Supplemental Materials

Table S1. Sequences of oligonucleotide primers for QRT-PCR.

Gene Names	Sequence (5' → 3')	NCBI Reference Sequence	Amplicon size (bp)
GADPH	AAGGTCGGTGTGAACGGATT CAACAATCTCCACTTTGCCACT	NM_001289726.1	82
β-actin	CAAGAGAGGTATCCTGACCT TGATCTGGGTCATCTTTTCAC	NM_007393.5	188
HIF-1α	GCACGACTTGATTTTCTCCCT AAAGGCAGCTTGTATCCTCTGA	XM_017314961.2	119
EPO	CCAATTCCTCCCAGCCACCA AGCTCCCAGTACCCGAAGCA	NM_007942.2	98
LDH-A	TATCTTGACCTACGTGGCTT GCGCTGAATCCAGATTGCAAC	NM_010699.2	83
ET-1	TCTTCCAGGTCCAAGCGTTC TTGGCAGAAATTCCAGCACT	NM_010104.4	114
VEGF	AACCTCACCAAAGCCAGCAC TTTCCCTTTCCTCGAACTGA	NM_001025250.3	118
Flk-1	ATTTCACCTGGCACTCTCCAC AAACATCTTCGCCACAGTCCC	NM_010612.3	95
bFGF	GAAGAGCGACCCACACGTGTCA AGCAGCCGTCCATCTTCCTT	NM_008006.2	114
Glut1	GTGTTCTACTACTCACAGAGCA TCTACAACAAACAGCGACACC	NM_011400.3	119
pdk1	TTTGGTTACGGATTGCCCAT TAGATAACCGCATCTGTCCC	NM_013743.2	101
l1cam	GTGACCCAATGCCAACAGACC GGTATACTCGCCATCGTCCT	NM_001374694.1	95
Flt1	CCTGCAACATTGAAGTCTGCT CCTGCATCCTCGGTTGTCAC	NM_010228.4	80
PPARα	ACATTTCCCTGTTTGTGGCTG TGCAACTTCTCAATGTAGCCTA	NM_011144.6	82
PPARγ	TCTTAACTGCCGGATCCACA TGAGACATCCCCACAGCAA	NM_001127330.2	84

RXR	GTCCACCAGCAGTGCCAACGA CCCCATGTTTGCCTCCACGTA	NM_011305.3	103
APOA1	AAGATGAACCCCAGTCCCAA CTCTGCCGCTGTCTTTGACC	NM_009692.4	81
APOA2	TATGCAGAGCCTGTTCACT AATCTCTGAGGTCTTGGCCTT	NM_013474.2	85
APOC3	AAGCCTCCAAGACGGTCCA TAAACTTGCTCCAGTAGCCTT	NM_001289755.1	120
APOA4	CCCAGCTAAGCAACAATGCC TAGCATCCCCAAGTTTGTCC	NM_007468.2	102
APOA5	GGCTTTTCGGCATGACACCT TGGTGCTGAATTTCCTCTGT	NM_080434.4	81
HMGCS2	AAACAACCAGCCTTTCACCCTC AACATCAACCGAGCCAGGGA	NM_008256.4	96
ELOVL6	AAGTTTGCCATGTTCATCACCT GCTGCATCCAGTTGAAGACCA	NM_130450.2	88
FASN	CACCGTGACCATCTCTGGAC ACCTCCTTGGCAAACACACC	NM_007988.3	84
SREBP1	GCACACAAAAGCAAATCACT TCATGCCCTCCATAGACACA	NM_011480.4	82
THRSP	TATCCCAAGAACTGCCTGCT GGGATCATCACCACCTGCTC	NM_009381.3	80
CYP7A1	AGCAAACACCATTCCTGCAAC TCACTTCTTCAGAGGCTGCTT	NM_007824.3	86
CYP8B1	GCCAGTACTTCACCTTTGTCA CAAACACCTTGAGCACCAGT	NM_010012.3	114
CYP27A1	CCCTTTTGGAAGCGATACCTG CATCTGGCCCAGTTTCCTGT	NM_024264.5	115
HSD3B7	AATCCCTACACGCTGGCTA GGTCCTGCTCTCTTCCCAT	NM_133943.2	108
AKR1D1	AACATTCCACTCATTGGGCTT TACCCCTCATCAATAGCTGTC	NM_145364.2	95
ACBP	CGCCTCAAGACTCAGCCAAC TTTACATCGCCCACAGTAGCTT	NM_001037999.2	80

FABP1	CCGCAATGAGTTCACCCTG TGCCTTTGAAAGTTGTCACCA	NM_017399.5	116
ACS	AGTGGAACTACAGGCAACCC TGAATGCACTCTCTGTTGCTT	NM_001302163.1	97
FATP1	GCTTTCTGCGTATCGTCTGCAA CAGCTCTAGCCGAACACGAA	NM_011977.4	80
FATP4	TCGACGGGTACCTCAACCAG TAACCCAGCTCATCCATCACC	NM_011989.5	115
SCP-X	TCTCAGATCGGACCACTCCA TTCTTTCCCAGCATACCCAA	NM_011327.4	110
ACADL	CTTTTCCTCGGAGCATGACA CCAGCTTTCTCCCATTCTGTGT	NM_007381.4	93
ACOX1	AAGCCTACAAGCTACGTGCAG CACGCCACTTCCTTGCTCT	NM_015729.3	94
CPT1A	TCGGCAGACCTATTTTGCAC TATATCCCTGTTCCGATTCGT	NM_013495.2	101
CPT2	ACTGATACCAAGGCTAGACACC TTCCCATCTTGATCGAGGACA	NM_009949.2	80
ECH1	TTTCTGCCTGTGACATTCGCTA CCTACATCAGCAGCCAAGCC	NM_016772.1	85
MCAD	GCCCATCTGACATTGCCAAC CACAGAGCCATCTCCCTCGT	NM_007662.2	116
HADHA	CCGCAGCTTTACAACGTCT GAATAACTGCCACATCCCCTT	NM_178878.3	80
EHHADH	CGGTCAATGCCATCAGTCCA TCCACAGATCACTATGGCTCT	NM_023737.3	98
ADFP	ACCTGATTGAATTCGCCAGGA CCACCCACGAGACATAGAGC	NM_007408.3	87
PLIN4	CCCCTCATCTAAAGTGTCCACC ATGTCCTTGTCTCCAGCTGT	NM_001372234.1	93
LPL	AAGACTCGCTCTCAGATGCC TGCCGTACAGAGAAATCTCG	NM_008509.2	115
LXR	AGCCTCCGTACTTTGAGCAG AGTCACTCGTGGACATCCCAG	NM_013839.4	110

ABCA1	TCCCTGCTACACTGGTCA TCGACCACCCATACAGCAAG	NM_013454.3	111
ACACA	TTTGACCTTACTGCCATCCCA TTCTGTGCCTACTTCCACCT	XM_030245461.1	81
ACACB	AAACGACCATATTCGACGTCCT GTAAACCTCCAGGGACGCCAT	NM_133904.2	80
ACLY-	CCCCAGTGAACAACAGACCT ATCTTGCCTTCTGGGTGCTT	NM_001199296.1	81
FXR	TCTGCTCACAGCGATCGTC TGGTACATCTTGCACAGCTT	NM_001163700.1	120
BSEP	TCAACAGCTCCTTCAACCAG CCAACTCCTGCGTAGATGCC	NM_021022.3	103
FGF14	GTACCGAGAACCATCCTTGC TTGTTGACTGGTTTGCCTCC	NM_010201.4	114
SHP	AAGAACATTCCAGGCACCCTT CCACGGGTCACCTCAGCAA	NM_011850.3	109
SLC51A	TCAAGTGATGAACTGCCACA GCGAACAAGCCTCATACCCAA	NM_145932.3	110
SLC51B	TCCTGGCAAACAGAAATCGAA TCTCTCTTAGGAAGACCTGGC	NM_178933.2	114
NTCP	GTTGCTGCTCATCATGCTCT TATGGCGATGATCACCCCTT	NM_001177561.1	94

Table S2. Total Variance Explained of PCA

Total Variance Explained (HIF-1α system target genes)

Component	Initial Eigenvalues			Extraction Sums of Squared Loadings		
	Total	% of Variance	Total	% of Variance	Total	% of Variance
1	8.355	75.955	75.955	8.355	75.955	75.955
2	1.006	9.150	85.105	1.006	9.150	85.105
3	.849	7.717	92.822	.849	7.717	92.822
4	.279	2.534	95.356			
5	.215	1.956	97.312			
6	.117	1.065	98.376			
7	.094	.858	99.235			
8	.057	.515	99.750			
9	.014	.123	99.873			
10	.012	.112	99.985			
11	.002	.015	100.000			

Extraction Method: Principal Component Analysis (PCA).

Table S3. Total Variance Explained of PCA

Total Variance Explained (PPARα/γ system target genes)

Component	Initial Eigenvalues			Extraction Sums of Squared Loadings		
	Total	% of Variance	Total	% of Variance	Total	% of Variance
1	22.787	67.021	67.021	22.787	67.021	67.021
2	5.565	16.367	83.389	5.565	16.367	83.389
3	1.686	4.959	88.348	1.686	4.959	88.348
4	1.166	3.429	91.777			
5	.776	2.282	94.059			
6	.581	1.708	95.768			
7	.336	.989	96.757			
8	.227	.669	97.425			
9	.199	.586	98.011			
10	.167	.492	98.504			
11	.113	.331	98.835			
12	.106	.310	99.145			
13	.090	.265	99.410			
14	.062	.181	99.591			
15	.043	.126	99.717			
16	.034	.100	99.817			
17	.026	.076	99.893			
18	.020	.059	99.952			
19	.014	.040	99.992			
20	.003	.008	100.000			
21	7.603E-16	2.236E-15	100.000			
22	5.977E-16	1.758E-15	100.000			
23	5.327E-16	1.567E-15	100.000			
24	3.838E-16	1.129E-15	100.000			
25	2.747E-16	8.080E-16	100.000			
26	1.866E-16	5.490E-16	100.000			
27	7.799E-17	2.294E-16	100.000			
28	-1.247E-17	-3.667E-17	100.000			
29	-6.143E-17	-1.807E-16	100.000			
30	-1.645E-16	-4.838E-16	100.000			
31	-4.092E-16	-1.203E-15	100.000			
32	-4.138E-16	-1.217E-15	100.000			
33	-4.536E-16	-1.334E-15	100.000			
34	-8.189E-16	-2.408E-15	100.000			

Extraction Method: Principal Component Analysis (PCA).