**Supporting online material**

**Materials and Methods**

**Generation of mice lacking XBP1 in the liver (Xbp1Δ).** $Xbp1^{flox}$ mice harboring loxP sites in the first and second intron of the Xbp1 gene (*S1*) were crossed with Mx1-cre mice (*S2*) that express interferon-dependent cre recombinase. 5-6 weeks old mice were intraperitoneally injected 1 or 3 times with 250 μg of poly(I:C) each time with 2 days intervals to induce the cre expression. Mice were used for experiments at least 2-3 weeks after the final poly(I:C) injection. Cre-mediated recombination removes exon 2 of Xbp1 gene to induce alternative splicing between exon 1 and 3 of XBP1 mRNA, resulting in a reading frame shift and introduction of a translational termination codon. Intraperitoneal poly(I:C) injection efficiently deleted the floxed exon 2 in liver as determined by Southern blot (Fig. S1a). The XBP1Δ mRNA was slightly smaller than the WT mRNA due to the lack of exon 2, as confirmed by Northern blot, RT-PCR and DNA sequencing analysis of the mutant transcript (Fig. S1b). Lack of XBP1 protein in Xbp1Δ liver was confirmed by Western blot (Fig. S1c). Mice backcrossed for more than five generations onto C57BL/6 background were used in most experiments, except for those in Table S1, Figure 2a and 2b, where mice on a SV129 and C57BL/6 mixed background were used. Sex-matched $Xbp1^{f/f}$ littermates injected with poly(I:C) were used as WT controls throughout the study.

**Tunicamycin injection.** Tunicamycin diluted in 150 mM dextrose at 100 μg/ml was intraperitoneally injected at 1g/Kg body weight.

**Diet studies.** Mice were housed in a specific pathogen free facility at the Harvard School of Public Health on a 12h light/dark cycle and had free access to standard rodent chow diet or 60% fructose diet (Harlan Teklad TD.8820).

**Northern blot and real time PCR analysis.** Total RNA isolation, Northern blot and real time PCR analysis were performed as described previously (***S3, S4***). Primers for the real time PCR analysis are described in supplementary table 2 or elsewhere (*S4*). Probes for Northern blot were generated with PCR amplified cDNA pieces for each gene by using primers shown in supplementary table 3. IRE1 splicing of XBP-1 mRNA was measured by RT-PCR analysis as described previously (*S5*).

**Nuclear extracts and Western blot**. Nuclear extracts from the liver were prepared as described with modifications (*S6*). Briefly, pieces of the liver (~0.5 g) were homogenized in 3 ml homogenization buffer (10 mM Hepes, pH 7.9, 10 mM KCl, 0.1 mM EDTA, 0.74 mM Spermidine, 1 mM DTT, 0.3 M sucrose, protease inhibitor mix (Roche)) with Polytron, mixed with 6 ml of the cushion buffer (10 mM Hepes, pH 7.9, 0.1 mM EDTA, 0.74 mM Spermidine, 1 mM DTT, 2.2 M sucrose, 2 μg/ml aprotinin, 2 μg/ml leupeptin) and then overlayed on 2 ml cushion buffer. Nuclei were precipitated by 60 min centrifugation at 77,000g, and lysed in RIPA buffer (50 mM Tris pH 7.4, 150 mM NaCl, 1 mM EDTA, 1% Triton X-100, 1% sodium deoxycholate, 0.1% SDS). Lysates were briefly sonicated and cleared by centrifugation for 5 min. Nuclear extracts from cultured hepatocytes were prepared as described previously (*S7*). Western blot analyses on nuclear extracts were performed with rabbit polyclonal anti-XBP-1, ATF6α (gift of Dr. K. Mori),

Sp1 (Santa cruz), SREBP-1 and SREBP-2 antibodies (gift of Dr. J. Goldstein). IRE1α proteins in the liver were detected by Western blot with rabbit polyclonal anti-IRE1α antibody (gift of the Mannkind Corp.) following immunoprecipitation with the same antibody from 500 μg of the liver lysates prepared in a lysis buffer (1% NP-40, 30 mM Tris, pH 7.5, 150 mM NaCl, 50 mM sodium fluoride, 10 mM sodium orthophosphate, 1 μg/ml aprotinin, 2 μg/ml leupeptin). In some experiments, immunoprecipitation products were resuspended in a buffer for λ phosphatase (NEB) treatment for 30 min before Western blot analysis. Whole liver lysates prepared in 1% NP-40 lysis buffer were used for the western blot of total JNK with specific antibody (Cell signaling). JNK kinase activity in liver lysates was measured using the SAPK/JNK kinase assay kit (Cell Signaling). ApoB-100 protein species in plasma were detected by using monoclonal ApoB-100 antibody (*S8*).

**Histology and TEM.** Pieces of the liver fixed in 10% neutral buffered formalin were embedded in paraffin and stained with hematoxylin and eosin. Frozen sections were stained with oil Red O. TEM was performed as described previously (*S4*).

**Blood chemistries and lipid analysis.** Plasma triglyceride and cholesterol levels in the fed state were measured by using commercial kits (Sigma, TR0100; Roche Diagnostics; Molecular probes, A12216). Blood glucose concentrations were measured by using ACCU-Check glucometer (Roche). Serum ALT and albumin levels were measured by using commercial reagents (Bioquant). For VLDL secretion assays, mice were fasted for 4 hrs, and retro-orbitally injected with 0.5 mg/Kg Tyloxapol (Sigma). Tail bleedings were performed at indicated time points for plasma triglyceride measurements. The distribution of cholesterol in plasma was determined by fast performance liquid chromatography (FPLC) separation followed by TG and cholesterol assays of each fraction as described previously (*S9*). Lipid composition in the liver was determined by TrueMass Lipomics analysis (Lipomics) after pooling liver pieces from 4 mice/group.

**Mouse primary hepatocytes and pulse-chase experiments.** Mouse primary hepatocytes were isolated by perfusion followed by collagenase digestion by using commercial reagents (Invitrogen). Cells were resuspended in M199 media supplemented with 5% fetal bovine serum, plated at a density of $1.2x10^6$ cells per 60 mm positively-charged Primaria® dish (Becton Dickinson) and allowed to attach for 6~7 hrs. Cells were washed and cultured for 30 min in methionine and cysteine-free DMEM supplemented with 10% dialysed fetal bovine serum, and then labeled with the same media containing 100 μCi/ml $^{35}$S-methionine/cysteine for 30 min. Media was changed with M199 containing both methionine and cysteine and 5% fetal bovine serum. Media and cells were harvested at the indicated times for immunoprecipitation. Cells were lysed in a buffer containing 1% NP-40, 30 mM Tris, pH 7.5, 150 mM NaCl. ApoB protein species were immunoprecipitated with goat anti-ApoB antibody (Chemicon), washed three times with lysis buffer, and run on 5% SDS-PAGE gels. Gels were treated with Amplify® (Amersham), dried and exposed to a phosphorimager screen.

**Lipid synthesis.** The rates of fatty acids and sterol synthesis were measured as described previously (*S10*). Primary hepatocytes plated in 60 mm dishes were cultured in the presence of 1.5 μl of [1-$^{14}$C]acetate (57.5 mCi/mmol, Sigma) for 17 h. Cells were washed

twice with PBS, resuspended in 1 ml PBS and mixed with 2.5 ml of 7% potassium hydroxide in 70% methanol. After incubation for 3h at 95 ºC, sterols were extracted three times with 3.5 ml petroleum ether. The remaining aqueous phase was mixed with 0.47 ml of sulfuric acid and extracted three times with 3.5 ml petroleum ether for fatty acids. The organic phase was dried under low heat, and measured for [$^{14}$C] level using a liquid scintillation counter.

**Recombinant adenoviruses.** XBP-1s cDNA was cloned into pAdTRACK-cmv shuttle vector (*S11*). Recombinant adenoviral DNA was generated by homologous recombination by transforming BJ5183-AD1 competent cells (Stratagene) with the shuttle vector. Adenoviral DNAs were linearized using PacI and then transfected into HEK-293 cells with Lipofectamine 2000 reagents (Invitrogen) to produce recombinant viruses. Infected cells were lysed by three cycles of freezing and thawing and then centrifuged. Viral titer was determined by infecting HEK-293 cells with serially diluted viral stock and counting GFP positive cells 24 hrs after infection. Primary hepatocytes were infected with recombinant adenoviruses at 2 or 10 pfu per cell. Total RNAs were prepared from virus-infected hepatocytes 24 hrs later by using Trizol reagent (Invitrogen).

**Chromatin immunoprecipitation (CHIP) assay.** Nuclei were isolated from ~0.5g of liver tissue by centrifugation on 2.2 M sucrose cushion as described above. CHIP assays were performed as described previously (*S12*) with some modifications. Briefly, purified nuclei were resuspended in 1 ml PBS containing 1.4% formaldehyde and incubated at room temperature for 15 min to cross-link protein to DNA. Cross-linked nuclei were washed twice with PBS and once with IP buffer (1% NP-40, 30 mM Tris, pH 7.5, 150 mM NaCl, 1 μg/ml aprotinin, 2 μg/ml leupeptin). Lysates were sonicated and immunoprecipitated with rabbit polyclonal anti-XBP-1 antibody or control rabbit serum. Immune complexes were precipitated by using protein A-agarose (Roche) and washed 5 times with IP buffer. Immunoprecipitated genomic DNA was eluted by boiling for 10 min in 10% Chlex 100 beads (Bio-Rad) and then used for real time PCR with primers designed to amplify proximal promoter regions (Supplementary Table 4). Acc2 promoter II was predicted by aligning the mouse genomic DNA sequences with the reported human Acc2 promoter sequences (*S13*).

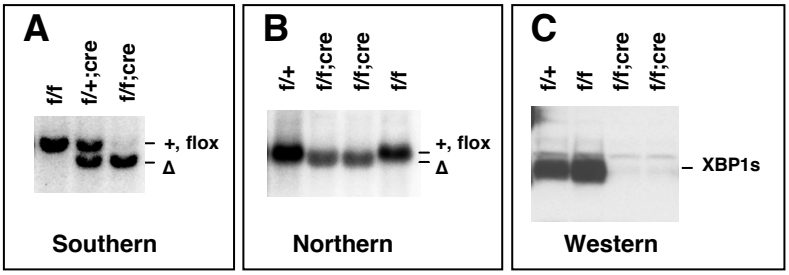


**Fig. S1. Characterization of Xbp1Δ mice.** (A) Southern blot analysis of the genomic DNA from liver. Xbp1$^{f/f}$, Xbp1$^{f/+}$;Mx1-cre and Xbp1$^{f/f}$;Mx1-cre mice were injected three times with poly(I:C) and genomic DNA was prepared two weeks later. Bands representing the floxed, WT (+), and deleted allele of the Xbp1 gene by cre-mediated recombination are indicated. (B) Northern blot analysis of the RNA from mice with indicated genotypes. Total liver RNAs were prepared two weeks after poly(I:C) injections. The mutant XBP-1 mRNA from the Xbp1Δ allele is smaller than the WT due to the lack of the floxed exon 2 sequences (97 nt). (C) Liver nuclear extracts were prepared from poly(I:C) injected mice as in (B) and subjected to a western blot analysis with anti-XBP1 antibody.

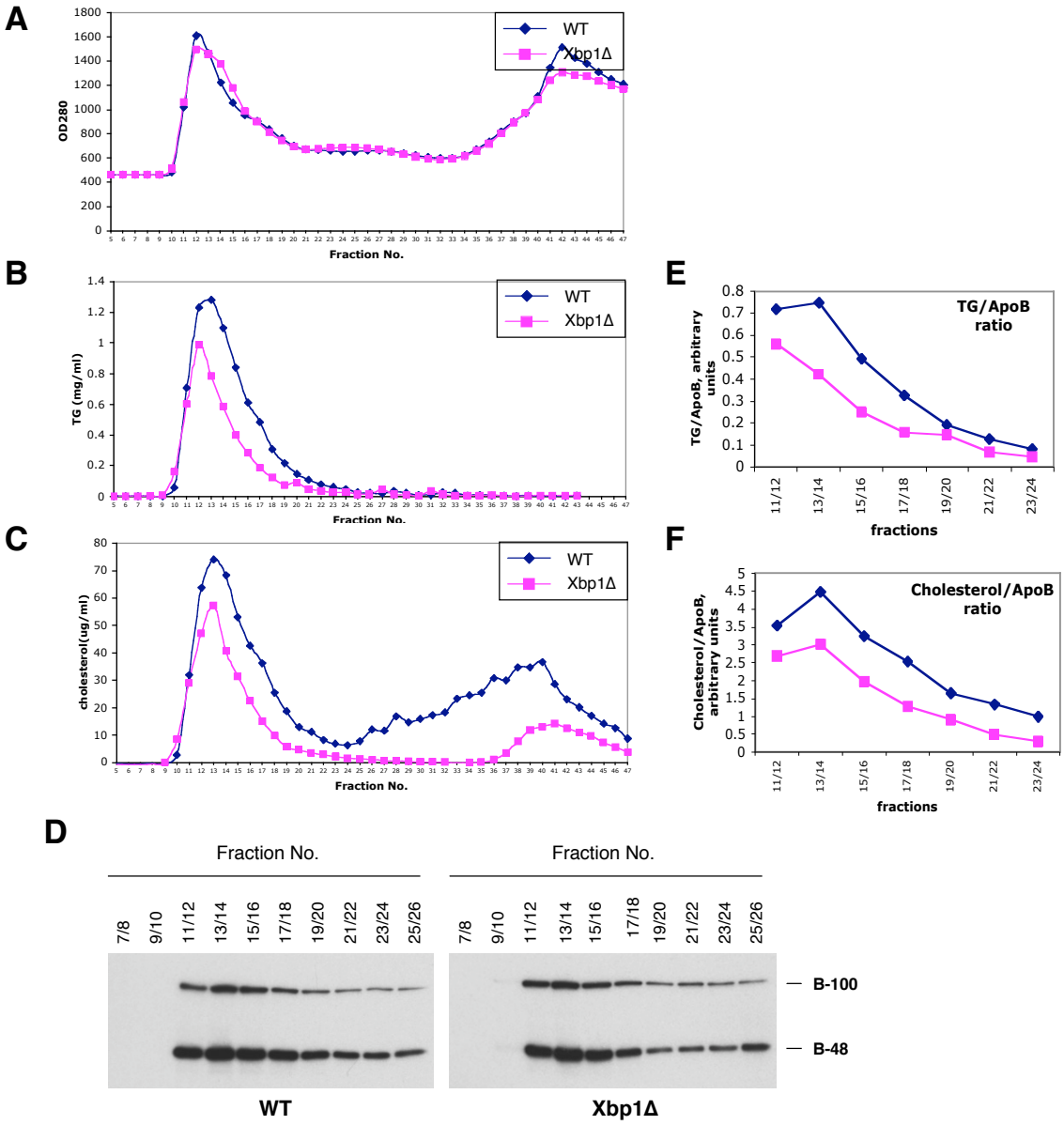


**Fig. S2. FPLC analysis of lipoprotein particles.** Mice were fasted overnight and injected with Tyloxapol 3h prior to sacrifice to enrich plasma VLDL. Plasma pooled from two mice was fractionated by FPLC. Concentrations of total protein (A), TG (B) and cholesterol (C) in each fraction were determined. (D) Levels of apoB protein species were measured by western blot after combining neighboring two fractions as indicated. Concentrations of TG (E) and cholesterol (F) in each pooled fraction were plotted against total apoB content.

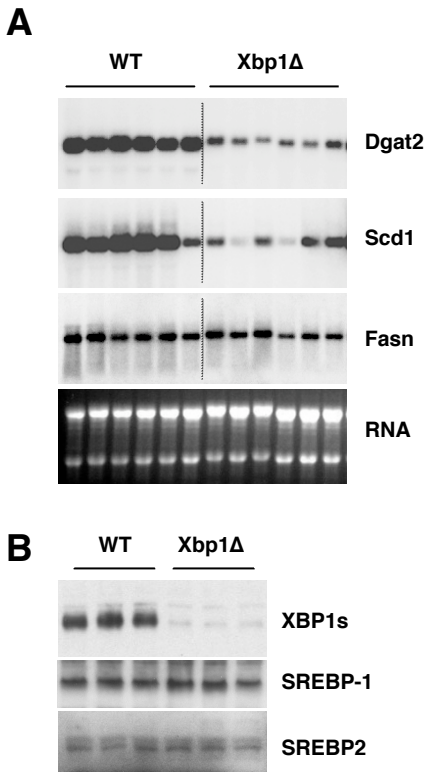


**Fig. S3. Expression of lipogenic genes and SREBP1 in the XBP1 deficient liver.** Total RNAs were prepared from livers of mice fed a standard rodent chow diet. (A) Northern blot analysis was performed to measure the expression of Dgat2, Scd1 and Fasn genes. Ethidium bromide staining of the gel is shown as a loading control. (B) Liver nuclear extracts were subjected to western blot analysis with anti-XBP1 and anti-SREBP-1 antibodies.

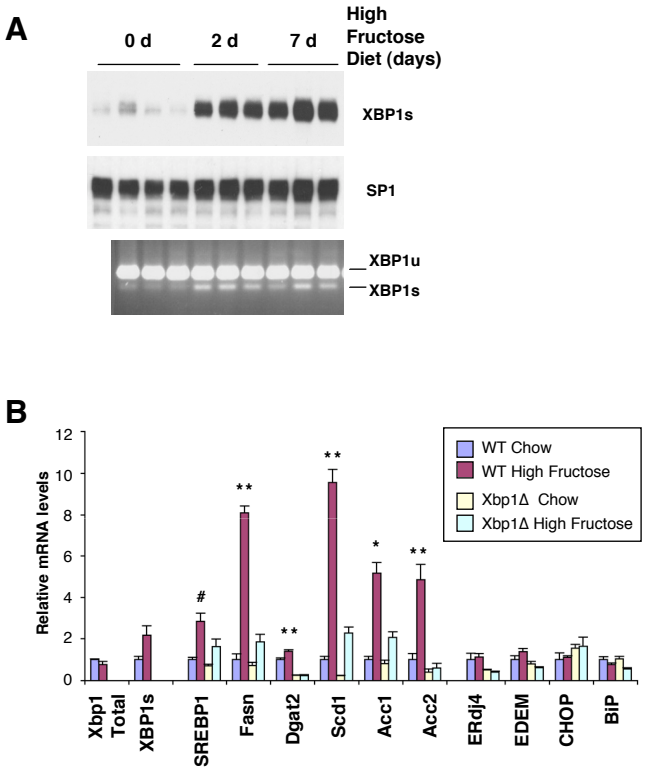


**Figure S4. XBP1 activated by high fructose diet feeding, directly induces lipogenic genes in the liver.** (A) XBP1s protein in the liver of mice fed high fructose diet was measured by Western blot. IRE1 splicing of XBP1 mRNA was measured by RT-PCR. (B) Expression of lipogenic genes was measured in the liver of mice fed standard chow or high fructose diet for 7 days. Values represent the abundance of each mRNA relative to WT mice fed chow diet. N=3-6. T tests were performed between high fructose diet-fed WT and Xbp1Δ mice #, p=0.05.

Table S1. Changes in physiologic parameters by poly(I:C) treatment in WT and Xbp1Δ mice

| | Before poly(I:C) | | After poly(I:C) | |
|---|---|---|---|---|
| | Xbp1ff | Xbp1ff;Mxcre | Xbp1ff | Xbp1ff;Mxcre |
| Body weight (g) | ND | ND | 42.0±1.1 | 39.7±0.8 |
| Liver weight (g) | ND | ND | 2.07±0.14 | 1.97±0.11 |
| Liver/body | ND | ND | 0.051±0.002 | 0.050±0.002 |
| Serum ALT (IU/L) | ND | ND | 53±6 | 57±5 |
| Plasma insulin, fed (ng/ml) | ND | ND | 1.1±0.06 | 1.0±0.18 |
| Blood glucose, fed (mg/dl) | ND | ND | 124±4 | 128±4 |
| Serum protein (mg/ml) | 39.8±0.6 | 39.5±0.7 | 40.7±1.3 | 34.5±0.5[a] |
| Serum albumin (mg/ml) | 28.5±0.4 | 28.6±0.3 | 29.4±0.7 | 23.6±0.4[b] |

Male mice (5~6 weeks old, n=6~12) were injected with poly(I:C) three times, and fed a chow diet ad libitum. Experiments were performed three weeks after the last injection of poly(I:C). Values represent mean ± SEM. Statistical significances of differences between WT and Xbp1Δ were determined by student T tests. a, p=0.0003; b, p=0.00001.

**Table S2.** Expression of UPR related genes in XBP1 deficient liver. Total RNAs from the WT and Xbp1Δ liver were subjected to microarray analyses by using Affymetrx mouse 430A Chip. Data were analyzed by GCOS1.4 software (Affymetrix).

| Probe Set ID | WT | | Xbp1Δ | | Fold change KO/WT | Differece Call | Gene Symbol | Gene Title |
|---|---|---|---|---|---|---|---|---|
| | Signal | Detection | Signal | Detection | | | | |
| 1417191 | 1460 | P | 823 | P | 0.5 | D | Dnajb9 | DnaJ (Hsp40) homolog, subfamily B, member 9 |
| 1419162 | 691 | P | 409 | P | 0.6 | D | Dnajc3 | DnaJ (Hsp40) homolog, subfamily C, member 3 |
| 1419163 | 591 | P | 535 | P | 0.7 | D | Dnajc3 | DnaJ (Hsp40) homolog, subfamily C, member 3 |
| 1433887 | 1617 | P | 1159 | P | 0.7 | D | Dnajc3 | DnaJ (Hsp40) homolog, subfamily C, member 3 |
| 1449372 | 1075 | P | 666 | P | 0.6 | D | Dnajc3 | DnaJ (Hsp40) homolog, subfamily C, member 3 |
| 1449373 | 303 | P | 157 | P | 0.5 | D | Dnajc3 | DnaJ (Hsp40) homolog, subfamily C, member 3 |
| 1416064 | 5019 | P | 4514 | P | 0.8 | D | Hspa5 | heat shock 70kD protein 5 (glucose-regulated protein) |
| 1427464 | 3969 | P | 2659 | P | 0.6 | D | Hspa5 | heat shock 70kD protein 5 (glucose-regulated protein) |
| 1417516 | 144 | A | 154 | M | 1.1 | NC | Ddit3 | DNA-damage inducible transcript 3 |
| 1438992 | 600 | P | 398 | P | 0.8 | D | Atf4 | activating transcription factor 4 |
| 1439258 | 9 | A | 7 | A | 1.4 | NC | Atf4 | activating transcription factor 4 |
| 1448135 | 1044 | P | 705 | P | 0.8 | D | Atf4 | activating transcription factor 4 |
| 1435444 | 267 | P | 277 | P | 0.9 | NC | Atf6 | activating transcription factor 6 |
| 1424065 | 995 | P | 1034 | P | 0.8 | D | Edem1 | ER degradation enhancer, mannosidase alpha-like 1 |
| 1451218 | 856 | P | 703 | P | 0.8 | D | Edem1 | ER degradation enhancer, mannosidase alpha-like 1 |
| 1423423 | 2938 | P | 3015 | P | 1.1 | NC | Pdia3 | protein disulfide isomerase associated 3 |
| 1416497 | 579 | P | 286 | P | 1.5 | I | Pdia4 | protein disulfide isomerase associated 4 |
| 1424650 | 1694 | P | 1571 | P | 1.0 | NC | Pdia5 | protein disulfide isomerase associated 5 |
| 1423648 | 1462 | P | 1942 | P | 0.7 | D | Pdia6 | protein disulfide isomerase associated 6 |
| 1437465 | 3727 | P | 4989 | P | 0.7 | D | P4hb | prolyl 4-hydroxylase, beta polypeptide |
| 1448411 | 95 | P | 142 | P | 1.1 | NC | Wfs1 | Wolfram syndrome 1 homolog (human) |
| 1415827 | 1955 | P | 1368 | P | 0.8 | D | D3Ucla1 | DNA segment, Chr 3, University of California at Los Angeles 1 |
| 1415828 | 1694 | P | 1316 | P | 0.7 | D | D3Ucla1 | DNA segment, Chr 3, University of California at Los Angeles 1 |
| 1423648 | 1942 | P | 1462 | P | 0.7 | D | Pdia6 | protein disulfide isomerase associated 6 |
| 1423151 | 462 | P | 352 | P | 0.8 | D | Dnajb11 | DnaJ (Hsp40) homolog, subfamily B, member 11 |
| 1435626 | 4291 | P | 4512 | P | 1.1 | NC | Herpud1 | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-l |
| 1448185 | 5550 | P | 4911 | P | 0.9 | NC | Herpud1 | homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-l |
| 1449519 | 21 | A | 10 | A | 0.3 | NC | Gadd45a | growth arrest and DNA-damage-inducible 45 alpha |
| 1428529 | 254 | P | 178 | P | 0.8 | NC | 2810026 | RIKEN cDNA 2810026P18 gene |
| 1428112 | 1938 | P | 933 | P | 0.5 | D | Armet | arginine-rich, mutated in early stage tumors |
| 1419029 | 146 | P | 139 | P | 1.0 | NC | Ero1l | ERO1-like (S. cerevisiae) |
| 1419030 | 183 | P | 233 | P | 1.4 | NC | Ero1l | ERO1-like (S. cerevisiae) |
| 1415889 | 4739 | P | 3855 | P | 0.9 | NC | Tra1 | tumor rejection antigen gp96 |
| 1438040 | 2794 | P | 2270 | P | 0.9 | NC | Tra1 | tumor rejection antigen gp96 |
| 1417354 | 571 | P | 337 | P | 0.7 | D | Sil1 | endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae) |
| 1421240 | 41 | A | 55 | A | 1.2 | NC | Ern1 | endoplasmic reticulum (ER) to nucleus signalling 1 |
| 1423246 | 113 | P | 73 | P | 0.7 | NC | Txndc4 | thioredoxin domain containing 4 (endoplasmic reticulum) |
| 1423247 | 1022 | P | 488 | P | 0.5 | D | Txndc4 | thioredoxin domain containing 4 (endoplasmic reticulum) |
| 1415738 | 863 | P | 726 | P | 1.2 | NC | Txndc12 | thioredoxin domain containing 12 (endoplasmic reticulum) |
| 1424674 | 71 | P | 102 | P | 1.3 | NC | Slc39a6 | solute carrier family 39 (metal ion transporter), member 6 |
| 1424675 | 29 | A | 48 | A | 1.2 | NC | Slc39a6 | solute carrier family 39 (metal ion transporter), member 6 |
| 1431886 | 2 | A | 4 | A | 1.3 | NC | Ern1 | endoplasmic reticulum (ER) to nucleus signalling 1 |
| 1450176 | 23 | P | 76 | P | 1.6 | NC | Ern1 | endoplasmic reticulum (ER) to nucleus signalling 1 |
| 1450139 | 4 | A | 5 | A | 2.1 | NC | Ern2 | endoplasmic reticulum (ER) to nucleus signalling 2 |
| 1451896 | 147 | P | 142 | P | 1.2 | NC | Cherp | calcium homeostasis endoplasmic reticulum protein |
| 1453634 | 323 | P | 357 | P | 0.9 | NC | Erp29 | endoplasmic reticulum protein 29 |
| 1418932 | 291 | P | 253 | P | 0.9 | NC | Nfil3 | nuclear factor, interleukin 3, regulated |
| 1416059 | 671 | P | 585 | P | 0.9 | NC | Sec23b | SEC23B (S. cerevisiae) |
| 1416189 | 1634 | P | 1028 | P | 0.6 | D | Sec61a1 | Sec61 alpha 1 subunit (S. cerevisiae) |
| 1416190 | 310 | P | 212 | P | 0.8 | D | Sec61a1 | Sec61 alpha 1 subunit (S. cerevisiae) |
| 1416191 | 469 | P | 372 | P | 0.8 | D | Sec61a1 | Sec61 alpha 1 subunit (S. cerevisiae) |
| 1417083 | 1724 | P | 1134 | P | 0.7 | D | Sec61b | Sec61 beta subunit |
| 1423090 | 1584 | P | 653 | P | 0.5 | D | Sec61g | SEC61, gamma subunit |
| 1419819 | 612 | P | 549 | P | 0.8 | D | Sec63 | SEC63-like (S. cerevisiae) |
| 1424924 | 638 | P | 463 | P | 0.8 | D | Sec63 | SEC63-like (S. cerevisiae) |
| 1424925 | 293 | P | 229 | P | 0.7 | D | Sec63 | SEC63-like (S. cerevisiae) |
| 1424926 | 303 | P | 212 | P | 0.9 | NC | Sec63 | SEC63-like (S. cerevisiae) |
| 1415692 | 2926 | P | 3060 | P | 1.0 | NC | Canx | calnexin |
| 1422845 | 1234 | P | 1034 | P | 0.9 | D | Canx | calnexin |
| 1428935 | 140 | P | 198 | P | 1.1 | NC | Canx | calnexin |
| 1417606 | 3181 | P | 4327 | P | 1.3 | I | Calr | calreticulin |
| 1433806 | 2476 | P | 3117 | P | 1.3 | I | Calr | calreticulin |
| 1456170 | 2387 | P | 3134 | P | 1.3 | NC | Calr | calreticulin |

A, absent; P; present; D, decreased; I, increased, NC, no change

Table S3. Sequences of real time PCR primers

| Gene | Forward | Reverse | Source |
|---|---|---|---|
| XBP1s | AAGAACACGCTTGGGAATGG | CTGCACCTGCTGCGGAC | This study |
| Dgat2 | TTCCTGGCATAAGGCCCTATT | AGTCTATGGTGTCTCGGTTGAC | This study |
| Scd1 | AGATCTCCAGTTCTTACACGACCAC | GACGGATGTCTTCTTCCAGGTG | Ref. S14 |
| Acc2 | GGGCTCCCTGGATGACAAC | TTCCGGGAGGAGTTCTGGA | Ref. S14 |
| SREBP-1 | CAGCTCAGAGCCGTGGTGA | TTGATAGAAGACCGGTAGCGC | Ref. S14 |
| ChREBP | CCAGCCTCAAGGTGAGCAAA | CATGTCCCGCATCTGGTCA | PrimerBank* |
| Fasn | GGAGGTGGTGATAGCCGGTAT | TGGGTAATCCATAGAGCCCAG | PrimerBank |
| PGC1a | TATGGAGTGACATAGAGTGTGCT | CCACTTCAATCCACCCAGAAAG | PrimerBank |
| PGC1b | TCCTGTAAAAGCCCGGAGTAT | GCTCTGGTAGGGGCAGTGA | PrimerBank |
| Acc1 | ATTGGGCACCCCAGAGCTA | CCCGCTCCTTCAACTTGCT | Ref. S14 |
| Crat | AGGGTCAGCTTCGGTTTGCT | GCAGCGTCTCATTGTCAATCA | This study |
| Gck | TGAGCCGGATGCAGAAGGA | GCAACATCTTTACACTGGCCT | PrimerBank |
| Pklr | TCAAGGCAGGGATGAACATTG | CACGGGTCTGTAGCTGAGTG | PrimerBank |
| PEPCK | GTCACCATCACTTCCTGGAAGA | GGTGCAGAATCGCGAGTTG | PrimerBank |
| G6P | GACCTCAGGAACGCCTTCTATG | ATTGATGCCCACAGTCTCTTGA | PrimerBank |
| Gys2 | TTGCCTCCTGTGACCACTCA | CCGATTCGTCTAATGGTGCTG | PrimerBank |
| Hmgcs | GTGGCACCGGATGTCTTTG | ACTCTGACCAGATACCACGTT | PrimerBank |
| Hmgcr | AGCTTGCCCGAATTGTATGTG | TCTGTTGTGAACCATGTGACTTC | PrimerBank |

*http://pga.mgh.harvard.edu/primerbank/

Table S4. Sequences of primers for  Nothern blot probes

| Gene | Forward | Reverse | Amplicon |
|---|---|---|---|
| Dgat2 | TTCCTGGCATAAGGCCCTATT | AACTTCTTCTGGACCCATCGG | 0.35 kb |
| Scd1 | CCAGTTCTTACACGACCAC | GACGGATGTCTTCTTCCAGGTG | 0.1 kb |
| Fasn | TCTCTCCAAGTTCGACGCCT | GGCAATGCTTGGTCCTTTGA | 0.3 kb |

Table S5. Sequences of primers use for CHIP analysis

| Gene | Forward | Reverse | Position* |
|---|---|---|---|
| Dgat2 | TTTGGTGTTTGGAGACAGGGT | AGAGTTTGAAGCCAGCCCAG | 0.8 kb |
| Acc2 | GAACGGTTGCATGAGTGTGAA | GGCTTGCTACACGTCCGTACT | 0.4 kb |
| Scd1 | GCTAGAGGCAGAGGGAACAGC | CTGTGAAGCCCGTCTTGTCAT | 0.5 kb |
| ERdj4 | AGTGACGCAAGGACCAAACG | CTACACGAAACGCTTCCCCA | 0.2 kb |

*Distance from the transcription start site

**Supporting references**


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