## **SUPPLEMENTAL INFORMATION:**

## Rosiglitazone remodels the lipid droplets and britens human visceral and subcutaneous adipocytes ex vivo

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Su	oplemental	Table S1.	<b>Characteristics of</b>	subjects
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ID	Procedure	Age (years)	Sex	Race	BMI (kg/m <sup>2</sup> )	Meds
1	Ovarian cystectomy	35	F	AA	25.0	
2	TAH laproscopic	46	F	Н	27.0	
3	Gastric Bypass	47	F	AA	51.0	Simvastatin
4	TAH laproscopic	39	F	Н	31.0	
5	Hysteroscopy	31	F	Н	29.0	
6	TAH laproscopic	48	F	Н	23.0	Simvastatin
7	Gastric Bypass	31	Μ	Н	63.0	
8	Panniculectomy	27	F	AA	29.0	
9	Gastric Bypass	31	F	AA	49.0	
10	Gastric Bypass	64	F	С	44.9	Synthroid
11	Panniculectomy	31	F	AA	24.0	
12	Gastric Bypass	28	F	AA	37.5	
13	Gastric Bypass	62	Μ	С	36.0	Lipitor
14	Gastric Bypass	45	F	С	39.0	
15	Gastric Bypass	33	F	Н	43.0	
16	Gastric Bypass	29	F	Н	45.0	Metformin
17	Nephrectomy donor	50	F	С	23.0	
18	Gastric Bypass	25	Μ	Н	55.8	
19	Gastric Bypass	31	F	Н	51.7	Simvastatin
20	Gastric Bypass	33	F	С	45.8	
21	Gastric Bypass	27	F	С	39.7	Levothyroxine
22	Sleeve Gastrectomy	45	Μ	AA	52.4	
23	Sleeve Gastrectomy	30	F	AA	56.1	Albuterol, Nystatin
24	Gastric Bypass	46	Μ	Н	45.8	
25	Sleeve Gastrectomy	42	Μ	С	42.1	
26	Sleeve Gastrectomy	29	F	С	40.3	
27	Sleeve Gastrectomy	38	F	С	41.5	
28	Gastric Bypass	39	F	С	42.0	
29	Gastric Bypass	42	F	Н	46.3	
30	Panniculectomy	47	F	Н	45.7	
31	Sleeve Gastrectomy	31	F	С	38.1	
32	Gastric Bypass	45	F	С	42.1	
33	Gastric Bypass	31	F	С	42.1	
34	Abdominoplasty	53	F	AA	33.5	
35	TAH laproscopic	59	F	С	31.0	
36	TAH laproscopic	62	F	С	31.4	
37	Gastric Bypass	57	F	С	53.8	
38	TAH laproscopic	53	F	AA	53.3	
39	Abdominoplasty	71	F	С	29.0	Synthroid

BMI, Body Mass Index; TAH, total abdominal hysterectomy; AA, African American; C, Caucasian; H, Hispanic



Supplemental Figure S1. Remodeling of lipid droplets and rearrangement of mitochondria in rosi-britened human adipocytes isolated from cultured abdominal subcutaneous adipose tissues.

Isolated adipocytes from abdominal subcutaneous adipose tissues that were cultured with or without rosi for 7d were used for confocal imaging after staining with LipidTOX-Deep Red, Mitotracker-Green and DAPI. Adipocytes isolated from control (A) and rosi-treated (B) adipose tissues. White bars = 10 micrometers.

## **A** KEGG pathways associated with transcripts induced by Rosi (FDR < 0.05)

Term ID	Term	Genes in terms	P Value	Genes
hsa01100	Metabolic pathway	114	6.24E-11	AGPAT3, AGK, MLYCD, HK2, MOGAT3, MGLL, PEMT, ACAT1, RDH10, ACAA1, ACAA2, ACADS, ACADM, ACADVL, CTP1A, CPT2, EHHADH, HADH, ACACA, ACSL3, ACSL4, MECR, TECR
hsa00071	Fatty acid degradation	15	2.25E-08	ACAT1, ACAA1, ACAA2, ACADS, ACADM, ACADVL, CTP1A, CPT2, EHHADH, HADH
hsa00190	Oxidative phosphorylation	24	2.68E-07	ATP5B, ATP5F1, ATP5C1, NDUFS2, NDUFS7, NDUFS8, SDHB, COX7B, COX11, UQCRC2
hsa00280	BCAA degradation	14	4.55E-07	HMGCS1, HIBCH, ACAT1, ACAA1, ACADS, ACADM
hsa03320	PPAR signaling pathway	14	3.18E-05	UCP1, FABP3, ACAA1, ACADM, ACSL3, ACSL4, CPT1A, CPT2, PLTP
hsa00062	Fatty acid elongation	8	2.05E-04	ELOVL3, SLC27A3, ACACA, ACOT4, MECR, TECR
hsa03010	Ribosome	18	6.32E-04	RPL3, RPL9, MRPS2, MRPS9, MRPS11
hsa04146	Peroxisome	13	1.10E-03	PHYH, EHHADH, AGPS, CRAT, CAT, FAR2, PEX3, MLYCD

## **B** KEGG pathways associated with transcripts suppressed by Rosi (FDR < 0.05)

Term ID	Term	Genes in terms	P Value	Genes
hsa04060	Cytokine-cytokine receptor interaction	33	2.96E-08	LEP, TNF, CCL2, CCL1, CCL11, CCR1, CCR3, IL1R1, IL6R, TGFB3, TGFBR2, SAA1
hsa04062	Chemokine signaling pathway	23	6.28E-05	CCL2, CCL1, CCL11, CCR1, CCR3
hsa04510	Focal adhesion	23	2.83E-04	CAV1, CCND1, COL1A1, COL3A1, HGF, FGF, IGF1, ITGA5, PGF
hsa04610	Complement and coagulation cascades	12	3.58E-04	F13A1, A2M, C1QA, C1QC, C3, C7, CFB
hsa04640	Hematopoietic cell lineage	12	2.13E-03	CD3, CD14, IL1R1, IL6R1, TNF
hsa04064	NF-kappa B signaling pathway	12	2.57E-03	CCL19, CCL21, NFKBIA, ICAM1, TRAK4, TNFSF14



Supplemental Figure S2. Rosi-mediated regulation of omental human adipose tissue gene expression.

After treating with omental adipose tissues with or without rosi (1  $\mu$ M) for 7 days, RNA was purified for microarray and differential mRNA expression between control and rosi treated samples were determined. (A) Up- or (B) down-regulated genes were subjected to functional categorization using DAVID and significantly enriched (p < 0.01) pathways extracted from the KEGG database are displayed. (C) Log<sub>2</sub> fold changes in the rosi-treated vs. control samples and the corresponding significance values presented as log<sub>10</sub>(FDRq). The grey line indicates the cutoff values for FDRq < 0.05. In total, 902 (right) and 777 (left) genes were identified that had been induced or suppressed by rosi treatment, respectively. The most significantly affected genes are labelled.