

SUPPLEMENTARY DATA

**Supplementary Table 1. Primer sequences used for RT-qPCR validation of the microarray data**

<b>Gene</b>	<b>Primer direction</b>	<b>Primer sequence</b>
Glyceraldehyde 3-phosphate dehydrogenase ( <i>Gapdh</i> )	Forward	5'-ACAATGAATACGGCTACAGCAACAG-3'
	Reverse	5'-GGTGGTCCAGGGTTTCTTACTCC-3'
Cell death-inducing DFFA-like effector a ( <i>Cidea</i> )	Forward	5'-TTTCAAACCATGACCGAAGTAGCC-3'
	Reverse	5'-CCTCCAGCACCAGCGTAACC-3'
Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha ( <i>Pparg1a</i> , <i>PGC1α</i> )	Forward	5'-AAGTGTGGA ACTCTCTGGA ACTG-3'
	Reverse	5'-GGGTTATCTTGGTTGGCTTTATG-3'
Peroxisome proliferative activated receptor, gamma, coactivator 1 beta ( <i>Pparg1b</i> , <i>PGC1β</i> )	Forward	5'-GGTCCCTGGCTGACATTCAC-3'
	Reverse	5'-GGCACATCGAGGGCAGAG-3'
Carnitine palmitoyltransferase I alpha ( <i>Cpt1a</i> )	Forward	5'-ATCTGGATGGCTATGGTCAAGGTC-3'
	Reverse	5'-GTGCTGTCATGCGTTGGAAGTC-3'
Insulin receptor substrate 2 ( <i>Irs2</i> )	Forward	5'-CCCATGTCCCGCCGTGAAG-3'
	Reverse	5'-CTCCAGTGCCAAGGTCTGAAGG-3'
β3-adrenoceptor ( <i>Adrb3</i> )	Forward	5'-CTTCACTCTCTGCTGGTTGC-3'
	Reverse	5'-AAGGCAGAATTGGCATAACC-3'
Phosphoenolpyruvate carboxykinase 1 ( <i>Pck1</i> )	Forward	5'-TGCCTCTCTCCACACCATTGC-3'
	Reverse	5'-TGCCTTCCACGAACTTCCTCAC-3'

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**Supplementary Table 2. Transcriptional pattern related with lipid metabolism in the liver of C57BL/6J mice fed with normal diet and high-fat diet with or without luteolin treatment**

	ND	HFD	LU
<i>Fatty acid and lipid transporter</i>			
Lrp4	1.00 ± 0.01	1.06 ± 0.02*	1.32 ± 0.05 <sup>§§</sup>
Ldlr	1.01 ± 0.11	0.78 ± 0.03	1.06 ± 0.04 <sup>§§</sup>
Pcsk9	1.22 ± 0.56	0.34 ± 0.00	0.45 ± 0.02 <sup>§§</sup>
Stab1	1.01 ± 0.08	0.75 ± 0.02*	0.92 ± 0.04 <sup>§</sup>
Vldlr	1.01 ± 0.09	2.11 ± 0.03 <sup>***</sup>	1.66 ± 0.06 <sup>§§</sup>
<i>Fatty acid synthesis</i>			
Acaa2	1.00 ± 0.01	0.80 ± 0.02 <sup>***</sup>	0.60 ± 0.02 <sup>§§</sup>
Acacb	1.03 ± 0.19	0.33 ± 0.03*	0.26 ± 0.02
Acot1	1.00 ± 0.03	0.45 ± 0.03 <sup>***</sup>	0.22 ± 0.01 <sup>§§§</sup>
Acot3	1.00 ± 0.06	0.35 ± 0.06 <sup>***</sup>	0.32 ± 0.04
Acot4	1.00 ± 0.04	0.61 ± 0.05 <sup>**</sup>	0.54 ± 0.02
Decr2	1.00 ± 0.04	0.91 ± 0.04	0.57 ± 0.02 <sup>§§</sup>
Echdc2	1.00 ± 0.04	0.85 ± 0.02*	0.84 ± 0.03
Echs1	1.00 ± 0.05	0.82 ± 0.01*	0.92 ± 0.04 <sup>§</sup>
Fads1	1.01 ± 0.07	0.69 ± 0.04*	0.66 ± 0.04
Fads2	1.00 ± 0.03	0.66 ± 0.02 <sup>***</sup>	0.70 ± 0.02
<i>Lipogenesis</i>			
Acat3	1.00 ± 0.05	1.25 ± 0.04*	0.92 ± 0.04 <sup>§§</sup>
Acs11	1.00 ± 0.03	0.75 ± 0.02 <sup>**</sup>	0.61 ± 0.04 <sup>§</sup>
Acs15	1.01 ± 0.08	0.76 ± 0.02*	0.54 ± 0.01 <sup>§§§</sup>
Adrp	1.00 ± 0.05	0.85 ± 0.02*	0.48 ± 0.00 <sup>§§§</sup>
Agpat2	1.00 ± 0.05	0.93 ± 0.02	0.71 ± 0.00 <sup>§§§</sup>
Agpat6	1.00 ± 0.06	0.67 ± 0.01 <sup>**</sup>	0.68 ± 0.05
Agpat9	1.00 ± 0.06	1.05 ± 0.04	0.73 ± 0.01 <sup>§§</sup>
Dgat2	1.00 ± 0.06	1.24 ± 0.03*	1.21 ± 0.02
Gpam	1.00 ± 0.05	0.86 ± 0.01*	0.61 ± 0.01 <sup>§§§</sup>
Mttp	1.01 ± 0.07	0.76 ± 0.03*	0.60 ± 0.02 <sup>§§</sup>
Ppap2a	1.00 ± 0.02	0.92 ± 0.01 <sup>**</sup>	0.60 ± 0.02 <sup>§§§</sup>
Ppapdc1	1.00 ± 0.05	0.75 ± 0.03*	0.70 ± 0.01
Ppapdc1b	1.00 ± 0.04	0.69 ± 0.02 <sup>**</sup>	0.58 ± 0.03 <sup>§</sup>
<i>Fatty acid oxidation</i>			
Acadl	1.00 ± 0.04	1.07 ± 0.01	1.26 ± 0.01 <sup>§§§</sup>
Acox1	1.01 ± 0.09	1.47 ± 0.05*	1.72 ± 0.05 <sup>§</sup>

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Cpt1a	1.00 ± 0.02	0.70 ± 0.02 <sup>***</sup>	0.73 ± 0.01
Cyp4a12a	1.00 ± 0.04	0.54 ± 0.08 <sup>**</sup>	0.60 ± 0.06
Cyp4a12b	1.00 ± 0.07	0.50 ± 0.10 <sup>*</sup>	0.77 ± 0.03
Hadh	1.00 ± 0.04	1.16 ± 0.06	1.50 ± 0.09 <sup>§</sup>
Scp2	1.00 ± 0.04	1.26 ± 0.05 <sup>*</sup>	1.65 ± 0.05 <sup>§§</sup>
<b><i>Lipolysis</i></b>			
Lpl	1.01 ± 0.07	4.50 ± 0.47 <sup>**</sup>	6.36 ± 0.17 <sup>§</sup>
Mgl1	1.00 ± 0.04	0.68 ± 0.02 <sup>**</sup>	0.47 ± 0.03 <sup>§§</sup>
Pnpla2	1.00 ± 0.04	0.82 ± 0.02 <sup>*</sup>	0.82 ± 0.01
<b><i>Cholesterol synthesis</i></b>			
Acat1	1.00 ± 0.07	0.57 ± 0.02 <sup>**</sup>	0.59 ± 0.02
Hsd17b7	1.00 ± 0.00	0.50 ± 0.02 <sup>***</sup>	0.42 ± 0.02
Lss	1.06 ± 0.27	0.65 ± 0.02	0.67 ± 0.02
Nsdhl	1.03 ± 0.17	0.68 ± 0.01	0.55 ± 0.01 <sup>§§§</sup>
Pmvk	1.01 ± 0.11	0.68 ± 0.03 <sup>*</sup>	0.65 ± 0.02
Tm7sf2	1.00 ± 0.06	0.59 ± 0.02 <sup>**</sup>	0.60 ± 0.00
<b><i>Bile acid synthesis</i></b>			
Cyp39a1	1.00 ± 0.04	0.68 ± 0.04 <sup>**</sup>	0.62 ± 0.04
<b><i>Biliary cholesterol excretion</i></b>			
Abcg5	1.00 ± 0.02	2.93 ± 0.04 <sup>***</sup>	3.16 ± 0.05 <sup>§</sup>
Abcg8	1.00 ± 0.01	2.56 ± 0.12 <sup>***</sup>	3.60 ± 0.35 <sup>§</sup>
<b><i>Transcription regulator</i></b>			
Cidea	1.00 ± 0.06	14.35 ± 1.97 <sup>**</sup>	2.83 ± 0.21 <sup>§§</sup>
Pparg	1.01 ± 0.09	1.53 ± 0.05 <sup>**</sup>	1.51 ± 0.07
Ppargc1b (PGC1β)	1.01 ± 0.07	0.91 ± 0.07	1.34 ± 0.07 <sup>§</sup>
Srebf1	1.00 ± 0.07	2.11 ± 0.07 <sup>***</sup>	2.36 ± 0.04

Data shown as means ± S.E. ND vs HFD; \*p<0.05, \*\*p<0.01, \*\*\*p<0.001. HFD vs LU; §p<0.05, §§p<0.01, §§§p<0.001.

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**Supplementary Table 3. Transcriptional pattern related with lipid metabolism in the epididymal white adipose tissue of C57BL/6J mice fed with normal diet and high-fat diet with or without luteolin treatment**

	ND	HFD	LU
<i>Fatty acid and lipid transporter</i>			
Cd36	1.00 ± 0.04	1.05 ± 0.05	1.60 ± 0.03 <sup>\$\$\$</sup>
Fabp4 (aP2)	1.00 ± 0.03	0.83 ± 0.06	1.47 ± 0.04 <sup>\$\$\$</sup>
Ffar3	1.00 ± 0.01	0.85 ± 0.03 <sup>**</sup>	1.20 ± 0.02 <sup>\$\$\$</sup>
Lpl	1.01 ± 0.09	0.89 ± 0.04	1.10 ± 0.05 <sup>§</sup>
Stab1	1.00 ± 0.06	1.42 ± 0.02 <sup>**</sup>	1.37 ± 0.02
Vldlr	1.00 ± 0.04	1.07 ± 0.00 <sup>c</sup>	0.85 ± 0.01 <sup>\$\$\$</sup>
<i>Fatty acid synthesis</i>			
Acacb	1.02 ± 0.13	0.40 ± 0.03 <sup>**</sup>	0.60 ± 0.04 <sup>§§</sup>
Acot3	1.00 ± 0.03	0.71 ± 0.01 <sup>***</sup>	0.69 ± 0.01
Acot4	1.00 ± 0.06	0.43 ± 0.02 <sup>***</sup>	0.53 ± 0.01 <sup>§§</sup>
Echdc2	1.00 ± 0.04	0.59 ± 0.03 <sup>***</sup>	0.93 ± 0.03 <sup>§§</sup>
Echdc3	1.00 ± 0.02	0.69 ± 0.02 <sup>***</sup>	0.87 ± 0.04 <sup>§§</sup>
Echs1	1.00 ± 0.01	0.69 ± 0.04 <sup>**</sup>	0.87 ± 0.03 <sup>§</sup>
Fasn	1.04 ± 0.19	0.77 ± 0.09	1.09 ± 0.05 <sup>§</sup>
Mcat	1.00 ± 0.06	0.68 ± 0.01 <sup>***</sup>	0.83 ± 0.02 <sup>§§</sup>
Mecr2	1.00 ± 0.05	0.80 ± 0.01 <sup>*</sup>	0.99 ± 0.02 <sup>\$\$\$</sup>
Scd2	1.05 ± 0.22	2.41 ± 0.29 <sup>*</sup>	1.89 ± 0.08
<i>Lipogenesis</i>			
Acs15	1.00 ± 0.03	1.39 ± 0.03 <sup>***</sup>	1.15 ± 0.03 <sup>§§</sup>
Adrp	1.00 ± 0.07	1.82 ± 0.04 <sup>***</sup>	1.41 ± 0.06 <sup>§§</sup>
Agpat6	1.00 ± 0.07	0.70 ± 0.01 <sup>*</sup>	0.84 ± 0.01 <sup>\$\$\$</sup>
Agpat9	1.00 ± 0.05	0.65 ± 0.03 <sup>**</sup>	0.65 ± 0.04
Dgat1	1.00 ± 0.05	0.73 ± 0.01 <sup>**</sup>	1.05 ± 0.06 <sup>§§</sup>
Gpam	1.01 ± 0.12	0.73 ± 0.01	0.70 ± 0.01
Ppap2a	1.00 ± 0.02	1.18 ± 0.04 <sup>*</sup>	0.91 ± 0.03 <sup>§§</sup>
<i>Fatty acid oxidation</i>			
Acadl	1.00 ± 0.03	0.94 ± 0.03	1.20 ± 0.05 <sup>§§</sup>
Acads	1.00 ± 0.05	0.72 ± 0.03 <sup>**</sup>	1.02 ± 0.01 <sup>§§</sup>
Acadsb	1.00 ± 0.03	0.66 ± 0.03 <sup>***</sup>	0.94 ± 0.03 <sup>§§</sup>
Acadv1	1.00 ± 0.05	0.73 ± 0.01 <sup>**</sup>	0.96 ± 0.01 <sup>\$\$\$</sup>
Cpt1b	1.00 ± 0.02	1.79 ± 0.05 <sup>***</sup>	1.75 ± 0.05
Cpt2	1.01 ± 0.09	0.79 ± 0.03	1.01 ± 0.01 <sup>§§</sup>

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Hadh	1.00 ± 0.00	0.88 ± 0.02 <sup>**</sup>	1.24 ± 0.04 <sup>§§§</sup>
Scp2	1.00 ± 0.02	0.67 ± 0.01 <sup>***</sup>	0.74 ± 0.03
<b><i>Lipolysis</i></b>			
Lipe	1.00 ± 0.07	0.70 ± 0.03 <sup>*</sup>	0.90 ± 0.01 <sup>§§</sup>
Pnpla2	1.00 ± 0.03	0.74 ± 0.01 <sup>***</sup>	0.93 ± 0.01 <sup>§§§</sup>
<b><i>Cholesterol synthesis</i></b>			
Dhcr7	1.01 ± 0.09	1.55 ± 0.13 <sup>*</sup>	1.26 ± 0.03
Dhcr24	1.00 ± 0.05	1.24 ± 0.04 <sup>*</sup>	1.10 ± 0.01 <sup>§</sup>
Hsd17b7	1.01 ± 0.08	1.60 ± 0.09 <sup>**</sup>	1.32 ± 0.01 <sup>§</sup>
Lss	1.01 ± 0.09	1.35 ± 0.10	1.15 ± 0.03
Nsdhl	1.01 ± 0.08	1.37 ± 0.10 <sup>*</sup>	1.10 ± 0.03 <sup>§</sup>
Pmvk	1.00 ± 0.03	0.83 ± 0.03 <sup>*</sup>	0.94 ± 0.03 <sup>§</sup>
Sc4mol	1.00 ± 0.05	1.51 ± 0.06 <sup>**</sup>	1.16 ± 0.01 <sup>§§</sup>
Sqle	1.01 ± 0.12	1.29 ± 0.09	1.01 ± 0.03 <sup>§</sup>
<b><i>Bile acid synthesis</i></b>			
Cyp27a1	1.00 ± 0.05	0.66 ± 0.02 <sup>*</sup>	0.93 ± 0.01 <sup>§§§</sup>
<b><i>Transcription regulator</i></b>			
Adrb3	1.01 ± 0.11	0.36 ± 0.01 <sup>**</sup>	0.63 ± 0.02 <sup>§§§</sup>
Pparg	1.01 ± 0.09	1.53 ± 0.05 <sup>**</sup>	1.51 ± 0.07
Rxra (RXR $\alpha$ )	1.00 ± 0.06	0.62 ± 0.01 <sup>**</sup>	0.84 ± 0.01 <sup>§§§</sup>
Rxrb (RXR $\beta$ )	1.00 ± 0.03	0.79 ± 0.01 <sup>**</sup>	0.91 ± 0.01 <sup>§§§</sup>
Rxrg (RXR $\gamma$ )	1.00 ± 0.05	0.83 ± 0.04	1.02 ± 0.00 <sup>§§</sup>
Ppargc1a (PGC-1 $\alpha$ )	1.00 ± 0.05	0.71 ± 0.03 <sup>**</sup>	0.96 ± 0.02 <sup>§§</sup>
Ppargc1b (PGC-1 $\beta$ )	1.01 ± 0.10	0.88 ± 0.03	1.15 ± 0.01 <sup>§§§</sup>
Mlxipl (Chrebp)	1.00 ± 0.07	0.74 ± 0.02 <sup>*</sup>	1.15 ± 0.00 <sup>§§§</sup>
Pck1	1.00 ± 0.04	0.41 ± 0.04 <sup>***</sup>	0.66 ± 0.03 <sup>§§</sup>

Data shown as means ± S.E. ND vs HFD; \*p<0.05, \*\*p<0.01, \*\*\*p<0.001. HFD vs LU; §p<0.05, §§p<0.01, §§§p<0.001.

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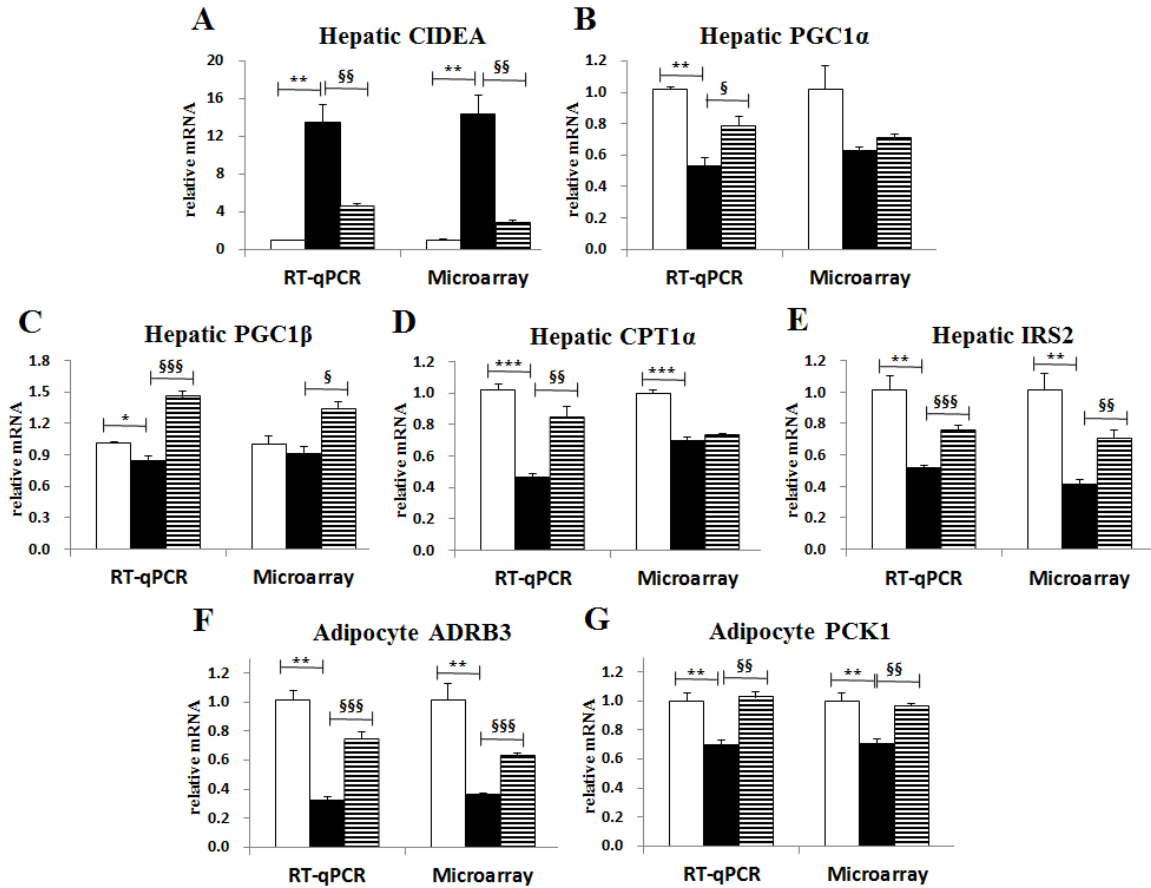
**Supplementary Table 4. Effect of luteolin treatment on transcriptional pattern related with TCA cycle in adipose tissue of C57BL/6J mice.**

	ND	HFD	LU
Pdha1	1.00 ± 0.02	0.66 ± 0.00 <sup>***</sup>	0.67 ± 0.00
Pdhb	1.00 ± 0.06	0.74 ± 0.04 <sup>*</sup>	0.97 ± 0.04 <sup>§</sup>
Pcx	1.00 ± 0.07	0.67 ± 0.03 <sup>**</sup>	0.88 ± 0.03 <sup>§§</sup>
Cs	1.00 ± 0.04	0.78 ± 0.02 <sup>**</sup>	0.95 ± 0.01 <sup>§§</sup>
Aco1	1.00 ± 0.01	0.75 ± 0.02 <sup>***</sup>	0.93 ± 0.03 <sup>§§</sup>
Aco2	1.00 ± 0.05	0.66 ± 0.02 <sup>**</sup>	0.87 ± 0.00 <sup>§§§</sup>
Idh2	0.99 ± 0.02	0.89 ± 0.02 <sup>*</sup>	1.15 ± 0.02 <sup>§§§</sup>
Idh3b	1.00 ± 0.02	0.73 ± 0.01 <sup>***</sup>	0.84 ± 0.03 <sup>§</sup>
Idh3g	1.00 ± 0.01	0.79 ± 0.02 <sup>***</sup>	0.95 ± 0.02 <sup>§§</sup>
Ogdh	1.00 ± 0.03	0.81 ± 0.03 <sup>**</sup>	0.94 ± 0.01 <sup>§§</sup>
Dlst	1.00 ± 0.03	0.71 ± 0.01 <sup>***</sup>	0.87 ± 0.02 <sup>§§</sup>
Suclg2	1.00 ± 0.06	0.67 ± 0.02 <sup>**</sup>	0.83 ± 0.01 <sup>§§</sup>
Sdhb	1.00 ± 0.01	0.75 ± 0.02 <sup>***</sup>	0.87 ± 0.02 <sup>§</sup>
Sdhc	1.00 ± 0.03	0.77 ± 0.01 <sup>***</sup>	1.00 ± 0.03 <sup>§§§</sup>
Fn1	1.01 ± 0.11	1.22 ± 0.05	0.67 ± 0.02 <sup>§§§</sup>
Mdh1	1.00 ± 0.03	0.99 ± 0.04	1.26 ± 0.03 <sup>§§</sup>
Mdh2	1.00 ± 0.05	0.82 ± 0.01 <sup>*</sup>	0.95 ± 0.02 <sup>§§</sup>

Data shown as means ± S.E. ND vs HFD; \*p<0.05, \*\*p<0.01, \*\*\*p<0.001. HFD vs LU; §p<0.05, §§p<0.01, §§§p<0.001.

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**Supplementary Figure 1. Real-time RT-qPCR validation.** Microarray and RT-qPCR data shown as means  $\pm$  S.E. ND vs HFD; \* $p$ <0.05, \*\* $p$ <0.01, \*\*\* $p$ <0.001. HFD vs LU; § $p$ <0.05, §§ $p$ <0.01, §§§ $p$ <0.001. White bar = ND group; black bar = HFD group; stripe bar = LU group.



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**Supplementary Figure 2. Effect of luteolin treatment on hepatic metabolites expressions using PLS-DA in C57BL/6J mice fed a high-fat diet. (A) PLS-DA scores scatter plot. (B) Validation plot.**

