

Table S1. A list of differentially expressed genes¹ in RNA sequencing dataset

Gene symbol	Fold change	P-value
<i>Tmc7</i>	-8.696	0.00766
<i>Rgs3</i>	-6.826	0.00312
<i>Gopc</i>	-5.313	0.00214
<i>Cnbd2</i>	-5.176	0.01026
<i>Eef2k</i>	-4.981	0.00250
<i>Fabp5</i>	-4.881	0.03206
<i>Dnm2</i>	-4.564	0.00250
<i>Me1</i>	-4.563	0.01045
<i>St3gal5</i>	-4.538	0.00298
<i>Man2b1</i>	-4.125	0.01554
<i>Dctn4</i>	-4.094	0.03106
<i>Hmgcl</i>	-4.062	0.01787
<i>Amfr</i>	-4.043	0.00515
<i>Ddc</i>	-3.896	0.01715
<i>Prkag1</i>	-3.890	0.00390
<i>Tmem245</i>	-3.854	0.03777
<i>Serpina1a</i>	-3.808	0.03518
<i>Aspg</i>	-3.737	0.03287
<i>Serpina3a</i>	-3.715	0.01926
<i>Onecut1</i>	-3.693	0.04203
<i>TrnS2</i>	-3.615	0.03711
<i>Gstm6</i>	-3.610	0.02624
<i>Ppp2cb</i>	-3.597	0.01545
<i>Ugt1a7c</i>	-3.553	0.01225
<i>Aacs</i>	-3.547	0.01346
<i>Gpatch8</i>	-3.543	0.02193
<i>Bag2</i>	-3.474	0.00053
<i>Rsph1</i>	-3.450	0.02809
<i>Orai1</i>	-3.444	0.01262
<i>Rtn3</i>	-3.443	0.00188
<i>Tmem53</i>	-3.390	0.03934
<i>Clec2d</i>	-3.382	0.04926
<i>Vps53</i>	-3.366	0.00210
<i>S100a10</i>	-3.292	0.00529
<i>Slc50a1</i>	-3.234	0.02470
<i>Ihh</i>	-3.203	0.04394
<i>Rxra</i>	-3.199	0.01079
<i>Elovl2</i>	-3.167	0.02657

<i>Rps4x</i>	-3.152	0.00687
<i>Srebf2</i>	-3.064	0.00399
<i>Cdkn2aipnl</i>	-3.052	0.03147
<i>Stam</i>	-2.977	0.01036
<i>Wdr5b</i>	-2.968	0.04049
<i>Cebpa</i>	-2.938	0.03513
<i>Mob4</i>	-2.883	0.02727
<i>Cyp2c68</i>	-2.880	0.03067
<i>Acaca</i>	-2.855	0.01196
<i>Usp39</i>	-2.838	0.00818
<i>Tbc1d32</i>	-2.832	0.04589
<i>Blvra</i>	-2.822	0.03946
<i>Snrpf</i>	-2.751	0.01925
<i>Btafl</i>	-2.736	0.03662
<i>Tkfc</i>	-2.727	0.00417
<i>Plpp5</i>	-2.727	0.03715
<i>Nudcd1</i>	-2.704	0.04575
<i>Yipf3</i>	-2.670	0.02526
<i>Fdx1l</i>	-2.669	0.00698
<i>Calm1</i>	-2.659	0.03733
<i>Fasn</i>	-2.652	0.03175
<i>Zfp180</i>	-2.623	0.04431
<i>Sdhb</i>	-2.563	0.04137
<i>C1s2</i>	-2.537	0.03181
<i>Arhgef11</i>	-2.533	0.03831
<i>Arhgap15os</i>	-2.497	0.04012
<i>Srgap3</i>	-2.469	0.02968
<i>Ryk</i>	-2.462	0.04867
<i>Prkar1a</i>	-2.450	0.01945
<i>Tm6sf2</i>	-2.412	0.03439
<i>Sf3b2</i>	-2.400	0.04698
<i>Urah</i>	-2.373	0.00939
<i>Scd3</i>	-2.310	0.01819
<i>Trim34a</i>	-2.275	0.01030
<i>Thrsp</i>	-2.237	0.04215
<i>Rnf181</i>	-2.233	0.01102
<i>Mtg1</i>	-2.226	0.04726
<i>Mpc1</i>	-2.193	0.01321
<i>Dusp22</i>	-2.188	0.04920
<i>Dnajc7</i>	-2.186	0.02859
<i>Wdr70</i>	-2.163	0.01798

<i>Swi5</i>	-2.159	0.02130
<i>Copz1</i>	-2.157	0.02307
<i>Rrbp1</i>	-2.150	0.04093
<i>Wdr6</i>	-2.144	0.03727
<i>Rps15</i>	-2.144	0.01192
<i>Hsd3b7</i>	-2.144	0.01456
<i>Pmvk</i>	-2.107	0.03961
<i>Tma16</i>	-2.083	0.04844
<i>Mycn</i>	-2.080	0.02839
<i>Slc25a11</i>	-2.063	0.00480
<i>Ces2a</i>	-2.057	0.00189
<i>Gja4</i>	2.009	0.00270
<i>Mup-ps16</i>	2.011	0.04858
<i>Tia1</i>	2.014	0.04227
<i>Enc1</i>	2.020	0.04158
<i>Dgcr14</i>	2.041	0.03075
<i>Inafm1</i>	2.056	0.04793
<i>Cngb1</i>	2.111	0.02270
<i>Scamp3</i>	2.123	0.02600
<i>Ngrn</i>	2.129	0.01282
<i>Zfp608</i>	2.150	0.02774
<i>Mansc4</i>	2.157	0.00786
<i>Pde4a</i>	2.160	0.00634
<i>Rbm3</i>	2.162	0.03389
<i>Gpr137c</i>	2.162	0.01115
<i>Ccnh</i>	2.177	0.01316
<i>Pdk3</i>	2.205	0.02368
<i>Spag1</i>	2.218	0.00483
<i>Uimc1</i>	2.221	0.00553
<i>Nle1</i>	2.312	0.02224
<i>Ciapi1</i>	2.313	0.00004
<i>Hsf2</i>	2.322	0.03259
<i>Simc1</i>	2.332	0.01828
<i>Ptprcap</i>	2.340	0.01870
<i>Ppp1r3fos</i>	2.348	0.04604
<i>Osbp15</i>	2.352	0.04332
<i>Pcp4l1</i>	2.379	0.04499
<i>Ccdc73</i>	2.396	0.04686
<i>Mustn1</i>	2.401	0.03134
<i>Fam104a</i>	2.420	0.04288
<i>Rtn1</i>	2.421	0.01884

<i>Tmem194b</i>	2.467	0.02851
<i>Mkln1os</i>	2.535	0.04120
<i>Neurl4</i>	2.555	0.00997
<i>G0s2</i>	2.587	0.02171
<i>Slamf8</i>	2.645	0.02847
<i>Fstl4</i>	2.670	0.03646
<i>Atad3aos</i>	2.741	0.02023
<i>Mocs1</i>	2.840	0.02320
<i>Tuba1a</i>	2.870	0.00568
<i>Rrnad1</i>	2.895	0.02550
<i>Fam83f</i>	3.043	0.00100
<i>Hes1</i>	3.045	0.01572
<i>Micalcl</i>	3.086	0.00819
<i>Dlg4</i>	3.097	0.00512
<i>Adat3</i>	3.113	0.01602
<i>Trbc2</i>	3.142	0.04632
<i>Apold1</i>	3.166	0.02553
<i>Ppp1r1c</i>	3.208	0.00553
<i>Lpcat2</i>	3.224	0.03083
<i>Igkc</i>	3.390	0.02047
<i>Aard</i>	3.470	0.01320
<i>Gjc3</i>	3.511	0.00132
<i>Cirbp</i>	3.545	0.02555
<i>Trim34b</i>	3.629	0.01340
<i>Krt23</i>	3.670	0.01669
<i>Ccdc159</i>	3.745	0.00855
<i>Dusp1</i>	3.809	0.02923
<i>Zfp36</i>	3.849	0.02651
<i>Cyp4a14</i>	3.926	0.01863
<i>Dlg1</i>	4.203	0.01470
<i>Fbxo44</i>	4.267	0.01264
<i>Hba-a2</i>	4.298	0.02169
<i>Plscr2</i>	4.481	0.00334
<i>Junb</i>	4.602	0.00091
<i>Ier2</i>	4.620	0.01199
<i>Gdf15</i>	4.716	0.03223
<i>Hba-a1</i>	5.127	0.01746
<i>Adam15</i>	5.165	0.00623
<i>Hddc3</i>	5.299	0.00050
<i>Igha</i>	6.433	0.00767
<i>Hbb-bs</i>	6.530	0.00815

<i>Ighv1-81</i>	9.549	0.03563
<i>Fos</i>	10.774	0.04110
<i>Egr1</i>	16.496	0.00299
<i>Mettl7a2</i>	23.132	0.01850
<i>Sult2a3</i>	31.485	0.02596
<i>Gdpd3</i>	81.848	0.02006

¹ Genes passed following criteria were selected as differentially expressed genes: Fold change > ± 2 , and P-value < 0.05

Table S2. DAVID GO terms for biological process

Category ¹	Terms ²	Count ³	%	P-Value
GOTERM_BP_FAT	Lipid Metabolic Process	21	12.7	5.30E-04
GOTERM_BP_FAT	Organonitrogen Compound Biosynthetic Process	21	12.7	1.70E-03
GOTERM_BP_FAT	Amide Biosynthetic Process	16	9.6	8.20E-04
GOTERM_BP_FAT	Organic Acid Metabolic Process	16	9.6	1.90E-03
GOTERM_BP_FAT	Response to Organic Cyclic Compound	16	9.6	6.70E-03
GOTERM_BP_FAT	Cellular Amide Metabolic Process	16	9.6	8.60E-03
GOTERM_BP_FAT	Carboxylic Acid Metabolic Process	15	9.0	2.00E-03
GOTERM_BP_FAT	Oxoacid Metabolic Process	15	9.0	2.10E-03
GOTERM_BP_FAT	Hemopoiesis	15	9.0	5.70E-03
GOTERM_BP_FAT	Cellular Lipid Metabolic Process	15	9.0	7.10E-03
GOTERM_BP_FAT	Hematopoietic or Lymphoid Organ Development	15	9.0	8.90E-03
GOTERM_BP_FAT	Translation	14	8.4	2.20E-03
GOTERM_BP_FAT	Peptide Biosynthetic Process	14	8.4	2.90E-03
GOTERM_BP_FAT	Cofactor Metabolic Process	11	6.6	4.20E-04
GOTERM_BP_FAT	Lipid Biosynthetic Process	11	6.6	6.80E-03
GOTERM_BP_FAT	Monocarboxylic Acid Metabolic Process	11	6.6	7.50E-03

¹ Functional Annotation Tool (FAT) GO category inside a cluster

² GO terms inside each cluster

³ Gene count in differentially expressed genes

Table S3. Annotation clusters of DAVID GO terms for biological process

Annotation Cluster 1	Enrichment Score ¹ : 3.2	Count ²	P-Value
GOTERM_BP_FAT	Acyl-CoA Metabolic Process	6	3.20E-04
GOTERM_BP_FAT	Thioester Metabolic Process	6	3.20E-04
GOTERM_BP_FAT	Cofactor Metabolic Process	11	4.20E-04
GOTERM_BP_FAT	Acetyl-CoA Metabolic Process	4	1.20E-03
GOTERM_BP_FAT	Coenzyme Metabolic Process	9	1.90E-03
Annotation Cluster 2	Enrichment Score: 2.53	Count	P-Value
GOTERM_BP_FAT	Lipid Metabolic Process	21	5.30E-04
GOTERM_BP_FAT	Lipid Biosynthetic Process	11	6.80E-03
GOTERM_BP_FAT	Cellular Lipid Metabolic Process	15	7.10E-03
Annotation Cluster 3	Enrichment Score: 2.49	Count	P-Value
GOTERM_BP_FAT	Amide Biosynthetic Process	16	8.20E-04
GOTERM_BP_FAT	Organonitrogen Compound Biosynthetic Process	21	1.70E-03
GOTERM_BP_FAT	Translation	14	2.20E-03
GOTERM_BP_FAT	Peptide Biosynthetic Process	14	2.90E-03
GOTERM_BP_FAT	Regulation of Translation	9	5.80E-03
GOTERM_BP_FAT	Cellular Amide Metabolic Process	16	8.60E-03
GOTERM_BP_FAT	Regulation of Cellular Amide Metabolic Process	9	8.70E-03
Annotation Cluster 4	Enrichment Score: 2.48	Count	P-Value
GOTERM_BP_FAT	Organic Acid Metabolic Process	16	1.90E-03
GOTERM_BP_FAT	Carboxylic Acid Metabolic Process	15	2.00E-03

GOTERM_BP_FAT	Oxoacid Metabolic Process	15	2.10E-03
GOTERM_BP_FAT	Cellular Lipid Metabolic Process	15	7.10E-03
GOTERM_BP_FAT	Monocarboxylic Acid Metabolic Process	11	7.50E-03
Annotation Cluster 5	Enrichment Score: 2.14	Count	P-Value
GOTERM_BP_FAT	Hemopoiesis	15	5.70E-03
GOTERM_BP_FAT	Myeloid Cell Differentiation	9	7.50E-03
GOTERM_BP_FAT	Hematopoietic or Lymphoid Organ Development	15	8.90E-03

¹ Minimum enrichment score threshold was set to 0.75.

² Gene count in differentially expressed genes

Table S4. A list of representative terms in Kyoto Encyclopedia of Gene and Genomes (KEGG) pathways

Category	Term	Count	P-value
KEGG_PATHWAY	AMPK Signaling Pathway	6	0.005
KEGG_PATHWAY	Fatty Acid Metabolism	4	0.010
KEGG_PATHWAY	PPAR Signaling Pathway	4	0.034
KEGG_PATHWAY	Insulin Signaling Pathway	5	0.035
KEGG_PATHWAY	African Trypanosomiasis	3	0.038
KEGG_PATHWAY	Chemical Carcinogenesis	4	0.048
KEGG_PATHWAY	Malaria	3	0.067
KEGG_PATHWAY	cAMP Signaling Pathway	5	0.096

Table S5. A list of TaqMan primers

Primer	Manufacturer	Assay ID	RefSeq/ Accession number
β -Actin (<i>Actb</i>)	Life Technologies	Mm02619580_g1	NM_007393
Acetyl CoA carboxylase alpha (<i>Acaca</i>)		Mm01304257_m1	NM_133360.2
Fatty acid synthase (<i>Fasn</i>)		Mm00662319_m1	NM_007988.3
Stearoyl-CoA Desaturase-1 (<i>Scd1</i>)		Mm00772290_m1	NM_009127.4
Retinoid X receptor alpha (<i>Rxra</i>)		Mm00441185_m1	NM_001290481.1
Thyroid hormone responsive (<i>Thrsp</i>)		Mm01273967_m1	NM_009381.2
Malic enzyme (<i>Me1</i>)		Mm00782380_s1	NM_001198933.1
CD36 antigen (<i>Cd36</i>)		Mm00432403_m1	NM_001159555.1
Solute carrier family 27 member 1 (<i>Slc27a1</i>)		Mm00449511_m1	NM_011977.3
Sterol regulatory element binding transcription factor 1 (<i>Srebf1</i>)		Mm00550338_m1	NM_011480.3
Peroxisome proliferator activated receptor alpha (<i>Ppara</i>)		Mm00440939_m1	NM_001113418.1
Sirtuin 1 (<i>Sirt1</i>)		Mm01168521_m1	NM_001159589.1
Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha (<i>Ppargc1</i>)		Mm01208835_m1	NM_008904.2
ELOVL family member 6 (<i>Elovl6</i>)		Mm00851223_s1	NM_130450.2
Diacylglycerol O-acyltransferase 2 (<i>Dgat2</i>)		Mm00499536_m1	NM_026384.3
Acyl-CoA oxidase 1, palmitoyl (<i>Acox1</i>)		Mm01246834_m1	NM_001271898.1