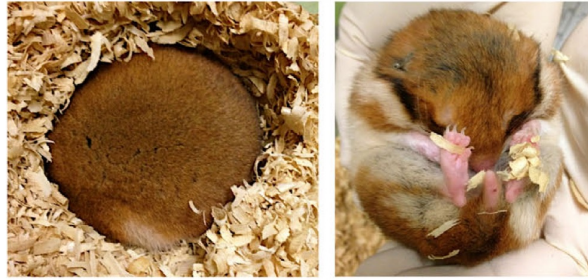
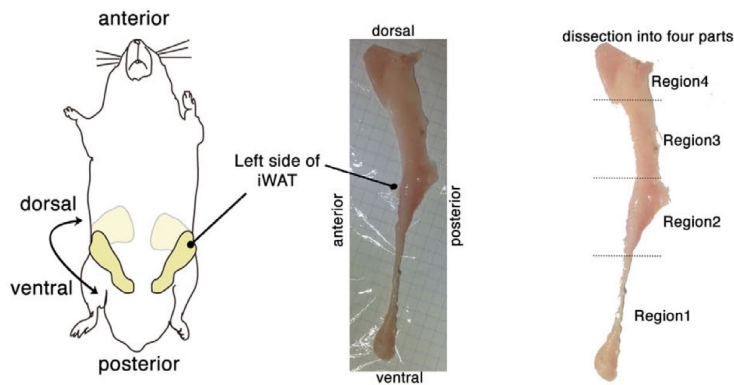


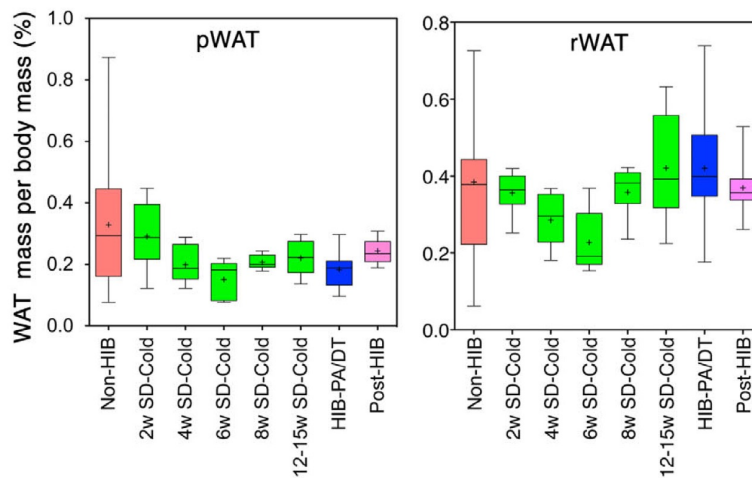
A



B

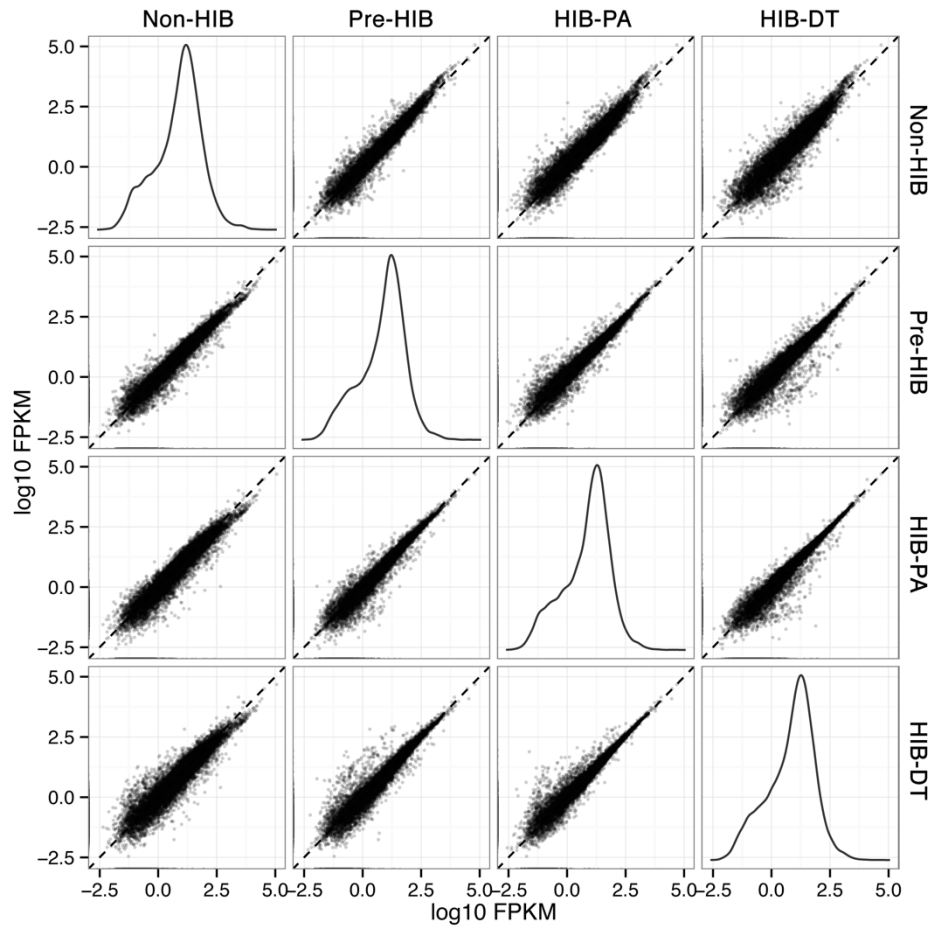


C



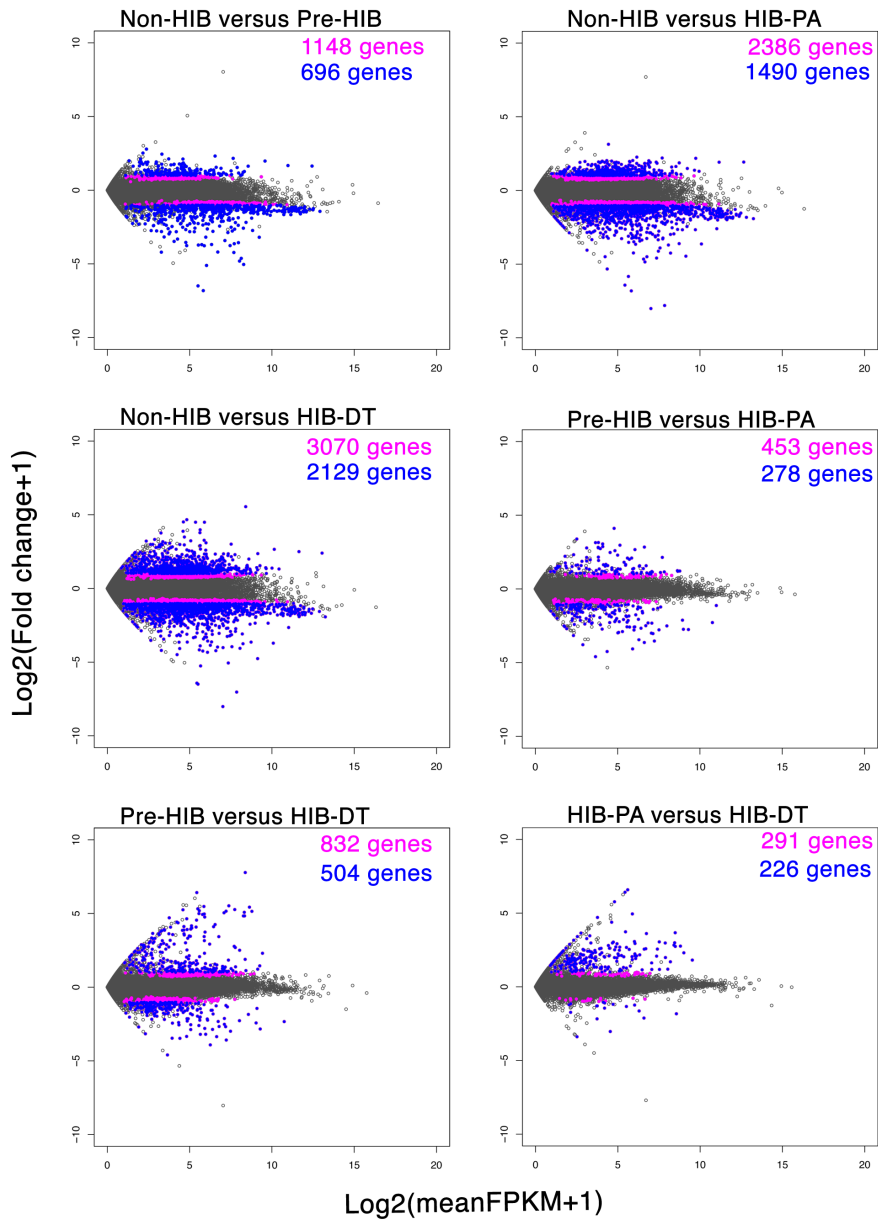
Supplementary Figure S1

(A) Dorsal view (left) and ventral view (right) of a Syrian hamster in deep torpor during HIB. (B) Anatomical location and morphology of iWAT in Syrian hamsters. Isolated iWAT was divided into four regions for histological analysis. (C) Mass of perigonadal WAT (pWAT) and retroperitoneal WAT (rWAT) before and after SD-Cold exposure. They tended to be gradually decreased during 6 weeks after the exposure and rWAT seemed to be recovered before hibernation.



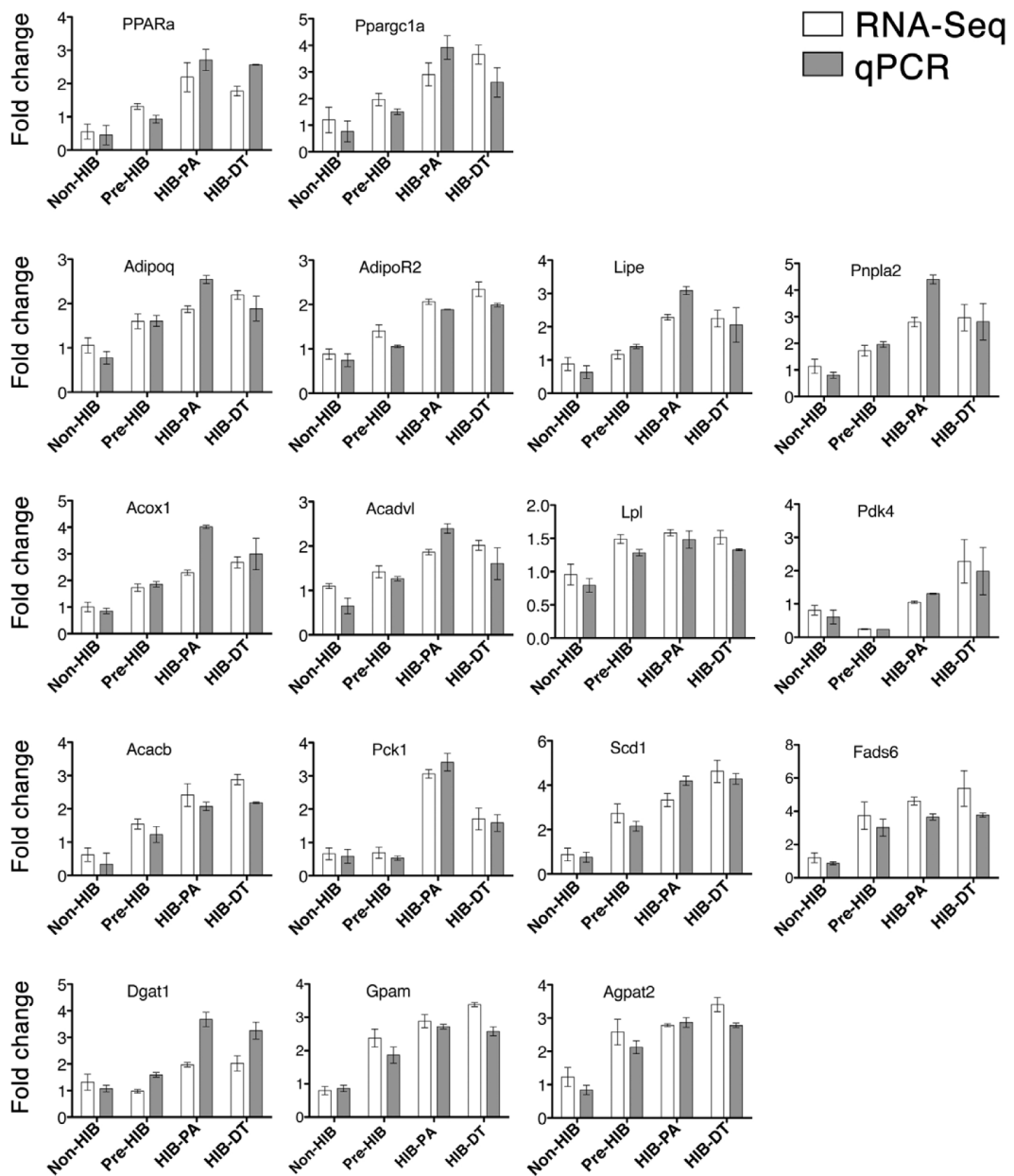
Supplementary Figure S2

Correlation plot of log₁₀ FPKM values for genes between each combination of experimental groups. Each dot depicts a transcript. Although the majority of transcripts distributed on the lines representing similar expression levels between each state, a subset of gene transcripts deviated from the lines, which was differentially expressed in a state against its comparison.



Supplementary Figure S3

MA plot of the log2 fold change of all genes. Magenta indicate differentially expressed genes (DEGs) with q -value less than 0.01. Blue indicate DEGs which exhibited more than twofold change between any groups with q -value \leq 0.01.



Supplementary Figure S4

qPCR validation of RNA-seq results for genes related to PPAR signaling, adipocytokine signaling, an lipid metabolism. RNA-seq fold change is shown in grey, and qPCR fold change is shown in white. Bar plots represent mean values of three animals for each group. Error bars represent the standard errors.

experimental_group	# of reads	reads%
Non-HIB_0	10.5M	7.4
Non-HIB_1	9.1M	6.4
Non-HIB_2	11.2M	8
Pre-HIB_0	12.9M	9.1
Pre-HIB_1	10.2M	7.2
Pre-HIB_2	8.4M	5.9
HIB-PA_0	11.0M	7.8
HIB-PA_1	14.5M	10.3
HIB-PA_2	13.0M	9.2
HIB-DT_0	13.1M	9.3
HIB-DT_1	9.9M	7
HIB-DT_2	17.5M	12.4
total	141.3M	100

Supplementary Table S1

Number and percentage of reads of each experimental replicate are shown.

experimental_group	Left reads input	Left reads mapped	Left read mapping rate	Right reads input	Right reads mapped	Right read mapping rate	Overall read mapping rate	Aligned pairs	concordant pair alignment rate
Non-HIB_0	10497844	9361593	89.2%	10497844	9215922	87.8%	88.5%	8806077	82.5%
Non-HIB_1	9052271	8085261	89.3%	9052271	7976527	88.1%	88.7%	7637573	82.9%
Non-HIB_2	11241435	9849686	87.6%	11241435	9720276	86.5%	87.0%	9294496	81.1%
Pre-HIB_0	12909112	11462898	88.8%	12909112	11279833	87.4%	88.1%	10770300	81.9%
Pre-HIB_1	10195308	9125317	89.5%	10195308	8995870	88.2%	88.9%	8609289	83.2%
Pre-HIB_2	8373014	7477147	89.3%	8373014	7349723	87.8%	88.5%	7022702	82.6%
HIB-PA_0	11035715	9790922	88.7%	11035715	9638372	87.3%	88.0%	9234726	82.4%
HIB-PA_1	14546869	12993700	89.3%	14546869	12809297	88.1%	88.7%	12248053	83.0%
HIB-PA_2	12957685	10167477	78.5%	12957685	10017146	77.3%	77.9%	9517384	72.2%
HIB-DT_0	13081729	11640439	89.0%	13081729	11443238	87.5%	88.2%	10936298	82.2%
HIB-DT_1	9907019	8823817	89.1%	9907019	8695970	87.8%	88.4%	8282862	82.3%
HIB-DT_2	17535458	15264335	87.0%	17535458	15024224	85.7%	86.4%	14329131	80.3%

Supplementary Table S2

Mapping rate of left, right, and overall reads of each experimental replicate are shown.

A

Term	Count	%	P-Value	Genes
hsa04910:Insulin signaling pathway	7	0.262	0.02471	PRKAR2A, EXOC7, RHOQ, MTOR, RPS6, RAPGEF1, CALM2
hsa04640:Hematopoietic cell lineage	5	0.187	0.054938	CD38, CD3G, CD3D, CD2, CD7

B

Term	Count	%	P-Value	Genes
hsa04662:B cell receptor signaling pathway	11	0.252	2.27E-06	PIK3CG, RAC2, RASGRP3, NFKBIE, PIK3CD, PLCG2, NFAT5, CD22, PIK3AP1, BLNK, SYK
hsa04660:T cell receptor signaling pathway	9	0.206	0.001518	PIK3CG, ITK, CD8A, NFKBIE, PIK3CD, CBL, NFAT5, MAP3K14, LCP2
hsa04670:Leukocyte transendothelial migration	9	0.206	0.002666	PIK3CG, ITK, RAC2, PIK3CD, PLCG2, MYL9, TXK, ACTN3, MYL9
hsa04666:Fc gamma R-mediated phagocytosis	7	0.16	0.01267	PIK3CG, DOCK2, RAC2, PIK3CD, PLCG2, PPAP2A, SYK
hsa04062:Chemokine signaling pathway	10	0.229	0.013731	PIK3CG, ITK, DOCK2, CCR6, RAC2, CXCR5, PREX1, PIK3CD, CXCR2, PLCB2
hsa04370:VEGF signaling pathway	6	0.137	0.018093	PIK3CG, RAC2, PIK3CD, PLCG2, NFAT5, HSPB1
hsa04664:Fc epsilon RI signaling pathway	6	0.137	0.021097	PIK3CG, RAC2, PIK3CD, PLCG2, LCP2, SYK
hsa00250:Alanine, aspartate and glutamate metabolism	4	0.092	0.02467	ADSSL1, GFPT1, IL4I1, GPT

Supplementary Table S3

(A and B) KEGG pathway analysis results for the top 300 genes that contributed most to PC1 (A) and PC2 (B).

Term	Count	%	PValue	Genes
hsa03010:Ribosome	56	5.19	2.13E-40	RPL18, RPL17, RPL36A, RPL19, RPS27L, RPL22L1, RPS3, RPS3A, RPLP1, RPL10, FAU, RPL12, RPS27A, RPS4X, RPS18, RPS19, RPS16, RPS15, RPS12, RPS13, RPS10, RPS11, UBA52, RPL27A, RPS15A, RPL36, RPL37, RPL38, RPS25, RPS26, RPL30, RPS27, RPS28, RPL32, RPL7, RPL9, RPL34, RPL3, RPL5, RPL10A, RPL4, RPS23, RPSA, RPL26, RPL27, RPL23A, RPL24, RPS6, RPS8, RPL28, RPL29, RPS7, RPL23, RPL13A, RPL22, RPL21
hsa05340:Primary immunodeficiency	13	1.205	6.94E-06	CIITA, PTPRC, CD8A, CD3D, CD3E, CD40LG, TNFRSF13C, IL2RG, CD40, IL7R, ADA, BLNK, BTK
hsa04620:Toll-like receptor signaling pathway	18	1.668	0.001861695	PIK3CG, LY96, TBK1, TLR1, PIK3CD, TLR2, TLR3, TLR4, CD40, TLR6, TLR7, CXCL10, FOS, CD86, CD80, TICAM2, IL1B, SPP1
hsa04060:Cytokine-cytokine receptor interaction	35	3.244	0.00197654	IL1R2, CCL2, CCR1, IL18, IL21R, CCL8, CXCR3, IL7R, TNFRSF4, CXCL10, CCL24, CXCR5, CXCR4, TNFRSF18, IL1B, IL2RG, FAS, IL13RA1, LTB, CD27, FLT3, TNFRSF13C, CCL19, HGF, CD40, CCL11, TNFRSF9, CCR7, CCR6, CCR5, RELT, CXCL14, CXCL13, CD40LG, CCR2
hsa04640:Hematopoietic cell lineage	16	1.483	0.002370268	IL1R2, CD3G, CD3D, CD8A, FLT3, CD3E, FCER2, MME, ITGA4, IL7R, CD38, MS4A1, CD2, CD22, IL1B, CD7
hsa04062:Chemokine signaling pathway	26	2.41	0.005127849	CCL2, FGR, CCR1, CCL8, GNG11, CXCR3, CXCL10, CCL24, CXCR5, CXCR4, GNG2, SHC2, PIK3CG, ITK, HCK, PIK3CD, CCL19, CCL11, CCR7, CCR6, CCR5, CXCL14, CXCL13, GNG10, CCR2, RAP1A
hsa04110:Cell cycle	18	1.668	0.016467932	CDK1, CDC14A, RBL1, TTK, ATR, PTTG1, CDC26, MCM4, ATM, RBX1, CCNB1, CCNB2, MAD2L1, PCNA, BUB1, BUB1B, CCNA2, STAG2
hsa00520:Amino sugar and nucleotide sugar metabolism	9	0.834	0.018832504	GALK2, PGM3, UAP1, GNPDA1, GNPDA2, HK3, HEXB, NPL, NANP
hsa05310:Asthma	7	0.649	0.022176973	FCER1A, CCL11, CD40LG, PRG2, FCER1G, MS4A2, CD40
hsa04662:B cell receptor signaling pathway	12	1.112	0.029791741	PIK3CG, FOS, DAPP1, RASGRP3, NFKBIE, PIK3CD, CD22, PIK3AP1, CD79B, CD72, BLNK, BTK
hsa00740:Riboflavin metabolism	5	0.463	0.031351503	TYR, ENPP3, ACP5, MTMR7, PHPT1
hsa04660:T cell receptor signaling pathway	15	1.39	0.040135789	PIK3CG, ITK, PTPRC, CD3G, CD3D, CD8A, NFKBIE, CD3E, PIK3CD, CD247, FOS, LAT, CD40LG, NCK1, GRAP2

Supplementary Table S4

KEGG pathway analysis results for Cluster 8 (1528 genes) in Figure 3D.

Term	Count	%	PValue	Genes
hsa04510:Focal adhesion	34	3.895	2.34E-08	TLN1, TLN2, DIAPH1, BCAR1, ITGB4, MYL9, LAMB2, DOCK1, LAMB1, THBS1, RAPGEF1, THBS2, COL4A2, TNXB, FLT1, COL4A1, ACTN4, ITGA3, FLNB, FLNA, KDR, LAMA2, VWF, LAMA1, LAMA3, ITGA6, LAMA5, JUN, ITGA7, PDGFRB, MAPK9, RELN, LAMC1, PARVA
hsa04512:ECM-receptor interaction	20	2.291	1.63E-07	COL4A2, TNXB, COL4A1, DAG1, ITGB4, HSPG2, ITGA3, LAMA2, LAMA1, VWF, LAMA3, LAMB2, ITGA6, LAMA5, ITGA7, RELN, LAMC1, LAMB1, THBS1, THBS2
hsa03320:PPAR signaling pathway	14	1.604	1.19E-04	CPT1B, PPARA, ACOX1, SLC27A1, RXRA, SCD, EHHADH, CPT1A, PCK1, ACOX3, SORBS1, HMGCS2, PLIN1, ANGPTL4
hsa04270:Vascular smooth muscle contraction	18	2.062	1.87E-04	ADCY3, ADCY4, ACTA2, GNA11, ADCY5, ADCY6, GNA12, PRKCE, ARHGEF12, ITPR2, ARHGEF11, MYL9, GNAQ, ADCY9, MYH11, PLA2G6, ADRA1A, CACNA1D
hsa05200:Pathways in cancer	36	4.124	2.14E-04	FGFR1, FOXO1, ZBTB16, TCF7L2, TCF7L1, LAMB2, CDKN2B, LAMB1, FGF1, TRAF3, APC, COL4A2, PLD1, BCR, COL4A1, EPAS1, RXRA, FZD1, ITGA3, FZD4, FZD7, LAMA2, JUP, CCDC6, LAMA1, CDKN1A, LAMA3, ITGA6, LAMA5, JUN, PDGFRB, MAPK9, PTCH1, MTOR, LAMC1, ABL1
hsa05222:Small cell lung cancer	14	1.604	8.82E-04	COL4A2, COL4A1, RXRA, ITGA3, LAMA2, LAMA1, LAMA3, LAMB2, ITGA6, CDKN2B, LAMA5, LAMC1, LAMB1, TRAF3
hsa04520:Adherens junction	13	1.489	0.001299535	PTPRB, FGFR1, PTPRM, ACTN4, SORBS1, BAIAP2, WASF1, WASF2, LMO7, TCF7L2, MLLT4, TCF7L1, FARP2
hsa04920:Adipocytokine signaling pathway	12	1.375	0.001326729	CPT1B, PPARA, IRS2, RXRA, ADIPOR2, MAPK9, MTOR, ACACB, PPARGC1A, CPT1A, PCK1, PTPN11
hsa04910:Insulin signaling pathway	18	2.062	0.001685581	IRS2, HK2, FOXO1, RHOQ, IGF2, ACACB, PPARGC1A, RPTOR, PCK1, PRKAR2A, SORBS1, GYS1, FASN, MAPK9, SH2B2, MTOR, RAPGEF1, LIPE
hsa04810:Regulation of actin cytoskeleton	24	2.749	0.002597504	FGFR1, SSH1, ACTN4, DIAPH1, BAIAP2, BCAR1, WASF1, WASF2, GNA12, ITGB4, IGF2, ITGA3, ARHGEF12, MYL9, DOCK1, ITGA6, ITGA7, PDGFRB, MYH14, FGF1, PIP4K2C, MYH10, SLC9A1, APC
hsa04912:GnRH signaling pathway	14	1.604	0.003674139	ADCY3, ADCY4, PLD1, GNA11, ADCY5, ADCY6, ITPR2, MAP3K4, GNAQ, ADCY9, JUN, PLA2G6, MAPK9, CACNA1D
hsa05412:Arrhythmic right ventricular cardiomyopathy (ARVC)	12	1.375	0.00373146	JUP, LAMA2, ATP2A2, ACTN4, ITGA6, ITGA7, DAG1, ITGB4, ITGA3, CACNA1D, TCF7L2, TCF7L1
hsa00564:Glycerophospholipid metabolism	11	1.26	0.004988476	GPD2, CDS2, CPT1B, GPD1, PLD1, LCAT, PLA2G6, PHOSPHO1, GPAM, PNPLA3, AGPAT2
hsa05414:Dilated cardiomyopathy	13	1.489	0.005938652	ADCY3, LAMA2, ADCY4, ITGA6, ADCY9, ATP2A2, ADCY5, ADCY6, ITGA7, DAG1, ITGB4, ITGA3, CACNA1D
hsa04360:Axon guidance	16	1.833	0.006636561	ABLIM1, PLXNA2, NTN4, L1CAM, DPYSL2, ARHGEF12, NTN1, EPHB1, SEMA6A, EPHA4, SEMA6B, UNC5B, SEMA3G, SRGAP3, EFNA5, ABL1
hsa04144:Endocytosis	20	2.291	0.008728296	PLD1, FLT1, LDLR, ASAP2, ASAP1, CXCR2, ASAP3, KDR, HSPA1L, RAB11FIP3, HSPA2, ARRB1, PDCD6IP, SMURF1, GRK5, AGAP1, ARAP3, EHD2, IQSEC1, EPN2
hsa02010:ABC transporters	8	0.916	0.011732413	ABCB9, ABCC3, ABCC4, ABCB10, ABCB1, ABCG4, ABCB6, ABCA3
hsa04916:Melanogenesis	12	1.375	0.025562408	ADCY3, ADCY4, GNAO1, GNAQ, ADCY9, ADCY5, ADCY6, FZD1, FZD4, TCF7L2, TCF7L1, FZD7
hsa04710:Circadian rhythm	4	0.458	0.034885909	CRY2, PER2, PER1, PER3

Supplementary Table S5

KEGG pathway analysis results for Cluster 5 (990 genes) in Figure 3D.

Gene	Forward (5'→3')	Reverse (5'→3')	NCBI Reference Sequence
PPARa	AAGCTGTCCAGGCTCCGAGG	CGGGGCAGCTGACTGATGAGG	NM_001281543.1
Ppargc1a	AAGGGGCTGGTTGCCTGCAT	CATCCAGCTCCTGAATGACGCC	XM_005068779.3
Adipoq	AGGAGAGCCGGGAGAAAGCG	AACGCTGGGGACGGTGACTC	XM_021227970.1
AdipoR2	GGCAGATCGGCTGGCTAATGC	ACGTTCTGGGATGCGGGCAG	XM_021224762.1
Lipe	GCATTGTGCCCTGCTCGGTT	CAGTGACGCAGAGGTTGCCG	XM_013125988.2
Pnpla2	GCAGGGCTACAGAGACGGACT	TTTCCTGGGGGACAACCGGG	XM_005064203.3
Acox1	CGAGGGCGACCTGAGCCTTT	GCTCTTGCTGCTCTGCGGTG	XM_005069904.2
Acadvl	GCAGGCGGGACGTAAAGAGGA	CCGCCCCACACTCGGAGTTA	XM_005067510.3
Lpl	TCCATGGCTGGACGGTGACA	CGATGACGTTGGAGTCGGGC	XM_013117159.2
Pdk4	CGGCAAGAGTTGCCCGTGAG	CAGCTGCACGGAGGGGGTAT	XM_005082915.3
Acacb	GGACAGCTGAAGGCCCGAGA	CCAGCATGTGGCCTGGTGTG	XM_021232318.1
Pck1	CCAAAACCGCCTCAGCCAG	TTCATGCACCCCGGAACT	XM_005074472.3
Scd1	ACGGGAGAAGCAGAAGACCGT	CCTGGTAGCTGGGGTCGTGT	NM_001281585.1
Fads6	GAAGTGCCCGTGCCTCAACC	AACGCTCGAGAGCGACCAGT	XM_005069942.3
Dgat1	GCCGAAGAGGAGGTGCGAGA	CTTTGTCGGGGTCGGGACT	XM_005085991.3
Gpam	CTCAGCAGACCCAGACGG	GGAAGTCTGCTGCCTGAGC	XM_013111923.2
Agpat2	GGAGCTGGGGGAAGACAGGT	GTGGGGAGCAGGATAAGGCGT	XM_005083644.3
Ucp1	GGGCAACCTACCGAGGTCGT	GGTCCCAGTGTAGCGGGTT	NM_001281332.1
Prdm16	CATGGGCTTCGACCACACC	GCCCCTTCCCAAAGTTGGC	XM_021232554.1
Atp2a2	GCTCACACAAAGACGGTGGAG	CCCATCTCTCCTTGAGCTTCT	ENSMAUT00000028608.1
Ppia1	GCAGACAAAGTCCAAAGACAGCA	TCCTGGGATAATTCTGTGAAAGGAG	XM_005086775.3

Supplementary Table S6

List of real-time PCR primers listed 5' to 3'.

Gene Symbol	Gene Name
4E-BP2	Eukaryotic translation initiation factor 4E binding protein 2
Acacb	Acetyl-CoA carboxylase beta
Acot2	Acyl-CoA thioesterase 2
Acox1	Acyl-CoA oxidase 1
Adipoq	Adiponectin
AdipoR2	Adiponectin receptor 2
Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2
Akt	v-akt murine thymoma viral oncogene homolog 1
Angptl4	Angiopoietin like 4.
Atp2a2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
Camkk2	Calcium/calmodulin dependent protein kinase kinase 2
Cd40	CD40 molecule
Clstn2	Calsynenin 2
Cpt1a/1b	Carnitine palmitoyltransferase 1 alpha/beta
Deptor	DEP domain containing MTOR interacting protein
Dgat1	Diacylglycerol O-acyltransferase 1
Ebf3	EBF transcription factor 3.
Ehhadh	Enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase
Eif4e3	Eukaryotic translation initiation factor 4E family member 3.
Fads6	Fatty acid desaturase 6
Fasn	Fatty acid synthase
Fbxo31	F-box protein 31
Gpm	Glycerol-3-phosphate acyltransferase
Gpd1	Glycerol-3-phosphate dehydrogenase 1
Gys1	Glycogen synthase 1
Hmgcs2	3-hydroxy-3-methylglutaryl-CoA synthase 2
Hspb7	Heat shock protein family B (small) member 7
InsR	Insulin receptor
Irs2	Insulin receptor substrate 2
Lamtor2/3/5	Late endosomal/lysosomal adaptor 2/3/5, MAPK and MTOR activator 2/3/5
Lipe	Lipase E hormone sensitive type
Mgl1	Monoglyceride lipase
mTOR	Mechanistic target of rapamycin
Oplah	5-oxoprolinase
Orm1	Orosomucoid 1
Pck1	Phosphoenolpyruvate carboxykinase 1
Pdk1	Pyruvate dehydrogenase kinase 1
Pdk4	Pyruvate dehydrogenase kinase 4
PI3K	Phosphoinositide 3-kinase
Plin1/5	Perilipin 1/5 hormone sensitive type
Pnpla2/3	Patatin like phospholipase domain containing 2/3
Ppara	Peroxisome proliferator activated receptor alpha
Ppargc1a	Peroxisome proliferator-activated receptor gamma coactivator 1-alpha
Ppargc1b	Peroxisome proliferator-activated receptor gamma coactivator 1-beta
Prdm16	PR domain 16
Prkar2a	Protein kinase cAMP-dependent type II regulatory subunit alpha
Pten	Phosphatase and Tensin Homolog Deleted from Chromosome 10
Pygl	Glycogen phosphorylase L
Rapgef1	Rap guanine nucleotide exchange factor 1
Raptor	Regulatory associated protein of MTOR complex 1
Rheb	Ras homolog enriched in brain
Rhoq	Ras homolog family member Q
Rictor	RPTOR independent companion of MTOR complex 2
Rragd	Ras related GTP binding D
Rxra	Retinoid X receptor alpha
Scd1	Stearoyl-Coenzyme A desaturase 1
Sesn2	Sestrin 2
Sh2b2	SH2B adaptor protein 2
Slc27a1	Solute carrier family 27 member 1
Sorbs1	Sorbin and SH3 domain containing 1
Sp100	SP100 nuclear antigen
Spare11	SPARC like 1
Syne2	Spectrin repeat containing nuclear envelope protein 2
Tlr4	Toll like receptor 4
Tnfrsf9	TNF receptor superfamily member 9
Tsc2	TSC complex subunit 2
Ucp1	Uncoupling protein 1

Supplementary Table S7

Gene symbols and gene names described in this study.