Supporting Information

Contents

Supporting Materials and Methods

Cell lines and treatment

LO2 cells were purchased from Zhong Qiao Xin Zhou Biotechnology Co.,Ltd., Shanghai, and Huh7 cells were purchased from the Cell Bank of the Chinese Academy of Sciences. Cells were cultured in Dulbecco's modified Eagle's medium (DMEM, Gibco) supplemented with 10% fetal bovine serum (FBS, Excell, China) in a 5% CO_2 incubator at 37^{o}C. All cell identities were confirmed and cultured as recommended by the suppliers. Mycoplasma determination was performed by Shanghai Biowing Applied Biotechnology Co..

The cellular lipid accumulation model was induced by free fatty acid (FFA, including palmitate and oleic acid at a final ratio of 1:2 and a final concentration of 0.2 mM; Sigma-Aldrich), which was added to the medium for 24 h. For knockdown, cells were seeded in 6-well culture plates and transiently transfected with siRNA oligonucleotides at 30 pmol per well with RNAiMAX (Life Technology) according to the manufacturer's instructions. mGPDH-specific, Cyp-D-specific, thyroid receptor (TR)α-specific, TRβ-specific and corresponding negative control siRNAs were synthesized by QIAGEN and RIBOBIO. For overexpression, cells were seeded in 6-well culture plates and transfected with 1 μg plasmid using Lipofectamine 3000 Reagent (Invitrogen) according to the manufacturer's instructions. pCMV3-N-GFPSpark-mGPDH and control vector plasmids were generated by Sino Biological. Insulin and tauroursodeoxycholic acid (TUDCA) were purchased from Sigma-Aldrich. 1,2-bis (2-aminophenoxy) ethane N,N,N´,N´-tetraacetic acid acetoxymethyl ester (BAPTA-AM) was purchased from TCI, and cyclosporine A (CsA) was purchased from Aladdin. MG-132 was purchased from Santa Cruz Biotechnology.

RNA-seq analysis

Total RNA was harvested from cells with Trizol (Takara) and quantified by a NanoDrop2000. RNA integrity and gDNA contamination were tested by denaturing agarose gel electrophoresis, and the sequencing library was determined by an Agilent 2100 Bioanalyzer using the Agilent DNA 1000 Chip Kit (Agilent). RNA-seq analyses were performed by KangChen Biotech., Shanghai, using the Illumina HiSeq 4000 platform.

Mitochondrial calcium flux assays

Mitochondria were isolated using a mitochondria isolation kit (Mitochondrial Isolation Kit, Beyotime) following the manufacturer's recommendations. Mitochondria (2 mg protein/ml) and the calcium-sensitive dye Arsenazo III (30 μM) were added to a medium containing mannitol (195 mM), sucrose (25 mM), Hepes (40 mM at pH 7.2), $CaCl_2$ (60 nmol mg/protein) and rotenone (13 μM). Potassium succinate (3.33 mM) and FCCP (1 μM) were used to induce influx and efflux. Calcium flux was estimated by monitoring the difference in the absorbance of Arsenazo III between 675 nm and 685 nm according to a previously described method.[1, 2]

Ubiquitination and half-life assays

Ubiquitination and half-life assays were performed according to our previous protocol.[3] Briefly, for the ubiquitination assay, cells were transfected by an mGPDH plasmid with hemagglutinin (HA)-tagged ubiquitin for 24 h and then treated with FFA and MG-132 (10 μM). Cells were harvested, and the lysates were incubated with anti-Cyp-D antibody at 4 ^{o}C overnight. Immunoprecipitated proteins were analyzed by immunoblotting with an antibody directed against the HA epitope. To measure Cyp-D protein half-life, cells were treated with mGPDH plasmid and FFA, and then cycloheximide (CHX, 25 μM) was added to block protein synthesis. Total lysates were collected at the indicated time points after CHX administration and subjected to immunoblot analysis.

mGPDH activity and G3P content assays

Mitochondria were isolated using a mitochondria isolation kit (Mitochondrial Isolation Kit, Beyotime) following the manufacturer's recommendations. mGPDH activity was detected using 2,6-dichloroindophenol (DCIP, Sigma) as the electron acceptor, and the loss of absorbance at 600 nm was measured. The reaction buffer consisted of 50 mM KH_2PO_4/K_2HPO_4 buffer (pH 7.5), 9.3 μM antimycin A, 5 μM rotenone and 50 μM DCIP. G3P content was determined using the G3P Colorimetric Assay Kit (Abnova) according to its protocol.

Metabolic and liver function assays

Levels of TG, total cholesterol (TC), nonesterified fatty acid (NEFA), low-density lipoprotein cholesterol (LDL), high-density lipoprotein cholesterol (HDL), alanine aminotransferase (ALT) and aspartate aminotransferase (AST) were measured using corresponding commercial determination kits (all from Nanjing Jiancheng) with liver tissue or serum samples. Serum β-hydroxybutyric acid

concentrations were measured using an ELISA kit from MSK Bio. Cellular TG levels were measured using a commercial TG Quantification Colorimetric Kit (Biovision) according to the manufacturer's protocol.

Western blot and antibodies

For protein extraction, cells were lysed in sample buffer (50 mM Tris-HCl [pH 6.8], 2% SDS, 10% glycerol, 100 mM dithiothreitol, and 0.1% bromophenol blue), tissue lysates were prepared as previously described,[3] and protein concentrations were measured using the BCA Protein Assay Kit (Beyotime). Extracted protein lysates were resolved by SDS-PAGE and immunoblotted with the indicated primary antibodies (1:500-1:10,000) and their corresponding HRP-conjugated secondary antibodies. Blots were developed with chemiluminescent HRP substrate (Millipore) and imaged using a fusion FX5s system (Vilber Lourmat). The following antibodies were used: mGPDH (D-12), GAPDH (V-18), β-actin (C-2), ATF4 (B-3), TRα1/β1 (C1), and FASN (G-11) from Santa-Cruz Biotechnology; Akt, p-Akt (Ser473), IRS1, p-IRS1 (Ser307), elF2α, p-elF2α (Ser51), XBP1s, CHOP, VDAC, p38 (L53F8), p-p38 (D3F9), ERK (137F5), p-ERK (20G11) and p-JNK (81E11) from Cell Signaling Technology; OTC from Proteintech; and mGPDH, Cyp-D and ANT-1 from Abcam.

Hematoxylin and eosin (H&E), oil red o and immunohistochemical (IHC) analyses

H&E, oil red o and IHC staining were carried out as we previously described.[3, 4] Briefly, for H&E analysis, tissue sections were prepared using paraffin, and these paraffinized sections were subjected to H&E staining. For oil red o analysis, tissue sections were prepared using the Tissue-Tek OCT compound (Sakura Finetek), and cells were fixed in formaldehyde solution. These frozen liver sections or fixed cells were subjected to oil red o staining. For IHC staining, tissue sections were prepared using paraffin, and these paraffinized sections were subjected to IHC staining using indicated antibodies. Digital images were obtained with a light microscope (Olympus).

ROS assay

ROS levels were measured in fresh liver tissue by using a ROS assay kit (GENMED SCIENTIFICS INC. U.S.A) according to the manufacturer's instructions. We also performed DHE and MitoSox Red staining in frozen liver sections to measure ROS levels according to a previous description.[5, 6] Briefly, cryosections of livers were rehydrated in PBS and then incubated in dihydroethidium (DHE, Invitrogen)

or MitoSox Red (Invitrogen) solution, washed with PBS and placed on coverslips. Images were acquired using a fluorescence microscope (Olympus).

ATP content and cell oxygen consumption rate (OCR) measurement

The ATP contents in liver tissue were assessed according to the manufacturer's instructions (Beyotime). The bioenergetics of isolated mitochondria was measured using a Seahorse XF96 extracellular flux analyzer (Seahorse Biosciences) according to previous literature[7] with modifications. In brief, isolated mouse liver mitochondria were seeded in each well of an XF 96-well microplates (Seahorse Bioscience). After obtaining a baseline measurement, the OCR was measured after the sequential addition of 1 μM oligomycin, 1.5 μM FCCP, 1 μM rotenone plus 1 μM antimycin A, and 10 mM G3P. Basal, maximal and G3P stimulated respiration were calculated at baseline and after FCCP and G3P injection, respectively.

Human tissues

The experimental protocols were approved by the Ethics Committee of Xinqiao Hospital, and were consistent with the Declaration of Helsinki (clinical trial register no. ChiCTR-ROC-17010719). All samples were collected from patients hospitalized at Chongqing Medical University, and written consent was obtained from each participant. The procedure was carried out in a manner similar to that in our previous study.[4] Briefly, liver samples were obtained from individuals with NAFLD who underwent percutaneous liver biopsy, and control samples were collected from liver transplant donors. The diagnostic criteria for NAFLD were as follows: i) performed a physical examination, laboratory investigation, and liver biopsy. ii) Other causes of liver disease were ruled out, such as current or past excessive alcohol consumption (defined as average daily consumption of alcohol > 20 g for males or > 10 g for females), chronic hepatitis C or B, autoimmune, celiac disease, genetic disorders based on self-reports, or if laboratory and/or histopathological data showed causes of liver disease other than NAFLD. All liver specimens were snap frozen after resection and stored at -80 ^{o}C.

Supporting figure legend

Supporting Fig. S1. Increased TG in KO mice fed with chow diet. (A-F) Liver-specific mGPDH knockout (KO) and cre-control (control) mice were fed with chow diet. Hepatic mGPDH mRNA (left)

and protein (right) expression levels were detected by qRT-PCR and western blot, respectively (A). The body weight (BW) (left) and ratio of liver weight to BW (LW/BW) (right) (B), liver lipid content (TG, TC and NEFA) (C), serum lipid profiles (TG, TC, LDL, HDL and NEFA) (D), β-hydroxybutyric acid (E), and H&E and oil red o staining of liver sections (F) were determined. Scale bar: 200 or 100 μm. n = 6 mice per group. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$, $^{***}P < 0.001$.

Supporting Fig. S2. Increased hepatic steatosis in HFD-fed mGPDH$^{+/-}$ heterozygous mice. (A) mRNA (upper panel) and protein (lower panel) expression of mGPDH in liver-specific hemizygous mGPDH knockout mice (KO/+). (B) mRNA (upper panel) and protein (lower panel) in mice fed the HFD for 12 weeks HFD. (C-G) KO/+ and cre-control (control) mice were fed with HFD for 12 weeks, BW and LW/BW (C), liver lipid content (TG, TC and NEFA) (D), serum lipid profiles (TG, TC, LDL, HDL and NEFA) (E), serum levels of β-hydroxybutyric acid (F), and H&E and oil red o staining of liver sections (G) were shown. Scale bar: 200 or 100 μm. n = 4 mice per group for A,C-G, n = 6 mice per group for B. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$, $^{***}P < 0.001$.

Supporting Fig. S3. mGPDH decreases TG content and lipid droplet accumulation under basal conditions. (A and B) LO2 and Huh7 cells were transfected with siRNA or plasmid for mGPDH inhibition or overexpression, the TG contents of treated cells were determined enzymatically (A), and oil red o staining is shown (B). n = 3. Scale bar: 20 μm. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$.

Supporting Fig. S4. mGPDH does not affect β-hydroxybutyrate, inflammation and insulin signaling. (A-C) LO2 cells were transfected with siRNA or plasmid for mGPDH and then treated with FFA for 24 h. β-hydroxybutyric acid concentrations were determined enzymatically (A). The mRNA levels of genes related to inflammation (IL-1β, TNFα, MCP-1 and IL-10) were determined by qRT-PCR in treated LO2 cells and KO and control mice fed with HFD (B). The expression of proteins related to insulin signaling (p-IRS1 and p-AKT) was detected by western blot in LO2 cells (C). n = 3 for cells, n = 6 for mice. Data are presented as the mean ± S.E.M. n.s., not significant.

Supporting Fig. S5. ER stress induced by mGPDH suppression occurs via Cyp-D-controlled mPTP activation. (A) LO2 cells transfected with mGPDH siRNA were treated with FFA and BAPTA-AM (25 μM) for 24 h, and ER stress markers were determined. (B and C) LO2 cells transfected with mGPDH siRNA or plasmid were treated with FFA for 24 h. Mitochondrial Ca^{2+} uptake (B) and

release (C) were determined using arsenazo III. (D) LO2 cells transfected with mGPDH siRNA were treated with FFA and CsA (2.5 μM) for 24 h, and ER stress markers were determined. (E and F) LO2 cells were transfected with mGPDH siRNA or plasmid and then treated with FFA for 24 h. The mRNA (E) and protein (F) expressions of Cyp-D, ANT-1 and VDAC were determined. (G and H) LO2 cells were treated with FFA for 24 h and G3P (10 mM) during the last 10 min. The protein expression of Cyp-D (G) and mRNA levels of ER stress markers (H) were shown. (I) Cyp-D protein levels were assessed in KO and control mice fed with HFD. (J) LO2 cells cotransfected with mGPDH siRNA and Cyp-D siRNA were treated with FFA for 24 h, and ER stress markers were determined. (K-N) KO and control mice were fed with HFD for 8 weeks and injected with AAV8-Cyp-D-shRNA at the fifth week of HFD feeding via the tail vein. ER stress markers (K), LW/BW (L), liver lipid contents (M), and H&E and oil red o staining of liver sections (N) were shown. Scale bars: 100 μm. n = 6 mice per group for I, n = 4 mice per group for K-N, n = 3 for A-H and J. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, n.s., not significant.

Supporting Fig. S6. The effect of mGPDH knockout on MAP Kinases. KO and control mice fed with HFD, and the MAP Kinases in livers were determined by western blot. n = 6 mice per group. Data are presented as the mean ± S.E.M.

Supporting Fig. S7. The effect of mGPDH downregulation on ATP levels and mitochondrial bio energetics. (A) Hepatic ATP content of KO and control mice fed with HFD. (B) The mitochondria were isolated from KO and control mice fed with HFD, and the oxygen consumption rate (OCR) was measured in the presence of oligomycin (Oligo), FCCP, rotenone (Rot) and antimycin (AA), and glycerol-3-phosphate (G3P). n = 6 for A, n = 10 for B. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$, $^{***}P < 0.001$.

Supporting Fig. S8. mGPDH regulates Cyp-D through the ubiquitination-proteasomal degradation pathway. (A-C) LO2 cells were transfected by mGPDH and hemagglutinin (HA)-tagged ubiquitin (Ub) plasmids as indicated and then treated with FFA for 24 h and the proteasomal inhibitor MG-132 (10 μM) during the last 4 h. Cyp-D protein (A) and ubiquitination (B) were detected by immunoblotting and immunoprecipitation analysis. The half-life of the Cyp-D protein was determined

by pulse-chase assay with protein synthesis inhibitor CHX (25 μM) administration (C). *n* = 3 for A-C. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$, n.s., not significant.

Supporting Fig. S9. Thyroid hormone receptor is not involved in the suppression of hepatocellular mGPDH under HFD conditions. (A-C) Serum thyroid hormone (T3, T4 and TSH) levels (A) and the mRNA (B) and protein (C) expression of thyroid hormone receptors (TRs, TRα and TRβ) were measured by using thyroid hormone assay kits, qRT-PCR and western blot in ob/ob mice. (D-F) Serum thyroid hormone levels (D) and the mRNA (E) and protein (F) expression of TRs were measured in HFD-fed mice. (G) C57BL/6J mice were treated with saline (Veh) or TR antagonist 1-850 (10 nmol per mouse per day) for 20 days, and mGPDH mRNA levels were determined. (H) LO2 cells were transfected with siRNA for TRα or TRβ and then treated with or without FFA for 24 h; mRNA levels of mGPDH were assessed by qRT-PCR. *n* = 6 mice per group for A-G, *n* = 3 for H. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, n.s., not significant.

Supporting Fig. S10. The effects of mGPDH knockout on hepatic ROS levels. (A and B) ROS levels in fresh liver tissue and cryosections were tested by using a ROS assay kit (A) and performing DHE and MitoSox Red staining (B) in normal chow (NC)- and HFD-fed C57BL/6J mice. (C and D) ROS levels in fresh liver tissue and cryosections were tested by using a ROS assay kit (C) and performing DHE and MitoSox Red staining (D) in NC- and HFD-fed liver-specific mGPDH KO and control mice. Scale bar: 100 μm. *n* = 6 mice per group. Data are presented as the mean ± S.E.M. $^{*}P < 0.05$, $^{***}P < 0.001$.

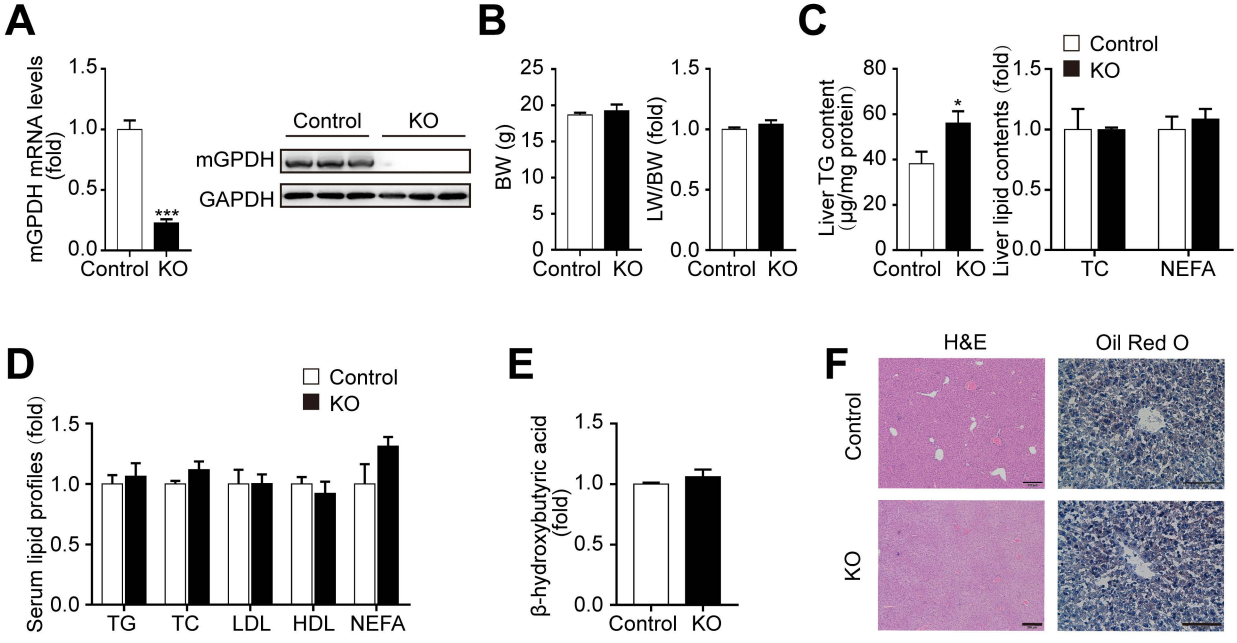
Supporting Fig. S11. AAV8-mGPDH leads to mGPDH overexpress exclusively in the liver. (A-C) Eight-week-old ob/ob mice were injected with AAV8-mGPDH (mGPDH) or AAV8-GFP (Veh) via the tail vein. Eight weeks later, the mRNA (A and B) and protein (C) expression of mGPDH in the indicated tissues or livers was determined by qRT-PCR and western blot. (D-F) C57BL/6J mice were fed with HFD for 12 weeks, and at the fifth week of HFD feeding were injected with AAV8-mGPDH or Veh via the tail vein. The mRNA (D and E) and protein (F) expression of mGPDH in the indicated tissues or livers is shown. *n* = 6 mice per group for A-C, *n* = 5 mice per group for D-F. Data are presented as the mean ± S.E.M. $^{**}P < 0.01$, $^{***}P < 0.001$ compared with the Veh group.

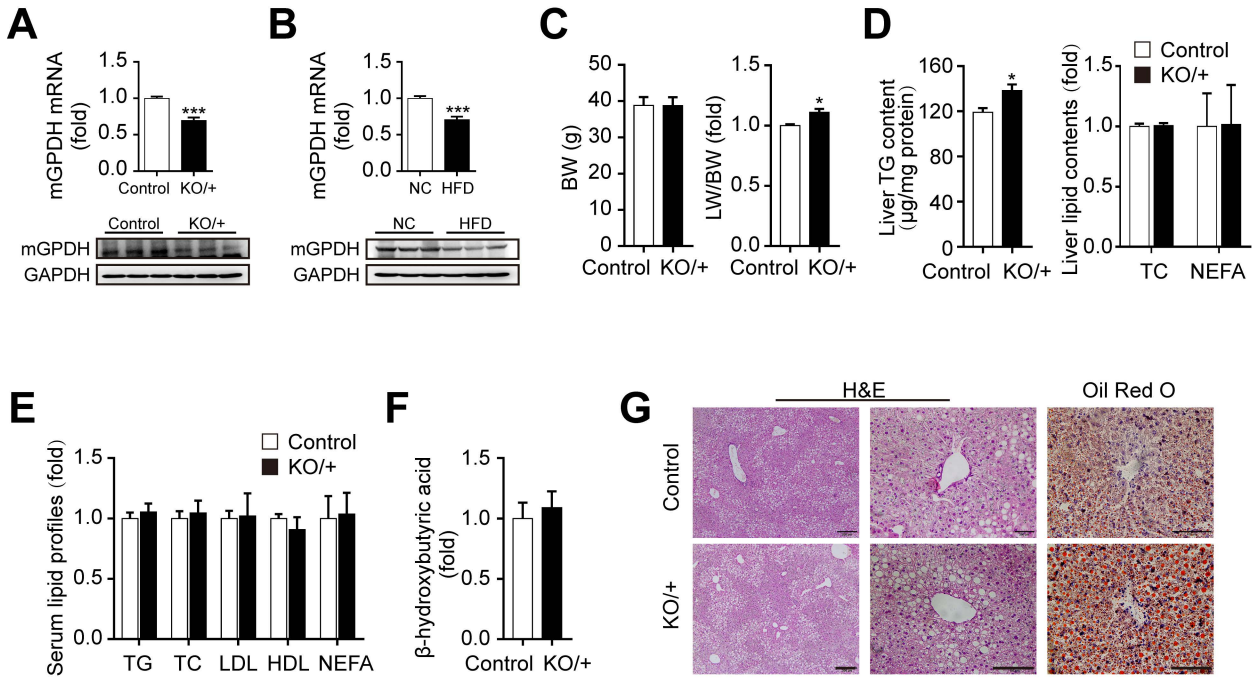
Supporting Fig. S12. AAV8-mGPDH does not change serum lipid profiles and β-hydroxybutyrate in NAFLD mice. (A and B) Eight-week-old ob/ob mice were injected with AAV8-mGPDH (mGPDH)

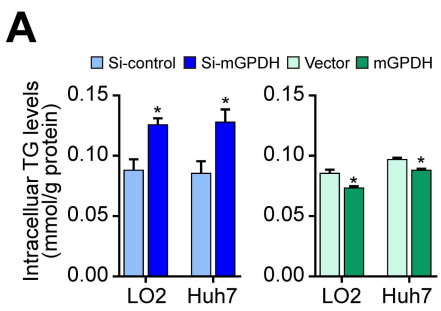
and AAV8-GFP (Veh) via the tail vein. Eight weeks later, serum lipid profiles (A) and β-hydroxybutyrate concentrations (B) were determined enzymatically. (C and D) C57BL/6J mice were fed with HFD for 12 weeks and at the fifth week of HFD feeding were injected with AAV8-mGPDH or Veh via the tail vein. Serum lipid profiles (C) and β-hydroxybutyrate concentrations (D) were tested. *n* = 6 per group for A and B, *n* = 5 per group for C and D. Data are presented as the mean ± S.E.M.

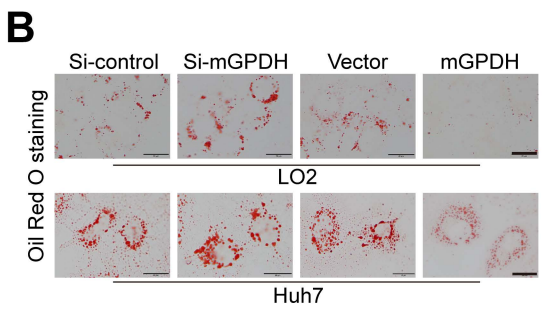
References in supporting information

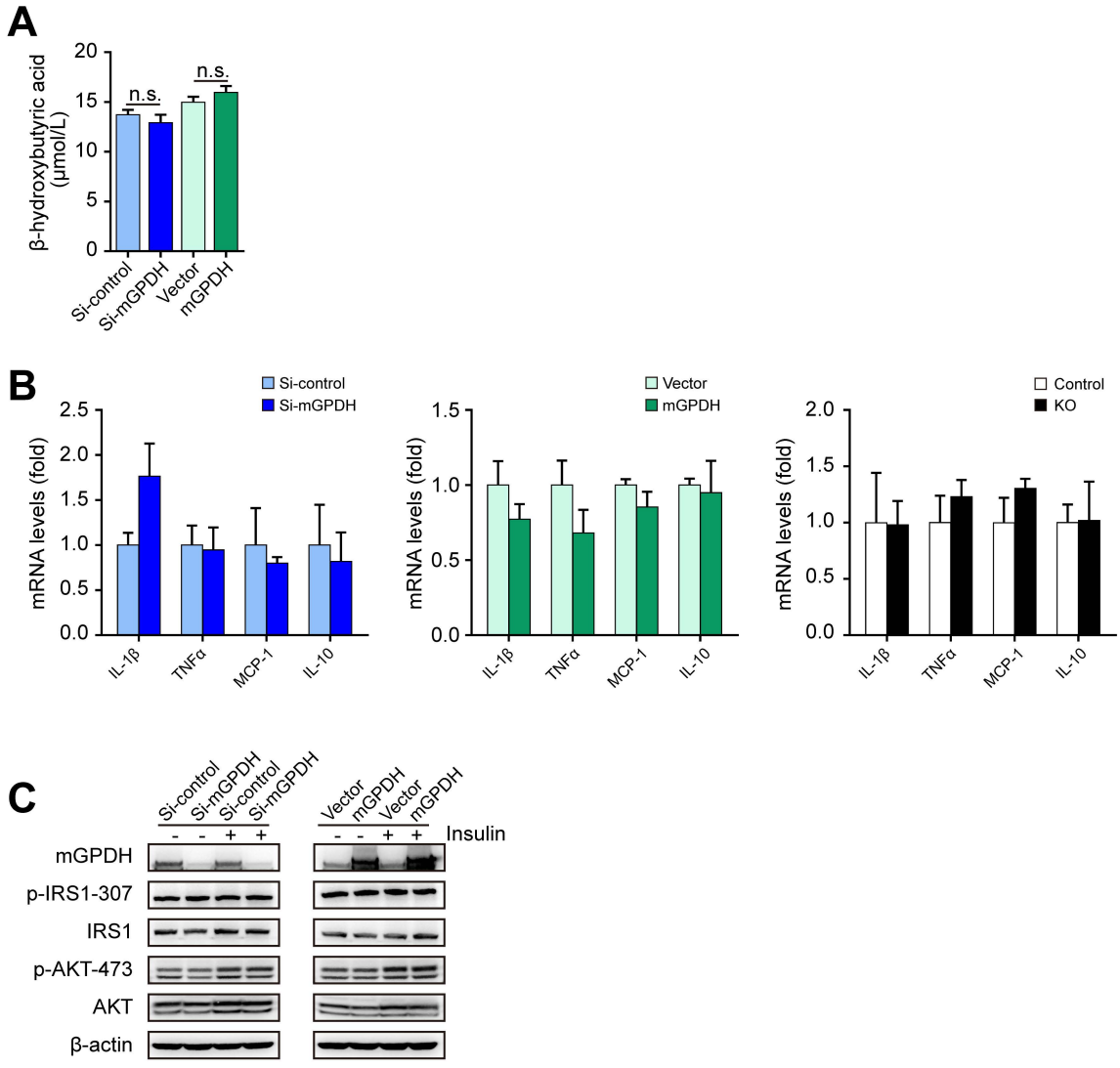
1. Xu W, Liu L, Charles IG, Moncada S. Nitric oxide induces coupling of mitochondrial signalling with the endoplasmic reticulum stress response. Nature Cell Biology 2004;6:1129-1134.
2. Andrade Pires AD, Jabor GG, Rodrigues NG, Echevarria A, Moretto RC, Merlin Rocha ME, et al. Antioxidant effect of 1,3,4-thiadiazolium mesoionic derivatives on isolated mitochondria. European Journal of Pharmacology 2016;770:78-84.
3. Wang H, Liu X, Long M, Huang Y, Zhang L, Zhang R, et al. NRF2 activation by antioxidant antidiabetic agents accelerates tumor metastasis. Sci Transl Med 2016;8:334ra351.
4. Liao X, Song L, Zhang L, Wang H, Tong Q, Xu J, et al. LAMP3 regulates hepatic lipid metabolism through activating PI3K/Akt pathway. Molecular and Cellular Endocrinology 2018;470:160-167.
5. Kohli R, Kirby M, Xanthakos SA, Softic S, Feldstein AE, Saxena V, et al. High-fructose, medium chain trans fat diet induces liver fibrosis and elevates plasma coenzyme Q9 in a novel murine model of obesity and nonalcoholic steatohepatitis. Hepatology 2010;52:934-944.
6. Wang X, Du H, Shao S, Bo T, Yu C, Chen W, et al. Cyclophilin D deficiency attenuates mitochondrial perturbation and ameliorates hepatic steatosis. Hepatology 2018;68:62-77.
7. Figarola JL, Singhal J, Tompkins JD, Rogers GW, Warden C, Horne D, et al. SR4 Uncouples Mitochondrial Oxidative Phosphorylation, Modulates AMP-dependent Kinase (AMPK)-Mammalian Target of Rapamycin (mTOR) Signaling, and Inhibits Proliferation of HepG2 Hepatocarcinoma Cells. J Biol Chem 2015;290:30321-30341.

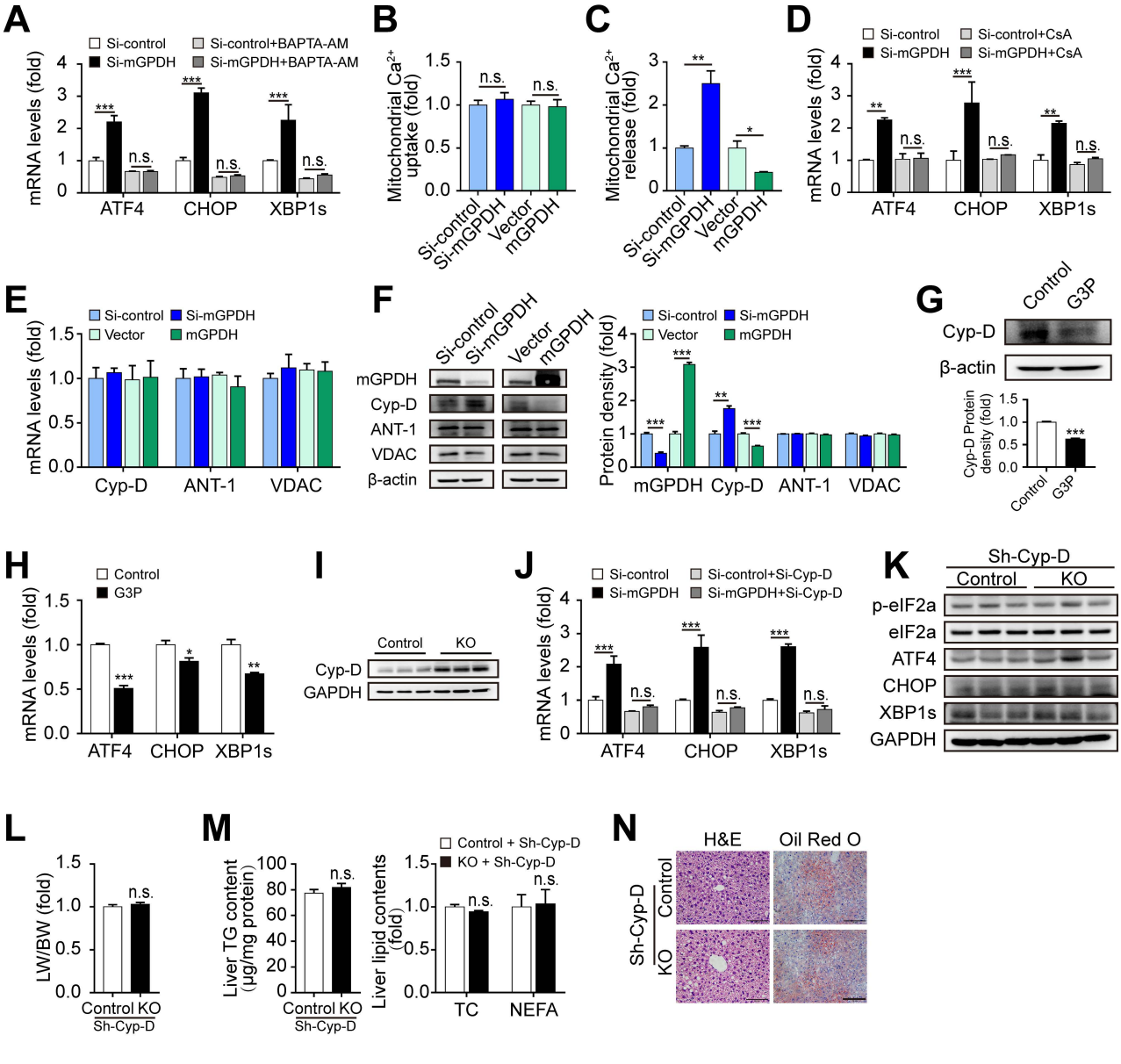

A
mGPDH mRNA levels (fold)
1.5
1.0
0.5
0.0
***
Control
KO
Control
KO
mGPDH
GAPDH
B
BW (g)
25
20
15
10
5
0
Control
KO
LW/BW (fold)
1.5
1.0
0.5
0.0
Control
KO
C
Liver TG content (μg/mg protein)
80
60
40
20
0
*
Control
KO
Liver lipid contents (fold)
1.5
1.0
0.5
0.0
Control
KO
TC
NEFA
D
Serum lipid profiles (fold)
Control
KO
1.5
1.0
0.5
0.0
TG
TC
LDL
HDL
NEFA
E
β-hydroxybutyric acid (fold)
1.5
1.0
0.5
0.0
Control
KO
F
H&E
Oil Red O
Control
KO

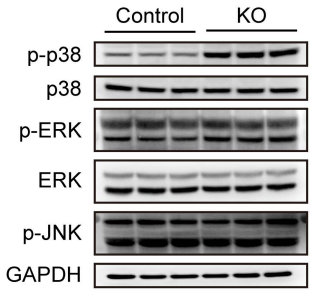

A
mGPDH mRNA (fold)
1.5
1.0
0.5
0.0
***
Control
KO/+
Control
KO/+
mGPDH
GAPDH
B
mGPDH mRNA (fold)
1.5
1.0
0.5
0.0
***
NC
HFD
NC
HFD
mGPDH
GAPDH
C
BW (g)
50
40
30
20
10
0
Control
KO/+
LW/BW (fold)
1.5
1.0
0.5
0.0
*
Control
KO/+
D
Liver TG content (μg/mg protein)
160
120
80
40
0
*
Control
KO/+
Liver lipid contents (fold)
1.5
1.0
0.5
0.0
Control
KO/+
TC
NEFA
E
Serum lipid profiles (fold)
1.5
1.0
0.5
0.0
Control
KO/+
TG
TC
LDL
HDL
NEFA
F
β-hydroxybutyric acid (fold)
1.5
1.0
0.5
0.0
Control
KO/+
G
H&E
Oil Red O
Control
KO/+

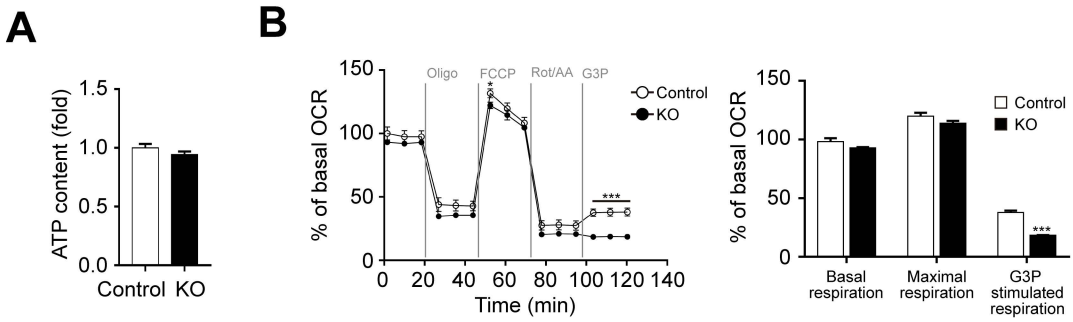

A
Si-control
Si-mGPDH
Vector
mGPDH
Intracellular TG levels (mmol/g protein)
0.15
0.10
0.05
0.00
*
LO2
Huh7

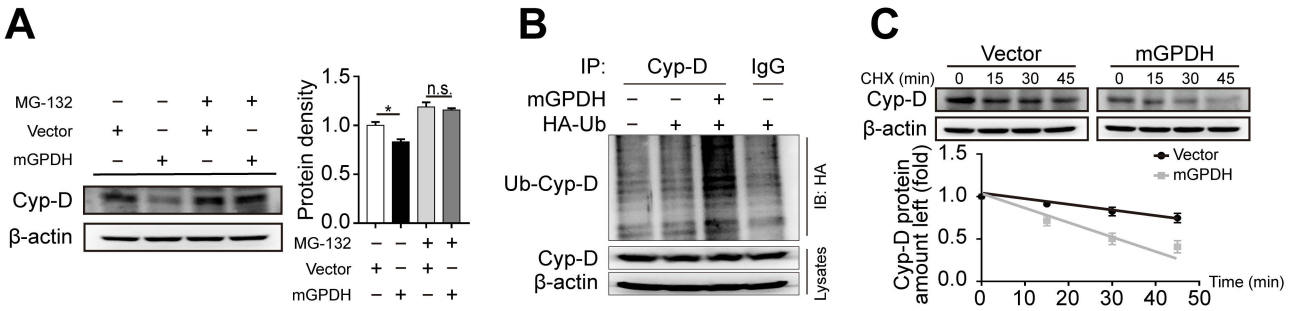

B
Si-control
Si-mGPDH
Vector
mGPDH
Oil Red O staining
LO2
Huh7

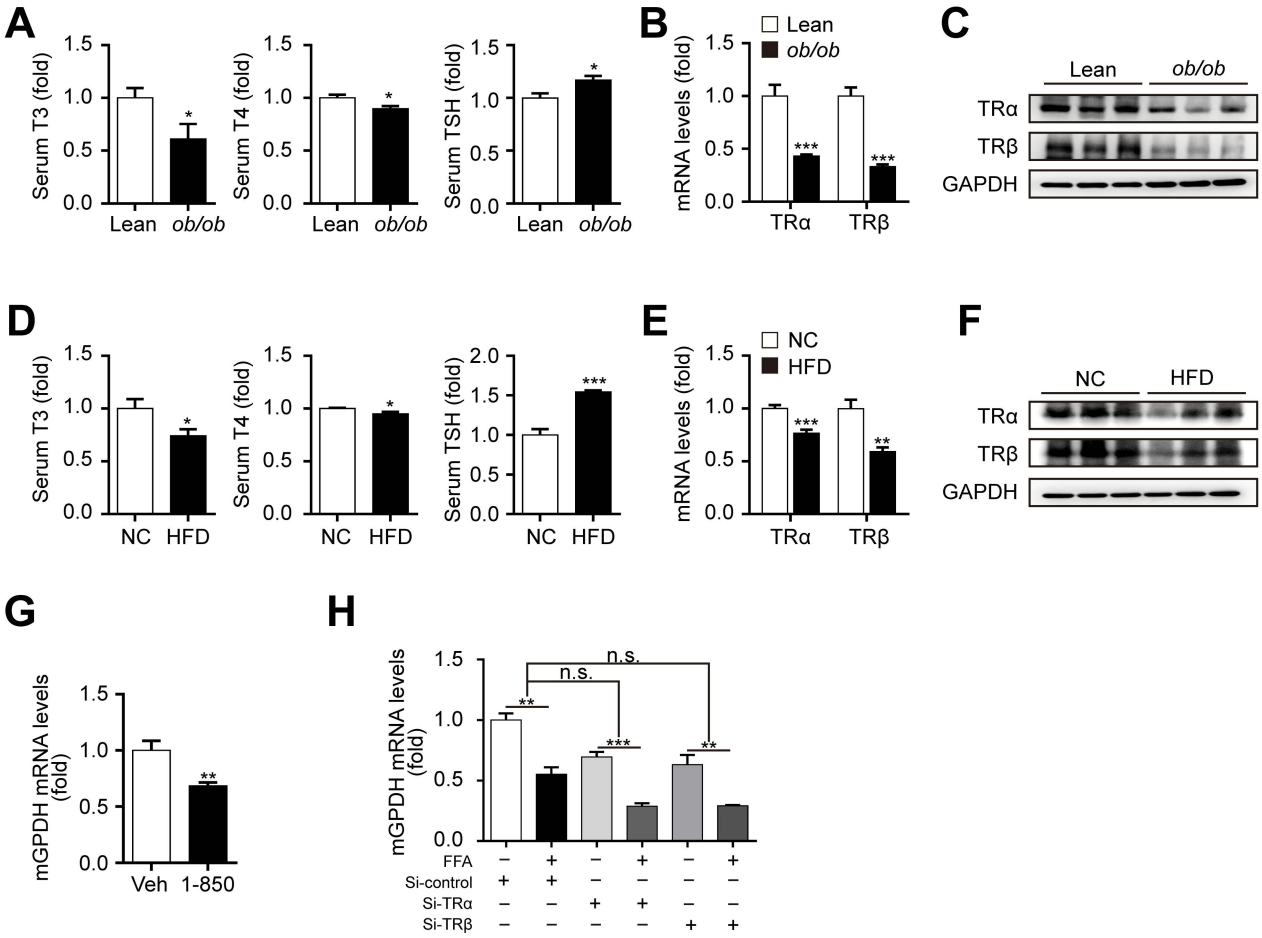

A
β-hydroxybutyric acid (μmol/L)
20
15
10
5
0
n.s.
n.s.
Si-control
Si-mGPDH
Vector
mGPDH
B
Si-control
Si-mGPDH
mRNA levels (fold)
2.5
2.0
1.5
1.0
0.5
0.0
IL-1β
TNFα
MCP-1
IL-10
Vector
mGPDH
1.5
1.0
0.5
0.0
Control
KO
2.0
C
Si-control
Si-mGPDH
Si-control
Si-mGPDH
Vector
mGPDH
Vector
mGPDH
- - + +
Insulin
mGPDH
p-IRS1-307
IRS1
p-AKT-473
AKT
β-actin

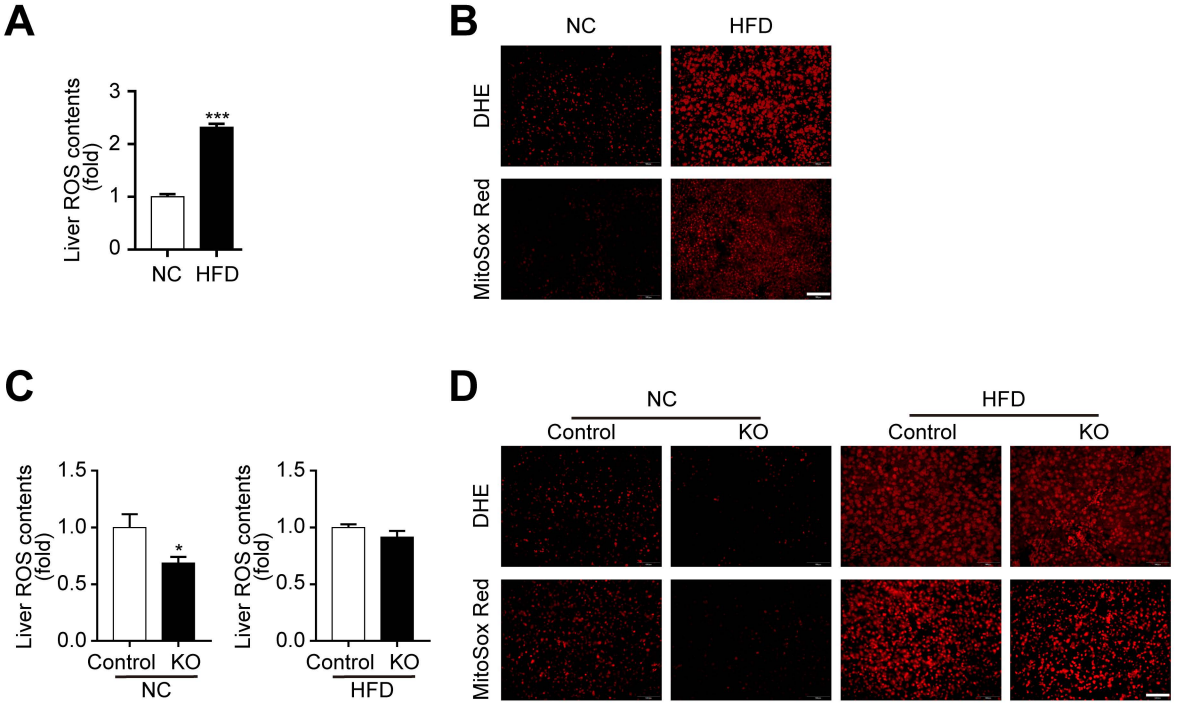

A
Si-control
Si-control+BAPTA-AM
Si-mGPDH
Si-mGPDH+BAPTA-AM
mRNA levels (fold)
ATF4
CHOP
XBP1s
B
Mitochondrial Ca2+ uptake (fold)
Si-control
Si-mGPDH
Vector
mGPDH
C
Mitochondrial Ca2+ release (fold)
D
Si-control+CsA
Si-mGPDH+CsA
E
Cyp-D
ANT-1
VDAC
F
Protein density (fold)
G
Control
G3P
Cyp-D
β-actin
Cyp-D Protein density (fold)
H
I
Sh-Cyp-D
KO
GAPDH
J
Si-control+Si-Cyp-D
Si-mGPDH+Si-Cyp-D
K
p-eIF2a
eIF2a
L
LW/BW (fold)
M
Liver TG content (μg/mg protein)
Liver lipid contents (fold)
Control + Sh-Cyp-D
KO + Sh-Cyp-D
TC
NEFA
N
H&E
Oil Red O

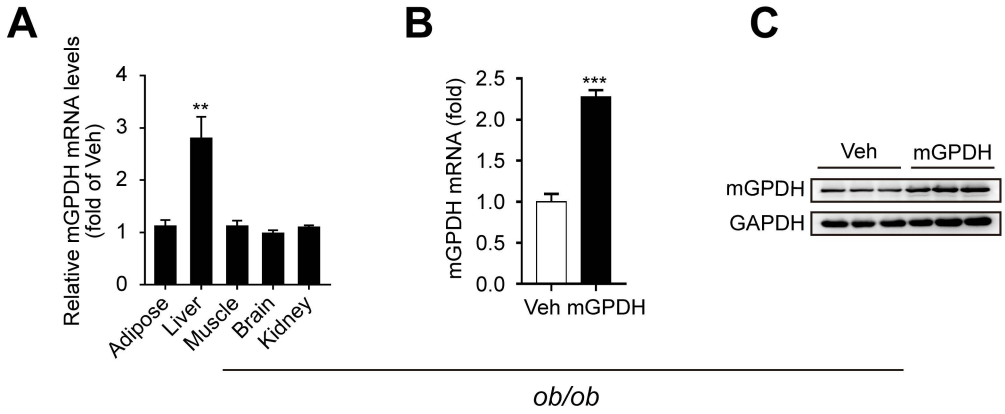

Control
KO
p-p38
p38
p-ERK
ERK
p-JNK
GAPDH

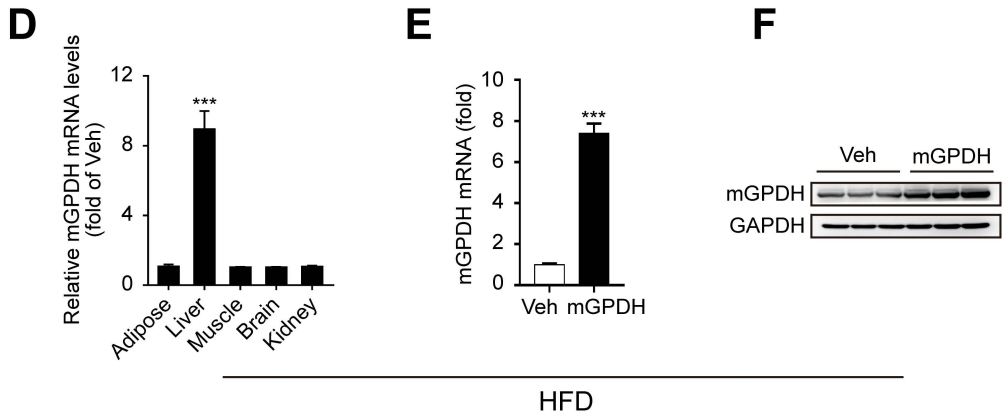

A
B
ATP content (fold)
1.5
1.0
0.5
0.0
Control
KO
% of basal OCR
150
100
50
0
Oligo
FCCP
Rot/AA
G3P
Control
KO
*
***
0
20
40
60
80
100
120
140
Time (min)
% of basal OCR
150
100
50
0
Control
KO
***
Basal respiration
Maximal respiration
G3P stimulated respiration

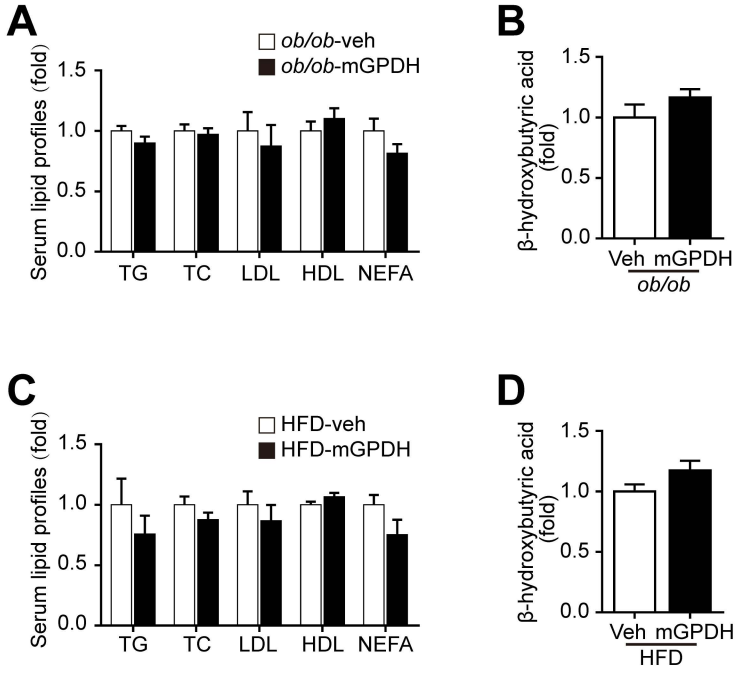

A
MG-132 – – + +
Vector + – + –
mGPDH – + – +
Cyp-D
β-actin
Protein density
1.5
1.0
0.5
0.0
*
n.s.
MG-132 – – + +
Vector + – + –
mGPDH – + – +
B
IP: Cyp-D IgG
mGPDH – – + –
HA-Ub – + + +
Ub-Cyp-D
IB: HA
Cyp-D
β-actin
Lysates
C
Vector
mGPDH
CHX (min) 0 15 30 45 0 15 30 45
Cyp-D
β-actin
Cyp-D protein amount left (fold)
1.5
1.0
0.5
0.0
Vector
mGPDH
0 10 20 30 40 50
Time (min)


A
Serum T3 (fold)
Serum T4 (fold)
Serum TSH (fold)
Lean
ob/ob
B
Lean
ob/ob
mRNA levels (fold)
TRα
TRβ
C
Lean
ob/ob
TRα
TRβ
GAPDH
D
Serum T3 (fold)
Serum T4 (fold)
Serum TSH (fold)
NC
HFD
E
NC
HFD
mRNA levels (fold)
TRα
TRβ
F
NC
HFD
TRα
TRβ
GAPDH
G
mGPDH mRNA levels (fold)
Veh
1-850
H
mGPDH mRNA levels (fold)
n.s.
n.s.
FFA
Si-control
Si-TRα
Si-TRβ


A
Liver ROS contents (fold)
3
2
1
0
***
NC
HFD
B
NC
HFD
DHE
MitoSox Red
C
Liver ROS contents (fold)
1.5
1.0
0.5
0.0
*
Control
KO
NC
Liver ROS contents (fold)
1.5
1.0
0.5
0.0
Control
KO
HFD
D
NC
HFD
Control
KO
Control
KO
DHE
MitoSox Red


A
Relative mGPDH mRNA levels (fold of Veh)
4
3
2
1
0
**
Adipose
Liver
Muscle
Brain
Kidney
B
mGPDH mRNA (fold)
2.5
2.0
1.5
1.0
0.5
0.0
***
Veh
mGPDH
C
Veh
mGPDH
mGPDH
GAPDH
ob/ob


D
Relative mGPDH mRNA levels (fold of Veh)
12
8
4
0
***
Adipose
Liver
Muscle
Brain
Kidney
E
mGPDH mRNA (fold)
10
8
6
4
2
0
***
Veh
mGPDH
F
Veh
mGPDH
mGPDH
GAPDH
HFD


A
ob/ob-veh
ob/ob-mGPDH
Serum lipid profiles (fold)
1.5
1.0
0.5
0.0
TG
TC
LDL
HDL
NEFA
B
β-hydroxybutyric acid (fold)
1.5
1.0
0.5
0.0
Veh
mGPDH
ob/ob
C
HFD-veh
HFD-mGPDH
Serum lipid profiles (fold)
1.5
1.0
0.5
0.0
TG
TC
LDL
HDL
NEFA
D
β-hydroxybutyric acid (fold)
1.5
1.0
0.5
0.0
Veh
mGPDH
HFD

Supporting Table S1. List of primers.

Primers		
m-mGPDH	Forward	TTTCTTCTTGCCTTGGGAGA
	Reverse	AGTTCCGCACTTCATTCAGG
h-mGPDH	Forward	CGGACAACATAACGATGCAC
	Reverse	CTGTCTGGGGGTCTGTCTTC
m-GAPDH	Forward	TGAACGGGAAGCTCACTG
	Reverse	TCCACCACCCTGTTGCTG
h-GAPDH	Forward	GGGTGTGAACCACGAGAAAT
	Reverse	CCTTCCACAATGCCAAAGTT
m- PPARγ	Forward	TGGACACCATACTTGAGCAGA
	Reverse	CAGGAGCAGAGCAAAGAGGT
h-PPARγ	Forward	CATAAAGTCCTTCCCGCTGA
	Reverse	TCTGTGATCTCCTGCACAGC
m-SREBP1c	Forward	CACTTCTGGAGACATCGCAAAC
	Reverse	ATGGTAGACAACAGCCGCATC
h-SREBP1c	Forward	TGAGGACAGCAAGGCAAAG
	Reverse	CAGGACAGGCAGAGGAAGAC
m-ACACA	Forward	CGAAGGGCTTACATTGCCTA
	Reverse	GGATGTTCCCTCTGTTTGGA
h-ACACA	Forward	TTCTGCACACGTTCCTTGTC
	Reverse	TGCAGCAGCAACACTGAAAT
m-FASN	Forward	AAGTTGCCCGAGTCAGAGAA
	Reverse	GACCGCTTGGGTAATCCATA
h-FASN	Forward	GTCCACCAGCAACATCAGC
	Reverse	GTTCTCCAGCAAGCCATCTC
m-SCD-1	Forward	TGTCTCGGTGTGTGTCGGAGT
	Reverse	TGTACCACTACCTGCCTGCATG
h-SCD-1	Forward	TCCAGAGGAGGTACTACAAACCT
	Reverse	GCACCACAGCATATCGCAAG
m-PGC-1α	Forward	TCTCAGTAAGGGGCTGGTTG
	Reverse	TTCCGATTGGTCGCTACACC
h-PGC-1α	Forward	TCCTTTGGGGTCTTTGAGAA
	Reverse	GGCACGCAATCCTATTCATT

m-ACOX1	Forward	CTGCGGTCCCTTGACCTTTT
	Reverse	TGCATCCATTTCTCCTGCTGA
h-ACOX1	Forward	CTGTGAGGCACCAGTCTGAA
	Reverse	AGGTGAAAGCCTTCAGTCCA
m-CPT-1α	Forward	TCAAGCCAGACGAAGAACATC
	Reverse	TGGTAGGAGAGCAGCACCTT
h-CPT-1α	Forward	GCACATCGTCGTGTACCATC
	Reverse	AATAGGCCTGACGACACCTG
m-CD36	Forward	ATTCCCTTGGCAACCAACCA
	Reverse	CAGCCAGGACTGCACCAATA
h-CD36	Forward	ACGCTGAGGACAACACAGTCT
	Reverse	GCCACAGCCAGATTGAGAAC
m-FATP1	Forward	ACTCTGCAAAGGGCTCATCC
	Reverse	GCACGCATGCTGTAGGAATG
h-FATP1	Forward	ACGCGATATACCAGGAGCTG
	Reverse	ATCTTGAAGGTGCCTGTGGT
m-Apoa4	Forward	GCCTGAGGGAGAAGGTCAAC
	Reverse	CTCTCCAGAGGTTTGGGCTG
h-Apoa4	Forward	GAACGTGGAGGAGCTCAAGG
	Reverse	CCTGCGTGTCCTGAGCATAG
m-MTTP	Forward	GCGGGAATGGTTAGTGGCTA
	Reverse	GAGCCTCCAGGTTGTCCTTC
h-MTTP	Forward	CTTCCTGGCCTTCATTCAGC
	Reverse	AGCAGAGGTGACAGCATCCA
m-IL-1β	Forward	CCAGGATGAGGACATGAGCA
	Reverse	CGGAGCCTGTAGTGCAGTTG
h-IL-1β	Forward	CCACAGACCTTCCAGGAGAA
	Reverse	GTGATCGTACAGGTGCATCG
m-TNFα	Forward	ACTGGCAGAAGAGGCACTCC
	Reverse	GCCACAAGCAGGAATGAGAA
h-TNFα	Forward	GGCGTGGAGCTGAGAGATAA
	Reverse	TTGATGGCAGAGAGGAGGTT
m-MCP-1	Forward	ACAAGAGGATCACCAGCAGC
	Reverse	GGACCCATTCCTTCTTGGGG

h-MCP-1	Forward	ATAGCAGCCACCTTCATTCC
	Reverse	CGAGCCTCTGCACTGAGAT
m-IL-10	Forward	AGGCGCTGTCATCGATTTCT
	Reverse	AGGAAGAACCCCTCCCATCA
h-IL-10	Forward	CTGCCTAACATGCTTCGAGA
	Reverse	CCCTTAAAGTCCTCCAGCAA
m-ATF4	Forward	CATGACCGAGATGAGCTTCCTGAAC
	Reverse	CCGCCTTGTCGCTGGAGAAC
h-ATF4	Forward	TCCAACAACAGCAAGGAGGA
	Reverse	CCAACGTGGTCAGAAGGTCA
m-CHOP	Forward	CCAACAGAGGTCACACGCACATC
	Reverse	TCGTTCTCCTGCTCCTTCTCCTTC
h-CHOP	Forward	TTCTCTGGCTTGGCTGACTG
	Reverse	TCCTCCTCTTCCTCCTGAGC
m-XBP1s	Forward	AGAACCAGGAGTTAAGAACACGCTTG
	Reverse	GAGGCAACAGTGTCAGAGTCCATG
h-XBP1s	Forward	GGCATTCTGGACAACTTGGA
	Reverse	GGAGGCTGGTAAGGAACTGG
h-ATF6	Forward	CAGTCTCGTCTCCTCGGTCA
	Reverse	AGTGGCTCCGCTGAAGAGAG
m-Cyp-D	Forward	TGGCTCTCAGTTCTTTATCTGC
	Reverse	ACATCCATGCCCTCTTTGAC
h-Cyp-D	Forward	CCAAAGACAGCTGAGAACTTCA
	Reverse	GTGCTTCAGTGTAAAGTTCTCG
m-VDAC	Forward	AGTAACACTCGCTTCGGAATAG
	Reverse	TGGTTTTAGGGTCTGAGTGTAC
h-VDAC	Forward	CAACTCCAGCCTGATAGGTTTA
	Reverse	TGCTTGAAATTCCAGTCCTAGA
m-ANT-1	Forward	AAAGGCATCATTGATTGTGTCG
	Reverse	GTACTTGTCTTTGAAGGCGAA
h-ANT-1	Forward	GGATCATTGATTGTGTGGTGAG
	Reverse	CCTAAGAAGAGCTGCTTGTACT
m-OTC	Forward	GTGGGAAGCCAGTCCAAAGT
	Reverse	TCTGGAGCACAGGTGAGTAGT

h-OTC	Forward	TGAAAGTCTCACGGACACGG
	Reverse	AATGTCCAGTCAGAGGCAGC
m-TRα	Forward	TGAGCACTACGTCAACCACC
	Reverse	TGCCCCCTTGTACAGAATCG
h-TRα	Forward	CCAAGCTGCTGATGAAGGGT
	Reverse	CTTGGAGACTTCCCGCTTCAC
m-TRβ	Forward	GCGCTCTGATCCGTGTTTTC
	Reverse	AGGCAGGCTTCAGACATTCC
h-TRβ	Forward	AGGGCACTGGTAATTTGGCT
	Reverse	TGGCTTTGTCACCACACACT

Supporting Table S2. All differential expressed genes in mGPDH over-expressed LO2 cells.

Up-regulated:

No.	Track_id	Gene_Name	Locus	log2(fold_change)	Fold_Change
1	ENSG00000143878.9_1	RHOB	chr2:20646835-20649206	6.420935657	85.682915
2	ENSG00000126945.8_2	HNRNPH2	chrX:100663283-100669121	6.091912309	68.210045
3	ENSG00000155876.5_2	RRAGA	chr9:19049393-19050981	6.084787791	67.874031
4	ENSG00000124942.13_2	AHNAK	chr11:62201014-62323707	5.435343158	43.27143792
5	ENSG00000145337.4_2	PYURF	chr4:89442136-89444964	5.288005632	39.07044093
6	ENSG00000171223.5_1	JUNB	chr19:12902310-12904129	5.127670255	34.960896
7	ENSG00000184897.5_1	H1FX	chr3:129033614-129035120	4.512381811	22.82245067
8	ENSG00000176903.4_1	PNMA1	chr14:74178486-74181075	4.373624967	20.729666
9	ENSG00000185745.9_1	IFIT1	chr10:91152303-91166243	4.19454019	18.30975003
10	ENSG00000184207.8_1	PGP	chr16:2261998-2264808	4.05868499	16.66425585
11	ENSG00000121966.6_1	CXCR4	chr2:136871919-136875735	3.956884573	15.52890903
12	ENSG00000180185.11_1	FAHD1	chr16:1876942-1890208	3.956239784	15.52197019
13	ENSG00000183978.7_1	COA3	chr17:40947165-40950722	3.933361709	15.27776615
14	ENSG00000177733.6_2	HNRNPA0	chr5:137081340-137090065	3.919611718	15.132849
15	ENSG00000259956.1_1	RBM15B	chr3:51428699-51435339	3.640250837	12.468801
16	ENSG00000141232.4_2	TOB1	chr17:48939584-48945339	3.635230514	12.42548719
17	ENSG00000170881.4_2	RNF139	chr8:125486979-125500155	3.630887314	12.3881368
18	ENSG00000260027.4_2	HOXB7	chr17:46684589-46710934	3.602963821	12.15066881
19	ENSG00000186222.4_2	BLOC1S4	chr4:6717782-6719398	3.595681599	12.089491
20	ENSG00000171421.12_2	MRPL36	chr5:1798500-1801480	3.5608755	11.8013132
21	ENSG00000119938.8_1	PPP1R3C	chr10:93388199-93392811	3.528248395	11.53741725
22	ENSG00000205138.3_1	SDHAF1	chr19:36486101-36487217	3.508420032	11.379932
23	ENSG00000255112.2_2	CHMP1B	chr18:11851395-11854448	3.403014368	10.57814219
24	ENSG00000137124.7_2	ALDH1B1	chr9:38392661-38398658	3.293668399	9.806024724
25	ENSG00000273604.1_1	C17orf96	chr17:36827956-36831674	3.274532728	9.676818
26	ENSG00000175283.7_1	DOLK	chr9:131707809-131709898	3.047016391	8.265009
27	ENSG00000268861.6_2	CTD-2207O23.3	chr19:7447720-7537363	2.971646183	7.844308
28	ENSG00000204899.5_1	MZT1	chr13:73282495-73301825	2.931321131	7.628086116
29	ENSG00000168264.10_1	IRF2BP2	chr1:234740015-234745271	2.914533607	7.539838423
30	ENSG00000180008.8_1	SOCS4	chr14:55493948-55516206	2.866268684	7.291768118
31	ENSG00000171443.6_1	ZNF524	chr19:56111388-56114504	2.83091331	7.115244386
32	ENSG00000054598.6_1	FOXC1	chr6:1610207-1614132	2.82077998	7.065442803
33	ENSG00000215251.3_2	FASTKD5	chr20:3127165-3140543	2.761168271	6.779450168
34	ENSG00000205269.5_1	TMEM170B	chr6:11538511-11583757	2.740369492	6.682414587
35	ENSG00000110917.7_1	MLEC	chr12:121124672-121139667	2.686353546	6.436844184
36	ENSG00000163960.11_1	UBXN7	chr3:196074533-196159345	2.663467589	6.335539992
37	ENSG00000179886.5_1	TIGD5	chr8:144680005-144685394	2.602436688	6.073115
38	ENSG00000094916.14_2	CBX5	chr12:54624724-54673917	2.593361666	6.035033028
39	ENSG00000179859.8_2	AC025335.1	chr17:7816642-7819594	2.578885656	5.974780266
40	ENSG00000104472.9_2	CHRAC1	chr8:141521397-141527236	2.557274423	5.885946474
41	ENSG00000143942.4_1	CHAC2	chr2:53994929-54002333	2.529436946	5.773463081
42	ENSG00000168461.12_2	RAB31	chr18:9708162-9862548	2.504447906	5.674321547
43	ENSG00000245848.2_1	CEBPA	chr19:33790840-33793470	2.473757564	5.554887
44	ENSG00000111911.6_1	HINT3	chr6:126277927-126301390	2.463061803	5.513856814
45	ENSG00000272414.5_2	FAM47E-STBD1	chr4:77172874-77232282	2.440426677	5.428022411

46	ENSG00000164284.14_1	GRPEL2	chr5:148724993-148734146	2.439123831	5.42312277
47	ENSG00000175895.3_1	PLEKHF2	chr8:96146032-96168912	2.408881495	5.310624393
48	ENSG00000171314.8_1	PGAM1	chr10:99185917-99193198	2.39995107	5.277852637
49	ENSG00000120742.10_1	SERP1	chr3:150259781-150321015	2.378101651	5.198522521
50	ENSG00000178074.5_2	C2orf69	chr2:200775979-200820658	2.35648542	5.121212488
51	ENSG00000105810.9_1	CDK6	chr7:92234235-92465908	2.352686668	5.10774559
52	ENSG00000180398.11_1	MCFD2	chr2:47129009-47168994	2.352094453	5.105649331
53	ENSG00000137168.7_1	PPIL1	chr6:36822603-36842800	2.347606928	5.089792805
54	ENSG00000166619.12_2	BLCAP	chr20:36120874-36156333	2.331731126	5.034090408
55	ENSG00000241360.1_2	PDXP	chr22:38054734-38062941	2.315759047	4.978665356
56	ENSG00000188211.8_1	NCR3LG1	chr11:17373273-17398888	2.280804379	4.859488205
57	ENSG00000185115.5_2	NSMCE3	chr15:29557196-29562033	2.273128235	4.833701
58	ENSG00000179833.4_1	SERTAD2	chr2:64858755-64978139	2.22584226	4.677839166
59	ENSG00000120137.6_2	PANK3	chr5:167975500-168006605	2.225564471	4.676938542
60	ENSG00000002834.17_2	LASP1	chr17:37026112-37078023	2.214698812	4.641846488
61	ENSG00000178449.8_2	COX14	chr12:50505762-50514240	2.208131575	4.620764537
62	ENSG00000164983.7_1	TMEM65	chr8:125318430-125384933	2.19383831	4.575211097
63	ENSG00000165169.10_1	DYNLT3	chrX:37696010-37706890	2.171383236	4.50455077
64	ENSG00000076554.15_2	TPD52	chr8:80946980-81143467	2.155939392	4.456587377
65	ENSG00000196821.9_1	C6orf106	chr6:34555065-34664636	2.143523774	4.418399209
66	ENSG00000168282.5_1	MGAT2	chr14:50087513-50090199	2.130547418	4.378836
67	ENSG00000160888.6_1	IER2	chr19:13261229-13265722	2.095097303	4.272549786
68	ENSG00000168040.4_1	FADD	chr11:70049269-70053496	2.068683483	4.19503685
69	ENSG00000177946.5_1	CENPBD1	chr16:90036199-90038942	2.068537024	4.194611
70	ENSG00000198681.6_2	MAGEA1	chrX:152481520-152486115	2.054732084	4.154664798
71	ENSG00000213463.4_2	SYNJ2BP	chr14:70833213-70883778	2.0506675	4.142976108
72	ENSG00000243927.5_2	MRPS6	chr21:35445524-35515334	2.035176507	4.098728722
73	ENSG00000244509.3_1	APOBEC3C	chr22:39410088-39416357	2.020943814	4.058492124
74	ENSG00000119396.10_2	RAB14	chr9:123940415-123985292	2.020185871	4.05636049
75	ENSG00000176125.4_1	UFSP1	chr7:100486344-100487339	2.016645716	4.046419
76	ENSG00000237190.3_1	CDKN2AIPNL	chr5:133737778-133747589	2.008342851	4.023198306
77	ENSG00000176018.12_1	LYSMD3	chr5:89811428-89825401	2.004363989	4.012117864
78	ENSG00000152642.10_2	GPD1L	chr3:32147181-32210205	1.986473571	3.96267204
79	ENSG00000184785.5_1	SMIM10	chrX:134124968-134126503	1.962648592	3.897769
80	ENSG00000270757.1_2	HSPE1-MOB4	chr2:198365137-198415450	1.953924143	3.874269041
81	ENSG00000215012.8_2	C22orf29	chr22:19833661-19842419	1.946359682	3.854008309
82	ENSG00000184675.9_1	AMER1	chrX:63404997-63425624	1.938848575	3.833995318
83	ENSG00000153989.7_1	NUS1	chr6:117996665-118031803	1.935304117	3.824587401
84	ENSG00000185432.11_1	METTL7A	chr12:51317255-51326300	1.926860631	3.802269075
85	ENSG00000158825.5_1	CDA	chr1:20915441-20945401	1.926800143	3.802109661
86	ENSG00000106080.10_1	FKBP14	chr7:30050203-30066300	1.920311797	3.785048528
87	ENSG00000181744.8_1	C3orf58	chr3:143690640-143767561	1.915556338	3.772592667
88	ENSG00000259040.5_2	BLOC1S5-TXNDC5	chr6:7881755-8064597	1.909430854	3.756608714
89	ENSG00000115963.13_1	RND3	chr2:151324709-151395525	1.899657159	3.731245169
90	ENSG00000150991.14_2	UBC	chr12:125396150-125401914	1.899343172	3.730433194
91	ENSG00000148175.12_1	STOM	chr9:124101266-124132582	1.886733141	3.697969027
92	ENSG00000006831.9_1	ADIPOR2	chr12:1797740-1897844	1.876150904	3.670943485
93	ENSG00000213214.4_1	ARHGEF35	chr7:143883176-143892748	1.85367315	3.614192
94	ENSG00000169813.16_2	HNRNPF	chr10:43881065-43904614	1.853197598	3.61300086

95	ENSG00000127423.10_1	AUNIP	chr1:26158404-26185949	1.840364894	3.581005897
96	ENSG00000185262.8_1	UBALD2	chr17:74261283-74267380	1.835852547	3.569823009
97	ENSG00000182512.4_1	GLRX5	chr14:95999840-96011061	1.831401642	3.558826602
98	ENSG00000185875.12_1	THNSL1	chr10:25305587-25315593	1.829722368	3.554686596
99	ENSG00000188997.7_2	KCTD21	chr11:77882295-77899868	1.82093243	3.533094727
100	ENSG00000139146.13_2	FAM60A	chr12:31433518-31479992	1.76875503	3.407597721
101	ENSG00000113369.8_1	ARRDC3	chr5:90664541-90679176	1.76468643	3.398001359
102	ENSG00000117000.8_1	RLF	chr1:40627045-40706593	1.7512431	3.366485148
103	ENSG00000131873.5_1	CHSY1	chr15:101715928-101792137	1.749259244	3.361859061
104	ENSG00000139921.12_1	TMX1	chr14:51706880-51724264	1.743127943	3.347601833
105	ENSG00000196636.7_1	SDHAF3	chr7:96745902-96811075	1.740982121	3.342626411
106	ENSG00000113638.13_2	TTC33	chr5:40512435-40756077	1.735941091	3.330967068
107	ENSG00000179195.15_2	ZNF664	chr12:124456392-124499986	1.733042908	3.324282314
108	ENSG00000100528.11_1	CNIH1	chr14:54890278-54908149	1.727630775	3.311834948
109	ENSG00000116191.17_2	RALGPS2	chr1:178694282-178890976	1.711329204	3.274623867
110	ENSG00000165410.14_1	CFL2	chr14:35175975-35184029	1.707006885	3.264827764
111	ENSG00000145780.7_1	FEM1C	chr5:114856605-114880591	1.703794293	3.257565738
112	ENSG00000147853.16_2	AK3	chr9:4709559-4742043	1.69010046	3.226791723
113	ENSG00000106636.7_2	YKT6	chr7:44240567-44253893	1.684640215	3.214602194
114	ENSG00000112335.14_1	SNX3	chr6:108532426-108582464	1.680767541	3.205984702
115	ENSG00000152683.14_2	SLC30A6	chr2:32390910-32449448	1.67346481	3.189797436
116	ENSG00000110104.11_1	CCDC86	chr11:60609544-60618554	1.672929465	3.188614008
117	ENSG00000082497.11_1	SERTAD4	chr1:210406144-210419976	1.672730702	3.188174736
118	ENSG00000100410.7_1	PHF5A	chr22:41855721-41864729	1.669883331	3.181888608
119	ENSG00000115520.8_1	COQ10B	chr2:198318147-198340032	1.669577115	3.181213316
120	ENSG00000205213.13_1	LGR4	chr11:27387508-27494322	1.643786009	3.124847986
121	ENSG00000113719.15_2	ERGIC1	chr5:172261278-172379688	1.635577979	3.107120039
122	ENSG00000106537.7_1	TSPAN13	chr7:16793160-16824161	1.633459971	3.102561851
123	ENSG00000081087.14_2	OSTM1	chr6:108362613-108487058	1.631608306	3.098582339
124	ENSG00000196743.8_2	GM2A	chr5:150591711-150650001	1.631077724	3.097442979
125	ENSG00000175606.10_2	TMEM70	chr8:74884672-74895018	1.617526285	3.068484477
126	ENSG00000171862.9_2	PTEN	chr10:89622870-89731687	1.615913927	3.06505705
127	ENSG00000100418.7_1	DESI1	chr22:41994032-42017100	1.613829357	3.060631504
128	ENSG00000186480.12_2	INSIG1	chr7:155089486-155101945	1.606819736	3.045796885
129	ENSG00000175215.10_2	CTDSP2	chr12:58213710-58240522	1.605144012	3.042261174
130	ENSG00000108825.17_2	PTGES3L-AARSD1	chr17:41102543-41132545	1.605092581	3.042152722
131	ENSG00000204315.3_1	FKBPL	chr6:32096484-32098068	1.604179395	3.040227732
132	ENSG00000165175.15_1	MID1IP1	chrX:38660685-38665790	1.603244781	3.038258835
133	ENSG00000158604.14_2	TMED4	chr7:44617493-44621886	1.600498921	3.032481662
134	ENSG00000120075.5_2	HOXB5	chr17:46668619-46671323	1.584439293	2.998912217
135	ENSG00000123836.14_1	PFKFB2	chr1:207207711-207254369	1.576953982	2.983392889
136	ENSG00000172007.5_1	RAB33B	chr4:140374386-140397763	1.576906077	2.983293827
137	ENSG00000142751.14_1	GPN2	chr1:27202624-27216788	1.576883501	2.983247144
138	ENSG00000114933.15_2	INO80D	chr2:206858445-206951027	1.575849144	2.981109037
139	ENSG00000134533.6_2	RERG	chr12:15260717-15501609	1.565517471	2.959836473
140	ENSG00000129480.12_2	DTD2	chr14:31915242-31926716	1.558274548	2.945014114
141	ENSG00000132912.12_1	DCTN4	chr5:150088002-150138671	1.54839115	2.924907804
142	ENSG00000158769.17_2	F11R	chr1:160965001-160991138	1.54598755	2.920038823
143	ENSG00000275993.2_1	CH507-42P11.8	chr21:44834402-44847008	1.53406064	2.895998068

144	ENSG00000124164.15_1	VAPB	chr20:56964178-57026157	1.532672314	2.893212548
145	ENSG00000129055.12_1	ANAPC13	chr3:134196548-134205558	1.526520196	2.880901223
146	ENSG00000129128.12_1	SPCS3	chr4:177241115-177253396	1.52132257	2.870540817
147	ENSG00000162433.14_2	AK4	chr1:65613232-65697828	1.514809248	2.857610424
148	ENSG00000112078.13_1	KCTD20	chr6:36410544-36458920	1.502205603	2.832754552
149	ENSG00000164188.8_2	RANBP3L	chr5:36248536-36302216	1.498911474	2.826293856
150	ENSG00000155959.10_1	VBP1	chrX:154425284-154468098	1.494670947	2.817998702
151	ENSG00000109062.10_2	SLC9A3R1	chr17:72744752-72765492	1.49327432	2.815272006
152	ENSG00000236104.2_2	ZBTB22	chr6:33282183-33285719	1.492567496	2.813893051
153	ENSG00000006625.17_2	GGCT	chr7:30536237-30544460	1.488451922	2.805877301
154	ENSG00000137492.7_2	THAP12	chr11:76061000-76092015	1.482673692	2.794661777
155	ENSG00000147536.11_1	GINS4	chr8:41386725-41402565	1.458525013	2.748272412
156	ENSG00000143401.14_2	ANP32E	chr1:150190717-150208504	1.452840847	2.737465622
157	ENSG00000213064.9_1	SFT2D2	chr1:168195176-168222263	1.450875702	2.733739364
158	ENSG00000177721.4_2	ANXA2R	chr5:43039183-43043272	1.446873693	2.726166531
159	ENSG00000131446.16_2	MGAT1	chr5:180211782-180242652	1.446651176	2.725746087
160	ENSG00000206075.13_2	SERPINB5	chr18:61143994-61172318	1.437439401	2.708397328
161	ENSG00000122140.10_1	MRPS2	chr9:138391830-138396519	1.437116242	2.707790724
162	ENSG00000106799.12_1	TGFBR1	chr9:101866320-101916474	1.436085305	2.705856452
163	ENSG00000160113.5_2	NR2F6	chr19:17342692-17356749	1.434390326	2.702679288
164	ENSG00000152104.11_2	PTPN14	chr1:214522039-214725792	1.424507696	2.684228885
165	ENSG00000120948.15_2	TARDBP	chr1:11072401-11086477	1.423206107	2.681808286
166	ENSG00000104442.9_1	ARMC1	chr8:66514691-66546452	1.421203071	2.67808745
167	ENSG00000165434.7_1	PGM2L1	chr11:74041363-74109518	1.406179835	2.650344384
168	ENSG00000102931.7_2	ARL2BP	chr16:57279010-57287547	1.393997266	2.628058274
169	ENSG00000158470.5_1	B4GALT5	chr20:48249482-48330415	1.393995561	2.628055168
170	ENSG00000171475.13_1	WIPF2	chr17:38375556-38440388	1.388062258	2.617269087
171	ENSG00000180773.14_2	SLC36A4	chr11:92877337-92931130	1.384431398	2.610690433
172	ENSG00000160209.18_1	PDXK	chr21:45138975-45182188	1.382992765	2.608088391
173	ENSG00000085719.12_2	CPNE3	chr8:87526656-87573726	1.379635354	2.602025957
174	ENSG00000170145.4_1	SIK2	chr11:111473115-111601577	1.37786695	2.59883844
175	ENSG00000111331.12_1	OAS3	chr12:113376157-113411054	1.377583016	2.598327018
176	ENSG00000105855.9_1	ITGB8	chr7:20370325-20455377	1.373047206	2.590170749
177	ENSG00000110042.7_1	DTX4	chr11:58938903-58976060	1.372194369	2.588640043
178	ENSG00000268533.1_2	AC004076.7	chr19:57905551-57949825	1.355227612	2.558374761
179	ENSG00000052802.12_2	MSMO1	chr4:166248775-166264312	1.352653635	2.55381432
180	ENSG00000143190.21_2	POU2F1	chr1:167190066-167396582	1.349885073	2.548918197
181	ENSG00000112210.11_1	RAB23	chr6:57051790-57087112	1.348118501	2.545798971
182	ENSG00000177853.14_2	ZNF518A	chr10:97889472-97965044	1.337211178	2.526624337
183	ENSG00000166130.14_1	IKBIP	chr12:99007183-99038891	1.334274556	2.521486595
184	ENSG00000162512.15_2	SDC3	chr1:31342314-31381608	1.3341299	2.521233785
185	ENSG00000003989.16_2	SLC7A2	chr8:17354597-17428082	1.327910935	2.510388998
186	ENSG00000101447.13_1	FAM83D	chr20:37554955-37581749	1.326177269	2.507374111
187	ENSG00000115884.10_1	SDC1	chr2:20400558-20425194	1.325325773	2.505894666
188	ENSG00000147533.16_1	GOLGA7	chr8:41347915-41368499	1.324207782	2.50395352
189	ENSG00000135956.8_1	TMEM127	chr2:96914254-96931732	1.321569497	2.499378675
190	ENSG00000204389.9_2	HSPA1A	chr6:31783241-31785723	1.320398597	2.497350987
191	ENSG00000133393.12_1	FOPNL	chr16:15959577-15982482	1.31950318	2.495801472
192	ENSG00000078401.6_1	EDN1	chr6:12290596-12297427	1.315960498	2.489680301

193	ENSG00000166881.9_2	NEMP1	chr12:57449426-57481846	1.30999824	2.479412375
194	ENSG00000111843.13_1	TMEM14C	chr6:10723148-10731362	1.308748504	2.477265511
195	ENSG00000185551.13_2	NR2F2	chr15:96869167-96883492	1.303536573	2.468332201
196	ENSG00000099795.6_1	NDUFB7	chr19:14676890-14682874	1.300171759	2.462581991
197	ENSG00000198961.9_1	PJA2	chr5:108670410-108745695	1.297487643	2.458004647
198	ENSG00000198252.11_1	STYX	chr14:53196898-53241716	1.293978825	2.45203373
199	ENSG00000155621.14_1	C9orf85	chr9:74526426-74600970	1.289745065	2.444848494
200	ENSG00000282936.1_1	CTC-281F24.5	chr17:6540100-6543636	1.288496771	2.442734
201	ENSG00000102780.16_2	DGKH	chr13:42614172-42830714	1.287501911	2.441050111
202	ENSG00000122873.11_1	CISD1	chr10:60028818-60049346	1.287210028	2.440556291
203	ENSG00000118985.15_1	ELL2	chr5:95220802-95297775	1.280791435	2.429722302
204	ENSG00000120709.10_1	FAM53C	chr5:137667624-137685418	1.273016724	2.416663702
205	ENSG00000108829.9_2	LRRC59	chr17:48452420-48474914	1.272350837	2.415548528
206	ENSG00000173598.13_2	NUDT4	chr12:93771659-93801922	1.270132949	2.411837903
207	ENSG00000187325.4_1	TAF9B	chrX:77385245-77395203	1.2694224	2.410650329
208	ENSG00000198663.16_2	C6orf89	chr6:36839646-36896740	1.26413344	2.401828998
209	ENSG00000133678.13_2	TMEM254	chr10:81838402-81852313	1.258149579	2.391887572
210	ENSG00000168564.5_1	CDKN2AIP	chr4:184365744-184369351	1.256756135	2.389578455
211	ENSG00000127334.10_2	DYRK2	chr12:68042118-68059186	1.254771883	2.386294138
212	ENSG00000153944.10_2	MSI2	chr17:55333212-55762046	1.251386976	2.380701886
213	ENSG00000184209.14_2	SNRNP35	chr12:123942188-123957701	1.250974343	2.380021065
214	ENSG00000152492.13_1	CCDC50	chr3:191046866-191116459	1.250712445	2.379589051
215	ENSG00000084652.15_1	TXLNA	chr1:32645287-32663886	1.250411354	2.379092481
216	ENSG00000141026.5_1	MED9	chr17:17380300-17396540	1.248539086	2.376006999
217	ENSG00000008086.11_2	CDKL5	chrX:18443703-18671749	1.248320008	2.375646222
218	ENSG00000117697.14_1	NSL1	chr1:212899495-212965124	1.242740139	2.36647575
219	ENSG00000132356.11_1	PRKAA1	chr5:40759481-40798476	1.233242089	2.350947121
220	ENSG00000092847.11_2	AGO1	chr1:36335409-36396129	1.232333242	2.349466573
221	ENSG00000109519.12_1	GRPEL1	chr4:7060633-7069924	1.230228702	2.346041773
222	ENSG00000150779.11_1	TIMM8B	chr11:111955524-111957522	1.230001547	2.345672414
223	ENSG00000155858.5_1	LSM11	chr5:157170703-157187717	1.229752051	2.345266794
224	ENSG00000008282.8_1	SYPL1	chr7:105730949-105753022	1.226992467	2.340785061
225	ENSG00000124783.12_2	SSR1	chr6:7268539-7347679	1.225868931	2.338962823
226	ENSG00000058091.16_2	CDK14	chr7:90095738-90839905	1.2241556	2.336186742
227	ENSG00000116273.5_1	PHF13	chr1:6673745-6684093	1.220625072	2.330476672
228	ENSG00000052723.11_1	SIKE1	chr1:115312100-115323306	1.217454883	2.325361288
229	ENSG00000173917.10_1	HOXB2	chr17:46618256-46622351	1.212364204	2.317170502
230	ENSG00000173889.15_1	PHC3	chr3:169804520-169899537	1.208669661	2.311244139
231	ENSG00000183723.12_2	CMTM4	chr16:66648653-66730610	1.20264423	2.301611334
232	ENSG00000121417.13_1	ZNF211	chr19:58141763-58154147	1.202511984	2.301400363
233	ENSG00000173744.17_2	AGFG1	chr2:228336868-228425930	1.197484841	2.293394975
234	ENSG00000104756.15_1	KCTD9	chr8:25285363-25315992	1.197135146	2.292839146
235	ENSG00000132603.13_2	NIP7	chr16:69373333-69377014	1.193811419	2.28756291
236	ENSG00000164466.12_2	SFXN1	chr5:174904065-174956745	1.193490858	2.287054679
237	ENSG00000108064.10_2	TFAM	chr10:60144782-60158981	1.191405799	2.283751694
238	ENSG00000167074.14_1	TEF	chr22:41763337-41795330	1.190796784	2.282787842
239	ENSG00000177981.10_2	ASB8	chr12:48541571-48574996	1.186006569	2.275220816
240	ENSG00000097033.14_1	SH3GLB1	chr1:87170253-87213867	1.173057681	2.254890977
241	ENSG00000140382.14_2	HMG20A	chr15:77712754-77777949	1.172026952	2.253280551

242	ENSG00000141574.7_2	SECTM1	chr17:80278900-80291950	1.168991267	2.248544236
243	ENSG00000273439.1	ZNF8	chr19:58790318-58807254	1.168125276	2.247194932
244	ENSG00000186908.14_2	ZDHHC17	chr12:77157368-77247476	1.167929616	2.246890186
245	ENSG00000198081.10_2	ZBTB14	chr18:5289018-5297052	1.166464434	2.244609432
246	ENSG00000259529.1_2	RP11-468E2.4	chr14:24620427-24636611	1.159592346	2.233942955
247	ENSG00000154511.11_1	FAM69A	chr1:93298294-93427079	1.154319905	2.225793737
248	ENSG00000165660.7_1	FAM175B	chr10:126490354-126525239	1.154292885	2.225752051
249	ENSG00000182318.5_1	ZSCAN22	chr19:58838385-58853698	1.147617323	2.215476959
250	ENSG00000096063.15_2	SRPK1	chr6:35800743-35889119	1.147561207	2.215390787
251	ENSG00000116205.11_2	TCEANC2	chr1:54519260-54578192	1.146452397	2.213688761
252	ENSG00000115159.15_1	GPD2	chr2:157291802-157470247	1.145537931	2.212286038
253	ENSG00000104419.14_2	NDRG1	chr8:134249414-134314265	1.144738157	2.211059972
254	ENSG00000169570.9_2	DTWD2	chr5:118173017-118324240	1.14365445	2.209399717
255	ENSG00000235878.4	AP001468.1	chr21:47612391-47613673	1.140445624	2.204491056
256	ENSG00000005073.5_1	HOXA11	chr7:27221129-27224842	1.140249073	2.20419074
257	ENSG00000125954.12_2	CHURC1-FNTB	chr14:65381203-65528521	1.139159213	2.20252625
258	ENSG00000070444.14_1	MNT	chr17:2287354-2304412	1.136132711	2.197910608
259	ENSG00000196247.11_2	ZNF107	chr7:64126461-64171960	1.129974351	2.188548492
260	ENSG00000198856.12_1	OSTC	chr4:109571740-109588976	1.129870451	2.188390883
261	ENSG00000213593.9_2	TMX2	chr11:57480072-57508445	1.128686716	2.18659604
262	ENSG00000167130.17_2	DOLPP1	chr9:131843379-131852717	1.128395795	2.186155155
263	ENSG00000164011.17_1	ZNF691	chr1:43312244-43318148	1.127540393	2.184859325
264	ENSG00000135913.10_1	USP37	chr2:219314974-219433084	1.127375447	2.184609541
265	ENSG00000084112.14_2	SSH1	chr12:109171968-109251366	1.126497769	2.183280916
266	ENSG00000214871.3	AC005082.1	chr7:23210760-23234503	1.124316709	2.179982735
267	ENSG00000134321.11_1	RSAD2	chr2:7005937-7038370	1.122339236	2.176996724
268	ENSG00000139644.12_2	TMBIM6	chr12:50101508-50158717	1.116025906	2.167490854
269	ENSG00000104381.12_1	GDAP1	chr8:75233365-75401107	1.115932151	2.167350002
270	ENSG00000179562.2_1	GCC1	chr7:127220672-127233665	1.115172336	2.166208838
271	ENSG00000170345.9_2	FOS	chr14:75745477-75748933	1.113978148	2.164416505
272	ENSG00000118260.14_2	CREB1	chr2:208394461-208468155	1.113473341	2.163659297
273	ENSG00000105085.10_2	MED26	chr19:16685718-16739873	1.11145308	2.160631562
274	ENSG00000258315.5_2	C17orf49	chr17:6917814-6920844	1.110955788	2.159886929
275	ENSG00000198466.11_2	ZNF587	chr19:58361225-58376480	1.10968395	2.157983673
276	ENSG00000148154.9_1	UGCG	chr9:114659046-114697649	1.107142433	2.154185419
277	ENSG00000235750.9_1	KIAA0040	chr1:175126123-175162135	1.105359841	2.151525353
278	ENSG00000114503.10_2	NCBP2	chr3:196662273-196669468	1.103378423	2.148572445
279	ENSG00000130332.14_2	LSM7	chr19:2321516-2328619	1.103060595	2.148099165
280	ENSG00000204568.11_1	MRPS18B	chr6:30585486-30594172	1.099103967	2.142216018
281	ENSG00000251201.8_2	TMED7-TICAM2	chr5:114914339-114961858	1.097939256	2.140487271
282	ENSG00000135069.13_1	PSAT1	chr9:80912059-80945009	1.097675208	2.140095546
283	ENSG00000132109.9_1	TRIM21	chr11:4406127-4414926	1.097028807	2.139136888
284	ENSG00000168275.14_1	COA6	chr1:234509202-234519795	1.094498552	2.135388474
285	ENSG00000101928.12_1	MOSPD1	chrX:134021656-134049297	1.094460314	2.135331878
286	ENSG00000158406.4_1	HIST1H4H	chr6:26277837-26285866	1.092759152	2.132815473
287	ENSG00000124839.12_1	RAB17	chr2:238482965-238510257	1.092305463	2.132144865
288	ENSG00000103966.10_2	EHD4	chr15:42188137-42264776	1.091199634	2.130511198
289	ENSG00000143363.15_2	PRUNE1	chr1:150980896-151008189	1.089539835	2.128061486
290	ENSG00000164764.10_2	SBSPON	chr8:73976775-74036323	1.087982924	2.125766187

291	ENSG00000165879.8_1	FRAT1	chr10:99079024-99081672	1.083278054	2.118845
292	ENSG00000067082.14_1	KLF6	chr10:3818188-3827473	1.081568161	2.116335216
293	ENSG00000168438.14_1	CDC40	chr6:110501344-110575478	1.081447082	2.11615761
294	ENSG00000163041.9_1	H3F3A	chr1:226249552-226259702	1.076780535	2.109323736
295	ENSG00000115310.17_2	RTN4	chr2:55199323-55339757	1.075463096	2.107398425
296	ENSG00000119048.7_2	UBE2B	chr5:133706870-133727683	1.074815052	2.106452015
297	ENSG00000179454.13_1	KLHL28	chr14:45393522-45511525	1.073032106	2.103850377
298	ENSG00000215193.12_2	PEX26	chr22:18560686-18613905	1.072896443	2.103652552
299	ENSG00000182551.13_1	ADI1	chr2:3501132-3523507	1.072859451	2.103598613
300	ENSG00000270276.2_1	HIST2H4B	chr1:149825607-149832776	1.071765597	2.102004266
301	ENSG00000175073.7_1	VCPIP1	chr8:67540722-67579452	1.066914044	2.094947434
302	ENSG00000134247.9_1	PTGFRN	chr1:117452679-117532980	1.065835895	2.09338243
303	ENSG00000108582.11_1	CPD	chr17:28705923-28797007	1.064696226	2.091729398
304	ENSG00000142166.12_2	IFNAR1	chr21:34696782-34732168	1.062211513	2.088129973
305	ENSG00000148672.8_1	GLUD1	chr10:88810243-88854623	1.059101345	2.083633221
306	ENSG00000142892.14_2	PIGK	chr1:77554675-77685115	1.05881911	2.08322564
307	ENSG00000145332.13_1	KLHL8	chr4:88081255-88161466	1.058192465	2.082320972
308	ENSG00000163788.13_1	SNRK	chr3:43328004-43466256	1.057975773	2.082008232
309	ENSG00000169239.12_2	CA5B	chrX:15706953-15806532	1.057271147	2.080991608
310	ENSG00000141378.14_1	PTRH2	chr17:57751997-57784987	1.056171624	2.079406223
311	ENSG00000212747.4_1	FAM127C	chrX:134154534-134156559	1.055476112	2.078404
312	ENSG00000101413.11_1	RPRD1B	chr20:36661948-36756182	1.050086253	2.070653641
313	ENSG00000171861.10_2	MRM3	chr17:685513-695749	1.047238828	2.066570853
314	ENSG00000124201.14_1	ZNFX1	chr20:47854483-47894963	1.045202937	2.063656623
315	ENSG00000079950.13_1	STX7	chr6:132767006-132834337	1.042542118	2.059854048
316	ENSG00000256206.2_2	RP11-140L24.4	chr11:14515329-14541890	1.042478616	2.059763383
317	ENSG00000219607.3_1	PPP1R3G	chr6:5084815-5089721	1.040415544	2.05682
318	ENSG00000163069.12_1	SGCB	chr4:52886872-52904648	1.023556923	2.032924904
319	ENSG00000168569.7_2	TMEM223	chr11:62539101-62559493	1.021603454	2.030174102
320	ENSG00000184208.10_1	C22orf46	chr22:42084943-42094140	1.019137431	2.026706855
321	ENSG00000167112.9_2	TRUB2	chr9:131067440-131085021	1.017430662	2.024310594
322	ENSG00000106688.11_1	SLC1A1	chr9:4490444-4587469	1.017115743	2.023868764
323	ENSG00000126775.8_2	ATG14	chr14:55833110-55878576	1.016158799	2.022526771
324	ENSG00000168769.13_2	TET2	chr4:106067032-106200973	1.014695042	2.020475758
325	ENSG00000145623.12_2	OSMR	chr5:38845960-38945698	1.009804381	2.013638047
326	ENSG00000101945.16_1	SUV39H1	chrX:48553945-48567403	1.008840275	2.012292848
327	ENSG00000149016.15_2	TUT1	chr11:62342517-62359649	1.007766799	2.010796104
328	ENSG00000158042.8_1	MRPL17	chr11:6702013-6704632	1.004446231	2.006173293
329	ENSG00000131115.15_1	ZNF227	chr19:44711700-44741421	1.001175201	2.001629838
330	ENSG00000114450.9_2	GNB4	chr3:179113877-179169378	1.001147717	2.001591707
331	ENSG00000204175.5_1	GPRIN2	chr10:46994087-47000573	0.999892023	1.999850318
332	ENSG00000100266.18_2	PACSIN2	chr22:43231418-43411151	0.996100707	1.994601731
333	ENSG00000168917.8_1	SLC35G2	chr3:136537489-136574734	0.994486894	1.992371797
334	ENSG00000138376.10_2	BARD1	chr2:215590370-215674435	0.993113325	1.990475791
335	ENSG00000125449.6_1	ARMC7	chr17:73106047-73126360	0.990723247	1.987180948
336	ENSG00000150051.13_2	MKX	chr10:27961804-28034989	0.990700854	1.987150104
337	ENSG00000185736.15_2	ADARB2	chr10:1223258-1779670	0.990165389	1.986412697
338	ENSG00000154114.12_2	TBCEL	chr11:120894781-120961484	0.99013108	1.986365459
339	ENSG00000125629.14_1	INSIG2	chr2:118846028-118868573	0.981716189	1.974813194

340	ENSG00000152952.11_1	PLOD2	chr3:145787227-145881440	0.978419194	1.970305301
341	ENSG00000151743.10_2	AMN1	chr12:31824071-31882108	0.975353798	1.966123299
342	ENSG00000005020.12_2	SKAP2	chr7:26706681-27034858	0.967602272	1.955587749
343	ENSG00000147548.16_2	WHSC1L1	chr8:38127215-38239790	0.965286167	1.952450763
344	ENSG00000230567.3	FAM203B	chr8:145437880-145440835	0.964649783	1.951589712
345	ENSG00000169981.10_2	ZNF35	chr3:44690219-44702283	0.964382337	1.951227961
346	ENSG00000111775.2_2	COX6A1	chr12:120875893-120878545	0.963505061	1.950041816
347	ENSG00000203811.1_1	HIST2H3C	chr1:149811110-149812765	0.961300306	1.947064
348	ENSG00000171159.4_1	C9orf16	chr9:130922539-130926207	0.961291716	1.947052407
349	ENSG00000124466.8_1	LYPD3	chr19:43964939-43969812	0.959854574	1.945113815
350	ENSG00000131069.19_2	ACSS2	chr20:33459949-33515765	0.95981122	1.945055363
351	ENSG00000172840.6_2	PDP2	chr16:66912492-66929657	0.959242762	1.944289113
352	ENSG00000134108.12_1	ARL8B	chr3:5163905-5222597	0.957390505	1.941794469
353	ENSG00000173852.14_2	DPY19L1	chr7:34968488-35077883	0.957170532	1.941498419
354	ENSG00000183542.5_2	KLRC4	chr12:10559981-10562356	0.956561534	1.940679036
355	ENSG00000178878.12_2	APOLD1	chr12:12878851-12982909	0.955511456	1.939267009
356	ENSG00000099219.13_1	ERMP1	chr9:5765076-5833117	0.954221918	1.937534391
357	ENSG00000163738.18_2	MTHFD2L	chr4:74979891-75168816	0.951053741	1.933284209
358	ENSG00000173011.11_2	TADA2B	chr4:7043626-7059679	0.949141804	1.930723813
359	ENSG00000135373.12_1	EHF	chr11:34642640-34682604	0.948463926	1.929816839
360	ENSG00000169519.20_2	METTL15	chr11:28129795-28548588	0.948091667	1.929318952
361	ENSG00000101782.14_2	RIOK3	chr18:21032787-21066567	0.947654123	1.928733912
362	ENSG00000241127.7_2	YAE1D1	chr7:39605975-39649919	0.946720171	1.927485718
363	ENSG00000169100.13_1_PAR_Y	SLC25A6	chrY:1455045-1461617	0.946636501	1.927373936
364	ENSG00000253368.3_1	TRNP1	chr1:27320198-27327389	0.946425769	1.927092429
365	ENSG00000012963.14_2	UBR7	chr14:93673401-93695561	0.944009545	1.923867638
366	ENSG00000215712.10_2	TMEM242	chr6:157710418-157744633	0.941486572	1.920506134
367	ENSG00000241258.6_2	CRCP	chr7:65579591-65619555	0.941263744	1.92020953
368	ENSG00000178252.17_2	WDR6	chr3:49044495-49053386	0.940881594	1.91970096
369	ENSG00000146007.10_2	ZMAT2	chr5:140078265-140086261	0.938933271	1.917110203
370	ENSG00000115540.14_2	MOB4	chr2:198380295-198418423	0.933701214	1.91017023
371	ENSG00000076248.10_1	UNG	chr12:109535379-109548797	0.933285155	1.909619436
372	ENSG00000101557.14_2	USP14	chr18:158383-214629	0.929918659	1.905168577
373	ENSG00000066583.11_1	ISOC1	chr5:128430444-128449721	0.929359035	1.904429702
374	ENSG00000233608.3_1	TWIST2	chr2:239756673-239832239	0.928388098	1.903148448
375	ENSG00000143590.13_2	EFNA3	chr1:155051348-155060014	0.926422049	1.900556678
376	ENSG00000119640.8_1	ACYP1	chr14:75519924-75536186	0.92450716	1.898035742
377	ENSG00000175602.3_1	CCDC85B	chr11:65657583-65659106	0.923949336	1.897302
378	ENSG00000175893.11_1	ZDHHC21	chr9:14611069-14693469	0.923904167	1.897242599
379	ENSG00000171970.12_2	ZNF57	chr19:2900896-2918474	0.923496154	1.896706111
380	ENSG00000105722.9_2	ERF	chr19:42751724-42759309	0.922950959	1.895989479
381	ENSG00000196154.11_2	S100A4	chr1:153516089-153522612	0.921540676	1.894136992
382	ENSG00000198146.4_2	ZNF770	chr15:35270542-35280488	0.918863463	1.890625296
383	ENSG00000169991.10_2	IFFO2	chr1:19230775-19283180	0.917073414	1.888280925
384	ENSG00000121060.15_2	TRIM25	chr17:54965270-54991399	0.914487639	1.884899547
385	ENSG00000175305.17_2	CCNE2	chr8:95891998-95908906	0.913440872	1.883532428
386	ENSG00000137449.15_1	CPEB2	chr4:15004298-15071777	0.909990137	1.879032652
387	ENSG00000198040.10_2	ZNF84	chr12:133613878-133639890	0.90602442	1.873874612
388	ENSG00000161888.11_2	SPC24	chr19:11242196-11266484	0.905035945	1.87259115

389	ENSG00000176095.11_1	IP6K1	chr3:49761727-49823975	0.905000097	1.872544621
390	ENSG00000144736.13_1	SHQ1	chr3:72798428-72911065	0.904710433	1.872168689
391	ENSG00000197355.10_1	UAP1L1	chr9:139971953-139978991	0.904620166	1.872051555
392	ENSG00000203618.5_2	GP1BB	chr22:19710468-19712294	0.904181172	1.871482
393	ENSG00000145040.3_2	UCN2	chr3:48599160-48601206	0.902441781	1.869227
394	ENSG00000166166.12_1	TRMT61A	chr14:103995521-104003410	0.902281292	1.869019074
395	ENSG00000185947.14_2	ZNF267	chr16:31885079-31928678	0.900493136	1.866703943
396	ENSG00000173848.18_1	NET1	chr10:5454514-5500426	0.900060863	1.866144708
397	ENSG00000143443.9_1	C1orf56	chr1:151020216-151024462	0.899956188	1.866009315
398	ENSG00000196793.13_1	ZNF239	chr10:44051792-44070066	0.899870244	1.865898156
399	ENSG00000164715.5_1	LMTK2	chr7:97736197-97838945	0.89661201	1.861688901
400	ENSG00000157181.15_2	C1orf27	chr1:186344970-186390510	0.889447368	1.852466391
401	ENSG00000203852.3_1	HIST2H3A	chr1:149824181-149825836	0.888942315	1.851818
402	ENSG00000129355.6_1	CDKN2D	chr19:10677138-10679735	0.888504889	1.851256612
403	ENSG00000117479.12_2	SLC19A2	chr1:169433147-169455241	0.887648296	1.850157765
404	ENSG00000177683.13_2	THAP5	chr7:108194987-108210194	0.886652994	1.848881798
405	ENSG00000150782.11_1	IL18	chr11:112013974-112034840	0.886417535	1.84858007
406	ENSG00000140265.12_1	ZSCAN29	chr15:43650370-43663223	0.885998688	1.848043465
407	ENSG00000182208.12_1	MOB2	chr11:1490687-1522477	0.884127785	1.845648454
408	ENSG00000047644.18_2	WWC3	chrX:9983602-10112518	0.882172555	1.84314881
409	ENSG00000173451.6_2	THAP2	chr12:72056789-72074419	0.881492469	1.842280156
410	ENSG00000068366.19_2	ACSL4	chrX:108867473-108976632	0.880471056	1.840976303
411	ENSG00000163257.10_1	DCAF16	chr4:17802278-17812381	0.879436831	1.839657034
412	ENSG00000243335.8_2	KCTD7	chr7:66093868-66276174	0.87696749	1.83651094
413	ENSG00000001167.14_1	NFYA	chr6:41040684-41067715	0.87632281	1.835690464
414	ENSG00000033100.15_2	CHPF2	chr7:150929575-150935913	0.876110455	1.835420283
415	ENSG00000154127.9_1	UBASH3B	chr11:122526383-122685181	0.871439567	1.829487511
416	ENSG00000239305.6_2	RNF103	chr2:86830516-86850989	0.868530022	1.825801623
417	ENSG00000135900.3_1	MRPL44	chr2:224822121-224832431	0.866632615	1.823401939
418	ENSG00000187607.15_2	ZNF286A	chr17:15602891-15624101	0.866328949	1.82301818
419	ENSG00000278845.4_1	MRPL45	chr17:36452989-36479101	0.865858012	1.822423192
420	ENSG00000105514.7_2	RAB3D	chr19:11432722-11456946	0.865697928	1.822220984
421	ENSG00000065923.9_2	SLC9A7	chrX:46458687-46618607	0.863778479	1.819798203
422	ENSG00000142867.12_1	BCL10	chr1:85731931-85742773	0.863547913	1.819507393
423	ENSG00000180834.7_2	MAP6D1	chr3:183533664-183543382	0.858619175	1.813301942
424	ENSG00000135316.17_2	SYNCRIP	chr6:86317503-86353510	0.857847831	1.812332709
425	ENSG00000204822.6_2	MRPL53	chr2:74699085-74700449	0.855419269	1.809284484
426	ENSG00000136867.10_1	SLC31A2	chr9:115913222-115926417	0.855209557	1.809021504
427	ENSG00000008083.13_1	JARID2	chr6:15246527-15522271	0.8540683	1.807591026
428	ENSG00000196459.13_1	TRAPPC2	chrX:13730363-13752754	0.852633929	1.805794758
429	ENSG00000144746.6_1	ARL6IP5	chr3:69134095-69155217	0.847773154	1.799720854
430	ENSG00000164176.12_2	EDIL3	chr5:83236373-83680611	0.847167304	1.798965232
431	ENSG00000257529.5_2	RPL36A-HNRNPH2	chrX:100645999-100667285	0.844351754	1.795457812
432	ENSG00000257923.9_2	CUX1	chr7:101459184-101927249	0.844009651	1.795032109
433	ENSG00000165406.15_1	MARCH8	chr10:45950033-46090354	0.843879578	1.794870278
434	ENSG00000169032.9_1	MAP2K1	chr15:66679155-66784650	0.842284313	1.79288669
435	ENSG00000163291.14_1	PAQR3	chr4:79808281-79860592	0.842278372	1.792879307
436	ENSG00000168528.11_1	SERINC2	chr1:31882412-31907527	0.842112097	1.792672684
437	ENSG00000268313.1	AC119673.1	chr1:205682497-205684153	0.839159032	1.789007

438	ENSG00000258643.5_2	BCL2L2-PABPN1	chr14:23776044-23794578	0.837594734	1.787068251
439	ENSG00000115183.13_2	TANC1	chr2:159825146-160089170	0.836509943	1.785725023
440	ENSG00000167394.12_1	ZNF668	chr16:31072164-31085641	0.834667286	1.783445694
441	ENSG00000104998.3_1	IL27RA	chr19:14142560-14164028	0.833988787	1.782607137
442	ENSG00000164663.14_2	USP49	chr6:41757634-41863099	0.832564648	1.780848326
443	ENSG00000171004.17_2	HS6ST2	chrX:131760044-132095423	0.831754107	1.779848084
444	ENSG00000147862.10	NFIB	chr9:14081842-14398982	0.830361245	1.778130544
445	ENSG00000104549.11_1	SQLE	chr8:126010739-126034525	0.830272444	1.778021099
446	ENSG00000143727.15_1	ACP1	chr2:264140-278283	0.830037939	1.777732112
447	ENSG00000137413.15_1	TAF8	chr6:42018251-42055199	0.830003986	1.777690274
448	ENSG00000146674.14_2	IGFBP3	chr7:45951844-45961473	0.827995998	1.77521775
449	ENSG00000134278.15_2	SPIRE1	chr18:12446511-12658133	0.82781799	1.774998728
450	ENSG00000198265.11_2	HELZ	chr17:65066554-65242105	0.824067458	1.770390308
451	ENSG00000160051.11_1	IQCC	chr1:32671262-32674288	0.823426548	1.769603995
452	ENSG00000100320.22_2	RBFOX2	chr22:36134783-36424473	0.819835834	1.765205117
453	ENSG00000080603.16_2	SRCAP	chr16:30709530-30752730	0.819681212	1.76501594
454	ENSG00000108671.9_2	PSMD11	chr17:30771279-30810336	0.815963363	1.760473319
455	ENSG00000053372.4_1	MRTO4	chr1:19578033-19586622	0.815256839	1.759611382
456	ENSG00000163814.7_1	CDCP1	chr3:45123770-45187914	0.814677296	1.758904673
457	ENSG00000179304.16_2	FAM156B	chrX:52920336-52937587	0.814497686	1.75868571
458	ENSG00000141526.15_2	SLC16A3	chr17:80186273-80219005	0.813796341	1.757830959
459	ENSG00000160446.18_1	ZDHHC12	chr9:131483148-131486406	0.809743398	1.752899639
460	ENSG00000135341.17_1	MAP3K7	chr6:91223292-91296764	0.80872879	1.751667306
461	ENSG00000106615.9_1	RHEB	chr7:151163098-151217206	0.806462886	1.748918288
462	ENSG00000107789.15_1	MINPP1	chr10:89264632-89313217	0.804658295	1.746732026
463	ENSG00000138685.12_2	FGF2	chr4:123747863-123819391	0.802636358	1.744285696
464	ENSG00000109332.19_2	UBE2D3	chr4:103715540-103790053	0.800649302	1.741884907
465	ENSG00000126804.13_2	ZBTB1	chr14:64970430-65000408	0.798840148	1.739701934
466	ENSG00000107036.11_1	RIC1	chr9:5629025-5776557	0.797127957	1.73763848
467	ENSG00000163026.11_2	WDCP	chr2:24252210-24272445	0.79634049	1.736690283
468	ENSG00000123395.14_1	ATG101	chr12:52463030-52471278	0.796176983	1.736493467
469	ENSG00000170631.14_2	ZNF16	chr8:146155744-146176274	0.795390481	1.735547055
470	ENSG00000147459.17_1	DOCK5	chr8:25042238-25275598	0.792197123	1.731709727
471	ENSG00000150768.15_1	DLAT	chr11:111895538-111935114	0.787438671	1.726007425
472	ENSG00000177463.15_2	NR2C2	chr3:14989091-15095107	0.786494496	1.724878205
473	ENSG00000246705.4_2	H2AFJ	chr12:14927317-14930936	0.786241847	1.724576167
474	ENSG00000160870.12_2	CYP3A7	chr7:99302660-99332819	0.783077591	1.720797807
475	ENSG00000158290.16_1	CUL4B	chrX:119658464-119709649	0.78025731	1.717437157
476	ENSG00000101132.9_1	PFDN4	chr20:52824386-52844591	0.780061338	1.71720388
477	ENSG00000141759.14_1	TXNL4A	chr18:77730811-77793949	0.779728292	1.71680751
478	ENSG00000205339.9_1	IPO7	chr11:9406169-9469673	0.779296023	1.716293187
479	ENSG00000277258.4_1	PCGF2	chr17:36890150-36906070	0.777607757	1.714285926
480	ENSG00000137710.14_2	RDX	chr11:110045605-110167447	0.776047199	1.712432592
481	ENSG00000173641.17_2	HSPB7	chr1:16340523-16346089	0.774598278	1.710713633
482	ENSG00000161981.10_1	SNRNP25	chr16:103010-107669	0.773385092	1.70927567
483	ENSG00000225828.1_2	FAM229A	chr1:32826871-32829879	0.771017867	1.706473329
484	ENSG00000205643.10_1	CDPF1	chr22:46639908-46646576	0.769286564	1.704426708
485	ENSG00000054965.10_1	FAM168A	chr11:73111532-73309234	0.769021571	1.704113669
486	ENSG00000143933.16_2	CALM2	chr2:47387221-47403740	0.768448313	1.703436671

487	ENSG00000188015.9_2	S100A3	chr1:153519805-153521848	0.767909962	1.702801141
488	ENSG00000105976.14_2	MET	chr7:116312444-116438440	0.767674168	1.702522858
489	ENSG00000131931.8_1	THAP1	chr8:42691817-42698468	0.765619277	1.70009961
490	ENSG00000136146.14_2	MED4	chr13:48627459-48669267	0.764015774	1.69821106
491	ENSG00000162430.16_2	SEPN1	chr1:26126667-26144715	0.761183865	1.694880861
492	ENSG00000196139.13_2	AKR1C3	chr10:5077546-5149878	0.761139245	1.694828442
493	ENSG00000113312.10_1	TTC1	chr5:159436120-159492550	0.761065008	1.694741233
494	ENSG00000108239.8_1	TBC1D12	chr10:96162261-96295687	0.760287178	1.693827759
495	ENSG00000168118.11_2	RAB4A	chr1:229406809-229441641	0.758968848	1.692280651
496	ENSG00000144744.16_1	UBA3	chr3:69103881-69129559	0.758802668	1.692085734
497	ENSG00000178177.15_2	LCORL	chr4:17842822-18023499	0.758291223	1.691485984
498	ENSG00000213585.10_1	VDAC1	chr5:133307606-133340824	0.756383226	1.689250434
499	ENSG00000085662.13_1	AKR1B1	chr7:134127102-134144036	0.756311343	1.689166268
500	ENSG00000036054.12_1	TBC1D23	chr3:99979844-100044095	0.754384022	1.686911189
501	ENSG00000133997.11_2	MED6	chr14:71047974-71067407	0.752770517	1.685025609
502	ENSG00000204116.11_2	CHIC1	chrX:72783036-72906937	0.74896535	1.680587141
503	ENSG00000130312.6_1	MRPL34	chr19:17403418-17417652	0.747456116	1.678829961
504	ENSG00000152433.14_2	ZNF547	chr19:57874845-57890933	0.744169859	1.675010175
505	ENSG00000177842.11_1	ZNF620	chr3:40547483-40560227	0.741881935	1.672355935
506	ENSG00000147421.17_2	HMBOX1	chr8:28747911-28922281	0.741248957	1.671622355
507	ENSG00000181192.11_2	DHTKD1	chr10:12110971-12165224	0.739647553	1.669767868
508	ENSG00000187134.13_2	AKR1C1	chr10:5005445-5025475	0.735294507	1.664737268
509	ENSG00000134440.11_2	NARS	chr18:55267888-55289445	0.735287851	1.664729588
510	ENSG00000275778.1_2	PRH1-PRR4	chr12:10998448-11324197	0.731668172	1.660558066
511	ENSG00000109189.12_1	USP46	chr4:53457138-53525502	0.730001656	1.658640996
512	ENSG00000229117.8_1	RPL41	chr12:56510370-56511727	0.7288848	1.657357463
513	ENSG00000125945.14_1	ZNF436	chr1:23685941-23695935	0.725176103	1.65310241
514	ENSG00000157823.16_2	AP3S2	chr15:90373831-90437870	0.719816703	1.64697277
515	ENSG00000263155.5_2	MYZAP	chr15:57884139-57977562	0.719363681	1.646455684
516	ENSG00000272674.3_2	PCDHB16	chr5:140560980-140565974	0.719301743	1.646385
517	ENSG00000133731.9_1	IMPA1	chr8:82570196-82598928	0.719079748	1.646131681
518	ENSG00000143847.15_1	PPFIA4	chr1:202995626-203047868	0.719020312	1.646063866
519	ENSG00000154370.14_2	TRIM11	chr1:228581374-228594541	0.718328704	1.645274954
520	ENSG00000100483.13_1	VCPKMT	chr14:50575350-50583318	0.717207092	1.643996345
521	ENSG00000115657.12_2	ABCB6	chr2:220074490-220083712	0.71689824	1.643644437
522	ENSG00000181029.8_2	TRAPPC5	chr19:7745729-7752589	0.714723556	1.641168712
523	ENSG00000131467.10_1	PSME3	chr17:40976402-40995775	0.714222965	1.640599353
524	ENSG00000123562.16_2	MORF4L2	chrX:102930424-102943086	0.713129868	1.63935678
525	ENSG00000141560.14_1	FN3KRP	chr17:80674559-80688204	0.711693219	1.637725106
526	ENSG00000147124.12_1	ZNF41	chrX:47305278-47342345	0.709532128	1.635273705
527	ENSG00000164073.9_1	MFSD8	chr4:128838960-128887150	0.709525005	1.635265632
528	ENSG00000152620.12_1	NADK2	chr5:36192694-36242381	0.708941239	1.634604079
529	ENSG00000248109.2_2	CTC-295J13.3	chr5:147601213-147623143	0.707196153	1.632628054
530	ENSG00000177076.5_1	ACER2	chr9:19409057-19452018	0.706764392	1.632139524
531	ENSG00000198862.13_2	LTN1	chr21:30300466-30365277	0.70668224	1.632046587
532	ENSG00000125901.5_1	MRPS26	chr20:3026591-3028900	0.70634604	1.631666306
533	ENSG00000121774.17_1	KHDRBS1	chr1:32479430-32526451	0.706281299	1.631593086
534	ENSG00000151690.14_2	MFSD6	chr2:191273081-191373931	0.705009981	1.630155942
535	ENSG00000105656.12_2	ELL	chr19:18553473-18632937	0.704172303	1.629209693

536	ENSG00000251537.4_2	RP11-385D13.1	chr17:15474805-15554967	0.704153208	1.629188129
537	ENSG00000213185.6_2	FAM24B	chr10:124608594-124639157	0.703829916	1.628823088
538	ENSG00000143033.17_1	MTF2	chr1:93544792-93604638	0.702798701	1.627659247
539	ENSG00000268885.1	AC026740.1	chr5:667759-668839	0.700761806	1.625362828
540	ENSG00000280789.1_2	PAGR1	chr16:29827273-29831438	0.700251097	1.624787558
541	ENSG00000119820.10_2	YIPF4	chr2:32502979-32541663	0.699564295	1.624014254
542	ENSG00000143153.12_1	ATP1B1	chr1:169074935-169101960	0.699306736	1.62372435
543	ENSG00000134882.15_2	UBAC2	chr13:99853028-100038688	0.69794742	1.622195189
544	ENSG00000100211.10_1	CBY1	chr22:39052641-39069859	0.69498934	1.618872471
545	ENSG00000146243.13_1	IRAK1BP1	chr6:79577189-79656157	0.694559675	1.618390409
546	ENSG00000173457.10_2	PPP1R14B	chr11:64011952-64014413	0.694271454	1.61806712
547	ENSG00000196422.10_1	PPP1R26	chr9:138370925-138380739	0.693957792	1.617715368
548	ENSG00000169689.14_2	STRA13	chr17:79976578-79981983	0.692949029	1.616584623
549	ENSG00000136514.2_1	RTP4	chr3:187086120-187089864	0.690261058	1.613575471
550	ENSG00000074356.16_1	NCBP3	chr17:3705459-3749545	0.6897381	1.612990678
551	ENSG00000186130.4_1	ZBTB6	chr9:125670335-125675609	0.68959362	1.61282915
552	ENSG00000185658.13_2	BRWD1	chr21:40556102-40693485	0.688725967	1.611859469
553	ENSG00000280987.3_2	MATR3	chr5:138609441-138667366	0.688149801	1.611215873
554	ENSG00000198908.11_1	BHLHB9	chrX:101975616-102008468	0.685717537	1.608501785
555	ENSG00000116815.15_2	CD58	chr1:117057157-117113661	0.685321494	1.608060287
556	ENSG00000143507.17_1	DUSP10	chr1:221874766-221915518	0.684509605	1.60715559
557	ENSG00000198160.14_1	MIER1	chr1:67390578-67454302	0.684422305	1.607058342
558	ENSG00000185728.16_2	YTHDF3	chr8:64081112-64125344	0.682644388	1.60507909
559	ENSG00000167118.10_1	URM1	chr9:131133598-131154295	0.68258665	1.605014855
560	ENSG00000116984.12_2	MTR	chr1:236958581-237067281	0.68172642	1.604058125
561	ENSG00000198315.10_1	ZKSCAN8	chr6:28109688-28127250	0.681649016	1.603972065
562	ENSG00000198930.12_1	CSAG1	chrX:151903228-151909518	0.680103989	1.602255241
563	ENSG00000105887.10_2	MTPN	chr7:135611509-135662101	0.679961248	1.602096721
564	ENSG00000119231.10_2	SENP5	chr3:196594727-196661585	0.67963969	1.601739674
565	ENSG00000163428.3_1	LRRC58	chr3:120043356-120068186	0.678739039	1.600740046
566	ENSG00000154328.15_1	NEIL2	chr8:11627148-11644855	0.678241932	1.600188577
567	ENSG00000198743.6_2	SLC5A3	chr21:35445870-35478561	0.678147051	1.600083342
568	ENSG00000111700.12_2	SLCO1B3	chr12:20963636-21069845	0.677561351	1.599433877
569	ENSG00000187626.8_1	ZKSCAN4	chr6:28212401-28220002	0.677346095	1.599195253
570	ENSG00000156642.16_1	NPTN	chr15:73852355-73926475	0.676521673	1.598281661
571	ENSG00000136152.14_1	COG3	chr13:46039033-46110765	0.674892707	1.596478038
572	ENSG00000272962.1	SLC5A3	chr21:35445870-35478561	0.673334748	1.59475494
573	ENSG00000183840.6_2	GPR39	chr2:133174147-133404132	0.672615377	1.593959946
574	ENSG00000146477.5_1	SLC22A3	chr6:160769300-160873613	0.672273424	1.593582185
575	ENSG00000205060.10_1	SLC35B4	chr7:133974084-134001803	0.671480606	1.592706689
576	ENSG00000119328.11_1	FAM206A	chr9:111696461-111713024	0.670216615	1.591311879
577	ENSG00000180758.11_2	GPR157	chr1:9160364-9189229	0.669308138	1.590310132
578	ENSG00000168077.13_1	SCARA3	chr8:27491385-27534293	0.667648847	1.588482115
579	ENSG00000081386.12_1	ZNF510	chr9:99518147-99540411	0.66617137	1.586856169
580	ENSG00000147642.16_2	SYBU	chr8:110586207-110704020	0.665185176	1.585771801
581	ENSG00000115073.7_1	ACTR1B	chr2:98272426-98280570	0.66404809	1.584522439
582	ENSG00000180318.3_1	ALX1	chr12:85673885-85695562	0.663372479	1.583780584
583	ENSG00000163344.5_1	PMVK	chr1:154897210-154909467	0.663180178	1.583569492
584	ENSG00000173535.13_1	TNFRSF10C	chr8:22941868-22974950	0.661567632	1.581800475

585	ENSG00000129003.15_2	VPS13C	chr15:62144588-62352672	0.658769986	1.57873605
586	ENSG00000159921.14_1	GNE	chr9:36214438-36277053	0.656994384	1.57679421
587	ENSG00000118200.14_2	CAMSAP2	chr1:200708686-200829832	0.654704701	1.574293685
588	ENSG00000196648.6	GOLGA6L9	chr15:83098710-83108085	0.65436826	1.573926597
589	ENSG00000115419.12_2	GLS	chr2:191745553-191830278	0.653659503	1.57315356
590	ENSG00000197063.10_2	MAFG	chr17:79876146-79885590	0.652673628	1.572078902
591	ENSG00000135919.12_2	SERPINE2	chr2:224839829-224904036	0.651355044	1.570642721
592	ENSG00000122884.12_1	P4HA1	chr10:74766975-74856732	0.650261997	1.569453186
593	ENSG00000155324.9_2	GRAMD3	chr5:125695824-125832186	0.650176391	1.569360061
594	ENSG00000122481.16_2	RWDD3	chr1:95699711-95712781	0.649643315	1.56878029
595	ENSG00000173928.2_1	SWSAP1	chr19:11485361-11487627	0.649401631	1.568517506
596	ENSG00000164056.10_1	SPRY1	chr4:124317950-124324915	0.64923112	1.568332135
597	ENSG00000153214.9_2	TMEM87B	chr2:112812800-112876895	0.64778302	1.566758717
598	ENSG00000118518.15_2	RNF146	chr6:127587755-127609712	0.647278996	1.566211445
599	ENSG00000145908.12_1	ZNF300	chr5:150273954-150284545	0.647059563	1.565973244
600	ENSG00000154122.12_2	ANKH	chr5:14704913-14871887	0.646920547	1.565822356
601	ENSG00000123094.15_2	RASSF8	chr12:26111962-26232825	0.646828829	1.565722814
602	ENSG00000170471.14_2	RALGAPB	chr20:37101459-37207504	0.646600419	1.565474946
603	ENSG00000134294.13_1	SLC38A2	chr12:46751972-46766650	0.646104011	1.564936383
604	ENSG00000130921.7_1	C12orf65	chr12:123717463-123742506	0.646101865	1.564934055
605	ENSG00000025156.12_1	HSF2	chr6:122720691-122754264	0.646042788	1.564869974
606	ENSG00000143321.18_1	HDGF	chr1:156711899-156736717	0.645218322	1.563975944
607	ENSG00000198554.11_2	WDHD1	chr14:55405668-55493823	0.644886956	1.563616762
608	ENSG00000159674.11_2	SPON2	chr4:1160720-1202750	0.643068692	1.561647339
609	ENSG00000100225.17_1	FBXO7	chr22:32870663-32894816	0.642473264	1.56100295
610	ENSG00000131480.8_1	AOC2	chr17:40996617-41002724	0.64191405	1.560397995
611	ENSG00000181577.15_1	C6orf223	chr6:43968317-43973695	0.641663359	1.560126875
612	ENSG00000081181.7_1	ARG2	chr14:68086515-68118437	0.640713215	1.55909973
613	ENSG00000243646.9_2	IL10RB	chr21:34638663-34682492	0.639077562	1.557333105
614	ENSG00000065600.12_1	TMEM206	chr1:212537273-212588243	0.6381106	1.556289657
615	ENSG00000166266.13_1	CUL5	chr11:107879459-107978503	0.637767249	1.555919315
616	ENSG00000173546.7_1	CSPG4	chr15:75966663-76005189	0.636234511	1.554267164
617	ENSG00000115128.6_1	SF3B6	chr2:24290454-24299313	0.636132455	1.55415722
618	ENSG00000164134.12_1	NAA15	chr4:140222609-140341187	0.635981151	1.553994234
619	ENSG00000163125.15_1	RPRD2	chr1:150335567-150449042	0.635839771	1.553841955
620	ENSG00000131389.16_1	SLC6A6	chr3:14444076-14530857	0.633818499	1.551666486
621	ENSG00000173915.13_2	USMG5	chr10:105148798-105156223	0.632498854	1.550247812
622	ENSG00000165730.14_1	STOX1	chr10:70587298-70655188	0.632353031	1.550091127
623	ENSG00000114120.11_2	SLC25A36	chr3:140660672-140698775	0.632202938	1.549929869
624	ENSG00000244462.7_2	RBM12	chr20:34236847-34252878	0.631221972	1.548876346
625	ENSG00000185722.16_2	ANKFY1	chr17:4067201-4167272	0.630901295	1.548532106
626	ENSG00000162063.12_2	CCNF	chr16:2479395-2508855	0.629640953	1.547179895
627	ENSG00000204186.7_1	ZDBF2	chr2:207139387-207179152	0.629417014	1.546939756
628	ENSG00000276418.5_2	RP11-26J3.4	chr8:80831095-80993010	0.62905924	1.546556178
629	ENSG00000101974.14_1	ATP11C	chrX:138808505-139027435	0.628491476	1.54594766
630	ENSG00000135686.12_1	KLHL36	chr16:84682131-84701292	0.628365482	1.545812655
631	ENSG00000257594.3_2	GALNT4	chr12:89913185-89918583	0.626984646	1.54433383
632	ENSG00000179152.19_1	TCAIM	chr3:44379611-44450943	0.626867959	1.544208928
633	ENSG00000169641.13_2	LUZP1	chr1:23410516-23504301	0.626488742	1.543803081

634	ENSG00000173726.10_1	TOMM20	chr1:235272651-235292251	0.62530387	1.54253569
635	ENSG00000169184.5_1	MN1	chr22:28144265-28197486	0.62457574	1.541757367
636	ENSG00000141741.11_1	MIEN1	chr17:37884749-37887040	0.623753526	1.540878946
637	ENSG00000112312.9_2	GMNN	chr6:24775159-24786327	0.621708557	1.538696353
638	ENSG00000262560.1_2	RP11-296A16.1	chr15:44064815-44091331	0.621387529	1.538354
639	ENSG00000112365.4_2	ZBTB24	chr6:109783797-109804440	0.621287995	1.53824787
640	ENSG00000111540.15_1	RAB5B	chr12:56367697-56390467	0.620418722	1.537321302
641	ENSG00000214113.10_1	LYRM4	chr6:5102827-5261172	0.619985369	1.536859595
642	ENSG00000074527.11_1	NTN4	chr12:96051583-96184930	0.61966286	1.536516075
643	ENSG00000137075.17_1	RNF38	chr9:36336393-36487545	0.618624732	1.535410833
644	ENSG00000166272.16_1	WBP1L	chr10:104503727-104576024	0.618540072	1.535320735
645	ENSG00000167508.11_2	MVD	chr16:88718343-88729569	0.617355661	1.534060798
646	ENSG00000069482.6_1	GAL	chr11:68451247-68458643	0.616422	1.53306833
647	ENSG00000111181.12_1	SLC6A12	chr12:299243-323736	0.615998082	1.532617923
648	ENSG00000158435.7_1	CNOT11	chr2:101869264-101886778	0.615326002	1.531904118
649	ENSG00000040341.17_2	STAU2	chr8:74332604-74659943	0.615137678	1.531704162
650	ENSG00000196730.12_2	DAPK1	chr9:90112143-90323548	0.612778354	1.529201324
651	ENSG00000196652.11_1	ZKSCAN5	chr7:99102274-99132323	0.61265906	1.529074881
652	ENSG00000130348.11_2	QRSL1	chr6:107077453-107116292	0.611103835	1.527427427
653	ENSG00000017797.11_2	RALBP1	chr18:9475007-9538114	0.610435222	1.52671971
654	ENSG00000068354.15_2	TBC1D25	chrX:48397845-48420997	0.609214985	1.52542895
655	ENSG00000111142.13_2	METAP2	chr12:95867296-95909615	0.608163583	1.524317659
656	ENSG00000085721.12_1	RRN3	chr16:15153879-15188174	0.607914596	1.524054607
657	ENSG00000139211.6_1	AMIGO2	chr12:47469490-47473734	0.607182655	1.523281585
658	ENSG00000181852.17_2	RNF41	chr12:56595959-56615717	0.60663284	1.52270117
659	ENSG00000125814.17_1	NAPB	chr20:23355156-23402156	0.603700052	1.519608884
660	ENSG00000066557.5_1	LRRC40	chr1:70610488-70671303	0.60354819	1.519448935
661	ENSG00000169100.13_1	SLC25A6	chrX:1505045-1511617	0.602175601	1.518004009
662	ENSG00000118418.14_1	HMGN3	chr6:79910962-79944455	0.601844761	1.517655939
663	ENSG00000172888.11_1	ZNF621	chr3:40566369-40616176	0.601229198	1.51700853
664	ENSG00000143870.12_2	PDIA6	chr2:10923517-10978103	0.600571494	1.516317106
665	ENSG00000152242.10_2	C18orf25	chr18:43753519-43846954	0.599873722	1.515583902
666	ENSG00000110395.6_2	CBL	chr11:119076986-119184636	0.599189623	1.514865411
667	ENSG00000136937.12_2	NCBP1	chr9:100395908-100436030	0.597879224	1.513490085
668	ENSG00000070540.12_1	WIPI1	chr17:66417089-66453654	0.597786013	1.513392303
669	ENSG00000114346.13_1	ECT2	chr3:172468472-172539264	0.597458881	1.51304918
670	ENSG00000112419.14_2	PHACTR2	chr6:143857982-144152322	0.597294461	1.512876752
671	ENSG00000157693.14_1	C9orf91	chr9:117373486-117408702	0.596433872	1.511974567
672	ENSG00000148297.15_2	MED22	chr9:136205160-136214986	0.595452106	1.510946006
673	ENSG00000176105.13_2	YES1	chr18:721588-812547	0.592101435	1.507440893
674	ENSG00000188243.12_1	COMMD6	chr13:76099355-76123575	0.59148786	1.506799918
675	ENSG00000243244.5_2	STON1	chr2:48756522-48825652	0.590908615	1.506195056
676	ENSG00000197622.12_1	CDC42SE1	chr1:151023447-151042801	0.590867859	1.506152507
677	ENSG00000173041.11_1	ZNF680	chr7:63980262-64023484	0.590265535	1.505523821
678	ENSG00000163923.9_2	RPL39L	chr3:186838736-186898696	0.59022716	1.505483775
679	ENSG00000173894.10_1	CBX2	chr17:77751931-77761782	0.590112247	1.505363865
680	ENSG00000116455.13_2	WDR77	chr1:111982512-111991998	0.589524723	1.504750946
681	ENSG00000176386.8_1	CDC26	chr9:116018115-116037869	0.588881514	1.504080219
682	ENSG00000095303.14_2	PTGS1	chr9:125132809-125157982	0.588754195	1.503947489

683	ENSG00000116661.9_1	FBXO2	chr1:11708424-11715842	0.587492671	1.502632978
684	ENSG00000172159.15_1	FRMD3	chr9:85857905-86153461	0.585656593	1.500721836
685	ENSG00000100906.10_1	NFKBIA	chr14:35870717-35873955	0.585540827	1.500601418

Down-regulated:

No.	Track_id	Gene_Name	Locus	log2(fold_change)	Fold_Change
1	ENSG00000198727.2	MT-CYB	chrM:14747-15887	-10.513634	0.000684039
2	ENSG00000169564.6_2	PCBP1	chr2:70314586-70316335	-7.260181889	0.006523302
3	ENSG00000204388.6_2	HSPA1B	chr6:31795512-31798032	-7.021933907	0.007694622
4	ENSG00000136026.13_2	CKAP4	chr12:106631655-106698057	-4.963434422	0.032052164
5	ENSG00000277443.2_2	MARCKS	chr6:114178541-114184648	-4.915367713	0.033138045
6	ENSG00000181218.5_1	HIST3H2A	chr1:228644680-228645574	-4.792656474	0.036080009
7	ENSG00000189241.6_2	TSPYL1	chr6:116597741-116601066	-4.694541092	0.038619115
8	ENSG00000270170.1_1	NCBP2-AS2	chr3:196669494-196670411	-4.529595344	0.043296813
9	ENSG00000124659.6_1	TBCC	chr6:42712219-42713834	-4.273310735	0.051713661
10	ENSG00000198890.7_2	PRMT6	chr1:107599301-107601916	-4.114363943	0.057736844
11	ENSG00000176396.10_2	EID2	chr19:40029345-40030973	-4.00557964	0.062258747
12	ENSG00000170385.9_1	SLC30A1	chr1:211744910-211752084	-3.970734081	0.063780796
13	ENSG00000182154.7_1	MRPL41	chr9:140445651-140447007	-3.800949827	0.071746396
14	ENSG00000148730.6_1	EIF4EBP2	chr10:72164135-72188374	-3.721500134	0.075808313
15	ENSG00000132467.3_1	UTP3	chr4:71554196-71556268	-3.713788839	0.076214598
16	ENSG00000124766.6_2	SOX4	chr6:21592999-21598850	-3.622690506	0.081182326
17	ENSG00000277150.1_1	F8A3	chrX:154686575-154688333	-3.600933612	0.082415893
18	ENSG00000238227.7_2	C9orf69	chr9:139006427-139010709	-3.334717177	0.099117446
19	ENSG00000233276.3_1	GPX1	chr3:49394609-49396033	-3.328512383	0.099544652
20	ENSG00000263020.6_2	XXbac-BPG32J3.22	chr6:31633879-31641323	-3.320521523	0.100097544
21	ENSG00000168286.2_1	THAP11	chr16:67875985-67878098	-3.245559856	0.105436051
22	ENSG00000160131.13_1	VMA21	chrX:150564987-150577836	-3.114887408	0.115431797
23	ENSG00000143742.12_1	SRP9	chr1:225965515-225978168	-2.975837927	0.127111113
24	ENSG00000100092.20_2	SH3BP1	chr22:38030661-38062939	-2.952866454	0.129151253
25	ENSG00000170677.5_2	SOCS6	chr18:67956137-67997436	-2.949660787	0.129438546
26	ENSG00000184557.4_2	SOCS3	chr17:76352859-76356158	-2.937610634	0.130524213
27	ENSG00000198816.6_2	ZNF358	chr19:7580178-7585912	-2.921922039	0.131951345
28	ENSG00000164967.9_1	RPP25L	chr9:34610483-34612101	-2.897270922	0.134225351
29	ENSG00000135045.6_1	C9orf40	chr9:77561497-77567802	-2.881448919	0.135705498
30	ENSG00000177485.6_2	ZBTB33	chrX:119384607-119392253	-2.806186425	0.142972895
31	ENSG00000180964.16_1	TCEAL8	chrX:102507923-102510131	-2.800642692	0.143523343
32	ENSG00000273841.4_2	TAF9	chr5:68660570-68665840	-2.794534501	0.144132292
33	ENSG00000243317.7_1	C7orf73	chr7:135347244-135378166	-2.789921722	0.144593868
34	ENSG00000261652.2_1	C15orf65	chr15:55700746-55710962	-2.789750673	0.144611013
35	ENSG00000174579.3_2	MSL2	chr3:135867764-135916083	-2.75787446	0.147841739
36	ENSG00000152778.8_1	IFIT5	chr10:91174343-91180758	-2.662743786	0.157918951
37	ENSG00000185085.2_2	INTS5	chr11:62414320-62420774	-2.653060566	0.158982451
38	ENSG00000165997.4_1	ARL5B	chr10:18948334-18970568	-2.620839866	0.162573062
39	ENSG00000142684.8_2	ZNF593	chr1:26496362-26497364	-2.593407311	0.165693934
40	ENSG00000176410.7_1	DNAJC30	chr7:73095299-73097783	-2.580816495	0.167146321
41	ENSG00000183508.4_1	FAM46C	chr1:118148556-118170994	-2.578331563	0.167434466
42	ENSG00000169504.14_1	CLIC4	chr1:25071848-25170815	-2.565678581	0.168909388
43	ENSG00000119917.13_1	IFIT3	chr10:91087651-91100728	-2.561067399	0.169450124

44	ENSG00000126821.7_1	SGPP1	chr14:64150932-64194757	-2.515042637	0.174943063
45	ENSG00000166848.5_1	TERF2IP	chr16:75681684-75795770	-2.505664486	0.176083974
46	ENSG00000154978.12_1	VOPP1	chr7:55503749-55640681	-2.5019185	0.176541773
47	ENSG00000170779.10_1	CDCA4	chr14:105475910-105487485	-2.499017755	0.176897093
48	ENSG00000091542.8_1	ALKBH5	chr17:18086392-18113268	-2.498058773	0.177014718
49	ENSG00000176907.4_1	C8orf4	chr8:40010974-40012827	-2.42523719	0.186179071
50	ENSG00000173674.10_1	EIF1AX	chrX:20142636-20159962	-2.365834049	0.194005028
51	ENSG00000167552.13_1	TUBA1A	chr12:49578579-49583107	-2.345829449	0.196713865
52	ENSG00000136720.6_1	HS6ST1	chr2:128994290-129076151	-2.337848759	0.197805061
53	ENSG00000170270.4_1	C14orf142	chr14:93669239-93673439	-2.336287998	0.198019169
54	ENSG00000267303.1_2	CTD-2369P2.12	chr19:10426147-10431354	-2.306728867	0.202118199
55	ENSG00000135070.14_2	ISCA1	chr9:88879461-88898017	-2.28988133	0.204492335
56	ENSG00000181817.5_1	LSM10	chr1:36856839-36863493	-2.262375132	0.208428558
57	ENSG00000258790.1_2	RP11-561B11.2	chr14:35591755-35786680	-2.251801487	0.209961762
58	ENSG00000255439.6_2	RP11-196G11.1	chr16:31094760-31106277	-2.241453772	0.211473124
59	ENSG00000116199.11_1	FAM20B	chr1:178994939-179045697	-2.23660827	0.212184581
60	ENSG00000185950.8_1	IRS2	chr13:110405045-110438915	-2.207603493	0.216493634
61	ENSG00000119922.9_2	IFIT2	chr10:91043451-91069033	-2.196387875	0.21818323
62	ENSG00000124767.6_1	GLO1	chr6:38643701-38670917	-2.182040416	0.220363866
63	ENSG00000176788.8_2	BASP1	chr5:17065707-17276952	-2.171480855	0.221982699
64	ENSG00000255302.4_2	EID1	chr15:49170083-49172380	-2.169197327	0.222334336
65	ENSG00000115944.14_2	COX7A2L	chr2:42560686-42652228	-2.161445853	0.223532134
66	ENSG00000197579.7_1	TOPORS	chr9:32540542-32552551	-2.142883169	0.226426831
67	ENSG00000130513.6_2	GDF15	chr19:18485541-18499986	-2.107802446	0.232000136
68	ENSG00000188060.6_1	RAB42	chr1:28918712-28921955	-2.094095803	0.234214808
69	ENSG00000063322.13_1	MED29	chr19:39881943-39891277	-2.075878614	0.237191035
70	ENSG00000165244.6_1	ZNF367	chr9:99148223-99180611	-2.06507849	0.238973328
71	ENSG00000168092.13_1	PAFAH1B2	chr11:117014983-117047610	-2.053074965	0.24096993
72	ENSG00000180667.10_1	YOD1	chr1:207217194-207226325	-2.044546011	0.242398721
73	ENSG00000205765.8_1	C5orf51	chr5:41904290-41921738	-2.031798004	0.244550106
74	ENSG00000147955.16_1	SIGMAR1	chr9:34634719-34637806	-1.993816459	0.251073826
75	ENSG00000155868.7_2	MED7	chr5:156564423-156586030	-1.988285353	0.252038258
76	ENSG00000162702.7_1	ZNF281	chr1:200374068-200379184	-1.980214079	0.253452258
77	ENSG00000233493.3_1	TMEM238	chr19:55890613-55895966	-1.970865955	0.255099866
78	ENSG00000109089.7_1	CDR2L	chr17:72983727-73001895	-1.960059587	0.257017841
79	ENSG00000269711.1_2	CTD-3214H19.16	chr19:7743387-7747740	-1.945205775	0.259677735
80	ENSG00000196659.9_1	TTC30B	chr2:178413726-178417742	-1.945199781	0.259678814
81	ENSG00000179431.6_1	FJX1	chr11:35639967-35642416	-1.934535373	0.261605473
82	ENSG00000136193.16_2	SCRN1	chr7:29959719-30029905	-1.922036021	0.263881841
83	ENSG00000166275.15_2	BORCS7	chr10:104613980-104624718	-1.913858321	0.265381863
84	ENSG00000168209.4_1	DDIT4	chr10:74033678-74035794	-1.913558496	0.265437021
85	ENSG00000104140.6_1	RHOV	chr15:41164412-41166487	-1.902554343	0.267469382
86	ENSG00000276023.4_1	DUSP14	chr17:35849937-35873603	-1.896419678	0.268609144
87	ENSG00000113384.13_1	GOLPH3	chr5:32124810-32174456	-1.886508335	0.270460847
88	ENSG00000108179.13_1	PPIF	chr10:81107225-81115093	-1.881708753	0.271362119
89	ENSG00000196976.7_2	LAGE3	chrX:153706108-153707596	-1.874613326	0.272700013
90	ENSG00000165152.8_2	TMEM246	chr9:104235453-104295819	-1.868040907	0.273945174
91	ENSG00000101346.12_2	POFUT1	chr20:30795683-30826470	-1.85565244	0.276307678
92	ENSG00000166228.8_1	PCBD1	chr10:72642037-72648541	-1.848391051	0.277701899

93	ENSG00000101152.10_1	DNAJC5	chr20:62526535-62567384	-1.838397873	0.279632146
94	ENSG00000170540.14_2	ARL6IP1	chr16:18802989-18813000	-1.838159812	0.279678293
95	ENSG00000176422.13_2	SPRYD4	chr12:56862351-56873491	-1.824179492	0.282401667
96	ENSG00000074071.14_2	MRPS34	chr16:1821891-1823156	-1.819376332	0.283343433
97	ENSG00000159873.9_1	CCDC117	chr22:29168662-29185289	-1.814617266	0.28427965
98	ENSG00000142686.7_1	C1orf216	chr1:36179476-36185073	-1.807823443	0.285621514
99	ENSG00000177051.5_2	FBXO46	chr19:46213887-46234162	-1.802983071	0.286581409
100	ENSG00000184857.7_1	TMEM186	chr16:8874241-8891505	-1.794208397	0.288329749
101	ENSG00000163807.5_1	KIAA1143	chr3:44779153-44803154	-1.782764152	0.290626034
102	ENSG00000182307.12_1	C8orf33	chr8:146277764-146281416	-1.781925209	0.290795085
103	ENSG00000160007.17_2	ARHGAP35	chr19:47421933-47508334	-1.777107223	0.29176784
104	ENSG00000125827.8_1	TMX4	chr20:7957995-8000476	-1.772850552	0.292629972
105	ENSG00000198680.4_1	TUSC1	chr9:25676387-25678438	-1.771137837	0.292977578
106	ENSG00000041353.9_2	RAB27B	chr18:52385091-52562747	-1.76718075	0.293782273
107	ENSG00000171206.13_1	TRIM8	chr10:104404253-104418164	-1.763337828	0.294565867
108	ENSG00000128272.14_1	ATF4	chr22:39915700-39918690	-1.757020835	0.295858483
109	ENSG00000099864.17_2	PALM	chr19:708939-748329	-1.75228172	0.296831947
110	ENSG00000132825.6_1	PPP1R3D	chr20:58511723-58515352	-1.729262136	0.301606174
111	ENSG00000107295.9_1	SH3GL2	chr9:17579080-17797127	-1.727226158	0.30203211
112	ENSG00000168061.14_2	SAC3D1	chr11:64808373-64812300	-1.721580303	0.303216401
113	ENSG00000162734.12_2	PEA15	chr1:160175127-160185166	-1.716942069	0.304192804
114	ENSG00000179604.9_1	CDC42EP4	chr17:71279763-71308314	-1.708768927	0.305921005
115	ENSG00000122042.9_1	UBL3	chr13:30338508-30424821	-1.707149348	0.306264627
116	ENSG00000183513.8_1	COA5	chr2:99215773-99224978	-1.702006515	0.307358329
117	ENSG00000069011.15_1	PITX1	chr5:134363425-134370503	-1.70165184	0.3074339
118	ENSG00000084090.13_2	STARD7	chr2:96850597-96874563	-1.681654201	0.311725007
119	ENSG00000100941.8_1	PNN	chr14:39644387-39652422	-1.680237483	0.312031269
120	ENSG00000147883.10_1	CDKN2B	chr9:22002902-22009362	-1.670354718	0.314176087
121	ENSG00000127526.14_1	SLC35E1	chr19:16660642-16683193	-1.666883449	0.314932936
122	ENSG00000266472.5_1	MRPS21	chr1:150266140-150281414	-1.660345848	0.3163633
123	ENSG00000274211.4_2	SOCS7	chr17:36508111-36561846	-1.653541696	0.317858881
124	ENSG00000267426.5_2	RP11-552F3.12	chr17:73894726-73926210	-1.647016265	0.31929984
125	ENSG00000137040.9_2	RANBP6	chr9:6011043-6015625	-1.646043982	0.3195151
126	ENSG00000112697.15_1	TMEM30A	chr6:75962640-75994684	-1.64582581	0.319563422
127	ENSG00000254505.9_2	CHMP4A	chr14:24678789-24683075	-1.645519347	0.319631313
128	ENSG00000105058.11_1	FAM32A	chr19:16296191-16302857	-1.639028708	0.321072563
129	ENSG00000164430.15_2	MB21D1	chr6:74123238-74161999	-1.630987804	0.322867067
130	ENSG00000237172.3_1	B3GNT9	chr16:67182008-67185117	-1.62905626	0.323299625
131	ENSG00000064666.14_2	CNN2	chr19:1026580-1039067	-1.628646994	0.323391352
132	ENSG00000211448.11_2	DIO2	chr14:80663870-80854100	-1.621011995	0.325107333
133	ENSG00000112308.12_1	C6orf62	chr6:24705089-24721064	-1.616020572	0.326234085
134	ENSG00000128016.5_1	ZFP36	chr19:39897453-39900052	-1.614846638	0.326499653
135	ENSG00000162757.4_1	C1orf74	chr1:209952553-209957904	-1.589884526	0.332198042
136	ENSG00000224420.3_2	ADM5	chr19:50191921-50193832	-1.58072545	0.334313739
137	ENSG00000181827.14_2	RFX7	chr15:56379478-56535464	-1.578972268	0.334720248
138	ENSG00000156853.12_2	ZNF689	chr16:30613879-30635333	-1.578105114	0.334921497
139	ENSG00000104147.8_1	OIP5	chr15:41601466-41624819	-1.571258279	0.336514767
140	ENSG00000198113.2_1	TOR4A	chr9:140172201-140177093	-1.563699453	0.338282523
141	ENSG00000180530.10_2	NRIP1	chr21:16333556-16438257	-1.558585407	0.33948379

142	ENSG00000174282.11_1	ZBTB4	chr17:7362685-7387582	-1.541029365	0.343640179
143	ENSG00000140743.7_2	CDR2	chr16:22357257-22448486	-1.536090163	0.34481868
144	ENSG00000142669.14_2	SH3BGRL3	chr1:26605667-26608013	-1.529820772	0.346320388
145	ENSG00000232434.2_1	C9orf172	chr9:139738867-139743253	-1.502991452	0.352821051
146	ENSG00000125148.6_1	MT2A	chr16:56642111-56643409	-1.502538492	0.352931843
147	ENSG00000177427.12_2	MIEF2	chr17:18163848-18169866	-1.498543813	0.353910431
148	ENSG00000181274.6_1	FRAT2	chr10:99092254-99094466	-1.476559	0.359344871
149	ENSG00000143079.14_1	CTTNBP2NL	chr1:112938803-113006078	-1.469872138	0.361014293
150	ENSG00000104221.12_1	BRF2	chr8:37700786-37707422	-1.469139834	0.361197589
151	ENSG00000198551.9_2	ZNF627	chr19:11670189-11729950	-1.467698591	0.361558603
152	ENSG00000136238.17_1	RAC1	chr7:6414154-6443608	-1.467617521	0.361578921
153	ENSG00000183309.11_1	ZNF623	chr8:144718183-144738588	-1.464375563	0.362392358
154	ENSG00000091436.16_1	AC013461.1	chr2:173940163-174132738	-1.454294777	0.36493343
155	ENSG00000173272.14_2	MZT2A	chr2:132222473-132250316	-1.452223036	0.365457859
156	ENSG00000143545.8_1	RAB13	chr1:153954093-153958834	-1.45163135	0.365607774
157	ENSG00000137331.11_1	IER3	chr6:30710976-30712331	-1.449218007	0.366219875
158	ENSG00000255508.7_2	RP11-864I4.1	chr11:62327075-62359003	-1.443031389	0.367793684
159	ENSG00000080371.5_1	RAB21	chr12:72148654-72194065	-1.441168925	0.368268798
160	ENSG00000116251.9_2	RPL22	chr1:6241329-6269449	-1.432322718	0.370533858
161	ENSG00000158710.14_1	TAGLN2	chr1:159887897-159895522	-1.431823094	0.370662201
162	ENSG00000134086.7_1	VHL	chr3:10182692-10193904	-1.43001327	0.371127479
163	ENSG00000184900.15_1	SUMO3	chr21:46225532-46238694	-1.425530745	0.372282384
164	ENSG00000164713.9_1	BRI3	chr7:97881691-97939753	-1.41500909	0.375007385
165	ENSG00000196981.3_2	WDR5B	chr3:122131179-122134898	-1.414955985	0.375021189
166	ENSG00000213977.7_2	TAX1BP3	chr17:3566190-3571976	-1.413604938	0.375372551
167	ENSG00000130772.13_1	MED18	chr1:28655513-28662478	-1.412339478	0.375701953
168	ENSG00000123728.9_1	RAP2C	chrX:131337052-131353508	-1.397719735	0.379528535
169	ENSG00000130803.14_1	ZNF317	chr19:9251056-9274100	-1.394578183	0.380355881
170	ENSG00000171016.11_1	PYGO1	chr15:55831088-55881145	-1.392165005	0.38099263
171	ENSG00000204070.9_2	SYS1	chr20:43990577-44005438	-1.391162269	0.381257528
172	ENSG00000206418.3_1	RAB12	chr18:8609443-8639379	-1.388899021	0.381856101
173	ENSG00000176842.14_2	IRX5	chr16:54964774-54968397	-1.388437865	0.38197818
174	ENSG00000004799.7_1	PDK4	chr7:95212811-95225803	-1.383585416	0.383265112
175	ENSG00000182253.14_1	SYNM	chr15:99638420-99675798	-1.373309	0.386004882
176	ENSG00000164978.17_1	NUDT2	chr9:34329504-34343711	-1.371306516	0.386541035
177	ENSG00000134308.13_1	YWHAQ	chr2:9724101-9771143	-1.370384569	0.386788131
178	ENSG00000126878.12_1	AIF1L	chr9:133971863-133998539	-1.370324394	0.386804264
179	ENSG00000109787.12_1	KLF3	chr4:38665817-38702663	-1.353718981	0.3912821
180	ENSG00000118804.8_2	STBD1	chr4:77227179-77232752	-1.347602959	0.392944385
181	ENSG00000180818.4_2	HOXC10	chr12:54378849-54384063	-1.346427363	0.393264711
182	ENSG00000204576.11_1	PRR3	chr6:30524663-30531500	-1.344525329	0.393783528
183	ENSG00000155090.14_1	KLF10	chr8:103661007-103668130	-1.344260079	0.393855935
184	ENSG00000134109.10_1	EDEM1	chr3:5229331-5261642	-1.340689332	0.394831957
185	ENSG00000214357.8_1	NEURL1B	chr5:172068269-172118543	-1.339185551	0.395243721
186	ENSG00000198420.9_2	TCAF1	chr7:143548468-143599291	-1.336805043	0.395896428
187	ENSG00000167397.14_2	VKORC1	chr16:31102163-31107301	-1.335666703	0.396208929
188	ENSG00000117036.11_1	ETV3	chr1:157090983-157108266	-1.331718886	0.397294607
189	ENSG00000161671.16_2	EMC10	chr19:50979657-50994127	-1.330796931	0.397548579
190	ENSG00000151014.5_1	NOCT	chr4:139936943-139967093	-1.33079092	0.397550235

191	ENSG00000184117.11_2	NIPSNAP1	chr22:29950797-29977326	-1.328796457	0.398100212
192	ENSG00000119862.12_2	LGALSL	chr2:64681103-64688515	-1.327268829	0.398521972
193	ENSG00000197933.12_2	ZNF823	chr19:11832080-11849824	-1.326250004	0.398803505
194	ENSG00000173950.15_2	XXYLT1	chr3:194789008-194991896	-1.326066796	0.398854153
195	ENSG00000012174.11_2	MBTPS2	chrX:21857754-21903542	-1.323049319	0.399689251
196	ENSG00000184787.18_1	UBE2G2	chr21:46188495-46221934	-1.322281152	0.399902124
197	ENSG00000155115.6_1	GTF3C6	chr6:111279763-111289093	-1.320880376	0.400290595
198	ENSG00000113583.7_1	C5orf15	chr5:133291193-133304478	-1.320650178	0.400354471
199	ENSG00000127804.12_2	METTL16	chr17:2308856-2415185	-1.31515914	0.401881162
200	ENSG00000204103.3_1	MAFB	chr20:39314488-39317880	-1.310897312	0.403070104
201	ENSG00000105974.11_2	CAV1	chr7:116164839-116201238	-1.310065752	0.403302498
202	ENSG00000135766.8_1	EGLN1	chr1:231499497-231560790	-1.307855136	0.403920945
203	ENSG00000038210.12_2	PI4K2B	chr4:25235597-25280714	-1.30687862	0.404194439
204	ENSG00000102221.13_2	JADE3	chrX:46771711-46920641	-1.306616636	0.404267845
205	ENSG00000196937.10_2	FAM3C	chr7:120988905-121036418	-1.300046714	0.406113048
206	ENSG00000169139.11_1	UBE2V2	chr8:48920960-48977268	-1.297313442	0.406883183
207	ENSG00000089902.9_1	RCOR1	chr14:103058998-103196913	-1.292805869	0.408156441
208	ENSG00000177951.17_1	BET1L	chr11:167784-207428	-1.28992645	0.408971878
209	ENSG00000174007.7_1	CEP19	chr3:196433148-196439164	-1.289465844	0.409102471
210	ENSG00000180855.15_2	ZNF443	chr19:12540521-12551926	-1.287452259	0.409673858
211	ENSG00000141639.11_2	MAPK4	chr18:48086448-48258194	-1.284165466	0.410608254
212	ENSG00000143367.15_2	TUFT1	chr1:151512781-151556059	-1.281625193	0.411331883
213	ENSG00000179010.14_1	MRFAP1	chr4:6641818-6644472	-1.281336186	0.411414291
214	ENSG00000100335.13_2	MIEF1	chr22:39895437-39914137	-1.277728617	0.412444351
215	ENSG00000141034.9_2	GID4	chr17:17942606-17971718	-1.27352307	0.413648407
216	ENSG00000186193.8_1	SAPCD2	chr9:139956576-139965040	-1.269209012	0.414887181
217	ENSG00000127452.8_1	FBXL12	chr19:9920943-9938492	-1.268164041	0.415187801
218	ENSG00000060491.16_1	OGFR	chr20:61436187-61445352	-1.267944219	0.415251067
219	ENSG00000161179.13_2	YDJC	chr22:21982378-21984353	-1.262683132	0.416768131
220	ENSG00000133059.16_1	DSTYK	chr1:205111633-205180694	-1.259115987	0.417799889
221	ENSG00000197965.11_2	MPZL1	chr1:167690429-167761156	-1.25684039	0.418459414
222	ENSG00000214717.10_2_PAR_Y	ZBED1	chrY:2354455-2369008	-1.248419081	0.420909191
223	ENSG00000196449.3_1	YRDC	chr1:38268616-38273857	-1.238527588	0.42380497
224	ENSG00000109618.11_1	SEPSECS	chr4:25121636-25162064	-1.238085094	0.423934977
225	ENSG00000142544.6_1	CTU1	chr19:51600863-51611627	-1.234448382	0.42500497
226	ENSG00000106049.8_1	HIBADH	chr7:27565061-27702614	-1.230220898	0.426252175
227	ENSG00000106299.7_1	WASL	chr7:123321989-123389121	-1.226356232	0.427395543
228	ENSG00000101000.5_1	PROCR	chr20:33759876-33804043	-1.224350563	0.427990132
229	ENSG00000114988.11_2	LMAN2L	chr2:97371666-97405801	-1.215664342	0.43057476
230	ENSG00000147164.11_1	SNX12	chrX:70276182-70293276	-1.214474921	0.430929891
231	ENSG00000099968.17_1	BCL2L13	chr22:18111621-18213621	-1.207584292	0.43299303
232	ENSG00000250067.11_2	YJEFN3	chr19:19639670-19648390	-1.202497703	0.434522352
233	ENSG00000198060.9_1	MARCH5	chr10:94050920-94113721	-1.201030785	0.434964395
234	ENSG00000179387.9_2	ELMOD2	chr4:141445312-141474924	-1.196170256	0.436432288
235	ENSG00000088356.5_1	PDRG1	chr20:30532145-30539895	-1.195470295	0.436644086
236	ENSG00000164695.4_1	CHMP4C	chr8:82644669-82671750	-1.194076575	0.437066111
237	ENSG00000152484.13_1	USP12	chr13:27640279-27746033	-1.192096959	0.43766625
238	ENSG00000113552.15_2	GNPDA1	chr5:141371314-141392606	-1.188840742	0.438655195
239	ENSG00000136295.14_1	TTYH3	chr7:2671585-2704436	-1.18592271	0.439543328

240	ENSG00000204271.11_2	SPIN3	chrX:57002803-57021970	-1.180715532	0.441132656
241	ENSG00000171848.13_1	RRM2	chr2:10262455-10271546	-1.18065906	0.441149924
242	ENSG00000100811.11_2	YY1	chr14:100704635-100749129	-1.17766718	0.442065735
243	ENSG00000176890.15_1	TYMS	chr18:657604-673578	-1.174363322	0.443079252
244	ENSG00000134686.17_2	PHC2	chr1:33789224-33896653	-1.171696105	0.443899163
245	ENSG00000065559.14_2	MAP2K4	chr17:11924141-12047147	-1.170424223	0.444290678
246	ENSG00000136999.4_1	NOV	chr8:120428546-120436593	-1.168412302	0.444910699
247	ENSG00000150776.17_1	C11orf57	chr11:111944810-111955874	-1.168182432	0.444981594
248	ENSG00000006695.10_1	COX10	chr17:13972813-14111994	-1.167030107	0.445337157
249	ENSG00000142556.18_2	ZNF614	chr19:52516018-52533493	-1.164558191	0.446100852
250	ENSG00000247077.6_2	PGAM5	chr12:133287405-133299320	-1.161486265	0.447051745
251	ENSG00000184731.5_1	FAM110C	chr2:38814-46870	-1.156246264	0.448678431
252	ENSG00000159228.12_1	CBR1	chr21:37442239-37445464	-1.154935335	0.449086315
253	ENSG00000103111.14_2	MON1B	chr16:77224732-77236302	-1.152084994	0.449974454
254	ENSG00000101444.12_2	AHCY	chr20:32868074-32899608	-1.146048796	0.45186108
255	ENSG00000136197.12_2	C7orf25	chr7:42948325-42951904	-1.145468419	0.452042894
256	ENSG00000280071.3_2	CH507-9B2.3	chr21:45553509-45602558	-1.144227329	0.452431935
257	ENSG00000186666.5_1	BCDIN3D	chr12:50229822-50236912	-1.143963356	0.452514725
258	ENSG00000186432.8_2	KPNA4	chr3:160212783-160283376	-1.140660089	0.453552012
259	ENSG00000181894.14_1	ZNF329	chr19:58637619-58666477	-1.140636281	0.453559497
260	ENSG00000134352.19_1	IL6ST	chr5:55230923-55290821	-1.135902635	0.455050122
261	ENSG00000169964.6_2	TMEM42	chr3:44903361-44907162	-1.135048975	0.45531946
262	ENSG00000134986.13_2	NREP	chr5:110998318-111333161	-1.122530637	0.45928748
263	ENSG00000061794.12_2	MRPS35	chr12:27863706-27909228	-1.118206171	0.460666256
264	ENSG00000029993.14_1	HMGB3	chrX:150148982-150159248	-1.115014779	0.461686426
265	ENSG00000177383.4_2	MAGEF1	chr3:184428155-184429790	-1.113584492	0.462144368
266	ENSG00000123505.15_2	AMD1	chr6:111195973-111216916	-1.113569761	0.462149087
267	ENSG00000138071.13_2	ACTR2	chr2:65454887-65498387	-1.109890301	0.46332926
268	ENSG00000188277.9_1	C15orf62	chr15:41062278-41064647	-1.109118474	0.463577203
269	ENSG00000064652.10_1	SNX24	chr5:122179134-122365049	-1.105374982	0.464781651
270	ENSG00000007376.7_1	RPUSD1	chr16:834974-838397	-1.104094399	0.465194389
271	ENSG00000072954.6_1	TMEM38A	chr19:16771938-16800840	-1.103699242	0.465321824
272	ENSG00000171425.9_2	ZNF581	chr19:56146825-56156988	-1.096846079	0.467537478
273	ENSG00000198182.12_2	ZNF607	chr19:38187264-38210691	-1.096341991	0.467700867
274	ENSG00000176058.11_2	TPRN	chr9:140086069-140098645	-1.093888603	0.468496897
275	ENSG00000102554.13_1	KLF5	chr13:73629114-73651680	-1.090683187	0.469538972
276	ENSG00000213689.10_2	TREX1	chr3:48507210-48509044	-1.090109306	0.469725784
277	ENSG00000196072.11_1	BLOC1S2	chr10:102033037-102046469	-1.089284417	0.469994436
278	ENSG00000103353.15_2	UBFD1	chr16:23568683-23585710	-1.088321523	0.470308228
279	ENSG00000103152.11_2	MPG	chr16:127006-135852	-1.086055582	0.471047489
280	ENSG00000158792.15_1	SPATA2L	chr16:89762751-89768113	-1.085644932	0.471181587
281	ENSG00000100422.13_1	CERK	chr22:47080308-47134158	-1.084377686	0.471595649
282	ENSG00000162419.12_1	GMEB1	chr1:28995244-29045865	-1.084191467	0.471656525
283	ENSG00000167625.10_2	ZNF526	chr19:42724423-42732353	-1.084079392	0.471693167
284	ENSG00000186665.9_2	C17orf58	chr17:65987217-65992547	-1.082915705	0.472073792
285	ENSG00000105879.11_1	CBLL1	chr7:107384142-107402112	-1.082674269	0.4721528
286	ENSG00000150907.7_2	FOXO1	chr13:41044090-41240734	-1.079568694	0.47317026
287	ENSG00000177674.15_2	AGTRAP	chr1:11796141-11814859	-1.075762407	0.474420282
288	ENSG00000122958.14_1	VPS26A	chr10:70883268-70932617	-1.075135096	0.474626614

289	ENSG00000175087.9_1	PDIK1L	chr1:26437656-26452034	-1.074931123	0.474693723
290	ENSG00000213096.10_2	ZNF254	chr19:24216207-24312763	-1.072951152	0.475345645
291	ENSG00000174206.12_1	C12orf66	chr12:64580096-64616076	-1.070044608	0.476304271
292	ENSG00000104228.12_1	TRIM35	chr8:27142404-27168836	-1.0671895	0.477247816
293	ENSG00000089818.16_1	NECAP1	chr12:8234807-8250367	-1.065779305	0.477714541
294	ENSG00000183741.11_1	CBX6	chr22:39257455-39268319	-1.064197509	0.478238603
295	ENSG00000266967.6_2	AARSD1	chr17:41102543-41116515	-1.063179608	0.478576145
296	ENSG00000119812.18_2	FAM98A	chr2:33808725-33824449	-1.063168964	0.478579676
297	ENSG00000124657.1_1	OR2B6	chr6:27925019-27925960	-1.062428459	0.478825384
298	ENSG00000213920.8_2	MDP1	chr14:24683143-24685276	-1.061267052	0.479211006
299	ENSG00000163171.7_1	CDC42EP3	chr2:37869025-37965611	-1.057761741	0.480376759
300	ENSG00000164265.8_1	SCGB3A2	chr5:147250245-147261754	-1.056722606	0.480722886
301	ENSG00000261915.6_2	RP11-542C16.2	chr17:7215980-7222493	-1.050634109	0.482755932
302	ENSG00000112242.14_2	E2F3	chr6:20402137-20493946	-1.046919121	0.484000646
303	ENSG00000146223.14_1	RPL7L1	chr6:42847356-42857663	-1.044706656	0.484743462
304	ENSG00000110651.11_2	CD81	chr11:2397407-2418649	-1.044377613	0.484854032
305	ENSG00000119414.11_1	PPP6C	chr9:127908852-127952218	-1.044170385	0.484923681
306	ENSG00000165355.7_2	FBXO33	chr14:39866873-39901704	-1.04154303	0.485807602
307	ENSG00000119335.16_2	SET	chr9:131445703-131458679	-1.040755394	0.4860729
308	ENSG00000116857.16_2	TMEM9	chr1:201103900-201140702	-1.039421073	0.486522667
309	ENSG00000165704.14_1	HPRT1	chrX:133594183-133654543	-1.037888029	0.487039933
310	ENSG00000105438.8_1	KDELR1	chr19:48885827-48894810	-1.034247141	0.488270614
311	ENSG00000107371.12_2	EXOSC3	chr9:37766975-37801434	-1.031187096	0.489307365
312	ENSG00000164008.14_2	C1orf50	chr1:43232940-43241418	-1.029202234	0.489981018
313	ENSG00000119541.9_2	VPS4B	chr18:61056423-61089716	-1.028526184	0.490210678
314	ENSG00000164823.9_1	OSGIN2	chr8:90914087-90940116	-1.026974534	0.490738194
315	ENSG00000011052.21_2	NME1-NME2	chr17:49230951-49249105	-1.026869726	0.490773846
316	ENSG00000170584.10_1	NUDCD2	chr5:162873532-162887146	-1.026824881	0.490789102
317	ENSG00000106367.13_2	AP1S1	chr7:100797678-100804877	-1.022428941	0.492286834
318	ENSG00000167513.8_1	CDT1	chr16:88869621-88875666	-1.021262692	0.49268495
319	ENSG00000160803.7_1	UBQLN4	chr1:156005092-156023585	-1.019186016	0.493394652
320	ENSG00000180776.15_2	ZDHHC20	chr13:21946712-22033509	-1.016837444	0.494198506
321	ENSG00000283149.1_1	RP11-134F2.8	chr3:186299784-186314892	-1.016005592	0.494483542
322	ENSG00000250722.5_2	SEPP1	chr5:42799982-42887494	-1.015663401	0.494600841
323	ENSG00000100219.16_2	XBP1	chr22:29190543-29196585	-1.010623761	0.496331608
324	ENSG00000100324.13_1	TAB1	chr22:39795746-39833065	-1.010328236	0.496433288
325	ENSG00000267645.5_2	RP11-577H5.5	chr7:102277496-102312088	-1.009344593	0.496771877
326	ENSG00000114383.9_2	TUSC2	chr3:50357458-50365682	-1.009147344	0.496839801
327	ENSG00000116704.7_1	SLC35D1	chr1:67465015-67519782	-1.008933854	0.496913329
328	ENSG00000179151.11_2	EDC3	chr15:74922899-74988633	-1.006864122	0.497626727
329	ENSG00000117280.12_1	RAB29	chr1:205737114-205744588	-1.002283961	0.499209066
330	ENSG00000085491.15_1	SLC25A24	chr1:108676658-108743471	-1.001694836	0.499412959
331	ENSG00000173581.7_2	CCDC106	chr19:56152428-56164527	-0.997715086	0.500792518
332	ENSG00000197766.7_1	CFD	chr19:859643-863630	-0.996496733	0.501215615
333	ENSG00000139233.6_2	LLPH	chr12:66510335-66524548	-0.993680093	0.502195117
334	ENSG00000135801.9_1	TAF5L	chr1:229728858-229761794	-0.992301681	0.502675165
335	ENSG00000173480.10_2	ZNF417	chr19:58411664-58427978	-0.992237121	0.50269766
336	ENSG00000184709.7_2	LRRC26	chr9:140063210-140064503	-0.9921175	0.502739343
337	ENSG00000167202.11_2	TBC1D2B	chr15:78276378-78370066	-0.991080519	0.503100832

338	ENSG00000104687.12_1	GSR	chr8:30535578-30585443	-0.985908437	0.504907692
339	ENSG00000204366.3_1	ZBTB12	chr6:31867384-31869769	-0.982127287	0.506232737
340	ENSG00000076067.11_1	RBMS2	chr12:56915713-56989980	-0.982114552	0.506237206
341	ENSG00000147586.9_2	MRPS28	chr8:80830952-80942524	-0.978681982	0.507443118
342	ENSG00000082213.17_2	C5orf22	chr5:31532373-31555165	-0.978584004	0.507477581
343	ENSG00000164105.3_1	SAP30	chr4:174291120-174298683	-0.974796464	0.508811624
344	ENSG00000163900.10_1	TMEM41A	chr3:185194284-185216845	-0.97311086	0.509406453
345	ENSG00000168899.4_1	VAMP5	chr2:85811531-85820535	-0.971404478	0.510009322
346	ENSG00000168566.12_1	SNRNP48	chr6:7590432-7612200	-0.971238192	0.510068109
347	ENSG00000182141.10_2	ZNF708	chr19:21473962-21512227	-0.969907231	0.510538891
348	ENSG00000178691.10_1	SUZ12	chr17:30264037-30328064	-0.96815788	0.511158324
349	ENSG00000164024.7	METAP1	chr4:99916771-99983964	-0.965919743	0.511951929
350	ENSG00000172757.12_2	CFL1	chr11:65590493-65629497	-0.962237515	0.513260266
351	ENSG00000139990.17_1	DCAF5	chr14:69517598-69619867	-0.958676686	0.514528649
352	ENSG00000198176.12_1	TFDP1	chr13:114239036-114295785	-0.95797686	0.514778299
353	ENSG00000164631.18_1	ZNF12	chr7:6728064-6746554	-0.954087505	0.516167959
354	ENSG00000164294.13_1	GPX8	chr5:54455946-54462899	-0.953526857	0.516368587
355	ENSG00000043355.11_2	ZIC2	chr13:100634026-100639027	-0.953236567	0.516472498
356	ENSG00000115275.11_2	MOGS	chr2:74688184-74692537	-0.952922935	0.516584788
357	ENSG00000118898.15_2	PPL	chr16:4932508-5010742	-0.952620997	0.516692914
358	ENSG00000102871.15_1	TRADD	chr16:67188083-67194201	-0.951341917	0.517151212
359	ENSG00000120327.6_2	PCDHB14	chr5:140602504-140607331	-0.951322953	0.51715801
360	ENSG00000120509.10_1	PDZD11	chrX:69506445-69510364	-0.95085034	0.517327454
361	ENSG00000189280.3_1	GJB5	chr1:35220648-35224113	-0.949628255	0.51776586
362	ENSG00000005100.12_2	DHX33	chr17:5344232-5372380	-0.947760088	0.518436757
363	ENSG00000169955.7_2	ZNF747	chr16:30541688-30546668	-0.946942272	0.518730725
364	ENSG00000112425.13_1	EPM2A	chr6:145822719-146057160	-0.945736688	0.519164381
365	ENSG00000181938.13_1	GINS3	chr16:58328984-58440048	-0.944704397	0.519535992
366	ENSG00000167220.11_2	HDHD2	chr18:44633774-44676891	-0.942841671	0.52020722
367	ENSG00000161021.11_2	MAML1	chr5:179159851-179223512	-0.942711428	0.520254186
368	ENSG00000203668.2_2	CHML	chr1:241792155-241803556	-0.942399196	0.520366793
369	ENSG00000166823.5_1	MESP1	chr15:90291892-90294541	-0.94184317	0.520567385
370	ENSG00000215033.3	AL603965.1	chr10:47746962-47770871	-0.938881858	0.521637012
371	ENSG00000148331.11_1	ASB6	chr9:132396883-132404448	-0.937144506	0.522265566
372	ENSG00000174151.14_2	CYB561D1	chr1:110036674-110045554	-0.937074966	0.522290741
373	ENSG00000135002.11_2	RFK	chr9:79000433-79009433	-0.935897331	0.522717248
374	ENSG00000185818.7_1	NAT8L	chr4:2061239-2070816	-0.935317247	0.522927466
375	ENSG00000198498.9_2	TMA16	chr4:164415594-164441691	-0.934001389	0.523404637
376	ENSG00000145293.15_2	ENOPH1	chr4:83351715-83382244	-0.928834217	0.52528263
377	ENSG00000133193.12_1	FAM104A	chr17:71203492-71232892	-0.928763147	0.525308507
378	ENSG00000189159.15_2	HN1	chr17:73131343-73164376	-0.927115652	0.525908729
379	ENSG00000111707.11_1	SUDS3	chr12:118814185-118855836	-0.923100444	0.52737444
380	ENSG00000104205.12_2	SGK3	chr8:67624653-67774257	-0.918546429	0.529041782
381	ENSG00000215020.3	AL591684.1	chr10:48255279-48279199	-0.916453714	0.529809745
382	ENSG00000136048.13_2	DRAM1	chr12:102271129-102405908	-0.910193931	0.532113558
383	ENSG00000102390.10_2	PBDC1	chrX:75392771-75398039	-0.909039782	0.532539417
384	ENSG00000131370.15_1	SH3BP5	chr3:15296360-15382875	-0.907849103	0.532979112
385	ENSG00000147471.11_2	PROSC	chr8:37620111-37637285	-0.907200412	0.533218813
386	ENSG00000166595.11_2	FAM96B	chr16:66965958-66968326	-0.902785944	0.534852895

387	ENSG00000203667.9_1	COX20	chr1:244998624-245008359	-0.896848731	0.537058544
388	ENSG00000142178.7_1	SIK1	chr21:44834395-44847008	-0.896308015	0.537259869
389	ENSG00000079462.7_1	PAFAH1B3	chr19:42801185-42807698	-0.895252507	0.537653084
390	ENSG00000250021.7_2	C15orf38-AP3S2	chr15:90377540-90456114	-0.893017703	0.538486581
391	ENSG00000136371.10_2	MTHFS	chr15:80125927-80189721	-0.892256971	0.538770599
392	ENSG00000107829.13_1	FBXW4	chr10:103370421-103455052	-0.891939658	0.538889112
393	ENSG00000139173.9_1	TMEM117	chr12:44229770-44783545	-0.891025505	0.539230683
394	ENSG00000198892.6_1	SHISA4	chr1:201857808-201861434	-0.889601165	0.539763316
395	ENSG00000162704.15_2	ARPC5	chr1:183589981-183604892	-0.888843861	0.540046725
396	ENSG00000176182.5_1	MYPOP	chr19:46393278-46405862	-0.888625859	0.540128336
397	ENSG00000157657.14_2	ZNF618	chr9:116638562-116818871	-0.884013669	0.54185785
398	ENSG00000140497.16_2	SCAMP2	chr15:75136071-75165706	-0.881589518	0.542769095
399	ENSG00000106605.10_2	BLVRA	chr7:43798279-43846941	-0.879520184	0.543548176
400	ENSG00000112972.14_2	HMGCS1	chr5:43289497-43313614	-0.879146771	0.543688881
401	ENSG00000235863.3_1	B3GALT4	chr6:33244909-33252609	-0.878526809	0.543922568
402	ENSG00000117318.8_1	ID3	chr1:23884409-23886285	-0.877837586	0.54418248
403	ENSG00000213347.10_2	MXD3	chr5:176728462-176739758	-0.876307115	0.544760077
404	ENSG00000106266.9_2	SNX8	chr7:2291405-2393953	-0.876197762	0.544801371
405	ENSG00000197324.8_2	LRP10	chr14:23340822-23350789	-0.875502363	0.545064036
406	ENSG00000139505.11_1	MTMR6	chr13:25820339-25862147	-0.874118797	0.545587011
407	ENSG00000156973.13_1	PDE6D	chr2:232597135-232650982	-0.873474175	0.545830844
408	ENSG00000177311.11_2	ZBTB38	chr3:141043055-141168634	-0.871860249	0.5464418
409	ENSG00000128626.11_1	MRPS12	chr19:39421188-39423802	-0.86884647	0.547584506
410	ENSG00000082196.20_2	C1QTNF3	chr5:34019553-34043937	-0.868836214	0.547588398
411	ENSG00000155287.10_1	SLC25A28	chr10:101370279-101380366	-0.868704573	0.547638366
412	ENSG00000164438.5_1	TLX3	chr5:170736288-170739138	-0.867185261	0.548215392
413	ENSG00000142961.14_2	MOB3C	chr1:47073387-47082563	-0.865670049	0.548791466
414	ENSG00000277462.1_2	ZNF670	chr1:247200086-247242057	-0.863554092	0.549596952
415	ENSG00000198931.10_1	APRT	chr16:88875747-88878352	-0.863013724	0.549802845
416	ENSG00000143811.17_2	PYCR2	chr1:226107577-226112040	-0.862115644	0.550145204
417	ENSG00000100605.16_2	ITPK1	chr14:93403259-93582665	-0.862069936	0.550162634
418	ENSG00000198162.12_2	MAN1A2	chr1:117910071-118071494	-0.861377371	0.550426803
419	ENSG00000146834.13_1	MEPCE	chr7:100026413-100031749	-0.857660999	0.551846526
420	ENSG00000164296.6_1	TIGD6	chr5:149372681-149380730	-0.854849313	0.552923075
421	ENSG00000260007.2_2	RP11-315D16.2	chr15:68476370-68522056	-0.853269907	0.553528726
422	ENSG00000158234.12_2	FAIM	chr3:138327448-138352218	-0.853036374	0.553618334
423	ENSG00000151532.13_1	VTI1A	chr10:114206756-114578503	-0.852839109	0.553694037
424	ENSG00000090776.5_1	EFNB1	chrX:68048840-68061990	-0.851879397	0.554062489
425	ENSG00000175793.11_2	SFN	chr1:27189629-27190948	-0.851145222	0.554344518
426	ENSG00000184378.2_2	ACTRT3	chr3:169484709-169487683	-0.849333684	0.555041025
427	ENSG00000181690.7_1	PLAG1	chr8:57073463-57123883	-0.848138083	0.555501194
428	ENSG00000025293.16_2	PHF20	chr20:34359896-34538303	-0.84355816	0.557267468
429	ENSG00000117593.9_1	DARS2	chr1:173793641-173827684	-0.843199365	0.557406077
430	ENSG00000196670.13_1	ZFP62	chr5:180274611-180288285	-0.841407398	0.558098859
431	ENSG00000115808.11_1	STRN	chr2:37070783-37193615	-0.84102379	0.558247276
432	ENSG00000149084.12_2	HSD17B12	chr11:43702108-43878167	-0.84019868	0.558566641
433	ENSG00000106608.16_2	URGCP	chr7:43915493-43966010	-0.838883695	0.559075994
434	ENSG00000265241.6_2	RBM8A	chr1:145507415-145517375	-0.835222513	0.560496585
435	ENSG00000162236.11_2	STX5	chr11:62574369-62599560	-0.834511798	0.56077277

436	ENSG00000067167.7_1	TRAM1	chr8:71485677-71520622	-0.833792568	0.561052403
437	ENSG00000103343.12_2	ZNF174	chr16:3451235-3459370	-0.833753438	0.561067621
438	ENSG00000175334.7_1	BANF1	chr11:65769550-65771620	-0.832482508	0.561562106
439	ENSG00000132768.13_1	DPH2	chr1:44435672-44439041	-0.830728211	0.562245373
440	ENSG00000066027.11_2	PPP2R5A	chr1:212458879-212535205	-0.830071945	0.562501191
441	ENSG00000187514.15_2	PTMA	chr2:232571605-232578251	-0.82937162	0.562774311
442	ENSG00000144567.10_2	FAM134A	chr2:220040947-220050201	-0.827087946	0.563665844
443	ENSG00000163013.11_1	FBXO41	chr2:73481810-73511559	-0.826787776	0.563783134
444	ENSG00000108788.11_1	MLX	chr17:40719086-40725257	-0.826417435	0.563927876
445	ENSG00000180957.17_2	PITPNB	chr22:28247657-28316122	-0.825884999	0.564136036
446	ENSG00000132773.11_1	TOE1	chr1:45805342-45809647	-0.823445009	0.56509095
447	ENSG00000140262.17_1	TCF12	chr15:57210821-57591479	-0.822678174	0.565391393
448	ENSG00000108578.14_1	BLMH	chr17:28575213-28619074	-0.819093471	0.566797983
449	ENSG00000154710.15_2	RABGEF1	chr7:66147151-66276451	-0.817764455	0.56732036
450	ENSG00000219200.6	RNASEK	chr17:6915736-6917851	-0.817570648	0.567396577
451	ENSG00000276966.2_1	HIST1H4E	chr6:26204780-26206266	-0.814554525	0.568584027
452	ENSG00000205903.6_2	ZNF316	chr7:6676953-6696063	-0.813935933	0.568827874
453	ENSG00000255641.1_2	RP11-277P12.6	chr12:10564911-10588600	-0.813796475	0.568882862
454	ENSG00000132359.14_2	RAP1GAP2	chr17:2658999-2941033	-0.813335666	0.569064597
455	ENSG00000070367.15_1	EXOC5	chr14:57667225-57735726	-0.81323765	0.56910326
456	ENSG00000132004.12_1	FBXW9	chr19:12798867-12807457	-0.811762557	0.569685441
457	ENSG00000153071.14_2	DAB2	chr5:39371777-39462402	-0.810796872	0.570066895
458	ENSG00000075223.13_1	SEMA3C	chr7:80371854-80551675	-0.809612985	0.570534888
459	ENSG00000114850.6_1	SSR3	chr3:156257929-156272973	-0.807535978	0.571356863
460	ENSG00000151748.14_2	SAV1	chr14:51098776-51135049	-0.805195742	0.572284429
461	ENSG00000105329.9_1	TGFB1	chr19:41807492-41859816	-0.804027755	0.57274793
462	ENSG00000185220.11_1	PGBD2	chr1:249200395-249214145	-0.803989218	0.57276323
463	ENSG00000058804.11_1	NDC1	chr1:54231133-54304533	-0.803701917	0.572877302
464	ENSG00000077684.15_2	JADE1	chr4:129730778-129796379	-0.800401356	0.574189416
465	ENSG00000172346.14_1	CSDC2	chr22:41956767-41973745	-0.798682778	0.574873814
466	ENSG00000108669.16_2	CYTH1	chr17:76670130-76778379	-0.798517052	0.574939855
467	ENSG00000129521.13_2	EGLN3	chr14:34393437-34931980	-0.797943633	0.575168418
468	ENSG00000120784.15_2	ZFP30	chr19:38104650-38183238	-0.797631314	0.575292946
469	ENSG00000148153.13_1	INIP	chr9:115446206-115480516	-0.796506855	0.575741513
470	ENSG00000109586.11_1	GALNT7	chr4:174089904-174245118	-0.796374073	0.575794505
471	ENSG00000182149.20_2	IST1	chr16:71879899-71965102	-0.796042948	0.575926676
472	ENSG00000168792.4_1	ABHD15	chr17:27887565-27894155	-0.791931231	0.577570423
473	ENSG00000212127.5_2	TAS2R14	chr12:11090005-11324172	-0.791457809	0.577759984
474	ENSG00000108061.11_1	SHOC2	chr10:112679305-112773425	-0.791429278	0.57777141
475	ENSG00000122870.11_2	BICC1	chr10:60272900-60591197	-0.79096912	0.577955724
476	ENSG00000132275.10_1	RRP8	chr11:6616305-6624850	-0.789486621	0.578549931
477	ENSG00000175063.16_1	UBE2C	chr20:44441215-44445596	-0.789230858	0.578652506
478	ENSG00000198363.16_2	ASPH	chr8:62413115-62627199	-0.788908178	0.578781945
479	ENSG00000114166.7_1	KAT2B	chr3:20081515-20195896	-0.788070291	0.579118186
480	ENSG00000142871.16_2	CYR61	chr1:86046444-86049645	-0.787178011	0.579476471
481	ENSG00000172795.15_1	DCP2	chr5:112312399-112356667	-0.786272072	0.579840467
482	ENSG00000141580.15_2	WDR45B	chr17:80572438-80606429	-0.783267764	0.581049201
483	ENSG00000104899.6_2	AMH	chr19:2249308-2252072	-0.781733552	0.581667438
484	ENSG00000128886.11_2	ELL3	chr15:44064798-44069741	-0.780586032	0.58213028

485	ENSG00000278535.4_2	DHRS11	chr17:34948228-34957235	-0.780262462	0.582260856
486	ENSG00000130813.17_2	C19orf66	chr19:10196798-10203928	-0.780239665	0.582270057
487	ENSG00000132541.10_2	RIDA	chr8:99114572-99129469	-0.779748992	0.582468125
488	ENSG00000106524.8_1	ANKMY2	chr7:16639401-16685442	-0.778534666	0.582958599
489	ENSG00000072042.12_2	RDH11	chr14:68143518-68162531	-0.778164082	0.583108362
490	ENSG00000203724.10_1	C1orf53	chr1:197871777-197876497	-0.776779987	0.583668054
491	ENSG00000113460.12_1	BRIX1	chr5:34915481-34926101	-0.775126023	0.584337579
492	ENSG00000103855.17_1	CD276	chr15:73976307-74006859	-0.774429319	0.584619834
493	ENSG00000127080.9_1	IPPK	chr9:95375466-95432547	-0.77399053	0.584797671
494	ENSG00000273173.5_2	SNURF	chr15:25200133-25222997	-0.771288536	0.585893953
495	ENSG00000139291.13_2	TMEM19	chr12:72079867-72098826	-0.768873878	0.586875392
496	ENSG00000143147.14_1	GPR161	chr1:168048781-168106905	-0.767981265	0.587238612
497	ENSG00000262664.2_2	OVCA2	chr17:1945230-1946724	-0.767469851	0.587446816
498	ENSG00000173320.10_2	STOX2	chr4:184719175-184944679	-0.766536735	0.587826891
499	ENSG00000111678.10_1	C12orf57	chr12:7052141-7055166	-0.765511657	0.588244709
500	ENSG00000212719.10_2	C17orf51	chr17:21428051-21477722	-0.765174603	0.588382155
501	ENSG00000169851.15_2	PCDH7	chr4:30722037-31148427	-0.764925583	0.588483723
502	ENSG00000157326.18_1	DHRS4	chr14:24422795-24438488	-0.763158317	0.589205043
503	ENSG00000097007.17_2	ABL1	chr9:133589333-133763062	-0.762313432	0.5895502
504	ENSG00000173757.9_2	STAT5B	chr17:40351186-40428725	-0.760786053	0.590174686
505	ENSG00000127870.16_2	RNF6	chr13:26706253-26796630	-0.759528822	0.590689216
506	ENSG00000130766.4_1	SESN2	chr1:28586038-28609002	-0.757550982	0.591499567
507	ENSG00000070423.17_1	RNF126	chr19:647526-663277	-0.757004172	0.5917238
508	ENSG00000167333.12_2	TRIM68	chr11:4619902-4629489	-0.755529134	0.592329099
509	ENSG00000196236.12_1	XPNPEP3	chr22:41253081-41328819	-0.755122827	0.59249594
510	ENSG00000075234.16_2	TTC38	chr22:46663858-46689905	-0.755041987	0.592529141
511	ENSG00000136869.13_1	TLR4	chr9:120466610-120479149	-0.75425927	0.592850698
512	ENSG00000141384.12_2	TAF4B	chr18:23805900-23971649	-0.753337717	0.593229515
513	ENSG00000100138.13_1	SNU13	chr22:42069934-42086508	-0.752026146	0.593769072
514	ENSG00000136436.14_2	CALCOCO2	chr17:46908350-46943884	-0.751870637	0.593833078
515	ENSG00000123297.17_2	TSFM	chr12:58176372-58201854	-0.750909767	0.594228717
516	ENSG00000229809.8_1	ZNF688	chr16:30580667-30584055	-0.750228869	0.594509237
517	ENSG00000187193.8_2	MT1X	chr16:56716336-56718108	-0.747161086	0.595774761
518	ENSG00000040633.12_2	PHF23	chr17:7138347-7143041	-0.746827261	0.595912634
519	ENSG00000109184.14_1	DCUN1D4	chr4:52709166-52783003	-0.746380277	0.596097291
520	ENSG00000176209.11_1	SMIM19	chr8:42396298-42410336	-0.744664828	0.596806508
521	ENSG00000066322.13_2	ELOVL1	chr1:43829068-43833745	-0.7432932	0.597374185
522	ENSG00000175595.14_1	ERCC4	chr16:14014014-14046202	-0.739834815	0.59880791
523	ENSG00000174652.17_1	ZNF266	chr19:9523274-9546254	-0.739743563	0.598845787
524	ENSG00000178229.7_1	ZNF543	chr19:57831877-57842144	-0.739019724	0.599146319
525	ENSG00000181450.17_2	ZNF678	chr1:227751244-227865144	-0.738086563	0.599533983
526	ENSG00000170619.9_2	COMMD5	chr8:146066427-146079121	-0.737150863	0.599922954
527	ENSG00000146676.7_2	PURB	chr7:44915892-44924960	-0.737142458	0.599926449
528	ENSG00000196417.12_2	ZNF765	chr19:53893046-53933666	-0.734315833	0.601103017
529	ENSG00000118689.14_1	FOXO3	chr6:108881038-109005977	-0.73426552	0.601123981
530	ENSG00000178605.13_1_PAR_Y	GTPBP6	chrY:171196-180884	-0.73239975	0.601901889
531	ENSG00000101347.8_1	SAMHD1	chr20:35518632-35580246	-0.731665546	0.602208282
532	ENSG00000152475.6_1	ZNF837	chr19:58878985-58892427	-0.731135424	0.602429606
533	ENSG00000167778.8_1	SPRYD3	chr12:53458100-53473204	-0.729996966	0.602905182

534	ENSG00000134250.18_2	NOTCH2	chr1:120454176-120612240	-0.72823759	0.603640877
535	ENSG00000176894.9_2	PXMP2	chr12:133264192-133281577	-0.725810778	0.604657139
536	ENSG00000163818.16_2	LZTFL1	chr3:45864808-45957534	-0.725374646	0.604839956
537	ENSG00000145569.5_1	FAM105A	chr5:14581884-14615116	-0.724922939	0.605029361
538	ENSG00000164070.11_2	HSPA4L	chr4:128702976-128761888	-0.721792973	0.606343414
539	ENSG00000248871.1_2	TNFSF12-TNFSF13	chr17:7452416-7464918	-0.720966591	0.606690829
540	ENSG00000065970.8_1	FOXJ2	chr12:8185299-8208099	-0.720705448	0.606800657
541	ENSG00000198382.8_2	UVRAG	chr11:75526212-75854239	-0.720400579	0.606928899
542	ENSG00000120324.8_1	PCDHB10	chr5:140571926-140575215	-0.720289849	0.606975484
543	ENSG00000141569.10_1	TRIM65	chr17:73876416-73893084	-0.719356387	0.60736834
544	ENSG00000087301.8_2	TXNDC16	chr14:52897308-53019240	-0.719202884	0.607432968
545	ENSG00000124257.6_1	NEURL2	chr20:44517264-44519926	-0.718449228	0.60775037
546	ENSG00000124107.5_1	SLPI	chr20:43880880-43883205	-0.717002356	0.608360186
547	ENSG00000102974.14_1	CTCF	chr16:67596310-67673086	-0.716423719	0.608604236
548	ENSG00000242372.6_2	EIF6	chr20:33866710-33872788	-0.715017069	0.609197924
549	ENSG00000214194.8_2	LINC00998	chr7:112756773-112758668	-0.714637194	0.609358353
550	ENSG00000137834.14_2	SMAD6	chr15:66994566-67075186	-0.71429075	0.6095047
551	ENSG00000181027.10_2	FKRP	chr19:47249303-47280245	-0.713125774	0.609997073
552	ENSG00000167807.15_2	CTD-2369P2.10	chr19:10416103-10426685	-0.713068295	0.610021377
553	ENSG00000147400.8_1	CETN2	chrX:151995517-151999321	-0.712390119	0.610308201
554	ENSG00000134153.9_2	EMC7	chr15:34376218-34394149	-0.711738828	0.610583781
555	ENSG00000216490.3_2	IFI30	chr19:18283972-18288927	-0.710687637	0.611028832
556	ENSG00000277971.1_2	XXbac-B562F10.12	chr22:20783528-20800907	-0.708359143	0.612015822
557	ENSG00000147394.18_1	ZNF185	chrX:152082986-152142024	-0.706698084	0.612720878
558	ENSG00000137825.10_2	ITPKA	chr15:41785591-41795749	-0.703874057	0.613921433
559	ENSG00000099860.8_2	GADD45B	chr19:2476120-2478257	-0.701868577	0.614775434
560	ENSG00000143252.14_1	SDHC	chr1:161284047-161345130	-0.701025357	0.615134861
561	ENSG00000076351.12_2	SLC46A1	chr17:26721775-26734215	-0.69783168	0.616498086
562	ENSG00000185009.12_1	AP3M1	chr10:75880013-75910821	-0.697816369	0.616504628
563	ENSG00000051180.16_1	RAD51	chr15:40986972-41024537	-0.697762786	0.616527527
564	ENSG00000198682.12_1	PAPSS2	chr10:89419370-89507462	-0.697326036	0.616714197
565	ENSG00000107951.8	MTPAP	chr10:30598730-30663377	-0.694603266	0.617879209
566	ENSG00000131148.8_2	EMC8	chr16:85805364-85833214	-0.694280575	0.618017427
567	ENSG00000119900.7_1	OGFRL1	chr6:71998506-72018653	-0.69420092	0.61805155
568	ENSG00000155744.9_1	FAM126B	chr2:201838441-201936394	-0.69380181	0.618222553
569	ENSG00000035403.16_2	VCL	chr10:75754951-75881121	-0.693367789	0.618408567
570	ENSG00000168301.12_2	KCTD6	chr3:58477841-58488087	-0.692053423	0.618972224
571	ENSG00000179091.4_1	CYC1	chr8:145149930-145152428	-0.691061254	0.61939805
572	ENSG00000164687.10_1	FABP5	chr8:82192598-82197012	-0.690879189	0.619476221
573	ENSG00000259075.6_2	POC1B-GALNT4	chr12:89913185-89920039	-0.690408126	0.619678523
574	ENSG00000112852.6_2	PCDHB2	chr5:140474163-140478287	-0.689309002	0.620150808
575	ENSG00000010072.15_1	SPRTN	chr1:231472850-231490769	-0.688362754	0.620557692
576	ENSG00000116514.16_1	RNF19B	chr1:33402046-33430286	-0.68779919	0.62080015
577	ENSG00000158796.16_1	DEDD	chr1:161090764-161102478	-0.687446011	0.620952143
578	ENSG00000062370.16_2	ZNF112	chr19:44830708-44871377	-0.687045892	0.621124383
579	ENSG00000159388.5_1	BTG2	chr1:203274619-203278730	-0.686351748	0.621423305
580	ENSG00000163251.3_1	FZD5	chr2:208627310-208634287	-0.6857554	0.621680228
581	ENSG00000167565.12_2	SERTAD3	chr19:40946751-40950612	-0.685641332	0.621729383
582	ENSG00000255152.8_2	MSH5-SAPCD1	chr6:31707797-31732628	-0.68543605	0.621817856

583	ENSG00000132383.11_1	RPA1	chr17:1732996-1803376	-0.685098192	0.621963493
584	ENSG00000011304.18_2	PTBP1	chr19:797075-812327	-0.685014192	0.621999708
585	ENSG00000164291.16_1	ARSK	chr5:94890778-94940768	-0.6850015	0.62200518
586	ENSG00000196411.9_1	EPHB4	chr7:100400187-100425143	-0.684649128	0.622157121
587	ENSG00000010704.18_2	HFE	chr6:26087509-26098571	-0.684438236	0.622248074
588	ENSG00000163975.11_2	MELTF	chr3:196715492-196756687	-0.681789313	0.623391629
589	ENSG00000173418.11_1	NAA20	chr20:19997760-20014299	-0.681157831	0.623664553
590	ENSG00000203778.7_1	FAM229B	chr6:112408802-112423993	-0.679338777	0.624451411
591	ENSG00000133328.3_1	HRASLS2	chr11:63320242-63330855	-0.678619233	0.624762933
592	ENSG00000116922.14_2	C1orf109	chr1:38147242-38157921	-0.676105005	0.625852676
593	ENSG00000151881.14_2	TMEM267	chr5:43444354-43483995	-0.67602201	0.625888681
594	ENSG00000020256.19_2	ZFP64	chr20:50668202-50820847	-0.675839928	0.625967679
595	ENSG00000112941.13_2	PAPD7	chr5:6713120-6757161	-0.675367769	0.626172576
596	ENSG00000213995.11_2	NAXD	chr13:111267807-111292340	-0.675210254	0.626240946
597	ENSG00000131504.15_1	DIAPH1	chr5:140894583-140998622	-0.675100739	0.626288486
598	ENSG00000148341.17_1	SH3GLB2	chr9:131769315-131790582	-0.675089425	0.626293397
599	ENSG00000155366.16_2	RHOC	chr1:113243728-113250056	-0.672923439	0.627234388
600	ENSG00000249115.8_2	HAUS5	chr19:36103646-36116251	-0.672534711	0.627403416
601	ENSG00000072210.18_2	ALDH3A2	chr17:19551449-19580911	-0.671856875	0.627698264
602	ENSG00000140718.19_2	FTO	chr16:53735604-54192424	-0.671760087	0.627740377
603	ENSG00000144048.10_1	DUSP11	chr2:73989311-74007284	-0.66934697	0.628791242
604	ENSG00000197037.10_2	ZSCAN25	chr7:99214569-99230030	-0.6685306	0.629147154
605	ENSG00000198874.12_1	TYW1	chr7:66460160-66704506	-0.665538667	0.630453265
606	ENSG00000100767.15_2	PAPLN	chr14:73704205-73741348	-0.665157001	0.630620074
607	ENSG00000134852.14_2	CLOCK	chr4:56294070-56413305	-0.663575575	0.631311714
608	ENSG00000164088.17_2	PPM1M	chr3:52279809-52284613	-0.662776175	0.631661622
609	ENSG00000148803.11_2	FUOM	chr10:135168658-135171539	-0.661049658	0.632418003
610	ENSG00000131788.15_2	PIAS3	chr1:145575233-145586546	-0.657569667	0.633945329
611	ENSG00000159069.13_2	FBXW5	chr9:139834887-139839148	-0.656285608	0.634509818
612	ENSG00000100221.10_2	JOSD1	chr22:39081548-39097561	-0.65627002	0.634516674
613	ENSG00000163453.11_1	IGFBP7	chr4:57896939-57976551	-0.656065204	0.634606761
614	ENSG00000125656.8_2	CLPP	chr19:6361463-6368919	-0.655990689	0.634639539
615	ENSG00000111880.15_1	RNGTT	chr6:89319991-89673440	-0.654907059	0.635116405
616	ENSG00000154380.17_2	ENAH	chr1:225674537-225840844	-0.654407766	0.635336247
617	ENSG00000114648.11_1	KLHL18	chr3:47324407-47388306	-0.654321351	0.635374304
618	ENSG00000100994.11_2	PYGB	chr20:25228705-25278650	-0.653464036	0.635751984
619	ENSG00000106144.19_1	CASP2	chr7:142985308-143004789	-0.653256743	0.635843338
620	ENSG00000173267.13_1	SNCG	chr10:88718375-88723017	-0.652773825	0.636056212
621	ENSG00000175879.8_1	HOXD8	chr2:176994422-176997423	-0.65213045	0.636339927
622	ENSG00000175115.11_2	PACS1	chr11:65837834-66012218	-0.650922579	0.636872914
623	ENSG00000168818.9_2	STX18	chr4:4417469-4544073	-0.650201488	0.637191317
624	ENSG00000163235.15_2	TGFA	chr2:70674412-70781325	-0.649546289	0.637480762
625	ENSG00000119661.14_1	DNAL1	chr14:74111578-74170435	-0.649298881	0.637590094
626	ENSG00000198223.16_2	CSF2RA	chrX:1387693-1429274	-0.648514767	0.637936722
627	ENSG00000043093.13_2	DCUN1D1	chr3:182655862-182703741	-0.647764804	0.63826843
628	ENSG00000136982.5_2	DSCC1	chr8:120846216-120868250	-0.647082322	0.638570441
629	ENSG00000104691.14_2	UBXN8	chr8:30589764-30624522	-0.64610342	0.639003873
630	ENSG00000072736.18_2	NFATC3	chr16:68118654-68263162	-0.643190758	0.640295263
631	ENSG00000157193.15_2	LRP8	chr1:53708036-53793742	-0.642952239	0.640401131

632	ENSG00000110344.9_1	UBE4A	chr11:118230300-118269926	-0.641912553	0.640862806
633	ENSG00000243667.6_2	WDR92	chr2:68350068-68384692	-0.641716417	0.640949938
634	ENSG00000174917.8_1	C19orf70	chr19:5678432-5680907	-0.640893977	0.641315429
635	ENSG00000101079.20_1	NDRG3	chr20:35280169-35374481	-0.640782095	0.641365166
636	ENSG00000104880.17_2	ARHGEF18	chr19:7459999-7537363	-0.639850962	0.641779244
637	ENSG00000213145.9_2	CRIP1	chr14:105952654-105955284	-0.639562736	0.641907474
638	ENSG00000104081.13_2	BMF	chr15:40380091-40401093	-0.639195617	0.642070839
639	ENSG00000118707.9_2	TGIF2	chr20:35201891-35222353	-0.638790556	0.642251137
640	ENSG00000110583.12_1	NAA40	chr11:63706431-63724800	-0.638534557	0.642365111
641	ENSG00000103429.10_1	BFAR	chr16:14726672-14763093	-0.638354603	0.642445242
642	ENSG00000116525.13_1	TRIM62	chr1:33611003-33647660	-0.637790094	0.642696671
643	ENSG00000165072.9_2	MAMDC2	chr9:72658497-72841886	-0.637256917	0.642934237
644	ENSG00000165886.4_1	UBTD1	chr10:99258625-99330966	-0.635793671	0.643586661
645	ENSG00000198522.13_2	GPN1	chr2:27851114-27874375	-0.635426166	0.643750625
646	ENSG00000160271.14_2	RALGDS	chr9:135973107-136024721	-0.634947787	0.64396412
647	ENSG00000002919.14_1	SNX11	chr17:46180719-46200436	-0.634558019	0.644138121
648	ENSG00000262484.1_1	CCER2	chr19:39399620-39402798	-0.63442702	0.644196613
649	ENSG00000183671.12_2	GPR1	chr2:207040040-207082771	-0.634102937	0.644341339
650	ENSG00000125970.11_2	RALY	chr20:32581452-32696114	-0.632987497	0.644839714
651	ENSG00000128699.13_2	ORMDL1	chr2:190635049-190649097	-0.631053846	0.645704575
652	ENSG00000132376.19_2	INPP5K	chr17:1397865-1420182	-0.630048041	0.646154898
653	ENSG00000141627.13_2	DYM	chr18:46567844-46987717	-0.629783823	0.646273247
654	ENSG00000165637.13_1	VDAC2	chr10:76969912-76991206	-0.629575952	0.646366373
655	ENSG00000075303.12_1	SLC25A40	chr7:87462883-87505672	-0.629558586	0.646374153
656	ENSG00000215271.7_2	HOMEZ	chr14:23741631-23768656	-0.62811658	0.647020541
657	ENSG00000196689.11_2	TRPV1	chr17:3468738-3512705	-0.626781854	0.647619417
658	ENSG00000159128.14_2	IFNGR2	chr21:34775202-34851655	-0.626060444	0.647943336
659	ENSG00000175874.9_1	CREG2	chr2:101962013-102004057	-0.626031062	0.647956532
660	ENSG00000041802.10_1	LSG1	chr3:194361517-194393206	-0.623711332	0.648999228
661	ENSG00000146802.12_1	TMEM168	chr7:112402437-112430647	-0.6235765	0.649059886
662	ENSG00000213648.10_2	SULT1A4	chr16:29471210-29476297	-0.623474318	0.649105858
663	ENSG00000187098.14_2	MITF	chr3:69788586-70017488	-0.623004265	0.649317382
664	ENSG00000168872.16_2	DDX19A	chr16:70380732-70407286	-0.622312465	0.649628817
665	ENSG00000140995.16_2	DEF8	chr16:90014333-90034468	-0.622277899	0.649644382
666	ENSG00000166510.13_1	CCDC68	chr18:52568740-52626739	-0.621133887	0.650159733
667	ENSG00000088205.12_1	DDX18	chr2:118572226-118589955	-0.620558975	0.650418873
668	ENSG00000156030.13_2	ELMSAN1	chr14:74181825-74256988	-0.62051663	0.650437964
669	ENSG00000188610.8	FAM72B	chr1:120837756-120855681	-0.620421853	0.650480695
670	ENSG00000133740.10_1	E2F5	chr8:86089460-86129387	-0.620368034	0.650504962
671	ENSG00000099256.18_1	PRTFDC1	chr10:25137536-25241533	-0.620337086	0.650518916
672	ENSG00000120705.12_2	ETF1	chr5:137841784-137878989	-0.620071568	0.650638651
673	ENSG00000123213.22_2	NLN	chr5:65018023-65167553	-0.617892363	0.651622189
674	ENSG00000196757.7_2	ZNF700	chr19:12035883-12061588	-0.616461668	0.652268712
675	ENSG00000115738.9_1	ID2	chr2:8818975-8824583	-0.615832142	0.652553394
676	ENSG00000154146.12_1	NRGN	chr11:124609742-124617106	-0.614845479	0.65299983
677	ENSG00000115649.15_1	CNPPD1	chr2:220036619-220042828	-0.614099192	0.653337705
678	ENSG00000197930.12_2	ERO1A	chr14:53106634-53162618	-0.61394093	0.65340938
679	ENSG00000165948.10_2	IFI27L1	chr14:94547628-94570192	-0.612159246	0.654216819
680	ENSG00000178773.14_2	CPNE7	chr16:89642176-89663654	-0.612016879	0.654281381

681	ENSG00000150457.8_1	LATS2	chr13:21547171-21635686	-0.61078168	0.6548418
682	ENSG00000140836.14_2	ZFHX3	chr16:72816784-73093597	-0.610713446	0.654872772
683	ENSG00000125741.4_2	OPA3	chr19:46030685-46105470	-0.610701835	0.654878043
684	ENSG00000141750.6_1	STAC2	chr17:37366789-37382125	-0.610253467	0.655081601
685	ENSG00000132613.14_1	MTSS1L	chr16:70695107-70719969	-0.609745589	0.655312252
686	ENSG00000100983.9_1	GSS	chr20:33516233-33543620	-0.609416366	0.655461811
687	ENSG00000204237.4_2	OXLD1	chr17:79632066-79633665	-0.608279448	0.655978553
688	ENSG00000160190.13_2	SLC37A1	chr21:43916118-44001550	-0.607240471	0.656451135
689	ENSG00000133884.9_1	DPF2	chr11:65101225-65120720	-0.606393133	0.656836802
690	ENSG00000161921.14_1	CXCL16	chr17:4636821-4643217	-0.606182301	0.656932797
691	ENSG00000108679.12_2	LGALS3BP	chr17:76967320-76976191	-0.604431385	0.657730563
692	ENSG00000143570.17_2	SLC39A1	chr1:153931575-153940660	-0.604118441	0.657873251
693	ENSG00000125968.8_1	ID1	chr20:30193086-30194318	-0.603393954	0.658203702
694	ENSG00000197502.1	AL627171.1	chr14:50300810-50311552	-0.60296325	0.658400232
695	ENSG00000135441.7_2	BLOC1S1	chr12:56109821-56113871	-0.602231209	0.658734398
696	ENSG00000161513.11_1	FDXR	chr17:72858619-72869156	-0.601374563	0.659125658
697	ENSG00000167705.11_2	RILP	chr17:1549439-1553371	-0.601319386	0.659150867
698	ENSG00000172992.11_1	DCAKD	chr17:43100708-43138477	-0.601093569	0.659254048
699	ENSG00000172531.14_1	PPP1CA	chr11:67165654-67188654	-0.600001137	0.659753435
700	ENSG00000266086.1_2	RP11-159D12.5	chr17:56066399-56082614	-0.599751812	0.659867463
701	ENSG00000135480.14_2	KRT7	chr12:52626304-52645970	-0.599659768	0.659909564
702	ENSG00000228672.3_1	PROB1	chr5:138726281-138731402	-0.599228277	0.660106964
703	ENSG00000169891.17_1	REPS2	chrX:16964814-17171403	-0.598398305	0.660486828
704	ENSG00000170264.12_1	FAM161A	chr2:62051989-62081278	-0.598299689	0.660531977
705	ENSG00000196812.4_1	ZSCAN16	chr6:28092338-28097860	-0.597842848	0.660741173
706	ENSG00000188959.9_1	C9orf152	chr9:112952328-112970469	-0.59752419	0.660887132
707	ENSG00000138613.13_2	APH1B	chr15:63568217-63601325	-0.597054791	0.661102195
708	ENSG00000171174.9	RBKS	chr2:28004231-28113965	-0.595673501	0.661735462
709	ENSG00000197746.13_1	PSAP	chr10:73576055-73611132	-0.594695958	0.662183993
710	ENSG00000160352.11	ZNF714	chr19:21264965-21308073	-0.594419806	0.662310757
711	ENSG00000065243.19_2	PKN2	chr1:89149905-89301938	-0.594288013	0.662371263
712	ENSG00000132286.11_2	TIMM10B	chr11:6502677-6505909	-0.594283699	0.662373243
713	ENSG00000177839.6_2	PCDHB9	chr5:140566701-140571114	-0.594228151	0.662398747
714	ENSG00000110057.7_2	UNC93B1	chr11:67758575-67772452	-0.591011869	0.663877118
715	ENSG00000007866.18_2	TEAD3	chr6:35441374-35464853	-0.589580775	0.664535983
716	ENSG00000184281.14_2	TSSC4	chr11:2421718-2425108	-0.589321362	0.664655485
717	ENSG00000175582.19_1	RAB6A	chr11:73386683-73472182	-0.589007064	0.664800299
718	ENSG00000099804.8_1	CDC34	chr19:531712-542092	-0.587673346	0.665415166
719	ENSG00000029639.10_1	TFB1M	chr6:155578643-155635627	-0.587469644	0.665509126
720	ENSG00000166016.5_2	ABTB2	chr11:34172535-34379555	-0.586713116	0.665858201

Supporting Table S3. Top 10 terms of GO_BP analysis in mGPDH over-expressed LO2 cells.

GO.ID	Term	Ontology	Count	Pop. Hits	List. Total	Pop. Total	Fold. Enrichment	P value	FDR	Enrichment. Score	Gene. Ratio	GENES
GO:0044237	Cellular metabolic process	Biological proc	6735	9979	9801	16672	1.148068734	4E-171	3E-167	170.3630809	0.6871748	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0034641	Cellular nitrogen compound metabolic process	Biological proc	4554	6338	9801	16672	1.222244534	2E-162	6E-159	161.7362646	0.4646465	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0006807	Nitrogen compound metabolic process	Biological proc	4795	6778	9801	16672	1.203384351	2E-151	4E-148	150.6818211	0.4892358	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0044260	Cellular macromolecule metabolic process	Biological proc	5655	8217	9801	16672	1.170675784	9E-150	1E-146	149.0679567	0.5769819	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0044238	Primary metabolic process	Biological proc	6667	9992	9801	16672	1.134998643	6E-143	8E-140	142.2169079	0.6802367	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0008152	Metabolic process	Biological proc	7119	10818	9801	16672	1.119410376	1E-137	1E-134	136.9930892	0.7263545	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0006139	Nucleobase-containing compound metabolic process	Biological proc	4054	5647	9801	16672	1.221190084	4E-135	3E-132	134.4299425	0.4136313	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0071704	Organic substance metabolic process	Biological proc	6894	10449	9801	16672	1.122312661	1E-131	1E-128	130.8647744	0.7033976	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0046483	Heterocycle metabolic process	Biological proc	4114	5771	9801	16672	1.212636191	6E-129	4E-126	128.2232406	0.4197531	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE
GO:0006725	Cellular aromatic compound metabolic process	Biological proc	4137	5819	9801	16672	1.20935687	2E-126	9E-124	125.8225949	0.4220998	SIRT1//LIG4//APTX//TDP1//XRCC1//ALYRE

Supporting Table S4.Top 10 terms of KEGG analysis for all differentially expressed genes in mGPDH over-expressed LO2 cells.

Down-regulated pathway:

Pathway ID	Definition	Size	Enrichment Score	P value	FDR	Selection Counts	Selection Size	Count	Gene Ratio	Genes
hsa04141	Protein processing in endoplasmic reticulum	5869	3.93206	0.000117	0.00117	16	197	165	0.081	ATF4//HSPA1B//SSR3//UBE2G2//XBP1//MOGS//EDEM1//MAN1A2//CKAP4//HSPA4L//TRAM1//ERO1A//MBTPS2//YOD1//UBQLN4//DNAJC5
hsa04350	TGF-beta signaling pathway	5869	2.72635	0.001878	0.00939	9	197	84	0.046	AMH//CDKN2B//E2F5//ID1//ID2//ID3//SMAD6//TFDP1//TGFB1
hsa04130	SNARE interactions in vesicular transport	5869	2.18408	0.006545	0.02182	5	197	36	0.025	STX5//VAMP5//BET1L//STX18//VTI1A
hsa05130	Pathogenic Escherichia coli infection	5869	1.97255	0.010652	0.02663	6	197	56	0.03	ABL1//TLR4//TUBA1A//WASL//ARPC5//YWHAQ
hsa05131	Shigellosis	5869	1.79923	0.015877	0.03175	6	197	61	0.03	ABL1//DIAPH1//RAC1//VCL//WASL//ARPC5
hsa04110	Cell cycle	5869	1.63797	0.023016	0.03663	9	197	124	0.046	ABL1//CDKN2B//E2F3//E2F5//SFN//GADD45B//TFDP1//TGFB1//YWHAQ
hsa05211	Renal cell carcinoma	5869	1.53301	0.029308	0.03663	6	197	70	0.03	RAC1//TGFA//TGFB1//VHL//EGLN1//EGLN3
hsa05212	Pancreatic cancer	5869	1.53301	0.029308	0.03663	6	197	70	0.03	E2F3//RAC1//RAD51//RALGDS//TGFA//TGFB1
hsa00562	Inositol phosphate metabolism	5869	1.38276	0.041423	0.04584	5	197	57	0.025	ITPK1//ITPKA//INPP5K//PI4K2B//IPPK
hsa05200	Pathways in cancer	5869	1.33877	0.045838	0.04584	17	197	326	0.086	ABL1//CDKN2B//CSF2RA//E2F3//FOXO1//MITF//RAC1//RAD51//RALGDS//STAT5B//TGFA//TGFB1//VHL//FZD5//PIAS3//EGLN1//EGLN3

Up-regulated pathway:

Pathway ID	Definition	Size	Enrichment Score	P value	FDR	Selection Counts	Selection Size	Count	Gene Ratio	Genes
hsa00750	Vitamin B6 metabolism	5869	3.2476	0.0006	0.0062	3	184	6	0.0163	PDXK//PSAT1//PDXP
hsa00471	D-Glutamine and D-glutamate metabolism	5869	2.2498	0.0056	0.0213	2	184	4	0.0109	GLS//GLUD1
hsa03040	Spliceosome	5869	2.2025	0.0063	0.0213	10	184	127	0.0543	HSPA1A//NCBP1//TXNL4A//NCBP2//CDC40//SF3B6//PPIL1//LSM7//PHF5A//ZMAT2
hsa00620	Pyruvate metabolism	5869	2.1108	0.0077	0.0213	5	184	40	0.0272	ACYP1//ALDH1B1//AKR1B1//DLAT//ACSS2
hsa04144	Endocytosis	5869	1.6292	0.0235	0.0412	12	184	201	0.0652	CBL//HSPA1A//MET//RAB4A//RAB5B//TGFBR1//CXCR4//RNF41//RAB31//EHD4//SH3GLB1//CHMP1B
hsa04120	Ubiquitin mediated proteolysis	5869	1.5954	0.0254	0.0412	9	184	135	0.0489	CBL//UBE2B//UBE2D3//CUL5//CUL4B//UBA3//ANAPC13//FBXO2//CDC26
hsa00330	Arginine and proline metabolism	5869	1.5811	0.0262	0.0412	5	184	54	0.0272	ALDH1B1//ARG2//GLS//GLUD1//P4HA1
hsa00910	Nitrogen metabolism	5869	1.4704	0.0339	0.0414	3	184	23	0.0163	GLS//GLUD1//CA5B
hsa04964	Proximal tubule bicarbonate reclamation	5869	1.4704	0.0339	0.0414	3	184	23	0.0163	ATP1B1//GLS//GLUD1
hsa04380	Osteoclast differentiation	5869	1.3267	0.0471	0.0479	8	184	128	0.0435	CREB1//FOS//IFNAR1//JUNB//NFKBIA//MAP2K1//MAP3K7//TGFBR1

Supporting Table S5. Differential changed genes regarding "protein processing in endoplasmic reticulum" item of KEGG analysis

No.	Track_id	Gene_Name	log2(fold_change)	Fold_Change
1	ENSG00000204388.6_2	HSPA1B	-7.021933907	0.007694622
2	ENSG00000136026.13_2	CKAP4	-4.963434422	0.032052164
3	ENSG00000180667.10_1	YOD1	-2.044546011	0.242398721
4	ENSG00000101152.10_1	DNAJC5	-1.838397873	0.279632146
5	ENSG00000128272.14_1	ATF4	-1.757020835	0.295858483
6	ENSG00000134109.10_1	EDEM1	-1.340689332	0.394831957
7	ENSG00000012174.11_2	MBTPS2	-1.323049319	0.399689251
8	ENSG00000184787.18_1	UBE2G2	-1.322281152	0.399902124
9	ENSG00000160803.7_1	UBQLN4	-1.019186016	0.493394652
10	ENSG00000100219.16_2	XBP1	-1.010623761	0.496331608
11	ENSG00000115275.11_2	MOGS	-0.952922935	0.516584788
12	ENSG00000198162.12_2	MAN1A2	-0.861377371	0.550426803
13	ENSG00000067167.7_1	TRAM1	-0.833792568	0.561052403
14	ENSG00000114850.6_1	SSR3	-0.807535978	0.571356863
15	ENSG00000164070.11_2	HSPA4L	-0.721792973	0.606343414
16	ENSG00000197930.12_2	ERO1A	-0.61394093	0.65340938