

Supplemental Table 1. Functional Categorization of Genes using the Database for Annotation, Visualization, and Integrated Discovery (DAVID)

Gene Group 1	Enrichment Score: 14.07	ACUTE PHASE RESPONSE	Full Gene Name
1		NM_001085	serpin peptidase inhibitor, clade a (alpha-1 antiproteinase, antitrypsin), member 3
2		NM_000608	orosomuroid 2
3		NM_000607	orosomuroid 1
4		NM_004673	angiopoietin-like 1
5		NM_001012631	interleukin 32
6		NM_001147	angiopoietin 2
7		NM_001039659	interleukin 18 binding protein
8		NM_007115	tumor necrosis factor, alpha-induced protein 6
Gene Group 2	Enrichment Score: 12.41	CHEMOKINE	
1		NM_002982	chemokine (c-c motif) ligand 2
2		NM_020530	oncostatin m
3		NM_002996	chemokine (c-x3-c motif) ligand 1
4		NM_001511	chemokine (c-x-c motif) ligand 1 (melanoma growth stimulating activity, alpha)
5		NM_002090	chemokine (c-x-c motif) ligand 3
6		NM_002089	chemokine (c-x-c motif) ligand 2
7		NM_005623	chemokine (c-c motif) ligand 8
8		NM_002416	chemokine (c-x-c motif) ligand 9
9		NM_001565	chemokine (c-x-c motif) ligand 10
10		NM_005409	chemokine (c-x-c motif) ligand 11
11		NM_002984	chemokine (c-c motif) ligand 4
12		NM_000600	interleukin 6
13		NM_001200	bone morphogenetic protein 2
Gene Group 3	Enrichment Score: 7.79	CELL ADHESION	
1		NM_134470	interleukin 1 receptor accessory protein
2		NM_014718	calsyntenin 3
3		NM_001065	tumor necrosis factor receptor superfamily, member 1a
4		NM_003037	signaling lymphocytic activation molecule family member 1
5		NM_000201	intercellular adhesion molecule 1 (cd54), human rhinovirus receptor
6		NM_001024912	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
7		NM_000873	intercellular adhesion molecule 2
8		NM_003004	secreted and transmembrane 1
9		NM_001147	angiopoietin 2
10		NM_002999	syndecan 4 (amphiglycan, ryudocan)
11		NM_002996	chemokine (c-x3-c motif) ligand 1
12		NM_133327	sema domain, transmembrane domain (tm), and cytoplasmic domain, (semaphorin) 6b
13		NM_000450	selectin e (endothelial adhesion molecule 1)

14		NM_080682	vascular cell adhesion molecule 1
15		NM_014734	kiaa0247
16		NM_052815	immediate early response 3
17		NM_052884	sialic acid binding ig-like lectin 11
18		NM_002346	lymphocyte antigen 6 complex, locus e
19		NM_015259	inducible t-cell co-stimulator ligand
20		NM_178232	hyaluronan and proteoglycan link protein 3
21		NM_020125	slam family member 8
22		NM_001031726	chromosome 19 open reading frame 12
23		NM_174918	mast cell-expressed membrane protein 1
Gene Group 4	Enrichment Score: 6.58	T CELL ACTIVATOR	
1		NM_015259	inducible t-cell co-stimulator ligand
2		NM_003807	tumor necrosis factor (ligand) superfamily, member 14
3		NM_172174	interleukin 15
4		NM_000417	interleukin 2 receptor, alpha
5		NM_003004	secreted and transmembrane 1
6		NM_014143	cd274 antigen
7		NM_005755	epstein-barr virus induced gene 3
Gene Group 5	Enrichment Score: 4.18	METAL-BINDING	
1		NM_005953	metallothionein 2a
2		NM_005952	metallothionein 1x
3		NM_176870, NM_005950	metallothionein 1g
4		NM_005949	metallothionein 1f (functional)
5		NM_175617	metallothionein 1e (functional)
Gene Group 6	Enrichment Score: 2.73	LIPID METABOLISM	
1		NM_145343	apolipoprotein l, 1
2		NM_145642	tnf-inducible protein cg12-1
3		NM_145660	apolipoprotein l, 4
4		NM_145637	apolipoprotein l, 2

Supplemental Table 2: Summary of Peak Fold-Change of Prioritized Genes

Gene Symbol	Full Gene Name	Adipose Discovery*	Adipose Validation*	Primary Adipocytes*	M1 Macrophages†	M2 Macrophages†
ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif, 1	4.72(2.76-8.08)	1.71(1.39-2.11)	0.56(0.42-0.75)	not detected	not detected
ADAMTS3	ADAM metalloproteinase with thrombospondin type 1 motif, 3	4.28(2.17-8.44)	1.35(0.68-2.66)	1.36(0.34-5.51)	not detected	0.26(0.1-0.64)
ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9	5.78(3.88-8.62)	1.41(1.11-1.8)	0.43(0.19-0.98)	not detected	1.08(0.4-2.92)
ANGPT2	angiopoietin 2	3.14(1.72-5.77)	1.83(1.04-3.2)	1.62(1.33-1.98)	0.98(0.15-6.57)	8.22(2.09-32.28)
ANGPTL1	angiopoietin-like 1	2.46(1.48-4.09)	1.16(0.96-1.41)	1.2(1.01-1.42)	not detected	0.83(0.26-2.61)
APOL1	apolipoprotein L, 1	3.44(2.7-4.38)	1.18(0.62-2.24)	1.93(1.26-2.98)	4.88(1.45-16.35)	0.44(0.24-0.8)
APOL2	apolipoprotein L, 2	2.93(2.39-3.59)	1.22(0.72-2.05)	1.14(0.65-2.03)	2.38(0.64-8.89)	5.24(4.12-6.66)
APOL3	apolipoprotein L, 3	2.77(2.13-3.6)	1.69(1.11-2.57)	1.97(1.23-3.14)	16.06(2.24-115.09)	0.75(0.38-1.47)
APOL4	apolipoprotein L, 4	2.85(1.57-5.22)	1.21(0.89-1.65)	0.16(0.07-0.4)	8.64(0.35-215.43)	1.4(0.89-2.21)
BMP2	bone morphogenetic protein 2	5.58(3.66-8.5)	2.72(1.69-4.37)	6.03(0.8-45.36)	9.21(3.33-25.53)	2.43(1.79-3.29)
C19ORF12	chromosome 19 open reading frame 12	2.29(1.44-3.17)	1.87(1.45-2.42)	0.7(0.51-0.95)	1.47(0.22-10.08)	0.45(0.08-2.47)
C19orf59	chromosome 19 open reading frame 59	13.43(3.63-49.6)	1.48(0.79-2.78)	not detected	2.31(1.62-3.28)	not detected
C1QTNF1	C1q and tumor necrosis factor related protein 1	2.49(1.65-3.75)	1.21(0.85-1.73)	1.25(0.8-1.93)	29.88(18.11-49.3)	0.06(0.05-0.08)
CCL2(MCP1)	chemokine (C-C motif) ligand 2	30.07(14.41-62.76)	8.01(4.29-14.96)	20.49(13.87-30.26)	5.53(1.68-18.22)	0.44(0.38-0.52)
CCL4	chemokine (C-C motif) ligand 4	15.04(7.19-31.47)	1.23(0.72-2.1)	not detected	9.81(7.17-13.41)	not detected
CCL8	chemokine (C-C motif) ligand 8	21.72(9.99-47.21)	3.42(1.89-6.16)	11.21(7.86-15.98)	70.57(30.9-161.16)	not detected
CD14	CD14 molecule	3.01(1.94-4.67)	1.17(0.84-1.61)	1.34(0.9-2.02)	1.65(0.49-5.58)	7.6(3.95-14.61)
CD274	CD274 molecule	8.88(4.72-16.7)	2.51(1.54-4.11)	8.86(3.35-23.48)	35.17(12.08-102.4)	0.71(0.14-3.69)

CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	5.73(3.36-10.03)	1.88(1.4-2.53)	not detected	0.33(0.16-0.66)	0.28(0.05-1.61)
CLSTN3	calsyntenin 3	2.26(1.6-3.18)	1.15(0.95-1.39)	6.7(3.98-11.28)	14.93(5.52-40.37)	1.1(0.42-2.85)
CRISP3	cysteine-rich secretory protein 3	9.03(3.89-20.97)	not detected(-)	not detected	not detected	1.11(0.36-3.42)
CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	2.71(1.91-3.83)	1.4(1.17-1.68)	1.32(1.02-1.7)	14.04(4.2-46.97)	not detected
CX3CL1	chemokine	32.79(20.65-52.06)	12.52(6.3-24.9)	11.68(2.65-51.47)	not detected	0.22(0.09-0.5)
CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	12.04(4.93-29.38)	3.91(1.92-7.97)	112.9(80.85-157.8)	12.25(4.12-36.44)	2.66(2.01-3.53)
CXCL10	chemokine (C-X-C motif) ligand 10	261.9(107.1-640.5)	5.69(2.46-13.19)	13.98(3.96-49.32)	37.86(5.2-275.56)	0.53(0.17-1.67)
CXCL11	chemokine (C-X-C motif) ligand 11	155.3(60.58-398.2)	4.23(1.87-9.59)	1.48(0.73-3)	61.35(6.57-573.05)	0.1(0.05-0.2)
CXCL2	chemokine (C-X-C motif) ligand 2	18.96(10.95-32.8)	13.66(5.43-34.4)	61.98(25.96-148)	12.25(2.52-59.65)	0.78(0.4-1.51)
CXCL3	chemokine (C-X-C motif) ligand 3	15.1(7.54-30.21)	6.59(3.08-14.1)	64.94(34.53-122.1)	23.5(4.88-113.17)	0.32(0.18-0.56)
CXCL9	chemokine (C-X-C motif) ligand 9	7.89(3.42-18.19)	1.95(1.24-3.07)	not detected	34.42(26.05-45.49)	not detected
DIO3	deiodinase, iodothyronine, type III	2.53(1.58-4.04)	1.65(1.21-2.26)	0.37(0.22-0.64)	not detected	not detected
EBI3	Epstein-Barr virus induced gene 3	6.64(4.77-9.26)	2.36(1.48-3.77)	6.62(3.4-12.88)	103.47(19.3-554.7)	0.07(0.01-0.34)
EGFLAM	EGF-like, fibronectin type III and laminin G domains	4.82(3.01-7.71)	0.85(0.61-1.2)	1.11(0.74-1.67)	not detected	not detected
FAM107A	family with sequence similarity 107, member A	6.62(4.23-10.4)	2.46(1.7-3.56)	18.74(11.57-30.36)	4.3(0.15-123.63)	0.29(0.16-0.52)
GCA	granulocyte, EF-hand calcium binding protein	2.29(1.29-4.04)	0.79(0.65-0.95)	1.43(1.12-1.83)	0.64(0.32-1.27)	not detected
GPX3	glutathione peroxidase 3 (plasma)	3.13(2.23-4.38)	1.4(0.99-1.96)	1.01(0.77-1.33)	1.52(0.93-2.48)	0.29(0.19-0.44)
HAPLN3	hyaluronan and proteoglycan	13.79(9.53-	2.73(1.65-4.52)	1.45(1.07-1.97)	22.27(8.83-	0.85(0.59-1.23)

	link protein 3	19.95)			56.16)	
HP	haptoglobin	12.14(5.48-26.88)	2.07(0.47-9.16)	1.66(0.63-4.4)	not detected	0.1(0.05-0.2)
HPR	haptoglobin-related protein	7.58(3.62-16.26)	1.6(1.3-1.97)	1.78(1.22-2.58)	2.79(0.59-13.16)	0.37(0.27-0.51)
ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	34.19(22.53-51.87)	10.1(5.16-19.74)	3.17(1.71-5.86)	23.06(19.22-27.67)	0.92(0.89-0.95)
ICAM2	intercellular adhesion molecule 2	1.86(1.37-2.52)	1.04(0.6-1.79)	2.96(1.72-5.08)	10.01(5.78-17.32)	not detected
ICOSLG	inducible T-cell co-stimulator ligand	2.78(2.1-3.68)	1.8(1.44-2.24)	2.34(1.01-5.4)	1.4(0.55-3.57)	2.96(0.27-32.01)
IER3	immediate early response 3	5.66(3.66-8.75)	1.84(1.4-2.41)	11.04(5.98-20.4)	14.21(6.53-30.95)	0.14(0.07-0.27)
IL15	interleukin 15	2.82(1.46-5.46)	1.37(1.04-1.8)	2.66(2.11-3.37)	not detected	0.8(0.28-2.25)
IL18BP	interleukin 18 binding protein	2.96(1.87-4.67)	1.23(0.78-1.38)	1.06(0.72-1.56)	5(0.65-38.67)	1.42(1.17-1.73)
IL1RAP	interleukin 1 receptor accessory protein	4.13(2.44-6.98)	1.26(0.79-2.01)	1.75(1.35-2.26)	1.57(0.45-5.42)	not detected
IL2RA	interleukin 2 receptor, alpha	4.41(2.29-8.49)	2.53(1.51-4.23)	not detected	1.88(0-1990.27)	0.37(0.09-1.5)
IL32	interleukin 32	10.14(5.25-19.56)	2.46(1.64-3.7)	9.06(5.76-14.27)	6.72(3.42-13.18)	0.08(0.02-0.31)
IL6	interleukin 6 (interferon, beta 2)	70.9(27.54-182.51)	4.46(2.31-8.62)	19.41(7.71-48.87)	178(65.81-481.51)	not detected
ISG15	ISG15 ubiquitin-like modifier	4.7(2.13-10.4)	1.6(1.07-2.38)	1.5(1.12-2.01)	21.66(1.76-267.05)	0.83(0.76-0.91)
ISG20	interferon stimulated exonuclease gene 20kDa	18.76(7.85-44.86)	1.73(0.5-1.34)	2.12(1.5-3)	7102(3710-13595)	0.92(0.26-3.3)
KIAA0247	KIAA0247	2.66(1.92-3.68)	1.67(1.23-2.28)	1.51(1.24-1.85)	4.92(0.47-51.67)	0.68(0.44-1.04)
LBP	lipopolysaccharide binding protein	4.62(2.54-8.42)	1.21(0.89-1.64)	2.52(0.77-8.27)	1.38(0.36-5.33)	0.75(0.39-1.43)
LCN6	lipocalin 6	3.63(2.63-5)	2.08(0.47-1.96)	not detected	not detected	0.06(0.01-0.23)
LITAF	lipopolysaccharide-induced TNF factor	2.34(1.64-3.34)	1.17(0.91-1.49)	1.23(0.99-1.52)	3.72(2.76-5.01)	0.07(0.01-0.44)
LRG1	leucine-rich alpha-2-glycoprotein 1	58.76(20.95-164.8)	4.7(2.31-9.53)	9.86(3.38-28.8)	1.72(0.59-5.01)	0.59(0.31-1.13)
LY6E	lymphocyte antigen 6 complex, locus E	2.23(1.22-4.06)	1.23(0.92-1.63)	1.13(0.87-1.47)	39.53(24.14-64.71)	not detected
MT1E	metallothionein 1E	5.67(4.3-7.48)	2.81(1.46-5.42)	2.89(1.48-5.64)	7.27(3.96-13.34)	1.09(0.03-34.49)

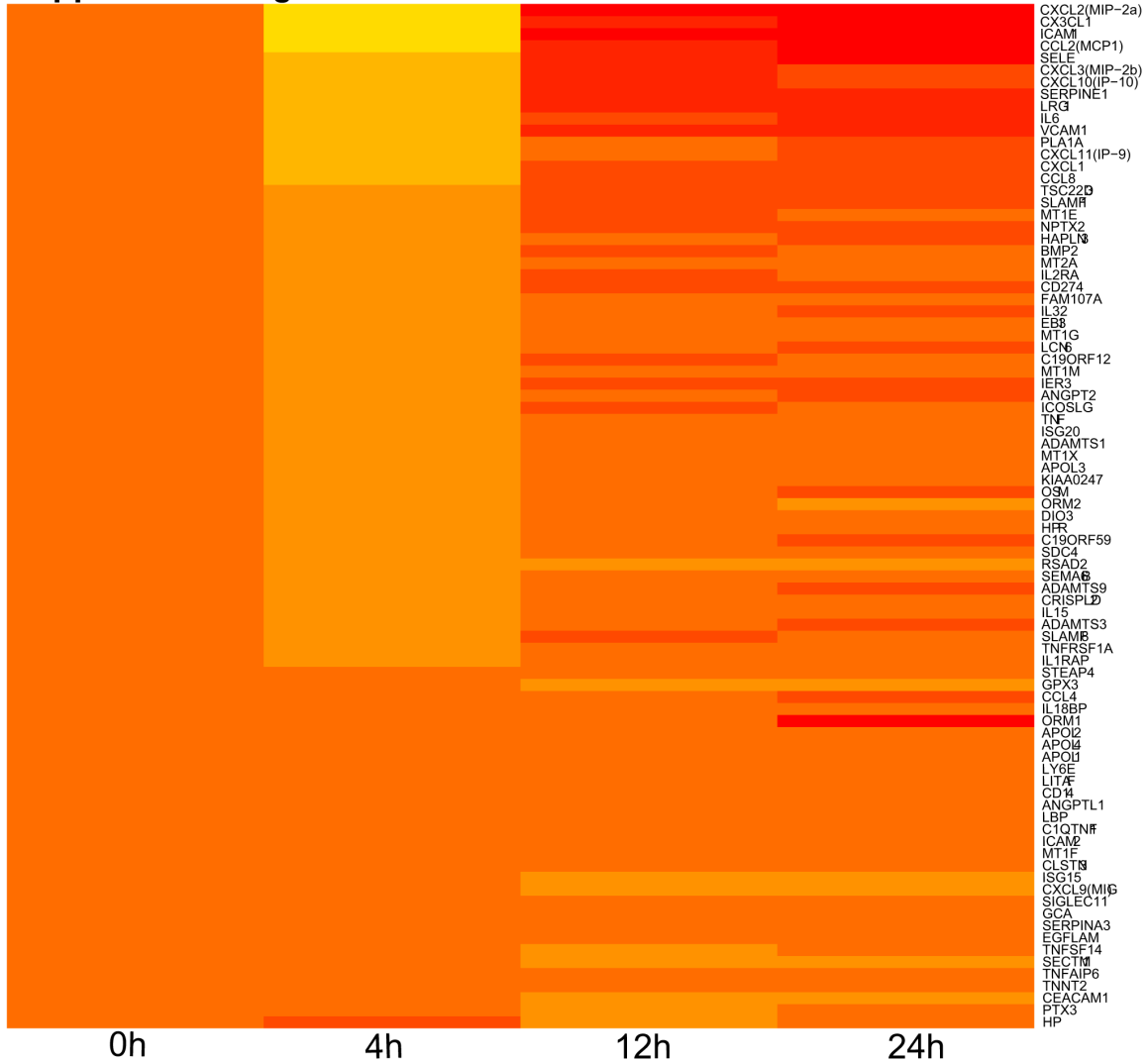
MT1F	metallothionein 1F	4.97(3.43-7.21)	1.19(0.89-1.58)	9.22(1.45-58.64)	6.19(2.66-14.41)	0.38(0.23-0.63)
MT1G	metallothionein 1G	9.98(6.92-14.4)	2.15(0.55-2.18)	4.11(0.74-22.9)	6.63(3.78-11.63)	0.04(0.01-0.16)
MT1M	metallothionein 1M	13.41(8.66-20.89)	1.86(0.54-1.58)	6.64(2.82-15.61)	9.78(4.31-22.18)	4.59(2.42-8.69)
MT1X	metallothionein 1X	6.41(4.64-8.85)	1.7(0.8-1.46)	7.45(3.75-14.79)	2.89(0.89-9.43)	0.8(0.15-4.3)
MT2A	metallothionein 2A	6.81(5.06-9.17)	2.58(0.56-1.8)	6.13(4.45-8.45)	6.72(3.42-13.18)	1.47(0.36-5.99)
NPTX2	neuronal pentraxin II	23.23(12.5-43.2)	2.78(1.19-6.5)	1.42(0.64-3.13)	1.86(0.85-4.07)	0.23(0.12-0.44)
ORM1	orosomuroid 1	12.77(4.84-33.66)	1.22(0.21-4.01)	2.45(0.83-7.27)	8.26(3.52-19.4)	3.23(1.72-6.05)
ORM2	orosomuroid 2	10.91(4.16-28.97)	1.66(0.18-6.35)	2.17(1.2-3.91)	7.84(3.58-17.16)	0.64(0.51-0.81)
OSM	oncostatin M	4.73(2.52-8.87)	1.67(0.83-3.35)	0.15(0-22.62)	15.67(4.89-50.24)	1.66(0.91-3.03)
PLA1A	phospholipase A1 member A	37.8(18.55-77.02)	4.35(2.57-7.35)	4.21(2.87-6.18)	91.21(50.75-163.9)	8.3(5.72-12.05)
PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	32.21(9.69-107.04)	2.86(0.83-9.94)	2.05(1.63-2.58)	1.51(0.89-2.56)	2.46(0.48-12.75)
RSAD2	radical S-adenosyl methionine domain containing 2	6.66(2.89-15.38)	1.82(1.08-3.07)	0.42(0.23-0.78)	80.87(7.55-865.93)	0.44(0.29-0.66)
SDC4	syndecan 4	2.79(1.88-4.13)	1.48(1.15-1.91)	2.08(1.44-3.02)	3.7(0.02-586.37)	0.91(0.36-2.35)
SECTM1	secreted and transmembrane 1	3.82(1.81-8.05)	1.4(0.97-2)	1.38(0.93-2.05)	3.42(0.08-138.52)	1.36(0.43-4.33)
SELE	selectin E (endothelial adhesion molecule 1)	19.75(8.85-44.08)	7.35(3.23-16.74)	11.87(2.99-47.1)	2.75(0-905678.38)	not detected
SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	3.47(2.27-5.32)	1.44(1.02-2.03)	1.23(0.43-3.51)	0.99(0.04-21.94)	0.11(0-773.7)
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 3	26.54(11.27-62.52)	1.22(0.57-2.62)	0.7(0.46-1.07)	not detected	0.11(0.04-0.34)
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	10.38(5.16-20.86)	4.77(1.92-11.87)	4.44(3.12-6.33)	3.86(2.58-5.77)	0.07(0.01-0.44)
SIGLEC11	sialic acid binding Ig-like lectin 11	3.41(2.1-5.55)	1.14(0.87-1.48)	not detected	0.68(0.33-1.43)	1.79(0.69-4.62)

SLAMF1	signaling lymphocytic activation molecule family member 1	6.12(3.33-11.26)	2.98(0.31-28.52)	not detected	32.21(7.28-142.52)	0.73(0.73-0.73)
SLAMF8	SLAM family member 8	5.12(2.13-12.41)	1.32(0.99-1.75)	12.47(6.96-22.32)	2.1(1.47-3)	0.23(0.09-0.58)
STEAP4	STEAP family member 4	3.79(2.54-5.67)	1.24(0.63-1.31)	5.99(4.33-8.29)	not detected	9.17(0.54-156.3)
TNFAIP6	tumor necrosis factor, alpha-induced protein 6	3.69(2.12-6.42)	1.74(0.42-0.7)	11.71(1.87-73.2)	5.44(2.11-14.02)	0.58(0.17-1.92)
TNFα	tumor necrosis factor alpha	18.18(7.95-41.61)	0.76(0.58-1.12)	28.27(18.21-43.87)	35.56(24.62-51.34)	not detected
TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	2.18(1.69-2.8)	1.3(0.65-1.69)	1.27(0.72-2.24)	5.22(1.73-15.74)	3.06(0.43-21.73)
TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	6.23(2.8-13.89)	2.12(1.06-4.23)	8.25(5.83-11.67)	0.89(0.29-2.69)	0.12(0.04-0.37)
TNNT2	troponin T type 2 (cardiac)	2.5(1.86-3.37)	1.03(0.53-2)	1.97(0.05-76.38)	not detected	0.3(0.21-0.42)
TSC22D3	TSC22 domain family, member 3	2.28(1.64-3.18)	3.12(1.94-5.03)	0.3(0.26-0.35)	4.41(1.06-18.35)	0.49(0.29-0.83)
VCAM1	vascular cell adhesion molecule 1	6.34(3.66-10.97)	4.35(2.8-6.78)	2.56(1.43-4.57)	36.64(8.43-159.26)	0.66(0.39-1.13)

Data are presented as mean fold-change (GEE for Discovery and Validation Studies, geometric mean for Adipocyte, M1, and M2 macrophage studies) and 95% confidence intervals. *For Discovery, Validation, and primary adipocyte studies, the timepoint of peak mRNA modulation (positive or negative direction) was used. †Fold Change in M1 and M2 Macrophages vs. Resting Macrophages

Supplemental Figure 1: Endotoxin-induced adipose mRNA fold-change in Discovery Study
 Heatmap depicting mean log₁₀ expression changes of 86 high-priority genes in human adipose tissue before and 4, 12, and 24 hours after 3 ng/kg endotoxin (Discovery Study), as determined by microarray analysis. NCBI Gene ID names are listed on the right, ranked in order of log₁₀ fold-change at 4h. Time 0 values are set to 1 (log₁₀ changes = 0). All fold-change values had p values <1x10⁻⁵. Color coding: 0 is set to orange as seen at baseline, yellow indicates upregulation, red indicated downregulation.

Supplemental Figure 1



Supplemental Figure 2: Endotoxin-induced adipose mRNA fold-change in Validation Study Heatmap depicting mean log10 expression changes of 85 detectable high-priority genes in human adipose tissue before and 4, 12, and 24 hours after 0.6 ng/kg endotoxin (Validation Study), as determined by quantitative PCR. NCBI Gene ID names are listed on the right, ranked in order of log10 fold-change at 4h. Time 0 values are set to 1 (log10 changes = 0). Color coding: 0 is set to orange as seen at baseline, yellow indicates upregulation, red indicated downregulation.

Supplemental Figure 2

