

RBP name	Average CPM
Hdlbp	11.03
Pabpc1	11.03
Srrm2	10.87
Zfp36l1	10.66
Hnrnpa2b1	10.42
Hnrnpa3	10.24
Ncl	10.14
Ankrd17	10.02
Fus	9.98
Eif4b	9.91
Hnrnpf	9.87
Csde1	9.81
Zfp36l2	9.76
Zfr	9.71
Pcbp2	9.69
Hnrnpk	9.68
Ybx1	9.65
Srsf5	9.60
Nono	9.42
Hnrnph1	9.27
Hnrnpa1	9.28
Bicc1	9.25
Igf2bp2	9.19
Rbfox2	9.20
Tnrc6b	9.17
Rbm39	9.13
Syncrip	9.12
Zc3hav1	9.09
Sfpq	9.06
Supt6	8.98
Mbnl1	8.94
Rbms1	8.93
Rbm25	8.89
Larp1	8.87
Ewsr1	8.86
Larp4	8.79
Mbnl2	8.72

Qk	8.69
Hnrnpd	8.66
Ssb	8.61
Hnrnpdl	8.61
Pcbp1	8.60
Matr3	8.60
Parp14	8.51
Hnrnpab	8.56
Zfp638	8.56
Srrm1	8.55
Zc3h7b	8.55
Pum2	8.54
Hnrnpm	8.50
Sf1	8.52
Eif4h	8.51
Rbm3	8.47
Fmr1	8.42
Ptbp1	8.45
Hnrnpl	8.44
Rc3h2	8.41
Rbms2	8.37
Khsrp	8.36
G3bp2	8.35
Rbms3	8.32
Srsf11	8.31
Srsf6	8.27
Tra2b	8.23
Acin1	8.21
Srsf1	8.14
Srsf3	8.10
Sfswap	8.08
Eif3b	8.09
Taf15	8.06
Rbm5	8.08
Zc3h14	8.07
Spen	8.04
Ankhd1	8.03
Ptbp3	8.02
Hnrnpc	8.00
Srrt	8.00
Tia1	8.00

Marf1	7.99
Khdrbs1	7.94
Zc3h15	7.92
Ccar1	7.91
Raly	7.88
Celf1	7.88
Ythdc1	7.86
Tardbp	7.86
Hnrnpr	7.78
Scaf8	7.85
Helz	7.76
Cstf2t	7.74
Rc3h1	7.73
Srsf10	7.72
Pum1	7.71
Tnrc6a	7.70
Snrnp70	7.71
Safb	7.67
Fubp3	7.64
Upf1	7.65
Hnrnpa0	7.61
U2surp	7.62
Zc3h13	7.60
Ybx3	7.61
Ythdf3	7.60
Igf2bp3	7.61
Ppargc1a	7.56
Cnot4	7.48
Ireb2	7.57
Tnrc6c	7.54
Fubp1	7.51
Fxr1	7.50
Rbm17	7.43
Hnrnph2	7.47
Rbm33	7.43
Pum3	7.46
Rbpms	7.46
Rbm28	7.45
Setd1a	7.40
Ppp1r10	7.40
Rbm6	7.39

Cherp	7.36
Larp4b	7.39
Celf2	7.35
Dazap1	7.34
Tra2a	7.30
Puf60	7.33
Rbm26	7.32
G3bp1	7.32
Zc3h18	7.30
Cpsf6	7.29
U2af2	7.30
Ro60	7.28
Poldip3	7.25
Parp12	7.26
Cpsf7	7.26
Safb2	7.19
Rbmxl1	7.22
Pabpc4	7.19
Snrpd3	7.21
Pabpn1	7.19
Tiparp	7.18
Srsf2	7.18
Cpeb4	7.13
Grsf1	7.14
Aco1	7.13
Zfp36	7.11
Ttc14	7.02
Scaf4	7.06
Zc3h4	7.05
Pdcd11	7.02
Rbm27	6.98
Sart3	6.94
Zc3h7a	6.95
Srek1	6.95
Eif2s1	6.94
Ythdf1	6.89
Mex3a	6.87
Mex3c	6.88
Myef2	6.88
Rbm10	6.86
Samd4	6.84

Srsf9	6.82
Raver1	6.84
Tial1	6.80
Ptbp2	6.79
Rbm15	6.77
Elavl1	6.74
Htatsf1	6.59
Dhx57	6.73
Synj1	6.70
Pprc1	6.65
Akap1	6.62
Srsf4	6.62
HnrnpII	6.58
Slbp	6.63
Zc3h12a	6.59
Zrsr2	6.59
Enox1	6.57
Dhx8	6.55
Ythdf2	6.52
Pnpt1	6.50
Rbm18	6.47
Prpf3	6.48
Sf3a1	6.32
Ppil4	6.45
Cpne1	6.42
Rbm8a	6.41
Snrpc	6.38
Sugp1	6.38
Pcbp4	6.36
Snrpd1	6.17
Larp7	6.31
U2af1	6.34
Sltm	6.29
Snrpb2	6.27
Rbm22	6.31
Upf3b	6.29
Fxr2	6.26
Tmem63a	6.27
Cstf2	6.30
Msi2	6.25
Zcrb1	6.26

Tep1	6.26
Eif3g	6.26
Snrpa	6.17
Alyref	6.17
Mcm3ap	6.18
Rbm7	6.13
Uhmk1	6.11
Rnps1	5.91
Parn	6.11
Pspc1	6.08
Nifk	6.08
Nol8	6.05
Unk	6.02
Thumpd3	5.85
Snrpf	5.99
Mex3d	5.96
Krr1	6.03
Igf2bp1	6.01
Rrp7a	5.95
Sf3b6	5.95
Sf3b4	5.90
Trmt1l ENSMUSG00000053286	5.86
Dus3l	5.83
Srsf7	5.88
Eif2d	5.85
Snrpb	5.85
Slirp	5.83
Prr3	5.57
Zc3h6	5.76
Lsm2	5.75
Srbd1	5.71
Rbm14	5.28
Zgpat	5.66
Rbm45	5.55
Mkrn1	5.65
Rbm4b	5.55
Sugp2	5.46
Dkc1	5.62
Gtf3a	5.60
Zc3hav1l	5.61
Lsm8	5.52

Thumpd1	5.55
Alkbh8	5.55
RbmX	5.51
Gm7964	5.25
Trmt1	5.46
Lsm3	5.51
Nelfe	5.46
Hnrnph3	5.42
Zrsr1	5.33
Rbm12b2	5.33
Zcchc17	5.33
Rbm42	5.37
Tut1	5.31
Rbm19	5.23
Trmt2a	5.30
Aptx	5.06
Samd14	5.24
Toe1	4.99
Lsm4	5.08
Clasrp	5.17
Carhsp1	5.16
Nip7	5.14
Lsm1	5.11
Zc3h3	5.08
Lsm6	5.05
Rbm41	5.03
Tdrkh	5.01
Zc3h12c	4.96
Cpsf4	4.89
Mkrn2	4.96
Cirbp	4.96
Synj2	4.92
Naa38	4.68
Rbm34	4.88
Mthfsd	4.84
Snrpg	4.80
Trnau1ap	4.79
Rbm43	4.73
Ascc1	4.66
Cpeb2	4.69
Cpeb3	4.51

Dgkq	4.63
Zc3h12b	4.55
Lemd3	4.47
Ppie	4.54
Nufip1	4.50
Polr2g	4.50
Pno1	4.40
Snrnp35	4.32
Mcts1	4.06
Pcbp3	4.34
Nupl2	3.66
Kin	4.06
Snrpd2	4.14
Lsm10	4.14
RbmX2	4.16
Larp6	4.13
Mcts2	3.83
Ythdc2	3.95
Mex3b	3.73
U2af1l4	3.84
Rnpc3	3.72
Rbm47	3.79
Celf5	3.79
Unkl	3.61
Ppargc1b	3.70
Nop9	3.70
Leng9	3.62
Mbnl3	3.45
Lsm7	2.60
Rexo5	3.30
Enox2	3.30
Thumpd2	3.30
Akap17b	3.19
Zc3h8	2.95
Dnajc17	3.06
Snrpert	2.67
Zc3h10	2.72
Rbm38	2.72
Alyref2	2.72
Gm2531	2.24
Nsun6	2.18

Csdc2	2.18
Lsm11	2.57
Gm38393	2.44
Celf4	2.05
Rbpms2	2.37
Rbm20	2.37
Gm9833	2.01
Msi1	2.01
Rnf113a1	1.90
Rdm1	2.10
Cpeb1	1.70
Pabpc1l	1.70
Gm7846	1.67
Zmat5	1.67
Rbm12b1	1.43
Gm7353	1.00
Rcan2	1.00
Mkrn3	1.00
Ybx2	1.00
Elavl3	1.00
Gm10110	1.00
Zfp239	1.00
Gm11847	1.00
E130201H02Rik	1.00
Gm8991	1.00
Zc3h12d	1.00
Nova2	1.00
Rbfox3	1.00
Dnd1	1.00

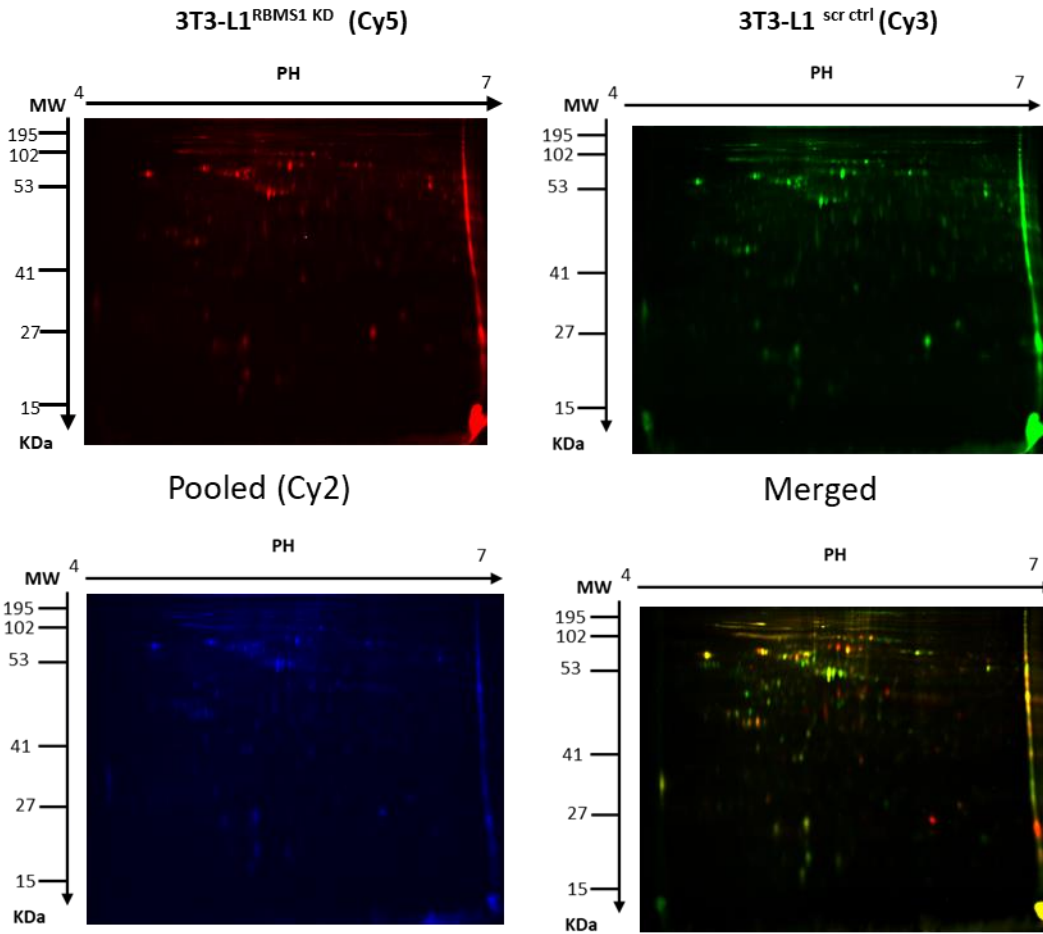
Supplemental table 1- The expression of RNA binding proteins (RBPs) in 3T3-L1 cells before differentiation

SI no.	Gene name	log2FoldChange	padj
1	Chrdl1	-2.094018	4.76E-24
2	Acta1	-3.878189	5.76E-14
3	Rasd1	-3.410705	5.76E-14
4	Egfr	-1.983423	8.78E-13
5	Col15a1	-4.253132	5.04E-11
6	Tsnax	-2.015381	5.70E-11
7	Nid2	-1.66705	3.56E-10
8	Smarca2	-1.516036	6.80E-10
9	Ptprm	-1.714339	2.12E-09
10	Cdo1	-1.452151	6.16E-09
11	P3h3	-2.827604	1.56E-08
12	Sfrp2	-3.092906	2.64E-08
13	Cgnl1	-1.638247	2.64E-08
14	Sowahc	-1.188336	3.93E-08
15	Grb10	-2.746397	1.24E-07
16	Col23a1	-2.185516	3.64E-07
17	Ptgfr	-1.535763	3.64E-07
18	Gstk1	-1.989428	5.97E-07
19	Dusp1	-2.081596	6.78E-07
20	Anxa5	-0.9307908	7.49E-07
21	Adgrl2	-1.800786	7.91E-07
22	Ndrp2	-3.620184	9.39E-07
23	Lum	-1.76132	1.52E-06
24	Thrsp	-1.644268	1.52E-06
25	Mest	-7.027225	3.16E-06

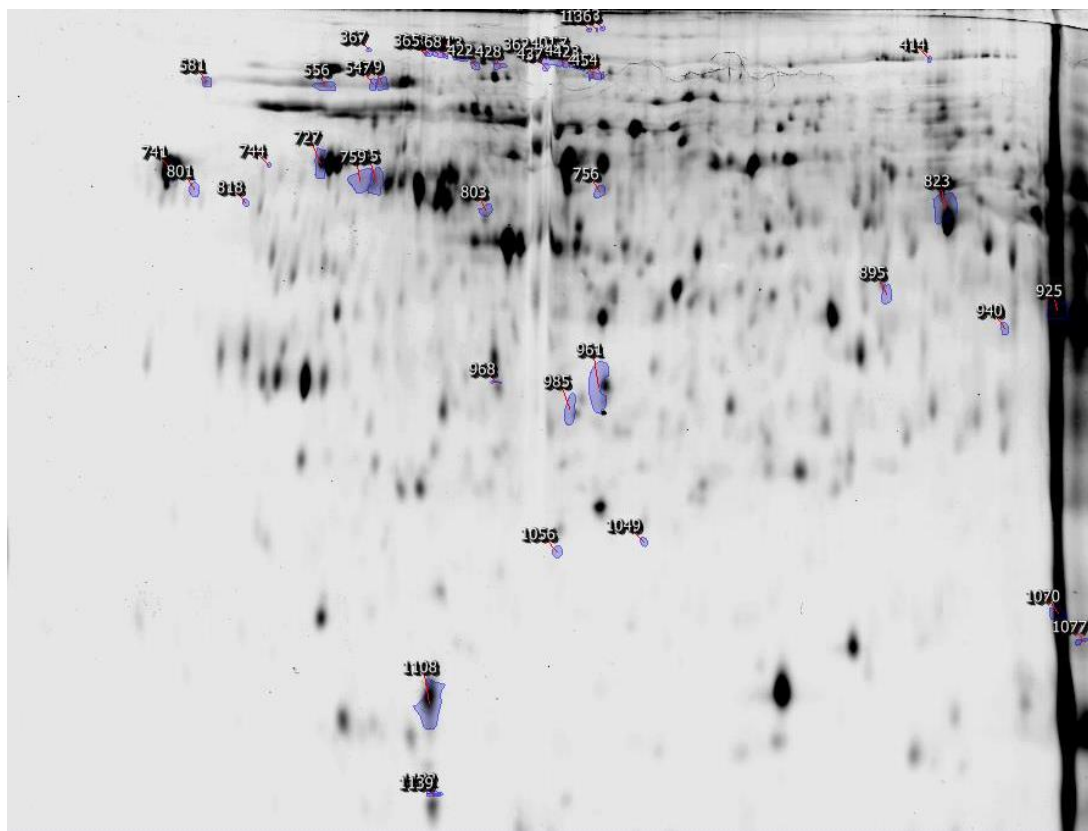
Supplemental table 2- Top 25 most significant downregulated genes in 3T3-L1 cells after Rbms1 knockdown

SI no.	Gene name	log2FoldChange	padj
1	Gm773	3.074423	7.77E-09
2	Pcyox1	0.8887469	6.78E-07
3	Sox11	2.662427	0.0000165
4	Gm6741	5.583851	0.0000462
5	Gabre	1.507848	0.0000514
6	Rgs17	1.580638	0.0001187
7	Rnf128	2.136338	0.00019
8	Pltp	1.321833	0.0002167
9	Bhlhe41	1.333575	0.0002597
10	Plxna4	1.636459	0.0003476
11	Parvb	1.365159	0.0004506
12	Cyp2e1	4.228098	0.0007373
13	Tmem151a	2.270955	0.0008204
14	Sh3tc1	1.283811	0.0010148
15	Spire1	1.066147	0.0016558
16	Tmeff1	0.8412142	0.0022858
17	Stbd1	1.440143	0.0035328
18	Uck2	0.6788502	0.0044207
19	Six4	0.894881	0.0050981
20	Fmr1	0.705129	0.0052473
21	Unc5b	0.6861495	0.0063002
22	Xpr1	0.6040634	0.0064142
23	Prelp	0.6562632	0.0066922
24	Slc5a7	2.137867	0.0071061
25	Bid	0.8591196	0.0081103

Supplemental table 3- Top 25 most significant downregulated genes in 3T3-L1 cells after Rbms1 knockdown



Supplemental figure 1 (S1)- A representative image showing the protein separation pattern is shown in the 3T3-L1^{RBMS1 KD} and 3T3-L1^{scr ctrl} adipocytes.



Supplemental figure 2 (S2)- A representative image protein spots on the gel

SI no:	Spot No ^a	Accession No ^b	Protein Name	MASCOT ID	P value (ANOVA)	Ratio ^c	Pi ^d	MW ^e	Cov%	Score ^f	EXP
1	1056	Q9DCX2	ATP synthase subunit d, mitochondrial	ATP5H_MOUSE	0.002	-5.04062	5.52	18738	61	57	↓
2	410	P63017	Heat shock cognate 71 kDa protein	HSP7C_MOUSE	0.003	-3.93272	5.37	70827	26	67	↓
3	404	Q8BZQ7	Anaphase-promoting complex subunit 2	ANC2_MOUSE	0.005	-4.76049	5.21	95261	9	57	↓
4	370	P11499	Heat shock protein HSP 90-beta	HS90B_MOUSE	0.005	-4.78179	4.97	83273	39	121	↓
5	744	Q9ET22	Dipeptidyl peptidase 2	DPP2_MOUSE	0.005	-5.30529	5.17	56234	26	200	↓
6	925	P08249	Malate dehydrogenase, mitochondrial	MDHM_MOUSE	0.006	14.29734	8.93	35589	30	58	↑
7	423	P63260	Actin, cytoplasmic 2	ACTG_MOUSE	0.007	-2.93406	5.31	41766	38	57	↓
8	1070	Q6DFW0	Guanine nucleotide exchange factor C9orf72 homolog	CI072_MOUSE	0.007	18.47058	5.4	47284	132	57	↑
9	756	Q3TDX8	Cytochrome b5 reductase 4	NB5R4_MOUSE	0.008	2.964571	6.3	60543	94	80	↑
10	368	P20152	Vimentin	VIME_MOUSE	0.009	-7.76575	5.06	53655	70	347	↓
11	411	P38647	Stress-70 protein, mitochondrial	GRP75_MOUSE	0.01	-2.82905	5.91	73483	44	179	↓
12	895	Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial	3HIDH_MOUSE	0.01	-2.50973	8.37	35417	32	58	↓
13	371	Q6P1G2	Lysine-specific demethylase 2B	KDM2B_MOUSE	0.01	-5.04869	8.66	149638	15	57	↓
14	1132	P07091	Protein S100-A4	S10A4_MOUSE	0.012	-3.89148	5.23	11714	43	70	↓
15	961	P67778	Prohibitin 1	PHB_MOUSE	0.013	-1.98007	5.57	29802	63	99	↓
16	143	Q02566	Myosin-6	MYH6_MOUSE	0.013	4.335798	5.57	223426	36	57	↑
17	362	Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2_MOUSE	0.014	-5.1482	5.66	29627	13	57	↓
18	428	Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUS1_MOUSE	0.018	-2.0888	5.51	79698	34	67	↓
19	727	P56480	ATP synthase subunit beta, mitochondrial	ATPB_MOUSE	0.019	-1.81516	5.19	56265	63	165	↓
20	759	Q6P1Y8	Type II inositol 3,4-bisphosphate 4-phosphatase	INP4B_MOUSE	0.02	-2.4315	5.69	100465	20	57	↓
21	369	Q05920	Pyruvate carboxylase, mitochondrial	PYC_MOUSE	0.021	-4.49871	6.25	129602	29	151	↓
22	373	Q6P1Y8	Type II inositol 3,4-bisphosphate 4-phosphatase	INP4B_MOUSE	0.023	-3.874	5.69	100465	15	57	↓
23	1139	Q05920	Pyruvate carboxylase, mitochondrial	PYC_MOUSE	0.026	-3.76159	6.25	129602	22	117	↓
24	365	Q8BY02	NF-kappa-B-repressing factor	NKRF_MOUSE	0.027	-5.21235	9.08	77658	17	57	↓
25	367	Q9JL25	Regulator of G-protein signaling 1	RGS1_MOUSE	0.03	-3.67879	9.2	24091	41	68	↓
26	414	Q8BHX1	HAUS augmin-like complex subunit 1	HAUS1_MOUSE	0.03	-3.92161	5.56	31359	30	62	↓
27	549	Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2_MOUSE	0.037	1.832763	5.66	29627	13	57	↑
28	741	P14211	Calreticulin	CALR_MOUSE	0.039	-2.17188	4.33	47965	27	85	↓
29	765	Q922R8	Protein disulfide-isomerase A6	PDIA6_MOUSE	0.039	-1.8828	5	48070	34	94	↓
30	422	P20152	Vimentin	VIME_MOUSE	0.04	-2.07737	5.06	53655	48	172	↓
31	1108	P16045	Galectin-1	LEG1_MOUSE	0.044	-2.03928	5.32	14856	42	59	↓
32	803	P63260	Actin, cytoplasmic 2	ACTG_MOUSE	0.047	-2.45903	5.31	41766	60	127	↓
33	136	Q32MG2	Protein chibby homolog 2	SPERT_MOUSE	0.048	3.585876	6.28	51833	21	57	↑

34	556	P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	0.049	3.408055	8.49	43204	27	57	↑
35	861	P14206	40S ribosomal protein SA	RSSA_MOUSE	0.05	7.282463	4.8	32817	49	74	↑
36	985	B2RVL6	Zinc finger CCHC domain-containing protein 24	ZCH24_MOUSE	0.051	-1.8505	8.98	26943	33	57	↓
37	1077	Q6P1Y8	Type II inositol 3,4-bisphosphate 4-phosphatase	INP4B_MOUSE	0.058	-4.71116	5.69	104465	15	57	↓

Supplementary Table S4: Differentially abundant proteins between RBMS1 Knockdown vs. Scramble Control . MALDI-TOF mass spectrometry was utilized to identify and analyze the protein spots from the 2D-DIGE gels

^aSpot numbers matched those included in the 2D-image

^bProtein accession number for SWISSPROT Database

^cProtein expression between RBMS1 knockdown vs scramble control (positive values demonstrate an increase in the protein abundance in RBMS1 knockdown; negative values demonstrate a decrease in the protein abundance in RBMS1 knockdown)

^dTheoretical isoelectric point

^eTheoretical molecular weight

^fMASCOT score

Supplementary Table S5: Sequences of the forward and reverse primers for mouse species ordered from Macrogen and used in the quantitative real time PCR (qRT-PCR).

Gene Name	Forward (5'-3')	Reverse (5'-3')
Actin	ATGACCCAAGCCGAGAAGG	CGGCCAAGTCTTAGAGTTGTTG
Hsl	GGCAGTGGTGTGTAAGTAGGATTG	ATCCATGCTGTGTGAGAACGC
Adipocnectin	AACTTGTGCAGGTTGGATGG	CGATACACATAAGCGGCTT
Atgl	GGAACCAAAGGACCTGATGACC	ACATCAGGCAGCCACTCCAACA
Ppar γ2	GCATGGTGCCTTCGCTGA	TGGCATCTCTGTGTCAACCATG
C/ebp α	CAAGAACAGCAACGAGTACCG	GTCAGTGGTCAACTCCAGCAC
RBMS1	CTGAGCAAGACAAACCTCTACAT	GGCCTTATCCAAAATCGCCTT

Supplementary Table S6: The list of primary and secondary antibodies used in this study.

Serial	Antibody name	Host/Isotype	Type	Reference
1	RBMS1	Rabbit/ IgG	Primary Antibody	Abcam(ab150353)
2	beta Actin Control Antibody (BA3R)	Mouse/ IgG2b	Primary Antibody	Invitrogen (MA5-15739)
3	alfa Tubulin	Mouse/ IgG1	Primary Antibody	Invitrogen (A11126)
4	GAPDH Loading Control Monoclonal Antibody (GA1R)	Mouse / IgG1	Primary Antibody	Invitrogen (MA5-15738)
5	PPAR gamma monoclonal Antibody	Rabbit/ IgG	Primary Antibody	Invitrogen (PA3-821A)
6	C/ebp α	Rabbit/ IgG	Primary Antibody	Cell Signaling Technology (8178S)
7	ATGL (30A4) Rabbit mAb	Rabbit/ IgG	Primary Antibody	Cell Signaling Technology (2439S)
8	Adiponectin	Mouse / IgG	Primary Antibody	Invitrogen (MA1-054)
9	HSL (hormone-sensitive lipase)	Rabbit/ IgG	Primary Antibody	Cell Signaling Technology (4107S)
10	Goat Anti mouse	Goat / IgG	Secondary antibody	Invitrogen (31430)
11	Goat Anti Rabbit	Goat / IgG	Secondary antibody	Invitrogen (31460)