

## Supplementary Information

**Table S1.** Upregulated transcripts in SCAAT of obese vs. lean subjects classified according to GO biological process criteria.

GO biological process	Gene symbol	Gene name	SLR		Reference sequence
			Mean	SD	
Cell cycle	<i>EGFL6</i>	EGF-like-domain, multiple 6	3.13	0.79	NM_015507
Cell growth and cell proliferation	<i>LTBP2</i>	Latent transforming growth factor beta binding protein 2	0.62	0.30	NM_000428
	<i>PALLD</i>	Palladin, cytoskeletal associated protein	1.10	0.22	NM_016081
	<i>TAGLN</i>	Transgelin	0.90	0.35	NM_003186
	<i>ACP5</i>	Acid phosphatase 5, tartrate resistant	1.58	0.53	NM_001611
	<i>GPNMB</i>	Glycoprotein (transmembrane) nmb	0.53	0.17	NM_002510
Immune and inflammation response	<i>CHI3L1/YKL40</i>	Chitinase 3-like 1 or human cartilage glycoprotein-39	1.28	0.53	NM_001276
	<i>SPP1</i>	Secreted phosphoprotein 1	1.78	0.43	NM_000582
	<i>CTGF</i>	Connective tissue growth factor	1.25	0.19	NM_001901
	<i>TPSAB1</i>	Tryptase alpha/beta 1	0.95	0.06	NM_003294
Chemokine receptor activity	<i>DARC</i>	Duffy blood group, chemokine receptor	0.80	0.16	NM_002036
	<i>ALCAM</i>	Activated leukocyte cell adhesion molecule	0.73	0.33	NM_001627
	<i>C1S</i>	Complement component 1, s subcomponent	0.58	0.25	NM_001734
	<i>MIF</i>	Macrophage migration inhibitory factor	0.58	0.10	NM_002415
	<i>HLA-DQA1</i>	Major histocompatibility complex, class II, DQ alpha 1	0.90	0.79	NM_002122
	<i>DEFA1</i>	Defensin, alpha 1, myeloid-related sequence	1.25	0.71	NM_004084
	<i>SAA2</i>	Serum amyloid A2	0.93	0.91	NM_030754
	<i>HLA-DRB4</i>	Major histocompatibility complex, class II, DR beta 4	4.05	0.51	NM_021983
	<i>SPON2</i>	Spondin 2, extracellular matrix protein	0.75	0.19	NM_012445
	<i>TUBB2</i>	Tubulin, beta 2	0.75	0.17	NM_001069
	<i>ITGB5</i>	Integrin, beta 5	0.68	0.37	NM_002213
	<i>TNMD</i>	Tenomodulin	1.53	0.56	NM_022144
	<i>IGLC1</i>	immunoglobulin lambda constant 1	0.68	0.66	X57812
Proteolysis and peptidolysis	<i>CD59</i>	CD59 molecule, complement regulatory protein	0.40	0.24	NM_000611
	<i>CTSB</i>	Cathepsin B	0.65	0.45	NM_001908
	<i>MMP9</i>	Matrix metalloproteinase 9	1.30	0.67	NM_004994

Table S1. Cont.

GO biological process	Gene symbol	Gene name	SLR		Reference sequence
			Mean	SD	
Signal transduction	<i>EIF5A</i>	Eukaryotic translation initiation factor 5A	1.70	0.98	NM_001970
	<i>WISP2</i>	WNT1 inducible signaling pathway protein 2	1.55	0.37	NM_003881
	<i>CNKSR2</i>	Connector enhancer of kinase suppressor of Ras 2	1.38	0.38	NM_014927
	<i>CRYAB</i>	Crystallin, alpha B	0.78	0.74	NM_001885
	<i>MEN1</i>	Multiple endocrine neoplasia I	0.53	0.86	NM_000244
Stress response	<i>NQO1</i>	NAD(P)H dehydrogenase, quinone 1	1.30	0.41	NM_000903
	<i>UCHL1</i>	Ubiquitin carboxyl-terminal esterase L1	1.10	0.58	NM_004181
	<i>HSPB7</i>	Heat shock 27 kda protein family, member 7	0.78	0.46	NM_014424
Transport	<i>SLC5A3</i>	Solute carrier family 5, member 3	0.53	0.38	NM_006933
	<i>MAP1B</i>	Microtubule-associated protein 1B	0.78	0.43	NM_005909
	<i>SVEP1</i>	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	3	1.87	NM_153366.3

SLR: Signal Log Ratio; SD: Standard Deviation.

**Table S2.** Downregulated transcripts in SCAAT of obese vs. lean subjects classified according to GO biological process criteria.

GO biological process	Gene symbol	Gene name	SLR		Reference sequence
			Mean	SD	
Cell cycle	<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene homolog B	-3.38	0.26	NM_006732
	<i>CDKN2C</i>	Cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	-1.20	0.47	NM_001262
	<i>CIDEA</i>	Cell death-inducing DFFA-like effector a	-1.13	0.38	NM_001279
	<i>DUSP6</i>	Dual specificity phosphatase 6	-1.00	0.77	NM_001946
	<i>ARMCX2</i>	Armadillo repeat containing, X linked 2	-0.93	0.31	NM_014782
	<i>PLAGL1</i>	Pleiomorphic adenoma gene-like 1	-0.65	0.17	NM_002656
	<i>CCNG2</i>	Cyclin G2	-0.65	0.26	NM_004354
	<i>RAD21</i>	RAD21 homolog (S. Pombe)	-0.53	0.17	NM_006265
Cell growth and cell proliferation	<i>CYR61</i>	Cysteine-rich, angiogenic inducer, 61	-1.68	0.38	NM_001554
	<i>S100B</i>	S100 calcium binding protein, Beta	-0.90	0.50	NM_006272
	<i>LRIG1</i>	Leucine-rich repeats and immunoglobulin-like domains 1	-0.88	0.22	NM_015541
Immune and inflammation response	<i>CA3</i>	Carbonic anhydrase III, muscle specific	-2.05	0.77	NM_005181
	<i>ZFP36</i>	Zinc finger protein 36, C3H type, homolog (mouse)	-0.93	0.75	NM_003407
	<i>MUT</i>	Methylmalonyl Coenzyme A mutase	-0.80	0.73	NM_000255
	<i>CAPN7</i>	Calpain 7	-0.70	0.24	NM_014296
	<i>IER2</i>	Immediate early response 2	-0.63	0.15	NM_004907
	<i>NID1</i>	Nidogen 1	-0.60	0.55	NM_002508
	<i>CXCL14</i>	Chemokine (C-X-C motif) ligand 14	-0.60	0.35	NM_004887
	<i>CD302</i>	CD302 molecule	-0.53	0.13	NM_014880
	<i>DDIT4</i>	DNA-damage inducible transcript 4	-0.53	0.26	NM_019058
	<i>NID2</i>	Nidogen 2 (osteonidogen)	-0.53	0.49	NM_007361
	<i>RGCC</i>	Regulator of cell cycle	-0.50	0.49	NM_014059
	<i>TCRA/TCRD</i>	T cell receptor alpha delta locus	-0.50	0.39	NG_001332.2
	<i>PTENP1</i>	Phosphatase and tensin homolog pseudogene 1	-0.45	0.34	NG_001337.2
<i>SATI</i>	Spermidine/spermine N1-acetyltransferase, transcript variant 1	-0.55	0.10	NM_002970	

Table S2. Cont.

GO biological process	Gene symbol	Gene name	SLR		Reference sequence
			Mean	SD	
	<i>FOS</i>	v-FOS FBJ murine osteosarcoma viral oncogene	-2.75	2.10	NM_005252
	<i>EGR1</i>	Early growth response 1	-1.58	0.28	NM_001964
	<i>DDX3X</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	-0.33	0.17	NM_001356
	<i>CLMN</i>	Calmin (calponin-like, transmembrane	-1.18	0.44	NM_024734
	<i>CITED2</i>	Cbp/p300-interacting transactivator	-1.05	0.26	NM_006079
	<i>HLF</i>	Hepatic leukemia factor	-0.98	0.49	NM_002126
	<i>GNAI1</i>	Guanine nucleotide binding protein (G protein)	-0.95	0.31	NM_002069
	<i>NR3C1</i>	Nuclear receptor subfamily 3, group C, member 1	-0.90	0.18	NM_000176
	<i>SVIL</i>	Supervillin	-0.90	0.45	NM_003174
	<i>TJP2</i>	Tight junction protein 2 (zona occludens 2)	-0.88	0.28	NM_004817
	<i>TWIST1</i>	Twist homolog	-0.88	0.28	NM_000474
	<i>KLF4</i>	Kruppel-like factor 4 (gut)	-0.83	0.31	NM_004235
	<i>NR1P1</i>	Nuclear receptor interacting protein 1	-0.80	0.44	NM_003489
Signal transduction	<i>ATF2</i>	Activating transcription factor 2	-0.75	0.26	NM_001880
	<i>SPRY1</i>	Sprouty homolog 1, antagonist of FGF signaling (Drosophila)	-0.70	0.29	NM_005841
	<i>RHOB</i>	Ras homolog gene family, member B	-0.68	0.19	NM_004040
	<i>ANK2</i>	Ankyrin 2	-0.68	0.22	NM_001148
	<i>CXCR7</i>	Chemokine (C-X-C motif) receptor 7	-0.68	0.57	NM_020311
	<i>JUN</i>	Jun proto-oncogene	-0.68	0.31	NM_002228
	<i>GLUL</i>	Glutamate-ammonia ligase (glutamine synthetase)	-0.68	0.05	NM_002065
	<i>EIF3K</i>	Eukaryotic translation initiation factor 3, subunit K	-0.48	0.10	NM_013234
	<i>EIF3L</i>	Eukaryotic translation initiation factor 3, subunit L	-0.48	0.10	NM_016091
	<i>NR1D1</i>	Nuclear receptor subfamily 1, group D, member 1	-0.48	0.38	NM_021724
	<i>TIMP4</i>	Metallopeptidase inhibitor 4	-0.48	0.45	NM_003256
	<i>RAPGEF2</i>	Rap guanine nucleotide exchange factor (GEF) 2	-0.38	0.10	NM_014247
	<i>MYOD1</i>	Myogenic differentiation 1	-0.30	0.16	NM_002478
	<i>AGTR1</i>	Angiotensin II receptor, type 1	-0.10	0.39	NM_000685

Table S2. Cont.

GO biological process	Gene symbol	Gene name	SLR		Reference sequence
			Mean	SD	
Stress response	<i>GHR</i>	Growth hormone receptor	-0.73	0.33	NM_000163
	<i>VEGFA</i>	Vascular endothelial growth factor A	-1.53	0.58	NM_003376
	<i>NDRG4</i>	NDRG family member 4	-1.50	0.64	NM_020465
	<i>NET1</i>	Neuroepithelial cell transforming gene 1	-0.88	0.22	NM_005863
	<i>IGF1</i>	Insulin-like growth factor 1 (somatomedin C)	-0.98	0.13	NM_000618
	<i>DPYD</i>	Dihydropyrimidine dehydrogenase	-0.35	0.29	NM_000110
	<i>DUSP1</i>	Dual specificity phosphatase 1	-0.85	0.79	NM_004417
	<i>TCF7L2</i>	Transcription factor 7-like 2 (T-cell specific, HMG-box)	-0.30	0.24	NM_030756
	<i>HMGB2</i>	High-mobility group box 2	-0.28	0.17	NM_002129
Transport	<i>SLC39A14</i>	carrier family 39 (zinc transporter), member 14	-0.35	0.29	NM_001128431
	<i>SLC19A2</i>	Solute carrier family 19 (thiamine transporter), member 2	-0.93	0.13	NM_006996

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