## Zhao *et al.* Supplementary Data

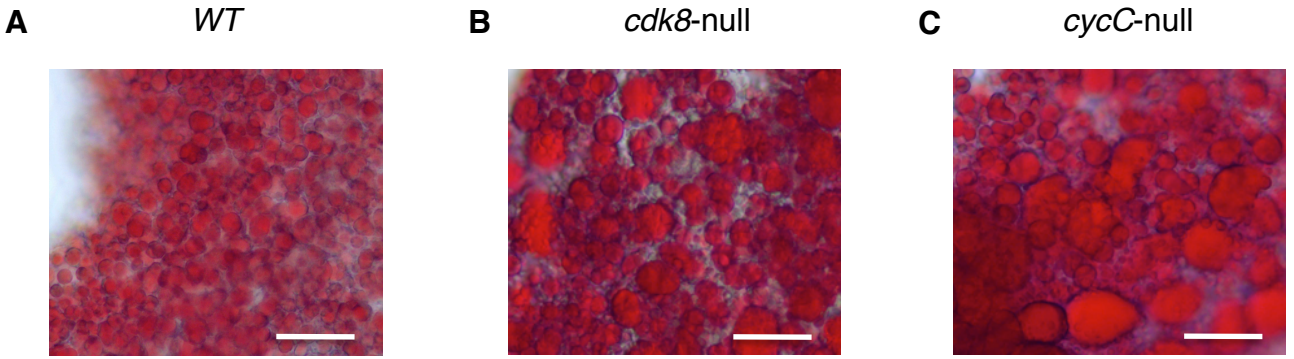


**Figure S1.** Representative images of Oil Red O staining for wild-type (*WT*) (*w1118*) (**A**), *cdk8*-null (*k185*) (**B**) and *cycC*-null (*y5*) (**C**) *Drosophila* larvae (Bar=0.1mm).

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**Table S1.** A list of genes that are significantly up-regulated in cdk8- and cycC mutants by microarray analysis

| # | Gene names | Gene symbols | Fold change * | |
|---|---|---|---|---|
| | | | ***cdk8/cont*** | ***cycC/cont*** |
| 1 | *Maltase (Larval visceral protein D)* | *LvpD (CG8694)* | 7.754 | 9.758 |
| 2 | *bubblegum (long chain fatty acid CoA ligase)* | *bgm (CG4501)* | 4.645 | 3.064 |
| 3 | *Maltase (Larval visceral protein L)* | *LvpL (CG8695)* | 4.303 | 17.820 |
| 4 | *Fatty acid synthetase* | *dFAS (CG3523)* | 4.212 | 2.505 |
| 5 | *Acetyl-CoA carboxylase* | *dACC (CG11198)* | 3.558 | 2.159 |
| 6 | *malic enzyme* | *Men (CG10120)* | 3.391 | 2.983 |
| 7 | *acetyl CoA oxidase* | *Acox57D-d (CG9709)* | 3.355 | 2.107 |
| 8 | *Cytochrome b5-related* | *Cyt-b5-r (CG13279)* | 3.301 | 5.009 |
| 9 | *Acetyl CoA synthetase* | *dACS (CG9390)* | 3.182 | 1.835 |
| 10 | *Maltase (Larval visceral protein H)* | *LvpH (CG8696)* | 3.053 | 4.590 |
| 11 | *acetyl CoA oxidase* | *Acox57D-p (CG9707)* | 2.748 | 1.562 |
| 12 | *Fatty acid transport protein* | *dFATP (CG7400)* | 2.401 | 2.408 |
| 13 | *aldolase* | *Ald (CG6058)* | 2.175 | 2.131 |
| 14 | *hoepel (citrate membrane transporter)* | *hoe1 (CG12787)* | 2.123 | 2.250 |
| 15 | *Fatty acyl CoA synthetase (Acsl)* | *l(2)44DEa (CG8732)* | 1.800 | 1.490 |
| 16 | *Lipase 2* | *Lip2 (CG17116)* | 1.714 | 3.527 |
| 17 | *Glycerol kinase* | *Gyk (CG18374)* | 1.554 | 1.621 |
| | *SCAP* | *dSCAP (CG33131)* | 1.256 | 1.511 |
| | *SREBP* | *dSREBP (CG8522)* | 1.401 | 1.179 |
| | *Cyclin-dependent kinase 8* | *dCdk8 (CG10572)* | 0.198 | 0.999 |
| | *Cyclin C* | *dCycC (CG7281)* | 0.968 | 0.096 |
| | *Rp49 (the ribosomal protein 49)* | *RpL32 (CG7939)* | 0.993 | 1.109 |

* Fold changes are calculated by the ratio between *cdk8* (or *cycC*) null mutants and the control larvae.

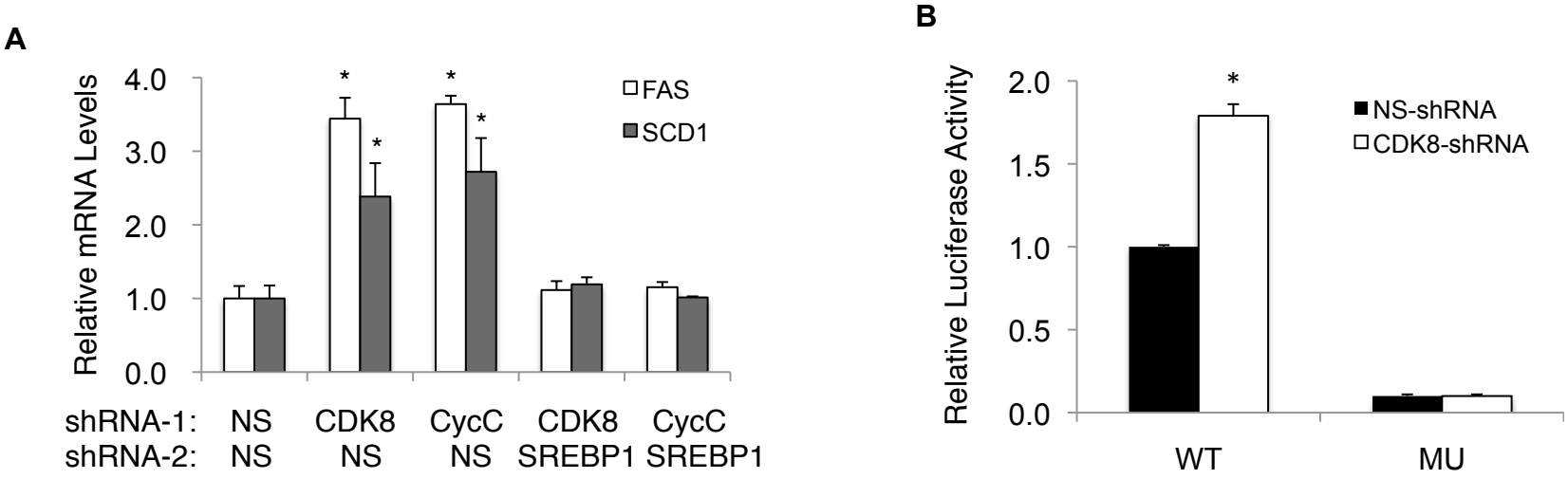


**Figure S2.** SREBP1-dependent regulation of CDK8 on gene expression. **A.** mRNA levels of endogenous SREBP-target genes (FAS and SCD1) in HepG2 cells were detected by qRT-PCR after treatments of the indicated combinations of lentiviral shRNAs. Cyclophilin B served as the invariant control and the mRNA levels of each gene were normalized with those in NS-shRNA-treated sample. Data represent Mean ± S.D. of three independent treatments. *p<0.01 *vs.* NS-shRNA. **B.** Effect of CDK8 knockdown by lentiviral shRNA on the SREBP1-target promoter activity in HEK293 cells measured by dual luciferase assays. The expression of firefly luciferase was controlled by a promoter region of rat SREBP-1c that contains either wildtype (WT) or point-mutated (MU) SREBP1-binding sites. The minimal promoter-driven renilla luciferase served as the invariant control. Firefly luciferase activity was first normalized by corresponding renilla luciferase activity, and then normalized by the WT promoter activity with the treatment of lentiviral NS-shRNA (non-silencing shRNA).

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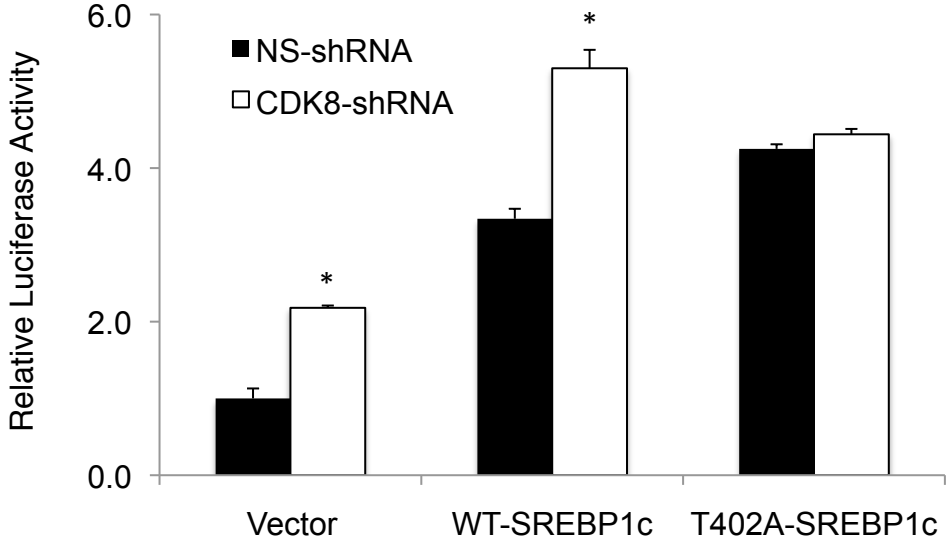


**Figure S3.** Effect of CDK8 knockdown by lentiviral shRNA on the transcription activities of wildtype (WT) or T402A mutated SREBP-1c in HEK293 cells as measured by dual luciferase assays. The expression of firefly luciferase was controlled by a promoter region of rat fatty acid synthase (FAS). The minimal promoter-driven renilla luciferase served as the invariant control. Firefly luciferase activity was first normalized by corresponding renilla luciferase activity, and then normalized by the promoter activity with the treatment of lentiviral NS-shRNA (non-silencing shRNA) and vector. Data represent Mean ± S.D. of three independent treatments. For CDK8-shRNA, *$p<0.01$ *vs.* NS-shRNA.

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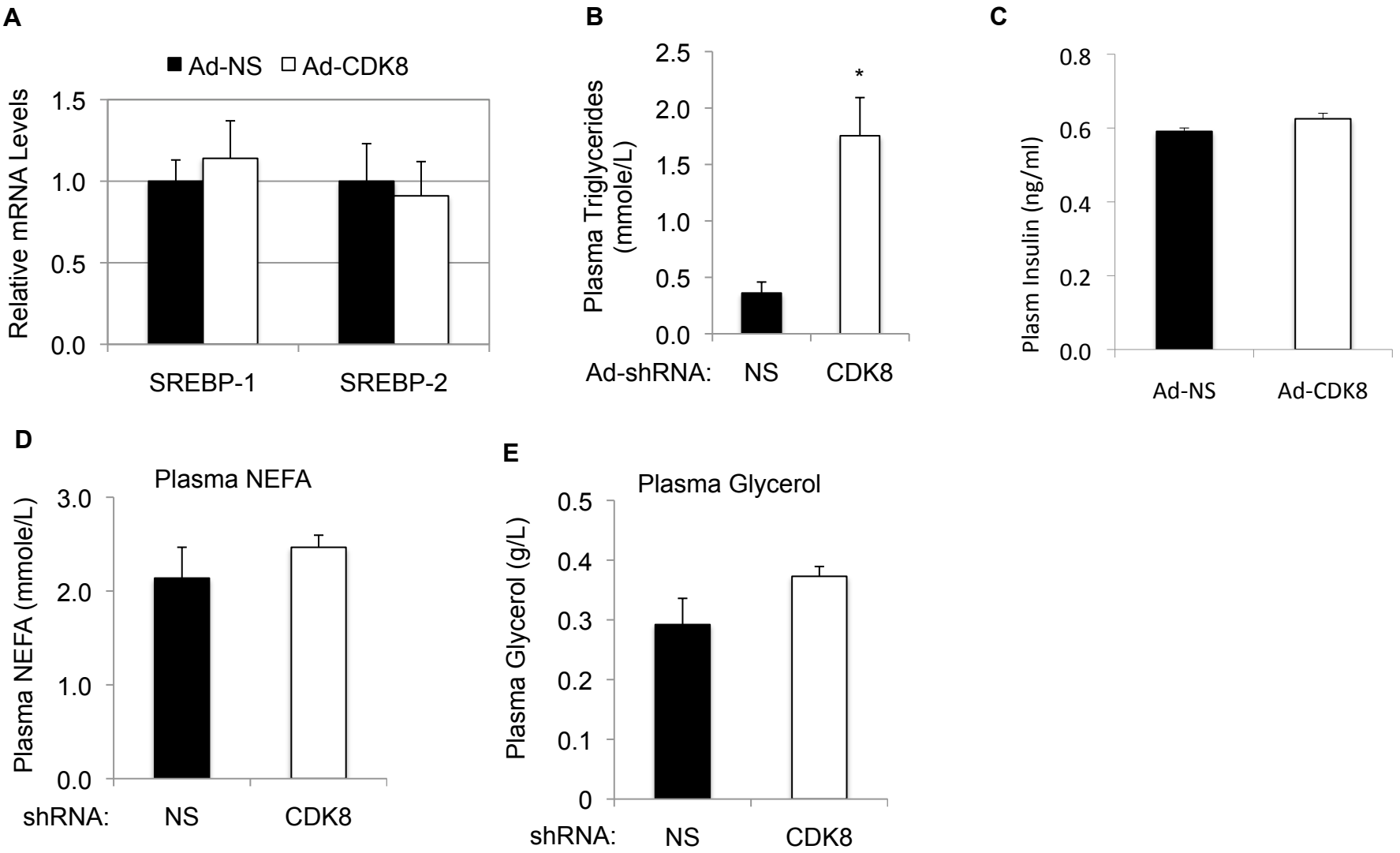


**Figure S4.** Effects of CDK8 knockdown by tail-vein injection of adenoviruses (Ad) expressing shRNA against CDK8 in mouse livers on **A**. The mRNA levels of indicated genes in liver; Plasma levels of triglycerides (**B**); insulin (**C**); non-esterified fatty acids (NEFA) (**D**) and glycerol (**E**). Data represent Mean ± S.D. (N=6). NS-shRNA, shRNA against non-silencing (NS) sequence, *p<0.01 vs NS.

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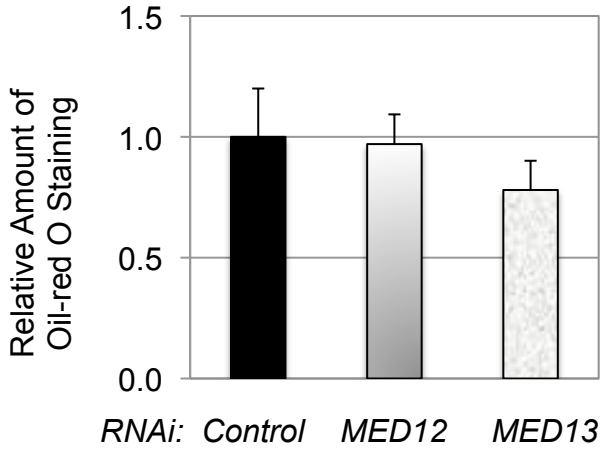


**Figure S5.** Effect of fat-body specific knockdown of MED12 or MED13 on lipid levels in *Drosophila* larvae by quantitative measurement of Oil Red O staining. Data represent Mean ± S.D., * $p<0.01$ *vs* wild-type larvae (n=3 groups with 10 larvae per group).

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**Table S2.** Primers for quantitative PCR

| Gene Name | Forward Primer | Reverse Primer |
|---|---|---|
| ***Drosophila*** | | |
| ACC | 5'-TAACCCGCGCTACATGGAAA | 5'-TCGTCTTGACCAGGTCCTTCTC |
| ACS | 5'-TTCCGGCAAGATTATGCGTC | 5'-CAGTTGCTCCACAATTTGCTCA |
| Bgm | 5'-CCAGTGCGGCAGCTCCCATGTC | 5'-GTGGCAACCGGCCGTCTCCG |
| Cyt-b5r | 5'-CGCCACACCAACATCCTCTACT | 5'-CACGCAGATCCAAATGCCTAA |
| FAS | 5'-CGAATCCATCAATATGCCCG | 5'-ACATAGTGACCACCACCCAGGT |
| Fatp | 5'-GAAATCCTTCTCGCGAATTCCT | 5'-GGAGATGAAAGCCATATCGCC |
| Rp49 | 5'-ACAGGCCCAAGATCGTGAAGA | 5'-CGCACTCTGTTGTCGATACCCT |
| | | |
| ***Human*** | | |
| FAS | 5'-TGATCCGGGAGCCGAAGCCA | 5'-GCCACTGGGCCTCGGGGATA |
| ACC | 5'-TGCCAGTGCCTGGAGGACCA | 5'-ATGACCCCAGCCAGCCCACA |
| ACLY | 5'-AACGCCAGCGGGAGCACATC | 5'-TTGCAGGCGCCACCTCATCG |
| SCD1 | 5'-CCGGACACGGTCACCCGTTG | 5'-CGCCTTGCACGCTAGCTGGT |
| CypB | 5'-CGGTGAGCGCTTCCCCGATG | 5'-CTGACCCAGCCAGGCCCGTA |
| | | |
| ***Rat*** | | |
| FAS | 5'-TGCTGCATGCCAGTGGACGG | 5'-GGGCATGGCTGCTGTAGGGG |
| ACC | 5'-AGGGCAAAGGGACTGGTGTTCAGAT | 5'-GCCAACGGAGATGGTTCATCCATTA |
| ACLY | 5'-CCACCGGCCCATTCCCAACC | 5'-CCTGCTGGGTGCTGGTGTCG |
| SCD1 | 5'-AGCTCAGCCAAATGCTGTGTTGTC | 5'-TGCCTTGATCAGTCACAGACACCT |
| CypB | 5'-GACGGACAGCCGGGACAAGC | 5'-AGGGATGAGGTCCCCGAGGC |

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**Table S2.** Primers for quantitative PCR (continue)

| | | |
|---|---|---|
| ***Mouse*** | | |
| FAS | 5'-CACTGCATTGACGGCCGGGT | 5'-GGACAAGCCCAGGCTGCGAG |
| ACC | 5'-CTGGAGCTAAACCAGCACTCCCGAT | 5'-GAGCTGACGGAGGCTGGTGACA |
| ACLY | 5'-GCTGTGCAGGGCATGCTGGA | 5'-CCATGGCAGCCACTGAGGGC |
| SCD1 | 5'- GCCAGACCGGGCTGAACACC | 5'- TGGTGTAGGCGAGTGGCGGA |
| L-PK | 5'-GCAGCAGTATGGAAGGGCCAGC | 5'-CCATAGCTGCGGGCAGTTGCT |
| SREBP-1 | 5'- CCAGCGGCTGCCTTCACACA | 5'- CCAGCCGAAAAGCGAGGCCA |
| SREBP-2 | 5'- TGGGGGCTGTCGGGTGTCAT | 5'- AGTCCCCCGTGAGGTCCAGC |
| CypB | 5'-TGAAGGTGCTCTTCGCCGCC | 5'-TCGTTGGCCACGGAGGGTCC |
| | | |
| ***Others*** | | |
| FF-Luc | 5'-CGGGCGCGGTCGGTAAAGTT | 5'-CGCCCAGCGTTTTCCCGGTAT |
| RN-Luc | 5'-CCGCAGTGGTGGGCCAGATG | 5'-AGAAGAGGCCGCGTTACCATGT |

**Abbreviations**:
ACC: Acetyl-CoA Carboxylase;
ACS: Acetyl-CoA Synthase;
CypB: Cyclophilin B;
FAS: Fatty Acid Synthase;
FF-Luc: Firefly Luciferase;
RN-Luc: Renilla Luciferase;
SCD1: Stearoyl-Coenzyme A Desaturase 1;
SREBP1: Sterol Regulatory Element Binding Factor 1;
SREBP2: Sterol Regulatory Element Binding Factor 2.
ACLY: ATP Citrate Lyase;
Bgm: Bubblegum;
Cyt-b5r: Cytochrome b5-related;
Fatp: Fatty acid (long chain) transport protein;
L-PK: Pyruvate Kinase (liver and red blood cell);
Rp49: Ribosomal protein L32;