

Supplemental Table 1. The selected genes involved in fatty acid, glucose, and cholesterol metabolism in lipid-loaded HepG2 cells treated with linalool (LN) and fenofibrate (FF)

Gene symbol	Gene description	Group (fold of control)	
		LN	FF
<i>Fatty acid metabolism</i>			
<i>Elovl3</i>	Elongation of very long chain fatty acids protein 3	0.63	0.87
<i>Ppara</i>	Peroxisome proliferator-activated receptor alpha	1.41	1.98
<i>Aldh6a1</i>	Methylmalonate-semialdehyde dehydrogenase	1.19	1.61
<i>Srebp-1c</i>	Sterol regulatory element-binding protein 1c	0.92	0.63
<i>Acadvl</i>	Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	1.19	2.58
<i>Echs1</i>	Enoyl-CoA hydratase, mitochondrial precursor	1.55	1.64
<i>Acox1</i>	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase)	1.19	1.73
<i>Acaal</i>	3-ketoacyl-CoA thiolase, peroxisomal precursor (Acetyl-CoA acyltransferase)	1.41	1.80
<i>Acat1</i>	Acetyl-CoA acetyltransferase, mitochondrial precursor	1.27	2.00
<i>Acadm</i>	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	1.46	2.39
<i>Hadhb</i>	Trifunctional enzyme subunit beta, mitochondrial precursor (TP-beta) (Acetyl-CoA acyltransferase)	1.32	2.43
<i>Cpt1a</i>	Carnitine O-palmitoyltransferase I, liver isoform	0.99	0.94
<i>Cpt2</i>	Carnitine O-palmitoyltransferase 2, mitochondrial precursor	1.02	0.71
<i>Fabp1</i>	Fatty acid binding protein 1, liver	1.70	1.80
<i>Pck2</i>	Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	2.08	1.67
<i>Hadh</i>	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor	1.26	2.32
<i>Acc1</i>	Acetyl-CoA carboxylase 1	0.96	0.50

Supplemental Table 1. Continued

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<i>Glucose metabolism</i>			
<i>Pk</i>	Pyruvate kinase	0.90	0.77
<i>Gck</i>	Glucokinase (Hexokinase-4)	0.91	0.71
<i>Suclg1</i>	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor	1.4	2.07
<i>Pfkl</i>	6-phosphofructokinase, liver type	0.70	0.71
<i>Mdh</i>	Malate dehydrogenase	1.82	2.73
<i>Sdhb</i>	Succinate dehydrogenase	1.37	2.39
<i>Suclg2</i>	Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor	1.01	1.02
<i>Idh3b</i>	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial precursor	1.16	1.90
<i>Idh2</i>	Isocitrate dehydrogenase [NADP], mitochondrial precursor (Oxalosuccinate decarboxylase)	1.06	1.04
<i>Mdh2</i>	Malate dehydrogenase, mitochondrial precursor	0.88	0.94
<i>Ogdhl</i>	Oxoglutarate dehydrogenase-like	0.97	0.92
<i>Aco1</i>	Iron-responsive element-binding protein 1 (IRE-BP 1) (Aconitate hydratase)	1.57	0.68
<i>Aco2</i>	Aconitate hydratase, mitochondrial precursor (Citrate hydrolyase)	1.50	2.76
<i>Pgm1</i>	Phosphoglucomutase-1	1.52	2.36
<i>Fbp1</i>	Fructose-1,6-bisphosphatase 1	1.20	0.61
<i>Fbp2</i>	Fructose-1,6-bisphosphatase isozyme 2	1.32	0.86
<i>Hkdc1</i>	Hexokinase domain containing 1	0.82	0.95

Supplemental Table 1. Continued

Gene symbol	Gene description	Group (fold of control)
		LN
<i>Cholesterol metabolism</i>		
<i>Hsd17b4</i>	Peroxisomal multifunctional enzyme type 2 (17-beta-hydroxysteroid dehydrogenase 4)	1.44
<i>Cyp27a1</i>	Cytochrome P450 27, mitochondrial precursor	1.52
<i>Hsd3b7</i>	3 beta-hydroxysteroid dehydrogenase type 7	1.49
<i>Akr1d1</i>	3-oxo-5-beta-steroid 4-dehydrogenase (Aldo-keto reductase family 1 member D1)	1.46
<i>Mcee</i>	Methylmalonyl-CoA epimerase, mitochondrial precursor	0.58
<i>Sqle</i>	Squalene monooxygenase	1.79
<i>Dhcr7</i>	7-dehydrocholesterol reductase	2.24
<i>Cel</i>	Bile salt-activated lipase precursor (BAL)	1.35
<i>Insig2</i>	Insulin induced protein 2	1.57
<i>Soat2</i>	Sterol O-acyltransferase 2 (Acyl coenzyme A:cholesterol acyltransferase 2)	1.21
<i>Apoa1</i>	Apolipoprotein A-I	2.16
<i>Lipa</i>	Lysosomal acid lipase/cholesteryl ester hydrolase precursor	1.56
<i>Mbtps1</i>	Membrane-bound transcription factor site-1 protease precursor (Site-1 protease)	0.94