected with specific siRNA against GPS2, SMRT or NCOR1 for 48 h and then gene expression profiles of GPS2, SMRT and NCOR1 were analyzed by qPCR. (D-F) Validation using 2 single siRNAs (#1 and #2) and 1 pool of four sequences (#3) targeting GPS2, SMRT or NCOR1. Gene expression and protein levels were quantified by qPCR and western blotting. IL6 mRNA expression was also quantified to confirm our findings.



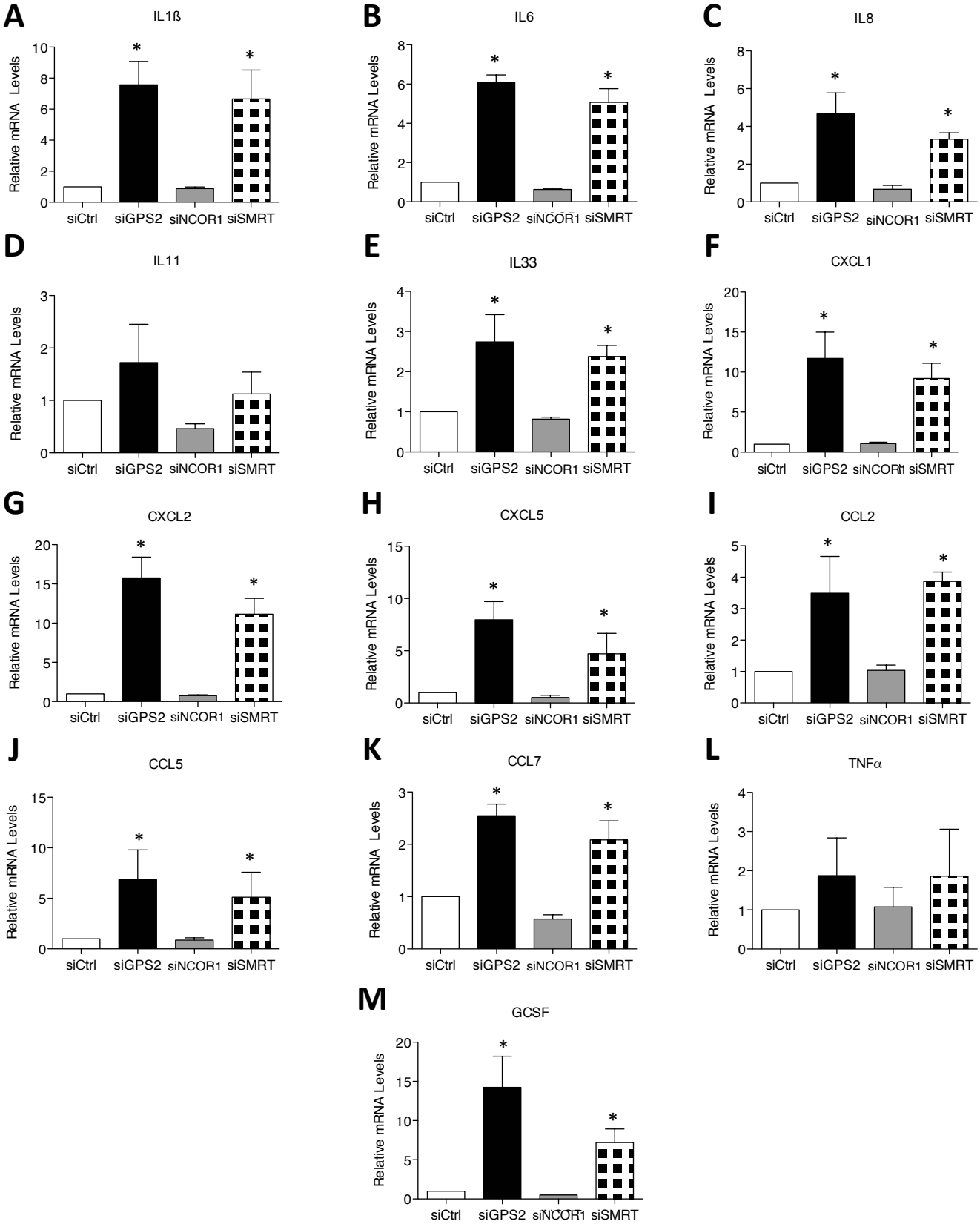
Supplemental Figure 5

(A-C) Unbiased microarray analysis (GO) of the up-regulated genes upon depletion of GPS2, SMRT and NCOR1 in pre-adipocytes. See Figure 3 for experimental details. A Summary of the top 10 common up-regulated genes is given in Supplemental Table 7.



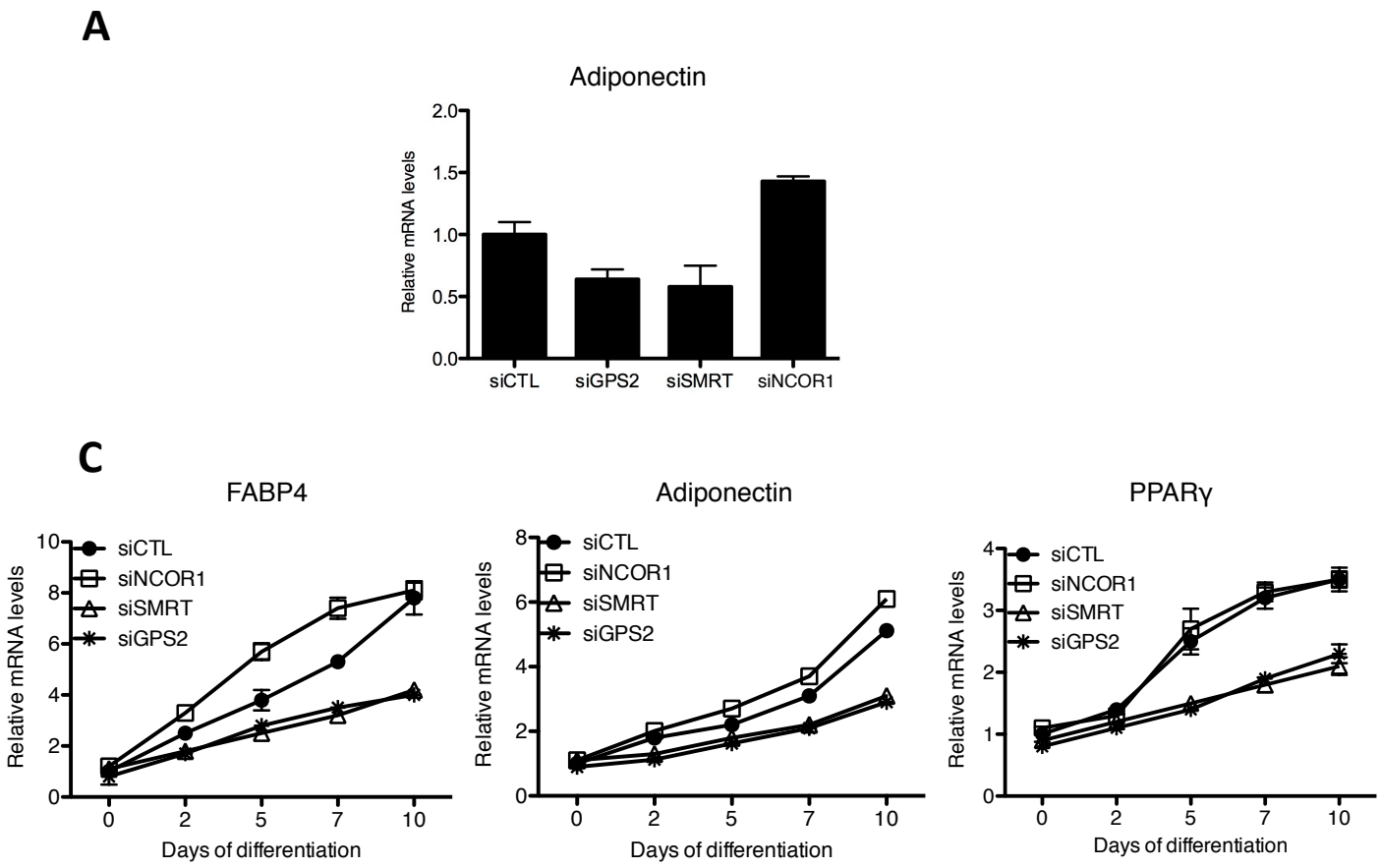
Supplemental Figure 6

(A-C) Unbiased microarray analysis (KEGG) of the up-regulated genes upon siRNA depletion of GPS2, SMRT. See Figure 3 for experimental details.



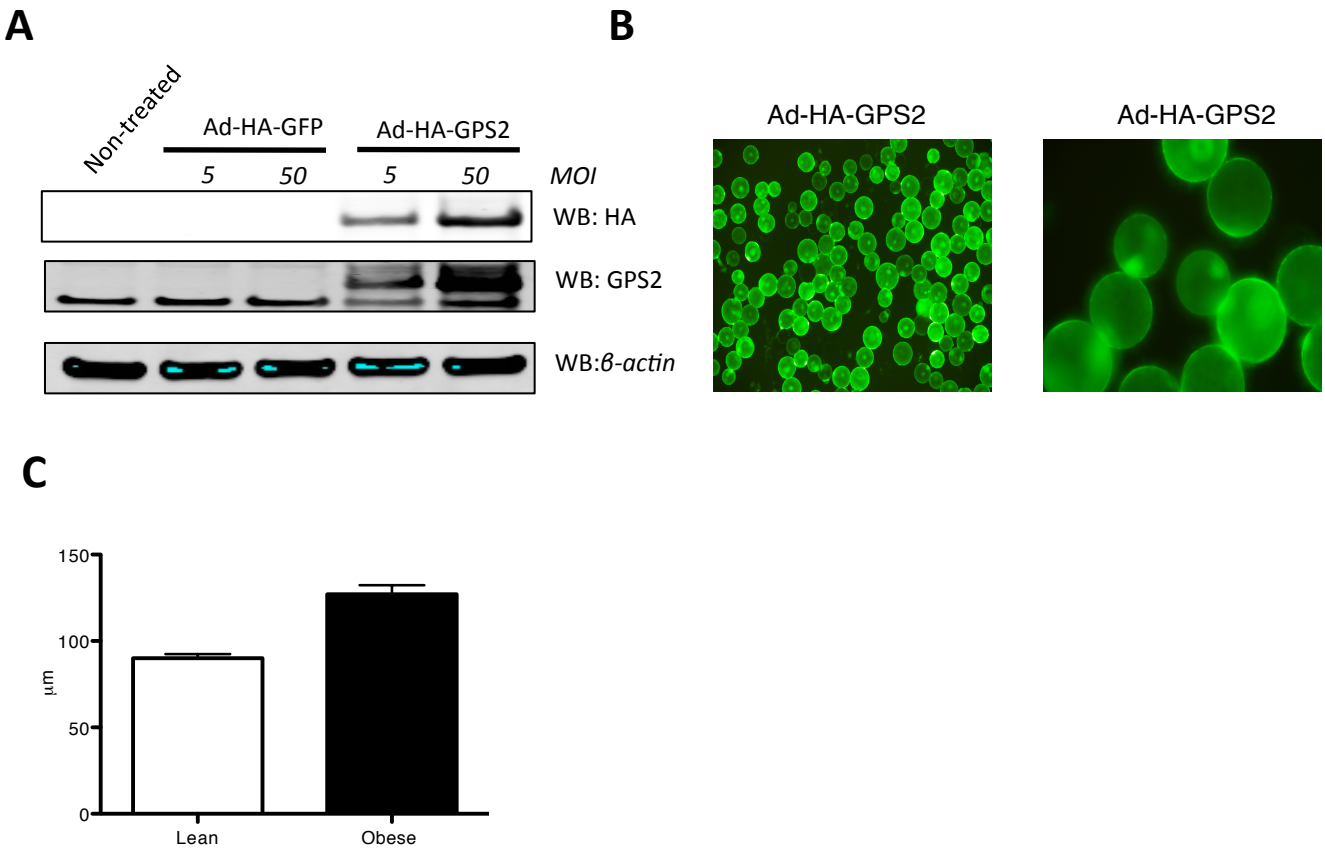
Supplemental Figure 7

Quantitation of the regulated genes presented in the color map in Figure 4 B. mRNA expression profiles of inflammatory genes from human adipocytes depleted for GPS2, SMRT and NCOR1 as measured by qPCR. Data are representative for 8 different experiments. (* = $p < 0.05$)



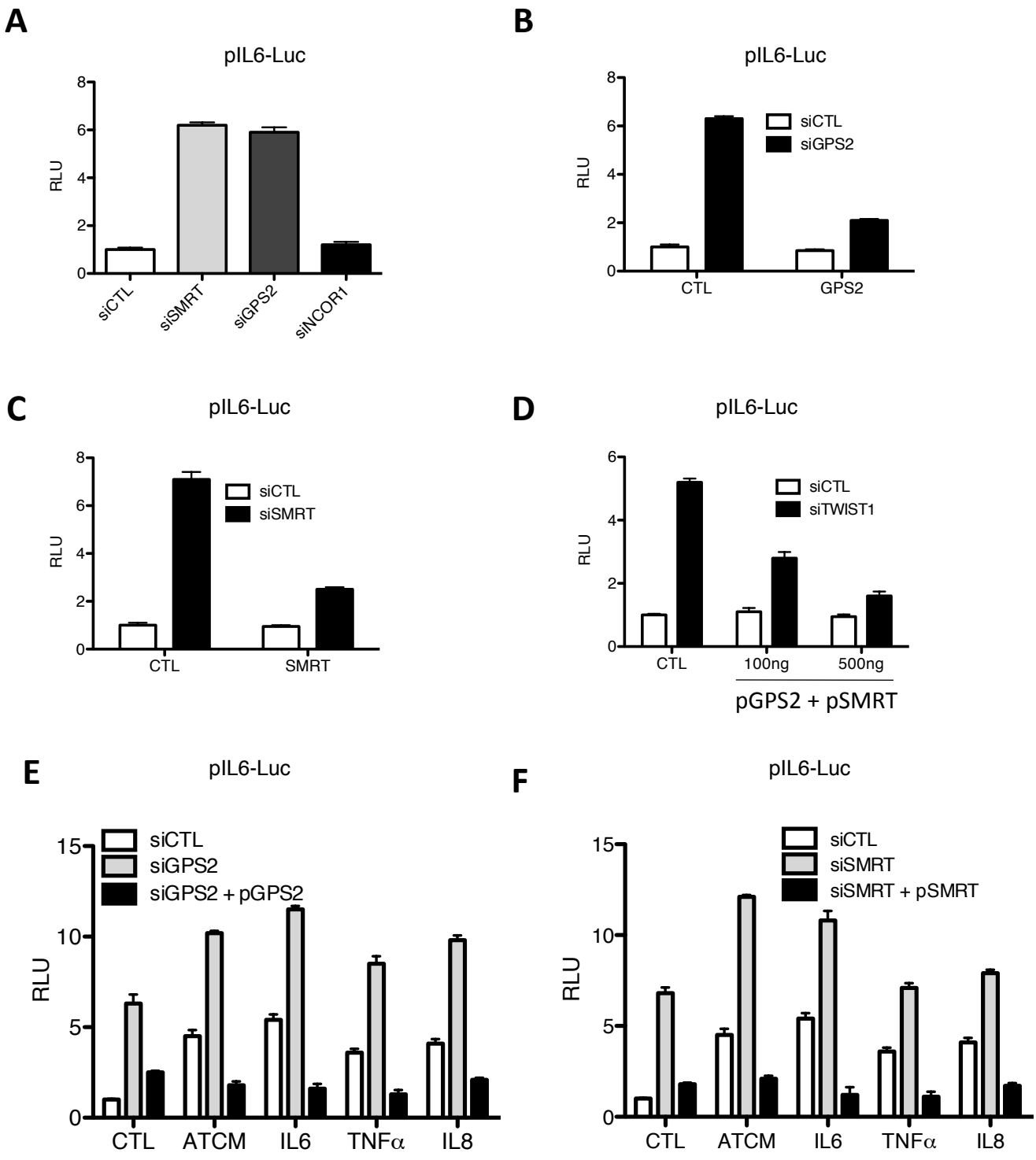
Supplemental Figure 8

(A) Regulation of adiponectin mRNA expression upon siRNA GPS2, SMRT and NCOR1 in human adipocytes. (B) Regulation of FABP4, adiponectin and PPARg expression during adipogenesis of isolated human pre-adipocytes upon siRNA-mediated depletion of GPS2, SMRT and NCOR1.



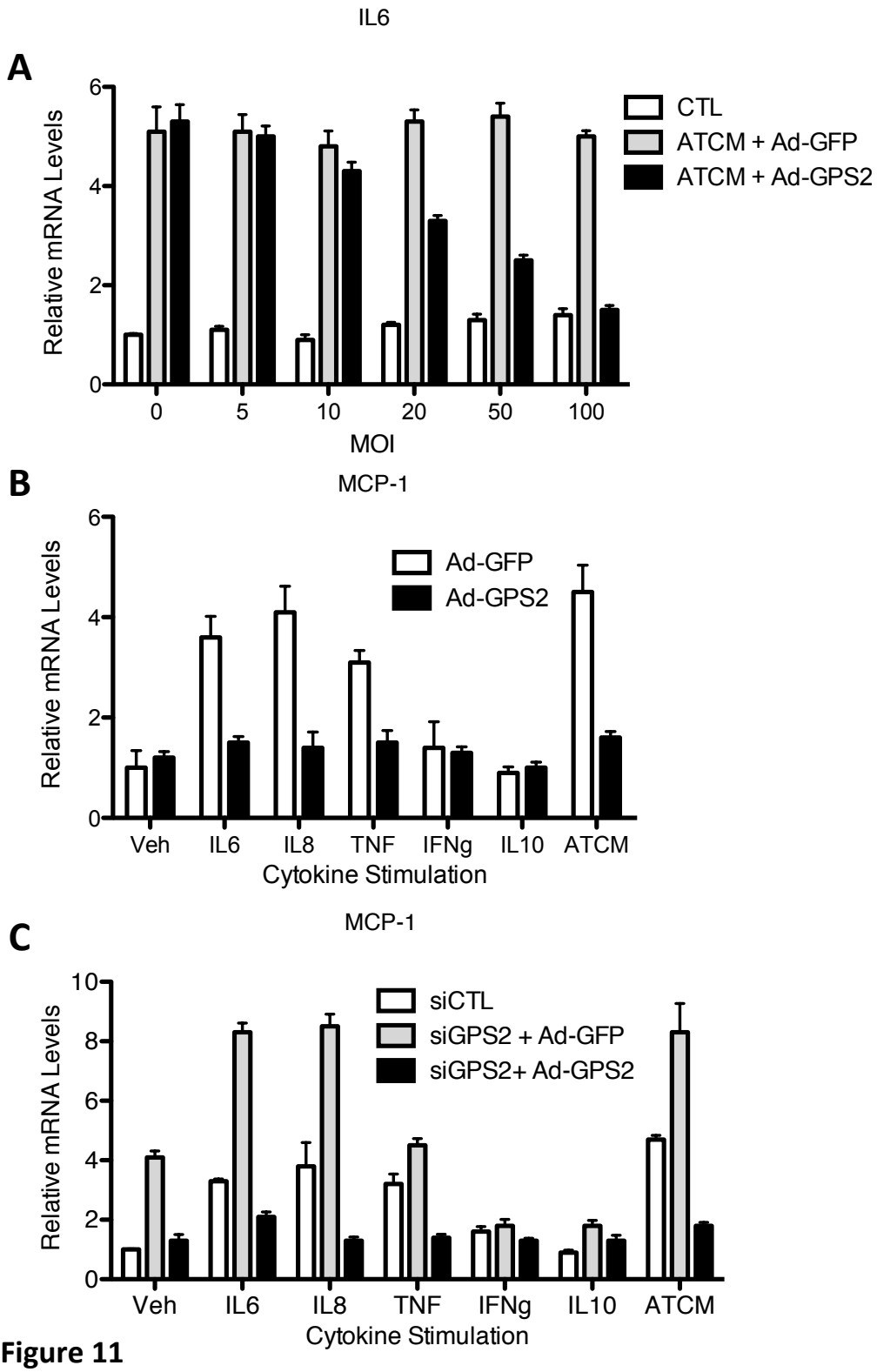
Supplemental Figure 9

Validation of adenoviral expression of HA-GPS2 and GFP in isolated human preadipocytes and human mature by GFP fluorescence. (A,B) Mature adipocytes: Validation of HA-GPS2 expression by western blotting (anti-GPS2 blots: lower mobility band marks endogenous GPS2, higher mobility band HA-tagged GPS2) and of transfection efficiency by GFP fluorescence. (C) Measurement of average adipocyte size in non obese and obese subjects.



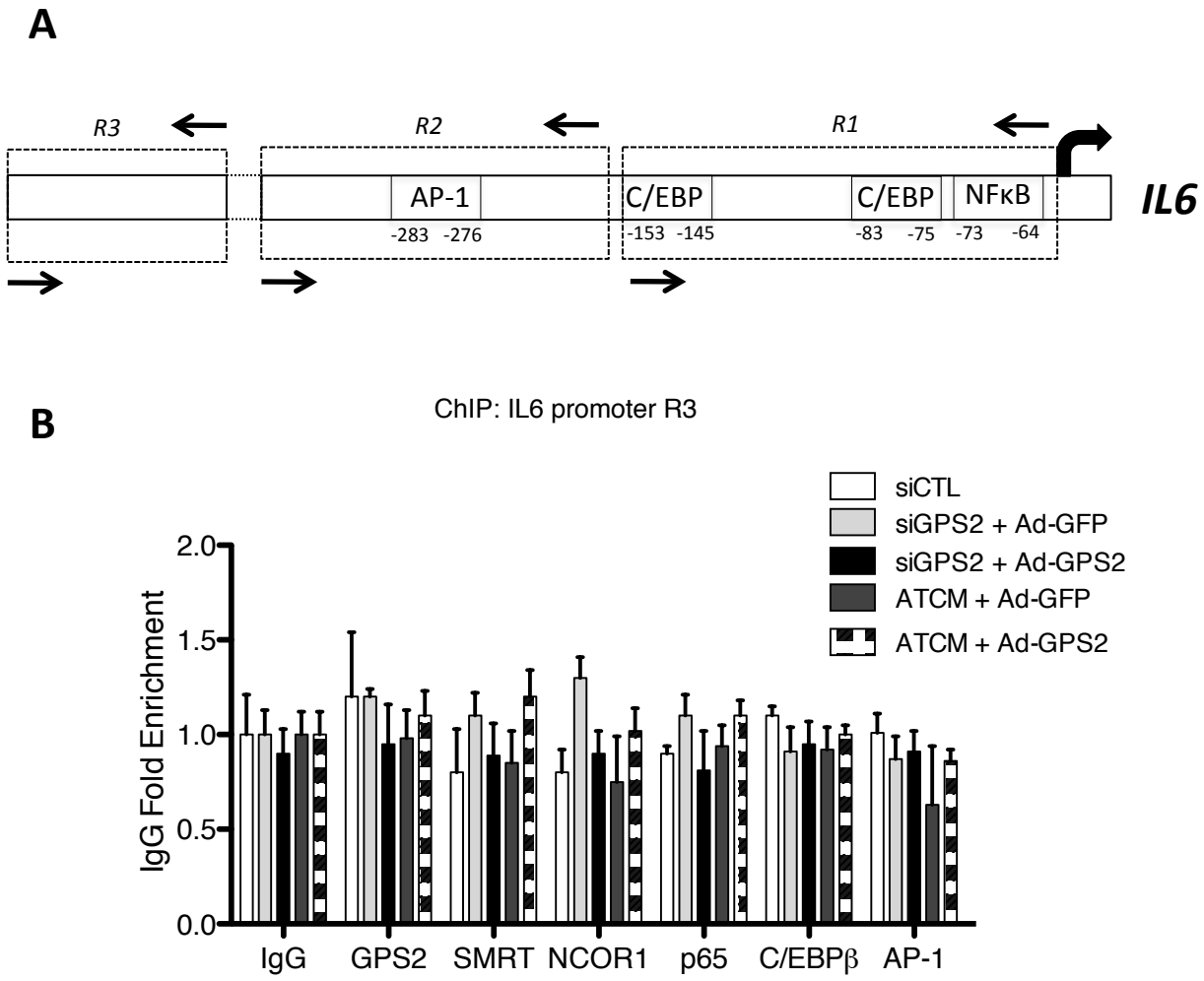
Supplemental Figure 10

Analysis of IL6 promoter activity in isolated human adipocytes using a luciferase reporter. (A) Activity of a transfected IL6 reporter was analyzed upon siRNA-mediated depletion of GPS2, SMRT and NCOR (random siRNA as control). (B-C) IL6 promoter activity was analyzed upon siRNA depletion of GPS2 (B) and SMRT (C) and overexpression of pGPS2 (B), pSMRT or empty (as control) plasmids. (D) IL6 promoter activity was analyzed upon siRNA depletion of TWIST1 and plasmid-mediated overexpression of GPS2 and SMRT (empty plasmids as control). (E-F) IL6 promoter activity was studied upon siRNA-mediated depletion of GPS2 or SMRT in conjunction with treatment by cytokines or adipose tissue-conditioned media (ATCM).



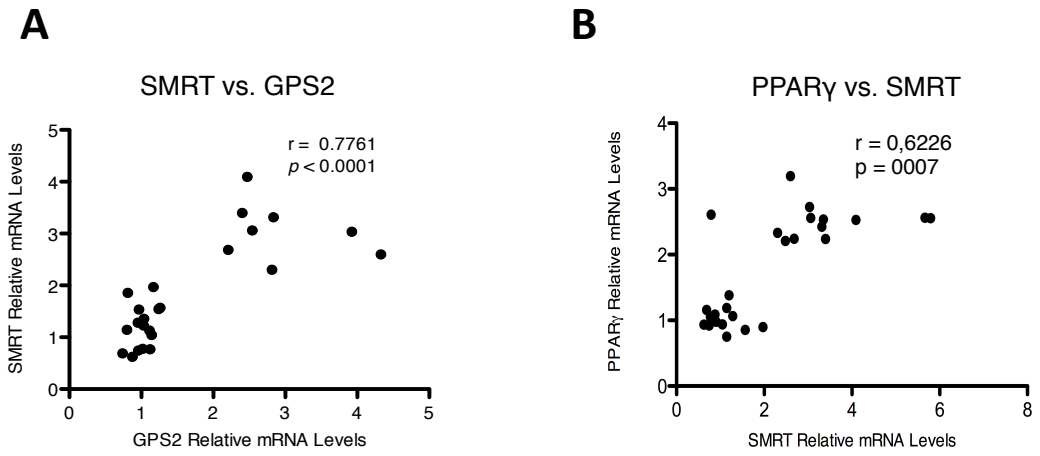
Supplemental Figure 11

(A) Dose (MOI)-dependent adenoviral expression of HA-GPS2 or GFP (as control) was performed in human adipocytes upon treatment with adipose tissue-conditioned media (ATCM). IL6 mRNA expression was analyzed by qPCR (B) Adenoviral expression of HA-GPS2 or GFP (as control) was performed in human adipocytes upon treatment with cytokines or adipose tissue-conditioned media (ATCM). MCP-1 (CCL2) mRNA expression was analyzed by qPCR. (C) Adenoviral expression of HA-GPS2 or GFP (as control) was performed in human adipocytes upon siRNA-mediated depletion of GPS2, and/or treatment with cytokines or adipose tissue-conditioned media (ATCM). MCP-1 (CCL2) gene expression was analyzed by qPCR. Data are representative of 5 different experiments.



Supplemental Figure 12

Schematic representation of the human IL6 promoter. (A) Highlighted are the suspected binding sites for inflammatory transcription factors and the location of ChIP primers specific for regions R1, R2 and R3 (control promoter region without suspected binding sites). (B) ChIP analysis of the indicated factors onto the non-responsive control region R3 in human adipocytes, similar to the assays described in Figure 6 D, E. Data are representative of 4 different experiments.



Supplemental Figure 13

Correlation between mRNA expression of SMRT and GPS2 (A) or SMRT and PPARγ (B) in human subcutaneous adipose tissue of obese subjects before and 6 month after gastric bypass surgery (n=14). Correlations were analyzed using Spearman statistical test. P-value *=p<0.05; r= Spearman coefficient.

Supplemental Table 1: Transcription factor profiling in human adipocytes

Table representing data of DNA-binding of the 47 transcription factors studied. Results represent luminescence intensity associated with the binding of transcription factors upon our experimental conditions outlined in Figure 6 A. Experiment was performed with a pool of 4 nuclear extracts.

	siCTL		siGPS2		siSMRT	
	RLU	Fold Change to CTL	RLU	Fold Change to CTL	RLU	Fold Change to CTL
AP1	1997	1	4210	2.108162243	4123	2.064596895
AP2	2154	1	2272	1.054781801	2213	1.027390901
AR	4579	1	4565	0.996942564	3057	0.667613016
ATF2	1720	1	3442	2.001162791	3746	2.177906977
Brn-3	2145	1	1825	1.061046512	1763	1.025
C/EBP	1123	1	3145	2.800534283	3214	2.861976848
CAR	1532	1	1776	1.15926893	1778	1.160574413
CBF	1498	1	1558	1.040053405	1560	1.041388518
CDP	2219	1	2056	0.926543488	2019	0.909869311
CREB	1857	1	1831	0.985998923	1830	0.98546042
E2F1	2869	1	2897	1.009759498	1858	0.647612409
EGR	1658	1	1703	1.027141134	1760	1.061519903
ER	1725	1	3754	2.176231884	3589	2.08057971
Ets	1856	1	3529	1.901400862	3301	1.778556034
FAST-1	1607	1	2146	1.335407592	2109	1.312383323
GAS/ISRE	1621	1	2852	1.759407773	3100	1.912399753
GATA	1628	1	1875	1.151719902	1816	1.115479115
GR/PR	1498	1	1453	0.969959947	1416	0.945260347
HIF	1421	1	3788	2.66572836	3520	2.477128783
HNF4	1538	1	1425	0.926527958	1432	0.931079324
IRF	1326	1	1325	0.999245852	1450	1.093514329
MEF2	1805	1	1998	1.106925208	1864	1.032686981
myb	1387	1	1231	0.887527037	1222	0.881038212
Myc-Max	1581	1	1328	0.8399747	1311	0.829222011
NF-1	1924	1	1949	1.012993763	1920	0.997920998
NFAT	1350	1	2846	2.108148148	2621	1.941481481
NF-E2	3154	1	3183	1.009194673	3312	1.050095117
NFkB	1259	1	2871	2.280381255	2751	2.185067514
OCT4	1247	1	1058	0.848436247	1000	0.801924619
p53	1954	1	1521	0.778403275	1542	0.789150461
PAX-5	1553	1	1916	1.233741146	1985	1.278171281
Pbx1	1952	1	1990	1.019467213	1812	0.928278689
Pit	1625	1	1943	1.195692308	1941	1.194461538
PXR	2004	1	2067	1.031437126	2261	1.128243513
SMAD	1487	1	1622	1.090786819	1613	1.084734364
sp1	7114	1	2848	0.400337363	2214	0.311217318
SRF	1345	1	1213	0.901858736	1352	1.005204461
SATB1	2481	1	2108	0.849657396	2213	0.891979041
STAT1	5721	1	5823	1.017829051	5201	0.9091068
STAT3	1759	1	4191	2.382603752	3954	2.247868107
STAT4	1457	1	2164	1.485243651	2154	1.478380233
STAT5	1857	1	2216	1.193322563	2248	1.210554658
STAT6	3641	1	2431	0.667673716	3216	0.883273826
TCF.LEF	1607	1	1873	1.165525825	1851	1.151835719
TR	1398	1	1762	1.26037196	1217	0.870529328
YYI	2014	1	2086	1.035749752	2134	1.05958292
TFIID	3609	1	7210	1.997783319	7423	2.056802438

Supplemental Table 2: Transcription factor profiling in human adipocytes under inflammatory conditions

Table representing data of DNA-binding of the 47 transcription factors studied. Results represent luminescence intensity associated with the binding of transcription factors upon our experimental conditions outlined in Figure 6 B. Experiment was performed with a pool of 4 nuclear extracts.

	CTL		siGPS2+ Ad-GFP		siGPS2 + Ad-GPS2		ATCM + Ad-GFP		ATCM + Ad-GPS2	
	RLU	Fold Change to CTL	RLU	Fold Change to CTL	RLU	Fold Change to CTL	RLU	Fold Change to CTL	RLU	Fold Change to CTL
AP1	2068	1	4003	1.9357	1415	0.6842	5316	2.5706	1862	0.9004
AP2	2250	1	1372	0.6098	1613	0.7169	1281	0.5693	1245	0.5533
AR	5035	1	4215	0.8371	3097	0.6151	3211	0.6377	3591	0.7132
ATF2	1600	1	3442	2.1513	1346	0.8413	3197	1.9981	1238	0.7738
Brn-3	2150	1	1825	1.1406	2083	1.3019	1771	1.1069	1912	1.1950
C/EBP	1272	1	3260	2.5629	2014	1.5833	3095	2.4332	1913	1.5039
CAR	1609	1	1776	1.1038	1718	1.0677	1840	1.1436	1753	1.0895
CBF	1573	1	1558	0.9905	1460	0.9282	1517	0.9644	1499	0.9530
CDP	2384	1	1828	0.7668	1319	0.5533	2017	0.8461	2346	0.9841
CREB	1804	1	1884	1.0443	1460	0.8093	1334	0.7395	1092	0.6053
E2F1	2976	1	2563	0.8612	1858	0.6243	2307	0.7752	1676	0.5632
EGR	1439	1	1403	0.9750	1260	0.8756	1502	1.0438	1534	1.0660
ER	1825	1	3567	1.9545	1589	0.8707	1670	0.9151	1147	0.6285
Ets	1629	1	3372	2.0700	1592	0.9773	3107	1.9073	1341	0.8232
FAST-1	1709	1	1946	1.1387	1604	0.9386	1885	1.1030	1665	0.9743
GAS/ISRE	1801	1	2501	1.3887	1466	0.8140	2756	1.5303	1354	0.7518
GATA	1627	1	2059	1.2655	1418	0.8715	1487	0.9140	1568	0.9637
GR/PR	1594	1	1646	1.0326	1296	0.8130	1346	0.8444	1893	1.1876
HIF	1372	1	3482	2.5379	1520	1.1079	3263	2.3783	1286	0.9373
HNF4	1509	1	1485	0.9841	1215	0.8052	1469	0.9735	1609	1.0663
IRF	1512	1	1494	0.9881	1466	0.9696	1382	0.9140	1401	0.9266
MEF2	1785	1	2098	1.1754	2867	1.6062	2394	1.3412	2476	1.3871
myb	1315	1	1561	1.1871	1406	1.0692	1691	1.2859	1699	1.2920
Myc-Max	1637	1	1688	1.0312	1628	0.9945	2235	1.3653	1842	1.1252
NF-1	1858	1	1749	0.9413	1520	0.8181	1909	1.0274	1594	0.8579
NFAT	1378	1	2646	1.9202	1278	0.9274	2920	2.1190	1492	1.0827
NF-E2	3261	1	3383	1.0374	3298	1.0113	2807	0.8608	2523	0.7737
NFkB	1348	1	2646	1.9629	1201	0.8909	2421	1.7960	1125	0.8346
OCT4	1387	1	1758	1.2675	1900	1.3699	1442	1.0397	1672	1.2055
p53	1712	1	1834	1.0713	2262	1.3213	2229	1.3020	1855	1.0835
PAX-5	1667	1	1916	1.1494	3457	2.0738	1774	1.0642	3905	2.3425
Pbx1	1934	1	2390	1.2358	1712	0.8852	2089	1.0801	2018	1.0434
Pit	1409	1	1743	1.2370	1284	0.9113	1472	1.0447	1603	1.1377
PXR	1901	1	2022	1.0637	1260	0.6628	1777	0.9348	1898	0.9984
SMAD	1327	1	1533	1.1552	1502	1.1319	1257	0.9472	1000	0.7536
sp1	6897	1	2848	0.4129	6217	0.9014	3747	0.5433	6354	0.9213
SRF	1363	1	1439	1.0558	2382	1.7476	2008	1.4732	1367	1.0029
SATB1	2387	1	2204	0.9233	1756	0.7357	2208	0.9250	1904	0.7977
STAT1	6101	1	6201	1.0164	5160	0.8458	4447	0.7289	4357	0.7141
STAT3	1940	1	3831	1.9747	1436	0.7402	3960	2.0412	1364	0.7031
STAT4	1242	1	2025	1.6304	1125	0.9058	1855	1.4936	1719	1.3841
STAT5	1813	1	1898	1.0469	1448	0.7987	1948	1.0745	1505	0.8301
STAT6	3562	1	2162	0.6070	1290	0.3622	1795	0.5039	1857	0.5213
TCF.LEF	1503	1	1831	1.2182	1310	0.8716	1514	1.0073	1506	1.0020
TR	1442	1	1819	1.2614	2217	1.5374	2178	1.5104	1973	1.3682
YYI	1949	1	2007	1.0298	1882	0.9656	1652	0.8476	2188	1.1226
TFIID	3404	1	7009	2.0590	2152	0.6322	9424	2.7685	1857	0.5455

Supplemental Table 3: Source of all siRNAs

siRNA	***#1***	***#2***	***#3***	***Supplier***
siGPS2	*D-004329-05*	*L-004329-09*	*L-004329-00*	*Dharmacon*
siSMRT	*L-020145-11*	*L-020145-13*	*L-020145-01*	*Dharmacon*
siNCOR	*L-003518-06*	*L-003518-08*	*L-003518-00*	*Dharmacon*
siTWIST1	*l-006434-00*	-	-	*Sigma*
siCTL	*D-0012110-02-05*	-	-	*Dharmacon*

Supplemental Table 4: Primers for ChIP experiments

Promoter	*Forward*	*Reverse*
SMRT-promoter	5'-GAGTCTGCAGTGTGTTCGCC-3'	5'-TCGCGTTTCAGCTATTAAAT-3'
SMRT-enhancer	5'-CACTCACTGCTGTTACT-3'	5'-GAAGCCTTATCAACTCAAGC-3'
GPS2-promoter	5'-TGCCTGATCCTATATGTGGG-3'	5'-ACCTCGTGAGCTCAAGCGAT-3'
GPS2-enhancer	5'-GATTACAGTGTGGGTCACCA-3'	5'-TCCATAATCACAGCCTCCTG-3'
IL6 R1	5'CGTCCACATTGCACAATCTTA-3'	5'-CATCTCCAGTCCTATATTTA-3'
IL6 R2	5'TGCATGACTTCAGCTTTACTC-3'	5'-GCAGAACCACTCTTCCTTTAC-3'
IL6 R3	5'-GGGCTTCTGAACCAGCTTGA-3'	5'-CAGGACGGCTCTAGGCTC-3'
TWIST1	5'-CCTGTAGCGGAAGATGCAAAC-3'	5'-ATTCCGTCGCCGAGTGATTT-3'

Supplemental Table 5: List of antibodies used for ChIP experiments

Antibody	***Catalog #***	***Supplier***
GPS2	*(aa 1-105)*	*Custom-made (this study)*
NCOR	*06-892*	*Upstate*
HADC3 (B-12)	*Sc-17795*	*Santa Cruz*
POL2	*Sc-9001*	*Santa Cruz*
IgG	*Sc-2027*	*Santa Cruz*
PPARγ (H-100)	*Sc-7126*	*Santa Cruz*
acH3	*ab 1791*	*Abcam*
Me2H3K4	*ab7766*	*Abcam*
Me3H3K9	*06-599*	*Upstate*
TWIST1	*T6451*	*Sigma*
P65	ab19870	*Abcam*
C/EBPβ	sc-7962	*Santa Cruz*
c-Jun	ab31419	*abcam*

Supplemental Table 6: Primer used for qPCR

Gene	*Forward*	*Reverse*
Adiponectin	AGAGATGGCACCCCTGGT	CACCGATGTCTCCCTTAGGA
Leptin	TTGTCACCAGGATCAATGACA	GTCCAAACCGGTGACTTTCT
IL6	GCCCAGCTATGAACTCCTTCT	GAAGGCAGCAGGCAACAC
IL1β	CTGTCCTGCGTGTTGAAAGA	TTGGGTAATTTTTGGGATCTACA
IL8	AGACAGCAGAGCACACAAGC	ATGGTTCCTTCCGGTGGT
IL11	TATCCACTTGAGGGCGATTT	CTGCCCCAGTTACCCAAG
IL33	AGCAAAGTGGAAGAACACAGC	CTTCTTTGGCCTTCTGTTGG
CXCL1	TCATCGAAAAGATGCTGAACA	TTCAGGAACAGCCACCAGT
CXCL2	CATCGAAAAGATGCTGAAAAATG	TTCAGGAACAGCCACCAATA
CXCL5	AAATGAGCACGCATGGAAA	TCTTCCCTGGGTTCAGAGAC
CCL2	TTCTGTGCCTGCTGCTCAT	GGGGCATTGATTGCATCT
CCL5	ACACCAGTGGCAAGTGCTC	ACACACTTGGCGGTTCTTTC
CCL7	GAAAGCCTCTGCAGCACTTC	AATCTGTAGCAGCAGGTAGTTGAA
TNFα	CAGCCTCTTCTCCTTCCTGA	GCCAGAGGGCTGATTAGAGA
GCSF	TCCAGGAGAAGCTGGTGAGT	CCAGAGAGTGTCCGAGCAG
GPS2	GCTGCACCGCACATTATG	CATCATCTTATCCACCTCTTCTTCCT
NCOR	CCCAGGAGAAACTGCAGACCTGT	CTGATTCCTGCTGTGGCGATA
SMRT	GGTACCCATTTGGAATCACGGGCTGC	AAGCTTCCACACACACAGACACGCAC
TBLR1	TTAGCAAGTGCATCCTTTGATTCT	TCTTGGTGTGGTCTTCTTCCT
TBL1	ATTGACGTCCCGAGTAACAAAGAC	CGTAGCCAAGAGTGTTCCATTG

Supplemental Table 7:
Summary of the top 10 common up-regulated genes upon siRNA depletion of GPS2, SMRT and NCOR1 in human pre-adipocytes.

	siGPS2 (fold change)	siSMRT (fold change)	siNCOR1 (fold change)
CXCL2	7.69	9.3	1.26
IL1ß	2.25	2.3	0.69
IL6	2.74	2.63	0.85
NFkBIZ	2.7	2.35	1.15
NFkB1A	2.64	2.71	1.18
TNFAIP3	3.83	2.86	0.98
ANXA1	2.21	1.77	2.08
BIRC3	5.5	4.94	1.65
TNFAIP8	2.2	1.94	0.84
TNFRSF10B	1.85	2.01	1.52

Supplemental Table 8:
Regulation of various PPARγ target genes involved in adipogenesis that were identified in our microarray study.

	siGPS2		siSMRT		siNCOR1	
Gene	**fold change**	**p value**	**fold change**	**p value**	**fold change**	**p value**
FABP4	0.73	0.166	0.78	0.195	1.22	0.1511
PLIN	0.87	0.287	0.82	0.090	1.18	0.2846
LPL	0.52	0.392	0.51	0.364	1.13	0.1347
FAS	0.93	0.256	1.03	0.586	1.08	0.2088
ACC	0.93	0.106	0.85	**0.035**	1.3	**0.0002**
SREBP1c	0.77	**0.003**	0.74	**0.003**	1.36	0.0079
SCD	0.86	0.058	0.82	0.113	1.15	0.0330