(A) Gluconeogenesis

Gene	Description	C	HS	HS-HF
PC	pyruvate carboxylase	-0,22	-0,24	-0,22
Got1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	0,64	0,91	0,57
Got2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	-0,09	-0,06	-0,18
Me1	malic enzyme 1, NADP(+)-dependent, cytosolic	-0,78	-0,56	-0,58
Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	0,20	0,51	0,19
Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial	0,25	0,06	0,01
Mdh1	malate dehydrogenase 1, NAD (soluble)	-0,11	0,22	-0,03
Mdh1b	malate dehydrogenase 1B, NAD (soluble)	-0,21	-0,06	-0,17
Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	-0,11	-0,03	-0,06
Bpgm	2,3-bisphosphoglycerate mutase	0,27	0,04	0,13
Sds	serine dehydratase	0,60	0,62	0,31
Pck1	phosphoenolpyruvate carboxykinase 1 (soluble)	0,35	0,46	0,39
Eno1	enolase 1, (alpha)	-0,26	0,07	0,05
Eno2	enolase 2, gamma, neuronal	-0,11	0,02	-0,18
Pgk1	phosphoglycerate kinase 1	-0,07	0,03	0,01
Pgk2	phosphoglycerate kinase 2	-0,18	0,08	0,05
Tpi1	triosephosphate isomerase 1	0,15	-0,18	-0,03
Aldoa	aldolase A, fructose-bisphosphate	0,14	0,47	0,60
Aldob	aldolase B, fructose-bisphosphate	-0,03	-0,02	-0,06
Aldoc	aldolase C, fructose-bisphosphate	-0,11	0,05	-0,27
Fbp1	fructose-1,6-bisphosphatase 1	-0,06	-0,10	-0,03
Fbp2	fructose-1,6-bisphosphatase 2	0,17	0,11	0,06
Gpi	glucose phosphate isomerase	-0,07	0,00	0,05
G6pc	glucose-6-phosphatase, catalytic subunit	-0,02	0,04	0,38

(A) Fatty acid and triglyglyceride synthesis

Gene	Description	C	HS	HS-HF
Srebf1	sterol regulatory element binding transcription factor 1	-0,47	-0,34	-0,50
Gk	glycerol kinase	-0,42	-0,35	-0,32
Pklr	pyruvate kinase, liver and RBC	-0,51	-0,50	-0,50
Acaca	acetyl-coenzyme A carboxylase alpha	-0,50	-0,37	-0,74
Acacb	acetyl-Coenzyme A carboxylase beta	0,52	0,36	-0,03
Fasn	Fatty acid synthase	NA	NA	NA
Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	-0,92	0,09	0,03
Scd1	stearoyl-Coenzyme A desaturase 1	-1,09	-0,34	-1,37
Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	0,01	0,36	0,32
Dgat1	diacylglycerol O-acyltransferase homolog 1 (mouse)	0,05	0,06	-0,11
Dgat2	diacylglycerol O-acyltransferase homolog 2 (mouse)	-0,01	-0,03	-0,17
Gnpat	glyceronephosphate O-acyltransferase	0,01	0,27	0,01
Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	-0,18	-0,02	0,19
Gk2	glycerol kinase 2	0,01	-0,05	-0,11
Agpat1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	-0,08	0,26	0,32
Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	0,19	0,08	0,00
Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	-0,19	-0,26	-0,27
Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	-0,10	-0,03	0,04
Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	0,12	-0,05	0,07
Ppap2a	phosphatidic acid phosphatase type 2A	0,09	0,44	-0,06
Ppap2b	phosphatidic acid phosphatase type 2B	0,10	-0,03	-0,05
Ppap2c	phosphatidic acid phosphatase type 2c	0,08	-0,18	0,01

(B) Fatty acid oxidation

Gene	Description	C	HS	HS-HF
Acss2	acyl-CoA synthetase short-chain family member 2	0,11	0,02	-0,09
Acsl1	acyl-CoA synthetase long-chain family member 1	0,02	0,05	0,06
Acsl3	acyl-CoA synthetase long-chain family member 3	0,41	0,12	0,35
Acsl4	acyl-CoA synthetase long-chain family member 4	0,13	0,16	0,13
Acsl5	acyl-CoA synthetase long-chain family member 5	0,19	0,11	-0,05
Acsl6	acyl-CoA synthetase long-chain family member 6	-0,08	-0,12	-0,02
Crat	carnitine acetyltransferase	0,13	0,06	0,56
Cpt1a	carnitine palmitoyltransferase 1a, liver	0,11	0,26	0,31
Chkb	choline kinase beta	-0,19	0,03	-0,12
Cpt2	carnitine palmitoyltransferase 2	-0,09	0,12	0,21
Slc25a20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-0,02	0,11	0,12
Cpt1b	carnitine palmitoyltransferase 1b, muscle	0,27	0,18	0,42
Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	-0,17	-0,18	0,00
Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, beta subunit	-0,49	-0,36	-0,31
Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit	-0,07	-0,18	-0,02
Acadl	acyl-Coenzyme A dehydrogenase, long-chain	-0,17	-0,18	0,00
Acadm	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	-0,08	-0,02	-0,06
Acsbg1	acyl-CoA synthetase bubblegum family member 1	0,03	0,02	-0,09
Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	-0,04	0,21	0,12
Hadh	hydroxyacyl-CoA dehydrogenase	0,13	0,09	-0,03
Eci1	enoyl-Coenzyme A delta isomerase 1	-0,20	-0,11	-0,17
Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	-0,38	-0,13	0,32
Acaa1a	acetyl-Coenzyme A acyltransferase 1A	-0,16	-0,08	0,10
Acaa1b	acetyl-Coenzyme A acyltransferase 1B	-0,05	-0,04	0,04
Acaa2	acetyl-Coenzyme A acyltransferase 2	-0,84	-0,14	0,48
Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	-0,17	-0,12	-0,38
Acox2	acyl-Coenzyme A oxidase 2, branched chain	0,05	0,10	0,16
Acox3	acyl-Coenzyme A oxidase 3, pristanoyl	0,03	0,11	-0,09

(C) Ketogenesis

Gene	Description	C	HS	HS-HF
Acat1	acetyl-coenzyme A acetyltransferase 1	-0,12	-0,20	-0,31
Acat3	acetyl-Coenzyme A acetyltransferase 3	0,03	0,26	-0,41
Bdh1	3-hydroxybutyrate dehydrogenase, type 1	-0,10	-0,13	-0,25
Bdh2	3-hydroxybutyrate dehydrogenase, type 2	0,19	0,55	0,39
Hmgcl	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	-0,30	0,04	-0,05
Hmgcll1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	-0,13	0,07	0,23
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	0,35	0,06	0,49
Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	-0,11	-0,07	-0,02

(E) Cholesterol metabolism

Gene	Description	C	HS	HS-HF
Fdps	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase)	0,21	0,06	0,40
Fdft1	farnesyl diphosphate farnesyl transferase 1	0,27	-0,06	0,02
Sqle	squalene epoxidase	1,41	0,48	0,88
Lss	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	0,10	0,07	-0,02
Cyp51	cytochrome P450, family 51	0,58	0,04	0,20
Tm7sf2	transmembrane 7 superfamily member 2	1,10	0,61	0,69
Sc4mol	sterol-C4-methyl oxidase-like	0,82	0,10	0,06
Nsdhl	NAD(P) dependent steroid dehydrogenase-like	-0,01	-0,01	0,02
Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	0,45	0,14	0,11
Ebp	emopamil binding protein (sterol isomerase)	0,33	0,18	0,12
Dhcr24	24-dehydrocholesterol reductase	0,48	0,07	-0,18
Sc5dl	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	0,06	0,04	0,03
Dhcr7	7-dehydrocholesterol reductase	0,67	0,35	0,48
Abca1	ATP-binding cassette, subfamily A (ABC1), member 1	0,02	0,01	-0,19
Lcat	lecithin cholesterol acyltransferase	-0,07	-0,19	-0,11
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	0,35	0,06	0,49
Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0,27	0,08	0,11
Pmvk	phosphomevalonate kinase	0,10	0,28	0,12
Mvd	mevalonate (diphospho) decarboxylase	-0,12	0,09	0,23

(F) Bile acid synthesis

Gene	Description	C	HS	HS-HF
Cyp7a1	cytochrome P450, family 7, subfamily a, polypeptide 1	0,27	0,27	-0,29
Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	-0,04	-0,32	-0,12
Cyp8b1	cytochrome P450, family 8, subfamily b, polypeptide 1	0,21	0,37	0,21
Akr1d1	aldo-keto reductase family 1, member D1	-0,08	-0,01	-0,10
Akr1c1	aldo-keto reductase family 1, member C1	0,27	0,93	0,35
Akr1c2	aldo-keto reductase family 1, member C2	0,26	-0,19	-0,09
Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	0,14	0,20	0,13
Slc27a5	solute carrier family 27 (fatty acid transporter), member 5	-0,18	-0,10	-0,20
Amacr	alpha-methylacyl-CoA racemase	0,10	0,18	0,16
Scp2	sterol carrier protein 2	-0,03	0,13	-0,04
Baat	bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase)	-0,27	-0,08	-0,13

Supplemental figure 3: Complete list of genes in relevant pathways encoding enzyme or proteins involved in gluconeogenesis (C), fatty acid and triglyceride synthesis (D), fatty acid oxidation (E), ketogenesis (F), cholesterol metabolism (G) and bile acid synthesis (H). Fold changes are based on signal log ratios for each of the background diets (HP-NP). Values >0 represent increase in gene expression under HP compared to NP conditions while values <0 represent decrease in gene expression under HP conditions.