

UP780, a Chromone-Enriched *Aloe* Composition, Enhances Adipose Insulin Receptor Signaling and Decreases Liver Lipid Biosynthesis

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ABSTRACT

Nutrigenomic studies were conducted to uncover the mechanism of action for the hypoglycemic and insulin sensitizing effects of UP780. From high fat diet-induced obesity mouse model for UP780, livers and white adipose tissues (WAT) from groups of lean control, high fat diet (HFD), and HFD treated with UP780 were collected for microarray study. Microarray generated gene expression changes were applied to Ingenuity Pathway Analysis for changes in canonical metabolic and signaling pathways. Microarray was validated by quantitative reverse transcriptase-polymerase chain reaction (QPCR), Western blots, liver triglyceride, liver cholesterol, liver steatosis, and insulin ELISA. UP780 treatment decreased liver gene expressions for multiple enzymes involved in fatty acid biosynthesis and triglyceride production. UP780 treatment increased gene expressions globally for the insulin receptor signaling pathway in WAT. Both liver triglyceride and liver cholesterol levels were significantly reduced by UP780 over HFD. The reduction of liver fat was confirmed by microscopic analysis of liver steatosis. Finally, UP780 significantly decreased fasting plasma insulin level over HFD. The mechanism of action for UP780 indicated a reduction of liver fat accumulation and an enhancement in adipose tissue insulin signaling pathway. This provided mechanistic explanation for the *in vivo* UP780 effects of enhanced insulin sensitivity and decreased blood glucose in mouse diabetes and prediabetes models.

Keywords: Nutrigenomics; Insulin Signaling Pathway; Liver Fatty Acid Biosynthesis; Liver Steatosis; Aloe Vera

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1. INTRODUCTION

Diabetes and prediabetes have become epidemic globally. In recent US surveys, 26.9% of the population aged 65 years and older had diabetes and 35% of those 20 years or older had prediabetes [1]. WHO of the United Nations estimated in 2011 that 346 million people worldwide had diabetes, and that number was likely to double by 2030 [2]. Complications of diabetes include heart disease, stroke, hypertension, blindness, kidney disease, neuropathy, amputation, and dental disease. Economic burden of diabetes was high, in US, the 2007 direct and indirect cost of diabetes amounted to \$174 billion [1].

The culprit for the epidemic of type II diabetes and prediabetes/metabolic syndrome is obesity. Obesity predisposes patients to a complex metabolic pathology, characterized by a cluster of closely related clinical features of central obesity, hyperglycemia, insulin resistance, dyslipidaemia and hypertension [3]. Metabolic syndrome is associated with increased risk of type II diabetes and cardiovascular disease; cardiovascular diseases ultimately are responsible for a large proportion of diabetic mortality [4]. The epidemics in type II diabetes calls for interventions at the stage of metabolic syndrome, with diet, exercise, and medications/dietary supplements targeting insulin resistance, to decrease the societal burden from diabetes.

For thousands of years, herbal medicine was the only treatment available to mankind. What is old is not necessarily worthless in the modern world. Recently, traditional herbal medicines with a history in diabetic treatment, now as nutritional supplements or as alternate medicines, were rediscovered by the medical world for obesity, metabolic syndrome, and diabetes: *Aloe vera* leaf gel [5], berberine [6,7], bitter melon [8], ginsenoside Rb1

[9], genistein [10], and cinnamon [11], to name a few. In addition, resveratrol from red grape was recently discovered to improve obesity and aging related disorders [12].

Aloe vera inner leaf gel and whole leaf extract had been reported to produce a hypoglycemic effect in diabetic animal models of alloxan-induced diabetic mice [13-15] and type I/type II diabetic rats [16,17]. UP780, the *Aloe vera* inner leaf gel extract standardized with aloesin, was found to decrease fasting blood glucose levels and insulin resistance in mouse diet-induced obesity (DIO) model and *db* diabetic model [18]. Significantly, UP780 was the subject of a double blind, placebo controlled clinical pilot study of prediabetic patients. After eight weeks of treatment, UP780 significantly reduced fasting blood glucose, insulin, HbA1c, fructosamine, and urinary F2-isoprostanes compared to placebo [19].

Although aloe was traditionally used for diabetes treatment, and shown to reduce blood glucose, improve lipid profile, and provide anti-oxidants in diabetic animal models [13,15-17,20,21], there is a paucity of aloe mechanism of action study. From the UP780 prediabetic DIO mouse study [18], livers and white adipose tissues (WAT) collected from the DIO animals were used in a nutrigenomic study. By microarray/pathway analysis and QPCR gene expression, UP780 decreased fatty acid biosynthesis and triglyceride production in liver and increased insulin receptor signaling pathway in WAT. The microarray and QPCR gene expression data was validated by Western blot, liver triglyceride/cholesterol, liver steatosis, and plasma insulin ELISA.

2. MATERIALS AND METHODS

2.1. Composition of UP780

UP780 is a combination of *Aloe vera* inner leaf gel powder (QMatrix[®]) standardized to contain 2% - 4% aloesin. QMatrix[®] is produced from *Aloe vera* gel carbon-filtered to remove anthraquinone, which has laxative effect [22]. Aloesin, an aromatic chromone isolated from *Aloe ferox*, was discovered by high throughput screening of 2059 plant extracts to increase adiponectin secretion from differentiated 3T3-L1 adipocytes [18]. In the preparation of QMatrix[®], aloesin was removed by carbon filtration. Aloesin was added to QMatrix[®] with an expectation of broadening the aloe action for glycemic control. GW1929 is a specific non-thiazolidinedione, tyrosine-derived agonist of peroxisome proliferatoractivated receptor gamma (PPAR α , Tocris Bioscience). Thiazolidinedione class PPAR agonists are standard medicines for type II diabetes [23].

2.2. Methods

Methods for tissue collection from DIO mice, RNA ex-

traction, microarray, Ingenuity Pathway Analysis, real-time RT-QPCR, Western blot, liver triglyceride and cholesterol assays, liver steatosis, and plasma insulin ELISA are described in the supplemental materials.

3. RESULTS

3.1. Microarray/QPCR and UP780 Mechanism of Action

HFD feeding of C57BL/6J mice is known to induce gene expression variations in organs that respond to high caloric intake such as liver, fat, and muscle [12]. It was of great interest to observe the effects of UP780 treatment over HFD-induced changes in gene expressions. Microarray gene expression variations were applied to the construction of a hypothesis for UP780 mechanism of action, based on the canonical metabolic and signaling pathway analysis, and taken into account of known gene functions [24,25]. The large volume of pathway analysis results were allocated to the supplemental materials. Only key genes involved in the interpretation of biological significance of UP780 were validated by QPCR (**Table 1**). An equivalent **Table 2** was generated for WAT. Concordance between liver microarray and liver QPCR was good, 11 out of 14, when the genes loosely categorized as Signaling were not counted (**Table 1**) Concordance between WAT microarray and QPCR was excellent, 11 out of the 13 key genes tested (**Table 2**)

The liver key gene list in **Table 1** emphasized the metabolic pathways. Liver responds to the nutritional state of the body by modifying the enzyme/gene activities involved in metabolism, either by protein phosphorylation or by gene expression variation. With liver, genes encoding relevant members of metabolic pathways of fatty acid biosynthesis, fatty acid metabolism, glycolysis/gluconeogenesis, and fat transport were all found to be strikingly up-regulated by HFD and down-regulated by UP780 (**Table 1**). The hypoglycemic effect of UP780 suggested a decreased gluconeogenesis pathway. Many genes in glycolysis/gluconeogenesis pathway were up-regulated by HFD and down-regulated by UP780 (**Table 1, Supplement Figure 5** and **Supplement Table 1**). While this may suggest a decrease of gluconeogenesis by UP780, close examination of the functions of the genes involved indicated contradictions that cannot be resolved by gene expression data alone. In particular, phosphoenolpyruvate carboxykinase (PEPCK) is a rate-limiting enzyme for gluconeogenesis. The cytosolic PEPCK1 was up-regulated by HFD/UP780, opposing gluconeogenesis as a mechanism of hypoglycemic control. Effect of UP780 on carbohydrate metabolism in liver will need further studies.

Strong evidence of UP780-modulated metabolic pathways in support of UP780 insulin-sensitizing effect was

Table 1. Liver gene expression variations from microarray and QPCR. For microarray, up-regulations ≥ 0.8 and with a p-value < 0.05 are highlighted with red and marked with “ $\uparrow +$ ”, down-regulations ≤ -0.8 and with a p-value < 0.05 are highlighted with green and marked by “ $\downarrow -$ ”. For QPCR, up- and down-regulations over 2 fold difference are highlighted with red and green, respectively. Concordances in between microarray and QPCR are marked with •.

Genes	Description	Microarray (Fold Change)			QPCR (Relative Expression)		
		LUP-LV	LUP-LC	LV-LC	LC	LV	LUP
Fatty Acid Biosynthesis							
ACC1	ACACA, Acetyl-CoA carboxylase 1	$\downarrow -1.80$	$\downarrow -1.36$	$\uparrow +1.32$			
ACC2	ACACB, Acetyl-CoA carboxylase 2	$\downarrow -3.11$	$\downarrow -2.82$	$\uparrow +1.10$	1.00 ± 0.13	0.81 ± 0.06	0.33 ± 0.16 •
ACSL3	Acyl-CoA synthetase long chain 3	$\downarrow -1.77$	$\downarrow -1.43$	$\uparrow +1.24$			
FASN	Fatty acid synthase	$\downarrow -3.89$	$\downarrow -2.53$	$\uparrow +1.54$	1.00 ± 0.02	0.93 ± 0.03	0.35 ± 0.01 •
FADS1	Fatty acid desaturase 1	$\downarrow -1.90$	$\downarrow -1.32$	$\uparrow +1.43$			
FADS2	Fatty acid desaturase 2	$\downarrow -3.48$	$\downarrow -1.32$	$\uparrow +2.79$			
SCD1	Stearoyl-CoA desaturase	$\downarrow -4.50$	$\downarrow -4.25$	$\uparrow +1.07$	1.00 ± 0.00	0.98 ± 0.02	0.26 ± 0.01 •
ELOV5	Elongation of long chain fatty acids 5	$\downarrow -2.44$	$\downarrow -1.34$	$\uparrow +1.83$			
ELOV6	Elongation of long chain fatty acids 6	$\downarrow -2.89$	$\downarrow -2.39$	$\uparrow +1.25$			
Fatty Acid Metabolism							
ACOX1	Acyl-CoA oxidase 1, palmitoyl	$\downarrow -1.87$	$\downarrow -1.15$	$\uparrow +1.62$	1.00 ± 0.01	1.12 ± 0.02	0.92 ± 0.02
ACOT1	Acyl-CoA thioesterase 1, peroxisome	$\downarrow -6.42$	$\downarrow -3.26$	$\uparrow +2.53$			
CPT1A	Carnitine palmitoyl transferase 1A	$\downarrow -1.78$	$\uparrow +1.21$	$\uparrow +2.16$	1.00 ± 0.04	1.43 ± 0.04	1.06 ± 0.05 •
CRAT	Carnitine acetyltransferase	$\downarrow -2.41$	$\downarrow -1.10$	$\uparrow +2.18$			
HAO2	Hydroxyacid oxidase 2, peroxisome	$\downarrow -2.33$	$\downarrow -1.15$	$\uparrow +2.03$			
Steroid Biosynthesis							
FDPS	Farnesyl diphosphate synthase	$\downarrow -1.39$	$\downarrow -1.99$	$\downarrow -1.43$			
HMGCR	3-Hydroxy-3-methylglutaryl-CoA reductase	$\downarrow -1.19$	$\downarrow -2.26$	$\downarrow -1.90$	1.00 ± 0.03	0.41 ± 0.01	0.47 ± 0.01 •
MVD	Mevalonate decarboxylase	$\downarrow -2.70$	$\downarrow -2.51$	$\uparrow +1.07$			
Bile Acid Biosynthesis							
CYP7A1	Cytochrome P450 7A1	$\uparrow +2.77$	$\downarrow -2.45$	$\downarrow -4.89$	1.06 ± 0.42	0.07 ± 0.03	0.97 ± 0.02 •
CYP7B1	Cytochrome P450 7B1	$\uparrow +2.76$	$\uparrow +2.30$	$\downarrow -1.22$	1.00 ± 0.50	0.56 ± 0.02	2.53 ± 0.08 •
Fat Transport							
APOA4	Apolipoprotein A4, chylomicron	$\downarrow -3.48$	$\uparrow +2.41$	$\uparrow +8.40$			
CD36	Fat transporter	$\downarrow -3.29$	$\downarrow -1.34$	$\uparrow +2.45$	1.00 ± 0.07	1.98 ± 0.08	0.98 ± 0.04 •
FABP4	Fatty acid binding protein 4	$\uparrow +1.07$	$\uparrow +2.70$	$\uparrow +2.52$	1.00 ± 0.04	0.54 ± 0.08	2.77 ± 0.03
FABP5	Fatty acid binding protein 5	$\uparrow +2.63$	$\downarrow -1.49$	$\downarrow -3.91$	1.00 ± 0.06	0.08 ± 0.01	0.64 ± 0.14 •
LDLR	LDL receptor	$\downarrow -2.75$	$\downarrow -1.54$	$\uparrow +1.67$			
Glycolysis/Gluconeogenesis							
ALDH1B1	Aldehyde dehydrogenase 1B1	$\downarrow -3.04$	$\downarrow -1.77$	$\uparrow +1.72$			
GCK	Glucokinase, MODY2	$\downarrow -2.29$	$\uparrow +1.13$	$\uparrow +2.04$			
GYS2	Glycogen synthase 2	$\downarrow -1.40$	$\uparrow +1.05$	$\uparrow +1.47$	1.00 ± 0.09	1.08 ± 0.06	1.14 ± 0.03
HK1	Hexokinase 1	$\downarrow -2.55$	$\downarrow -1.77$	$\downarrow -1.39$			
PDK4	Pyruvate dehydrogenase kinase 4	$\downarrow -2.59$	$\downarrow -1.41$	$\uparrow +1.83$	1.03 ± 0.32	1.70 ± 0.44	0.11 ± 0.04 •
PKLR	Pyruvate kinase, liver & RBC	$\downarrow -2.26$	$\downarrow -1.54$	$\uparrow +1.62$			
PEPCK1	PCK1, Phosphoenolpyruvate carboxykinase 1	$\uparrow +1.09$	$\uparrow +2.34$	$\uparrow +2.23$	1.00 ± 0.04	1.73 ± 0.05	2.72 ± 0.08 •
Signaling							
AMPK $\alpha 2$	PRKAA2, AMP-activated kinase $\alpha 2$	$\downarrow -1.60$	$\downarrow -1.49$	$\uparrow +1.07$	1.00 ± 0.02	0.85 ± 0.13	0.96 ± 0.03
AMPK $\gamma 2$	PRKAG2, AMP-activated kinase $\gamma 2$	$\downarrow -1.40$	$\downarrow -1.38$	$\downarrow -1.01$	1.00 ± 0.05	0.79 ± 0.11	0.75 ± 0.01
SLC2A2	GLUT2, solute carrier family 2, member 2	$\downarrow -1.50$	$\downarrow -1.37$	$\uparrow +1.09$	1.00 ± 0.02	0.84 ± 0.06	0.77 ± 0.04
HNF4A	Hepatocyte nuclear factor 4 α	$\downarrow -1.18$	$\downarrow -1.27$	$\downarrow -1.07$	1.00 ± 0.04	0.74 ± 0.04	1.06 ± 0.04
mTOR	FRAP1, FK506 binding protein 12, rapamycin-associated protein 1	$\downarrow -1.10$	$\uparrow +1.18$	$\uparrow +1.43$	1.00 ± 0.06	0.93 ± 0.01	0.88 ± 0.04
PGC1A	PPAR γ coactivator 1A	$\downarrow -1.66$	$\downarrow -1.45$	$\uparrow +1.22$	1.46 ± 1.46	1.13 ± 0.79	2.53 ± 0.54
PGC1B	PPAR γ coactivator 1B	$\downarrow -2.32$	$\downarrow -1.59$	$\uparrow +1.46$	1.08 ± 0.55	1.05 ± 0.26	1.32 ± 0.07
PPAR α	Peroxisome proliferator-activated receptor	$\downarrow -2.41$	$\uparrow +1.07$	$\uparrow +2.25$	1.00 ± 0.09	1.42 ± 0.03	1.44 ± 0.05
PPAR δ	Peroxisome proliferators-activated receptor	$\downarrow -1.11$	$\uparrow +1.07$	$\uparrow +1.22$	1.00 ± 0.05	1.12 ± 0.08	0.99 ± 0.14
SREBF1	Sterol regulatory element binding factor 1	$\downarrow -2.40$	$\downarrow -1.58$	$\uparrow +1.52$	1.00 ± 0.09	0.92 ± 0.04	0.88 ± 0.09

LUP: Livers from UP780 treated DIO mice. **LV:** Livers from high fat diet, HFD, treated DIO mice. **LC:** Livers from lean control mice.

Table 2. WAT gene expression variations from microarray and QPCR. For microarray, up-regulations ≥ 0.8 and with a p-value < 0.05 are highlighted with red and marked with “ $\uparrow +$ ”, down-regulations ≤ -0.8 and with a p-value < 0.05 are highlighted with green and marked with “ $\downarrow -$ ”. For QPCR, up- and down-regulations over 2 fold difference are highlighted with red and green, respectively. Concordances in between microarray and QPCR are marked with •.

Gene	Description	Microarray (Fold Change)			QPCR (Relative Expression)		
		FUP/FV	FUP/FC	FV/FC	FC	FV	FUP
Insulin Receptor Signaling							
EIF4EBP1	Eukaryotic translation initiation factor 4E binding protein 1	$\uparrow +2.16$	$\uparrow +1.02$	$\downarrow -2.23$			
FOXO1	Forkhead box O1	$\uparrow +1.58$	$\downarrow -1.25$	$\downarrow -1.97$			
FRAP1	FK506 binding protein 12-rapamycin associated protein 1, mTOR	$\downarrow -1.77$	$\downarrow -1.10$	$\uparrow +1.92$			
GYS1	Glycogen synthase 1 (muscle)	$\uparrow +2.14$	$\downarrow -1.17$	$\downarrow -2.50$			
GYS2	Glycogen synthase 2 (liver)	$\downarrow -3.18$	$\uparrow +1.75$	$\uparrow +5.58$			
IGF1R	Insulin-like growth factor 1 receptor	$\uparrow +1.68$	$\downarrow -1.21$	$\downarrow -2.03$			
INSR	Insulin receptor	$\uparrow +1.59$	$\downarrow -1.21$	$\downarrow -1.92$	1.00 ± 0.07	0.24 ± 0.07	0.30 ± 0.22
IRS1	Insulin receptor substrate 1	$\uparrow +2.62$	$\downarrow -1.60$	$\downarrow -4.19$	1.01 ± 0.18	0.58 ± 0.05	1.06 ± 0.08
PIK3CA	Phosphoinositide-3-kinase, catalytic, p110	$\uparrow +1.56$	$\downarrow -1.19$	$\downarrow -1.76$			
PIK3R1	Phosphoinositide-3-kinase, regulatory 1, p85	$\uparrow +1.55$	$\downarrow -1.62$	$\downarrow -2.64$			
PRKCH	Protein kinase C, eta	$\downarrow -1.67$	$\uparrow +2.00$	$\uparrow +3.02$			
SLC2A4	GLUT4, solute carrier family 2, member 4	$\uparrow +2.58$	$\downarrow -1.31$	$\downarrow -2.31$	1.00 ± 0.06	0.64 ± 0.05	0.87 ± 0.05
STXBP4	Syntaxin binding protein 4	$\uparrow +1.81$	$\downarrow -1.08$	$\downarrow -1.96$			
VAMP2	Synaptobrevin 2	$\uparrow +1.38$	$\downarrow -1.38$	$\downarrow -1.90$			
Cell Cycle							
BRCA1	Breast cancer 1, early onset	$\downarrow -3.30$	$\uparrow +1.79$	$\uparrow +5.91$			
CCNB1	Cyclin B1	$\downarrow -2.97$	$\uparrow +2.32$	$\uparrow +6.89$			
CCNB2	Cyclin B2	$\downarrow -2.87$	$\uparrow +2.43$	$\uparrow +6.97$			
CCNE1	Cyclin E1	$\downarrow -1.59$	$\uparrow +1.44$	$\uparrow +2.29$			
CDC2	Cell division cycle 2, G1 to S and G2 to M	$\downarrow -2.63$	$\uparrow +2.38$	$\uparrow +6.27$			
CDK6	Cyclin-dependent kinase 6	$\downarrow -1.70$	$\uparrow +1.55$	$\uparrow +2.31$			
CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	$\downarrow -1.60$	$\uparrow +2.77$	$\uparrow +4.43$			
CDKN1B	Cyclin-dependent kinase inhibitor 1B (p27, Kip1)	$\uparrow +1.31$	$\downarrow -1.35$	$\downarrow -1.77$			
CDKN2B	Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	$\downarrow -2.02$	$\uparrow +1.02$	$\uparrow +2.06$			
E2F1	E2F transcription factor 1	$\downarrow -1.28$	$\uparrow +1.58$	$\uparrow +1.87$			
E2F6	E2F transcription factor 6	$\downarrow -2.24$	$\uparrow +2.08$	$\uparrow +4.66$			
RB1	Retinoblastoma 1 (including osteosarcoma)	$\downarrow -1.57$	$\uparrow +1.40$	$\uparrow +2.19$			
SIRT1	Sirtuin	$\uparrow +1.28$	$\downarrow -1.37$	$\downarrow -1.75$			
TOP2A	Topoisomerase (DNA) II alpha 170 kDa	$\downarrow -2.89$	$\uparrow +2.12$	$\uparrow +6.12$			
Metabolism							
ACACA	ACC1, acetyl-Coenzyme A carboxylase alpha	$\uparrow +1.84$	$\downarrow -4.20$	$\downarrow -3.32$	1.04 ± 0.32	0.04 ± 0.01	0.51 ± 0.10

Continued

ACACB	ACC2, acetyl-Coenzyme A carboxylase beta	↑ +2.24	↑ +1.04	↓ -2.15			
ADIPOQ	Adiponectin	↑ +1.15	↓ -1.03	↓ -1.18	1.00 ± 0.12	0.63 ± 0.15	1.01 ± 0.17
ALDOB	Aldolase B, fructose bisphosphate	↑ +2.74	↓ -2.76	↓ -7.57	1.00 ± 0.10	0.006 ± 0.003	0.016 ± 0.004
CPT1A	Carnitine palmitoyltransferase 1A (liver)	↑ +1.05	↑ +1.49	↑ +1.42			
FABP4	Fatty acid binding protein 4	↑ +3.41	↓ -1.19	↓ -4.05	1.00 ± 0.03	1.21 ± 0.26	1.41 ± 0.29
FASN	Fatty acid synthase	↑ +1.14	↓ -1.39	↓ -1.59	1.00 ± 0.02	0.54 ± 0.13	0.64 ± 0.14
LEP	Leptin	↓ -1.17	↑ +1.59	↑ +1.51	1.05 ± 0.36	2.84 ± 0.13	1.77 ± 0.15
PEPCK1	PCK1, Phosphoenolpyruvate carboxykinase 1	↑ +4.57	↑ +1.13	↓ -4.69	1.00 ± 0.06	0.25 ± 0.11	1.46 ± 0.11
SLC27A1	FATP1, fatty acid transporter	↑ +1.76	↑ +1.54	↓ -1.14			
UCP2	Uncoupling protein 2	↓ -1.45	↑ +1.79	↑ +2.58	1.03 ± 0.29	1.78 ± 0.18	1.49 ± 0.22
Nuclear Receptors							
AR	Androgen receptor	↑ +1.82	↓ -1.36	↓ -2.48			
ESR1	Estrogen receptor 1	↑ +1.43	↓ -1.47	↓ -2.10			
NR3C1	Glucocorticoid receptor	↑ +3.97	↓ -1.46	↓ -2.72	1.02 ± 0.21	0.60 ± 0.04	0.98 ± 0.29
NCOR1	Nuclear receptor co-repressor 1	↑ +1.82	↓ -1.51	↓ -2.19			
THRA	Throid hormone receptor alpha	↑ +1.41	↓ -1.47	↓ -2.07			
PGC1A	PPAR γ coactivator 1A	↑ +1.16	↓ -1.37	↓ -1.77			
PGC1B	PPAR γ coactivator 1B	↑ +1.14	↓ -1.70	↓ -1.68			
PPAR γ	Peroxisome proliferator-activated receptor	↑ +1.18	↓ -1.43	↓ -1.68	1.00 ± 0.08	0.68 ± 0.14	0.80 ± 0.13
Immunity/inflammation							
CCL3	Chemokine (C-C motif) ligand 3	↓ -2.49	↑ +2.84	↑ +7.07			
CCL13	Chemokine (C-C motif) ligand 13	↓ -2.69	↑ +3.21	↑ +8.63			
CERK	Ceramide kinase	↓ -1.40	↑ +1.61	↑ +2.25			
CXCL3	Chemokine (C-X-C motif) ligand 3	↑ +1.04	↑ +2.68	↑ +2.57			
CXCR4	Chemokine (C-X-C motif) ligand 4	↓ -1.32	↑ +1.74	↑ +2.29			
FOS	v-fos FBJ viral oncogen homolog	↓ -2.13	↑ +1.65	↑ +3.51			
IL1R2	Interleukin 1 receptor, type II	↓ -2.74	↑ +1.24	↑ +3.38			
IL1RN	Interleukin 1 receptor antagonist	↓ -3.49	↑ +9.85	↑ +24.08			
SPHK1	Sphingosine kinase 1	↓ -2.25	↑ +1.59	↑ +3.58			

FUP: Fat tissues from UP780 treated DIO mice. **FV:** Fat tissues from high fat diet, HFD, treated DIO mice. **FC:** Fat tissues from lean control mice.

found in lipid biosynthesis (**Figure 1**). First, the fatty acid biosynthesis depends on two major cytoplasmic enzymes, acetyl-CoA carboxylase (ACC1) and fatty acid synthase (FASN). Both ACC1 and FASN were decreased by UP780 (**Table 1** and **Figure 1**). Second, the pentose phosphate pathway, which produces NADPH for fatty acid biosynthesis, was also down-regulated by UP780 (**Supplement Table 1**). Third, fatty acid desaturases (SCD1 and FADS1/2) and fatty acid elongases (ELOV5/6) were decreased by UP780, strongly supporting the mechanism that UP780 decreased liver fatty acid and tri-glyceride biosyntheses (**Table 1** and **Figure 1**). Free fatty

acid infusion in human induced systemic insulin resistance [26], UP780 could enhance systemic insulin sensitivity by a reduced lipotoxicity, resulting in enhanced blood glucose control.

Pathway analysis also suggested a cholesterol lowering effect by UP780, by 1) decreasing the rate-limiting enzyme HMG-CoA reductase (HMGCR) for cholesterol biosynthesis, 2) increasing the bile acid biosynthesis enzymes CYP7A1 and CYP7B1 for increased elimination of cholesterol through gut, and 3) decreasing apolipoprotein B for decreased LDL level (**Table 1** and **Figure 1**).

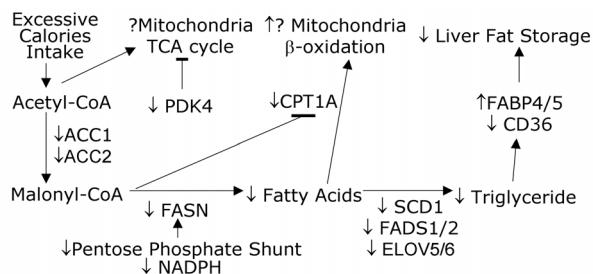


Figure 1. Liver metabolism modulated by UP780 over high fat diet. A schematic diagram is constructed to illustrate the influences exerted by UP780 to the metabolism of carbohydrates and lipids in liver.

Increased mitochondrial β -oxidation is a prominent mechanism of glycemic control [27]. The rate-limiting enzyme for mitochondrial fatty acid β -oxidation, carnitine palmitoyl transferase 1A (CPT1A), was decreased from HFD-elevated level (2-fold) by UP780 to lean control level, suggesting decreased β -oxidation. CPT1A activity is regulated by the feedback metabolite malonyl-CoA. Malonyl-CoA concentration in mitochondria depends on the mitochondrial ACC2. ACC2 expression in UP780 liver was ~3-fold lower than in HFD, suggesting increased β -oxidation (**Table 1**). The overall activity of fatty acid β -oxidation in liver might well be increased; a mechanism that will support a role of UP780 in better lipid metabolism control but will need further study (**Table 1** and **Figure 1**).

Microarray analysis of WAT gene expression offered a clear explanation for the insulin sensitizing effect by UP780. Key genes in the insulin receptor signaling pathway were globally decreased by HFD and globally increased by UP780 (**Table 2** and **Supplement Figure 6**). Among these key genes, insulin receptor (INSR), IRS-1, and glucose transporter 4 (GLUT4) were validated by QPCR (**Table 2**). With DIO mouse model, HFD feeding was known to induce insulin resistance [12]. Insulin activates INSR tyrosine kinase, which by phosphorylation of the IRS proteins, transduces insulin signal through protein kinases to the translocation of GLUTs to plasma membrane, thereafter increases glucose uptake. This increased glucose uptake from blood in WAT increases the usage of glucose for lipid biosynthesis and energy storage [28]. Lowered plasma glucose enhances systemic insulin sensitivity. The concerted down-regulation of insulin signaling pathway by HFD and opposing upregulation by UP780 strongly pointed to a reversal of insulin-resistance as an important mechanism underlying the UP780 normalization of glycemic control and insulin sensitivity.

Two more categories in WAT gene list were regulated similarly to the insulin receptor pathway: those involved in metabolism and nuclear receptor/co-activator/co-repressor. Again, multiple gene expression variations were

confirmed by QPCR (**Table 2**). Of note was adiponectin (ADIPOQ) gene expression, reduced by HFD and restored to control level by UP780 (**Table 2** QPCR).

HFD is also known to induce adipose tissue inflammation and secretion of inflammatory cytokines such as TNF- α [29]. Many inflammatory genes were among the highest of up-regulated genes by HFD, with UP780 reducing these gene expressions (**Table 2**). Similarly, many genes in the cell cycle pathway were up-regulated by HFD and decreased by UP780 (**Table 2**).

3.2. Functional Validation

Quantification at mRNA levels, although powerful in generating a global pattern of UP780 mechanism of action, is limited in depicting protein levels. Western blotting therefore was used to validate at the protein level for liver FASN (**Figure 2(a)**, upper). After normalization with β -actin loading control (**Figure 2(a)**, lower) to lean control = 1, HFD decreased FASN to 0.7, UP780 further decreased FASN to 0.5, and GW1929 to 0.6. Therefore liver FASN protein levels by Western blot correlated to microarray and QPCR data (**Table 1** and **Figure 2(a)**).

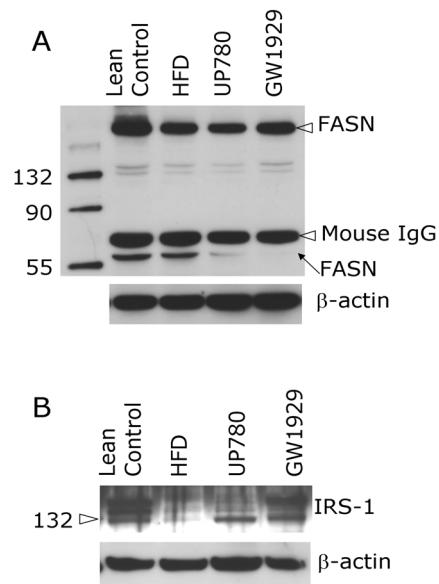


Figure 2. Western blotting for protein expression levels modified by UP780. (A) Liver proteins were probed with a mouse monoclonal anti-FASN antibody. A fulllength 270 kD FASN and a smaller 60 kD degradation fragment were reproducible in Western blots. The blot was re-probed with anti- α -actin antibody for protein loading control. (B) WAT Western blot was probed for IRS-1 protein levels and re-probed for α -actin loading control. Three protein bands 132 kD and up were reproducibly observed. Positions of molecular weight markers are either shown in A or marked in B at the left.

For WAT, IRS-1 protein level in the insulin signaling pathway was validated by Western blot (**Figure 2(b)**). IRS-1 proteins were dramatically decreased by HFD, much more than the 42% reduction by QPCR (**Figure 2(b)** and **Table 2**). UP780 restored some of the IRS-1 proteins (**Figure 2(b)**, upper). Quantification was not attempted even though β -actin loading control was available (**Figure 2(b)**, lower) due to background interference.

Liver triglyceride and cholesterol levels were measured from liver lipid extracts to validate the UP780 mechanism of action. HFD increased liver triglyceride level 12-fold above lean control. UP780 treatment decreased liver triglyceride level to 60% of HFD (**Figure 3(a)**) with statistical significance of $P = 0.029$ by T-test. Liver cholesterol levels were not dramatically changed by HFD over lean control. HFD increased liver cholesterol 25% over lean control. In correlation to microarray pathway analysis, UP780 decreased liver cholesterol to 65% of HFD with statistical significance of $P = 0.016$ by T-test (**Figure 3(b)**).

Morphology of hepatosteatosis was examined (**Figure 4**). In lean control liver, lipid droplet was not visible. Vast amount of lipid droplets (black arrowheads) were observed in HFD liver sections. The liver functional unit of liver parenchyma is centered around the central vein (indicated in **Figure 4**) with nutrient supply from hepatic artery and portal vein reaching first to the hepatocytes distal from the central vein [30]. It was clear from **Figure 4** that in HFD liver more lipid droplets and ballooning were observed in hepatocytes distal from central vein than proximal. Lipid droplets disappeared almost completely in the UP780-treated livers. When observed, the number of lipid droplets per cell in UP780 livers was much lower than HFD. Lymphocytes (white arrowhead) infiltration into liver was observed in HFD liver, not in lean control liver, and infrequently in UP780 liver (not shown).

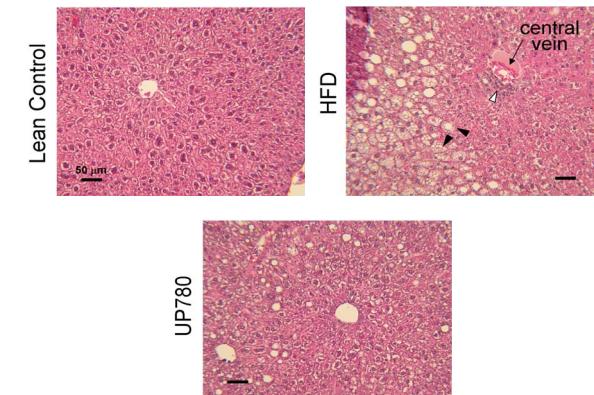


Figure 4. Liver steatosis. Formalin-fixed liver thin sections were stained with hematoxylin-eosin. Liver steatosis analyses were done for individual animals for each treatment group. Representative photomicrographs were shown. Black arrowheads, lipid droplets and ballooning. White arrowhead, inflammation. Central vein was indicated on the HFD liver, and existed in lean control and UP780 liver sections. Scale bars, 50 μ m.

infiltration into liver was observed in HFD liver, not in lean control liver, and infrequently in UP780 liver (not shown).

Improvement of insulin sensitivity should be accompanied by decreased fasting plasma insulin levels; therefore fasting plasma insulin levels were measured for baseline, week-7 and week-10. In **Figure 5**, data were plotted by individual animals within the treatment groups. Lean control fasting plasma insulin levels were similarly low at baseline, week-7, and week-10. For HFD, week-7 showed higher fasting plasma insulin levels, but by week-10, two animals showed decreased fasting plasma insulin levels. After 18 weeks of high fat feeding, these two animals probably developed pancreatic islet degeneration. GW1929 was as expected. For the UP780 group, plasma insulin levels were decreased by week-7, and trended to decrease further at week-10 (**Figure 5**). Two-way ANOVA statistical analysis indicated that UP780 significantly decreased fasting plasma insulin compared to HFD, with $P = 0.05$, and GW1929 with $P = 4.67E-6$.

4. DISCUSSION

Microarray pathway analysis and validation indicated the mechanism of the UP780 effects in increasing insulin sensitivity and decreasing plasma glucose [18] by decreasing liver fatty acid and triglyceride biosynthesis, increasing liver mitochondria fatty acid α -oxidation (possibly), and increasing WAT insulin signaling pathway (therefore increasing insulin sensitivity).

UP780 was discovered by high throughput screening of differentiated 3T3-L1 adipocytes that identified botanic substances capable of increasing adiponectin secretion [18]. Adiponectin together with leptin, another adi-

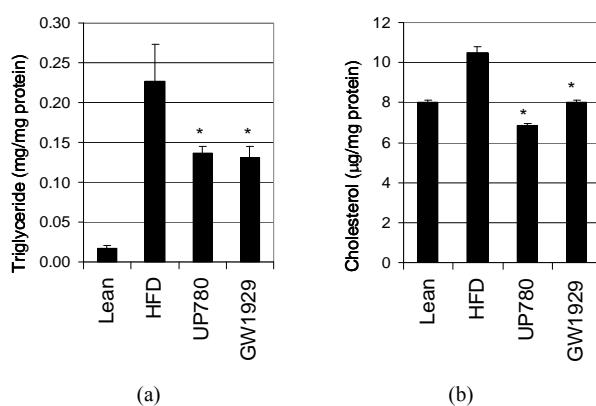


Figure 3. UP780 decreased liver triglyceride and cholesterol over HFD. Total lipids extracted from liver were used for (a) triglyceride and (b) cholesterol assays. Liver triglyceride and liver cholesterol were assayed in replicates and in dilutions, and independently multiple times. Representative assays were displayed. *indicated T-test P value < 0.05 compared to HFD.

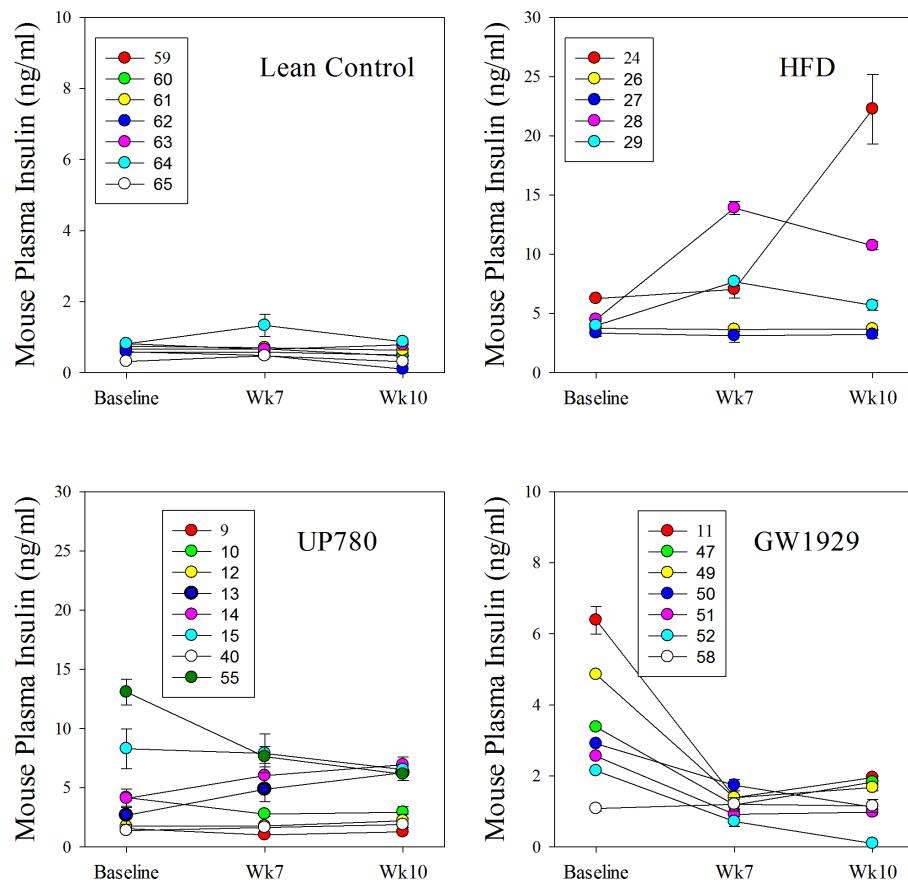


Figure 5. Fasting plasma insulin. Plasma insulin levels were plotted by individual animals per treatment groups of week-0, week-7 and week-10 plasma samples, using SigmaPlot. The animal numbers indicated were from experimental assignments. The treatment groups of lean control, HFD, UP780, and GW1929 were indicated in the plots. Each plasma sample was assayed in dilutions and in duplicates, and sometimes in repeats, therefore each data point contained >2 individual measurements. Statistical analysis was by 2-way ANOVA comparing UP780/GW groups to HFD group, with *indicate $P \leq 0.05$ and **indicated $P \leq 0.01$.

pokine, in an insulin-resistant lipoatrophic mouse model completely reversed insulin resistance, but only partially by adiponectin or leptin alone [31]. In obese and diabetic rodents and humans, adiponectin levels were decreased, which were reversed with weight loss and diabetic treatments [31]. Adiponectin, together with adiponectin receptors AdipoR1 and AdipoR2, sensitizes tissues to insulin through regulation of glucose and fatty acid metabolism, activation of AMP-activated protein kinase (AMPK), activation of PPAR α signaling pathway, and conversion of the toxic ceramide to beneficial sphingosine through a ceramidase domain in AdipoR1/2 [32, 33]. This UP780 nutrigenomic study was successful in demonstrating decreased liver fatty acid biosynthesis and increased WAT insulin sensitivity, in line with adiponectin mechanism. Activation of AMPK by aloe, furthermore, was demonstrated by western blots of AMPK phosphorylation in WAT of DIO model [34]. Increased adiponectin gene expression in WAT by UP780 (**Table 2**)

correlated with its discovery by screening.

Multiple animal/human studies agreed on the hypoglycemic effect of aloe [5, 13-17, 19, 35-39] but not the lipid-lowering effects. A double-blind, placebo-controlled pilot clinic trial by Devaraj *et al.* showed significant cholesterol/LDL reduction by Qmatrix® but not triglyceride, while UP780 caused no change to either blood triglyceride or cholesterol level [19]. Clinic trial by Hu-seini *et al.* claimed that aloe gel reduced both blood cholesterol and triglyceride, but the conclusion should be dismissed due to faulty statistical data analysis [38]. Clinic trial by Yagi *et al.* showed reduced blood triglyceride, but not cholesterol, by a high molecular weight fraction of *Aloe vera* gel. The Yagi study was not blinded and was without placebo control [39]. The Yongchai-yudha *et al.*/Bunyapraphatsara *et al.* clinic studies of *Aloe vera* juice also showed reduced blood triglyceride, but not cholesterol; the studies were single-blinded and placebo-controlled [36, 37].

In UP780 DIO studies [18], blood triglyceride levels could be significantly reduced in one experiment but not another, including the experiment that livers were collected for triglyceride and cholesterol assays (**Figure 3**) and for liver steatosis photomicrography (**Figure 4**). Such was the variation observed for animal DIO model where diet was strictly controlled. Fasting blood triglyceride and cholesterol levels are influenced by diet and additional environmental factors, which is difficult to control in clinic trials. Compounded with the variations in aloe preparations and the human genomes, modification of *Aloe vera* gel to blood lipid levels may have too much variation to be detected reliably. Perhaps, future clinic studies of *Aloe vera* gel effect to liver steatosis will achieve more uniform results.

5. ACKNOWLEDGEMENTS

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SUPPLEMENTAL MATERIALS

1. MATERIALS AND METHODS

1.1. Tissue Collection from Dio Mouse Model

DIO mice were as described in the companion paper [1]. Lean, HFD, UP780, and GW1929 fasting blood samples were taken before treatment (baseline), during treatment (7 weeks), and at the time of euthanasia (10 weeks). Mice were anesthetized with CO₂; liver and visceral WAT tissues were collected within 5 minutes of euthanasia. For RNA isolation, 5 mm tissue strips were preserved in RNAlater (Ambion). For Western blots, triglyceride and cholesterol assays, tissues were snap frozen in liquid nitrogen and stored at -80°C. For histology, one lobe of the livers were fixed in 10% formalin/phosphate buffered saline (SIGMA) and stored at 4°C. Fixed livers were thin sectioned and stained with hematoxylin-eosin for microscopic observations.

1.2. RNA Extraction

For total RNA extraction, RNEasy kit was used for total liver RNA extraction, and RNEasy for Fatty Tissue kit was used for WAT RNA extraction (Qiagen). RNA qualities were determined with glyoxal agarose gel electrophoresis (Ambion). When genomic DNA was observed, a second extraction was carried out.

1.3. Microarray

Affymetrix mouse genome 430 2.0 array was used for

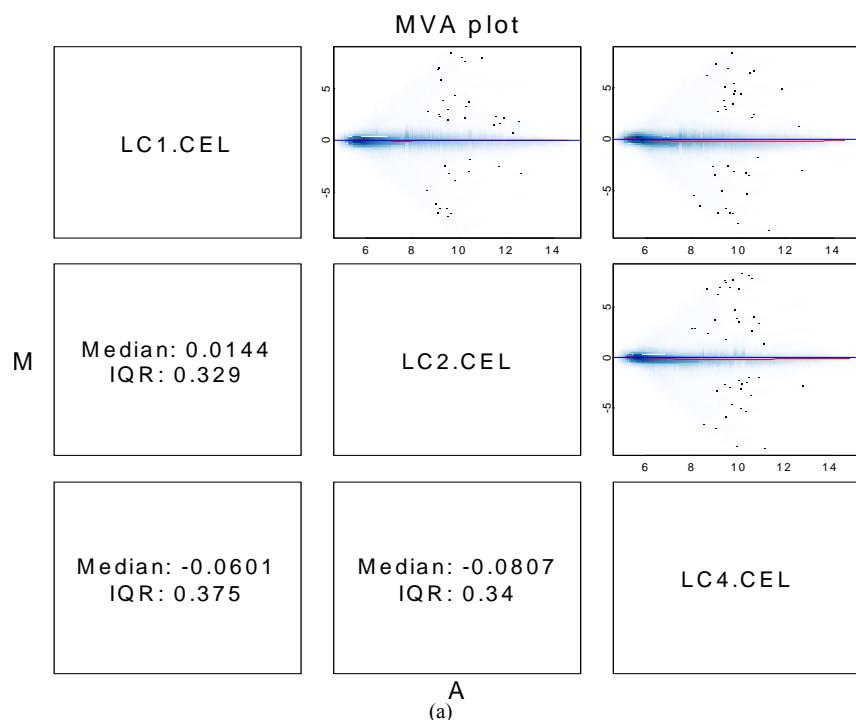
microarray analysis of liver and WAT gene expression. Microarray procedures followed the standard protocol of Affymetrix GeneChip one-cycle target preparation [2]. The mouse samples were coded LC, LV, and LUP for livers of lean-control, HFD, and UP780, respectively, and FC, FV, and FUP for WAT. Three mice per treatment group, 3 treatment groups, and 2 tissues, in total 18 microarray chips were used. All microarray datasets passed quality controls, including GCOS [3] and Bioconductor package affy [4] (**Supplement Figures 1 and 2**). Details of microarray data analysis followed published procedures [5,6].

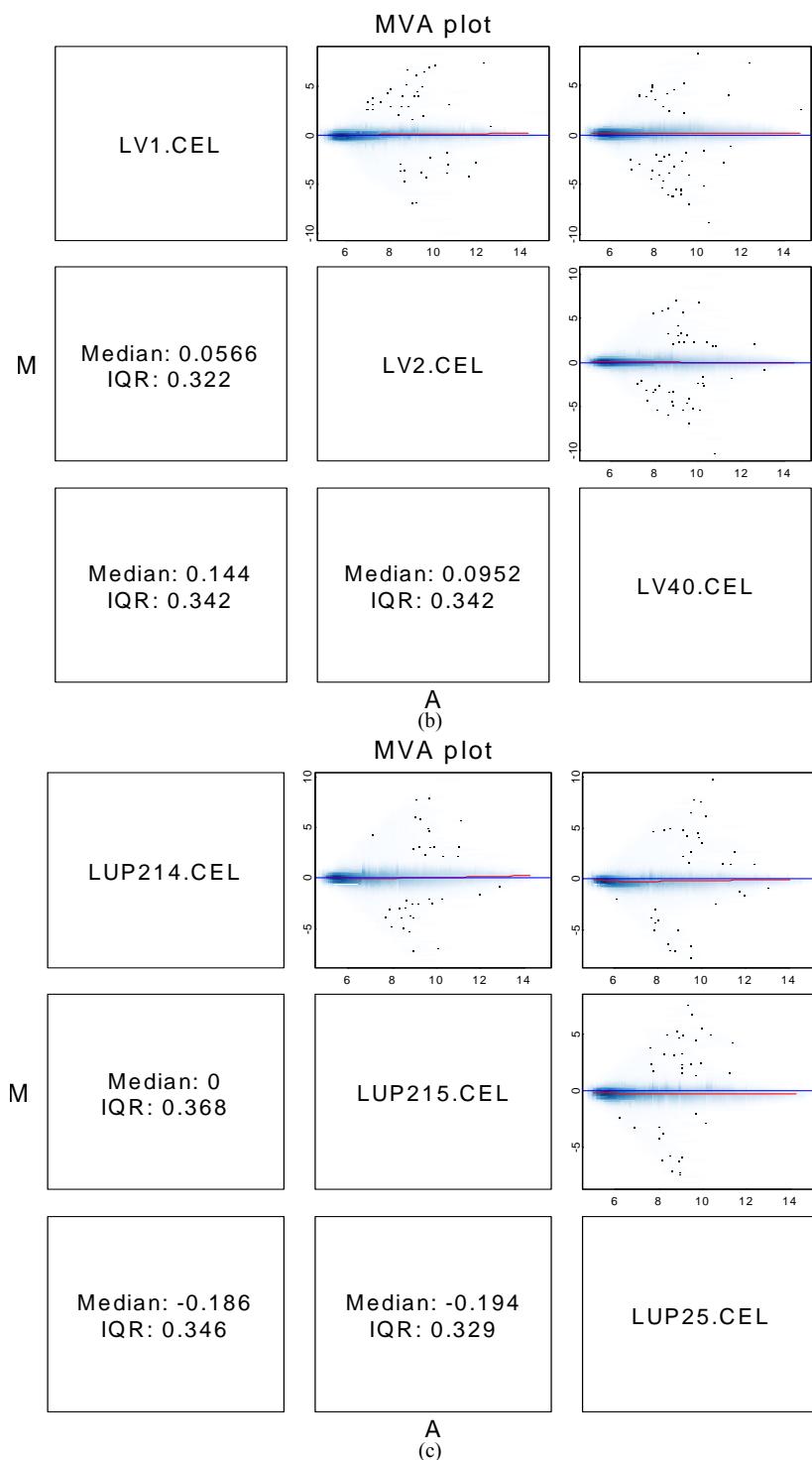
1.4. Pathway Analysis

Analysis of microarray data, in the range of 45,000 probe sets, benefited greatly from the Ingenuity pathway analysis (IPA) software to develop a sense of the biological significance. The microarray analysis results by Bioconductor of eBayes-adjusted p-values, log₂ fold changes, and log₂ expression values were uploaded into the IPA server. Cutoff criteria of $p \leq 0.05$, log₂ fold change ≥ 0.8 , and log₂ intensity ≥ 3.5 were applied. Furthermore, due to multiple probe sets per gene minimal p-value was set to resolve among multiple probe sets. IPA results of canonical pathways were further analyzed in detail. Information of gene functions were from IPA and OMIM databases [7,8].

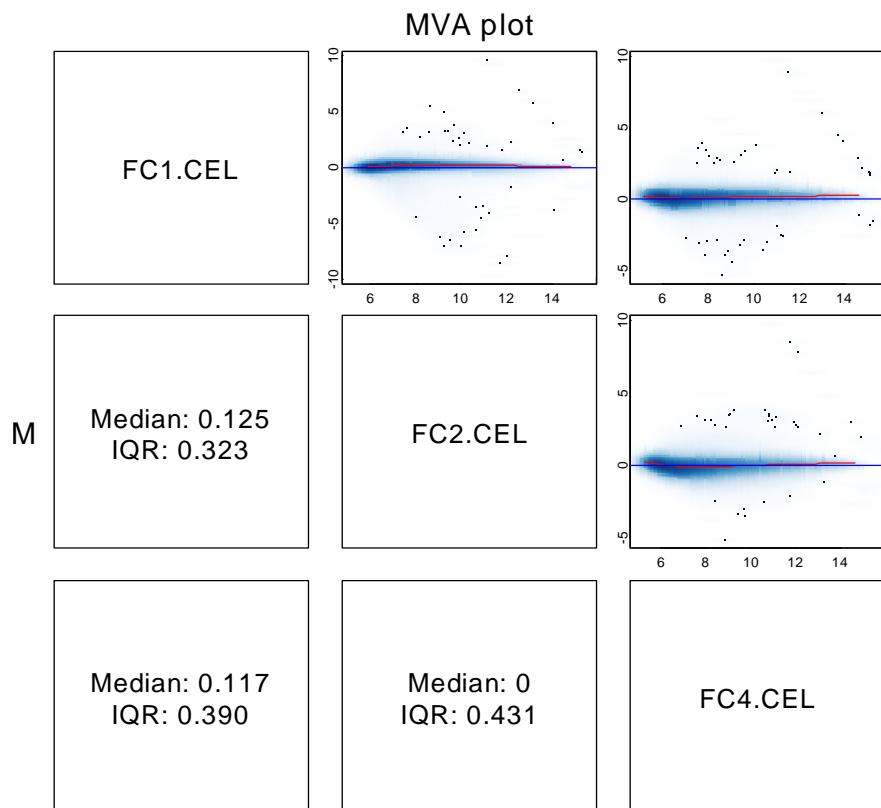
1.5. Real-Time QPCR

Total RNAs in excess of the needs for microarray were

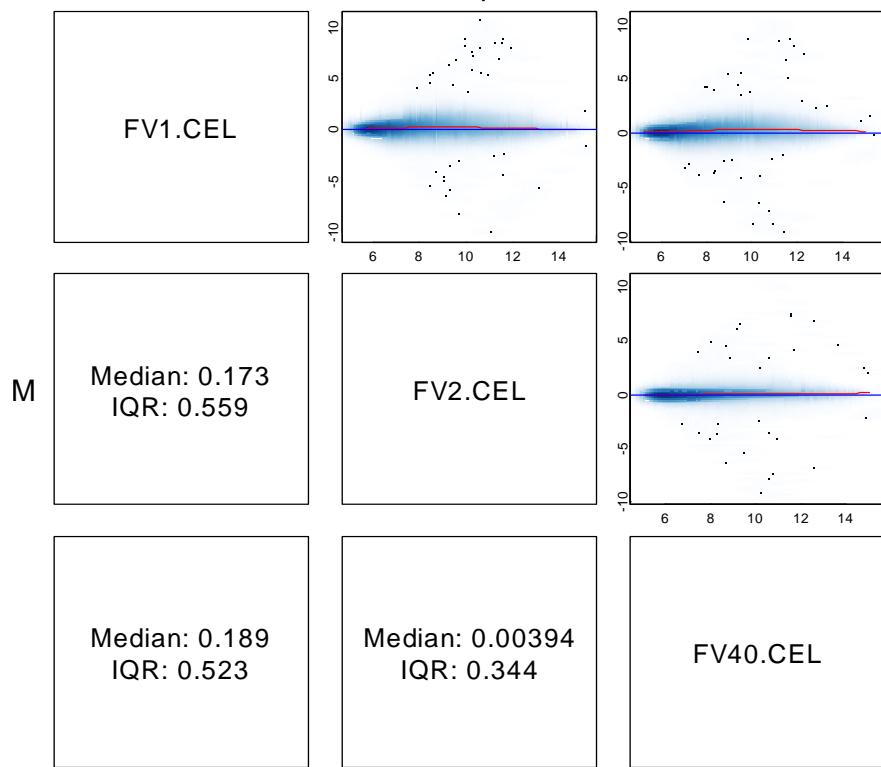




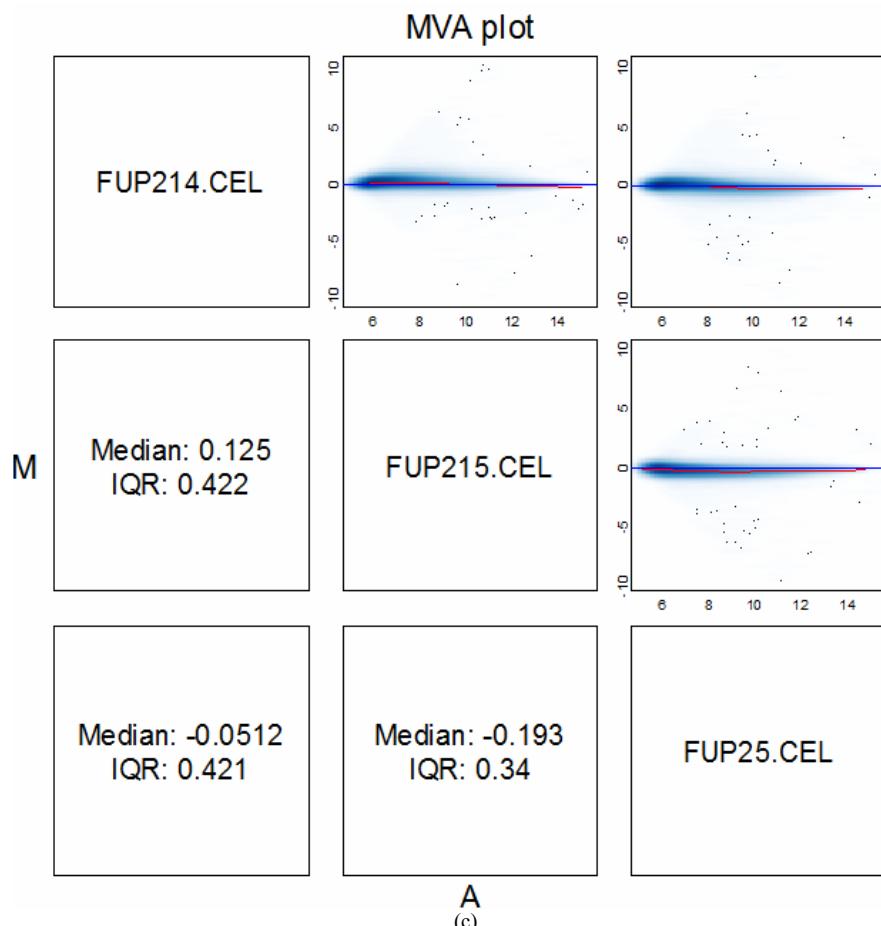
Supplement Figure 1. Microarray data quality control plots for the nine liver microarray chips. Probe level data/object (before gcrma, affy preprocessing of background subtraction, normalization, and summarization of intensities) from the Bioconductor affy package was used for quality control plots. MVA plots were used for assessing the three biological replicates each for A. lean control (LC1, LC2, and LC4), B. HFD (LV1, LV2, and LV40), and C. HFD + UP780 (LUP25, LUP214, and LUP215) chips. The MVA plots of all pairwise comparisons were particularly useful in diagnosing problems in replicate sets of arrays. The plots indicated tight correlation among the replicate sets of arrays. Based on these quality control plots, the nine liver microarray chips were judged to be of good quality.



A
(a)
MVA plot



A
(b)



Supplement Figure 2. Microarray data quality control plots for the nine WAT microarray chips. Probe level data/object from affy package (before germa preprocessing of background subtraction, normalization, and summarization of intensities), the Bioconductor affy package was used for quality control plots. MVA plots were used for assessing the three biological replicates each for A. lean control (FC1, FC2, and FC4), B. HFD (FV1, FV2, and FV40), and C. HFD + UP780 (FUP25, FUP214, and FUP215) chips. The MVA plots of all pairwise comparisons were particularly useful in diagnosing problems in replicate sets of arrays. The plots indicated tight correlation among the replicate sets of arrays. Based on these quality control plots, the nine WAT microarray chips were judged to be of good quality.

combined for QPCR. Superscript III reverse transcriptase (Invitrogen) was used for cDNA synthesis. The ABI TaqMan Gene Expression assays for the selected genes were confirmed by RefSeq accession numbers before use, to ensure the sequences used by the Affymetrix mouse genome 430 2.0 array and the ABI TaqMan Gene Expression assays were compatible. Thermal cycling and fluorescence detection was performed by an ABI 7700 Sequence Detector. The relative quantification method of $\Delta\Delta CT$ was used for data analysis. Most QPCR runs were multiplex reactions and each plate contained at least one control cDNA (the lean control) and each well contained the GAPDH internal control. Singleplex QPCR was used for abundant transcripts such as adiponectin with GAPDH

controls in separate wells. QPCR reactions were run in triplicates and results expressed as mean \pm S.D.

1.6. Western Blot

Mouse liver and WAT were homogenized in RIPA buffer (50 mM Tris.HCl pH 7.4, 150 mM NaCl, 1% Triton X-100, 0.25% deoxycholate, supplemented with a protease inhibitor cocktail (Roche) and a phosphatase inhibitor cocktail (Pierce)) and debris removed by centrifugation at 5000 g for 5 min. Protein concentrations were determined by BCA protein assay (Pierce). Twenty five μ g of liver proteins and 50 μ g of WAT proteins were used per lane for 4% - 12% Bis-Tris gel electrophoresis (Invitrogen). The proteins were electroporated onto PVDF

membranes and immunoblotted: mouse monoclonal antibody specific for fatty acid synthase (FASN) at 1:1000 dilution, rabbit polyclonal antibody specific for insulin receptor substrate-1 (IRS-1) at 1:200 dilution, and secondary HRP-conjugated antibodies at 1:3000 dilution for anti-mouse IgG and 1:5000 dilution for anti-rabbit IgG (Santa Cruz); detected with ECL-Plus chemiluminescence solution and ECL film (GE Healthcare). For quantification, ECL films were scanned and the band intensities analyzed with NIH ImageJ software.

1.7. Liver Triglyceride and Cholesterol Assays

Liver homogenates and protein BCA assay were as described for Western blot. Liver homogenates were mixed with two volumes of methanol and chloroform (1:3, by volume) and shook vigorously for 10 minutes, then centrifuged for 15 minutes at 14,000 rpm. The organic layers were transferred to clean tubes. Extraction was repeated and the two organic fractions combined. The organic fractions were dried under N₂ gas, then resuspended in ethanol. The extracted lipids were assayed in duplicate using triglyceride assay kits (Cayman Chemicals and Sigma-Aldrich) and a cholesterol assay kit (Cayman Chemicals). Each assay plate included a standard curve (Cayman Chemicals). Several dilutions for each sample were tested. The total liver triglyceride and cholesterol concentrations were normalized by protein concentrations in the initial liver homogenates, and expressed as mean ± S.D. Statistical analysis used T-test.

1.8. Insulin ELISA Assay

Plasma samples collected at baseline, week-7 and week-10 of treatments were used for mouse insulin ELISA (Crystal Chem). A standard curve was included in every assay plate and all samples were assayed in duplicates. For assay results that fell outside the range of the standard curves, ELISA assays were repeated with dilutions. SigmaPlot was used for standard curve-fitting (logistic 4-parameter) and X-Y conversion. Results were expressed as mean ± S.D. Statistical analysis used 2-way ANOVA (SigmaStat).

2. RESULTS AND DISCUSSIONS

2.1. Microarray Data Analysis

The nine-chip datasets from tissue samples (liver or WAT) were read-in together using the Bioconductor affy package [5] as one object, so that the subsequent preprocessing steps could be conducted as one experiment. The pre-processing steps of background correction, normalization, and summarization of the expression values were carried out using the gcrma package, taking advantage of the

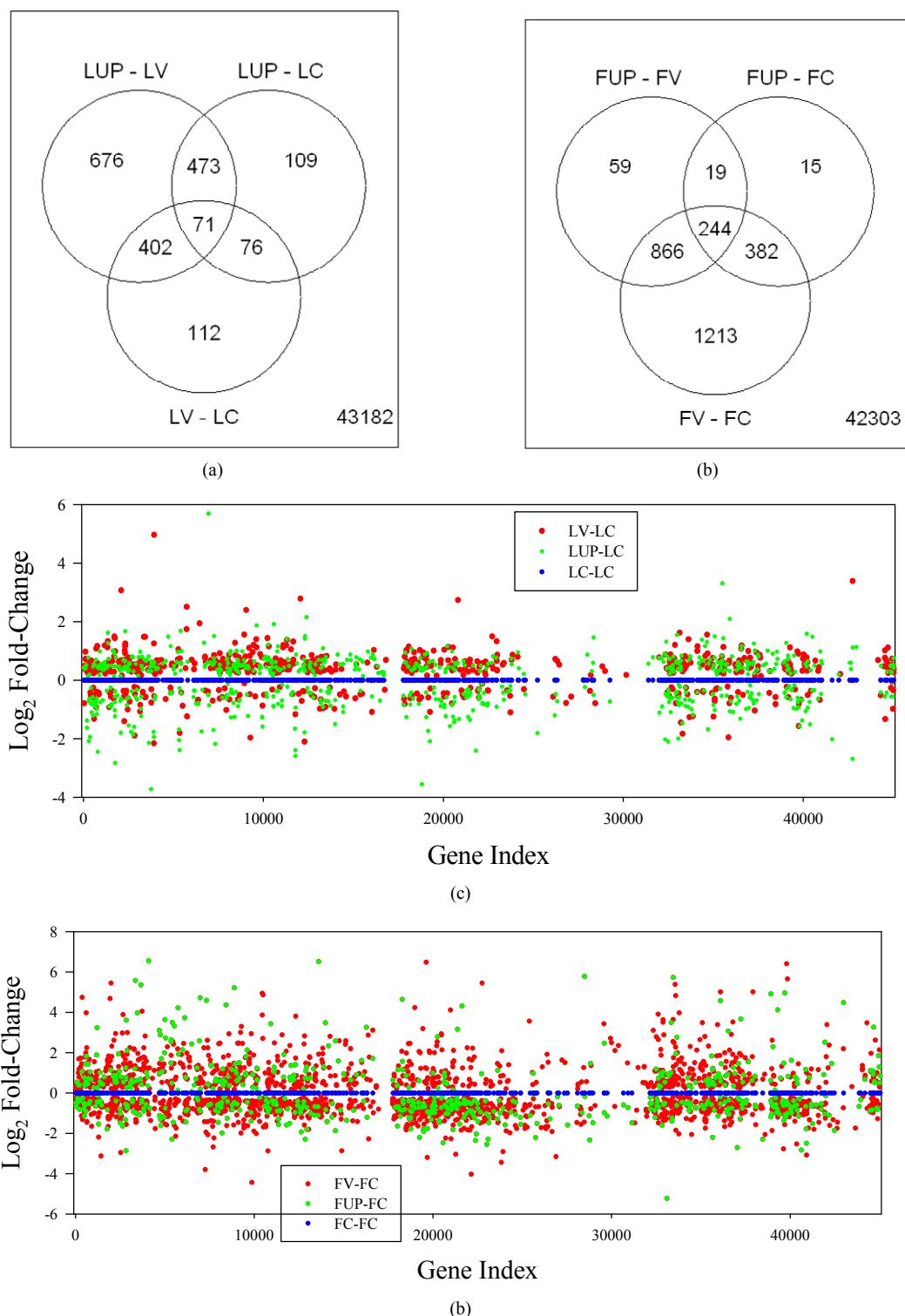
background adjustment feature with probe GC-content sequence information [9]. The expression values generated by gcrma were summarized as log2 transformed expression values. Statistical analyses for differential expressions by Student's T-test were calculated by using the linear model as implemented in the limma package [6]. Three contrasts, HFD + UP780 vs. HFD, HFD + UP780 vs. lean control, and HFD vs. lean control, were computed using the lmfit function, followed by the eBayes function to adjust the standard errors of the log2-fold changes for the 3 contrasts, or false discovery rate (FDR) [6]. The analysis results of adjusted p-values, log2 fold changes, and log2 expression values were uploaded to the Ingenuity IPA [8] website for pathway analysis.

Global views of gene expression variations influenced by HFD and by UP780 on top of HFD were extracted from the results of limma linear model fits [6]. In **Supplement Figures 3(a) and (b)**, Venn diagrams show the number of significant gene expression variations scored by limma and the number of overlapping genes shared by the comparisons between lean control (LC and FC), HFD (LV and FV), and HFD+UP780 (LUP and FUP). The distributions of up- or down-regulations are plotted in **Supplement Figure 3(c)** for liver and **Supplement Figure 3(d)** for WAT. Among the 729 LUP-LC significant genes, 425 were up-regulated and 304 were down regulated. Among the 661 LV-LC significant genes, 486 were up-regulated and 175 were down regulated (**Supplement Figure 3(c)**). Apparently in liver, HFD tends to induce gene expression levels and UP780 tends to reduce gene expression levels. This trend became clear when individual genes in significant metabolic and signaling pathways were examined (**Table 1** and **Supplement Tables 1 and 2**).

From WAT far more genes were scored significant, and had larger fold-changes as compared to liver (**Supplement Figure 3(c) and (d)**). Among the 660 FUP-FC significant genes, 278 were up-regulated and 382 were down-regulated. Among the 2705 significant FV-FC genes, 1025 were up-regulated and 1680 were down-regulated (**Supplement Figure 3(d)**). The large gene number difference between FUP-FC and FV-FC suggested that in WAT, HFD caused wide-spread and strong gene expression regulations, and UP780 treatment decreased globally these gene expression regulations to be closer to the lean control.

2.2. IPA Pathway Analysis

The pathways were ranked by right-tailed Fisher's exact test for the significance of changes between two contrasts, taken into consideration 1) the number of genes that passed the cutoff and were also in the pathway, 2)



Supplement Figure 3. Gene Expression variations by linear model fit. Significant gene expression variations were data exported from limma linear model fit. Venn diagrams show the numbers of genes with differential expression from the three comparisons and the gene numbers of overlapping distribution between and among the three comparisons, A liver, B WAT. The differentially expressed genes in individual comparisons of Venn diagrams were plotted to show the distribution of up- or down-regulated genes influenced by HFD and by HFD + UP780, using the lean controls as the baseline, C liver, D WAT. Gene index was numbered according to the gene-ID list of the Affymetrix mouse genome 430.2 chip.

Supplement Table 1.

Name	Description	RefSeq ID	LUP/LV			LUP/LC			LV/LC		
			p-value	Log ₂ Ratio	Intensity	p-value	Log ₂ Ratio	Intensity	p-value	Log ₂ Ratio	Intensity
Pyruvate Metabolism											
ACACB	acetyl-Coenzyme A carboxylase beta	NM_133904	0.01	-1.641	5.459	0.015	-1.498	6.957	0.762	0.143	7.1
ACAT2	acetyl-Coenzyme A acetyltransferase 2 acyl-CoA	NM_009338	0.035	-0.586	10.935	0.005	-0.927	11.862	0.117	0.152	12.068
ACSL3	acyl-CoA synthetase long-chain family member 3 acyl-CoA synthetase	NM_001033606	0.011	-0.825	7.664	0.064	-0.519	8.184	0.233	0.305	8.489
ACSS2	short-chain family member 2 acylphosphatase 1, erythrocyte (common) type	NM_019811	0.313	-0.529	11.218	0.02	-1.499	12.717	0.054	-1.03	11.548
ACYP1	aldo-keto reductase family 1, member B1 (aldose reductase)	NM_025421	0.004	1.214	7.721	0.013	0.937	6.784	0.234	-0.386	7.339
AKR1B1	aldehyde dehydrogenase 1 family, member B1	NM_009658	0.002	0.852	7.936	0.026	0.472	7.464	0.018	-0.587	5.291
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
DLAT	dihydrolipoamide S-acetyltransferase	NM_145614	0.003	-0.895	8.757	0.003	-0.903	9.66	0.803	0.084	7.625
ME1	NADP(+) -dependent, cytosolic nudix (nucleoside diphosphate linked moiety X)-type motif 7	NM_008615	0.012	-1.137	11.44	0.017	-1.058	12.499	0.7	-0.172	11.28
NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	NM_024437	0.001	1.083	14.423	0.028	0.565	13.857	0.039	-0.518	13.34
PC	pyruvate carboxylase	NM_008797	0.011	-0.632	11.029	0.043	0.45	10.579	0.001	1.081	11.66
PKLR	pyruvate kinase, liver and RBC	NM_001099779	0.006	-1.179	9.396	0.142	-0.626	8.63	0.049	0.7	10.574
Glycolysis/Gluconeogenesis											
ACSL3	acyl-CoA synthetase long-chain family member 3	NM_001033606	0.011	-0.825	7.664	0.064	-0.519	8.184	0.233	0.305	8.489
ACSS2	acyl-CoA synthetase short-chain family member 2	NM_019811	0.313	-0.529	11.218	0.02	-1.499	12.717	0.054	-1.03	11.548
ACYP1	acylphosphatase 1, erythrocyte (common) type	NM_025421	0.004	1.214	7.721	0.013	0.937	6.784	0.234	-0.386	7.339
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
ALDOC	aldolase C, fructose-bisphosphate 2,3-bisphosphoglycerate mutase	NM_009657	0.544	0.214	8.518	0.066	-0.744	9.262	0.027	-0.958	8.304
BPGM	2,3-bisphosphoglycerate mutase	NM_007563	0.004	-1.09	7.804	0.001	-1.632	9.436	0.072	-0.542	8.894
DLAT	dihydrolipoamide S-acetyltransferase	NM_145614	0.003	-0.895	8.757	0.003	-0.903	9.66	0.803	0.084	7.625
G6PC	glucose-6-phosphatase, catalytic subunit	NM_008061	0.098	-0.641	12.013	0.641	0.161	11.851	0.049	0.803	12.654

Continued

GCK	glucokinase (hexokinase 4)	NM_010292	0.008	-1.193	8.679	0.511	0.182	8.288	0.007	1.03	9.318
GPI	glucose phosphate isomerase	NM_008155	0.001	-0.85	11.57	0.224	-0.209	11.779	0.005	0.642	12.42
HK1	hexokinase 1	NM_010438	0	-1.348	3.313	0.006	-0.826	4.139	0.015	-0.475	12.23
PFKL	phosphofructokinase, liver	NM_008826	0.024	-0.734	8.904	0.205	0.363	7.152	0.006	1.005	9.638
PGM1	phosphoglucomutase 1	NM_025700	0.003	-0.889	10.729	0.142	-0.326	11.054	0.026	0.564	11.618
PGM3	phosphoglucomutase 3	NM_028352	0.271	-0.381	6.948	0.038	0.827	6.122	0.008	1.208	7.329
PKLR	pyruvate kinase, liver and RBC	NM_001099779	0.006	-1.179	9.396	0.142	-0.626	8.63	0.049	0.7	10.574
Fatty Acid Biosynthesis											
ACACB	acetyl-Coenzyme A carboxylase beta	NM_133904	0.01	-1.641	5.459	0.015	-1.498	6.957	0.762	0.143	7.1
ACSL3	acyl-CoA synthetase long-chain family member 3	NM_001033606	0.011	-0.825	7.664	0.064	-0.519	8.184	0.233	0.305	8.489
FASN	fatty acid synthase	NM_007988	0.002	-1.961	11.054	0.012	-1.338	12.392	0.154	0.623	13.015
Androgen/Estrogen Metabolism											
ARSA	arylsulfatase A	NM_009713	0.038	-0.805	8.473	0.053	-0.735	9.208	0.827	0.07	9.279
ARSB	arylsulfatase B	NM_009712	0.006	-1.032	7.29	0.073	-0.555	7.845	0.112	0.477	8.322
ARSG	arylsulfatase G	NM_028710	0.908	-0.019	8.523	0	1.165	7.359	0	1.184	8.542
CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	NM_007825	0.005	1.464	12.838	0.013	1.203	11.635	0.404	-0.286	12.756
HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	NM_008292	0.007	-0.66	12.308	0.41	0.149	12.159	0.003	0.809	12.968
HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	NM_010476	0.041	-0.668	7.674	0.018	-0.827	8.501	0.555	-0.152	10.318
STS	steroid sulfatase (microsomal), isozyme S	NM_009293	0.016	-0.995	7.962	0.175	-0.466	8.428	0.13	0.53	8.957
SULF2	sulfatase 2	NM_028072	0.023	-1.178	3.59	0.126	-0.497	6.836	0.058	0.912	4.768
UGT2B10	UDP glucuronosyltransferase 2 family, polypeptide B10	NM_053215	0.024	1.63	4.538	0.104	1.041	3.497	0.322	-0.589	2.908
UGT2B17	UDP glucuronosyltransferase 2 family, polypeptide B17	NM_133894	0.007	3.388	8.373	0.107	1.639	6.734	0.075	-0.247	13.76
Pentose Phosphate Shunt											
ALDOC	aldolase C, fructose-bisphosphate	NM_009657	0.544	0.214	8.518	0.066	-0.744	9.262	0.027	-0.958	8.304
GPI	glucose phosphate isomerase	NM_008155	0.001	-0.85	11.57	0.224	-0.209	11.779	0.005	0.642	12.42
PFKL	phosphofructokinase, liver	NM_008826	0.024	-0.734	8.904	0.205	0.363	7.152	0.006	1.005	9.638
PGD	phosphogluconate dehydrogenase	NM_001081274	0.026	-1.181	7.348	0.114	-0.745	8.093	0.147	0.549	8.851
PGM1	phosphoglucomutase 1	NM_025700	0.003	-0.889	10.729	0.142	-0.326	11.054	0.026	0.564	11.618
PGM3	phosphoglucomutase 3	NM_028352	0.271	-0.381	6.948	0.038	0.827	6.122	0.008	1.208	7.329
RPIA	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)	NM_009075	0.004	-1.074	5.833	0.045	-0.6	6.433	0.094	0.474	6.907
TKT	transketolase (Wernicke-Korsakoff syndrome)	NM_009388	0.001	-1.35	8.781	0.012	-0.852	9.633	0.06	0.537	11.842
Glycerophospholipid Metabolism											
AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	NM_053014	0.004	-1.809	7.367	0.159	-0.655	8.022	0.005	0.633	10.017
CHKA	choline kinase alpha	NM_001025566	0.036	-0.578	2.754	0.298	0.287	7.425	0.017	0.812	8.237

Continued

GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	NM_008149	0.013	-1.213	11.802	0.05	-0.862	12.663	0.36	0.351	13.015
GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	NM_010271	0.003	-0.861	10.337	0.258	-0.227	10.565	0.012	0.634	11.199
GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	NM_010274	0.004	-0.871	8.968	0.254	-0.011	2.295	0.002	0.989	9.839
GRN	granulin	NM_008175	0.014	-0.862	10.889	0.094	-0.501	11.391	0.11	0.493	10.695
LIPG	lipase, endothelial	NM_010720	0.075	-0.718	3.694	0.193	0.422	5.104	0.012	1.016	6.12
MGLL	monoglyceride lipase	NM_011844	0.003	-0.801	11.244	0.112	0.317	10.927	0.001	1.118	12.045
PCYT1A	phosphate cytidylyltransferase 1, choline, alpha	NM_009981	0.001	-1.323	6.718	0.007	-0.806	7.524	0.043	0.517	8.041
PIGF	phosphatidylinositol glycan anchor biosynthesis, class F	NM_008838	0.001	1.213	7.798	0.011	0.726	7.072	0.052	-0.488	6.585
PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	NM_008869	0.004	1.111	5.765	0.013	0.879	4.886	0.396	-0.232	4.654
PPAP2B	phosphatidic acid phosphatase type 2B	NM_080555	0.014	-0.831	10.244	0.057	-0.573	10.817	0.305	0.181	11.441
Xenobiotic Metabolism by P450											
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	NM_007812	0.503	-0.321	11.504	0.02	-1.399	12.903	0.052	-1.078	11.825
CYP2B6 (includes EG:1555)	cytochrome P450, family 2, subfamily B, polypeptide 6	NM_009998	0.026	-0.948	2.434	0.002	-1.753	4.175	0.044	-0.546	2.408
CYP2B9	cytochrome P450, family 2, subfamily b, polypeptide 9	NM_010000	0.001	-5.322	2.896	0.684	-0.354	3.249	0.001	4.969	8.218
CYP2C38	cytochrome P450, family 2, subfamily c, polypeptide 38	NM_010002	0.001	-2.033	7.649	0.015	-1.247	8.896	0.079	0.786	9.682
CYP2C54	cytochrome P450, family 2, subfamily c, polypeptide 54	NM_206537	0.019	0.494	13.689	0.088	-0.32	14.01	0.002	-0.815	13.195
CYP2C55	cytochrome P450, family 2, subfamily c, polypeptide 55	NM_028089	0.479	0.214	6.431	0	-1.945	8.376	0	-2.158	6.217
CYP2D13	cytochrome P450, family 2, subfamily d, polypeptide 13	NR_003552	0.005	0.973	6.427	0.044	0.582	5.845	0.141	-0.391	5.454
CYP2G1P	cytochrome P450, family 2, subfamily G, polypeptide 1 pseudogene	NM_013809	0.874	0.037	3.222	0.002	-1.19	4.411	0.001	-1.227	3.185
GSTA4	glutathione S-transferase A4	NM_010357	0.417	0.149	10.43	0.003	-0.779	11.209	0.001	-0.928	10.281
GSTA5	glutathione S-transferase A5	NM_008181	0.133	-1.013	7.634	0.001	-2.393	10.925	0.004	-1.8	9.126
GSTM1 (includes EG:14862)	glutathione S-transferase, mu 1	NM_010358	0	-0.86	13.665	0	-1.256	7.021	0.016	-0.409	6.612
GSTM1 (includes EG:2944)	glutathione S-transferase M1	NM_008183	0.001	-0.997	8.965	0	-1.162	10.127	0.332	-0.165	9.962
GSTM3 (includes EG:14864)	glutathione S-transferase, mu 3	NM_010359	0.016	-1.416	9.939	0.001	-2.399	12.338	0.061	-0.982	11.356
GSTM4	glutathione S-transferase M4	NM_026764	0.097	-0.469	9.231	0.002	-1.226	10.456	0.019	-0.757	9.699
GSTM5	glutathione S-transferase M5	NM_008184	0.376	-0.149	10.351	0.002	-0.818	11.169	0.005	-0.669	10.501
GSTT3	glutathione S-transferase, theta 3	NM_133994	0.002	-1.072	8.57	0.001	-1.275	9.845	0.366	-0.203	9.642
MGST3	microsomal glutathione S-transferase 3	NM_025569	0.131	-0.459	7.726	0.009	-0.982	8.708	0.093	-0.523	8.185
UGT2B10	UDP glucuronosyltransferase 2 family, polypeptide B10	NM_053215	0.024	1.63	4.538	0.104	1.041	3.497	0.322	-0.589	2.908
UGT2B17	UDP glucuronosyltransferase 2 family, polypeptide B17	NM_133894	0.007	3.388	8.373	0.107	1.639	6.734	0.075	-0.247	13.76
Fatty Acid Metabolism											
ACAA1B	acetyl-Coenzyme A acyltransferase 1B	NM_130864	0.002	-0.912	12.809	0.048	-0.279	14.769	0.027	0.441	14.5

Continued

ACAD11	acyl-Coenzyme A dehydrogenase family, member 11	NM_028721	0.018	-0.542	12.11	0.174	0.262	11.847	0.003	0.804	12.651
ACAT2	acetyl-Coenzyme A acetyltransferase 2	NM_009338	0.035	-0.586	10.935	0.005	-0.927	11.862	0.117	0.152	12.068
ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	NM_015729	0.002	-0.901	13.03	0.298	-0.207	13.236	0.008	0.694	13.93
ACSL3	acyl-CoA synthetase long-chain family member 3	NM_001033606	0.011	-0.825	7.664	0.064	-0.519	8.184	0.233	0.305	8.489
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
CPT1A	carnitine palmitoyltransferase 1A (liver)	NM_013495	0.008	-0.834	11.137	0.252	0.279	10.858	0.002	1.114	11.972
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	NM_007812	0.503	-0.321	11.504	0.02	-1.399	12.903	0.052	-1.078	11.825
CYP2B6 (includes EG:1555)	cytochrome P450, family 2, subfamily B, polypeptide 6	NM_009998	0.026	-0.948	2.434	0.002	-1.753	4.175	0.044	-0.546	2.408
CYP2B9	cytochrome P450, family 2, subfamily b, polypeptide 9	NM_010000	0.001	-5.322	2.896	0.684	-0.354	3.249	0.001	4.969	8.218
CYP2C38	cytochrome P450, family 2, subfamily c, polypeptide 38	NM_010002	0.001	-2.033	7.649	0.015	-1.247	8.896	0.079	0.786	9.682
CYP2C54	cytochrome P450, family 2, subfamily c, polypeptide 54	NM_206537	0.019	0.494	13.689	0.088	-0.32	14.01	0.002	-0.815	13.195
CYP2C55	cytochrome P450, family 2, subfamily c, polypeptide 55	NM_028089	0.479	0.214	6.431	0	-1.945	8.376	0	-2.158	6.217
CYP2D13	cytochrome P450, family 2, subfamily d, polypeptide 13	NR_003552	0.005	0.973	6.427	0.044	0.582	5.845	0.141	-0.391	5.454
CYP2G1P	cytochrome P450, family 2, subfamily G, polypeptide 1 pseudogene	NM_013809	0.874	0.037	3.222	0.002	-1.19	4.411	0.001	-1.227	3.185
CYP4A14	cytochrome P450, family 4, subfamily a, polypeptide 14	NM_007822	0.04	-1.506	11.52	0.364	-0.571	12.091	0.159	0.934	13.026
HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	NM_008292	0.007	-0.66	12.308	0.41	0.149	12.159	0.003	0.809	12.968
Bile Acid Biosynthesis											
ACAA1B	acyl-Coenzyme A acyltransferase 1B	NM_130864	0.002	-0.912	12.809	0.048	-0.279	14.769	0.027	0.441	14.5
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	NM_007824	0.064	1.472	9.635	0.082	-1.292	7.267	0.012	-2.291	8.163
CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	NM_007825	0.005	1.464	12.838	0.013	1.203	11.635	0.404	-0.286	12.756
Glycerolipid Metabolism											
AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3	NM_053014	0.004	-1.809	7.367	0.159	-0.655	8.022	0.005	0.633	10.017
AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	NM_009658	0.002	0.852	7.936	0.026	0.472	7.464	0.018	-0.587	5.291
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949

Continued

ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	NM_008149	0.013	-1.213	11.802	0.05	-0.862	12.663	0.36	0.351	13.015
LIPG	lipase, endothelial	NM_010720	0.075	-0.718	3.694	0.193	0.422	5.104	0.012	1.016	6.12
MGLL	monoglyceride lipase	NM_011844	0.003	-0.801	11.244	0.112	0.317	10.927	0.001	1.118	12.045
MOGAT1	monoacylglycerol O-acyltransferase 1	NM_026713	0.074	-1.178	3.038	0.654	0.259	2.779	0.038	1.438	4.217
PPAP2B	phosphatidic acid phosphatase type 2B	NM_080555	0.014	-0.831	10.244	0.057	-0.573	10.817	0.305	0.181	11.441
Aminosugar Metabolism											
CYB561	cytochrome b-561	NM_007805	0.036	-0.666	5.122	0.272	0.303	4.819	0.008	0.969	5.788
CYB5R3	cytochrome b5 reductase 3	NM_029787	0.009	-0.809	11.975	0.03	-0.605	12.58	0.231	0.235	13.42
GCK	glucokinase (hexokinase 4)	NM_010292	0.008	-1.193	8.679	0.511	0.182	8.288	0.007	1.03	9.318
GFPT1	glutamine-fructose-6-phosphate transaminase 1	NM_013528	0.024	-0.809	6.724	0.272	0.001	2.286	0.044	0.169	2.533
HK1	hexokinase 1	NM_010438	0	-1.348	3.313	0.006	-0.826	4.139	0.015	-0.475	12.23
NQO1	NAD(P)H dehydrogenase, quinone 1	NM_008706	0.064	-0.883	3.705	0.035	-1.056	4.761	0.677	-0.172	4.589
PDE2A	phosphodiesterase 2A, cGMP-stimulated phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_001008548	0.001	-1.426	4.773	0.002	-1.319	6.092	0.653	0.116	9.205
PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_019840	0.004	-0.967	2.681	0.254	-0.007	2.321	0.009	0.808	3.647
PDE7B	phosphodiesterase 7B	NM_013875	0.002	-0.826	5.305	0.07	-0.349	5.655	0.023	0.476	6.131
PGM3	phosphoglucomutase 3	NM_028352	0.271	-0.381	6.948	0.038	0.827	6.122	0.008	1.208	7.329
Sphingolipid Metabolism											
ARSA	arylsulfatase A	NM_009713	0.038	-0.805	8.473	0.053	-0.735	9.208	0.827	0.07	9.279
ARSB	arylsulfatase B	NM_009712	0.006	-1.032	7.29	0.073	-0.555	7.845	0.112	0.477	8.322
ARSG	arylsulfatase G	NM_028710	0.908	-0.019	8.523	0	1.165	7.359	0	1.184	8.542
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	NM_007811	0.022	-1.991	5.192	0.001	-3.72	8.911	0.037	-1.729	7.183
PPAP2B	phosphatidic acid phosphatase type 2B	NM_080555	0.014	-0.831	10.244	0.057	-0.573	10.817	0.305	0.181	11.441
SULF2	sulfatase 2	NM_028072	0.023	-1.178	3.59	0.126	-0.497	6.836	0.058	0.912	4.768
VNN1	vanin 1	NM_011704	0.059	-0.882	9.365	0.086	0.764	10.887	0.004	1.658	10.247
Glutathione Metabolism											
ACSS2	acyl-CoA synthetase short-chain family member 2	NM_019811	0.313	-0.529	11.218	0.02	-1.499	12.717	0.054	-1.03	11.548
GSTA4	glutathione S-transferase A4	NM_010357	0.417	0.149	10.43	0.003	-0.779	11.209	0.001	-0.928	10.281
GSTA5	glutathione S-transferase A5	NM_008181	0.133	-1.013	7.634	0.001	-2.393	10.925	0.004	-1.8	9.126
GSTM1 (includes EG:14862)	glutathione S-transferase, mu 1	NM_010358	0	-0.86	13.665	0	-1.256	7.021	0.016	-0.409	6.612
GSTM1 (includes EG:2944)	glutathione S-transferase M1	NM_008183	0.001	-0.997	8.965	0	-1.162	10.127	0.332	-0.165	9.962
GSTM3 (includes EG:14864)	glutathione S-transferase, mu 3	NM_010359	0.016	-1.416	9.939	0.001	-2.399	12.338	0.061	-0.982	11.356

Continued

GSTM4	glutathione S-transferase M4	NM_026764	0.097	-0.469	9.231	0.002	-1.226	10.456	0.019	-0.757	9.699
GSTM5	glutathione S-transferase M5	NM_008184	0.376	-0.149	10.351	0.002	-0.818	11.169	0.005	-0.669	10.501
GSTT3	glutathione S-transferase, theta 3	NM_133994	0.002	-1.072	8.57	0.001	-1.275	9.845	0.366	-0.203	9.642
MGST3	microsomal glutathione S-transferase 3	NM_025569	0.131	-0.459	7.726	0.009	-0.982	8.708	0.093	-0.523	8.185
PGD	phosphogluconate dehydrogenase	NM_001081274	0.026	-1.181	7.348	0.114	-0.745	8.093	0.147	0.549	8.851
Biosynthesis of Steroid											
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	NM_138656	0.022	-1.991	5.192	0.001	-3.72	8.911	0.037	-1.729	7.183
CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	NM_007811	0.005	1.464	12.838	0.013	1.203	11.635	0.404	-0.286	12.756
DHCR7	7-dehydrocholesterol reductase	NM_146006	0.085	-0.676	9.689	0.022	-1.006	10.694	0.289	0	2.285
FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	NM_007825	0.072	-0.476	11.331	0.004	-0.996	12.327	0.055	-0.52	11.807
HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	NM_134469	0.428	-0.254	6.79	0.007	-1.179	7.969	0.02	-0.925	7.044
IDI1	isopentenyl-diphosphate delta isomerase 1	NM_008706	0.14	0.561	10.519	0.226	-0.446	10.965	0.022	-1.007	9.958
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	NM_145360	0.412	0.04	2.469	0.023	-1.037	6.498	0.04	-0.889	5.609
MVD	mevalonate (diphospho) decarboxylase	NM_008255	0.005	-1.431	6.181	0.008	-1.329	7.51	0.776	0.102	7.613
NQO1	NAD(P)H dehydrogenase, quinone 1	NM_026784	0.064	-0.883	3.705	0.035	-1.056	4.761	0.677	-0.172	4.589
PMVK	phosphomevalonate kinase	NM_007856	0.941	0.026	8.598	0.041	-0.87	9.467	0.037	-0.896	8.571
Tryptophan Metabolism											
ACAT2	acetyl-Coenzyme A acetyltransferase 2	NM_009338	0.035	-0.586	10.935	0.005	-0.927	11.862	0.117	0.152	12.068
AFMID	arylformamidase	NM_027827	0.008	0.527	6.536	0.001	-0.78	8.825	0	-1.084	6.009
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	NM_007812	0.503	-0.321	11.504	0.02	-1.399	12.903	0.052	-1.078	11.825
CYP2B6 (includes EG:1555)	cytochrome P450, family 2, subfamily B, polypeptide 6	NM_009998	0.026	-0.948	2.434	0.002	-1.753	4.175	0.044	-0.546	2.408
CYP2B9	cytochrome P450, family 2, subfamily b, polypeptide 9	NM_010000	0.001	-5.322	2.896	0.684	-0.354	3.249	0.001	4.969	8.218
CYP2C38	cytochrome P450, family 2, subfamily c, polypeptide 38	NM_010002	0.001	-2.033	7.649	0.015	-1.247	8.896	0.079	0.786	9.682
CYP2C54	cytochrome P450, family 2, subfamily c, polypeptide 54	NM_206537	0.019	0.494	13.689	0.088	-0.32	14.01	0.002	-0.815	13.195
CYP2C55	cytochrome P450, family 2, subfamily c, polypeptide 55	NM_028089	0.479	0.214	6.431	0	-1.945	8.376	0	-2.158	6.217
CYP2D13	cytochrome P450, family 2, subfamily d, polypeptide 13	NR_003552	0.005	0.973	6.427	0.044	0.582	5.845	0.141	-0.391	5.454
CYP2G1P	cytochrome P450, family 2, subfamily G, polypeptide 1 pseudogene	NM_013809	0.874	0.037	3.222	0.002	-1.19	4.411	0.001	-1.227	3.185

Continued

CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	NM_007825	0.005	1.464	12.838	0.013	1.203	11.635	0.404	-0.286	12.756
DHCR24	24-dehydrocholesterol reductase	NM_053272	0.007	-1.058	11.196	0.037	-0.704	11.9	0.231	0.354	12.254
HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	NM_008292	0.007	-0.66	12.308	0.41	0.149	12.159	0.003	0.809	12.968
NEDD4	neural precursor cell expressed, developmentally down-regulated 4	NM_010890	0.003	-1.586	7.541	0.021	-1.061	8.602	0.127	0.433	11.085
SYVN1	synovial apoptosis inhibitor 1, synoviolin	NM_028769	0.031	-1.076	8.032	0.79	0.104	7.534	0.031	1.079	9.109
Linoleic Acid Metabolism											
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	NM_007812	0.503	-0.321	11.504	0.02	-1.399	12.903	0.052	-1.078	11.825
CYP2B6 (includes EG:1555)	cytochrome P450, family 2, subfamily B, polypeptide 6	NM_009998	0.026	-0.948	2.434	0.002	-1.753	4.175	0.044	-0.546	2.408
CYP2B9	cytochrome P450, family 2, subfamily b, polypeptide 9	NM_010000	0.001	-5.322	2.896	0.684	-0.354	3.249	0.001	4.969	8.218
CYP2C38	cytochrome P450, family 2, subfamily c, polypeptide 38	NM_010002	0.001	-2.033	7.649	0.015	-1.247	8.896	0.079	0.786	9.682
CYP2C54	cytochrome P450, family 2, subfamily c, polypeptide 54	NM_206537	0.019	0.494	13.689	0.088	-0.32	14.01	0.002	-0.815	13.195
CYP2C55	cytochrome P450, family 2, subfamily c, polypeptide 55	NM_028089	0.479	0.214	6.431	0	-1.945	8.376	0	-2.158	6.217
CYP2D13	cytochrome P450, family 2, subfamily d, polypeptide 13	NR_003552	0.005	0.973	6.427	0.044	0.582	5.845	0.141	-0.391	5.454
CYP2G1P	cytochrome P450, family 2, subfamily G, polypeptide 1 pseudogene	NM_013809	0.874	0.037	3.222	0.002	-1.19	4.411	0.001	-1.227	3.185
FADS1	fatty acid desaturase 1	NM_146094	0.005	-0.924	12.436	0.106	-0.405	12.841	0.051	0.519	13.36
FADS2	fatty acid desaturase 2	NM_019699	0.001	-1.798	10.549	0.243	-0.399	10.947	0.002	1.482	11.893
GRN	granulin	NM_008175	0.014	-0.862	10.889	0.094	-0.501	11.391	0.11	0.493	10.695
PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	NM_008869	0.004	1.111	5.765	0.013	0.879	4.886	0.396	-0.232	4.654
Butanoate Metabolism											
AACS	acetoacetyl-CoA synthetase	NM_030210	0.007	-1.215	7.416	0.002	-1.513	8.93	0.254	-0.082	2.284
ACAT2	acetyl-Coenzyme A acetyltransferase 2	NM_009338	0.035	-0.586	10.935	0.005	-0.927	11.862	0.117	0.152	12.068
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
BDH1	3-hydroxybutyrate dehydrogenase, type 1	NM_001122683/// NM_175177	0.008	-0.95	11.488	0.024	0.646	7.796	0.001	1.188	8.984
HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	NM_008292	0.007	-0.66	12.308	0.41	0.149	12.159	0.003	0.809	12.968
Galactose Metabolism											
AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	NM_009658	0.002	0.852	7.936	0.026	0.472	7.464	0.018	-0.587	5.291
G6PC	glucose-6-phosphatase, catalytic subunit	NM_008061	0.098	-0.641	12.013	0.641	0.161	11.851	0.049	0.803	12.654
GCK	glucokinase (hexokinase 4)	NM_010292	0.008	-1.193	8.679	0.511	0.182	8.288	0.007	1.03	9.318
HK1	hexokinase 1	NM_010438	0	-1.348	3.313	0.006	-0.826	4.139	0.015	-0.475	12.23

Continued

PFKL	phosphofructokinase, liver	NM_008826	0.024	-0.734	8.904	0.205	0.363	7.152	0.006	1.005	9.638
PGM1	phosphoglucomutase 1	NM_025700	0.003	-0.889	10.729	0.142	-0.326	11.054	0.026	0.564	11.618
PGM3	phosphoglucomutase 3	NM_028352	0.271	-0.381	6.948	0.038	0.827	6.122	0.008	1.208	7.329
Nicotinate Nicotinamide Metabolism											
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	NM_009873	0.039	1.332	6.144	0.254	0.007	2.284	0.218	-0.704	4.812
NMNAT1	nicotinamide nucleotide adenyllyltransferase 1	NM_009874	0.003	0.944	6.387	0.004	0.875	5.512	0.736	-0.069	5.443
PRKCE	protein kinase C, epsilon	NM_133435	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287
CDK6	cyclin-dependent kinase 6	NM_008795	0.003	-1.2	5.302	0.015	-0.841	6.143	0.202	0.359	6.501
PCTK3	PCTAIRE protein kinase 3	NM_011104	0.001	-1.343	5.872	0.005	-0.883	6.756	0.065	0.46	7.216
CDK7	cyclin-dependent kinase 7	NM_016979	0.006	0.792	8.031	0.005	0.807	7.224	0.254	-0.047	2.306
PRKX	protein kinase, X-linked	NM_013830	0.001	-1.187	3.965	0.004	-0.887	4.851	0.184	0.3	5.152
Arachidonic Acid Metabolism											
ACSS2	acyl-CoA synthetase short-chain family member 2	NM_019811	0.313	-0.529	11.218	0.02	-1.499	12.717	0.054	-1.03	11.548
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	NM_007812	0.503	-0.321	11.504	0.02	-1.399	12.903	0.052	-1.078	11.825
CYP2B6 (includes EG:1555)	cytochrome P450, family 2, subfamily B, polypeptide 6	NM_009998	0.026	-0.948	2.434	0.002	-1.753	4.175	0.044	-0.546	2.408
CYP2B9	cytochrome P450, family 2, subfamily b, polypeptide 9	NM_010000	0.001	-5.322	2.896	0.684	-0.354	3.249	0.001	4.969	8.218
CYP2C38	cytochrome P450, family 2, subfamily c, polypeptide 38	NM_010002	0.001	-2.033	7.649	0.015	-1.247	8.896	0.079	0.786	9.682
CYP2C54	cytochrome P450, family 2, subfamily c, polypeptide 54	NM_206537	0.019	0.494	13.689	0.088	-0.32	14.01	0.002	-0.815	13.195
CYP2C55	cytochrome P450, family 2, subfamily c, polypeptide 55	NM_028089	0.479	0.214	6.431	0	-1.945	8.376	0	-2.158	6.217
CYP2G1P	cytochrome P450, family 2, subfamily G, polypeptide 1 pseudogene	NM_013809	0.874	0.037	3.222	0.002	-1.19	4.411	0.001	-1.227	3.185
PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	NM_008869	0.004	1.111	5.765	0.013	0.879	4.886	0.396	-0.232	4.654
Inositol Phosphate Metabolism											
CDK6	cyclin-dependent kinase 6	NM_009873	0.003	-1.2	5.302	0.015	-0.841	6.143	0.202	0.359	6.501
CDK7	cyclin-dependent kinase 7	NM_009874	0.006	0.792	8.031	0.005	0.807	7.224	0.254	-0.047	2.306
PCTK3	PCTAIRE protein kinase 3	NM_008795	0.001	-1.343	5.872	0.005	-0.883	6.756	0.065	0.46	7.216
PRKCE	protein kinase C, epsilon	NM_011104	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287
PRKX	protein kinase, X-linked	NM_016979	0.001	-1.187	3.965	0.004	-0.887	4.851	0.184	0.3	5.152
PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	NM_008960	0.005	-0.489	10.369	0.026	-0.982	10.268	0.124	0.204	10.859
Taurine Hypotaurine Metabolism											
ACSS2	acyl-CoA synthetase short-chain family member 2	NM_019811	0.313	-0.529	11.218	0.02	-1.499	12.717	0.054	-1.03	11.548
CSAD	cysteine sulfenic acid decarboxylase	NM_144942	0.409	0.315	10.032	0.002	-1.786	11.818	0.001	-2.101	9.717

Supplement Table 2.

Name	Description	RefSeq ID	LUP/LV		LUP/LC		LV/LC		
			p-value	Log ₂ Ratio	Intensity	p-value	Log ₂ Ratio	Intensity	p-value
LPS/IL-1 Mediated Inhibition of RXR Function									
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019
FABP5L2	fatty acid binding protein 5-like 2	NM_010634	0.055	1.243	12.168	0.383	-0.575	10.635	0.017
GSTA4	glutathione S-transferase A4	NM_010357	0.417	0.149	10.43	0.003	-0.779	11.209	0.001
ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	NM_015729	0.002	-0.901	13.03	0.298	-0.207	13.236	0.008
GSTM1 (includes EG:2944)	glutathione S-transferase M1	NM_008183	0.001	-0.997	8.965	0	-1.162	10.127	0.332
CD14	CD14 molecule	NM_009841	0.045	1.027	6.315	0.115	0.755	5.56	0.534
HS6ST1	heparan sulfate 6-O-sulfotransferase 1	NM_015818	0.013	-0.997	7.551	0.185	-0.433	7.983	0.098
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001
FMO1	flavin containing monooxygenase 1	NM_010231	0	-1.137	10.033	0.004	-0.751	10.784	0.063
SOD3	superoxide dismutase 3, extracellular	NM_011435	0	-0.89	6.429	0.088	-0.258	6.687	0.002
FABP2	fatty acid binding protein 2, intestinal	NM_007980	0.594	-0.145	12.165	0.035	0.693	11.471	0.017
SLCO1A2	solute carrier organic anion transporter family, member 1A2	NM_030687	0.034	-1.539	8.012	0.025	-1.668	9.68	0.828
GSTA5	glutathione S-transferase A5	NM_008181	0.133	-1.013	7.634	0.001	-2.393	10.925	0.004
GSTM5	glutathione S-transferase M5	NM_008184	0.376	-0.149	10.351	0.002	-0.818	11.169	0.005
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13	NM_007812	0.503	-0.321	11.504	0.02	-1.399	12.903	0.052
CYP4A14	cytochrome P450, family 4, subfamily a, polypeptide 14	NM_007822	0.04	-1.506	11.52	0.364	-0.571	12.091	0.159
FABP4	fatty acid binding protein 4, adipocyte	NM_024406	0.254	0.099	2.383	0.001	1.431	6.908	0.004
GSTM4	glutathione S-transferase M4	NM_026764	0.097	-0.469	9.231	0.002	-1.226	10.456	0.019
GALNAC4S-6ST	B cell RAG associated protein	NM_029935	0.004	-0.648	4.748	0.001	-0.814	5.562	0.29
SREBF1	sterol regulatory element binding transcription factor 1	NM_011480	0.003	-1.265	11.29	0.043	-0.663	11.952	0.06
GSTM3 (includes EG:14864)	glutathione S-transferase, mu 3	NM_010359	0.016	-1.416	9.939	0.001	-2.399	12.338	0.061
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_008306	0.003	-1.331	6.396	0.02	-0.872	7.268	0.152
ABCC3	microsomal glutathione S-transferase 3	NM_029600	0.021	-1.024	9.496	0.048	-0.82	10.315	0.227
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	NM_007824	0.064	1.472	9.635	0.082	-1.292	7.267	0.012
MGST3	glutathione S-transferase, mu 1	NM_025569	0.131	-0.459	7.726	0.009	-0.982	8.708	0.093
GSTM1 (includes EG:14862)	interleukin 1 receptor, type I	NM_010358	0	-0.86	13.665	0	-1.256	7.021	0.016
PPARA	peroxisome proliferator-activated receptor alpha	NM_001113418	0.008	-1.269	9.622	0.757	0.095	9.613	0.012
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645
								-0.195	4.865

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SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	NM_026935	0.027	-0.873	6.347	0.137	-0.52	6.867	0.289	0.353	7.22
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424
FMO5	flavin containing monooxygenase 5	NM_010232	0.001	-0.887	11.336	0.038	-0.37	11.706	0.006	0.695	10.173
FABP7	fatty acid binding protein 7, brain	NM_021272	0.002	0.876	7.398	0.387	0.161	7.237	0.005	-0.715	6.521
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ACSL3	acyl-CoA synthetase long-chain family member 3	NM_001033606	0.011	-0.825	7.664	0.064	-0.519	8.184	0.233	0.305	8.489
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
PLTP	phospholipid transfer protein	NM_011125	0.027	-1.201	9.997	0.011	-1.493	11.49	0.51	-0.292	11.198
CPT1A	carnitine palmitoyltransferase 1A (liver)	NM_013495	0.008	-0.834	11.137	0.252	0.279	10.858	0.002	1.114	11.972
Aryl Hydrocarbon Receptor Signaling											
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
BAX	BCL2-associated X protein	NM_007527	0.003	-0.844	6.969	0.173	-0.28	7.248	0.02	0.564	7.812
CCND1	cyclin D1	NM_007631	0	-1.599	5.005	0	-1.239	6.244	0.041	0.355	7.465
CCND2	cyclin D2	NM_009829	0.001	-0.606	4.175	0.001	-0.944	5.89	0.132	-0.175	2.597
CDK6	cyclin-dependent kinase 6	NM_009873	0.003	-1.2	5.302	0.015	-0.841	6.143	0.202	0.359	6.501
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
ESR1	estrogen receptor 1	NM_007956	0.012	-0.862	8.244	0.02	-0.763	9.007	0.622	-0.111	4.922
FASN	fatty acid synthase	NM_007988	0.002	-1.961	11.054	0.012	-1.338	12.392	0.154	0.623	13.015
GSTA4	glutathione S-transferase A4	NM_010357	0.417	0.149	10.43	0.003	-0.779	11.209	0.001	-0.928	10.281
GSTA5	glutathione S-transferase A5	NM_008181	0.133	-1.013	7.634	0.001	-2.393	10.925	0.004	-1.8	9.126
GSTM1 (includes EG:14862)	glutathione S-transferase, mu 1	NM_010358	0	-0.86	13.665	0	-1.256	7.021	0.016	-0.409	6.612
GSTM1 (includes EG:2944)	glutathione S-transferase M1	NM_008183	0.001	-0.997	8.965	0	-1.162	10.127	0.332	-0.165	9.962
GSTM3 (includes EG:14864)	glutathione S-transferase, mu 3	NM_010359	0.016	-1.416	9.939	0.001	-2.399	12.338	0.061	-0.982	11.356
GSTM4	glutathione S-transferase M4	NM_026764	0.097	-0.469	9.231	0.002	-1.226	10.456	0.019	-0.757	9.699
GSTM5	glutathione S-transferase M5	NM_008184	0.376	-0.149	10.351	0.002	-0.818	11.169	0.005	-0.669	10.501
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
MGST3	microsomal glutathione S-transferase 3	NM_025569	0.131	-0.459	7.726	0.009	-0.982	8.708	0.093	-0.523	8.185
NFIA	nuclear factor I/A	NM_001122952	0.008	-1.234	7.955	0.026	-0.941	8.896	0.09	0.275	2.694

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NFIB	nuclear factor I/B	NM_001113209	0.001	-0.8	8.03	0.005	-0.622	8.652	0.064	0.59	3.579
NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	NM_008688	0.002	-2.153	2.894	0.067	-1.007	10.325	0.009	1.488	6.18
NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	NM_001081981	0.013	-0.839	9.742	0.049	-0.287	4.334	0.261	0.3	10.581
NQO1	NAD(P)H dehydrogenase, quinone 1	NM_008706	0.064	-0.883	3.705	0.035	-1.056	4.761	0.677	-0.172	4.589
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.003	-1.221	5.919	0.031	-0.715	6.634	0.095	0.506	7.14
SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	NM_011417	0.003	-1.241	7.787	0.363	-0.302	5.462	0.004	1.198	9.028
LXR/RXR Activation											
APOA4	apolipoprotein A-IV	NM_007468	0.003	-1.8	11.795	0.014	1.271	10.524	0	3.071	13.595
CD14	CD14 molecule	NM_009841	0.045	1.027	6.315	0.115	0.755	5.56	0.534	-0.272	5.288
CD36	CD36 molecule (thrombospondin receptor)	NM_007643	0.014	-1.72	5.253	0.432	-0.427	5.68	0.042	1.293	6.973
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	NM_007824	0.064	1.472	9.635	0.082	-1.292	7.267	0.012	-2.291	8.163
FASN	fatty acid synthase	NM_007988	0.002	-1.961	11.054	0.012	-1.338	12.392	0.154	0.623	13.015
HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	NM_008255	0.428	-0.254	6.79	0.007	-1.179	7.969	0.02	-0.925	7.044
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
IL1R1	interleukin 1 receptor, type I	NM_001123382	0.029	1.579	7.292	0.07	1.228	6.064	0.555	-0.351	5.713
LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	NM_010700	0.005	-1.457	9.068	0.121	-0.625	9.692	0.043	0.743	3.31
MSR1	macrophage scavenger receptor 1	NM_001113326	0.001	1.087	6.778	0.014	0.588	6.19	0.027	-0.499	5.691
PLTP	phospholipid transfer protein	NM_011125	0.027	-1.201	9.997	0.011	-1.493	11.49	0.51	-0.292	11.198
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	NM_009127	0.003	-2.169	9.694	0.003	-2.087	11.781	0.596	0.101	15.081
SREBF1	sterol regulatory element binding transcription factor 1	NM_011480	0.003	-1.265	11.29	0.043	-0.663	11.952	0.06	0.602	12.555
Xenobiotic Metabolism Signaling											
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_029600	0.021	-1.024	9.496	0.048	-0.82	10.315	0.227	-0.126	2.463
ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_028270	0.008	-1.606	6.814	0.094	-0.827	7.641	0.111	0.779	8.419
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.008	-0.808	8.158	0.09	-0.422	8.58	0.114	0.387	8.966
CAMK1D	calcium/calmodulin-dependent protein kinase ID	NM_177343	0.04	-0.702	6.781	0.006	-1.12	7.901	0.172	-0.418	7.483
CES1 (includes EG:12623)	carboxylesterase 1	NM_021456	0.159	-0.509	9.847	0.02	-0.988	10.835	0.182	-0.478	10.357
CES2 (includes EG:234671)	carboxylesterase 2	NM_145603	0.207	0.338	10.019	0.037	-0.632	10.651	0.006	-0.97	9.681
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313

Continued

CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	NM_010121	0.014	-0.805	5.143	0.817	-0.058	5.2	0.019	0.748	5.948
FMO1	flavin containing monooxygenase 1	NM_010231	0	-1.137	10.033	0.004	-0.751	10.784	0.063	0.386	11.171
FMO5	flavin containing monooxygenase 5	NM_010232	0.001	-0.887	11.336	0.038	-0.37	11.706	0.006	0.695	10.173
GALNAC4S -6ST	B cell RAG associated protein	NM_029935	0.004	-0.648	4.748	0.001	-0.814	5.562	0.29	-0.166	5.396
GSTA4	glutathione S-transferase A4	NM_010357	0.417	0.149	10.43	0.003	-0.779	11.209	0.001	-0.928	10.281
GSTA5	glutathione S-transferase A5	NM_008181	0.133	-1.013	7.634	0.001	-2.393	10.925	0.004	-1.8	9.126
GSTM1 (includes EG:14862)	glutathione S-transferase, mu 1	NM_010358	0	-0.86	13.665	0	-1.256	7.021	0.016	-0.409	6.612
GSTM1 (includes EG:2944)	glutathione S-transferase M1	NM_008183	0.001	-0.997	8.965	0	-1.162	10.127	0.332	-0.165	9.962
GSTM3 (includes EG:14864)	glutathione S-transferase, mu 3	NM_010359	0.016	-1.416	9.939	0.001	-2.399	12.338	0.061	-0.982	11.356
GSTM4	glutathione S-transferase M4	NM_026764	0.097	-0.469	9.231	0.002	-1.226	10.456	0.019	-0.757	9.699
GSTM5	glutathione S-transferase M5	NM_008184	0.376	-0.149	10.351	0.002	-0.818	11.169	0.005	-0.669	10.501
HS6ST1	heparan sulfate 6-O-sulfotransferase 1	NM_015818	0.013	-0.997	7.551	0.185	-0.433	7.983	0.098	0.565	8.548
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
KEAP1	kelch-like ECH-associated protein 1	NM_001110305 ///NM_001110306 ///NM_001110307 /// NM_016679	0.005	-0.977	5.151	0.041	-0.593	5.744	0.054	0.26	9.147
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	NM_001025577	0.007	-0.852	4.264	0.001	-1.235	5.499	0.081	-0.334	5.989
MGST3	microsomal glutathione S-transferase 3	NM_025569	0.131	-0.459	7.726	0.009	-0.982	8.708	0.093	-0.523	8.185
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	NM_008306	0.003	-1.331	6.396	0.02	-0.872	7.268	0.152	0.458	7.726
NQO1	NAD(P)H dehydrogenase, quinone 1	NM_008706	0.064	-0.883	3.705	0.035	-1.056	4.761	0.677	-0.172	4.589
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.003	-1.221	5.919	0.031	-0.715	6.634	0.095	0.506	7.14
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	NM_012024	0	-0.905	7.187	0	-0.59	7.777	0.001	0.314	8.091
PRKCE	protein kinase C, epsilon	NM_011104	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287
SOD3	superoxide dismutase 3, extracellular	NM_011435	0	-0.89	6.429	0.088	-0.258	6.687	0.002	0.631	7.319
SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	NM_026935	0.027	-0.873	6.347	0.137	-0.52	6.867	0.289	0.353	7.22
UGT2B10	UDP glucuronosyltransferase 2 family, polypeptide B10	NM_053215	0.024	1.63	4.538	0.104	1.041	3.497	0.322	-0.589	2.908
UGT2B17	UDP glucuronosyltransferase 2 family, polypeptide B17	NM_133894	0.007	3.388	8.373	0.107	1.639	6.734	0.075	-0.247	13.76
NRF2-mediated Oxidative Stress Response											
ACTG1	actin, gamma 1	NM_009609	0.002	-0.945	11.935	0.88	0.028	11.907	0.001	0.973	12.88
GSTA4	glutathione S-transferase A4	NM_010357	0.417	0.149	10.43	0.003	-0.779	11.209	0.001	-0.928	10.281
GSTM1 (includes EG:2944)	glutathione S-transferase M1	NM_008183	0.001	-0.997	8.965	0	-1.162	10.127	0.332	-0.165	9.962

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DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	NM_025384	0.001	0.817	11.075	0.013	0.51	10.565	0.082	-0.306	10.258
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
FMO1	flavin containing monooxygenase 1	NM_010231	0	-1.137	10.033	0.004	-0.751	10.784	0.063	0.386	11.171
SOD3	superoxide dismutase 3, extracellular	NM_011435	0	-0.89	6.429	0.088	-0.258	6.687	0.002	0.631	7.319
GSTA5	glutathione S-transferase A5	NM_008181	0.133	-1.013	7.634	0.001	-2.393	10.925	0.004	-1.8	9.126
GSTM5	glutathione S-transferase M5	NM_008184	0.376	-0.149	10.351	0.002	-0.818	11.169	0.005	-0.669	10.501
VCP	valosin-containing protein	NM_009503	0.001	-0.821	11.941	0.361	-0.144	12.085	0.003	0.677	12.762
NQO1	NAD(P)H dehydrogenase, quinone 1	NM_008706	0.064	-0.883	3.705	0.035	-1.056	4.761	0.677	-0.172	4.589
GSTM4	glutathione S-transferase M4	NM_026764	0.097	-0.469	9.231	0.002	-1.226	10.456	0.019	-0.757	9.699
GSTM3 (includes EG:14864)	glutathione S-transferase, mu 3	NM_010359	0.016	-1.416	9.939	0.001	-2.399	12.338	0.061	-0.982	11.356
DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14	XM_001473173	0.003	-1.225	4.7	0.216	-0.361	5.062	0.016	0.864	5.925
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	NM_001025577	0.007	-0.852	4.264	0.001	-1.235	5.499	0.081	-0.334	5.989
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313
PRKCE	protein kinase C, epsilon	NM_011104	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	NM_009716	0.011	0.869	9.16	0.017	0.784	8.377	0.734	-0.076	10.489
MGST3	microsomal glutathione S-transferase 3	NM_025569	0.131	-0.459	7.726	0.009	-0.982	8.708	0.093	-0.523	8.185
GSTM1 (includes EG:14862)	glutathione S-transferase, mu 1	NM_010358	0	-0.86	13.665	0	-1.256	7.021	0.016	-0.409	6.612
JUND	jun D proto-oncogene	NM_010592	0.002	-0.832	9.321	0.115	-0.309	9.63	0.02	0.523	10.153
EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	NM_010121	0.014	-0.805	5.143	0.817	-0.058	5.2	0.019	0.748	5.948
BACH1	BTB and CNC homology 1, basic leucine zipper t ranscription factor 1	NM_007520	0.009	-0.761	4.05	0.004	-0.915	4.965	0.038	-0.575	8.737
KEAP1	kelch-like ECH-associated protein 1	NM_001110305	0.005	-0.977	5.151	0.041	-0.593	5.744	0.054	0.26	9.147
GSK3B	glycogen synthase kinase 3 beta	NM_019827	0.003	-1.35	4.392	0.027	-0.818	5.21	0.108	0.627	6.711
PXR/RXR Activation											
ABCC3	ATP-binding cassette, sub-familyC (CFTR/MRP), member3	NM_029600	0.021	-1.024	9.496	0.048	-0.82	10.315	0.227	-0.126	2.463
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	NM_007437	0.048	-0.654	11.296	0.516	0.184	11.112	0.019	0.838	11.949
CPT1A	carnitine palmitoyltransferase 1A (liver)	NM_013495	0.008	-0.834	11.137	0.252	0.279	10.858	0.002	1.114	11.972
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	NM_009993	0.069	0.399	12.721	0.003	-0.847	13.568	0	-1.246	12.323
CYP2B6 (includes EG:1555)	cytochrome P450, family 2, subfamily B, polypeptide 6	NM_009998	0.026	-0.948	2.434	0.002	-1.753	4.175	0.044	-0.546	2.408
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	NM_007824	0.064	1.472	9.635	0.082	-1.292	7.267	0.012	-2.291	8.163
FOXO3	forkhead box O3	NM_019740	0.01	-0.858	7.286	0.043	-0.591	7.877	0.091	-0.29	4.357

Continued

G6PC	glucose-6-phosphatase, catalytic subunit	NM_008061	0.098	-0.641	12.013	0.641	0.161	11.851	0.049	0.803	12.654
GSTA5	glutathione S-transferase A5	NM_008181	0.133	-1.013	7.634	0.001	-2.393	10.925	0.004	-1.8	9.126
GSTM1 (includes EG:14862)	glutathione S-transferase, mu 1	NM_010358	0	-0.86	13.665	0	-1.256	7.021	0.016	-0.409	6.612
GSTM1 (includes EG:2944)	glutathione S-transferase M1	NM_008183	0.001	-0.997	8.965	0	-1.162	10.127	0.332	-0.165	9.962
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424
PPARA	peroxisome proliferator-activated receptor alpha	NM_001113418	0.008	-1.269	9.622	0.757	0.095	9.613	0.012	1.168	10.89
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	NM_008854	0.001	-0.837	6.149	0.164	-0.235	6.384	0.006	0.603	6.986
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	NM_009127	0.003	-2.169	9.694	0.003	-2.087	11.781	0.596	0.101	15.081
FXR/RXR Activation											
ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	NM_008830	0.131	-0.345	11.391	0.016	0.651	10.74	0.002	0.996	11.736
APOB	apolipoprotein B (including Ag(x) antigen)	NM_009693	0.025	-1.82	9.83	0.701	-0.068	13.11	0.015	2.064	11.65
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	NM_007824	0.064	1.472	9.635	0.082	-1.292	7.267	0.012	-2.291	8.163
FASN	fatty acid synthase	NM_007988	0.002	-1.961	11.054	0.012	-1.338	12.392	0.154	0.623	13.015
G6PC	glucose-6-phosphatase, catalytic subunit	NM_008061	0.098	-0.641	12.013	0.641	0.161	11.851	0.049	0.803	12.654
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424
OSTBETA	organic solute transporter beta	NM_178933	0	0.803	3.951	0	0.834	3.117	0.692	0.031	3.148
PKLR	pyruvate kinase, liver and RBC	NM_001099779	0.006	-1.179	9.396	0.142	-0.626	8.63	0.049	0.7	10.574
PLTP	phospholipid transfer protein	NM_011125	0.027	-1.201	9.997	0.011	-1.493	11.49	0.51	-0.292	11.198
PPARA	peroxisome proliferator-activated receptor alpha	NM_001113418	0.008	-1.269	9.622	0.757	0.095	9.613	0.012	1.168	10.89
SLC22A7	solute carrier family 22 (organic anion transporter), member 7	NM_144856	0.304	0.502	10.384	0.014	1.509	8.875	0.064	1.007	9.882
SREBF1	sterol regulatory element binding transcription factor 1	NM_011480	0.003	-1.265	11.29	0.043	-0.663	11.952	0.06	0.602	12.555
VLDLR	very low density lipoprotein receptor	NM_013703	0.032	-1.159	3.548	0.1	-0.816	4.363	0.09	0.481	2.856
PPARα/RXRα Activation											
ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	NM_015729	0.002	-0.901	13.03	0.298	-0.207	13.236	0.008	0.694	13.93
CD36	CD36 molecule (thrombospondin receptor)	NM_007643	0.014	-1.72	5.253	0.432	-0.427	5.68	0.042	1.293	6.973
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313
CYP2C38	cytochrome P450, family 2, subfamily c, polypeptide 38	NM_010002	0.001	-2.033	7.649	0.015	-1.247	8.896	0.079	0.786	9.682
CYP2C54	cytochrome P450, family 2, subfamily c, polypeptide 54	NM_206537	0.019	0.494	13.689	0.088	-0.32	14.01	0.002	-0.815	13.195
CYP2C55	cytochrome P450, family 2, subfamily c, polypeptide 55	NM_028089	0.479	0.214	6.431	0	-1.945	8.376	0	-2.158	6.217
FASN	fatty acid synthase	NM_007988	0.002	-1.961	11.054	0.012	-1.338	12.392	0.154	0.623	13.015

Continued

GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	NM_008139	0.001	-0.923	5.957	0.011	-0.605	6.563	0.043	0.514	6.285
GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	NM_010271	0.003	-0.861	10.337	0.258	-0.227	10.565	0.012	0.634	11.199
GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	NM_010274	0.004	-0.871	8.968	0.254	-0.011	2.295	0.002	0.989	9.839
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
IL1R1	interleukin 1 receptor, type I	NM_001123382	0.029	1.579	7.292	0.07	1.228	6.064	0.555	-0.351	5.713
ITGB5	integrin, beta 5	NM_010580	0.003	-0.94	9.049	0.075	-0.432	9.482	0.032	0.474	9.953
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424
PPARA	peroxisome proliferator-activated receptor alpha	NM_001113418 // NM_011144	0.008	-1.269	9.622	0.757	0.095	9.613	0.012	1.168	10.89
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha		0.001	-0.837	6.149	0.164	-0.235	6.384	0.006	0.603	6.986
SMAD3	SMAD family member 3	NM_016769	0.005	-0.99	4.439	0.105	-0.438	4.877	0.052	0.552	5.429
Integrin Signaling											
ACTG1	actin, gamma 1	NM_009609	0.002	-0.945	11.935	0.88	0.028	11.907	0.001	0.973	12.88
ARF3	ADP-ribosylation factor 3	NM_007478	0.003	-0.805	8.165	0.181	-0.288	6.881	0.014	0.586	8.97
ARHGAP26	Rho GTPase activating protein 26	NM_175164	0.023	0.742	7.574	0.007	0.98	6.594	0.1	0.476	4.812
CAPN8	calpain 8	NM_130890	0.023	1.148	4.258	0.009	1.428	2.83	0.491	0.28	3.11
CAV1	caveolin 1, caveolae protein, 22 kDa	NM_007616	0.018	0.872	7.171	0.008	1.046	6.125	0.549	0.174	6.3
GSK3B	glycogen synthase kinase 3 beta	NM_019827	0.003	-1.35	4.392	0.027	-0.818	5.21	0.108	0.627	6.711
ITGB5	integrin, beta 5	NM_010580	0.003	-0.94	9.049	0.075	-0.432	9.482	0.032	0.474	9.953
MYL9 (includes EG:98932)	myosin, light polypeptide 9, regulatory	XM_485171	0.008	-0.851	3.726	0.005	-0.95	4.676	0.67	-0.1	4.577
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	NM_008960	0.005	-0.489	10.369	0.026	-0.982	10.268	0.124	0.204	10.859
PXN	paxillin	NM_011223	0.002	-1.146	9.179	0.031	-0.633	9.812	0.064	0.513	10.325
RAP1B	RAP1B, member of RAS oncogene family	NM_024457	0.001	1.046	9.914	0.02	0.595	9.319	0.055	-0.451	8.868
RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	NM_001039086	0.031	-0.855	4.558	0.586	-0.178	4.736	0.069	0.677	5.413
RHOJ	ras homolog gene family, member J	NM_023275	0.001	-1.553	4.105	0.011	-0.882	4.987	0.033	0.671	5.658
RHOU	ras homolog gene family, member U	NM_133955	0	-1.221	8.933	0.021	-0.436	9.368	0.001	0.785	10.154
RND2	Rho family GTPase 2	NM_009708	0.009	-0.583	7.485	0.001	-0.859	8.343	0.128	-0.276	8.067
VCL	vinculin	NM_009502	0.007	-0.852	7.954	0.158	-0.352	8.305	0.061	0.501	8.806
WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	NM_009515	0.022	0.807	4.52	0.064	0.597	3.923	0.46	-0.21	3.713
WASL (includes EG:8976)	Wiskott-Aldrich syndrome-like	NM_028459	0.001	-0.808	6.796	0.016	-0.251	9.173	0.007	0.549	7.604
ZYX	zyxin	NM_011777	0.003	-1.279	6.549	0.007	-1.097	7.646	0.538	0.182	7.828
RXR Activation											

Continued

CCNH	cyclin H	NM_023243	0.003	0.911	7.331	0.052	0.479	6.852	0.043	-0.306	8.953
CDK7	cyclin-dependent kinase 7	NM_009874	0.006	0.792	8.031	0.005	0.807	7.224	0.254	-0.047	2.306
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313
CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_007788	0.001	-1.087	7.111	0.015	-0.604	7.715	0.036	0.483	8.198
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	NM_007811	0.022	-1.991	5.192	0.001	-3.72	8.911	0.037	-1.729	7.183
DUSP1	dual specificity phosphatase 1	NM_013642	0.005	-1.426	7.398	0.586	0.197	7.201	0.003	1.623	8.824
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
NR2F2	nuclear receptor subfamily 2, group F, member 2	NM_009697	0.004	-0.885	7.792	0.01	-0.725	8.518	0.067	0.101	2.422
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.003	-1.221	5.919	0.031	-0.715	6.634	0.095	0.506	7.14
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
PRKACA	protein kinase, cAMP- dependent, catalytic, alpha	NM_008854	0.001	-0.837	6.149	0.164	-0.235	6.384	0.006	0.603	6.986
PRKCE	protein kinase C, epsilon	NM_011104	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287
PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	NM_008960	0.005	-0.489	10.369	0.026	-0.982	10.268	0.124	0.204	10.859
RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	NM_021557	0.697	-0.143	8.321	0.02	-1.089	9.41	0.034	-0.945	8.464
RDH16 (includes EG:19683)	retinol dehydrogenase 16	NM_009040	0.031	-0.978	8.001	0.066	-0.783	8.784	0.6	0.195	8.979
SMAD3	SMAD family member 3	NM_016769	0.005	-0.99	4.439	0.105	-0.438	4.877	0.052	0.552	5.429
SMAD6	SMAD family member 6	NM_008542	0.015	-0.906	4.742	0.069	-0.595	5.337	0.294	0.311	5.647
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	NM_011416	0.023	-0.889	4.837	0.436	0.004	2.325	0.063	0.674	5.726
SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	NM_011417	0.003	-1.241	7.787	0.363	-0.302	5.462	0.004	1.198	9.028
STAT5A	signal transducer and activator of transcription 5A	NM_011488	0.009	-0.68	2.856	0.116	0.493	5.449	0.003	0.83	3.536
P53 Signaling											
BAX	BCL2-associated X protein	NM_007527	0.003	-0.844	6.969	0.173	-0.28	7.248	0.02	0.564	7.812
CCND1	cyclin D1	NM_007631	0	-1.599	5.005	0	-1.239	6.244	0.041	0.355	7.465
CCND2	cyclin D2	NM_009829	0.001	-0.606	4.175	0.001	-0.944	5.89	0.132	-0.175	2.597
FASN	fatty acid synthase	NM_007988	0.002	-1.961	11.054	0.012	-1.338	12.392	0.154	0.623	13.015
GSK3B	glycogen synthase kinase 3 beta	NM_019827	0.003	-1.35	4.392	0.027	-0.818	5.21	0.108	0.627	6.711
HIPK2	homeodomain interacting protein kinase 2	NM_010433	0.013	-1.579	6.149	0.105	-0.872	7.021	0.04	0.571	5.961
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
PLAGL1	pleiomorphic adenoma gene-like 1	NM_009538	0.002	-1.83	3.904	0.093	-0.729	4.633	0.023	1.101	5.734
PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	NM_008960	0.005	-0.489	10.369	0.026	-0.982	10.268	0.124	0.204	10.859
TP53BP2	tumor protein p53 binding protein, 2	NM_173378	0.001	-0.835	4.35	0.169	0.145	6.649	0.003	0.695	5.185

Continued

Nucleotide Excision Repair Pathway												
CCNH	cyclin H	NM_023243	0.003	0.911	7.331	0.052	0.479	6.852	0.043	-0.306	8.953	
CDK7	cyclin-dependent kinase 7	NM_009874	0.006	0.792	8.031	0.005	0.807	7.224	0.254	-0.047	2.306	
ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	NM_028042	0.027	0.855	5.184	0.055	0.703	4.481	0.133	-0.152	3.782	
POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220 kDa	NM_009089	0.025	-1.022	5.64	0.618	-0.183	5.822	0.051	0.839	6.661	
POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33 kDa	NM_009090	0.005	0.856	9.071	0.058	0.467	8.604	0.1	-0.389	8.215	
RPA3	replication protein A3, 14 kDa	NM_026632	0.012	1.006	8.22	0.228	0.387	7.833	0.074	-0.619	7.215	
ERK/MAPK Signaling												
PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	NM_026731	0.014	0.868	5.672	0.052	0.618	5.054	0.371	-0.25	4.805	
YWHAG	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, gamma polypeptide	NM_018871	0.001	-0.917	8.857	0.032	-0.405	9.262	0.012	0.512	9.774	
MKNK2	MAP kinase interacting serine/threonine kinase 2	NM_021462	0.005	-1.582	9.258	0.012	-1.316	10.574	0.323	0.335	5.522	
RAP1B	RAP1B, member of RAS oncogene family	NM_024457	0.001	1.046	9.914	0.02	0.595	9.319	0.055	-0.451	8.868	
DUSP1	dual specificity phosphatase 1	NM_013642	0.005	-1.426	7.398	0.586	0.197	7.201	0.003	1.623	8.824	
PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	NM_012024	0	-0.905	7.187	0	-0.59	7.777	0.001	0.314	8.091	
RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	NM_001039086	0.031	-0.855	4.558	0.586	-0.178	4.736	0.069	0.677	5.413	
PRKCE	protein kinase C, epsilon	NM_011104	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287	
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	NM_008854	0.001	-0.837	6.149	0.164	-0.235	6.384	0.006	0.603	6.986	
PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234	
ESR1	estrogen receptor 1	NM_007956	0.012	-0.862	8.244	0.02	-0.763	9.007	0.622	-0.111	4.922	
PXN	paxillin	NM_011223	0.002	-1.146	9.179	0.031	-0.633	9.812	0.064	0.513	10.325	
MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1	NM_019920	0.01	0.805	9.796	0.053	0.53	9.265	0.263	-0.275	8.991	
ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	NM_009716	0.011	0.869	9.16	0.017	0.784	8.377	0.734	-0.076	10.489	
MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	NM_008709	0.127	-0.768	4.113	0.234	-0.054	2.357	0.035	1.167	4.881	
PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	NM_008869	0.004	1.111	5.765	0.013	0.879	4.886	0.396	-0.232	4.654	
ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	NM_013508	0.01	-0.603	5.567	0.002	-0.849	6.415	0.033	0.455	4.877	
RPS6KA1	ribosomal protein S6 kinase, 90 kDa, polypeptide 1	NM_009097	0.007	-1.049	5.943	0.209	-0.369	6.312	0.04	0.681	6.993	
PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	NM_016854	0.292	-0.276	11.789	0.063	0.63	7.723	0.014	0.805	12.065	
Hepatic Cholestasis												

Continued

ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	NM_008830	0.131	-0.345	11.391	0.016	0.651	10.74	0.002	0.996	11.736
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_029600	0.021	-1.024	9.496	0.048	-0.82	10.315	0.227	-0.126	2.463
CD14	CD14 molecule	NM_009841	0.045	1.027	6.315	0.115	0.755	5.56	0.534	-0.272	5.288
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	NM_007824	0.064	1.472	9.635	0.082	-1.292	7.267	0.012	-2.291	8.163
CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	NM_007825	0.005	1.464	12.838	0.013	1.203	11.635	0.404	-0.286	12.756
ESR1	estrogen receptor 1	NM_007956	0.012	-0.862	8.244	0.02	-0.763	9.007	0.622	-0.111	4.922
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
IL1R1	interleukin 1 receptor, type I	NM_001123382	0.029	1.579	7.292	0.07	1.228	6.064	0.555	-0.351	5.713
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424
PPARA	peroxisome proliferator-activated receptor alpha	NM_001113418	0.008	-1.269	9.622	0.757	0.095	9.613	0.012	1.168	10.89
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	NM_008854	0.001	-0.837	6.149	0.164	-0.235	6.384	0.006	0.603	6.986
PRKCE	protein kinase C, epsilon	NM_011104	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287
SLC22A7	solute carrier family 22 (organic anion transporter), member 7	NM_144856	0.304	0.502	10.384	0.014	1.509	8.875	0.064	1.007	9.882
SLCO1A2	solute carrier organic anion transporter family, member 1A2	NM_030687	0.034	-1.539	8.012	0.025	-1.668	9.68	0.828	-0.129	9.551
SREBF1	sterol regulatory element binding transcription factor 1	NM_011480	0.003	-1.265	11.29	0.043	-0.663	11.952	0.06	0.602	12.555
Glucocorticoid Receptor Signaling											
AR	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	NM_013476	0.007	-0.93	3.522	0.002	-1.25	4.772	0.061	-0.626	5.533
CCL5	chemokine (C-C motif) ligand 5	NM_013653	0.603	0.125	4.088	0.008	-0.878	4.965	0.004	-1.003	3.963
CCNH	cyclin H	NM_023243	0.003	0.911	7.331	0.052	0.479	6.852	0.043	-0.306	8.953
CDK7	cyclin-dependent kinase 7	NM_009874	0.006	0.792	8.031	0.005	0.807	7.224	0.254	-0.047	2.306
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313
DUSP1	dual specificity phosphatase 1	NM_013642	0.005	-1.426	7.398	0.586	0.197	7.201	0.003	1.623	8.824
ESR1	estrogen receptor 1	NM_007956	0.012	-0.862	8.244	0.02	-0.763	9.007	0.622	-0.111	4.922
FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	NM_010186	0.003	1	6.698	0.1	0.421	6.276	0.037	-0.579	5.698
GTF2A2	general transcription factor II A, 2, 12 kDa	NM_001039519	0.003	1.047	9.899	0.048	0.562	9.337	0.077	-0.485	8.852
HSPA4	heat shock 70 kDa protein 4	NM_008300	0.011	-0.424	9.2	0.15	-0.194	9.394	0.016	1.251	7.18
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.003	-1.221	5.919	0.031	-0.715	6.634	0.095	0.506	7.14
PBX1	pre-B-cell leukemia homeobox 1	NM_008783	0.004	-1.118	5.635	0.042	-0.63	6.265	0.093	0.488	6.753

Continued

PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
POLR2A	(DNA directed) polymerase (RNA) II, polypeptide A, 220 kDa	NM_009089	0.025	-1.022	5.64	0.618	-0.183	5.822	0.051	0.839	6.661
POLR2C	(DNA directed) polymerase (RNA) II, polypeptide C, 33 kDa	NM_009090	0.005	0.856	9.071	0.058	0.467	8.604	0.1	-0.389	8.215
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	NM_008854	0.001	-0.837	6.149	0.164	-0.235	6.384	0.006	0.603	6.986
SMAD3	SMAD family member 3	NM_016769	0.005	-0.99	4.439	0.105	-0.438	4.877	0.052	0.552	5.429
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	NM_011416	0.023	-0.889	4.837	0.436	0.004	2.325	0.063	0.674	5.726
SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	NM_011417	0.003	-1.241	7.787	0.363	-0.302	5.462	0.004	1.198	9.028
STAT5A	signal transducer and activator of transcription 5A	NM_011488	0.009	-0.68	2.856	0.116	0.493	5.449	0.003	0.83	3.536
TBP	TATA box binding protein	NM_013684	0.004	0.863	6.324	0.002	0.98	5.344	0.576	0.117	5.461
NFkB Signaling											
CARD10	caspase recruitment domain family, member 10	NM_130859	0	-1.27	5.419	0.001	-0.993	6.413	0.142	0.276	6.689
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313
CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_007788	0.001	-1.087	7.111	0.015	-0.604	7.715	0.036	0.483	8.198
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	NM_007912	0.009	1.053	10.54	0.035	1.053	9.481	0.039	-0.733	9.487
GSK3B	glycogen synthase kinase 3 beta	NM_019827	0.003	-1.35	4.392	0.027	-0.818	5.21	0.108	0.627	6.711
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
IL1R1	interleukin 1 receptor, type I	NM_001123382	0.029	1.579	7.292	0.07	1.228	6.064	0.555	-0.351	5.713
KLK1B4	kallikrein 1-related peptidase b4	NM_010915	0.202	-0.411	4.457	0.03	-0.808	5.265	0.216	-0.397	4.869
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	NM_008809	0	-1.144	5.035	0.007	-0.598	5.633	0.01	0.546	6.179
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	NM_008854	0.001	-0.837	6.149	0.164	-0.235	6.384	0.006	0.603	6.986
TGFA	transforming growth factor, alpha	NM_031199	0.011	-0.891	6.539	0.051	-0.604	7.143	0.254	-0.099	2.284
TRAF3	TNF receptor-associated factor 3	NM_001048206	0.018	-1.553	4.619	0.272	-0.176	2.538	0.014	1.636	6.172
IL-10 Signaling											
BLVRA	biliverdin reductase A	NM_026678	0.000	0.840	9.077	0.001	0.535	8.542	0.015	-0.305	8.237
CD14	CD14 molecule	NM_009841	0.045	1.027	6.315	0.115	0.755	5.560	0.534	-0.272	5.288
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_010188	0.001	1.333	7.116	0.038	0.542	6.574	0.008	-0.791	5.783
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.060	0.645	-0.195	4.865
IL1R1	interleukin 1 receptor, type I	NM_001123382 /// NM_008362	0.029	1.579	7.292	0.070	1.228	6.064	0.555	-0.351	5.713
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.390	0.233	4.849	0.001	1.438	6.287
SOCS3	suppressor of cytokine signalling 3	NM_007707	0.006	0.900	5.801	0.000	1.482	4.318	0.039	0.582	4.901

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PTEN Signaling													
BCL2L11	BCL2-like 11 (apoptosis facilitator)	NM_009754	0.006	-1.103	3.951	0.193	-0.311	2.762	0.035	0.715	5.053		
CCND1	cyclin D1	NM_007631	0	-1.599	5.005	0	-1.239	6.244	0.041	0.355	7.465		
CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_007788	0.001	-1.087	7.111	0.015	-0.604	7.715	0.036	0.483	8.198		
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	NM_007912	0.009	1.053	10.54	0.035	1.053	9.481	0.039	-0.733	9.487		
FOXO3	forkhead box O3	NM_019740	0.01	-0.858	7.286	0.043	-0.591	7.877	0.091	-0.29	4.357		
GSK3B	glycogen synthase kinase 3 beta	NM_019827	0.003	-1.35	4.392	0.027	-0.818	5.21	0.108	0.627	6.711		
INPPL1	inositol polyphosphate phosphatase-like 1 platelet-derived growth	NM_001122739	0.006	-0.981	5.224	0.058	-0.561	5.785	0.132	0.42	6.205		
PDGFRB	factor receptor, beta polypeptide	NM_008809	0	-1.144	5.035	0.007	-0.598	5.633	0.01	0.546	6.179		
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234		
PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	NM_008960	0.005	-0.489	10.369	0.026	-0.982	10.268	0.124	0.204	10.859		
Estrogen Receptor Signaling													
CCNH	cyclin H	NM_023243	0.003	0.911	7.331	0.052	0.479	6.852	0.043	-0.306	8.953		
CDK7	cyclin-dependent kinase 7	NM_009874	0.006	0.792	8.031	0.005	0.807	7.224	0.254	-0.047	2.306		
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313		
ESR1	estrogen receptor 1	NM_007956	0.012	-0.862	8.244	0.02	-0.763	9.007	0.622	-0.111	4.922		
G6PC	glucose-6-phosphatase, catalytic subunit	NM_008061	0.098	-0.641	12.013	0.641	0.161	11.851	0.049	0.803	12.654		
HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37 kDa)	NM_001077265	0.004	-0.918	7.372	0.064	-0.283	4.374	0.064	0.472	8.289		
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424		
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.003	-1.221	5.919	0.031	-0.715	6.634	0.095	0.506	7.14		
POLR2A	polymerase (RNA) II (DNA directed)	NM_009089	0.025	-1.022	5.64	0.618	-0.183	5.822	0.051	0.839	6.661		
POLR2C	polymerase (RNA) II (DNA directed)	NM_009090	0.005	0.856	9.071	0.058	0.467	8.604	0.1	-0.389	8.215		
SMARCA4	polypeptide C, 33 kDa SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	NM_011417	0.003	-1.241	7.787	0.363	-0.302	5.462	0.004	1.198	9.028		
TBP	TATA box binding protein	NM_013684	0.004	0.863	6.324	0.002	0.98	5.344	0.576	0.117	5.461		
14-3-3 mediated Signaling													
AKT1S1	AKT1 substrate 1 (proline-rich)	NM_026270	0.013	-1.145	7.536	0.155	-0.541	8.077	0.094	0.464	5.732		
BAX	BCL2-associated X protein	NM_007527	0.003	-0.844	6.969	0.173	-0.28	7.248	0.02	0.564	7.812		
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	NM_007912	0.009	1.053	10.54	0.035	1.053	9.481	0.039	-0.733	9.487		
GSK3B	glycogen synthase kinase 3 beta	NM_019827	0.003	-1.35	4.392	0.027	-0.818	5.21	0.108	0.627	6.711		

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JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	NM_008809	0	-1.144	5.035	0.007	-0.598	5.633	0.01	0.546	6.179
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
PRKCE	protein kinase C, epsilon	NM_011104	0.003	-0.784	4.509	0.003	-0.802	5.311	0.254	0.003	2.287
RPS6KA1	ribosomal protein S6 kinase, 90 kDa, polypeptide 1	NM_009097	0.007	-1.049	5.943	0.209	-0.369	6.312	0.04	0.681	6.993
SNCA	synuclein, alpha (non A4 component of amyloid precursor)	NM_001042451	0.022	-1.043	8.316	0.003	-1.596	9.912	0.126	-0.59	9.648
TUBB2A	tubulin, beta 2A	NM_009450	0	-1.35	10.868	0.454	0.196	4.976	0	1.32	12.219
YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	NM_018871	0.001	-0.917	8.857	0.032	-0.405	9.262	0.012	0.512	9.774
PPAR Signaling											
CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	NM_001025432	0.005	-1.363	5.911	0.161	-0.511	6.422	0.018	0.027	2.313
IL1B	interleukin 1, beta	NM_008361	0.006	1.642	6.506	0.011	1.447	5.06	0.645	-0.195	4.865
IL1R1	interleukin 1 receptor, type I	NM_001123382	0.029	1.579	7.292	0.07	1.228	6.064	0.555	-0.351	5.713
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
NR0B2	nuclear receptor subfamily 0, group B, member 2	NM_011850	0.012	-1.395	9.029	0.062	-0.913	9.942	0.275	0.482	10.424
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.003	-1.221	5.919	0.031	-0.715	6.634	0.095	0.506	7.14
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	NM_008809	0	-1.144	5.035	0.007	-0.598	5.633	0.01	0.546	6.179
PPARA	peroxisome proliferator-activated receptor alpha	NM_001113418	0.008	-1.269	9.622	0.757	0.095	9.613	0.012	1.168	10.89
STAT5A	signal transducer and activator of transcription 5A	NM_011488	0.009	-0.68	2.856	0.116	0.493	5.449	0.003	0.83	3.536
TR/RXR Activation											
CYP7A1	cytochrome P450, family 7, subfamily A, polypeptide 1	NM_007824	0.064	1.472	9.635	0.082	-1.292	7.267	0.012	-2.291	8.163
DIO1	deiodinase, iodothyronine, type I	NM_007860	0.11	0.418	12.432	0	1.671	10.761	0.001	1.253	12.014
FASN	fatty acid synthase	NM_007988	0.002	-1.961	11.054	0.012	-1.338	12.392	0.154	0.623	13.015
G6PC	Glucose-6-phosphatase, catalytic subunit	NM_008061	0.098	-0.641	12.013	0.641	0.161	11.851	0.049	0.803	12.654
LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	NM_010700	0.005	-1.457	9.068	0.121	-0.625	9.692	0.043	0.743	3.31
ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	NM_008615	0.012	-1.137	11.44	0.017	-1.058	12.499	0.7	-0.172	11.28
PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
RCAN2	regulator of calcineurin 2	NM_030598	0	-2.667	5.18	0.018	-0.922	6.101	0.001	1.746	7.847
SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	NM_011400	0.034	-0.838	4.409	0.04	-0.799	5.208	0.693	0.09	4.814
SREBF1	sterol regulatory element binding transcription factor 1	NM_011480	0.003	-1.265	11.29	0.043	-0.663	11.952	0.06	0.602	12.555
THRSP	thyroid hormone responsive (SPOT14 homolog, rat)	NM_009381	0.099	-0.67	13.337	0.042	-0.883	14.219	0.477	-0.35	11.878
UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	NM_011671	0.032	-0.608	6.714	0.007	-0.881	7.595	0.26	-0.273	7.322

Cell Cycle: G1/S Checkpoint Regulation

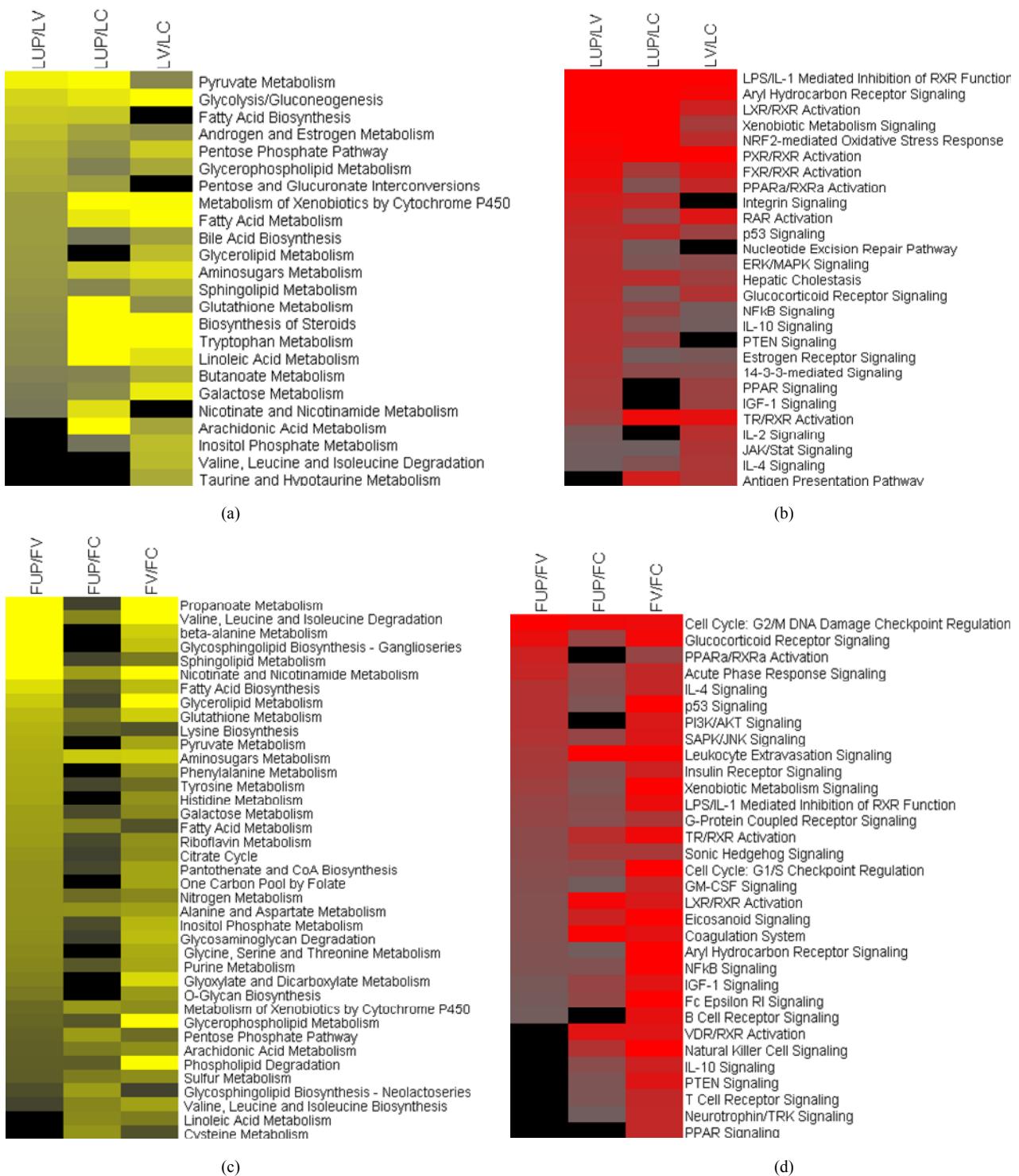
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CCND1	cyclin D1	NM_007631	0	-1.599	5.005	0	-1.239	6.244	0.041	0.355	7.465
CCND2	cyclin D2	NM_009829	0.001	-0.606	4.175	0.001	-0.944	5.89	0.132	-0.175	2.597
CDK6	Cyclin-dependent kinase 6	NM_009873	0.003	-1.2	5.302	0.015	-0.841	6.143	0.202	0.359	6.501
GSK3B	glycogen synthase kinase 3 beta	NM_019827	0.003	-1.35	4.392	0.027	-0.818	5.21	0.108	0.627	6.711
SMAD3	SMAD family member 3	NM_016769	0.005	-0.99	4.439	0.105	-0.438	4.877	0.052	0.552	5.429
IL-2 Signaling											
CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_007788	0.001	-1.087	7.111	0.015	-0.604	7.715	0.036	0.483	8.198
JUN	jun oncogene	NM_010591	0.003	-1.205	5.081	0.39	0.233	4.849	0.001	1.438	6.287
PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
STAT5A	signal transducer and activator of transcription 5A	NM_011488	0.009	-0.68	2.856	0.116	0.493	5.449	0.003	0.83	3.536
JAK/Stat Signaling											
PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
SOCS2	suppressor of cytokine signaling 2	NM_007706	0.003	2.46	8.84	0.254	0.074	2.291	0.005	-1.893	6.011
SOCS3	suppressor of cytokine signaling 3	NM_007707	0.006	0.9	5.801	0	1.482	4.318	0.039	0.582	4.901
STAT5A	signal transducer and activator of transcription 5A	NM_011488	0.009	-0.68	2.856	0.116	0.493	5.449	0.003	0.83	3.536
IL-4 Signaling											
HLA-DMA	major histocompatibility complex, class II, DM alpha	NM_010386	0.068	0.532	5.799	0.308	-0.268	6.068	0.015	-0.8	5.268
HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	NM_207105	0.793	-0.127	6.424	0.025	-1.355	7.779	0.036	-1.228	6.551
HLA-DRB1	major histocompatibility complex, class II, DR beta 1	NM_010382	0.903	-0.068	8.855	0.045	-1.327	10.182	0.054	-1.26	8.923
IL13RA1	interleukin 13 receptor, alpha 1	NM_133990	0.007	1.088	7.898	0.049	0.681	7.217	0.116	-0.452	7.264
INPPL1	inositol polyphosphate phosphatase-like 1	NM_001122739	0.006	-0.981	5.224	0.058	-0.561	5.785	0.132	0.42	6.205
PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.001	-1.124	6.417	0.061	-0.437	3.074	0.003	0.891	7.234
Antigen Presentation Pathway											
CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	NM_001042605	0.219	-0.511	9.262	0.017	-1.202	10.464	0.112	-0.691	9.773
HLA-DMA	major histocompatibility complex, class II, DM alpha	NM_010386	0.068	0.532	5.799	0.308	-0.268	6.068	0.015	-0.8	5.268
HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	NM_207105	0.793	-0.127	6.424	0.025	-1.355	7.779	0.036	-1.228	6.551
HLA-DRB1	major histocompatibility complex, class II, DR beta 1	NM_010382	0.903	-0.068	8.855	0.045	-1.327	10.182	0.054	-1.26	8.923

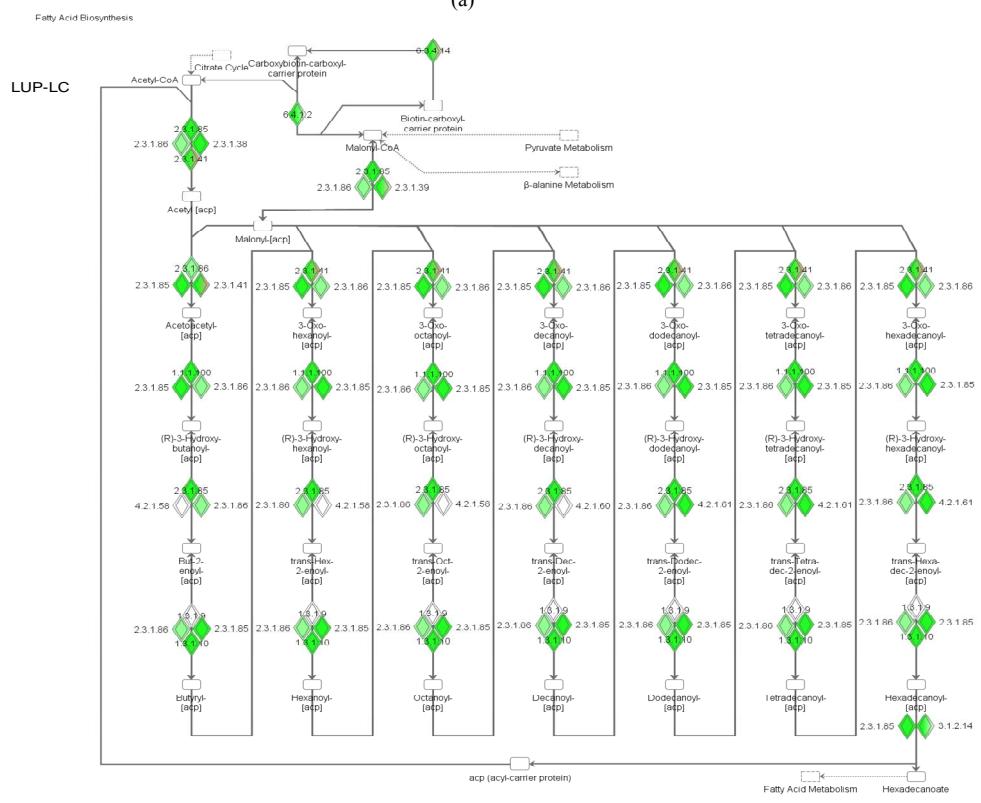
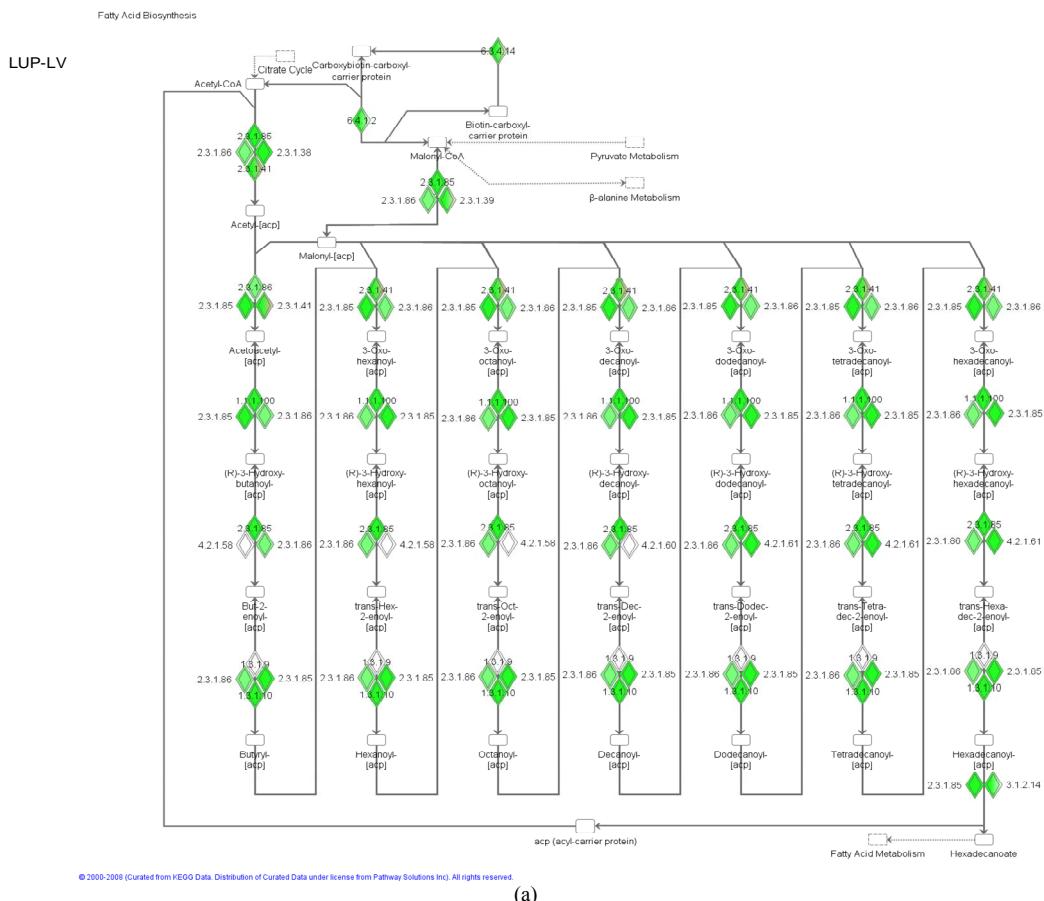
the total number of genes known to be associated with that pathway, 3) the total number of eligible genes included in the analysis, and 4) the total number of genes in the input data. Tables of $-\log(p\text{-value})$, to rank the significance, were exported from IPA into JavaTreeView [10] to generate heatmaps (**Supplement Figure 4**). IPA presents pathway analysis data in part as interactive graphs. Pathway graphs deemed to be highly significant to UP780 mechanism of action are illustrated in the **Supplement Figures 5** and **6**. In addition, genes included in the significant pathways from all three contrasts

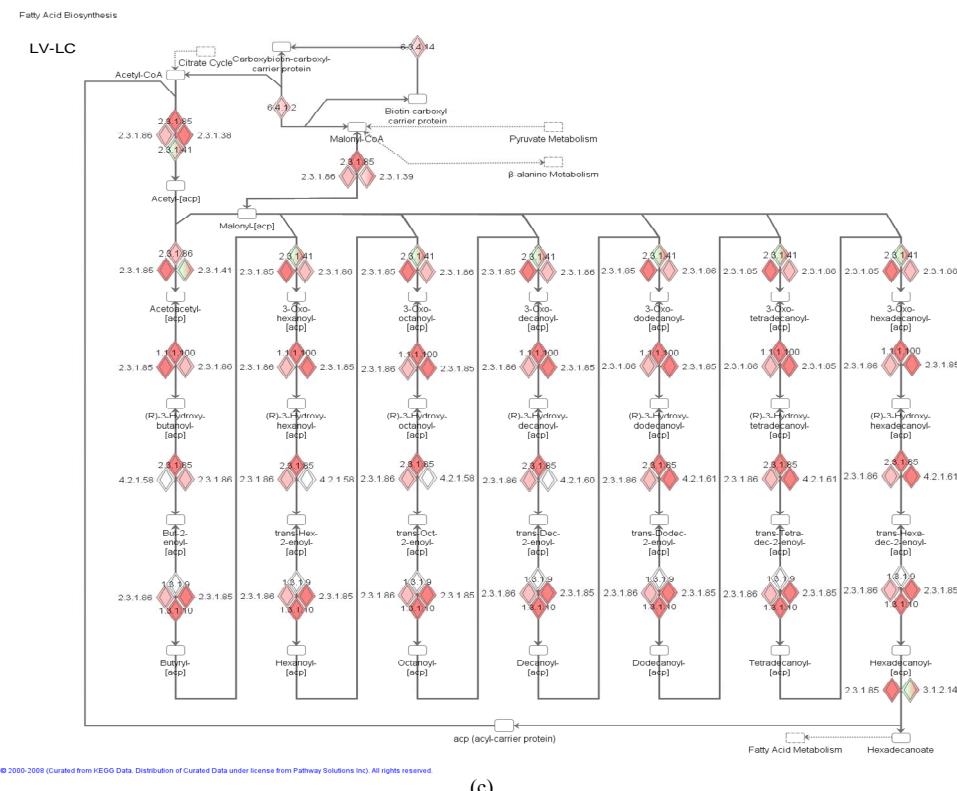
were exported to Excel as **Supplement Tables 1-4**.

From the Ingenuity pathway analysis result of significant Canonical Pathways, the p-values derived from the evaluation of the pathways in association with the gene expression variations were $-\log_{10}$ transformed and plotted as heatmaps [10], for liver metabolic pathways (**Supplement Figure 4(a)**) and signaling pathways (**Supplement Figure 4(b)**) and for WAT metabolic pathways (**Supplement Figure 4(c)**) and signaling pathways (**Supplement Figure 4(d)**). The complete gene lists for individual pathways in **Supplement Figure 4** are supplied as

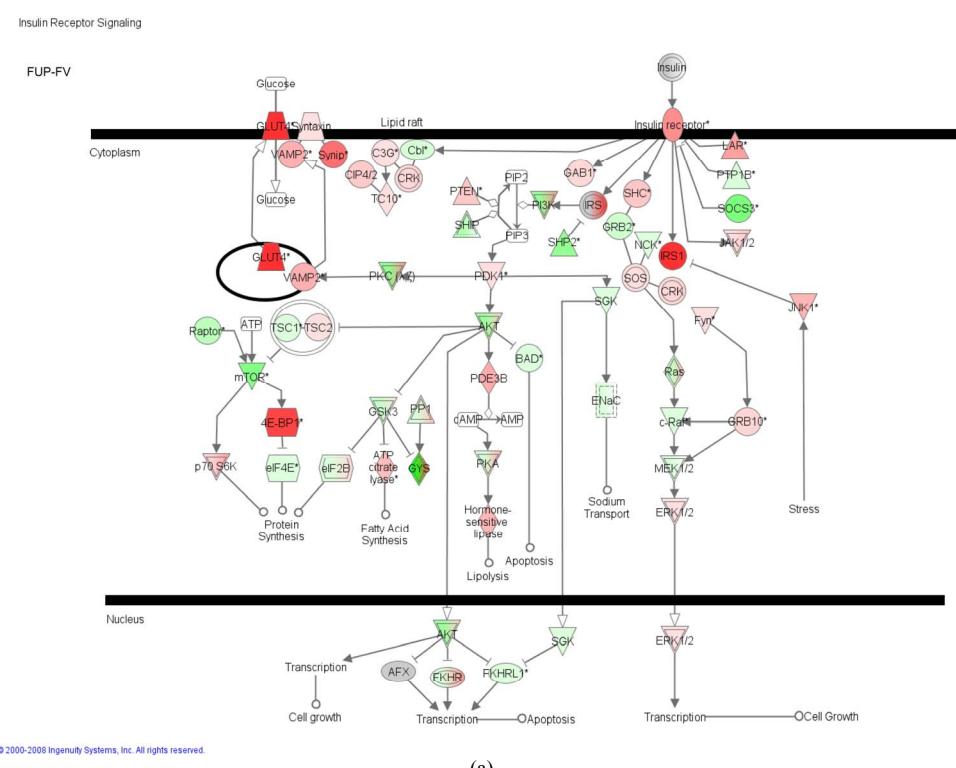


Supplement Figure 4. Significant pathways with gene expression variations measured by microarrays. Heatmaps [10] were used to illustrate the metabolic and signaling canonical pathways that passed at least one of the IPA statistic tests at $p < 0.05$ for gene expression variations in between contrasting RNA samples of HFD + UP780 vs. HFD, HFD + UP780 vs. lean control, and HFD vs. lean control. The color gradients correspond to the $-\log_{10}$ transformed p-values from the IPA pathway analysis of one-tailed Fisher's exact tests, with yellow for the metabolic pathways and red for the signaling pathways, and black denoting missing values. A. liver metabolic pathways; B. liver signaling pathways; C. WAT metabolic pathways; and D. WAT signaling pathways. C is an exception in that the cutoff value for \log_2 ratio was set at 0.5 instead of 0.8 when conducting the IPA pathway analysis, as described in materials and methods.

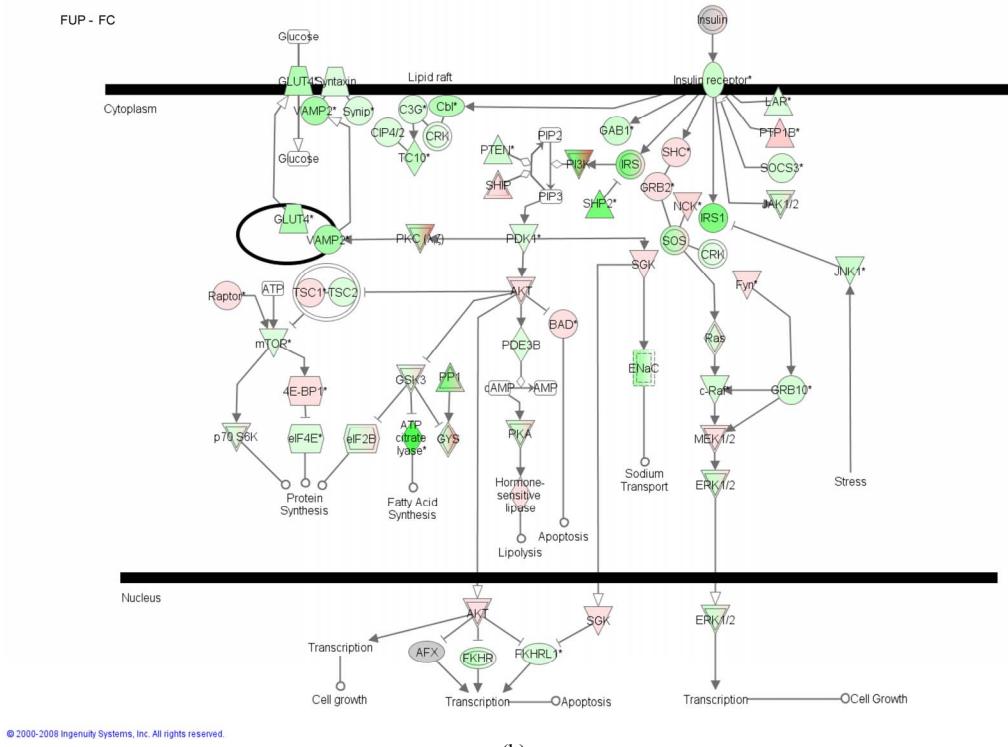




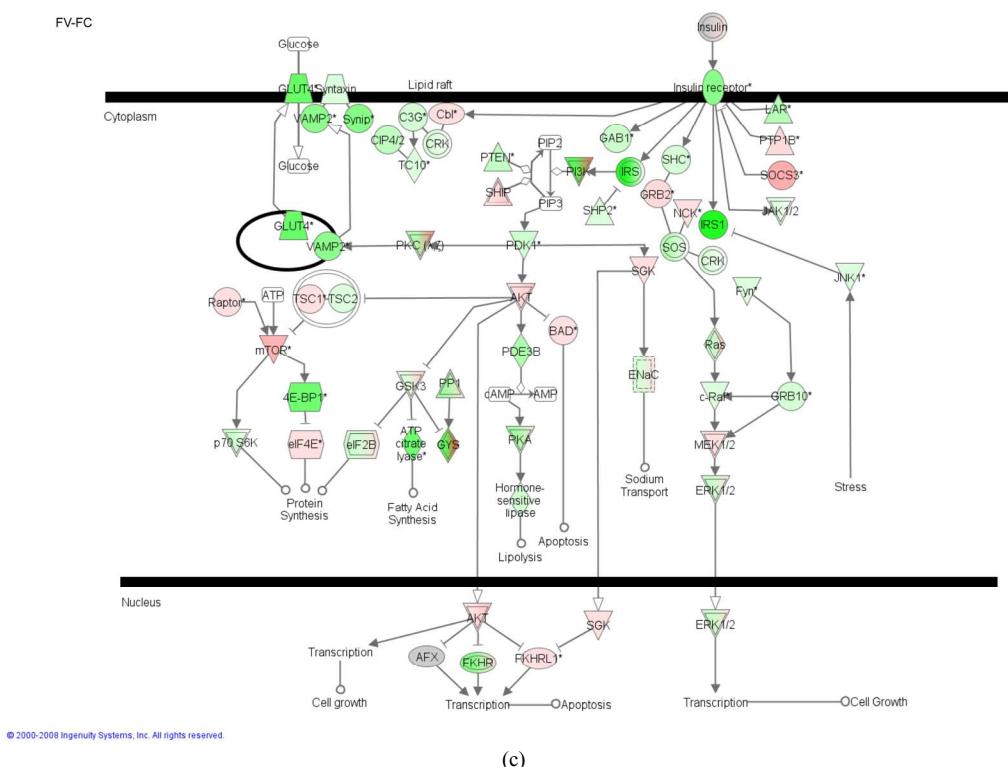
Supplement Figure 5. Liver canonical pathway of fatty acid biosynthesis. Fatty acid biosynthesis pathway figures for comparisons A, LUP-LV, B, LUP-LC, and C, LV-LC were overlaid with red (up-regulation) and green (down-regulation) according to the values of \log_2 ratio, with color gradient denoting the scale of up- or down-regulation. The figures were exported from the Ingenuity Pathway Analysis.



Insulin Receptor Signaling



Insulin Receptor Signaling



Supplement Figure 6. WAT canonical pathway of insulin receptor signaling. Insulin receptor signaling pathway figures for comparisons A, FUP-FV, B, FUP-FC, and C, FV-FC were overlaid with red (up-regulation) and green (down-regulation) according to the values of \log_2 ratio, with color gradient denoting the scale of up- or down-regulation. The figures were exported from the Ingenuity Pathway Analysis.

Supplement Table 3.

Name	Description	RefSeq ID	FUP/FV		FUP/FC		FV/FC		
			p-value	Log Ratio	Intensity	p-value	Log Ratio	Intensity	p-value
Propanoate Metabolism									
ACACA	acetyl-Coenzyme A carboxylase alpha	NM_133360	0.034	0.833	12.656	0.009	-2.07	5.182	0.001
ACACB	acetyl-Coenzyme A carboxylase beta	NM_133904	0.03	1.164	9.508	0.893	0.059	9.449	0.036
ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	NM_028037	0.008	0.906	8.387	0.37	0.068	2.183	0.003
ACAD11	A dehydrogenase family, member 11	NM_028721	0.009	0.587	12.508	0.376	0.185	13.851	0.03
ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	NM_025862	0.005	0.537	9.194	0.004	-0.559	9.753	0
ACADS	B A dehydrogenase, short/branched chain acyl-CoA synthetase	NM_025826	0.023	0.505	12.485	0.09	-0.338	12.823	0.002
ACSM5	medium-chain acyl-CoA synthetase family member 5	NM_178758	0.029	1.781	6.683	0.783	-0.181	6.864	0.019
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	NM_134042	0.002	0.503	12.566	0.009	-0.359	12.925	0
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	NM_138600	0.063	0.448	12.281	0.129	-0.346	12.627	0.006
DHCR24	24-dehydrocholesterol reductase	NM_053272	0.012	-0.788	8.527	0.869	0.039	8.489	0.009
ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NM_053119	0.041	0.411	13.874	0.457	-0.127	14.001	0.014
EHHADH	enoyl-Coenzyme A hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	NM_023737	0.044	0.605	10.052	0.57	0.145	9.907	0.103
GCDH	glutaryl-Coenzyme A dehydrogenase	NM_001044744	0.046	0.491	10.413	0.859	-0.037	10.45	0.036
HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	NM_146108	0.041	0.509	12.605	0.496	-0.303	6.948	0.017
IVD	isovaleryl Coenzyme A dehydrogenase	NM_019826	0.013	0.847	13.68	0.052	-0.55	11.655	0.001
LDHB	lactate dehydrogenase B	NM_008492	0.078	0.391	13.627	0.192	-0.278	12.671	0.016
MUT	methylmalonyl Coenzyme A mutase	NM_008650	0.007	0.455	13.304	0.255	-0.003	2.125	0.004
PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	NM_025835	0.015	0.852	12.85	0.714	-0.099	12.95	0.009
SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	NM_011507	0.036	0.729	10.32	0.106	-0.329	12.734	0.004
Valine, Leucine and Isoleucine Degradation									
9330129D05RIK	RIKEN cDNA 9330129D05 gene	XM_488540	0.003	1.082	9.448	0.298	0.26	9.188	0.011
ACAA1B	acyl-Coenzyme A acyltransferase 1B	NM_130864	0.138	-0.285	13.107	0.009	0.617	12.489	0.001
ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	NM_028037	0.008	0.906	8.387	0.37	0.068	2.183	0.003

Continued

ACAD11	acyl-Coenzyme A dehydrogenase family, member 11	NM_028721	0.009	0.587	12.508	0.376	0.185	13.851	0.03	-0.442	11.922
ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	NM_025862	0.005	0.537	9.194	0.004	-0.559	9.753	0	-1.097	8.657
ACADS	acyl-Coenzyme A dehydrogenase, short/branched chain	NM_025826	0.023	0.505	12.485	0.09	-0.338	12.823	0.002	-0.843	11.98
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	NM_134042	0.002	0.503	12.566	0.009	-0.359	12.925	0	-0.862	12.064
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	NM_138600	0.063	0.448	12.281	0.129	-0.346	12.627	0.006	-0.793	11.833
BCAT1	branched chain aminotransferase 1, cytosolic	NM_001024468	0.448	-0.618	7.92	0.018	0.877	3.754	0.007	1.091	4.845
BCAT2	branched chain aminotransferase 2, mitochondrial	NM_009737	0.1	0.513	8.935	0.339	-0.276	9.211	0.024	-0.789	8.422
BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide dihydrolipoamide	NM_007533	0.037	0.655	13.087	0.968	-0.01	13.097	0.035	-0.666	12.431
DBT	branched chain transacylase E2	NM_010022	0.024	0.641	10.512	0.138	-0.369	10.882	0.003	-1.01	9.871
ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NM_053119	0.041	0.411	13.874	0.457	-0.127	14.001	0.014	-0.539	13.463
EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	NM_023737	0.044	0.605	10.052	0.57	0.145	9.907	0.103	-0.46	9.447
GCDH	glutaryl-Coenzyme A dehydrogenase	NM_001044744	0.046	0.491	10.413	0.859	-0.037	10.45	0.036	-0.528	9.922
HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	NM_146108	0.041	0.509	12.605	0.496	-0.303	6.948	0.017	-0.641	12.096
HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	NM_145942	0.253	0.256	12.31	0.013	0.699	11.61	0.023	0.659	14.896
HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	NM_008256	0.006	1.257	11.845	0.031	0.868	10.978	0.258	-0.39	10.588
IVD	isovaleryl Coenzyme A dehydrogenase	NM_019826	0.013	0.847	13.68	0.052	-0.55	11.655	0.001	-1.253	10.402
MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	NM_023644	0.027	0.444	13.701	0.321	-0.168	13.868	0.007	-0.612	13.256
MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	NM_030026	0.009	0.521	12.3	0.096	-0.275	12.575	0.001	-0.796	11.779
MUT	methylmalonyl Coenzyme A mutase	NM_008650	0.007	0.455	13.304	0.255	-0.003	2.125	0.004	-0.527	12.849
PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	NM_025835	0.015	0.852	12.85	0.714	-0.099	12.95	0.009	-0.951	11.999
Beta-Alanine Metabolism											
9330129D05RIK	RIKEN cDNA 9330129D05 gene	XM_488540	0.003	1.082	9.448	0.298	0.26	9.188	0.011	-0.822	8.366

Continued

ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	NM_028037	0.008	0.906	8.387	0.37	0.068	2.183	0.003	-1.1	7.481
ACAD11	acyl-Coenzyme A dehydrogenase family, member 11	NM_028721	0.009	0.587	12.508	0.376	0.185	13.851	0.03	-0.442	11.922
ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	NM_025862	0.005	0.537	9.194	0.004	-0.559	9.753	0	-1.097	8.657
ACADS	acyl-Coenzyme A dehydrogenase, short/branched chain	NM_025826	0.023	0.505	12.485	0.09	-0.338	12.823	0.002	-0.843	11.98
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	NM_134042	0.002	0.503	12.566	0.009	-0.359	12.925	0	-0.862	12.064
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	NM_138600	0.063	0.448	12.281	0.129	-0.346	12.627	0.006	-0.793	11.833
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	NM_009675	0.005	0.53	14.416	0.186	-0.191	14.607	0.001	-0.721	13.886
DPYD	dihydropyrimidine dehydrogenase	NM_170778	0.013	0.637	9.48	0.055	-0.441	9.921	0.001	-1.078	8.843
ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NM_053119	0.041	0.411	13.874	0.457	-0.127	14.001	0.014	-0.539	13.463
EHHADH	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	NM_023737	0.044	0.605	10.052	0.57	0.145	9.907	0.103	-0.46	9.447
GCDH	glutaryl-Coenzyme A dehydrogenase	NM_001044744	0.046	0.491	10.413	0.859	-0.037	10.45	0.036	-0.528	9.922
HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	NM_146108	0.041	0.509	12.605	0.496	-0.303	6.948	0.017	-0.641	12.096
IVD	isovaleryl Coenzyme A dehydrogenase	NM_019826	0.013	0.847	13.68	0.052	-0.55	11.655	0.001	-1.253	10.402
SMS	spermine synthase	NM_009214	0.01	-0.441	7.06	0.012	0.423	6.637	0	0.864	7.501
Glycosphingolipid Biosynthesis—Ganmglioseries											
B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1	NM_008080	0.023	-0.826	8.162	0.138	0.472	7.69	0.003	1.299	8.988
CHI3L3	chitinase 3-like 3	NM_009892	0.047	-0.997	6.054	0.078	0.85	5.203	0.003	1.847	7.05
DBT	dihydrolipoamide branched chain transacylase E2	NM_010022	0.024	0.641	10.512	0.138	-0.369	10.882	0.003	-1.01	9.871
GLB1	galactosidase, beta 1	AW553762	0.044	0.917	7.97	0.004	0.282	10.92	0.001	0.369	11.288
GLB1L	galactosidase, beta 1-like	BB207162	0.005	0.636	8.014	0.207	-0.019	2.343	0.006	-0.615	7.378
GLB1L2	galactosidase, beta 1-like 2	NM_153803	0.028	0.508	14.096	0.033	-0.47	13.134	0.002	-0.879	12.256
ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	NM_009179	0.004	0.964	7.715	0.099	-0.416	7.643	0.002	-1.051	6.751
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	NM_009178	0.006	1.037	9.968	0.253	-0.011	2.324	0.003	-1.234	8.931

Continued

ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2, 3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	NM_011373	0.005	−0.842	5.309	0.059	0.467	4.842	0.001	1.309	6.151
ST8SIA4	ST8 alpha-N-acetyl-neuraminate alpha-2, 8-sialyltransferase 4	NM_009183	0.049	−1.529	2.759	0.64	0.31	2.449	0.025	1.839	4.287
Sphingolipid Metabolism											
ASAH2	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	NM_018830	0.002	0.564	9.084	0.039	−0.286	9.37	0	−0.849	8.52
CERK (includes EG:64781)	ceramide kinase	NM_145475	0.153	−0.486	9.449	0.059	0.686	8.763	0.007	1.172	9.935
GALC	galactosylceramidase	NM_008079	0.198	−0.391	10.185	0.002	1.087	4.748	0.002	1.059	5.806
GLA	galactosidase, alpha	NM_013463	0.045	−1.008	8.5	0.051	0.969	7.53	0.002	1.977	9.508
GLB1	galactosidase, beta 1	---	0.044	0.917	7.97	0.004	0.282	10.92	0.001	0.369	11.288
GLB1L	galactosidase, beta 1-like	---	0.005	0.636	8.014	0.207	−0.019	2.343	0.006	−0.615	7.378
GLB1L2	galactosidase, beta 1-like 2	NM_153803	0.028	0.508	14.096	0.033	−0.47	13.134	0.002	−0.879	12.256
KDSR	3-ketodihydrosphingosine reductase	NM_027534	0.004	0.76	9.115	0.093	−0.337	9.452	0.001	−1.097	8.355
PPAP2A	phosphatidic acid phosphatase type 2A	NM_008247	0.154	−0.308	11.42	0.309	0.21	11.209	0.033	0.518	11.728
SPHK1	sphingosine kinase 1	NM_011451	0.017	−1.173	4.766	0.113	0.668	4.098	0.002	1.841	5.939
SULF1	sulfatase 1	NM_172294	0.074	0.661	11.097	0.284	−0.315	2.943	0.049	−0.753	10.436
SULF2	sulfatase 2	NM_028072	0.002	0.66	12.889	0.545	0.245	8.922	0.003	−0.627	12.229
UGCG	UDP-glucose ceramide glucosyltransferase	NM_011673	0.001	0.744	7.738	0.121	0.247	7.49	0.01	−0.368	6.274
VNN1	vanin 1	NM_011704	0.003	0.913	9.747	0.019	0.614	9.133	0.173	−0.3	8.834
VNN2	vanin 2	NM_011979	0.005	1.429	10.815	0.745	−0.118	10.932	0.004	−1.547	9.386
Nicotine and Nicotinamide Metabolism											
ACVR2A	activin A receptor, type IIA	NM_007396	0.06	−0.395	5.998	0.109	0.322	5.676	0.005	0.717	6.393
AKT2	v-akt murine thymoma viral oncogene homolog 2	NM_001110208	0.02	0.692	11.06	0.489	0.164	10.896	0.016	−0.439	13
ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	NM_009703	0.038	0.376	10.45	0.258	0.245	11.406	0.02	−0.912	3.647
BST1	bone marrow stromal cell antigen 1	NM_009763	0.186	−0.466	8.101	0.32	0.338	7.763	0.041	0.804	8.566
CD38	CD38 molecule	NM_007646	0.002	1.162	7.285	0.035	−0.377	10.359	0	−1.043	9.315
CDC2	cell division cycle 2, G1 to S and G2 to M	NM_007659	0.013	−1.395	8.342	0.02	1.253	7.088	0	2.648	9.736
CDK6	cyclin-dependent kinase 6	NM_009873	0.024	−0.762	9.029	0.093	0.629	7.834	0.003	1.211	9.791
CDK7	cyclin-dependent kinase 7	NM_009874	0.043	−0.591	5.752	0.161	−0.283	6.617	0.023	−0.533	6.084
CSNK1D	casein kinase 1, delta	NM_027874	0.036	0.593	10.45	0.253	−0.043	2.526	0.026	−0.345	9.897
EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	NM_011163	0.034	0.58	6.376	0.261	0.163	6.524	0.088	−0.433	5.796
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	NM_008813	0.046	−1.405	5.35	0.185	0.845	4.505	0.007	2.25	6.755

Continued

ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	NM_015744	0	0.634	13.733	0	-0.484	5.976	0	-1.215	13.099
ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	NM_134005	0.096	0.472	7.501	0.253	-0.175	8.227	0.031	-0.667	7.029
ENPP5	Ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	NM_032003	0.02	0.663	11.621	0.352	-0.216	11.837	0.006	-0.879	10.958
GRK5	G protein-coupled receptor kinase 5	NM_018869	0.166	-0.242	10.366	0.028	0.436	9.93	0.004	0.678	10.608
IRAK1	interleukin-1 receptor-associated kinase 1	NM_008363	0.008	0.417	11.985	0.062	-0.131	8.168	0.003	-0.53	11.568
MAPK9	mitogen-activated protein kinase 9	NM_016961	0.06	0.215	7.449	0.012	-0.33	7.779	0.001	-0.545	7.234
NAMPT	nicotinamide phosphoribosyltransferase NIMA (never in mitosis gene a)	NM_021524	0.026	0.207	7.355	0.001	-0.512	10.566	0	-0.529	7.147
NEK2	related kinase 2	---	0.253	0.012	2.135	0.051	1.088	3.839	0.024	1.33	5.169
NMNAT1	nicotinamide nucleotide adenylyltransferase 1	NM_133435	0.039	-0.298	6.904	0.011	0.409	6.495	0.001	0.708	7.203
NMNAT3 (includes EG:349565)	nicotinamide nucleotide adenylyltransferase 3	NM_144533	0.801	-0.051	6.603	0.025	-0.574	7.177	0.035	-0.522	6.654
NNT	nicotinamide nucleotide transhydrogenase	NM_008710	0.086	0.251	9.147	0.002	-0.481	7.964	0	-0.66	7.304
NTSE	5'-nucleotidase, ecto (CD73)	NM_011851	0.002	1.233	5.667	0.003	-1.063	6.73	0	-2.296	4.434
PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	NM_011035	0.036	-0.962	7.984	0.301	0.477	7.838	0.013	1.446	9.283
PCTK3	PCTAIRE protein kinase 3	NM_008795	0.052	-1.766	6.542	0.001	3.965	2.577	0	5.73	8.308
PIM1	pim-1 oncogene	NM_008842	0.032	-1.3	3.545	0.459	0.18	8.558	0.06	1.086	4.845
PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	NM_001013367	0.009	0.408	6.52	0.001	-0.631	7.151	0	-1.039	6.112
PRKCD	protein kinase C, delta	NM_011103	0.15	-0.273	11.239	0.033	0.451	10.788	0.004	0.724	11.512
PRKCH	protein kinase C, eta	NM_008856	0.087	-0.743	10.472	0.027	0.997	7.892	0.003	1.594	9.486
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	NM_013830	0.008	0.345	8.006	0.071	-0.264	9.994	0.002	-0.563	8.844
VNN1	vanin 1	NM_011704	0.003	0.913	9.747	0.019	0.614	9.133	0.173	-0.3	8.834
VNN2	vanin 2	NM_011979	0.005	1.429	10.815	0.745	-0.118	10.932	0.004	-1.547	9.386
Fatty Acid Biosynthesis											
ACACA	acetyl-Coenzyme A carboxylase alpha	NM_133360	0.034	0.833	12.656	0.009	-2.07	5.182	0.001	-1.73	11.823
ACACB	acetyl-Coenzyme A carboxylase beta	NM_133904	0.03	1.164	9.508	0.893	0.059	9.449	0.036	-1.106	8.344
FASN	fatty acid synthase	NM_007988	0.262	0.185	14.606	0.017	-0.48	15.086	0.004	-0.665	14.421
MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	NM_030026	0.009	0.521	12.3	0.096	-0.275	12.575	0.001	-0.796	11.779
PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	NM_025835	0.015	0.852	12.85	0.714	-0.099	12.95	0.009	-0.951	11.999
Glycerolipid Metabolism											
ADHFE1	alcohol dehydrogenase, iron containing, 1	NM_175236	0.024	0.506	13.325	0.188	-0.253	13.578	0.004	-0.76	12.819

Continued

	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) aldo-keto reductase family 1, member B10 (aldose reductase)	NM_026792	0.006	-0.453	10.34	0.243	0.2	9.39	0.002	0.574	10.793
AKR1B10		NM_172398	0.026	-0.34	11.359	0.023	0.349	11.01	0.001	0.69	11.699
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	NM_138600	0.063	0.448	12.281	0.129	-0.346	12.627	0.006	-0.793	11.833
APOC2	apolipoprotein C-II	NM_009695	0.187	-0.44	9.316	0.073	0.639	8.677	0.01	1.08	9.756
CERK (includes EG:64781)	ceramide kinase	NM_145475	0.153	-0.486	9.449	0.059	0.686	8.763	0.007	1.172	9.935
DAGLB	diacylglycerol lipase, beta	NM_144915	0.054	-0.527	10.114	0.08	0.466	9.649	0.004	0.992	10.641
DGKZ	diacylglycerol kinase, zeta 104 kDa	NM_138306	0.106	-0.399	11.397	0.017	0.6	7.504	0.004	0.841	8.345
GK	glycerol kinase	NM_008194	0.03	-0.897	7.821	0.564	0.193	6.204	0.018	1.006	7.21
GLA	galactosidase, alpha	NM_013463	0.045	-1.008	8.5	0.051	0.969	7.53	0.002	1.977	9.508
GLB1	galactosidase, beta 1	---	0.044	0.917	7.97	0.004	0.282	10.92	0.001	0.369	11.288
GLB1L	galactosidase, beta 1-like	---	0.005	0.636	8.014	0.207	-0.019	2.343	0.006	-0.615	7.378
GLB1L2	galactosidase, beta 1-like 2	NM_153803	0.028	0.508	14.096	0.033	-0.47	13.134	0.002	-0.879	12.256
GLYCTK	glycerate kinase	NM_001039586	0.155	-0.622	3.75	0.069	0.844	2.906	0.008	1.466	4.371
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	NM_008149	0.019	0.977	9.215	0.15	-0.377	13.572	0.005	-1.326	8.238
LIPA	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	NM_001111100	0.044	-0.971	9.896	0.027	0.828	12.45	0.002	1.498	13.949
LIPF	lipase, gastric	NM_026334	0.21	-1.319	8.153	0.01	3.418	4.734	0.002	4.738	9.472
MGLL	monoglyceride lipase	NM_011844	0.003	0.274	14.677	0.019	0.185	14.492	0.017	0.819	5.255
MOGAT1	monoacylglycerol O-acyltransferase 1 patatin-like phospholipase domain containing 3	NM_026713	0.045	1.23	10.98	0.274	-0.589	11.569	0.009	-1.819	9.75
PNPLA3	phosphatidic acid phosphatase type 2A	NM_054088	0.309	0.351	9.154	0.157	-0.51	9.663	0.033	-0.861	8.803
PPAP2A	sphingosine kinase 1	NM_008247	0.154	-0.308	11.42	0.309	0.21	11.209	0.033	0.518	11.728
SPHK1	similar to aldo-keto reductase family 1, member B10	NM_011451	0.017	-1.173	4.766	0.113	0.668	4.098	0.002	1.841	5.939
TCAG7.1260		NM_008012	0.059	-0.593	12.179	0.599	0.143	12.036	0.027	0.736	12.772
Glutathione Metabolism											
G6PD2	glucose-6-phosphate dehydrogenase 2	NM_008062	0.086	0.208	11.592	0.001	0.59	11.002	0.009	0.381	11.384
GCLM	glutamate-cysteine ligase, modifier subunit	NM_008129	0.138	-0.358	10.577	0.366	-0.214	7.458	0.04	0.546	10.935
GGT6	gamma-glutamyltransferase 6	NM_027819	0.002	-1.32	4.6	0.123	0.479	4.12	0	1.799	5.919
GPX3	glutathione peroxidase 3 (plasma)	NM_001083929	0.008	0.692	15.37	0.063	-0.41	15.78	0.001	-1.102	14.677
GSTA3	glutathione S-transferase A3	NM_001077353	0.061	0.953	11.415	0.127	-0.725	9.233	0.006	-1.656	7.577

Continued

GSTA4	glutathione S-transferase A4	NM_010357	0.04	0.853	11.386	0.122	-0.589	11.975	0.004	-1.441	10.533
GSTO1	glutathione S-transferase omega 1	NM_010362	0.102	-0.283	10.549	0.006	0.463	12.792	0.001	0.673	13.464
GSTT1	glutathione S-transferase theta 1	NM_008185	0.013	0.59	12.791	0.026	-0.502	13.293	0.001	-1.092	12.201
GSTT2	glutathione S-transferase theta 2	NM_010361	0.006	0.683	11.146	0.63	-0.086	11.232	0.004	-0.77	10.463
GSTT3	glutathione S-transferase, theta 3	NM_133994	0.022	0.862	8.133	0.007	-1.124	9.257	0	-1.987	7.271
H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	NM_173371	0.002	0.688	14.002	0.939	-0.011	14.013	0.002	-0.699	13.314
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	NM_173011	0.014	0.505	13.076	0.951	0.01	13.067	0.016	-0.496	12.571
LNPEP	leucyl/cystinyl aminopeptidase	NM_172827	0.002	0.539	11.772	0.05	-0.046	2.178	0	-0.787	11.232
LTC4S	leukotriene C4 synthase	NM_008521	0.665	-0.042	14.476	0	0.748	13.728	0	0.79	14.517
MGST2	microsomal glutathione S-transferase 2	NM_174995	0.043	-0.457	10.739	0.327	0.192	10.547	0.011	0.649	11.196
PGDS	prostaglandin D2 synthase, hematopoietic	NM_019455	0.112	-1.715	7.268	0.103	1.77	5.498	0.009	3.485	8.984
RAB15	RAB15, member RAS oncogene family	NM_134050	0.18	-0.669	7.353	0.106	0.837	6.516	0.014	1.507	8.023
TRHDE	thyrotropin-releasing hormone degrading enzyme	NM_146241	0.118	0.991	4.864	0.058	-1.27	6.134	0.006	-2.261	3.873
Lysine Biosynthesis											
AASDHPPT	amino adipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	NM_026276	0.017	0.56	7.337	0.036	-0.463	7.8	0.001	-1.024	6.777
VNN1	vanin 1	NM_011704	0.003	0.913	9.747	0.019	0.614	9.133	0.173	-0.3	8.834
VNN2	vanin 2	NM_011979	0.005	1.429	10.815	0.745	-0.118	10.932	0.004	-1.547	9.386
Pyruvate Metabolism											
ACACA	acetyl-Coenzyme A carboxylase alpha	NM_133360	0.034	0.833	12.656	0.009	-2.07	5.182	0.001	-1.73	11.823
ACACB	acetyl-Coenzyme A carboxylase beta	NM_133904	0.03	1.164	9.508	0.893	0.059	9.449	0.036	-1.106	8.344
ACSM5	acyl-CoA synthetase medium-chain family member 5	NM_178758	0.029	1.781	6.683	0.783	-0.181	6.864	0.019	-1.963	4.901
AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	NM_172398	0.026	-0.34	11.359	0.023	0.349	11.01	0.001	0.69	11.699
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	NM_138600	0.063	0.448	12.281	0.129	-0.346	12.627	0.006	-0.793	11.833
BCKDHA	branched chain keto acid dehydrogenase E1, alpha polypeptide	NM_007533	0.037	0.655	13.087	0.968	-0.01	13.097	0.035	-0.666	12.431
LDHB	lactate dehydrogenase B	NM_008492	0.078	0.391	13.627	0.192	-0.278	12.671	0.016	-0.608	13.236
LDHD	lactate dehydrogenase D	NM_027570	0.033	0.88	9.491	0.574	-0.179	9.868	0.055	-0.762	8.611
NKD1	naked cuticle homolog 1 (<i>Drosophila</i>) nudix (nucleoside diphosphate linked moiety X)-type motif 7	NM_027280	0.147	-0.383	8.007	0.177	0.353	6.959	0.021	0.703	8.389
NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	NM_024437	0.001	-0.568	11.735	0.058	0.313	12.288	0	0.776	12.302

Continued

PC	pyruvate carboxylase	NM_008797	0.053	0.355	14.585	0.334	-0.157	14.741	0.013	-0.511	14.23
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	NM_011044	0.002	2.193	12.827	0.783	0.181	12.921	0.002	-2.229	10.633
PDHA1 (includes EG:5160)	pyruvate dehydrogenase (lipoamide) alpha 1	NM_008810	0.012	0.255	14.666	0.003	-0.349	15.014	0	-0.603	14.411
PDHB	pyruvate dehydrogenase (lipoamide) beta	NM_024221	0.306	0.149	14.083	0.019	-0.774	10.036	0.006	-0.541	13.934
RWDD2B	RWD domain containing 2B	NM_016924	0.014	-0.6	7.627	0.747	0.061	7.566	0.009	0.661	8.227
TCAG7.1260	similar to aldo-keto reductase family 1, member B10	NM_008012	0.059	-0.593	12.179	0.599	0.143	12.036	0.027	0.736	12.772
Aminosugars Metabolism											
CHI3L3	chitinase 3-like 3	NM_009892	0.047	-0.997	6.054	0.078	0.85	5.203	0.003	1.847	7.05
CMAH	cytidine monophosphate-N-acetylneuraminate hydroxylase(CMP-N-acetylneuraminate monooxygenase) pseudogene	NM_001111110	0.038	0.563	5.526	0.181	-0.07	3.162	0.13	-0.375	4.964
CMAS	cytidine monophosphate N-acetylneuraminate acid synthetase	NM_009908	0.102	-0.223	11.727	0.034	0.314	11.413	0.003	0.537	11.95
CYB561	cytochrome b-561	BE133856	0.231	0.052	2.178	0.146	0.39	9.951	0.049	0.571	10.522
HK1	hexokinase 1	NM_010438	0.042	0.813	7.697	0.195	0.464	7.233	0.316	-0.349	6.884
HK2	hexokinase 2	NM_013820	0.31	0.195	11.454	0.024	-0.519	11.973	0.006	-0.713	11.259
HK3	hexokinase 3 (white cell)	NM_001033245	0.03	-0.966	8.121	0.017	1.122	6.999	0.001	2.087	9.086
NANS	N-acetylneuraminic acid synthase (sialic acid synthase)	NM_053179	0.002	-0.663	9.19	0.025	0.229	11.614	0	0.545	12.159
PDE1A	phosphodiesterase 1A, calmodulin-dependent	NM_001009978	0.003	1.239	8.699	0.059	-0.608	9.306	0	-1.847	7.46
PDE2A	phosphodiesterase 2A, cGMP-stimulated	NM_001008548	0.148	-0.252	10.092	0.004	0.683	9.41	0.001	0.935	10.345
PDE3B	phosphodiesterase 3B, cGMP-inhibited	NM_011055	0.003	0.491	13.119	0.129	-0.179	13.298	0	-0.67	12.628
PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_019840	0	1.104	8.99	0.001	0.883	8.107	0.222	-0.222	7.885
PDE7A	phosphodiesterase 7A	NM_001122759	0.14	-0.436	8.998	0.003	1.237	8.55	0.001	1.448	9.997
PDE7B	phosphodiesterase 7B	NM_013875	0.11	-0.672	9.416	0.113	0.666	8.75	0.009	1.339	10.088
PDE8B	phosphodiesterase 8B	NM_172263	0.043	-1.083	3.146	0.803	0.111	3.035	0.03	1.194	4.229
PGM3	phosphoglucomutase 3	NM_028352	0.135	0.35	8.521	0.451	-0.164	8.685	0.044	-0.514	8.172
RENBP	renin binding protein	NM_023132	0.019	-0.632	10.641	0.029	0.571	10.07	0.001	1.204	11.273
UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1	NM_133806	0.006	0.434	10.855	0.123	-0.229	9.853	0.002	-0.547	10.421
Phenylalanine Metabolism											
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	NM_026316	0.017	-0.56	7.848	0.046	0.431	7.417	0.001	0.992	8.409
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	NM_009675	0.005	0.53	14.416	0.186	-0.191	14.607	0.001	-0.721	13.886
DBT	dihydrolipoamide branched chain transacylase E2	NM_010022	0.024	0.641	10.512	0.138	-0.369	10.882	0.003	-1.01	9.871

Continued

DHCR24	24-dehydrocholesterol reductase	NM_053272	0.012	-0.788	8.527	0.869	0.039	8.489	0.009	0.827	9.315
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	NM_010324	0.798	-0.052	9.489	0.038	0.51	8.978	0.026	0.563	9.541
MAOA	monoamine oxidase A	NM_173740	0.01	-0.523	12.262	0.582	-0.229	7.565	0.008	0.559	12.784
MAOB	monoamine oxidase B	NM_172778	0.038	0.463	12.2	0.035	-0.473	12.673	0.002	-0.936	11.737
MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	NM_010798	0.049	-0.256	13.282	0.037	0.277	13.005	0.002	0.534	13.539
Tyrosine Metabolism											
ADHFE1	alcohol dehydrogenase, iron containing, 1	NM_175236	0.024	0.506	13.325	0.188	-0.253	13.578	0.004	-0.76	12.819
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	NM_026316	0.017	-0.56	7.848	0.046	0.431	7.417	0.001	0.992	8.409
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	NM_009675	0.005	0.53	14.416	0.186	-0.191	14.607	0.001	-0.721	13.886
BCKDHA	branched chain keto acid dehydrogenase	NM_007533	0.037	0.655	13.087	0.968	-0.01	13.097	0.035	-0.666	12.431
DBT	E1, alpha polypeptide dihydrolipoamide branched chain transacylase E2	NM_010022	0.024	0.641	10.512	0.138	-0.369	10.882	0.003	-1.01	9.871
FRRS1	ferric-chelate reductase 1	NM_001113478	0.039	-0.542	9.868	0.038	0.545	9.323	0.002	1.087	10.41
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	NM_010324	0.798	-0.052	9.489	0.038	0.51	8.978	0.026	0.563	9.541
MAOA	monoamine oxidase A	NM_173740	0.01	-0.523	12.262	0.582	-0.229	7.565	0.008	0.559	12.784
MAOB	monoamine oxidase B	NM_172778	0.038	0.463	12.2	0.035	-0.473	12.673	0.002	-0.936	11.737
MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	NM_010798	0.049	-0.256	13.282	0.037	0.277	13.005	0.002	0.534	13.539
Histidine Metabolism											
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	NM_026316	0.017	-0.56	7.848	0.046	0.431	7.417	0.001	0.992	8.409
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	NM_138600	0.063	0.448	12.281	0.129	-0.346	12.627	0.006	-0.793	11.833
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	NM_009675	0.005	0.53	14.416	0.186	-0.191	14.607	0.001	-0.721	13.886
DBT	dihydrolipoamide branched chain transacylase E2	NM_010022	0.024	0.641	10.512	0.138	-0.369	10.882	0.003	-1.01	9.871
HARS2	histidyl-tRNA synthetase 2, mitochondrial (putative)	NM_080636	0.014	0.56	9.206	0.522	0.12	5.406	0.02	-0.516	8.646
HNMT	histamine N-methyltransferase	NM_080462	0.018	0.452	11.034	0.211	-0.199	11.233	0.003	-0.651	10.582
MAOA	monoamine oxidase A	NM_173740	0.01	-0.523	12.262	0.582	-0.229	7.565	0.008	0.559	12.784
MAOB	monoamine oxidase B	NM_172778	0.038	0.463	12.2	0.035	-0.473	12.673	0.002	-0.936	11.737
PRPS1	phosphoribosyl pyrophosphate synthetase 1	NM_021463	0.038	-0.472	13.71	0.005	0.76	12.225	0	1.185	13.41

Continued**Galactose Metabolism**

AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	NM_172398	0.026	-0.34	11.359	0.023	0.349	11.01	0.001	0.69	11.699
GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	NM_008064	0.003	0.668	10.984	0.395	0.133	10.851	0.006	-0.318	9.011
GLA	galactosidase, alpha	NM_013463	0.045	-1.008	8.5	0.051	0.969	7.53	0.002	1.977	9.508
GLB1	galactosidase, beta 1	AW553762	0.044	0.917	7.97	0.004	0.282	10.92	0.001	0.369	11.288
GLB1L	galactosidase, beta 1-like	BB207162	0.005	0.636	8.014	0.207	-0.019	2.343	0.006	-0.615	7.378
GLB1L2	galactosidase, beta 1-like 2	NM_153803	0.028	0.508	14.096	0.033	-0.47	13.134	0.002	-0.879	12.256
HK1	hexokinase 1	NM_010438	0.042	0.813	7.697	0.195	0.464	7.233	0.316	-0.349	6.884
HK2	hexokinase 2	NM_013820	0.31	0.195	11.454	0.024	-0.519	11.973	0.006	-0.713	11.259
HK3	hexokinase 3 (white cell)	NM_001033245	0.03	-0.966	8.121	0.017	1.122	6.999	0.001	2.087	9.086
PFKM	phosphofructokinase, muscle	NM_021514	0.031	0.497	9.384	0.311	-0.198	9.582	0.007	-0.694	8.888
PGM1	phosphoglucomutase 1	NM_025700	0.07	0.346	13.557	0.353	-0.16	13.716	0.018	-0.506	13.21
PGM3	phosphoglucomutase 3	NM_028352	0.135	0.35	8.521	0.451	-0.164	8.685	0.044	-0.514	8.172
TCAG7.1260	similar to aldo-keto reductase family 1, member B10	NM_008012	0.059	-0.593	12.179	0.599	0.143	12.036	0.027	0.736	12.772
UGP2	UDP-glucose pyrophosphorylase 2	NM_139297	0.009	0.325	13.374	0.002	-0.468	11.745	0	-0.747	10.998

Fatty Acid Metabolism

9330129D05RIK	RIKEN cDNA 9330129D05 gene	XM_488540	0.003	1.082	9.448	0.298	0.26	9.188	0.011	-0.822	8.366
ACAA1B	acetyl-Coenzyme A acyltransferase 1B	NM_130864	0.138	-0.285	13.107	0.009	0.617	12.489	0.001	0.902	13.391
ACAD10	acyl-Coenzyme A dehydrogenase family, member 10	NM_028037	0.008	0.906	8.387	0.37	0.068	2.183	0.003	-1.1	7.481
ACAD11	acyl-Coenzyme A dehydrogenase family, member 11	NM_028721	0.009	0.587	12.508	0.376	0.185	13.851	0.03	-0.442	11.922
ACAD8	acyl-Coenzyme A dehydrogenase family, member 8	NM_025862	0.005	0.537	9.194	0.004	-0.559	9.753	0	-1.097	8.657
ACADS8	acyl-Coenzyme A dehydrogenase, short/branched chain	NM_025826	0.023	0.505	12.485	0.09	-0.338	12.823	0.002	-0.843	11.98
ACOX3	acyl-Coenzyme A oxidase 3, pristanoyl	NM_030721	0.324	0.182	7.467	0.014	0.571	6.896	0.061	0.388	7.285
ADHFE1	alcohol dehydrogenase, iron containing, 1	NM_175236	0.024	0.506	13.325	0.188	-0.253	13.578	0.004	-0.76	12.819
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	NM_009656	0.022	0.533	8.298	0.104	-0.302	13.448	0.003	-0.756	12.692
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	NM_138600	0.063	0.448	12.281	0.129	-0.346	12.627	0.006	-0.793	11.833
CPT1A	carnitine palmitoyltransferase 1A (liver)	NM_013495	0.609	0.073	12.711	0.005	0.578	12.134	0.009	0.505	12.638
CYP2C44	cytochrome P450, family 2, subfamily c, polypeptide 44	NM_001001446	0.001	-2.814	5.549	0.002	2.405	3.144	0	5.219	8.363
CYP2C70	cytochrome P450, family 2, subfamily c, polypeptide 70	NM_145499	0.038	-1.289	2.723	0.426	0.418	2.305	0.012	1.707	4.012

Continued

CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6	NM_019823	0.001	1.07	8.348	0.004	-0.434	9.841	0	-0.98	8.862
CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	NM_007817	0.443	0.79	4.829	0.003	-4.431	9.26	0.001	-5.221	4.039
CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	NM_010008	0.088	0.283	7.918	0.127	-0.246	8.165	0.008	-0.53	7.635
CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	NM_007823	0.108	0.195	10.787	0.001	0.599	10.188	0.007	0.404	10.592
ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	NM_053119	0.041	0.411	13.874	0.457	-0.127	14.001	0.014	-0.539	13.463
EHHADH	glutaryl-Coenzyme A dehydrogenase	NM_023737	0.044	0.605	10.052	0.57	0.145	9.907	0.103	-0.46	9.447
GCDH	isovaleryl Coenzyme A dehydrogenase	NM_001044744	0.046	0.491	10.413	0.859	-0.037	10.45	0.036	-0.528	9.922
IVD	solute carrier family 27 (fatty acid transporter), member 1	NM_019826	0.013	0.847	13.68	0.052	-0.55	11.655	0.001	-1.253	10.402
SLC27A1		NM_011977	0.004	0.813	11.768	0.016	0.619	11.149	0.342	-0.194	10.955
Riboflavin Metabolism											
ACP6	acid phosphatase 6, lysophosphatidic acid phosphatase/ectonucleotide	NM_019800	0.542	0.128	8.704	0.037	-0.526	9.229	0.016	-0.654	8.575
ENPP1	pyrophosphatase/phosphodiesterase 1 ectonucleotide	NM_008813	0.046	-1.405	5.35	0.185	0.845	4.505	0.007	2.25	6.755
ENPP2	pyrophosphatase/phosphodiesterase 2 (autotaxin) ectonucleotide	NM_015744	0	0.634	13.733	0	-0.484	5.976	0	-1.215	13.099
ENPP3	pyrophosphatase/phosphodiesterase 3 ectonucleotide	NM_134005	0.096	0.472	7.501	0.253	-0.175	8.227	0.031	-0.667	7.029
ENPP5	pyrophosphatase/phosphodiesterase 5 (putative function) phosphatidic acid phosphatase type 2 domain containing 2	NM_032003	0.02	0.663	11.621	0.352	-0.216	11.837	0.006	-0.879	10.958
PPAPDC2		NM_028922	0.032	0.671	8.277	0.071	-0.532	8.809	0.002	-1.203	7.606
Citrate Cycle											
ACLY	ATP citrate lyase	NM_134037	0.311	0.38	12.337	0.003	-0.937	14.13	0.001	-1.142	12.988
ACO1	aconitase 1, soluble	NM_007386	0.014	0.295	12.258	0.008	-0.335	12.593	0	-0.63	11.963
ACO2	aconitase 2, mitochondrial dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	NM_080633	0.02	0.576	13.986	0.254	0.005	2.126	0.017	-0.603	13.41
DLST		NM_030225	0.002	0.639	5.389	0.078	-0.247	13.008	0.001	-0.676	4.75
IDH2	isocitrate dehydrogenase 2 (NADP ⁺), mitochondrial	NM_173011	0.014	0.505	13.076	0.951	0.01	13.067	0.016	-0.496	12.571
PC	pyruvate carboxylase	NM_008797	0.053	0.355	14.585	0.334	-0.157	14.741	0.013	-0.511	14.23
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble) succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	NM_011044	0.002	2.193	12.827	0.783	0.181	12.921	0.002	-2.229	10.633
SDHA		NM_023281	0.003	0.428	13.729	0.069	-0.199	13.927	0	-0.626	13.301
SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	NM_011507	0.036	0.729	10.32	0.106	-0.329	12.734	0.004	-0.776	11.958
Pantothenate and CoA Biosynthesis											
BCAT1	branched chain aminotransferase 1, cytosolic	NM_001024468	0.448	-0.618	7.92	0.018	0.877	3.754	0.007	1.091	4.845

Continued

BCAT2	branched chain aminotransferase 2, mitochondrial	NM_009737	0.1	0.513	8.935	0.339	-0.276	9.211	0.024	-0.789	8.422
DPYD	dihydropyrimidine dehydrogenase	NM_170778	0.013	0.637	9.48	0.055	-0.441	9.921	0.001	-1.078	8.843
ENPP1	Ectonucleotide pyrophosphatase/phosphodiesterase 1 ectonucleotide	NM_008813	0.046	-1.405	5.35	0.185	0.845	4.505	0.007	2.25	6.755
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	NM_015744	0	0.634	13.733	0	-0.484	5.976	0	-1.215	13.099
ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3 ectonucleotide	NM_134005	0.096	0.472	7.501	0.253	-0.175	8.227	0.031	-0.667	7.029
ENPP5	pyrophosphatase/phosphodiesterase 5 (putative function)	NM_032003	0.02	0.663	11.621	0.352	-0.216	11.837	0.006	-0.879	10.958
One Carbon Pool by Folate											
EHD4	EH-domain containing 4 phosphoribosylglycinamide formyltransferase,	NM_133838	0.045	-0.472	11.346	0.344	0.193	11.152	0.012	0.666	11.818
GART	phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	NM_010256	0.026	0.733	6.031	0.158	-0.407	6.439	0.004	-1.14	5.299
MTFMT	mitochondrial methionyl-tRNA formyltransferase	NM_027134	0.024	0.535	8.713	0.644	0.157	4.964	0.036	-0.479	8.178
MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1,	NM_138745	0.192	0.277	10.105	0.171	-0.293	10.398	0.022	-0.571	9.827
MTHFD1L	methylene tetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	NM_172308	0.146	-0.408	4.851	0.24	0.319	4.531	0.024	0.727	5.258
MTHFD2	methylene tetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	NM_008638	0.027	-0.616	8.241	0.174	0.329	7.912	0.004	0.945	8.857
PDPK	pyruvate dehydrogenase phosphatase regulatory subunit	BB667201	0.002	0.442	10.152	0.006	-0.341	10.493	0	-0.783	9.71
TYMS	thymidylate synthetase	NM_021288	0.03	-0.55	8.022	0.275	0.235	7.787	0.006	0.785	8.572
Nitrogen Metabolism											
ASNS	asparagine synthetase	NM_012055	0.012	0.543	12.503	0.022	-0.475	12.978	0.001	-1.018	11.96
CA13	carbonic anhydrase XIII	NM_024495	0.508	0.178	3.418	0.017	-0.632	7.984	0.014	-0.661	7.323
CA3	carbonic anhydrase III, muscle specific	NM_007606	0.008	0.174	15.645	0.208	-0.833	12.791	0.003	-2.866	9.925
CA4	carbonic anhydrase IV	NM_007607	0.031	0.707	9.466	0.016	0.832	8.634	0.547	0.17	8.01
CA5B	carbonic anhydrase VB, mitochondrial	NM_019513	0.015	0.974	11.934	0.189	-0.239	11.687	0.006	-1.222	10.96
CA8	carbonic anhydrase VIII	NM_007592	0.207	0.339	5.473	0.24	-0.312	5.786	0.034	-0.651	5.135
CA9	carbonic anhydrase IX	NM_139305	0.104	-1.251	3.229	0.462	0.517	2.712	0.035	1.768	4.48

Continued

CTH	cystathionase (cystathionine gamma-lyase)	NM_145953	0.02	-0.699	9.125	0.268	0.276	8.849	0.005	0.975	9.824
PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	BB667201	0.002	0.442	10.152	0.006	-0.341	10.493	0	-0.783	9.71
PTPRG	protein tyrosine phosphatase, receptor type, G	NM_008981	0.001	0.499	8.83	0.009	-0.328	9.158	0	-0.827	8.331
VNN1	vanin 1	NM_011704	0.003	0.913	9.747	0.019	0.614	9.133	0.173	-0.3	8.834
VNN2	vanin 2	NM_011979	0.005	1.429	10.815	0.745	-0.118	10.932	0.004	-1.547	9.386
Alanine and Aspartate Metabolism											
ADSL	adenylosuccinate lyase	NM_009634	0.198	0.28	10.082	0.214	-0.269	10.351	0.029	-0.55	9.801
ADSSL1	adenylosuccinate synthase like 1	NM_007421	0.023	-0.956	9.522	0.016	1.041	8.481	0.001	1.996	10.477
ASNS	asparagine synthetase	NM_012055	0.012	0.543	12.503	0.022	-0.475	12.978	0.001	-1.018	11.96
ASS1	argininosuccinate synthetase 1	NM_007494	0.002	-1.845	6.465	0.694	0.154	6.31	0.002	1.999	8.309
CRAT	carnitine acetyltransferase	NM_007760	0.003	0.607	11.47	0.312	0.123	4.974	0.002	-0.617	10.863
DDO	D-aspartate oxidase	NM_027442	0.043	0.662	7.798	0.144	-0.436	8.234	0.005	-1.099	7.136
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	NM_010324	0.798	-0.052	9.489	0.038	0.51	8.978	0.026	0.563	9.541
GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	NM_173866	0.02	0.917	11.372	0.027	-0.589	11.014	0.001	-1.195	9.819
PC	pyruvate carboxylase	NM_008797	0.053	0.355	14.585	0.334	-0.157	14.741	0.013	-0.511	14.23
PDHA1 (includes EG:5160)	pyruvate dehydrogenase (lipoamide) alpha 1	NM_008810	0.012	0.255	14.666	0.003	-0.349	15.014	0	-0.603	14.411
PDHB	pyruvate dehydrogenase (lipoamide) beta	NM_024221	0.306	0.149	14.083	0.019	-0.774	10.036	0.006	-0.541	13.934
Inositol Phosphate Metabolism											
ACVR2A	activin A receptor, type IIA	NM_007396	0.06	-0.395	5.998	0.109	0.322	5.676	0.005	0.717	6.393
AKT2	v-akt murine thymoma viral oncogene homolog 2	NM_00111020	0.02	0.692	11.06	0.489	0.164	10.896	0.016	-0.439	13
ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	NM_009703	0.038	0.376	10.45	0.258	0.245	11.406	0.02	-0.912	3.647
CDC2	cell division cycle 2, G1 to S and G2 to M	NM_007659	0.013	-1.395	8.342	0.02	1.253	7.088	0	2.648	9.736
CDK6	cyclin-dependent kinase 6	NM_009873	0.024	-0.762	9.029	0.093	0.629	7.834	0.003	1.211	9.791
CDK7	cyclin-dependent kinase 7	NM_009874	0.043	-0.591	5.752	0.161	-0.283	6.617	0.023	-0.533	6.084
CSNK1D	casein kinase 1, delta	NM_027874	0.036	0.593	10.45	0.253	-0.043	2.526	0.026	-0.345	9.897
EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	NM_011163	0.034	0.58	6.376	0.261	0.163	6.524	0.088	-0.433	5.796
GRK5	G protein-coupled receptor kinase 5	NM_018869	0.166	-0.242	10.366	0.028	0.436	9.93	0.004	0.678	10.608
INPP1	inositol polyphosphate-1-phosphatase	NM_008384	0.012	0.798	8.696	0.987	0.004	8.692	0.013	-0.794	7.898
INPP5D	inositol polyphosphate-5-phosphatase, 145 kDa	NM_001110192	0.028	-0.539	7.477	0.083	0.388	6.693	0.006	0.776	8.016
INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	NM_033134	0.036	0.373	8.194	0.202	-0.2	8.394	0.006	-0.573	7.821
IRAK1	interleukin-1 receptor-associated kinase 1	NM_008363	0.008	0.417	11.985	0.062	-0.131	8.168	0.003	-0.53	11.568

Continued

MAPK9	mitogen-activated protein kinase 9 NIMA (never in mitosis gene a)-related kinase 2	NM_016961 BB203873	0.06 0.253	0.215 0.012	7.449 2.135	0.012 0.051	-0.33 1.088	7.779 3.839	0.001 0.024	-0.545 1.33	7.234 5.169
NEK2	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	NM_011035	0.036	-0.962	7.984	0.301	0.477	7.838	0.013	1.446	9.283
PCTK3	PCTAIRE protein kinase 3	NM_008795	0.052	-1.766	6.542	0.001	3.965	2.577	0	5.73	8.308
PI4K2A	phosphatidylinositol 4-kinase type 2 alpha	NM_145501	0.013	-0.277	11.346	0.002	0.453	7.825	0	0.619	11.623
PI4K2B	phosphatidylinositol 4-kinase type 2 beta	NM_025951	0.056	-0.355	8.647	0.018	0.693	6.639	0.002	0.749	9.001
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIM1	pim-1 oncogene	NM_008842	0.032	-1.3	3.545	0.459	0.18	8.558	0.06	1.086	4.845
PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	NM_008844	0.057	-0.483	9.721	0.647	0.1	9.621	0.029	0.582	10.204
PLCB4	phospholipase C, beta 4	NM_013829	0.015	1.036	4.286	0.28	-0.212	10.733	0.01	-1.154	3.251
PLCD1	phospholipase C, delta 1	NM_019676	0.013	0.645	10.652	0.094	-0.374	11.027	0.001	-1.019	10.007
PLCD3	phospholipase C, delta 3	NM_152813	0.056	0.609	6.56	0.478	-0.196	6.756	0.02	-0.806	5.951
PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	NM_172285	0.014	-0.475	9.296	0.439	0.116	9.181	0.005	0.591	9.771
PLCL2	phospholipase C-like 2	NM_013880	0.031	-0.398	9.447	0.301	0.161	9.285	0.007	0.559	9.844
PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	NM_001013367	0.009	0.408	6.52	0.001	-0.631	7.151	0	-1.039	6.112
PRKCD	protein kinase C, delta	NM_011103	0.15	-0.273	11.239	0.033	0.451	10.788	0.004	0.724	11.512
PRKCH	protein kinase C, eta	NM_008856	0.087	-0.743	10.472	0.027	0.997	7.892	0.003	1.594	9.486
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	NM_013830	0.008	0.345	8.006	0.071	-0.264	9.994	0.002	-0.563	8.844
Glycosaminoglycan Degradation											
AFP	alpha-fetoprotein	NM_007423	0.068	-1.708	2.718	0.114	0.381	3.333	0.022	0.631	3.964
CHI3L3	chitinase 3-like 3	NM_009892	0.047	-0.997	6.054	0.078	0.85	5.203	0.003	1.847	7.05
GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)	NM_016722	0.129	-0.279	9.491	0.08	0.334	9.157	0.008	0.613	9.77
GLB1	galactosidase, beta 1	AW553762	0.044	0.917	7.97	0.004	0.282	10.92	0.001	0.369	11.288
GLB1L	galactosidase, beta 1-like	BB207162	0.005	0.636	8.014	0.207	-0.019	2.343	0.006	-0.615	7.378
GLB1L2	galactosidase, beta 1-like 2	NM_153803	0.028	0.508	14.096	0.033	-0.47	13.134	0.002	-0.879	12.256
GUSB	glucuronidase, beta	NM_010368	0.101	-0.432	12.27	0.023	0.747	10.177	0.002	1.093	12.702
IDS	iduronate 2-sulfatase (Hunter syndrome)	NM_001038990	0.025	0.303	7.605	0.028	-0.268	12.593	0.001	-0.527	12.066
MGEA5	meningioma expressed antigen 5 (hyaluronidase)	NM_023799	0.004	0.38	10.546	0.074	-0.234	12.444	0.001	-0.535	10.166
SULF1	sulfatase 1	NM_172294	0.074	0.661	11.097	0.284	-0.315	2.943	0.049	-0.753	10.436
SULF2	sulfatase 2	NM_028072	0.002	0.66	12.889	0.545	0.245	8.922	0.003	-0.627	12.229

Supplement Table 4.

Name	Description	RefSeq ID	FUP/FV			FUP/FC			FV/FC				
			p-value	Log Ratio	Intensity	p-value	Log Ratio	Intensity	p-value	Log Ratio	Intensity		
Cell Cycle: G2/M DNA Damage Checkpoint Regulation													
BRCA1	breast cancer 1, early onset	NM_009764	0.045	-1.721	4.598	0.265	0.843	3.755	0.009	2.564	6.318		
CCNB1	cyclin B1	NM_172301	0.026	-1.571	5.055	0.064	1.214	3.841	0.002	2.785	6.626		
CCNB2	cyclin B2	NM_007630	0.016	-1.52	7.083	0.031	1.282	5.8	0.001	2.802	8.602		
CDC2	cell division cycle 2, G1 to S and G2 to M	NM_007659	0.013	-1.395	8.342	0.02	1.253	7.088	0	2.648	9.736		
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_001111099	0.026	-0.679	9.893	0.001	1.468	8.425	0	2.146	10.571		
SKP2	S-phase kinase-associated protein 2 (p45)	NM_013787	0.214	-0.599	3.876	0.138	0.737	3.139	0.02	1.337	4.476		
TOP2A	topoisomerase (DNA) II alpha 170 kDa	NM_011623	0.023	-1.53	6.184	0.076	1.083	5.1	0.002	2.614	7.714		
UBD	ubiquitin D	NM_023137	0.022	-2.072	12.159	0.001	4.475	7.683	0	6.547	14.23		
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	BF714941	0.012	1.219	5.874	0.053	-0.267	8.76	0.003	-1.598	4.655		
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_011740	0.008	-0.876	7.273	0.447	-0.188	7.461	0.024	0.688	8.148		
Glucocorticoid Receptor Signaling													
AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	NM_007428	0.012	1.903	12.813	0.207	-0.772	13.584	0.002	-2.674	10.91		
AR	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	NM_013476	0.001	0.866	10.48	0.031	-0.445	10.925	0	-1.311	9.615		
BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672		
CCL13	chemokine (C-C motif) ligand 13	NM_011333	0.001	-1.425	10.787	0	1.683	9.103	0	3.109	12.212		
CCL3	chemokine (C-C motif) ligand 3	NM_011337	0.033	-1.316	4.068	0.019	1.505	2.563	0.001	2.821	5.383		
CD163	CD163 molecule	NM_053094	0.072	0.681	10.343	0.108	-0.591	10.934	0.006	-1.272	9.662		
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_001111099	0.026	-0.679	9.893	0.001	1.468	8.425	0	2.146	10.571		
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	NM_009876	0.223	0.223	9.726	0.008	-0.634	10.36	0.002	-0.857	9.503		
CXCL3	chemokine (C-X-C motif) ligand 3	NM_009140	0.919	0.061	4.962	0.048	1.422	3.541	0.055	1.361	4.901		
ESR1	estrogen receptor 1	NM_007956	0.041	0.52	6.097	0.033	-0.551	6.648	0.002	-1.071	5.577		

Continued

FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	NM_010186	0.048	-1.167	6.736	0.224	0.613	9.285	0.015	1.513	10.798
FKBP5	FK506 binding protein 5	NM_010220	0.049	0.842	7.948	0.226	-0.249	11.349	0.054	-0.439	10.909
FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	NM_010234	0.077	-1.089	10.759	0.207	0.725	10.034	0.012	1.813	11.848
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	NM_019777	0.013	-0.555	8.531	0.029	0.456	8.075	0.001	1.012	9.086
IL1R2	interleukin 1 receptor, type II	NM_010555	0.002	-1.453	2.719	0.318	0.305	2.413	0.001	1.759	4.172
IL1RN	interleukin 1 receptor antagonist	NM_001039701	0.005	-1.805	2.203	0	3.3	3.963	0	4.59	8.553
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256
NCOR1	nuclear receptor co-repressor 1	NM_011308	0.002	0.864	8.333	0.039	-0.595	5.03	0.001	-1.134	7.47
NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NM_008173_0	0	0.988	8.946	0.001	-0.542	12.348	0	-1.444	7.958
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.002	0.675	10.356	0.004	-0.572	10.928	0	-1.247	9.681
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	NM_011044	0.002	2.193	12.827	0.783	0.181	12.921	0.002	-2.229	10.633
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_008871	0.044	-1.615	8.757	0.403	0.578	8.179	0.013	2.194	10.373
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	NM_011416	0	0.519	9.873	0.001	-0.325	10.198	0	-0.844	9.354
TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68 kDa	NM_027427	0.006	1.104	4.151	0.173	-0.647	3.913	0.031	-0.753	3.047
TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65 kDa	NM_146092	0.061	-0.401	7.943	0.057	0.411	7.532	0.003	0.812	8.343
TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31 kDa	NM_001001176	0.006	0.868	8.582	0.081	-0.448	9.03	0.001	-1.316	7.713
TGFB3	transforming growth factor, beta 3	NM_009368	0.001	0.495	10.669	0.009	-0.337	11.006	0	-0.832	10.174

Continued

TGFBR2	transforming growth factor, beta receptor II (70/80 kDa)	NM_009371	0.001	0.966	9.972	0.218	0.228	9.744	0.004	-0.739	9.005
TRA@	T cell receptor alpha locus	XM_001471582	0.038	-1.438	8.857	0.035	1.472	7.385	0.002	2.909	10.295
VCAM1	vascular cell adhesion molecule 1	NM_011693	0.078	-0.706	6.165	0.225	0.452	5.714	0.013	1.158	6.872
PPARα/RXRα Activation											
ACVR1C	activin A receptor, type IC	NM_001033369	0.001	0.859	8.051	0.002	-0.725	8.777	0	-1.584	7.192
ADCY7	adenylate cyclase 7	NM_001037723	0.08	-0.758	10.645	0.204	0.467	7.078	0.019	1.034	8.113
BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672
CYP2C44	cytochrome P450, family 2, subfamily c, polypeptide 44	NM_001001446	0.001	-2.814	5.549	0.002	2.405	3.144	0	5.219	8.363
CYP2C70	cytochrome P450, family 2, subfamily c, polypeptide 70	NM_145499	0.038	-1.289	2.723	0.426	0.418	2.305	0.012	1.707	4.012
GK	glycerol kinase	NM_008194	0.03	-0.897	7.821	0.564	0.193	6.204	0.018	1.006	7.21
GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	NM_010274	0.008	1.084	5.657	0.001	-1.621	7.277	0	-2.704	4.573
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	NM_019777	0.013	-0.555	8.531	0.029	0.456	8.075	0.001	1.012	9.086
IL1R2	interleukin 1 receptor, type II	NM_010555	0.002	-1.453	2.719	0.318	0.305	2.413	0.001	1.759	4.172
INSR	insulin receptor	NM_001033381	0	0.668	9.937	0.022	-0.275	10.212	0	-0.943	9.269
IRS1	insulin receptor substrate 1	NM_010570	0.006	1.387	11.258	0.089	-0.681	11.939	0.001	-2.067	9.872
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256
NCOR1	nuclear receptor co-repressor 1	NM_011308	0.002	0.864	8.333	0.039	-0.595	5.03	0.001	-1.134	7.47
PLCB4	phospholipase C, beta 4	NM_013829	0.015	1.036	4.286	0.28	-0.212	10.733	0.01	-1.154	3.251
PLCD1	phospholipase C, delta 1	NM_019676	0.013	0.645	10.652	0.094	-0.374	11.027	0.001	-1.019	10.007
PLCD3	phospholipase C, delta 3	NM_152813	0.056	0.609	6.56	0.478	-0.196	6.756	0.02	-0.806	5.951
SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	NM_011977	0.004	0.813	11.768	0.016	0.619	11.149	0.342	-0.194	10.955
TGFB3	transforming growth factor, beta 3	NM_009368	0.001	0.495	10.669	0.009	-0.337	11.006	0	-0.832	10.174
TGFBR2	transforming growth factor, beta receptor II (70/80 kDa)	NM_009371	0.001	0.966	9.972	0.218	0.228	9.744	0.004	-0.739	9.005

Acute Phase Response Signaling

Continued

AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	NM_007428	0.012	1.903	12.813	0.207	-0.772	13.584	0.002	-2.674	10.91				
BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672				
C2	complement component 2	NM_013484	0.005	0.859	12.656	0.057	-0.441	14.039	0.001	-1.319	11.797				
CP	ceruloplasmin (ferroxidase)	NM_001042611	0.003	0.867	11.589	0.016	-0.513	11.028	0	-1.278	10.722				
FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	NM_010234	0.077	-1.089	10.759	0.207	0.725	10.034	0.012	1.813	11.848				
FRAP1	FK506 binding protein 12-rapamycin associated protein 1	NM_020009	0.05	-0.825	4.157	0.274	-0.144	10.371	0.031	0.938	4.981				
HMOX1	heme oxygenase (decyclining) 1	NM_010442	0.242	-0.495	9.717	0.194	0.557	9.16	0.032	1.052	10.212				
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	NM_019777	0.013	-0.555	8.531	0.029	0.456	8.075	0.001	1.012	9.086				
IL1RN	interleukin 1 receptor antagonist	NM_001039701	0.005	-1.805	2.203	0	3.3	3.963	0	4.59	8.553				
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887				
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256				
NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NM_008173	0	0.988	8.946	0.001	-0.542	12.348	0	-1.444	7.958				
ORM1	orosomucoid 1	NM_011016	0.001	-1.35	6.237	0	1.542	4.695	0	2.892	7.587				
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11				
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764				
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017				
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112				
RBP7	retinol binding protein 7, cellular	NM_022020	0.209	0.547	10.121	0.008	1.48	8.64	0.052	0.934	9.574				
SAA2	serum amyloid A2	NM_011315	0.015	-2.323	11.267	0.738	0.245	11.022	0.01	2.568	13.59				
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	NM_009243	0.002	-1.046	4.653	0.264	0.242	4.411	0	1.288	5.699				
SERpine1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_008871	0.044	-1.615	8.757	0.403	0.578	8.179	0.013	2.194	10.373				
SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	NM_011340	0.57	0.092	13.765	0.001	0.924	12.841	0.001	0.757	13.916				

Continued

TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	NM_008764	0.147	0.525	6.2	0.075	-0.675	6.875	0.008	-1.2	5.675
P53 Signaling											
BAX	BCL2-associated X protein	NM_007527	0.033	-0.451	11.466	0.056	0.386	11.079	0.002	0.837	11.917
BIRC5	baculoviral IAP repeat-containing 5 (survivin)	NM_001012273	0.03	-1.655	6.71	0.074	1.274	5.436	0.002	2.929	8.366
BRCA1	breast cancer 1, early onset	NM_009764	0.045	-1.721	4.598	0.265	0.843	3.755	0.009	2.564	6.318
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_001111099	0.026	-0.679	9.893	0.001	1.468	8.425	0	2.146	10.571
E2F1	E2F transcription factor 1	NM_007891	0.085	-0.354	6.977	0.016	0.663	8.141	0.002	0.904	7.331
GADD45B	growth arrest and DNA-damage-inducible, beta	NM_008655	0.003	-0.949	10.17	0.089	0.407	9.762	0	1.356	11.118
HDAC9	histone deacetylase 9	NM_024124	0.11	-0.461	8.363	0.131	0.43	7.933	0.011	0.891	8.824
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PLAGL1	pleiomorphic adenoma gene-like 1	NM_009538	0.002	1.079	13.007	0.029	-0.604	13.61	0	-1.683	11.928
RB1	retinoblastoma 1 (including osteosarcoma)	NM_009029	0.038	-0.65	4.483	0.098	0.483	4.001	0.003	1.133	5.134
SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	NM_019812	0.103	0.352	7.59	0.048	-0.451	8.041	0.004	-0.804	7.237
THBS1	thrombospondin 1	NM_011580	0.001	1.08	11.08	0.199	0.399	11.387	0.002	-0.984	10
WT1	Wilms tumor 1	NM_144783	0.047	0.689	8.517	0.041	-0.721	9.238	0.002	-1.411	7.827
IL-4 Signaling											
FRAP1	FK506 binding protein 12-rapamycin associated protein 1	NM_020009	0.05	-0.825	4.157	0.274	-0.144	10.371	0.031	0.938	4.981
HLA-DMB	major histocompatibility complex, class II, DM beta	NM_010387	0.004	-1.038	9.338	0.03	0.435	11.761	0	1.094	12.855
HMGAI	high mobility group AT-hook 1	NM_001025427	0.028	-0.867	10.864	0.023	0.911	9.953	0.001	1.778	11.731
IRS1	insulin receptor substrate 1	NM_010570	0.006	1.387	11.258	0.089	-0.681	11.939	0.001	-2.067	9.872

Continued

NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NM_008173	0	0.988	8.946	0.001	-0.542	12.348	0	-1.444	7.958
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PI3K/AKT Signaling											
BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_001111099	0.026	-0.679	9.893	0.001	1.468	8.425	0	2.146	10.571
CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	NM_009875	0.125	0.39	8.696	0.093	-0.436	9.132	0.009	-0.826	8.306
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	NM_007918	0.016	1.108	9.708	0.838	0.03	14.414	0.013	-1.158	8.599
FOXO1	forkhead box O1	NM_019739	0.007	0.656	10.756	0.1	-0.323	11.079	0.001	-0.979	10.1
FRAP1	FK506 binding protein 12-rapamycin associated protein 1	NM_020009	0.05	-0.825	4.157	0.274	-0.144	10.371	0.031	0.938	4.981
GYS1	glycogen synthase 1 (muscle)	NM_030678	0.011	1.096	7.294	0.493	-0.225	7.52	0.005	-1.321	6.199
GYS2	glycogen synthase 2 (liver)	NM_145572	0.005	-1.67	8.426	0.085	0.809	7.617	0.001	2.479	10.096
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	NM_019777	0.013	-0.555	8.531	0.029	0.456	8.075	0.001	1.012	9.086
MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	NM_011162	0.007	1.17	7.242	0.05	-0.722	7.964	0.001	-1.892	6.071
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PPP2R3A (includes EG:5523)	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	XM_001474396	0.007	0.486	6.878	0.004	-0.55	7.428	0	-1.036	6.392
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	BF714941	0.012	1.219	5.874	0.053	-0.267	8.76	0.003	-1.598	4.655
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_011740	0.008	-0.876	7.273	0.447	-0.188	7.461	0.024	0.688	8.148

Continued**SAPK/JNK Signaling**

GNG2	guanine nucleotide binding protein (G protein), gamma 2	NM_001038637	0.008	-1.146	8.658	0.135	0.514	8.144	0.001	1.661	9.804
GNG7	guanine nucleotide binding protein (G protein), gamma 7	NM_001038655	0.016	0.966	6.278	0.645	-0.142	6.42	0.008	-1.109	5.311
IRS1	insulin receptor substrate 1	NM_010570	0.006	1.387	11.258	0.089	-0.681	11.939	0.001	-2.067	9.872
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
MAP3K13	mitogen-activated protein kinase kinase kinase 13	XM_001480812	0.1	0.676	4.22	0.443	0	2.122	0.05	-0.85	3.543
MAP3K3	mitogen-activated protein kinase kinase kinase 3	NM_011947	0.049	-2.011	5.549	0.137	-1.412	6.962	0.092	-0.237	9.719
MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	NM_008279	0.2	-0.252	7.733	0.002	0.867	6.866	0.001	1.119	7.985
MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	NM_011162	0.007	1.17	7.242	0.05	-0.722	7.964	0.001	-1.892	6.071
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
TRA@	T cell receptor alpha locus	XM_001471582	0.038	-1.438	8.857	0.035	1.472	7.385	0.002	2.909	10.295
TRG@	T cell receptor gamma locus	NM_011558	0.262	0.396	3.995	0.072	-0.695	4.69	0.013	-1.09	3.599

Leukocyte Extravasation Signaling

ACTN1	actinin, alpha 1	NM_134156	0.032	-0.786	5.706	0.04	0.743	8.142	0.002	1.523	6.492
ACTN3	actinin, alpha 3	NM_013456	0.221	0.612	7.425	0.03	-1.26	8.685	0.005	-1.873	6.813
ARHGAP4	Rho GTPase activating protein 4	NM_138630	0.022	-0.612	5.938	0.262	0.249	5.689	0.005	0.861	6.55
ARHGAP6	Rho GTPase activating protein 6	NM_009707	0.08	-0.982	5.421	0.688	0.199	5.222	0.044	1.181	6.404
ARHGAP9	Rho GTPase activating protein 9	NM_146011	0.027	-0.886	9	0.032	0.848	8.152	0.001	1.735	9.887
BTK	Bruton agammaglobulinemia tyrosine kinase	NM_013482	0.009	-1.057	9.376	0.607	0.153	9.223	0.005	1.21	10.433
CD44	CD44 molecule (Indian blood group)	NM_001039150	0.036	-0.906	10.775	0.019	1.077	6.791	0.001	1.916	8.707
CLDN12	claudin 12	NM_022890	0.035	0.523	7.849	0.039	-0.504	8.353	0.002	-1.027	7.326
CLDN5	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)	NM_013805	0.029	1.096	12.816	0.045	0.977	11.839	0.771	-0.119	11.72
CTNNA1	catenin (cadherin-associated protein), alpha 1, 102 kDa	NM_009818	0.03	0.666	5.007	0.129	-0.096	13.283	0.005	-1.025	4.342

Continued

CXCR4	chemokine (C-X-C motif) receptor 4	NM_009911	0.413	-0.397	7	0.125	0.8	6.2	0.037	1.198	7.397
CYBA	cytochrome b-245, alpha polypeptide	NM_007806	0.068	-0.399	13.656	0.025	0.532	13.123	0.002	0.932	14.055
CYBB	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	NM_007807	0.045	-0.569	10.756	0.087	0.461	10.295	0.004	1.03	11.325
DLC1	deleted in liver cancer 1	NM_015802	0.051	0.403	12.01	0.007	-0.554	9.799	0.001	-0.823	8.976
ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	NM_008404	0.077	-0.456	13.308	0.011	0.774	12.534	0.001	1.229	13.764
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256
MMP11	matrix metallopeptidase 11 (stromelysin 3)	NM_008606	0.139	-0.636	7.553	0.418	0.326	7.227	0.041	0.962	8.189
MMP12	matrix metallopeptidase 12 (macrophage elastase)	NM_008605	0.447	-0.687	13.129	0.012	2.956	10.173	0.005	3.643	13.816
MMP13	matrix metallopeptidase 13 (collagenase 3)	NM_008607	0.082	-1.477	2.74	0.546	0.455	2.285	0.033	1.932	4.217
MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	NM_010809	0.207	-1.303	5.923	0.193	1.348	4.574	0.027	2.651	7.226
MMP9	matrix metallopeptidase 9 (gelatinase B, 92 kDa gelatinase, 92 kDa type IV collagenase)	NM_013599	0.081	2.265	7.787	0.268	-1.057	9.127	0.019	-3.411	5.522
NCF1C	neutrophil cytosolic factor 1C pseudogene	NM_010876	0.157	-0.222	11.784	0.003	1.001	7.382	0.001	0.766	12.007
NCF2	neutrophil cytosolic factor 2 (65 kDa, chronic granulomatous disease, autosomal 2)	NM_010877	0.021	-0.644	10.281	0.059	0.483	9.798	0.001	1.126	10.924
NCF4	neutrophil cytosolic factor 4, 40 kDa	NM_008677	0.024	-0.596	9.787	0.028	0.575	9.212	0.001	1.171	10.383
PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	NM_001032378	0.011	0.891	9.643	0.142	0.424	9.219	0.112	-0.467	8.752
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PRKCH	protein kinase C, eta	NM_008856	0.087	-0.743	10.472	0.027	0.997	7.892	0.003	1.594	9.486
PRKD1	protein kinase D1	NM_008858	0	0.377	10.713	0	-0.515	11.227	0	-0.892	10.336
RDX	radixin	NM_001104616	0	1.015	7.9	0.003	-0.276	12.632	0	-0.645	11.988
SELPLG	selectin P ligand	NM_009151	0.01	-0.604	11.224	0.187	0.248	10.976	0.002	0.852	11.828
TEC	tec protein tyrosine kinase	NM_001113460	0.039	-0.422	10.126	0.005	0.697	9.429	0	1.119	10.548

Continued

TIMP1	TIMP metallopeptidase inhibitor 1	NM_001044384	0.023	-1.025	9.675	0.032	0.94	8.734	0.001	1.965	10.699
TIMP3	TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)	NM_011595	0	1.066	9.076	0.393	-0.121	12.275	0	-1.012	8.01
TIMP4	TIMP metallopeptidase inhibitor 4	NM_080639	0.018	0.772	13.367	0.404	-0.217	13.585	0.006	-0.99	12.595
VAV1	vav 1 guanine nucleotide exchange factor	NM_011691	0.044	-0.704	5.755	0.209	0.391	5.363	0.007	1.095	6.458
VAV3	vav 3 guanine nucleotide exchange factor	NM_020505	0.072	-0.768	8.743	0.116	0.582	3.591	0.009	1.336	9.51
VCAM1	vascular cell adhesion molecule 1	NM_011693	0.078	-0.706	6.165	0.225	0.452	5.714	0.013	1.158	6.872
WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	NM_009515	0.028	-0.623	8.982	0.066	0.485	8.497	0.002	1.107	9.604

Insulin Receptor Signaling

ACLY	ATP citrate lyase	NM_134037	0.311	0.38	12.337	0.003	-0.937	14.13	0.001	-1.142	12.988
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	NM_007918	0.016	1.108	9.708	0.838	0.03	14.414	0.013	-1.158	8.599
FOXO1	forkhead box O1	NM_019739	0.007	0.656	10.756	0.1	-0.323	11.079	0.001	-0.979	10.1
FRAP1	FK506 binding protein 12-rapamycin associated protein 1	NM_020009	0.05	-0.825	4.157	0.274	-0.144	10.371	0.031	0.938	4.981
GYS1	glycogen synthase 1 (muscle)	NM_030678	0.011	1.096	7.294	0.493	-0.225	7.52	0.005	-1.321	6.199
GYS2	glycogen synthase 2 (liver)	NM_145572	0.005	-1.67	8.426	0.085	0.809	7.617	0.001	2.479	10.096
INSR	insulin receptor	NM_001033381	0	0.668	9.937	0.022	-0.275	10.212	0	-0.943	9.269
IRS1	insulin receptor substrate 1	NM_010570	0.006	1.387	11.258	0.089	-0.681	11.939	0.001	-2.067	9.872
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PRKCH	protein kinase C, eta	NM_008856	0.087	-0.743	10.472	0.027	0.997	7.892	0.003	1.594	9.486
SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	NM_009204	0.029	1.368	12.889	0.309	-0.393	12.374	0.014	-1.205	11.169
STXBP4	syntaxin binding protein 4	---	0.003	0.858	5.13	0.567	-0.11	5.239	0.002	-0.968	4.271
VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	NM_009497	0.079	0.464	7.815	0.081	-0.46	8.274	0.005	-0.924	7.351

Xenobiotic Metabolism Signaling

Continued

ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	NM_011076	0.006	0.761	5.988	0.157	-0.401	8.141	0.001	-1.052	5.227
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	NM_026316	0.017	-0.56	7.848	0.046	0.431	7.417	0.001	0.992	8.409
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	NM_134042	0.002	0.503	12.566	0.009	-0.359	12.925	0	-0.862	12.064
ARNT	aryl hydrocarbon receptor nuclear translocator	NM_001037737	0.01	0.831	6.119	0.002	-0.259	8.705	0	-0.425	8.28
CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	NM_001025438	0.062	0.087	2.365	0.496	-0.25	7.43	0.038	-0.902	6.528
CES1 (includes EG:1066)	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	NM_053200	0.007	1.036	13.647	0.27	-0.33	13.056	0.002	-1.382	11.674
CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	NM_021439	0.112	-0.274	2.418	0.025	0.687	8.607	0.01	0.85	9.457
CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	NM_010828	0.028	0.615	11.678	0.162	-0.343	12.022	0.004	-0.958	11.064
CUL3	cullin 3	NM_016716	0.001	0.599	8.051	0.017	-0.329	8.38	0	-0.928	7.452
FMO1	flavin containing monooxygenase 1	NM_010231	0.033	0.909	13.444	0.163	-0.526	13.971	0.004	-1.435	12.536
FMO5	flavin containing monooxygenase 5	NM_010232	0	1.169	6.838	0.077	-0.228	7.066	0	-1.396	5.669
GSTA3	glutathione S-transferase A3	NM_001077353	0.061	0.953	11.415	0.127	-0.725	9.233	0.006	-1.656	7.577
GSTA4	glutathione S-transferase A4	NM_010357	0.04	0.853	11.386	0.122	-0.589	11.975	0.004	-1.441	10.533
GSTT1	glutathione S-transferase theta 1	NM_008185	0.013	0.59	12.791	0.026	-0.502	13.293	0.001	-1.092	12.201
HMOX1	heme oxygenase (decycling) 1	NM_010442	0.242	-0.495	9.717	0.194	0.557	9.16	0.032	1.052	10.212
KEAP1	kelch-like ECH-associated protein 1	NM_001110305	0.017	0.972	9.352	0.174	0.466	8.886	0.145	-0.505	8.381
LIPA	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	NM_001111100	0.044	-0.971	9.896	0.027	0.828	12.45	0.002	1.498	13.949
MAOB	monoamine oxidase B	NM_172778	0.038	0.463	12.2	0.035	-0.473	12.673	0.002	-0.936	11.737
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
MAP3K3	mitogen-activated protein kinase kinase kinase 3	NM_011947	0.049	-2.011	5.549	0.137	-1.412	6.962	0.092	-0.237	9.719
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NM_019408	0.3	-0.283	8.379	0.045	0.625	7.754	0.01	0.908	8.662

Continued

NRIP1	nuclear receptor interacting protein 1	NM_173440	0.002	0.675	10.356	0.004	-0.572	10.928	0	-1.247	9.681
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PPP2R3A (includes EG:5523)	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	XM_001474396	0.007	0.486	6.878	0.004	-0.55	7.428	0	-1.036	6.392
PRKCH	protein kinase C, eta	NM_008856	0.087	-0.743	10.472	0.027	0.997	7.892	0.003	1.594	9.486
PRKD1	protein kinase D1	NM_008858	0	0.377	10.713	0	-0.515	11.227	0	-0.892	10.336
SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	NM_133670	0.054	0.635	13.709	0.529	-0.179	13.888	0.022	-0.814	13.073
SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	NM_023135	0.056	0.446	10.503	0.004	-0.856	11.36	0	-1.303	10.057
LPS/IL-1 Mediated Inhibition of RXR Function											
ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	NM_011076	0.006	0.761	5.988	0.157	-0.401	8.141	0.001	-1.052	5.227
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	NM_009593	0.097	-0.535	11.624	0.022	0.827	10.798	0.002	1.361	12.159
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	NM_026316	0.017	-0.56	7.848	0.046	0.431	7.417	0.001	0.992	8.409
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	NM_134042	0.002	0.503	12.566	0.009	-0.359	12.925	0	-0.862	12.064
APOC2	apolipoprotein C-II	NM_009695	0.187	-0.44	9.316	0.073	0.639	8.677	0.01	1.08	9.756
APOC4 (includes EG:346)	apolipoprotein C-IV	NM_007385	0	-2.248	2.126	0.996	0.001	2.125	0	2.249	4.375
CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	NM_021439	0.112	-0.274	2.418	0.025	0.687	8.607	0.01	0.85	9.457
FABP4	fatty acid binding protein 4, adipocyte	NM_024406	0.001	1.771	10.72	0.438	-0.247	10.967	0	-2.018	8.949
FABP5	fatty acid binding protein 5 (psoriasis-associated)	NM_010634	0.018	-0.471	13.231	0.007	0.594	12.636	0	1.065	13.702
FABP7	fatty acid binding protein 7, brain	NM_021272	0.032	-1.602	5.956	0.017	1.882	4.074	0.001	3.484	7.558
FMO1	flavin containing monooxygenase 1	NM_010231	0.033	0.909	13.444	0.163	-0.526	13.971	0.004	-1.435	12.536

Continued

FMO5	flavin containing monooxygenase 5	NM_010232	0	1.169	6.838	0.077	-0.228	7.066	0	-1.396	5.669
GSTA3	glutathione S-transferase A3	NM_001077353	0.061	0.953	11.415	0.127	-0.725	9.233	0.006	-1.656	7.577
GSTA4	glutathione S-transferase A4	NM_010357	0.04	0.853	11.386	0.122	-0.589	11.975	0.004	-1.441	10.533
GSTT1	glutathione S-transferase theta 1	NM_008185	0.013	0.59	12.791	0.026	-0.502	13.293	0.001	-1.092	12.201
HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	NM_008256	0.006	1.257	11.845	0.031	0.868	10.978	0.258	-0.39	10.588
IL1R2	interleukin 1 receptor, type II	NM_010555	0.002	-1.453	2.719	0.318	0.305	2.413	0.001	1.759	4.172
MAOB	monoamine oxidase B	NM_172778	0.038	0.463	12.2	0.035	-0.473	12.673	0.002	-0.936	11.737
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
NR1H4	nuclear receptor subfamily 1, group H, member 4	NM_009108	0.042	0.573	5.143	0.183	-0.337	5.48	0.006	-0.91	4.57
PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	NM_011864	0.002	0.526	11.338	0.007	-0.403	11.74	0	-0.928	10.812
SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	NM_011977	0.004	0.813	11.768	0.016	0.619	11.149	0.342	-0.194	10.955
SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-prefering, member 1	NM_133670	0.054	0.635	13.709	0.529	-0.179	13.888	0.022	-0.814	13.073
SULT1E1	sulfotransferase family 1E, estrogen-prefering, member 1	NM_023135	0.056	0.446	10.503	0.004	-0.856	11.36	0	-1.303	10.057
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	NM_008764	0.147	0.525	6.2	0.075	-0.675	6.875	0.008	-1.2	5.675

G-Protein Coupled Receptor Signaling

ADCY7	adenylate cyclase 7	NM_001037723	0.08	-0.758	10.645	0.204	0.467	7.078	0.019	1.034	8.113
ADRB3	adrenergic, beta-3-, receptor	NM_013462	0.018	1.981	12.716	0.733	-0.187	13.423	0.012	-1.83	11.592
BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672
CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	NM_001025438	0.062	0.087	2.365	0.496	-0.25	7.43	0.038	-0.902	6.528
DUSP9	dual specificity phosphatase 9	NM_029352	0.446	-0.308	4.25	0.007	2.199	3.445	0.005	2.294	5.74
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	NM_008311	0.022	-3.244	3.063	0.477	0.81	2.252	0.008	4.055	6.307
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	NM_019777	0.013	-0.555	8.531	0.029	0.456	8.075	0.001	1.012	9.086
P2RY1	purinergic receptor P2Y, G-protein coupled, 1	NM_008772	0.017	-0.513	7.303	0	1.407	5.895	0	1.92	7.816

Continued

P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	NM_183168	0.047	-0.82	11.171	0.169	0.518	10.653	0.006	1.338	11.991
PDE1A	phosphodiesterase 1A, calmodulin-dependent	NM_001009978	0.003	1.239	8.699	0.059	-0.608	9.306	0	-1.847	7.46
PDE2A	phosphodiesterase 2A, cGMP-stimulated	NM_001008548	0.148	-0.252	10.092	0.004	0.683	9.41	0.001	0.935	10.345
PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_019840	0	1.104	8.99	0.001	0.883	8.107	0.222	-0.222	7.885
PDE7A	phosphodiesterase 7A	NM_001122759	0.14	-0.436	8.998	0.003	1.237	8.55	0.001	1.448	9.997
PDE8B	phosphodiesterase 8B	NM_172263	0.043	-1.083	3.146	0.803	0.111	3.035	0.03	1.194	4.229
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PLCB4	phospholipase C, beta 4	NM_013829	0.015	1.036	4.286	0.28	-0.212	10.733	0.01	-1.154	3.251
RGS18	regulator of G-protein signaling 18	NM_022881	0.026	-0.815	9.106	0.629	0.151	8.392	0.016	0.915	9.921
RGS2	regulator of G-protein signaling 2, 24 kDa	NM_009061	0.02	-1.28	7.699	0.337	0.422	9.278	0.007	1.42	10.466
RGS4	regulator of G-protein signaling 4	NM_009062	0.004	1.013	6.633	0.074	0.496	6.137	0.065	-0.517	5.619

TR/RXR Activation

ACACA	acetyl-Coenzyme A carboxylase alpha	NM_133360	0.912	0.064	3.113	0.009	-2.07	5.182	0.008	-2.134	3.048
BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672
F10	coagulation factor X	NM_007972	0.11	-0.315	3.27	0.002	1.908	6.065	0	1.201	3.585
FRAP1	FK506 binding protein 12-rapamycin associated protein 1	NM_020009	0.05	-0.825	4.157	0.274	-0.144	10.371	0.031	0.938	4.981
KLF9	Kruppel-like factor 9	NM_010638	0.003	0.552	12.606	0.002	-0.476	13.011	0	-0.861	12.15
LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	NM_010700	0	-0.928	9.28	0.237	-0.036	3.487	0	0.9	10.207
NCOR1	nuclear receptor co-repressor 1	NM_011308	0.002	0.864	8.333	0.039	-0.595	5.03	0.001	-1.134	7.47
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	NM_011044	0.002	2.193	12.827	0.783	0.181	12.921	0.002	-2.229	10.633
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11

Continued

PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	NM_178060	0.011	0.496	11.44	0.007	-0.551	11.991	0	-1.047	10.944
UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	NM_011671	0.056	-0.533	12.598	0.009	0.836	11.761	0.001	1.369	13.13

Sonic Hedgehog Signaling

C2	complement component 2	NM_013484	0.005	0.859	12.656	0.057	-0.441	14.039	0.001	-1.319	11.797
C3AR1	complement component 3a receptor 1	NM_009779	0.037	-1.017	11.903	0.062	1.088	10.166	0.003	1.917	11.113
C5AR1	complement component 5a receptor 1	NM_008555	0.996	-0.002	3.631	0.012	-1.298	4.929	0.012	-1.296	3.633
CCNB1	cyclin B1	NM_007577	0.094	-0.801	8.231	0.072	0.665	9.86	0.011	1.095	10.955
CDC2	cell division cycle 2, G1 to S and G2 to M	NM_001081125	0.61	-0.109	3.313	0.019	-1.043	7.217	0.011	-1.2	6.017
GLI2	GLI-Kruppel family member GLI2	NM_172301	0.026	-1.571	5.055	0.064	1.214	3.841	0.002	2.785	6.626
MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	NM_007659	0.013	-1.395	8.342	0.02	1.253	7.088	0	2.648	9.736

Cell Cycle: G1/S Checkpoint Regulation

CCNE1	cyclin E1	NM_007633	0.071	-0.671	7.728	0.14	0.523	7.205	0.008	1.194	8.398
CDK6	cyclin-dependent kinase 6	NM_009873	0.024	-0.762	9.029	0.093	0.629	7.834	0.003	1.211	9.791
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_001111099	0.026	-0.679	9.893	0.001	1.468	8.425	0	2.146	10.571
CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	NM_009875	0.125	0.39	8.696	0.093	-0.436	9.132	0.009	-0.826	8.306
CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	NM_007670	0	-1.013	9.99	0.835	0.032	9.957	0	1.045	11.003
E2F1	E2F transcription factor 1	NM_007891	0.085	-0.354	6.977	0.016	0.663	8.141	0.002	0.904	7.331
E2F6	E2F transcription factor 6	NM_033270	0.009	-1.162	7.857	0.014	1.06	6.797	0	2.222	9.019
HDAC11	histone deacetylase 11	NM_144919	0.015	0.825	6.416	0.229	-0.036	2.48	0.017	-0.8	5.59

Continued

HDAC9	histone deacetylase 9	NM_024124	0.11	-0.461	8.363	0.131	0.43	7.933	0.011	0.891	8.824
RB1	retinoblastoma 1 (including osteosarcoma)	NM_009029	0.038	-0.65	4.483	0.098	0.483	4.001	0.003	1.133	5.134
SKP2	S-phase kinase- associated protein 2 (p45)	NM_013787	0.214	-0.599	3.876	0.138	0.737	3.139	0.02	1.337	4.476
TGFB3	transforming growth factor, beta 3	NM_009368	0.001	0.495	10.669	0.009	-0.337	11.006	0	-0.832	10.174
GM-CSF Signaling											
BCL2A1	BCL2-related protein A1	NM_007534	0.11	-0.784	10.911	0.058	0.973	9.938	0.005	1.756	11.694
CAMK2D	calcium/calmodulin- dependent protein kinase (CaM kinase) II delta	NM_001025438	0.062	0.087	2.365	0.496	-0.25	7.43	0.038	-0.902	6.528
HCK	hemopoietic cell kinase	NM_010407	0.016	-0.964	9.879	0.063	0.663	9.216	0.001	1.627	10.843
LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	NM_001111096	0.047	-0.516	10.223	0.211	0.291	9.933	0.008	0.806	10.739
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PIM1	pim-1 oncogene	NM_008842	0.032	-1.3	3.545	0.459	0.18	8.558	0.06	1.086	4.845
RUNX1	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	NM_001111021	0.024	-0.812	4.622	0.246	0.506	4.344	0.01	1.447	5.791
LXR/RXR Activation											
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	NM_009593	0.097	-0.535	11.624	0.022	0.827	10.798	0.002	1.361	12.159
ACACA	acetyl-Coenzyme A carboxylase alpha	NM_133360	0.912	0.064	3.113	0.009	-2.07	5.182	0.008	-2.134	3.048
APOC2	apolipoprotein C-II	NM_009695	0.187	-0.44	9.316	0.073	0.639	8.677	0.01	1.08	9.756
APOC4 (includes EG:346)	apolipoprotein C-IV	NM_007385	0	-2.248	2.126	0.996	0.001	2.125	0	2.249	4.375
CCL7	chemokine (C-C motif) ligand 7	NM_013654	0.009	-1.626	10.311	0.008	1.689	8.623	0	3.314	11.937
IL1R2	interleukin 1 receptor, type II	NM_010555	0.002	-1.453	2.719	0.318	0.305	2.413	0.001	1.759	4.172
IL1RN	interleukin 1 receptor antagonist	NM_001039701	0.005	-1.805	2.203	0	3.3	3.963	0	4.59	8.553
LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	NM_010700	0	-0.928	9.28	0.237	-0.036	3.487	0	0.9	10.207

Continued

MMP9	matrix metallopeptidase 9 (gelatinase B, 92 kDa gelatinase, 92 kDa type IV collagenase)	NM_013599	0.081	2.265	7.787	0.268	-1.057	9.127	0.019	-3.411	5.522
MSR1	macrophage scavenger receptor 1	NM_001113326	0.027	-0.972	2.914	0.009	1.537	4.507	0.001	1.778	10.468
NCOR1	nuclear receptor co-repressor 1	NM_011308	0.002	0.864	8.333	0.039	-0.595	5.03	0.001	-1.134	7.47
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	NM_008764	0.147	0.525	6.2	0.075	-0.675	6.875	0.008	-1.2	5.675
Eicosanoid Signaling											
ALOX15	arachidonate 15-lipoxygenase	NM_009660	0.211	0.694	8.642	0.154	-0.808	9.45	0.022	-1.501	7.949
FPRL1 (includes EG:2358)	formyl peptide receptor 2	NM_008039	0.266	-0.346	6.049	0.104	0.539	5.51	0.019	0.885	6.396
LAMB2	laminin, beta 2 (laminin S)	NM_008483	0.027	0.608	7.677	0.346	-0.215	7.893	0.007	-0.824	7.069
PGDS	prostaglandin D2 synthase, hematopoietic	NM_019455	0.112	-1.715	7.268	0.103	1.77	5.498	0.009	3.485	8.984
PLA2G2D	phospholipase A2, group IID	NM_011109	0.091	1.338	7.413	0.107	-1.261	8.674	0.007	-2.6	6.075
PLA2G2E	phospholipase A2, group IIE	NM_012044	0.229	-0.454	10.054	0.004	1.54	8.514	0.001	1.993	10.508
PLA2G5	phospholipase A2, group V	NM_001122954	0.039	-1.49	3.435	0.094	1.126	2.309	0.003	2.615	4.924
PNPLA3	patatin-like phospholipase domain containing 3	NM_054088	0.309	0.351	9.154	0.157	-0.51	9.663	0.033	-0.861	8.803
PTGER2	prostaglandin E receptor 2 (subtype EP2), 53 kDa	NM_008964	0.159	-0.436	7.244	0.011	0.975	6.269	0.002	1.41	7.68
PTGER4	prostaglandin E receptor 4 (subtype EP4)	AV230399	0.464	0.151	3.121	0.019	1.147	3.326	0.031	1.011	4.337
PTGES	prostaglandin E synthase	NM_022415	0.044	1.004	11.72	0.026	-1.15	9.87	0.007	-1.59	10.716
PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	NM_008969	0.013	0.674	10.601	0.108	-0.393	9.35	0.002	-0.96	9.927
TBXAS1	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)	NM_011539	0.095	-0.414	10.7	0.023	0.63	10.07	0.002	1.044	11.113
WISP2	WNT1 inducible signaling pathway protein 2	NM_016873	0.038	-2.08	9.333	0.004	3.495	5.837	0	5.576	11.413
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_011740	0.008	-0.876	7.273	0.447	-0.188	7.461	0.024	0.688	8.148
Coagulation System											
F10	coagulation factor X	NM_007972	0.11	-0.315	3.27	0.002	1.908	6.065	0	1.201	3.585
F2R	coagulation factor II (thrombin) receptor	NM_010169	0.159	-0.587	10.428	0.116	0.669	9.76	0.013	1.256	11.015
F7	coagulation factor VII (serum prothrombin conversion accelerator)	NM_010172	0.232	-1.265	10.19	0.005	4.092	6.099	0.001	5.356	11.455

Continued

PLAUR	plasminogen activator, urokinase receptor	NM_011113	0.009	-0.415	9.151	0	0.855	8.296	0	1.27	9.565
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	NM_009243	0.002	-1.046	4.653	0.264	0.242	4.411	0	1.288	5.699
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	NM_008871	0.044	-1.615	8.757	0.403	0.578	8.179	0.013	2.194	10.373
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	NM_011576	0.045	0.771	8.877	0.004	-0.514	9.297	0.002	-1.422	9.384
THBD	thrombomodulin	NM_009378	0.001	0.777	12.751	0.001	-0.829	13.58	0	-1.606	11.974

Aryl Hydrocarbon Receptor Signaling

ALDH3B1	aldehyde dehydrogenase 3 family, member B1	NM_026316	0.017	-0.56	7.848	0.046	0.431	7.417	0.001	0.992	8.409
ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	NM_172532	0.012	0.802	10.108	0.459	-0.18	10.288	0.004	-0.982	9.306
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	NM_134042	0.002	0.503	12.566	0.009	-0.359	12.925	0	-0.862	12.064
ARNT	aryl hydrocarbon receptor nuclear translocator	NM_001037737	0.01	0.831	6.119	0.002	-0.259	8.705	0	-0.425	8.28
BAX	BCL2-associated X protein	NM_007527	0.033	-0.451	11.466	0.056	0.386	11.079	0.002	0.837	11.917
CCNA2	cyclin A2	NM_009828	0.02	-1.43	7.361	0.015	1.519	5.842	0.001	2.949	8.79
CCNE1	cyclin E1	NM_007633	0.071	-0.671	7.728	0.14	0.523	7.205	0.008	1.194	8.398
CDK6	cyclin-dependent kinase 6	NM_009873	0.024	-0.762	9.029	0.093	0.629	7.834	0.003	1.211	9.791
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_001111099	0.026	-0.679	9.893	0.001	1.468	8.425	0	2.146	10.571
CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	NM_009875	0.125	0.39	8.696	0.093	-0.436	9.132	0.009	-0.826	8.306
E2F1	E2F transcription factor 1	NM_007891	0.085	-0.354	6.977	0.016	0.663	8.141	0.002	0.904	7.331
ESR1	estrogen receptor 1	NM_007956	0.041	0.52	6.097	0.033	-0.551	6.648	0.002	-1.071	5.577
FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	NM_010234	0.077	-1.089	10.759	0.207	0.725	10.034	0.012	1.813	11.848
GSTA3	glutathione S-transferase A3	NM_001077353	0.061	0.953	11.415	0.127	-0.725	9.233	0.006	-1.656	7.577
GSTA4	glutathione S-transferase A4	NM_010357	0.04	0.853	11.386	0.122	-0.589	11.975	0.004	-1.441	10.533
GSTT1	glutathione S-transferase theta 1	NM_008185	0.013	0.59	12.791	0.026	-0.502	13.293	0.001	-1.092	12.201
HSPB2	heat shock 27 kDa protein 2	NM_024441	0.003	-0.869	8.93	0.083	0.393	8.537	0	1.262	9.799
NFIA	nuclear factor I/A	NM_001122952	0.002	0.799	6.289	0.004	-0.657	6.946	0	-1.456	5.49

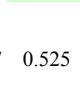
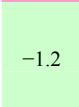
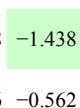
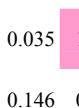
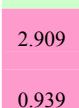
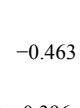
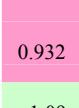
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NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NM_019408	0.3	-0.283	8.379	0.045	0.625	7.754	0.01	0.908	8.662
NR2F1	nuclear receptor subfamily 2, group F, member 1	NM_010151	0.022	0.744	5.675	0.052	-0.594	6.269	0.001	-1.338	4.931
NRIP1	nuclear receptor interacting protein 1	NM_173440	0.002	0.675	10.356	0.004	-0.572	10.928	0	-1.247	9.681
RB1	retinoblastoma 1 (including osteosarcoma)	NM_009029	0.038	-0.65	4.483	0.098	0.483	4.001	0.003	1.133	5.134
TGFB3	transforming growth factor, beta 3	NM_009368	0.001	0.495	10.669	0.009	-0.337	11.006	0	-0.832	10.174

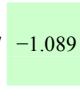
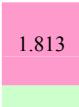
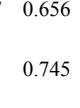
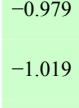
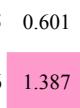
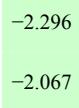
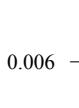
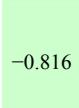
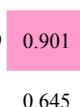
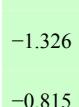
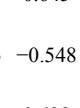
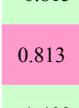
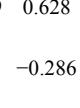
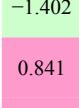
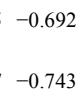
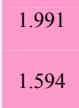
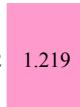
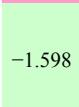
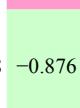
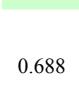
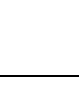
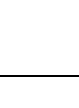
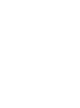
NFkB Signaling

BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672
BMP4	bone morphogenetic protein 4	NM_007554	0.004	1.211	10.683	0.476	-0.209	10.892	0.002	-1.421	9.471
CARD10	caspase recruitment domain family, member 10	NM_130859	0.006	0.725	11.039	0.286	-0.209	11.248	0.002	-0.934	10.315
CD40	CD40 molecule, TNF receptor superfamily member 5	NM_011611	0.005	-0.654	7.344	0.168	0.241	7.103	0.001	0.895	7.998
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	NM_007912	0.251	0.419	4.992	0.095	-0.381	9.611	0.024	-0.976	4.573
IL1R2	interleukin 1 receptor, type II	NM_010555	0.002	-1.453	2.719	0.318	0.305	2.413	0.001	1.759	4.172
IL1RN	interleukin 1 receptor antagonist	NM_001039701	0.005	-1.805	2.203	0	3.3	3.963	0	4.59	8.553
INSR	insulin receptor	NM_001033381	0	0.668	9.937	0.022	-0.275	10.212	0	-0.943	9.269
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
MAP3K3	mitogen-activated protein kinase kinase kinase 3	NM_011947	0.049	-2.011	5.549	0.137	-1.412	6.962	0.092	-0.237	9.719
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NM_019408	0.3	-0.283	8.379	0.045	0.625	7.754	0.01	0.908	8.662
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
TLR1	toll-like receptor 1	NM_030682	0.043	-1.217	7.019	0.195	0.699	6.32	0.007	1.916	8.236
TLR7	toll-like receptor 7	NM_133211	0.083	-0.704	3.197	0.405	0.317	7.567	0.042	0.904	8.47
TLR8	toll-like receptor 8	NM_133212	0.048	-1.566	5.652	0.104	1.213	4.438	0.004	2.779	7.218

Continued

TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	NM_009399	0.046	 -0.864	2.489	0.385	0.345	4.948	0.018	 1.169	6.117
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	NM_008764	0.147	 0.525	6.2	0.075	-0.675	6.875	0.008	 -1.2	5.675
TRA@	T cell receptor alpha locus	XM_001471582	0.038	 -1.438	8.857	0.035	 1.472	7.385	0.002	 2.909	10.295
TRAF3	TNF receptor-associated factor 3	NM_001048206	0.046	 -0.562	3.927	0.146	0.376	3.551	0.005	 0.939	4.489
TRAF5	TNF receptor-associated factor 5	NM_011633	0.001	 -0.463	7.543	0	0.469	7.074	0	 0.932	8.006
TRG@	T cell receptor gamma locus	NM_011558	0.262	 0.396	3.995	0.072	-0.695	4.69	0.013	 -1.09	3.599

IGF-1 Signaling

FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	NM_010234	0.077	 -1.089	10.759	0.207	0.725	10.034	0.012	 1.813	11.848
FOXO1	forkhead box O1	NM_019739	0.007	 0.656	10.756	0.1	-0.323	11.079	0.001	 -0.979	10.1
IGF1R	insulin-like growth factor 1 receptor	NM_010513	0.01	 0.745	8.221	0.228	-0.275	8.496	0.002	 -1.019	7.476
IGFBP2	insulin-like growth factor binding protein 2, 36 kDa	NM_008342	0.005	 0.601	6.253	0	 -1.694	7.948	0	 -2.296	5.652
IRS1	insulin receptor substrate 1	NM_010570	0.006	 1.387	11.258	0.089	-0.681	11.939	0.001	 -2.067	9.872
NEDD4	neural precursor cell expressed, developmentally down-regulated 4	NM_010890	0	 0.709	12.25	0.006	-0.107	12.357	0	 -0.816	11.541
NOV	nephroblastoma overexpressed gene	NM_010930	0.089	 0.901	7.881	0.379	-0.424	8.306	0.024	 -1.326	6.98
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	 0.645	6.755	0.127	-0.249	7.833	0	 -0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	 -0.548	6.216	0.256	-0.386	9.26	0.012	 0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	 0.628	9.645	0.001	-0.697	13.043	0	 -1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	 -0.286	7.827	0.06	 0.555	7.271	0.012	 0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	 -0.692	7.33	0.022	 1.299	6.031	0.003	 1.991	8.022
PRKCH	protein kinase C, eta	NM_008856	0.087	 -0.743	10.472	0.027	 0.997	7.892	0.003	 1.594	9.486
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	BF714941	0.012	1.219	5.874	0.053	-0.267	8.76	0.003	-1.598	4.655
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	NM_011740	0.008	-0.876	7.273	0.447	-0.188	7.461	0.024	0.688	8.148

Fc Epsilon RI Signaling

Continued

BTK	Bruton agammaglobulinemia tyrosine kinase	NM_013482	0.009	-1.057	9.376	0.607	0.153	9.223	0.005	1.21	10.433
FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	NM_010184	0.05	-1.043	7.485	0.808	0.109	7.375	0.035	1.152	8.528
FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	NM_010185	0.032	-0.573	14.157	0.256	0.26	13.897	0.006	0.833	14.73
LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76 kDa)	NM_010696	0.082	-0.362	9.448	0.03	0.488	8.96	0.002	0.85	9.809
LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	NM_001111096	0.047	-0.516	10.223	0.211	0.291	9.933	0.008	0.806	10.739
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
PLA2G2D	phospholipase A2, group IID	NM_011109	0.091	1.338	7.413	0.107	-1.261	8.674	0.007	-2.6	6.075
PLA2G2E	phospholipase A2, group IIE	NM_012044	0.229	-0.454	10.054	0.004	1.54	8.514	0.001	1.993	10.508
PLA2G5	phospholipase A2, group V	NM_001122954	0.039	-1.49	3.435	0.094	1.126	2.309	0.003	2.615	4.924
PRKCH	protein kinase C, eta	NM_008856	0.087	-0.743	10.472	0.027	0.997	7.892	0.003	1.594	9.486
PRKD1	protein kinase D1	NM_008858	0	0.377	10.713	0	-0.515	11.227	0	-0.892	10.336
VAV1	vav 1 guanine nucleotide exchange factor	NM_011691	0.044	-0.704	5.755	0.209	0.391	5.363	0.007	1.095	6.458
VAV3	vav 3 guanine nucleotide exchange factor	NM_020505	0.072	-0.768	8.743	0.116	0.582	3.591	0.009	1.336	9.51

B Cell Receptor Signaling

BCL2A1	BCL2-related protein A1	NM_007534	0.11	-0.784	10.911	0.058	0.973	9.938	0.005	1.756	11.694
BCL3	B-cell CLL/lymphoma 3	NM_033601	0.03	-0.392	8.281	0.002	0.684	7.596	0	1.076	8.672
BLNK	B-cell linker	NM_008528	0.054	-1.111	11.996	0.09	0.942	11.054	0.004	2.053	13.107
BTK	Bruton agammaglobulinemia tyrosine kinase	NM_013482	0.009	-1.057	9.376	0.607	0.153	9.223	0.005	1.21	10.433
CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	NM_001025438	0.062	0.087	2.365	0.496	-0.25	7.43	0.038	-0.902	6.528
CARD10	caspase recruitment domain family, member 10	NM_130859	0.006	0.725	11.039	0.286	-0.209	11.248	0.002	-0.934	10.315

Continued

FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_010188	0.051	-0.467	12.2	0.125	0.343	11.857	0.005	0.81	12.667
FRAP1	FK506 binding protein 12-rapamycin associated protein 1	NM_020009	0.05	-0.825	4.157	0.274	-0.144	10.371	0.031	0.938	4.981
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	NM_019777	0.013	-0.555	8.531	0.029	0.456	8.075	0.001	1.012	9.086
LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	NM_001111096	0.047	-0.516	10.223	0.211	0.291	9.933	0.008	0.806	10.739
MAP2K7	mitogen-activated protein kinase kinase 7	NM_001042557	0.114	0.613	4.499	0.271	0.348	3.444	0.032	-0.912	3.887
MAP3K13	mitogen-activated protein kinase kinase kinase 13	XM_001480812	0.1	0.676	4.22	0.443	0	2.122	0.05	-0.85	3.543
MAP3K3	mitogen-activated protein kinase kinase kinase 3	NM_011947	0.049	-2.011	5.549	0.137	-1.412	6.962	0.092	-0.237	9.719
MAPK14	mitogen-activated protein kinase 14	NM_011951	0.002	0.846	7.58	0.062	-0.064	12.45	0	-0.194	12.256
PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	NM_031376	0.056	-1.386	6.584	0.312	0.652	5.932	0.013	2.038	7.97
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_008839	0.001	0.645	6.755	0.127	-0.249	7.833	0	-0.815	6.11
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	NM_001029837	0.053	-0.548	6.216	0.256	-0.386	9.26	0.012	0.813	6.764
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	NM_001024955	0.009	0.628	9.645	0.001	-0.697	13.043	0	-1.402	9.017
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_181585	0.281	-0.286	7.827	0.06	0.555	7.271	0.012	0.841	8.112
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	NM_177320	0.155	-0.692	7.33	0.022	1.299	6.031	0.003	1.991	8.022
VAV1	vav 1 guanine nucleotide exchange factor	NM_011691	0.044	-0.704	5.755	0.209	0.391	5.363	0.007	1.095	6.458
VAV3	vav 3 guanine nucleotide exchange factor	NM_020505	0.072	-0.768	8.743	0.116	0.582	3.591	0.009	1.336	9.51

Supplement Tables 1-4. Heatmaps in **Supplement Figure 4** listed the pathways by rank order of statistical significance.

2.3. Comparison to Similar Microarray Data

Microarray results a few years ago were notorious for data variability when comparing similar studies from different laboratories. To confirm our microarray result to the published gene expression studies, two similar liver microarray datasets from similar DIO mouse models [11, 12] were compared to our LC/LV/LUP dataset. Side-by-side comparisons were remarkably similar. One dataset, that of the resveratrol treated DIO model [11], was identical to our experimental design of lean control, HFD, and HFD+resveratrol treatments. Not only were the comparisons between lean control and HFD similar, but also the comparisons between LUP vs. LV and HFD + resveratrol vs. HFD similar. Resveratrol, a phenolic compound from grape, activates sirtuin, a protein known from yeast, *Drosophila*, and *C. elegans* to prolong life

span when sirtuin activity is heightened in response to caloric restriction [11]. The similarity between UP780 and resveratrol was observed in both the highest differential gene expressions and in the significant metabolic and signaling pathways. Resveratrol was discovered through high throughput screening for sirtuin activation [11], while UP780's discovery was designed not to be specific for enzymatic modification, but for increased adiponectin secretion from differentiate 3T3-L1 adipocytes [1].

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