Supplemental Table 1. TaqMan Assays and Primers used for reverse transcription-quantitative PCR (RT-qPCR).

Gene Symbol	**Reference Sequence**	**TaqMan Assay ID**	
CYP2B6	**NM_000767**	Hs04183483_g1	
PLIN2	**NM_001122**	Hs000605340_m1	
NR0B2 (SHP)	**NM_021969**	Hs00222677_m1	
		Forward primer (5’ to 3’)	**Reverse Primer (5’ to 3’)**
ACAA2	**NM_006111**	CAGGGAATGCATCGGGTGTA	GCCCACAATTCTTGCCAGTG
ACOT12	**NM_130767**	TGCTCAAGTGGATCGACACC	TCCAACTCTAGCTGTCTCCTCA
ACOX1	**NM_004035**	CTTCAACCCGGAGCTGCTTA	ATGTTCTCGATCCGGCG
ACOX2	**NM_003500**	ACAGAGGGGAGCCAGGTTCTT	ATCCCCCAATGACACTCGGT
CPT1A	**NM_001876**	CTTTGGACCGGTTGCTGATG	GTGCCTTCCAAAGCGATGAG
CYP1A2	**NM_000761.4**	AGCACCTGCCTCTACAGTTGG	TTTTCAGGCCTTTGGGGACC
CYP2B6	**NM_000767**	AGCTTCATGACCGAGCCAAA	CTGTGTCCTTGGGGATGATGT
CYP2E1	**NM_000773.3**	ACTCCCTGGCTCCAGCTTTA	TCTCTGTCCCCGCAAAGAAC
CYP3A4	**NM_017460.5**	TACCCAATAAGGCACCACCC	AATGTGCAGGAAAGCATCTGA
EHHADH	**NM_001966**	AAAAGTGGTTTGCCTGACGG	AAGTCGTACTGATCGCGTTG
HADHA	**NM_000182**	GGAGGACTTGAGGTTGCCAT	TAAGGCCCCCAGCAAAACTT
HADHB	**NM_000183**	CCCCAGCTGTCCAGACCAAA	CCGATGCAACAAACCCGTAA
NR0B2 (SHP)	**NM_021969**	GTGGCTTCATGCTGTCTGG	CTGGCACATCGGGGTTGA
PLIN2	**NM_001122**	GGCGAGGCGGGGTTTATAG	CCACACTCGGTTGTGGATCA

Supplemental Table 2. Customized PCR array genes, functional classifications, and treatment-induced fold changes.

Gene Symbol	Gene Name	FOH	OA	OA+ FOH	CITCO	GW4064	GW7647	OA+ CITCO	OA+ GW4064	OA+ GW7647
Fatty Acid Uptake/Transport										
CD36	CD36 molecule (thrombospondin receptor)	1.1	1.6	1.2	-1.4	-1.1	3.3	1.6	1.3	5.1
FABP1	Fatty acid binding protein 1, liver	1.9	-1.3	1.2	-1.0	-1.7	2.8	1.4	-3.7	1.8
LIPC	Lipase, hepatic	1.3	-1.1	-1.0	-1.2	-2.4	1.2	1.5	-4.0	1.1
SCP2	Sterol carrier protein 2	1.2	-1.1	-1.1	-1.0	1.1	1.0	1.2	-1.9	-1.2
SLC27A1	Solute carrier family 27 (fatty acid transporter), member 1	-1.2	-1.2	1.3	1.1	1.1	1.0	-1.6	-3.1	-1.3
SLC27A2	Solute carrier family 27 (fatty acid transporter), member 2	1.7	-1.2	1.1	1.2	1.3	2.2	1.8	-1.4	1.4
Mitochondrial Fatty Acid Oxidation										
ACAA1	Acetyl-CoA acyltransferase 1	-1.1	-1.0	1.3	1.0	-1.1	2.0	-1.2	1.1	1.6
ACAA2	Acetyl-CoA acyltransferase 2	1.3	1.3	1.7	-1.1	1.1	2.0	1.7	-1.4	1.9
ACADL	Acyl-CoA dehydrogenase, long chain	1.1	-1.1	-1.1	-1.2	-1.4	-1.2	1.1	-2.3	-1.3
ACADM	Acyl-CoA dehydrogenase, C-4 to C-12 straight chain	1.2	1.1	1.3	-1.1	-1.3	1.3	1.1	-2.1	1.2
ACADS	Acyl-CoA dehydrogenase, C-2 to C-3 short chain	1.4	1.3	2.2	1.4	1.3	2.5	1.4	-2.4	1.8
ACADVL	Acyl-CoA dehydrogenase, very long chain	1.0	1.1	1.1	1.1	1.2	1.8	1.0	-1.3	1.5
ACAT1	Acetyl-CoA Acetyltransferase 1	1.3	1.1	1.1	-1.1	-1.4	1.1	1.5	-2.2	1.0
ACSL3	Acyl-CoA synthetase long-chain family member 3	1.2	-1.2	-1.1	1.0	1.3	1.5	1.1	-1.4	1.2
ACSL4	Acyl-CoA synthetase long-chain family member 4	-1.1	-1.0	1.4	1.2	-1.0	1.7	-1.1	-2.5	1.3
ACSL5	Acyl-CoA synthetase long-chain family member 5	1.2	1.1	1.5	1.1	1.6	1.8	1.3	-1.2	1.6
CPT1A	Carnitine palmitoyltransferase 1A (liver)	1.1	1.2	1.7	1.2	1.1	1.8	1.2	-1.7	1.6
CPT2	Carnitine palmitoyltransferase 2	-1.0	-1.1	1.1	1.4	1.2	2.0	-1.3	-1.9	1.3
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	1.2	-1.2	-1.4	-1.0	1.0	1.1	1.3	-1.6	-1.1

Gene Symbol	**Gene Name**	**FOH**	**OA**	**OA+ FOH**	**CITCO**	**GW4064**	**GW7647**	**OA+ CITCO**	**OA+ GW4064**	**OA+ GW7647**
ECHS1	Enoyl CoA hydratase, short chain, 1, mitochondrial	-1.1	-1.0	1.1	1.1	1.0	1.3	-1.1	-2.0	-1.1
HADH	Hydroxyacyl-CoA dehydrogenase	1.2	-1.0	1.0	-1.0	-1.0	1.4	1.3	-2.1	1.2
HADHA	Hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	1.1	1.2	1.3	1.1	1.1	2.3	1.4	-1.3	2.1
HADHB	Hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	1.3	1.6	1.5	1.1	1.0	2.5	1.9	-1.0	2.3
SLC24A20	Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-1.0	1.2	1.3	1.2	-1.0	2.0	1.2	-1.5	1.7
<u>Peroxisomal β-Oxidation</u>										
ACOT4	Acyl-CoA thioesterase 4	1.1	-1.2	-1.0	1.3	1.1	1.3	1.3	-1.7	1.4
ACOT8	Acyl-CoA thioesterase 8	-1.2	-1.1	1.2	1.2	1.1	1.1	-1.3	-2.2	-1.2
ACOX1	Acyl-CoA oxidase 1, palmitoyl	1.1	-1.1	1.3	1.2	1.0	1.4	-1.0	-2.1	1.3
ACOX2	Acyl-CoA oxidase 2, branched chain	1.7	-1.4	-1.2	1.0	-2.9	1.3	1.1	-6.6	-1.3
ECH1	Enoyl CoA hydratase 1, peroxisomal	1.3	-1.0	-1.0	-1.0	-1.2	1.6	-1.1	-2.0	-1.1
EHHADH	Enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	-1.0	-1.0	1.2	1.1	-1.2	1.3	-1.1	-2.7	1.0
<u>Microsomal ω-Oxidation</u>										
CYP2E1	Cytochrome P450, family 2, subfamily E, polypeptide 1	-1.4	1.3	2.2	-1.0	-6.0	-1.1	1.4	-9.6	-1.1
CYP4A11	Cytochrome P450, family 4, subfamily A, polypeptide 11	-1.0	-1.1	1.1	-1.1	-1.8	2.1	-1.1	-3.0	1.4
<u>Fatty Acid Biosynthesis</u>										
ACACA	Acetyl-CoA carboxylase alpha	-1.2	-1.2	1.2	-1.0	-1.0	-1.0	-1.4	-2.4	-1.2
ACACB	Acetyl-CoA carboxylase beta	1.0	-1.2	1.1	1.1	1.2	1.0	-1.5	-2.4	1.1
ACLY	ATP citrate lyase	1.0	-1.2	1.1	1.1	1.2	1.0	-1.2	-2.0	-1.1
ELOVL1	ELOVL fatty acid elongase 1	1.1	1.0	-1.2	1.3	1.4	1.4	1.1	-1.2	1.1

Gene Symbol	Gene Name	FOH	OA	OA+ FOH	CITCO	GW4064	GW7647	OA+ CITCO	OA+ GW4064	OA+ GW7647
ELOVL5	ELOVL fatty acid elongase 5	-1.1	-1.1	1.0	1.1	1.2	1.3	1.0	-1.6	1.2
ELOVL6	ELOVL fatty acid elongase 6	1.0	1.1	1.4	1.3	1.2	1.2	-1.2	-1.8	1.2
FASN	Fatty acid synthase	1.1	-1.2	1.3	1.1	1.1	1.1	-1.2	-2.4	1.4
MCAT	Malonyl CoA:ACP acyltransferase (mitochondrial)	-1.2	1.0	1.2	1.2	-1.0	1.1	-1.5	-2.0	-1.1
MECR	Mitochondrial trans-2-enoyl-CoA reductase	-1.0	1.0	-1.1	1.1	1.2	1.3	1.0	-1.6	1.1
PECR	Peroxisomal trans-2-enoyl-CoA reductase	-1.1	-1.3	-1.2	1.2	-1.1	1.1	-1.2	-2.5	-1.3
SCD	Stearoyl-CoA desaturase	1.2	-2.0	-1.4	1.2	-1.4	1.6	-2.0	-6.2	-1.5
SCD5	Stearoyl-CoA desaturase 5	-1.2	-1.4	-1.3	1.1	1.2	1.2	-1.2	-2.1	-1.3
TECR	Trans-2,3-enoyl-CoA reductase	-1.1	-1.1	1.0	1.1	1.1	1.2	1.1	-1.7	1.1
<u>Fatty Acid Metabolism (Other)</u>										
ACAT2	Acetyl-CoA Acetyltransferase 2	1.3	1.1	1.1	-1.1	-1.0	-1.1	1.4	-1.6	1.0
ACOT1	Acyl-CoA thioesterase 1	1.1	1.1	1.3	1.4	1.2	1.6	-1.1	-2.0	1.1
ACOT6	Acyl-CoA thioesterase 6	-1.1	-1.1	-1.3	-1.3	-1.6	-1.2	1.5	-8.6	-1.2
ACOT7	Acyl-CoA thioesterase 7	1.0	-1.1	-1.2	1.3	1.4	1.2	1.3	-1.4	1.2
ACOT12	Acyl-CoA thioesterase 12	1.6	1.8	3.9	1.1	-1.6	1.3	2.0	-2.6	1.6
COX10	Cytochrome C oxidase assembly homolog 10	-1.3	-1.1	1.1	1.2	1.1	1.3	-1.0	-2.0	1.2
<u>Triglyceride Biosynthesis</u>										
LPIN1	Lipin 1	-1.2	-1.1	1.3	-1.0	-1.3	1.1	-1.1	-2.8	1.0
LPIN2	Lipin 2	-1.1	-1.2	1.2	-1.0	-1.4	1.0	-1.3	-4.3	-1.2
LPIN3	Lipin 3	-1.3	-1.3	1.1	-1.2	-1.4	-1.2	-1.3	-3.4	-1.2
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	-1.1	-1.1	-1.3	1.3	1.6	1.4	-1.0	-1.4	-1.1
AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2	1.0	1.4	1.2	1.5	1.7	2.2	1.7	1.0	1.7
AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6	-1.2	1.0	1.4	1.0	1.2	1.1	-1.0	-2.1	1.1
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	-1.2	1.3	1.2	1.3	1.4	1.4	1.1	-1.5	1.7
DGAT1	Diacylglycerol O-acyltransferase 1	-1.3	-1.2	-1.0	-1.0	-2.0	1.1	-1.2	-3.0	-1.2
DGAT2	Diacylglycerol O-acyltransferase 2	-1.1	1.1	1.3	1.2	-1.4	1.3	-1.1	-3.0	1.0

Gene Symbol	Gene Name	FOH	OA	OA+ FOH	CITCO	GW4064	GW7647	OA+ CITCO	OA+ GW4064	OA+ GW7647
SREBF1	Sterol regulatory element binding transcription factor 1	-1.1	-1.6	-1.0	1.1	-1.2	1.2	-1.8	-4.9	-1.7
MTTP	Microsomal triglyceride transfer protein large subunit	-1.0	-1.3	-1.1	1.2	-1.3	-1.1	-1.1	-3.6	-1.4
Cholesterol Metabolism										
DHDDS	Dehydrodolichyl diphosphate synthase complex subunit	-1.0	1.2	1.2	1.1	1.3	1.5	-1.0	-1.8	1.3
FDFT1	Farnesyl-diphosphate farnesyltransferase 1	1.4	-1.0	1.0	1.1	1.2	1.2	1.4	-1.3	1.1
FDPS	Farnesyl diphosphate synthase	1.3	-1.1	-1.2	1.1	1.1	1.2	-1.0	-1.6	-1.0
FNTA	Farnesyltransferase, CAAX box, alpha	-1.2	-1.1	1.3	1.1	-1.1	1.3	-1.1	-2.5	1.0
FNTB	Farnesyltransferase, CAAX box, beta	-1.3	-1.1	1.2	1.2	1.2	1.2	-1.1	-2.1	1.0
GGPS1	Geranylgeranyl diphosphate synthase 1	1.1	-1.1	-1.1	1.0	1.1	1.0	-1.0	-1.7	-1.1
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	1.1	1.2	1.4	1.1	1.3	1.1	1.3	-1.1	1.4
PDSS1	Prenyl (decaprenyl) diphosphate synthase, subunit 1	1.4	1.2	1.0	-1.1	-1.3	1.0	1.6	-1.7	1.1
PPAPDC2	Phosphatidic acid phosphatase type 2 domain containing 2	-1.1	-1.2	1.1	1.1	1.1	1.0	-1.2	-2.1	-1.3
RABGGTA	Rab geranylgeranyltransferase, alpha subunit	-1.1	-1.2	-1.4	1.2	1.2	1.2	1.1	-1.5	-1.1
RABGGTB	Rab geranylgeranyltransferase, beta subunit	1.2	-1.2	-1.3	-1.1	-1.0	1.1	1.4	-1.5	-1.0
Carbohydrate Metabolism										
MLXIPL	MLX interacting protein-like	-1.1	-1.2	-1.5	1.3	-1.7	1.0	-1.3	-2.8	-1.4
PCK1	Phosphoenolpyruvate carboxykinase 1 (soluble)	-1.5	1.8	4.0	1.4	-5.4	3.5	2.5	-5.7	4.2
Inflammation										
IL6	Interleukin 6 (interferon, beta 2)	-1.1	-1.9	1.1	-1.0	-1.0	-1.3	-1.5	-4.5	-2.6
Nuclear Receptors										
NR1H4	Nuclear receptor subfamily 1, group H, member 4	-1.3	-1.4	1.1	1.1	-1.5	-1.4	-1.4	-3.1	1.0

Gene Symbol	Gene Name	FOH	OA	OA+ FOH	CITCO	GW4064	GW7647	OA+ CITCO	OA+ GW4064	OA+ GW7647
NR1I3	Nuclear receptor subfamily 1, group I, member 3	1.0	-1.0	1.2	1.0	-1.5	1.1	-1.2	-6.3	-2.8
PPARA	Peroxisome proliferator-activated receptor alpha	1.0	1.1	1.7	1.1	1.1	-1.1	-1.4	-2.6	-1.2
PPARG	Peroxisome proliferator-activated receptor gamma	1.4	1.1	1.3	-1.2	1.6	1.0	1.1	-1.4	-1.1
Nuclear Receptor Target Genes (Positive Controls)										
CYP2B6	Cytochrome P450, family 2, subfamily B, polypeptide 6	2.1	-1.5	2.3	9.9	-1.6	1.0	4.2	-4.6	-1.9
NR0B2 (SHP)	Nuclear receptor subfamily 0, group B, member 2	-1.3	-1.3	-1.7	1.1	5.0	-1.4	-1.2	2.3	-1.9
PLIN2	Perilipin 2	1.3	1.5	1.8	-1.0	1.3	3.8	1.9	1.1	3.9
Apolipoproteins										
APOA5	Apolipoprotein A5	1.3	2.6	4.3	1.1	1.6	2.0	3.2	1.5	2.6
APOB	Apolipoprotein B	-1.0	-1.5	1.1	-1.1	-1.4	-1.2	-1.4	-3.7	-1.3
APOC4	Apolipoprotein C4	-1.4	-1.2	-1.1	-1.1	1.7	-1.5	-1.7	-2.1	-1.7
APOE	Apolipoprotein E	1.1	-1.1	1.1	-1.0	-1.2	1.1	-1.2	-2.0	-1.3

Genes whose expression changed by at least 1.3-fold relative to control in response to farnesol treatment, alone and/or in combination with oleic acid, are indicated by grey shading. Values for the FOH, OA, and OA+FOA treatment groups are the fold changes relative to FF-BSA+ EtOH treated controls. Values for the CITCO, GW4064, GW7647, OA+CITCO, OA+GW4064, and OA+GW7647 treatment groups are the fold changes relative to FF-BSA+ DMSO-treated controls.