**Supplementary Materials.** DNA methylation alters transcriptional rates of differentially expressed genes and contributes to pathophysiology in mice fed a high fat diet by Zhang et al.



Figure S1. Characterization of mice on a high fat diet. C57BL/6 mice were placed on a high fat or normal chow diet for 14 weeks. A. Average weight of the animals over the coursed of the experiment. B. Food intake was measured in grams. C. An intraperitoneal glucose tolerance test was performed and blood glucose was measured for the times indicated. (data are the mean +/- SEM, \*, P < 0.05)

# Figure S2.

DifMeth +/- 10,000 bp from TSS



**Figure S2.** Analysis of differentially expressed genes with differentially methylated CpGs after 14 weeks on a high fat diet. A. 8870 significantly differentially methylated CpGs, representing 6180 genes, were found within 10,000 bp of transcription start sites (TSS). When intersected with the top 600 differentially expressed RNAs, 147 genes were found in common. Numbers of genes found to be increased or decreased with corresponding hypermethylated or hypomethylated CpGs are shown (lists of those genes in are found in supplementary tables 5-8). Note that many genes have multiple differentially methylated CpGs, and genes may have CpGs that are both hypo- and hypermethylated. B. Toppgene [1] analysis of disease prioritization showing number of genes in common with the training set and the p Value. Diseases correlating with altered genes from the high fat diet include cirrhosis, cancer, hypertensive disease, dyslipidemia and diabetes – all consistent with the development of the metabolic syndrome [2].

Name	Left primer	Right primer				
pre-mRNA						
Slc16a5	GCATGGCGGATTAACTCATT	GGTAGCGTTCTCCATTTTGG				
Gnmt	GAGGCCTAAGCAGATGGTGT	GGGCAGCCCAACCTTATAGT				
PhIda1	TCCGTGTCCTTTCTTTCCAG	GCTTCCTGCAACTGTGATGA				
Foxa3	TTCGCCTTTCTCTTTCTCCA	CCTCGGCTCTTGGTGTACTT				
Onecut 1	GGCTGTGAGGAATGGTTGAC	TTGGACGGACGCTTATTTTC				
ChIP						
Phlda1 promoter	CCTGCCTGGATCTGCTACC	GCAGGTTCTGGAAACTCCTG				
Phida1 EXON1	GAAGGATGCTGGAGAACAGC	ACTAGGTTGGGACGGTTCG				
Phida1 EXON2	TCCGTGTCCTTTCTTTCCAG	GCTTCCTGCAACTGTGATGA				
Onecut1 promoter	CCTCGGTTCATTTGTGCTG	GGCTCGGTTACTGTTGCAGA				
Onecut1 Exon1	ACAAGATGCTCACCCCAAAT	ATCTCTTCCATCTGCCCTGA				
Onecut1 Exon2	GAAAATAAGCGTCCGTCCAA	AAGTGCTCGATGAGGACGAT				
Onecut1 Exon2 end	GGAAAATAAGCGTCCGTCCA	TTCCTCCCTCATGCTTTGGT				
Foxa3 Exon1	GGGGCTAGTGCCTGTAGAGA	ATCCCCGAGGACACACC				
Foxa3 Exon2	TTGAACCCACTCAGC TCTCC	CCTTTGCCATCTCTTTTCCA				
Foxa3 Exon2 end	TTCCTTTCTTTCCACGGTTG	GTGCCTTTTTAATGGCCAAA				
Foxa3 promoter	TTCCTTTCTTTCCACGGTTG	GGATAACGGGAAAGTCATCG				
mRNA						
β-actin	AGCCATGTACGTAGCCATCC	CTCTCAGCTGTGGTGGTGAA				
Gnmt	AAGAGGGCTTCAGCGTGATG	CTGGCAAGTGAGCAAAACTGT				
Slc16a5	ATCACGGTAGTGGGCTTGTAT	TGGAGTAAGATGCCACCGAAG				
SIc25a3	CATCACCAAGAAGCACCTGA	GTACCCTTATAGCCCGCACA				
Irx3	GACGAGGAAGAGAGCAAACG	TCGTCCGAGTCGCTAGTTTT				
Cish	TCGGGAAGTGGATGCTTATC	AAACTCCAGACACCCCACTG				
Socs2	TGGCTGCTCAAGATCAAATG	TGTCCTCCTGGAAATGGAAG				

Foxa1	CAGCACAAGCTGGACTTCAA	AGCACGGGTCTGGAATACAC
Foxa2	GACATACCGACGCAGCAGCTACA	GGCACCTTGAGAAAGCAGTC
Onecut1	GGCAACGTGAGCGGTAGTTT	TTGCTGGGAGTTGTGAATGCT
Phida1	GGGCTACTGCTCATACCGC	AAAAGTGCAATTCCTTCAGCTT
Foxa3	CTACATGACCTTGAACCCACTC	GGGCTACATACCCGGAAGC

## Supplemental Table 2. Summary statistic for RNA-seq

Library	total reads	aligned reads	% aligned
normal			
1_1BC	42,315,569	36,343,322	0.858864074
1_1LC	21,658,077	17,575,957	0.811519739
1_1NC	59,685,957	50,084,723	0.839137471
1_1RC	34,954,648	28,458,348	0.81415061
2_1LC	31,907,946	26,294,512	0.824074104
2_1NC	31,732,872	26,096,217	0.822371735
2_1RC	53,368,278	42,173,702	0.790239138
high fat			
1_4BC	53,863,635	43,665,966	0.810676183
1_4LC	37,439,032	28,227,112	0.753948767
1_4NC	38,131,178	29,035,979	0.761476055
1_4RC	34,835,729	26,676,785	0.765788051
2_4LC	20,302,121	17,692,470	0.871459194
2_4NC	41,644,336	36,539,067	0.877407842
2_4RC	23,634,778	19,678,396	0.832603378

Ouppie	mentai	Table J.	Summ	ary Otati	31103 101		letinyi-o	-4		
Sample ID	#reads	# pairs	# pairs removed after trimming	#pairs remaining	<ul> <li># Paired</li> <li>end</li> <li>alignment</li> <li>with</li> <li>unique</li> <li>best hit</li> </ul>		# duplicated pairs	pairs analyzed	% pairs analyzed	approximate fold coverage (52Mb capture)
Normal										
G1_1RC	108,787,410	54,393,705	1,213,575	53,180,130	36,727,668	69.1%	11,143,605	25,584,063	47.03%	
G1_1LC	128,228,736	64,114,368	1,450,274	62,664,094	43,654,179	69.7%	9,550,798	34,103,381	53.19%	131.16685
G2_1LC	124,264,108	62,132,054	1,400,257	60,731,797	42,685,346	70.3%	1,270,902	41,414,444	66.66%	159.2863231
G1_1NC	120,760,734	60,380,367	1,392,279	58,988,088	40,589,058	68.8%	4,894,023	35,695,035	59.12%	137.2885962
G2_1RC	117,629,094	58,814,547	1,343,298	57,471,249	38,964,159	67.8%	11,124,280	27,839,879	47.34%	107.0764577
G2_1NC	113,885,548	56,942,774	1,297,220	55,645,554	38,621,945	69.4%	9,178,454	29,443,491	51.71%	113.2441962
G1_1BC	116,203,544	58,101,772	1,318,334	56,783,438	39,496,146	69.6%	9,994,402	29,501,744	50.78%	113.4682462
High Fat										
G1_4NC	169,802,970	84,901,485	2,034,858	82,866,627	57,067,889	68.9%	14,046,240	43,021,649	50.67%	165.4678808
G1_4BC	157,695,914	78,847,957	1,957,171	76,890,786	52,182,910	67.9%	9,264,249	42,918,661	54.43%	165.0717731
G1_4RC	186,815,332	93,407,666	2,058,068	91,349,598	62,090,548	68.0%	29,997,052	32,093,496	34.36%	123.4365231
G2_4RC	149,406,108	74,703,054	1,618,152	73,084,902	51,158,472	70.0%	24,190,973	26,967,499	36.10%	103.72115
G2_4LC	131,049,978	65,524,989	1,534,427	63,990,562	42,881,093	67.0%	12,239,682	30,641,411	46.76%	117.8515808
G2_4NC	98,751,052	49,375,526	1,176,190	48,199,336	33,022,488	68.5%	10,364,887	22,657,601	45.89%	87.14461923

## Supplemental Table 3. Summary Statistics for DNA Methyl-Seq

## Supplemental Table 4. Characterization of differentially methylated genes in the study

id	chr	start	end	pva	alue qvalue	meth.diff	avg_meth_lowfat	avg_meth_highfat	dist.to.feature	feature.	feature.C	pGi	shores prom	exon	intron	gene.ID	symbol	name
Phlda1																		
chr10.1110	11chr10	111,017,921	11101792	1 2.	38E-05 0.00244909	7.124120684	8.95280642	8 15.0246797	73 74581	uc007haf.2	+	0	0 0	0	0	NM_009344	PhIda1	pleckstrin homology-like domain, family A, member 1
chr10.1110	01.chr10	111,017,958	11101795	8 1.	.69E-08 2.45E-05	8.704192235	5.97505599	4 13.9856575	2 74618	uc007haf.2	+	0	0 0	0	0	NM_009344	Phlda1	pleckstrin homology-like domain, family A, member 1
chr10.1110	)1:chr10	111,011,760	11101176	0 0.000	021261 0.00906516	9.038730448	84.4753721	5 92.1559311	1 68420	uc007haf.2	+	0	0 0	0	0	NM_009344	Phida1	pleckstrin homology-like domain, family A, member 1
chr10.1110	11.chr10	111,017,408	11101073	5 2. 8 2.	59E-05 0.00257468	10.9912854	24,78574	20.400945	73413	uc007haf.2	+	0	0 0	0	0	NM 009344	Phida1	pleckstrin homology-like domain, family A, member 1 pleckstrin homology-like domain, family A, member 1
chr10.1109	4ichr10	110,942,377	11094237	7 9.	.06E-06 0.00136654	11.09434445	28.8455115	7 38.7430159	965	uc007haf.2	+	0	1 1	0	0	NM 009344	Phida1	pleckstrin homology-like domain, family A, member 1
chr10.1109	51chr10	110,958,950	11095895	0 6.	.59E-06 0.00111365	12.95675199	10.2277432	9 24.4353843	6 15610	uc007haf.2	+	0	0 0	0	0	NM_009344	PhIda1	pleckstrin homology-like domain, family A, member 1
chr10.1109	4ichr10	110,942,365	11094236	5 9.	.39E-10 3.55E-06	13.02640376	15.8172380	5 29.1092186	52 -977	uc007haf.2	+	0	1 1	0	0	NM_009344	PhIda1	pleckstrin homology-like domain, family A, member 1
chr10.1109	Michr10	110,942,402	11094240	2 2.	45E-07 0.00013859	14.01076995	29.0307124	5 41.1015597	74 -940 26 75170	uc007haf.2	+	0	1 1	0	0	NM_009344	Phida1	pleckstrin homology-like domain, family A, member 1
chr10.1110	)2(chr10	111,018,519	11101851	9 2. 1 8.	44E-15 6.84E-10	16.74478812	50.4829136	6 66.8594067	73179	uc007haf.2	+	0	0 0	0	0	NM 009344	Phida1	pleckstrin homology-like domain, family A, member 1 pleckstrin homology-like domain, family A, member 1
foxa3																-		
IOAUS																		
chr7.19608	4!chr7	19,608,459	1960845	9 6.	.73E-05 0.00459166	6.127486852	14.8592584	2 20.9128301	430	uc009fkd.1	-	0	1 1	0	1	NM_008260	Foxa3	forkhead box A3
chr7.19599	11chr7	19,599,167	1959916	77.	.94E-05 0.00504945	7.259532821	25.4774583	3 32.1698842	9722	uc009fkd.1	-	0	1 0	1	0	NM_008260	Foxa3	forkhead box A3
chr7 19608	salchr7	19,608,402	1960840	22. 61	51E-05 0.000579	7.423638206	13.8322456	3 20.8/6225t 8 16 5701136	3 487 52 763	uc009fkd.1		0	1 1	0	1	NM_008260	Foxa3	forkhead box A3
chr7.19608	31chr7	19,608,383	1960838	3 9.	99E-16 1.67E-10	8.664900254	2.98990732	4 11.4041951	4 506	uc009fkd.1	-	0	1 1	ō	1	NM 008260	Foxa3	forkhead box A3
chr7.19607	4(chr7	19,607,400	1960740	0 9.	97E-05 0.00578528	11.18748863	21.6729413	3 31.7848090	1489	uc009fkd.1	-	0	0 0	0	1	NM_008260	Foxa3	forkhead box A3
Hip1R																		
chr5.12442 chr5.12442	13:chr5	124,423,345	12442334	53. 33.	60E-08 4.01E-05	13.35209506	2.02866948	5 15.0001515 7 24.9526380	-292 06 -294	uc008zos.2 uc008zos.2	+	0	1 1	0	0	NM_145070 NM_145070	Hip1r Hip1r	huntingtin interacting protein 1 related huntingtin interacting protein 1 related
Notch3												-			-			
chr17.3229	9(chr17	32,299,055	3229905	5 6.	40E-05 0.00444968	6.920659062	9.91259510	2 18.0842589	92 4743	uc008bvx.1	-	0	1 0	0	1	NM_008716	Notch3	notch 3
chr17.3229	9(chr17	32,299,029	3229902	9 2.	53E-05 0.00253878	7.857087301	17.071300	1 24.9617303	4769	uc008bvx.1	-	0	1 0	0	1	NM_008716	Notch3	notch 3
chr17.3230	Alchr17 Michr17	32,304,013	3230401	38. 81	59E-09 5 14E-06	20 37066778	34.0024779	3 51.3/54825	-217	uc008bvx.1		0	1 1	0	0	NM_008716	Notch3	notch 3
Scara5		,,																
JCaraJ																		
chr14.6628	5/chr14	66,285,498	6628549	8 8.	34E-05 0.00521098	16.50025602	36.0756420	8 52.6755445	54 260	uc007ujn.2	+	0	0 1	1	0	NM_028903	Scara5	scavenger receptor class A, member 5 (putative)
chr14.6628	5!chr14	66,285,536	6628553	6 5.	.39E-05 0.00401093	18.12356227	61.4156251	2 78.4435045	59 298	uc007ujn.2	+	0	0 1	1	0	NM_028903	Scara5	scavenger receptor class A, member 5 (putative)
chr14.6628	Sichr14	66,285,367	6628536	71.	.62E-08 2.38E-05	23.82998572	27.1640359	1 48.3717135 41.906022/	58 129 14 96	uc007ujn.2	+	0	0 1	1	0	NM_028903	Scara5	scavenger receptor class A, member 5 (putative)
UII 14.0028	5:CHI 14	00,265,554	0026555	4 7.	.192-08 0.272-03	24.37303834	23.3676019	6 41.6909224	96	00070J1.2	*	0	0 1	1	0	NINI_028905	Scalab	scavenger receptor class A, member 5 (putative)
Sik3																		
chr9 45906	4'chr9	45,906,411	4590641	1 8	63E-05 0.0053186	-11.59606171	75.0433084	3 62 93780	-24889	uc009pha.1	+	0	0 0	0	1	NM 027498	Sik3	SIK family kinase 3
chr9.45928	11chr9	45,928,124	4592812	4 2.	32E-06 0.00057943	-10.78195489	67.9878254	5 59.1070785	-3176	uc009pha.1	+	0	0 0	0	1	NM 027498	Sik3	SIK family kinase 3
chr9.45823	11(chr9	45,823,169	4582316	9 0.00	015931 0.00763012	6.779763659	18.3728179	3 25.7026252	24 2268	uc009pgz.2	+	0	1 0	0	1	NM_027498	Sik3	SIK family kinase 3
chr9.45934	19:chr9	45,934,916	4593491	6 5.	.87E-05 0.00422418	12.28092349	46.0992797	6 56.8931786	58 <u>3618</u>	uc009pha.1	+	0	0 0	0	1	NM_027498	Sik3	SIK family kinase 3
chr9.45820	)2(chr9	45,820,204	4582020	4 1.	12E-07 8.32E-05	15.84850341	33.4983347	2 49.0386687	73 <mark>-699</mark>	uc009pgz.2	+	0	1 1	0	0	NM_027498	Sik3	SIK family kinase 3
Trdmt1																		
chr2.13466	8ichr2	13,466,821	1346682	1 5.	78E-06 0.00102802	-22.74819198	74.7703985	4 56.0628171	-531	uc008ika.2		0	0 1	0	0	NM 010067	Trdmt1	tRNA aspartic acid methyltransferase 1
chr2.13461	7:chr2	13,461,735	1346173	5 3.	70E-05 0.00317994	-13.98828887	96.6378066	4 82.8251718	4557	uc008ika.2	-	0	0 0	0	1	NM_010067	Trdmt1	tRNA aspartic acid methyltransferase 1
chr2.13466	521chr2	13,466,277	1346627	79.	90E-08 7.70E-05	6.462585034		0 6.47173897	15	uc008ika.2	-	0	0 1	1	0	NM_010067	Trdmt1	tRNA aspartic acid methyltransferase 1
Onecut	1																	
chr9.74702	??!chr9	74,702,752	7470275	2 3.	30E-06 0.00071941	-13.6037793	68.0659006	6 54.5742948	8 6484	uc009qrg.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74702	9(chr9	74,702,905	7470290	5 3.	83E-06 0.00078914	-11.42312764	70.1481359	7 58.8498656	6637	uc009qrg.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74702	9ichr9	74,702,921	7470292	1 3.	83E-06 0.00078987	-10.88286128	75.3252076	3 65.047734	13 6653	uc009qrg.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74705	8:chr9	74,705,813	7470581	3 0.000	010811 0.00607044	-10.15015781	77.7172574	5 68.1024990	Jb -3915	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74700	7.chr9	74,700,890	7470089	8 0.00	022102 0.00928511	-7.374090772	70.6300244	3 63,0132800	4022	uc009qrg.1	+	0	0 0	0	1	NM 008262	Onecut1	one cut domain, family member 1
chr9.74697	5-chr9	74,697,545	7469754	5 1.	41E-06 0.00042508	5.245693871	2.35242024	5 7.0877888	1277	uc009qrg.1	+	õ	1 0	õ	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74716	55:chr9	74,716,533	7471653	3 1.	18E-05 0.00160781	6.053683609	4.95726179	7 11.5487119	6807	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74716	ilichr9	74,716,189	7471618	9 2.	.02E-07 0.00012214	7.206803147	4.18887831	6 11.176136	6463	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74716	551chr9	74,716,597	7471659	71.	.03E-05 0.00147575	7.960234342	14.1583713	8 22.057332	6871	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74716 chr9.74716	44chr9	74,716,466	74/1646	ь 9. 0.0.00	461-05 0.00560599	8.088585188	/.46373826	/ 14.1258297 3 20.262077	rb 6740 71 6764	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1 one cut domain, family member 1
chr9.74705	i0.chr9	74,705.028	7470502	8 8	54E-06 0.00131669	11.00665091	39.1705373	5 49.9876791	18 -4700	uc009arh.1	+	0	0 0	0	1	NM 008262	Onecut1	one cut domain, family member 1
chr9.74716	51chr9	74,716,585	7471658	5 4.	59E-11 4.69E-07	12.0929867	13.4273021	1 25.9301963	6859	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74718	7ichr9	74,718,788	7471878	8 1.	85E-05 0.00210484	12.16118754	31.6579742	8 44.888724	9062	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74698	1:chr9	74,698,113	7469811	3 2.	27E-05 0.00238063	14.33769384	48.9385969	4 64.6321378	32 1845	uc009qrg.1	+	0	1 0	0	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74698	V:chr9	74,698,733	7469873	3 0.000	010034 0.0058072	14.67352092	15.9769003	1 32.359289	2465	uc009qrg.1	+	0	1 0	1	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74718	7fchr9	74,096,087	7409808	, 5. 3 8	46E-11 7.25E-07	18,21378612	45.2621314 58 5625487	4 76.2028585	9037	uc009qrg.1	+	0	0 0	0	1	NM 008262	Onecut1	one cut domain, family member 1
chr9.74718	7/chr9	74,718,740	7471874	0 1.	18E-12 3.66E-08	21.7035792	25.609366	4 46.0556184	9014	uc009qrh.1	+	ō	0 0	õ	1	NM_008262	Onecut1	one cut domain, family member 1
chr9.74718	71chr9	74,718,722	7471872	2 1.	73E-10 1.13E-06	21.91051933	26.9490830	4 46.9579707	8996	uc009qrh.1	+	0	0 0	0	1	NM_008262	Onecut1	one cut domain, family member 1

C	
Supplementary Lanie 5 Genes with Hypermethylate	
Supplementary rable 5. denes with hypermethylate	

Acot4	Cidea	Gngt1	Ntrk2	Rtn4	Tpm2
Ar	Corin	Kbtbd11	Osbpl3	Sh2d4a	Trdmt1
Car3	Cpeb1	Lgals1	Pax8	Slc13a4	Unc13a
Cdca2	Cxcl11	Mab21l3	Pdlim2	Slc22a26	Wfdc2
Cenpf	Cyp26a1	Mfap3l	Plscr2	Smc2	Zfp442
Cenpw	Fsip1	Mogat1	Prrx1	Snai2	
Cep55	Gadd45b	Nebl	Raet1d	Sult1c2	

### Supplementary Table 6. Genes with Hypermethylated CpGs decreased expression.

3930402G	Co das A	De et 1	E	L La	1 1		Comine ( o	CudE - 1	Nime 1
23111	Cadm4	Dact1	гохаз	нр	Leprei	Phidal	Serpinala	Srd5a1	XIrp1
AI118078	Cd4	Dnajc12	Fzd5	Hspa5	Llgl2	Pitx3	Serpina1e	Srgap3	Zbtb7c
Abtb2	Chrna2	Dpy19l3	Fzd7	Hyal1	Lrfn3	Plcxd2	Shb	Susd4	Zfhx3
Adcy1	Cldn1	Efna3	Got1	ld2	Myo1e	Prhoxnb	Sidt2	Syvn1	Zfp217
Agap2	Cobl	Egfr	Grm8	ld3	Nudt7	Qsox1	Sik3	Tbc1d30	Zfp568
Ankrd33b	Creld2	Erbb3	H13	lgfbp2	Oaf	Rcl1	Slc13a2	Tgm1	Zfp598
Apoa1	Crip2	Fabp5	Hhex	ll22ra1	Onecut1	Rnase4	Slc25a34	Tnfaip8l1	Zfpm1
Arid5b	Crybb3	Fga	Hip1r	Irf6	Orm1	Scara5	Socs3	Tspan9	
Atp2a2	Cyp1a2	Fgb	Hist2h3c2	lrs2	Pck1	Sel1l3	Sorbs3	Usp6nl	
C8b	Cyp21a1	Fkbp11	Норх	Lad1	Pde9a	Serpina10	Sox12	Vtn	

#### Supplementary Table 6. Genes with Hypomethylated CpGs increased expression.

A530016L24Rik	Aatk	B430212C06Rik	Caprin2	Car3	Fam126a	Far1
Mad2l1	Mpped2	Nebl	Pdlim2	Pdxp	Rtn4	Smc2
Stap1	Stil	Tpm2	Trdmt1	Tsc22d1	Unc13a	

#### Supplementary Table 6. Genes with Hypomethylated CpGs decreased expression.

Ada	Ccdc11	Cd276	Cish	Crip2	Dact1	Fzd7	Gfra1	Gm11194	lfitm2
lgfbp2	Mycl1	Myo1e	Onecut1	Pck1	Pitx3	Sel1l3	Serpine2	Sik3	Slc41a3
Slco2a1	Tmem120 b	Tnk2	Tspan9	Tuba8	Tuft1	Wnk4	Zfp217	Zfpm1	

Supplemental Table 9. Characteristics of genes differentially methylated and expressed in liver after a high fat diet.

Gene	DNA Methylation HF vs SC	RNAseq HF vs SC	RT-PCR HF vs SC	Function/ Role in Obesity/Diabetes
Foxa3	6.12*	0.64*	0.26*	Development, glucose homeostasis in adult liver
Hip1R	13.35*	0.54*	0.75	Huntington's interacting protein 1 related, endocytosis
Notch3	20.37*	0.53*	0.72	Hypertension
Phlda1	13.03*	0.27*	0.33*	Associated with steatosis: KO animals have liver steatosis
Scara5	-22.75*	1.61*	0.62	Scavenger receptor
Sik3	15.85*	0.63*	0.78	Salt inducible kinase 3, member of AMPK family
Trdmt1	23.83*	0.20*	0.61	tRNA aspartic acid methyl-transferase 1
Onecut1	21.7*	0.22*	0.41	Liver development

Mean of fold change comparing high fat diet (HF) to standard chow diet (SC) using data from RNAseq or RT-PCR. For DNA Methyl-seq, data are relative differences in percentage methylation in CpGs within 1,000 bp of the TSS of the indicated gene. The *Phlda1* assignation was a CpG ~10,000 bp from the TSS. n=7, \* p < 0.05

References for Supplemental Material.

[1] Chen, J., Bardes, E. E., Aronow, B. J., and Jegga, A. G., 2009. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. *Nucleic acids research* 37: W305-311

[2] Kaur, J., 2014. A comprehensive review on metabolic syndrome. *Cardiology research and practice* 2014: 943162