Cytoplasmic polyadenylation element binding protein deficiency stimulates PTEN and Stat3 mRNA translation and induces hepatic insulin resistance

Ilya M. Alexandrov  
*University of Massachusetts Medical School, ilya.alexandrov@umassmed.edu*

Maria Ivshina  
*University of Massachusetts Medical School, Mariya.Ivshina@umassmed.edu*

Dae Young Jung  
*University of Massachusetts Medical School, DaeYoung.Jung@umassmed.edu*

*See next page for additional authors*

Follow this and additional works at: [http://escholarship.umassmed.edu/pgfe_pp](http://escholarship.umassmed.edu/pgfe_pp)  
Part of the [Genetics and Genomics Commons](http://escholarship.umassmed.edu/pgfe_pp)

Repository Citation  
Alexandrov, Ilya M.; Ivshina, Maria; Jung, Dae Young; Friedline, Randall H.; Ko, Hwi Jin; Xu, Mei; O'Sullivan-Murphy, Bryan; Bortell, Rita; Huang, Yen-Tsung; Urano, Fumihiko; Kim, Jason K.; and Richter, Joel D., "Cytoplasmic polyadenylation element binding protein deficiency stimulates PTEN and Stat3 mRNA translation and induces hepatic insulin resistance" (2012). Program in Gene Function and Expression Publications and Presentations. Paper 183.  
[http://escholarship.umassmed.edu/pgfe_pp/183](http://escholarship.umassmed.edu/pgfe_pp/183)

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in Program in Gene Function and Expression Publications and Presentations by an authorized administrator of eScholarship@UMMS. For more information, please contact Lisa.Palmer@umassmed.edu.
Cytoplasmic polyadenylation element binding protein deficiency stimulates PTEN and Stat3 mRNA translation and induces hepatic insulin resistance

Authors
Ilya M. Alexandrov, Maria Ivshina, Dae Young Jung, Randall H. Friedline, Hwi Jin Ko, Mei Xu, Bryan O'Sullivan-Murphy, Rita Bortell, Yen-Tsung Huang, Fumihiko Urano, Jason K. Kim, and Joel D. Richter

Comments
Copyright: © 2012 Alexandrov et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Rights and Permissions
Citation: Alexandrov IM, Ivshina M, Jung DY, Friedline R, Ko HJ, et al. (2012) Cytoplasmic Polyadenylation Element Binding Protein Deficiency Stimulates PTEN and Stat3 mRNA Translation and Induces Hepatic Insulin Resistance. PLoS Genet 8(1): e1002457. doi:10.1371/journal.pgen.1002457 Link to article on publisher’s site

This article is available at eScholarship@UMMS: http://escholarship.umassmed.edu/pgfe_pp/183
Cytoplasmic Polyadenylation Element Binding Protein Deficiency Stimulates PTEN and Stat3 mRNA Translation and Induces Hepatic Insulin Resistance

Ilya M. Alexandrov, Maria Ivshina, Dae Young Jung, Randall Friedline, Hwi Jin Ko, Mei Xu, Bryan O’Sullivan-Murphy, Rita Bortell, Yen-Tsung Huang, Fumihiko Urano, Jason K. Kim, Joel D. Richter

1 Program in Molecular Medicine, University of Massachusetts Medical School, Worcester, Massachusetts, United States of America, 2 Research Computing, Information Service Department, University of Massachusetts Medical School, Worcester, Massachusetts, United States of America, 3 Program in Gene Function and Expression, University of Massachusetts Medical School, Worcester, Massachusetts, United States of America, 4 Departments of Epidemiology and Biostatistics, Harvard University, Boston, Massachusetts, United States of America, 5 Department of Medicine, Division of Endocrinology, Metabolism, and Diabetes, University of Massachusetts Medical School, Worcester, Massachusetts, United States of America

Abstract

The cytoplasmic polyadenylation element binding protein CPEB1 (CPEB) regulates germ cell development, synaptic plasticity, and cellular senescence. A microarray analysis of mRNAs regulated by CPEB unexpectedly showed that several encoded proteins are involved in insulin signaling. An investigation of Cpeb1 knockout mice revealed that the expression of two particular negative regulators of insulin action, PTEN and Stat3, were aberrantly increased. Insulin signaling to Akt was attenuated in livers of CPEB–deficient mice, suggesting that they might be defective in regulating glucose homeostasis. Indeed, when the Cpeb1 knockout mice were fed a high-fat diet, their livers became insulin-resistant. Analysis of HepG2 cells, a human liver cell line, depleted of CPEB demonstrated that this protein directly regulates the translation of PTEN and Stat3 mRNAs. Our results show that CPEB regulated translation is a key process involved in insulin signaling.

Introduction

The maintenance of glucose homeostasis requires that organisms respond to changing environmental conditions by balancing pancreatic insulin secretion with the ability of tissues, particularly liver, muscle, and fat, to respond to hormone-induced signaling by importing or secreting glucose [1,2]. Obesity and other insults that promote diabetes do so by causing inflammation and insulin resistance, which is characterized by the inability of tissues to transduce insulin/insulin receptor interactions into elevated glucose uptake in muscle and adipose tissue and/or efficient insulin-induced hepatic insulin resistance. This event allows Gld2 to polyadenylate the RNA by precluding the eIF4E-eIF4G interaction that is necessary to recruit the 40S ribosomal unit to the 5' end of the mRNA. Because Maskin is tethered to CPE, only CPE-containing RNAs are repressed. CPEB-induced stimulated (i.e., deprepressed) translation is initiated when CPEB is phosphorylated on S174 or T171 (species-dependent), which expels PARN from the ribonucleoprotein complex. This event allows Gld2 to polyadenylate the RNA by
null
immunoprecipitated with CPEB but not CPEBAZF, suggesting that they might be direct targets of CPEB regulation.

**CPEB represses the translation of Stat3 and PTEN mRNAs**

Because of their central role in insulin signaling and their robust change in KO liver, we focused on PTEN and Stat3 as possible direct targets of CPEB regulation. The 3' UTRs of both RNAs contain conserved CPEs (Figure 5A, 5B), indicating that CPEB association with these transcripts as demonstrated in Figure 4E is probably direct. Depletion of CPEB from HepG2 cells resulted in elevated amounts of Stat3 and PTEN when examined by western blotting (Figure 5C, 5D; Figure 5E and 5F show that CPEB depletion had no effect on Stat3 or PTEN mRNA levels). However, because western blots reflect steady state protein levels and not necessarily protein synthesis, control and CPEB-depleted cells were pulse-labeled with 35S-methionine for 15 minutes, followed by Stat3 and PTEN immunoprecipitation and SDS-PAGE analysis. Figure 5G and 5H show that de novo labeling of Stat3 and PTEN mimics the western analysis of these proteins, and indicates that their mRNAs are under direct translational control by CPEB. As a control, Figure 5G shows that 35S-methionine labeled tubulin was unaffected by CPEB depletion. To buttress the conclusion that CPEB regulates Stat3 and PTEN at the translational level, the 3' UTRs of these mRNAs, containing or lacking the CPEs, were appended to firefly luciferase RNA (Figure 5I). These reporters, which together with Renilla luciferase RNA that served as an internal reference standard, were electroporated into control or CPEB-depleted HepG2 cells. The depletion of CPEB resulted in ~50% increase of firefly luciferase RNA translation when the reporter contained either the Stat3 or PTEN 3' UTRs. Moreover, nearly identical expression levels were observed when the CPEs were mutated, irrespective of whether the cells contained CPEB (Figure 5J, 5K, upper graph). There was no detectable difference in the stabilities of any of the electroporated RNAs (Figure 5J, 5K, lower panel). Finally, the polysome sedimentation profiles in Figure S1C show that CPEB represses translation of Stat3 and PTEN mRNAs, but not IRS1 or PDK1 mRNAs. Taken together, the data in Figure 5 as well as in Figure S1C demonstrate that CPEB acts directly on Stat3 and PTEN mRNAs to repress their translation.

**Figure 1. Analysis of polysome sucrose gradients reveals CPEB control of insulin signaling.** Extracts prepared from WT and CPEB KO MEFs were centrifuged through sucrose gradients; the fractions containing polysomes were pooled, the RNA extracted, and used to probe microarrays. A functional annotation analysis reveals changes in the translation of a number of mRNAs involved in insulin signaling. doi:10.1371/journal.pgen.1002457.g001
Cpeb1 knockout mice are insulin-resistant

Although the data in Figure 2 demonstrate that the Cpeb1 KO mice have substantial alterations in the levels of insulin signaling proteins, the animals are normal in size and mass. However, because neither of these observations speaks directly to possible changes in glucose metabolism, we subjected the animals to a glucose tolerance test (GTT), which measures glucose clearance from the blood. In this regard, the WT and KO animals were indistinguishable (Figure 6A). On the other hand, serum insulin levels measured during the GTT were significantly higher in the KO mice, which would indicate insulin resistance. To examine this possibility, we performed an insulin tolerance test (ITT). After a 5 hour fast, animals were injected with insulin, which was followed by serum glucose determination 0–60 minutes later. Compared to WT, the KO animals had
significantly higher levels of glucose (Figure 6A); these data, together with those showing that insulin-injected KO animals have very low levels of phospho-Akt, indicate that the absence of CPEB induces insulin resistance. We also examined insulin secretion from isolated pancreatic islets from WT and CPEB KO mice; when challenged with glucose, we detected no statistical difference between the two groups of animals (data not shown).

We measured the levels of a number of cytokines and hormones and found that IL6 (NM_031168.1) was elevated by ~5 fold in KO mouse serum (Figure S2A). Increased amounts of this cytokine often correlate with insulin resistance and diabetes [14]. This observation supports the notion that the KO animals have an activated inflammatory Jak-Stat signaling pathway, which is further indicated by enhanced Stat3 phosphorylation and Socs3

**Figure 3. CPEB mediates insulin signaling in the liver.** (A) Western blot and quantification of total and phospho-Akt (serine 473 and threonine 308) from liver of WT and Cpeb1 KO mice, some of which were injected with insulin. The pAkt (Ser473) and pAkt (Thr308) data were analyzed with ANOVA with \( p < 0.05, *; p < 0.01, ** \). Data are represented as mean +/- SEM. In this and all panels, at least 3 animals per group were used for the experiment. (B,C) Phospho-Akt (threonine 308) in CPEB KO fat and muscle, respectively. Analysis as in panel A. (D) Examination of insulin signaling molecules in WT and CPEB KO liver. Analysis as in panel A.

doi:10.1371/journal.pgen.1002457.g003
expression in the liver (Figure 2). Because inflammation can exacerbate insulin resistance, CPEB might control the expression of a number of molecules in several tissues to ensure that proper glucose levels are maintained.

To determine whether the insulin resistance can be magnified by metabolic insult, WT and Cpeb1 KO mice were fed a high fat diet (HFD) for 7 weeks, which elicited obesity in both groups of animals (whole body mass); there was also no difference in fat or lean mass between the genotypes (Figure 6B). To investigate organ-specific effects of CPEB deletion on insulin action, we performed a 2-hr hyperinsulinemic-euglycemic clamp in conscious WT and KO mice. The steady-state glucose infusion rate to maintain euglycemia during clamps was reduced by 50\% in the KO animals, although this was not statistically significant (p = 0.197). In addition, insulin-stimulated whole body glucose turnover, glycolysis, and glycogen plus lipid synthesis were unaffected in the Cpeb1 KO mice (Figure 6C). However, hepatic insulin action, expressed as insulin-mediated percent suppression of hepatic glucose production (HGP), was significantly compromised in the Cpeb1 KO mice (Figure 6C). The cause of this decrease in basal HGP is not clear, but because fasting levels of glucose and insulin are not affected by genotype, it may indicate, for example, aberrant gluconeogenesis. Finally, analysis of WT and KO liver following the euglycemic clamp demonstrates that although Akt was strongly phosphorylated in WT animals following insulin administration as expected, this was not the case with the Cpeb1 KO liver (Figure 6D). We also measured fasting glucose and insulin levels in WT and KO mice fed normal chow and a high fat diet (Figure S2B). As expected, glucose levels for both genotypes increased on a high fat diet. Relative to WT, insulin levels in the CPEB KO animals were elevated on normal chow, but did not change further on a high fat diet. These data demonstrate that Cpeb1 KO mice fed a HFD developed defects in insulin signaling and hepatic insulin resistance.

Discussion

Although the inflammatory response is known to be regulated by 3’UTR binding proteins that affect translation and stability [15], there is a paucity of information regarding such proteins in insulin resistance or diabetes. Our data indicate that CPEB integrates the expression of several mRNAs involved in insulin signaling. Coordinate posttranscriptional regulation of factors in a given signal transduction pathway, or coordinate regulation of multiple processing steps (e.g., splicing, export, localization, and translation) of a given RNA are two examples of a ribonome regulon [16,17]; see also [18]). Post-transcriptional regulons mediate the inflammatory

Figure 4. CPEB depletion in HepG2 cells results in aberrant insulin signaling. (A) HepG2 cells were infected with lentiviruses expressing a control shRNA or one directed against CPEB; extracted RNA was then assessed for CPEB RNA, and tubulin as a control. (B) HepG2 cells were co-infected with the lentiviruses noted above as well as a retrovirus expressed FLAG-CPEB; western blots were probed for the FLAG epitope and tubulin. (C) HepG2 cells infected with lentivirus expressing control or CPEB shRNA were treated with insulin and western blotted for phospho (S473 and T308) and total Akt. The pAkt (Ser473) and pAkt (Thr308) data were analyzed with ANOVA (p < 0.05, *). All experiments were performed 3 times. (D) HepG2 cells co-infected with the viruses noted above were western blotted for phospho (S473) and total Akt. The pAkt (Ser473) data was analyzed by ANOVA (p < 0.05). (E) HepG2 cells infected with virus expressing FLAG-CPEB or FLAG-CPEBΔZF, which lacks two zinc fingers and cannot bind RNA, followed by FLAG co-immunoprecipitation and analysis of Stat3, PTEN, PDK1, IRS1, IRS2, and Socs3 RNAs by quasi-quantitative RT-PCR. Input represents 10% of total. At least 3 animals per group were used for the experiment.

doi:10.1371/journal.pgen.1002457.g004
Figure 5. CPEB controls the synthesis of Stat3 and PTEN. (A and B) 3' UTR sequences of Stat3 and PTEN from human, mouse and cow. The nucleotides in bold represent putative CPEs. (C and D) Western blots of Stat3 and PTEN following CPEB depletion in HepG2 cells. In panels C-H, tubulin served as a negative or input control. (E and F) Quasi-quantitative RT-PCR for Stat3 and PTEN RNAs following CPEB depletion. (G and H)
HepG2 cells depleted of CPEB were pulse labeled with $^{35}$S-methionine for 15 min followed by Stat3, PTEN and tubulin (as a control) immunoprecipitation and SDS-PAGE analysis. These same proteins were also analyzed by western blots. (I) Representation of Renilla and firefly luciferase RNAs that were electroporated into HepG2 cells. Renilla luciferase RNA, which contained an irrelevant 3' UTR, served as a normalization control. Firefly luciferase contained the Stat3 or PTEN 3' UTRs as noted in panels A and B; in some cases, the CPEs in these 3' UTRs were mutated. (J and K) The firefly and Renilla RNAs noted above were electroporated into HepG2 cells, some of which were depleted of CPEB. Firefly luciferase was normalized to the Renilla luciferase transfection control; luciferase activity derived from all RNAs was then made relative to the control shRNA. The Stat3 and PTEN data were analyzed with ANOVA; p values were 0.009 and 0.005, respectively. The asterisk refers to statistical significance (p<0.05). Data are represented as mean +/- SEM. The firefly and Renilla luciferase RNAs were also analyzed for relative stability by quasi-quantitative RT-PCR; all the RNAs had similar stabilities. At least 3 animals were used for each experiment. 

Figure 6. Cpeb1 KO mice are insulin-resistant. (A) WT and KO mice were fed a normal chow diet and then examined for glucose tolerance test, serum insulin levels, and insulin tolerance. ANOVA values are as indicated in the figure. (B) Measurements for lean mass, fat mass, and total body mass of WT and Cpeb1 KO mice fed a high fat diet. (C) Animals fed a high fat diet were subjected to euglycemic clamp analysis that determined glucose infusion rate (GIR), glucose turnover, whole body glycolysis, glycogen synthesis, hepatic glucose production (HGP), and liver insulin action (the ratio of basal to clamped HGP). The HGP data were analyzed with ANOVA with a value of 0.006. The asterisks in this panel as well as panel D refer to statistical significance (p<0.05). (D) Following the euglycemic clamp, liver proteins from WT and KO animals were probed on western blots for total and phospho-Akt (S473 and T308). The pAkt (Ser473) and pAkt (Thr308) data were analyzed with ANOVA with suggestive values of 0.01999 and 0.08335 values respectively. Data are represented as mean +/- SEM. At least 3 animals per group were used for the Western blots and at least 6 animals per group were used to measure the physiological parameters.
While not all of these mRNAs are likely to be directly regulated by CPEB (indeed, two of them, IRS2 and Socs3, do not co-IP with CPEB), the preponderance of CPEs suggests that CPEB influences the expression of many of them.

Although CPEB was first described as an mRNA stimulatory factor by way of inducing poly(A) tail length [23,26], recent evidence shows that it can also repress translation [12]. Presumably, the factors with which CPEB associates in any given cell determines whether it will stimulate or repress translation. In the liver, at least for the messages we examined, CPEB seems to repress translation; when it is not present in KO mice, the synthesis of certain proteins such as PTEN and Stat3 are elevated. However, it should be borne in mind that translational repression is often reversible. It is possible that under some conditions, CPEB would be released from the RNA, which would elicit enhanced translation. Irrespective of how CPEB regulates translation, why would the insulin signaling cascade be controlled by this protein? We propose that CPEB acts as a rheostat to modulate the levels of insulin signaling proteins in response to particular environmental cues. For example, CPEB activity might be turned up or down in response to a high fat diet, and thereby modulate the degree of insulin sensitivity. If such is the case, then CPEB performance could play a central role in glucose homeostasis.

Materials and Methods

Animals

Male C57BL/6 Cpeb1 KO mice (12 weeks old) (Tay and Richter, 2001) were fed normal chow diet or a high fat diet (HFD; 55% fat by calories, Harlan Teklad) for 7 weeks. Mostly littermates were used for all experiments, in some cases mice with +/-1 week of birth date were used.

Ethics statement

The animals, which were housed in the UMass Medical School animal facility, were used according to guidelines approved the Institutional Animal Care and Use Committee and fully comply with all applicable Federal and State requirements.

Reagents and antibodies

Mouse CPEB (WT and ΔZF) was cloned into a FLAG containing vector (Nagaoka and Richter, submitted). PTEN and Stat3 3’ UTRs (nucleotides 1–90 and 1–195, respectively) were cloned into EcoRI-Xhol sites of pcDNA3.1+ vector containing firefly luciferase. In some cases, the CPEs were mutated to C or G in place of T. Renilla luciferase (pRL-TK; Promega) was used as a control vector in the luciferase experiments. Antibodies to PTEN (Cell Signaling), Akt1, and pAkt473 (Cell Signaling) were a generous gift from M. Sherman. Antibodies to Socs3 (Cell Signaling) and pAkt308 (Cell Signaling) were a generous gift from R. Davis. IRS2 and IR antibody was a generous gift from M. White. Antibodies to PDK1 (Genetex), IRS1 (Upstate), tubulin (Sigma), were purchased from the indicated commercial sources. Antibodies to Stat3, pStat3, GSK-3, pGSK-3, FOXO, pFOXO, pIRS-1 were obtained from Cell Signaling. See Protocol S1 for additional information.

Biochemical assays and cell culture

Mouse tissues (liver, fat- white adipose tissue only, muscle) and HepG2 cells were lysed in buffer (50 mM Tris-HCl (pH 7.4), 0.25 M NaCl, 1 mM MgCl2, 0.1 mM CaCl2, 1% NP-40, 0.5% deoxycholate, 0.1% SDS) with protease inhibitor (Complete, Roche) and phosphatase inhibitors (vanadate and fluoride, NEB). Western blots were performed with these samples using ECL (Perkin-Elmer), or Femto-ECL (Pierce) detection systems. RNP co-immunoprecipitation using Dynabeads (Invitrogen) was performed in the same buffer with RNAse inhibitor (RNAsOut, Invitrogen) and antibody against the FLAG epitope (Sigma). The RNA was extracted from the final precipitate (or from total RNA) with Trizol (Invitrogen) and subjected to quantitative RT-PCR (Quantitect RT kit, Qiagen).

Firefly luciferase RNAs appended with Stat3 or PTEN 3’ UTRs containing or lacking CPEs were synthesized in vitro with T7 RNA polymerase (mMessage Machine kit; Ambion). Control Renilla luciferase RNA containing an irrelevant 3’ UTR was polyadenylated with E. coli polya polymerase (NEB). Each of the firefly luciferase RNAs together with the Renilla luciferase RNA was used to transfect with lipofectamine 2000 or nucleofec (with Amaxa nucleofector) HepG2 human hepatocarcinoma cells (ATCC #CRL-10741) that were grown to 50% confluency. Some of these cells were also infected with lentivirus harboring control or CPEB shRNA as described by Udagawa et al. (submitted). Infectivity was monitored by GFP, which was encoded by the virus. After infection, fresh DMEM with 10% FBS was added. Luciferase activity was determined 12 hr after cell transduction with a Dual-Luciferase Reporter Assay System (Promega) and normalized to the Renilla control. Luminescence was detected with a SAFIRE multimode microplate reader (Tecan).

Glucose and insulin tolerance tests and plasma serum analysis

Glucose tolerance (GTT) and insulin tolerance tests (ITT) were performed using methods described previously [27]. Serum insulin concentrations during the GTT were determined using an insulin ELISA (Crystal Chem). Blood glucose was measured using an Ascensia Breeze 2 glucometer (Bayer). Statistical analysis was done with GraphPad Prism (version 5.0).
performed by ANOVA. Serum adiponectines, cytokines, and insulin were measured by ELISA using a Luminex 200 luminometer (Millipore).

Hyperinsulinemic-euglycemic clamp
Hyperinsulinemic-euglycemic clamps were performed at the UMass Mouse Phenotyping Center. Mice were fed normal chow or a HFD for 7 weeks. Whole body fat and lean mass were non-invasively measured using proton magnetic resonance spectroscopy (1H-MRS) (Echo Medical Systems). Following an overnight fast, a 2 h body hyperinsulinemic-euglycemic clamp was performed with a primed and continuous infusion of human insulin (150 mU/kg body; 2.5 mU/kg/min), Humulin; Eli Lilly, and 20% glucose was infused to maintain euglycemia (Kim et al., 2004). Whole body glucose turnover and glucose uptake in 20% glucose was infused to maintain euglycemia (Kim et al., 2004).

Bioinformatics Resources 6.7, Panther pathway annotation with biologic triplicates. The data were analyzed with DAVID Medical School Genomics Core facility with Affymetrix GeneChip fractions, pooled, and subjected to microarray analysis by UMass RPM in a SW41 rotor. The RNA was isolated from polysomal fractions of CPEB in WT and KO liver. (B) Western blots of insulin signaling molecules, and tubulin as a control, in muscle and fat derived from untreated and insulin treated WT and CPEB KO mice. (C) HepG2 cells infected with virus expressing FLAG-CPEB or FLAG-CPEBZF, which lacks two zinc fingers and cannot bind RNA, followed by FLAG communoprecipitation and Western blot analysis with anti-FLAG antibody. Input represents 10% of total. (D) Sedimentation profiles on polyosm sucrose gradients of Stat3, PTEN, IRS1, and PKD1 mRNAs from WT and CPEBKO liver. The 80S monosome is indicated. RNAs were quantified by quasi-quantitative RT-PCR. Each experiment was performed with 3 different animals of each genotype. (TIF)

Figure S2 CPEB control of IL6 and insulin levels. (A) IL6 levels in serum from WT and CPEB KO mice on a normal and high fat diet. The asterisk refers to statistical significance (p<0.05, Student’s t test). (B) Glucose and insulin levels in WT and CPEB KO mice when fed normal chow (left panels) or a high fat diet (right panels). The asterisk refers to statistical significance (p<0.05, Student’s t test). (TIF)

Protocol S1 Primers for sequences used in this study. (DOCX)

Table S1 Identification of sequences from polysomal fractions of WT and CPEB KO MEFs based on microarray analysis. Extracts from mouse embryo fibroblasts (MEFs) were centrifuged through sucrose gradients and the RNA from fractions containing polysomes was extracted and analyzed by microarrays on an Affymetrix platform. (DOC)

Acknowledgments
We thank Tatsushi Udagawa, Ivan Alexandrov, Michael Sherman, Mariano Sadagurski, Moris Nechama, Shashi Kaushal, Vladimir Gabai, Anatoli Merin, Julia Yaqoglu, and Natalia Naumova for reagents and/or advice; Mike Czech for reading the manuscript; and Elena Philippova, Meghna Jane, and Nemisha Dawra for technical help.

Author Contributions
Conceived and designed the experiments: IMA MI DYJ RF HJK BO-M RB. Analyzed the data: IMA MI RF FU JKK JDR. Performed the experiments: IMA MI DYJ RF HJK BO-M RB. Acknowledgments

Supporting Information
Figure S1 CPEB mediates liver insulin signaling. (A) Western blot of CPEB in WT and KO liver. (B) Western blots of insulin signaling molecules, and tubulin as a control, in muscle and fat derived from untreated and insulin treated WT and CPEB KO mice. (C) HepG2 cells infected with virus expressing FLAG-CPEB or FLAG-CPEBZF, which lacks two zinc fingers and cannot bind RNA, followed by FLAG communoprecipitation and Western blot analysis with anti-FLAG antibody. Input represents 10% of total. (D) Sedimentation profiles on polyosm sucrose gradients of Stat3, PTEN, IRS1, and PKD1 mRNAs from WT and CPEBKO liver. The 80S monosome is indicated. RNAs were quantified by quasi-quantitative RT-PCR. Each experiment was performed with 3 different animals of each genotype. (TIF)

Figure S2 CPEB control of IL6 and insulin levels. (A) IL6 levels in serum from WT and CPEB KO mice on a normal and high fat diet. The asterisk refers to statistical significance (p<0.05, Student’s t test). (B) Glucose and insulin levels in WT and CPEB KO mice when fed normal chow (left panels) or a high fat diet (right panels). The asterisk refers to statistical significance (p<0.05, Student’s t test). (TIF)

Protocol S1 Primers for sequences used in this study. (DOCX)

Table S1 Identification of sequences from polysomal fractions of WT and CPEB KO MEFs based on microarray analysis. Extracts from mouse embryo fibroblasts (MEFs) were centrifuged through sucrose gradients and the RNA from fractions containing polysomes was extracted and analyzed by microarrays on an Affymetrix platform. (DOC)

Acknowledgments
We thank Tatsushi Udagawa, Ivan Alexandrov, Michael Sherman, Mariano Sadagurski, Moris Nechama, Shashi Kaushal, Vladimir Gabai, Anatoli Merin, Julia Yaqoglu, and Natalia Naumova for reagents and/or advice; Mike Czech for reading the manuscript; and Elena Philippova, Meghna Jane, and Nemisha Dawra for technical help.

Author Contributions
Conceived and designed the experiments: IMA MI FY JKK JDR. Performed the experiments: IMA MI FYJ RF HJK BO-M RB. Analyzed the data: IMA MI RF FU JKK JDR. Contributed reagents/materials/analysis tools: MX. Wrote the paper: IMA MI JDR.

References
1. White MF, Kahn CR (1994) The insulin signaling system. J Biol Chem 269: 1–4.
2. Kahn SE, Hull RL, Utschneider KM (2006) Mechanisms linking obesity to insulin resistance and type 2 diabetes. Nature 444: 840–846.
3. Ueki K, Kondo T, Kahn CR (2004) Suppressor of cytokine signaling 1 (SOCS-1) and SOCS-3 cause insulin resistance through inhibition of tyrosine phosphorylation of insulin receptor substrate proteins by discrete mechanisms. Mol Cell Biol 24: 5434–5446.
4. Kim JH, Kim JE, Liu HY, Cao W, Chen J (2008) Regulation of interleukin-6-induced hepatic insulin resistance by mammalian target of rapamycin through translational control of cell division. Cell 103: 435–447.
5. Alarcon JM, Rodgrign M, Theis M, Huang YS, Kandel ER, et al. (2004) Selective modulation of some forms of schaffer collateral-CA1 synaptic plasticity in mice with a disruption of the CPEB-1 gene. Learn Mem 11: 318–327.
6. Wu L, Wells D, Tay J, Mendis D, Abbott MA, et al. (1998) CPEB-mediated cytoplasmic polyadenylation and the regulation of experience-dependent translation of alpha-CaMKII mRNA at synapses. Neuron 21: 1129–1139.
7. Groisman I, Huang YS, Mendez R, Cao Q, Theurkauf W, et al. (2000) CPEB, maspin, and cyclin B1 mRNA at the mitotic apparatus: implications for local translational control of cell division. Cell 103: 415–427.
8. Groisman I, Ishihara M, Marin V, Kennedy NJ, Davis RJ, et al. (2006) Control of cellular senescence by CPEB. Genes Dev 20: 2701–2712.
9. Burns DM, Richter JD (2008) CPEB regulation of human cellular senescence, energy metabolism, and p53 mRNA translation. Genes Dev 22: 3449–3460.
10. Feve B, Bastard JP (2009) The role of interleukins in insulin resistance and type 2 diabetes mellitus. Nat Rev Endocrinol 5: 305–311.
11. Alarcon JM, Hodgman R, Theis M, Huang YS, Kandel ER, et al. (2004) Selective modulation of some forms of schaffer collateral-CA1 synaptic plasticity in mice with a disruption of the CPEB-1 gene. Learn Mem 11: 318–327.
17. Morris AR, Mukherjee N, Keene JD. Systematic analysis of posttranscriptional gene expression. Wiley Interdiscip Rev Syst Biol Med 2: 162–180.

18. Maniatis T, Reed R (2002) An extensive network of coupling among gene expression machines. Nature 416: 499–506.

19. Licatalosi DD, Darnell RB. RNA processing and its regulation: global insights into biological networks. Nat Rev Genet 11: 75–87.

20. Licatalosi DD, Mele A, Fak JJ, Ule J, Kayikci M, et al. (2008) HITS-CLIP yields genome-wide insights into brain alternative RNA processing. Nature 456: 464–469.

21. Boettger T, Beetz N, Kostin S, Schneider J, Kruger M, et al. (2009) Acquisition of the contractile phenotype by murine arterial smooth muscle cells depends on the Mir143/145 gene cluster. J Clin Invest 119: 2634–2647.

22. Liu N, Olson EN. MicroRNA regulatory networks in cardiovascular development. Dev Cell 18: 510–525.

23. Wang S, Aurora AB, Johnson BA, Qi X, McAnally J, et al. (2008) The endothelial-specific microRNA miR-126 governs vascular integrity and angiogenesis. Dev Cell 15: 261–271.

24. Herranz H, Cohen SM. MicroRNAs and gene regulatory networks: managing the impact of noise in biological systems. Genes Dev 24: 1339–1344.

25. Paris J, Swenson K, Pwnica-Worms H, Richter JD (1993) Maturation-specific polyadenylation: in vitro activation by p53/cdk2 and phosphorylation of a 58-kD CPE-binding protein. Genes Dev 5: 1697–1708.

26. Hake LE, Richter JD (1994) CPEB is a specificity factor that mediates cytoplasmic polyadenylation during Xenopus oocyte maturation. Cell 79: 617–627.

27. Mori A, Sakamoto K, McManus EJ, Alessi DR (2005) Role of the PDK1-PKB-GSK3 pathway in regulating glycogen synthase and glucose uptake in the heart. FEBS Lett 579: 3632–3638.

28. Kim HJ, Higashimori T, Park SY, Choi H, Dong J, et al. (2004) Differential effects of interleukin-6 and -10 on skeletal muscle and liver insulin action in vivo. Diabetes 53: 1060–1067.

29. Huang da W, Sherman BT, Lempicki RA (2009) Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. Nucleic Acids Res 37: 1–13.

30. Nottrott S, Simard MJ, Richter JD (2006) Human let-7a miRNA blocks protein production on actively translating polyribosomes. Nat Struct Mol Biol 13: 1108–1114.

31. Burns D, D’Ambrosio A, Nottrott S, Richter JD (2011) CPEB and two poly(A) polymerases control miR-122 stability and p53 mRNA translation. Nature 473: 105–108.

32. Huang da W, Sherman BT, Lempicki RA (2009) Systematic and integrative analysis of large gene lists using DAVID Bioinformatics Resources. Nature Protoc 4: 44–57.