Supplemental Table 1. List of primer sequences and PCR conditions

Gene access No.	Gene	Primers	Sequences (5' -> 3')	Tm (°C)	Cycles	Product size
NM_001008533.2	A1R	F R	TGTGACCACCACCCAGAGTA GCAGAGACTGGGACAAGGAG	55	30	285
NM_009630.2	A2AR	F R	GAAGCAGATGGAGAGCCAAC GAGAGGATGATGGCCAGGTA	55	30	206
NM_007413.3	A2BR	F R	CCTTTGGCATTGGATTGACT AAAATGCCCACGATCATAGC	55	30	330
NM_009631.3	A3R	F R	TCATACCGGAAGGAATGAGC AGCTTGACCACCCAGATGAC	55	30	273
NM_011144.3	PPARα	F R	GAACCCAAGTTTGACTTCGCT CCTATGTTTAGAAGGCCAGGC	55	30	136
NM_013495.1	CPT 1	F R	CGCACGGAAGGAAAATGG TGTGCCCAATATTCCTGG	55	30	207
NM_008642.1	MTP	F R	CACACAACTGGCCTCTCATTAAAT TGCCCCCATCAAGAAACACT	55	30	79
J05029	LCAD	F R	AAGGATTTATTAAGGGCAAGAAGC GGAAGCGGAGGCGGAGTC	55	30	380
NM_007382.2	MCAD	F R	TGGAGACATTGCCAATCAGC ACCATAGAGCTGAAGACAGG	55	30	355
NM_011146.2	PPARγ	F R	TGGGTGAAACTCTGGGAGAT CCATAGTGGAAGCCTGATGC	55	30	454
NM_009024.2	RXR	F R	TGCGTCCCAATCCCCAGATA ATCCAGCTCCCCCAATACAC	55	30	157
NM_009883.2	C/EBP	F R	CTGAGCGACGAGTACAAGAT CTGCTTGAACAAGTTCCG	55	30	191
NM_008509.2	LPL	F R	ACTTGTCATCTCATTCCTGG GCACCCAACTCTCATACATT	55	30	20
NM_024406.1	aP2	F R	ACATGAAAGTGGGAGTG AAGTACTCTCTGACCGGATG	55	30	20
NM_007988.3	FAS	F R	TTGCCCGAGTCAGAGAACC CGTCCACAATAGCTTCATAGC	55	30	171
NM_030682.1	TLR1	F R	TCTCTGAAGGCTTTGTCGATACA GACAGAGCCTGTAAGCATATTCG	55	35	426
NM_011905.2	TLR2	F R	TCTAAAGTCGATCCGCGACAT TACCCAGCTCGCTCACTACGT	55	35	344

Supplemental Table 1. (*continued*)

Gene access No.	Gene	Primers	Sequences (5' -> 3')	Tm (°C)	Cycles	Product size
NM_126166.3	TLR3	F R	TTGTCTTCTGCACGAACCTG CGCAACGCAAGGATTTTATT	55	35	217
NM_021297	TLR4	F R	ACCTCTGCCTTCACTACAGA AGGGACTTCTCAACCTTCTC	55	35	223
NM_016928.2	TLR5	F R	ACTGAATTCCTTAAGCGACGTA AGAAGATAAAGCCGTGCGAAA	55	35	401
NM_011604.2	TLR6	F R	AACAGGATACGGAGCCTTGA CCAGGAAAGTCAGCTTCGTC	55	35	199
NM_133211.3	TLR7	F R	TTCCGATACGATGAATATGCACG TGAGTTTGTCCAGAAGCCGTAAT	55	35	199
NM_133212.2	TLR8	F R	GGCACAACTCCCTTGTGATT CATTTGGGTGCTGTTGTTTG	55	35	412
NM_031178.1	TLR9	F R	ATGGTTCTCCGTCGAAGGACT GAGGCTTCAGCTCACAGGG	60	35	118
NM_205823.1	TLR12	F R	ATACCCAAATACGGATGAGC GGCAGCCCAGTGATAAGG	55	33	421
NM_205820.1	TLR13	F R	CAAAGACGCCTTCACTCC CAAAGACGCCTTCACTCC	55	33	284
NM_008489.2	LBP	F R	CAAACTCTGCCAGTCACA GGACATTGGCACCCAAGT	55	30	786
NM_009841.3	CD14	F R	TGAGTATTGCCCAAGCACACT GTAACTGAGATCCAGCACGCT	55	30	389
NM_010851.2	MyD88	F R	AAGAAAGTGAGTCTCCCCTC TCCCATGAAACCTCTAACAC	55	30	149
NM_054096.1	MAL	F R	GTGGCCGCTGGAGCAAAGAC TTGCCTCTGCCATCCACATA	55	35	370
NM_174989.3	TRIF	F R	ATG GAT AAC CCA GGG CCT T TTC TGG TCA CTG CAG GGG AT	55	30	528
NM_009424.2	TRAF6	F R	GCA CAA GTG CCC AGT TGA CAA TGA AGT GTC GTG CCA AGT GAT TCC TCT	55	35	689
NM_008390.1	IRF1	F R	AGCTGTGTGCAGATGTTAGCC CGTGAAGACATGTTGTATGCC	55	30	478
NM_016849.3	IRF3	F R	ACATCTCCAACAGCCAGCCTAT AGTCCATGTCCTCCACCAAGTC	55	30	80

Supplemental Table 1. (*continued*)

Gene access No.	Gene	Primers	Sequences (5' -> 3')	Tm (°C)	Cycles	Product size
NM_012057.2	IRF5	F R	AATACCCCACCACCTTTTGA TTGAGATCCGGGTTTGAGAT	55	33	191
NM_016850.2	IRF7	F R	CAGCGAGTGCTGTTTGGAGAC AAGTTCGTACACCTTATGCGG	55	30	350
NM_008689.2	p50	F R	CGCCAAAGTATAAGGATGTC GTAGAGAAAGGGTTTCGGTT	55	30	104
NM_009045	p65	F R	AGCACAGATACCACCAAGAC TCAGCCTCATAGTAGCCATC	55	30	158
NM_013693.2	TNFα	F R	TGTCTCAGCCTCTTCTCATT AGATGATCTGAGTGTGAGGG	55	30	156
NM_031168.1	IL-6	F R	ATGAAGTTCCTCTCTGCAAGAGACT CACTAGGTTTGCCGAGTAGATCTC	55	35	638
NM_010502.2	IFNα	F R	ATGGCTAG(G/A)CTCTGTGCTTTCCT GGGCTCTCCAGA(T/C)TTCTGCTCTG	55	35	500
NM_010510.1	IFNβ	F R	CCA CAG CCC TCT CCA TCA ACT ATA AGC AGC TCT TCA ACT GGA GAG CAG TTG AGG	55	35	372
NM_008352.2	IL-12-p40	F R	ATC GTT TTG CTG GTG TCT CC CTT TGT GGC AGG TGT ACT GG	55	30	321
NM_009140.2	CXCL2	F R	GTG CCT CGC TGT CTG AGA GTT AGT TCC CAA CTC ACC CTC TCC	55	35	277
NM_028320.3	adipoR1	F R	ACGTTGGAGAGTCATCCCGTAT CTCTGTGTGGATGCGGAAGAT	55	30	133
NM_197985.3	adipoR2	F R	TCCCAGGAAGATGAAGGGTTTAT TTCCATTCGTTCGATAGCATGA	55	30	378
NM_019812.1	SRIT1	F R	AGC TCC TTG GAG ACT GCG AT ATG AAG AGG TGT TGG TGG CA	55	30	170
NM_008904.1	PGC1α	F R	TAAATCTGCGGGATGATGGA GTTTCGTTCGACCTGCGTAA	55	30	109
NM_011480.2	SREBP-1c	F R	GGAGCCATGGATTGCACATT AGGAAGGCTTCCAGAGAGGA	55	30	102
XM001091567	GAPDH	F R	AGA ACA TCA TCC CTG CAT CC TCC ACC ACC CTG TTG CTG TA	55	30	367