

Supplemental Table 1. Hepatic transcripts differentially regulated by high fat diet ($Q < 0.05$, $n = 24$ microarrays). Livers were collected from randomly selected PyMT negative, non-tumor bearing- F2 female sib-pairs fed opposing diets ($n = 12$ mice fed HFD, $n = 12$ mice fed MCD). Annotation was performed with Ingenuity Pathway Analysis Knowledge Base.

*Positive fold change is significant fold change increase in high fat diet relative to matched control diet. Negative fold change is significant fold change increase in matched control diet relative to high fat diet.

†Identification of transcript by RefSeq or Illumina probe ID where RefSeq was not available.

‡Highlights significant transcripts that appear in duplicate due to the redundancy of transcript representation on Illumina Bead Chips.

§Official symbolic name of transcript

||Official descriptive name of transcript

	A	B	C	D	E
1	Fold Change*	ID†	Notes‡	Molecules§	Description
2	1.218	68464		1110004M10RIK	RIKEN cDNA 1110004M10 gene
3	-0.683	NM_026947.2		1810022C23RIK	RIKEN cDNA 1810022C23 gene
4	1.294	329406		5230400M03RIK	RIKEN cDNA 5230400M03 gene
5	1.346	AK052127		5830411K21RIK	RIKEN cDNA 5830411K21 gene
6	1.437	77339		9430051O21RIK	RIKEN cDNA 9430051O21 gene
7	1.184	NM_177159		9530091C08RIK	RIKEN cDNA 9530091C08 gene
8	-0.555	NM_030210.1		AACS	acetoacetyl-CoA synthetase
9	1.526	XM_358306.1		ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
10	-0.554	NM_133904		ACACB	acetyl-Coenzyme A carboxylase beta
11	-0.816	NM_025988.1		ACBD4	acyl-Coenzyme A binding domain containing 4
12	1.179	NM_178758.2		ACSM5	acyl-CoA synthetase medium-chain family member 5
13	-0.512	NM_019811.2		ACSS2	acyl-CoA synthetase short-chain family member 2
14	-0.826	NM_028717.2		ALS2	amyotrophic lateral sclerosis 2 (juvenile)
15	-0.838	NM_027799.1		ANKRD40	ankyrin repeat domain 40
16	1.469	XM_128064.4		APOL9A	apolipoprotein L 9a
17	1.521	NM_173743.2		APOL9B	apolipoprotein L 9b
18	-0.784	NM_175105.2		AQP11	aquaporin 11
19	-0.911	NM_146045.1		B4GALT7	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)
20	1.168	BC002245		BC002245	cDNA sequence BC002245
21	-0.745	NM_018772.1		BRI3	brain protein I3
22	1.189	AK049694		C10ORF97	chromosome 10 open reading frame 97
23	-0.886	329478		C130078N14	hypothetical protein C130078N14
24	-0.865	XM_133786.5		C16ORF52	chromosome 16 open reading frame 52
25	-0.676	NM_153577.1		C19ORF46	chromosome 19 open reading frame 46
26	-0.825	NM_029021.1		C20ORF123	chromosome 20 open reading frame 123
27	1.663	NM_009780.1		C4B	complement component 4B (Chido blood group)
28	1.219	XM_128587.4		C6ORF106	chromosome 6 open reading frame 106
29	-0.776	NM_009801.3		CA2	carbonic anhydrase II
30	-0.838	XM_355539.1		CAMTA1	calmodulin binding transcription activator 1
31	1.188	XM_147426.3		CCDC131	coiled-coil domain containing 131
32	1.265	AK013634		CCNT2	cyclin T2
33	-0.808	NM_145822.1		CD3EAP	CD3e molecule, epsilon associated protein
34	-0.760	NM_007657.2		CD9	CD9 molecule
35	-0.854	NM_025584.1		CD99	CD99 antigen
36	-0.790	NM_007543.2		CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21
37	1.261	NM_025639.2	D	CENPM	centromere protein M
38	1.282	NM_178269.1	D	CENPM	centromere protein M
39	1.516	XM_356125.1		CES3	carboxylesterase 3 (brain)
40	1.194	76499		CLASP2	cytoplasmic linker associated protein 2
41	-0.820	NM_171826		CLDND1	claudin domain containing 1
42	1.384	NM_016751.2		CLEC4F	C-type lectin domain family 4, member F

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43	-0.782	NM_009944.2		COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
44	1.191	AK020013		CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa
45	-0.693	NM_029787.2	D	CYB5R3	cytochrome b5 reductase 3
46	-0.776	NM_029787.2	D	CYB5R3	cytochrome b5 reductase 3
47	1.487	NM_009993.2		CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2
48	-0.859	XM_129747.4		CYP20A1	cytochrome P450, family 20, subfamily A, polypeptide 1
49	1.757	NM_007813.1		CYP2B13	cytochrome P450, family 2, subfamily b, polypeptide 13
50	1.218	NM_010000.1		CYP2B9	cytochrome P450, family 2, subfamily b, polypeptide 9
51	1.445	NM_010001.1		CYP2C37	cytochrome P450, family 2, subfamily c, polypeptide 37
52	1.749	NM_134144.1		CYP2C50	cytochrome P450, family 2, subfamily c, polypeptide 50
53	2.059	NM_206537.1		CYP2C54	cytochrome P450, family 2, subfamily c, polypeptide 54
54	-0.588	XM_283309.2		CYP2D40	cytochrome P450, family 2, subfamily d, polypeptide 40
55	1.261	NM_026819.2		DHRS1	dehydrogenase/reductase (SDR family) member 1
56	-0.837	XM_135485		DHRSX	dehydrogenase/reductase (SDR family) X-linked
57	-0.787	NM_145614.2		DLAT	dihydrolipoamide S-acetyltransferase
58	1.604	NM_181680		DSG1C	desmoglein 1 gamma
59	-0.888	XM_127250.4		E2F3	E2F transcription factor 3
60	-0.859	NM_025344		EIF3F	eukaryotic translation initiation factor 3, subunit F
61	-0.862	NM_023314.2		EIF4E2	eukaryotic translation initiation factor 4E family member 2
62	-0.245	NM_130450.1		ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-east)
63	1.139	AK088491.1		ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)
64	1.299	AK046967		ENSMUSG00000063087	predicted gene, ENSMUSG000000063087
65	-0.548	NM_010634.1		FABP5L2	fatty acid binding protein 5-like 2
66	1.633	NM_183278.1		FAM25A	family with sequence similarity 25, member A
67	1.230	NM_133858.2		FAM63A	family with sequence similarity 63, member A
68	-0.665	NM_020013.2		FGF21	fibroblast growth factor 21
69	1.296	NM_010236.1		FPGS	folylpolyglutamate synthase
70	-0.630	NM_008062.1		G6PD	glucose-6-phosphate dehydrogenase
71	-0.771	NM_008064.2		GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)
72	-0.845	NM_139272.2		GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase (NAc-T2)
73	-0.692	NM_145741.2		GDF10	growth differentiation factor 10
74	-0.721	NM_011819.1		GDF15	growth differentiation factor 15
75	1.205	AK089856		GOLGA7	golgi autoantigen, golgin subfamily a, 7
76	1.491	NM_016696.1		GPC1	glypican 1
77	-0.774	NM_010274.2		GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
78	-0.668	NM_008155.1		GPI	glucose phosphate isomerase
79	-0.873	NM_016886.1		GRIA3	glutamate receptor, ionotropic, AMPA 3
80	1.246	AK037997		GRIPAP1	GRIP1 associated protein 1

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81	-0.753	NM_021296		GRPEL2	GrpE-like 2, mitochondrial (E. coli)
82	2.553	NM_029555		GSTK1	glutathione S-transferase kappa 1
83	1.291	NM_178747.2		GULO	gulonolactone (L-) oxidase
84	-0.833	NM_020586.1		HERPUD2	HERPUD family member 2
85	-0.747	NM_008235.2		HES1	hairy and enhancer of split 1, (Drosophila)
86	-0.862	NM_178922.2		HIC2	hypermethylated in cancer 2
87	1.499	NM_001012306.1		HSD3B3	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3
88	1.195	NM_012057.1		IRF5	interferon regulatory factor 5
89	-0.832	NM_019715.1		KCMF1	potassium channel modulatory factor 1
90	-0.735	XM_203753.2		KDSR	3-ketodihydrosphingosine reductase
91	1.240	NM_172615.1		KIAA0226	KIAA0226
92	-0.651	NM_010915.1		KLK1B4	kallikrein 1-related peptidase b4
93	1.149	NM_008455		KLKB1	kallikrein B, plasma (Fletcher factor) 1
94	1.253	AK042286		LINGO4	leucine rich repeat and Ig domain containing 4
95	1.342	NM_008502.1		LLGL1	lethal giant larvae homolog 1 (Drosophila)
96	-0.855	NM_026506.1		LOC100130932	similar to Sm protein G
97	-0.830	NM_027733.2		LOC202051	hypothetical protein LOC202051
98	-0.643	XM_885191.2		LOC440498	hypothetical gene supported by AK001829
99	-0.845	NM_174992.2		LOC57228	small trans-membrane and glycosylated protein
100	1.282	XM_128721.2		LONP1	lon peptidase 1, mitochondrial
101	1.164	AK045341		LPP	LIM domain containing preferred translocation partner in lipoma
102	-0.819	NM_013587.1		LRPAP1	low density lipoprotein receptor-related protein associated protein 1
103	-0.448	NM_198119.1		LRRC24	leucine rich repeat containing 24
104	-0.708	NM_175124.3		LRRC28	leucine rich repeat containing 28
105	1.151	NM_138680.1		LUC7L2	LUC7-like 2 (S. cerevisiae)
106	-0.793	NM_011844.3		MGLL	monoglyceride lipase
107	-0.813	NM_010798.1		MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)
108	1.902	NM_008645.2	D	MUG1	murinoglobulin 1
109	1.391	NM_008645	D	MUG1	murinoglobulin 1
110	1.257	NM_139300		MYLK	myosin light chain kinase
111	-0.767	NM_026703.1		NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
112	1.290	AK034793		NFIB	nuclear factor I/B
113	1.444	AK006371		NNMT	nicotinamide N-methyltransferase
114	1.389	AK088505.1		OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
115	-0.704	NM_011014.1		OPRS1	opioid receptor, sigma 1
116	-0.761	NM_008773.2		P2RY2	purinergic receptor P2Y, G-protein coupled, 2
117	-0.799	NM_148917.1		PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)
118	-0.761	NM_008810.2		PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1
119	-0.678	NM_013743.1		PDK4	pyruvate dehydrogenase kinase, isozyme 4
120	-0.869	NM_026131.2		PDLIM7	PDZ and LIM domain 7 (enigma)

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1	Fold Change*	ID†	Notes‡	Molecules§	Description
121	-0.463	NM_026018.1		PDZK1IP1	PDZK1 interacting protein 1
122	-0.802	AK014543		PGRMC2	progesterone receptor membrane component 2
123	1.268	NM_008835.1		PHXR4	per-hexamer repeat gene 4
124	-0.850	NM_019640.2		PITPNB	phosphatidylinositol transfer protein, beta
125	-0.739	NM_011125.1		PLTP	phospholipid transfer protein
126	1.165	NM_172775.1		PLXNB1	plexin B1
127	-0.795	NM_025928.1		PMF1	polyamine-modulated factor 1
128	-0.797	NM_027241.1		POLR3GL	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like
129	1.181	XM_889570.2		POU5F2	POU domain class 5, transcription factor 2
130	-0.820	NM_133819		PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15B
131	-0.862	NM_017374.2		PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
132	1.227	NM_029239.2		PRKD3	protein kinase D3
133	1.436	NM_178047.2		PROM2	prominin 2
134	1.187	AK019450		PTPRB	protein tyrosine phosphatase, receptor type, B
135	-0.730	NM_008990.2		PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)
136	-0.850	NM_198163.1		RAB35	RAB35, member RAS oncogene family
137	-0.799	NM_009010.2		RAD23A	RAD23 homolog A (S. cerevisiae)
138	-0.614	NM_207649.1		RCAN2	regulator of calcineurin 2
139	-0.618	NM_009040.1		RDH16	retinol dehydrogenase 16
140	1.100	AK020104		RNF170	ring finger protein 170
141	1.698	XM_133272		RNF170	ring finger protein 170
142	-0.718	NM_025786.1		RNF186	ring finger protein 186
143	-0.802	NM_134064.1		RNF44	ring finger protein 44
144	-0.533	NM_009127.2		SCD	stearoyl-CoA desaturase (delta-9-desaturase)
145	1.299	NM_146013.1		SEC14L4	SEC14-like 4 (S. cerevisiae)
146	-0.798	XM_131192.5		SEC24B	SEC24 related gene family, member B (S. cerevisiae)
147	-0.399	NM_177920.4	D	SERPINA7	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 7
148	-0.670	NM_177920	D	SERPINA7	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 7
149	1.125	NM_018877.1		SETDB1	SET domain, bifurcated 1
150	-0.801	NM_009172.1		SIAH1	seven in absentia homolog 1 (Drosophila)
151	-0.762	NM_022411.1		SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2
152	1.211	NM_054055.1		SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
153	-0.860	NM_007451.2		SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
154	1.211	NM_177732.2		SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1
155	-0.859	NM_019810.2		SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1
156	-0.805	NM_022316.1		SMOC1	SPARC related modular calcium binding 1
157	-0.861	NM_009225.1		SNRPB	small nuclear ribonucleoprotein polypeptides B and B1
158	1.322	NM_175229.2		SRRM2	serine/arginine repetitive matrix 2
159	-0.728	NM_145933.2		ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1

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160	-0.603	NM_026935.3		SULT1C2	sulfotransferase family, cytosolic, 1C, member 2
161	1.459	NM_020564.1		SULT5A1	sulfotransferase family 5A, member 1
162	1.264	NM_009306		SYT1	synaptotagmin I
163	-0.712	NM_013769.1		TJP3	tight junction protein 3 (zona occludens 3)
164	1.227	AK087243		TMCC1	transmembrane and coiled-coil domain family 1
165	-0.847	NM_173453.1		TMEM11	transmembrane protein 11
166	1.415	NM_144916.1		TMEM150	transmembrane protein 150
167	1.180	AK081890		TMEM164	transmembrane protein 164
168	-0.629	NM_175507.2		TMEM20	transmembrane protein 20
169	1.225	NM_178577.3		TMEM205	transmembrane protein 205
170	-0.792	NM_013749.1		TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A
171	-0.769	AK012264		TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)-like
172	-0.698	AK029485		TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)-like
173	-0.817	XM_127105.4		TTC7B	tetratricopeptide repeat domain 7B
174	-0.755	NM_011673		UGCG	UDP-glucose ceramide glucosyltransferase
175	-0.654	NM_013701.1	D	UGT1A3	UDP glucuronosyltransferase 1 family, polypeptide A3
176	-0.608	NM_013701.1	D	UGT1A3	UDP glucuronosyltransferase 1 family, polypeptide A3
177	-0.549	NM_201643		UGT1A4	UDP glucuronosyltransferase 1 family, polypeptide A4
178	-0.601	NM_011697.1		VEGFB	vascular endothelial growth factor B
179	-0.788	NM_016852.1		WBP2	WW domain binding protein 2
180	-0.844	NM_018871.2		YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma peptide
181	1.547	NM_009539.2		ZAP70	zeta-chain (TCR) associated protein kinase 70kDa
182	-0.872	NM_026025		ZCRB1	zinc finger CCHC-type and RNA binding motif 1
183	-0.803	NM_025428.1		ZDHHC12	zinc finger, DHHC-type containing 12
184	-0.861	NM_007496.1		ZFH3	zinc finger homeobox 3
185	-0.786	NM_009569.1		ZFPM1	zinc finger protein, multitype 1
186	-0.835	NM_175477.2		ZNF574	zinc finger protein 574
187	-0.910	XM_355639.1		ZNF664	zinc finger protein 664
188	-0.815	NM_199143.1		ZNRF2	zinc and ring finger 2
189	1.319	XM_357173.1			This ID not mapped to the IPAKB
190	1.269	XM_356927.1			This ID not mapped to the IPAKB
191	-0.815	XM_355879.1			This ID not mapped to the IPAKB
192	1.168	XM_133707.3			This ID not mapped to the IPAKB
193	-0.330	XM_147335			This ID not mapped to the IPAKB
194	1.201	AK042521			This ID not mapped to the IPAKB
195	1.224	AK044567			This ID not mapped to the IPAKB
196	1.209	AK04526			This ID not mapped to the IPAKB
197	1.201	AK049777			This ID not mapped to the IPAKB
198	1.247	AK051902			This ID not mapped to the IPAKB
199	1.367	XM_132843			This ID not mapped to the IPAKB

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1	Fold Change*	ID†	Notes‡	Molecules§	Description
200	1.321	Birc1cl			This ID not mapped to the IPAKB
201	1.573	Mug-ps1			This ID not mapped to the IPAKB
202	1.874	NM_027147.1			This ID not mapped to the IPAKB
203	1.259	5330406M23Rik			This ID not mapped to the IPAKB
204	1.952	NM_027147.1			This ID not mapped to the IPAKB
205	1.285	NM_175422.2			This ID not mapped to the IPAKB
206	1.273	NM_133946.1			This ID not mapped to the IPAKB
207	-0.841	XM_365085			This ID not mapped to the IPAKB
208	1.295	4933411D12Rik			This ID not mapped to the IPAKB
209	1.171	9430064K01Rik			This ID not mapped to the IPAKB
210	1.388	9930031P18Rik			This ID not mapped to the IPAKB
211	1.258	C130040J23Rik			This ID not mapped to the IPAKB
212	1.313	4731420N21			This ID not mapped to the IPAKB