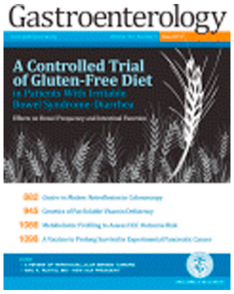

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Activation of autophagy, observed in liver tissues from patients with Wilson disease and from Atp7b-deficient animals, protects hepatocytes from copper-induced apoptosis

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ABSTRACT

BACKGROUND AND AIMS. Wilson disease is an inherited disorder of copper metabolism that leads to copper accumulation and toxicity in liver and brain. It is caused by mutations in the ATPase copper transporting beta gene (*ATP7B*), which encodes a protein that transports copper out of heaptocytes into the bile. We studied ATP7B-deficient cells and animals to identify strategies to reduce copper toxicity in patients with Wilson disease.

METHODS. We used RNA-seq to compare gene expression patterns between wild-type and ATP7B-knockout HepG2 cells exposed to copper. We collected blood and liver tissues from *Atp7b*$^{-/-}$ and *Atp7b*$^{+/-}$ (control) rats (LPP) and mice; some mice were given 5 daily injections of an autophagy inhibitor (spautin-1) or vehicle. We obtained liver biopsies from 2 patients with Wilson disease in Italy and liver tissues from patients without Wilson disease (control). Liver tissues were analyzed by immunohistochemistry, immunofluorescence, cell viability, and apoptosis assays, as well as by electron and confocal microscopy. Proteins were knocked down in cell lines using small interfering RNAs. Levels of copper were measured in cell lysates, blood samples, liver homogenates, and subcellular fractions by spectroscopy.

RESULTS. Following exposure to copper, ATP7B-knockout cells had significant increases in expression of 103 genes that regulate autophagy (including *MAP1LC3A,* known as *LC3*), compared with wild-type cells. Electron and confocal microscopy revealed more autophagic structures in the cytoplasm of ATP7B-knockout cells than wild-type cells following copper exposure. Hepatocytes in liver tissues from patients with Wilson disease, as well as *Atp7b*$^{-/-}$ mice and rats (but not controls), had multiple autophagosomes. In ATP7B-knockout cells, mTOR had reduced activity and was dissociated from lysosomes; this resulted in translocation of the mTOR substrate transcription factor EB (TFEB) to the nucleus, and activation of autophagy-related genes. In wild-type HepG2 cells (but not ATP7B-knockout cells), exposure to copper and amino acids induced recruitment of mTOR to lysosomes. Pharmacologic inhibitors of autophagy or knockdown of autophagy proteins ATG7 and ATG13 induced and accelerated death of ATP7B-knockout HepG2 cells, compared to wild-type cells. Autophagy protected ATP7B-knockout cells from copper-induced death.

CONCLUSION. ATP7B-deficient hepatocytes, such as in those in patients with Wilson disease, activate autophagy in response to copper overload to prevent copper-induced apoptosis. Agents designed to activate this autophagic pathway might reduce copper toxicity in patients with Wilson disease.

Key words: Cu, metal toxicity, copper homeostasis, mitophagy

INTRODUCTION

Wilson disease belongs to a cohort of relatively frequent inherited liver disorders with an incidence of 1:7,000-30,000 live births [1]. It is caused by toxic Cu overload in the liver due to mutations in the *ATP7B* gene encoding a Cu pump that is expressed mainly in hepatocytes and normally drives the excretion of excess Cu into the bile. Cu accumulation can be highly toxic due to the ability of Cu to directly damage different intracellular components or to disrupt the redox balance [2, 3].

Understanding the mechanisms that either promote or counteract Cu toxicity is of great importance as it has the potential to reveal possible therapeutic targets for Wilson disease. Cells utilize a vast repertoire of tools to combat Cu toxicity. Relocation of the efflux transporters ATP7A/B promotes Cu removal to the extracellular space [4, 5]. Another well-documented response to Cu includes down-regulation or internalization of the Cu influx transporter CTR1 [6, 7] and up-regulation of metallothioneins, which capture and store excess Cu ions [8, 9]. Finally, a growing body of evidence suggests that quality control pathways such as proteasomal degradation [8, 9] or autophagy [10-12] might be involved in the degradation of Cu-damaged proteins or larger cellular components, respectively. ATP7B-deficient hepatocytes lack the most effective weapon against Cu toxicity (i.e., the Cu efflux transporter ATP7B) and therefore have to rely on alternative mechanisms to survive Cu overload. Indeed, increased metallothionein expression [9] and down-regulation of the Cu influx transporter CTR1 [6] have been documented for ATP7B-deficient hepatocytes. However, other mechanisms that allow hepatocytes to combat Cu toxicity during development of Wilson disease remain to be identified. To find such mechanisms we analyzed the global transcriptional response of ATP7B-deficient hepatic cells to Cu and observed a striking induction of numerous autophagy-related genes. These transcriptional changes were mirrored by an activation of autophagy that helps ATP7B-deficient hepatocytes to attenuate Cu toxicity. Taken together, our findings underscore the novel role of autophagy as a pro-survival mechanism in the pathogenesis of Wilson disease.

MATERIALS AND METHODS

Antibodies and other reagents

The full list of antibodies, siRNAs and primers is provided in Supplementary Methods.

Cell culture, construction of recombinant adenoviruses

Wild-type HepG2 cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% FCS, 2 mM L-glutamine, and 1% penicillin and streptomycin. ATP7B-ko HepG2 cells [13] were grown in RPMI medium supplemented with 10% FCS, 2 mM L-glutamine, and 1% penicillin and streptomycin. To transduce WT or ATP7B-ko cells, adenoviruses that contained ATP7B-GFP, TFEB or α-fetoprotein were used at a MOI of 1,000 particles per cell.

Animals

The *Atp7b*$^{-/-}$ (LPP) rat strain [14] was provided by Jimo Borjigin (University of Michigan, Ann Arbor, USA). The *Atp7b*$^{-/-}$ mice [15] were obtained from The Jackson Laboratory through re-derivation. Animal studies were carried out in accordance with the ARRIVE guidelines and with the Italian (authorization #726/2018-PR) and German (authorization #AZ 55.2-1-54-2532-162-2014) Ministries of Health regulations for animal procedures. Rat and murine strains were housed at the Helmholtz Center (Munich, Germany) and TIGEM (Pozzuoli, Italy) animal facilities, respectively. Animals used for this study were either 80-100 (*Atp7b*$^{-/-}$ rats) or 90-100 (*Atp7b*$^{-/-}$ mice) days of age. Both males and females mice were used, as no sex-related differences were observed in phenotypes. Heterozygous (*Atp7b*$^{+/-}$) controls were age-matched and obtained from both littermates and separate litters that were co-housed. Animals were kept on an *ad-libitum* Altromin 1314 diet and tap water. Spautin-1 (10 mg/kg) and control vehicle were supplied to *Atp7b*$^{-/-}$ and *Atp7b*$^{+/-}$ mice by intraperitoneal injection once a day for 5 days. Animals were treated, sacrificed and tissues collected during light cycle hours.

Wilson disease patient biopsies

Liver biopsies from Wilson disease patients were obtained in the 'Federico II' University Hospital (Naples, Italy) during the course of Wilson disease diagnosis confirmation.

Patient #1 has milder loss of ATP7B function than Patient #2 (see Supplementary Methods). Tiny pieces of healthy liver tissue were obtained during liver transplantation surgery in Bambino Gesù Children's Hospital (Rome, Italy) and used for comparison. Liver samples were fixed with 1% glutaraldehyde and prepared for electron microscopy analysis.

Isolation of subcellular fractions

To prepare mitochondrial and cytosolic extracts, cells were homogenized and mitochondrial and cytosolic extracts obtained using the Qproteome Mitochondria Isolation Kit (QIAGEN). Mitochondria and lysosomes from rat liver homogenates were purified by differential and density gradient centrifugation using either Percoll (GE Healthcare Europe) or Nycodenz (Axis-Shield). Purity of organelle fractions was controlled by immunobloting (see Supplementary Methods) and electron microscopy.

RNA interference

Small interfering RNAs (siRNAs) that targeted PINK1, BNIP3L, FUNDC1, ATG7, and ATG13 (Sigma-Aldrich) were used to suppress the corresponding gene. The efficiency of silencing were determined by qRT-PCR (see Supplementary Methods).

Immunofluorescence and immunohistochemistry

Immunofluorescence [16], mitochondrial membrane potential [17] assays are described in Supplementary Methods. To evaluate lysosomal acidification or proteolytic activity, the cells were loaded with LysoTracker Red (Life Technologies) or with DQ-BSA (Thermo Fisher) and Magic Red (ImmunoChemistry Technologies), respectively, according to the manufacture’s instructions. Acquisition and quantification of the LysoTracker or the DQ-BSA and Magic Red signals was performed using a confocal microscope (Zeiss LSM 700) equipped with Zen 2012 software (see Supplementary Methods). The immuno-histochemical staining of LC3 [18] was performed on rat tissue sections using Novolink kit (Menarini Diagnostics).

Cell viability and apoptosis assay

Wild-type and ATP7B-ko cells were grown in 24-well plates and treated with 0.25, 0.5, and 1 mM $CuCl_2$ for 24 h. To induce autophagy, the cells were starved or transduced with adenoviruses carrying TFEB. ATG7- or ATG13-specific siRNAs or 50 µM spautin were used to inhibit autophagy, while mitophagy was suppressed using PINK1-, FUNDC1- or BNIP3L-specific siRNAs. To analyze apoptosis, treated and control cells were incubated with CellEvent Reagent (Life Technologies) and observed by confocal microscopy (Zeiss LSM 700). The numbers of apoptotic (CellEvent-positive) nuclei were quantified in 10 equal fields of view, and expressed as a percentage of the total cell nuclei (stained with Hoechst). To measure cell viability, the numbers of cells in treated specimens were calculated in 10 equal fields using nuclear staining, and then normalized to the numbers of cells in the similar field in untreated specimens.

Electron microscopy

Electron microscopy (EM) of the cells, tissues and organelle fractions was performed as described previously [16, 17] (see Supplementary Methods).

Metal content determination

Cu in cell lysates, blood, liver homogenates, and subcellular fractions was analyzed after wet washing of the samples with nitric acid by inductively coupled plasma optical emission spectroscopy (Ciros Vision, Spectro Analytical Instruments GmbH) or atomic adsorption spectroscopy (ZEEnit 650P, Analytik Jena).

Aminotransferase activities

To evaluate the extent of liver damage in spautin-1-treated and control mice, serum activities of alanine transaminase (ALT) and aspartate transaminase (AST) were measured with ALT-RF/AST-RF kits (Olveks diagnosticum) according to the manufacture’s instructions.

QuantSeq 3’ mRNA analysis

Three biological replicates of ATP7B-ko and WT HepG2 were incubated with 0.5 mM $CuCl_2$ for 24h and their transcriptional response to the metal was analyzed using QuantSeq 3’ mRNA sequencing [19]. Total RNA was extracted using the RNeasy Mini Kit

(Qiagen) according to the manufacturer's instructions from ATP7B-ko and from WT cells treated with Cu. RNA extracted from untreated cells was used as control. Total RNA was prepared using the QuantSeq 3'mRNA-Seq Library prep kit (Lexogen) according to the manufacturer's instructions. Amplified cDNA fragments were sequenced in single-end mode using the NextSeq500 (Illumina) with a read length of 75 base pairs. Analysis of the sequence reads and gene ontology enrichment analysis of modulated transcripts is described in Supplementary Methods.

Statistical analysis

Data are expressed as means ± standard deviation collected from multiple independent experiments performed on different days. Statistical significance for all data, except the QuantSeq and bioinformatics analysis (see Supplementary Methods), was computed using Student's two-tailed t-tests (significances: $^{*}p < 0.05$, $^{**}p < 0.01$, and $^{***}p < 0.001$ in all figures).

RESULTS

Loss of ATP7B and Cu overload trigger autophagy in hepatic cells, in the liver of *Atp7b*$^{-/-}$ animals, and in patients with Wilson disease.

To investigate which mechanisms might be activated in ATP7B-deficient hepatocytes to protect against Cu toxicity in Wilson disease, we employed an *ATP7B* knockout (ATP7B-ko) HepG2 cell line [13]. Control (wild-type; WT) and ATP7B-ko HepG2 cells were incubated with Cu for 24 h and their transcriptional responses were analyzed using QuantSeq 3' mRNA sequencing, which allows precise measurements of quantitative differences in gene expression [19]. We found that Cu increased the expression levels of 1,244 genes in ATP7B-ko cells versus 480 in control cells (Fig. 1A; GEO Series accession number GSE107323). Gene Ontology Enrichment Analysis (GOEA) showed that ATP7B-deficient cells exhibited Cu-dependent activation of autophagic genes (Supplementary Tables 1, 2), indicating that autophagy constitutes an important part of the transcriptional response to Cu under ATP7B loss. To define this further, we first specified the subsets of genes differentially expressed in WT and ATP7B-ko cells (Supplementary Tables 3, 4) and then subjected these sets to GOEA (Supplementary

Tables 5, 6). This revealed that autophagy was specifically and positively regulated in ATP7B-ko (but not in WT) cells exposed to Cu (Supplementary Table 6). This finding was further supported by analysis of the individual genes that are known to be relevant to autophagy (see Supplementary Methods). ATP7B-ko cells showed specific and statistically significant ($p = 2.6E-05$) activation of 103 autophagic genes in response to Cu (Fig. 1A, B; Supplementary Table 7; Supplementary Fig. 1).

Next, we analyzed the distribution of the *bona fide* autophagy marker MAP1LC3B (also known as LC3) in WT and ATP7B-ko cells under steady-state conditions and upon exposure to Cu. Incubation with Cu resulted in an increased number of LC3-positive cytoplasmic puncta in both WT and ATP7B-ko cells (Fig. 1C, D). However, the number of Cu-induced LC3 puncta was significantly higher in ATP7B-deficient cells (Fig. 1D). In parallel, immunoblotting revealed stronger LC3 (and LC3-II) signals in both WT and ATP7B-ko cells upon Cu treatment (Fig. 1E). Again, ATP7B-ko cells were more susceptible to Cu-mediated induction of autophagy compared to WT cells, because even low Cu concentrations triggered substantial increases in LC3 levels in these cells (Fig. 1E).

Importantly, under basal conditions (i.e., without Cu stimulation), ATP7B-ko cells also showed a higher number of LC3-positive dots than WT cells (Fig. 1C left column and Fig. 1D). This could be explained by the fact that even under basal conditions ATP7B-ko cells accumulate Cu (Fig. 1F), which can stimulate autophagy. The increase in LC3 puncta might represent accumulation of autophagic structures due to either acceleration of their biogenesis or due to inefficient completion of the autophagic flux [20]. To discriminate between these possibilities, we employed Bafilomycin A1, which neutralizes lysosomal pH and inhibits fusion with autophagosomes and/or lysosomal degradation. The incubation of ATP7B-ko cells with Bafilomycin A1 increased the numbers of LC3 puncta and overall LC3 amounts (Supplementary Fig. 2A-C). Importantly, the magnitude of the increase in LC3 puncta was substantially higher in ATP7B-ko cells (Supplementary Fig. 2A, B) indicating that biogenesis of autophagosomes proceeds at a higher rate in ATP7B-deficient cells. This conclusion was further substantiated by labeling the cells with WIPI2, a protein that is associated with autophagosome formation [20, 21]. Here, ATP7B-ko cells showed increased numbers of WIPI2 spots, and hence of newly forming autophagosomes (Supplementary Fig. 2D, E).

In line with these observations, EM revealed numerous autophagic structures in the cytoplasm of ATP7B-ko cells, in contrast to a scarcity of autophagic vacuoles in WT cells (Fig. 2A, B, black arrows; Fig. 2C). Even phagophores (which represent forming autophagosomes [20]) were frequently observed in ATP7B-ko cells (Fig. 2B, white arrow) but were hardly detectable in WT cells. Activation of autophagy in ATP7B-ko cells was further validated by immunoblotting, which displayed higher LC3 levels upon ATP7B depletion (Fig. 2D). Moreover, stimulation of autophagy by cell starvation led to higher rates of LC3 (and in particular of LC3-II) increase in ATP7B-ko cells (Fig. 2D). These observations indicate that depletion of ATP7B, and hence absence of efficient Cu efflux, causes activation of autophagy.

In Wilson disease, hepatocytes are constantly exposed to increasing Cu levels. We thus investigated whether autophagy activation occurs in the livers of the *bona fide* Wilson disease animal models, *Atp7b*$^{-/-}$ rats and mice [14, 15]. Immunohistochemical staining of liver sections yielded stronger LC3-specific signals in the hepatocytes of *Atp7b*$^{-/-}$ rats compared to those of control animals (Fig. 2E). Accordingly, EM revealed numerous autophagic structures in the livers of *Atp7b*$^{-/-}$ rats, while the hepatocytes in control liver tissue rarely exhibited autophagosome or autolysosome profiles (Fig. 2F, G). A similar trend with an increase in the number of autophagic structures (Supplementary Fig. 3A-E) and in LC3 expression (Supplementary Fig. 3F) was documented in *Atp7b*$^{-/-}$ mice.

While the number of human patient samples is limited, we nevertheless observed that liver samples from patients with Wilson disease exhibited multiple autophagosomes in their hepatocytes whereas autophagic structures in healthy liver tissue were scarce (Supplementary Fig. 4A-C, arrows). Interestingly, the patients investigated were heterogeneous for their levels of ATP7B dysfunction (see Supplementary Methods). Here, the patient with mutations resulting in an almost full loss of ATP7B catalytic activity (designated as patient 2) exhibited a higher number of autophagic structures in hepatocytes as compared to the patient with partial ATP7B dysfunction (designated as patient 1; Supplementary Fig. 4B, C, D).

Taken together, these observations demonstrate that hepatic cells activate autophagy in response to the loss of ATP7B function and Cu overload.

Activation of autophagy in ATP7B-deficient cells involves the mTORC1/TFEB signaling pathway

Which mechanisms might contribute to autophagy activation in ATP7B-deficient cells? Previous studies have indicated that the kinase mTOR (mechanistic target of rapamycin) might be involved in autophagic responses to Cu [12]. mTOR, as part of the mTOR complex 1 (mTORC1), inhibits autophagy and its activity correlates with its recruitment to lysosomes when amino acids are abundant in the cell [22, 23]. To track recruitment of mTOR to lysosomes, a mixture of amino acids was added to cell cultures [22]. This resulted in substantial overlap of the mTOR-specific immunofluorescence signal with LAMP1-positive structures in WT cells (Fig. 3A, B). In sharp contrast, colocalization between mTOR and LAMP1 was decreased in ATP7B-ko cells, both under steady state conditions and upon Cu treatment (Fig. 3A, B, Supplementary Fig. 5 A-D). Furthermore, the ability of amino acids to stimulate mTOR binding to lysosomes was strongly inhibited in Cu-treated ATP7B-ko cells, while the combination of amino acids and Cu induced a massive recruitment of mTOR to the lysosomes in WT cells (Fig. 3B; Supplementary Fig. 5 E, F). These findings suggest that ATP7B loss and the resulting Cu overload interfere with the activation of mTOR-dependent signaling at lysosomal membranes.

In parallel, we performed immunoblot analyses to monitor the phosphorylation of 4E-BP1, which is a substrate of mTORC1 activation. The phospho-4E-BP1 levels decreased in ATP7B-ko cells suggesting inhibition of mTORC1 (Fig. 3C, D). Of note, the exposure to Cu resulted in a remarkable reduction in phospho-4E-BP1, especially in ATP7B-ko cells (Fig. 3C, D) indicating mTORC1 deactivation.

Loss of mTOR activity at the lysosomes promotes dephosphorylation of transcription factor EB (TFEB), and its translocation to the nucleus where TFEB transactivates a wide range of autophagy-related genes [23]. Indeed, immunofluorescence analysis revealed increased nuclear localization of TFEB in ATP7B-ko cells (Fig. 3E). Accordingly, numerous TFEB target genes [24, 25] (including autophagic) were activated in ATP7B-ko cells in response to Cu (Fig. 3F; Supplementary Table 8).

Next, we investigated why the balance of mTORC1/TFEB signaling at lysosomes was shifted toward TFEB activation. Usually, this occurs upon cell starvation and/or lysosome dysfunction [23]. This prompted us to investigate lysosomal structure and function in ATP7B-ko cells. EM of ATP7B-ko cells revealed larger, irregularly shaped lysosomes that were filled with ‘undigested’ membrane material while WT cells contained regular LAMP1-positive multivesicular bodies and lysosomes (Fig. 4A, B). To understand whether these morphologically abnormal lysosomes were fully functional we used LysoTracker, which indicated reduced lysosomal acidification in ATP7B-ko cells (Fig. 4C, arrows and Fig. 4D). Furthermore lysosomal cleavage of fluorogenic substrates (Magic Red or DQ-BSA) was reduced in ATP7B-ko cells (Fig. 4E, F; Supplementary Fig. 6A, B). To access the degree of lysosome dysfunction in ATP7B-ko cells, we tested whether the lysosomal blocker Bafilomycin A1 further worsens lysosomal activity and whether ATP7B-GFP expression rescues lysosome function. Exposure of ATP7B-ko cells to Bafilomycin A1 impaired the digestion of Magic Red and LC3 as well as reducing the acidification of lysosomes, while expression of ATP7B-GFP normalized lysosomal pH and activity (Supplementary Fig. 6 C-H).

Altogether, these findings indicate that ATP7B loss only partially impairs lysosomal function, but that this is sufficient to trigger the TFEB signaling cascade that then favors the activation of autophagy.

Autophagy attenuates copper toxicity in ATP7B-deficient cells and animals.

Under a wide range of pathological conditions, autophagy sequesters and turns over toxic intracellular components, such as protein aggregates and damaged organelles, thereby promoting cell survival [26, 27]. We thus reasoned that autophagy might counteract Cu-mediated damage in a similar way in Wilson disease, and consequently investigated how modulation of autophagy impacts on the resistance of ATP7Bdeficient cells to Cu. Inhibition of autophagy with specific inhibitor spautin-1 [28] or depletion of ATG7/ATG13 [21] substantially accelerated the death of ATP7B-ko cells, even at the lowest (0.25 mM) Cu concentration used (Fig. 5A-C). In contrast, activation of autophagy with starvation (Fig. 5A-C) or TFEB overexpression (Fig. 5D, E) favored the survival of ATP7B-ko cells in high Cu, and significantly reduced apoptosis.

In addition, the impact of autophagy inhibition was investigated in *Atp7b*$^{-/-}$ mice by injection of spautin-1, whose ability to attenuate autophagy in the liver was confirmed by EM and Western blot (Supplementary Fig. 7A-D). Spautin-1 caused a statistically significant increase in serum ALT and AST levels pointing to accelerated liver damage in *Atp7b*$^{-/-}$ mice, while ALT and AST values remained invariable in spautin-1-injected control animals (Supplementary Fig. 7E). Correspondingly, spautin-1 injection in *Atp7b*$^{-/-}$ mice triggered significant elevation of serum Cu levels (Supplementary Fig. 7F), which could be attributed to release of Cu from damaged hepatocytes as happens in WD patients with acute liver failure [29].

Thus, our *in vitro* and *in vivo* findings suggest that autophagy acts as an important pro-survival mechanism that protects ATP7B-deficient cells from Cu toxicity.

Autophagy targets mitochondria in ATP7B-deficient cells

Recent reports have suggested that mitochondria are particularly sensitive to Cu overload in cells lacking Cu efflux transporters [17, 30]. Indeed, we found that hepatocytes from *Atp7b*$^{-/-}$ rats accumulate significant amounts of Cu in their mitochondria (Fig. 6A). Interestingly, Cu accumulation in the mitochondria and lysosomes from *Atp7b*$^{-/-}$ rats occurred with similar magnitude, which paralleled disease progression (Fig. 6A). Thus, increased lysosomal Cu might occur due to sequestration of damaged and Cu-loaded mitochondria through autophagic flux in an attempt to minimize the consequences of a loss in the integrity of mitochondria.

To investigate this hypothesis, we analyzed the ultrastructure of mitochondria and autophagosomes in *Atp7b*$^{-/-}$ rat livers. Mitochondria in hepatocytes from *Atp7b*$^{-/-}$ rats exhibited seriously compromised morphology (Fig. 6B) with various aberrations (Fig.

6C). Autophagosomes in hepatocytes from control animals were relatively rare (Fig. 6D) and only a few of these contained recognizable mitochondrial remnants. In contrast, *Atp7b*$^{-/-}$ hepatocytes frequently contained autophago(lyso)somes with mitochondria inside (Fig. 6D, E). Of note, similar mitochondrial damage and elevated capture of mitochondria by autophagosomes were also apparent in liver biopsy samples from patients with Wilson disease (Supplementary Fig. 4B, C, F, G) and in *Atp7b*$^{-/-}$ mice (Supplementary Fig. 3B and 7A). Most importantly, and in strong agreement with the above hypothesis, inhibition of autophagy with spautin-1 significantly worsened the overall ultrastructure of mitochondria in *Atp7b*$^{-/-}$ mice (Supplementary Fig. 7B). Finally, immuno-blot analysis revealed a higher signal of the mitophagy marker parkin in the mitochondrial fraction from *Atp7b*$^{-/-}$ rat livers (Fig. 6F) and an overall reduction in the levels of major mitochondrial proteins in liver lysates (Supplementary Fig. 8A) indicating accelerated autophagic clearance of mitochondria upon ATP7B loss.

Specific activation of mitophagy was further confirmed in ATP7B-ko cells. We found that LC3-positive spots did not exhibit significant colocalization with the mitochondrial marker mitofusin 2 in WT cells even upon Cu stimulation, while numerous LC3 structures that contained mitofusin 2 were observed in Cu-treated ATP7B-ko cells (Fig. 7A). EM revealed that exposure of ATP7B-ko cells to Cu caused mitochondrial aberrations (Supplementary Fig. 9A) and appearance of abnormal mitochondria inside autophagosomes (Fig. 7B, C). We also noted that mitophagic structures were frequently located near lysosomes (Fig. 7B) and that autolysosomes often contained recognizable mitochondria in their interior (Fig. 2B; empty arrowhead). This indicated that these engulfed mitochondria were efficiently delivered to lysosomal compartments in ATP7B-ko cells.

In parallel, rapid loss of mitochondrial potential (Supplementary Fig. 9B, C) and induction of mitochondrial pro-apoptotic genes (Supplementary Fig. 9D; Supplementary Table 9) were observed in Cu-treated ATP7B-ko cells. Usually, loss of membrane potential leads to rapid turnover of damaged mitochondria via PINK1/parkin-mediated mitophagy [21, 31]. Indeed, exposure of ATP7B-ko cells to Cu increased expression of PINK1, BNIP3L (known as NIX) and several other mitophagy-associated genes (Fig. 7D;

Supplementary Table 9). Notably, even under basal conditions parkin was detected in mitochondrial fractions from untreated ATP7B-ko cells but not in those from WT cells (Fig. 7E). This indicates that mitochondrial function is partially compromised by ATP7B loss even in the absence of a large Cu challenge. Incubation of ATP7B-ko cells with Cu further stimulated parkin binding to mitochondria, and resulted in the appearance of autophagic markers in mitochondrial fractions (Fig. 7E). Mitochondria from WT cells exhibited a milder, although still appreciable, increase in parkin, LC3, and p62 upon exposure to Cu (Fig. 7E). Finally, the levels of several *bona fide* mitochondrial markers were decreased in ATP7B-ko cells, while Cu treatment led to a further decrease (Supplementary Fig. 8B), suggesting that active turnover of mitochondria by mitophagy occurs in ATP7B-deficient cells.

Considering that mitochondrial damage can trigger the release of pro-apoptotic factors and cell death [21, 31], we asked whether sequestration of damaged mitochondria by mitophagy operates as a protective mechanism in ATP7B-deficient cells. ATP7B-ko cells were depleted for the main regulators of different mitophagy pathways, PINK1, BNIP3L or FUNDC1 [21, 31], using RNAi and then exposed to Cu. PINK1 and BNIP3L depletion significantly reduced viability and increased apoptosis of ATP7B-ko cells in response to Cu (Supplementary Fig. 10). These data strongly support the idea that mitophagy counteracts Cu toxicity in the context of ATP7B loss.

DISCUSSION

The protective function of autophagy has been documented in a wide range of disorders, including conditions in which oxidative damage precipitates cell death and organismal disease [26, 27]. In contrast, the role of autophagy in Wilson disease has remained obscure although recent reports document activation of autophagy by Cu salts or Cu-containing anticancer compounds [10-12]. Here, we report on several novel findings demonstrating that autophagy operates as a pro-survival mechanism in Wilson disease.

We consistently observed *in vitro* and *in vivo* that ATP7B-deficient hepatic cells contain numerous autophagic structures including phagophores/isolation membranes whose presence reflects efficient induction of autophagosomal biogenesis [20, 21].

Correspondingly, ATP7B-ko cells respond to Cu challenges with significant up-regulation of genes and signaling mechanisms that support and sustain autophagy. Most importantly, this autophagy activation increased the resistance of ATP7B-deficient cells to Cu, while inhibition of autophagy promoted Cu toxicity in ATP7B-deficient cells and in *Atp7b*$^{-/-}$ mice. These findings may explain the clinical observation that undernourishment (which stimulates autophagy [21, 25]) caused a significantly milder clinical phenotype in one of a pair of monozygotic Wilson Disease twins [32]. Thus, autophagy emerges as a yet unconsidered quality control mechanism that aids in hepatocyte protection by removing toxic cell components damaged by excess Cu.

Another intriguing and novel aspect consists in the differences in the autophagic response to Cu between healthy and ATP7B-deficient cells. Loss of ATP7B function apparently causes hepatocytes to mount an autophagic response even when they are kept under normal culture conditions (but still accumulate Cu due to impaired efflux). As a consequence, lower concentrations of Cu were required to stimulate autophagy in ATP7B-ko cells compared to WT cells. The substrate of autophagy represents another striking difference between healthy and Wilson disease hepatocytes. Loss of ATP7B results in selective capture of mitochondria by autophagosomes, indicating activation of mitophagy. In contrast, we did not detect any specific sequestration of mitochondria by autophagosomes in control hepatocytes. This latter finding is in line with a recent report showing that Cu triggers autophagy in normal cells but that this response does not involve mitophagy [12].

Why are mitochondria preferentially subjected to autophagy in ATP7B-deficient cells? Loss of ATP7B-mediated hepatic efflux of Cu leads to failure of mitochondria to handle massively incoming Cu, which damages mitochondrial proteins and membranes [33]. In strong agreement, we consistently observed typical Wilson disease-type mitochondrial structural defects in ATP7B-deficient cells and in hepatocytes from Wilson disease patients and from *Atp7b*$^{-/-}$ rodents. Damaged mitochondria represent a serious danger to the cell due to the leakage of pro-apoptotic factors from their interior. This is why loss of transmembrane potential activates PINK1, which subsequently recruits parkin to convert mitochondria into substrates for autophagic sequestration [21, 31]. Indeed, we observed that suppression of mitophagy through silencing of PINK1 substantially reduced the viability of ATP7B-ko cells exposed to Cu. In addition, we also found that BNIP3L (NIX) helps ATP7B-deficient cells to tolerate elevated Cu, indicating that crosstalk between the PINK1 and NIX mitophagy pathways [31] might be involved in the response to Cu overload. From these results, a picture emerges in which the selective degradation of copper-burdened mitochondria is activated in ATP7B-deficient hepatocytes as a cellular countermeasure against Cu-induced death. Strong support for this conclusion comes from our *in vivo* studies in $Atp7b^{-/-}$ mice. Here, blocking autophagy via the specific inhibitor spautin-1 strongly aggravated mitochondrial impairment paralleled by severe liver damage.

In addition to mitochondrial damage, our findings further suggest that additional cellular signaling mechanisms may contribute to the activation of autophagy in Wilson disease. A recent study indicated that autophagy activation by Cu involves the p38 and/or JNK MAP kinase pathways, which usually participate in responses to oxidative stress and regulate several autophagy effectors [10, 11]. Indeed, both oxidative stress and MAP kinase genes were up-regulated in ATP7B-ko cells upon Cu exposure (see Supplementary Table 2). Moreover, the p38 and JNK pathways are known to be induced in cells that express ATP7B mutants [34, 35] indicating that these pathways may contribute to the induction of autophagy in our settings as well. Finally, we observed that activation of mTORC1 was inhibited and TFEB was activated in ATP7B-ko cells thus favoring a stimulation of autophagy. Such modulation of mTORC1/TFEB signaling is likely to be caused by partially dysfunctional lysosomes, which require ATP7B for several activities [16, 36]. In the long run, this lysosome dysfunction could lead to a sort of mild lysosomal storage disease (LSD)-like phenotype, hampering the eventual use of autophagy as a therapeutic approach in Wilson disease. However, TFEB overactivation has been used in various LSDs as an effective strategy to promote cellular clearance through accelerated autophagic sequestration, flux and further lysosomal exocytosis of toxic material [23]. Along this line, we found that TFEB overexpression dramatically increased resistance of ATP7B-ko cells to Cu. Thus, activation of pro-autophagic signaling pathways allows ATP7B-deficient cells to sequester and neutralize components damaged by excess Cu, and hence to attenuate the potentially lethal effects of Cu toxicity.

In conclusion, our study provides compelling evidence in favor of a pro-survival function of autophagy in Wilson disease. These findings may be also considered in the broader context of metabolic disorders that arise from the accumulation of metals in the liver and in other tissues. Cu, manganese and iron accumulation were shown for the liver of patients with MEDNIK syndrome, inherited hypermanganesemia, and hemochromatosis, respectively [37-39]. As in Wilson disease, excessive accumulation of these metals has a devastating impact on redox homeostasis [37-39] and can therefore harm cellular components, including mitochondria. In this context, it is tempting to speculate that autophagy and mitophagy play a key role in protection against pathogenic processes inflicted by transitional metals. Therefore, the potential of autophagy for the reduction of metal toxicity should be explored in Wilson disease and in several other disorders of metal metabolism.

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Author names in bold designate shared co-first authorship

FIGURE LEGENDS

Figure 1. ATP7B-deficient cells exhibit stronger activation of autophagy in response to Cu.

(A) WT and ATP7B-ko HepG2 cells were prepared for RNA-Seq analysis directly and after 24 h incubation with 0.5 mM $CuCl_2$. The graphs show statistically significant changes in gene expression induced by Cu treatment in each cell line. Green circles, down-regulated autophagy genes; red circles, up-regulated autophagy genes. (**B**) Venn diagram showing overlap between the induced autophagy genes in Cu-treated WT and ATP7B-ko cells. (**C**) Cells were treated with Cu as indicated in panel A. Untreated (-Cu) and 0.5 mM $CuCl_2$-treated (+Cu) WT and ATP7B-ko cells were fixed and labeled with an antibody against LC3 to reveal autophagosomes (arrows) (**D**) Number of LC3-positive structures per cell for WT and ATP7B-ko cells before and after Cu treatment (as indicated; n = 50 cells). (**E**) WT and ATP7B-ko cells were treated with different concentrations of $CuCl_2$ (as indicated) for 24 h. Western blots show that Cu treatment leads to a greater increase in LC3 levels in ATP7B-ko cells than in WT cells. **(F)** ICP-OES analysis (see methods) shows that untreated ATP7B-ko cells contain higher amounts of Cu compared to untreated WT cells (n = 3 experiments). Scale bar: 10 µm (C).

Figure 2. Loss of ATP7B results in activation of autophagy *in vitro* and *in vivo*.

(A, B) Immuno-EM of WT and ATP7B-ko cells labeled with an antibody against LAMP1. Autophagic structures are highlighted in either blue WT or red ATP7B-ko color and indicated by arrows. White arrow and arrowheads indicate phagophore- and lysosome-like structures, respectively. **(C)** Quantification shows an increase in the number of both autophagosomes and autolysosomes in ATP7B-ko cells (n = 20 fields). (**D**) Cells were starved with HBSS for the indicated time. Western blot showing more rapid and greater LC3 increase in ATP7B-ko cells with respect to WT cells. (**E**) Liver sections from $Atp7b^{+/-}$ and $Atp7b^{-/-}$ rats labeled with an antibody against LC3. A srtonger LC3 signal was detected in $Atp7b^{-/-}$ rats (arrows). (**F**) EM of liver tissue shows autophagosomes (arrows) in $Atp7b^{+/-}$ rats (blue) and in $Atp7b^{-/-}$ rats (red, arrows). (**G**) Quantification reveals a significantly higher number of autophagosomes (per 25 μm^2 field of view) in the liver of $Atp7b^{-/-}$ rats (n = 20 fields). Scale bar: 500 nm (A, B, F), 40 µm (E).

Figure 3. Impact of ATP7B loss on the mTORC1/TFEB signaling machinery.

(A) Cells were starved and then incubated with a mixture of amino acids for 1 h at 37 °C. After fixation, the cells were labeled to reveal lysosomes containing mTOR and LAMP1 (arrows). (**B**) Untreated and Cu-treated (0.5 mM for 24h) WT and ATP7B-ko cells were stimulated with amino acids as described in panel A and analyzed by confocal microscopy (see Supplementary Fig. 5). Graph shows that under all conditions colocalization of LAMP1 with mTOR was lower in ATP7B-ko cells (n = 50 cells). (**C-F**) Cells were incubated in medium without and with 0.5 mM $CuCl_2$ for 24 h. (**C**) Western blot shows protein levels of ATP7B, mTOR, phosphorylated 4E-BP1 (p-4E-BP1), and total 4E-BP1. Phosphorylated 4E-BP1 levels were significantly reduced in ATP7B-ko cells. (**D**) Normalized intensities of p-4E-BP1 under different conditions corresponding to panel C (n = 3 experiments). (**E**) Cells were fixed and labeled with an antibody against TFEB. Untreated and Cu-treated ATP7B-ko cell populations exhibit higher numbers of cells with nuclear localization of TFEB (arrows). Percentage of cells with nuclear localization of TFEB is indicated in each panel for each condition. (**F**) Quant-Seq analysis of TFEB-associated genes shows mRNA-fold changes (FC) in response to the Cu treatment for WT and ATP7B-ko cells. Higher expression of numerous TFEB-dependent genes was observed in ATP7B-ko cells treated with Cu. Scale bar: 10 µm (A), 8.5 µm (E).

Figure 4. Lack of ATP7B affects the ultrastructure and function of lysosomes.

(**A**) Immuno-EM for WT and ATP7B-ko cells labeled with an antibody against LAMP1. Compared to typical lysosomes in WT cells (highlighted in blue and indicated by arrows), large irregular lysosome-like structures containing LAMP1 were detected in ATP7B-ko cells (highlighted in red and indicated by arrows). **(B)** Quantification shows a larger diameter of lysosomes in ATP7B-ko cells (n = 50 lysosomes). (**C**) WT and ATP7B-deficient cells loaded with 200 nM Lysotracker, fixed and labeled with an antibody against LAMP1. Very few LAMP1-positive structures showed an intense LysoTracker signal in ATP7B-ko cells with respect to WT cells (arrows). (**D**) Mean fluorescence (AU) of LysoTracker in the two cell types (n = 50 cells). (**E**) WT and ATP7B-ko cells loaded with the fluorogenic substrate Magic Red. The numbers and fluorescence intensities of the Magic Red spots were reduced in ATP7B-ko cells (arrows). (**F**) Mean fluorescence (AU) of Magic Red in the two cell types (n = 50 cells). Scale bar: 700 nm (A), 10 µm (C, E).

Figure 5. Autophagy increases tolerance of ATP7B-deficient cells to Cu. (**A**) Cells were treated for 24 h with 0.5 mM $CuCl_2$ either in the presence of spautin or HBSS. During the last 30 min of treatment, the cells were incubated with Cell Event reagent to detect apoptotic cells. Phase contrast images (left column) show overall morphology of WT and ATP7B-ko cells, and the overlap with the apoptotic marker in green (right column). Spautin accelerated cell death, while starvation promoted survival of ATP7B-ko cells and reduced apoptosis under high Cu. (**B, C**) The graphs show quantification (see Supplemenary Methods) of viability (B) and apoptosis (C) of WT and ATP7B-ko cells at different $CuCl_2$ concentrations, combined with starvation, spautin treatment or incubation with pools of ATG7-specific (siATG7) or ATG13-specific (siATG13) siRNAs. (**D, E**) ATP7B-ko cells were infected with adenovirus carrying TFEB (activator of autophagy) or AFP (negative control) and treated with different concentrations of $CuCl_2$ for 24 h. TFEB overexpression increased the viability (D) and reduced apoptosis (E) of ATP7B-ko cells. Scale bar: 60 µm (A).

Figure 6. Loss of ATP7B leads to activation of mitophagy in *Atp7b*$^{-/-}$ rats. (**A**) Cytosolic, mitochondrial, and lysosomal fractions were isolated from livers of *Atp7b*$^{+/-}$ and *Atp7b*$^{-/-}$ rats. *Atp7b*$^{-/-}$ rats were divided into two groups on the basis of disease progression (see Methods). The subcellular fractions were subjected to ICP-OES of Cu. In *Atp7b*$^{-/-}$ cells, Cu levels in hepatic mitochondria and lysosomes were higher than in cytosol and continued to increase with disease progression (n = 37 rats for *Atp7b*$^{+/-}$, 24 for *Atp7b*$^{-/-}$ affected, and 21 for *Atp7b*$^{-/-}$ disease groups). (**B**) EM of liver tissue from *Atp7b*$^{+/-}$ and *Atp7b*$^{-/-}$ rats. Rats lacking Atp7b showed abnormal mitochondria (e.g., swelling of intermembrane space; arrowheads). (**C**) Image gallery shows different mitochondrial ultrastructure abnormalities in the liver of *Atp7b*$^{-/-}$ rats. (**D**) Autophagosomes containing cytosol and

ER membranes are indicated by arrowheads. Autophagosomes with incorporated mitochondria (arrows) were observed in hepatocytes of *Atp7B*$^{-/-}$ rats. (**E**) A large proportion (>50%) of autophagosomes contained mitochondria in the liver of *Atp7b*$^{-/-}$ rats (n = 20 fields of view). **F**. Western blot showing elevated levels of Parkin in the mitochondrial fraction of *Atp7b*$^{-/-}$ rats. Scale bar: 600 nm (B), 500 nm (C, D).

Figure 7. **Cu overload induces mitophagy in ATP7B-deficient cells.**

(A) Untreated and 0.5 mM $CuCl_2$-treated cells (24 h treatment) were fixed and labeled with antibodies against LC3 and mitofusin 2. LC3 did not colocalize with mitofusin in WT and untreated ATP7B-ko cells (red, green arrows). Yellow arrows indicate colocalization with mitofusin 2 upon Cu overload in ATP7B-ko cells. (**B**) EM image of ATP7B-ko cells treated with 0.5 mM $CuCl_2$ for 24 h. Numerous autophagosomes contained mitochondria (arrowheads) and were in close proximity to lysosomes (arrows). (**C**) The graph shows the percent of autophagosomes that contained mitochondria in WT and ATP7B-ko cells (n = 50 cells). (**D)** Quant-Seq analysis of mitophagy-associated genes shows mRNA fold change (FC) in response to Cu treatment (0.5 mM $CuCl_2$ for 24 h) in ATP7B-deficient and WT cells. Higher expression of numerous mitophagy-associated genes was observed for ATP7B-ko cells treated with Cu. (**E**) Cells were treated as indicated in (A). Western blot showed levels of different proteins in mitochondrial and cytosolic extracts from WT and ATP7B-ko cells. The mitochondrial fraction exhibited an increase in the mitophagy marker parkin, and general autophagy markers LC3 and p62 in Cu-treated cells, while a decrease in cytosolic parkin occurs upon Cu treatment indicating parkin recruitment from the cytosol to mitochondria. ATP7B-ko cells show stronger elevation of mitochondrial parkin, LC3 and p62 in response to Cu. Scale bar: 10 µm (A), 500 nm (B).

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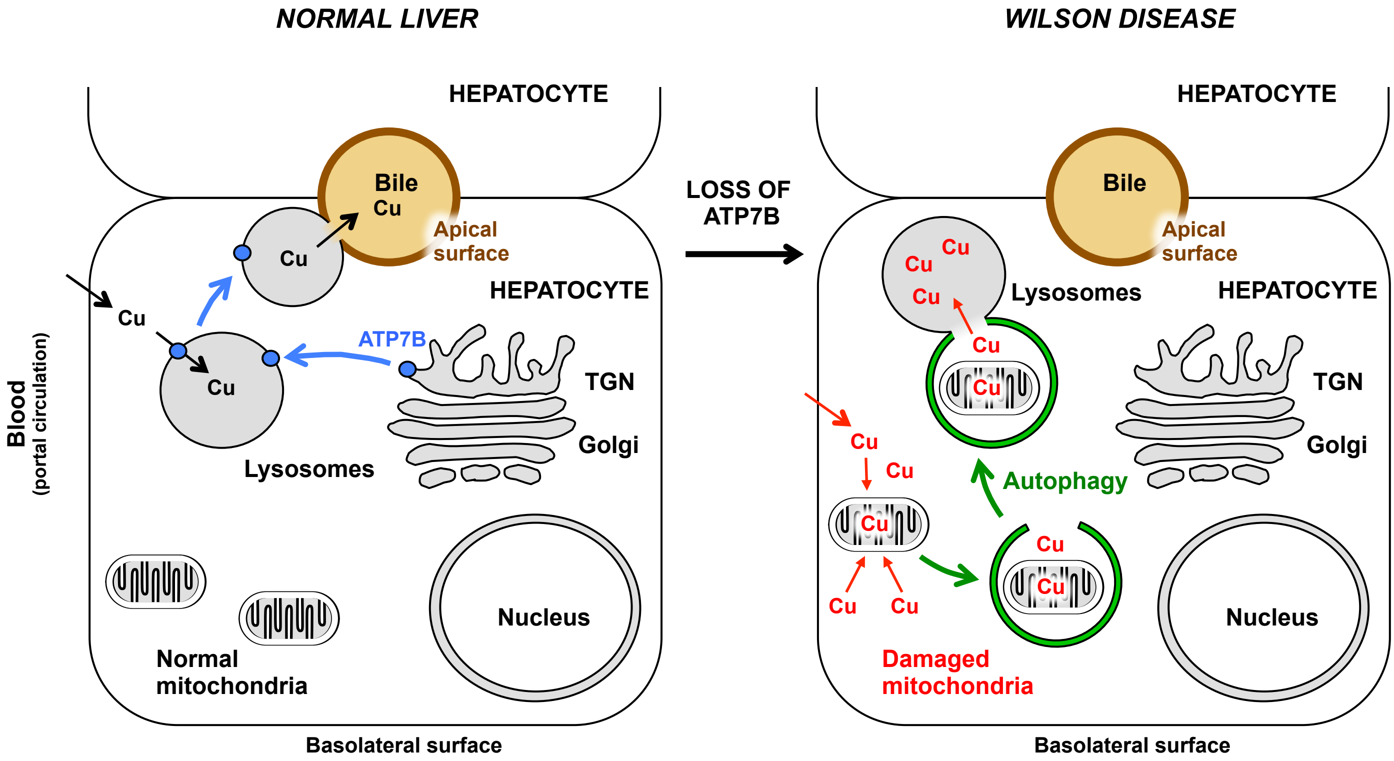
Graphic abstract. Polishchuk et al.



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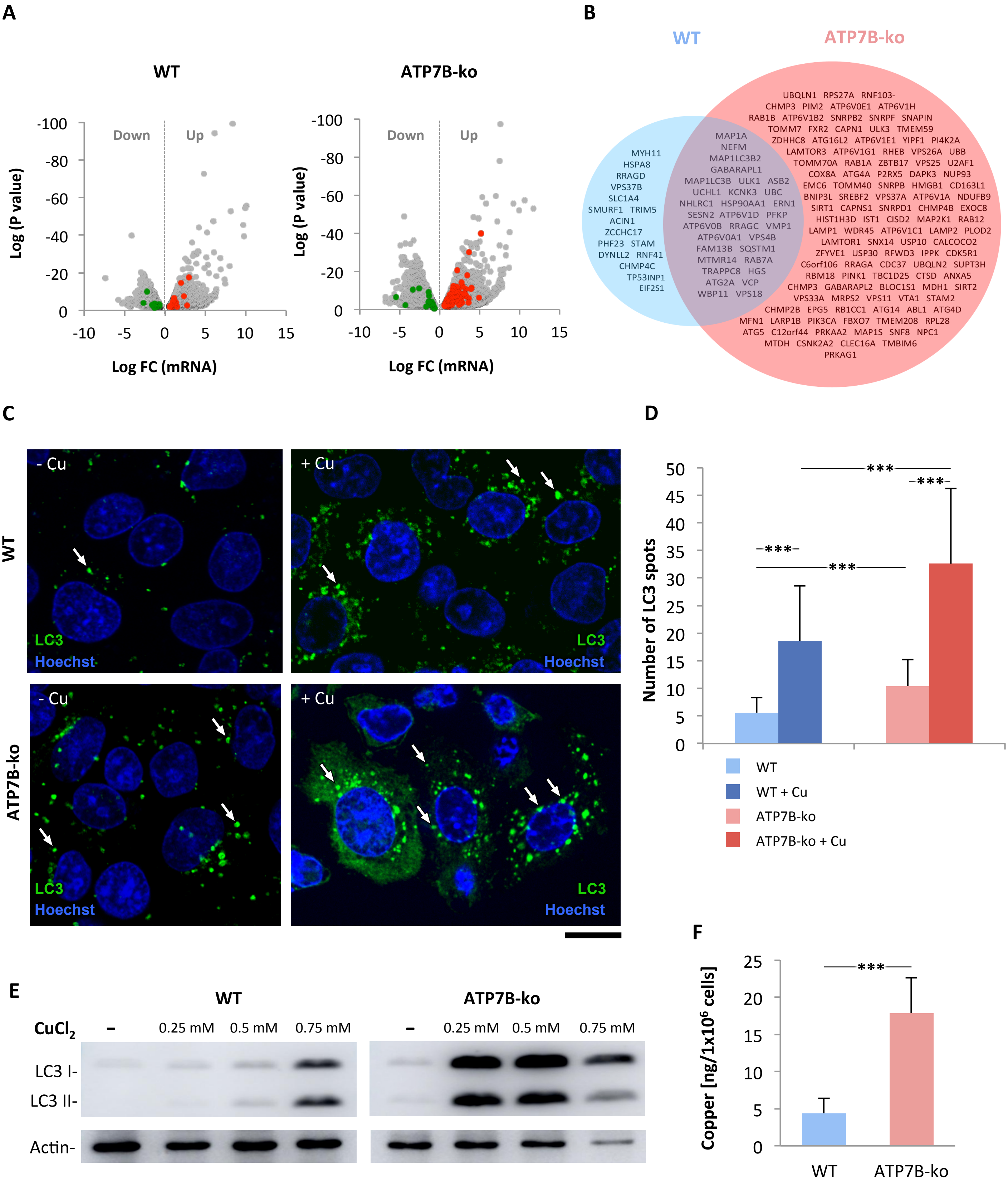

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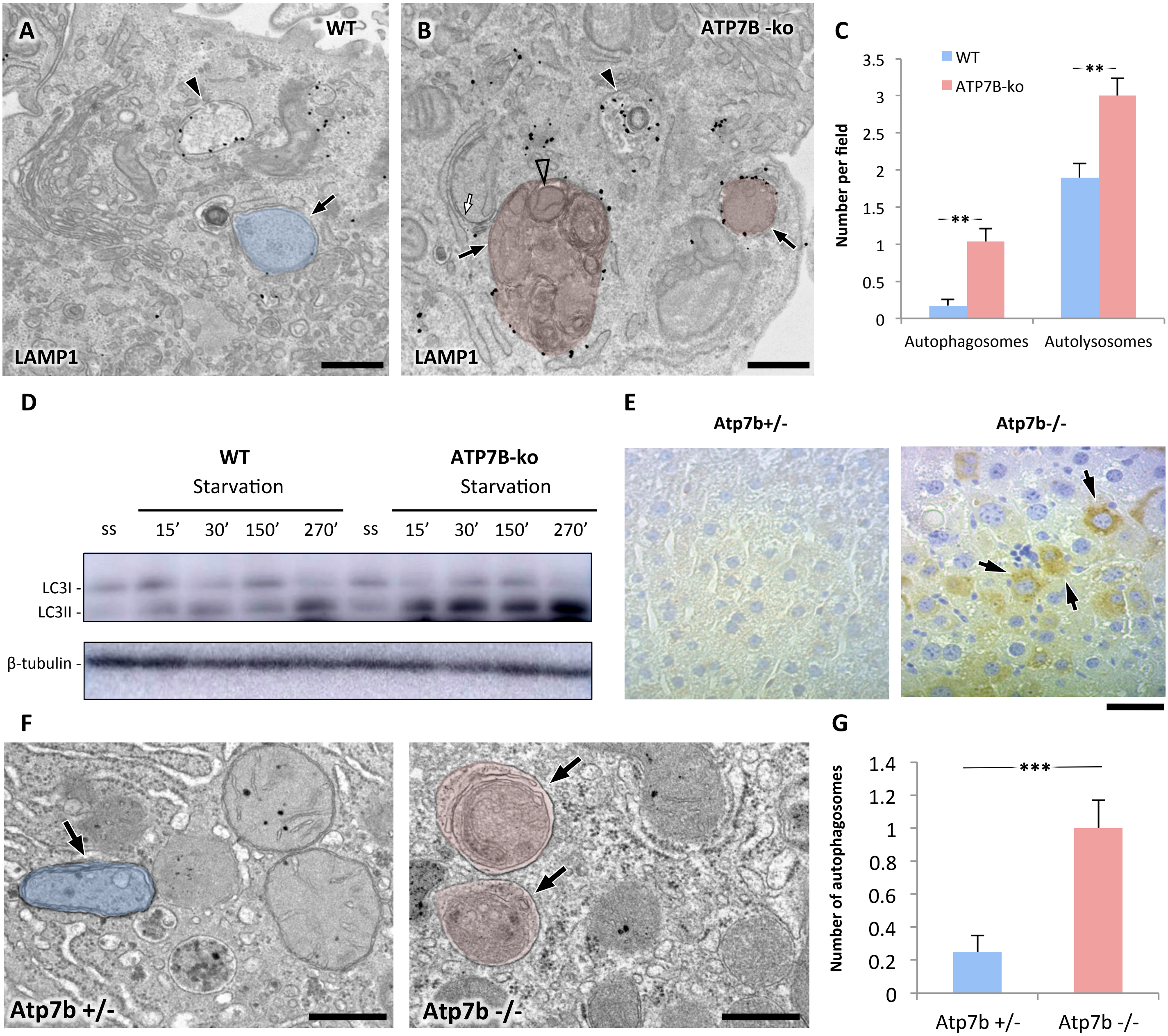

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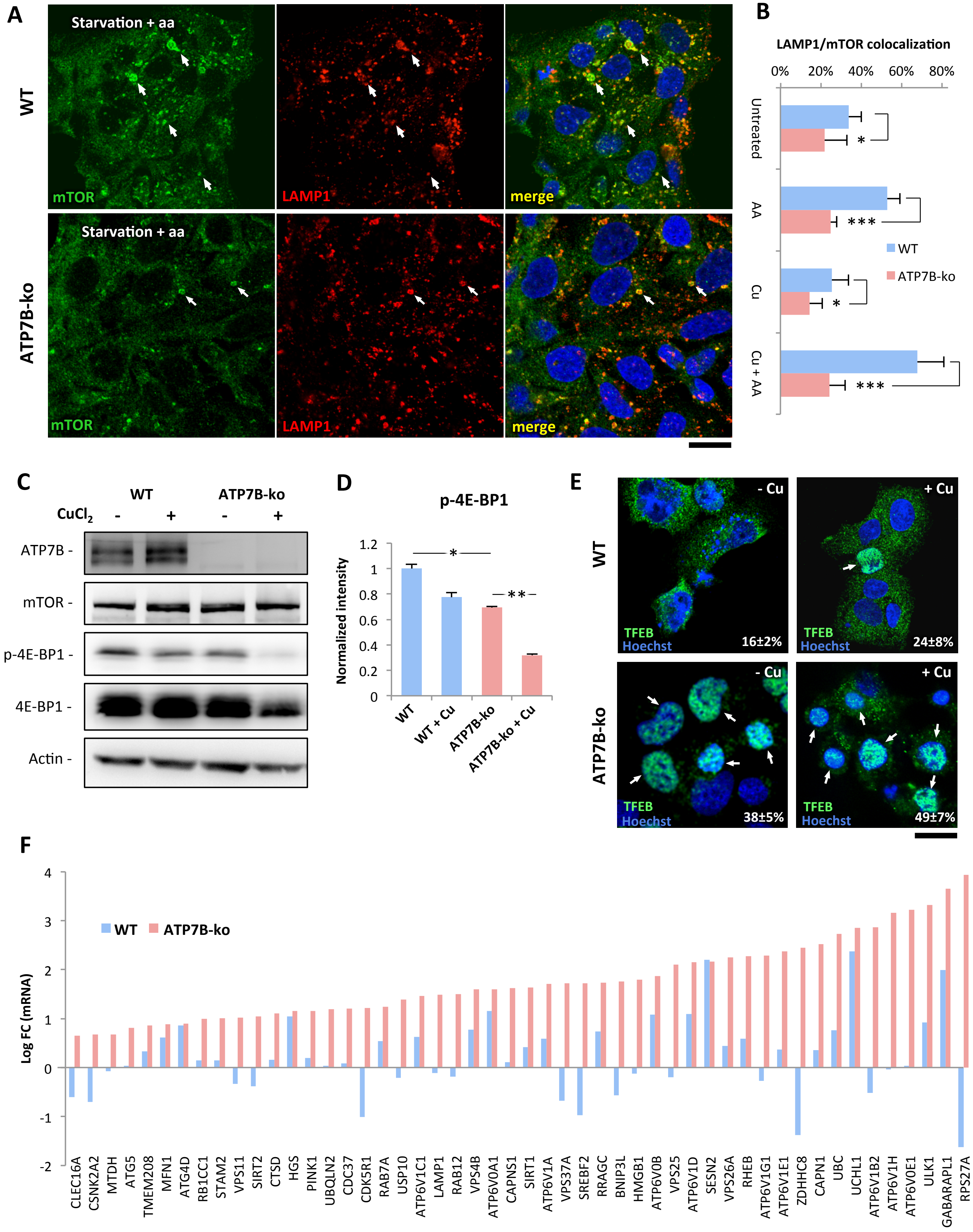

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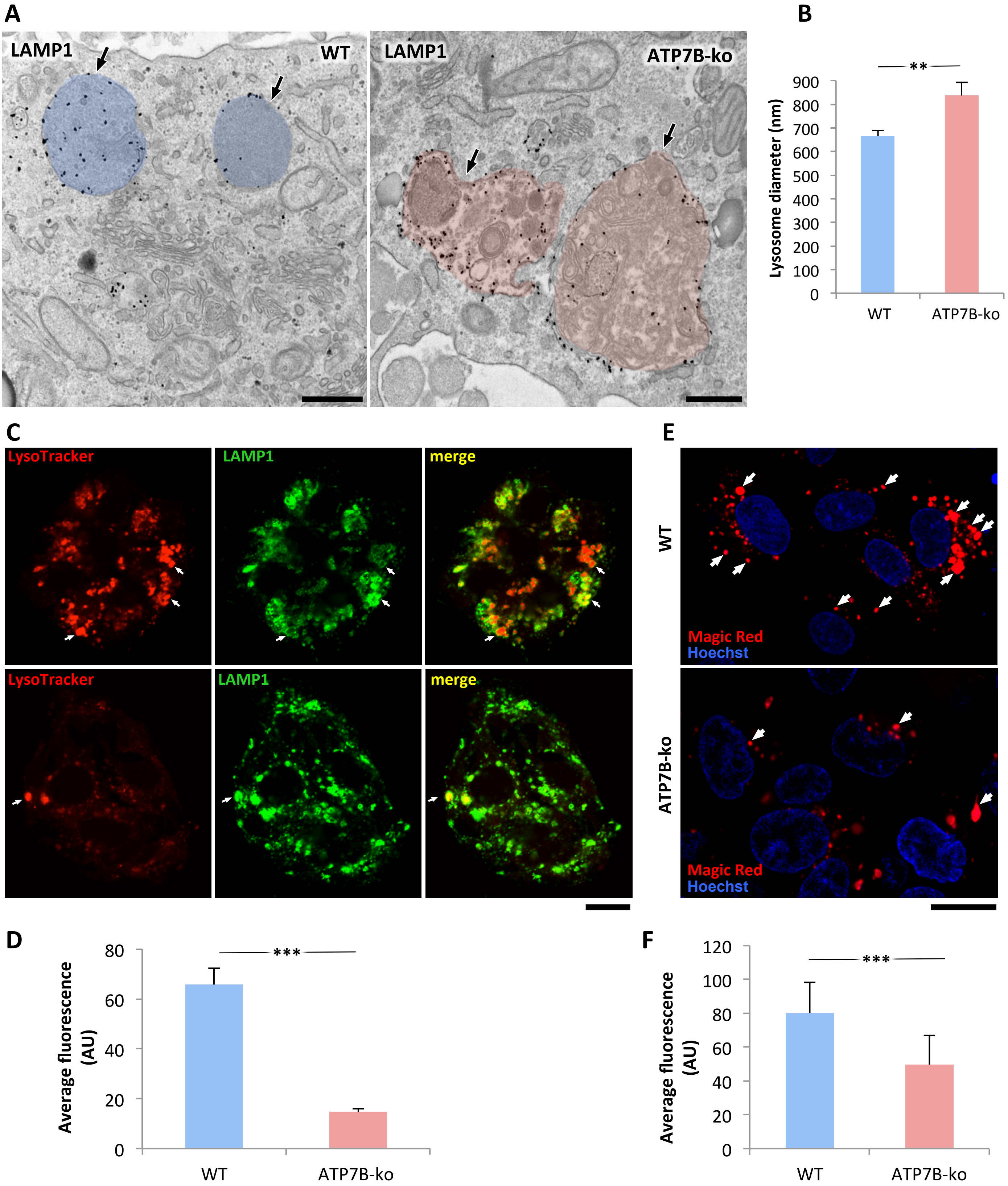

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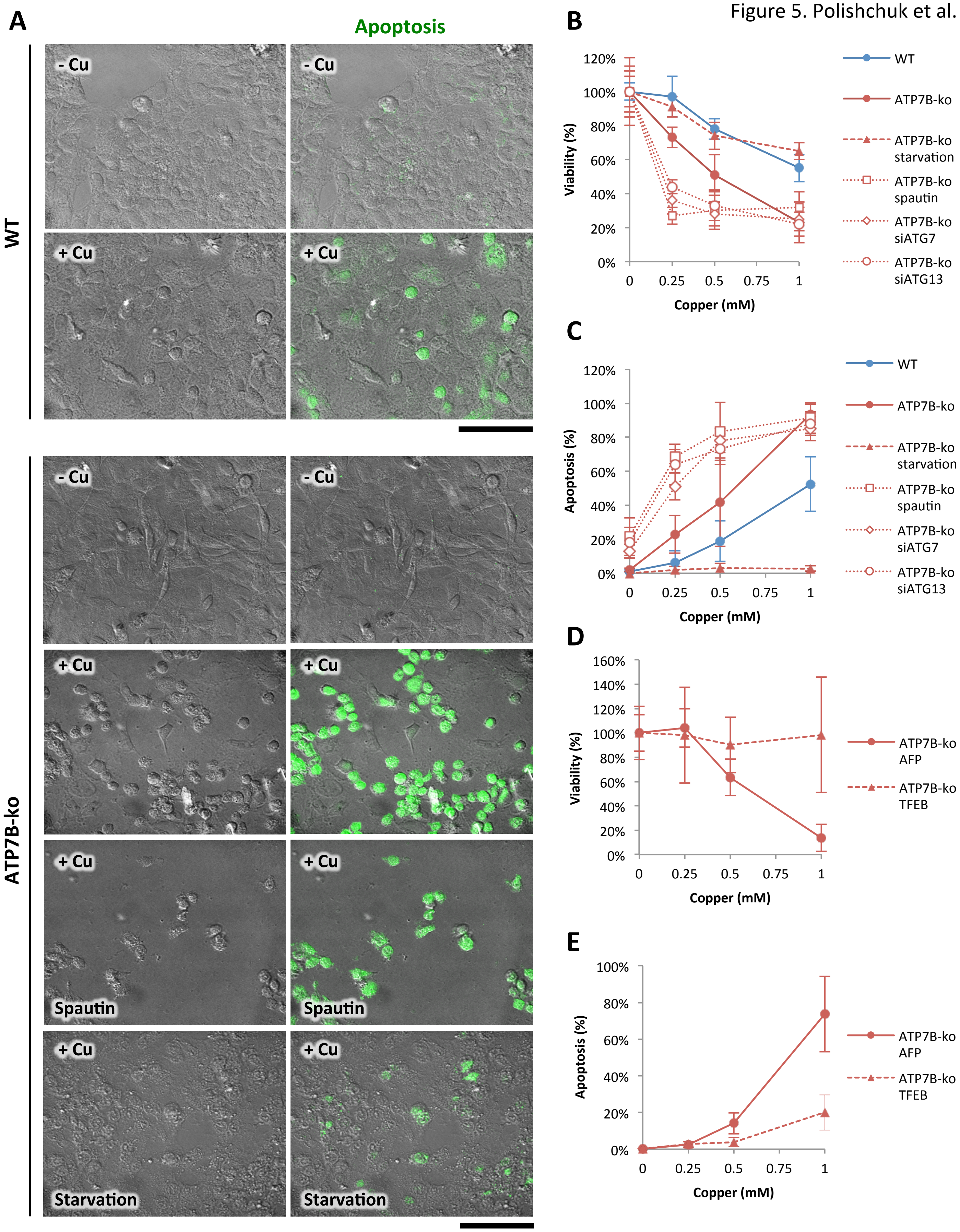

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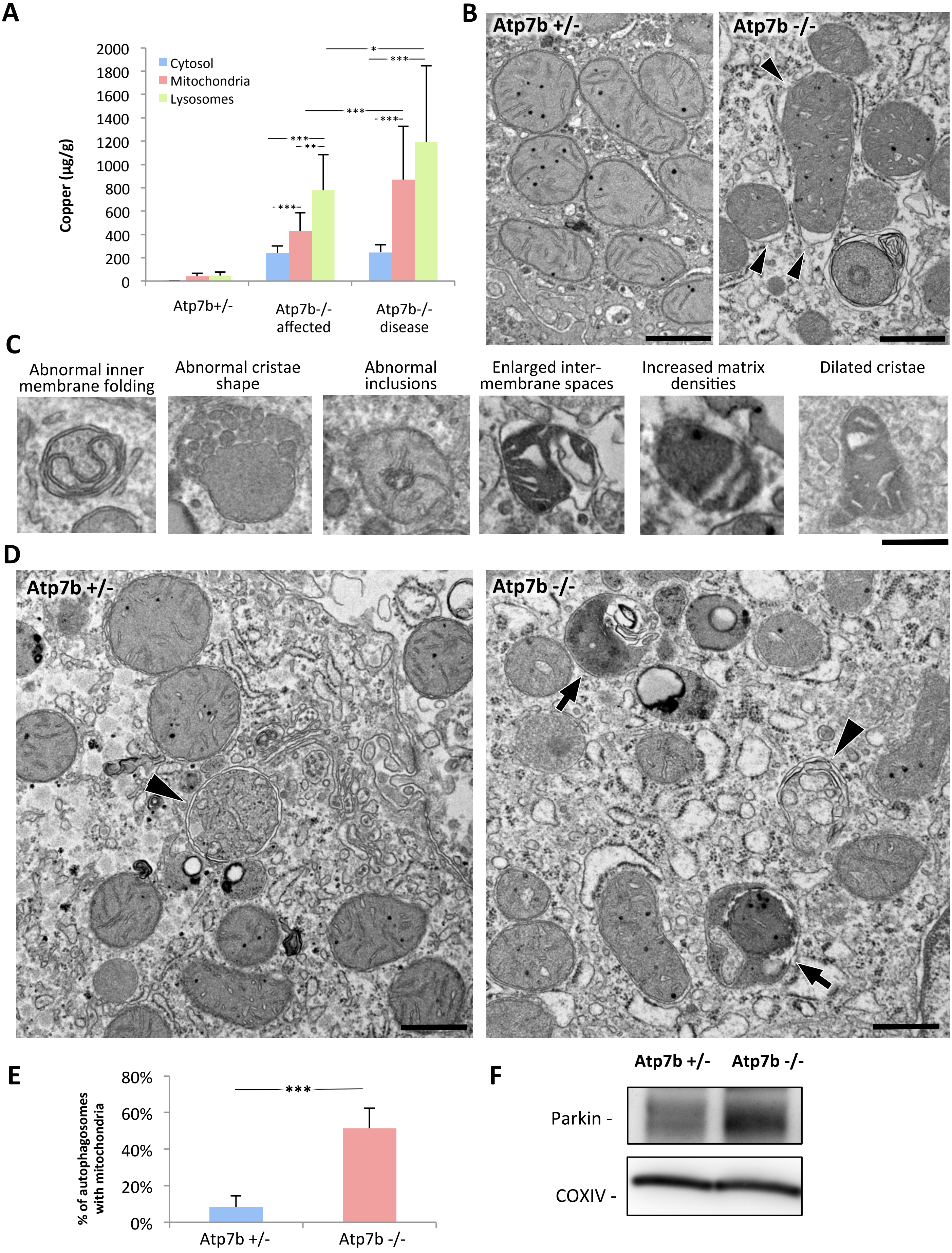

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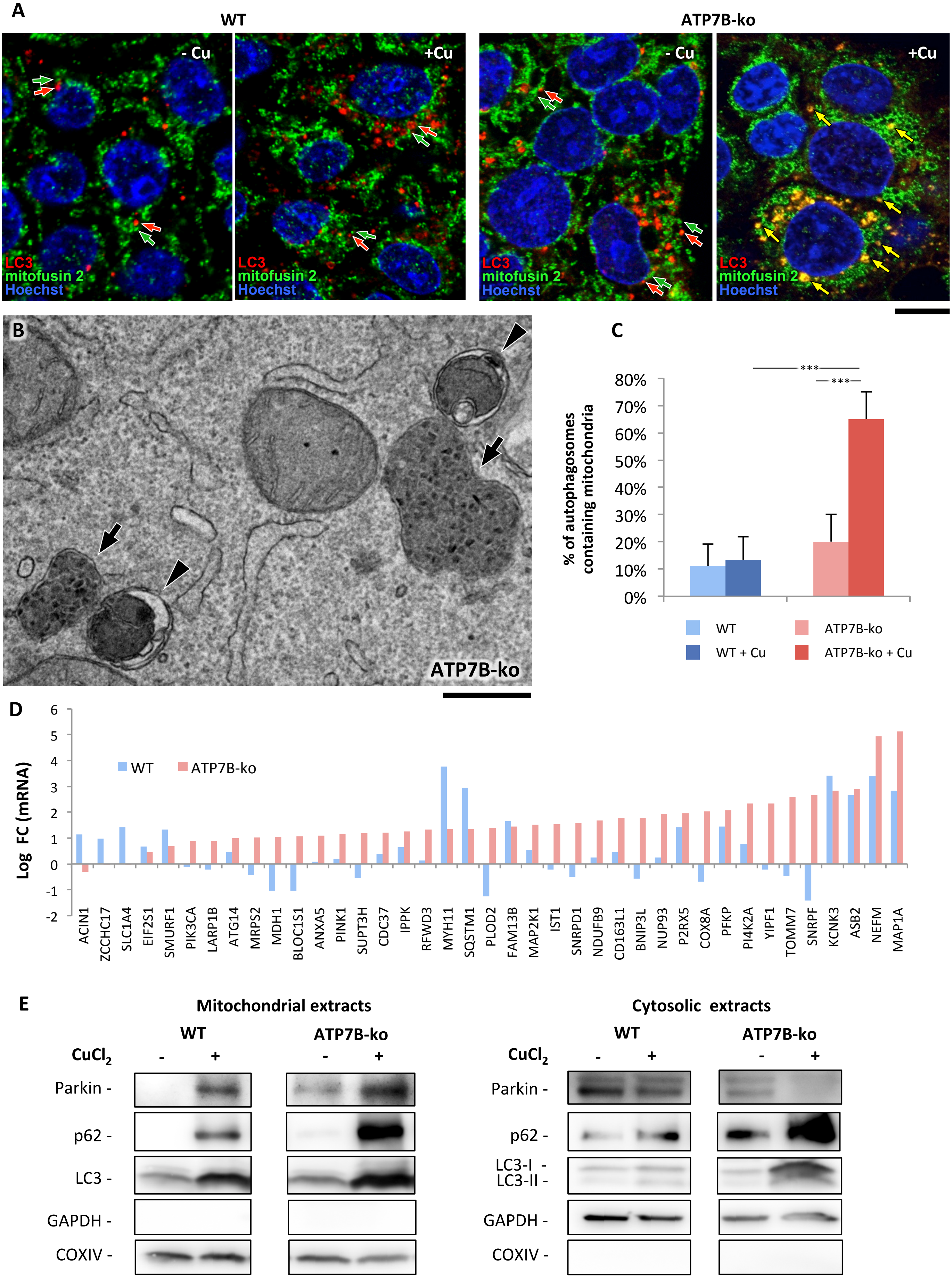

SUPPLEMENTARY MATERIALS AND METHODS

Antibodies

The following antibodies were used: Anti-LAMP1 (Developmental Studies Hybridoma Bank); anti-p62 (Abnova); anti-LC3B (Novus or Nanotools)**;** anti-GAPDH (Santa Cruz); anti-parkin, anti-CoxIV, anti-mTOR, anti-TFEB, anti-4E-BP1 and anti-phosphorylated-4E-BP1 (Cell Signaling Technology); UQCRC2, MTCO1, SDHB, NDUFB8, anti-mitofusin 2 and anti-ATP7B (Abcam); Alexa Fluor 488, 568 goat anti-rabbit, goat anti-mouse, goat anti-rat, donkey anti-sheep (Life Technologies).

Cell culture and recombinant adenoviruses

Wild-type HepG2 cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% fetal calf serum (decomplemented at 56 °C for 30 min), 2 mM L-glutamine, and 1% penicillin and streptomycin. ATP7B-ko HepG2 cells [1] were grown in RPMI medium supplemented with 10% fetal calf serum, 2 mM L-glutamine, and 1% penicillin and streptomycin. To transduce WT or ATP7B-ko cells, adenoviruses that contained ATP7B-GFP, TFEB or α-fetoprotein were used at a MOI of 1,000 particles per cell.

Animals

The *Atp7b*$^{-/-}$ (LPP) rat strain [2] was provided by Jimo Borjigin (University of Michigan, Ann Arbor, USA). The *Atp7b*$^{-/-}$ mice [3] were obtained from The Jackson Laboratory through re-derivation. Animal studies were carried out in accordance with the ARRIVE guidelines and with the Italian (authorization #726/2018-PR) and German (authorization #AZ 55.2-1-54-2532-162-2014) Ministries of Health regulations for animal procedures. Rat and murine strains were housed at the Helmholtz Center (Munich, Germany) and TIGEM (Pozzuoli, Italy) animal facilities, respectively. Animals used for this study were either 80-100 (*Atp7b*$^{-/-}$ rats) or 90-100 (*Atp7b*$^{-/-}$ mice) days of age. Both males and females mice were used, as no sex-related differences were observed in phenotypes. Heterozygous (*Atp7b*$^{+/-}$) controls were age-matched and obtained from both littermates and separate litters that were co-housed. The animals were maintained on an *ad-libitum* Altromin 1314 diet (Altromin Spezialfutter GmbH, Seelenkamp, Germany) and tap water. The basic copper content of this standard diet was 13 mg/kg. Spautin-1 (10 mg/kg) and control vehicle were supplied to *Atp7b*$^{-/-}$ and *Atp7b*$^{+/-}$ mice by intraperitoneal injection once a day for 5 days. Animals were treated, sacrificed and tissues collected during light cycle hours. For Cu measurements, Atp7b-/- rats were divided into two groups with different degrees of disease progression, as those 'affected' (with AST blood levels <200 U/mL) and 'diseased' (with AST blood levels >200 U/mL).

Wilson disease patient biopsies

Liver biopsies from patients with Wilson disease were obtained in the 'Federico II' University Hospital (Naples, Italy) during the course of their Wilson disease diagnosis confirmation. The patient denoted as Patient #1 was compound heterozygous with two mutations in the promoter region of *ATP7B* (484C>T; 441/-427del15nt), which resulted in a mild loss of ATP7B function as judged from their slightly decreased ceruloplasmin levels (18 mg/dL *vs*. 20-40 mg/dL in normal healthy subjects). Genetic analysis of the patient denoted as Patient #2 revealed compound heterozygosity with two missense *ATP7B* mutations (P840L; N1270S) that led to almost complete loss of Cu-transporting activity of the corresponding ATP7B protein product [4]. Indeed, the loss of ATP7B function in patient #2 resulted in a significant decrease in ceruloplasmin levels (to 2 mg/dL). Small pieces of biopsy healthy liver tissue were obtained during liver transplantation surgery in Bambino Gesù Children's Hospital (Rome, Italy) and used for comparison. Liver samples were fixed with 1% glutaraldehyde and prepared for electron microscopy analysis.

Isolation of subcellular fractions

To characterize the levels of the proteins parkin, LC3, p62, and COXIV in mitochondrial and cytosolic extracts, the cells were homogenized in RIPA buffer in the presence of a protease inhibitor cocktail (Roche). The mitochondrial and cytosolic extracts were obtained from cultured cells using mitochondria isolation kits (Qproteome; Qiagen), according to the manufacturer protocol. The mitochondria and lysosomes from rat liver homogenates were purified by differential and density gradient centrifugation using either Percoll (GE Healthcare Europe) or Nycodenz (Axis-Shield) [5, 6]. The protein concentrations in the subcellular fractions were determined using a commercial protein assay (Bio-Rad). A total of 30 µg protein from each sample was loaded onto SDS-polyacrylamide gels. Purity of subcellular fractions was controlled by electron microscopy and by immunobloting with following markers: Lamp 2 for lysosomes, Hsp60 and citrate synthase (CS) for mitochondria, Bip for ER and GAPDH for cytosol.

Western blotting

To characterize the total protein levels of ATP7B, UQCRC2, MTCO1, SDHB, NDUFB8, mTOR, 4E-BP1, and phosphorylated 4E-BP1, the cells were collected in lysis buffer that contained 10 mM Tris/HCl, pH 8, 0.2% SDS. Here, a total of 40 µg protein from each sample was loaded onto the SDS-polyacrylamide gels. The proteins of interest in subcellular fractions, total cell or tissue lysates were detected using horseradish-peroxidase-conjugated goat anti-mouse or anti-rabbit IgG antibodies (GE Healthcare), and visualized (Luminata Crescendo substrate; Millipore; or Super Signal West Femto substrate; Thermo Scientific), according to manufacturer protocols. Western blotting images were acquired using the Chemidoc-It imaging system (UVP), and the band intensities were calculated using the ImageJ software.

RNA interference

Small interfering RNAs (siRNAs) that targeted PINK1, BNIP3L, FUNDC1, ATG7, and ATG13 were from Sigma-Aldrich. The following siRNAs were used:
siRNA PINK1 #1 GGACGCUGUUCCUCGUUAU
siRNA PINK1 #2 AAGCCACCAUGCCUACAUU
siRNA ATG7 #1 ASUAAUGUCCUUGGGAGCUUC
siRNA ATG7 #2 ASUGAACUCCAAUGUUAAGCG
siRNA ATG13 #1 GAAGAAUGUCCGCGAGUUU
siRNA ATG13 #2 CCAUACAGACAGCGAGAUC
siRNA FUNDC1 #1 GCAGCACCUGAAAUCAACA
siRNA BNIP3L #1 GACCAUAGCUCUCAGUCAG
siRNA BNIP3L #2 CAACAACAACUGCGAGGAA

Each siRNA was used to suppress the corresponding gene either alone or paired with another siRNA. The efficiencies of silencing were determined by qRT-PCR. A scrambled siRNA was used as the negative control.

RNA preparation and qRT-PCR

Total RNAs from WT and ATP7B-ko cells (untreated or silenced for PINK1, ATG7, or ATG13) were purified (QIAshredder; Qiagen) and their RNA was extracted (RNeasy Protect mini kits; Qiagen) using standard conditions. Total RNA (1 µg) was reverse-transcribed (QuantiTect Reverse Transcription kits; Qiagen), according to the manufacturer instructions. qRT-PCR was performed using specific primers (see below) and Light Cycler 480 Syber Green MasterMix (Roche) for cDNA amplification, and LightCycler 480 II (Roche) for signal detection. qRT-PCR results were analyzed using the comparative Ct method, normalized against the housekeeping gene β-actin.

The specific primers used were:
β-ACTIN forward (5'-AAGAGCTACGAGCTGCCTGA-3')
β-ACTIN reverse (5'-GACTCCATGCCCAGGAAGG-3')
PINK1 forward (5'-TGGTCGACTACCCTGATGTG-3')
PINK1 reverse (5'-CGCAGGGTACAGGGATAGTT-3')
ATG7 forward (5'-ACAGATGGAGTAGCAGTTTCC-3')
ATG7 reverse (5'-ACATTCACTGAGGTTCACCAT-3')
ATG13 forward (5'-TCCAGACAGTTCGTGTTGGG-3')
ATG13 reverse (5'-CTCAAATTGCCTGGTAGACATGA-3')
FUNDC1 forward (5'-TCAGATTGCTAGTCATAGTGGC-3')
FUNDC1 reverse (5'-TGCTTTGTTCGCTCGTTTCT-3')
BNIP3L forward (5'-CGCCCCTGCACAACAAC-3')
BNIP3L reverse (5'-TCATTGCCATTGCTGCTG-3')

Immunofluorescence and immunohistochemistry

For immunofluorescence, the cells were fixed for 10 min with 4% paraformaldehyde in 0.2 M HEPES, followed by incubation with blocking/permeabilizing solution: 0.5% bovine serum albumin (BSA), 0.1% saponin, 50 mM NH_4Cl in PBS for 30 min. Primary and secondary antibodies were diluted in blocking/permeabilizing solution, and added to the cells for 1 h or 45 min, respectively. Samples were examined under a confocal microscope (Zeiss LSM 700) equipped with a 63×1.4 NA oil objective. Colocalization between specific markers was quantified using the Zeiss Zen 2012 software.

To evaluate lysosomal acidification, the cells were loaded with 200 nM LysoTracker Red (Life Technologies) for 1 h at 37 °C. Then the cells were fixed, labeled with an antibody against LAMP1, and analyzed. The LysoTracker fluorescent signal inside the cells was measured using the Zeiss Zen 2012 software, and is reported in arbitrary units (AU).

DQ™ Green self-quenched BSA (Thermo Fisher) or Magic Red cathepsin activity kits (ImmunoChemistry Technologies) were used to analyze the proteolytic activity of the lysosomes. The cells were loaded with 50 µM DQ-BSA for 30 min or 1 h, at 37 °C. Magic Red solution was prepared at a dilution 1:20 and added to the cells, together with Hoechst nuclear stain (1:1000), for 30 min at 37 °C. The DQ-BSA and Magic Red signals were observed using a confocal microscope (Zeiss LSM 700), with the appropriate filter sets. The numbers of green DQ-BSA spots were counted in 50 cells per condition, using the ImageJ software. The Magic Red fluorescent signal inside the cells was measured using the Zeiss Zen 2012 software and is reported in arbitrary units (AU).

The immuno-histochemical staining of LC3 was performed on rat tissue sections using Novolink kit (Menarini Diagnostics), as described previously [7]. In brief, deparaffinized tissue sections were incubated in citrate buffer at 95 °C, then cooled and mounted on slides. These were then washed twicewith 0.1% Tween 20 in PBS. After blocking of the endogenous peroxidase activity and the nonspecific sites, the slides were incubated with a primary antibody specific for LC3 (Nanotools), which was dissolved in 1% BSA in TBS. The bound antibody was revealed, and the sections were counterstained according to the instruction in the Novolink kit.

Cell viability and apoptosis assay

Wild-type and ATP7B-ko cells were grown in 24-well plates and treated with 0.25, 0.5, and 1 mM $CuCl_2$ for 24 h. To induce autophagy, the cells were starved with Hank's balanced salt solution (HBSS) or transduced with adenoviruses carrying TFEB. ATG7-specific or ATG13-specific siRNAs or 50 µM spautin were used to inhibit autophagy, while mitophagy was suppressed using PINK1-, FUNDC1- or BNIP3L-specific siRNAs. To analyze cell apoptosis, treated and control cells were incubated with 6 µM CellEvent Caspase-3/7 Green Detection Reagent (Life Technologies) for 30 min, then fixed and labeled with Hoechst 33342. After activation of Caspase-3/7, the apoptotic cells contained nuclei of green color produced by binding of the CellEvent dye to DNA. The cells were observed by using an appropriate filter set under confocal microscope (Zeiss LSM 700). The numbers of apoptotic nuclei (visualized using the CellEvent reagent) were quantified in 10 equal fields of view, and expressed as a percentage of the total cell nuclei (stained with Hoechst). To measure cell viability, the numbers of cells in treated specimens were calculated in 10 equal fields using nuclear staining, and then normalized to the numbers of cells in the similar field in untreated specimens.

Mitochondrial membrane potential assay

The fluorescent dye tetramethylrhodamine (TMRE; ethyl ester; Life Technologies) was used to characterize mitochondrial membrane potential in WT and ATP7B-ko cells treated with $CuCl_2$. TMRE is a cell-permeant, positively charged, red-orange dye that readily accumulates in active mitochondria, due to their relative negative charge. An uncoupler of oxidative phosphorylation, carbonyl cyanide 4-(trifluoromethoxy) phenylhydrazone) (FCCP), was used as a positive control for membrane potential loss. FCCP eliminates the mitochondrial membrane potential and TMRE staining. The cells were loaded with 250 nM TMRE or 30 µM FCCP in the presence of Hoechst for 30 min at 37 °C. Then the cells were monitored using a Zeiss LSM 700 confocal microscope equipped with an appropriate filter set. The TMRE fluorescent signal inside the cells was measured using the Zeiss Zen 2012 software, and is reported in arbitrary units (AU).

Electron microscopy

Electron microscopy of the cells, tissues and organelle fractions was performed as described previously [8, 9] (see Supplementary Methods). For pre-embedding immuno-electron microscopy, the cells were fixed, permeabilized, and labeled as described previously [8]. Briefly, the cells were fixed with a mixture of 4% paraformaldehyde and 0.05% glutaraldehyde in 0.2 M HEPES for 10 min, and then with 4% paraformaldehyde alone for 30 min, followed by an incubation with blocking/ permeabilizing solution for 30 min. Primary anti-LAMP1 antibodies and 1.4-nm gold-conjugated Fab' fragment of anti-rabbit IgGs were diluted in blocking/permeabilizing solution and added to the cells overnight and for 2 h, respectively. GoldEnhance EM kit was used to enhance the ultrasmall gold particles. The cells were scraped, pelleted, post-fixed in OsO_4 and uranyl acetate, and embedded in Epon. For routine electron miscoscopy, the samples were fixed in 1% glutaraldehyde, and post-fixed and embedded as indicated above. From each sample, thin 60-nm sections were cut using Leica EM UC7 (Leica Mycrosystems). Electron miscorscopy images were acquired from thin sections under an electron microscope (Tecnai G2 Spirit BioTwin; FEI) equipped with a VELETTA CCD digital camera (Soft Imaging Systems GmbH). Morphometric analysis was performed using the iTEM software (Soft Imaging Systems GmbH, Munster, Germany). The numbers of autophagosomes were counted on thin sections that were acquired with the same magnification, from within a 25 μm^2 field of view. Electron microscopy of organelle fractions was performed as described previously [9].

Metal content determination

Cu in cell lysates, blood, liver homogenates, and subcellular fractions was analyzed after wet washing of the samples with 65% nitric acid by inductively coupled plasma optical emission spectroscopy (Ciros Vision, Spectro Analytical Instruments GmbH) or atomic adsorption spectroscopy (ZEEnit 650P, Analytik Jena).

Aminotransferase activities

To evaluate the extent of liver damage in spautin-1-treated and control mice, serum activities of alanine transaminase (ALT) and aspartate transaminase (AST) were measured with ALT-RF/AST-RF kits (Olveks diagnosticum) according to the manufacture’s instructions.

Preparation of the QuantSeq 3’-mRNA sequencing library

Three biological replicates of WT and ATP7B-ko cells were incubated with 0.5 mM $CuCl_2$ for 24 h, and the transcriptional responses were analyzed using QuantSeq 3’-mRNA sequencing. Total RNA was extracted from WT and ATP7B-ko cells treated with Cu, using RNeasy mini kits (Quiagen), according to the manufacturer instructions. RNA was extracted from untreated cells as the controls. Total RNA (100 ng) from each sample was prepared using QuantSeq 3'-mRNA-Seq Library prep kits (Lexogen), according to the manufacturer instructions. The amplified fragments of cDNA were sequenced in single-end mode using NextSeq500 (Illumina), with a read length of 75 base pairs.

QuantSeq 3’ mRNA sequencing data processing and analysis.

The sequence reads were trimmed using the Trim Galore software (https://www.bioinformatics.babraham.ac.uk/projects/trim_galore/), to remove adapter sequences and low-quality end bases. They were then aligned on the hg19 reference sequence using STAR [10]. The expression levels of genes were determined with htseq-count [11] using the Gencode v19 gene model [12]. The data have been deposited in NCBI Gene Expression Omnibus (GEO), and are accessible through the GEO Series accession number GSE107323. Differential expression analysis was performed using EdgeR [13], a statistical package based on generalized linear models that is suitable for multifactorial experiments. The threshold for statistical significance chosen was a false discovery rate (FDR)<0.05; a further filtering was performed by selection genes with a Log2 fold-change (LogFC) >2 for up-regulated genes, and LogFC <-2 for down-regulated genes.

Gene Ontology Enrichment Analysis (GOEA) [14] was then performed on both the up-regulated and down-regulated genes using the DAVID online tool (DAVID Bioinformatics Resources 6.8), restricting the output to Biological Process terms (BP_FAT). The threshold for statistical significance of the GOEA was FDR<0.1 and an enrichment score ≥1.5. Supplementary Table 1 summarizes the results from the GOEA analysis on the 480 (up-regulated) and 240 (down-regulated) genes from the WT+Cu *versus* WT dataset. Supplementary Table 2 summarizes the results from the GOEA analysis on the 1244 (up-regulated) and 681 (down-regulated) genes from the ATP7B-ko+Cu *versus* ATP7B-ko dataset. Then the list of 5973 total differentially expressed genes from ATP7B-ko+Cu *versus* ATP7B-ko was crossed examined with the list of 3208 total differentially expressed genes in the WT+Cu *versus* WT dataset (the threshold for this comparison was FDR<0.05). Thus the 1526 genes (Supplementary Table 3) and 4291 genes (Supplementary Table 4) that were specifically regulated in the WT+Cu *versus* WT dataset and specifically regulated in the ATP7B-ko+Cu *versus* ATP7B-ko dataset, respectively, were defined. GOEA with the restricted output to BP_FAT terms was then performed on these lists of genes, dividing the analysis according to the up-regulated and down-regulated genes. Supplementary Tables 5 summarizes the results of the GOEA analysis on the 663 and 863 genes specifically up-regulated and down-regulated in the WT+Cu *versus* WT dataset following the comparison. Supplementary Tables 6 summarizes the results of the GOEA analysis on the 2337 and 1954 genes specifically up-regulated and down-regulated in the ATP7B-ko+Cu *versus* ATP7B-ko dataset following the comparison.

Identification of autophagic genes regulated by the loss of ATP7B and Cu overload in hepatic cells

The list of well-known autophagic genes was downloaded from the Molecular Signatures Database (MSigDB) [15]. This list was crossed checked with the total list of the 5973 differentially expressed genes in the ATP7B-ko+Cu *versus* ATP7B-ko, and with the total list of the 3208 differentially expressed genes in the WT+Cu *versus* WT dataset (threshold: false discovery rate <0.05). Here, 86 and 184 autophagic genes were differentially expressed in the WT+Cu *versus* WT dataset and the ATP7B-ko+Cu *versus* ATP7B-ko dataset, respectively. In detail, 49 autophagic genes were regulated in both datasets, while 37 (out of 86) were regulated specifically for WT+Cu *versus* WT and 135 (out of 184) were regulated specifically for ATP7B-ko+Cu *versus* ATP7B-ko (Supplementary Figure 1; Supplementary Table 7). The significance of the enrichment of the autophagic genes was calculated by using the hypergeometric test, and this reached significance only for positive regulation of the 103 (out of 135) specific autophagic induced genes in the ATP7B-ko+Cu *versus* ATP7B-ko dataset (p = 2.6E-05). These autophagic genes that were regulated in the two datasets (Supplementary Table 7) were then linked to the TFEB regulation (Supplementary Table 8). For each gene, the regulation mediated by TFEB in published microarray studies [16-19] [16-19], and direct binding of TFEB to gene promoter [20] was indicated.

Identification of mitophagy genes regulated by the loss of ATP7B and Cu overload in hepatic cells

Three lists of known mitophagy-related genes were downloaded from MSigDB for three sub-categories: “regulation of mitophagy”, “macromitophagy”, and “positive regulation of release of cytochrome c from mitochondria”. The three lists were merged into one list, excluding the redundancy of genes annotated in more than one of these three categories. This list was then cross checked with the genes up-regulated (threshold FDR<0.05) for ATP7B-ko+Cu *versus* ATP7B-ko and WT+Cu *versus* WT, separately. We were thus able to define 10 genes that were up-regulated in both datasets, as 11 specifically in WT+Cu *versus* WT, and 43 specifically in ATP7B-ko+Cu *versus* ATP7B-ko (see Supplementary Table 9).

Statistical analysis

The data are expressed as means ± standard deviation. The data presented in the Figures were collected from multiple independent experiments performed on different days. Statistical significance for all of the data, except the QuantSeq and bioinformatics analysis, was computed using Student’s two-tailed t-tests. p <0.05 was considered statistically significant. For all of the Figures (significances: *p <0.05, **p <0.01, and ***p <0.001).

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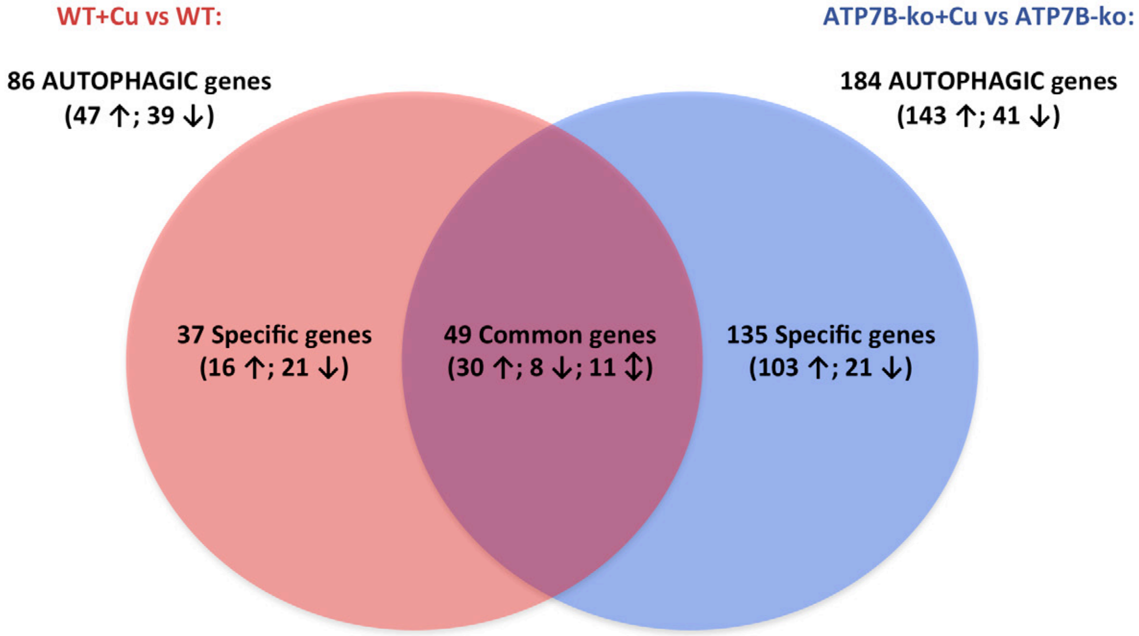
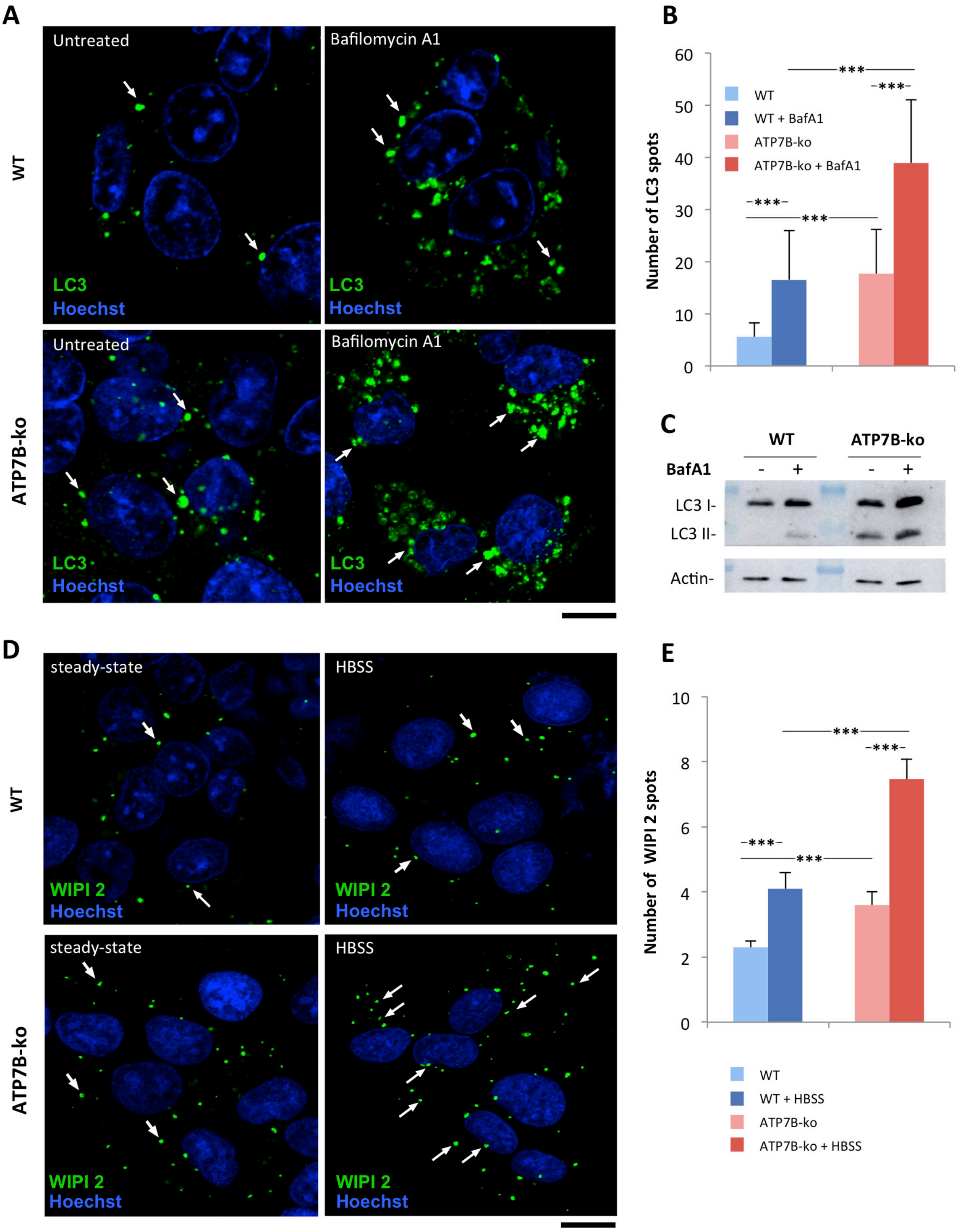


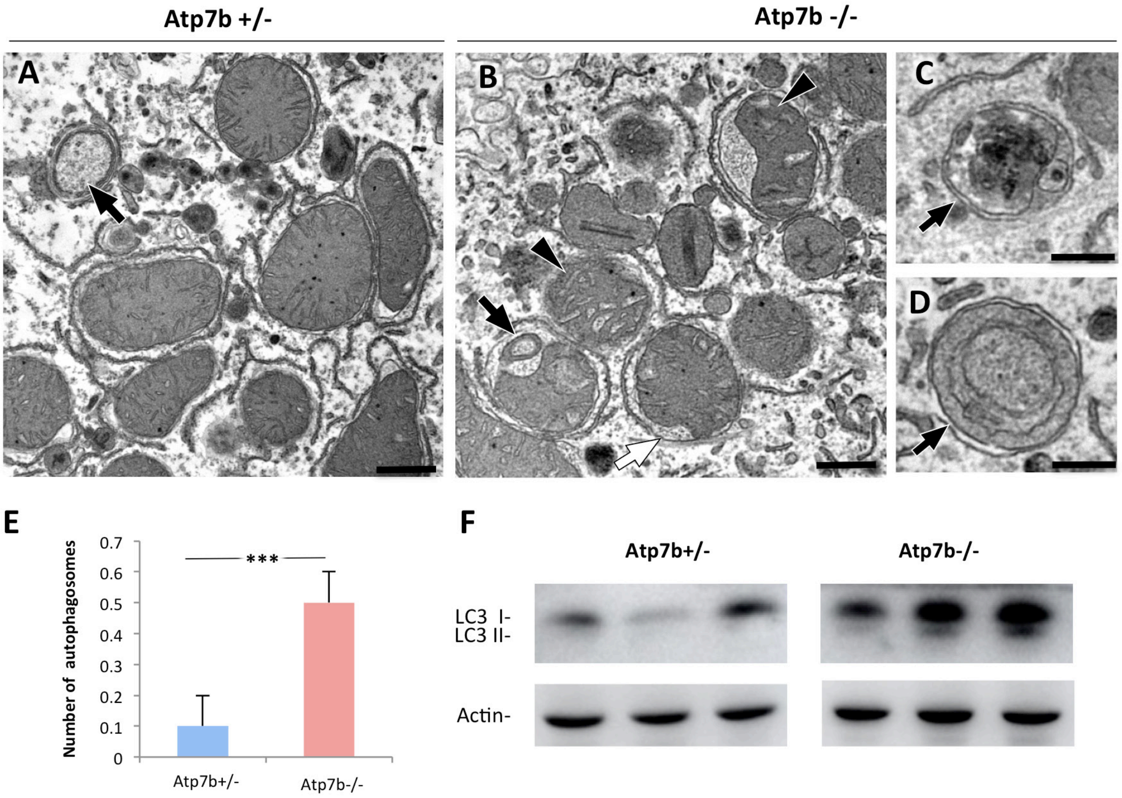
Supplementary Figure 1. Impact of Cu on autophagic genes in ATP7B-deficient and control HepG2 cells.
A Venn diagram was generated to compare the lists of 86 and 184 autophagic genes that showed significantly modulated expression under Cu treatment in the WT cells (WT+Cu *vs*. WT dataset) and in the ATP7B-ko cells (ATP7B-ko+Cu *vs*. ATP7B-ko dataset), respectively (see also Supplementary Table 7). The diagram shows that Cu specifically changes the expression of 135 autophagic genes (103 up-regulated; 22 down-regulated) in ATP7B-ko cells, while only 37 autophagic transcripts (16 up-regulated; 21 down-regulated) were specifically regulated by Cu in WT cells. The expression of 49 autophagic genes was modulated by Cu in both cell types (30 up-regulated; 8 down-regulated; 11 regulated in opposite directions). The positive regulation of the 103 specific autophagic genes in the ATP7B-ko cell dataset is statistically significant (p = 2.6E-05; hypergeometric test; see Methods).



Supplementary Figure 2. ATP7B loss leads to activation of autophagosome biogenesis.

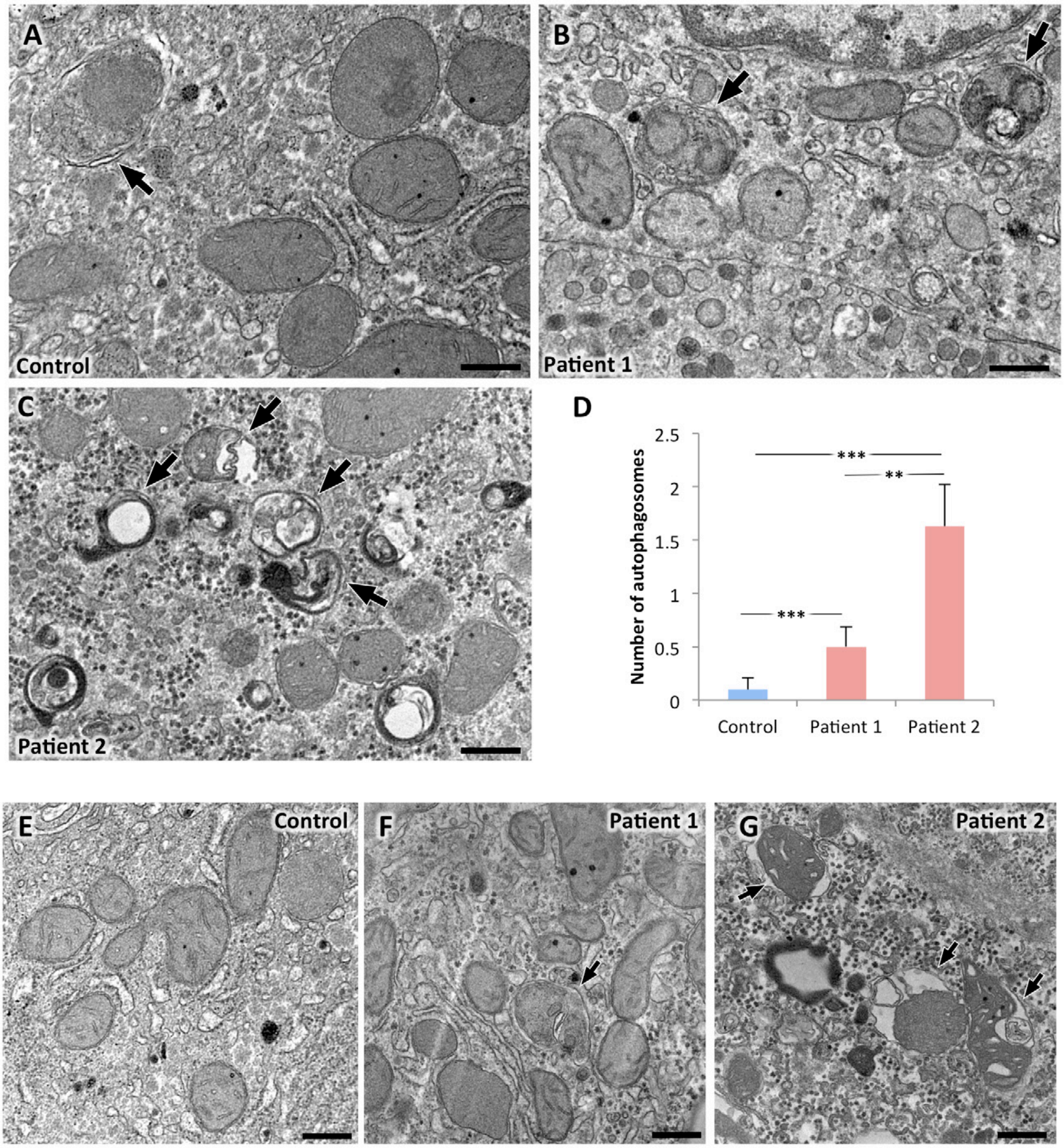
(A) WT and ATP7B-ko cells were treated with 200 nM Bafilomycin A1 for 2 h at 37 °C. Bafilomycin A1 treatment led to a more substantial increase in the number of LC3 spots (arrows) in ATP7B-ko cells compared to WT cells. (**B**) Quantification of the number of LC3-positive structures per cell in WT and ATP7B-ko cells before and after Bafilomycin A1 treatment (***p <0.001; t-test; n = 50 cells). **(C)** WT and ATP7B-ko cells were treated with Bafilomycin A1 as in panel A. Western blot shows higher LC3-I and LC3-II levels in untreated ATP7B-ko cells than in untreated WT cells, while Bafilomycin A1 induces an increase in LC3-I and LC3-II amounts in both cell types. (**D**) WT and ATP7B-ko cells were fixed directly or after 4 h of starvation in HBSS and stained for WIPI2. ATP7B-ko cells exhibited higher number of WIPI2 spots (arrows) than control WT cells under both steady state and starvation conditions, indicating accelerated autophagosome biogenesis. (**E**) Quantification of the number of WIPI2-positive dots per cell in WT and ATP7B-ko cells before and after starvation with HBSS (***p <0.001; t-test, n = 50 cells). Scale bar: 8 µm (A, D)

Sup. Figure 3. Polishchuk et al.



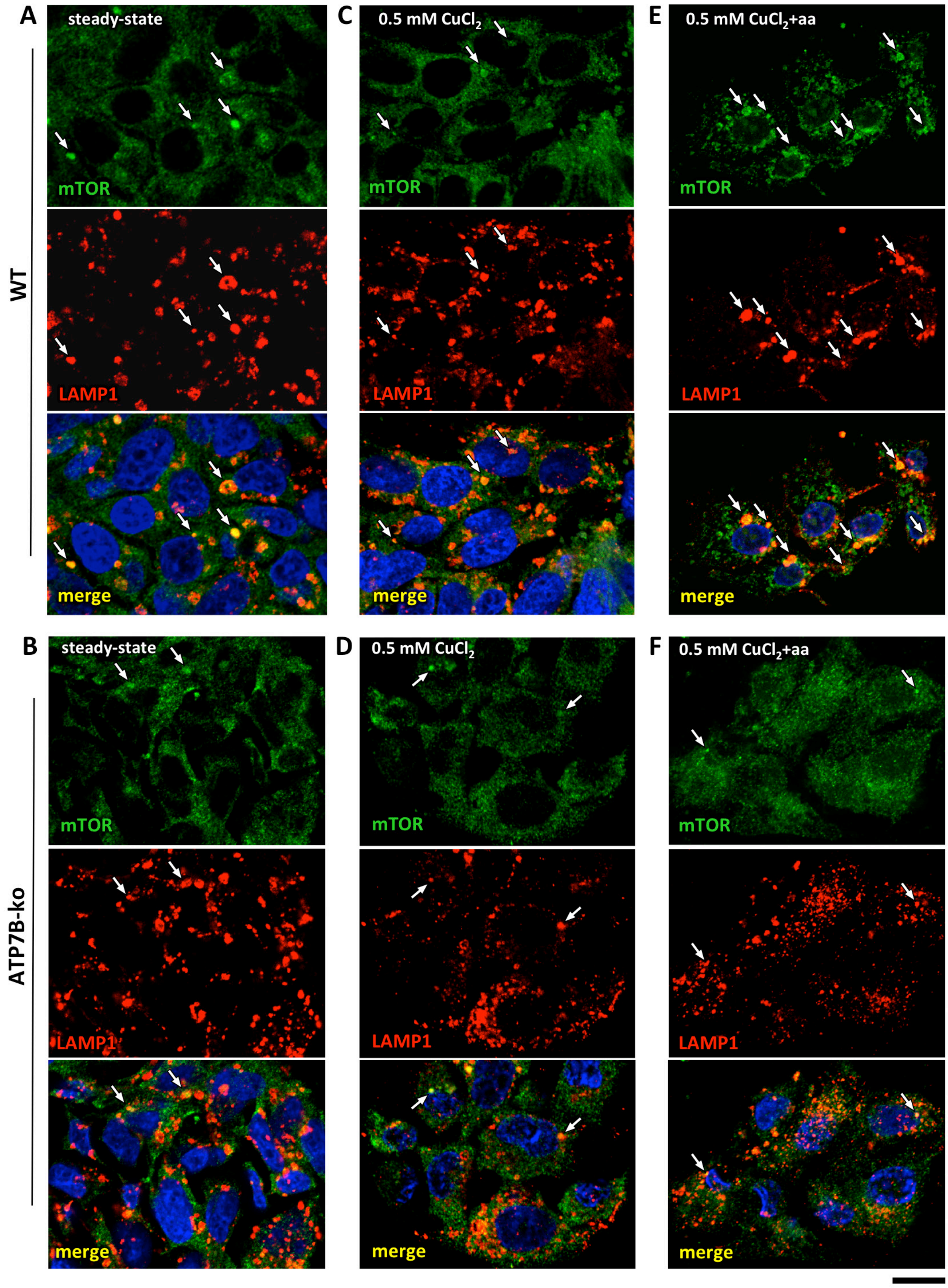
Supplementary Figure 3. Activation of autophagy in Atp7b-/- mice.

(A-D) Liver tissue specimens from Atp7b$^{+/-}$ (A) or from Atp7b$^{-/-}$ (B-D) mice were analyzed using EM. Arrows indicate autophagosomes, which were more numerous in Atp7b$^{-/-}$ mice. White arrow in panel B shows a phagophore-like structure engulfing mitochondria. Aberrant mitochondria with swollen cristae and inter-membrane space are indicated by arrowheads in panel B. Panels C and D display individual autophagosomes at higher magnification. **(E)** Quantification reveals a higher number of autophagosomes per field of view in Atp7b$^{-/-}$ mice (***p <0.001; t-test, n = 20 fields). **(F)** Western blot of liver tissue lysates shows higher LC3 levels in Atp7b$^{-/-}$ mice than Atp7b$^{+/-}$ mice (3 different animals are shown for each genotype). Scale bar: 500 nm (A, B), 300 nm (C, D).

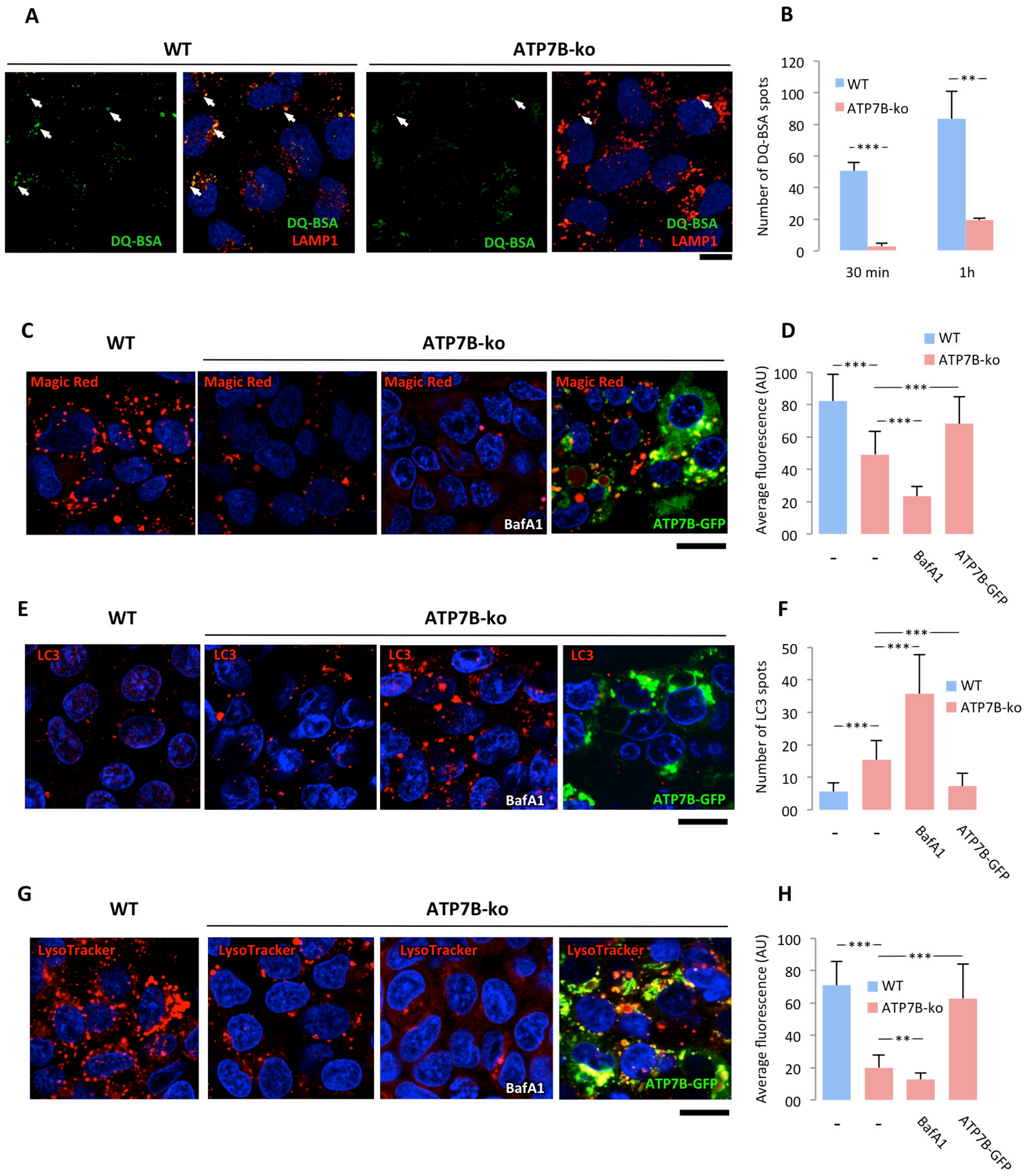


Supplementary Figure 4. Ultrastructure of hepatocytes in control liver sample and tissue biopsies from Wilson disease patients.

EM images were obtained from thin sections of control liver sample from a healthy subject (A, E) and liver biopsies from two WD patients (B, C, F, G). Patient 1 (B, F) exhibits a milder clinical phenotype than patient 2 (C, G) (see Methods). Arrows in panels A-C indicate autophagic structures, which appeared to be more numerous in liver samples from WD patients. The graph in panel D shows the number of autophagosomes per field of view in the liver tissue from the healthy subject (Control) and two WD patients (***$p<0.001$, t-test, n=20 fields). Images in panels E-G display the ultrastructure of hepatic mitochondria. Arrows in F and G indicate aberrant mitochondria, which appear to be more numerous in WD Patient 2 who has a more severe clinical phenotype (F). Scale bar: 500 nm (A-C, E-G)



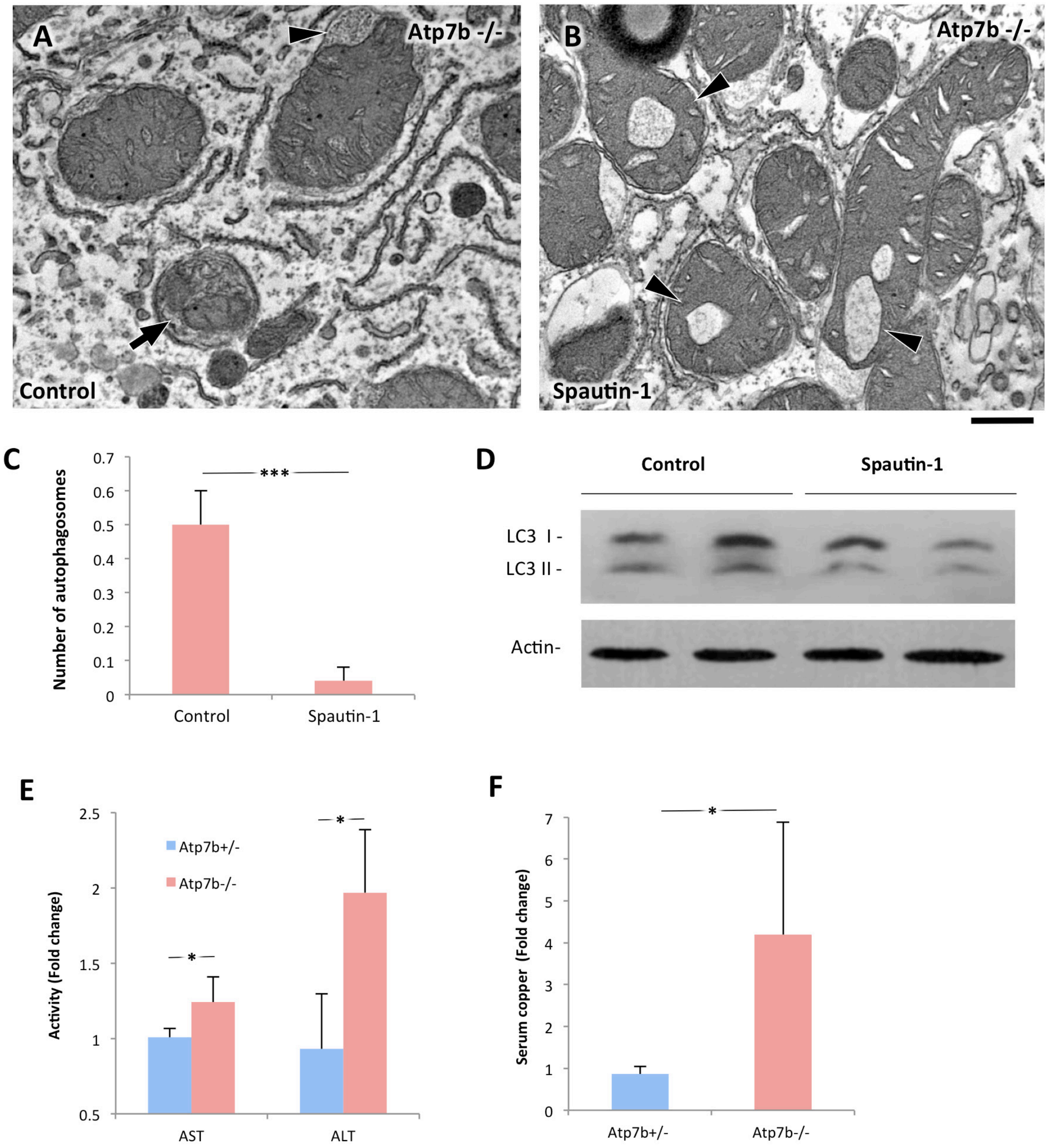
Supplementary Figure 5. Association of mTOR with lysosomes in WT and ATP7B-ko HepG2 cells.
WT and ATP7B-ko were treated as indicated in the panels, fixed and labeled for mTOR and LAMP1. **(A, B)** Under steady-state conditions some lysosomes with mTOR (A, arrows) were detected in WT cells, while the number of lysosomes containing mTOR was lower (B, arrows) in ATP7B-ko cells. **(C, D**) The cells were treated with 0.5 mM CuCl$_2$ for 24 h. Cu treatment alone did not stimulate translocation of mTOR to the lysosomes either in WT or in ATP7B-ko cells. Lysosomes containing both LAMP1 and mTOR are indicated by arrows. (**E, F**) The cells were first treated with 0.5 mM CuCl$_2$ for 24 h, then starved with medium containing dialyzed FBS for 1 h and finally incubated with a mixture of amino acids for 1 h to observe translocation of mTOR to the lysosomes. Stimulation of Cu-treated WT cells with amino acids caused evident translocation of mTOR to the lysosomes (E, arrows), while only a few lysosomes received mTOR in Cu-treated ATP7B-ko cells after amino acid stimulation (F, arrows). Scale bar: 10 µm (A-F).



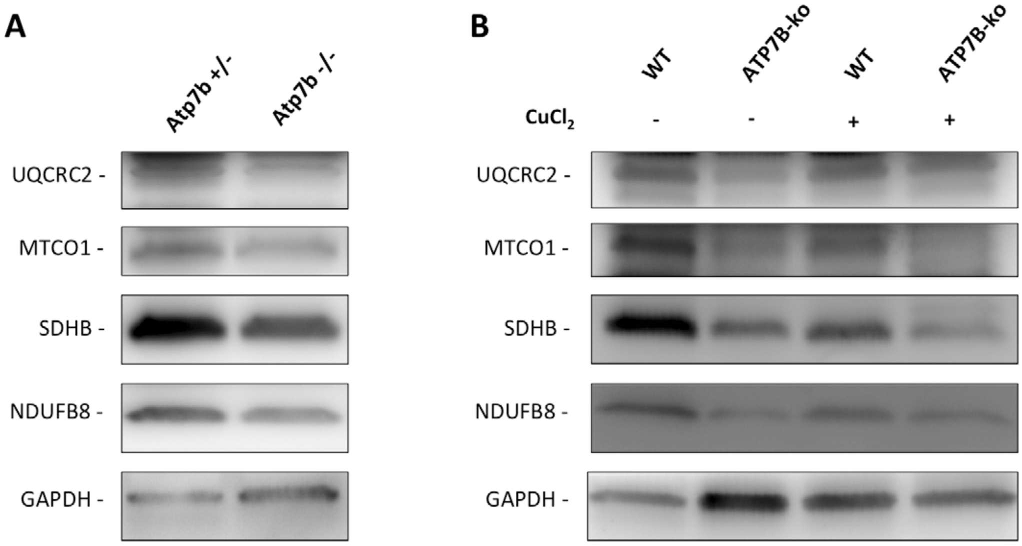
Supplementary Figure 6. Impact of ATP7B loss on activity of lysosomes.

(A) WT and ATP7B-ko cells were loaded with 50 µM DQ-BSA for 30 min or 1 h. The cells were then fixed, labeled with an antibody against LAMP1, and analyzed. The number of BSA spots decreased in ATP7B-ko cells (arrows). **(B)** Quantification of the number of DQ-BSA spots per cell in WT and ATP7B-ko cells 30 min or 1h after DQ-BSA addition (***p <0.001, **p <0.01; t-tests, n = 50 cells). **(C-H)** ATP7B-ko cells were fixed directly, 2h after treatment with 200nM Baf1A, or 24h after infection with Adeno-ATP7B-GFP. The cells were loaded before fixation with Magic Red (C, D), LysoTracker (G, H) or stained after fixation for LC3 (E, F). WT cells were used as control. **(C)** BafA1 reduced fluorescence of Magic Red (and hence proteolytic activity of lysosomes) in ATP7B-ko cells, while expression of ATP7B-GFP increased the Magic Red signal to levels comparable to those in WT cells. **(D)** Quantification of average Magic Red fluorescence per cell (***p <0.001; t-tests, n = 50 cells). **(E)** In ATP7B-ko cells, BafA1 caused an increase in the number of LC3 spots likely due to reduced turnover of LC3 in lysosomes. In contrast, expression of ATP7B-GFP reduced the number of LC3 puncta to normal levels, indicating rescue of LC3 degradation in lysosomes. **(F)** Quantification of the number of LC3 spots per cell (***p <0.001; t-tests, n = 50 cells). **(G)** BafA1-treated ATP7B-ko cells exhibited reduced fluorescence of LysoTracker (indicating reduced acidification of lysosomes), while expression of ATP7B-GFP recovers the LysoTracker signal to levels similar to those in WT cells. **(H)** Quantification of average LysoTracker fluorescence per cell (***p <0.001, **p <0.01; t-tests, n = 50 cells). Scale bar: 10 µm (A) 15 µm (C, E, G).

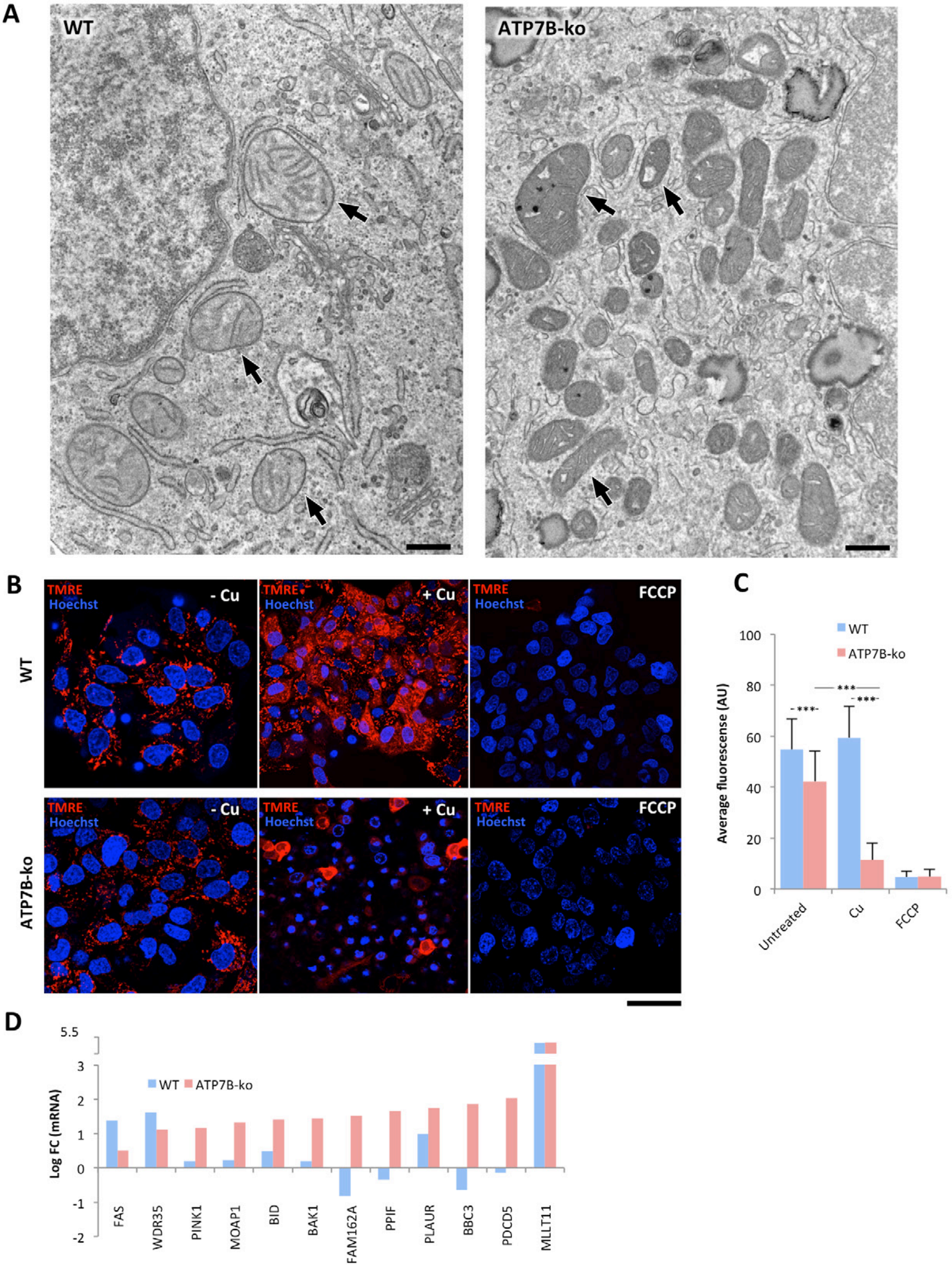
Sup. Figure 7. Polishchuk et al.



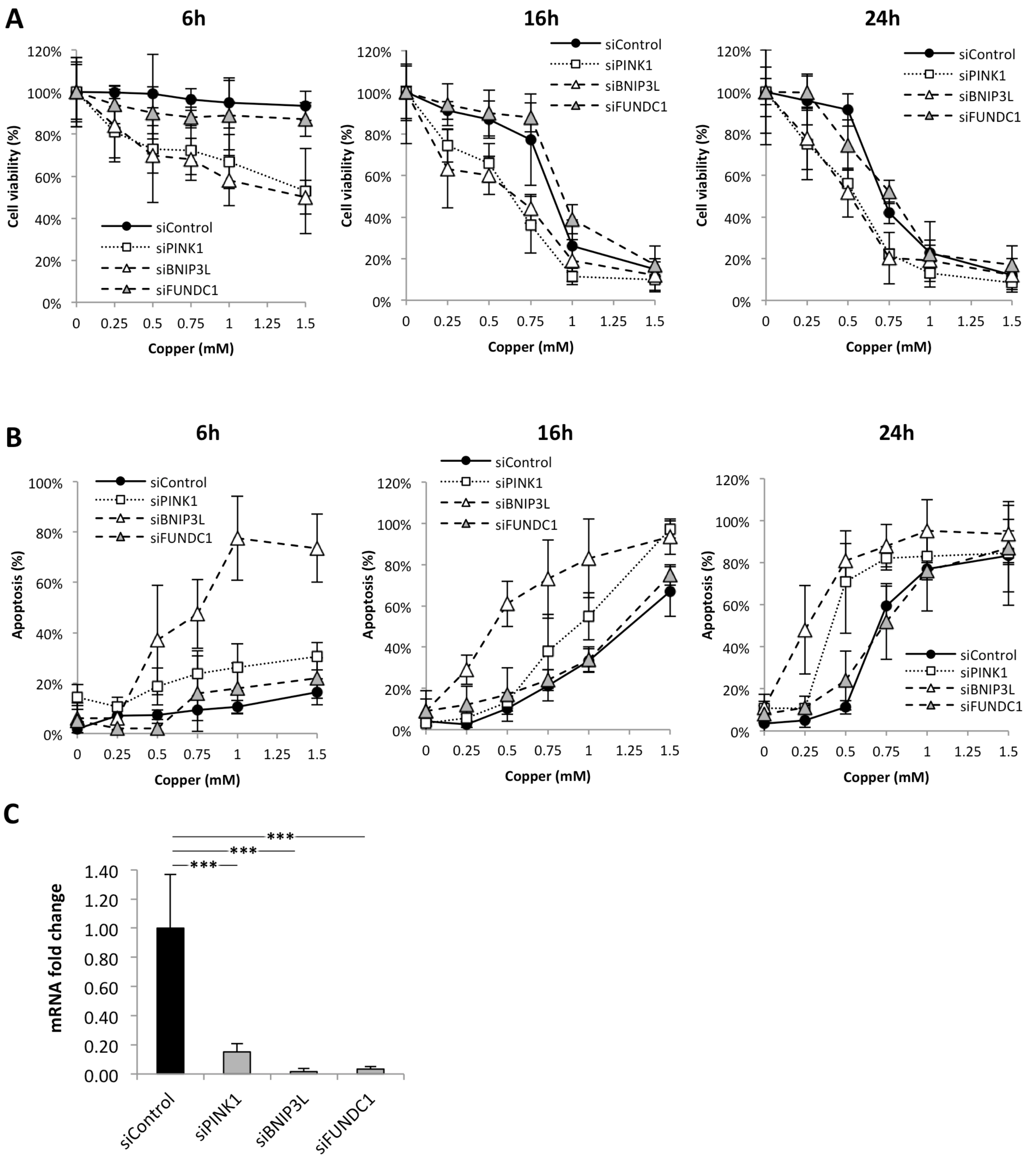
Supplementary Figure 7. A specific inhibitor of autophagy promotes liver (hepatic) damage in Atp7b-/- mice. Atp7b+/- and Atp7b-/- mice were injected either with spautin-1 or with control vehicle (see Methods). Liver tissue (A-D) and blood (E, F) were collected for further analysis. **(A, B)** Representative EM image of liver sections shows an autophagosome containing a mitochondrion (A, arrow) in Atp7b-/- mice injected with control vehicle, while autophagosomes were very scarce in spautin-1-treated Atp7b-/- mice (B). Arrowheads in A and B indicate damaged mitochondria, whose number increased significantly after spautin-1 injection. **(C)** Quantification reveals a decrease in the number of autophagosomes per field of view after spautin-1 treatment in Atp7b$^{-/-}$ mice (***p <0.001; t-test, n = 20 fields). **(D)** Western blot of liver tissue lysates shows a reduction in the LC3 (and LC3-II) signal after spautin-1 injection (2 different animals are shown for each condition). **(E)** The graph shows fold changes in serum AST and ALT activities (see methods) after spautin-1 injection in Atp7b+/- or Atp7b-/- mice. A significant increase in both AST and ALT activities was detected in response to spautin-1 in Atp7b-/- mice (*p <0.05; t-test, n = 5 animals). **(F)** Quantification indicates fold change in serum Cu levels (measured using AAS) after spautin-1 injection in Atp7b+/- or Atp7b-/- mice. Atp7b-/- mice exhibit a significant elevation in serum Cu after spautin-1 treatment (*p <0.05; t-test, n = 5 animals). Scale bar: 500 nm (A, B).



Supplementary Figure 8. Impact of ATP7B loss on specific mitochondrial proteins.
(**A**) Abundance of the mitochondrial proteins UQCRC2, MTCO1, SDHB, and NDUFB8 was evaluated by Western blot in Atp7b$^{+/-}$ and Atp7b$^{-/-}$ rats. A substantial reduction in the expression of mitochondrial markers was detected in Atp7b$^{-/-}$ rats compared to control Atp7b$^{+/-}$ rats. (**B**) WT and ATP7B-ko HepG2 cells were prepared for Western blot directly or after treatment with 0.5 mM $CuCl_2$. Immunolabeling revealed that ATP7B-ko cells showed reduced UQCRC2, MTCO1, SDHB and NDUFB8 signals, while $CuCl_2$ treatment led to further decreases in the levels of these mitochondrial proteins.



Supplementary Figure 9. Cu induces mitochondrial damage in ATP7B-deficient cells.
(**A**) Representative electron microscopy images show ultrastructure of mitochondria (arrows) in WT and ATP7B-ko cells. Cells lacking ATP7B exhibit a darker matrix, swollen cristae, and other aberrations. (**B**) WT and ATP7B-ko cells untreated and treated with 0.5 mM $CuCl_2$ or 30 µM FCCP were labeled with the membrane potential dye TMRE. The TMRE fluorescent signal was significantly reduced in ATP7B-ko cells treated with Cu. FCCP led to a complete loss of TMRE fluorescence in both cell types, indicating the specificity of the fluorescent dye. (**C**) Quantification of TMRE fluorescence in WT and ATP7B-ko cells under the conditions described in B (***p <0.001; t-test, n = 50 cells). (**D**) Quant-Seq analysis of genes that are associated with cytochome C release shows that mRNA fold-change (FC) in response to Cu treatment (0.5 $CuCl_2$; 24 h) was increased mainly in ATP7B-ko cells. Scale bar: 500 nm (A); 35 µm (B).



Supplementary Figure 10. Depletion of PINK1 decreases resistance of ATP7B-deficient cells to Cu.
(**A**) ATP7B-ko cells were silenced with PINK1- (siPINK1), BNIP3L- (siBNIP3L), FUNDC1-specific or scramble (siControl) siRNAs for 48 h and then treated with different concentrations of $CuCl_2$ for 6h, 16h and 24h. The graphs show that PINK1- and BNIP3L-specific siRNA reduce viability (see methods) of ATP7B-ko cells at different Cu concentrations. (**B**) Cells were treated as indicated in panel A. The graphs show higher apoptosis (see methods) in PINK1- and BNIP3L silenced ATP7B-ko cells upon exposure to Cu. (**C**) Quantitative RT-PCR shows a decrease in PINK1-, BNIP3L- or FUNDC1 mRNA after incubation of ATP7B-ko cells with the corresponding siRNA (*** p<0.001, t-test, n=3 experiments).

SUPPLEMENTARY TABLE 1

Complete list of biological processes (BPs) related to the gene ontology enrichment analysis GOEA for the genes significantly up-regulated and down-regulated by copper (Cu) treatment in control HepG2 cells.

GOEA was performed on up- and down-regulated genes (threshold of FDR<0,05and LogFC>2) in the QuantSeq experiment on control hepatocytes treated with Cu. The data in this table were collected using DAVID on tool restricting the output to BP_FAT terms: the up-regulated and down-regulated BPs are highlighted in red and in green, respectively.

UP-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 4.452428233062466

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0071294~cellular response to zinc ion	9	MT1M, MT2A, MT1E, MT1B, MT1H, MT1X, MT1G, KCNK3, MT1F	4.05E
GOTERM_BP_FAT	GO:0071241~cellular response to inorganic substance	15	MT1M, CPNE7, FOSB, MMP3, JUNB, MT1X, KCNK3, FOS, HMOX1, MT2A, MT1E, MT1B, MT1H, MT1G, MT1F	2.98E
GOTERM_BP_FAT	GO:0071248~cellular response to metal ion	14	MT1M, CPNE7, FOSB, MT1X, KCNK3, JUNB, FOS, HMOX1, MT2A, MT1E, MT1B, MT1H, MT1G, MT1F	3.31E
GOTERM_BP_FAT	GO:0010043~response to zinc ion	9	MT1M, MT2A, MT1E, MT1B, MT1H, MT1X, MT1G, KCNK3, MT1F	0.00346
GOTERM_BP_FAT	GO:0071276~cellular response to cadmium ion	6	HMOX1, MT1E, MT1H, MT1X, MT1G, MT1F	0.00906
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	20	MT1M, GNAO1, CRYAB, CPNE7, FOSB, MMP3, JUNB, MT1X, KCNK3, HSPH1, FOS, HMOX1, MT2A, MT1E, TXNRD1,	0.30669
GOTERM_BP_FAT	GO:1990267~response to transition metal nanoparticle	10	MT1M, HMOX1, MT2A, MT1E, MT1B, MT1H, MT1X, MT1G, KCNK3, MT1F	0.44651
GOTERM_BP_FAT	GO:0045926~negative regulation of growth	13	MT1M, CRYAB, SESN2, MT1X, SQSTM1, MT2A, MT1E, MT1B, SEMA4D, MT1H, MT1G, SEMA4A, MT1F	0.79244
GOTERM_BP_FAT	GO:0046686~response to cadmium ion	6	HMOX1, MT1E, MT1H, MT1X, MT1G, MT1F	1.00530
GOTERM_BP_FAT	GO:0010038~response to metal ion	14	MT1M, CPNE7, FOSB, MT1X, KCNK3, JUNB, FOS, HMOX1, MT2A, MT1E, MT1B, MT1H, MT1G, MT1F	2.24409

Annotation Cluster 2 Enrichment Score: 1.7450245310206967

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0032461~positive regulation of protein oligomerization	4	CCK, HRK, PMAIP1, MMP3	8.40395

Annotation Cluster 3 Enrichment Score: 1.5589602033654324

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0034097~response to cytokine	25	CSF3, TRAF1, EGR1, GNAO1, NMI, SOCS2, IL1RL1, SYNJ1, TNFSF15, TNFSF14, LRRC15, JUNB, MT1X, CCL26, FOS, T	3.52856

DOWN-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 4.0892452339059755

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006629~lipid metabolic process	39	ACOX2, ABHD6, EDN1, ACOT2, KITLG, GPD1L, TTR, AGT, APOC3, NUDT7, ATP8B1, PCSK9, SCARB1, APOM, GAL3S	8.31E
GOTERM_BP_FAT	GO:0032787~monocarboxylic acid metabolic process	21	ACOX2, ACSM2B, SULT2A1, FAXDC2, ACSM2A, OGDHL, EDN1, HAL, ACOT2, FADS2, PPARGC1A, PCK1, P2RX7, AP	0.00207
GOTERM_BP_FAT	GO:0006082~organic acid metabolic process	26	ACOX2, EDN1, OGDHL, ACOT2, PAH, MSRA, APOC3, ATP8B1, GNMT, ACSM2B, ALDH6A1, SULT2A1, FAXDC2, ACS	0.01015
GOTERM_BP_FAT	GO:0019752~carboxylic acid metabolic process	24	ACOX2, ACSM2B, ALDH6A1, SULT2A1, FAXDC2, ACSM2A, OGDHL, EDN1, HAL, ACOT2, FADS2, PAH, PPARGC1A, P	0.02130
GOTERM_BP_FAT	GO:0043436~oxoacid metabolic process	24	ACOX2, ACSM2B, ALDH6A1, SULT2A1, FAXDC2, ACSM2A, OGDHL, EDN1, HAL, ACOT2, FADS2, PAH, PPARGC1A, P	0.02346
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	20	ACSM2B, ACOX2, MOGAT2, FAXDC2, SPTLC3, ABHD6, ACSM2A, EDN1, FADS2, PPARGC1A, PCK1, GPD1L, P2RX7,	0.03891
GOTERM_BP_FAT	GO:0072330~monocarboxylic acid biosynthetic process	10	ACSM2B, ACOX2, FAXDC2, APOC3, EDN1, ACSM2A, FADS2, CYP8B1, AKR1D1, SLC27A2	0.22973
GOTERM_BP_FAT	GO:0055114~oxidation-reduction process	24	ACOX2, ALDH6A1, AIFM3, FAXDC2, OGDHL, HR, FADS2, PAH, PPARGC1A, GPD1L, MSRA, G6PC, DHRS4, SDHC, CY	0.30802
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	11	ACSM2B, ACOX2, FAXDC2, APOC3, EDN1, ACSM2A, FADS2, PAH, CYP8B1, AKR1D1, SLC27A2	0.66598
GOTERM_BP_FAT	GO:0044283~small molecule biosynthetic process	15	ACOX2, ACSM2B, FAXDC2, ACSM2A, EDN1, FADS2, PAH, PPARGC1A, PCK1, G6PC, C1QTNF3, APOC3, CYP8B1, SLC	0.89694
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	11	ACSM2B, ACOX2, FAXDC2, APOC3, EDN1, ACSM2A, FADS2, PAH, CYP8B1, AKR1D1, SLC27A2	1.06157
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	12	ACSM2B, ACOX2, FAXDC2, APOC3, EDN1, ACSM2A, ACOT2, FADS2, FABP1, CYP4F3, PPARGC1A, SLC27A2	2.47406
GOTERM_BP_FAT	GO:0006699~bile acid biosynthetic process	4	ACOX2, CYP8B1, AKR1D1, SLC27A2	4.56929
GOTERM_BP_FAT	GO:0006694~steroid biosynthetic process	7	ACOX2, FAXDC2, CYP8B1, AKR1D1, PPARGC1A, SLC27A2, CYP19A1	6.86533

Annotation Cluster 2 Enrichment Score: 4.0768221241579266

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0055088~lipid homeostasis	10	CEBPA, ACOX2, G6PC, C1QTNF3, APOC3, ACSM2A, PCSK9, SCARB1, APOM, ANGPTL4	0.0092
GOTERM_BP_FAT	GO:0070328~triglyceride homeostasis	5	C1QTNF3, APOC3, ACSM2A, SCARB1, ANGPTL4	0.62108
GOTERM_BP_FAT	GO:0055090~acylglycerol homeostasis	5	C1QTNF3, APOC3, ACSM2A, SCARB1, ANGPTL4	0.62108

Annotation Cluster 3 Enrichment Score: 4.072699695944865

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	15	CEBPA, ACOX2, G6PC, DHRS4, SULT2A1, FAXDC2, AGT, ATP8B1, PCSK9, SCARB1, CYP8B1, PPARGC1A, AKR1D1, SL	0.00172
GOTERM_BP_FAT	GO:1901615~organic hydroxy compound metabolic process	14	CEBPA, MOGAT2, FAXDC2, PAH, PCK1, TTR, DHRS4, PCSK9, SCARB1, CYP4F3, DIO1, CYP8B1, AKR1D1, CYP19A1	0.55767
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	7	CEBPA, FAXDC2, PCSK9, SCARB1, CYP8B1, AKR1D1, CYP19A1	3.76578

Annotation Cluster 4 Enrichment Score: 3.1136278144844955

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006639~acylglycerol metabolic process	10	GPD1L, MOGAT2, G6PC, ABHD6, APOC3, PCSK9, DGKK, FABP1, SCARB1, PCK1	0.00615
GOTERM_BP_FAT	GO:0006638~neutral lipid metabolic process	10	GPD1L, MOGAT2, G6PC, ABHD6, APOC3, PCSK9, DGKK, FABP1, SCARB1, PCK1	0.00659
GOTERM_BP_FAT	GO:0006641~triglyceride metabolic process	8	GPD1L, MOGAT2, G6PC, APOC3, PCSK9, FABP1, SCARB1, PCK1	0.16252
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	13	MOGAT2, ABHD6, DGKK, KITLG, PCK1, TMEM150A, GPD1L, G6PC, APOC3, PCSK9, FABP1, SCARB1, PLA2G4D	0.96160

Annotation Cluster 5 Enrichment Score: 2.915379788021445

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0019752~carboxylic acid metabolic process	24	ACOX2, ACSM2B, ALDH6A1, SULT2A1, FAXDC2, ACSM2A, OGDHL, EDN1, HAL, ACOT2, FADS2, PAH, PPARGC1A, P	0.02130
GOTERM_BP_FAT	GO:0043436~oxoacid metabolic process	24	ACOX2, ACSM2B, ALDH6A1, SULT2A1, FAXDC2, ACSM2A, OGDHL, EDN1, HAL, ACOT2, FADS2, PAH, PPARGC1A, P	0.02346
GOTERM_BP_FAT	GO:0044712~single-organism catabolic process	22	ACOX2, ALDH6A1, SULT2A1, ENPP3, ABHD6, OGDHL, HAL, PDE3A, COL2A1, PAH, PPARGC1A, MMP11, P2RX7, G6	0.23368
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	9	ACOX2, ALDH6A1, SULT2A1, HAL, FABP1, CYP4F3, PAH, AKR1D1, SLC27A2	3.65659
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	10	ACOX2, SULT2A1, ABHD6, APOC3, FABP1, SCARB1, CYP4F3, AKR1D1, SLC27A2, PLA2G4D	5.82510
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	8	ACOX2, ALDH6A1, SULT2A1, HAL, FABP1, PAH, AKR1D1, SLC27A2	6.74757

Annotation Cluster 6 Enrichment Score: 2.22443433942156

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008209~androgen metabolic process	4	SCARB1, AKR1D1, PPARGC1A, CYP19A1	4.56929
GOTERM_BP_FAT	GO:0042445~hormone metabolic process	8	TTR, DHRS4, AGT, SCARB1, DIO1, AKR1D1, PPARGC1A, CYP19A1	4.64447
GOTERM_BP_FAT	GO:0034754~cellular hormone metabolic process	6	TTR, DHRS4, SCARB1, AKR1D1, PPARGC1A, CYP19A1	8.44636

Annotation Cluster 7 Enrichment Score: 2.140451773487501

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0007586~digestion	8	MOGAT2, P2RX7, SULT2A1, HAMP, FABP1, SCARB1, AKR1D1, PPARGC1A	2.59433
GOTERM_BP_FAT	GO:0050892~intestinal absorption	4	MOGAT2, HAMP, FABP1, SCARB1	8.01141

Annotation Cluster 8 Enrichment Score: 2.137651710809531

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008643~carbohydrate transport	8	RFT1, G6PC, AGT, SLC2A2, SLC2A14, EDN1, SLC5A9, KLF15	2.24339
GOTERM_BP_FAT	GO:0015758~glucose transport	7	G6PC, AGT, SLC2A2, SLC2A14, EDN1, SLC5A9, KLF15	2.30474
GOTERM_BP_FAT	GO:0008645~hexose transport	7	G6PC, AGT, SLC2A2, SLC2A14, EDN1, SLC5A9, KLF15	2.51230
GOTERM_BP_FAT	GO:0015749~monosaccharide transport	7	G6PC, AGT, SLC2A2, SLC2A14, EDN1, SLC5A9, KLF15	2.51230

Annotation Cluster 9 Enrichment Score: 1.8261160877563443

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0015748~organophosphate ester transport	6	P2RX7, G6PC, SLC35B2, APOC3, ATP8B1, SCARB1	2.88299

Annotation Cluster 10 Enrichment Score: 1.7364812506248282

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0055088~lipid homeostasis	10	CEBPA, ACOX2, G6PC, C1QTNF3, APOC3, ACSM2A, PCSK9, SCARB1, APOM, ANGPTL4	0.0092
GOTERM_BP_FAT	GO:0034369~plasma lipoprotein particle remodeling	4	AGT, APOC3, SCARB1, APOM	3.25432
GOTERM_BP_FAT	GO:0034367~macromolecular complex remodeling	4	AGT, APOC3, SCARB1, APOM	3.25432
GOTERM_BP_FAT	GO:0034368~protein-lipid complex remodeling	4	AGT, APOC3, SCARB1, APOM	3.25432
GOTERM_BP_FAT	GO:0097006~regulation of plasma lipoprotein particle levels	5	AGT, APOC3, PCSK9, SCARB1, APOM	4.55944
GOTERM_BP_FAT	GO:0034384~high-density lipoprotein particle clearance	3	APOC3, SCARB1, APOM	6.31186
GOTERM_BP_FAT	GO:0034381~plasma lipoprotein particle clearance	4	APOC3, PCSK9, SCARB1, APOM	7.36166
GOTERM_BP_FAT	GO:0071827~plasma lipoprotein particle organization	4	AGT, APOC3, SCARB1, APOM	8.69147
GOTERM_BP_FAT	GO:0055092~sterol homeostasis	5	G6PC, APOC3, PCSK9, SCARB1, APOM	8.99645
GOTERM_BP_FAT	GO:0042632~cholesterol homeostasis	5	G6PC, APOC3, PCSK9, SCARB1, APOM	8.99645

Annotation Cluster 11 Enrichment Score: 1.6913029208310866

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006820~anion transport	13	SLC38A4, FXYD3, CLCN2, SLC22A7, ENPP3, EDN1, SLC26A3, P2RX7, CA9, SLC2A2, ATP8B1, FABP1, SLC27A2	5.60860

Annotation Cluster 13 Enrichment Score: 1.5268110759756994

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	7	CEBPA, FAXDC2, PCSK9, SCARB1, CYP8B1, AKR1D1, CYP19A1	3.76578

Annotation Cluster 15 Enrichment Score: 1.5031679529098019

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0036293~response to decreased oxygen levels	11	CA9, CTGF, SLC6A4, EDN1, FABP1, WTIP, CCNA2, PPARGC1A, CITED2, PCK1, ANGPTL4	1.66895
GOTERM_BP_FAT	GO:0070482~response to oxygen levels	11	CA9, CTGF, SLC6A4, EDN1, FABP1, WTIP, CCNA2, PPARGC1A, CITED2, PCK1, ANGPTL4	2.65386
GOTERM_BP_FAT	GO:0071456~cellular response to hypoxia	7	CA9, EDN1, FABP1, CCNA2, PPARGC1A, CITED2, PCK1	4.21825
GOTERM_BP_FAT	GO:0001666~response to hypoxia	10	CA9, SLC6A4, EDN1, FABP1, WTIP, CCNA2, PPARGC1A, CITED2, PCK1, ANGPTL4	4.87406
GOTERM_BP_FAT	GO:0036294~cellular response to decreased oxygen levels	7	CA9, EDN1, FABP1, CCNA2, PPARGC1A, CITED2, PCK1	5.42572
GOTERM_BP_FAT	GO:0071453~cellular response to oxygen levels	7	CA9, EDN1, FABP1, CCNA2, PPARGC1A, CITED2, PCK1	7.55552

SUPPLEMENTARY TABLE 2

Complete list of BPs related to the GOEA for the genes significantly up-regulated and down-regulated by Cu treatment in ATP7B-ko HepG2 cells.

GOEA was performed on up- and down-regulated genes (threshold of FDR<0,05 and LogFC>2) in the QuantSeq experiment on ATP7B-deficient HepG2 cells treated with Cu. The data in this table were collected by using DAVID online tool restricting the output to BP_FAT terms: the BPs up-regulated and down-regulated are highlighted in red and in green, respectively.

UP-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 7.25740230044955

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006614~SRP-dependent cotranslational protein targeting to membrane	31	RPL18, SRP14, RPL36A, RPL15, SRP19, RPS29, RPL7, RPL9, RPLP0, RPL10, RPL11, RPL10A,	1.95E-12
GOTERM_BP_FAT	GO:0006613~cotranslational protein targeting to membrane	32	RPL18, SRP14, RPL36A, RPL15, SRP19, RPS29, RPL7, RPLP0, RPL9, RPL10, RPL11, RPL10A,	1.95E-12
GOTERM_BP_FAT	GO:0045047~protein targeting to ER	32	RPL18, SRP14, RPL36A, RPL15, SRP19, RPS29, RPL7, RPL9, RPLP0, RPL10, RPL11, RPL10A,	2.82E-12
GOTERM_BP_FAT	GO:0072599~establishment of protein localization to endoplasmic reticulum	32	RPL18, SRP14, RPL36A, RPL15, SRP19, RPS29, RPL7, RPL9, RPLP0, RPL10, RPL11, RPL10A,	8.68E-12
GOTERM_BP_FAT	GO:0070972~protein localization to endoplasmic reticulum	34	RPL18, SRP14, RPL36A, RPL15, SRP19, UBAC2, RPS29, RPL7, RPLP0, RPL9, RPL10, RPL11,	3.58E-11
GOTERM_BP_FAT	GO:0019083~viral transcription	37	RPL18, POLR2G, POLR2F, RPL36A, POLR2K, RPL15, TRIM11, PFN1, RPS29, RPL7, RAE1, RP	1.06E-08
GOTERM_BP_FAT	GO:0019080~viral gene expression	37	RPL18, POLR2G, POLR2F, RPL36A, POLR2K, RPL15, TRIM11, PFN1, RPS29, RPL7, RAE1, RP	6.34E-08
GOTERM_BP_FAT	GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	29	RPL18, RPL36A, RPL15, RPL7, RPS29, RPL9, RPLP0, RPL10, RPL11, RPL10A, RPS21, RPS23,	8.78E-08
GOTERM_BP_FAT	GO:0033365~protein localization to organelle	97	RPL18, SRP14, RPL36A, IL18, RPL15, SAE1, PMAIP1, SRP19, FLCN, PRDX1, AKR1C3, HSPH1	9.20E-08
GOTERM_BP_FAT	GO:0072594~establishment of protein localization to organelle	78	RPL18, SRP14, RPL36A, IL18, RPL15, SAE1, PMAIP1, SRP19, PRDX1, AKR1C3, HSPH1, STA	1.90E-07
GOTERM_BP_FAT	GO:0044033~multi-organism metabolic process	38	RPL18, POLR2G, POLR2F, RPL36A, POLR2K, RPL15, TRIM11, PFN1, RPS29, RPL7, RAE1, RP	3.89E-07
GOTERM_BP_FAT	GO:0006612~protein targeting to membrane	35	RPL18, SRP14, RPL36A, RPL15, PIP5K1A, SRP19, GOLGA7, RPS29, RPL7, RPLP0, RPL9, RPL	8.25E-07
GOTERM_BP_FAT	GO:0000956~nuclear-transcribed mRNA catabolic process	35	RPL18, POLR2G, RPL36A, RPL15, ZFP36L1, RPS29, RPL7, RPLP0, RPL9, ZC3H12A, RPL10, R	7.35E-06
GOTERM_BP_FAT	GO:0006401~RNA catabolic process	39	RPL18, POLR2G, RPL36A, RPL15, OAS2, ZFP36L1, RPS29, RPL7, RPLP0, RPL9, ZC3H12A, R	8.64E-06
GOTERM_BP_FAT	GO:0006413~translational initiation	33	RPL18, POLR2G, RPL36A, RPL15, RPS29, RPL7, RPLP0, RPL9, CDC123, RPL10, RPL11, RPL1	1.11E-05
GOTERM_BP_FAT	GO:0006402~mRNA catabolic process	36	RPL18, POLR2G, RPL36A, RPL15, ZFP36L1, RPS29, RPL7, RPLP0, RPL9, ZC3H12A, RPL10, R	1.32E-05
GOTERM_BP_FAT	GO:0016072~rRNA metabolic process	41	RPL18, RPL36A, GAR1, RPL15, PIN4, EBNA1BP2, RPS29, RPL7, RPLP0, RPL9, RPL10, RPL11	1.55E-05
GOTERM_BP_FAT	GO:0090150~establishment of protein localization to membrane	49	RPL18, SRP14, RPL36A, RPL15, PMAIP1, PIP5K1A, SRP19, LRRC15, GOLGA7, TMEM59, RP	1.69E-05
GOTERM_BP_FAT	GO:0034655~nucleobase-containing compound catabolic process	50	RPL18, RPL36A, HINT1, RPL15, RPLP0, RPL10, DERA, RPL11, DEDD2, RPS27A, RPL35A, M	1.73E-05
GOTERM_BP_FAT	GO:1902582~single-organism intracellular transport	75	RPL18, SRP14, RPL36A, IL18, RPL15, UCHL1, STOML2, AP3S1, PIP5K1A, SRP19, PRDX1, R	1.74E-05
GOTERM_BP_FAT	GO:0006364~rRNA processing	39	RPL18, RPL36A, GAR1, RPL15, PIN4, EBNA1BP2, RPS29, RPL7, RPLP0, RPL9, RPL10, RPL11	7.37E-05
GOTERM_BP_FAT	GO:0046700~heterocycle catabolic process	51	RPL18, RPL36A, HINT1, RPL15, HMOX1, RPLP0, RPL10, DERA, RPL11, DEDD2, RPS27A, RP	8.28E-05
GOTERM_BP_FAT	GO:0006605~protein targeting	73	RPL18, SRP14, RPL36A, IL18, RPL15, SAE1, PIP5K1A, SRP19, PRDX1, AKR1C3, GOLGA7, ST	1.21E-04
GOTERM_BP_FAT	GO:0044270~cellular nitrogen compound catabolic process	51	RPL18, RPL36A, HINT1, RPL15, HMOX1, RPLP0, RPL10, DERA, RPL11, DEDD2, RPS27A, RP	1.41E-04
GOTERM_BP_FAT	GO:0019439~aromatic compound catabolic process	51	RPL18, RPL36A, HINT1, RPL15, HMOX1, RPLP0, RPL10, DERA, RPL11, DEDD2, RPS27A, RP	2.07E-04
GOTERM_BP_FAT	GO:0019058~viral life cycle	53	RPL18, RPL36A, CHMP5, CHMP7, RPL15, RAB1B, LRRC15, RAB1A, SLC1A5, RAE1, RPLP0,	3.39E-04
GOTERM_BP_FAT	GO:1901361~organic cyclic compound catabolic process	52	RPL18, RPL36A, HINT1, RPL15, HMOX1, RPLP0, RPL10, DERA, RPL11, DEDD2, RPS27A, RP	4.09E-04
GOTERM_BP_FAT	GO:0051641~cellular localization	192	RPL18, SRP14, RPL36A, CHMP5, IL18, RPL15, CHMP7, EIF5A, SNRPD2, RAB1B, STOML2, S	4.28E-04
GOTERM_BP_FAT	GO:0008104~protein localization	186	RPL18, SRP14, RPL36A, CHMP5, IL18, RPL15, CHMP7, EIF5A, RAB1B, SAE1, ANKRD1, PMA	4.87E-04
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	132	RPL18, SRP14, RPL36A, IL18, RPL15, EIF5A, SAE1, PMAIP1, SRP19, FLCN, FNTA, STARD7,	0.00100442
GOTERM_BP_FAT	GO:0042254~ribosome biogenesis	42	RPL18, RPL36A, GAR1, RPL15, PIN4, EBNA1BP2, RPS29, RRN3, RPL7, RPLP0, RPL9, RPL10,	0.0011679
GOTERM_BP_FAT	GO:0033036~macromolecule localization	206	RPL18, CHMP5, RPL15, CHMP7, EDN1, RAB1B, STOML2, RAB1A, RAE1, RPLP0, U2AF1, RP	0.00150514
GOTERM_BP_FAT	GO:0034613~cellular protein localization	130	RPL18, SRP14, RPL36A, IL18, RPL15, EIF5A, SAE1, PMAIP1, SRP19, FLCN, FNTA, STARD7,	0.00182362
GOTERM_BP_FAT	GO:0046907~intracellular transport	129	RPL18, SRP14, RPL36A, CHMP5, IL18, RPL15, RAB1B, SNRPD2, STOML2, EIF5A, SAE1, SRP	0.00245502
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	156	RPL18, SRP14, RPL36A, CHMP5, IL18, RPL15, CHMP7, EIF5A, RAB1B, SAE1, ANKRD1, PMA	0.00258682
GOTERM_BP_FAT	GO:0034470~ncRNA processing	47	RPL18, RPL36A, GAR1, RPL15, PIN4, EBNA1BP2, TRMT44, RPS29, RPL7, RPLP0, RPL9, CTU	0.00314445
GOTERM_BP_FAT	GO:0043604~amide biosynthetic process	71	RPL18, RPL36A, SGMS2, RPL15, EIF5A, IGHMBP2, RPLP0, RPL10, RPL11, YRDC, MRPL39,	0.00329689
GOTERM_BP_FAT	GO:1902580~single-organism cellular localization	96	RPL18, SRP14, RPL36A, IL18, SYNJ1, UCHL1, RPL15, AP3S1, STOML2, PMAIP1, PIP5K1A, S	0.00371777
GOTERM_BP_FAT	GO:0072657~protein localization to membrane	52	RPL18, SRP14, RPL36A, RPL15, PIP5K1A, PMAIP1, LRRC15, SRP19, GOLGA7, FNTA, TMEM	0.00691756
GOTERM_BP_FAT	GO:0043043~peptide biosynthetic process	65	RPL18, RPL36A, RPL15, EIF5A, IGHMBP2, RPLP0, RPL10, RPL11, YRDC, MRPL39, MRPL34,	0.00700091
GOTERM_BP_FAT	GO:0006412~translation	63	RPL18, RPL36A, RPL15, EIF5A, IGHMBP2, RPLP0, RPL10, RPL11, YRDC, MRPL39, MRPL34,	0.00766177
GOTERM_BP_FAT	GO:0006396~RNA processing	81	RPL18, RPL36A, ZMAT5, GAR1, RPL15, SNRPD2, BUD31, RBM4B, EBNA1BP2, RPLP0, CTU	0.01258815
GOTERM_BP_FAT	GO:0015031~protein transport	142	RPL18, SRP14, RPL36A, CHMP5, IL18, CHMP7, RPL15, EIF5A, RAB1B, SAE1, ANKRD1, SRP	0.01558537
GOTERM_BP_FAT	GO:0051649~establishment of localization in cell	151	RPL18, SRP14, RPL36A, CHMP5, IL18, RPL15, CHMP7, EIF5A, SNRPD2, RAB1B, STOML2, S	0.01570883
GOTERM_BP_FAT	GO:0034660~ncRNA metabolic process	56	RPL18, RPL36A, GAR1, RPL15, EBNA1BP2, RPLP0, CTU2, RPL10, RPL11, YRDC, MRPL39, R	0.02885477
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	63	RPL18, RPL36A, ZMAT5, RPL15, SNRPD2, BUD31, RBM4B, RPLP0, U2AF1, RPL10, ZRSR1,	0.03375934
GOTERM_BP_FAT	GO:0016032~viral process	83	RPL18, RPL36A, CHMP5, RPL15, CHMP7, RAB1B, PMAIP1, LRRC15, MMP1, RAB1A, RTN3,	0.03469301
GOTERM_BP_FAT	GO:0044403~symbiosis, encompassing mutualism through parasitism	85	RPL18, RPL36A, CHMP5, RPL15, CHMP7, RAB1B, PMAIP1, LRRC15, MMP1, RAB1A, RTN3,	0.03881524
GOTERM_BP_FAT	GO:0044419~interspecies interaction between organisms	85	RPL18, RPL36A, CHMP5, RPL15, CHMP7, RAB1B, PMAIP1, LRRC15, MMP1, RAB1A, RTN3,	0.03881524
GOTERM_BP_FAT	GO:0044764~multi-organism cellular process	83	RPL18, RPL36A, CHMP5, RPL15, CHMP7, RAB1B, PMAIP1, LRRC15, MMP1, RAB1A, RTN3,	0.0453292
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	86	RPL18, SRP14, RPL36A, IL18, RPL15, AP3S1, EIF5A, SAE1, PIP5K1A, SRP19, PRDX1, AKR1C	0.04789453
GOTERM_BP_FAT	GO:0022613~ribonucleoprotein complex biogenesis	48	RPL18, RPL36A, STRAP, GAR1, RPL15, SNRPD2, PIN4, EBNA1BP2, RPS29, RRN3, RPL7, RPL	0.08385318
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	81	RPL18, RPL36A, SGMS2, RPL15, EIF5A, IGHMBP2, RBM4B, PICALM, RPLP0, RPL10, YRDC,	0.26680088
GOTERM_BP_FAT	GO:0044802~single-organism membrane organization	72	RPL18, SRP14, RPL36A, RPL15, CHMP7, STOML2, PIP5K1A, PMAIP1, SRP19, LRRC15, GOL	0.37367884
GOTERM_BP_FAT	GO:1901566~organonitrogen compound biosynthetic process	104	RPL18, RPL36A, SGMS2, EDN1, RPL15, STOML2, EIF5A, FLCN, IGHMBP2, ELOVL5, RPLP0,	0.46847939
GOTERM_BP_FAT	GO:0061024~membrane organization	82	RPL18, SRP14, RPL36A, CHMP5, RPL15, CHMP7, STOML2, RAB1B, PIP5K1A, PMAIP1, SRP	0.47232881
GOTERM_BP_FAT	GO:0006518~peptide metabolic process	67	RPL18, RPL36A, RPL15, EIF5A, IGHMBP2, PICALM, RPLP0, RPL10, RPL11, YRDC, MRPL39,	0.94140138

Annotation Cluster 2 Enrichment Score: 5.390958697534641

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0070887~cellular response to chemical stimulus	204	OSER1, EDN1, FSTL3, B2M, RAE1, RPLP0, SERPINE1, H2AFZ, HTRA3, GNG5, C5AR1, RAN,	3.32E-05
GOTERM_BP_FAT	GO:0010033~response to organic substance	212	RPL15, EDN1, FSTL3, B2M, RAE1, RPLP0, SERPINE1, H2AFZ, HTRA3, GNG5, C5AR1, CRYAB	1.17E-04
GOTERM_BP_FAT	GO:0071310~cellular response to organic substance	169	GABRB3, IL18, EDN1, FSTL3, CBX3, ANKRD1, FLCN, B2M, FNTA, CDKN2B, RAE1, RPLP0, SE	7.17E-04
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	111	GABRB3, EDN1, FSTL3, CBX3, ANKRD1, FLCN, FNTA, CDKN2B, RPLP0, HTRA3, GNG5, RPS2	1.96852508
GOTERM_BP_FAT	GO:0071495~cellular response to endogenous stimulus	86	ATP6V0E1, GABRB3, EDN1, FSTL3, CBX3, AP3S1, ANKRD1, FLCN, BUD31, AKR1C3, MAX,	5.60812914

Annotation Cluster 3 Enrichment Score: 4.224078268194712

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008219~cell death	151	GABRB3, EDN1, JAG2, EIF5A, ANKRD1, PMAIP1, MMP3, FLCN, UBQLN1, IL11, CLPTM1L,	0.00426242
GOTERM_BP_FAT	GO:0006915~apoptotic process	137	GABRB3, EDN1, JAG2, EIF5A, ANKRD1, PMAIP1, FLCN, UBQLN1, IL11, CLPTM1L, SHB, FNT	0.00598663
GOTERM_BP_FAT	GO:0012501~programmed cell death	143	GABRB3, EDN1, JAG2, EIF5A, ANKRD1, PMAIP1, FLCN, UBQLN1, IL11, CLPTM1L, TOP1, SH	0.00788541
GOTERM_BP_FAT	GO:0010941~regulation of cell death	118	GABRB3, EDN1, ANKRD1, PMAIP1, MMP3, UBQLN1, FLCN, IL11, PICALM, CDKN2D, SERPI	0.03917157
GOTERM_BP_FAT	GO:0042981~regulation of apoptotic process	109	GABRB3, EDN1, ANKRD1, PMAIP1, UBQLN1, FLCN, IL11, CDKN2D, SERPINE1, ROBO4, TPT	0.10191642
GOTERM_BP_FAT	GO:0097190~apoptotic signaling pathway	55	HINT1, PMAIP1, UBQLN1, FLCN, HSPH1, TMEM109, RRN3, BAG3, HMOX1, CDKN2D, TICA	0.10606556
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	109	GABRB3, EDN1, ANKRD1, PMAIP1, UBQLN1, FLCN, IL11, CDKN2D, SERPINE1, ROBO4, TPT	0.15183093
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptotic process	65	NUAK2, GABRB3, EDN1, IL11, HSPH1, RRN3, CDKN2D, HMOX1, BAG3, SERPINE1, TPT1, R	2.46814967
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	65	NUAK2, GABRB3, EDN1, IL11, HSPH1, RRN3, CDKN2D, HMOX1, BAG3, SERPINE1, TPT1, R	3.50165834
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	69	NUAK2, GABRB3, EDN1, IL11, HSPH1, TMEM109, RRN3, BAG3, HMOX1, CDKN2D, SERPIN	3.99407366

Annotation Cluster 4 Enrichment Score: 3.703779366832255

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0071294~cellular response to zinc ion	10	MT1M, MT1A, MT2A, MT1E, MT1B, MT1H, MT1X, MT1G, KCNK3, MT1F	3.73E-04
GOTERM_BP_FAT	GO:0071276~cellular response to cadmium ion	9	AKR1C3, SUMO1, MT1A, HMOX1, MT1E, MT1H, MT1X, MT1G, MT1F	0.00196006
GOTERM_BP_FAT	GO:0046686~response to cadmium ion	11	AKR1C3, SUMO1, MT1A, SLC30A1, HMOX1, MT1E, MT1H, MT1X, MT1G, MT1F, B2M	0.13269139
GOTERM_BP_FAT	GO:0071248~cellular response to metal ion	20	MT1M, EDN1, FSTL3, FOSB, JUNB, MT1X, KCNK3, B2M, AKR1C3, FOS, SUMO1, MT1A, JU	0.15854847
GOTERM_BP_FAT	GO:0071241~cellular response to inorganic substance	21	MT1M, EDN1, FSTL3, FOSB, MMP3, JUNB, MT1X, KCNK3, B2M, AKR1C3, FOS, SUMO1, M	0.43196206
GOTERM_BP_FAT	GO:0010043~response to zinc ion	11	MT1M, MT1A, SLC30A1, MT2A, MT1E, MT1B, MT1H, MT1X, MT1G, KCNK3, MT1F	0.96928181

Annotation Cluster 5 Enrichment Score: 3.5246479791950236

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	101	RPL18, SGSH, SCPEP1, RPL36A, COPS3, RPL15, UCHL1, PMAIP1, MYLIP, UBQLN1, KLHL28,	3.02E-07
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	112	SCPEP1, RPL18, RPL36A, RPL15, MYLIP, PMAIP1, UBQLN1, SERPINE2, RPLP0, RPL10, RPL1	1.15E-05
GOTERM_BP_FAT	GO:0051443~positive regulation of ubiquitin-protein transferase activity	22	BMI1, TRIB3, CDC20, SKP1, UBE2N, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, P	1.81E-04
GOTERM_BP_FAT	GO:0031398~positive regulation of protein ubiquitination	30	BMI1, TRIB3, FKBP1A, SPRTN, NHLRC1, UBQLN1, PSMB4, PSMB7, PSMB1, TICAM1, PSM	2.26E-04

GOTERM_BP_FAT	GO:0002223~stimulatory C-type lectin receptor signaling pathway	22	NFKBIA, SKP1, UBE2N, PSMA1, PSMB4, NRAS, PSMB7, PSMD13, UBE2D2, PSMB1, PSMC4	2.56E-04
GOTERM_BP_FAT	GO:0002220~innate immune response activating cell surface receptor signaling pathwa	22	NFKBIA, SKP1, UBE2N, PSMA1, PSMB4, NRAS, PSMB7, PSMD13, UBE2D2, PSMB1, PSMC4	3.59E-04
GOTERM_BP_FAT	GO:1903322~positive regulation of protein modification by small protein conjugation o	31	BMI1, TRIB3, FKBP1A, SPRTN, NHLRC1, UBQLN1, PSMB4, PSMB7, PSMB1, TICAM1, ZC3H	4.28E-04
GOTERM_BP_FAT	GO:1904668~positive regulation of ubiquitin protein ligase activity	19	CDC20, SKP1, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5, UBC,	4.63E-04
GOTERM_BP_FAT	GO:0051437~positive regulation of ubiquitin-protein ligase activity involved in regulatio	18	CDC20, SKP1, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5, UBC,	7.49E-04
GOTERM_BP_FAT	GO:1904666~regulation of ubiquitin protein ligase activity	19	CDC20, SKP1, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5, UBC,	9.86E-04
GOTERM_BP_FAT	GO:0031145~anaphase-promoting complex-dependent catabolic process	18	CDC20, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5, UBC, PSMD	0.00134589
GOTERM_BP_FAT	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	45	SYVN1, ABTB2, UCHL1, TRIB3, RFFL, NHLRC1, UBQLN1, PSMB4, RNF126, PSMB7, UBE2D3	0.0014746
GOTERM_BP_FAT	GO:0002479~antigen processing and presentation of exogenous peptide antigen via MH	16	NCF2, ITGB5, HLA-F, B2M, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11,	0.00153685
GOTERM_BP_FAT	GO:0071356~cellular response to tumor necrosis factor	34	ZFAND6, TNFRSF21, TNFRSF12A, EDN1, ANKRD1, RFFL, CCL26, ZFP36L1, CALCA, PSMB4,	0.00158682
GOTERM_BP_FAT	GO:0050852~T cell receptor signaling pathway	27	TNFRSF21, STOML2, NFKBIA, SHB, PSMB4, PSMB7, UBE2D2, PSMB1, PSMD3, UBE2D1, T	0.00160104
GOTERM_BP_FAT	GO:0051438~regulation of ubiquitin-protein transferase activity	22	BMI1, TRIB3, CDC20, SKP1, UBE2N, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, P	0.00228262
GOTERM_BP_FAT	GO:0033209~tumor necrosis factor-mediated signaling pathway	24	TNFRSF21, TNFRSF12A, CD40, RFFL, BIRC3, PSMA1, PSMB4, TNFRSF9, PSMB7, PSMD13,	0.0023182
GOTERM_BP_FAT	GO:0042590~antigen processing and presentation of exogenous peptide antigen via MH	16	NCF2, ITGB5, HLA-F, B2M, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11,	0.00290658
GOTERM_BP_FAT	GO:0034612~response to tumor necrosis factor	35	ZFAND6, TNFRSF21, TNFRSF12A, EDN1, ANKRD1, RFFL, CCL26, GCH1, ZFP36L1, CALCA, P	0.00309343
GOTERM_BP_FAT	GO:0010498~proteasomal protein catabolic process	46	SYVN1, ABTB2, UCHL1, TRIB3, RFFL, NHLRC1, PMAIP1, UBQLN1, PSMB4, RNF126, PSMB7	0.00433047
GOTERM_BP_FAT	GO:0051436~negative regulation of ubiquitin-protein ligase activity involved in mitotic	16	CDC20, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PSMD	0.00771718
GOTERM_BP_FAT	GO:0044248~cellular catabolic process	128	SCPEP1, RPL18, RPL36A, GNPDA1, RPL15, MYLIP, PMAIP1, UBQLN1, RPLP0, MIOX, DERA,	0.00828893
GOTERM_BP_FAT	GO:0000209~protein polyubiquitination	33	SYVN1, RFFL, NHLRC1, MYLIP, PSMB4, RNF126, PSMB7, UBE2D3, UBE2D2, PSMB1, RNF1	0.00914903
GOTERM_BP_FAT	GO:0051439~regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	16	CDC20, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PSMD	0.00927325
GOTERM_BP_FAT	GO:2000060~positive regulation of protein ubiquitination involved in ubiquitin-depend	18	CDC20, SKP1, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5, UBC,	0.01058867
GOTERM_BP_FAT	GO:1904667~negative regulation of ubiquitin protein ligase activity	16	CDC20, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PSMD	0.01110317
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	41	UCHL1, DUSP10, TRIB3, SFN, LRRC15, GPRC5A, PAQR3, PSMB4, SHB, PSMB7, PSMB1, CD	0.01452378
GOTERM_BP_FAT	GO:0038095~Fc-epsilon receptor signaling pathway	26	PPP3R1, NFKBIA, FOS, PSMB4, PSMB7, UBE2D2, PSMB1, PSMD3, TRAF6, UBE2D1, RPS27	0.01901247
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	58	COPS3, UCHL1, MYLIP, UBQLN1, KLHL28, PSMD3, KLHL21, FBXL15, KLHL20, RPS27A, PSM	0.02294758
GOTERM_BP_FAT	GO:1903320~regulation of protein modification by small protein conjugation or remova	34	BMI1, TRIB3, FKBP1A, SPRTN, NHLRC1, UBQLN1, PSMB4, PSMB7, PSMB1, TICAM1, PSMD	0.02374394
GOTERM_BP_FAT	GO:0038061~NIK/NF-kappaB signaling	19	SKP1, BIRC3, PSMA1, PSMB4, PSMB7, PSMD13, TNFRSF10B, PSMC4, PSMB1, PSMD11, P	0.02605402
GOTERM_BP_FAT	GO:1903052~positive regulation of proteolysis involved in cellular protein catabolic pro	25	TRIB3, UBQLN1, PSMB4, SUMO1, PSMB7, PSMB1, RNF166, PSMD3, UBE2D1, RPS27A, PS	0.02619061
GOTERM_BP_FAT	GO:0031396~regulation of protein ubiquitination	32	BMI1, TRIB3, FKBP1A, SPRTN, NHLRC1, UBQLN1, PSMB4, PSMB7, PSMB1, TICAM1, PSMD	0.02655232
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	57	COPS3, UCHL1, MYLIP, UBQLN1, KLHL28, PSMD3, KLHL21, FBXL15, KLHL20, RPS27A, PSM	0.03040391
GOTERM_BP_FAT	GO:0051444~negative regulation of ubiquitin-protein transferase activity	16	CDC20, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PSMD	0.03573223
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	56	COPS3, UCHL1, MYLIP, UBQLN1, KLHL28, PSMD3, KLHL21, FBXL15, KLHL20, RPS27A, PSM	0.04083011
GOTERM_BP_FAT	GO:2000058~regulation of protein ubiquitination involved in ubiquitin-dependent prote	18	CDC20, SKP1, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5, UBC,	0.04462137
GOTERM_BP_FAT	GO:1903364~positive regulation of cellular protein catabolic process	25	TRIB3, UBQLN1, PSMB4, SUMO1, PSMB7, PSMB1, RNF166, PSMD3, UBE2D1, RPS27A, PS	0.10623938
GOTERM_BP_FAT	GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic p	28	SYVN1, ABTB2, MYLIP, RFFL, PSMB4, RNF126, PSMB7, PSMB1, KLHL28, KLHL21, PSMD3,	0.10672855
GOTERM_BP_FAT	GO:0044772~mitotic cell cycle phase transition	50	CHMP7, CCNE2, PPP1R1C, CDKN2B, CDKN2D, PSMD3, FBXL15, CDCA5, RPS27A, PSMD9,	0.11489296
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	60	SCPEP1, COPS3, UCHL1, MYLIP, PMAIP1, UBQLN1, KLHL28, PSMD3, KLHL21, FBXL15, KLH	0.11688945
GOTERM_BP_FAT	GO:0090263~positive regulation of canonical Wnt signaling pathway	19	WNT2B, JUP, PSMA1, PSMB4, PSMB7, PSMD13, CTDNEP1, PSMB1, PSMC4, PSMD11, NR	0.14190112
GOTERM_BP_FAT	GO:0034097~response to cytokine	69	IL18, EDN1, SYNJ1, ANKRD1, LRRC15, B2M, FOS, RPLP0, IL4R, PSMD3, FOSL1, TUBA1B, R	0.19074377
GOTERM_BP_FAT	GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	16	NCF2, ITGB5, HLA-F, B2M, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11,	0.19406342
GOTERM_BP_FAT	GO:0038093~Fc receptor signaling pathway	29	PPP3R1, NFKBIA, ACTG1, FOS, PSMB4, PSMB7, UBE2D2, PSMB1, PSMD3, BRK1, UBE2D1,	0.203588
GOTERM_BP_FAT	GO:0006521~regulation of cellular amino acid metabolic process	12	PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5, PSMD3, PSME3, PS	0.21140836
GOTERM_BP_FAT	GO:0033238~regulation of cellular amine metabolic process	14	NR4A2, HPRT1, PSMB4, PSMA1, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, PSM	0.25624087
GOTERM_BP_FAT	GO:0060071~Wnt signaling pathway, planar cell polarity pathway	17	RYK, PSMA1, PFN1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PS	0.33005213
GOTERM_BP_FAT	GO:0090090~negative regulation of canonical Wnt signaling pathway	22	EGR1, SDHAF2, DDIT3, PSMA1, PSMB4, RGS20, PSMB7, PSMD13, PSMB1, PSMC4, PSMD	0.36913657
GOTERM_BP_FAT	GO:0050851~antigen receptor-mediated signaling pathway	27	TNFRSF21, STOML2, NFKBIA, SHB, PSMB4, PSMB7, UBE2D2, PSMB1, PSMD3, UBE2D1, T	0.41845665
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	60	SCPEP1, COPS3, UCHL1, MYLIP, PMAIP1, UBQLN1, KLHL28, PSMD3, KLHL21, FBXL15, KLH	0.42748916
GOTERM_BP_FAT	GO:0090175~regulation of establishment of planar polarity	17	RYK, PSMA1, PFN1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PS	0.45746009
GOTERM_BP_FAT	GO:0043488~regulation of mRNA stability	20	RBM24, EXOSC3, ZFP36L1, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11,	0.50312871
GOTERM_BP_FAT	GO:0044770~cell cycle phase transition	50	CHMP7, CCNE2, PPP1R1C, CDKN2B, CDKN2D, PSMD3, FBXL15, CDCA5, RPS27A, PSMD9,	0.51434153
GOTERM_BP_FAT	GO:0043487~regulation of RNA stability	20	RBM24, EXOSC3, ZFP36L1, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11,	0.91924552
GOTERM_BP_FAT	GO:0060828~regulation of canonical Wnt signaling pathway	27	SDHAF2, PSMB4, PSMB7, PSMB1, NRARP, PSMD3, EMD, RPS27A, PSMD9, EGR1, DDIT3,	0.9935512
GOTERM_BP_FAT	GO:0002758~innate immune response-activating signal transduction	27	NFKBIA, UBQLN1, PSMB4, UBE2D3, PSMB7, UBE2D2, PSMB1, TICAM1, PSMD3, UBE2D1,	1.12594868
GOTERM_BP_FAT	GO:0030163~protein catabolic process	66	SCPEP1, COPS3, UCHL1, MYLIP, PMAIP1, UBQLN1, SERPINE2, KLHL28, PSMD3, KLHL21, F	1.26529694
GOTERM_BP_FAT	GO:1901990~regulation of mitotic cell cycle phase transition	32	SFN, ZFP36L1, RPA2, PSMB4, PSMB7, PSMB1, CDKN2B, PPP1R1C, PSMD3, UBE2D1, CDC	1.28603092
GOTERM_BP_FAT	GO:0031331~positive regulation of cellular catabolic process	29	POLR2G, ABHD5, TRIB3, UBQLN1, ZFP36L1, PSMB4, SUMO1, PSMB7, RNF166, PSMB1, P	1.30679458
GOTERM_BP_FAT	GO:0007164~establishment of tissue polarity	17	RYK, PSMA1, PFN1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PS	1.47984265
GOTERM_BP_FAT	GO:0001736~establishment of planar polarity	17	RYK, PSMA1, PFN1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PS	1.47984265
GOTERM_BP_FAT	GO:0001738~morphogenesis of a polarized epithelium	18	RYK, PSMA1, PFN1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PS	1.63935199
GOTERM_BP_FAT	GO:0002218~activation of innate immune response	27	NFKBIA, UBQLN1, PSMB4, UBE2D3, PSMB7, UBE2D2, PSMB1, TICAM1, PSMD3, UBE2D1,	1.71789451
GOTERM_BP_FAT	GO:0030178~negative regulation of Wnt signaling pathway	23	EGR1, SDHAF2, DDIT3, PSMA1, PSMB4, RGS20, PSMB7, PSMD13, PSMB1, PSMC4, PSMD	2.13431654
GOTERM_BP_FAT	GO:1901987~regulation of cell cycle phase transition	33	SFN, ZFP36L1, RPA2, PSMB4, PSMB7, PSMB1, CDKN2B, PPP1R1C, CDKN2D, PSMD3, UBE	2.13867939
GOTERM_BP_FAT	GO:0071345~cellular response to cytokine stimulus	58	IL18, EDN1, ANKRD1, LRRC15, B2M, RPLP0, IL4R, PSMD3, TUBA1B, RPS27A, PSMD9, EGR	2.24216432
GOTERM_BP_FAT	GO:0060070~canonical Wnt signaling pathway	29	SDHAF2, PSMB4, PSMB7, PSMB1, NRARP, PSMD3, RPS27A, PSMD9, EGR1, RYK, NR4A2,	2.51424856
GOTERM_BP_FAT	GO:1903050~regulation of proteolysis involved in cellular protein catabolic process	25	TRIB3, UBQLN1, PSMB4, SUMO1, PSMB7, PSMB1, RNF166, PSMD3, UBE2D1, RPS27A, PS	2.53031965
GOTERM_BP_FAT	GO:0045732~positive regulation of protein catabolic process	27	TRIB3, MYLIP, UBQLN1, PSMB4, SUMO1, PSMB7, RNF166, PSMB1, SEC22B, PSMD3, UBE	2.55289501
GOTERM_BP_FAT	GO:0030177~positive regulation of Wnt signaling pathway	19	WNT2B, JUP, PSMA1, PSMB4, PSMB7, PSMD13, CTDNEP1, PSMB1, PSMC4, PSMD11, NR	2.78632287
GOTERM_BP_FAT	GO:0002768~immune response-regulating cell surface receptor signaling pathway	37	TNFRSF21, PPP3R1, NFKBIA, STOML2, ACTG1, PSMB4, FOS, SHB, PSMB7, UBE2D2, PSMB	2.82002172
GOTERM_BP_FAT	GO:0035567~non-canonical Wnt signaling pathway	19	RYK, PPP3R1, PSMA1, PSMB4, PFN1, PSMB7, PSMD13, PSMB1, PSMC4, PSMD11, PSMA5	2.9964168
GOTERM_BP_FAT	GO:0032446~protein modification by small protein conjugation	69	BMI1, UFC1, SAE1, LRR1, MYLIP, SPRTN, UBQLN1, TOP1, RAE1, KLHL28, MED27, TICAM1,	3.04285534
GOTERM_BP_FAT	GO:0045862~positive regulation of proteolysis	34	CCK, TRIB3, PMAIP1, UBQLN1, PSMB4, PSMB7, SUMO1, PICALM, PSMB1, RNF166, PSMD	3.12559264
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	43	CKS1B, CHMP5, EDN1, SAE1, ASNS, SFN, HECA, ZFP36L1, RPA2, PSMB4, SHB, PSMB7, PSM	3.33872041
GOTERM_BP_FAT	GO:1903362~regulation of cellular protein catabolic process	26	TRIB3, MYLIP, UBQLN1, PSMB4, SUMO1, PSMB7, RNF166, PSMB1, PSMD3, UBE2D1, RPS	3.84186591
GOTERM_BP_FAT	GO:0016567~protein ubiquitination	61	BMI1, SAE1, LRR1, MYLIP, SPRTN, UBQLN1, KLHL28, TICAM1, MED27, PSMD3, KLHL21, F	3.86460956
GOTERM_BP_FAT	GO:0070647~protein modification by small protein conjugation or removal	77	BMI1, COPS3, UCHL1, UFC1, SAE1, LRR1, SPRTN, MYLIP, UBQLN1, TOP1, RAE1, KLHL28,	4.81185687
GOTERM_BP_FAT	GO:0002478~antigen processing and presentation of exogenous peptide antigen	19	NCF2, ITGB5, DCTN6, HLA-F, B2M, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PS	4.86316204
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	41	POLR2G, EIF5A, SESN2, ZNF706, ZFP36L1, PSMB4, RBM4B, PSMB7, PSMB1, CDC123, PSM	5.0536975
GOTERM_BP_FAT	GO:0009896~positive regulation of catabolic process	31	POLR2G, ABHD5, TRIB3, MYLIP, UBQLN1, ZFP36L1, PSMB4, SUMO1, PSMB7, PSMB1, RN	6.70148251
GOTERM_BP_FAT	GO:0031397~negative regulation of protein ubiquitination	16	CDC20, PSMA1, PSMB4, PSMB7, PSMD13, PSMC4, PSMB1, PSMD11, PSMA5, UBC, PSMD	6.89525128
GOTERM_BP_FAT	GO:0019884~antigen processing and presentation of exogenous antigen	19	NCF2, ITGB5, DCTN6, HLA-F, B2M, PSMA1, PSMB4, PSMB7, PSMD13, PSMB1, PSMC4, PS	7.573238
GOTERM_BP_FAT	GO:2000027~regulation of organ morphogenesis	25	B4GALT1, RYK, PDGFA, EDN1, SOX8, WNT2B, PSMA1, PSMB4, PFN1, PSMB7, PSMD13, P	8.17106413
GOTERM_BP_FAT	GO:0080134~regulation of response to stress	91	PDGFA, IL18, EDN1, ANKRD1, PMAIP1, MMP3, UBQLN1, PRDX1, B2M, HSPH1, LBH, SERP	8.19959391
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	43	KRT6A, PDGFA, EDN1, JAG2, SDC4, SOX8, SRF, PSMB4, PFN1, PSMB7, PSMB1, NRARP, PS	9.52243209

Annotation Cluster 6 Enrichment Score: 3.150160293353892

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006914~autophagy	44	ATP6V0E1, UCHL1, RAB1B, ATP6V1B2, NHLRC1, ATP6V1G1, UBQLN1, SESN2, FLCN, ZBTB	0.05565227
GOTERM_BP_FAT	GO:0016241~regulation of macroautophagy	16	ATP6V0E1, UCHL1, RAB1B, ATP6V1H, ATP6V1B2, ATP6V1G1, SESN2, ATP6V1D, CAPN1,	4.75233923
GOTERM_BP_FAT	GO:0010506~regulation of autophagy	26	ATP6V0E1, UCHL1, RAB1B, ATP6V1G1, ATP6V1B2, FLCN, ZBTB17, SESN2, MAP1LC3B, TM	9.3472162

Annotation Cluster 7 Enrichment Score: 3.0770077569126846

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	95	EDN1, UCHL1, FSTL3, UBQLN1, LRRC15, FLCN, IL11, HSPH1, SERPINE2, RRN3, HEY1, HMO	0.11303917
GOTERM_BP_FAT	GO:0023057~negative regulation of signaling	95	EDN1, UCHL1, FSTL3, UBQLN1, LRRC15, FLCN, IL11, HSPH1, SERPINE2, RRN3, HEY1, HMO	0.12605194
GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	86	UCHL1, FSTL3, UBQLN1, LRRC15, FLCN, HSPH1, SERPINE2, RRN3, HEY1, HMOX1, CDKN2D	0.45619516
GOTERM_BP_FAT	GO:0009966~regulation of signal transduction	183	PDGFA, IL18, FAM110C, EDN1, FSTL3, JAG2, ANKRD1, PMAIP1, FLCN, UBQLN1, IL11, SHB	1.05305401
GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	98	PDGFA, EDN1, FSTL3, UBQLN1, FLCN, SERPINE2, CDKN2D, SERPINE1, TPT1, HTRA3, RPS2	4.28699917
GOTERM_BP_FAT	GO:0023051~regulation of signaling	197	ATP1B2, CHMP5, FAM110C, EDN1, FSTL3, SHB, SERPINE2, SERPINE1, HTRA3, ARC, C5AR1	5.12487176
GOTERM_BP_FAT	GO:0010646~regulation of cell communication	194	FAM110C, EDN1, FSTL3, SHB, SERPINE2, SERPINE1, HTRA3, ARC, C5AR1, PIM3, CD40, PIN	5.46858801

Annotation Cluster 8 Enrichment Score: 2.918984351983277

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044085~cellular component biogenesis	206	RPL18, HCCS, CHMP5, FAM110C, PDLIM5, EDN1, RPL15, CHMP7, AURKC, RAB1B, STOML	0.01541509

GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	175	HCCS, MORF4L1, CHMP5, MORF4L2, CHMP7, AURKC, NDUFAB1, CBX3, EIF5A, STOML2, F	0.07202074
GOTERM_BP_FAT	GO:0071822~protein complex subunit organization	126	HCCS, CHMP5, CHMP7, NDUFAB1, RAB1B, STOML2, EIF5A, PMAIP1, MMP3, SRP19, MM	0.11247507
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	120	HCCS, NDUFAB1, SNRPD2, RAB1B, STOML2, PMAIP1, MMP3, SRP19, MMP1, RAB1A, IGH	2.57680311
GOTERM_BP_FAT	GO:0006461~protein complex assembly	103	HCCS, NDUFAB1, RAB1B, STOML2, PMAIP1, MMP3, SRP19, MMP1, RAB1A, IGHMBP2, PI	3.7527528
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	103	HCCS, NDUFAB1, RAB1B, STOML2, PMAIP1, MMP3, SRP19, MMP1, RAB1A, IGHMBP2, PI	3.81535936
GOTERM_BP_FAT	GO:0022607~cellular component assembly	169	HCCS, CHMP5, PDGFA, LRTM2, CHMP7, EDN1, AURKC, NDUFAB1, SNRPD2, RAB1B, STO	8.65239661

Annotation Cluster 9 Enrichment Score: 2.8113154223381662

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0034645~cellular macromolecule biosynthetic process	330	RPL18, RPL15, EDN1, FSTL3, STOML2, SPRTN, SIN3B, PICALM, RPLP0, SERPINE1, INSIG1,	0.00607987
GOTERM_BP_FAT	GO:0034654~nucleobase-containing compound biosynthetic process	288	RPL18, RPL15, EDN1, FSTL3, STOML2, SPRTN, SIN3B, PICALM, RAE1, RPLP0, SERPINE1, IN	0.03103797
GOTERM_BP_FAT	GO:0019438~aromatic compound biosynthetic process	291	RPL18, RPL15, EDN1, FSTL3, STOML2, SPRTN, SIN3B, PICALM, RAE1, RPLP0, SERPINE1, IN	0.04046398
GOTERM_BP_FAT	GO:0018130~heterocycle biosynthetic process	290	RPL18, RPL15, EDN1, FSTL3, STOML2, SPRTN, SIN3B, PICALM, RAE1, RPLP0, SERPINE1, IN	0.04363118
GOTERM_BP_FAT	GO:0010467~gene expression	340	RPL18, RPL15, EDN1, FSTL3, STOML2, SIN3B, PICALM, SERPINE2, RAE1, RPLP0, SERPINE1	0.04993063
GOTERM_BP_FAT	GO:0031325~positive regulation of cellular metabolic process	198	EDN1, FSTL3, RAB1B, STOML2, SPRTN, RAB1A, PICALM, INSIG1, SERPINE1, H2AFZ, C5AR1	0.06037214
GOTERM_BP_FAT	GO:0009893~positive regulation of metabolic process	208	EDN1, FSTL3, RAB1B, STOML2, MYLIP, SPRTN, RAB1A, PICALM, INSIG1, SERPINE1, H2AFZ	0.144154
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	256	RPL18, RPL15, EDN1, FSTL3, SIN3B, PICALM, RAE1, RPLP0, INSIG1, SERPINE1, MED27, H2	0.22505146
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	193	EDN1, FSTL3, RAB1B, STOML2, SPRTN, MYLIP, RAB1A, PICALM, SERPINE1, INSIG1, H2AFZ	0.49382133
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	125	PDGFA, IL18, EDN1, MORF4L2, FSTL3, STOML2, EIF5A, ANKRD1, FLCN, IL11, BATF, GABPE	0.63793834
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	127	PDGFA, IL18, EDN1, MORF4L2, FSTL3, STOML2, EIF5A, ANKRD1, FLCN, IL11, BATF, GABPE	0.64047595
GOTERM_BP_FAT	GO:0016070~RNA metabolic process	294	RPL18, RPL15, EDN1, FSTL3, SIN3B, PICALM, RAE1, RPLP0, SERPINE1, INSIG1, MED27, U2	0.72027373
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	127	PDGFA, IL18, EDN1, MORF4L2, FSTL3, STOML2, EIF5A, ANKRD1, FLCN, IL11, BATF, GABPE	0.72629038
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	116	PDGFA, IL18, EDN1, MORF4L2, FSTL3, STOML2, EIF5A, ANKRD1, FLCN, IL11, BATF, GABPE	0.94235779
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase-containing compound metabolic proces	119	PDGFA, IL18, EDN1, MORF4L2, FSTL3, STOML2, ANKRD1, FLCN, IL11, BATF, GABPB1, PIC	1.19113835
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	101	IL18, EDN1, MORF4L2, FSTL3, ANKRD1, FLCN, IL11, BATF, GABPB1, PICALM, CDKN2B, SE	3.87802861
GOTERM_BP_FAT	GO:1902680~positive regulation of RNA biosynthetic process	98	IL18, EDN1, MORF4L2, FSTL3, ANKRD1, FLCN, IL11, BATF, GABPB1, PICALM, CDKN2B, SE	4.28699917
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	123	IL18, EDN1, MORF4L2, FSTL3, ANKRD1, FLCN, CBX6, IL11, BATF, GABPB1, SIN3B, CDKN2B	8.10770509
GOTERM_BP_FAT	GO:0051171~regulation of nitrogen compound metabolic process	270	EDN1, FSTL3, STOML2, SIN3B, PICALM, SERPINE1, INSIG1, MED27, H2AFZ, HTRA3, ZNF39	8.71818661

Annotation Cluster 10 Enrichment Score: 2.374788602332973

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0035966~response to topologically incorrect protein	25	HERPUD1, HSP90AA1, SYVN1, UFD1L, ASNS, ZBTB17, SERPINH1, DDIT3, RNF126, HSPH1,	0.12625118
GOTERM_BP_FAT	GO:0006986~response to unfolded protein	22	HERPUD1, HSP90AA1, SYVN1, ASNS, ZBTB17, SERPINH1, DDIT3, HSPH1, CTH, DNAJB9, SE	0.65638993
GOTERM_BP_FAT	GO:0036499~PERK-mediated unfolded protein response	7	HERPUD1, ATF3, TMEM33, ASNS, IGFBP1, PPP1R15A, DDIT3	1.19563653
GOTERM_BP_FAT	GO:0034976~response to endoplasmic reticulum stress	26	SYVN1, UFC1, TRIB3, ASNS, PMAIP1, ZBTB17, SESN2, UBQLN1, UBAC2, TMEM33, SDF2, H	9.3472162

Annotation Cluster 11 Enrichment Score: 2.364698909661039

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB signaling	27	ZFAND6, IL18, NFKBIA, TFG, FKBP1A, PRDX1, TMEM9B, HMOX1, TICAM1, ZC3H12A, TRA	0.81991721
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling	21	GOLT1B, IL18, TFG, FKBP1A, CD40, PIM2, BIRC3, AJUBA, UBE2N, CCR7, CTH, TNFRSF10B,	3.33184448
GOTERM_BP_FAT	GO:0007249~I-kappaB kinase/NF-kappaB signaling	26	IL18, NFKBIA, TFG, FKBP1A, PRDX1, TMEM9B, HMOX1, TICAM1, ZC3H12A, TRAF6, TRAF5	5.26348552

Annotation Cluster 12 Enrichment Score: 2.3149399812594837

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0043620~regulation of DNA-templated transcription in response to stress	15	EGR1, CEBPB, SESN2, DDIT3, RGS14, UBE2D3, UBE2D2, ATF3, JUN, HMOX1, UBC, UBB, U	0.03141166
GOTERM_BP_FAT	GO:0043618~regulation of transcription from RNA polymerase II promoter in response	14	EGR1, CEBPB, SESN2, DDIT3, UBE2D3, UBE2D2, ATF3, JUN, HMOX1, UBC, UBB, UBE2D1,	0.0627299

Annotation Cluster 13 Enrichment Score: 2.22002725826548

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0042981~regulation of apoptotic process	109	GABRB3, EDN1, ANKRD1, PMAIP1, UBQLN1, FLCN, IL11, CDKN2D, SERPINE1, ROBO4, TPT	0.10191642
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	109	GABRB3, EDN1, ANKRD1, PMAIP1, UBQLN1, FLCN, IL11, CDKN2D, SERPINE1, ROBO4, TPT	0.15183093

Annotation Cluster 14 Enrichment Score: 2.061799976563238

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0031668~cellular response to extracellular stimulus	22	GABARAPL1, NUAK2, CBL, NR4A2, PIM1, ASNS, MAP1LC3B2, PMAIP1, SRF, WNT2B, AKR1	2.11605024
GOTERM_BP_FAT	GO:0071496~cellular response to external stimulus	27	NUAK2, ASNS, ANKRD1, PMAIP1, SRF, AKR1C3, MAX, FOS, CDKN2B, MAP1LC3B, HMOX1,	2.55289501
GOTERM_BP_FAT	GO:0031669~cellular response to nutrient levels	19	GABARAPL1, NUAK2, CBL, PIM1, ASNS, MAP1LC3B2, PMAIP1, SRF, WNT2B, AKR1C3, MA	3.97226441

Annotation Cluster 15 Enrichment Score: 2.0043744143496194

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044772~mitotic cell cycle phase transition	50	CHMP7, CCNE2, PPP1R1C, CDKN2B, CDKN2D, PSMD3, FBXL15, CDCA5, RPS27A, PSMD9,	0.11489296
GOTERM_BP_FAT	GO:0044770~cell cycle phase transition	50	CHMP7, CCNE2, PPP1R1C, CDKN2B, CDKN2D, PSMD3, FBXL15, CDCA5, RPS27A, PSMD9,	0.51434153
GOTERM_BP_FAT	GO:1901990~regulation of mitotic cell cycle phase transition	32	SFN, ZFP36L1, RPA2, PSMB4, PSMB7, PSMB1, CDKN2B, PPP1R1C, PSMD3, UBE2D1, CDC	1.28603092
GOTERM_BP_FAT	GO:1901987~regulation of cell cycle phase transition	33	SFN, ZFP36L1, RPA2, PSMB4, PSMB7, PSMB1, CDKN2B, PPP1R1C, CDKN2D, PSMD3, UBE	2.13867939
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	43	CKS1B, CHMP5, EDN1, SAE1, ASNS, SFN, HECA, ZFP36L1, RPA2, PSMB4, SHB, PSMB7, PS	3.33872041
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	74	CHMP5, EDN1, AURKC, SAE1, FLCN, CCNE2, SHB, PPP1R1C, CDKN2B, CDKN2D, PSMD3, K	3.94098377
GOTERM_BP_FAT	GO:1903047~mitotic cell cycle process	67	CHMP5, CHMP7, EDN1, AURKC, CCNE2, PPP1R1C, CDKN2B, RAE1, OIP5, CDKN2D, PSMD	7.62760769

Annotation Cluster 16 Enrichment Score: 1.897550804460445

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0045445~myoblast differentiation	12	CXCL14, KCNAB1, IL18, HINFP, DLL1, ASB2, ID3, MBNL1, SOX8, SRF, IFRD1, DDIT3	3.08214864

Annotation Cluster 17 Enrichment Score: 1.7022120599348385

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	35	OSER1, TRA2B, EDN1, ROMO1, MMP3, SESN2, UBQLN1, GCLM, PRDX1, PXN, GCH1, AKR1	7.49449276

Annotation Cluster 18 Enrichment Score: 1.6820320427702862

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051128~regulation of cellular component organization	157	PDGFA, CHMP5, PDLIM5, FAM110C, LRTM2, EDN1, EIF5A, RAB1B, STOML2, SAE1, ANKR	2.08548557

Annotation Cluster 19 Enrichment Score: 1.6813677470313535

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	53	PDGFA, EDN1, JAG2, ANKRD1, SDC4, HEY1, PSMD3, RPS27A, PSMD9, CYR61, ACTA1, EFN	1.70834051
GOTERM_BP_FAT	GO:2000027~regulation of organ morphogenesis	25	B4GALT1, RYK, PDGFA, EDN1, SOX8, WNT2B, PSMA1, PSMB4, PFN1, PSMB7, PSMD13, PS	8.17106413
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	43	KRT6A, PDGFA, EDN1, JAG2, SDC4, SOX8, SRF, PSMB4, PFN1, PSMB7, PSMB1, NRARP, PS	9.52243209

Annotation Cluster 20 Enrichment Score: 1.643790014949071

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0022411~cellular component disassembly	43	CHMP5, CHMP7, SYNJ1, EIF5A, MMP3, DDR2, MMP1, TIMP1, MRPL13, LAMB3, TOMM7,	5.01295921

Annotation Cluster 21 Enrichment Score: 1.6220767626667298

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0071560~cellular response to transforming growth factor beta stimulus	25	STRAP, EDN1, ITGB5, FKBP1A, ANKRD1, FLCN, PXN, ZFP36L1, FOS, FNTA, CDKN2B, HTRA	0.85813783
GOTERM_BP_FAT	GO:0071559~response to transforming growth factor beta	25	STRAP, EDN1, ITGB5, FKBP1A, ANKRD1, FLCN, PXN, ZFP36L1, FOS, FNTA, CDKN2B, HTRA	0.98297726
GOTERM_BP_FAT	GO:0070848~response to growth factor	54	IER2, EDN1, FSTL3, ANKRD1, FLCN, FOS, FNTA, CDKN2B, ZYX, HTRA3, FBXL15, RPS27A, C	1.53626841
GOTERM_BP_FAT	GO:0071363~cellular response to growth factor stimulus	52	EDN1, FSTL3, ANKRD1, FLCN, FOS, FNTA, CDKN2B, ZYX, HTRA3, FBXL15, RPS27A, CYR61,	1.89700814
GOTERM_BP_FAT	GO:0071495~cellular response to endogenous stimulus	86	ATP6V0E1, GABRB3, EDN1, FSTL3, CBX3, AP3S1, ANKRD1, FLCN, BUD31, AKR1C3, MAX, F	5.60812914
GOTERM_BP_FAT	GO:0007179~transforming growth factor beta receptor signaling pathway	18	DAND5, STRAP, CBL, ITGB5, FKBP1A, FLCN, PXN, FOS, FNTA, CDKN2B, JUN, UBC, UBB, HT	9.15848091

Annotation Cluster 22 Enrichment Score: 1.6135344288120044

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:2001233~regulation of apoptotic signaling pathway	35	SYVN1, TNFRSF12A, PPP3R1, RFFL, PMAIP1, SFN, FLCN, UBQLN1, GCLM, HSPH1, RRN3, H	4.28151167

Annotation Cluster 23 Enrichment Score: 1.606069456180373

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	41	UCHL1, DUSP10, TRIB3, SFN, LRRC15, GPRC5A, PAQR3, PSMB4, SHB, PSMB7, PSMB1, CD	0.01452378
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	107	PDGFA, FAM110C, IL18, EDN1, JAG2, ANKRD1, PMAIP1, FLCN, IL11, SHB, TMEM9B, CDK	0.52313962
GOTERM_BP_FAT	GO:0035556~intracellular signal transduction	180	PDGFA, IL18, FAM110C, EDN1, RRAD, RAB1B, ANKRD1, PMAIP1, FLCN, UBQLN1, RAB1A,	0.74384913
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	51	UCHL1, FLCN, LRRC15, SHB, HSPH1, PPP1R1C, CDKN2B, TMEM59, CDKN2D, PSMD3, RPS	0.99913773
GOTERM_BP_FAT	GO:0009966~regulation of signal transduction	183	PDGFA, IL18, FAM110C, EDN1, FSTL3, JAG2, ANKRD1, PMAIP1, FLCN, UBQLN1, IL11, SHB	1.05305401
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	112	PDGFA, IL18, FAM110C, EDN1, JAG2, ANKRD1, PMAIP1, FLCN, IL11, SHB, TMEM9B, SERP	1.53310488
GOTERM_BP_FAT	GO:0023056~positive regulation of signaling	112	PDGFA, IL18, FAM110C, EDN1, JAG2, ANKRD1, PMAIP1, FLCN, IL11, SHB, TMEM9B, SERP	1.90445962
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	73	BMI1, PDGFA, IL18, EDN1, UCHL1, LRRC15, SDC4, DDR2, CCNE2, SHB, HSPH1, PPP1R1C,	3.38943028
GOTERM_BP_FAT	GO:0000165~MAPK cascade	65	PDGFA, IL18, EDN1, UCHL1, FLCN, PRDX1, IL11, HSPH1, PSMD3, ARHGAP8, RPS27A, PSM	4.84040156
GOTERM_BP_FAT	GO:0023051~regulation of signaling	197	ATP1B2, CHMP5, FAM110C, EDN1, FSTL3, SHB, SERPINE2, SERPINE1, HTRA3, ARC, C5AR1	5.12487176
GOTERM_BP_FAT	GO:0010646~regulation of cell communication	194	FAM110C, EDN1, FSTL3, SHB, SERPINE2, SERPINE1, HTRA3, ARC, C5AR1, PIM3, CD40, PI	5.46858801
GOTERM_BP_FAT	GO:0032269~negative regulation of cellular protein metabolic process	74	EDN1, UCHL1, LRRC15, FLCN, SHB, HSPH1, PICALM, SERPINE2, PPP1R1C, CDKN2B, TME	5.82422716
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	77	EDN1, UCHL1, LRRC15, FLCN, SHB, HSPH1, PICALM, SERPINE2, PPP1R1C, CDKN2B, TME	7.19130323
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	135	PDGFA, IL18, FAM110C, EDN1, JAG2, STOML2, ANKRD1, PMAIP1, MMP3, FLCN, UBQLN1	8.74287198
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	153	PDGFA, IL18, EDN1, EIF5A, MYLIP, SPRTN, PMAIP1, FLCN, UBQLN1, IL11, SHB, FNTA, PIC	9.80006312

Annotation Cluster 24 Enrichment Score: 1.5635270032256903

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	33	KCNAB1, PDLIM5, IL18, MORF4L2, EDN1, UCHL1, ANKRD1, SOX8, SRF, ZFP36L1, ACTG1,	6.7495698

Annotation Cluster 25 Enrichment Score: 1.5597241389029672

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0016236~macroautophagy	22	LAMTOR3, GABARAPL1, RAB1B, SNAPIN, MAP1LC3B2, SESN2, UBQLN1, RNF103-CHMP3,	5.38696054

Annotation Cluster 26 Enrichment Score: 1.548273864428586

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0061061~muscle structure development	49	JPH2, KCNAB1, IL18, PDLIM5, UCHL1, MORF4L2, EDN1, FKBP1A, ANKRD1, SRF, SOX8, AC	4.39752705

Annotation Cluster 27 Enrichment Score: 1.5183982814561725

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	41	POLR2G, EIF5A, SESN2, ZNF706, ZFP36L1, PSMB4, RBM4B, PSMB7, PSMB1, CDC123, PS	5.0536975

DOWN-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 6.20143299215114

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006629~lipid metabolic process	75	ALDH8A1, PTGES2, STAR, NAAA, EHHADH, ARSI, TTPA, ARSK, ACOT1, ST6GALNAC4, PTG	3.51E-06
GOTERM_BP_FAT	GO:0044255~cellular lipid metabolic process	58	ALDH8A1, PTGES2, STAR, EHHADH, ARSI, ARSK, ACOT1, ST6GALNAC4, PTGES, MCEE, AP	5.96E-04
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	33	ALDH8A1, PTGES2, STAR, ST6GALNAC4, PTGES, APOA5, PLA2G1B, INPP5E, PCYT2, LIPT2,	0.81565729

Annotation Cluster 2 Enrichment Score: 4.491230859297726

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0032787~monocarboxylic acid metabolic process	43	ALDH8A1, CYP2U1, ACADSB, PTGES2, STAR, EHHADH, ACOT1, AGXT, GALK1, PTGES, MC	4.45E-06
GOTERM_BP_FAT	GO:0019752~carboxylic acid metabolic process	50	ALDH8A1, CYP2U1, ACADSB, PTGES2, STAR, GLUD2, EHHADH, ACOT1, AGXT, ARG1, GAL	4.01E-04
GOTERM_BP_FAT	GO:0043436~oxoacid metabolic process	50	ALDH8A1, CYP2U1, ACADSB, PTGES2, STAR, GLUD2, EHHADH, ACOT1, AGXT, ARG1, GAL	4.80E-04
GOTERM_BP_FAT	GO:0006082~organic acid metabolic process	53	ALDH8A1, PTGES2, STAR, CNDP2, EHHADH, ACOT1, AGXT, PTGES, MCEE, APOA5, ATP8B	4.81E-04
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	27	CYP2U1, ACADSB, PTGES2, EHHADH, ACOT1, PTGES, MCEE, APOA5, PLA2G1B, CYGB, LIP	0.01514204
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	33	ALDH8A1, PTGES2, STAR, ST6GALNAC4, PTGES, APOA5, PLA2G1B, INPP5E, PCYT2, LIPT2,	0.81565729
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	19	ACSM2B, ALDH8A1, PTGES2, STAR, FAXDC2, GLUD2, ACSM2A, AMACR, CDO1, AGXT, ML	1.13851411
GOTERM_BP_FAT	GO:0072330~monocarboxylic acid biosynthetic process	14	ACSM2B, PTGES2, STAR, FAXDC2, ACSM2A, AMACR, AGXT, PTGES, MLYCD, APOA5, PLA2	3.19360386
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	17	ACSM2B, PTGES2, STAR, FAXDC2, GLUD2, ACSM2A, AMACR, AGXT, MLYCD, PTGES, APO	4.04199302
GOTERM_BP_FAT	GO:0044283~small molecule biosynthetic process	25	ALDH8A1, ACSM2B, PTGES2, STAR, FAXDC2, GLUD2, AMACR, ACSM2A, GPER1, CDO1, A	6.87484334

Annotation Cluster 3 Enrichment Score: 2.6429665397303688

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006687~glycosphingolipid metabolic process	9	ENPP7, ST6GALNAC4, BAX, ARSI, SUMF1, ARSA, ARSK, SMPD2, NEU4	1.35015631
GOTERM_BP_FAT	GO:0006664~glycolipid metabolic process	11	PGAP3, ENPP7, PIGZ, ST6GALNAC4, BAX, ARSI, SUMF1, ARSA, ARSK, SMPD2, NEU4	2.60002453
GOTERM_BP_FAT	GO:1903509~liposaccharide metabolic process	11	PGAP3, ENPP7, PIGZ, ST6GALNAC4, BAX, ARSI, SUMF1, ARSA, ARSK, SMPD2, NEU4	3.13433191
GOTERM_BP_FAT	GO:0006643~membrane lipid metabolic process	14	PGAP3, ENPP7, PIGZ, SPTLC3, ARSI, ARSK, ALDH3B1, ST6GALNAC4, BAX, ARSA, SUMF1, B	6.99441271

Annotation Cluster 4 Enrichment Score: 2.546345097661939

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044282~small molecule catabolic process	27	ACADSB, GLUD2, EHHADH, SNX17, FUT6, AGXT, ARG1, GALK1, GALM, MCEE, HAAO, GST	0.00422217
GOTERM_BP_FAT	GO:0044712~single-organism catabolic process	45	ACADSB, ENPP7, GLUD2, FUT6, SNX17, EHHADH, AGXT, STUB1, GALK1, ARG1, GALM, NT	0.03860327
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	19	AADAT, ACADSB, SULT2A1, ACADS, GLUD2, EHHADH, BCKDHB, AMACR, HAL, CRAT, CDO	0.06882506
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	17	AADAT, ACADSB, SULT2A1, ACADS, GLUD2, EHHADH, AMACR, HAL, CRAT, CDO1, AGXT,	0.15113288
GOTERM_BP_FAT	GO:1901565~organonitrogen compound catabolic process	24	AADAT, HYAL1, PAOX, NUDT18, ACADSB, ENPP7, GLUD2, CNDP2, BCKDHB, HAL, PDE4C,	0.27576213
GOTERM_BP_FAT	GO:1901605~alpha-amino acid metabolic process	14	AADAT, ADSSL1, GLUD2, HAL, CDO1, AGXT, ARG1, HAAO, GSTZ1, GPT, GAMT, DAO, GN	4.80688314
GOTERM_BP_FAT	GO:1901606~alpha-amino acid catabolic process	8	AADAT, ARG1, GLUD2, HAAO, GSTZ1, GPT, DAO, AGXT	8.16721782

Annotation Cluster 5 Enrichment Score: 2.3619764055836705

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0015711~organic anion transport	20	SLC38A4, RAB3A, SLC13A5, SLCO4C1, SLC22A9, SLC6A12, SLC22A7, MPC1, STARD10, SLC	3.34165134
GOTERM_BP_FAT	GO:0015849~organic acid transport	11	ARG1, SLC38A4, SLC13A5, SLC22A9, SLC6A12, ATP8B1, ACE2, SLC51B, SLCO2B1, SLC27A	3.53637243
GOTERM_BP_FAT	GO:0006820~anion transport	24	FXYD1, SLC38A4, RAB3A, SLC13A5, SLCO4C1, SLC22A9, SLC6A12, SLC22A7, MPC1, STARD	8.2547594

Annotation Cluster 6 Enrichment Score: 2.0629261720152567

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0030195~negative regulation of blood coagulation	8	KNG1, F12, FGG, FGA, SERPINF2, KLKB1, TMPRSS6, PROC	0.41589437
GOTERM_BP_FAT	GO:1900047~negative regulation of hemostasis	8	KNG1, F12, FGG, FGA, SERPINF2, KLKB1, TMPRSS6, PROC	0.41589437
GOTERM_BP_FAT	GO:0050819~negative regulation of coagulation	8	KNG1, F12, FGG, FGA, SERPINF2, KLKB1, TMPRSS6, PROC	0.70615702
GOTERM_BP_FAT	GO:0030193~regulation of blood coagulation	10	KNG1, DMTN, F12, FGG, FGA, SERPINF2, KLKB1, F7, TMPRSS6, PROC	0.8368805
GOTERM_BP_FAT	GO:1900046~regulation of hemostasis	10	KNG1, DMTN, F12, FGG, FGA, SERPINF2, KLKB1, F7, TMPRSS6, PROC	0.8368805
GOTERM_BP_FAT	GO:0072378~blood coagulation, fibrin clot formation	6	KNG1, F12, FGG, FGA, KLKB1, F7	0.91620825
GOTERM_BP_FAT	GO:0031638~zymogen activation	7	F12, FGG, FGA, SERPINF2, KLKB1, CYFIP2, CTSH	0.95662914
GOTERM_BP_FAT	GO:0042730~fibrinolysis	6	F12, FGG, FGA, SERPINF2, KLKB1, TMPRSS6	1.1083265
GOTERM_BP_FAT	GO:0050818~regulation of coagulation	10	KNG1, DMTN, F12, FGG, FGA, SERPINF2, KLKB1, F7, TMPRSS6, PROC	1.28042667
GOTERM_BP_FAT	GO:0061045~negative regulation of wound healing	8	KNG1, F12, FGG, FGA, SERPINF2, KLKB1, TMPRSS6, PROC	2.15005336
GOTERM_BP_FAT	GO:0051604~protein maturation	18	TMPRSS2, F12, TFR2, F7, STUB1, PROC, C8A, C8B, FGG, FGA, SERPINF2, KLKB1, TYSND1,	2.2394957
GOTERM_BP_FAT	GO:0031639~plasminogen activation	5	F12, FGG, FGA, SERPINF2, KLKB1	2.79578343
GOTERM_BP_FAT	GO:0016485~protein processing	16	C8A, C8B, F12, TMPRSS2, FGG, FGA, SERPINF2, KLKB1, TYSND1, CYFIP2, ACE2, F7, CASP1,	3.74559167
GOTERM_BP_FAT	GO:1903035~negative regulation of response to wounding	8	KNG1, F12, FGG, FGA, SERPINF2, KLKB1, TMPRSS6, PROC	4.43625613

Annotation Cluster 7 Enrichment Score: 2.0162242046508387

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0019395~fatty acid oxidation	10	ACADSB, MLYCD, ACADS, EHHADH, AMACR, TYSND1, CYGB, CRAT, PPARGC1A, PHYH	2.04547064
GOTERM_BP_FAT	GO:0034440~lipid oxidation	10	ACADSB, MLYCD, ACADS, EHHADH, AMACR, TYSND1, CYGB, CRAT, PPARGC1A, PHYH	2.36908932
GOTERM_BP_FAT	GO:0030258~lipid modification	16	ACADSB, KLB, ERBB3, ACADS, EHHADH, ERBB2, AMACR, CRAT, PHYH, PPARGC1A, MLYC	9.69309693

Annotation Cluster 8 Enrichment Score: 1.8043294148572133

Category	Term	Count	Genes	FDR

GOTERM_BP_FAT	GO:0015914~phospholipid transport	9	ABCG8, ATP9A, ATP10A, APOA5, ATP8B1, STARD10, ABCA2, MTTP, ABCB4	0.48461847
GOTERM_BP_FAT	GO:0015748~organophosphate ester transport	10	ABCG8, G6PC, ATP9A, ATP10A, APOA5, ATP8B1, STARD10, ABCA2, MTTP, ABCB4	0.76545302
GOTERM_BP_FAT	GO:0006869~lipid transport	20	OSBP2, SLC22A9, STAR, ATP10A, ABCA2, STARD10, SLCO2B1, FZD4, MTTP, ABCB4, ABCG	1.69580493
GOTERM_BP_FAT	GO:0010876~lipid localization	21	OSBP2, SLC22A9, STAR, ATP10A, ABCA2, STARD10, SLCO2B1, FZD4, MTTP, ABCB4, ABCG	2.06236221

SUPPLEMENTARY TABLE 3.

Complete list of genes specifically regulated by Cu only in control HepG2 cells.

Significant transcriptional responses to Cu were detected using QuantSeq and compared in control HepG2 and ATP7B-ko HepG2 cells. The table shows the genes, which were significantly (FDR<0,05) up-regulated (red) or down-regulated (green) only in control HepG2 cells.

UP-REGULATED GENES

EnsemblID	GeneSymbol	logFC specific WT+Cu vs WT	FDR specific WT+Cu vs WT
ENSG00000266401.1	RP11-874J12.4	5.501874869	2.06E-05
ENSG00000118160.9	SLC8A2	5.404686921	0.000139388
ENSG00000272141.1	RP11-465B22.8	5.39037471	7.96E-05
ENSG00000196312.7	HIATL2	5.185354298	0.000161381
ENSG00000027075.9	PRKCH	5.167978511	0.000285924
ENSG00000228313.3	CTD-2555K7.4	5.106841772	0.002799715
ENSG00000225807.1	RP11-44M6.1	5.074513123	6.43E-07
ENSG00000240211.1	RP11-758P17.3	4.949007047	0.009239985
ENSG00000243499.1	RPS6P21	4.943223996	0.001890565
ENSG00000259460.1	RP11-128A17.1	4.892191507	0.00078358
ENSG00000271781.1	CTD-2589H19.6	4.882784635	0.001953998
ENSG00000263307.1	RP11-166B2.8	4.760099511	0.003759658
ENSG00000242992.2	FTH1P4	4.757869573	0.011683927
ENSG00000272733.1	KB-208E9.1	4.662292575	0.007240484
ENSG00000123685.4	BATF3	4.600504578	0.020443221
ENSG00000228695.5	CES1P1	4.589886491	7.29E-08
ENSG00000269896.1	RP4-740C4.6	4.546391104	0.003989761
ENSG00000172818.5	OVOL1	4.543247596	0.004084156
ENSG00000213212.3	NCLP1	4.394924377	0.023848753
ENSG00000196189.8	SEMA4A	4.368945615	0.013128062
ENSG00000135605.8	TEC	4.364568542	0.01005794
ENSG00000169169.10	CPT1C	4.352081109	0.01409343
ENSG00000251442.1	RP11-792D21.2	4.333629677	0.00648918
ENSG00000063015.15	SEZ6	4.330867703	0.029860364
ENSG00000112182.10	BACH2	4.326201124	0.012782656
ENSG00000269834.1	CTD-3018O17.3	4.213344806	0.000150787
ENSG00000182404.6	RP1-86D1.3	4.098425405	0.019854877
ENSG00000186977.2	KRTAP19-5	4.089545207	0.024702524
ENSG00000142227.6	EMP3	4.075538129	0.01641879
ENSG00000197114.7	ZGPAT	4.065681149	0.034709873
ENSG00000172346.10	CSDC2	4.058886399	0.025991251
ENSG00000213144.2	RP11-64B16.2	4.003224068	0.000679903
ENSG00000258441.1	LINC00641	3.946436423	6.19E-08
ENSG00000223573.2	TINCR	3.861630232	0.000585476
ENSG00000226835.1	RP11-148B18.3	3.810746149	0.04547642
ENSG00000273076.1	RP3-508I15.22	3.810283399	0.003147631

ENSG00000229423.2	RPL27AP8	3.791311503	0.045435637
ENSG00000114529.8	C3orf52	3.782370934	0.031329202
ENSG00000267462.1	RP11-866E20.3	3.779728638	0.03245495
ENSG00000133392.12	MYH11	3.77605636	0.03362839
ENSG00000123329.13	ARHGAP9	3.740446664	0.000873667
ENSG00000102524.7	TNFSF13B	3.725426627	0.002558039
ENSG00000270408.1	JAG1	3.717246891	0.003832794
ENSG00000170049.5	KCNAB3	3.674642165	0.000593256
ENSG00000113249.8	HAVCR1	3.673928552	0.01552669
ENSG00000242366.2	UGT1A8	3.600737799	0.000584701
ENSG00000228857.2	AC104653.1	3.578357076	3.80E-09
ENSG00000269423.1	CTC-273B12.6	3.568718575	2.02E-06
ENSG00000112149.5	CD83	3.543048829	0.003067291
ENSG00000173267.9	SNCG	3.495565003	0.000102139
ENSG00000181634.7	TNFSF15	3.482513821	0.002608843
ENSG00000176945.12	MUC20	3.476028781	0.000221056
ENSG00000111424.6	VDR	3.42359234	0.004537564
ENSG00000214212.4	C19orf38	3.413677883	0.0001443
ENSG00000249877.1	RP11-706F1.2	3.375892488	0.022812053
ENSG00000268375.1	CTD-2568A17.8	3.363768354	0.016220339
ENSG00000056558.6	TRAF1	3.346959927	0.006723266
ENSG00000243244.1	STON1	3.336991944	0.004902634
ENSG00000178773.10	CPNE7	3.324714656	0.001127425
ENSG00000099957.12	P2RX6	3.307787845	0.028165937
ENSG00000099998.13	GGT5	3.253413396	0.005580184
ENSG00000256229.3	ZNF486	3.24317626	4.98E-05
ENSG00000171786.5	NHLH1	3.215623442	0.008359513
ENSG00000161677.7	JOSD2	3.200740285	0.008377061
ENSG00000116852.10	KIF21B	3.182260586	0.018151482
ENSG00000256294.3	ZNF225	3.168493161	0.009388171
ENSG00000267473.1	AC005789.11	3.151464393	3.62E-05
ENSG00000266088.1	RP5-1028K7.2	3.086664815	0.013355641
ENSG00000173480.6	ZNF417	3.079407107	0.029384658
ENSG00000087258.9	GNAO1	3.06434515	0.024861041
ENSG00000224722.3	RP11-255B23.1	3.017144354	0.003299466
ENSG00000269399.1	CTD-3222D19.7	2.990098969	5.04E-06
ENSG00000261519.2	Y_RNA	2.978159381	0.036095906
ENSG00000091536.12	MYO15A	2.97179863	0.047761622
ENSG00000267475.1	CTD-2538C1.2	2.955495079	0.00012397
ENSG00000187720.10	THSD4	2.952785384	0.047257168
ENSG00000128965.7	CHAC1	2.947085519	0.008746599
ENSG00000271533.1	RP3-368A4.6	2.945684026	0.030403193
ENSG00000083817.8	ZNF416	2.941269123	0.029594085
ENSG00000267222.1	RP11-194N12.2	2.891641613	0.009365501
ENSG00000132837.10	DMGDH	2.890703182	0.042218018
ENSG00000225177.1	RP11-390P2.4	2.887958918	1.88E-12

ENSG00000166750.5	SLFN5	2.885795752	0.007515128
ENSG00000163297.12	ANTXR2	2.852394311	4.19E-09
ENSG00000135502.12	SLC26A10	2.844483191	0.043165874
ENSG00000004776.7	HSPB6	2.841351857	0.040737248
ENSG00000255237.1	RP13-317D12.3	2.782198789	0.004698865
ENSG00000101443.13	WFDC2	2.77867872	0.045617955
ENSG00000186889.5	TMEM17	2.77867741	0.010115287
ENSG00000179698.9	KIAA1875	2.776957697	0.020043299
ENSG00000258768.2	CTD-2292M16.8	2.774985993	0.049018799
ENSG00000006062.9	MAP3K14	2.767927149	8.17E-06
ENSG00000260507.1	RP11-356C4.3	2.747959933	0.002629602
ENSG00000233822.3	HIST1H2BN	2.746942489	0.000169928
ENSG00000215769.4	hsa-mir-6080	2.743321986	0.046897263
ENSG00000273064.1	RP11-474G23.3	2.73152689	0.002405004
ENSG00000187796.9	CARD9	2.729254625	8.09E-05
ENSG00000229816.1	DDX50P1	2.71804503	0.039872089
ENSG00000224114.1	RP11-343H5.4	2.663140179	0.010800642
ENSG00000215154.2	AC141586.5	2.652042249	1.35E-05
ENSG00000172889.11	EGFL7	2.64445276	0.005541407
ENSG00000236404.4	RP11-125B21.2	2.62458692	0.034998141
ENSG00000261278.1	RP11-430C1.2	2.6184099	0.000369854
ENSG00000235005.1	RP11-195M16.1	2.615491249	6.08E-05
ENSG00000249129.1	SUDS3P1	2.606291821	0.046483447
ENSG00000059145.14	UNKL	2.599781471	6.87E-11
ENSG00000186026.6	ZNF284	2.598094407	0.035869182
ENSG00000106686.12	SPATA6L	2.598009366	0.023685295
ENSG00000161692.13	DBF4B	2.595051567	1.62E-05
ENSG00000230590.3	FTX	2.574688208	0.031329202
ENSG00000128165.7	ADM2	2.542387299	3.46E-11
ENSG00000130643.4	CALY	2.531333266	0.011631708
ENSG00000007372.16	PAX6	2.525360829	0.012698735
ENSG00000267042.1	CTD-3193K9.4	2.522584856	0.025745425
ENSG00000254676.1	RP11-727A23.4	2.506676629	0.027354163
ENSG00000048740.13	CELF2	2.500681394	0.006910465
ENSG00000230615.2	RP5-1198O20.4	2.498653865	0.003828832
ENSG00000258904.1	RP11-638I2.2	2.496904175	0.006563605
ENSG00000174194.11	AGAP8	2.496532761	0.038939996
ENSG00000260942.1	CAPN10-AS1	2.483217498	5.61E-07
ENSG00000234912.5	LINC00338	2.481291412	5.28E-06
ENSG00000101098.8	RIMS4	2.474997162	0.000439942
ENSG00000198744.5	RP5-857K21.11	2.460187347	2.20E-08
ENSG00000255198.3	SNHG9	2.446694382	3.48E-14
ENSG00000140450.7	ARRDC4	2.443184802	1.32E-06
ENSG00000103647.8	CORO2B	2.442730143	0.035340602
ENSG00000196361.5	ELAVL3	2.440523678	0.047213901
ENSG00000116883.8	RP11-268J15.5	2.437407341	0.012198975

ENSG00000150672.12	DLG2	2.430987519	0.001668708
ENSG00000265800.1	RP11-649A18.5	2.429081428	0.00034583
ENSG00000258450.1	RP11-649E7.7	2.410709048	0.018957363
ENSG00000130307.7	USHBP1	2.402288166	0.01363093
ENSG00000262902.1	RP11-750B16.1	2.398211832	0.024919547
ENSG00000154040.16	CABYR	2.394944404	0.041380815
ENSG00000224420.3	ADM5	2.388229032	0.011949395
ENSG00000167807.11	CTD-2369P2.10	2.386455533	0.00096394
ENSG00000269410.1	CTB-60E11.4	2.382864248	0.039067753
ENSG00000174353.13	STAG3L3	2.359494157	0.000322401
ENSG00000178150.4	ZNF114	2.335478765	3.30E-05
ENSG00000176826.11	FKBP9L	2.330341867	9.68E-06
ENSG00000204427.7	ABHD16A	2.320657764	0.020863528
ENSG00000266926.1	AC005943.4	2.313706233	0.00636312
ENSG00000225630.1	MTND2P28	2.302790762	0.000282878
ENSG00000197780.5	TAF13	2.302151766	1.06E-07
ENSG00000176593.3	CTD-2368P22.1	2.300423957	3.77E-05
ENSG00000260230.2	FRRS1L	2.295707028	0.001861289
ENSG00000226445.1	XXyac-YX65C7_A.2	2.291208149	0.020863528
ENSG00000205100.2	HSP90AA4P	2.286125912	0.000432354
ENSG00000119411.10	BSPRY	2.277834655	0.037302724
ENSG00000266179.2	RP11-1113L8.6	2.277819351	0.027580895
ENSG00000212694.4	AC084018.1	2.249468942	8.58E-06
ENSG00000100764.9	PSMC1	2.227045905	2.27E-06
ENSG00000249055.1	TBCAP3	2.216796531	0.010719067
ENSG00000182963.5	GJC1	2.192854352	0.012198975
ENSG00000270145.1	CTD-2267D19.6	2.187935141	0.01971825
ENSG00000241506.1	PSMC1P1	2.172330898	1.37E-05
ENSG00000186162.6	CIDECP	2.15713326	2.04E-06
ENSG00000166780.6	C16orf45	2.156741466	0.019729652
ENSG00000117036.7	ETV3	2.144937577	6.08E-05
ENSG00000130544.7	ZNF557	2.140704491	0.001801927
ENSG00000156515.17	HK1	2.13170888	1.56E-07
ENSG00000147852.11	VLDLR	2.123022754	1.86E-07
ENSG00000164620.4	RELL2	2.118722086	0.002148287
ENSG00000198804.2	MT-CO1	2.106972812	9.33E-12
ENSG00000273102.1	AP000569.9	2.102764756	0.031780369
ENSG00000170498.7	KISS1	2.08023762	0.002725851
ENSG00000213073.4	RP11-288H12.3	2.079427286	0.02005668
ENSG00000163093.7	BBS5	2.079068544	0.004094378
ENSG00000064547.9	LPAR2	2.075365172	0.014505049
ENSG00000267197.1	CTC-429L19.3	2.065355732	0.012103765
ENSG00000260742.1	RP11-366L5.1	2.056782559	0.001267357
ENSG00000214900.4	C14orf182	2.052049317	0.012197334
ENSG00000219626.4	FAM228B	2.050531884	0.03823488
ENSG00000224687.1	RASAL2-AS1	2.044760592	8.60E-05

ENSG00000269318.1	AC007292.3	2.023008869	0.008544917
ENSG00000196081.5	ZNF724P	2.020616281	3.74E-06
ENSG00000272769.1	RP11-725P16.2	2.01939342	0.024740233
ENSG00000253833.1	RP11-367E12.4	2.017372312	0.000686354
ENSG00000135378.3	PRRG4	2.002866726	0.044349126
ENSG00000112343.8	TRIM38	1.996129018	5.22E-14
ENSG00000214176.5	PLEKHM1P	1.984517773	0.025773095
ENSG00000178409.9	BEND3	1.983905332	0.016624469
ENSG00000102890.10	ELMO3	1.978704937	0.002319893
ENSG00000012822.11	CALCOCO1	1.977706122	0.001568153
ENSG00000198786.2	MT-ND5	1.968350182	7.43E-09
ENSG00000089199.5	CHGB	1.966860372	0.028954443
ENSG00000256045.1	MTRNR2L10	1.96158128	0.025674476
ENSG00000140682.14	TGFB1I1	1.953831453	0.001709598
ENSG00000150636.11	CCDC102B	1.950443798	0.025459252
ENSG00000197808.7	ZNF461	1.950434577	0.011941692
ENSG00000010310.4	GIPR	1.943865116	0.027136789
ENSG00000110987.4	BCL7A	1.942645056	1.42E-08
ENSG00000248932.1	RP11-319G6.1	1.933492887	0.048746778
ENSG00000260534.1	RP11-1006G14.4	1.925691579	0.024549845
ENSG00000167524.10	SGK494	1.918552772	0.011339548
ENSG00000132376.15	INPP5K	1.918437886	0.004686529
ENSG00000267632.1	RP11-400F19.18	1.916699223	0.001695264
ENSG00000087903.8	RFX2	1.913108056	1.78E-05
ENSG00000105329.5	TGFB1	1.912675372	8.89E-08
ENSG00000261596.1	CTB-31N19.3	1.904297094	0.00143359
ENSG00000048471.9	SNX29	1.893938018	0.020728025
ENSG00000254093.4	PINX1	1.89385942	0.001312532
ENSG00000179532.8	DNHD1	1.890108446	0.007881148
ENSG00000108852.10	MPP2	1.875258582	0.035631037
ENSG00000152439.8	ZNF773	1.875009079	1.15E-08
ENSG00000165643.6	SOHLH1	1.87117398	0.010401016
ENSG00000197291.4	RAMP2-AS1	1.86807609	0.03994699
ENSG00000198892.6	SHISA4	1.866668076	0.034895477
ENSG00000261824.2	LINC00662	1.858879418	5.28E-05
ENSG00000167548.10	KMT2D	1.856064589	0.002634587
ENSG00000255823.1	MTRNR2L8	1.85224728	0.046145936
ENSG00000213683.3	AC002056.3	1.851890865	0.04624228
ENSG00000099250.13	NRP1	1.851536502	5.00E-06
ENSG00000172167.3	MTBP	1.845165483	0.01348125
ENSG00000157601.9	MX1	1.838543805	0.002316091
ENSG00000261716.1	RP11-196G18.22	1.838194338	0.039233653
ENSG00000144852.12	NR1I2	1.837981147	0.000669342
ENSG00000142669.9	SH3BGRL3	1.830550083	9.63E-08
ENSG00000163481.3	RNF25	1.826851998	0.000205025
ENSG00000142396.6	ERVK3-1	1.816717046	0.000120515

ENSG00000271936.1	RP11-443B20.1	1.81335436	0.00113489
ENSG00000106258.9	CYP3A5	1.812280918	0.002454105
ENSG00000233085.1	XXyac-YX65C7_A.3	1.809227593	0.022742488
ENSG00000162734.8	PEA15	1.804584764	7.08E-06
ENSG00000135899.12	SP110	1.802147213	8.52E-08
ENSG00000236753.1	MKLN1-AS2	1.797682498	0.00021928
ENSG00000261118.1	RP11-104N10.1	1.796543136	0.01976013
ENSG00000121716.14	PILRB	1.768330903	0.007515128
ENSG00000127481.10	UBR4	1.755425464	7.56E-05
ENSG00000176473.9	WDR25	1.74986623	0.005889771
ENSG00000105426.10	PTPRS	1.749276149	0.000664212
ENSG00000131018.18	SYNE1	1.749080633	2.87E-05
ENSG00000182324.5	KCNJ14	1.740287093	0.001841633
ENSG00000134013.11	LOXL2	1.740027781	0.01104782
ENSG00000247627.2	MTND4P12	1.731189796	0.001959566
ENSG00000109971.9	HSPA8	1.727025877	2.20E-05
ENSG00000262251.1	RP11-199F11.2	1.72001773	0.00094256
ENSG00000109674.3	NEIL3	1.719631832	0.02252604
ENSG00000197321.10	SVIL	1.719192685	1.43E-05
ENSG00000249119.1	MTND6P4	1.704154041	0.000137189
ENSG00000240695.1	RP11-102M11.1	1.700496419	0.002083326
ENSG00000248527.1	MTATP6P1	1.698475941	0.018486768
ENSG00000124549.10	BTN2A3P	1.696408712	0.010025935
ENSG00000227992.1	AC108463.2	1.694393958	0.000546029
ENSG00000130787.9	HIP1R	1.679893146	0.020786135
ENSG00000227388.2	RP11-112J3.16	1.674694897	0.045608195
ENSG00000119917.9	IFIT3	1.667790142	0.02949282
ENSG00000025039.10	RRAGD	1.662803197	0.028565181
ENSG00000203832.6	NBPF20	1.661003708	0.023281135
ENSG00000170190.11	SLC16A5	1.645175035	0.002649755
ENSG00000118965.10	WDR35	1.623745194	0.026751225
ENSG00000198075.5	SULT1C4	1.618533649	0.033846129
ENSG00000198938.2	MT-CO3	1.617403532	0.000281598
ENSG00000203709.5	C1orf132	1.607987448	0.040214968
ENSG00000139722.2	VPS37B	1.607711049	0.000145051
ENSG00000168488.14	ATXN2L	1.603146797	0.000274959
ENSG00000215319.2	RP11-98L4.1	1.598408687	0.001010509
ENSG00000116922.10	C1orf109	1.598142742	2.17E-05
ENSG00000213928.4	IRF9	1.596243356	0.004446285
ENSG00000136010.9	ALDH1L2	1.5936386	0.002968086
ENSG00000260589.1	RP11-390B4.5	1.593085881	0.039547435
ENSG00000004700.11	RECQL	1.591566382	6.29E-05
ENSG00000173193.9	PARP14	1.577320122	1.59E-08
ENSG00000158615.8	PPP1R15B	1.566412521	0.000519247
ENSG00000164105.3	SAP30	1.564909327	2.02E-09
ENSG00000185753.8	CXorf38	1.561096055	0.003242013

ENSG00000175606.6	TMEM70	1.554576122	0.000201423
ENSG00000156931.11	VPS8	1.551027793	8.29E-06
ENSG00000173545.4	ZNF622	1.539054973	4.56E-06
ENSG00000204569.5	PPP1R10	1.534725185	7.43E-09
ENSG00000249592.1	RP11-440L14.1	1.528983393	0.042608901
ENSG00000143498.13	TAF1A	1.517609039	0.001715458
ENSG00000260796.1	RP11-1348G14.5	1.515668186	0.003394861
ENSG00000250251.2	PKD1P6	1.510638888	0.04897243
ENSG00000110628.9	SLC22A18	1.503395146	0.001077962
ENSG00000110200.4	ANAPC15	1.50176096	7.32E-05
ENSG00000181666.13	HKR1	1.497207393	0.039533655
ENSG00000180385.4	AC034193.5	1.486814354	7.53E-07
ENSG00000176274.6	SLC25A53	1.481941538	0.0209142
ENSG00000213658.6	LAT	1.474967902	0.048474554
ENSG00000176454.9	LPCAT4	1.471301956	0.030848504
ENSG00000127993.10	RBM48	1.464204256	0.000755725
ENSG00000251474.2	RPL32P3	1.463036188	0.001181263
ENSG00000237637.1	FRY-AS1	1.462776338	0.000436901
ENSG00000180573.8	HIST1H2AC	1.457049946	0.004051593
ENSG00000234106.3	RP11-288E14.2	1.453840616	0.02574232
ENSG00000092820.13	EZR	1.439718154	2.32E-06
ENSG00000269640.1	CTD-2521M24.9	1.439188594	0.000703836
ENSG00000124104.14	SNX21	1.438749659	0.008492611
ENSG00000013441.11	CLK1	1.436728997	2.97E-05
ENSG00000214367.3	HAUS3	1.425951971	0.008363494
ENSG00000115902.6	SLC1A4	1.424189018	2.14E-07
ENSG00000132688.10	NES	1.424185174	4.76E-06
ENSG00000160299.12	PCNT	1.419731325	0.000124631
ENSG00000165434.6	PGM2L1	1.418366418	1.60E-06
ENSG00000075391.12	RASAL2	1.411798035	0.000196263
ENSG00000213762.6	ZNF134	1.401378111	0.028557149
ENSG00000101901.6	ALG13	1.394866184	0.025357999
ENSG00000260852.1	FBXL19-AS1	1.39316241	0.02491757
ENSG00000120549.11	KIAA1217	1.390290587	0.000637289
ENSG00000197818.7	SLC9A8	1.389368018	0.000153571
ENSG00000159216.14	RUNX1	1.387796329	0.000351908
ENSG00000198805.7	PNP	1.387299986	0.001907142
ENSG00000074935.9	TUBE1	1.38577674	0.0042367
ENSG00000259529.1	RP11-468E2.4	1.38145815	0.032343731
ENSG00000105321.8	CCDC9	1.376011788	0.000911655
ENSG00000026103.15	FAS	1.373343015	0.008411405
ENSG00000145022.4	TCTA	1.363293184	0.002880323
ENSG00000140830.4	TXNL4B	1.363181817	0.000347993
ENSG00000157227.8	MMP14	1.355409909	0.000151214
ENSG00000243279.2	PRAF2	1.349640931	0.03823488
ENSG00000072786.8	STK10	1.34410724	0.000739084

ENSG00000160688.14	FLAD1	1.335146432	0.00024354
ENSG00000160183.9	TMPRSS3	1.329548209	0.016717718
ENSG00000114473.9	IQCG	1.329452036	0.035464789
ENSG00000111875.7	ASF1A	1.327842886	0.002122746
ENSG00000088305.14	DNMT3B	1.32756971	0.002651042
ENSG00000164171.6	ITGA2	1.323673772	0.000100617
ENSG00000198742.5	SMURF1	1.318073771	0.00011561
ENSG00000112081.12	SRSF3	1.317475056	7.50E-06
ENSG00000214021.11	TTLL3	1.316870657	0.00075664
ENSG00000111331.8	OAS3	1.312411902	0.000162611
ENSG00000112763.11	BTN2A1	1.305924996	0.00051924
ENSG00000179348.7	GATA2	1.30548024	0.001442391
ENSG00000170379.15	FAM115C	1.301732192	0.017303819
ENSG00000228502.1	EEF1A1P11	1.300032266	0.049668579
ENSG00000128692.7	EIF2S2P4	1.298446083	0.001858316
ENSG00000008128.18	CDK11A	1.298376945	0.000100708
ENSG00000132522.11	GPS2	1.298276785	0.001820489
ENSG00000078487.13	ZCWPW1	1.298240895	3.65E-05
ENSG00000168439.12	STIP1	1.297500272	0.000113787
ENSG00000269038.1	AP001462.6	1.296645019	0.043458093
ENSG00000243819.3	RN7SL832P	1.29655561	0.023964884
ENSG00000134955.7	SLC37A2	1.295972979	0.031780369
ENSG00000231742.1	RP11-112L6.4	1.287498341	0.045665098
ENSG00000170776.15	AKAP13	1.285479683	1.66E-05
ENSG00000173442.7	EHBP1L1	1.285416286	0.018563732
ENSG00000272578.1	AP000347.2	1.281930404	0.014505049
ENSG00000004478.5	FKBP4	1.273501332	3.64E-05
ENSG00000161960.10	EIF4A1	1.270199823	0.018317332
ENSG00000267858.1	AC016629.8	1.263493109	0.004084798
ENSG00000117461.10	PIK3R3	1.263011527	0.012747356
ENSG00000132256.14	TRIM5	1.255085371	0.00917115
ENSG00000183044.7	ABAT	1.251851956	4.97E-05
ENSG00000008710.13	PKD1	1.250283255	1.70E-05
ENSG00000107949.12	BCCIP	1.249927769	0.013152891
ENSG00000011243.13	AKAP8L	1.248757442	0.012375493
ENSG00000204519.6	ZNF551	1.248350002	0.000596583
ENSG00000099331.9	MYO9B	1.24629919	0.001230056
ENSG00000142546.9	NOSIP	1.241090736	0.00027232
ENSG00000256525.2	POLG2	1.240981114	0.003193919
ENSG00000100941.4	PNN	1.233719182	0.000649354
ENSG00000125812.11	GZF1	1.230650262	0.004815452
ENSG00000237037.5	NDUFA6-AS1	1.229185844	0.028015627
ENSG00000267680.1	ZNF224	1.225466512	0.023853877
ENSG00000254184.3	TYW1B	1.22348458	0.012731106
ENSG00000123810.3	B9D2	1.222588292	0.003135686
ENSG00000167394.8	ZNF668	1.218969553	0.010290913

ENSG00000203489.3	HMGB1P39	1.216133943	0.001512417
ENSG00000106462.6	EZH2	1.210939631	6.40E-05
ENSG00000177000.6	MTHFR	1.209540366	0.000724363
ENSG00000078124.7	ACER3	1.208254633	0.011999049
ENSG00000130054.4	FAM155B	1.194402875	0.001646179
ENSG00000264112.1	RP11-159D12.2	1.193768979	0.004327976
ENSG00000039560.9	RAI14	1.188593849	2.03E-07
ENSG00000122882.6	ECD	1.188103267	0.008848977
ENSG00000113141.11	IK	1.187735957	0.00266886
ENSG00000108509.16	CAMTA2	1.185600309	0.002094347
ENSG00000173120.10	KDM2A	1.179567075	0.000983891
ENSG00000100416.8	TRMU	1.179270097	0.000430798
ENSG00000198466.8	ZNF587	1.179246947	0.00233602
ENSG00000152443.8	ZNF776	1.177343752	0.008379801
ENSG00000013364.14	MVP	1.176342372	0.002010596
ENSG00000137364.4	TPMT	1.175006729	0.011119736
ENSG00000136490.4	LIMD2	1.170871176	0.003275226
ENSG00000176973.7	FAM89B	1.165062419	0.033690361
ENSG00000083312.13	TNPO1	1.162128644	6.94E-05
ENSG00000073605.14	GSDMB	1.159134073	0.040498925
ENSG00000176046.7	NUPR1	1.157702773	2.11E-05
ENSG00000100813.10	ACIN1	1.150634407	0.004820368
ENSG00000162129.8	CLPB	1.147618615	0.014520723
ENSG00000184208.10	C22orf46	1.143981697	0.007684395
ENSG00000160072.15	ATAD3B	1.142906282	0.01358663
ENSG00000240225.6	ZNF542	1.142430577	0.010604405
ENSG00000177082.8	WDR73	1.141620623	0.002604747
ENSG00000133789.10	SWAP70	1.14060206	0.000558851
ENSG00000109920.8	FNBP4	1.139942907	0.000253431
ENSG00000155366.12	RHOC	1.128047565	0.003513897
ENSG00000038382.13	TRIO	1.127403331	0.002076367
ENSG00000244165.1	P2RY11	1.123676306	0.049668579
ENSG00000177335.6	C8orf31	1.122693423	0.04624228
ENSG00000129566.8	TEP1	1.122663392	0.026503762
ENSG00000088448.10	ANKRD10	1.121955353	0.003832794
ENSG00000116560.6	SFPQ	1.121360512	3.03E-05
ENSG00000155100.6	OTUD6B	1.121343818	0.031298694
ENSG00000137760.10	ALKBH8	1.112025303	0.024596576
ENSG00000128512.15	DOCK4	1.111218186	0.024104377
ENSG00000184967.2	NOC4L	1.110600489	0.037443032
ENSG00000169871.8	TRIM56	1.110103993	0.005209427
ENSG00000052749.9	RRP12	1.109813181	0.018548497
ENSG00000133997.7	MED6	1.106542697	0.000744612
ENSG00000180957.13	PITPNB	1.106091254	0.006153562
ENSG00000103111.10	MON1B	1.10274144	0.00075664
ENSG00000164134.8	NAA15	1.102737193	0.000292162

ENSG00000172059.6	KLF11	1.101842259	0.043107197
ENSG00000128191.9	DGCR8	1.100882448	0.006102722
ENSG00000182841.8	RRP7B	1.098581391	0.019656097
ENSG00000104907.8	TRMT1	1.098346961	0.030364865
ENSG00000087191.8	PSMC5	1.09791881	0.002924713
ENSG00000022277.8	RTFDC1	1.095516492	0.001467646
ENSG00000173875.9	ZNF791	1.094761517	0.000896182
ENSG00000130119.11	GNL3L	1.09378245	0.005406216
ENSG00000160352.11	ZNF714	1.090329556	0.001740725
ENSG00000156873.11	PHKG2	1.086286807	0.00136403
ENSG00000272512.1	RP11-54O7.17	1.086136495	0.031835099
ENSG00000269028.2	MTRNR2L12	1.084201364	0.016453635
ENSG00000108591.5	DRG2	1.081431655	0.00685913
ENSG00000113838.8	TBCCD1	1.080671227	0.011513811
ENSG00000146063.14	TRIM41	1.07602783	0.004225315
ENSG00000113407.9	TARS	1.075876797	0.002257894
ENSG00000120519.10	SLC10A7	1.071336452	0.021910869
ENSG00000125841.8	NRSN2	1.068151659	0.02136483
ENSG00000104969.5	SGTA	1.068149749	0.014221417
ENSG00000087087.14	SRRT	1.067613783	0.000501315
ENSG00000266714.2	MYO15B	1.067343044	0.01636017
ENSG00000012211.8	PRICKLE3	1.066778383	0.011949395
ENSG00000107815.3	C10orf2	1.065984171	0.001650257
ENSG00000205940.7	HSP90AB2P	1.064675201	0.024382783
ENSG00000180008.8	SOCS4	1.062239666	0.032135324
ENSG00000145331.9	TRMT10A	1.062098422	0.000540963
ENSG00000124193.10	SRSF6	1.061767264	0.000132346
ENSG00000135930.9	EIF4E2	1.061006216	0.005104664
ENSG00000154553.9	PDLIM3	1.058601865	0.035114539
ENSG00000215421.5	ZNF407	1.056990691	0.026821836
ENSG00000013573.12	DDX11	1.053054961	0.01728009
ENSG00000214756.3	METTL12	1.052511179	0.010030396
ENSG00000168404.8	MLKL	1.050039891	0.049589191
ENSG00000166004.10	KIAA1731	1.047949057	0.002880148
ENSG00000130818.6	ZNF426	1.046487203	0.015062617
ENSG00000175213.2	ZNF408	1.04252612	0.019111696
ENSG00000101104.8	PABPC1L	1.037515331	0.018514172
ENSG00000055483.15	USP36	1.037318957	0.00101137
ENSG00000130589.12	HELZ2	1.035313529	0.002608843
ENSG00000198042.6	MAK16	1.032429411	0.001851807
ENSG00000179818.9	PCBP1-AS1	1.029583986	0.040600281
ENSG00000136271.6	DDX56	1.024197162	0.032462393
ENSG00000174799.6	CEP135	1.023424436	0.005134703
ENSG00000177337.3	DLGAP1-AS1	1.021003105	0.000939524
ENSG00000240682.5	ISY1	1.020576578	0.001659753
ENSG00000125843.6	AP5S1	1.020212753	0.005178601

ENSG00000085840.8	ORC1	1.020143414	0.010757225
ENSG00000198464.9	ZNF480	1.016495615	0.016258615
ENSG00000092020.6	PPP2R3C	1.014611357	0.004292764
ENSG00000163466.11	ARPC2	1.011420067	0.003277011
ENSG00000256087.2	ZNF432	1.010361912	0.026226758
ENSG00000196646.7	ZNF136	1.009099192	0.03422937
ENSG00000144040.8	SFXN5	1.007646604	0.006733792
ENSG00000196584.2	XRCC2	1.007441979	0.018178967
ENSG00000124201.10	ZNFX1	1.005286029	0.004982884
ENSG00000144468.12	RHBDD1	1.003457526	0.004833767
ENSG00000143013.8	LMO4	1.003356553	0.000202937
ENSG00000031698.8	SARS	0.999898109	0.002406058
ENSG00000198650.6	TAT	0.997112825	0.004752215
ENSG00000138231.8	DBR1	0.996666732	0.002368651
ENSG00000179151.7	EDC3	0.993968378	0.01636017
ENSG00000210144.1	MT-TY	0.993252398	0.007268801
ENSG00000109320.7	NFKB1	0.992646277	0.010658554
ENSG00000106346.7	USP42	0.990584557	0.005439467
ENSG00000100644.12	HIF1A	0.987873664	0.000390234
ENSG00000185019.12	UBOX5	0.986991695	0.041275629
ENSG00000006432.11	MAP3K9	0.983162803	0.012593392
ENSG00000105771.9	SMG9	0.982472901	0.004714612
ENSG00000090339.4	ICAM1	0.973553458	0.003298862
ENSG00000125651.9	GTF2F1	0.973228067	0.037175829
ENSG00000047621.7	C12orf4	0.973152792	0.020786135
ENSG00000087263.12	OGFOD1	0.972242769	0.012350677
ENSG00000163935.9	SFMBT1	0.971763335	0.001543684
ENSG00000121766.10	ZCCHC17	0.968142756	0.001897675
ENSG00000013503.5	POLR3B	0.966503865	0.002872486
ENSG00000109111.10	SUPT6H	0.963526517	0.014484014
ENSG00000213020.4	ZNF611	0.96123613	0.013136421
ENSG00000104643.5	MTMR9	0.961131657	0.011119736
ENSG00000187840.4	EIF4EBP1	0.959564923	0.01095097
ENSG00000169188.4	APEX2	0.957165743	0.002110105
ENSG00000066322.8	ELOVL1	0.95710226	0.000550616
ENSG00000173530.5	TNFRSF10D	0.955607245	0.000166634
ENSG00000137962.8	ARHGAP29	0.949880681	0.000181957
ENSG00000272216.1	LL22NC03-2H8.5	0.943778237	0.019854877
ENSG00000104689.5	TNFRSF10A	0.940504955	0.003137243
ENSG00000187961.9	KLHL17	0.939979126	0.00812124
ENSG00000112208.10	BAG2	0.936830495	0.005324684
ENSG00000104825.12	NFKBIB	0.936206235	0.002257894
ENSG00000145388.10	METTL14	0.935753175	0.007995448
ENSG00000023839.6	ABCC2	0.933294822	0.009754131
ENSG00000135164.14	DMTF1	0.929206725	0.035479204
ENSG00000125319.10	C17orf53	0.928401157	0.020004028

ENSG00000033050.3	ABCF2	0.926440946	0.020695983
ENSG00000173821.15	RNF213	0.923394589	0.001679093
ENSG00000106246.13	PTCD1	0.919285431	0.035314309
ENSG00000040633.8	PHF23	0.917418587	0.000455816
ENSG00000196123.8	KIAA0895L	0.915546678	0.023479064
ENSG00000083099.6	LYRM2	0.910177629	0.001298429
ENSG00000177469.12	PTRF	0.910141449	0.012326267
ENSG00000267321.1	RP11-1094M14.11	0.910053451	0.033993845
ENSG00000142751.10	GPN2	0.906489368	0.000987699
ENSG00000159079.14	C21orf59	0.906363423	0.016842026
ENSG00000055609.13	KMT2C	0.904609596	0.003426704
ENSG00000128563.9	PRKRIP1	0.904276536	0.004611563
ENSG00000260563.2	RP13-516M14.1	0.902507616	0.040909651
ENSG00000221963.5	APOL6	0.897473866	0.009100115
ENSG00000163113.10	OTUD7B	0.8924988	0.008379801
ENSG00000132024.13	CC2D1A	0.888893352	0.017465827
ENSG00000141378.13	PTRH2	0.888377269	0.036817316
ENSG00000099341.7	PSMD8	0.885137583	0.01005794
ENSG00000101363.8	MANBAL	0.884573675	0.008249117
ENSG00000134324.7	LPIN1	0.881642459	0.007540155
ENSG00000119707.9	RBM25	0.876940859	0.001226319
ENSG00000167460.10	TPM4	0.876561916	0.008481488
ENSG00000170871.7	KIAA0232	0.875786373	0.011592035
ENSG00000165732.8	DDX21	0.872702453	0.010812986
ENSG00000136147.12	PHF11	0.87246331	0.016740571
ENSG00000149346.10	SLX4IP	0.863076523	0.037826522
ENSG00000102753.5	KPNA3	0.861716692	0.000749425
ENSG00000168591.11	TMUB2	0.859066399	0.039872089
ENSG00000177455.7	CD19	0.85840696	0.011647543
ENSG00000188130.9	MAPK12	0.857245992	0.012795997
ENSG00000168040.4	FADD	0.855401921	0.01409343
ENSG00000087206.12	UIMC1	0.855275109	0.033561228
ENSG00000109606.8	DHX15	0.853949039	0.001755536
ENSG00000185163.5	DDX51	0.852765283	0.043827488
ENSG00000196396.5	PTPN1	0.852614252	0.013115473
ENSG00000067369.9	TP53BP1	0.850489068	0.008249117
ENSG00000167670.11	CHAF1A	0.849382827	0.01636017
ENSG00000157106.12	SMG1	0.848159409	0.031698713
ENSG00000071539.9	TRIP13	0.845457196	0.039629482
ENSG00000197948.6	FCHSD1	0.842435966	0.004549024
ENSG00000260482.1	CTD-2196E14.9	0.841142115	0.016041257
ENSG00000168769.8	TET2	0.839068848	0.039682347
ENSG00000168646.8	AXIN2	0.839049532	0.001889067
ENSG00000105127.4	AKAP8	0.837948957	0.022422117
ENSG00000153767.5	GTF2E1	0.836878032	0.008440045
ENSG00000176953.6	NFATC2IP	0.836778573	0.002195152

ENSG00000111371.11	SLC38A1	0.836109824	0.005223964
ENSG00000078140.9	UBE2K	0.834824313	0.006044094
ENSG00000169592.10	INO80E	0.834387779	0.012782656
ENSG00000203668.1	CHML	0.826996057	0.030380893
ENSG00000198105.7	ZNF248	0.825600255	0.041157739
ENSG00000165487.9	MICU2	0.822236209	0.023281135
ENSG00000155034.14	FBXL18	0.822213316	0.031122874
ENSG00000089723.5	OTUB2	0.820376966	0.01863998
ENSG00000023608.4	SNAPC1	0.819562588	0.0189869
ENSG00000161526.10	SAP30BP	0.814930049	0.024274684
ENSG00000162664.12	ZNF326	0.814852122	0.002368651
ENSG00000136738.10	STAM	0.812866667	0.022759497
ENSG00000241258.2	CRCP	0.812392794	0.008249117
ENSG00000003756.12	RBM5	0.812000923	0.032421198
ENSG00000119326.10	CTNNAL1	0.809157057	0.008377061
ENSG00000198730.3	CTR9	0.808250018	0.007827334
ENSG00000077782.15	FGFR1	0.807488847	0.003827872
ENSG00000198363.11	ASPH	0.806182872	0.004670796
ENSG00000156502.9	SUPV3L1	0.80443047	0.033919294
ENSG00000210082.2	MT-RNR2	0.802858879	0.04354996
ENSG00000039123.11	SKIV2L2	0.801692713	0.034775843
ENSG00000116539.6	ASH1L	0.799589538	0.010082823
ENSG00000141141.10	DDX52	0.796276531	0.002683059
ENSG00000087116.9	ADAMTS2	0.794086515	0.033836263
ENSG00000100994.7	PYGB	0.78772374	0.026397982
ENSG00000161217.7	PCYT1A	0.786198147	0.014091697
ENSG00000130305.12	NSUN5	0.784951449	0.01464118
ENSG00000125885.9	MCM8	0.783685912	0.029867822
ENSG00000114861.14	FOXP1	0.783330046	0.005075014
ENSG00000134202.6	GSTM3	0.781546195	0.026458667
ENSG00000053372.4	MRTO4	0.779223044	0.005410405
ENSG00000127564.12	PKMYT1	0.779074558	0.030486535
ENSG00000196586.9	MYO6	0.776158078	0.0037557
ENSG00000135951.10	TSGA10	0.772252801	0.044625794
ENSG00000131236.12	CAP1	0.772199519	0.012103765
ENSG00000028310.13	BRD9	0.771861922	0.022623585
ENSG00000264364.2	DYNLL2	0.770150796	0.011127765
ENSG00000108270.6	AATF	0.769631048	0.023043552
ENSG00000140416.15	TPM1	0.769024317	0.01394319
ENSG00000175854.7	SWI5	0.766459332	0.008514875
ENSG00000107290.9	SETX	0.764521549	0.015882918
ENSG00000089737.11	DDX24	0.763506736	0.005246699
ENSG00000138448.7	ITGAV	0.763102863	0.008547
ENSG00000145833.11	DDX46	0.762522365	0.004100493
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DOWN-REGULATED GENES

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ENSG00000132182.7	NUP210	-1.4147833	0.001996197
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ENSG00000158552.8	ZFAND2B	-1.42420028	5.67E-05
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ENSG00000271737.1	CTB-113I20.2	-1.456810506	0.031698713
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ENSG00000182979.13	MTA1	-1.484566631	6.51E-05
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ENSG00000171155.7	C1GALT1C1	-1.503637887	0.024200803
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ENSG00000172159.11	FRMD3	-2.417709568	1.26E-12
ENSG00000243364.3	EFNA4	-2.435254771	0.006847273
ENSG00000171766.11	GATM	-2.438735897	0.003277011
ENSG00000077152.5	UBE2T	-2.443399304	0.00162948
ENSG00000126231.9	PROZ	-2.443419588	0.000807436
ENSG00000146426.13	TIAM2	-2.450903547	0.003275226
ENSG00000186352.4	ANKRD37	-2.453043421	3.06E-15
ENSG00000235529.1	AGAP1-IT1	-2.468194437	0.015270817
ENSG00000250722.1	SEPP1	-2.47421777	6.28E-07
ENSG00000197536.6	C5orf56	-2.482604558	0.047874794
ENSG00000101447.9	FAM83D	-2.519465236	6.75E-05
ENSG00000141505.7	ASGR1	-2.521545714	5.11E-07
ENSG00000125968.7	ID1	-2.5226513	1.43E-08
ENSG00000255471.1	RP11-736K20.5	-2.527343875	0.000430798
ENSG00000254584.1	RP1-17K7.2	-2.535318885	0.04530072

ENSG00000091106.14	NLRC4	-2.536911799	0.009815778
ENSG00000203791.9	METTL10	-2.537877594	0.000957058
ENSG00000163586.5	FABP1	-2.563270786	2.16E-05
ENSG00000204444.6	APOM	-2.56649414	3.87E-05
ENSG00000245848.2	CEBPA	-2.570749631	2.38E-07
ENSG00000166924.4	NYAP1	-2.573155684	0.031433699
ENSG00000253304.1	TMEM200B	-2.601224198	0.012782656
ENSG00000272688.1	RP13-270P17.3	-2.615705934	0.004833767
ENSG00000188582.4	PAQR9	-2.632671565	0.00021896
ENSG00000165879.7	FRAT1	-2.63471988	0.000179086
ENSG00000234235.1	BOK-AS1	-2.645453213	0.03823488
ENSG00000146674.10	IGFBP3	-2.658576761	2.39E-10
ENSG00000111452.8	GPR133	-2.696981251	0.001440259
ENSG00000187736.8	NHEJ1	-2.700210709	0.0223294
ENSG00000255398.2	HCAR3	-2.702127	0.001024391
ENSG00000211452.6	DIO1	-2.703903784	0.026613365
ENSG00000213782.3	DDX47	-2.733511608	0.001732176
ENSG00000165246.8	NLGN4Y	-2.744403496	0.030114561
ENSG00000167664.4	TMIGD2	-2.781482465	0.000344941
ENSG00000186615.6	KTN1-AS1	-2.791979158	0.01835861
ENSG00000229119.3	CTB-63M22.1	-2.837926385	0.014830907
ENSG00000272043.1	RP11-44N11.3	-2.846036989	0.043827488
ENSG00000188747.4	NOXA1	-2.84625437	0.028698893
ENSG00000231007.4	CDC20P1	-2.846961285	0.026303922
ENSG00000216588.4	IGSF23	-2.849498089	0.028368537
ENSG00000267130.1	CTD-2540B15.9	-2.903447494	0.00202969
ENSG00000186732.9	MPPED1	-2.973991887	0.032362611
ENSG00000142279.8	WTIP	-3.000571192	0.000116019
ENSG00000107159.8	CA9	-3.012292524	0.0003093
ENSG00000090776.5	EFNB1	-3.014025008	0.000988436
ENSG00000123561.10	SERPINA7	-3.016826652	1.87E-09
ENSG00000132406.7	TMEM128	-3.160548453	8.16E-05
ENSG00000251580.1	RP11-539L10.3	-3.167720011	0.004116589
ENSG00000273314.1	RP5-1136G13.2	-3.177494152	0.010042794
ENSG00000159337.6	PLA2G4D	-3.228560212	0.013573775
ENSG00000136305.7	CIDEB	-3.246995888	8.60E-05
ENSG00000105290.7	APLP1	-3.248555865	0.003908946
ENSG00000099953.5	MMP11	-3.277401073	2.99E-07
ENSG00000162736.11	NCSTN	-3.286657749	7.29E-07
ENSG00000169507.5	SLC38A11	-3.291533784	0.007444512
ENSG00000187808.3	SOWAHD	-3.332742575	0.002604747
ENSG00000168301.8	KCTD6	-3.384268841	0.003588911
ENSG00000179636.10	TPPP2	-3.44406357	0.001753161
ENSG00000273355.1	RP11-672L10.6	-3.444857906	0.003966189
ENSG00000227403.1	AC009299.3	-3.467290042	0.006932232
ENSG00000157593.12	SLC35B2	-3.502547251	1.67E-05

ENSG00000180233.9	ZNRF2	-3.543481053	0.004555192
ENSG00000261455.1	LINC01003	-3.547163489	0.000441821
ENSG00000197444.5	OGDHL	-3.619294332	0.001479157
ENSG00000185338.4	SOCS1	-3.66011728	4.36E-08
ENSG00000182383.8	RPL27AP5	-3.676573437	0.0014824
ENSG00000172572.6	PDE3A	-3.758253496	0.002584848
ENSG00000104432.8	IL7	-4.202233351	0.03933527
ENSG00000226015.2	CCT8P1	-4.211947019	0.000256185
ENSG00000168306.8	ACOX2	-4.260131083	0.000272733
ENSG00000143036.12	SLC44A3	-4.262829175	0.036557908
ENSG00000186272.8	ZNF17	-4.345981312	0.024069326
ENSG00000185483.7	ROR1	-4.348298361	0.022409254
ENSG00000049130.9	KITLG	-4.348717736	0.016782176
ENSG00000114859.10	CLCN2	-4.47477165	0.031063525
ENSG00000234546.2	RP3-510D11.2	-4.484326621	0.020040931
ENSG00000169105.6	CHST14	-4.570661556	3.64E-05
ENSG00000167964.8	RAB26	-4.59680992	0.018716499
ENSG00000239779.2	WBP1	-4.712828853	0.005604132
ENSG00000082196.16	C1QTNF3	-5.165977198	0.000554962
ENSG00000091138.8	SLC26A3	-5.736634506	6.66E-05

SUPPLEMENTARY TABLE 4.

Complete list of genes specifically regulated by Cu only in ATP7B-ko HepG2 cells.

Significant transcriptional responses to Cu were detected using QuantSeq and compared in control HepG2 and ATP7B-ko HepG2 cells. The table shows the genes, which were significantly (FDR<0,05) up-regulated (red) or down-regulated (green) only in ATP7B-ko HepG2 cells.

UP-REGULATED GENES

EnsemblID	GeneSymbol	logFC specific ATP7B-KO+Cu	FDR specific ATP7B-KO+Cu
ENSG00000183508.4	FAM46C	7.835840547	1.16E-10
ENSG00000135898.5	GPR55	7.15203284	6.79E-11
ENSG00000126353.3	CCR7	6.851006136	7.34E-10
ENSG00000126856.9	PRDM7	6.805761987	2.03E-07
ENSG00000197580.7	BCO2	6.305248953	1.16E-05
ENSG00000169059.8	VCX3A	6.257394307	3.08E-05
ENSG00000110680.8	CALCA	6.108914433	6.78E-07
ENSG00000142871.11	CYR61	6.066571499	5.30E-13
ENSG00000111348.4	ARHGDIB	6.051491004	2.68E-06
ENSG00000267107.2	AC011526.1	6.044978387	6.30E-06
ENSG00000186462.7	NAP1L2	5.985887905	8.13E-06
ENSG00000187537.9	POTEM	5.93968232	3.58E-05
ENSG00000261481.1	RP11-77H9.6	5.923505062	1.06E-05
ENSG00000198062.10	POTEH	5.870202536	6.10E-05
ENSG00000125878.4	TCF15	5.856933496	2.16E-05
ENSG00000237330.2	RNF223	5.788280169	4.05E-05
ENSG00000229230.2	MT1P3	5.764210262	0.001512193
ENSG00000166206.9	GABRB3	5.719586086	1.71E-05
ENSG00000159556.5	ISL2	5.713479756	0.000197477
ENSG00000216436.2	HIST1H2APS1	5.657726742	0.000278536
ENSG00000110324.5	IL10RA	5.653434478	0.000249611
ENSG00000230450.1	NEK2P4	5.648343258	7.55E-05
ENSG00000227844.1	RP13-143G15.3	5.643334673	2.92E-05
ENSG00000158486.9	DNAH3	5.568194879	0.000205033
ENSG00000181847.7	TIGIT	5.562600184	4.98E-05
ENSG00000243710.3	WDR65	5.560825466	0.000122017
ENSG00000103196.7	CRISPLD2	5.478348361	0.000242701
ENSG00000135549.10	PKIB	5.477528806	0.000110988
ENSG00000189252.4	SPANXN3	5.476914484	8.53E-05
ENSG00000233894.1	RP4-650F12.2	5.476563015	0.000110504
ENSG00000261556.4	RP11-296I10.6	5.402352621	0.001221515
ENSG00000183206.12	POTEC	5.396623642	0.000800056
ENSG00000196639.6	HRH1	5.394564603	0.000528409
ENSG00000153234.9	NR4A2	5.388808692	0.000311922
ENSG00000143507.13	DUSP10	5.385224754	0.000409433
ENSG00000237639.2	RP11-368M16.5	5.384665737	0.000178639
ENSG00000047662.4	FAM184B	5.383782033	0.000212286
ENSG00000132357.9	CARD6	5.383003765	0.000537514
ENSG00000005513.9	SOX8	5.3819024	0.000357688
ENSG00000198719.7	DLL1	5.378412349	8.88E-08
ENSG00000198355.4	PIM3	5.352641408	4.11E-07

ENSG00000146039.6	SLC17A4	5.304853664	1.09E-05
ENSG00000152137.2	HSPB8	5.288623406	0.000311235
ENSG00000163273.3	NPPC	5.240582635	1.08E-09
ENSG00000182459.4	TEX19	5.206361956	2.41E-11
ENSG00000104435.9	STMN2	5.176371529	0.003288205
ENSG00000272518.1	RP11-26J3.3	5.082078186	0.002961436
ENSG00000236261.1	RP11-368M16.6	5.077071873	0.002188689
ENSG00000125780.11	TGM3	5.076671323	0.001945264
ENSG00000226721.2	EEF1DP2	5.075728591	0.001919712
ENSG00000204642.9	HLA-F	5.074045349	0.000897824
ENSG00000240751.1	RP11-553D4.2	5.07271331	0.000749592
ENSG00000239353.1	RP11-492E3.51	5.072706738	0.000747329
ENSG00000145107.11	TM4SF19	5.069295201	0.001298465
ENSG00000267809.1	NDUFV2P1	5.06698735	0.001461227
ENSG00000225793.2	RP1-234P15.4	5.063729658	0.001910304
ENSG00000271755.1	RP1-153G14.4	5.055437531	0.003755785
ENSG00000137267.5	TUBB2A	5.001929715	3.22E-13
ENSG00000175356.8	SCUBE2	4.969269254	0.004120818
ENSG00000184185.5	KCNJ12	4.956498865	3.67E-08
ENSG00000250548.2	RP11-47I22.2	4.956323543	0.00212786
ENSG00000259043.1	BRD7P1	4.955767396	0.00199766
ENSG00000152689.13	RASGRP3	4.952562287	0.001698463
ENSG00000179674.2	ARL14	4.951178772	0.001291668
ENSG00000204363.4	SPANXN5	4.951106829	0.001291668
ENSG00000120937.8	NPPB	4.950954416	0.001758241
ENSG00000249849.1	RP11-1101H11.1	4.94806927	0.002688202
ENSG00000257732.1	RP11-818F20.5	4.857908726	0.018236829
ENSG00000231416.1	RP11-422P24.9	4.831482938	0.008614639
ENSG00000228606.1	RP11-574F21.2	4.831143919	0.009423406
ENSG00000006327.9	TNFRSF12A	4.827747706	2.42E-09
ENSG00000159377.6	PSMB4	4.824691584	5.95E-10
ENSG00000149257.9	SERPINH1	4.823485476	7.19E-12
ENSG00000251410.1	AC007106.1	4.818109767	0.002239797
ENSG00000159231.5	CBR3	4.814761481	0.005874743
ENSG00000136866.9	ZFP37	4.709262867	7.25E-05
ENSG00000104883.3	PEX11G	4.67573098	0.006218387
ENSG00000234479.2	AP1B1P1	4.671882704	0.00388605
ENSG00000269971.1	RP3-426I6.5	4.671881478	0.00388484
ENSG00000065618.12	COL17A1	4.665946222	0.020657104
ENSG00000144485.6	HES6	4.648510809	3.10E-10
ENSG00000103269.9	RHBDL1	4.54687812	0.009459594
ENSG00000124496.8	TRERF1	4.515273233	0.009482609
ENSG00000269894.1	RP11-1020A11.1	4.509312849	0.01064911
ENSG00000130475.10	FCHO1	4.504104298	0.01081908
ENSG00000196431.3	CRYBA4	4.497108288	0.01770967
ENSG00000137270.10	GCM1	4.493961388	1.43E-06
ENSG00000169567.7	HINT1	4.484276431	3.47E-07
ENSG00000163395.12	IGFN1	4.455745614	2.73E-10
ENSG00000008018.8	PSMB1	4.447818642	1.06E-11
ENSG00000134686.12	PHC2	4.433742003	2.02E-07

ENSG00000173207.8	CKS1B	4.425041351	4.04E-06
ENSG00000250584.2	RP11-325I22.2	4.397594551	0.002867997
ENSG00000171858.13	RPS21	4.360502937	4.22E-07
ENSG00000235615.2	AJ239322.1	4.332686322	0.017918283
ENSG00000215559.4	ANKRD20A11P	4.332409327	0.017609222
ENSG00000241484.5	ARHGAP8	4.326987937	0.014354038
ENSG00000150722.6	PPP1R1C	4.323378472	0.018773462
ENSG00000230777.1	RP11-318C24.1	4.322749335	0.013245227
ENSG00000244716.2	RP11-20O24.4	4.311562768	0.019801785
ENSG00000004779.5	NDUFAB1	4.250690906	2.47E-08
ENSG00000159167.7	STC1	4.231814061	0.000113336
ENSG00000154133.10	ROBO4	4.220151297	4.34E-06
ENSG00000260896.1	RP11-314O13.1	4.178998359	0.001045994
ENSG00000164683.12	HEY1	4.177919199	9.97E-06
ENSG00000160161.5	CILP2	4.174857832	1.26E-05
ENSG00000119943.6	PYROXD2	4.122427631	0.037653893
ENSG00000155984.10	TMEM185A	4.120222299	0.03063586
ENSG00000248461.1	CTD-2207A17.1	4.111138237	0.031044656
ENSG00000226888.2	RP11-561G1.3	4.110990619	0.038809376
ENSG00000213741.4	RPS29	4.101473865	0.000311812
ENSG00000104808.3	DHDH	4.097630749	0.046083231
ENSG00000221823.6	PPP3R1	4.082204051	7.29E-09
ENSG00000116212.10	LRRC42	4.072236318	3.40E-06
ENSG00000205420.6	KRT6A	4.057177499	0.026389612
ENSG00000186480.8	INSIG1	4.055473845	0.000179044
ENSG00000189043.5	NDUFA4	4.049285758	2.11E-07
ENSG00000106153.12	CHCHD2	4.043243274	9.11E-11
ENSG00000135018.9	UBQLN1	3.995022287	1.43E-10
ENSG00000205362.6	MT1A	3.969948571	2.54E-07
ENSG00000112658.6	SRF	3.966834	4.13E-06
ENSG00000136930.8	PSMB7	3.938410697	3.70E-16
ENSG00000143947.8	RPS27A	3.934867238	5.82E-10
ENSG00000105011.4	ASF1B	3.933008877	0.000476795
ENSG00000110801.9	PSMD9	3.917610941	5.71E-07
ENSG00000151465.9	CDC123	3.906317134	3.39E-09
ENSG00000177156.6	TALDO1	3.898964482	9.42E-13
ENSG00000152117.13	AC093838.4	3.887770198	1.77E-08
ENSG00000237596.2	RP13-143G15.4	3.887160343	4.12E-05
ENSG00000127666.8	TICAM1	3.885481685	7.29E-05
ENSG00000156127.6	BATF	3.879573931	7.88E-11
ENSG00000227373.1	RP11-160H22.5	3.874491866	0.042840675
ENSG00000197472.10	ZNF695	3.873331328	1.76E-06
ENSG00000105640.8	RPL18A	3.870255539	1.31E-11
ENSG00000172264.12	MACROD2	3.868303117	0.044360082
ENSG00000198610.6	AKR1C4	3.867318072	0.043796499
ENSG00000110700.2	RPS13	3.843882872	9.24E-12
ENSG00000161040.12	FBXL13	3.84280294	0.000720746
ENSG00000166159.6	LRTM2	3.838593886	0.006538811
ENSG00000149596.6	JPH2	3.832078975	0.00020145
ENSG00000150782.7	IL18	3.831881359	0.000284376

ENSG00000260793.2	RP5-882C2.2	3.828453652	0.004826172
ENSG00000213337.4	ANKRD39	3.823387133	1.14E-07
ENSG00000187778.9	MCRS1	3.7917304	5.70E-08
ENSG00000173113.2	TRMT112	3.79060768	6.32E-08
ENSG00000165704.10	HPRT1	3.786149763	1.50E-06
ENSG00000005022.5	SLC25A5	3.786000494	0.00054455
ENSG00000074842.3	C19orf10	3.782359824	2.51E-06
ENSG00000104221.8	BRF2	3.782137464	1.51E-09
ENSG00000126453.5	BCL2L12	3.770912676	6.18E-10
ENSG00000197063.6	MAFG	3.769851094	7.24E-18
ENSG00000115009.7	CCL20	3.757832356	4.61E-08
ENSG00000239617.1	RP11-302B13.1	3.754953485	0.004716426
ENSG00000157379.9	DHRS1	3.742677917	2.75E-07
ENSG00000138772.8	ANXA3	3.731289927	7.25E-06
ENSG00000067798.9	NAV3	3.727369686	0.000892993
ENSG00000105136.15	ZNF419	3.723699053	3.33E-08
ENSG00000134871.13	COL4A2	3.721382226	3.28E-13
ENSG00000120129.5	DUSP1	3.71165344	1.41E-09
ENSG00000124688.9	MAD2L1BP	3.711637758	7.35E-06
ENSG00000251615.3	RP11-774O3.3	3.689042028	0.000182538
ENSG00000182117.4	NOP10	3.687027118	0.000117821
ENSG00000135404.7	CD63	3.682338712	2.21E-09
ENSG00000132581.5	SDF2	3.681377633	9.43E-10
ENSG00000197380.6	DACT3	3.662232975	3.01E-05
ENSG00000250461.1	RP11-631M6.2	3.654361544	0.002260107
ENSG00000116761.7	CTH	3.645150909	0.000149156
ENSG00000249884.4	RNF103-CHMP3	3.639505393	0.001098599
ENSG00000115484.10	CCT4	3.625538536	2.55E-10
ENSG00000189223.9	AC016683.6	3.62278287	3.90E-06
ENSG00000063169.6	GLTSCR1	3.622022712	0.000686563
ENSG00000257605.1	RP11-680A11.5	3.619192004	1.12E-05
ENSG00000165501.12	LRR1	3.618908006	3.10E-06
ENSG00000273284.1	RP11-888D10.4	3.61429276	0.000119955
ENSG00000137309.15	HMGA1	3.599411108	2.20E-13
ENSG00000149575.5	SCN2B	3.591594844	0.003288205
ENSG00000108344.10	PSMD3	3.584371091	4.58E-10
ENSG00000164032.7	H2AFZ	3.58424152	2.92E-08
ENSG00000173221.9	GLRX	3.582612699	2.47E-08
ENSG00000005108.11	THSD7A	3.568568355	0.018097269
ENSG00000272486.1	RP11-532M24.1	3.567135193	0.001434911
ENSG00000175984.10	DENND2C	3.563375272	0.002500117
ENSG00000169548.3	ZNF280A	3.561538784	5.66E-10
ENSG00000102934.5	PLLP	3.55950021	9.93E-05
ENSG00000116675.11	DNAJC6	3.547266145	0.000945854
ENSG00000101544.4	ADNP2	3.542962788	1.68E-11
ENSG00000129355.6	CDKN2D	3.540430182	1.72E-05
ENSG00000101928.8	MOSPD1	3.532346046	2.85E-08
ENSG00000153495.6	TEX29	3.520087913	0.007073608
ENSG00000181523.8	SGSH	3.513762876	0.000189776
ENSG00000141447.12	OSBPL1A	3.503182883	0.004518483

ENSG00000130513.6	GDF15	3.495571335	1.52E-09
ENSG00000099246.12	RAB18	3.486826996	3.45E-10
ENSG00000115541.6	HSPE1	3.470116491	7.00E-07
ENSG00000215251.3	FASTKD5	3.465162002	5.42E-10
ENSG00000122432.12	SPATA1	3.464780361	0.001164633
ENSG00000162385.6	MAGOH	3.462886154	1.01E-08
ENSG00000106803.5	SEC61B	3.454587552	1.56E-05
ENSG00000125877.8	ITPA	3.44817128	4.07E-10
ENSG00000138764.9	CCNG2	3.44393321	9.39E-07
ENSG00000186395.6	KRT10	3.431543846	3.03E-05
ENSG00000108106.9	UBE2S	3.423767439	0.000780191
ENSG00000066557.5	LRRC40	3.417336166	6.28E-05
ENSG00000109089.7	CDR2L	3.408367313	5.29E-05
ENSG00000183405.5	RPS7P1	3.405918216	0.000205602
ENSG00000025156.8	HSF2	3.405838658	2.60E-08
ENSG00000173320.5	STOX2	3.397193529	0.008063921
ENSG00000119414.7	PPP6C	3.386285844	5.17E-09
ENSG00000118939.13	UCHL3	3.385370629	9.63E-08
ENSG00000102096.9	PIM2	3.382259396	2.36E-06
ENSG00000005884.13	ITGA3	3.381625868	0.002744551
ENSG00000168288.8	MMADHC	3.375899365	6.66E-10
ENSG00000153310.14	FAM49B	3.375624441	1.97E-10
ENSG00000173418.7	NAA20	3.374372746	6.09E-06
ENSG00000051108.10	HERPUD1	3.370351039	4.34E-15
ENSG00000174109.3	C16orf91	3.369012734	0.000248702
ENSG00000220370.1	RP3-399J4.2	3.359351737	1.90E-05
ENSG00000156642.12	NPTN	3.351015774	2.36E-06
ENSG00000087494.11	PTHLH	3.349745873	0.018848461
ENSG00000151743.6	AMN1	3.349604131	1.06E-07
ENSG00000184731.5	FAM110C	3.337203166	9.14E-06
ENSG00000197608.7	ZNF841	3.329419178	5.91E-07
ENSG00000083842.8	ZNF8	3.323874539	5.63E-05
ENSG00000215021.4	PHB2	3.318746261	8.13E-08
ENSG00000165283.11	STOML2	3.317953263	1.14E-06
ENSG00000271795.1	CTC-251D13.1	3.316181979	0.00862695
ENSG00000089157.11	RPLP0	3.315906765	3.62E-08
ENSG00000099814.11	CEP170B	3.309623654	1.34E-09
ENSG00000171224.7	C10orf35	3.309553348	2.13E-08
ENSG00000167553.10	TUBA1C	3.303298941	4.61E-08
ENSG00000196878.8	LAMB3	3.298380457	5.01E-05
ENSG00000175003.8	SLC22A1	3.293182208	0.00449908
ENSG00000171246.5	NPTX1	3.288247598	0.00262859
ENSG00000272186.1	RP11-110I1.13	3.282864686	0.002145449
ENSG00000214189.4	ZNF788	3.271093586	0.006839547
ENSG00000232756.1	RP5-1185I7.1	3.260699811	0.016901397
ENSG00000101888.7	NXT2	3.258242095	1.30E-06
ENSG00000141933.8	TPGS1	3.257112484	0.032639148
ENSG00000109079.5	TNFAIP1	3.250158289	1.52E-09
ENSG00000099338.18	CATSPERG	3.240375851	0.026073307
ENSG00000154370.9	TRIM11	3.227935768	1.14E-10

ENSG00000166471.6	TMEM41B	3.222874089	2.29E-08
ENSG00000113732.4	ATP6V0E1	3.221928671	2.93E-07
ENSG00000108518.7	PFN1	3.221662177	1.32E-05
ENSG00000260060.1	RP11-388M20.1	3.219301545	0.011025924
ENSG00000153037.8	SRP19	3.218852706	0.000167369
ENSG00000156711.12	MAPK13	3.218666027	7.54E-07
ENSG00000139971.11	C14orf37	3.218503348	0.02047482
ENSG00000167977.4	KCTD5	3.207555051	9.75E-08
ENSG00000135900.3	MRPL44	3.199040557	9.57E-07
ENSG00000121895.7	TMEM156	3.198851263	0.000306896
ENSG00000187134.8	AKR1C1	3.197219276	1.33E-08
ENSG00000197457.5	STMN3	3.196498823	1.27E-05
ENSG00000133687.11	TMTC1	3.193995418	0.001294872
ENSG00000133800.4	LYVE1	3.193293421	3.49E-07
ENSG00000198860.7	TSEN15	3.19324392	2.53E-05
ENSG00000006837.7	CDKL3	3.187519554	0.00373232
ENSG00000213246.2	SUPT4H1	3.184297169	1.02E-12
ENSG00000175348.6	TMEM9B	3.178722065	4.48E-06
ENSG00000163807.4	KIAA1143	3.178512756	1.75E-10
ENSG00000204356.7	NELFE	3.167061495	4.85E-06
ENSG00000047249.12	ATP6V1H	3.166815336	2.71E-07
ENSG00000167103.7	PIP5KL1	3.160113567	0.018427259
ENSG00000111335.8	OAS2	3.157123418	0.043697816
ENSG00000268006.1	PTOV1-AS1	3.155368371	0.011335638
ENSG00000161970.8	RPL26	3.154512253	4.59E-07
ENSG00000253626.2	EIF5AL1	3.154040425	2.24E-07
ENSG00000159885.9	ZNF222	3.15365408	0.000808065
ENSG00000197927.8	C2orf27A	3.153565888	0.011301984
ENSG00000089335.16	ZNF302	3.153036423	0.000806731
ENSG00000002834.13	LASP1	3.150043829	1.87E-06
ENSG00000104497.9	SNX16	3.14954442	1.75E-05
ENSG00000165895.13	ARHGAP42	3.13747883	0.000150357
ENSG00000174903.10	RAB1B	3.137423089	7.55E-07
ENSG00000197020.6	ZNF100	3.134438923	7.00E-05
ENSG00000241837.2	ATP5O	3.131135768	9.31E-06
ENSG00000132661.3	NXT1	3.129158919	0.000115421
ENSG00000112237.8	CCNC	3.126775251	2.34E-09
ENSG00000205485.9	AC004980.7	3.117657549	3.64E-05
ENSG00000188042.5	ARL4C	3.115403286	0.046456122
ENSG00000133393.8	FOPNL	3.115340567	4.75E-07
ENSG00000122026.6	RPL21	3.110247822	6.82E-11
ENSG00000122497.13	NBPF14	3.107860645	0.016185314
ENSG00000261068.1	RP11-7K24.3	3.101091047	0.010751733
ENSG00000126391.9	FRMD8	3.093158749	2.89E-05
ENSG00000134668.8	SPOCD1	3.091069893	0.008756474
ENSG00000262484.1	CTC-360G5.1	3.090651209	0.020307805
ENSG00000088832.10	FKBP1A	3.090408524	2.12E-11
ENSG00000198840.2	MT-ND3	3.08792514	1.04E-07
ENSG00000180999.6	C1orf105	3.083123198	0.0063711
ENSG00000136653.15	RASSF5	3.081688611	0.0057306

ENSG00000148926.5	ADM	3.080936419	3.73E-11
ENSG00000120158.7	RCL1	3.080758481	2.01E-07
ENSG00000205809.5	KLRC2	3.066185442	0.000253253
ENSG00000099977.9	DDT	3.0628591	4.94E-10
ENSG00000004961.10	HCCS	3.056334755	1.76E-05
ENSG00000225405.3	RP11-84A1.1	3.053503806	7.39E-05
ENSG00000229186.3	ADAM1A	3.052509548	0.002153433
ENSG00000147883.9	CDKN2B	3.047852655	6.44E-05
ENSG00000196611.4	MMP1	3.036499399	8.68E-05
ENSG00000121931.11	LRIF1	3.032990127	7.72E-10
ENSG00000137767.9	SQRDL	3.03292388	6.64E-05
ENSG00000112306.7	RPS12	3.029767778	5.36E-08
ENSG00000166595.7	FAM96B	3.027982341	5.40E-05
ENSG00000169490.12	TM2D2	3.026984523	4.25E-06
ENSG00000129084.13	PSMA1	3.025386039	3.43E-07
ENSG00000242358.1	RPS21P4	3.024911235	1.03E-05
ENSG00000152601.13	MBNL1	3.024710923	2.40E-07
ENSG00000143632.10	ACTA1	3.020260987	1.34E-09
ENSG00000166173.9	LARP6	3.018941334	2.26E-05
ENSG00000161714.7	PLCD3	3.011552621	2.38E-06
ENSG00000232533.1	AC093673.5	3.000770973	0.000379513
ENSG00000258700.1	LINC00871	2.999055167	0.000262468
ENSG00000235162.4	C12orf75	2.995175612	6.70E-06
ENSG00000105146.8	AURKC	2.991610845	0.020362864
ENSG00000138495.2	COX17	2.98778974	1.04E-05
ENSG00000100632.6	ERH	2.984098247	4.91E-09
ENSG00000100285.9	NEFH	2.981259611	0.017131369
ENSG00000082515.12	MRPL22	2.978658321	1.36E-05
ENSG00000167618.5	LAIR2	2.975813315	1.45E-05
ENSG00000121270.11	ABCC11	2.975663097	0.000766249
ENSG00000172216.4	CEBPB	2.963353444	5.95E-06
ENSG00000167985.2	SDHAF2	2.958406424	5.47E-08
ENSG00000163291.10	PAQR3	2.957576067	8.61E-05
ENSG00000196139.7	AKR1C3	2.952242007	1.92E-07
ENSG00000125977.6	EIF2S2	2.94964398	1.61E-10
ENSG00000157045.4	NTAN1	2.948399589	4.65E-11
ENSG00000119280.12	C1orf198	2.946331717	1.76E-06
ENSG00000175895.3	PLEKHF2	2.945028291	0.000804748
ENSG00000134245.13	WNT2B	2.942186399	0.028342741
ENSG00000138326.14	RPS24	2.939531491	7.99E-07
ENSG00000104660.13	LEPROTL1	2.921112705	9.87E-07
ENSG00000087237.6	CETP	2.916018545	0.004895238
ENSG00000220842.5	RP11-572P18.1	2.914060639	4.83E-05
ENSG00000091622.11	PITPNM3	2.910264508	0.003753523
ENSG00000228818.1	RP11-567G24.1	2.910128305	0.043806738
ENSG00000146757.9	ZNF92	2.906024438	1.36E-06
ENSG00000272269.1	RP11-500C11.3	2.902900086	0.00026121
ENSG00000172530.15	BANP	2.899217933	1.36E-06
ENSG00000139514.8	SLC7A1	2.894179143	3.41E-08
ENSG00000151014.4	CCRN4L	2.88719445	0.048660377

ENSG00000261005.1	CTB-58E17.1	2.8856456	5.67E-05
ENSG00000189269.8	C22orf43	2.884573201	0.038359756
ENSG00000102898.7	NUTF2	2.876728866	1.15E-07
ENSG00000013288.4	MAN2B2	2.873389919	1.94E-05
ENSG00000129460.11	NGDN	2.868643961	2.83E-07
ENSG00000105193.4	RPS16	2.867421085	4.11E-08
ENSG00000147416.6	ATP6V1B2	2.861092976	7.00E-07
ENSG00000196072.7	BLOC1S2	2.860893703	3.93E-07
ENSG00000100711.9	ZFYVE21	2.859070592	0.000116271
ENSG00000164713.5	BRI3	2.85800836	4.24E-09
ENSG00000232388.2	LINC00493	2.852478957	0.000990434
ENSG00000267381.1	CTD-2086O20.3	2.851471308	0.035235529
ENSG00000172273.8	HINFP	2.848870948	0.000170799
ENSG00000228643.1	AC079779.4	2.847776685	0.014992341
ENSG00000146678.5	IGFBP1	2.843625027	7.61E-07
ENSG00000133134.7	BEX2	2.840264741	0.038677996
ENSG00000244313.2	RP11-425L10.1	2.836280915	2.49E-07
ENSG00000206149.6	HERC2P9	2.825380629	0.024998762
ENSG00000173915.8	USMG5	2.81757687	1.07E-05
ENSG00000163110.10	PDLIM5	2.814346554	1.43E-10
ENSG00000186577.7	C6orf1	2.798498646	9.19E-07
ENSG00000175841.7	FAM172BP	2.797787443	0.043025211
ENSG00000162298.12	SYVN1	2.793616689	0.001796007
ENSG00000108961.9	RANGRF	2.791776015	2.37E-05
ENSG00000164543.5	STK17A	2.791470205	1.82E-12
ENSG00000011009.6	LYPLA2	2.790759234	1.30E-10
ENSG00000125870.6	SNRPB2	2.788074521	1.60E-07
ENSG00000198736.7	MSRB1	2.78755936	6.50E-12
ENSG00000242951.1	RP11-507E23.1	2.785586866	0.005847707
ENSG00000224032.2	EPB41L4A-AS1	2.773225675	6.19E-06
ENSG00000063177.8	RPL18	2.77253265	5.17E-09
ENSG00000230002.2	ALMS1-IT1	2.772255273	5.57E-05
ENSG00000114354.8	TFG	2.771243475	1.08E-06
ENSG00000086827.4	ZW10	2.77091317	6.89E-07
ENSG00000165886.4	UBTD1	2.767945298	6.23E-09
ENSG00000023734.6	STRAP	2.765533473	1.12E-08
ENSG00000166136.11	NDUFB8	2.764646065	1.44E-08
ENSG00000166908.13	PIP4K2C	2.761663095	0.000546362
ENSG00000132471.7	WBP2	2.760227554	6.41E-07
ENSG00000242588.2	RP11-274B21.1	2.757797981	0.013058336
ENSG00000160179.14	ABCG1	2.757631474	0.045024537
ENSG00000171720.5	HDAC3	2.751674279	3.28E-06
ENSG00000132323.4	ILKAP	2.749122599	2.33E-08
ENSG00000128510.6	CPA4	2.736799941	0.000340433
ENSG00000116030.12	SUMO1	2.732473717	1.67E-07
ENSG00000018869.12	ZNF582	2.730821812	0.031771448
ENSG00000177025.3	C19orf18	2.730226687	8.53E-07
ENSG00000070404.5	FSTL3	2.727084831	1.53E-17
ENSG00000073921.13	PICALM	2.726678283	2.52E-08
ENSG00000106245.5	BUD31	2.723186153	1.10E-09

ENSG00000229833.5	PET100	2.721703719	0.00022407
ENSG00000063438.12	AHRR	2.717340941	0.000368373
ENSG00000100867.10	DHRS2	2.715837547	0.000502759
ENSG00000116791.9	CRYZ	2.714915454	2.16E-06
ENSG00000205639.5	MFSD2B	2.709627089	0.000537817
ENSG00000242125.2	SNHG3	2.706740168	4.39E-05
ENSG00000170638.5	TRABD	2.698045227	3.00E-05
ENSG00000132801.5	ZSWIM3	2.697975871	0.001463816
ENSG00000133818.8	RRAS2	2.691997617	6.26E-06
ENSG00000125995.11	ROMO1	2.691935551	4.20E-08
ENSG00000158825.5	CDA	2.69163896	0.005776791
ENSG00000113552.11	GNPDA1	2.691510256	2.16E-09
ENSG00000072401.10	UBE2D1	2.689936846	0.000162681
ENSG00000250616.2	RP11-455F5.3	2.687054847	0.000520653
ENSG00000137876.5	RSL24D1	2.685670386	2.33E-10
ENSG00000217555.8	CKLF	2.679729879	7.31E-07
ENSG00000112337.6	SLC17A2	2.678568795	0.003141669
ENSG00000085117.7	CD82	2.67440199	0.004256531
ENSG00000189143.8	CLDN4	2.673555422	2.13E-06
ENSG00000186468.8	RPS23	2.673182427	1.85E-06
ENSG00000162616.8	DNAJB4	2.672849459	3.79E-11
ENSG00000117450.9	PRDX1	2.667217242	4.83E-10
ENSG00000092203.9	TOX4	2.665868172	1.40E-11
ENSG00000160908.14	ZNF394	2.664904958	2.74E-06
ENSG00000160563.9	MED27	2.663892672	3.70E-10
ENSG00000147687.12	TATDN1	2.660013534	7.34E-08
ENSG00000236844.1	AC091633.2	2.657839142	1.05E-06
ENSG00000132432.9	SEC61G	2.657816358	0.000227044
ENSG00000091592.11	NLRP1	2.637922346	4.05E-07
ENSG00000163479.9	SSR2	2.637915631	1.23E-06
ENSG00000261690.1	AC009133.12	2.637240581	0.013350078
ENSG00000086065.9	CHMP5	2.636518813	1.09E-10
ENSG00000272218.1	RP11-11N5.3	2.634358626	0.039814263
ENSG00000267249.1	RP11-973H7.3	2.634137688	0.008302503
ENSG00000147604.9	RPL7	2.633175801	4.52E-08
ENSG00000094975.9	SUCO	2.623952826	2.52E-08
ENSG00000150527.12	CTAGE5	2.620342193	4.85E-05
ENSG00000143553.6	SNAPIN	2.620119022	0.006333634
ENSG00000272405.1	RP11-284F21.10	2.618126488	2.29E-07
ENSG00000221955.6	SLC12A8	2.614492616	0.001959974
ENSG00000196387.5	ZNF140	2.609626375	0.001028108
ENSG00000250321.1	RP11-478C6.4	2.609463977	2.74E-10
ENSG00000082781.7	ITGB5	2.607132995	1.37E-06
ENSG00000228399.1	RP4-575N6.2	2.606189723	0.024613223
ENSG00000114670.9	NEK11	2.603423446	0.000411458
ENSG00000172927.3	MYEOV	2.601455799	0.018552978
ENSG00000213300.4	HNRNPA3P6	2.601436813	0.001180525
ENSG00000110395.4	CBL	2.601324774	8.10E-08
ENSG00000089159.11	PXN	2.60124984	4.11E-08
ENSG00000168374.6	ARF4	2.598942148	2.90E-07

ENSG00000131174.4	COX7B	2.598480573	0.003267843
ENSG00000146386.7	ABRACL	2.594189692	5.46E-05
ENSG00000196683.6	TOMM7	2.591700883	1.76E-07
ENSG00000231940.1	RPS7P3	2.59113693	0.002286889
ENSG00000230629.2	RPS23P8	2.590836719	8.23E-05
ENSG00000124145.5	SDC4	2.587436618	7.14E-07
ENSG00000162604.8	TM2D1	2.585416666	0.000117003
ENSG00000178307.5	TMEM11	2.580384103	1.09E-05
ENSG00000104064.12	GABPB1	2.579954694	2.73E-05
ENSG00000145824.8	CXCL14	2.579051723	0.013096236
ENSG00000231609.1	AC009501.4	2.578153297	5.13E-05
ENSG00000143977.9	SNRPG	2.577688043	1.51E-07
ENSG00000109133.8	TMEM33	2.57745547	2.81E-06
ENSG00000132341.7	RAN	2.57612812	8.38E-05
ENSG00000013583.4	HEBP1	2.573633595	1.06E-05
ENSG00000028839.5	TBPL1	2.571460219	0.000242701
ENSG00000166455.9	C16orf46	2.570493181	0.000107518
ENSG00000120875.4	DUSP4	2.568475005	0.000246477
ENSG00000120265.12	PCMT1	2.566575239	1.71E-07
ENSG00000076321.6	KLHL20	2.56442301	0.000254268
ENSG00000122641.9	INHBA	2.555913949	0.044384151
ENSG00000092758.11	COL9A3	2.555906864	0.000501504
ENSG00000133318.9	RTN3	2.555358706	2.70E-06
ENSG00000225828.1	FAM229A	2.554144933	0.001003274
ENSG00000084090.9	STARD7	2.553322308	9.63E-08
ENSG00000234545.3	FAM133B	2.55031646	2.02E-06
ENSG00000204839.4	MROH6	2.549285389	0.000675784
ENSG00000109332.15	UBE2D3	2.54610104	9.07E-09
ENSG00000129245.7	FXR2	2.546084493	1.47E-07
ENSG00000203760.4	CENPW	2.541348599	2.83E-07
ENSG00000068697.6	LAPTM4A	2.540775767	5.05E-06
ENSG00000178498.11	DTX3	2.539730067	0.001172676
ENSG00000115540.10	MOB4	2.537815244	5.42E-05
ENSG00000162517.8	PEF1	2.534792603	0.000314703
ENSG00000077721.11	UBE2A	2.533925735	3.87E-05
ENSG00000158201.5	ABHD3	2.533231594	8.88E-07
ENSG00000169220.13	RGS14	2.531630114	0.003786144
ENSG00000142676.8	RPL11	2.530076277	2.70E-07
ENSG00000141753.5	IGFBP4	2.522341824	3.14E-05
ENSG00000123562.12	MORF4L2	2.521885261	2.72E-05
ENSG00000183741.7	CBX6	2.520992755	1.85E-07
ENSG00000014216.11	CAPN1	2.519737822	3.13E-07
ENSG00000124171.4	PARD6B	2.51682506	1.00E-08
ENSG00000167767.9	KRT80	2.506667358	0.000409433
ENSG00000104756.11	KCTD9	2.50579426	8.70E-08
ENSG00000140474.8	ULK3	2.502937252	0.000138238
ENSG00000196655.5	TRAPPC4	2.502096881	2.03E-05
ENSG00000145040.3	UCN2	2.50117055	0.01899395
ENSG00000132507.13	EIF5A	2.501099381	2.88E-05
ENSG00000086666.14	ZFAND6	2.500947482	5.03E-07

ENSG00000182899.10	RPL35A	2.499893138	8.48E-07
ENSG00000135845.5	PIGC	2.486375137	2.73E-05
ENSG00000116209.7	TMEM59	2.485692846	0.000112474
ENSG00000257433.1	RP1-197B17.3	2.482054253	0.016611262
ENSG00000228794.4	RP11-206L10.11	2.48024791	0.005562116
ENSG00000105583.5	WDR83OS	2.479428355	2.30E-08
ENSG00000256940.1	RP11-783K16.5	2.479296058	2.74E-05
ENSG00000174748.14	RPL15	2.479187578	7.27E-06
ENSG00000116668.8	SWT1	2.473500266	9.12E-05
ENSG00000167380.12	ZNF226	2.472410427	0.000164023
ENSG00000185641.5	CTD-2287O16.1	2.47018265	1.47E-05
ENSG00000117262.14	GPR89A	2.469865347	0.001369653
ENSG00000161647.14	MPP3	2.469401697	0.000918708
ENSG00000156261.8	CCT8	2.46930848	9.74E-07
ENSG00000127955.11	GNAI1	2.463258849	0.00013478
ENSG00000224856.2	RP4-796I17.5	2.461899627	0.001234976
ENSG00000272788.1	RP11-674N23.4	2.461419565	0.01444716
ENSG00000130985.12	UBA1	2.461303299	3.38E-05
ENSG00000123416.11	TUBA1B	2.459927003	8.62E-06
ENSG00000122565.14	CBX3	2.459601429	2.41E-08
ENSG00000131725.9	WDR44	2.45794935	8.89E-06
ENSG00000147669.6	POLR2K	2.457017203	3.11E-05
ENSG00000124614.9	RPS10	2.450741221	9.28E-08
ENSG00000099904.11	ZDHHC8	2.448513285	0.012280034
ENSG00000111361.8	EIF2B1	2.444822159	1.66E-06
ENSG00000125753.9	VASP	2.437073677	5.23E-07
ENSG00000112110.5	MRPL18	2.436330355	3.07E-07
ENSG00000259976.1	RP11-553L6.5	2.432607281	0.00051957
ENSG00000156026.10	MCU	2.432378082	4.87E-06
ENSG00000256969.1	RP11-320N7.2	2.432293527	0.000169313
ENSG00000112183.10	RBM24	2.431026937	0.0002877
ENSG00000168283.9	BMI1	2.430254828	9.94E-06
ENSG00000115268.5	RPS15	2.425269884	1.27E-07
ENSG00000177889.5	UBE2N	2.423456181	0.000251503
ENSG00000163785.8	RYK	2.422285702	3.35E-05
ENSG00000106089.7	STX1A	2.42195749	0.008373636
ENSG00000010072.11	SPRTN	2.418069142	2.78E-06
ENSG00000087086.9	FTL	2.417638488	1.19E-08
ENSG00000168010.6	ATG16L2	2.414940056	0.001033612
ENSG00000125952.14	MAX	2.410306736	3.09E-05
ENSG00000086200.12	IPO11	2.409183844	0.00022749
ENSG00000229344.1	RP5-857K21.7	2.408149039	0.000213075
ENSG00000145736.10	GTF2H2	2.407508376	0.002378573
ENSG00000204282.3	TNRC6C-AS1	2.405190595	0.004481934
ENSG00000242553.1	AP001432.14	2.404127963	0.030539801
ENSG00000203727.3	SAMD5	2.404073127	0.011572583
ENSG00000120963.7	ZNF706	2.401142917	0.000179475
ENSG00000103512.10	NOMO1	2.400878008	1.02E-06
ENSG00000100528.7	CNIH1	2.396752079	1.44E-05
ENSG00000102309.8	PIN4	2.389672868	0.000721656

ENSG00000100906.6	NFKBIA	2.389516697	9.73E-06
ENSG00000168496.3	FEN1	2.385145562	7.56E-05
ENSG00000167325.10	RRM1	2.38372107	2.81E-06
ENSG00000051009.6	FAM160A2	2.383638654	0.000845657
ENSG00000178741.7	COX5A	2.381212512	2.76E-05
ENSG00000103257.4	SLC7A5	2.380305428	6.58E-07
ENSG00000169019.9	COMMD8	2.378618045	0.000819113
ENSG00000121064.8	SCPEP1	2.377732101	7.85E-07
ENSG00000155085.11	AK9	2.376014982	0.006427574
ENSG00000131100.8	ATP6V1E1	2.37561804	1.22E-09
ENSG00000164825.3	DEFB1	2.375588591	0.01699371
ENSG00000182544.8	MFSD5	2.371100748	9.35E-05
ENSG00000147533.12	GOLGA7	2.370456774	2.48E-06
ENSG00000113558.14	SKP1	2.369853858	5.88E-09
ENSG00000166710.13	B2M	2.366613222	1.50E-06
ENSG00000137210.9	TMEM14B	2.365127624	1.37E-05
ENSG00000178127.8	NDUFV2	2.363009379	2.04E-06
ENSG00000230383.1	AC009245.3	2.360299049	0.02143874
ENSG00000135747.7	ZNF670	2.357906517	0.006077488
ENSG00000204272.6	RP11-622K12.1	2.357634897	0.01805161
ENSG00000100478.10	AP4S1	2.354170015	0.000752017
ENSG00000112245.6	PTP4A1	2.35405962	2.94E-06
ENSG00000070495.10	JMJD6	2.351645174	4.22E-09
ENSG00000141644.13	MBD1	2.349540921	1.09E-07
ENSG00000129474.11	AJUBA	2.349183805	0.000264115
ENSG00000107554.11	DNMBP	2.348200824	0.001378953
ENSG00000058799.9	YIPF1	2.347528243	1.87E-05
ENSG00000117395.6	EBNA1BP2	2.347414286	8.98E-09
ENSG00000172331.7	BPGM	2.346945152	0.000161452
ENSG00000189159.11	HN1	2.346481886	1.31E-08
ENSG00000175826.7	CTDNEP1	2.345139167	3.66E-06
ENSG00000116815.11	CD58	2.343540063	4.76E-05
ENSG00000197498.8	RPF2	2.342282041	2.89E-09
ENSG00000175691.8	ZNF77	2.342188854	0.000457215
ENSG00000221926.7	TRIM16	2.342138211	0.001947738
ENSG00000155252.12	PI4K2A	2.341573516	1.54E-06
ENSG00000230666.1	CEACAM22P	2.340884045	0.001038415
ENSG00000210107.1	MT-TQ	2.338809164	0.02119434
ENSG00000102805.9	CLN5	2.338784512	0.011786403
ENSG00000131746.8	TNS4	2.338711125	2.47E-05
ENSG00000108671.5	PSMD11	2.32945427	2.26E-10
ENSG00000182141.5	ZNF708	2.32919505	0.021970173
ENSG00000022840.11	RNF10	2.326081538	4.17E-08
ENSG00000214374.2	RPLP2P1	2.32242574	0.008324854
ENSG00000254999.2	BRK1	2.322101086	1.92E-07
ENSG00000105281.8	SLC1A5	2.321660692	2.72E-08
ENSG00000106829.14	TLE4	2.321578734	0.00038566
ENSG00000110442.7	COMMD9	2.321167223	3.88E-05
ENSG00000100319.11	ZMAT5	2.320199102	0.00026777
ENSG00000135074.11	ADAM19	2.313696371	0.001219925

ENSG00000105373.14	GLTSCR2	2.312337154	1.57E-07
ENSG00000102359.5	SRPX2	2.311967045	0.03309448
ENSG00000110906.8	KCTD10	2.309230093	9.81E-06
ENSG00000164978.13	NUDT2	2.306367199	0.000162214
ENSG00000109270.8	LAMTOR3	2.306306849	7.46E-10
ENSG00000223380.3	SEC22B	2.301470941	1.09E-05
ENSG00000151553.10	FAM160B1	2.301050307	0.004481401
ENSG00000174177.8	CTU2	2.298981025	0.000651994
ENSG00000113070.6	HBEGF	2.298810457	3.73E-09
ENSG00000186767.5	SPIN4	2.29748348	0.001620488
ENSG00000198440.5	ZNF583	2.297274903	0.035332195
ENSG00000146670.5	CDCA5	2.294472105	2.55E-07
ENSG00000236682.1	AC068282.3	2.293445423	0.019707547
ENSG00000118680.8	MYL12B	2.291982772	8.24E-08
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ENSG00000146066.2	HIGD2A	2.290784098	0.000138885
ENSG00000196976.5	LAGE3	2.289756704	0.005780658
ENSG00000124802.7	EEF1E1	2.287784257	1.11E-05
ENSG00000136888.6	ATP6V1G1	2.286736142	3.33E-08
ENSG00000029639.6	TFB1M	2.285225334	0.000329175
ENSG00000158480.6	SPATA2	2.28491141	2.40E-06
ENSG00000159596.6	TMEM69	2.28294599	0.001777527
ENSG00000197275.8	RAD54B	2.282845752	0.034447057
ENSG00000181610.8	MRPS23	2.279148735	1.54E-06
ENSG00000157778.4	PSMG3	2.278135875	3.69E-07
ENSG00000163435.11	ELF3	2.276445085	2.16E-11
ENSG00000197588.5	KLKP1	2.275194776	0.049194912
ENSG00000106615.5	RHEB	2.273360208	7.29E-05
ENSG00000140859.11	KIFC3	2.271776771	3.57E-05
ENSG00000133112.12	TPT1	2.269415674	4.12E-06
ENSG00000137936.12	BCAR3	2.269241299	0.004265602
ENSG00000136932.9	C9orf156	2.266948219	2.20E-05
ENSG00000228436.2	RP5-864K19.4	2.265142185	0.041199364
ENSG00000212802.3	RPL15P3	2.264510193	5.76E-05
ENSG00000108590.6	MED31	2.264162668	1.05E-06
ENSG00000056277.11	ZNF280C	2.262778226	0.004449762
ENSG00000173825.6	TIGD3	2.261598826	0.035598008
ENSG00000213130.3	EEF1DP5	2.260273613	0.005219739
ENSG00000184916.4	JAG2	2.259386565	0.022771185
ENSG00000147180.12	ZNF711	2.25856585	1.06E-05
ENSG00000163918.6	RFC4	2.258057197	0.000752946
ENSG00000259622.1	RP11-597K23.1	2.257426838	0.03188343
ENSG00000111711.5	GOLT1B	2.256396373	4.27E-05
ENSG00000263883.1	RP11-51F16.5	2.25590215	0.017074204
ENSG00000134049.3	IER3IP1	2.254766701	4.85E-05
ENSG00000101017.9	CD40	2.253677749	0.012327957
ENSG00000211455.3	STK38L	2.252564335	0.000159303
ENSG00000122958.10	VPS26A	2.250928841	1.55E-08
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ENSG00000177034.10	MTX3	2.246097336	0.026465413

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ENSG00000132718.7	SYT11	2.243729046	0.013514403
ENSG00000170542.5	SERPINB9	2.242647143	3.38E-06
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ENSG00000235770.1	LINC00607	2.240842199	0.0491887
ENSG00000175470.14	PPP2R2D	2.23894659	2.45E-07
ENSG00000164663.9	USP49	2.237782498	0.00017276
ENSG00000196449.3	YRDC	2.234267049	2.16E-09
ENSG00000146574.11	CCZ1B	2.234249327	0.004998537
ENSG00000184886.3	PIGW	2.228830832	0.000101298
ENSG00000101150.13	TPD52L2	2.226093134	1.15E-06
ENSG00000162614.14	NEXN	2.223690499	5.66E-09
ENSG00000168522.8	FNTA	2.223512846	6.77E-05
ENSG00000143106.8	PSMA5	2.223272806	0.000106475
ENSG00000142937.7	RPS8	2.221842723	2.02E-05
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ENSG00000141524.11	TMC6	2.218238756	4.94E-10
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ENSG00000160828.13	STAG3L2	2.216754198	0.00686343
ENSG00000131508.11	UBE2D2	2.215730079	1.09E-05
ENSG00000225648.1	SBDSP1	2.212547721	4.42E-05
ENSG00000161091.8	MFSD12	2.212314764	1.63E-08
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ENSG00000094841.9	UPRT	2.211036745	0.015687687
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ENSG00000242527.1	RP11-159H22.1	2.209158579	0.020134225
ENSG00000111215.7	PRR4	2.207607628	0.002065098
ENSG00000167130.13	DOLPP1	2.205624037	0.001815915
ENSG00000170315.9	UBB	2.203317304	1.18E-08
ENSG00000259820.1	AC083843.1	2.201061228	0.026513799
ENSG00000197756.5	RPL37A	2.201023764	1.06E-05
ENSG00000064419.9	TNPO3	2.198032428	5.02E-07
ENSG00000070423.13	RNF126	2.197579836	0.008470505
ENSG00000257815.1	RP11-611E13.2	2.197239	0.000683625
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ENSG00000060069.12	CTDP1	2.195028838	0.000135613
ENSG00000196155.8	PLEKHG4	2.194305093	0.000589916
ENSG00000125611.11	CHCHD5	2.192035781	0.002079623
ENSG00000135919.8	SERPINE2	2.19200285	9.43E-10
ENSG00000168917.8	SLC35G2	2.191104578	0.035551671
ENSG00000125743.6	SNRPD2	2.189877237	3.87E-07
ENSG00000090932.6	DLL3	2.189460484	0.010422029
ENSG00000171055.10	FEZ2	2.187685631	4.12E-06
ENSG00000125746.10	EML2	2.185940122	1.64E-05
ENSG00000131748.11	STARD3	2.184799904	1.59E-06
ENSG00000164603.7	C7orf60	2.181953938	0.000197477
ENSG00000102312.16	PORCN	2.181748841	0.003501439
ENSG00000100836.6	PABPN1	2.181416547	2.73E-07

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ENSG00000152454.3	ZNF256	2.1774428	0.019020204
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ENSG00000154719.9	MRPL39	2.175877281	0.006571508
ENSG00000008282.3	SYPL1	2.171727252	0.001837596
ENSG00000178440.5	LINC00843	2.170363848	0.045248368
ENSG00000100142.10	POLR2F	2.169655269	7.06E-05
ENSG00000114956.15	DGUOK	2.165844477	2.44E-05
ENSG00000134954.10	ETS1	2.165168047	0.043924398
ENSG00000173801.12	JUP	2.164121619	0.006151182
ENSG00000186184.11	POLR1D	2.163675125	7.05E-06
ENSG00000023330.10	ALAS1	2.163101995	1.18E-07
ENSG00000198900.5	TOP1	2.162833583	3.87E-11
ENSG00000144589.16	STK11IP	2.161673753	1.09E-07
ENSG00000175701.6	LINC00116	2.156558406	0.039689637
ENSG00000141030.8	COPS3	2.154706656	6.99E-07
ENSG00000138050.10	THUMPD2	2.153338831	0.000543396
ENSG00000213281.4	NRAS	2.152536984	8.02E-06
ENSG00000185467.7	KPNA7	2.151259526	0.035613384
ENSG00000100246.8	DNAL4	2.149165344	0.004342588
ENSG00000049656.9	CLPTM1L	2.148866503	0.001658489
ENSG00000154174.7	TOMM70A	2.148704532	5.59E-05
ENSG00000172977.8	KAT5	2.14722818	2.67E-06
ENSG00000143797.7	MBOAT2	2.145017938	0.03497459
ENSG00000205078.5	SYCE1L	2.144800111	0.041320885
ENSG00000198818.5	SFT2D1	2.144593537	4.42E-05
ENSG00000174021.6	GNG5	2.144458445	0.001726346
ENSG00000143398.15	PIP5K1A	2.142917991	1.68E-05
ENSG00000163682.11	RPL9	2.142500499	4.73E-05
ENSG00000109534.12	GAR1	2.141400657	0.000167943
ENSG00000109736.10	MFSD10	2.138467392	0.000122827
ENSG00000272145.1	RP4-739H11.4	2.137129598	0.006707156
ENSG00000142230.7	SAE1	2.133595091	3.49E-06
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ENSG00000013588.5	GPRC5A	2.130748128	0.001746573
ENSG00000111057.6	KRT18	2.130006474	2.28E-08
ENSG00000135631.11	RAB11FIP5	2.129856908	2.54E-06
ENSG00000168002.7	POLR2G	2.129797706	1.36E-05
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ENSG00000139350.7	NEDD1	2.128160291	0.001108674
ENSG00000100058.8	CRYBB2P1	2.127535393	7.11E-08
ENSG00000107872.8	FBXL15	2.12727566	0.00654862
ENSG00000179454.9	KLHL28	2.125321649	2.37E-06
ENSG00000116809.7	ZBTB17	2.120352631	1.07E-05
ENSG00000173465.3	SSSCA1	2.117867024	0.014323531
ENSG00000047634.10	SCML1	2.117830864	3.08E-05
ENSG00000110108.5	TMEM109	2.115242506	0.001521031
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ENSG00000092330.11	TINF2	2.113506538	1.52E-05

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ENSG00000239440.1	RP11-260O18.1	2.106121386	0.000450145
ENSG00000135624.11	CCT7	2.10552428	9.35E-07
ENSG00000005238.15	FAM214B	2.104082129	0.023706685
ENSG00000131475.2	VPS25	2.10344121	1.62E-07
ENSG00000226532.1	RP5-1052M9.1	2.101570653	1.36E-06
ENSG00000023445.9	BIRC3	2.100257183	4.15E-10
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ENSG00000181467.2	RAP2B	2.09697869	0.001485174
ENSG00000267041.1	ZNF850	2.095995586	0.024290394
ENSG00000133884.5	DPF2	2.09489772	0.000228573
ENSG00000124226.7	RNF114	2.093398533	1.60E-10
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ENSG00000104671.3	DCTN6	2.090644878	0.002331031
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ENSG00000120889.8	TNFRSF10B	2.089975705	0.000390192
ENSG00000139988.5	RDH12	2.08699204	0.018128528
ENSG00000136167.9	LCP1	2.086334295	0.014642314
ENSG00000123643.8	SLC36A1	2.085801917	0.000565478
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ENSG00000143222.7	UFC1	2.070218234	1.63E-08
ENSG00000177879.10	AP3S1	2.068569577	0.002669348
ENSG00000140319.6	SRP14	2.068414334	1.74E-08
ENSG00000159247.8	TUBBP5	2.067701101	0.013865046
ENSG00000185842.10	DNAH14	2.067373016	0.000165009
ENSG00000131979.14	GCH1	2.067004277	1.42E-05
ENSG00000128590.4	DNAJB9	2.065229516	0.000452764
ENSG00000196437.6	ZNF569	2.064621854	0.005690464
ENSG00000160201.7	U2AF1	2.063177239	2.33E-06
ENSG00000117748.5	RPA2	2.062348949	7.46E-05
ENSG00000231607.4	DLEU2	2.061153665	0.031771448
ENSG00000159840.11	ZYX	2.056620593	1.76E-05
ENSG00000114395.6	CYB561D2	2.055544481	0.014245467
ENSG00000012660.9	ELOVL5	2.053324387	8.77E-10
ENSG00000175376.4	EIF1AD	2.050395315	1.33E-08
ENSG00000215030.4	RPL13P12	2.049059897	4.71E-05
ENSG00000175104.10	TRAF6	2.048570641	0.01422153
ENSG00000073111.9	MCM2	2.047483082	0.004030839
ENSG00000154803.8	FLCN	2.047254811	1.10E-06
ENSG00000168273.3	SMIM4	2.047019228	0.001772723
ENSG00000170619.8	COMMD5	2.046094638	0.001417322
ENSG00000234518.1	PTGES3P1	2.0432883	8.59E-06
ENSG00000127511.5	SIN3B	2.040955642	1.33E-05
ENSG00000135205.10	CCDC146	2.039483091	0.024386228

ENSG00000187742.10	SECISBP2	2.039373656	2.53E-11
ENSG00000176340.3	COX8A	2.039100402	4.06E-05
ENSG00000104219.8	ZDHHC2	2.038374654	0.014986943
ENSG00000165355.7	FBXO33	2.038081281	9.15E-09
ENSG00000136699.15	SMPD4	2.037495285	4.57E-05
ENSG00000105185.7	PDCD5	2.035216943	0.000151439
ENSG00000158023.5	WDR66	2.029240725	0.023278037
ENSG00000106636.3	YKT6	2.027304178	1.59E-07
ENSG00000198176.8	TFDP1	2.025640679	0.001388543
ENSG00000181744.4	C3orf58	2.024767146	0.000250762
ENSG00000101844.13	ATG4A	2.022595971	0.000127567
ENSG00000180914.6	OXTR	2.022576421	0.041207922
ENSG00000133731.5	IMPA1	2.020038272	1.14E-05
ENSG00000136146.10	MED4	2.019525667	1.19E-06
ENSG00000241343.5	RPL36A	2.01841033	1.37E-06
ENSG00000114115.5	RBP1	2.017770293	3.07E-07
ENSG00000099625.8	C19orf26	2.016131759	0.002670644
ENSG00000129911.4	KLF16	2.014284023	0.005406449
ENSG00000107371.8	EXOSC3	2.010961779	0.001796372
ENSG00000165416.10	SUGT1	2.009524932	3.94E-07
ENSG00000170412.12	GPRC5C	2.00886828	5.65E-06
ENSG00000155256.13	ZFYVE27	2.008169498	0.000110504
ENSG00000148426.8	PROSER2	2.006769516	2.14E-05
ENSG00000171451.13	DSEL	2.004437009	0.006725898
ENSG00000154978.8	VOPP1	2.004205493	0.000715487
ENSG00000146072.6	TNFRSF21	2.003019184	1.93E-05
ENSG00000163605.10	PPP4R2	2.001331278	6.30E-06
ENSG00000131467.6	PSME3	2.000582782	2.46E-07
ENSG00000166986.8	MARS	1.996899941	1.43E-10
ENSG00000234093.2	RPS15AP11	1.996005035	0.035728854
ENSG00000151881.10	C5orf28	1.99560303	0.014637208
ENSG00000138297.9	TIMM23	1.992370414	0.000106408
ENSG00000162819.7	BROX	1.991768097	0.006707156
ENSG00000100591.3	AHSA1	1.989578989	2.51E-08
ENSG00000146648.11	EGFR	1.987673508	0.000336317
ENSG00000242071.2	RPL7AP6	1.985241223	0.048006388
ENSG00000104343.15	UBE2W	1.984996089	0.000103462
ENSG00000203819.6	HIST2H2BC	1.984047327	0.010121575
ENSG00000121274.8	PAPD5	1.980012985	9.72E-07
ENSG00000124767.6	GLO1	1.977724627	0.000418309
ENSG00000197647.7	ZNF433	1.975878759	0.018847021
ENSG00000105372.2	RPS19	1.973513107	4.06E-06
ENSG00000115944.10	COX7A2L	1.972651556	0.004158762
ENSG00000197345.8	MRPL21	1.972327138	3.67E-06
ENSG00000102471.9	NDFIP2	1.970589048	0.000288755
ENSG00000169087.6	HSPBAP1	1.968275173	0.027643159
ENSG00000219529.2	AP000580.1	1.967675891	7.04E-05
ENSG00000083454.17	P2RX5	1.967088143	0.04157126
ENSG00000197622.8	CDC42SE1	1.96695104	3.57E-05
ENSG00000122042.9	UBL3	1.966125691	1.13E-09

ENSG00000187688.10	TRPV2	1.966031003	1.21E-06
ENSG00000205937.7	RNPS1	1.965638446	1.67E-06
ENSG00000134308.9	YWHAQ	1.965261866	0.000178359
ENSG00000263731.1	RP11-498C9.15	1.964304587	0.016189289
ENSG00000117118.5	SDHB	1.964215476	0.000842049
ENSG00000140320.7	BAHD1	1.96119569	9.02E-05
ENSG00000156256.10	USP16	1.960898734	4.14E-06
ENSG00000124789.7	NUP153	1.958756776	7.18E-05
ENSG00000008405.7	CRY1	1.957535881	1.75E-08
ENSG00000100280.12	AP1B1	1.957147706	9.84E-07
ENSG00000149231.7	CCDC82	1.955723579	2.94E-08
ENSG00000261526.1	CTB-31O20.2	1.955495298	0.000142972
ENSG00000086619.9	ERO1LB	1.953970774	0.000245447
ENSG00000167657.7	DAPK3	1.953141207	0.000210566
ENSG00000170310.10	STX8	1.953014083	0.004131942
ENSG00000128463.8	EMC4	1.949361781	1.98E-06
ENSG00000085231.9	TAF9	1.946673155	0.001474786
ENSG00000260924.2	AC004463.6	1.941655079	0.031678993
ENSG00000117226.7	GBP3	1.940764945	0.011844444
ENSG00000210140.1	MT-TC	1.940401174	9.50E-07
ENSG00000146425.6	DYNLT1	1.94026336	0.003229289
ENSG00000139180.6	NDUFA9	1.940082458	6.03E-06
ENSG00000172046.14	USP19	1.93819197	4.83E-05
ENSG00000110321.11	EIF4G2	1.938104967	8.46E-05
ENSG00000231500.2	RPS18	1.937803753	4.04E-06
ENSG00000090013.5	BLVRB	1.93032186	6.09E-09
ENSG00000144659.6	SLC25A38	1.930178463	0.008527093
ENSG00000117592.8	PRDX6	1.927107233	2.90E-06
ENSG00000186222.3	BLOC1S4	1.92641742	0.021656592
ENSG00000235919.3	ASH1L-AS1	1.924304219	6.40E-06
ENSG00000158623.10	COPG2	1.923715714	0.001762457
ENSG00000183287.9	CCBE1	1.921616071	0.047314813
ENSG00000175324.5	LSM1	1.921498985	7.92E-05
ENSG00000183091.15	NEB	1.920445147	0.007816411
ENSG00000071082.6	RPL31	1.919627176	0.000178331
ENSG00000244306.5	CTD-2314B22.3	1.918152749	0.003649937
ENSG00000140465.9	CYP1A1	1.917515188	0.005150318
ENSG00000203879.7	GDI1	1.916633764	6.73E-07
ENSG00000012124.10	CD22	1.914450952	0.000213075
ENSG00000075618.13	FSCN1	1.913949293	0.000189863
ENSG00000227482.1	RP11-18B16.2	1.911766202	0.025800929
ENSG00000101745.11	ANKRD12	1.911184762	1.02E-07
ENSG00000151366.8	NDUFC2	1.910946077	1.83E-06
ENSG00000048162.15	NOP16	1.910058268	6.09E-06
ENSG00000154640.10	BTG3	1.909709936	6.62E-07
ENSG00000223482.3	NUTM2A-AS1	1.909078349	0.023965654
ENSG00000178567.5	EPM2AIP1	1.908364904	7.00E-07
ENSG00000167676.3	PLIN4	1.906627943	7.07E-05
ENSG00000179766.13	ATP8B5P	1.904425384	0.000146689
ENSG00000104852.10	SNRNP70	1.903807206	7.31E-05

ENSG00000067113.12	PPAP2A	1.902513886	0.010049318
ENSG00000137575.7	SDCBP	1.901969884	2.45E-08
ENSG00000254986.3	DPP3	1.9016665	0.001826877
ENSG00000168906.8	MAT2A	1.899195585	0.000336763
ENSG00000141428.12	C18orf21	1.898934633	0.002358678
ENSG00000196268.7	ZNF493	1.897426877	0.002708368
ENSG00000003402.15	CFLAR	1.89667657	2.01E-05
ENSG00000173626.5	TRAPPC3L	1.895853037	0.041150108
ENSG00000127774.6	EMC6	1.894358845	0.000190318
ENSG00000137504.9	CREBZF	1.892955617	5.59E-05
ENSG00000242338.2	BMS1P4	1.890838172	0.044591647
ENSG00000167182.11	SP2	1.887532969	0.034447057
ENSG00000196378.7	ZNF34	1.886454204	0.005881228
ENSG00000153561.8	RMND5A	1.886448278	0.000181067
ENSG00000134058.6	CDK7	1.886198591	5.82E-05
ENSG00000164548.6	TRA2A	1.883919324	6.92E-05
ENSG00000165609.8	NUDT5	1.883915582	0.00013201
ENSG00000143570.13	SLC39A1	1.882398644	6.67E-05
ENSG00000198146.4	ZNF770	1.879767195	5.93E-05
ENSG00000087842.6	PIR	1.877205085	0.001229217
ENSG00000197265.4	GTF2E2	1.876933383	3.32E-06
ENSG00000101079.16	NDRG3	1.876023858	2.27E-06
ENSG00000141338.9	ABCA8	1.875966403	0.037072169
ENSG00000105327.11	BBC3	1.871835823	0.005974006
ENSG00000101210.6	EEF1A2	1.869397527	0.022944541
ENSG00000105568.13	PPP2R1A	1.869056268	0.002165383
ENSG00000081721.7	DUSP12	1.868364576	0.015254807
ENSG00000213799.6	ZNF845	1.868307205	0.013612473
ENSG00000105643.5	ARRDC2	1.865608877	0.019590972
ENSG00000123106.6	CCDC91	1.865069059	2.79E-06
ENSG00000269958.1	RP11-73M18.8	1.864097176	0.000282949
ENSG00000121281.8	ADCY7	1.862411341	0.004050683
ENSG00000108294.4	PSMB3	1.862227491	5.07E-07
ENSG00000103363.10	TCEB2	1.862121925	2.89E-06
ENSG00000004455.12	AK2	1.860938677	2.95E-07
ENSG00000165233.13	C9orf89	1.854555936	0.001216728
ENSG00000118855.14	MFSD1	1.854143591	3.45E-05
ENSG00000186166.4	CCDC84	1.853934389	5.92E-05
ENSG00000117000.8	RLF	1.853268233	1.60E-07
ENSG00000127452.4	FBXL12	1.853262822	0.02483352
ENSG00000196459.9	TRAPPC2	1.852305794	0.000741514
ENSG00000165272.10	AQP3	1.850466566	0.015513358
ENSG00000106993.7	CDC37L1	1.85027958	1.08E-05
ENSG00000135069.9	PSAT1	1.849548775	0.009933584
ENSG00000175538.6	KCNE3	1.848912529	0.001114297
ENSG00000153485.5	TMEM251	1.842108605	0.030812453
ENSG00000167797.3	CDK2AP2	1.840990645	4.98E-05
ENSG00000236680.1	RP11-296P7.4	1.840823051	0.003605175
ENSG00000239969.1	RP11-163E9.2	1.840040637	0.020916153
ENSG00000150756.9	FAM173B	1.838250195	0.003750268

ENSG00000177548.8	RABEP2	1.837511616	0.000262902
ENSG00000118242.11	MREG	1.836839977	0.00286158
ENSG00000261189.1	RP3-512B11.3	1.835240959	0.012025575
ENSG00000185222.7	WBP5	1.83359213	1.18E-07
ENSG00000108828.11	VAT1	1.832730635	3.24E-07
ENSG00000221821.2	C6orf226	1.832454032	0.034823605
ENSG00000130255.8	RPL36	1.830913571	5.61E-06
ENSG00000181029.7	TRAPPC5	1.829073394	0.000407522
ENSG00000163281.7	GNPDA2	1.828998136	0.047408188
ENSG00000149273.10	RPS3	1.828038234	4.11E-05
ENSG00000006459.6	JHDM1D	1.826433632	8.28E-07
ENSG00000238172.1	RPS2P35	1.825652825	0.030806083
ENSG00000237238.2	BMS1P10	1.822624601	0.007379719
ENSG00000167967.11	E4F1	1.820543878	0.00063636
ENSG00000116604.13	MEF2D	1.819855464	0.000716288
ENSG00000111229.11	ARPC3	1.819349047	0.001111626
ENSG00000048828.12	FAM120A	1.81912058	0.000391614
ENSG00000264538.2	SUZ12P	1.819111171	0.000180618
ENSG00000121417.9	ZNF211	1.818780406	0.041077867
ENSG00000104695.8	PPP2CB	1.818661143	1.27E-09
ENSG00000127445.9	PIN1	1.818338155	0.001216728
ENSG00000239382.6	ALKBH6	1.817561344	0.005733461
ENSG00000196754.6	S100A2	1.817452145	0.008026189
ENSG00000110080.14	ST3GAL4	1.816757644	0.00233195
ENSG00000142507.5	PSMB6	1.816471409	9.96E-09
ENSG00000107362.9	ABHD17B	1.81554821	0.000848381
ENSG00000115514.7	TXNDC9	1.815297057	8.75E-05
ENSG00000163453.7	IGFBP7	1.81408836	0.03497459
ENSG00000214535.3	RPS15AP1	1.813507116	0.000654911
ENSG00000129968.11	ABHD17A	1.812522125	0.043803654
ENSG00000101182.10	PSMA7	1.81159329	2.40E-08
ENSG00000223891.1	OSER1-AS1	1.811389341	0.001036953
ENSG00000096088.12	PGC	1.811144682	0.004326149
ENSG00000182004.8	SNRPE	1.810843083	0.000187723
ENSG00000163376.7	KBTBD8	1.810306488	0.015718577
ENSG00000141452.5	C18orf8	1.810163414	0.002459557
ENSG00000149483.7	TMEM138	1.810089753	0.020297515
ENSG00000181026.13	AEN	1.80825668	1.39E-05
ENSG00000105835.7	NAMPT	1.807936602	0.00030413
ENSG00000148308.13	GTF3C5	1.807890469	1.95E-06
ENSG00000188846.9	RPL14	1.80627188	1.52E-05
ENSG00000047849.17	MAP4	1.805065706	6.30E-06
ENSG00000100600.10	LGMN	1.804933912	0.002874733
ENSG00000118579.7	MED28	1.804502281	1.93E-05
ENSG00000164983.6	TMEM65	1.803600595	0.000232721
ENSG00000140612.9	SEC11A	1.80103669	0.00047993
ENSG00000166886.8	NAB2	1.800748771	0.015453775
ENSG00000100991.7	TRPC4AP	1.799694069	0.000724231
ENSG00000125835.13	SNRPB	1.798506296	1.20E-05
ENSG00000182718.12	ANXA2	1.798029686	5.36E-05

ENSG00000189403.10	HMGB1	1.797107046	4.43E-06
ENSG00000011132.7	APBA3	1.795390787	0.00065047
ENSG00000073150.9	PANX2	1.788285071	5.10E-05
ENSG00000242615.1	CTC-359D24.3	1.78578581	0.011350334
ENSG00000179010.10	MRFAP1	1.784288851	0.000131198
ENSG00000158161.11	EYA3	1.783450437	0.000264766
ENSG00000116661.9	FBXO2	1.783232497	9.30E-07
ENSG00000182400.10	TRAPPC6B	1.783002981	1.25E-05
ENSG00000177733.4	HNRNPA0	1.779432484	0.000959315
ENSG00000243680.1	RPL37P23	1.779312786	0.016879221
ENSG00000101474.7	APMAP	1.779156107	0.000498715
ENSG00000173812.6	EIF1	1.777526548	3.57E-05
ENSG00000177675.4	CD163L1	1.777355652	0.008929979
ENSG00000117408.6	IPO13	1.777288163	0.014376124
ENSG00000144566.6	RAB5A	1.776975942	2.74E-05
ENSG00000111726.8	CMAS	1.776905958	0.000115266
ENSG00000179750.11	APOBEC3B	1.775786974	0.001108837
ENSG00000127837.5	AAMP	1.775057204	5.61E-05
ENSG00000197128.7	ZNF772	1.772925863	0.020502961
ENSG00000147164.7	SNX12	1.772227873	1.62E-05
ENSG00000132535.14	DLG4	1.767484368	1.64E-05
ENSG00000166012.10	TAF1D	1.767055839	4.77E-05
ENSG00000140157.10	NIPA2	1.765713201	0.000419846
ENSG00000104765.10	BNIP3L	1.76250051	0.000113874
ENSG00000149196.11	C11orf73	1.75988062	0.011350788
ENSG00000129657.10	SEC14L1	1.758140718	1.43E-05
ENSG00000165813.12	C10orf118	1.757355277	3.03E-08
ENSG00000164180.9	TMEM161B	1.756528127	7.06E-07
ENSG00000122203.10	KIAA1191	1.756032033	0.000910447
ENSG00000136235.11	GPNMB	1.755440079	0.04677212
ENSG00000134108.8	ARL8B	1.754048657	1.08E-06
ENSG00000099992.11	TBC1D10A	1.753517575	0.020848548
ENSG00000115875.14	SRSF7	1.753239136	6.57E-08
ENSG00000213939.4	RP11-314A20.1	1.751808509	0.012846328
ENSG00000126458.3	RRAS	1.751300348	0.000485089
ENSG00000177051.5	FBXO46	1.746407374	0.000345066
ENSG00000079689.9	SCGN	1.74629557	3.70E-06
ENSG00000131373.10	HACL1	1.74559161	0.007024832
ENSG00000139372.10	TDG	1.744070899	1.18E-05
ENSG00000136052.5	SLC41A2	1.743728061	0.024668485
ENSG00000089818.12	NECAP1	1.743419996	0.000870135
ENSG00000140497.12	SCAMP2	1.74242729	7.78E-06
ENSG00000011422.7	PLAUR	1.740177813	0.001367575
ENSG00000104408.5	EIF3E	1.739056845	0.000316754
ENSG00000197982.12	C1orf122	1.73840371	0.002546451
ENSG00000100325.10	ASCC2	1.736795237	0.011339062
ENSG00000115526.6	CHST10	1.732052408	0.004273929
ENSG00000268471.3	MIR4453	1.731808107	0.042344242
ENSG00000239704.6	CDRT4	1.731207382	0.010204345
ENSG00000156510.11	HKDC1	1.72932549	7.18E-09

ENSG00000075415.8	SLC25A3	1.72685388	3.24E-06
ENSG00000175105.5	ZNF654	1.726620233	0.001963263
ENSG00000130545.11	CRB3	1.725124252	0.032193858
ENSG00000132819.12	RBM38	1.725009852	0.04862463
ENSG00000213341.6	CHUK	1.72325606	2.18E-08
ENSG00000148634.11	HERC4	1.720898527	0.000279004
ENSG00000256683.2	ZNF350	1.720116902	0.003308207
ENSG00000221968.4	FADS3	1.718341544	0.001144498
ENSG00000106927.7	AMBP	1.717930389	5.35E-05
ENSG00000155975.5	VPS37A	1.717926838	0.001809337
ENSG00000141384.7	TAF4B	1.717840963	0.02119434
ENSG00000099869.6	IGF2-AS	1.717758138	0.032747125
ENSG00000123737.8	EXOSC9	1.717756377	4.45E-05
ENSG00000156831.3	NSMCE2	1.71765621	8.67E-05
ENSG00000080371.4	RAB21	1.716541323	2.42E-06
ENSG00000043355.6	ZIC2	1.716125608	0.003101958
ENSG00000163002.8	NUP35	1.715687623	0.002456348
ENSG00000154781.11	CCDC174	1.714828803	9.74E-08
ENSG00000165264.6	NDUFB6	1.714633886	0.016699988
ENSG00000081870.7	HSPB11	1.712004213	8.56E-05
ENSG00000101574.10	METTL4	1.711466308	0.016110903
ENSG00000181045.10	SLC26A11	1.710907743	1.32E-05
ENSG00000072062.9	PRKACA	1.71045841	0.000191009
ENSG00000272779.1	LL22NC03-80A10.6	1.709798752	0.010682864
ENSG00000114573.5	ATP6V1A	1.70830926	3.22E-06
ENSG00000162695.7	SLC30A7	1.708260911	2.13E-06
ENSG00000224596.3	ZMIZ1-AS1	1.706155795	0.027629842
ENSG00000128654.9	MTX2	1.705618116	0.021733077
ENSG00000184545.6	DUSP8	1.705328583	0.000400986
ENSG00000012983.7	MAP4K5	1.702053802	4.60E-05
ENSG00000129535.8	NRL	1.700535341	0.000793937
ENSG00000089060.7	SLC8B1	1.700370054	0.001495213
ENSG00000103174.7	NAGPA	1.700140448	0.011703409
ENSG00000065911.7	MTHFD2	1.699531075	7.66E-05
ENSG00000056050.6	C4orf27	1.696353695	0.012691696
ENSG00000100462.11	PRMT5	1.69606062	2.90E-05
ENSG00000166228.4	PCBD1	1.695669661	0.003018794
ENSG00000214413.3	BBIP1	1.693617727	6.80E-05
ENSG00000116957.8	TBCE	1.689976191	0.000458433
ENSG00000180098.5	TRNAU1AP	1.68988115	0.000442443
ENSG00000147684.3	NDUFB9	1.684881879	3.10E-06
ENSG00000129824.11	RPS4Y1	1.684168272	7.48E-07
ENSG00000189077.6	TMEM120A	1.683823967	0.001066764
ENSG00000168826.11	ZBTB49	1.683794687	0.022275942
ENSG00000149636.11	DSN1	1.683414631	0.000347649
ENSG00000186020.8	ZNF529	1.683326296	0.018609219
ENSG00000165490.8	C11orf82	1.682270332	0.001521031
ENSG00000018699.7	TTC27	1.681414804	0.001402085
ENSG00000156928.4	MALSU1	1.680715595	0.011189141
ENSG00000224057.1	EGFR-AS1	1.680035905	0.000183502

ENSG00000117228.9	GBP1	1.679703947	0.000284318
ENSG00000145632.10	PLK2	1.679571107	0.000107049
ENSG00000143384.8	MCL1	1.678526486	1.91E-05
ENSG00000255529.3	POLR2M	1.676920593	0.016559415
ENSG00000205336.7	GPR56	1.675826549	0.008637838
ENSG00000119048.3	UBE2B	1.675471055	1.04E-06
ENSG00000105856.9	HBP1	1.673713553	1.88E-07
ENSG00000135597.14	REPS1	1.673548996	0.000556425
ENSG00000243742.1	RPLP0P2	1.673527696	0.000514368
ENSG00000132153.10	DHX30	1.672063923	0.00011109
ENSG00000184900.11	SUMO3	1.671443912	1.13E-05
ENSG00000173674.6	EIF1AX	1.671413013	0.000472945
ENSG00000218208.1	RP11-367G18.2	1.671166345	0.043142174
ENSG00000210100.1	MT-TI	1.669001359	0.002459557
ENSG00000119318.8	RAD23B	1.667937742	6.79E-06
ENSG00000133131.10	MORC4	1.667325287	3.49E-05
ENSG00000154813.5	DPH3	1.667135941	7.99E-07
ENSG00000240344.4	PPIL3	1.666128683	5.59E-06
ENSG00000171960.6	PPIH	1.665385543	0.003909713
ENSG00000064995.12	TAF11	1.665357819	1.87E-05
ENSG00000111846.11	GCNT2	1.665326672	1.11E-08
ENSG00000106603.13	COA1	1.664976522	0.034307473
ENSG00000165637.9	VDAC2	1.663463235	2.18E-05
ENSG00000171903.12	CYP4F11	1.662680685	0.00032937
ENSG00000131503.16	ANKHD1	1.662594733	6.28E-05
ENSG00000000419.8	DPM1	1.662567886	0.000329876
ENSG00000125458.2	NT5C	1.661275547	0.00284357
ENSG00000164898.8	C7orf55	1.661274171	0.042737626
ENSG00000110330.4	BIRC2	1.660774365	0.002145911
ENSG00000081320.6	STK17B	1.659962685	4.92E-05
ENSG00000168255.14	POLR2J3	1.659207197	0.017149044
ENSG00000096968.8	JAK2	1.658986285	0.001696596
ENSG00000125356.6	NDUFA1	1.657020807	0.001796372
ENSG00000112972.10	HMGCS1	1.656050539	0.001264648
ENSG00000064726.5	BTBD1	1.653310249	0.001358386
ENSG00000150455.9	TIRAP	1.653117422	0.025541478
ENSG00000175183.5	CSRP2	1.653071358	0.015006149
ENSG00000127989.9	MTERF	1.652964961	0.012198997
ENSG00000171877.15	FRMD5	1.652196945	0.003958361
ENSG00000100353.13	EIF3D	1.651434256	7.08E-06
ENSG00000067064.6	IDI1	1.651199916	5.10E-05
ENSG00000068796.12	KIF2A	1.651191335	3.33E-05
ENSG00000108179.9	PPIF	1.651024929	0.001463214
ENSG00000102786.10	INTS6	1.650670043	0.000117078
ENSG00000166272.12	WBP1L	1.649241673	4.27E-05
ENSG00000158710.10	TAGLN2	1.647574401	1.27E-06
ENSG00000104691.10	UBXN8	1.647420159	9.12E-06
ENSG00000181315.6	ZNF322	1.645445087	0.005196385
ENSG00000272277.1	RP1-40E16.12	1.644721754	0.032486396
ENSG00000140471.12	LINS	1.644033962	0.012758452

ENSG00000117148.6	ACTL8	1.641626819	0.028055626
ENSG00000180953.7	ST20	1.641570301	0.042832732
ENSG00000114125.9	RNF7	1.641376787	2.40E-05
ENSG00000167862.5	ICT1	1.640385345	0.000425054
ENSG00000171649.7	ZIK1	1.639456962	0.039534521
ENSG00000114480.8	GBE1	1.638770341	3.47E-05
ENSG00000181019.8	NQO1	1.638568294	1.27E-05
ENSG00000147677.6	EIF3H	1.63854978	0.000403579
ENSG00000096717.7	SIRT1	1.637825178	4.16E-05
ENSG00000106588.6	PSMA2	1.634806444	0.00064669
ENSG00000260054.1	RP11-611L7.1	1.634707371	0.000105296
ENSG00000124562.5	SNRPC	1.634657047	1.98E-05
ENSG00000264644.1	KRT18P8	1.629701603	0.032630085
ENSG00000177954.7	RPS27	1.628312087	5.29E-06
ENSG00000102144.9	PGK1	1.62822381	0.000357923
ENSG00000170035.11	UBE2E3	1.626706535	5.29E-05
ENSG00000148943.7	LIN7C	1.626076733	0.000275655
ENSG00000197971.10	MBP	1.624645308	0.004534978
ENSG00000105248.11	CCDC94	1.622169168	1.63E-05
ENSG00000204869.4	IGFL4	1.621346797	0.031583965
ENSG00000126247.6	CAPNS1	1.620936874	7.72E-06
ENSG00000152778.7	IFIT5	1.620476403	0.037064299
ENSG00000116898.7	MRPS15	1.61990888	9.37E-05
ENSG00000271043.1	MTRNR2L2	1.61633253	0.009409957
ENSG00000137824.11	RMDN3	1.615871658	0.000917589
ENSG00000100129.13	EIF3L	1.615860644	1.45E-05
ENSG00000136021.13	SCYL2	1.612913742	4.12E-07
ENSG00000076201.10	PTPN23	1.612845613	1.51E-05
ENSG00000104881.10	PPP1R13L	1.611012	0.004438078
ENSG00000220804.4	AC093642.5	1.610274958	0.00082544
ENSG00000167578.12	RAB4B	1.609959397	0.006751669
ENSG00000161999.7	JMJD8	1.608790199	0.021739199
ENSG00000146556.10	WASH2P	1.605447213	0.036407661
ENSG00000185049.8	NELFA	1.605337623	0.003111612
ENSG00000164631.14	ZNF12	1.603804714	0.002629903
ENSG00000198498.5	TMA16	1.603716386	0.000193992
ENSG00000119965.8	C10orf88	1.600872032	0.013421499
ENSG00000137714.2	FDX1	1.59996511	0.018247079
ENSG00000240616.1	AD000092.3	1.599033826	0.033122416
ENSG00000169612.3	FAM103A1	1.598216274	0.025585649
ENSG00000174796.8	THAP6	1.597826356	0.00336558
ENSG00000161326.8	DUSP14	1.595450812	0.003934974
ENSG00000168216.6	LMBRD1	1.594304253	0.00404373
ENSG00000204178.5	TMEM57	1.591887791	3.32E-08
ENSG00000149308.12	NPAT	1.591626236	0.001891123
ENSG00000085063.10	CD59	1.590916437	4.73E-05
ENSG00000116478.7	HDAC1	1.590664856	0.000485233
ENSG00000164815.6	ORC5	1.588459685	0.017275287
ENSG00000164647.4	STEAP1	1.588208907	0.003278741
ENSG00000115128.6	SF3B14	1.587790047	0.000343421

ENSG00000132676.11	DAP3	1.587313531	9.72E-06
ENSG00000108064.6	TFAM	1.587009957	0.000101211
ENSG00000198876.8	DCAF12	1.586529099	0.000852104
ENSG00000167088.6	SNRPD1	1.585262917	0.00013449
ENSG00000173653.3	RCE1	1.585052666	0.01450008
ENSG00000101421.3	CHMP4B	1.583917557	1.48E-07
ENSG00000196505.6	GDAP2	1.583530749	7.87E-07
ENSG00000255302.3	EID1	1.581975053	0.000167875
ENSG00000109536.7	FRG1	1.581180857	9.97E-05
ENSG00000000460.12	C1orf112	1.580522699	0.001003274
ENSG00000170791.13	CHCHD7	1.580477475	3.18E-05
ENSG00000067560.6	RHOA	1.579560912	0.00508594
ENSG00000135047.10	CTSL	1.578878656	7.03E-08
ENSG00000144362.7	PHOSPHO2	1.57850696	0.026275581
ENSG00000139636.11	LMBR1L	1.578305949	1.82E-05
ENSG00000103855.13	CD276	1.578224221	0.000188505
ENSG00000138658.11	C4orf21	1.576712161	0.021209337
ENSG00000174111.8	SOCS7	1.576503923	0.03168992
ENSG00000132109.8	TRIM21	1.576087393	0.013416743
ENSG00000151657.7	KIN	1.575721258	9.94E-06
ENSG00000213609.3	RP11-170M17.2	1.575511454	0.026080863
ENSG00000153558.9	FBXL2	1.574520161	0.047844069
ENSG00000175322.7	ZNF519	1.57415033	0.018378112
ENSG00000148339.8	SLC25A25	1.573827344	0.000106694
ENSG00000150787.3	PTS	1.572201466	0.000184965
ENSG00000261188.1	CTA-445C9.14	1.570482786	0.00281538
ENSG00000185651.10	UBE2L3	1.569609468	0.001017263
ENSG00000169249.8	ZRSR2	1.567302976	9.63E-08
ENSG00000136521.8	NDUFB5	1.566330933	0.025334495
ENSG00000198455.3	ZXDB	1.565061623	0.009442147
ENSG00000116903.6	EXOC8	1.564259986	3.01E-06
ENSG00000130803.10	ZNF317	1.56375732	0.007454068
ENSG00000155090.10	KLF10	1.563057821	0.004237293
ENSG00000120686.7	UFM1	1.562957013	6.08E-05
ENSG00000138698.10	RAP1GDS1	1.561819816	0.001116948
ENSG00000156232.6	WHAMM	1.559619317	2.53E-05
ENSG00000102384.9	CENPI	1.559215706	0.001850441
ENSG00000166747.8	AP1G1	1.558496858	2.84E-05
ENSG00000132475.4	H3F3B	1.557997761	1.57E-07
ENSG00000082213.13	C5orf22	1.557329224	0.007175835
ENSG00000111364.11	DDX55	1.555347337	0.000952046
ENSG00000122257.14	RBBP6	1.55510883	1.52E-05
ENSG00000187626.7	ZKSCAN4	1.554424556	0.002249288
ENSG00000123843.8	C4BPB	1.554079175	0.032863233
ENSG00000033100.10	CHPF2	1.553970186	1.26E-05
ENSG00000139496.11	NUPL1	1.553330612	1.91E-05
ENSG00000099624.3	ATP5D	1.552624266	0.003181682
ENSG00000141552.13	ANAPC11	1.552471525	1.85E-05
ENSG00000204160.7	ZDHHC18	1.551467173	0.001196668
ENSG00000128578.5	STRIP2	1.551460151	0.026646532

ENSG00000124356.11	STAMBP	1.550938334	0.002594978
ENSG00000161547.10	SRSF2	1.550196449	0.000127894
ENSG00000136159.3	NUDT15	1.550095188	0.002787206
ENSG00000158122.7	AAED1	1.549536045	0.031423997
ENSG00000140988.11	RPS2	1.549082572	0.000492265
ENSG00000213699.4	SLC35F6	1.548091451	0.002316493
ENSG00000137494.9	ANKRD42	1.547879101	0.002484838
ENSG00000227615.1	RP11-864N7.2	1.547256716	3.60E-05
ENSG00000058804.10	NDC1	1.547125083	0.002811765
ENSG00000091732.11	ZC3HC1	1.54702297	0.000672571
ENSG00000110104.7	CCDC86	1.546921744	0.000301171
ENSG00000197142.6	ACSL5	1.545961967	3.18E-05
ENSG00000104047.10	DTWD1	1.545763714	0.038341997
ENSG00000177868.7	CCDC23	1.545481086	0.004120818
ENSG00000145425.5	RPS3A	1.545279341	0.000224969
ENSG00000197409.6	HIST1H3D	1.544530864	0.03093814
ENSG00000116752.5	BCAS2	1.543985555	0.000106285
ENSG00000112242.10	E2F3	1.541457158	1.98E-06
ENSG00000151632.12	AKR1C2	1.540206815	0.004375301
ENSG00000105866.9	SP4	1.540116109	0.012398988
ENSG00000233927.4	RPS28	1.53964639	1.78E-05
ENSG00000196547.10	MAN2A2	1.539603317	0.025397734
ENSG00000130165.6	ELOF1	1.538676633	5.69E-07
ENSG00000153015.11	CWC27	1.538035833	4.10E-05
ENSG00000116584.13	ARHGEF2	1.53792756	0.006846768
ENSG00000177888.7	ZBTB41	1.536352609	0.000127244
ENSG00000182149.16	IST1	1.536157095	3.45E-05
ENSG00000087053.14	MTMR2	1.53600402	0.001304862
ENSG00000126709.10	IFI6	1.535223147	0.006550566
ENSG00000100412.11	ACO2	1.534828988	3.12E-05
ENSG00000171453.13	POLR1C	1.534180953	0.000560022
ENSG00000197279.3	ZNF165	1.533034615	0.015309665
ENSG00000156172.5	C8orf37	1.530195545	0.037344463
ENSG00000145354.5	CISD2	1.528316856	0.000305007
ENSG00000105393.11	BABAM1	1.526707466	0.000275003
ENSG00000198258.6	UBL5	1.526133855	0.000486591
ENSG00000105732.9	ZNF574	1.525974944	0.003297863
ENSG00000179409.6	GEMIN4	1.525478018	0.003385928
ENSG00000176244.6	ACBD7	1.525271697	0.014555445
ENSG00000167528.8	ZNF641	1.521334085	0.026635493
ENSG00000123091.4	RNF11	1.521014227	0.000817958
ENSG00000165630.9	PRPF18	1.520986991	9.20E-07
ENSG00000114023.11	FAM162A	1.520186383	0.013789202
ENSG00000115738.5	ID2	1.519857656	2.73E-05
ENSG00000167283.3	ATP5L	1.518667699	0.000778287
ENSG00000171867.12	PRNP	1.518098031	0.000487788
ENSG00000072778.15	ACADVL	1.516928108	0.00051309
ENSG00000110047.13	EHD1	1.516755254	9.87E-07
ENSG00000168438.10	CDC40	1.516624549	5.93E-06
ENSG00000125304.8	TM9SF2	1.513957056	0.000485904

ENSG00000039523.13	FAM65A	1.512910188	0.020215911
ENSG00000147162.9	OGT	1.512070304	4.25E-06
ENSG00000169032.5	MAP2K1	1.510752336	0.000192942
ENSG00000134909.14	ARHGAP32	1.510155604	0.022850524
ENSG00000108474.12	PIGL	1.508735077	0.008459548
ENSG00000069399.8	BCL3	1.508507058	0.004180472
ENSG00000136802.7	LRRC8A	1.507414326	2.31E-07
ENSG00000135249.3	RINT1	1.507262341	0.013467601
ENSG00000143878.8	RHOB	1.50475609	0.001565853
ENSG00000138152.7	BTBD16	1.504424215	0.033909724
ENSG00000102978.8	POLR2C	1.504344022	0.000316838
ENSG00000206418.3	RAB12	1.503375218	0.000170819
ENSG00000196937.6	FAM3C	1.501277799	0.044808263
ENSG00000068438.10	FTSJ1	1.500845635	0.003496195
ENSG00000169021.4	UQCRFS1	1.500739899	0.009933584
ENSG00000261061.1	RP11-303E16.2	1.499891672	0.004923721
ENSG00000198060.5	MARCH5	1.499586275	0.01449178
ENSG00000089127.8	OAS1	1.499138919	0.000641916
ENSG00000122406.8	RPL5	1.499073501	0.000678748
ENSG00000181038.9	METTL23	1.498938446	0.007399102
ENSG00000181135.11	ZNF707	1.498401287	0.010178415
ENSG00000143183.12	TMCO1	1.495635183	7.27E-06
ENSG00000185728.12	YTHDF3	1.494685662	0.000239875
ENSG00000160746.8	ANO10	1.493795482	4.46E-05
ENSG00000113615.8	SEC24A	1.492846846	0.000721848
ENSG00000164045.7	CDC25A	1.492578936	0.002899621
ENSG00000100209.5	HSCB	1.491956557	0.002011159
ENSG00000180525.9	PRR26	1.490790553	0.0227323
ENSG00000185896.9	LAMP1	1.489583162	9.79E-06
ENSG00000198522.9	GPN1	1.489069348	0.000326622
ENSG00000160051.7	IQCC	1.488618598	0.03526086
ENSG00000158411.6	MITD1	1.488148259	0.000122979
ENSG00000166881.5	TMEM194A	1.484158406	0.029642273
ENSG00000142528.11	ZNF473	1.483002314	3.15E-05
ENSG00000196998.11	WDR45	1.481997814	0.017884002
ENSG00000165169.6	DYNLT3	1.480821436	0.005507449
ENSG00000171970.8	ZNF57	1.480800528	0.047070064
ENSG00000123728.5	RAP2C	1.480081718	0.014274326
ENSG00000185112.4	FAM43A	1.478058413	0.000242586
ENSG00000111906.13	HDDC2	1.476721438	0.003803454
ENSG00000245910.4	SNHG6	1.476666944	0.000387272
ENSG00000151247.8	EIF4E	1.474660014	0.000381861
ENSG00000162676.7	GFI1	1.474561384	0.018519352
ENSG00000159111.8	MRPL10	1.473040087	0.004624676
ENSG00000017260.15	ATP2C1	1.472863491	2.34E-07
ENSG00000173436.9	MINOS1	1.471014052	0.032531137
ENSG00000144554.6	FANCD2	1.46982156	0.000313305
ENSG00000087586.13	AURKA	1.469635709	0.000574706
ENSG00000155097.7	ATP6V1C1	1.4693747	3.90E-06
ENSG00000145623.8	OSMR	1.469276885	0.00685835

ENSG00000072110.9	ACTN1	1.467816599	2.68E-06
ENSG00000133895.10	MEN1	1.465493472	0.000565478
ENSG00000003400.10	CASP10	1.464755893	0.001161756
ENSG00000184831.9	APOO	1.459188838	0.0062282
ENSG00000129128.8	SPCS3	1.458908252	0.000458578
ENSG00000162972.6	C2orf47	1.458556668	0.009422531
ENSG00000122705.12	CLTA	1.458549733	8.76E-06
ENSG00000100056.7	DGCR14	1.458546741	0.000465609
ENSG00000124787.9	RPP40	1.458500409	0.001022538
ENSG00000113739.6	STC2	1.458161827	7.33E-05
ENSG00000225475.1	RP11-377K22.2	1.457424409	0.000354154
ENSG00000140950.11	TLDC1	1.4570423	0.006249514
ENSG00000166473.12	PKD1L2	1.455243745	0.023973634
ENSG00000130150.7	MOSPD2	1.453288454	0.035154894
ENSG00000149798.3	CDC42EP2	1.453028477	0.000128281
ENSG00000165632.7	TAF3	1.452592632	2.13E-05
ENSG00000005893.11	LAMP2	1.451970475	0.000112548
ENSG00000142627.9	EPHA2	1.451822561	0.001493519
ENSG00000121073.9	SLC35B1	1.451035855	3.52E-08
ENSG00000105699.12	LSR	1.450184954	0.000262885
ENSG00000064012.17	CASP8	1.448888177	0.001160136
ENSG00000170892.6	TSEN34	1.448131731	0.000426903
ENSG00000130413.11	STK33	1.446768676	0.032742684
ENSG00000169908.6	TM4SF1	1.44582946	0.000305007
ENSG00000030110.8	BAK1	1.44459274	0.000311922
ENSG00000163872.11	YEATS2	1.44340207	0.002769026
ENSG00000184203.3	PPP1R2	1.442909724	6.16E-05
ENSG00000170100.9	ZNF778	1.44040227	0.04625859
ENSG00000111641.6	NOP2	1.44025151	0.000105912
ENSG00000042286.10	AIFM2	1.437306552	4.86E-05
ENSG00000170270.4	C14orf142	1.43717126	0.04013782
ENSG00000103061.7	SLC7A6OS	1.43518646	2.42E-05
ENSG00000205352.6	PRR13	1.434403291	0.000103588
ENSG00000183527.7	PSMG1	1.433992667	0.012277333
ENSG00000115365.7	LANCL1	1.43345126	0.016060539
ENSG00000196911.5	KPNA5	1.432518185	0.000604886
ENSG00000152520.9	PAN3	1.432129713	0.006697615
ENSG00000181904.8	C5orf24	1.431507147	0.002316493
ENSG00000177410.8	ZFAS1	1.430542843	0.001412697
ENSG00000175061.13	C17orf76-AS1	1.430159404	0.000105142
ENSG00000132383.7	RPA1	1.429810105	0.007922935
ENSG00000105887.10	MTPN	1.428690227	3.20E-07
ENSG00000163507.9	KIAA1524	1.426541778	0.002044358
ENSG00000120885.15	CLU	1.425652514	1.35E-06
ENSG00000111237.14	VPS29	1.425432969	0.0001391
ENSG00000255242.1	C14orf169	1.424957367	0.009643434
ENSG00000141543.5	EIF4A3	1.424793986	0.000528409
ENSG00000070831.11	CDC42	1.423341408	0.021839002
ENSG00000131165.10	CHMP1A	1.42311406	1.79E-06
ENSG00000137168.7	PPIL1	1.420553196	0.000310815

ENSG00000143543.10	JTB	1.41982851	0.000690117
ENSG00000178694.5	NSUN3	1.419034975	0.001144417
ENSG00000070087.9	PFN2	1.417315317	5.36E-07
ENSG00000269858.1	EGLN2	1.417026753	0.00016632
ENSG00000127947.11	PTPN12	1.416789524	3.74E-05
ENSG00000268205.1	CTC-444N24.11	1.416496088	0.000445193
ENSG00000169635.5	HIC2	1.41622247	0.000291918
ENSG00000159459.7	UBR1	1.413867914	6.13E-05
ENSG00000107745.12	MICU1	1.413520782	1.04E-05
ENSG00000139289.9	PHLDA1	1.41312124	0.005015654
ENSG00000186871.5	ERCC6L	1.412240635	0.030086873
ENSG00000136986.5	DERL1	1.411969526	0.00210818
ENSG00000270019.1	RP11-141B14.1	1.411542287	0.018306261
ENSG00000260257.1	RP5-1085F17.3	1.410886537	0.000208311
ENSG00000151893.10	CACUL1	1.410431516	2.41E-05
ENSG00000108578.10	BLMH	1.409117922	0.001314716
ENSG00000262246.1	CORO7	1.40840751	0.003213706
ENSG00000015475.14	BID	1.408394824	4.40E-05
ENSG00000071994.6	PDCD2	1.406911783	0.003268372
ENSG00000149357.5	LAMTOR1	1.406655408	0.000547905
ENSG00000145592.9	RPL37	1.40405818	0.000819113
ENSG00000111727.7	HCFC2	1.403625801	0.002542441
ENSG00000144034.10	TPRKB	1.402732415	8.72E-05
ENSG00000107742.8	SPOCK2	1.402227414	0.003140079
ENSG00000166068.8	SPRED1	1.401921254	0.00265475
ENSG00000151923.13	TIAL1	1.399117263	0.000164985
ENSG00000148291.5	SURF2	1.399081168	0.021286637
ENSG00000156273.11	BACH1	1.398575652	0.000190473
ENSG00000131462.3	TUBG1	1.398045399	0.003297863
ENSG00000075975.11	MKRN2	1.397703162	0.000294397
ENSG00000138468.11	SENP7	1.396416582	0.00020686
ENSG00000149600.7	COMMD7	1.395485545	0.005155948
ENSG00000163611.7	SPICE1	1.395407729	0.006538811
ENSG00000143466.9	IKBKE	1.395063797	0.01374484
ENSG00000149489.4	ROM1	1.394080135	0.024278658
ENSG00000103005.7	USB1	1.39259787	0.000350611
ENSG00000109016.13	DHRS7B	1.390858491	0.000522476
ENSG00000161013.12	MGAT4B	1.390522471	0.000948501
ENSG00000117153.11	KLHL12	1.390213128	0.035762902
ENSG00000120709.6	FAM53C	1.390154615	0.000812198
ENSG00000173212.4	MAB21L3	1.389477483	6.86E-05
ENSG00000126756.7	UXT	1.388350573	0.000282784
ENSG00000135317.8	SNX14	1.386526288	0.002595541
ENSG00000103194.11	USP10	1.384602706	0.000129328
ENSG00000112996.5	MRPS30	1.384364986	0.002144381
ENSG00000143367.11	TUFT1	1.383606709	0.000160547
ENSG00000126249.3	PDCD2L	1.382206023	0.018890974
ENSG00000082258.8	CCNT2	1.382007739	0.000344807
ENSG00000169504.10	CLIC4	1.381410249	0.000569432
ENSG00000115073.6	ACTR1B	1.38086827	0.01369103

ENSG00000122912.10	SLC25A16	1.380235939	0.000212255
ENSG00000136436.10	CALCOCO2	1.379733845	6.32E-08
ENSG00000060138.8	YBX3	1.379255743	0.000301171
ENSG00000180992.5	MRPL14	1.379186073	0.000674548
ENSG00000172809.8	RPL38	1.377913836	0.000162566
ENSG00000126216.8	TUBGCP3	1.377272606	0.0065435
ENSG00000105402.3	NAPA	1.373609561	4.82E-06
ENSG00000121691.4	CAT	1.373189943	0.024532198
ENSG00000032389.8	TSSC1	1.370472821	0.012200913
ENSG00000263823.1	RP11-326K13.4	1.370034987	0.024693814
ENSG00000156471.8	PTDSS1	1.369200957	0.001361862
ENSG00000165861.9	ZFYVE1	1.368890467	0.004488482
ENSG00000197119.8	SLC25A29	1.367229791	0.005295504
ENSG00000197956.5	S100A6	1.367100674	0.000990003
ENSG00000136891.9	TEX10	1.366657543	0.001320661
ENSG00000115758.8	ODC1	1.366609032	1.47E-06
ENSG00000170855.3	TRIAP1	1.366200287	0.000863415
ENSG00000198612.6	COPS8	1.366159666	0.001870769
ENSG00000101310.10	SEC23B	1.363353513	0.000561766
ENSG00000153975.5	ZUFSP	1.361560075	0.000358063
ENSG00000006453.9	BAIAP2L1	1.360317665	3.24E-05
ENSG00000134597.9	RBMX2	1.360106209	0.008677902
ENSG00000124299.9	PEPD	1.358617578	0.010040037
ENSG00000108774.10	RAB5C	1.357657416	1.73E-05
ENSG00000131845.10	ZNF304	1.357645786	0.000986044
ENSG00000171848.9	RRM2	1.356160454	0.00036278
ENSG00000151500.10	THYN1	1.353550823	0.001299091
ENSG00000157214.9	STEAP2	1.351921391	0.001072566
ENSG00000146963.13	C7orf55-LUC7L2	1.351784812	0.001102375
ENSG00000143353.7	LYPLAL1	1.350801981	0.020609869
ENSG00000230076.1	AC016708.2	1.349899515	0.006826778
ENSG00000179021.5	C3orf38	1.349752484	0.011048353
ENSG00000104859.10	CLASRP	1.347564779	3.45E-05
ENSG00000172409.5	CLP1	1.347486244	0.016876006
ENSG00000147854.12	UHRF2	1.346863186	0.029272925
ENSG00000233461.1	RP11-295G20.2	1.346501332	0.010301524
ENSG00000189343.6	RPS2P46	1.346170483	0.002604755
ENSG00000223547.5	ZNF844	1.344710598	0.008634509
ENSG00000161036.6	LRWD1	1.344441608	0.005973643
ENSG00000160131.9	VMA21	1.340621	0.002610355
ENSG00000135093.8	USP30	1.339461497	0.00103494
ENSG00000034510.4	TMSB10	1.338760331	6.57E-06
ENSG00000074800.9	ENO1	1.336164369	9.05E-05
ENSG00000104812.10	GYS1	1.335865169	0.006210227
ENSG00000119421.5	NDUFA8	1.335027506	0.035948344
ENSG00000059691.7	PET112	1.334790479	0.005369475
ENSG00000181097.5	RP11-429J17.2	1.331988874	3.34E-05
ENSG00000075131.5	TIPIN	1.331658335	0.007765427
ENSG00000168411.9	RFWD3	1.32958772	0.00242826
ENSG00000111247.10	RAD51AP1	1.324855324	0.002776953

ENSG00000198356.7	ASNA1	1.324395371	0.000460055
ENSG00000083896.8	YTHDC1	1.323955695	8.86E-07
ENSG00000130684.9	ZNF337	1.323576162	0.029143117
ENSG00000137074.14	APTX	1.323126506	0.000728928
ENSG00000140299.7	BNIP2	1.320749014	3.67E-05
ENSG00000115756.8	HPCAL1	1.320707554	1.58E-06
ENSG00000142675.13	CNKSR1	1.320043824	0.042235224
ENSG00000197860.5	SGTB	1.318674404	0.000793423
ENSG00000165943.4	MOAP1	1.318074037	0.001881266
ENSG00000084072.12	PPIE	1.317252726	0.009465723
ENSG00000136830.7	FAM129B	1.315435402	0.003217472
ENSG00000081791.4	KIAA0141	1.315421602	0.001475656
ENSG00000181924.6	COA4	1.314633114	0.003090399
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ENSG00000104312.6	RIPK2	1.311649645	0.000475991
ENSG00000105339.6	DENND3	1.309203923	0.040503419
ENSG00000163866.8	SMIM12	1.308367423	0.011506911
ENSG00000124228.10	DDX27	1.307996416	2.37E-05
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ENSG00000088727.8	KIF9	1.306249145	0.000232989
ENSG00000152944.4	MED21	1.306148349	0.033908592
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ENSG00000052723.7	SIKE1	1.305411361	0.000485904
ENSG00000226243.1	RPL37AP1	1.30408767	0.031938083
ENSG00000160691.14	SHC1	1.303688731	5.45E-06
ENSG00000090520.6	DNAJB11	1.303002185	9.39E-05
ENSG00000101019.17	UQCC1	1.302698388	3.56E-05
ENSG00000090061.13	CCNK	1.30243246	1.33E-05
ENSG00000112742.5	TTK	1.301811061	0.00655211
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ENSG00000149792.4	MRPL49	1.289741037	0.037300498
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ENSG00000037474.10	NSUN2	1.287487268	0.00076593
ENSG00000164916.9	FOXK1	1.284619486	0.00070969
ENSG00000177674.11	AGTRAP	1.284018295	0.003737324
ENSG00000158290.12	CUL4B	1.283264365	0.003081999
ENSG00000134717.13	BTF3L4	1.28272978	0.017780741
ENSG00000100744.10	GSKIP	1.281923532	0.002063855
ENSG00000092445.7	TYRO3	1.280033316	0.003445939

ENSG00000084623.7	EIF3I	1.278680226	5.71E-07
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ENSG00000069248.9	NUP133	1.277400057	0.001513764
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ENSG00000164284.10	GRPEL2	1.275043956	0.012335092
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ENSG00000159842.10	ABR	1.270389659	0.018425664
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ENSG00000241553.8	ARPC4	1.262886909	0.000134266
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ENSG00000196756.7	SNHG17	1.258421178	0.014696786
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ENSG00000169756.12	LIMS1	1.254630566	0.000122386
ENSG00000147650.7	LRP12	1.253855172	0.020533732
ENSG00000145390.7	USP53	1.252546086	3.45E-05
ENSG00000143420.13	ENSA	1.25149673	0.001562744
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ENSG00000127080.5	IPPK	1.250148296	0.003213706
ENSG00000126790.7	L3HYPDH	1.250063718	0.032042823
ENSG00000100226.11	GTPBP1	1.250037092	0.002141055
ENSG00000130202.5	PVRL2	1.248561163	0.001850441
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ENSG00000165494.6	PCF11	1.245538976	1.20E-05
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ENSG00000161653.6	NAGS	1.2436343	0.044862605
ENSG00000026297.11	RNASET2	1.243226159	0.029405589
ENSG00000131148.4	EMC8	1.243185126	0.003201185
ENSG00000105137.8	SYDE1	1.242728549	0.016419856
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ENSG00000075426.7	FOSL2	1.238193992	0.000648773
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ENSG00000229994.1	RPL5P4	1.236689348	0.003857352
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ENSG00000160593.13	AMICA1	1.233301379	0.000568193
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ENSG00000068323.12	TFE3	1.231187792	6.68E-05
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ENSG00000172175.8	MALT1	1.229770174	0.000187657
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ENSG00000089876.7	DHX32	1.221136691	0.027683404
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ENSG00000114650.14	SCAP	1.204825763	0.038257176
ENSG00000133703.7	KRAS	1.204525431	0.002145449
ENSG00000158985.9	CDC42SE2	1.202930091	0.000507612
ENSG00000214517.4	PPME1	1.202783319	1.63E-06
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ENSG00000155876.4	RRAGA	1.201783049	0.034453747
ENSG00000033867.12	SLC4A7	1.201596225	2.05E-06
ENSG00000105401.2	CDC37	1.200532137	2.16E-05
ENSG00000163602.9	RYBP	1.199612147	1.04E-06
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ENSG00000094880.6	CDC23	1.198884947	0.007690344
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ENSG00000167600.9	CYP2S1	1.192794619	0.014642314
ENSG00000188021.7	UBQLN2	1.192569396	0.004945107
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ENSG00000196284.9	SUPT3H	1.1864235	0.001883994
ENSG00000092108.16	SCFD1	1.186380661	0.001011795
ENSG00000130021.9	HDHD1	1.185878788	0.03417524
ENSG00000175482.4	POLD4	1.184578432	0.001027898
ENSG00000101365.16	IDH3B	1.184434202	2.92E-05
ENSG00000180667.6	YOD1	1.184192111	0.024714557
ENSG00000164924.13	YWHAZ	1.18276545	2.48E-05
ENSG00000168958.15	MFF	1.18020214	0.01438065
ENSG00000010818.4	HIVEP2	1.177764481	0.002190612
ENSG00000119446.9	RBM18	1.177303573	0.000178911
ENSG00000113649.7	TCERG1	1.177080142	0.000613772
ENSG00000204370.4	SDHD	1.176858927	0.042235224
ENSG00000141994.11	DUS3L	1.174750015	0.042767792
ENSG00000150967.13	ABCB9	1.174293151	0.040862962
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ENSG00000183199.6	HSP90AB3P	1.172073594	2.46E-05
ENSG00000105298.9	CACTIN	1.17129268	0.014629134
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ENSG00000183891.5	TTC32	1.168727848	0.02170692
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ENSG00000119616.7	FCF1	1.166291601	9.42E-06
ENSG00000143155.8	TIPRL	1.162641378	0.027216383
ENSG00000158828.5	PINK1	1.161312007	0.001358656
ENSG00000149658.13	YTHDF1	1.160068732	0.000449015
ENSG00000088247.11	KHSRP	1.159821281	0.00170164
ENSG00000184451.5	CCR10	1.158721316	0.045019683
ENSG00000116489.8	CAPZA1	1.155809649	0.000319604
ENSG00000103978.11	TMEM87A	1.155304071	1.27E-06
ENSG00000152242.6	C18orf25	1.154844335	0.04721626
ENSG00000115419.8	GLS	1.154816375	4.29E-05
ENSG00000006194.6	ZNF263	1.154407796	0.000164927
ENSG00000135048.9	TMEM2	1.153152862	0.000540756
ENSG00000160058.14	BSDC1	1.15104404	1.95E-05
ENSG00000174840.8	PDE12	1.150799645	0.028830497
ENSG00000247077.2	PGAM5	1.149690811	0.016810502
ENSG00000133247.9	SUV420H2	1.146219802	0.03816482
ENSG00000257727.1	CNPY2	1.146025337	0.018384638
ENSG00000163728.6	TTC14	1.146001155	0.000433825

ENSG00000100852.8	ARHGAP5	1.144936227	5.90E-06
ENSG00000173039.14	RELA	1.144161795	0.000643321
ENSG00000175279.17	APITD1	1.144114248	0.0327054
ENSG00000068354.11	TBC1D25	1.142821449	0.049688463
ENSG00000142330.15	CAPN10	1.141569787	0.018427259
ENSG00000131469.8	RPL27	1.139544861	0.007854124
ENSG00000180190.7	TDRP	1.139174454	0.017007617
ENSG00000119682.12	AREL1	1.138676993	0.004970024
ENSG00000129472.8	RAB2B	1.138006441	0.007227712
ENSG00000135070.9	ISCA1	1.137296872	0.007036656
ENSG00000006118.10	TMEM132A	1.13667161	0.0494062
ENSG00000114942.9	EEF1B2	1.135741055	0.003193926
ENSG00000181544.9	FANCB	1.13515775	0.03093814
ENSG00000156463.13	SH3RF2	1.134584992	0.000916065
ENSG00000104529.13	EEF1D	1.134308027	0.003511676
ENSG00000031691.6	CENPQ	1.132740257	0.000122767
ENSG00000162923.10	WDR26	1.132720346	0.000274995
ENSG00000005486.12	RHBDD2	1.13244411	0.002484838
ENSG00000148399.7	DPH7	1.131979353	0.02636758
ENSG00000112378.11	PERP	1.129219619	0.001887241
ENSG00000149591.12	TAGLN	1.128285452	0.000980855
ENSG00000213551.4	DNAJC9	1.127537802	0.001349436
ENSG00000184220.6	CMSS1	1.127441163	0.003956213
ENSG00000119718.6	EIF2B2	1.126539905	0.008651309
ENSG00000210077.1	MT-TV	1.12496897	0.014637829
ENSG00000168003.12	SLC3A2	1.124265889	0.0002181
ENSG00000142731.6	PLK4	1.123844996	0.024668485
ENSG00000145741.11	BTF3	1.122625483	0.00081369
ENSG00000113810.11	SMC4	1.12236366	0.000213823
ENSG00000251062.1	CTD-2218G20.1	1.121775417	0.040228511
ENSG00000177105.9	RHOG	1.121544996	0.006384616
ENSG00000116260.12	QSOX1	1.120000848	5.67E-05
ENSG00000091073.15	DTX2	1.119545392	0.000191095
ENSG00000139116.13	KIF21A	1.119472002	2.48E-06
ENSG00000153187.12	HNRNPU	1.11867713	0.001324708
ENSG00000205659.6	LIN52	1.118510893	0.000193992
ENSG00000065135.7	GNAI3	1.117960284	0.000223814
ENSG00000114423.14	CBLB	1.117123748	0.023104336
ENSG00000144357.12	UBR3	1.11700077	0.000276405
ENSG00000119953.8	SMNDC1	1.116792874	6.05E-06
ENSG00000134294.9	SLC38A2	1.115637248	0.001341269
ENSG00000198301.7	SDAD1	1.115349004	0.000381963
ENSG00000127540.7	UQCR11	1.114834411	0.001716526
ENSG00000119760.11	SUPT7L	1.114247887	0.000887453
ENSG00000108433.11	GOSR2	1.112264682	2.80E-05
ENSG00000164182.6	NDUFAF2	1.111426718	0.00136031
ENSG00000196418.8	ZNF124	1.110829604	0.038311825
ENSG00000177181.10	RIMKLA	1.10828542	0.014289224
ENSG00000174227.11	PIGG	1.108258237	0.01117357
ENSG00000140307.6	GTF2A2	1.106010539	0.022436436

ENSG00000117984.8	CTSD	1.102286196	0.014152985
ENSG00000133872.9	TMEM66	1.101927059	0.004887841
ENSG00000164111.10	ANXA5	1.100929193	0.000703872
ENSG00000159256.8	MORC3	1.100668371	0.000528409
ENSG00000124209.3	RAB22A	1.100461711	0.000398609
ENSG00000169446.4	MMGT1	1.099685055	0.00136409
ENSG00000144036.10	EXOC6B	1.096505738	0.008491886
ENSG00000117614.5	SYF2	1.095396238	2.27E-06
ENSG00000171992.8	SYNPO	1.095330242	0.01824457
ENSG00000154642.6	C21orf91	1.095295326	0.047978985
ENSG00000165752.12	STK32C	1.095136011	0.005173231
ENSG00000115561.10	CHMP3	1.094769168	0.000610298
ENSG00000153391.11	INO80C	1.094612602	0.001515966
ENSG00000034713.3	GABARAPL2	1.093823344	0.000223265
ENSG00000173818.12	ENDOV	1.091567694	0.000297955
ENSG00000100445.12	SDR39U1	1.089559712	0.039819823
ENSG00000111737.7	RAB35	1.088189801	0.000109547
ENSG00000012963.9	UBR7	1.088160858	0.020380521
ENSG00000171169.8	NAIF1	1.088160817	0.042712907
ENSG00000138382.9	METTL5	1.087212614	0.010610357
ENSG00000162885.8	B3GALNT2	1.0871241	0.027721299
ENSG00000167601.7	AXL	1.087056947	0.027800603
ENSG00000157224.11	CLDN12	1.086291077	0.008745076
ENSG00000023191.12	RNH1	1.085065732	0.013193871
ENSG00000117632.16	STMN1	1.084245952	0.00145111
ENSG00000111321.6	LTBR	1.083983712	0.013753449
ENSG00000107929.10	LARP4B	1.079646215	0.000489169
ENSG00000172466.11	ZNF24	1.079358131	0.000460716
ENSG00000108039.13	XPNPEP1	1.076818331	0.012404541
ENSG00000062725.5	APPBP2	1.076278905	0.002738808
ENSG00000106392.6	C1GALT1	1.073950489	0.013810136
ENSG00000119640.4	ACYP1	1.073044714	0.014552788
ENSG00000101057.11	MYBL2	1.072486151	0.000621457
ENSG00000059769.15	DNAJC25	1.072284121	0.000456812
ENSG00000166451.9	CENPN	1.071501846	0.024202429
ENSG00000198920.5	KIAA0753	1.071379845	0.024586654
ENSG00000175137.9	SH3BP5L	1.071215875	0.000154631
ENSG00000054267.16	ARID4B	1.069839703	3.50E-05
ENSG00000111581.5	NUP107	1.069494086	0.00076939
ENSG00000118246.9	FASTKD2	1.068250346	0.010747732
ENSG00000125821.7	DTD1	1.067798704	0.025867536
ENSG00000063978.11	RNF4	1.066849937	0.015533681
ENSG00000083845.4	RPS5	1.065925869	0.004097371
ENSG00000132359.9	RAP1GAP2	1.065894641	0.043078253
ENSG00000090097.16	PCBP4	1.065645064	0.015820363
ENSG00000225528.1	RP3-370M22.8	1.065515065	0.013646627
ENSG00000270804.1	CTD-2583A14.11	1.064577287	0.036947133
ENSG00000141367.7	CLTC	1.06336357	0.000342362
ENSG00000182831.7	C16orf72	1.061775348	0.000101569
ENSG00000171984.10	C20orf196	1.061494782	0.007297927

ENSG00000116521.6	SCAMP3	1.060399688	0.003711634
ENSG00000104388.10	RAB2A	1.059704727	0.001114297
ENSG00000152332.11	UHMK1	1.056734595	0.000106475
ENSG00000214941.3	ZSWIM7	1.056198495	0.023264182
ENSG00000147202.13	DIAPH2	1.056193818	0.001489518
ENSG00000241878.5	PISD	1.055660687	0.000490803
ENSG00000110075.10	PPP6R3	1.05565176	0.003347636
ENSG00000113504.15	SLC12A7	1.055430343	0.024973846
ENSG00000176915.10	ANKLE2	1.05504261	0.001576042
ENSG00000023572.4	GLRX2	1.054790318	0.027904449
ENSG00000160588.5	MPZL3	1.054170683	0.012926925
ENSG00000150457.7	LATS2	1.051466208	0.002974381
ENSG00000171135.10	JAGN1	1.051276002	0.030263438
ENSG00000095203.10	EPB41L4B	1.050478219	0.047387514
ENSG00000113595.10	TRIM23	1.050267763	0.007757652
ENSG00000111678.6	C12orf57	1.047166315	0.008081356
ENSG00000137601.11	NEK1	1.046070506	0.00070448
ENSG00000156535.9	CD109	1.045326381	0.015305514
ENSG00000148688.9	RPP30	1.043783148	0.0032126
ENSG00000068903.15	SIRT2	1.043399186	0.011050209
ENSG00000134283.13	PPHLN1	1.043090411	0.000479456
ENSG00000163660.7	CCNL1	1.043047482	0.002974381
ENSG00000141480.13	ARRB2	1.042545109	0.044460992
ENSG00000166619.8	BLCAP	1.041097801	0.01804594
ENSG00000161996.13	WDR90	1.040127093	0.046093969
ENSG00000101856.8	PGRMC1	1.039274341	0.002419295
ENSG00000136770.6	DNAJC1	1.039217465	3.59E-05
ENSG00000165997.4	ARL5B	1.039090109	0.015274588
ENSG00000114026.17	OGG1	1.038353676	0.018808133
ENSG00000125656.4	CLPP	1.037737937	0.005261377
ENSG00000235954.2	TTC28-AS1	1.037714565	0.017180324
ENSG00000164346.5	NSA2	1.036044753	0.000180756
ENSG00000164463.8	CREBRF	1.035867278	0.010578077
ENSG00000167005.9	NUDT21	1.035836754	0.00136031
ENSG00000187239.12	FNBP1	1.035648759	0.003646483
ENSG00000180376.12	CCDC66	1.035549148	0.017959733
ENSG00000108298.5	RPL19	1.035303374	0.003352387
ENSG00000139719.5	VPS33A	1.035254788	0.031597739
ENSG00000111653.15	ING4	1.034778427	0.002815848
ENSG00000183779.5	ZNF703	1.03410586	0.006256036
ENSG00000185803.4	SLC52A2	1.033421428	0.004488482
ENSG00000165526.4	RPUSD4	1.033414574	0.003330809
ENSG00000122140.6	MRPS2	1.03324963	0.009455684
ENSG00000182208.8	MOB2	1.032493349	0.007555734
ENSG00000014138.4	POLA2	1.030984289	0.029650927
ENSG00000047346.8	FAM214A	1.030297017	0.020905617
ENSG00000081154.7	PCNP	1.029506101	0.007204723
ENSG00000226360.4	RPL10AP6	1.029370182	0.006571508
ENSG00000187145.10	MRPS21	1.028443012	0.004279424
ENSG00000049245.8	VAMP3	1.027125446	0.014086588

ENSG00000105854.8	PON2	1.026679442	0.025996431
ENSG00000113712.12	CSNK1A1	1.026179102	3.37E-05
ENSG00000156860.11	FBRS	1.023835742	8.97E-05
ENSG00000117691.5	NENF	1.023181134	0.006986606
ENSG00000160695.10	VPS11	1.023044152	0.030978334
ENSG00000009844.11	VTA1	1.023009905	0.002079898
ENSG00000131269.11	ABCB7	1.022497564	0.007583858
ENSG00000151576.6	QTRTD1	1.021685298	0.00304496
ENSG00000168036.12	CTNNB1	1.02034984	0.017192994
ENSG00000124784.4	RIOK1	1.019890938	0.001440814
ENSG00000141424.8	SLC39A6	1.0192466	0.000290677
ENSG00000134809.4	TIMM10	1.018326007	0.017733631
ENSG00000137409.14	MTCH1	1.018249238	0.000134661
ENSG00000096093.10	EFHC1	1.01796946	0.033979983
ENSG00000070501.7	POLB	1.015739591	0.014128794
ENSG00000135341.13	MAP3K7	1.014984086	0.01564016
ENSG00000115145.5	STAM2	1.014632396	0.008750587
ENSG00000197746.9	PSAP	1.014274911	0.000197477
ENSG00000083937.4	CHMP2B	1.013317141	0.001246002
ENSG00000115568.11	ZNF142	1.013241864	0.010535654
ENSG00000188342.7	GTF2F2	1.013116707	0.015723224
ENSG00000051128.14	HOMER3	1.012903675	0.011931265
ENSG00000101187.11	SLCO4A1	1.011955251	0.001397701
ENSG00000107862.4	GBF1	1.010919581	0.004611111
ENSG00000107669.13	ATE1	1.008998009	0.009744885
ENSG00000136536.10	MARCH7	1.008332269	0.000310537
ENSG00000167232.9	ZNF91	1.008164509	0.000894485
ENSG00000137710.10	RDX	1.008076271	0.00210673
ENSG00000077312.4	SNRPA	1.006502497	0.00486195
ENSG00000254901.3	MEF2BNB	1.003148496	0.014156709
ENSG00000115355.11	CCDC88A	1.002911918	0.001604056
ENSG00000086589.7	RBM22	1.002345118	5.35E-05
ENSG00000118900.10	UBN1	1.001282963	0.000993901
ENSG00000133193.8	FAM104A	1.001006859	0.000681674
ENSG00000139323.9	POC1B	1.000291284	0.038900648
ENSG00000152223.8	EPG5	0.999043223	0.039348385
ENSG00000154447.10	SH3RF1	0.998604692	0.000371465
ENSG00000023287.8	RB1CC1	0.997904431	1.55E-05
ENSG00000170185.5	USP38	0.997797368	0.042163259
ENSG00000136754.12	ABI1	0.995702141	0.011851624
ENSG00000103769.5	RAB11A	0.992998444	0.002600299
ENSG00000259494.1	MRPL46	0.9928737	0.006313386
ENSG00000130311.6	DDA1	0.992239132	3.04E-05
ENSG00000112305.10	SMAP1	0.992138129	0.005369475
ENSG00000120727.8	PAIP2	0.991959936	5.25E-05
ENSG00000151239.9	TWF1	0.990748959	0.020226618
ENSG00000126775.8	ATG14	0.989595801	0.008528194
ENSG00000029364.7	SLC39A9	0.989497052	0.014040245
ENSG00000122545.13	SEPT7	0.989439087	0.000206106
ENSG00000181991.11	MRPS11	0.989378952	0.001100491

ENSG00000174718.7	KIAA1551	0.988567748	0.015746258
ENSG00000092199.13	HNRNPC	0.98754214	0.001593062
ENSG00000114999.7	TTL	0.987359543	0.00325805
ENSG00000129625.8	REEP5	0.98685298	0.003542087
ENSG00000068912.9	ERLEC1	0.986258217	0.014397224
ENSG00000224470.3	ATXN1L	0.984703696	0.016408157
ENSG00000130024.10	PHF10	0.983823064	0.012474433
ENSG00000173660.7	UQCRH	0.983780803	0.001208038
ENSG00000062598.13	ELMO2	0.983547411	0.005116577
ENSG00000174579.3	MSL2	0.982539421	0.035516643
ENSG00000104381.8	GDAP1	0.980481114	0.023909956
ENSG00000104613.7	INTS10	0.977436122	0.00077485
ENSG00000157978.7	LDLRAP1	0.976190166	0.033562196
ENSG00000179262.5	RAD23A	0.974892122	0.006826234
ENSG00000178896.6	EXOSC4	0.974859147	0.011562651
ENSG00000169057.15	MECP2	0.974532662	0.005764204
ENSG00000116337.11	AMPD2	0.969982527	0.021780701
ENSG00000008394.8	MGST1	0.96902874	0.000601819
ENSG00000099817.7	POLR2E	0.96878333	0.007050211
ENSG00000106683.10	LIMK1	0.968178712	0.012849913
ENSG00000117519.11	CNN3	0.968035472	0.001318962
ENSG00000142186.12	SCYL1	0.967695627	0.001771892
ENSG00000039650.5	PNKP	0.96725093	0.016344198
ENSG00000128609.10	NDUFA5	0.965908434	0.00314719
ENSG00000181817.5	LSM10	0.965162499	0.028756634
ENSG00000105443.9	CYTH2	0.964959259	0.007407185
ENSG00000135316.13	SYNCRIP	0.963088145	0.00450642
ENSG00000112130.12	RNF8	0.960987179	0.023233106
ENSG00000213995.7	CARKD	0.960026337	0.043116826
ENSG00000076043.5	REXO2	0.959417365	0.007521303
ENSG00000175550.3	DRAP1	0.959323759	5.67E-05
ENSG00000153914.11	SREK1	0.95659771	0.000991642
ENSG00000148229.8	POLE3	0.95545876	0.004132264
ENSG00000110958.11	PTGES3	0.954381217	0.000193449
ENSG00000164022.12	AIMP1	0.954348662	0.011719812
ENSG00000122483.13	CCDC18	0.951120354	0.010286623
ENSG00000171566.7	PLRG1	0.949548304	0.000165334
ENSG00000229659.1	RP11-345K20.2	0.94852602	0.032705951
ENSG00000131013.3	PPIL4	0.946408421	0.000189819
ENSG00000159140.13	SON	0.946287264	0.000975256
ENSG00000196352.9	CD55	0.945992385	0.018650962
ENSG00000170142.7	UBE2E1	0.945858763	0.012479809
ENSG00000182768.7	NGRN	0.945094692	0.014347809
ENSG00000100220.7	RTCB	0.944988922	0.00077485
ENSG00000198887.7	SMC5	0.944377845	0.000765188
ENSG00000160336.10	ZNF761	0.943277065	0.010737547
ENSG00000161204.7	ABCF3	0.941882336	0.02296024
ENSG00000125814.13	NAPB	0.941637274	0.009599565
ENSG00000084733.6	RAB10	0.941523553	4.23E-05
ENSG00000164823.5	OSGIN2	0.941413315	0.032564424

ENSG00000197713.10	RPE	0.9411925	0.006673173
ENSG00000197223.7	C1D	0.940358344	0.002455069
ENSG00000153214.5	TMEM87B	0.939390409	0.005128686
ENSG00000198756.6	COLGALT2	0.939329215	0.014754141
ENSG00000067365.10	METTL22	0.938916226	0.00974016
ENSG00000138433.11	CIR1	0.938339466	0.000193449
ENSG00000153317.10	ASAP1	0.938071914	0.000433825
ENSG00000103642.7	LACTB	0.937344362	0.000627837
ENSG00000142657.16	PGD	0.936740942	0.009423836
ENSG00000123975.4	CKS2	0.93304186	0.000538014
ENSG00000214655.6	ZSWIM8	0.931793161	0.010811809
ENSG00000106524.4	ANKMY2	0.93148067	0.004240793
ENSG00000143621.12	ILF2	0.929260251	0.008145578
ENSG00000136813.10	KIAA0368	0.928607091	0.000967732
ENSG00000037241.3	RPL26L1	0.927772513	0.013680249
ENSG00000179335.14	CLK3	0.926789905	0.001834403
ENSG00000114982.13	KANSL3	0.925576612	0.009744885
ENSG00000072803.13	FBXW11	0.925120803	0.004804426
ENSG00000120253.9	NUP43	0.924900129	0.003332738
ENSG00000242247.6	ARFGAP3	0.924881226	0.014370408
ENSG00000131966.9	ACTR10	0.924542183	0.002146963
ENSG00000177119.11	ANO6	0.92165237	0.026934969
ENSG00000066697.10	MSANTD3	0.921581083	0.008957288
ENSG00000099968.13	BCL2L13	0.920780357	0.005021319
ENSG00000114315.3	HES1	0.920651897	0.00727521
ENSG00000141026.4	MED9	0.920511671	0.027991042
ENSG00000178950.12	GAK	0.918937985	0.000862738
ENSG00000162735.14	PEX19	0.918565196	0.007839174
ENSG00000163743.9	RCHY1	0.918500083	0.022043977
ENSG00000109917.6	ZNF259	0.918388452	0.002602731
ENSG00000147419.12	CCDC25	0.916539104	0.020898903
ENSG00000112079.8	STK38	0.916379755	0.01170164
ENSG00000136877.10	FPGS	0.915065093	0.026497196
ENSG00000097007.13	ABL1	0.913246899	0.017243763
ENSG00000196531.6	NACA	0.912935543	0.006036515
ENSG00000170448.7	NFXL1	0.911592133	0.002674106
ENSG00000176407.13	KCMF1	0.909793096	0.000184965
ENSG00000166199.8	ALKBH3	0.908768525	0.013411265
ENSG00000188971.4	RP11-427H3.3	0.908048537	0.000301186
ENSG00000115657.8	ABCB6	0.905244371	0.016871215
ENSG00000125772.8	GPCPD1	0.905054324	0.007701588
ENSG00000132912.8	DCTN4	0.903205279	0.003266488
ENSG00000173273.11	TNKS	0.902544055	0.009931991
ENSG00000101294.12	HM13	0.902339965	0.002655194
ENSG00000010270.9	STARD3NL	0.90168155	0.047972246
ENSG00000005801.12	ZNF195	0.901675722	0.014475293
ENSG00000123908.7	AGO2	0.90138216	0.001966585
ENSG00000130734.5	ATG4D	0.900414842	0.046551328
ENSG00000099804.4	CDC34	0.899985604	0.002922606
ENSG00000088205.8	DDX18	0.899291001	0.003808711

ENSG00000134480.9	CCNH	0.89864393	0.04033051
ENSG00000107937.14	GTPBP4	0.898353106	9.68E-05
ENSG00000115520.4	COQ10B	0.898292357	0.003732931
ENSG00000005700.10	IBTK	0.897779685	0.01872273
ENSG00000169607.8	CKAP2L	0.897761267	0.011025924
ENSG00000123159.11	GIPC1	0.897644574	0.006026776
ENSG00000119969.10	HELLS	0.895904434	0.027397671
ENSG00000138363.10	ATIC	0.895870216	0.028568125
ENSG00000136856.13	SLC2A8	0.894939624	0.008669259
ENSG00000120688.7	WBP4	0.894616917	0.016754903
ENSG00000136450.8	SRSF1	0.89411125	0.003374414
ENSG00000176261.11	ZBTB8OS	0.893672993	0.023773768
ENSG00000134186.7	PRPF38B	0.893059752	0.000235261
ENSG00000187189.9	TSPYL4	0.892738048	0.003332651
ENSG00000197045.8	GMFB	0.889099103	0.009933584
ENSG00000135932.6	CAB39	0.88678464	0.022103101
ENSG00000171109.14	MFN1	0.885748844	0.00262417
ENSG00000104375.11	STK3	0.884622127	0.016810502
ENSG00000144233.5	AMMECR1L	0.88049567	0.000415443
ENSG00000162623.11	TYW3	0.879783522	0.001014081
ENSG00000138709.13	LARP1B	0.879709925	0.03600277
ENSG00000120254.11	MTHFD1L	0.879662967	0.005244826
ENSG00000091651.4	ORC6	0.879495662	0.004288904
ENSG00000160957.8	RECQL4	0.879307283	0.011637741
ENSG00000082269.12	FAM135A	0.879157907	0.002740438
ENSG00000141985.5	SH3GL1	0.878511277	0.002128828
ENSG00000114346.9	ECT2	0.877902644	0.012849913
ENSG00000197122.7	SRC	0.877327636	0.007529096
ENSG00000121879.3	PIK3CA	0.875984307	0.003962691
ENSG00000164934.9	DCAF13	0.87567568	0.003066675
ENSG00000160789.15	LMNA	0.875516221	0.005819687
ENSG00000111412.4	C12orf49	0.874970927	0.026716178
ENSG00000135535.10	CD164	0.874868872	0.006031447
ENSG00000100911.9	PSME2	0.874171631	0.026040214
ENSG00000138621.7	PPCDC	0.872976589	0.040811126
ENSG00000142168.10	SOD1	0.872662783	0.000478476
ENSG00000162645.8	GBP2	0.871061507	0.007054258
ENSG00000179051.9	RCC2	0.869119542	0.015483069
ENSG00000119720.13	NRDE2	0.868827101	0.003496195
ENSG00000137947.7	GTF2B	0.868603267	0.024532198
ENSG00000239559.2	RPL37P2	0.867288942	0.025333661
ENSG00000121848.9	RNF115	0.86677391	0.000843818
ENSG00000104872.6	PIH1D1	0.866276844	0.042828518
ENSG00000147535.12	PPAPDC1B	0.865862012	0.019841379
ENSG00000213614.5	HEXA	0.864558471	0.004553801
ENSG00000168701.14	TMEM208	0.864227583	0.000157569
ENSG00000184640.13	SEPT9	0.861554515	0.033703501
ENSG00000143774.12	GUK1	0.861489132	0.018427259
ENSG00000226396.1	RPS14P3	0.86032445	0.008946457
ENSG00000130830.10	MPP1	0.859728665	0.024573946

ENSG00000134077.11	THUMPD3	0.859263625	0.025334495
ENSG00000095319.10	NUP188	0.858816722	0.013657218
ENSG00000133606.6	MKRN1	0.857899727	0.003133754
ENSG00000173145.7	NOC3L	0.857682133	0.011703409
ENSG00000226084.4	RP4-706A16.3	0.857345303	0.022237193
ENSG00000062582.9	MRPS24	0.856131987	0.015528353
ENSG00000166128.8	RAB8B	0.855479165	0.034325623
ENSG00000107341.4	UBE2R2	0.854977755	0.03996816
ENSG00000123815.7	ADCK4	0.854763532	0.04070528
ENSG00000093167.13	LRRFIP2	0.854593971	0.001957237
ENSG00000079332.10	SAR1A	0.852817581	0.000235742
ENSG00000135974.5	C2orf49	0.8518633	0.000539197
ENSG00000101558.9	VAPA	0.85184215	0.018971611
ENSG00000138180.11	CEP55	0.850090876	0.009465723
ENSG00000161813.16	LARP4	0.849872664	0.000604886
ENSG00000105171.5	POP4	0.849093879	0.018024168
ENSG00000082701.10	GSK3B	0.847942849	0.010401276
ENSG00000108107.8	RPL28	0.846470904	0.017959733
ENSG00000213593.5	TMX2	0.8460576	0.008685167
ENSG00000149806.6	FAU	0.845198523	0.006984137
ENSG00000156467.5	UQCRB	0.844783674	0.020933868
ENSG00000103121.4	CMC2	0.84466416	0.011953464
ENSG00000272449.1	RP3-395M20.12	0.844597291	0.048890437
ENSG00000140931.15	CMTM3	0.842747034	0.037441571
ENSG00000080802.14	CNOT4	0.842002567	0.02119434
ENSG00000033178.8	UBA6	0.841581432	0.001512193
ENSG00000146282.13	RARS2	0.840135763	0.004885667
ENSG00000116918.9	TSNAX	0.839806807	0.023434169
ENSG00000092140.10	G2E3	0.838859883	0.001084878
ENSG00000223959.4	AFG3L1P	0.836952915	0.023873248
ENSG00000164933.7	SLC25A32	0.832915691	0.009608067
ENSG00000180370.6	PAK2	0.831693088	0.001014122
ENSG00000121774.13	KHDRBS1	0.83152317	0.001513764
ENSG00000143379.8	SETDB1	0.831121337	0.045087843
ENSG00000125863.13	MKKS	0.830294225	0.024799944
ENSG00000126267.4	COX6B1	0.829936873	0.022603587
ENSG00000107262.12	BAG1	0.829031385	0.004673295
ENSG00000117360.8	PRPF3	0.828513548	0.014370408
ENSG00000124762.9	CDKN1A	0.828369063	0.024799944
ENSG00000166900.10	STX3	0.828306649	0.003568374
ENSG00000079950.9	STX7	0.828263025	0.0227323
ENSG00000171530.9	TBCA	0.828109182	0.003308207
ENSG00000126214.16	KLC1	0.827554947	0.001142102
ENSG00000114383.5	TUSC2	0.826851496	0.010015027
ENSG00000108424.5	KPNB1	0.824251779	0.018519352
ENSG00000080823.17	MOK	0.823546179	0.018773462
ENSG00000101773.12	RBBP8	0.823400693	0.019794128
ENSG00000100883.7	SRP54	0.822935047	0.019510913
ENSG00000183155.4	RABIF	0.822697025	0.012235047
ENSG00000100101.13	NOL12	0.821231041	0.005320367

ENSG00000135250.12	SRPK2	0.820669683	0.007379719
ENSG00000115761.11	NOL10	0.820590582	0.007037855
ENSG00000159176.9	CSRP1	0.820437852	0.037236232
ENSG00000168612.4	ZSWIM1	0.820085308	0.037300498
ENSG00000155229.16	MMS19	0.818338752	0.015896542
ENSG00000272330.1	AC002044.4	0.817699001	0.046083231
ENSG00000018510.8	AGPS	0.817265651	0.020811338
ENSG00000141522.7	ARHGDIA	0.816753621	0.003458506
ENSG00000159346.8	ADIPOR1	0.816387542	0.01045566
ENSG00000101457.8	DNTTIP1	0.815440953	0.008651545
ENSG00000155329.7	ZCCHC10	0.813845401	0.014136054
ENSG00000214832.4	UPF3AP2	0.812907605	0.04119009
ENSG00000134697.8	GNL2	0.812671297	0.000435223
ENSG00000139318.7	DUSP6	0.811712323	0.002079623
ENSG00000198477.3	ZNF280B	0.811638132	0.008290352
ENSG00000171475.9	WIPF2	0.811490476	0.009459594
ENSG00000164253.8	WDR41	0.811450875	0.008212282
ENSG00000174444.10	RPL4	0.811324876	0.013715873
ENSG00000166226.8	CCT2	0.810999136	0.002399071
ENSG00000057663.8	ATG5	0.810730323	0.038341997
ENSG00000104341.12	LAPTM4B	0.810668227	0.005969841
ENSG00000086712.8	TXLNG	0.808829289	0.008454939
ENSG00000122566.16	HNRNPA2B1	0.801693915	0.007651223
ENSG00000117682.12	DHDDS	0.800384171	0.020506768
ENSG00000089280.14	FUS	0.799232497	0.003979084
ENSG00000077157.16	PPP1R12B	0.798568752	0.039585468
ENSG00000269821.1	KCNQ1OT1	0.797367619	0.003352264
ENSG00000168092.9	PAFAH1B2	0.797308588	0.024026331
ENSG00000122696.8	SLC25A51	0.797280613	0.041683443
ENSG00000011295.11	TTC19	0.796416479	0.025133032
ENSG00000136603.9	SKIL	0.795718345	0.008603276
ENSG00000121579.8	NAA50	0.795009453	0.035712129
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ENSG00000132436.7	FIGNL1	0.792267774	0.035332195
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ENSG00000107438.4	PDLIM1	0.789453516	0.04708618
ENSG00000198034.6	RPS4X	0.789434791	0.024172407
ENSG00000114019.10	AMOTL2	0.789066651	0.034522719
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ENSG00000008838.13	MED24	0.787168592	0.029059527
ENSG00000162409.6	PRKAA2	0.786605948	0.004076836
ENSG00000130479.6	MAP1S	0.781054356	0.016540714
ENSG00000103168.12	TAF1C	0.780179674	0.002553986
ENSG00000151062.10	CACNA2D4	0.77947635	0.019007941
ENSG00000101247.13	NDUFAF5	0.779453674	0.037327512
ENSG00000158850.10	B4GALT3	0.778846587	0.025471769
ENSG00000020426.6	MNAT1	0.778189706	0.028662859
ENSG00000107968.5	MAP3K8	0.778069014	0.038359756
ENSG00000101132.5	PFDN4	0.777104895	0.001003274

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ENSG00000112695.7	COX7A2	0.770662713	0.017781605
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ENSG00000134900.7	TPP2	0.77033441	0.031060844
ENSG00000230989.2	HSBP1	0.767981127	0.009508027
ENSG00000078304.15	PPP2R5C	0.766772931	0.016270992
ENSG00000121644.14	DESI2	0.766590751	0.042015199
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ENSG00000152683.10	SLC30A6	0.762551704	0.025367166
ENSG00000103496.10	STX4	0.762131875	0.00150661
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ENSG00000184164.10	CRELD2	0.761677563	0.045019683
ENSG00000066427.17	ATXN3	0.758812899	0.008564736
ENSG00000091009.6	RBM27	0.757659499	0.002659836
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ENSG00000110841.9	PPFIBP1	0.753634702	0.014925757
ENSG00000108953.12	YWHAE	0.752527006	0.017793885
ENSG00000078687.12	TNRC6C	0.751947853	0.019720706
ENSG00000126934.9	MAP2K2	0.751802586	0.014245467
ENSG00000198815.4	FOXJ3	0.751410747	0.022510527
ENSG00000153815.12	CMIP	0.750456458	0.021379159
ENSG00000141140.12	MYO19	0.75004877	0.006671834
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ENSG00000075624.9	ACTB	0.746162913	0.008936444
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ENSG00000112851.10	ERBB2IP	0.743739069	0.009459622
ENSG00000169251.8	NMD3	0.74339422	0.008953704
ENSG00000140367.7	UBE2Q2	0.741198619	0.031242846
ENSG00000075790.6	BCAP29	0.741123149	0.048607954
ENSG00000124172.5	ATP5E	0.740637122	0.022165104
ENSG00000257923.5	CUX1	0.739387055	0.003858519
ENSG00000123130.12	ACOT9	0.739138753	0.01530687
ENSG00000205871.4	RPS3AP47	0.738379264	0.027461737
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ENSG00000084073.4	ZMPSTE24	0.737404694	0.043602978
ENSG00000172869.10	DMXL1	0.736153013	0.044062106

ENSG00000136940.9	PDCL	0.735774003	0.023930725
ENSG00000105221.12	AKT2	0.735505831	0.040873225
ENSG00000198646.9	NCOA6	0.733476432	0.042951712
ENSG00000171206.9	TRIM8	0.732796875	0.027557439
ENSG00000167323.5	STIM1	0.732581419	0.04280328
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ENSG00000157540.15	DYRK1A	0.731182258	0.023192665
ENSG00000109475.12	RPL34	0.7307491	0.02797146
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ENSG00000120306.5	CYSTM1	0.729826848	0.049866978
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ENSG00000168566.11	SNRNP48	0.724468513	0.002733808
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ENSG00000102172.11	SMS	0.721479644	0.017231128
ENSG00000124207.12	CSE1L	0.720843458	0.02598211
ENSG00000166266.9	CUL5	0.720127094	0.032522999
ENSG00000064932.11	SBNO2	0.720019335	0.022130289
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ENSG00000196792.7	STRN3	0.715329399	0.006150142
ENSG00000214113.6	LYRM4	0.713532309	0.017006453
ENSG00000074696.8	PTPLAD1	0.712579634	0.019520952
ENSG00000168137.11	SETD5	0.712530537	0.015160247
ENSG00000169714.12	CNBP	0.710392077	0.013837842
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ENSG00000169967.12	MAP3K2	0.703425276	0.020162261
ENSG00000168528.7	SERINC2	0.703382648	0.019390979
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ENSG00000196465.6	MYL6B	0.701542071	0.026646532
ENSG00000144867.7	SRPRB	0.700022968	0.007148264
ENSG00000171824.9	EXOSC10	0.695099963	0.021848399
ENSG00000162408.10	NOL9	0.693729478	0.02070244
ENSG00000137996.8	RTCA	0.693245281	0.016114193
ENSG00000109805.5	NCAPG	0.692976327	0.044386115
ENSG00000002919.10	SNX11	0.692079473	0.019161605
ENSG00000168564.5	CDKN2AIP	0.691006884	0.040928814
ENSG00000101189.5	MRGBP	0.690753841	0.02105904
ENSG00000101191.12	DIDO1	0.68894393	0.005325747
ENSG00000165055.11	METTL2B	0.687934143	0.016105481
ENSG00000149716.8	ORAOV1	0.687858168	0.032466078
ENSG00000101040.15	ZMYND8	0.686475764	0.018972668
ENSG00000011260.9	UTP18	0.685867158	0.040015552
ENSG00000141098.8	GFOD2	0.685624035	0.043577447

ENSG00000166233.8	ARIH1	0.684159993	0.016810502
ENSG00000141458.8	NPC1	0.68243368	0.030815529
ENSG00000159592.6	GPBP1L1	0.68154587	0.038691119
ENSG00000138592.9	USP8	0.680364969	0.00541211
ENSG00000120705.8	ETF1	0.677963196	0.012816518
ENSG00000065526.6	SPEN	0.677953086	0.021829214
ENSG00000147649.5	MTDH	0.676688003	0.013226522
ENSG00000141252.15	VPS53	0.67465413	0.018348932
ENSG00000198000.7	NOL8	0.674446039	0.02676976
ENSG00000186591.7	UBE2H	0.674264913	0.006421709
ENSG00000186866.12	POFUT2	0.67411661	0.044647431
ENSG00000198858.5	R3HDM4	0.673934495	0.038377918
ENSG00000112335.10	SNX3	0.672964214	0.007076103
ENSG00000113068.5	PFDN1	0.669433832	0.006138424
ENSG00000162909.13	CAPN2	0.666150579	0.045968598
ENSG00000163714.13	U2SURP	0.666045923	0.033908592
ENSG00000182199.6	SHMT2	0.664065452	0.022792571
ENSG00000150753.7	CCT5	0.662824536	0.009328914
ENSG00000182087.8	TMEM259	0.662063905	0.024655469
ENSG00000150459.8	SAP18	0.659262841	0.021359512
ENSG00000038532.10	CLEC16A	0.656265949	0.03922933
ENSG00000139644.8	TMBIM6	0.65522552	0.01713509
ENSG00000145907.10	G3BP1	0.654178425	0.036155946
ENSG00000181061.9	HIGD1A	0.65322552	0.024385753
ENSG00000115649.11	CNPPD1	0.652978963	0.036353611
ENSG00000113387.7	SUB1	0.651090163	0.040937418
ENSG00000107223.8	EDF1	0.650478409	0.017007617
ENSG00000136522.9	MRPL47	0.649370617	0.040355857
ENSG00000118217.5	ATF6	0.649048437	0.02332453
ENSG00000061676.10	NCKAP1	0.647554549	0.025549934
ENSG00000184182.14	UBE2F	0.647250781	0.020696174
ENSG00000164163.6	ABCE1	0.646316595	0.033536897
ENSG00000166479.5	TMX3	0.644795217	0.026275581
ENSG00000131263.8	RLIM	0.640295543	0.026267343
ENSG00000228462.1	RP11-445N18.3	0.639674744	0.032466625
ENSG00000109790.12	KLHL5	0.638525578	0.024942083
ENSG00000068028.13	RASSF1	0.63797937	0.037682741
ENSG00000150093.14	ITGB1	0.637215464	0.046418706
ENSG00000171735.14	CAMTA1	0.636605897	0.044793511
ENSG00000058262.5	SEC61A1	0.636379151	0.040688239
ENSG00000008952.12	SEC62	0.636307613	0.009289942
ENSG00000067533.5	RRP15	0.634534458	0.018674726
ENSG00000095787.17	WAC	0.633576565	0.007187893
ENSG00000165417.7	GTF2A1	0.632541135	0.035029894
ENSG00000088833.13	NSFL1C	0.632281644	0.012907935
ENSG00000101391.16	CDK5RAP1	0.631708482	0.023930725
ENSG00000174173.6	TRMT10C	0.631373678	0.02084795
ENSG00000157827.15	FMNL2	0.630646912	0.041077867
ENSG00000171490.8	RSL1D1	0.626946007	0.022725532
ENSG00000168894.5	RNF181	0.625134737	0.021065078

ENSG00000144118.9	RALB	0.624019484	0.014555971
ENSG00000198162.8	MAN1A2	0.621391813	0.017770463
ENSG00000163510.9	CWC22	0.617857155	0.010982837
ENSG00000125450.6	NUP85	0.617135872	0.013848916
ENSG00000184863.6	RBM33	0.616081704	0.015955813
ENSG00000125686.7	MED1	0.615580185	0.045226143
ENSG00000101654.13	RNMT	0.614328829	0.023968825
ENSG00000164465.14	DCBLD1	0.61407218	0.02371306
ENSG00000029363.11	BCLAF1	0.609541332	0.017884002
ENSG00000070047.7	PHRF1	0.608194601	0.017865593
ENSG00000116754.9	SRSF11	0.59858863	0.015992284
ENSG00000180198.11	RCC1	0.59796199	0.043768762
ENSG00000111845.4	PAK1IP1	0.596172515	0.033338764
ENSG00000108559.7	NUP88	0.590448891	0.046657703
ENSG00000163798.9	SLC4A1AP	0.589685658	0.018778742
ENSG00000114416.13	FXR1	0.588811596	0.013223686
ENSG00000146083.7	RNF44	0.588413112	0.036349095
ENSG00000243147.3	MRPL33	0.587348723	0.028786533
ENSG00000198408.9	MGEA5	0.587100806	0.037194396
ENSG00000111786.4	SRSF9	0.5863347	0.047869094
ENSG00000198961.5	PJA2	0.585378895	0.035156556
ENSG00000127314.13	RAP1B	0.581217256	0.044544635
ENSG00000148498.11	PARD3	0.579200528	0.025541478
ENSG00000126698.6	DNAJC8	0.571407054	0.018755037
ENSG00000105723.7	GSK3A	0.571046261	0.038691119
ENSG00000106263.13	EIF3B	0.56849989	0.016007054
ENSG00000079785.10	DDX1	0.565009323	0.024659689
ENSG00000103591.8	AAGAB	0.562381968	0.045643191
ENSG00000171262.7	FAM98B	0.557654072	0.047849896
ENSG00000181929.7	PRKAG1	0.555964718	0.022448678
ENSG00000086102.14	NFX1	0.555819294	0.027960571
ENSG00000168214.16	RBPJ	0.5555005	0.040918175
ENSG00000109046.10	WSB1	0.554168898	0.030577376
ENSG00000147454.9	SLC25A37	0.553242035	0.04486091
ENSG00000240652.1	RP11-832N8.1	0.552773377	0.041121816
ENSG00000125351.6	UPF3B	0.549708086	0.048515651
ENSG00000167770.7	OTUB1	0.548518772	0.03469625
ENSG00000170144.14	HNRNPA3	0.548378928	0.033519149
ENSG00000144645.9	OSBPL10	0.548310595	0.041184858
ENSG00000170606.9	HSPA4	0.544818728	0.024037522
ENSG00000165733.7	BMS1	0.540058006	0.035328188
ENSG00000102024.13	PLS3	0.533353221	0.042050379
ENSG00000113643.4	RARS	0.532084752	0.030577376
ENSG00000136193.12	SCRN1	0.531486393	0.036529878
ENSG00000058272.11	PPP1R12A	0.501486626	0.047534945
ENSG00000079819.12	EPB41L2	0.479718712	0.042840675

DOWN-REGULATED GENES

ENSG00000204070.5	SYS1	-0.507911207	0.035328824
ENSG00000106771.8	TMEM245	-0.517117051	0.042586867
ENSG00000173486.8	FKBP2	-0.519610945	0.04492755

ENSG00000132300.14	PTCD3	-0.520001124	0.047729895
ENSG00000160209.14	PDXK	-0.536145726	0.045441092
ENSG00000117500.8	TMED5	-0.536498479	0.036855539
ENSG00000116750.9	UCHL5	-0.538938432	0.049178206
ENSG00000095380.10	NANS	-0.539402825	0.042946355
ENSG00000135486.13	HNRNPA1	-0.540850198	0.032863233
ENSG00000090863.7	GLG1	-0.544855923	0.022792571
ENSG00000090861.11	AARS	-0.546873071	0.039411021
ENSG00000132466.13	ANKRD17	-0.552343864	0.020285696
ENSG00000112200.12	ZNF451	-0.56224537	0.045010419
ENSG00000181222.10	POLR2A	-0.565013174	0.046875448
ENSG00000154380.12	ENAH	-0.569450265	0.049043263
ENSG00000184992.10	BRI3BP	-0.578103369	0.022331847
ENSG00000083168.5	KAT6A	-0.580295551	0.035150737
ENSG00000108264.12	TADA2A	-0.581013755	0.039942405
ENSG00000167693.12	NXN	-0.582150622	0.023996439
ENSG00000171067.6	C11orf24	-0.584906583	0.042931934
ENSG00000060749.10	QSER1	-0.584944872	0.024453256
ENSG00000008083.9	JARID2	-0.585630317	0.030518091
ENSG00000115661.9	STK16	-0.586500478	0.042264458
ENSG00000069329.11	VPS35	-0.587321501	0.04943219
ENSG00000128829.7	EIF2AK4	-0.587727781	0.023717789
ENSG00000101350.6	KIF3B	-0.587913796	0.03900335
ENSG00000130332.10	LSM7	-0.590128574	0.0386132
ENSG00000077684.11	PHF17	-0.592582948	0.049238512
ENSG00000147548.12	WHSC1L1	-0.598290476	0.03318224
ENSG00000164292.8	RHOBTB3	-0.598691026	0.008688983
ENSG00000123992.14	DNPEP	-0.599724454	0.032612144
ENSG00000183010.12	PYCR1	-0.60233064	0.038880771
ENSG00000144567.6	FAM134A	-0.603041359	0.028794763
ENSG00000089094.12	KDM2B	-0.603293277	0.025471769
ENSG00000180389.6	ATP5EP2	-0.60587768	0.036525044
ENSG00000006756.11	ARSD	-0.606728255	0.045791563
ENSG00000114993.11	RTKN	-0.607620377	0.026632091
ENSG00000134759.9	ELP2	-0.616566682	0.044046073
ENSG00000214078.7	CPNE1	-0.617204087	0.019795824
ENSG00000130956.9	HABP4	-0.617704666	0.019845578
ENSG00000153560.7	UBP1	-0.618146577	0.043098163
ENSG00000068079.3	IFI35	-0.620827496	0.027520252
ENSG00000157985.13	AGAP1	-0.622491108	0.020679771
ENSG00000122873.7	CISD1	-0.623188244	0.034080891
ENSG00000171492.10	LRRC8D	-0.625688348	0.030029338
ENSG00000147654.10	EBAG9	-0.626470865	0.044792029
ENSG00000151413.12	NUBPL	-0.627922229	0.032466078
ENSG00000118007.8	STAG1	-0.62871871	0.049399179
ENSG00000166170.9	BAG5	-0.628927472	0.012789627
ENSG00000147324.6	MFHAS1	-0.631639701	0.023233106
ENSG00000198648.6	STK39	-0.632685626	0.01851227
ENSG00000100354.16	TNRC6B	-0.632695109	0.039742589
ENSG00000115677.12	HDLBP	-0.634873011	0.044230353

ENSG00000153140.4	CETN3	-0.636766815	0.025153994
ENSG00000266402.2	SNORA76	-0.637146889	0.048914015
ENSG00000102974.10	CTCF	-0.639666784	0.02676976
ENSG00000162419.8	GMEB1	-0.641076388	0.02814819
ENSG00000119335.12	SET	-0.642016385	0.047267769
ENSG00000142444.6	C19orf52	-0.642152954	0.02513076
ENSG00000072210.14	ALDH3A2	-0.64243494	0.011575144
ENSG00000177106.10	EPS8L2	-0.643916931	0.019729777
ENSG00000144591.13	GMPPA	-0.64422234	0.031627806
ENSG00000163683.7	SMIM14	-0.644358843	0.038724285
ENSG00000119912.11	IDE	-0.64469766	0.049321409
ENSG00000180185.7	FAHD1	-0.64549169	0.010187679
ENSG00000115211.11	EIF2B4	-0.647747779	0.03955681
ENSG00000259806.2	CTD-2196E14.4	-0.64838929	0.046437638
ENSG00000228300.9	C19orf24	-0.65024652	0.038415728
ENSG00000127616.13	SMARCA4	-0.650617956	0.032410447
ENSG00000167515.6	TRAPPC2L	-0.651749172	0.027216383
ENSG00000013374.11	NUB1	-0.653652398	0.006577496
ENSG00000099940.7	SNAP29	-0.654614101	0.045318635
ENSG00000166902.4	MRPL16	-0.655144738	0.034041392
ENSG00000015171.14	ZMYND11	-0.655197536	0.021014506
ENSG00000161513.7	FDXR	-0.659869652	0.009459594
ENSG00000198663.12	C6orf89	-0.659968545	0.01211723
ENSG00000090432.5	MUL1	-0.661783303	0.048024216
ENSG00000138442.5	WDR12	-0.663103892	0.013119746
ENSG00000064545.10	TMEM161A	-0.663562115	0.039794682
ENSG00000135245.9	HILPDA	-0.664660565	0.030976114
ENSG00000125944.14	HNRNPR	-0.664903571	0.02774304
ENSG00000065000.11	AP3D1	-0.665442236	0.011953464
ENSG00000178988.10	MRFAP1L1	-0.665702052	0.022725532
ENSG00000065308.4	TRAM2	-0.666847223	0.021532141
ENSG00000180879.9	SSR4	-0.668543585	0.030405566
ENSG00000126768.8	TIMM17B	-0.668611915	0.022488449
ENSG00000140943.12	MBTPS1	-0.669574399	0.033527103
ENSG00000166598.8	HSP90B1	-0.669623039	0.032863233
ENSG00000105176.13	URI1	-0.670404823	0.010735106
ENSG00000205629.7	LCMT1	-0.672222226	0.024791081
ENSG00000078369.13	GNB1	-0.672226453	0.031426397
ENSG00000160223.12	ICOSLG	-0.672949071	0.048344711
ENSG00000072864.8	NDE1	-0.677617389	0.00933085
ENSG00000126777.13	KTN1	-0.679160139	0.036674111
ENSG00000170903.6	MSANTD4	-0.679390052	0.024714557
ENSG00000170017.8	ALCAM	-0.680642445	0.018410554
ENSG00000184708.13	EIF4ENIF1	-0.682268643	0.019960996
ENSG00000065268.6	WDR18	-0.682562912	0.021769176
ENSG00000198833.6	UBE2J1	-0.683754554	0.014415827
ENSG00000213585.6	VDAC1	-0.686391805	0.014860653
ENSG00000171316.7	CHD7	-0.686631811	0.006769081
ENSG00000121067.13	SPOP	-0.687890205	0.019249972
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ENSG00000147874.6	HAUS6	-0.691468682	0.026791726
ENSG00000100342.16	APOL1	-0.69191553	0.042586867
ENSG00000152127.4	MGAT5	-0.69371189	0.043953595
ENSG00000005436.9	GCFC2	-0.694029258	0.027757607
ENSG00000126778.7	SIX1	-0.694253364	0.01666805
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ENSG00000075711.16	DLG1	-0.695778332	0.027210181
ENSG00000168517.6	HEXIM2	-0.697012599	0.036525044
ENSG00000172269.12	DPAGT1	-0.698297848	0.011476147
ENSG00000132780.12	NASP	-0.699291108	0.022532957
ENSG00000124942.9	AHNAK	-0.699324955	0.03879497
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ENSG00000160439.11	RDH13	-0.703708531	0.018732748
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ENSG00000137171.10	KLC4	-0.710915691	0.020161105
ENSG00000225663.3	FAM195B	-0.711270189	0.014642314
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ENSG00000127589.4	TUBBP1	-0.712465834	0.016344198
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ENSG00000162929.9	KIAA1841	-0.714300649	0.036525044
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ENSG00000115827.9	DCAF17	-0.715370231	0.035655937
ENSG00000011426.6	ANLN	-0.715728044	0.038691119
ENSG00000172301.6	COPRS	-0.716496796	0.005590706
ENSG00000129422.9	MTUS1	-0.718978247	0.002559963
ENSG00000206053.8	HN1L	-0.719098459	0.008970036
ENSG00000085760.10	MTIF2	-0.720258463	0.006354999
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ENSG00000163527.5	STT3B	-0.721582914	0.007076984
ENSG00000140350.11	ANP32A	-0.722093234	0.022097363
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ENSG00000136935.9	GOLGA1	-0.722927186	0.033139303
ENSG00000108679.8	LGALS3BP	-0.72320837	0.00947864
ENSG00000072501.13	SMC1A	-0.724226536	0.01369103
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ENSG00000127423.6	AUNIP	-0.726384161	0.048262669
ENSG00000176410.7	DNAJC30	-0.727045932	0.015451781
ENSG00000096063.10	SRPK1	-0.727299921	0.013302218
ENSG00000267100.1	ILF3-AS1	-0.728598299	0.009339621
ENSG00000130227.12	XPO7	-0.728831711	0.01666805
ENSG00000158526.7	TSR2	-0.728890097	0.041665411
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ENSG00000169718.13	DUS1L	-0.756203416	0.00350061
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ENSG00000131149.13	GSE1	-0.758858717	0.009616963
ENSG00000101138.7	CSTF1	-0.759414692	0.004978836
ENSG00000134508.8	CABLES1	-0.761207522	0.005772243
ENSG00000255112.2	CHMP1B	-0.761653444	0.034129161
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ENSG00000164087.3	POC1A	-0.762999649	0.008836935
ENSG00000105677.7	TMEM147	-0.768919924	0.004690688
ENSG00000067248.5	DHX29	-0.769615605	0.021261109
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ENSG00000100697.10	DICER1	-0.771524712	0.003641847
ENSG00000103429.6	BFAR	-0.771924244	0.013245227
ENSG00000164244.16	PRRC1	-0.772216412	0.016090298
ENSG00000119777.14	TMEM214	-0.772552467	0.005843482
ENSG00000130939.14	UBE4B	-0.772918488	0.019595496
ENSG00000100116.12	GCAT	-0.773245416	0.028789516
ENSG00000014123.9	UFL1	-0.773629979	0.003577373
ENSG00000102738.6	MRPS31	-0.773754325	0.03828815
ENSG00000102893.11	PHKB	-0.774717086	0.005819532
ENSG00000178691.6	SUZ12	-0.775251096	0.012769754
ENSG00000151422.8	FER	-0.775351605	0.017171703
ENSG00000164944.7	KIAA1429	-0.775675761	0.038956721
ENSG00000143515.12	ATP8B2	-0.778088239	0.021882689

ENSG00000087365.10	SF3B2	-0.779169719	0.02047482
ENSG00000172939.4	OXSR1	-0.779453042	0.009248292
ENSG00000143641.8	GALNT2	-0.779886926	0.044893135
ENSG00000153029.10	MR1	-0.78015044	0.006668789
ENSG00000008382.11	MPND	-0.780222037	0.030260447
ENSG00000105696.4	TMEM59L	-0.782392853	0.005271709
ENSG00000117650.8	NEK2	-0.782775752	0.006874798
ENSG00000087884.10	AAMDC	-0.784599609	0.002450817
ENSG00000099204.14	ABLIM1	-0.785266594	0.002821221
ENSG00000168495.8	POLR3D	-0.786433645	0.017020559
ENSG00000049618.17	ARID1B	-0.786534021	0.001938955
ENSG00000198793.8	MTOR	-0.78666784	0.030849027
ENSG00000112983.13	BRD8	-0.787103962	0.013467601
ENSG00000116830.7	TTF2	-0.787638504	0.006677348
ENSG00000163624.5	CDS1	-0.78955472	0.026153665
ENSG00000131188.7	PRR7	-0.790643104	0.016782278
ENSG00000176102.7	CSTF3	-0.790740054	0.033155274
ENSG00000100304.12	TTLL12	-0.791104567	0.009500381
ENSG00000087269.11	NOP14	-0.792345496	0.009179237
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ENSG00000166548.11	TK2	-1.21864189	0.007793417
ENSG00000143374.10	TARS2	-1.219046256	0.001383968
ENSG00000103507.9	BCKDK	-1.220891165	3.61E-05
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ENSG00000225439.2	BOLA3-AS1	-1.226276632	0.011813566
ENSG00000126822.11	PLEKHG3	-1.226872436	0.001567001
ENSG00000196865.4	NHLRC2	-1.227171901	0.000700774
ENSG00000090920.9	FCGBP	-1.227457175	0.009315486
ENSG00000104884.10	ERCC2	-1.227737389	0.000513099
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ENSG00000122515.10	ZMIZ2	-1.229305941	0.002767227
ENSG00000196810.4	CTBP1-AS2	-1.229573745	0.018552978
ENSG00000067646.7	ZFY	-1.230694947	0.025350895
ENSG00000088888.13	MAVS	-1.233925119	2.25E-06
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ENSG00000104979.4	C19orf53	-1.237725121	0.000447651
ENSG00000180346.2	TIGD2	-1.237843839	0.004312954
ENSG00000250565.2	ATP6V1E2	-1.239574539	0.049862648
ENSG00000126215.9	XRCC3	-1.239794341	0.046892775
ENSG00000139597.12	N4BP2L1	-1.240299542	0.048703012
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ENSG00000172878.9	METAP1D	-1.245633582	0.016136374
ENSG00000092621.7	PHGDH	-1.248074663	0.000110504
ENSG00000092148.8	HECTD1	-1.249113902	9.94E-06
ENSG00000115685.10	PPP1R7	-1.249386292	8.31E-05
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ENSG00000185697.12	MYBL1	-1.254551024	0.023712304
ENSG00000141568.15	FOXK2	-1.255469747	0.000278536
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ENSG00000145990.6	GFOD1	-1.266933262	0.001289582
ENSG00000107789.11	MINPP1	-1.267169089	2.26E-05
ENSG00000184047.11	DIABLO	-1.268167549	0.004634721
ENSG00000158109.10	TPRG1L	-1.268886344	3.80E-06
ENSG00000104738.12	MCM4	-1.26955961	3.08E-05
ENSG00000180917.12	CMTR2	-1.271863746	0.019057642
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ENSG00000116691.6	MIIP	-1.274050005	0.001295087
ENSG00000173706.8	HEG1	-1.274639886	0.003467728
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ENSG00000162105.12	SHANK2	-1.279601092	0.007838971
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ENSG00000154080.8	CHST9	-1.283379837	0.006846768
ENSG00000009724.12	MASP2	-1.285227983	0.011025924
ENSG00000144021.2	CIAO1	-1.285870875	9.46E-08
ENSG00000099991.12	CABIN1	-1.286997538	5.50E-06
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ENSG00000136463.7	TACO1	-1.306472549	2.33E-06
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ENSG00000171219.8	CDC42BPG	-1.306933053	0.016810502
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ENSG00000171236.9	LRG1	-1.506606439	5.71E-07
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ENSG00000076662.5	ICAM3	-1.517648765	3.39E-06
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ENSG00000173662.15	TAS1R1	-1.531925475	5.33E-05
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ENSG00000273061.1	RP11-6J24.6	-1.543274691	0.011243495
ENSG00000144354.9	CDCA7	-1.543702153	6.32E-06
ENSG00000198929.8	NOS1AP	-1.544307561	9.16E-06
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ENSG00000064999.12	ANKS1A	-1.617380546	1.95E-05
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ENSG00000145494.7	NDUFS6	-1.781406883	1.10E-05
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ENSG00000141577.9	AZI1	-1.80343831	1.31E-05
ENSG00000157625.11	TAB3	-1.805555164	1.24E-06
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ENSG00000198189.6	HSD17B11	-1.822692717	9.28E-08
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ENSG00000156675.11	RAB11FIP1	-1.831478646	1.57E-07
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ENSG00000132530.12	XAF1	-1.844096647	0.018584253
ENSG00000136720.6	HS6ST1	-1.845298819	0.000280002
ENSG00000182809.6	CRIP2	-1.847711281	1.09E-05
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ENSG00000008283.11	CYB561	-1.876001116	4.71E-08
ENSG00000256235.1	SMIM3	-1.876206179	9.67E-08
ENSG00000108312.10	UBTF	-1.876362331	8.46E-09
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ENSG00000111877.13	MCM9	-1.881500812	0.004328917
ENSG00000167363.9	FN3K	-1.883044661	1.53E-07
ENSG00000167716.14	WDR81	-1.88314354	2.98E-05
ENSG00000158457.4	TSPAN33	-1.883963683	1.47E-05
ENSG00000184384.9	MAML2	-1.885217177	5.69E-06
ENSG00000095906.12	NUBP2	-1.889663398	1.77E-07
ENSG00000005206.12	SPPL2B	-1.889847196	4.08E-08
ENSG00000198208.7	RPS6KL1	-1.891825577	0.010289661
ENSG00000109667.7	SLC2A9	-1.892172169	0.000420185
ENSG00000127554.12	GFER	-1.893426162	1.69E-06
ENSG00000081913.9	PHLPP1	-1.893637025	2.16E-07
ENSG00000188833.5	ENTPD8	-1.894859219	0.048969644
ENSG00000125505.12	MBOAT7	-1.895185062	1.09E-07
ENSG00000127952.12	STYXL1	-1.898484909	3.95E-08
ENSG00000115884.6	SDC1	-1.899178812	1.63E-08
ENSG00000259926.1	RP11-44F14.5	-1.899545614	0.022103857
ENSG00000243199.1	RP11-408P14.1	-1.902416769	2.91E-05
ENSG00000164684.9	ZNF704	-1.903247527	1.09E-05
ENSG00000169692.8	AGPAT2	-1.904633846	3.47E-05
ENSG00000238105.3	GOLGA2B	-1.906199204	4.42E-05
ENSG00000038427.11	VCAN	-1.906263467	6.84E-05
ENSG00000155957.12	TMBIM4	-1.906788043	3.47E-08
ENSG00000241956.5	CTC-340A15.2	-1.907441894	0.049853721
ENSG00000165802.15	NSMF	-1.908881872	1.73E-06
ENSG00000183072.9	NKX2-5	-1.910912253	0.020983732
ENSG00000198945.3	L3MBTL3	-1.912631405	0.002832238
ENSG00000235106.4	LINC00094	-1.913039346	0.048976436
ENSG00000177352.9	CCDC71	-1.916608714	3.16E-10
ENSG00000052841.10	TTC17	-1.916998172	1.81E-05
ENSG00000132635.12	PCED1A	-1.917087832	3.30E-09
ENSG00000107902.9	LHPP	-1.919533394	0.00038709
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ENSG00000240602.3	RP11-64D22.2	-1.922021726	0.047189123
ENSG00000196535.10	MYO18A	-1.924104854	1.56E-06

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ENSG00000204371.7	EHMT2	-1.930241501	9.02E-07
ENSG00000075336.7	TIMM21	-1.930354679	3.20E-05
ENSG00000151224.8	MAT1A	-1.930385486	3.19E-10
ENSG00000126217.16	MCF2L	-1.931956852	3.44E-05
ENSG00000196083.5	IL1RAP	-1.933344666	1.81E-05
ENSG00000123243.10	ITIH5	-1.933978531	1.42E-06
ENSG00000265254.1	CTD-2350C19.2	-1.935012941	0.048824549
ENSG00000269609.1	RP11-18I14.10	-1.935697132	0.000258345
ENSG00000218902.3	PTMAP3	-1.937914842	0.046290439
ENSG00000136379.7	ABHD17C	-1.938345861	2.88E-08
ENSG00000229117.4	RPL41	-1.939661421	6.17E-05
ENSG00000114631.10	PODXL2	-1.939919611	0.001742011
ENSG00000078902.11	TOLLIP	-1.944064216	9.34E-08
ENSG00000143627.13	PKLR	-1.948372696	0.000998147
ENSG00000154511.7	FAM69A	-1.949554013	0.007948408
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ENSG00000060642.6	PIGV	-1.95071164	0.000153461
ENSG00000165730.10	STOX1	-1.953522346	0.00325805
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ENSG00000180530.5	NRIP1	-1.958176667	1.23E-09
ENSG00000178104.15	PDE4DIP	-1.958497877	0.00061661
ENSG00000257576.1	RP11-153M3.1	-1.960618675	0.003956641
ENSG00000182923.12	CEP63	-1.960857447	9.51E-09
ENSG00000106789.8	CORO2A	-1.962604127	1.13E-12
ENSG00000148584.10	A1CF	-1.964839729	8.39E-10
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ENSG00000085788.9	DDHD2	-1.971255585	3.19E-05
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ENSG00000090238.7	YPEL3	-1.976787099	1.04E-07
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ENSG00000229097.1	CALM2P2	-1.985926223	0.000137491
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ENSG00000005469.7	CROT	-1.988234174	2.42E-05
ENSG00000131797.8	CLUHP3	-1.988652127	5.13E-08
ENSG00000248275.1	TRIM52-AS1	-1.98884586	5.90E-05
ENSG00000198468.3	FLVCR1-AS1	-1.990665182	4.02E-06
ENSG00000168569.7	TMEM223	-1.99175847	2.60E-09
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ENSG00000106665.11	CLIP2	-1.999519704	8.14E-07
ENSG00000103051.14	COG4	-2.001570994	2.73E-07
ENSG00000107331.12	ABCA2	-2.001975244	0.000926281
ENSG00000214796.4	RP11-480I12.5	-2.002346387	0.000105297
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ENSG00000197258.5	EIF4BP6	-2.009374765	0.000212689
ENSG00000214530.3	STARD10	-2.010636943	4.37E-07
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ENSG00000120699.8	EXOSC8	-2.019026393	3.62E-06
ENSG00000166415.10	WDR72	-2.019073282	0.0333638
ENSG00000100299.13	ARSA	-2.020322708	1.32E-07
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ENSG00000141576.10	RNF157	-2.063966966	3.29E-11
ENSG00000178802.13	MPI	-2.065159429	8.05E-10
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ENSG00000084652.11	TXLNA	-2.205919804	1.80E-07
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ENSG00000142102.11	ATHL1	-2.217710316	1.41E-05
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ENSG00000161395.8	PGAP3	-2.22654874	7.29E-09
ENSG00000108813.9	DLX4	-2.228675895	0.011983213
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ENSG00000206190.7	ATP10A	-2.234965326	0.001211486
ENSG00000172831.7	CES2	-2.242601671	9.65E-14
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ENSG00000178531.4	CTXN1	-2.256053498	0.033453844
ENSG00000105647.10	PIK3R2	-2.260167786	3.06E-08
ENSG00000122378.9	FAM213A	-2.264819506	1.06E-09
ENSG00000196405.8	EVL	-2.266257316	2.26E-06
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ENSG00000139055.2	ERP27	-2.267025141	0.021829214
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ENSG00000136718.5	IMP4	-2.267536971	1.55E-07
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ENSG00000197061.3	HIST1H4C	-2.30401775	1.33E-08
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ENSG00000251602.2	RP11-521B24.3	-2.317437456	8.19E-08
ENSG00000136840.14	ST6GALNAC4	-2.323911801	4.44E-08
ENSG00000104518.6	GSDMD	-2.324308084	3.07E-08
ENSG00000177679.14	SRRM3	-2.325478974	0.005997995
ENSG00000162882.10	HAAO	-2.331398852	3.62E-08
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ENSG00000272791.1	RP11-464F9.22	-2.333158857	0.042391473
ENSG00000185100.6	ADSSL1	-2.334633876	0.008614639
ENSG00000115718.13	PROC	-2.336727244	2.26E-09
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ENSG00000147383.6	NSDHL	-2.344161377	2.87E-09
ENSG00000105649.5	RAB3A	-2.344584171	0.029775474
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ENSG00000245482.2	RP11-847H18.2	-2.358951034	0.035332195
ENSG00000246982.2	RP1-179N16.6	-2.361270704	0.003948472
ENSG00000042493.11	CAPG	-2.362699891	1.77E-08
ENSG00000167700.4	MFSD3	-2.36525715	2.53E-10
ENSG00000150764.9	DIXDC1	-2.368211488	9.76E-10
ENSG00000143434.11	SEMA6C	-2.36839162	4.71E-05
ENSG00000197846.3	HIST1H2BF	-2.368574698	0.001349436
ENSG00000108469.10	RECQL5	-2.386121428	1.18E-07
ENSG00000196532.4	HIST1H3C	-2.394394413	0.003521484
ENSG00000214914.3	RPL23AP3	-2.402888612	4.33E-05
ENSG00000147526.15	TACC1	-2.404445457	4.35E-11
ENSG00000110042.3	DTX4	-2.405510591	3.26E-09
ENSG00000146216.7	TTBK1	-2.408772383	0.038809376
ENSG00000237361.2	LINC01071	-2.410246938	4.37E-05
ENSG00000162545.5	CAMK2N1	-2.411770917	2.23E-10
ENSG00000181192.7	DHTKD1	-2.413808543	9.67E-11
ENSG00000137868.14	STRA6	-2.419839705	0.010298537
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ENSG00000116035.2	VAX2	-2.435160584	1.31E-06
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ENSG00000170430.9	MGMT	-2.467223647	6.17E-09
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ENSG00000233912.1	AC026202.3	-2.471782277	2.65E-05
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ENSG00000137561.4	TTPA	-2.493369848	1.09E-05
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ENSG00000257167.2	TMPO-AS1	-2.547170782	0.015821961
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ENSG00000163449.6	TMEM169	-3.578412117	5.49E-12
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ENSG00000138821.8	SLC39A8	-4.523504581	0.007556433
ENSG00000240685.1	RP11-286H14.6	-4.551885435	0.005884264
ENSG00000247033.1	RP11-252E2.1	-4.563855588	0.00984926
ENSG00000228146.2	CASP16	-4.594517903	0.000297418
ENSG00000010327.6	STAB1	-4.603578022	0.01445965
ENSG00000273033.1	RP11-67L2.2	-4.603983116	1.79E-06
ENSG00000167971.14	CASKIN1	-4.635576372	1.82E-05
ENSG00000183242.7	WT1-AS	-4.654625706	0.013501681
ENSG00000248015.2	AC005329.7	-4.659593568	5.17E-05
ENSG00000171119.2	NRTN	-4.759667373	8.23E-10
ENSG00000261302.1	RP11-343H19.1	-4.77147754	0.00708178
ENSG00000255128.1	HSPD1P3	-4.781662041	0.000197477
ENSG00000248956.1	HMGB1P44	-4.827485356	0.002167528
ENSG00000111181.8	SLC6A12	-4.866088764	0.011674022
ENSG00000173809.11	TDRD12	-4.911276775	0.001521031
ENSG00000232560.2	C21orf37	-4.94434789	0.001704804
ENSG00000230373.4	GOLGA6L5	-5.016040175	0.008227551
ENSG00000264443.1	RP4-594I10.3	-5.019662555	0.001109995
ENSG00000187792.3	ZNF70	-5.062220421	0.002358291
ENSG00000169856.7	ONECUT1	-5.257907709	5.81E-14
ENSG00000163083.5	INHBB	-5.295347283	0.00079885
ENSG00000203813.4	HIST1H3H	-5.423914879	3.92E-06
ENSG00000129596.4	CDO1	-5.521601961	0.000126436
ENSG00000196132.7	MYT1	-5.571259314	2.73E-05
ENSG00000175873.3	AC004840.9	-5.682325128	0.000386667
ENSG00000188987.2	HIST1H4D	-5.748577045	0.000258345
ENSG00000184792.11	OSBP2	-5.777652636	0.000343191
ENSG00000243910.3	TUBA4B	-5.814415718	2.73E-13
ENSG00000213759.4	UGT2B11	-5.889308278	0.000107759
ENSG00000261040.2	CTD-2319I12.1	-6.004920479	1.81E-05
ENSG00000205978.5	NYNRIN	-6.264227115	0.003167774
ENSG00000184227.3	ACOT1	-6.764349044	0.000281124

ENSG00000142273.6	CBLC	-6.765673731	4.44E-06

SUPPLEMENTARY TABLE 5

Significant biological processes (BPs) related to the GOEA for the genes, which were up-regulated or down-regulated by Cu only in control HepG2 cells.

GOEA was performed on genes, which were up- or down-regulated by Cu exclusively in control HepG2 cells (see Table 3). The data in this table were collected by using DAVID online tool restricting the output to BP_FAT terms: the BPs up-regulated and down-regulated are highlighted in red and in green, respectively.

UP-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 7.259837610585342

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0016070~RNA metabolic process	201	HKR1, NAA15, CLK1, SOHLH1, ZGPAT, ZNF776, DDX11, MAK16, MAP3K9, ZNF773, ZNF248, DHX3	2.20E-10
GOTERM_BP_FAT	GO:0010467~gene expression	216	HKR1, NAA15, CLK1, SOHLH1, ZGPAT, ZNF776, DDX11, MAK16, MAP3K9, ZNF773, ZNF248, DHX3	7.47E-09
GOTERM_BP_FAT	GO:0051171~regulation of nitrogen compound metabolic process	177	HKR1, DBF4B, LMO4, RBM5, NAA15, CLK1, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GT	1.18E-05
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	156	HKR1, LMO4, RBM5, NAA15, CLK1, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, ZN	2.23E-05
GOTERM_BP_FAT	GO:0006351~transcription, DNA-templated	151	HKR1, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, GTF2E1, ZGPAT, ZNF776, DDX11	2.29E-05
GOTERM_BP_FAT	GO:0010468~regulation of gene expression	173	HKR1, LMO4, RBM5, NAA15, CLK1, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, EI	4.21E-05
GOTERM_BP_FAT	GO:0097659~nucleic acid-templated transcription	155	HKR1, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, GTF2E1, ZGPAT, ZNF776, DDX11	4.77E-05
GOTERM_BP_FAT	GO:2000112~regulation of cellular macromolecule biosynthetic process	161	HKR1, DBF4B, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, EIF4EB	7.85E-05
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	158	HKR1, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, ZNF776, DDX11	9.47E-05
GOTERM_BP_FAT	GO:0019219~regulation of nucleobase-containing compound metabolic process	164	HKR1, DBF4B, LMO4, RBM5, NAA15, CLK1, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GT	1.04E-04
GOTERM_BP_FAT	GO:0010556~regulation of macromolecule biosynthetic process	164	HKR1, DBF4B, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, EIF4EB	1.09E-04
GOTERM_BP_FAT	GO:1903506~regulation of nucleic acid-templated transcription	148	HKR1, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, GTF2E1, ZGPAT, ZNF776, DDX11	1.93E-04
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-templated	147	HKR1, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, GTF2E1, ZGPAT, ZNF776, DDX11	2.30E-04
GOTERM_BP_FAT	GO:2001141~regulation of RNA biosynthetic process	148	HKR1, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, GTF2E1, ZGPAT, ZNF776, DDX11	2.70E-04
GOTERM_BP_FAT	GO:0034654~nucleobase-containing compound biosynthetic process	169	HKR1, XRCC2, LMO4, NAA15, JAG1, PNP, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, ZN	4.63E-04
GOTERM_BP_FAT	GO:0018130~heterocycle biosynthetic process	169	HKR1, XRCC2, LMO4, NAA15, JAG1, PNP, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, ZN	0.00108433
GOTERM_BP_FAT	GO:0019438~aromatic compound biosynthetic process	169	HKR1, XRCC2, LMO4, NAA15, JAG1, PNP, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1, ZN	0.00132472
GOTERM_BP_FAT	GO:0034645~cellular macromolecule biosynthetic process	186	HKR1, DBF4B, XRCC2, LMO4, NAA15, JAG1, SOHLH1, TGFB1, SETX, PNN, GATA2, ZGPAT, GTF2E1,	0.00176828
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	77	BACH2, TAF1A, HELZ2, LMO4, EZH2, PAX6, NFKB1, JAG1, SOHLH1, TGFB1, SETX, NFATC2IP, GATA	0.21589864
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	71	BACH2, HELZ2, LMO4, EZH2, PAX6, NFKB1, JAG1, SOHLH1, TGFB1, SETX, NFATC2IP, GATA2, ZGPA	4.83651148

Annotation Cluster 2 Enrichment Score: 4.10475595762814

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006396~RNA processing	53	RBM5, TRMT10A, TRMT1, SKIV2L2, TGFB1, SETX, PNN, DGCR8, MAK16, SRRM2, DBR1, DDX21, DH	7.57E-04
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	37	RBM5, SKIV2L2, PNN, SETX, SRRT, DDX46, ZNF326, SRRM2, ECD, EDC3, ISY1, DHX15, DBR1, SUPV	0.19341628
GOTERM_BP_FAT	GO:0006397~mRNA processing	29	RBM5, SKIV2L2, PNN, SETX, SRRT, DDX46, ZNF326, SRRM2, ECD, ISY1, DHX15, DBR1, ACIN1, RBM	0.20781346
GOTERM_BP_FAT	GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	21	TXNL4B, SF1, RBM5, SKIV2L2, PNN, SETX, SRSF3, SRRT, METTL14, DDX46, SRSF6, GTF2F1, SFPQ, S	0.43659561
GOTERM_BP_FAT	GO:0000398~mRNA splicing, via spliceosome	21	TXNL4B, SF1, RBM5, SKIV2L2, PNN, SETX, SRSF3, SRRT, METTL14, DDX46, SRSF6, GTF2F1, SFPQ, S	0.43659561
GOTERM_BP_FAT	GO:0000375~RNA splicing, via transesterification reactions	21	TXNL4B, SF1, RBM5, SKIV2L2, PNN, SETX, SRSF3, SRRT, METTL14, DDX46, SRSF6, GTF2F1, SFPQ, S	0.5188043
GOTERM_BP_FAT	GO:0008380~RNA splicing	25	TXNL4B, RBM5, AKAP8L, SF1, SKIV2L2, SETX, PNN, SRSF3, SRRT, DDX46, METTL14, SRSF6, ZNF32	0.55375332

Annotation Cluster 3 Enrichment Score: 2.511162553383309

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	77	BACH2, TAF1A, HELZ2, LMO4, EZH2, PAX6, NFKB1, JAG1, SOHLH1, TGFB1, SETX, NFATC2IP, GATA	0.21589864
GOTERM_BP_FAT	GO:2000113~negative regulation of cellular macromolecule biosynthetic process	60	BACH2, EZH2, PAX6, GNL3L, NFKB1, TGFB1, GATA2, ZGPAT, SAP30, EIF4EBP1, DGCR8, BCL7A, KD	0.25914145
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	62	BACH2, EZH2, PAX6, GNL3L, NFKB1, TGFB1, GATA2, ZGPAT, SAP30, EIF4EBP1, DGCR8, BCL7A, KD	0.51381314
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	64	BACH2, EZH2, PAX6, NFKB1, TGFB1, GATA2, ZGPAT, SAP30, EIF4EBP1, DGCR8, ACIN1, RANBP2, B	0.59289352
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	62	BACH2, EZH2, PAX6, GNL3L, NFKB1, TGFB1, GATA2, ZGPAT, SAP30, EIF4EBP1, DGCR8, BCL7A, KD	2.26631638
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	62	BACH2, EZH2, PAX6, GNL3L, NFKB1, TGFB1, GATA2, ZGPAT, SAP30, EIF4EBP1, DGCR8, ACIN1, BCL	2.34860444
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	61	BACH2, EZH2, PAX6, GNL3L, NFKB1, TGFB1, GATA2, ZGPAT, SAP30, EIF4EBP1, DGCR8, BCL7A, KD	2.50711455
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	71	BACH2, HELZ2, LMO4, EZH2, PAX6, NFKB1, JAG1, SOHLH1, TGFB1, SETX, NFATC2IP, GATA2, ZGPA	4.83651148
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-templated	47	FGFR1, HIST1H2AC, KMT2D, BACH2, EZH2, PAX6, NFKB1, TGFB1, GATA2, ZGPAT, VDR, SAP30, EZ	8.31889822

Annotation Cluster 4 Enrichment Score: 2.2385322102242426

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	77	BACH2, TAF1A, HELZ2, LMO4, EZH2, PAX6, NFKB1, JAG1, SOHLH1, TGFB1, SETX, NFATC2IP, GATA	0.21589864
GOTERM_BP_FAT	GO:0031325~positive regulation of cellular metabolic process	105	DBF4B, LMO4, NAA15, TNFSF15, JAG1, SOHLH1, TGFB1, SETX, GATA2, DDX11, MAP3K9, DHX36, F	1.62126335
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	104	DBF4B, LMO4, TNFSF15, NAA15, JAG1, SOHLH1, TGFB1, SETX, GATA2, DDX11, MAP3K9, DDX21, D	2.88469274
GOTERM_BP_FAT	GO:0009893~positive regulation of metabolic process	109	DBF4B, LMO4, NAA15, TNFSF15, JAG1, SOHLH1, TGFB1, SETX, GATA2, DDX11, MAP3K9, DDX21, D	4.04175294
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	71	BACH2, HELZ2, LMO4, EZH2, PAX6, NFKB1, JAG1, SOHLH1, TGFB1, SETX, NFATC2IP, GATA2, ZGPA	4.83651148
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	44	KMT2D, CAMTA2, HELZ2, LMO4, PAX6, NFKB1, JAG1, SOHLH1, CALCOCO1, TGFB1, SETX, NFATC2	8.39639183

Annotation Cluster 5 Enrichment Score: 1.9903654243983406

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	47	FGFR1, XRCC2, DBF4B, APEX2, EZH2, MUM1, GNL3L, BCCIP, TGFB1, SETX, FBXW7, MCM8, SWI5, I	0.66822605

Annotation Cluster 6 Enrichment Score: 1.955018768372042

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0034340~response to type I interferon	8	IFIT3, IRF9, TRIM56, UBE2K, OAS3, FADD, MX1, IP6K2	9.93088326

Annotation Cluster 7 Enrichment Score: 1.8664363507401125

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0022613~ribonucleoprotein complex biogenesis	27	ZNF622, TXNL4B, PDCD11, NOC4L, RBM5, SF1, GNL3L, SKIV2L2, MRTO4, SETX, OGFOD1, DDX56, I	1.47544319
GOTERM_BP_FAT	GO:0034660~ncRNA metabolic process	29	TRMT10A, SKIV2L2, TRMT1, NFKB1, GTF2E1, SRRT, DGCR8, MAK16, DDX11, DDX21, POLG2, TYW	4.05963626

Annotation Cluster 8 Enrichment Score: 1.6818286246689331

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0000245~spliceosomal complex assembly	7	TXNL4B, SRSF6, SF1, ISY1, RBM5, CELF2, SETX	7.64652747

Annotation Cluster 9 Enrichment Score: 1.6607368615049973

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	29	HIP1R, TNFSF15, RBM5, AKAP13, PTRH2, TGFB1, VDR, PEA15, FBXW7, DYNLL2, MAP3K9, TGM2, F	9.41206386

Annotation Cluster 11 Enrichment Score: 1.5854902068068506

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0034968~histone lysine methylation	10	KMT2D, BEND3, MTF2, KMT2C, EZH2, ASH1L, TET2, DNMT3B, CTR9, SUPT6H	3.1618268
GOTERM_BP_FAT	GO:0051568~histone H3-K4 methylation	7	KMT2D, BEND3, KMT2C, ASH1L, TET2, DNMT3B, CTR9	3.17770982
GOTERM_BP_FAT	GO:0018022~peptidyl-lysine methylation	10	KMT2D, BEND3, MTF2, KMT2C, EZH2, ASH1L, TET2, DNMT3B, CTR9, SUPT6H	6.35783853

Annotation Cluster 12 Enrichment Score: 1.5845016966095986

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008593~regulation of Notch signaling pathway	8	GATA2, FBXW7, PDCD10, EGFL7, CHAC1, JAG1, MMP14, STAT3	5.54951711

Annotation Cluster 13 Enrichment Score: 1.5334979107529148

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051568~histone H3-K4 methylation	7	KMT2D, BEND3, KMT2C, ASH1L, TET2, DNMT3B, CTR9	3.17770982

DOWN-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 13.212196031028144

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006082~organic acid metabolic process	99	BTD, IARS2, PDHB, INSIG2, PLOD1, SLC2A3, ELOVL2, SLC2A1, RGN, ELOVL7, PDHA1, GPT2, ACAA2	9.46E-15
GOTERM_BP_FAT	GO:0019752~carboxylic acid metabolic process	93	ACOX2, CPT2, BTD, AMT, OGDHL, IARS2, PDHB, AUH, AKT1, MTHFD1, MCCC2, INSIG2, PLOD1, SL	1.58E-14
GOTERM_BP_FAT	GO:0043436~oxoacid metabolic process	93	ACOX2, CPT2, BTD, AMT, OGDHL, IARS2, PDHB, AUH, AKT1, MTHFD1, MCCC2, INSIG2, PLOD1, SL	2.33E-14
GOTERM_BP_FAT	GO:0044282~small molecule catabolic process	48	ACOX2, IMPA2, CPT2, ECH1, PFKFB4, AMT, ESD, PAH, ACAT2, DTD2, PTEN, AUH, AFMID, AKT1, M	1.90E-09
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	37	ACOX2, CPT2, ECH1, AMT, PAH, DTD2, ACAT2, AUH, AFMID, AKT1, MCCC2, MTHFS, ASRGL1, ALD	8.00E-09
GOTERM_BP_FAT	GO:0032787~monocarboxylic acid metabolic process	62	ACOX2, CPT2, BTD, AMT, OGDHL, PDHB, AUH, AKT1, MCCC2, INSIG2, ELOVL2, RGN, ELOVL7, PDH	2.48E-08
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	40	ACOX2, CPT2, ECH1, APOC1, ACAT2, PDHB, AUH, AKT1, INSIG2, ELOVL2, RGN, BDH2, ELOVL7, PE	2.59E-04

Annotation Cluster 2 Enrichment Score: 9.519623335911675

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006629~lipid metabolic process	115	IMPAD1, RORC, PI4K2B, C14ORF1, PDHB, FDFT1, TTR, APOA2, SH3YL1, INSIG2, SULT1A1, ELOVL2,	4.91E-10
GOTERM_BP_FAT	GO:0044255~cellular lipid metabolic process	93	ARSB, ACOX2, IMPA2, IMPAD1, CPT2, PIP5K1B, PI4K2B, C14ORF1, PTEN, PDHB, AUH, FDFT1, CDS	2.94E-08
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	59	ACOX2, TM7SF2, PIP5K1B, PI4K2B, C14ORF1, PTEN, FDFT1, AKT1, CDS2, ST6GALNAC6, PIGK, SH3	3.55E-05
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	41	FGFR4, IMPAD1, IMPA2, ABHD6, SLC37A4, GPAA1, PIP5K1B, APOC1, KITLG, PI4K2B, OCRL, PTEN,	2.31E-04

Annotation Cluster 3 Enrichment Score: 7.3483381449056475

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044282~small molecule catabolic process	48	ACOX2, IMPA2, CPT2, ECH1, PFKFB4, AMT, ESD, PAH, ACAT2, DTD2, PTEN, AUH, AFMID, AKT1, M	1.90E-09
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	37	ACOX2, CPT2, ECH1, AMT, PAH, DTD2, ACAT2, AUH, AFMID, AKT1, MCCC2, MTHFS, ASRGL1, ALD	8.00E-09
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	33	ACOX2, CPT2, ECH1, AMT, PAH, DTD2, ACAT2, AUH, AKT1, MCCC2, ASRGL1, ALDH4A1, BDH2, PE	7.99E-08
GOTERM_BP_FAT	GO:0044712~single-organism catabolic process	78	ACOX2, IMPA2, CPT2, WFS1, AMT, OGDHL, ESD, PTEN, APOBEC3F, AUH, AFMID, AKT1, MCCC2, A	2.27E-07
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	40	ACOX2, CPT2, ECH1, APOC1, ACAT2, PDHB, AUH, AKT1, INSIG2, ELOVL2, RGN, BDH2, ELOVL7, PE	2.59E-04
GOTERM_BP_FAT	GO:0072329~monocarboxylic acid catabolic process	19	ACOX2, GCDH, ECI2, ACAA2, CPT2, ECH1, ACADM, DECR1, ACAT2, IDNK, CPT1A, AUH, AKT1, BDH	7.09E-04
GOTERM_BP_FAT	GO:0009062~fatty acid catabolic process	17	ACOX2, GCDH, ECI2, ACAA2, CPT2, ECH1, ACADM, DECR1, ACAT2, CPT1A, AUH, AKT1, BDH2, PEX	0.00134677
GOTERM_BP_FAT	GO:0006635~fatty acid beta-oxidation	15	ACOX2, GCDH, ECI2, ACAA2, CPT2, ECH1, ACADM, DECR1, ACAT2, CPT1A, AUH, AKT1, FABP1, BD	0.00193362
GOTERM_BP_FAT	GO:0019395~fatty acid oxidation	17	ACOX2, GCDH, ECI2, ACAA2, CPT2, ECH1, ACADM, DECR1, ACAT2, CPT1A, AUH, AKT1, DGAT2, BD	0.00456865
GOTERM_BP_FAT	GO:0030258~lipid modification	30	ACOX2, FGFR4, IMPAD1, IMPA2, CPT2, ECH1, PIP5K1B, APOC1, KITLG, PI4K2B, OCRL, ACAT2, PTE	0.00493937
GOTERM_BP_FAT	GO:0034440~lipid oxidation	17	ACOX2, GCDH, ECI2, ACAA2, CPT2, ECH1, ACADM, DECR1, ACAT2, CPT1A, AUH, AKT1, DGAT2, BD	0.00606494
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	23	ACOX2, GCDH, ACAA2, ECI2, CPT2, ECH1, ACADM, ABHD6, PNPLA2, DECR1, PNPLA4, ACAT2, CPT	0.01982597
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	30	ACOX2, CPT2, ECH1, ABHD6, APOC1, ACAT2, AUH, AKT1, APOA2, BDH2, SCARB1, PEX13, IAH1, G	0.04595291

Annotation Cluster 4 Enrichment Score: 5.6592314572118

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	33	ACOX2, CPT2, ECH1, AMT, PAH, DTD2, ACAT2, AUH, AKT1, MCCC2, ASRGL1, ALDH4A1, BDH2, PE	7.99E-08
GOTERM_BP_FAT	GO:0009063~cellular amino acid catabolic process	14	GCDH, SHMT1, ALDH6A1, AMT, QDPR, PAH, DTD2, AUH, MCCC2, ALDH4A1, PRODH2, ASRGL1, G	0.0778389
GOTERM_BP_FAT	GO:1901565~organonitrogen compound catabolic process	33	ARSB, AMT, ANPEP, PAH, DTD2, APOBEC3F, CPN1, AUH, AFMID, MCCC2, MTHFS, GPC3, NUDT7,	0.15317034
GOTERM_BP_FAT	GO:0006520~cellular amino acid metabolic process	25	AMT, FARS2, PAH, IARS2, DTD2, AUH, MTHFD1, MCCC2, PLOD1, SRR, ALDH4A1, ASRGL1, GPT2, G	0.34276248

Annotation Cluster 5 Enrichment Score: 5.399435806059737

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044283~small molecule biosynthetic process	52	ACOX2, TM7SF2, IMPAD1, IMPA2, LEPR, C14ORF1, FDFT1, MTHFD1, PLOD1, INSIG2, ELOVL2, RG	5.73E-06
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	40	ACOX2, CPT2, ECH1, APOC1, ACAT2, PDHB, AUH, AKT1, INSIG2, ELOVL2, RGN, BDH2, ELOVL7, PE	2.59E-04
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	29	ACOX2, APOC1, PAH, MTHFD1, INSIG2, PLOD1, ELOVL2, SRR, ALDH4A1, RGN, ELOVL7, ACSL3, GP	0.01439229
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	29	ACOX2, APOC1, PAH, MTHFD1, INSIG2, PLOD1, ELOVL2, SRR, ALDH4A1, RGN, ELOVL7, ACSL3, GP	0.04329616
GOTERM_BP_FAT	GO:0072330~monocarboxylic acid biosynthetic process	21	ACOX2, SCD, PRKAB2, MLXIPL, APOC1, FADS2, ACLY, ERLIN1, ACSM3, INSIG2, ELOVL2, SRR, RGN,	0.2605173
GOTERM_BP_FAT	GO:0006633~fatty acid biosynthetic process	17	SCD, PRKAB2, MLXIPL, APOC1, FADS2, ACLY, ERLIN1, ACSM3, INSIG2, ELOVL2, RGN, ELOVL7, LTA	0.8855994

Annotation Cluster 6 Enrichment Score: 5.204788007357046

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	41	FGFR4, IMPAD1, IMPA2, ABHD6, SLC37A4, GPAA1, PIP5K1B, APOC1, KITLG, PI4K2B, OCRL, PTEN,	2.31E-04
GOTERM_BP_FAT	GO:0006641~triglyceride metabolic process	18	SLC37A4, APOC1, PNPLA2, PNPLA4, CPT1A, PCK1, GPD1L, APOA2, INSIG2, LPCAT1, DGAT2, APOH	0.00297369
GOTERM_BP_FAT	GO:0006639~acylglycerol metabolic process	19	ABHD6, SLC37A4, APOC1, PNPLA2, PNPLA4, CPT1A, PCK1, GPD1L, APOA2, INSIG2, LPCAT1, DGAT	0.00479164
GOTERM_BP_FAT	GO:0006638~neutral lipid metabolic process	19	ABHD6, SLC37A4, APOC1, PNPLA2, PNPLA4, CPT1A, PCK1, GPD1L, APOA2, INSIG2, LPCAT1, DGAT	0.00542523

Annotation Cluster 7 Enrichment Score: 4.430487435105191

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006099~tricarboxylic acid cycle	10	SDHA, SUCLG2, SUCLG1, OGDHL, CS, IDH2, PDHA1, MDH2, PDHB, FH	0.00394838
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	28	ACADM, SUCLG2, LEPR, SUCLG1, OGDHL, SLC37A4, NDUFA7, CS, COX7C, BNIP3, GYG2, COQ9, PP	0.07301064
GOTERM_BP_FAT	GO:0009060~aerobic respiration	12	SDHA, UQCR10, SUCLG2, SUCLG1, OGDHL, CS, IDH2, PDHA1, MDH2, PDHB, SIRT3, FH	0.10471277
GOTERM_BP_FAT	GO:0045333~cellular respiration	19	SUCLG2, SUCLG1, NDUFA7, CS, OGDHL, COX7C, BNIP3, COQ9, PDHB, SIRT3, SDHA, IMMP2L, TRA	0.88679325

Annotation Cluster 8 Enrichment Score: 4.3281269412393675

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	47	FAM96A, PFKFB4, BTD, OGDHL, NFS1, RSAD1, SHPK, PDHB, PDSS2, AFMID, MTHFD1, GPD1L, MC	4.75E-07
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	40	PFKFB4, OGDHL, NFS1, SHPK, PDHB, PDSS2, AFMID, MTHFD1, GPD1L, MCCC2, MTHFS, ELOVL2, N	4.10E-06
GOTERM_BP_FAT	GO:0051188~cofactor biosynthetic process	27	FAM96A, NFS1, RSAD1, PDSS2, PDHB, AFMID, MTHFD1, MTHFS, ELOVL2, PNPO, SPR, BDH2, ELOV	1.30E-04
GOTERM_BP_FAT	GO:0009108~coenzyme biosynthetic process	23	PDK1, GCDH, NADK2, PCBD2, SCD, NFS1, QDPR, COQ9, ACLY, MPC2, PDSS2, PDHB, AFMID, COQ6	3.21E-04
GOTERM_BP_FAT	GO:0006790~sulfur compound metabolic process	39	ARSB, IMPAD1, FAM96A, ETHE1, NFS1, ESD, PDHB, HS2ST1, MTHFD1, SLC35B2, SULT1A1, CHST1	0.00109421
GOTERM_BP_FAT	GO:0006637~acyl-CoA metabolic process	16	PDK1, GCDH, SUCLG2, SUCLG1, SCD, ACLY, MPC2, PDHB, ACSM3, DGAT2, NUDT7, ELOVL2, ELOVL	0.02424604
GOTERM_BP_FAT	GO:0035383~thioester metabolic process	16	PDK1, GCDH, SUCLG2, SUCLG1, SCD, ACLY, MPC2, PDHB, ACSM3, DGAT2, NUDT7, ELOVL2, ELOVL	0.02424604
GOTERM_BP_FAT	GO:0044272~sulfur compound biosynthetic process	24	PDK1, GCDH, GSTA4, SCD, ESD, ACLY, MPC2, PDHB, HS2ST1, HAGH, SLC35B2, CHPF, CHST12, ELO	0.03958477
GOTERM_BP_FAT	GO:0071616~acyl-CoA biosynthetic process	11	PDK1, GCDH, SCD, ELOVL2, MPC2, ACLY, ELOVL7, PDHA1, ACSL4, ACSL3, PDHB	0.76387222
GOTERM_BP_FAT	GO:0035384~thioester biosynthetic process	11	PDK1, GCDH, SCD, ELOVL2, MPC2, ACLY, ELOVL7, PDHA1, ACSL4, ACSL3, PDHB	0.76387222
GOTERM_BP_FAT	GO:0035337~fatty-acyl-CoA metabolic process	8	GCDH, DGAT2, SCD, ELOVL2, ACLY, ELOVL7, ACSL4, ACSL3	8.30514002

Annotation Cluster 9 Enrichment Score: 4.144085457206467

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006066~alcohol metabolic process	34	TM7SF2, RBP4, IMPAD1, IMPA2, LEPR, APOC1, C14ORF1, OCRL, PTEN, FDFT1, TTR, APOA2, INSIG	2.78E-04
GOTERM_BP_FAT	GO:1901615~organic hydroxy compound metabolic process	42	TM7SF2, RBP4, IMPAD1, IMPA2, LEPR, APOC1, PAH, C14ORF1, OCRL, PTEN, FDFT1, TTR, APOA2,	6.89E-04
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	20	CEBPA, TM7SF2, SOAT2, ACAA2, LEPR, APOC1, ACLY, ERLIN1, C14ORF1, FDFT1, APOA2, NPC2, IN	0.0043497
GOTERM_BP_FAT	GO:1902652~secondary alcohol metabolic process	19	CEBPA, TM7SF2, SOAT2, ACAA2, LEPR, APOC1, ACLY, ERLIN1, C14ORF1, FDFT1, APOA2, NPC2, IN	0.00692419
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	18	CEBPA, TM7SF2, SOAT2, ACAA2, LEPR, APOC1, ACLY, ERLIN1, FDFT1, APOA2, NPC2, INSIG2, DHC	0.01401467
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	28	TM7SF2, ACOX2, FGFR4, LEPR, SLC37A4, APOC1, C14ORF1, FDFT1, APOA2, INSIG2, SULT1A1, DH	0.10030356
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	14	TM7SF2, ACAA2, IMPAD1, IMPA2, INSIG2, DHCR7, ERLIN1, ACLY, C14ORF1, SCP2, PTAFR, FDFT1,	0.820738
GOTERM_BP_FAT	GO:1902653~secondary alcohol biosynthetic process	9	TM7SF2, ACAA2, INSIG2, DHCR7, ACLY, ERLIN1, C14ORF1, FDFT1, DHCR24	1.91685739
GOTERM_BP_FAT	GO:1901617~organic hydroxy compound biosynthetic process	17	TM7SF2, TRPC1, ACAA2, IMPAD1, IMPA2, PAH, ACLY, ERLIN1, C14ORF1, FDFT1, PCK1, INSIG2, DH	3.30283703
GOTERM_BP_FAT	GO:0016126~sterol biosynthetic process	9	TM7SF2, ACAA2, INSIG2, DHCR7, ACLY, ERLIN1, C14ORF1, FDFT1, DHCR24	3.63914392
GOTERM_BP_FAT	GO:0006695~cholesterol biosynthetic process	8	TM7SF2, ACAA2, INSIG2, DHCR7, ACLY, ERLIN1, FDFT1, DHCR24	7.41733143

Annotation Cluster 10 Enrichment Score: 2.6624297472652643

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	41	FGFR4, IMPAD1, IMPA2, ABHD6, SLC37A4, GPAA1, PIP5K1B, APOC1, KITLG, PI4K2B, OCRL, PTEN,	2.31E-04
GOTERM_BP_FAT	GO:0045017~glycerolipid biosynthetic process	20	PGAP2, FGFR4, GPAA1, PIP5K1B, PI4K2B, OCRL, PTEN, SACM1L, PCK1, CDS2, GPD1L, PIGK, SH3YL	2.1235263
GOTERM_BP_FAT	GO:0046488~phosphatidylinositol metabolic process	19	PGAP2, IMPAD1, IMPA2, FGFR4, PLA2G16, GPAA1, PIP5K1B, KITLG, PI4K2B, OCRL, PTEN, SACM1L	4.11020051
GOTERM_BP_FAT	GO:0006650~glycerophospholipid metabolic process	23	PGAP2, IMPAD1, IMPA2, FGFR4, PLA2G16, LPGAT1, GPAA1, PIP5K1B, KITLG, PI4K2B, OCRL, PTEN,	7.37369204

Annotation Cluster 11 Enrichment Score: 2.4878625562648433

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0019217~regulation of fatty acid metabolic process	14	PDK1, PRKAB2, APOC1, MLXIPL, ERLIN1, PDHB, CPT1A, AKT1, INSIG2, DGAT2, RGN, FABP1, PDHA	0.11462912
GOTERM_BP_FAT	GO:0042180~cellular ketone metabolic process	24	PDK1, FGFR4, PRKAB2, MLXIPL, APOC1, ERLIN1, COQ9, CYP2W1, PDSS2, PDHB, CPT1A, COQ6, AF	0.2379247
GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	26	FGFR4, ABHD6, APOC1, RORC, PDHB, AKT1, APOA2, SORBS1, INSIG2, DHCR7, RGN, SCARB1, PDH	1.10525827
GOTERM_BP_FAT	GO:0046890~regulation of lipid biosynthetic process	15	FGFR4, ABHD6, PRKAB2, MLXIPL, APOC1, ERLIN1, AKT1, INSIG2, DGAT2, SORBS1, DHCR7, RGN, S	2.13166563
GOTERM_BP_FAT	GO:0042304~regulation of fatty acid biosynthetic process	7	INSIG2, PRKAB2, MLXIPL, APOC1, RGN, ERLIN1, CEACAM1	5.34987705

Annotation Cluster 12 Enrichment Score: 2.4014187607360484

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0005975~carbohydrate metabolic process	63	IMPA2, IMPAD1, LEPR, OGDHL, RORC, DPY19L4, PTEN, PDHB, HS2ST1, AKT1, ST6GALNAC6, SLC2	0.00274694
GOTERM_BP_FAT	GO:0044262~cellular carbohydrate metabolic process	29	IMPAD1, IMPA2, PFKFB4, LEPR, SLC37A4, RORC, PTEN, HS2ST1, AKT1, SORBS1, C1QTNF3, SLC2A1	0.02705125
GOTERM_BP_FAT	GO:0044723~single-organism carbohydrate metabolic process	51	IMPAD1, IMPA2, LEPR, OGDHL, DPY19L4, PTEN, PDHB, HS2ST1, AKT1, ST6GALNAC6, CHST12, SLC	0.09382439
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	22	RBP4, IMPAD1, IMPA2, ACADM, LEPR, WDR5, GYG2, HS2ST1, PCK1, AKT1, ST6GALNAC6, SORBS1,	0.18819463
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	19	PDK1, RBP4, ACADM, PFKFB4, LEPR, WDR5, SLC37A4, PDHB, CPT1A, PCK1, AKT1, SORBS1, C1QTN	2.61869546
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	21	PDK1, RBP4, ACADM, PFKFB4, LEPR, WDR5, SLC37A4, PDHB, CPT1A, PCK1, AKT1, SORBS1, C1QTN	7.05403933
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	20	PDK1, RBP4, ACADM, PFKFB4, LEPR, WDR5, SLC37A4, PDHB, CPT1A, PCK1, AKT1, SORBS1, C1QTN	8.74008727

Annotation Cluster 13 Enrichment Score: 2.342902266256128

Category	Term	Count	Genes	FDR

GOTERM_BP_FAT	GO:0000079~regulation of cyclin-dependent protein serine/threonine kinase activity	13	CEBPA, TFAP4, ATRAID, FAM58A, CCNG1, CDKN3, CDC25C, PTEN, AKT1, HHEX, CDKN1B, NR2F2,	0.90306223
GOTERM_BP_FAT	GO:1904029~regulation of cyclin-dependent protein kinase activity	13	CEBPA, TFAP4, ATRAID, FAM58A, CCNG1, CDKN3, CDC25C, PTEN, AKT1, HHEX, CDKN1B, NR2F2,	0.99867126
GOTERM_BP_FAT	GO:1904030~negative regulation of cyclin-dependent protein kinase activity	7	CEBPA, HHEX, CDKN1B, TFAP4, ATRAID, NR2F2, PTEN	3.29687208
GOTERM_BP_FAT	GO:0045736~negative regulation of cyclin-dependent protein serine/threonine kinase activity	7	CEBPA, HHEX, CDKN1B, TFAP4, ATRAID, NR2F2, PTEN	3.29687208
Annotation Cluster 14	Enrichment Score: 2.273266910060614			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:1901264~carbohydrate derivative transport	11	SLC29A1, RFT1, NPC2, SLC35B2, SLC50A1, SLC37A4, SLC35D2, SCARB1, SLC25A42, SLC28A1, SLC3	0.11143222
Annotation Cluster 15	Enrichment Score: 2.1184178358722026			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0035384~thioester biosynthetic process	11	PDK1, GCDH, SCD, ELOVL2, MPC2, ACLY, ELOVL7, PDHA1, ACSL4, ACSL3, PDHB	0.76387222
GOTERM_BP_FAT	GO:0071616~acyl-CoA biosynthetic process	11	PDK1, GCDH, SCD, ELOVL2, MPC2, ACLY, ELOVL7, PDHA1, ACSL4, ACSL3, PDHB	0.76387222
Annotation Cluster 16	Enrichment Score: 1.9757493699007203			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0055088~lipid homeostasis	23	CEBPA, ACOX2, GCDH, SOAT2, ACADM, SLC37A4, MLXIPL, PNPLA2, PNPLA4, USF2, ACSM3, APOA	2.26E-05
GOTERM_BP_FAT	GO:0055092~sterol homeostasis	12	ACSM3, SOAT2, APOA2, NPC2, HNF4A, DGAT2, SLC37A4, PCSK9, SCARB1, LIPC, APOM, LRP5	0.250314
GOTERM_BP_FAT	GO:0042632~cholesterol homeostasis	12	ACSM3, SOAT2, APOA2, NPC2, HNF4A, DGAT2, SLC37A4, PCSK9, SCARB1, LIPC, APOM, LRP5	0.250314
GOTERM_BP_FAT	GO:0034381~plasma lipoprotein particle clearance	8	APOA2, DGAT2, APOC1, PCSK9, SCARB1, LIPC, APOM, LRPAP1	0.63189199
GOTERM_BP_FAT	GO:0097006~regulation of plasma lipoprotein particle levels	10	SOAT2, APOA2, DGAT2, APOC1, PCSK9, SCARB1, LIPC, ACSL3, APOM, LRPAP1	1.06259575
GOTERM_BP_FAT	GO:0071827~plasma lipoprotein particle organization	7	SOAT2, APOA2, APOC1, SCARB1, LIPC, ACSL3, APOM	5.34987705
GOTERM_BP_FAT	GO:0034375~high-density lipoprotein particle remodeling	5	APOA2, APOC1, SCARB1, LIPC, APOM	5.76576589
GOTERM_BP_FAT	GO:0071825~protein-lipid complex subunit organization	7	SOAT2, APOA2, APOC1, SCARB1, LIPC, ACSL3, APOM	7.14530915
Annotation Cluster 17	Enrichment Score: 1.8818118870068332			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006767~water-soluble vitamin metabolic process	11	MTHFD1, MTHFS, MCCC2, SHMT1, BTD, SLC2A3, SLC2A1, PNPO, RGN, GSTO2, PCCB	7.76102159
Annotation Cluster 19	Enrichment Score: 1.775709400671332			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006820~anion transport	34	ARL6IP1, FXYD3, SEPT2, CPT2, CLCN2, CA14, ENPP3, SLC37A4, KCNJ10, BEST4, AKT1, TTYH3, SLC1	6.01987908
Annotation Cluster 20	Enrichment Score: 1.7539432269060056			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	47	FAM96A, PFKFB4, BTD, OGDHL, NFS1, RSAD1, SHPK, PDHB, PDSS2, AFMID, MTHFD1, GPD1L, MC	4.75E-07
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	40	PFKFB4, OGDHL, NFS1, SHPK, PDHB, PDSS2, AFMID, MTHFD1, GPD1L, MCCC2, MTHFS, ELOVL2, N	4.10E-06
GOTERM_BP_FAT	GO:0051188~cofactor biosynthetic process	27	FAM96A, NFS1, RSAD1, PDSS2, PDHB, AFMID, MTHFD1, MTHFS, ELOVL2, PNPO, SPR, BDH2, ELOV	1.30E-04
GOTERM_BP_FAT	GO:0009108~coenzyme biosynthetic process	23	PDK1, GCDH, NADK2, PCBD2, SCD, NFS1, QDPR, COQ9, ACLY, MPC2, PDSS2, PDHB, AFMID, COQ6	3.21E-04
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process	17	NADK2, PFKFB4, OGDHL, MLXIPL, COQ9, SHPK, MPC2, PDHB, PDSS2, AFMID, COQ6, GPD1L, P2RX	0.54952419
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	13	HAGH, P2RX7, BSG, PFKFB4, PGM1, OGDHL, SRR, MLXIPL, ENTPD5, MPC2, PDHA1, PDHB, PCK1	1.61270871
GOTERM_BP_FAT	GO:0072524~pyridine-containing compound metabolic process	15	NADK2, PFKFB4, OGDHL, MLXIPL, SHPK, MPC2, PDHB, AFMID, GPD1L, P2RX7, PGM1, ENTPD5, PN	2.66305839
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	14	NADK2, PFKFB4, OGDHL, MLXIPL, SHPK, MPC2, PDHB, AFMID, GPD1L, P2RX7, PGM1, ENTPD5, PD	4.2656106
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	14	NADK2, PFKFB4, OGDHL, MLXIPL, SHPK, MPC2, PDHB, AFMID, GPD1L, P2RX7, PGM1, ENTPD5, PD	4.2656106
Annotation Cluster 22	Enrichment Score: 1.669991864595567			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:1901605~alpha-amino acid metabolic process	18	GCDH, SHMT1, AMT, CRTAP, PRDX4, AFMID, MTHFD1, MTHFS, GLUL, PLOD1, P4HA1, SRR, PROD	7.71913706
Annotation Cluster 23	Enrichment Score: 1.6605260930668968			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008643~carbohydrate transport	17	SLC2A10, RFT1, SLC2A14, SLC37A4, SLC35A3, AKT1, SLC1A2, GPC3, SORBS1, SLC2A3, SLC2A2, SLC	2.39872206
GOTERM_BP_FAT	GO:0015758~glucose transport	13	SLC2A10, SLC2A14, SLC37A4, AKT1, SLC1A2, GPC3, SORBS1, SLC2A3, SLC2A2, SLC2A1, PLS1, SORT	7.79213654
GOTERM_BP_FAT	GO:0008645~hexose transport	13	SLC2A10, SLC2A14, SLC37A4, AKT1, SLC1A2, GPC3, SORBS1, SLC2A3, SLC2A2, SLC2A1, PLS1, SORT	8.88586452
GOTERM_BP_FAT	GO:0015749~monosaccharide transport	13	SLC2A10, SLC2A14, SLC37A4, AKT1, SLC1A2, GPC3, SORBS1, SLC2A3, SLC2A2, SLC2A1, PLS1, SORT	8.88586452
GOTERM_BP_FAT	GO:0034219~carbohydrate transmembrane transport	6	SLC2A10, SLC2A3, SLC2A2, SLC2A14, SLC2A1, SLC50A1	9.46173746
Annotation Cluster 24	Enrichment Score: 1.6508989886224241			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:1901566~organonitrogen compound biosynthetic process	91	MRPL42, GMPR2, WFS1, ATP5B, ESD, IARS2, AFMID, HS2ST1, AKT1, MTHFD1, ST6GALNAC6, GPC	0.04760857
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	61	MRPL42, ATP6AP2, ANPEP, IARS2, MTHFD1, AKT1, ST6GALNAC6, IMMP2L, MTG1, PCBP2, PROZ,	7.33598071
Annotation Cluster 26	Enrichment Score: 1.569747080078811			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0019637~organophosphate metabolic process	75	IMPA2, IMPAD1, GMPR2, WFS1, ATP5B, OGDHL, PIP5K1B, PI4K2B, PTEN, PDHB, FDFT1, AFMID, C	0.1406918
GOTERM_BP_FAT	GO:0055086~nucleobase-containing small molecule metabolic process	51	GMPR2, WFS1, ATP5B, OGDHL, APOBEC3F, PDHB, AFMID, MTHFD1, MCCC2, TTR, KDM1A, UQCR	1.15112709
GOTERM_BP_FAT	GO:0006753~nucleoside phosphate metabolic process	44	GMPR2, PFKFB4, WFS1, ATP5B, ENPP3, OGDHL, NFS1, COX7C, SHPK, PDHB, AFMID, APLP1, MTHF	9.8984156
Annotation Cluster 27	Enrichment Score: 1.5643696971553198			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0007067~mitotic nuclear division	37	KIF23, SNX18, KIF22, SEPT2, MPLKIP, CHEK2, PTTG1, CCNG1, FAM83D, SPC25, NLRC4, RAD21, CE	0.18002662
GOTERM_BP_FAT	GO:0048285~organelle fission	43	KIF23, SNX18, KIF22, SEPT2, MPLKIP, BNIP3, CHEK2, PTTG1, CCNG1, FAM83D, SPC25, NLRC4, RAD	4.12158875
GOTERM_BP_FAT	GO:0000280~nuclear division	40	KIF23, SNX18, KIF22, SEPT2, MPLKIP, CHEK2, PTTG1, CCNG1, FAM83D, SPC25, NLRC4, RAD21, CE	6.67211517
Annotation Cluster 28	Enrichment Score: 1.5155608886578102			
Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0034381~plasma lipoprotein particle clearance	8	APOA2, DGAT2, APOC1, PCSK9, SCARB1, LIPC, APOM, LRPAP1	0.63189199

SUPPLEMENTARY TABLE 6

Significant biological processes (BPs) related to the GOEA for the genes, which were up-regulated or down-regulated by Cu only in ATP7B-ko HepG2 cells.

GOEA was performed on genes, which were up- or down-regulated by Cu exclusively in ATP7B-ko HepG2 cells (see Table 4). The data in this table were collected by using DAVID online tool restricting the output to BP_FAT terms: the BPs up-regulated and down-regulated are highlighted in red and in green, respectively.

UP-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 21.2689780877919

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006396~RNA processing	240	RPL18, RPL19, RPL14, RPL15, SYNCRIP, NSRP1, RPLP0, INTS6, RPL26L1, U2AF1, RPP30, F	4.97E-36
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	185	RPL18, RPL36A, RPL19, RNMT, RPL14, RPL15, SNRPD1, SNRPD2, SYNCRIP, NSRP1, CACTI	1.98E-29
GOTERM_BP_FAT	GO:0045047~protein targeting to ER	59	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, RPS2, SRP19, RPS3, RPS3A, RPLP	2.27E-25
GOTERM_BP_FAT	GO:0072599~establishment of protein localization to endoplasmic reticulum	60	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, RPS2, SRP19, RPS3, RPS3A, RPLP	3.46E-25
GOTERM_BP_FAT	GO:0006614~SRP-dependent cotranslational protein targeting to membrane	56	RPL18, SRP14, RPL36A, RPL19, RPL14, RPL15, RPS2, SRP19, RPS3, RPS3A, RPLP0, RPL26L	9.16E-25
GOTERM_BP_FAT	GO:0022613~ribonucleoprotein complex biogenesis	141	RPL18, RPL36A, FASTKD2, RPL19, RPL14, MALSU1, RPL15, SNRPD1, SNRPD2, DDX27, EBN	9.90E-25
GOTERM_BP_FAT	GO:0006613~cotranslational protein targeting to membrane	58	RPL18, SRP14, RPL36A, RPL19, RPL14, RPL15, RPS2, SRP19, RPS3, RPS3A, RPLP0, RPL26L	1.16E-24
GOTERM_BP_FAT	GO:0070972~protein localization to endoplasmic reticulum	65	RPL18, SRP14, RPL36A, RPL19, RPL14, VAPA, CHMP4B, RPL15, RPS2, SRP19, RPS3, GBF1,	1.43E-24
GOTERM_BP_FAT	GO:0019080~viral gene expression	81	RPL18, CCNT2, RPL36A, RPL19, RPL14, RPL15, NUP188, RPS2, RPS3, TRIM8, RPS3A, RPLP	2.24E-24
GOTERM_BP_FAT	GO:0044033~multi-organism metabolic process	86	RPL18, CCNT2, RPL36A, RPL19, RPL14, RPL15, NUP188, RPS2, RPS3, CDC42, TRIM8, RPS3	2.91E-24
GOTERM_BP_FAT	GO:0019083~viral transcription	78	RPL18, CCNT2, RPL36A, RPL19, RPL14, RPL15, NUP188, RPS2, RPS3, TRIM8, RPS3A, RPLP	4.28E-24
GOTERM_BP_FAT	GO:0042254~ribosome biogenesis	108	RPL18, RPL36A, FASTKD2, RPL19, RPL14, MALSU1, RPL15, DDX27, EBNA1BP2, RPLP0, RP	7.90E-22
GOTERM_BP_FAT	GO:0034470~ncRNA processing	122	RPL18, RPL36A, RPL19, RPL14, RPL15, DDX27, EBNA1BP2, CLP1, RPLP0, INTS6, RPL26L1,	1.89E-21
GOTERM_BP_FAT	GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	60	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, RPS3, RPS3A, RPLP0, RPL26L1, FAU, RPL11,	2.69E-21
GOTERM_BP_FAT	GO:0006364~rRNA processing	92	RPL18, RPL36A, RPL19, RPL14, UTP18, GAR1, RPL15, RPS2, RPS3, DDX27, EBNA1BP2, DC	3.25E-20
GOTERM_BP_FAT	GO:0016032~viral process	212	RPL18, CHMP3, RPL19, VAPA, RPL14, CHMP5, RPL15, SYNCRIP, RAB1B, SLC52A2, RAB1A,	7.23E-20
GOTERM_BP_FAT	GO:0044419~interspecies interaction between organisms	216	RPL18, CHMP3, RPL19, VAPA, RPL14, CHMP5, RPL15, SYNCRIP, RAB1B, SLC52A2, RAB1A,	1.66E-19
GOTERM_BP_FAT	GO:0044403~symbiosis, encompassing mutualism through parasitism	216	RPL18, CHMP3, RPL19, VAPA, RPL14, CHMP5, RPL15, SYNCRIP, RAB1B, SLC52A2, RAB1A,	1.66E-19
GOTERM_BP_FAT	GO:0044764~multi-organism cellular process	212	RPL18, CHMP3, RPL19, VAPA, RPL14, CHMP5, RPL15, SYNCRIP, RAB1B, SLC52A2, RAB1A,	1.85E-19
GOTERM_BP_FAT	GO:0016072~rRNA metabolic process	92	RPL18, RPL36A, RPL19, RPL14, UTP18, GAR1, RPL15, RPS2, RPS3, DDX27, EBNA1BP2, DC	2.49E-19
GOTERM_BP_FAT	GO:0034660~ncRNA metabolic process	146	RPL18, RPL36A, RPL19, RPL14, RPL15, DDX27, EBNA1BP2, GTF2E2, CLP1, RPLP0, INTS6, F	3.20E-19
GOTERM_BP_FAT	GO:0006413~translational initiation	73	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, RPS3, RPS3A, EIF1AX, RPLP0, RPL26L1, FAU,	5.50E-19
GOTERM_BP_FAT	GO:0072594~establishment of protein localization to organelle	159	RPL18, SRP14, GRPEL2, RPL36A, CHERP, RPL19, RPL14, CHMP4B, IL18, RPL15, SAE1, CCT	7.31E-18
GOTERM_BP_FAT	GO:0006612~protein targeting to membrane	71	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, PIP5K1A, SRP19, RPS2, RPS3, MF	1.90E-17
GOTERM_BP_FAT	GO:0019058~viral life cycle	121	RPL18, RPL36A, RPL19, CHMP3, VAPA, RPL14, CHMP4B, CHMP5, RPL15, RAB1B, SLC52A	7.04E-17
GOTERM_BP_FAT	GO:0000956~nuclear-transcribed mRNA catabolic process	73	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L1, FAU,	1.70E-16
GOTERM_BP_FAT	GO:0006402~mRNA catabolic process	76	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L1, FAU,	2.08E-16
GOTERM_BP_FAT	GO:0090150~establishment of protein localization to membrane	104	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, SRP19, MFF, RPLP0, RPL26L1, FA	3.51E-16
GOTERM_BP_FAT	GO:0006401~RNA catabolic process	79	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L1, FAU,	7.98E-15
GOTERM_BP_FAT	GO:0006605~protein targeting	156	RPL18, SRP14, GRPEL2, RPL36A, CHERP, RPL19, RPL14, CHMP4B, IL18, RPL15, SAE1, SRP	1.94E-14
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	203	RPL18, RPL19, HM13, RPL14, RPL15, ERLEC1, CTNNB1, CRY2, HOMER3, RPLP0, RPL26L1,	6.85E-14
GOTERM_BP_FAT	GO:1902582~single-organism intracellular transport	152	RPL18, SRP14, GRPEL2, RPL36A, CHERP, RPL19, RPL14, CHMP4B, IL18, RPL15, STOML2, S	4.44E-13
GOTERM_BP_FAT	GO:0044802~single-organism membrane organization	177	RPL18, SRP14, RPL36A, CHMP3, RPL19, RPL14, CHMP4B, RPL15, STOML2, SRP19, ANKLE	1.33E-12
GOTERM_BP_FAT	GO:0072657~protein localization to membrane	117	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, SRP19, MFF, FNTA, RPLP0, RPL2	2.44E-12
GOTERM_BP_FAT	GO:1902580~single-organism cellular localization	205	RPL18, RPL19, RPL14, RPL15, STOML2, ITSN1, RAB1A, CTNNB1, CRY2, GAB2, RPLP0, INSI	1.31E-10
GOTERM_BP_FAT	GO:0034655~nucleobase-containing compound catabolic process	94	RPL18, RPL36A, RPL19, RPL14, HINT1, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L	2.52E-10
GOTERM_BP_FAT	GO:0046700~heterocycle catabolic process	98	RPL18, RPL36A, RPL19, RPL14, HINT1, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L	7.97E-10
GOTERM_BP_FAT	GO:0019439~aromatic compound catabolic process	99	RPL18, RPL36A, RPL19, RPL14, RPL15, CNOT4, RPLP0, RPL26L1, FAU, RPL11, LSM1, RPS2	1.95E-09
GOTERM_BP_FAT	GO:0044270~cellular nitrogen compound catabolic process	97	RPL18, RPL36A, RPL19, RPL14, HINT1, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L	5.75E-09
GOTERM_BP_FAT	GO:1901361~organic cyclic compound catabolic process	99	RPL18, RPL36A, RPL19, RPL14, RPL15, CNOT4, RPLP0, RPL26L1, FAU, RPL11, LSM1, RPS2	4.50E-08

Annotation Cluster 2 Enrichment Score: 18.66907071153011

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0046907~intracellular transport	323	RPL18, HM13, RPL19, CHMP3, VAPA, RPL14, CHMP5, RPL15, PTPN23, STOML2, RAB1B,	1.17E-25
GOTERM_BP_FAT	GO:0051641~cellular localization	437	RPL18, RPL19, RPL14, RPL15, VPS53, STOML2, ITSN1, NSRP1, CTNNB1, RPLP0, FAU, RPL1	3.66E-20
GOTERM_BP_FAT	GO:0051649~establishment of localization in cell	357	RPL18, HM13, RPL19, CHMP3, VAPA, RPL14, CHMP5, RPL15, PTPN23, STOML2, VPS53, R	3.65E-18
GOTERM_BP_FAT	GO:0072594~establishment of protein localization to organelle	159	RPL18, SRP14, GRPEL2, RPL36A, CHERP, RPL19, RPL14, CHMP4B, IL18, RPL15, SAE1, CCT	7.31E-18
GOTERM_BP_FAT	GO:0033365~protein localization to organelle	196	RPL18, RPL19, RPL14, VAPA, RPL15, AURKA, CCT2, CTNNB1, CRY2, GBF1, RPLP0, RPL26L	1.29E-17
GOTERM_BP_FAT	GO:0006612~protein targeting to membrane	71	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, PIP5K1A, SRP19, RPS2, RPS3, MF	1.90E-17
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	300	RPL18, HM13, RPL19, VAPA, RPL14, RPL15, CCT2, AURKA, ERLEC1, CTNNB1, CRY2, GBF1,	2.08E-17
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	356	RPL18, HM13, RPL19, CHMP3, RPL14, CHMP5, RPL15, PTPN23, RAB1B, VPS53, CCT2, VPS	2.94E-17
GOTERM_BP_FAT	GO:0034613~cellular protein localization	297	RPL18, HM13, RPL19, VAPA, RPL14, RPL15, CCT2, AURKA, ERLEC1, CTNNB1, CRY2, GBF1,	4.56E-17
GOTERM_BP_FAT	GO:0008104~protein localization	410	RPL18, RPL19, RPL14, RPL15, VPS53, CTNNB1, RPLP0, FAU, RPL11, JAGN1, CDCA5, MCRS	2.06E-16
GOTERM_BP_FAT	GO:0090150~establishment of protein localization to membrane	104	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, SRP19, MFF, RPLP0, RPL26L1, FA	3.51E-16
GOTERM_BP_FAT	GO:0033036~macromolecule localization	453	RPL18, RPL19, RPL14, RPL15, VPS53, STOML2, CTNNB1, RPLP0, FAU, RPL11, JAGN1, CDC	3.46E-15
GOTERM_BP_FAT	GO:0006605~protein targeting	156	RPL18, SRP14, GRPEL2, RPL36A, CHERP, RPL19, RPL14, CHMP4B, IL18, RPL15, SAE1, SRP	1.94E-14
GOTERM_BP_FAT	GO:0015031~protein transport	323	RPL18, HM13, RPL19, CHMP3, RPL14, CHMP5, RPL15, PTPN23, RAB1B, VPS53, VPS33A, F	2.41E-14
GOTERM_BP_FAT	GO:0061024~membrane organization	205	RPL18, CHMP3, RPL19, VAPA, RPL14, CHMP5, RPL15, RAB1B, STOML2, ANKLE2, RAB1A,	3.36E-14
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	203	RPL18, RPL19, HM13, RPL14, RPL15, ERLEC1, CTNNB1, CRY2, HOMER3, RPLP0, RPL26L1,	6.85E-14
GOTERM_BP_FAT	GO:1902582~single-organism intracellular transport	152	RPL18, SRP14, GRPEL2, RPL36A, CHERP, RPL19, RPL14, CHMP4B, IL18, RPL15, STOML2, S	4.44E-13
GOTERM_BP_FAT	GO:0044802~single-organism membrane organization	177	RPL18, SRP14, RPL36A, CHMP3, RPL19, RPL14, CHMP4B, RPL15, STOML2, SRP19, ANKLE	1.33E-12
GOTERM_BP_FAT	GO:0072657~protein localization to membrane	117	RPL18, SRP14, RPL36A, RPL19, RPL14, CHMP4B, RPL15, SRP19, MFF, FNTA, RPLP0, RPL2	2.44E-12
GOTERM_BP_FAT	GO:1902580~single-organism cellular localization	205	RPL18, RPL19, RPL14, RPL15, STOML2, ITSN1, RAB1A, CTNNB1, CRY2, GAB2, RPLP0, INSI	1.31E-10

Annotation Cluster 3 Enrichment Score: 17.44466002761763

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	185	RPL18, RPL36A, RPL19, RNMT, RPL14, RPL15, SNRPD1, SNRPD2, SYNCRIP, NSRP1, CACTI	1.98E-29
GOTERM_BP_FAT	GO:0008380~RNA splicing	105	SNRPD1, SNRPD2, SYNCRIP, NSRP1, CACTIN, SMNDC1, C7ORF55-LUC7L2, CLP1, DNAJC8,	6.79E-14
GOTERM_BP_FAT	GO:0006397~mRNA processing	117	RNMT, SNRPD1, SNRPD2, SYNCRIP, NSRP1, CACTIN, SMNDC1, C7ORF55-LUC7L2, CLP1, D	8.17E-14
GOTERM_BP_FAT	GO:0000375~RNA splicing, via transesterification reactions	83	SRSF1, ZMAT5, SNRPD1, SNRPD2, SYNCRIP, NSRP1, DGCR14, WBP4, BUD31, CACTIN, SM	2.00E-11
GOTERM_BP_FAT	GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	80	SRSF1, ZMAT5, SNRPD1, SNRPD2, SYNCRIP, NSRP1, DGCR14, WBP4, BUD31, CACTIN, C7	2.50E-10
GOTERM_BP_FAT	GO:0000398~mRNA splicing, via spliceosome	80	SRSF1, ZMAT5, SNRPD1, SNRPD2, SYNCRIP, NSRP1, DGCR14, WBP4, BUD31, CACTIN, C7	2.50E-10

Annotation Cluster 4 Enrichment Score: 17.406992201719106

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006412~translation	159	RPL18, MRPS36, RPL36A, RPL19, RPL14, MALSU1, RBM3, HBS1L, RPL15, EIF5A, SYNCRIP,	1.21E-19
GOTERM_BP_FAT	GO:0006413~translational initiation	73	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, RPS3, RPS3A, EIF1AX, RPLP0, RPL26L1, FAU,	5.50E-19
GOTERM_BP_FAT	GO:0043043~peptide biosynthetic process	159	RPL18, MRPS36, RPL36A, RPL19, RPL14, MALSU1, RBM3, HBS1L, RPL15, EIF5A, SYNCRIP,	8.56E-18
GOTERM_BP_FAT	GO:0006402~mRNA catabolic process	76	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L1, FAU,	2.08E-16
GOTERM_BP_FAT	GO:0043604~amide biosynthetic process	163	RPL18, MRPS36, RPL36A, RPL19, RPL14, MALSU1, RBM3, HBS1L, RPL15, EIF5A, SYNCRIP,	5.39E-15
GOTERM_BP_FAT	GO:0006401~RNA catabolic process	79	RPL18, RPL36A, RPL19, RPL14, RPL15, RPS2, CNOT4, RPS3, RPS3A, RPLP0, RPL26L1, FAU,	7.98E-15
GOTERM_BP_FAT	GO:0006518~peptide metabolic process	172	RPL18, MRPS36, RPL36A, HM13, RPL19, RPL14, MALSU1, RBM3, HBS1L, RPL15, EIF5A, SY	2.22E-13
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	192	RPL18, MRPS36, RPL36A, HM13, RPL19, RPL14, MALSU1, RBM3, HBS1L, RPL15, EIF5A, SY	2.35E-11
GOTERM_BP_FAT	GO:1901566~organonitrogen compound biosynthetic process	223	RPL18, RPL19, VAPA, ADCY7, RPL14, MALSU1, RPL15, SYNCRIP, STOML2, GOT1, EIF1AX,	7.96E-06

Annotation Cluster 5 Enrichment Score: 14.141146196892766

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0022613~ribonucleoprotein complex biogenesis	141	RPL18, RPL36A, FASTKD2, RPL19, RPL14, MALSU1, RPL15, SNRPD1, SNRPD2, DDX27, EBN	9.90E-25
GOTERM_BP_FAT	GO:0071826~ribonucleoprotein complex subunit organization	55	SRSF1, FASTKD2, HBS1L, SNRPD1, SNRPD2, C7ORF55-LUC7L2, CLP1, PRMT5, RPL11, FAM	5.15E-05
GOTERM_BP_FAT	GO:0022618~ribonucleoprotein complex assembly	53	SRSF1, FASTKD2, SNRPD1, SNRPD2, C7ORF55-LUC7L2, CLP1, PRMT5, RPL11, FAM103A1,	5.90E-05

Annotation Cluster 6 Enrichment Score: 11.424990837200601

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044085~cellular component biogenesis	486	RPL18, HCCS, RPL19, RPL14, MALSU1, RPL15, STOML2, MED24, CTNNB1, ACTG1, RPLP0,	4.29E-20
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	407	HCCS, MED24, STOML2, CTNNB1, MAP3K7, YEATS2, VMA21, RPL11, CAB39, OGT, DHX3	2.85E-15
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	289	HCCS, HM13, FASTKD2, CHMP3, STOML2, MED24, RAB1B, CCT2, RAB1A, CTNNB1, PICAL	1.40E-10

GOTERM_BP_FAT	GO:0022607~cellular component assembly	397	HCCS, MED24, STOML2, CTNNB1, ACTG1, VMA21, RPL11, CAB39, DHX30, PLS3, TBPL1, P	1.92E-08
GOTERM_BP_FAT	GO:0071822~protein complex subunit organization	269	HCCS, HM13, CHMP3, CHMP5, STOML2, MED24, RAB1B, CCT2, RAB1A, CTNNB1, PICAL	3.64E-07
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	175	HCCS, CHMP3, FASTKD2, CAPZA1, SNRPD1, NDUFAB1, SNRPD2, CCT2, SRP19, RAB1A, D	2.55E-06
GOTERM_BP_FAT	GO:0006461~protein complex assembly	229	HCCS, HM13, CHMP3, MED24, RAB1B, STOML2, CCT2, RAB1A, CTNNB1, PICALM, INSIG1	3.60E-05
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	229	HCCS, HM13, CHMP3, MED24, RAB1B, STOML2, CCT2, RAB1A, CTNNB1, PICALM, INSIG1	3.83E-05
GOTERM_BP_FAT	GO:0043623~cellular protein complex assembly	95	HCCS, NDUFAF5, CHMP3, KIAA0368, COA4, COA1, CAPZA1, NDUFAB1, PINK1, CCT2, CO	0.17975736

Annotation Cluster 7 Enrichment Score: 10.979576020352907

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:1903047~mitotic cell cycle process	185	CHMP3, CHMP4B, CHMP5, PPP2R5C, AURKC, TTK, AURKA, ANKLE2, CNOT4, CUL5, PPP1	2.29E-14
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	196	CHMP3, CHMP5, PPP2R5C, AURKC, AURKA, ANKLE2, CTNNB1, CUL5, PPP1R1C, NUP35,	4.01E-14
GOTERM_BP_FAT	GO:0007049~cell cycle	293	CHMP3, CHMP5, PPP2R5C, CNPPD1, AURKC, AURKA, ANKLE2, CTNNB1, CUL5, PPP1R1C,	6.66E-13
GOTERM_BP_FAT	GO:0022402~cell cycle process	241	CHMP3, CHMP5, PPP2R5C, AURKC, AURKA, ANKLE2, CTNNB1, CUL5, PPP1R1C, CAB39, N	1.23E-10
GOTERM_BP_FAT	GO:0044772~mitotic cell cycle phase transition	114	CHMP4B, PPP2R5C, TTK, AURKA, CNOT4, CUL5, CDKN2B, PPP1R1C, CDKN2D, ORC5, ORC	1.43E-09
GOTERM_BP_FAT	GO:0044770~cell cycle phase transition	117	CHMP4B, PPP2R5C, TTK, AURKA, CNOT4, CUL5, CDKN2B, PPP1R1C, CDKN2D, ORC5, ORC	8.71E-09
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	174	MOK, CHMP3, CHMP4B, CHMP5, PPP2R5C, CNPPD1, AURKC, TTK, AURKA, SAE1, FLCN, C	4.89E-07
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	99	CHMP3, CHMP5, CHMP4B, PPP2R5C, TTK, AURKA, SAE1, CNOT4, CTNNB1, CDKN2B, GB	1.22E-05
GOTERM_BP_FAT	GO:1901990~regulation of mitotic cell cycle phase transition	65	NBN, PPP2R5C, TTK, AURKA, CNOT4, TRIAP1, PRMT1, PPP1R1C, PLRG1, CDKN2B, PCBP4,	0.0019743
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	105	CHMP3, CHMP5, CHMP4B, PPP2R5C, AURKC, TTK, AURKA, FLCN, CNOT4, CTNNB1, CDK	0.00411031
GOTERM_BP_FAT	GO:1901987~regulation of cell cycle phase transition	67	NBN, PPP2R5C, TTK, AURKA, CNOT4, MEN1, TRIAP1, PRMT1, PPP1R1C, PLRG1, CDKN2B,	0.00650589

Annotation Cluster 8 Enrichment Score: 8.786937182351299

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0043603~cellular amide metabolic process	192	RPL18, MRPS36, RPL36A, HM13, RPL19, RPL14, MALSU1, RBM3, HBS1L, RPL15, EIF5A, S	2.35E-11
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	101	RBM3, MALSU1, TIRAP, SYNCRIP, EIF5A, CLP1, EIF1, EIF2B2, RPS27A, DNAJC1, SAMD4B,	2.88E-07
GOTERM_BP_FAT	GO:0006417~regulation of translation	69	RBM3, MALSU1, CPEB4, YBX3, PINK1, SYNCRIP, EIF5A, RPS3, QKI, EIF1, YRDC, EIF2B2, US	0.00330498
GOTERM_BP_FAT	GO:0034248~regulation of cellular amide metabolic process	73	RBM3, MALSU1, CPEB4, YBX3, PINK1, SYNCRIP, EIF5A, RPS3, PICALM, QKI, EIF1, YRDC, E	0.00507411

Annotation Cluster 9 Enrichment Score: 6.823214249865905

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:1903047~mitotic cell cycle process	185	CHMP3, CHMP4B, CHMP5, PPP2R5C, AURKC, TTK, AURKA, ANKLE2, CNOT4, CUL5, PPP1	2.29E-14
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	196	CHMP3, CHMP5, PPP2R5C, AURKC, AURKA, ANKLE2, CTNNB1, CUL5, PPP1R1C, NUP35,	4.01E-14
GOTERM_BP_FAT	GO:0022402~cell cycle process	241	CHMP3, CHMP5, PPP2R5C, AURKC, AURKA, ANKLE2, CTNNB1, CUL5, PPP1R1C, CAB39, N	1.23E-10
GOTERM_BP_FAT	GO:0051301~cell division	110	CHMP3, CHMP4B, CHMP5, AURKC, AURKA, ANKLE2, FLCN, TOP1, PPP1R1C, RALB, CDCA	3.27E-05
GOTERM_BP_FAT	GO:0007067~mitotic nuclear division	88	CLTA, CHMP3, CHMP4B, CHMP5, AURKC, TTK, AURKA, CLTC, ANKLE2, LATS1, SPICE1, LA	5.11E-05
GOTERM_BP_FAT	GO:0048285~organelle fission	108	CHMP3, CHMP4B, CHMP5, AURKC, TTK, AURKA, ANKLE2, SLC2A8, MFF, CDCA5, ZC3HC1,	0.00622749
GOTERM_BP_FAT	GO:0000280~nuclear division	101	CHMP3, CHMP5, CHMP4B, AURKC, TTK, AURKA, ANKLE2, SLC2A8, CDCA5, ZC3HC1, RAN,	0.01500565
GOTERM_BP_FAT	GO:0007059~chromosome segregation	61	MMS19, FAM96B, CHMP3, CHMP5, CHMP4B, AURKC, TTK, LATS1, SPICE1, RPS3, CTNNB	0.26843026
GOTERM_BP_FAT	GO:0000819~sister chromatid segregation	44	CHMP3, CHMP5, CHMP4B, AURKC, TTK, ANAPC10, CEP55, ANAPC11, LATS1, CTNNB1, C	0.5351203
GOTERM_BP_FAT	GO:0098813~nuclear chromosome segregation	50	CHMP3, CHMP5, CHMP4B, AURKC, TTK, SPICE1, LATS1, CTNNB1, NSMCE2, KPNB1, CDCA	3.25565906
GOTERM_BP_FAT	GO:0000070~mitotic sister chromatid segregation	28	CHMP3, CHMP5, CHMP4B, AURKC, TTK, ANAPC10, ANAPC11, CEP55, CHMP2B, NAA50,	7.57779433

Annotation Cluster 10 Enrichment Score: 6.115975927437178

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0007034~vacuolar transport	65	LEPROTL1, CHMP3, CHMP4B, AP1G1, RAB5C, CHMP5, VPS37A, PTPN23, VPS53, CLTC, V	1.09E-04
GOTERM_BP_FAT	GO:0016197~endosomal transport	56	LEPROTL1, CHMP3, CHMP5, RAB5C, AP1G1, CHMP4B, VPS37A, PTPN23, VPS53, CLTC, V	0.00115061
GOTERM_BP_FAT	GO:0016482~cytosolic transport	35	VPS29, STX8, CHMP3, AP1G1, SNX16, PTPN23, VPS53, RDX, SNX3, CLTC, SRC, MTMR2, R	0.02863558

Annotation Cluster 11 Enrichment Score: 5.948563247287321

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	191	CHMP3, CHMP4B, CHMP5, MALSU1, CAPZA1, TTK, STOML2, RAB1B, CCT2, SAE1, AURKA	2.36E-05
GOTERM_BP_FAT	GO:0051128~regulation of cellular component organization	333	CHMP3, CHMP5, PDLIM5, MALSU1, FAM110C, PTPN23, STOML2, RAB1B, CCT2, AURKA,	6.98E-04
GOTERM_BP_FAT	GO:0010638~positive regulation of organelle organization	107	STOML2, AURKA, SAE1, CCT2, CTNNB1, BAK1, MFF, ZNF304, STARD7, RALB, U2AF1, OGT	0.00196007
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organization	170	LRTM2, PTPN23, EIF5A, STOML2, CCT2, AURKA, SAE1, MMP1, B2M, CTNNB1, ZNF304,	0.79022989

Annotation Cluster 12 Enrichment Score: 5.192442132155562

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	162	HMGN1, MMS19, MORF4L2, STOML2, CCT2, SPRTN, FLCN, CTNNB1, BATF, ZNF304, TOP	0.00115839
GOTERM_BP_FAT	GO:0006974~cellular response to DNA damage stimulus	136	MMS19, HMGN1, PPP2R5C, MORF4L2, AURKA, SPRTN, CNOT4, BATF, BAK1, CRY2, CDK	0.00156336
GOTERM_BP_FAT	GO:0006281~DNA repair	85	BACH1, HMGN1, MMS19, NBN, FIGNL1, COPS3, MORF4L2, COPS8, TERF2IP, SPRTN, RPS	1.1586955

Annotation Cluster 13 Enrichment Score: 5.055638124677436

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0010467~gene expression	783	PPP2R5C, SYNCRIP, MED24, RCE1, MED21, MAP3K7, ZNF778, MED28, SERPINE2, RPLP0,	7.26E-20
GOTERM_BP_FAT	GO:0016070~RNA metabolic process	666	RPL18, RPL19, RPL14, RPL15, ZNF57, FSTL3, MED24, SYNCRIP, MED21, NSRP1, CTNNB1,	7.09E-12
GOTERM_BP_FAT	GO:0034645~cellular macromolecule biosynthetic process	687	RPL18, RPL19, RPL14, MALSU1, RPL15, ZNF57, FSTL3, STOML2, MED24, SYNCRIP, SPRTN	3.95E-08
GOTERM_BP_FAT	GO:0018130~heterocycle biosynthetic process	581	RPL18, RPL19, RPL14, ZNF57, RPL15, FSTL3, STOML2, MED24, SPRTN, MED21, CTNNB1,	0.00213637
GOTERM_BP_FAT	GO:0019438~aromatic compound biosynthetic process	582	RPL18, RPL19, RPL14, ZNF57, RPL15, FSTL3, STOML2, MED24, SPRTN, MED21, CTNNB1,	0.00231585
GOTERM_BP_FAT	GO:0034654~nucleobase-containing compound biosynthetic process	572	RPL18, RPL19, RPL14, ZNF57, RPL15, FSTL3, STOML2, MED24, SPRTN, MED21, CTNNB1,	0.00385112
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	511	RPL18, RPL19, RPL14, ZNF57, RPL15, FSTL3, MED24, MED21, CTNNB1, MAP3K7, ZNF778	0.03010818
GOTERM_BP_FAT	GO:0010468~regulation of gene expression	557	MALSU1, ZNF57, FSTL3, MED24, SYNCRIP, NSRP1, MED21, CTNNB1, MAP3K7, ZNF778, C	0.11117171
GOTERM_BP_FAT	GO:0051171~regulation of nitrogen compound metabolic process	560	MALSU1, ZNF57, FSTL3, STOML2, MED24, SYNCRIP, NSRP1, MED21, CTNNB1, MAP3K7,	0.25511034
GOTERM_BP_FAT	GO:2000112~regulation of cellular macromolecule biosynthetic process	494	MALSU1, ZNF57, FSTL3, STOML2, MED24, SYNCRIP, MED21, CTNNB1, MAP3K7, ZNF778,	7.835613
GOTERM_BP_FAT	GO:0010556~regulation of macromolecule biosynthetic process	507	MALSU1, ZNF57, FSTL3, STOML2, MED24, SYNCRIP, MED21, CTNNB1, MAP3K7, ZNF778,	8.37283358

Annotation Cluster 14 Enrichment Score: 4.628109356455101

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006353~DNA-templated transcription, termination	34	SRSF1, TAF1C, POLR2F, POLR2E, POLR2K, TAF1D, SRSF11, CLP1, PRMT5, CDC40, NUDT21	2.18E-05
GOTERM_BP_FAT	GO:0071426~ribonucleoprotein complex export from nucleus	34	SRSF1, NXT1, SDAD1, SRSF11, EIF5A, NUP188, NDC1, CDC40, U2AF1, NUP35, NMD3, PA	8.17E-04
GOTERM_BP_FAT	GO:0006403~RNA localization	49	SRSF1, EIF5A, CCT2, NUP188, U2AF1, QKI, NUP35, KHDRBS1, PABPN1, NUP133, NUP88,	0.00215913
GOTERM_BP_FAT	GO:0071166~ribonucleoprotein complex localization	34	SRSF1, NXT1, SDAD1, SRSF11, EIF5A, NUP188, NDC1, CDC40, U2AF1, NUP35, NMD3, PA	0.00339398
GOTERM_BP_FAT	GO:0051169~nuclear transport	88	SRSF1, CHERP, IL18, SNRPD1, EIF5A, SNRPD2, NUP188, NSRP1, PRDX1, CTNNB1, AKR1C3	0.00345725
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	86	SRSF1, CHERP, IL18, SNRPD1, EIF5A, SNRPD2, NUP188, NSRP1, PRDX1, CTNNB1, AKR1C3	0.00590134
GOTERM_BP_FAT	GO:0006369~termination of RNA polymerase II transcription	22	SRSF1, PABPN1, MAGOH, SRSF11, RNPS1, SRSF2, EIF4A3, PCF11, SRSF5, UPF3B, SRSF7,	0.00647942
GOTERM_BP_FAT	GO:0006406~mRNA export from nucleus	28	NXT1, SRSF1, SRSF11, EIF5A, NUP188, NDC1, CDC40, U2AF1, NUP35, PABPN1, NUP133,	0.04022959
GOTERM_BP_FAT	GO:0071427~mRNA-containing ribonucleoprotein complex export from nucleus	28	NXT1, SRSF1, SRSF11, EIF5A, NUP188, NDC1, CDC40, U2AF1, NUP35, PABPN1, NUP133,	0.04022959
GOTERM_BP_FAT	GO:0051028~mRNA transport	35	SRSF1, NXT1, SRSF11, EIF5A, NUP188, NXT2, NDC1, HNRNPA3, CDC40, U2AF1, QKI, TNK	0.04564528
GOTERM_BP_FAT	GO:0006405~RNA export from nucleus	31	NXT1, SRSF1, SRSF11, EIF5A, NUP188, NDC1, CDC40, U2AF1, NUP35, KHDRBS1, PABPN1	0.05325217
GOTERM_BP_FAT	GO:0051168~nuclear export	41	SRSF1, NXT1, SDAD1, SRSF11, EIF5A, NUP188, NDC1, CSE1L, CDC40, U2AF1, PRKACA, N	0.05840741
GOTERM_BP_FAT	GO:0050657~nucleic acid transport	39	SRSF1, NXT1, SRSF11, EIF5A, NUP188, NXT2, NDC1, HNRNPA3, CDC40, U2AF1, QKI, MRP	0.09441085
GOTERM_BP_FAT	GO:0050658~RNA transport	39	SRSF1, NXT1, SRSF11, EIF5A, NUP188, NXT2, NDC1, HNRNPA3, CDC40, U2AF1, QKI, MRP	0.09441085
GOTERM_BP_FAT	GO:0051236~establishment of RNA localization	39	SRSF1, NXT1, SRSF11, EIF5A, NUP188, NXT2, NDC1, HNRNPA3, CDC40, U2AF1, QKI, MRP	0.13868254
GOTERM_BP_FAT	GO:0015931~nucleobase-containing compound transport	41	SRSF1, NXT1, SRSF11, EIF5A, NUP188, NXT2, NDC1, HNRNPA3, SLC35B1, CDC40, U2AF1,	1.11310745
GOTERM_BP_FAT	GO:0031123~RNA 3'-end processing	26	SRSF1, SRSF11, CLP1, NUDT21, CDC40, ZNF473, U2AF1, RPS21, USB1, PABPN1, RPSA, EX	1.56712011
GOTERM_BP_FAT	GO:0031124~mRNA 3'-end processing	20	SRSF1, PABPN1, MAGOH, SRSF11, RNPS1, SRSF2, EIF4A3, PCF11, SRSF5, UPF3B, SRSF7,	5.88113585

Annotation Cluster 15 Enrichment Score: 4.583855861175966

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0022411~cellular component disassembly	97	MRPS36, CHMP5, CAPZA1, HBS1L, EIF5A, MMP1, MRPS30, CTNNB1, CISD2, FNTA, ATG5,	1.55E-04
GOTERM_BP_FAT	GO:0006414~translational elongation	38	MRPS36, EEF1B2, MRPS15, HBS1L, MRPS11, EIF5A, MRPS30, DTD1, MRPL10, MRPL14,	3.59E-04
GOTERM_BP_FAT	GO:0006415~translational termination	27	MRPS36, ABCE1, MRPS15, MRPS23, MRPS11, MRPS24, EIF5A, MRPL9, MRPS21, ETF1, M	0.02530253
GOTERM_BP_FAT	GO:0032984~macromolecular complex disassembly	52	MRPS36, CHMP5, CAPZA1, HBS1L, EIF5A, MRPS30, CTNNB1, DNAJC6, MRPL39, MRPL33,	0.10469984
GOTERM_BP_FAT	GO:0043241~protein complex disassembly	50	MRPS36, CHMP5, CAPZA1, EIF5A, MRPS30, CTNNB1, DNAJC6, MRPL39, MRPL33, KIF14,	0.14960359
GOTERM_BP_FAT	GO:0043624~cellular protein complex disassembly	41	MRPS36, MRPS15, MRPS11, CAPZA1, EIF5A, RDX, NAPA, NAPB, MRPS30, MRPL10, MRP	0.20115318
GOTERM_BP_FAT	GO:0070125~mitochondrial translational elongation	22	MRPS36, MRPS15, MRPS23, MRPS24, MRPS11, MRPL9, MRPS21, MRPS30, MRPL10, MR	0.67830262
GOTERM_BP_FAT	GO:0070126~mitochondrial translational termination	22	MRPS36, MRPS15, MRPS23, MRPS24, MRPS11, MRPL9, MRPS21, MRPS30, MRPL10, MR	0.80391471
GOTERM_BP_FAT	GO:0032543~mitochondrial translation	27	MRPS36, MRPS15, MALSU1, MRPS11, MRPS30, MRPL10, MRPL14, MRPL54, MRPL18, M	1.14996321

Annotation Cluster 16 Enrichment Score: 4.539853305754373

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006914~autophagy	100	CHMP3, CHMP4B, RAB1B, UBQLN2, UBQLN1, FLCN, VPS33A, RAB1A, CISD2, ATG5, U2AF	3.57E-10
GOTERM_BP_FAT	GO:0016236~macroautophagy	50	CHMP3, CHMP4B, PRKAG1, RAB1B, PINK1, UBQLN2, UBQLN1, VPS33A, RAB1A, ATG5, E	2.50E-04
GOTERM_BP_FAT	GO:0007033~vacuole organization	48	USP8, CHMP3, CHMP5, EXOC8, CHMP4B, SNX14, ATG14, STAM2, VPS37A, CALCOCO2, P	0.00782013
GOTERM_BP_FAT	GO:0000045~autophagosome assembly	17	GABARAPL2, CHMP4B, ATG14, PINK1, UBQLN1, RAB1A, SCFD1, ATG4D, ATG5, RB1CC1,	2.00180797
GOTERM_BP_FAT	GO:1905037~autophagosome organization	17	GABARAPL2, CHMP4B, ATG14, PINK1, UBQLN1, RAB1A, SCFD1, ATG4D, ATG5, RB1CC1,	2.87269261

Annotation Cluster 17 Enrichment Score: 4.3363381536429

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	230	RPL18, SCPEP1, RPL19, RPL14, PPP2R5C, RPL15, PTPN23, AURKA, ERLEC1, CTNNB1, CUL	2.01E-26
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	258	RPL18, SCPEP1, HM13, RPL19, RPL14, PGC, PPP2R5C, RPL15, PTPN23, AURKA, ERLEC1, C	1.71E-23
GOTERM_BP_FAT	GO:0032446~protein modification by small protein conjugation	182	MKRN1, MED24, LRR1, SAE1, AURKA, SPRTN, MED21, UBQLN1, CNOT4, CTNNB1, MKRN	4.44E-13
GOTERM_BP_FAT	GO:0070647~protein modification by small protein conjugation or removal	201	MED24, AURKA, SPRTN, MED21, CTNNB1, USP53, CUL5, G2E3, BTBD1, MED27, OGT, CR	2.22E-12
GOTERM_BP_FAT	GO:0030163~protein catabolic process	166	SCPEP1, HM13, CHMP4B, LGMN, PGC, PPP2R5C, PTPN23, AURKA, UBQLN2, UBQLN1, ER	9.98E-12
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	146	SCPEP1, CHMP4B, LGMN, PPP2R5C, PTPN23, AURKA, UBQLN2, UBQLN1, ERLEC1, CTNN	3.02E-11
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	131	PPP2R5C, PTPN23, AURKA, UBQLN2, UBQLN1, ERLEC1, CTNNB1, CUL5, BTBD1, RPS27A,	3.06E-11
GOTERM_BP_FAT	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	95	KIAA0368, PPP2R5C, AURKA, UBQLN2, RNF181, UBQLN1, RLIM, ERLEC1, CTNNB1, USP1	3.90E-11
GOTERM_BP_FAT	GO:0016567~protein ubiquitination	158	MKRN1, MED24, LRR1, SAE1, AURKA, SPRTN, MED21, UBQLN1, CNOT4, MKRN2, G2E3,	3.99E-11
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	140	SCPEP1, CHMP4B, LGMN, PPP2R5C, PTPN23, AURKA, UBQLN2, UBQLN1, ERLEC1, CTNN	7.08E-11
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	128	PPP2R5C, PTPN23, AURKA, UBQLN2, UBQLN1, ERLEC1, CTNNB1, CUL5, BTBD1, RPS27A,	1.34E-10
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	126	PPP2R5C, PTPN23, AURKA, UBQLN2, UBQLN1, ERLEC1, CTNNB1, CUL5, BTBD1, RPS27A,	2.50E-10
GOTERM_BP_FAT	GO:0010498~proteasomal protein catabolic process	97	PPP2R5C, AURKA, UBQLN2, UBQLN1, ERLEC1, CTNNB1, BTBD1, RPS27A, UBR3, SKP1, UB	5.79E-10
GOTERM_BP_FAT	GO:0044248~cellular catabolic process	272	RPL18, SCPEP1, RPL19, RPL14, RPL15, PPP2R5C, PTPN23, AURKA, GPCPD1, ERLEC1, CTN	1.53E-09
GOTERM_BP_FAT	GO:0000209~protein polyubiquitination	62	MKRN1, RNF181, RLIM, C18ORF25, TPP2, PSMD3, RPS27A, KLHL20, PSMD9, UBE2A, UB	6.63E-06
GOTERM_BP_FAT	GO:0042176~regulation of protein catabolic process	77	CREBRF, PINK1, AURKA, UBQLN2, UBQLN1, ERLEC1, TMF1, USP19, CDC42, SERPINE2, PS	1.84E-04
GOTERM_BP_FAT	GO:0038061~NIK/NF-kappaB signaling	33	HMGB1, TIRAP, COPS8, PSMA7, RPS3, MAP3K7, PSMB4, PSMB7, PSMB6, PSMB1, PSMB	2.25E-04
GOTERM_BP_FAT	GO:0031398~positive regulation of protein ubiquitination	46	BMI1, DERL1, CLU, PINK1, FKBP1A, ANAPC10, SPRTN, ANAPC11, PSMA7, UBQLN1, PIN1,	3.86E-04
GOTERM_BP_FAT	GO:0002223~stimulatory C-type lectin receptor signaling pathway	32	NFKBIA, PSMA7, SRC, MAP3K7, PSMB4, PSMB7, KRAS, UBE2D2, PSMB6, PSMB1, PAK2, P	4.87E-04
GOTERM_BP_FAT	GO:0002220~innate immune response activating cell surface receptor signaling pathway	32	NFKBIA, PSMA7, SRC, MAP3K7, PSMB4, PSMB7, KRAS, UBE2D2, PSMB6, PSMB1, PAK2, P	7.75E-04
GOTERM_BP_FAT	GO:0031396~regulation of protein ubiquitination	56	BMI1, PINK1, SPRTN, UBQLN1, RPS3, TICAM1, PSMD3, OGT, CRY1, RPS27A, PSMD9, GTP	0.00171635
GOTERM_BP_FAT	GO:1903320~regulation of protein modification by small protein conjugation or removal	59	BMI1, PINK1, SPRTN, UBQLN1, CTNNB1, RPS3, TICAM1, PSMD3, OGT, CRY1, RPS27A, PS	0.00280069
GOTERM_BP_FAT	GO:1903322~positive regulation of protein modification by small protein conjugation or removal	46	BMI1, DERL1, CLU, PINK1, FKBP1A, ANAPC10, SPRTN, ANAPC11, PSMA7, UBQLN1, PIN1,	0.0047566
GOTERM_BP_FAT	GO:1903050~regulation of proteolysis involved in cellular protein catabolic process	51	RAD23B, RAD23A, CLU, PINK1, GIPC1, KEAP1, AURKA, ANAPC10, UBQLN2, ANAPC11, PS	0.00531813
GOTERM_BP_FAT	GO:1903362~regulation of cellular protein catabolic process	54	PINK1, AURKA, UBQLN2, UBQLN1, TMF1, USP19, PSMD3, DDA1, PRKACA, VPS11, RPS27	0.0067681
GOTERM_BP_FAT	GO:0009894~regulation of catabolic process	92	CREBRF, PRKAG1, PINK1, AURKA, UBQLN2, UBQLN1, ERLEC1, TMF1, CDC42, USP19, SER	0.00702377
GOTERM_BP_FAT	GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	48	SYVN1, CACUL1, ABTB2, CLU, UBA6, KEAP1, ANAPC10, AURKA, ANAPC11, PSMA7, RNF1	0.02206456
GOTERM_BP_FAT	GO:0051438~regulation of ubiquitin-protein transferase activity	31	BMI1, PINK1, ANAPC10, ANAPC11, PSMA7, PIN1, PSMB4, PSMB7, PSMB6, PSMB1, PSM	0.0267459
GOTERM_BP_FAT	GO:0051444~negative regulation of ubiquitin-protein transferase activity	24	LIMK1, CDC23, ANAPC10, ANAPC11, PSMA7, CDK2, PSMA2, PSMA1, PSMB4, PSMB7, PS	0.02738023
GOTERM_BP_FAT	GO:0051443~positive regulation of ubiquitin-protein transferase activity	28	BMI1, PINK1, ANAPC10, ANAPC11, PSMA7, PIN1, PSMB4, PSMB7, PSMB6, PSMB1, PSM	0.03328586
GOTERM_BP_FAT	GO:0051436~negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	22	CDC23, ANAPC10, ANAPC11, PSMA7, CDK2, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PS	0.03986605
GOTERM_BP_FAT	GO:1903321~negative regulation of protein modification by small protein conjugation or remova	34	ANAPC10, ANAPC11, PSMA7, CTNNB1, RPS3, PSMB4, PSMB7, PSMB6, PSMB1, PSMB3, P	0.04599167
GOTERM_BP_FAT	GO:0051439~regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	22	CDC23, ANAPC10, ANAPC11, PSMA7, CDK2, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PS	0.05041156
GOTERM_BP_FAT	GO:1904667~negative regulation of ubiquitin protein ligase activity	22	CDC23, ANAPC10, ANAPC11, PSMA7, CDK2, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PS	0.06339097
GOTERM_BP_FAT	GO:0031145~anaphase-promoting complex-dependent catabolic process	23	CDC23, AURKA, ANAPC10, ANAPC11, PSMA7, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6,	0.07215442
GOTERM_BP_FAT	GO:1904666~regulation of ubiquitin protein ligase activity	24	CDC23, ANAPC10, SKP1, ANAPC11, PSMA7, CDK2, PSMA2, PSMA1, PSMB4, PSMB7, PSM	0.09763205
GOTERM_BP_FAT	GO:0002758~innate immune response-activating signal transduction	49	HMGB1, LGMN, TIRAP, NFKBIA, PSMA7, UBQLN1, CACTIN, SRC, SEC14L1, MAP3K7, PSM	0.1174523
GOTERM_BP_FAT	GO:0038093~Fc receptor signaling pathway	49	MAP3K7, ACTG1, CDC42, PAK2, GAB2, PIK3CA, PSMD3, SHC1, CHUK, RPS27A, PSMD9, L	0.1174523
GOTERM_BP_FAT	GO:0051437~positive regulation of ubiquitin-protein ligase activity involved in regulation of mito	22	CDC23, ANAPC10, SKP1, ANAPC11, PSMA7, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PS	0.12209693
GOTERM_BP_FAT	GO:1904668~positive regulation of ubiquitin protein ligase activity	23	CDC23, ANAPC10, SKP1, ANAPC11, PSMA7, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PS	0.13414903
GOTERM_BP_FAT	GO:0006508~proteolysis	239	SCPEP1, HM13, PGC, PPP2R5C, PTPN23, STOML2, AURKA, RCE1, ERLEC1, CTNNB1, BAK1	0.139981
GOTERM_BP_FAT	GO:0002218~activation of innate immune response	49	HMGB1, LGMN, TIRAP, NFKBIA, PSMA7, UBQLN1, CACTIN, SRC, SEC14L1, MAP3K7, PSM	0.24265277
GOTERM_BP_FAT	GO:1903052~positive regulation of proteolysis involved in cellular protein catabolic process	37	CLU, AURKA, ANAPC10, KEAP1, ANAPC11, UBQLN2, PSMA7, UBQLN1, PSMB4, ARIH1, S	0.25371525
GOTERM_BP_FAT	GO:1903364~positive regulation of cellular protein catabolic process	39	CLU, KEAP1, AURKA, RDX, ANAPC10, ANAPC11, UBQLN2, PSMA7, UBQLN1, PSMB4, ARI	0.32316877
GOTERM_BP_FAT	GO:0045862~positive regulation of proteolysis	64	PINK1, AURKA, UBQLN2, UBQLN1, RPS3, PDCD2, BAK1, PICALM, CASP8, CCBE1, PSMD3,	0.33719328
GOTERM_BP_FAT	GO:0031397~negative regulation of protein ubiquitination	30	ANAPC10, ANAPC11, PSMA7, RPS3, PSMB4, PSMB7, PSMB6, PSMB1, PSMB3, PSMD3, O	0.34220771
GOTERM_BP_FAT	GO:0050852~T cell receptor signaling pathway	36	TNFRSF21, NFKBIA, STOML2, PSMA7, MAP3K7, PSMB4, PSMB7, UBE2D2, PSMB6, PSMB	0.34284761
GOTERM_BP_FAT	GO:0006521~regulation of cellular amino acid metabolic process	17	ODC1, AZIN1, PSMA7, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PSMB1, PSMD11, PSMA	0.36940421
GOTERM_BP_FAT	GO:0031329~regulation of cellular catabolic process	66	PINK1, AURKA, UBQLN2, UBQLN1, TMF1, USP19, PSMD3, DDA1, PRKACA, VPS11, RPS27	0.48914006
GOTERM_BP_FAT	GO:0043488~regulation of mRNA stability	32	YWHAZ, YBX3, TIRAP, SYNCRIP, PSMA7, PSMB4, PSMB7, PSMB6, PSMB1, PCBP4, PSMB3	0.54289639
GOTERM_BP_FAT	GO:2000060~positive regulation of protein ubiquitination involved in ubiquitin-dependent protei	23	CLU, CDC23, ANAPC10, SKP1, ANAPC11, PSMA7, PSMA2, PSMA1, PSMB4, PSMB7, PSMB	0.68823765
GOTERM_BP_FAT	GO:0061136~regulation of proteasomal protein catabolic process	32	RAD23B, RAD23A, CLU, PINK1, AURKA, KEAP1, GIPC1, UBQLN2, UBQLN1, TMF1, ARIH1,	0.6990014
GOTERM_BP_FAT	GO:0002478~antigen processing and presentation of exogenous peptide antigen	34	CLTA, SEC24A, AP1B1, AP1G1, LGMN, ITGB5, CLTC, PSMA7, B2M, PSMB4, PSMB7, PSMB	0.88941155
GOTERM_BP_FAT	GO:0045089~positive regulation of innate immune response	53	AP1G1, LGMN, TIRAP, UBQLN1, CACTIN, MAP3K7, PAK2, CASP8, TICAM1, PSMD3, PRKA	0.89627804
GOTERM_BP_FAT	GO:0045732~positive regulation of protein catabolic process	48	CREBRF, CLU, EGLN2, KEAP1, RDX, ANAPC10, AURKA, UBQLN2, ANAPC11, TMEM259, PS	0.90143144
GOTERM_BP_FAT	GO:0043487~regulation of RNA stability	32	YWHAZ, YBX3, TIRAP, SYNCRIP, PSMA7, PSMB4, PSMB7, PSMB6, PSMB1, PCBP4, PSMB3	1.27411666
GOTERM_BP_FAT	GO:0019884~antigen processing and presentation of exogenous antigen	34	CLTA, SEC24A, AP1B1, AP1G1, LGMN, ITGB5, CLTC, PSMA7, B2M, PSMB4, PSMB7, PSMB	1.9200638
GOTERM_BP_FAT	GO:0033238~regulation of cellular amine metabolic process	19	ODC1, NR4A2, AZIN1, HPRT1, PSMA7, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PSMB1,	2.11578664
GOTERM_BP_FAT	GO:0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I,	17	ITGB5, PSMA7, HLA-F, B2M, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PSMB1, PSMD11,	2.40470182
GOTERM_BP_FAT	GO:0038095~Fc-epsilon receptor signaling pathway	35	PPP3R1, NFKBIA, PSMA7, MAP3K7, PSMB4, PSMB7, KRAS, UBE2D2, PSMB6, PSMB1, GA	2.66272
GOTERM_BP_FAT	GO:0030162~regulation of proteolysis	106	AURKA, UBQLN2, UBQLN1, BAK1, PICALM, SERPINE2, BTBD1, CDKN2D, CCBE1, PRKACA,	2.82493503
GOTERM_BP_FAT	GO:0060071~Wnt signaling pathway, planar cell polarity pathway	24	RYK, CLTC, PSMA7, PSMA2, CDC42, PSMA1, PFN1, PSMB4, PSMB7, PSMB6, PSMB1, ARR	2.90221696
GOTERM_BP_FAT	GO:2000058~regulation of protein ubiquitination involved in ubiquitin-dependent protein catabo	23	CLU, CDC23, ANAPC10, SKP1, ANAPC11, PSMA7, PSMA2, PSMA1, PSMB4, PSMB7, PSMB	3.03746715
GOTERM_BP_FAT	GO:0001738~morphogenesis of a polarized epithelium	28	CLTC, PSMA7, CDC42, PFN1, PSMB4, PSMB7, PSMB6, PSMB1, PSMB3, RAC1, RHOA, PSM	3.67447502
GOTERM_BP_FAT	GO:0001736~establishment of planar polarity	26	CLTC, PSMA7, CDC42, PFN1, PSMB4, PSMB7, PSMB6, PSMB1, PSMB3, RAC1, RHOA, PSM	3.74798008
GOTERM_BP_FAT	GO:0007164~establishment of tissue polarity	26	CLTC, PSMA7, CDC42, PFN1, PSMB4, PSMB7, PSMB6, PSMB1, PSMB3, RAC1, RHOA, PSM	3.74798008
GOTERM_BP_FAT	GO:0009896~positive regulation of catabolic process	56	CREBRF, AURKA, UBQLN2, UBQLN1, PSMD3, VPS11, RPS27A, PSMD9, AKT2, GTPBP1, SK	3.81736505
GOTERM_BP_FAT	GO:0042590~antigen processing and presentation of exogenous peptide antigen via MHC class I	17	ITGB5, PSMA7, HLA-F, B2M, PSMA2, PSMA1, PSMB4, PSMB7, PSMB6, PSMB1, PSMD11,	4.03430008
GOTERM_BP_FAT	GO:0090175~regulation of establishment of planar polarity	24	RYK, CLTC, PSMA7, PSMA2, CDC42, PSMA1, PFN1, PSMB4, PSMB7, PSMB6, PSMB1, ARR	4.22921769
GOTERM_BP_FAT	GO:0048002~antigen processing and presentation of peptide antigen	34	CLTA, SEC24A, AP1B1, AP1G1, LGMN, ITGB5, CLTC, PSMA7, B2M, PSMB4, PSMB7, PSMB	5.08360128
GOTERM_BP_FAT	GO:0045088~regulation of innate immune response	59	AP1G1, LGMN, TIRAP, UBQLN1, CACTIN, MAP3K7, PAK2, CASP8, TICAM1, PSMD3, PRKA	5.18358371
GOTERM_BP_FAT	GO:0031331~positive regulation of cellular catabolic process	47	HMGB1, POLR2G, CLU, KEAP1, RDX, ANAPC10, AURKA, ANAPC11, UBQLN2, PSMA7, UBC	5.30949483
GOTERM_BP_FAT	GO:0080134~regulation of response to stress	175	AP1G1, OSMR, IL18, PGC, LGMN, TIRAP, UBQLN2, UBQLN1, CACTIN, ERLEC1, B2M, MAP	6.95511683
GOTERM_BP_FAT	GO:0090263~positive regulation of canonical Wnt signaling pathway	25	PSMA7, SRC, PIN1, PSMB4, PSMB7, PSMB6, PSMB1, PSMB3, PSMD3, TNKS, RPS27A, PS	7.0125137

Annotation Cluster 18 Enrichment Score: 4.281194393949094

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0043484~regulation of RNA splicing	29	SRSF1, NSRP1, SF3B4, UHMK1, DAZAP1, CLK3, SNRNP70, KHDRBS1, RBM22, SRPK2, SRE	0.0352362
GOTERM_BP_FAT	GO:1903311~regulation of mRNA metabolic process	32	POLR2G, NSRP1, SF3B4, UHMK1, DAZAP1, TNRC6C, AGO2, SNRNP70, KHDRBS1, PABPN1	0.10102403
GOTERM_BP_FAT	GO:0048024~regulation of mRNA splicing, via spliceosome	21	KHDRBS1, SRPK2, SREK1, MAGOH, HNRNPA2B1, YTHDC1, SAP18, RNPS1, NSRP1, SF3B4,	0.10806302
GOTERM_BP_FAT	GO:0050684~regulation of mRNA processing	26	NSRP1, SF3B4, UHMK1, DAZAP1, SNRNP70, KHDRBS1, PABPN1, SRPK2, SREK1, TMBIM6,	0.30984386

Annotation Cluster 19 Enrichment Score: 3.891823132097787

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling	44	MTDH, VAPA, IL18, TIRAP, TFG, PINK1, FKBP1A, TERF2IP, CTNNB1, MAP3K7, TMEM9B, T	0.00267786
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB signaling	51	VAPA, IL18, TIRAP, PINK1, TERF2IP, PRDX1, CTNNB1, MAP3K7, TMEM9B, TRIM8, CASP8,	0.01470489
GOTERM_BP_FAT	GO:0007249~I-kappaB kinase/NF-kappaB signaling	50	MTDH, VAPA, IL18, TIRAP, PINK1, TFG, NFKBIA, FKBP1A, TERF2IP, PRDX1, CTNNB1, MAP	0.24779068

Annotation Cluster 20 Enrichment Score: 3.883550128133685

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:2000641~regulation of early endosome to late endosome transport	12	MTMR2, CHMP3, MAP2K1, MAP2K2, PTPN23, RDX, SNX3, SNX12, VPS11, RNF103-CHMP	9.94E-04
GOTERM_BP_FAT	GO:1903649~regulation of cytoplasmic transport	12	MTMR2, CHMP3, MAP2K1, MAP2K2, PTPN23, RDX, SNX3, SNX12, VPS11, RNF103-CHMP	0.00799909
GOTERM_BP_FAT	GO:0016482~cytosolic transport	35	VPS29, STX8, CHMP3, AP1G1, SNX16, PTPN23, VPS53, RDX, SNX3, CLTC, SRC, MTMR2, R	0.02863558
GOTERM_BP_FAT	GO:1903335~regulation of vacuolar transport	14	CHMP3, MAP2K1, MAP2K2, PTPN23, RDX, SNAPIN, SNX3, RNF103-CHMP3, SRC, MTMR2	0.03631423
GOTERM_BP_FAT	GO:0045022~early endosome to late endosome transport	12	MTMR2, FAM160A2, STX8, SNF8, SNX16, RAB5A, PTPN23, RDX, SNX3, SNX12, VPS11, RA	0.23117431
GOTERM_BP_FAT	GO:0098927~vesicle-mediated transport between endosomal compartments	12	MTMR2, FAM160A2, STX8, SNF8, SNX16, RAB5A, PTPN23, RDX, SNX3, SNX12, VPS11, RA	0.66233393

GOTERM_BP_FAT	GO:1903337~positive regulation of vacuolar transport	7	MTMR2, PTPN23, SNAPIN, RDX, VPS11, EHD1, RAB21	7.61821623

Annotation Cluster 21 Enrichment Score: 3.720595665687164

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0000462~maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LS	14	RPSA, UTP18, MRPS11, FCF1, BMS1, CCDC59, RPS8, DCAF13, RCL1, RPS19, RPS16, NGDN	0.21753894
GOTERM_BP_FAT	GO:0042274~ribosomal small subunit biogenesis	20	RPSA, UTP18, MRPS11, RPL38, FCF1, BMS1, RPS5, CCDC59, RPS8, DCAF13, RCL1, RPS27,	0.22900905
GOTERM_BP_FAT	GO:0030490~maturation of SSU-rRNA	15	RPSA, UTP18, MRPS11, FCF1, BMS1, CCDC59, RPS8, DCAF13, RCL1, RPS19, RPS28, RPS1	1.09458584

Annotation Cluster 22 Enrichment Score: 3.4672127583686696

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006900~membrane budding	33	PPP6C, SEC24A, CHMP3, VAPA, CHMP5, CHMP4B, VPS37A, TFG, RAB1B, NAPA, PPP6R3,	1.76E-04
GOTERM_BP_FAT	GO:0016050~vesicle organization	59	CHMP3, SEC24A, VAPA, AP1G1, CHMP5, CHMP4B, VPS37A, RAB1B, PINK1, MITD1, SDC4	0.02436094
GOTERM_BP_FAT	GO:0090114~COPII-coated vesicle budding	19	PPP6C, SEC24A, VAPA, TFG, RAB1B, NAPA, PPP6R3, RAB1A, SCFD1, CD59, TRAPPC6B, IN	0.38870512
GOTERM_BP_FAT	GO:0051656~establishment of organelle localization	72	CHMP3, SEC24A, CHMP4B, CHMP5, AP3S1, RAB1B, ITSN1, SPICE1, RAB1A, CTNNB1, CDC	0.47432816
GOTERM_BP_FAT	GO:0006888~ER to Golgi vesicle-mediated transport	37	PPP6C, ARFGAP3, IER3IP1, SEC24A, VAPA, TFG, RAB1B, NAPA, PPP6R3, WHAMM, RAB1A	0.51905314
GOTERM_BP_FAT	GO:0051640~organelle localization	81	SEC24A, CHMP3, CHMP4B, CHMP5, AP3S1, RAB1B, AURKA, ITSN1, SPICE1, VPS33A, RAB	0.58135529
GOTERM_BP_FAT	GO:0006901~vesicle coating	18	PPP6C, SEC24A, RAB1B, TFG, NAPA, PPP6R3, RAB1A, SCFD1, GBF1, CD59, TRAPPC6B, TR	0.80914991
GOTERM_BP_FAT	GO:0048199~vesicle targeting, to, from or within Golgi	18	PPP6C, SEC24A, RAB1B, TFG, NAPA, PPP6R3, RAB1A, SCFD1, GBF1, CD59, TRAPPC6B, TR	1.19921565
GOTERM_BP_FAT	GO:0048208~COPII vesicle coating	17	PPP6C, SEC24A, RAB1B, TFG, NAPA, PPP6R3, RAB1A, SCFD1, CD59, TRAPPC6B, TRAPPC5	1.65691894
GOTERM_BP_FAT	GO:0048207~vesicle targeting, rough ER to cis-Golgi	17	PPP6C, SEC24A, RAB1B, TFG, NAPA, PPP6R3, RAB1A, SCFD1, CD59, TRAPPC6B, TRAPPC5	1.65691894
GOTERM_BP_FAT	GO:0006903~vesicle targeting	19	PPP6C, SEC24A, RAB1B, TFG, NAPA, PPP6R3, RAB1A, SCFD1, GBF1, CD59, TRAPPC6B, TR	3.41908082

Annotation Cluster 23 Enrichment Score: 3.4615844082857357

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	33	BID, YWHAZ, MCL1, CLU, PPP3R1, PINK1, BAK1, MFF, TRIAP1, MOAP1, BLOC1S2, PPP2C	0.00313898
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	16	BID, CLU, LMNA, PINK1, ST20, PLAUR, PPIF, BAK1, MFF, TRIAP1, MOAP1, ARRB2, BBC3,	2.76828659
GOTERM_BP_FAT	GO:0090199~regulation of release of cytochrome c from mitochondria	13	BID, LMNA, PINK1, PLAUR, PPIF, BAK1, MFF, TRIAP1, MOAP1, ARRB2, BBC3, FAM162A,	4.94741715
GOTERM_BP_FAT	GO:0090200~positive regulation of release of cytochrome c from mitochondria	10	BID, PPIF, MFF, BAK1, MOAP1, BBC3, PINK1, FAM162A, PDCD5, PLAUR	4.96343328

Annotation Cluster 24 Enrichment Score: 3.4153150971974364

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006915~apoptotic process	259	CHMP3, PPP2R5C, AURKA, ITSN1, ANKLE2, CTNNB1, MAP3K7, BAK1, CLPTM1L, USP53, C	0.00145333
GOTERM_BP_FAT	GO:0012501~programmed cell death	267	CHMP3, PPP2R5C, AURKA, ITSN1, ANKLE2, CTNNB1, MAP3K7, BAK1, CLPTM1L, USP53,	0.00939363
GOTERM_BP_FAT	GO:0008219~cell death	279	CHMP3, VAPA, PPP2R5C, AURKA, ANKLE2, ITSN1, CTNNB1, MAP3K7, BAK1, CLPTM1L, U	0.01377001
GOTERM_BP_FAT	GO:0097190~apoptotic signaling pathway	100	PPP2R5C, UBQLN1, FLCN, CTNNB1, BAK1, MFF, CUL5, CDKN2D, TPT1, ZC3HC1, RELA, KIA	0.0256025
GOTERM_BP_FAT	GO:2001233~regulation of apoptotic signaling pathway	70	SH3RF1, FIGNL1, YBX3, PINK1, UBQLN1, FLCN, RPS3, CTNNB1, BAK1, TRIAP1, MFF, PAK2	0.0616224
GOTERM_BP_FAT	GO:0042981~regulation of apoptotic process	192	GABRB3, LGMN, AURKA, FLCN, UBQLN1, ITSN1, ANKLE2, CTNNB1, ZNF304, MFF, BAK1,	3.25944747
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	192	GABRB3, LGMN, AURKA, FLCN, UBQLN1, ITSN1, ANKLE2, CTNNB1, ZNF304, MFF, BAK1,	5.04173475
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptotic process	118	GABRB3, LGMN, AURKA, ANKLE2, ITSN1, CTNNB1, ZNF304, CDKN2D, TPT1, PIK3CA, NQC	5.50621655
GOTERM_BP_FAT	GO:0010941~regulation of cell death	203	AURKA, ITSN1, ANKLE2, CTNNB1, BAK1, PICALM, PIK3CA, HIGD1A, TYRO3, ZC3HC1, KIAA	5.62769697
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	118	GABRB3, LGMN, AURKA, ANKLE2, ITSN1, CTNNB1, ZNF304, CDKN2D, TPT1, PIK3CA, NQC	8.13787811
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	86	PINK1, FLCN, ITSN1, LATS1, LATS2, PDCD2, RPS3, CTNNB1, AKR1C3, BAK1, CDC42, MFF,	8.87294946
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	126	GABRB3, CHMP4B, LGMN, AURKA, ANKLE2, ITSN1, CTNNB1, ZNF304, ATG5, CDKN2D, TP	9.73295483

Annotation Cluster 25 Enrichment Score: 3.3323584562998003

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0042274~ribosomal small subunit biogenesis	20	RPSA, UTP18, MRPS11, RPL38, FCF1, BMS1, RPS5, CCDC59, RPS8, DCAF13, RCL1, RPS27,	0.22900905
GOTERM_BP_FAT	GO:0042255~ribosome assembly	17	RPSA, FASTKD2, MRPS11, RPL24, RPL38, RPS5, BMS1, RPF2, RPS27, RPS19, RPS28, RPS1	1.3633895
GOTERM_BP_FAT	GO:0000028~ribosomal small subunit assembly	9	RPSA, RPS27, RPS28, RPS19, MRPS11, RPS15, RPS10, RPL38, RPS5	2.520653

Annotation Cluster 26 Enrichment Score: 3.21324751707321

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006354~DNA-templated transcription, elongation	33	CCNT2, HMGN1, POLR2G, TAF1C, POLR2F, POLR2E, POLR2K, TAF1D, POLR2C, GTF2E2, G	0.00313898
GOTERM_BP_FAT	GO:0006368~transcription elongation from RNA polymerase II promoter	28	CCNT2, POLR2G, POLR2F, POLR2E, POLR2K, POLR2C, GTF2E2, GTF2A1, ELOF1, GTF2A2,	0.00991778
GOTERM_BP_FAT	GO:0016073~snRNA metabolic process	22	CCNT2, USB1, POLR2G, POLR2F, CCNK, POLR2E, EXOSC9, POLR2K, EXOSC4, EXOSC3, CDK	0.57012246
GOTERM_BP_FAT	GO:0050434~positive regulation of viral transcription	14	TAF11, PFN1, POLR2G, POLR2F, POLR2E, POLR2K, GTF2F2, NELFA, CHD1, SUPT4H1, NEL	0.90997956
GOTERM_BP_FAT	GO:0006352~DNA-templated transcription, initiation	41	POLR2G, TAF1C, HMGB1, E2F3, POLR2F, BCLAF1, POLR2E, POLR2K, TAF1D, MED24, POL	6.29795011
GOTERM_BP_FAT	GO:0042795~snRNA transcription from RNA polymerase II promoter	17	CCNT2, POLR2G, POLR2F, CCNK, POLR2E, POLR2K, CDK7, INTS10, POLR2C, GTF2B, TAF11	7.48700674
GOTERM_BP_FAT	GO:0009301~snRNA transcription	17	CCNT2, POLR2G, POLR2F, CCNK, POLR2E, POLR2K, CDK7, INTS10, POLR2C, GTF2B, TAF11	7.48700674

Annotation Cluster 27 Enrichment Score: 3.1192437624754197

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:2001233~regulation of apoptotic signaling pathway	70	SH3RF1, FIGNL1, YBX3, PINK1, UBQLN1, FLCN, RPS3, CTNNB1, BAK1, TRIAP1, MFF, PAK2	0.0616224
GOTERM_BP_FAT	GO:0097193~intrinsic apoptotic signaling pathway	51	NBN, FIGNL1, HINT1, PPP2R5C, YBX3, PINK1, FLCN, UBQLN1, RPS3, TRIAP1, BAK1, CUL5,	0.98301916
GOTERM_BP_FAT	GO:2001234~negative regulation of apoptotic signaling pathway	39	SH3RF1, SYVN1, MCL1, FIGNL1, CLU, YBX3, PINK1, SRC, CTNNB1, TRIAP1, RRN3, RB1CC1,	3.62073709
GOTERM_BP_FAT	GO:2001242~regulation of intrinsic apoptotic signaling pathway	30	BID, BCLAF1, SYVN1, MCL1, FIGNL1, CLU, YBX3, PINK1, FLCN, UBQLN1, SRC, RPS3, TRIAP	5.3216101
GOTERM_BP_FAT	GO:2001243~negative regulation of intrinsic apoptotic signaling pathway	21	HERPUD1, ARHGEF2, SYVN1, MCL1, FIGNL1, TMBIM6, CLU, YBX3, PINK1, VDAC2, BCL2L1	6.38030532

Annotation Cluster 28 Enrichment Score: 3.02541713962267

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0044772~mitotic cell cycle phase transition	114	CHMP4B, PPP2R5C, TTK, AURKA, CNOT4, CUL5, CDKN2B, PPP1R1C, CDKN2D, ORC5, ORC	1.43E-09
GOTERM_BP_FAT	GO:0044770~cell cycle phase transition	117	CHMP4B, PPP2R5C, TTK, AURKA, CNOT4, CUL5, CDKN2B, PPP1R1C, CDKN2D, ORC5, ORC	8.71E-09
GOTERM_BP_FAT	GO:0044843~cell cycle G1/S phase transition	61	BACH1, PPP2R5C, AURKA, LATS1, LATS2, CNOT4, MEN1, TRIAP1, PRMT1, CUL5, PPP1R1	4.69E-06
GOTERM_BP_FAT	GO:0000082~G1/S transition of mitotic cell cycle	55	BACH1, PPP2R5C, AURKA, LATS1, LATS2, CNOT4, TRIAP1, PRMT1, CUL5, PPP1R1C, PLRG	6.06E-05
GOTERM_BP_FAT	GO:1901990~regulation of mitotic cell cycle phase transition	65	NBN, PPP2R5C, TTK, AURKA, CNOT4, TRIAP1, PRMT1, PPP1R1C, PLRG1, CDKN2B, PCBP4,	0.0019743
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	105	CHMP3, CHMP5, CHMP4B, PPP2R5C, AURKC, TTK, AURKA, FLCN, CNOT4, CTNNB1, CDKN	0.00411031
GOTERM_BP_FAT	GO:1901987~regulation of cell cycle phase transition	67	NBN, PPP2R5C, TTK, AURKA, CNOT4, MEN1, TRIAP1, PRMT1, PPP1R1C, PLRG1, CDKN2B,	0.00650589
GOTERM_BP_FAT	GO:1902806~regulation of cell cycle G1/S phase transition	34	BID, PPP2R5C, RDX, AURKA, CNOT4, MEN1, RPA2, TRIAP1, PRMT1, CDKN2B, PLRG1, PPP	0.29453802
GOTERM_BP_FAT	GO:0045787~positive regulation of cell cycle	60	CCNT2, PPP2R5C, AURKC, AURKA, CNOT4, TRIAP1, USP19, CDC42, PRMT1, PPP1R1C, PL	0.71874167
GOTERM_BP_FAT	GO:2000045~regulation of G1/S transition of mitotic cell cycle	31	BID, PPP2R5C, RDX, AURKA, CNOT4, RPA2, TRIAP1, PRMT1, CDKN2B, PLRG1, PPP1R1C,	0.73640891
GOTERM_BP_FAT	GO:0007050~cell cycle arrest	45	ING4, NBN, PRKAG1, PPP2R5C, RRAGA, AURKA, UHMK1, CNOT4, TRIAP1, PRMT1, CUL5,	0.8037733
GOTERM_BP_FAT	GO:0030330~DNA damage response, signal transduction by p53 class mediator	24	ING4, NBN, PPP2R5C, AURKA, KAT5, SIRT1, CENPJ, CDK2, CNOT4, BATF, TRIAP1, PRMT1,	2.54627434
GOTERM_BP_FAT	GO:0042770~signal transduction in response to DNA damage	26	BID, ING4, NBN, PPP2R5C, AURKA, KAT5, SIRT1, CENPJ, CDK2, CNOT4, BATF, TRIAP1, CD	2.61589559
GOTERM_BP_FAT	GO:0045786~negative regulation of cell cycle	73	NBN, PRKAG1, PPP2R5C, TTK, AURKA, LATS1, LATS2, CNOT4, CTNNB1, MEN1, TRIAP1, P	6.37576197
GOTERM_BP_FAT	GO:0090068~positive regulation of cell cycle process	43	PPP2R5C, AURKC, GIPC1, RDX, AURKA, ANAPC11, CNOT4, TRIAP1, CDC42, USP19, PRMT	9.37755214

Annotation Cluster 29 Enrichment Score: 2.9540997070525825

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006368~transcription elongation from RNA polymerase II promoter	28	CCNT2, POLR2G, POLR2F, POLR2E, POLR2K, POLR2C, GTF2E2, GTF2A1, ELOF1, GTF2A2,	0.00991778
GOTERM_BP_FAT	GO:1903902~positive regulation of viral life cycle	25	POLR2G, POLR2F, CHMP3, POLR2E, VAPA, POLR2K, CHMP4B, RAD23A, POLR2C, CHMP2	0.12632423
GOTERM_BP_FAT	GO:0050434~positive regulation of viral transcription	14	TAF11, PFN1, POLR2G, POLR2F, POLR2E, POLR2K, GTF2F2, NELFA, CHD1, SUPT4H1, NEL	0.90997956
GOTERM_BP_FAT	GO:0048524~positive regulation of viral process	25	POLR2G, POLR2F, CHMP3, POLR2E, VAPA, POLR2K, CHMP4B, RAD23A, POLR2C, CHMP2	1.23575123
GOTERM_BP_FAT	GO:0046782~regulation of viral transcription	18	POLR2G, POLR2F, POLR2E, POLR2K, POLR2C, GTF2B, TRIM21, TRIM11, TAF11, PFN1, HD	1.44788185
GOTERM_BP_FAT	GO:0043902~positive regulation of multi-organism process	32	POLR2G, POLR2F, CHMP3, POLR2E, VAPA, POLR2K, CHMP4B, RAD23A, PGC, OXTR, AUR	2.74872419

Annotation Cluster 30 Enrichment Score: 2.865332038896476

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0034976~response to endoplasmic reticulum stress	50	CREBRF, HM13, SYVN1, DERL1, KIAA0368, TMX3, UFC1, UBQLN2, ZBTB17, UBQLN1, TM	0.75924707
GOTERM_BP_FAT	GO:0036498~IRE1-mediated unfolded protein response	19	SYVN1, TMBIM6, LMNA, SRPRB, ZBTB17, SEC62, ACADVL, BAK1, DNAJB9, SEC61B, DNAJ	1.04762709
GOTERM_BP_FAT	GO:0035966~response to topologically incorrect protein	37	CREBRF, DERL1, SYVN1, CLU, ZBTB17, SEC62, SERPINH1, RNF126, BAK1, DNAJB11, TMEM	1.6887609
GOTERM_BP_FAT	GO:0035967~cellular response to topologically incorrect protein	31	CREBRF, DERL1, SYVN1, ZBTB17, SEC62, RNF126, BAK1, DNAJB11, TMEM33, SHC1, YOD1	1.9160176
GOTERM_BP_FAT	GO:0030968~endoplasmic reticulum unfolded protein response	27	CREBRF, DERL1, SYVN1, ZBTB17, SEC62, BAK1, DNAJB11, TMEM33, SHC1, YOD1, SEC61A	5.45724118
GOTERM_BP_FAT	GO:0034620~cellular response to unfolded protein	27	CREBRF, DERL1, SYVN1, ZBTB17, SEC62, BAK1, DNAJB11, TMEM33, SHC1, YOD1, SEC61A	7.42870069
GOTERM_BP_FAT	GO:0006986~response to unfolded protein	32	CREBRF, DERL1, SYVN1, ZBTB17, SEC62, SERPINH1, BAK1, DNAJB11, TMEM33, HSPA4, H	9.32025809

Annotation Cluster 31 Enrichment Score: 2.8573972021621157

Category	Term	Count	Genes	FDR

GOTERM_BP_FAT	GO:0042775~mitochondrial ATP synthesis coupled electron transport	27	NDUFB5, NDUFB6, UQCRC1, NDUFB8, NDUFB9, COX7B, NDUFAB1, PINK1, COX7A2L, CO	0.00873146
GOTERM_BP_FAT	GO:0042773~ATP synthesis coupled electron transport	27	NDUFB5, NDUFB6, UQCRC1, NDUFB8, NDUFB9, COX7B, NDUFAB1, PINK1, COX7A2L, CO	0.01089082
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	29	ATP5D, NDUFB5, NDUFB6, UQCRC1, NDUFB8, NDUFB9, COX7B, NDUFAB1, PINK1, COX7	0.02926594
GOTERM_BP_FAT	GO:0045333~cellular respiration	40	NDUFB5, FASTKD2, UQCRC1, NDUFB6, NDUFB8, NDUFB9, COX7B, NDUFAB1, PINK1, CH	0.03074948
GOTERM_BP_FAT	GO:0022904~respiratory electron transport chain	29	NDUFB5, NDUFB6, UQCRC1, NDUFB8, NDUFB9, COX7B, NDUFAB1, PINK1, COX7A2L, UQ	0.0352362
GOTERM_BP_FAT	GO:0022900~electron transport chain	29	NDUFB5, NDUFB6, UQCRC1, NDUFB8, NDUFB9, COX7B, NDUFAB1, PINK1, COX7A2L, UQ	0.05060701
GOTERM_BP_FAT	GO:0046034~ATP metabolic process	50	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.05678296
GOTERM_BP_FAT	GO:0009144~purine nucleoside triphosphate metabolic process	54	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.09000076
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	53	PTGES3, FASTKD2, UQCRC1, NDUFAB1, PINK1, FLCN, UQCRFS1, COX5A, MTFR2, NDUFAF	0.13159936
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic process	55	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.1368032
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic process	55	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.15067774
GOTERM_BP_FAT	GO:0009205~purine ribonucleoside triphosphate metabolic process	52	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.17365834
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	56	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.22194861
GOTERM_BP_FAT	GO:0009199~ribonucleoside triphosphate metabolic process	52	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.30964133
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	67	PTGES3, ATP5D, FASTKD2, UQCRC1, GNPDA1, PRKAG1, NDUFAB1, PINK1, UQCRFS1, CO	0.32761214
GOTERM_BP_FAT	GO:0009123~nucleoside monophosphate metabolic process	57	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.41374372
GOTERM_BP_FAT	GO:0009141~nucleoside triphosphate metabolic process	55	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	0.41394899
GOTERM_BP_FAT	GO:0033108~mitochondrial respiratory chain complex assembly	23	NDUFA5, NDUFAF5, NDUFB5, NDUFB6, NDUFA8, COA4, NDUFA9, NDUFB8, COA1, NDUF	0.58265625
GOTERM_BP_FAT	GO:1901657~glycosyl compound metabolic process	71	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, COX5A, UQCRFS1	2.11452128
GOTERM_BP_FAT	GO:0009116~nucleoside metabolic process	66	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	5.3676192
GOTERM_BP_FAT	GO:0042278~purine nucleoside metabolic process	58	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	7.67155797
GOTERM_BP_FAT	GO:0006120~mitochondrial electron transport, NADH to ubiquinone	14	NDUFA4, NDUFA5, NDUFB5, NDUFB6, NDUFA8, NDUFB8, NDUFA9, NDUFB9, NDUFV2, N	8.96867342
GOTERM_BP_FAT	GO:0009119~ribonucleoside metabolic process	61	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	9.26404307
GOTERM_BP_FAT	GO:0046128~purine ribonucleoside metabolic process	57	ATP5D, ATP5E, UQCRC1, FIGNL1, PRKAG1, NDUFAB1, STOML2, PINK1, UQCRFS1, COX5A	9.9413295

Annotation Cluster 32 Enrichment Score: 2.699583427722618

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051276~chromosome organization	180	HMGN1, CHMP3, CHMP4B, CHMP5, MORF4L2, AURKC, CBX3, MED24, TTK, CCT2, AURK	0.02223848

Annotation Cluster 33 Enrichment Score: 2.621865486489641

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0090305~nucleic acid phosphodiester bond hydrolysis	49	AEN, CLP1, RPP30, KPNB1, TSEN15, RPS27A, PDE12, PAN3, EXOSC9, GEN1, NOL9, EXOSC	2.84555809
GOTERM_BP_FAT	GO:0090501~RNA phosphodiester bond hydrolysis	28	ENDOV, FCF1, BMS1, EXOSC10, CLP1, RNASET2, REXO2, RPP30, AGO2, RPS21, FEN1, TSE	4.09864482
GOTERM_BP_FAT	GO:0090502~RNA phosphodiester bond hydrolysis, endonucleolytic	17	RPSA, TSEN54, ENDOV, NOL9, FCF1, BMS1, RCL1, RNASET2, RPP30, AGO2, POP4, RPS21,	8.63362647

Annotation Cluster 34 Enrichment Score: 2.5845403776390348

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	33	BID, YWHAZ, MCL1, CLU, PPP3R1, PINK1, BAK1, MFF, TRIAP1, MOAP1, BLOC1S2, PPP2CE	0.00313898
GOTERM_BP_FAT	GO:0097345~mitochondrial outer membrane permeabilization	16	BID, YWHAZ, SLC25A5, PPP3R1, YWHAE, BAK1, MOAP1, BLOC1S2, BBC3, GSK3A, GSK3B,	1.2461692
GOTERM_BP_FAT	GO:1902108~regulation of mitochondrial membrane permeability involved in apoptotic process	17	BID, YWHAZ, SLC25A5, PPP3R1, YWHAE, BAK1, MOAP1, BLOC1S2, BBC3, GSK3A, GSK3B,	1.3633895
GOTERM_BP_FAT	GO:1902686~mitochondrial outer membrane permeabilization involved in programmed cell deat	16	BID, YWHAZ, SLC25A5, PPP3R1, YWHAE, BAK1, MOAP1, BLOC1S2, BBC3, GSK3A, GSK3B,	1.53675248
GOTERM_BP_FAT	GO:1902110~positive regulation of mitochondrial membrane permeability involved in apoptotic	16	BID, YWHAZ, SLC25A5, PPP3R1, YWHAE, BAK1, MOAP1, BLOC1S2, BBC3, GSK3A, GSK3B,	1.53675248
GOTERM_BP_FAT	GO:0007006~mitochondrial membrane organization	24	BID, YWHAZ, SLC25A5, TIMM10, PPP3R1, PINK1, YWHAE, PPIF, BAK1, MOAP1, TOMM7,	1.6914568
GOTERM_BP_FAT	GO:0035794~positive regulation of mitochondrial membrane permeability	16	BID, YWHAZ, SLC25A5, PPP3R1, YWHAE, BAK1, MOAP1, BLOC1S2, BBC3, GSK3A, GSK3B,	2.28992876
GOTERM_BP_FAT	GO:0046902~regulation of mitochondrial membrane permeability	18	BID, YWHAZ, SLC25A5, PPP3R1, YWHAE, PPIF, BAK1, MOAP1, BLOC1S2, BBC3, GSK3A, G	2.92197575
GOTERM_BP_FAT	GO:0090559~regulation of membrane permeability	18	BID, YWHAZ, SLC25A5, PPP3R1, YWHAE, PPIF, BAK1, MOAP1, BLOC1S2, BBC3, GSK3A, G	5.46268879

Annotation Cluster 35 Enrichment Score: 2.3848586821263518

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006997~nucleus organization	34	CHMP3, CHMP5, CHMP4B, NUP188, CEP55, ANKLE2, TMF1, CHMP2B, NDC1, SUMO1, RF	0.08439976
GOTERM_BP_FAT	GO:0075733~intracellular transport of virus	18	NUP133, NUP153, DERL1, NUP88, RAN, VPS37A, NUP85, NUP188, DYNLT1, NDC1, KPNA	1.73886589
GOTERM_BP_FAT	GO:0006998~nuclear envelope organization	21	PPP2R1A, NUP133, NUP153, CHMP4B, NUP88, TOR1AIP1, NSFL1C, LMNA, NUP85, NUP1	1.80312262
GOTERM_BP_FAT	GO:1902583~multi-organism intracellular transport	18	NUP133, NUP153, DERL1, NUP88, RAN, VPS37A, NUP85, NUP188, DYNLT1, NDC1, KPNA	2.07759809
GOTERM_BP_FAT	GO:1902581~multi-organism cellular localization	18	NUP133, NUP153, DERL1, NUP88, RAN, VPS37A, NUP85, NUP188, DYNLT1, NDC1, KPNA	2.07759809
GOTERM_BP_FAT	GO:0046794~transport of virus	18	NUP133, NUP153, DERL1, NUP88, RAN, VPS37A, NUP85, NUP188, DYNLT1, NDC1, KPNA	2.92197575
GOTERM_BP_FAT	GO:0044766~multi-organism transport	18	NUP133, NUP153, DERL1, NUP88, RAN, VPS37A, NUP85, NUP188, DYNLT1, NDC1, KPNA	5.46268879
GOTERM_BP_FAT	GO:1902579~multi-organism localization	18	NUP133, NUP153, DERL1, NUP88, RAN, VPS37A, NUP85, NUP188, DYNLT1, NDC1, KPNA	5.46268879
GOTERM_BP_FAT	GO:1900034~regulation of cellular response to heat	18	PTGES3, NUP133, NUP153, NUP88, NUP85, NUP188, HSBP1, SIRT1, YWHAE, NDC1, RPA	7.27235692

Annotation Cluster 36 Enrichment Score: 2.368294303990604

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006361~transcription initiation from RNA polymerase I promoter	12	MNAT1, TAF1C, POLR2F, POLR2E, RRN3, POLR2K, CCNH, POLR1D, TAF1D, POLR1C, CDK7	1.22268943
GOTERM_BP_FAT	GO:0006370~7-methylguanosine mRNA capping	12	MNAT1, POLR2G, POLR2F, RNMT, POLR2E, POLR2K, CCNH, GTF2F2, FAM103A1, CDK7, P	1.22268943
GOTERM_BP_FAT	GO:0009452~7-methylguanosine RNA capping	13	POLR2G, POLR2F, POLR2E, RNMT, POLR2K, CCNH, CDK7, POLR2C, GTF2H2, MNAT1, GTF	1.58154817
GOTERM_BP_FAT	GO:0036260~RNA capping	13	POLR2G, POLR2F, POLR2E, RNMT, POLR2K, CCNH, CDK7, POLR2C, GTF2H2, MNAT1, GTF	1.58154817
GOTERM_BP_FAT	GO:0006362~transcription elongation from RNA polymerase I promoter	11	MNAT1, TAF1C, POLR2F, POLR2E, POLR2K, CCNH, POLR1D, TAF1D, POLR1C, CDK7, GTF2	2.83971224
GOTERM_BP_FAT	GO:0006363~termination of RNA polymerase I transcription	11	MNAT1, TAF1C, POLR2F, POLR2E, POLR2K, CCNH, POLR1D, TAF1D, POLR1C, CDK7, GTF2	2.83971224

Annotation Cluster 37 Enrichment Score: 2.358433606878048

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0000079~regulation of cyclin-dependent protein serine/threonine kinase activity	24	CCNT2, EGFR, CKS1B, GTPBP4, CCNK, CCNH, CCNL1, CNPPD1, CCNC, ANAPC10, CDK7, LA	0.25082249
GOTERM_BP_FAT	GO:1904029~regulation of cyclin-dependent protein kinase activity	24	CCNT2, EGFR, CKS1B, GTPBP4, CCNK, CCNH, CCNL1, CNPPD1, CCNC, ANAPC10, CDK7, LA	0.29949088

Annotation Cluster 38 Enrichment Score: 2.25753534822317

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0007051~spindle organization	25	CHMP3, CHMP4B, CHMP5, AURKC, TTK, AURKA, CLTC, MYBL2, RCC1, SPICE1, RPS3, CHM	1.86881789
GOTERM_BP_FAT	GO:0051225~spindle assembly	21	CHMP3, CHMP5, CHMP4B, AURKC, AURKA, CLTC, RCC1, BIRC3, MYBL2, BIRC2, SPICE1, R	3.76444132

Annotation Cluster 39 Enrichment Score: 2.2311771400710634

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0071428~rRNA-containing ribonucleoprotein complex export from nucleus	7	ABCE1, RPSA, SDAD1, NUP88, RAN, RPS15, NMD3	1.94504182
GOTERM_BP_FAT	GO:0000054~ribosomal subunit export from nucleus	6	ABCE1, SDAD1, NUP88, RAN, RPS15, NMD3	5.24795027
GOTERM_BP_FAT	GO:0033753~establishment of ribosome localization	6	ABCE1, SDAD1, NUP88, RAN, RPS15, NMD3	5.24795027
GOTERM_BP_FAT	GO:0033750~ribosome localization	6	ABCE1, SDAD1, NUP88, RAN, RPS15, NMD3	5.24795027

Annotation Cluster 40 Enrichment Score: 2.0325400396666433

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0007080~mitotic metaphase plate congression	12	KIF14, CHMP1A, CHMP3, CHMP5, CHMP4B, RAB11A, CDC23, CEP55, KPNB1, CDCA5, ZW	3.50823392
GOTERM_BP_FAT	GO:0051310~metaphase plate congression	14	KIF14, CHMP3, CHMP4B, CHMP5, CENPQ, CDC23, CEP55, SPICE1, CHMP2B, CHMP1A, RA	3.58654166
GOTERM_BP_FAT	GO:0000920~cell separation after cytokinesis	8	CHMP1A, CHMP3, CHMP5, CHMP4B, MITD1, CEP55, RNF103-CHMP3, CHMP2B	4.39167436
GOTERM_BP_FAT	GO:0000070~mitotic sister chromatid segregation	28	CHMP3, CHMP5, CHMP4B, AURKC, TTK, ANAPC10, ANAPC11, CEP55, CHMP2B, NAA50,	7.57779433

Annotation Cluster 41 Enrichment Score: 1.9587150426036672

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051169~nuclear transport	88	SRSF1, CHERP, IL18, SNRPD1, EIF5A, SNRPD2, NUP188, NSRP1, PRDX1, CTNNB1, AKR1C3	0.00345725
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	86	SRSF1, CHERP, IL18, SNRPD1, EIF5A, SNRPD2, NUP188, NSRP1, PRDX1, CTNNB1, AKR1C3	0.00590134
GOTERM_BP_FAT	GO:0034504~protein localization to nucleus	67	CHERP, IL18, CCT2, NUP188, FLCN, PRDX1, CTNNB1, AKR1C3, CRY2, PLRG1, TRIM8, RHO	0.08737352
GOTERM_BP_FAT	GO:0051170~nuclear import	54	CHERP, IL18, SNRPD1, SNRPD2, NUP188, PRDX1, CTNNB1, AKR1C3, CRY2, RHOA, NUP35	0.89093405
GOTERM_BP_FAT	GO:0017038~protein import	58	GRPEL2, CHERP, IL18, NUP188, PRDX1, CTNNB1, AKR1C3, CRY2, RHOA, NUP35, KPNB1,	1.00865051
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	48	GPN1, CHERP, IL18, PPP3R1, NFKBIA, KEAP1, NUP188, POLA2, PRDX1, CTNNB1, AKR1C3,	5.58693212
GOTERM_BP_FAT	GO:0044744~protein targeting to nucleus	48	GPN1, CHERP, IL18, PPP3R1, NFKBIA, KEAP1, NUP188, POLA2, PRDX1, CTNNB1, AKR1C3,	5.58693212
GOTERM_BP_FAT	GO:1902593~single-organism nuclear import	48	GPN1, CHERP, IL18, PPP3R1, NFKBIA, KEAP1, NUP188, POLA2, PRDX1, CTNNB1, AKR1C3,	5.98837625

Annotation Cluster 42 Enrichment Score: 1.9061785539350695

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0038128~ERBB2 signaling pathway	12	EGFR, NRAS, CUL5, KRAS, USP8, PIK3CA, HBEGF, SHC1, UBB, RPS27A, SRC, CDC37	5.5222109
GOTERM_BP_FAT	GO:0038127~ERBB signaling pathway	29	CLTA, USP8, LGMN, STAM2, GPRC5A, PXN, CDC37, SRC, RNF126, CDC42, CUL5, KRAS, PI	6.99644072

Annotation Cluster 43 Enrichment Score: 1.8707092853213774

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006839~mitochondrial transport	54	BID, ATP5D, GRPEL2, ATP5E, YWHAZ, MTX3, MTX2, GDAP1, PPP3R1, TIMM10, PINK1, ST	0.1217042
GOTERM_BP_FAT	GO:1903827~regulation of cellular protein localization	94	CHERP, LEPROTL1, IL18, PINK1, SAE1, CCT2, CLTC, FLCN, PRDX1, ERLEC1, CTNNB1, CDC4	0.12629757
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	130	CHERP, CHMP3, IL18, PTPN23, SAE1, CCT2, FLCN, ERLEC1, CTNNB1, BAK1, MFF, GAB2, S	0.13952667
GOTERM_BP_FAT	GO:0010821~regulation of mitochondrion organization	45	BID, YWHAZ, MALSU1, PPP3R1, STOML2, PINK1, SAE1, FLCN, ZBTB17, TRIAP1, MFF, BAK	0.4476991
GOTERM_BP_FAT	GO:0010822~positive regulation of mitochondrion organization	35	BID, YWHAZ, PPP3R1, PINK1, STOML2, SAE1, ZBTB17, BAK1, MFF, PSMB7, MOAP1, UBE	1.29739344
GOTERM_BP_FAT	GO:0007006~mitochondrial membrane organization	24	BID, YWHAZ, SLC25A5, TIMM10, PPP3R1, PINK1, YWHAE, PPIF, BAK1, MOAP1, TOMM7,	1.6914568
GOTERM_BP_FAT	GO:0032386~regulation of intracellular transport	74	CREBRF, CHMP3, CHERP, IL18, PTPN23, PINK1, SAE1, PRDX1, ERLEC1, CDC42, MFF, GAB	4.85764996
GOTERM_BP_FAT	GO:1903829~positive regulation of cellular protein localization	59	CHERP, IL18, PINK1, SAE1, CCT2, MFF, CDC42, STARD7, TRIM8, CASP8, U2AF1, RHOA, PR	6.24614763
GOTERM_BP_FAT	GO:0070585~protein localization to mitochondrion	35	BID, GRPEL2, YWHAZ, MTX3, MTX2, GDAP1, PPP3R1, TIMM10, PINK1, SAE1, ZBTB17, M	7.81017803
GOTERM_BP_FAT	GO:1903749~positive regulation of establishment of protein localization to mitochondrion	24	BID, YWHAZ, ZDHHC8, PPP3R1, PINK1, SAE1, UBE2L3, ZBTB17, YWHAE, RPL28, UBL5, HE	8.37878981
GOTERM_BP_FAT	GO:0032880~regulation of protein localization	134	CHERP, IL18, SAE1, CCT2, FLCN, ERLEC1, CTNNB1, MFF, PICALM, STARD7, GBF1, RALB, U	9.90400607

Annotation Cluster 44 Enrichment Score: 1.8701059089873502

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0048261~negative regulation of receptor-mediated endocytosis	8	MTMR2, PICALM, SYT11, RAC1, DLG4, SDCBP, UBQLN2, ANXA2	6.23209257
GOTERM_BP_FAT	GO:0048259~regulation of receptor-mediated endocytosis	19	SYT11, CBL, UBQLN2, CD63, LDLRAP1, SRC, ANXA2, B2M, MTMR2, PICALM, SMAP1, ARR	7.00580908

Annotation Cluster 45 Enrichment Score: 1.8510831480266141

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0002756~MyD88-independent toll-like receptor signaling pathway	12	IKBKE, UBE2D3, UBE2D2, CASP8, TICAM1, UBB, TRAF6, BIRC3, UBE2D1, BIRC2, RPS27A,	0.90712153
GOTERM_BP_FAT	GO:0035666~TRIF-dependent toll-like receptor signaling pathway	11	IKBKE, UBE2D3, UBE2D2, CASP8, TICAM1, UBB, BIRC3, UBE2D1, BIRC2, RPS27A, CHUK	1.15866665

Annotation Cluster 46 Enrichment Score: 1.832547274571604

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0000460~maturation of 5.8S rRNA	13	EXOSC10, RCL1, RPSA, EXOSC9, NOL9, RRP15, EXOSC4, EXOSC3, MPHOSPH6, RPS21, FCF	0.27311036

Annotation Cluster 48 Enrichment Score: 1.7818380299836825

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0010824~regulation of centrosome duplication	12	CHMP1A, PLK4, CHMP3, NUBP1, PLK2, CHMP5, CHMP4B, GEN1, SPICE1, RNF103-CHMP	3.50823392
GOTERM_BP_FAT	GO:0046605~regulation of centrosome cycle	13	CHMP3, GEN1, CHMP4B, CHMP5, AURKA, SPICE1, CENPJ, RNF103-CHMP3, CHMP2B, PL	6.03929671
GOTERM_BP_FAT	GO:0032886~regulation of microtubule-based process	28	CHMP3, CHMP5, CHMP4B, AURKA, SPICE1, CTNNB1, RPS3, CHMP2B, NUBP1, NEFH, MK	9.15902953

Annotation Cluster 49 Enrichment Score: 1.778653265555076

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0071897~DNA biosynthetic process	42	PTGES3, NBN, GAR1, CCT2, SPRTN, TERF2IP, POLA2, SRC, CTNNB1, RPA1, MEN1, RPA2,	0.18894143
GOTERM_BP_FAT	GO:0007004~telomere maintenance via telomerase	17	GAR1, CCT2, PKIB, TERF2IP, NOP10, HNRNPU, SRC, CTNNB1, CCT7, PNKP, CCT5, ACD, CC	0.28979727
GOTERM_BP_FAT	GO:0010833~telomere maintenance via telomere lengthening	18	MCRS1, GAR1, CCT2, PKIB, TERF2IP, NOP10, HNRNPU, SRC, CTNNB1, CCT7, PNKP, CCT5,	0.53336939
GOTERM_BP_FAT	GO:0006278~RNA-dependent DNA biosynthetic process	18	PTGES3, GAR1, CCT2, PKIB, TERF2IP, NOP10, HNRNPU, SRC, CTNNB1, CCT7, PNKP, CCT5,	0.98784307
GOTERM_BP_FAT	GO:0033044~regulation of chromosome organization	52	NBN, TTK, PINK1, CCT2, TERF2IP, NAP1L2, FLCN, WBP2, CTNNB1, ZNF304, NSMCE2, OGT	1.15498006
GOTERM_BP_FAT	GO:0032200~telomere organization	31	PTGES3, NBN, GAR1, CCT2, TERF2IP, POLA2, SRC, CTNNB1, RPA1, RPA2, ACD, NSMCE2,	1.52512173
GOTERM_BP_FAT	GO:0000723~telomere maintenance	29	PTGES3, NBN, GAR1, CCT2, TERF2IP, POLA2, SRC, CTNNB1, RPA1, RPA2, ACD, NSMCE2,	1.52884755
GOTERM_BP_FAT	GO:1904356~regulation of telomere maintenance via telomere lengthening	15	MCRS1, PKIB, CCT2, HNRNPU, SRC, CTNNB1, CCT7, PNKP, CCT5, ACD, CCT4, CCT8, TNKS,	1.71312788
GOTERM_BP_FAT	GO:0032210~regulation of telomere maintenance via telomerase	14	PKIB, CCT2, HNRNPU, SRC, CTNNB1, CCT7, PNKP, CCT5, ACD, CCT4, CCT8, TNKS, HNRNP	1.8822562
GOTERM_BP_FAT	GO:0032204~regulation of telomere maintenance	18	MCRS1, NBN, PKIB, CCT2, TERF2IP, SRC, HNRNPU, CTNNB1, CCT7, PNKP, CCT5, CCT4, AC	2.07759809
GOTERM_BP_FAT	GO:0032205~negative regulation of telomere maintenance	10	NBN, MCRS1, ACD, TNKS, HNRNPC, TERF2IP, TINF2, SRC, HNRNPU, ERCC1	2.78930768
GOTERM_BP_FAT	GO:0051054~positive regulation of DNA metabolic process	37	HMGB1, NBN, STOML2, CCT2, SRC, CTNNB1, RPS3, ZNF304, PFN1, CDC42, ACD, RAC1, S	6.0414639

Annotation Cluster 50 Enrichment Score: 1.7586494018129026

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0036258~multivesicular body assembly	13	CHMP3, CHMP4B, CHMP5, STAM2, VTA1, VPS37A, RNF103-CHMP3, CHMP2B, CHMP1A,	0.13453046
GOTERM_BP_FAT	GO:0036257~multivesicular body organization	13	CHMP3, CHMP4B, CHMP5, STAM2, VTA1, VPS37A, RNF103-CHMP3, CHMP2B, CHMP1A,	0.19341618
GOTERM_BP_FAT	GO:0007032~endosome organization	19	FAM160A2, CHMP3, USP8, LAMTOR1, CHMP5, CHMP4B, EXOC8, STAM2, VTA1, VPS37A,	0.58729469
GOTERM_BP_FAT	GO:0019068~virion assembly	13	CHMP3, CHMP5, CHMP4B, VTA1, VPS37A, RAB1B, MITD1, RNF103-CHMP3, RAB1A, CH	1.58154817
GOTERM_BP_FAT	GO:0010824~regulation of centrosome duplication	12	CHMP1A, PLK4, CHMP3, NUBP1, PLK2, CHMP5, CHMP4B, GEN1, SPICE1, RNF103-CHMP	3.50823392
GOTERM_BP_FAT	GO:0000920~cell separation after cytokinesis	8	CHMP1A, CHMP3, CHMP5, CHMP4B, MITD1, CEP55, RNF103-CHMP3, CHMP2B	4.39167436
GOTERM_BP_FAT	GO:0046605~regulation of centrosome cycle	13	CHMP3, GEN1, CHMP4B, CHMP5, AURKA, SPICE1, CENPJ, RNF103-CHMP3, CHMP2B, PL	6.03929671
GOTERM_BP_FAT	GO:0046755~viral budding	9	CHMP1A, CHMP3, CHMP5, CHMP4B, VTA1, VPS37A, MITD1, RNF103-CHMP3, CHMP2B	8.64687854
GOTERM_BP_FAT	GO:1902592~multi-organism membrane budding	9	CHMP1A, CHMP3, CHMP5, CHMP4B, VTA1, VPS37A, MITD1, RNF103-CHMP3, CHMP2B	8.64687854
GOTERM_BP_FAT	GO:1902590~multi-organism organelle organization	9	CHMP1A, CHMP3, CHMP5, CHMP4B, VTA1, VPS37A, MITD1, RNF103-CHMP3, CHMP2B	8.64687854

Annotation Cluster 51 Enrichment Score: 1.752077408155834

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006399~tRNA metabolic process	38	FAM98B, TYW3, TRMT10C, DTD1, ZBTB8OS, CLP1, CTU2, RPP30, GTF3C5, YRDC, MRPL3	0.60826516
GOTERM_BP_FAT	GO:0008033~tRNA processing	28	FAM98B, TYW3, TRMT10C, ZBTB8OS, CLP1, CTU2, RPP30, YRDC, FTSJ1, CDK5RAP1, TPRK	0.73546579

Annotation Cluster 52 Enrichment Score: 1.631542783781426

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:1902532~negative regulation of intracellular signal transduction	70	STK38, FIGNL1, YBX3, PINK1, FLCN, MEN1, TRIAP1, SERPINE2, RRN3, CDKN2D, CASP8, TP	9.36672066

Annotation Cluster 53 Enrichment Score: 1.6309983090774625

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0040029~regulation of gene expression, epigenetic	47	BMI1, TAF1C, POLR2F, POLR2E, POLR2K, TAF1D, MORF4L2, ARID4B, RLIM, WBP2, CTNN	2.69841846
GOTERM_BP_FAT	GO:0016458~gene silencing	44	POLR2G, POLR2F, POLR2E, POLR2K, MORF4L2, TSNAX, NUP188, POLR2C, NDC1, ZNF304,	6.47421765

Annotation Cluster 54 Enrichment Score: 1.5599545287124454

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0051246~regulation of protein metabolic process	355	ADCY7, MALSU1, CNPPD1, SYNCRIP, AURKA, SPRTN, ANKLE2, ERLEC1, CTNNB1, MAP3K7	0.00113624
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	332	ADCY7, MALSU1, CNPPD1, SYNCRIP, AURKA, SPRTN, ANKLE2, CTNNB1, MAP3K7, BAK1,	0.00266368
GOTERM_BP_FAT	GO:0036211~protein modification process	509	HCCS, MED24, SPRTN, ANKLE2, MED21, CTNNB1, MAP3K7, USP53, CUL5, CLK3, PPP1R1	0.00334685
GOTERM_BP_FAT	GO:0006464~cellular protein modification process	509	HCCS, MED24, SPRTN, ANKLE2, MED21, CTNNB1, MAP3K7, USP53, CUL5, CLK3, PPP1R1	0.00334685
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	106	HMGN1, ADCY7, IL18, TIRAP, CCT2, CTNNB1, MAP3K7, BAK1, MAP3K8, RALB, PIK3CA, P	0.06214611
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	216	ADCY7, AURKA, SPRTN, ANKLE2, CTNNB1, MAP3K7, BAK1, PICALM, CCBE1, MAP3K8, PIK	0.13615796
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	144	HMGN1, STK38, ADCY7, IL18, CNPPD1, TIRAP, CCT2, CTNNB1, MAP3K7, BAK1, PPP1R1C,	0.27352272
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic process	202	ADCY7, AURKA, SPRTN, ANKLE2, CTNNB1, MAP3K7, BAK1, PICALM, CCBE1, MAP3K8, PIK	0.35292757
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	222	ADCY7, CNPPD1, SPRTN, ANKLE2, CTNNB1, MAP3K7, BAK1, CRY2, PPP1R1C, MAP3K8, PI	5.7531645

Annotation Cluster 55 Enrichment Score: 1.5243605691103472

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	87	RAB5C, RAB1B, FLCN, ITSN1, RAB1A, CDC42, ZNF304, ARHGAP5, GBF1, ARL14, RALB, RH	0.38062645
GOTERM_BP_FAT	GO:0007265~Ras protein signal transduction	54	ITSN1, FLCN, ZNF304, ARHGAP5, GBF1, RHOA, RALB, RHOB, RRAS, SHC1, OGT, KPNB1, C	4.27046656

DOWN-REGULATED BPs

Annotation Cluster 1 Enrichment Score: 4.907569784612656

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	43	PPARA, BCKDK, GLUD2, GCAT, ECHDC2, ECHS1, HADHA, ALDH3A2, FAH, GLDC, MUT, AK	0.00346282
GOTERM_BP_FAT	GO:0044282~small molecule catabolic process	58	PPARA, BCKDK, GCAT, ECHDC2, GLDC, FAH, MAT1A, APOE, MCEE, GSTZ1, DAO, HADH, D	0.003707
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	39	PPARA, BCKDK, GLUD2, GCAT, ECHDC2, ECHS1, HADHA, ALDH3A2, FAH, GLDC, MUT, AK	0.00447254
GOTERM_BP_FAT	GO:0006082~organic acid metabolic process	121	ALDH8A1, EIF6, TARS2, ALDH1L1, STAR, CNDP2, GCAT, GGT1, ACSS2, GLDC, FAH, MAT1	0.00737397
GOTERM_BP_FAT	GO:0043436~oxoacid metabolic process	112	ALDH8A1, EIF6, TARS2, STAR, GCAT, GGT1, ACSS2, GLDC, FAH, MAT1A, PLA2G1B, DAO,	0.01126822
GOTERM_BP_FAT	GO:0019752~carboxylic acid metabolic process	111	ALDH8A1, EIF6, TARS2, STAR, GCAT, GGT1, ACSS2, GLDC, FAH, MAT1A, PLA2G1B, DAO,	0.01412304
GOTERM_BP_FAT	GO:0032787~monocarboxylic acid metabolic process	79	ALDH8A1, EIF6, PPARA, D2HGDH, PTGES2, HNF1A, STAR, ECHDC2, ACOT1, GGT1, ACSS2,	0.06344698
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	53	EIF6, PPARA, PTGES2, HNF1A, ECHDC2, ACOT1, GGT1, ACSS2, GPX1, NDUFS6, LONP2, PT	0.81922251

GOTERM_BP_FAT	GO:0044712~single-organism catabolic process	103	GCAT, GLDC, FAH, APOB, APOE, MAT1A, PLA2G1B, DAO, HADH, DDAH1, HMGCL, AADAT	0.95295993

Annotation Cluster 2 Enrichment Score: 3.923887966923254

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006629~lipid metabolic process	162	EIF6, ALDH8A1, RARRES2, THRA, STAR, GGT1, RORA, ACSS2, APOB, NANS, APOE, LCAT, G	0.03130337
GOTERM_BP_FAT	GO:0044255~cellular lipid metabolic process	130	ALDH8A1, EIF6, RARRES2, STAR, GGT1, ACSS2, APOB, NANS, APOE, LCAT, GALR2, PLA2G	0.08860882
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	77	ALDH8A1, EIF6, PTGES2, HNF1A, STAR, PIP5K1C, GGT1, ACSS2, APOB, ST6GALNAC4, PIGI	4.71590849

Annotation Cluster 3 Enrichment Score: 3.6044798633641375

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	43	PPARA, BCKDK, GLUD2, GCAT, ECHDC2, ECHS1, HADHA, ALDH3A2, FAH, GLDC, MUT, AKI	0.00346282
GOTERM_BP_FAT	GO:0044282~small molecule catabolic process	58	PPARA, BCKDK, GCAT, ECHDC2, GLDC, FAH, MAT1A, APOE, MCEE, GSTZ1, DAO, HADH, D	0.003707
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	39	PPARA, BCKDK, GLUD2, GCAT, ECHDC2, ECHS1, HADHA, ALDH3A2, FAH, GLDC, MUT, AKI	0.00447254
GOTERM_BP_FAT	GO:0009062~fatty acid catabolic process	20	ECI1, PPARA, ACADS, AMACR, ECHS1, ECHDC2, CRAT, ACACB, LPIN2, HADHA, ALDH3A2,	0.34138572
GOTERM_BP_FAT	GO:0019395~fatty acid oxidation	21	ECI1, PPARA, ACADS, AMACR, ECHS1, ECHDC2, CRAT, ACACB, HADHA, POR, ALDH3A2, L	0.39478014
GOTERM_BP_FAT	GO:0072329~monocarboxylic acid catabolic process	22	ECI1, PPARA, ACADS, HOGA1, AMACR, ECHS1, ECHDC2, CRAT, ACACB, LPIN2, HADHA, AL	0.50984436
GOTERM_BP_FAT	GO:0034440~lipid oxidation	21	ECI1, PPARA, ACADS, AMACR, ECHS1, ECHDC2, CRAT, ACACB, HADHA, POR, ALDH3A2, L	0.52949684
GOTERM_BP_FAT	GO:0006635~fatty acid beta-oxidation	16	ECI1, PPARA, ACADS, AMACR, ECHS1, ECHDC2, CRAT, ACACB, HADHA, ABCD3, HSD17B4,	1.67214311

Annotation Cluster 4 Enrichment Score: 3.4807552037117446

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	43	PPARA, BCKDK, GLUD2, GCAT, ECHDC2, ECHS1, HADHA, ALDH3A2, FAH, GLDC, MUT, AKI	0.00346282
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	39	PPARA, BCKDK, GLUD2, GCAT, ECHDC2, ECHS1, HADHA, ALDH3A2, FAH, GLDC, MUT, AKI	0.00447254
GOTERM_BP_FAT	GO:1901606~alpha-amino acid catabolic process	16	AADAT, GLUD2, HOGA1, GCAT, DDO, GLDC, FAH, MAT1A, HAAO, GSTZ1, GPT, DAO, AHC	4.60547439
GOTERM_BP_FAT	GO:1901605~alpha-amino acid metabolic process	30	GLUD2, GCAT, GGT1, CAD, PSPH, FAH, GLDC, MUT, MAT1A, HAAO, GSTZ1, DAO, DDAH1,	7.19685711
GOTERM_BP_FAT	GO:0009063~cellular amino acid catabolic process	16	AADAT, BCKDK, GCAT, FTCD, CDO1, DDO, GLDC, FAH, MAT1A, GSTZ1, GPT, DAO, DDAH1	9.57102712

Annotation Cluster 5 Enrichment Score: 3.3791483583406468

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	127	XRCC3, DBF4, XRCC6, RPS27L, XRCC1, NONO, MC1R, ISG15, MIS18A, PLA2G1B, RDM1, P	0.03624946
GOTERM_BP_FAT	GO:0006281~DNA repair	74	XRCC3, FAM175A, XRCC6, TMEM161A, RPS27L, DEK, MLH3, XRCC1, NONO, MCM9, FAM	0.17180054
GOTERM_BP_FAT	GO:0033554~cellular response to stress	191	XRCC3, SEC31A, XRCC6, RPS27L, RORA, XRCC1, NONO, VPS13C, ISG15, MC1R, CUL7, APC	4.29029985

Annotation Cluster 6 Enrichment Score: 3.2684725193952713

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006325~chromatin organization	101	HMGN3, ZNF451, CBX4, CBX7, HIST1H2BO, USP27X, BRPF3, MIS18A, TADA2A, TADA2B,	0.09105367
GOTERM_BP_FAT	GO:0051276~chromosome organization	143	HMGN3, XRCC3, MAU2, CHMP6, ZNF451, XRCC6, CBX4, CBX7, HIST1H2BO, USP27X, BRP	0.16177744
GOTERM_BP_FAT	GO:0016569~covalent chromatin modification	70	ENY2, HMGN3, HNF1A, FAM175A, ZNF451, COPRS, CBX4, CTCF, DEK, CBX7, USP27X, PR	3.54738502

Annotation Cluster 7 Enrichment Score: 3.167454539889316

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	275	MRPL40, HGSNAT, XRCC3, OXA1L, HMGN3, MRPL41, SEC31A, CHMP6, XRCC6, TRAPPC2I	0.02574458
GOTERM_BP_FAT	GO:0044085~cellular component biogenesis	312	DLC1, HGSNAT, RAB3GAP2, OXA1L, XRCC3, SEC31A, SURF6, CHMP6, XRCC6, TRAPPC2L,	0.18123073
GOTERM_BP_FAT	GO:0022607~cellular component assembly	278	DLC1, HGSNAT, RAB3GAP2, OXA1L, XRCC3, SEC31A, CHMP6, XRCC6, TRAPPC2L, SYT7, M	0.80674601
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	188	HGSNAT, EIF6, XRCC3, KCNC4, OXA1L, THRA, SEC31A, CHMP6, IDE, ZNF451, XRCC6, TRAI	1.80161074
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	118	EIF6, OXA1L, XRCC3, THRA, IQGAP2, VTN, RPS27L, HIST1H2BO, DDX23, MIS18A, MLST8,	2.016698
GOTERM_BP_FAT	GO:0006461~protein complex assembly	161	HGSNAT, KCNC4, OXA1L, THRA, SEC31A, CHMP6, ZNF451, XRCC6, IDE, TRAPPC2L, IQGAF	2.56441207
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	161	HGSNAT, KCNC4, OXA1L, THRA, SEC31A, CHMP6, ZNF451, XRCC6, IDE, TRAPPC2L, IQGAF	2.65179939
GOTERM_BP_FAT	GO:0071822~protein complex subunit organization	181	MRPL40, HGSNAT, KCNC4, OXA1L, MRPL41, THRA, SEC31A, CHMP6, IDE, ZNF451, XRCC6	4.70119222

Annotation Cluster 8 Enrichment Score: 2.902255922156547

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0006281~DNA repair	74	XRCC3, FAM175A, XRCC6, TMEM161A, RPS27L, DEK, MLH3, XRCC1, NONO, MCM9, FAM	0.17180054
GOTERM_BP_FAT	GO:0006302~double-strand break repair	31	XRCC3, FAM175A, XRCC6, SHFM1, MGMT, POLA1, PRKDC, DEK, XRCC1, MCM9, HIST1H4	8.43490643
GOTERM_BP_FAT	GO:0006310~DNA recombination	37	XRCC3, XRCC6, SHFM1, POLA1, PRKDC, MLH3, XRCC1, NONO, STAT6, MCM9, FIGN, POL	9.79779267

Annotation Cluster 9 Enrichment Score: 2.64786181905258

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0040029~regulation of gene expression, epigenetic	44	EIF6, HIST1H2AB, POLR2L, TNRC18, HIST1H2AE, DICER1, DEK, CTCF, TRIM71, LIN28B, GP	0.11329515
GOTERM_BP_FAT	GO:0045814~negative regulation of gene expression, epigenetic	24	HIST1H2AB, DNMT3A, RBBP4, TNRC18, JARID2, HIST1H2AE, TRIM27, ATAD2, MBD3, H2	3.52196365

Annotation Cluster 10 Enrichment Score: 2.5380295129050703

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0001889~liver development	24	HNF1A, ONECUT1, JARID2, ARID5B, E2F8, ONECUT2, GFER, HFE, VTN, CAD, AK4, PRKCSH	1.90291868
GOTERM_BP_FAT	GO:0061008~hepaticobiliary system development	24	HNF1A, ONECUT1, JARID2, ARID5B, E2F8, ONECUT2, GFER, HFE, VTN, CAD, AK4, PRKCSH	2.60807661

Annotation Cluster 11 Enrichment Score: 1.8344394234792085

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:2000113~negative regulation of cellular macromolecule biosynthetic process	159	EIF6, THRA, CCDC85B, ZNF451, XRCC6, PASK, CBX4, CBX7, NONO, ATOH8, PITX1, EIF2B4,	0.08064969
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	172	NCBP2, EIF6, THRA, CCDC85B, ZNF451, XRCC6, CBX4, CBX7, NONO, CD46, ATOH8, PITX1,	0.26757618
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	165	EIF6, THRA, CCDC85B, ZNF451, XRCC6, PASK, CBX4, CBX7, NONO, CASP8AP2, ATOH8, PI	0.28878927
GOTERM_BP_FAT	GO:0034645~cellular macromolecule biosynthetic process	502	SCAF1, XRCC3, XRCC6, INTS2, RORA, MAMSTR, ZNF777, CDCA7, ISG15, MC1R, ZNF775, D	0.63236993
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	171	EIF6, THRA, CCDC85B, ZNF451, XRCC6, PASK, CBX4, CBX7, NONO, CASP8AP2, APOE, GAL	0.65625386
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	171	EIF6, THRA, CCDC85B, ZNF451, XRCC6, CBX4, CBX7, NONO, CASP8AP2, APOE, GALR2, AT	0.71936872
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	167	EIF6, THRA, CCDC85B, ZNF451, XRCC6, PASK, CBX4, CBX7, NONO, CASP8AP2, GALR2, AT	1.1940928
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-templated	131	THRA, CCDC85B, ZNF451, XRCC6, CBX4, CBX7, NONO, ATOH8, PITX1, S100A1, RARG, RR	1.82944321
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	91	ISX, PPARA, THRA, HNF1A, E2F8, NR6A1, DICER1, ZNF451, CBX4, CTCF, CBX7, ZNF205, A	2.93903986
GOTERM_BP_FAT	GO:1903507~negative regulation of nucleic acid-templated transcription	134	THRA, CCDC85B, ZNF451, XRCC6, CBX4, CBX7, NONO, CASP8AP2, ATOH8, PITX1, S100A1	3.08177294
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	198	HMGN3, GDF1, XRCC6, RORA, MAMSTR, MC1R, TRAK1, PLA2G1B, CREB3L4, WWOX, S10	3.21611096
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	196	SCAF1, HMGN3, GDF1, XRCC6, INTS2, RORA, MAMSTR, DHX38, MC1R, RBM8A, PLA2G1	3.69698803
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase-containing compound metabolic process	152	THRA, CCDC85B, ZNF451, XRCC6, CBX4, CBX7, NONO, CASP8AP2, GALR2, ATOH8, PITX1,	4.2603603
GOTERM_BP_FAT	GO:1902679~negative regulation of RNA biosynthetic process	134	THRA, CCDC85B, ZNF451, XRCC6, CBX4, CBX7, NONO, CASP8AP2, ATOH8, PITX1, S100A1	5.22326001
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	242	XRCC6, NONO, ISG15, APOE, CD46, PITX1, S100A1, EIF2B4, RARG, ANAPC5, RREB1, PTBP	6.28711718
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	137	THRA, CCDC85B, ZNF451, XRCC6, CBX4, CBX7, NONO, CASP8AP2, ATOH8, PITX1, S100A1	8.0433157

Annotation Cluster 12 Enrichment Score: 1.7818818042001734

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0008654~phospholipid biosynthetic process	36	MVD, GRB2, CHKB, PIP5K1C, SERINC5, ISYNA1, PIGM, FITM2, GGPS1, INPP5E, PCYT1B, I	0.90080759
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	77	ALDH8A1, EIF6, PTGES2, HNF1A, STAR, PIP5K1C, GGT1, ACSS2, APOB, ST6GALNAC4, PIGI	4.71590849
GOTERM_BP_FAT	GO:0090407~organophosphate biosynthetic process	70	PPCS, PIP5K1C, CAD, SLC26A2, PIGM, ATP5EP2, MC1R, APOE, FITM2, GALR2, PCYT2, AG	9.10855783

Annotation Cluster 13 Enrichment Score: 1.6936957103879555

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0071103~DNA conformation change	45	TNRC18, XRCC6, CTCF, HIST1H2BO, CHD8, SET, DDX3X, HIST1H4B, MIS18A, ANP32A, HIS	0.33438707
GOTERM_BP_FAT	GO:0006338~chromatin remodeling	30	HNF1A, TNRC18, DEK, CHD8, CHD7, HIST1H4B, MIS18A, ANP32A, HIST1H4E, PBRM1, AC	0.56083189
GOTERM_BP_FAT	GO:0043044~ATP-dependent chromatin remodeling	18	RBBP4, ANP32B, ANP32C, NASP, ANP32E, MBD3, RBBP7, CHD8, HIST1H4B, MIS18A, AN	1.03003507
GOTERM_BP_FAT	GO:0043486~histone exchange	14	RBBP4, ANP32B, ANP32C, NASP, ANP32E, RBBP7, HIST1H4B, MIS18A, ANP32A, HIST1H4	3.16442938
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	30	TNRC18, CTCF, HIST1H2BO, SET, HIST1H4B, MIS18A, ANP32A, HIST1H4E, HIST1H4C, HIS	5.34484711
GOTERM_BP_FAT	GO:0031497~chromatin assembly	27	TNRC18, CTCF, HIST1H2BO, SET, HIST1H4B, MIS18A, ANP32A, HIST1H4E, HIST1H4C, HIS	6.06601679
GOTERM_BP_FAT	GO:0006334~nucleosome assembly	25	HIST1H2BO, SET, HIST1H4B, MIS18A, HIST1H4E, ANP32A, HIST1H4C, HIST1H4D, HIST1H	6.51473608
GOTERM_BP_FAT	GO:0034728~nucleosome organization	28	CTCF, HIST1H2BO, SET, HIST1H4B, MIS18A, ANP32A, HIST1H4E, HIST1H4C, HIST1H4D, H	7.35474104
GOTERM_BP_FAT	GO:0006323~DNA packaging	31	TNRC18, CTCF, HIST1H2BO, SET, HIST1H4B, MIS18A, ANP32A, HIST1H4E, HIST1H4C, HIS	7.87372768
GOTERM_BP_FAT	GO:0071824~protein-DNA complex subunit organization	37	XRCC3, THRA, CTCF, HIST1H2BO, ERCC5, SET, HIST1H4B, MIS18A, ANP32A, HIST1H4E, HI	9.79779267
GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	34	XRCC3, THRA, HIST1H2BO, ERCC5, SET, HIST1H4B, MIS18A, ANP32A, HIST1H4E, HIST1H4	9.83236751

Annotation Cluster 15 Enrichment Score: 1.599532832046647

Category	Term	Count	Genes	FDR

GOTERM_BP_FAT	GO:0044283~small molecule biosynthetic process	63	ALDH8A1, PPARA, PTGES2, HNF1A, STAR, CAD, GGT1, PSPH, ACSS2, APOB, APOE, PTGES,	4.37842301

Annotation Cluster 16 Enrichment Score: 1.5851669494069638

Category	Term	Count	Genes	FDR
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	129	DLC1, RAB3GAP2, XRCC3, ZNF451, IQGAP2, TBC1D16, MVB12A, RUNDC1, VPS13C, CUL7	6.79784328
GOTERM_BP_FAT	GO:0051128~regulation of cellular component organization	240	DLC1, RAB3GAP2, XRCC3, SYT7, MVB12A, RUNDC1, CUL7, VPS13C, APOE, LCAT, MIS18A,	8.75555229

SUPPLEMENTARY TABLE 7

List of autophagic genes induced or suppressed by Cu in ATP7B-deficient and control HepG2 cells.

Significant differences in expression of 86 and 184 autophagic genes were found in the control cell (WT+Cu vs WT) dataset and in the ATP7B-deficient cell (ATP7B-KO+Cu vs ATP7B-KO) dataset, respectively. Among these genes, 49 exhibit transcriptional changes in both datasets, 37 only in control cells and 135 only in ATP7B-ko cells. Up-regulated or down-regulated genes

Autophagic genes	logFC (WT+Cu vs WT)	logFC (ATP7B-KO+Cu vs ATP7B-KO)
MAP1A	2.819528308	5.133741995
NEFM	3.394813846	4.941871213
UBQLN1		3.995022287
RPS27A		3.934867238
MAP1LC3B2	1.522064348	3.71210596
GABARAPL1	1.99152886	3.659882764
RNF103-CHMP3		3.639505393
MAP1LC3B	1.32870735	3.462988691
PIM2		3.382259396
ULK1	0.919289577	3.324693815
ATP6V0E1		3.221928671
ATP6V1H		3.166815336
RAB1B		3.137423089
ASB2	2.662655382	2.893258883
ATP6V1B2		2.861092976
UCHL1	2.379741454	2.853948262
KCNK3	3.415669658	2.834592736
SNRPB2		2.788074521
UBC	0.768844925	2.728165062
SNRPF	-1.416871476	2.672164231
SNAPIN		2.620119022
TOMM7		2.591700883
FXR2		2.546084493
CAPN1		2.519737822
NHLRC1	2.749877315	2.513795629
HSP90AA1	1.992149166	2.504001295
ULK3		2.502937252
TMEM59		2.485692846
ZDHHC8		2.448513285
ERN1	1.188074995	2.446119764
ATG16L2		2.414940056
ATP6V1E1		2.37561804
YIPF1		2.347528243
PI4K2A		2.341573516
LAMTOR3		2.306306849
ATP6V1G1		2.286736142
RHEB		2.273360208

VPS26A		2.250928841
UBB		2.203317304
SESN2	2.203416648	2.163096897
ATP6V1D	1.093045873	2.157841123
TOMM70A		2.148704532
RAB1A		2.131124552
ZBTB17		2.120352631
VPS25		2.10344121
PFKP	1.437374509	2.0835823
U2AF1		2.063177239
COX8A		2.039100402
ATG4A		2.022595971
P2RX5		1.967088143
DAPK3		1.953141207
NUP93	-1.255391445	1.949310999
EMC6		1.894358845
ATP6V0B	1.082550544	1.872234838
TOMM40	-1.224150789	1.835390231
SNRPB		1.798506296
HMGB1		1.797107046
CD163L1		1.777355652
BNIP3L		1.76250051
RRAGC	0.741668762	1.731154812
SREBF2	-0.97311099	1.725253147
VPS37A		1.717926838
ATP6V1A		1.70830926
NDUFB9		1.684881879
SIRT1		1.637825178
CAPNS1		1.620936874
VMP1	0.623331091	1.618361606
ATP6V0A1	1.153896475	1.601853819
VPS4B	0.773137518	1.597846534
SNRPD1		1.585262917
CHMP4B		1.583917557
EXOC8		1.564259986
HIST1H3D		1.544530864
IST1		1.536157095
CISD2		1.528316856
MAP2K1		1.510752336
RAB12		1.503375218
LAMP1		1.489583162
WDR45		1.481997814
ATP6V1C1		1.4693747
LAMP2		1.451970475
FAM13B	1.660615236	1.444574531
PLOD2	-1.254466059	1.408550345

LAMTOR1		1.406655408
SNX14		1.386526288
USP10		1.384602706
CALCOCO2		1.379733845
ZFYVE1		1.368890467
SQSTM1	2.940783004	1.358516268
USP30		1.339461497
RFWD3		1.32958772
MTMR14	0.729024614	1.305207248
IPPK		1.250148296
RAB7A	0.542537386	1.243443767
CDK5R1	-1.013655328	1.219300607
C6orf106		1.204953272
RRAGA		1.201783049
CDC37		1.200532137
UBQLN2		1.192569396
SUPT3H		1.1864235
RBM18		1.177303573
TRAPPC8	0.867418045	1.16680844
PINK1		1.161312007
HGS	1.04812842	1.157583517
TBC1D25		1.142821449
CTSD		1.102286196
ANXA5		1.100929193
CHMP3		1.094769168
GABARAPL2		1.093823344
BLOC1S1	-1.045468826	1.064596416
MDH1	-1.04107388	1.053536946
ATG2A	0.985023815	1.045394475
SIRT2		1.043399186
VPS33A		1.035254788
MRPS2		1.03324963
VPS11		1.023044152
VTA1		1.023009905
STAM2		1.014632396
CHMP2B		1.013317141
EPG5		0.999043223
RB1CC1		0.997904431
ATG14		0.989595801
VCP	1.116471208	0.977307752
ABL1		0.913246899
ATG4D		0.900414842
MFN1		0.885748844
LARP1B		0.879709925
PIK3CA		0.875984307
FBXO7	-1.242082554	0.872034883

TMEM208		0.864227583
RPL28		0.846470904
ATG5		0.810730323
C12orf44		0.790244512
PRKAA2		0.786605948
MAP1S		0.781054356
SNF8		0.747574778
WBP11	0.831404756	0.736688597
NPC1		0.68243368
MTDH		0.676688003
CSNK2A2	-0.703149684	0.67345737
CLEC16A		0.656265949
TMBIM6		0.65522552
PRKAG1		0.555964718
VTI1B	-0.703783794	-0.579065492
SNAP29		-0.654614101
VDAC1		-0.686391805
TBC1D5		-0.73817917
MTOR		-0.78666784
CHMP6		-0.801829383
HK2	-0.998689054	-0.814607321
WIPI2		-0.843301852
STK11		-0.844420371
CTSA		-0.893578949
STOM		-0.913877757
LRSAM1		-0.991550383
GABARAP		-1.005084025
RIMS3		-1.016939364
KRCC1		-1.144440894
HDAC6		-1.292276202
FIS1		-1.342481697
SPATA18	-2.70199473	-1.356989533
VPS41		-1.374565964
EI24	-0.752242692	-1.402717533
TP53INP2	-1.288171788	-1.414366967
ATG10		-1.45543086
REEP2	-0.918993944	-1.570278044
VPS18	1.003122464	-1.60593021
TM9SF1		-1.637266958
STX17		-1.70432167
TOLLIP		-1.944064216
NTHL1		-2.100361414
TXLNA		-2.205919804
PPARGC1A	-2.178925607	-2.369344725
HIST1H3C		-2.394394413
TOMM5		-2.434658521

PHYHIP		-2.45331985
MLST8		-2.453492994
TFEB		-2.493901854
CHST3		-2.555270827
C1orf210		-2.775917715
SCN1A	-1.598470633	-3.145702505
VPS37D		-3.374025602
OBSCN		-4.237984392
HIST1H3H		-5.423914879
MYH11	3.77605636	
HSPA8	1.727025877	
RRAGD	1.662803197	
VPS37B	1.607711049	
SLC1A4	1.424189018	
SMURF1	1.318073771	
TRIM5	1.255085371	
ACIN1	1.150634407	
ZCCHC17	0.968142756	
PHF23	0.917418587	
STAM	0.812866667	
DYNLL2	0.770150796	
RNF41	0.721328945	
CHMP4C	0.702817157	
TP53INP1	0.699963736	
EIF2S1	0.664880571	
BNIP3	-0.675323057	
TOMM20	-0.722652831	
C5	-0.749475122	
PEX13	-0.80427699	
NBR1	-0.932425843	
FANCL	-0.942315175	
ARSB	-0.975772529	
PDK1	-0.989477493	
MTSS1	-1.032131754	
TOMM22	-1.046350342	
SLC37A4	-1.046750632	
DYNLL1	-1.097735693	
LSM4	-1.11364342	
PRKAB2	-1.12047822	
PNPO	-1.13333008	
MYLK	-1.478056589	
TMEM39B	-1.489747779	
FANCF	-1.62338914	
TMEM203	-1.688387327	
USP13	-1.751892005	
FABP1	-2.563270786	

SUPPLEMENTARY TABLE 8

Relevance of Cu-sensitive autophagic genes to TFEB.

All the autophagic genes from **Supplementary Table 7** were linked to TFEB. For each gene we verified whether any regulation of the gene by TFEB was reported in published microarray experiments (refer to specific GEO accession number) and whether direct binding of TFEB to the gene promoter was detected by ChIP-seq (Palmieri et al., HMG 2011). The reported up-regulation or down-regulation by TFEB in published microarrays experiment (last column) is highlighted in red or in green, respectively.

Autophagic genes	logFC (WT+Cu vs WT)	logFC (ATP7B-KO+Cu vs ATP7B-KO)	Direct target of TFEB in ChIP-Seq experiments	Regulated by TFEB in published microarray data
ABL1		0.913246899	NO	NO
ACIN1	1.150634407		NO	NO
ANXA5		1.100929193	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
ARSB	-0.975772529		NO	NO
ASB2	2.662655382	2.893258883	NO	NO
ATG10		-1.45543086	NO	TFEB LIVER - (GSE35015)
ATG14		0.989595801	NO	NO
ATG16L2		2.414940056	NO	NO
ATG2A	0.985023815	1.045394475	NO	NO
ATG4A		2.022595971	NO	NO
ATG4D		0.900414842	NO	TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
ATG5		0.810730323	YES	NO
ATP6V0A1	1.153896475	1.601853819	NO	TFEB Hela - (GSE16267) TFEB MUSCLE - (GSE62975)
ATP6V0B	1.082550544	1.872234838	YES	TFEB LIVER - (GSE35015) TFEB Hela - (GSE16267) TFEB KIDNEY - KSP_P14 (GSE63376)
ATP6V0E1		3.221928671	YES	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
ATP6V1A		1.70830926	YES	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
ATP6V1B2		2.861092976	NO	TFEB LIVER - (GSE35015) TFEB Hela - (GSE16267) TFEB MUSCLE - (GSE62975)
ATP6V1C1		1.4693747	YES	TFEB LIVER - (GSE35015) TFEB Hela - (GSE16267) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P0 (GSE63376)
ATP6V1D	1.093045873	2.157841123	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
ATP6V1E1		2.37561804	YES	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
ATP6V1G1		2.286736142	YES	TFEB KIDNEY - KSP_P14 (GSE63376)
ATP6V1H		3.166815336	YES	TFEB Hela - (GSE16267) TFEB MUSCLE - KO(GSE62976) TFEB MUSCLE - (GSE62975)
BLOC1S1	-1.045468826	1.064596416	YES	NO
BNIP3	-0.675323057		NO	TFEB MUSCLE - (GSE62975)
BNIP3L		1.76250051	NO	TFEB KIDNEY - KSP_P14 (GSE63376)
C12orf44 (ATG101)		0.790244512	NO	NO
C1orf210		-2.775917715	NO	NO
C5	-0.749475122		NO	TFEB LIVER - (GSE35015)
C6orf106		1.204953272	NO	NO
CALCOCO2		1.379733845	NO	NO
CAPN1		2.519737822	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
CAPNS1		1.620936874	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
CD163L1		1.777355652	NO	NO
CDC37		1.200532137	NO	TFEB KIDNEY - KSP_P14 (GSE63376)
CDK5R1	-1.013655328	1.219300607	NO	TFEB MUSCLE - (GSE62975)
CHMP2B		1.013317141	NO	NO
CHMP3		1.094769168	NO	NO
CHMP4B		1.583917557	NO	NO
CHMP4C	0.702817157		NO	NO
CHMP6		-0.801829383	NO	TFEB LIVER - (GSE35015)
CHST3		-2.555270827	NO	NO
CISD2		1.528316856	NO	NO
CLEC16A		0.656265949	NO	TFEB LIVER - (GSE35015)

COX8A		2.039100402	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
CSNK2A2	-0.703149684	0.67345737	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
CTSA		-0.893578949	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
CTSD		1.102286196	NO	TFEB Hela - (GSE16267) TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P0 (GSE63376) TFEB KIDNEY - KSP_P14 (GSE63376)
DAPK3		1.953141207	NO	NO
DYNLL1	-1.097735693		NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
DYNLL2	0.770150796		NO	TFEB LIVER - (GSE35015)
EI24	-0.752242692	-1.402717533	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
EIF2S1	0.664880571		NO	TFEB MUSCLE - (GSE62975)
EMC6		1.894358845	NO	NO
EPG5		0.999043223	NO	NO
ERN1	1.188074995	2.446119764	NO	NO
EXOC8		1.564259986	NO	NO
FABP1	-2.563270786		NO	TFEB LIVER - (GSE35015)
FAM13B	1.660615236	1.444574531	NO	TFEB MUSCLE - (GSE62975)
FANCF	-1.62338914		NO	NO
FANCL	-0.942315175		NO	NO
FBXO7	-1.242082554	0.872034883	NO	NO
FIS1		-1.342481697	NO	NO
FXR2		2.546084493	NO	NO
GABARAP		-1.005084025	YES	TFEB LIVER - (GSE35015)
GABARAPL1	1.99152886	3.659882764	YES	TFEB LIVER - (GSE35015) TFEB KIDNEY - KSP_P14 (GSE63376)
GABARAPL2		1.093823344	NO	NO
HDAC6		-1.292276202	NO	NO
HGS	1.04812842	1.157583517	NO	TFEB MUSCLE - (GSE62975)
HIST1H3C		-2.394394413	NO	NO
HIST1H3D		1.544530864	NO	NO
HIST1H3H		-5.423914879	NO	NO
HK2	-0.998689054	-0.814607321	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P0 (GSE63376)
HMGB1		1.797107046	NO	TFEB MUSCLE - (GSE62975)
HSP90AA1	1.992149166	2.504001295	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P0 (GSE63376)
HSPA8	1.727025877		NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB MUSCLE - KO(GSE62976) TFEB KIDNEY - KSP_P14 (GSE63376)
IPPK		1.250148296	NO	NO
IST1		1.536157095	NO	NO
KCNK3	3.415669658	2.834592736	NO	TFEB LIVER - (GSE35015)
KRCC1		-1.144440894	NO	NO
LAMP1		1.489583162	YES	TFEB Hela - (GSE16267) TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
LAMP2		1.451970475	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB MUSCLE - KO(GSE62976) TFEB KIDNEY - KSP_P14 (GSE63376)
LAMTOR1		1.406655408	NO	NO
LAMTOR3		2.306306849	NO	NO
LARP1B		0.879709925	NO	TFEB MUSCLE - (GSE62975)
LRSAM1		-0.991550383	NO	NO
LSM4	-1.11364342		NO	TFEB MUSCLE - (GSE62975)
MAP1A	2.819528308	5.133741995	NO	NO
MAP1LC3B	1.32870735	3.462988691	NO	NO
MAP1LC3B2	1.522064348	3.71210596	NO	NO
MAP1S		0.781054356	YES	NO
MAP2K1		1.510752336	NO	NO
MDH1	-1.04107388	1.053536946	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB MUSCLE - KO(GSE62976)
MFN1		0.885748844	NO	TFEB LIVER - (GSE35015)

				TFEB MUSCLE - KO(GSE62976)
MLST8		-2.453492994	NO	TFEB KIDNEY - KSP_P14 (GSE63376)
MRPS2		1.03324963	NO	TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P0 (GSE63376) TFEB KIDNEY - KSP_P14 (GSE63376)
MTDH		0.676688003	NO	TFEB MUSCLE - (GSE62975)
MTMR14	0.729024614	1.305207248	NO	NO
MTOR		-0.78666784	NO	NO
MTSS1	-1.032131754		NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
MYH11	3.77605636		NO	TFEB MUSCLE - KO(GSE62976)
MYLK	-1.478056589		NO	TFEB MUSCLE - KO(GSE62976)
NBR1	-0.932425843		NO	TFEB LIVER - (GSE35015)
NDUFB9		1.684881879	NO	TFEB LIVER - (GSE35015)
NEFM	3.394813846	4.941871213	NO	NO
NHLRC1	2.749877315	2.513795629	NO	NO
NPC1		0.68243368	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB MUSCLE - KO(GSE62976)
NTHL1		-2.100361414	YES	NO
NUP93	-1.255391445	1.949310999	NO	TFEB MUSCLE - (GSE62975)
OBSCN		-4.237984392	NO	NO
P2RX5		1.967088143	NO	NO
PDK1	-0.989477493		NO	TFEB LIVER - (GSE35015)
PEX13	-0.80427699		NO	TFEB MUSCLE - (GSE62975)
PFKP	1.437374509	2.0835823	NO	TFEB LIVER - (GSE35015) TFEB KIDNEY - KSP_P14 (GSE63376)
PHF23	0.917418587		NO	NO
PHYHIP		-2.45331985	NO	NO
PI4K2A		2.341573516	NO	TFEB LIVER - (GSE35015)
PIK3CA		0.875984307	NO	TFEB MUSCLE - (GSE62975)
PIM2		3.382259396	NO	NO
PINK1		1.161312007	NO	TFEB MUSCLE - (GSE62975)
PLOD2	-1.254466059	1.408550345	NO	TFEB MUSCLE - (GSE62975)
PNPO	-1.13333008		YES	TFEB LIVER - (GSE35015)
PPARGC1A	-2.178925607	-2.369344725	YES	TFEB Hela - (GSE16267) TFEB LIVER - (GSE35015) TFEB KIDNEY - KSP_P0 (GSE63376) TFEB KIDNEY - KSP_P14 (GSE63376)
PRKAA2		0.786605948	NO	NO
PRKAB2	-1.12047822		NO	NO
PRKAG1		0.555964718	NO	NO
RAB12		1.503375218	NO	TFEB MUSCLE - (GSE62975)
RAB1A		2.131124552	NO	NO
RAB1B		3.137423089	NO	NO
RAB7A	0.542537386	1.243443767	YES	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
RB1CC1		0.997904431	NO	TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
RBM18		1.177303573	YES	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
REEP2	-0.918993944	-1.570278044	NO	NO
RFWD3		1.32958772	NO	NO
RHEB		2.273360208	NO	TFEB MUSCLE - (GSE62975)
RIMS3		-1.016939364	NO	NO
RNF103-CHMP3		3.639505393	NO	NO
RNF41	0.721328945		NO	TFEB MUSCLE - (GSE62975)
RPL28		0.846470904	NO	NO
RPS27A		3.934867238	NO	TFEB MUSCLE - (GSE62975)
RRAGA		1.201783049	NO	NO
RRAGC	0.741668762	1.731154812	YES	TFEB Hela - (GSE16267) TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
RRAGD	1.662803197		NO	TFEB MUSCLE - (GSE62975)
SCN1A	-1.598470633	-3.145702505	NO	NO
SESN2	2.203416648	2.163096897	NO	TFEB LIVER - (GSE35015)
SIRT1		1.637825178	YES	NO
SIRT2		1.043399186	NO	TFEB LIVER - (GSE35015)
SLC1A4	1.424189018		NO	TFEB LIVER - (GSE35015)
SLC37A4	-1.046750632		NO	TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
SMURF1	1.318073771		NO	NO
SNAP29		-0.654614101	NO	TFEB MUSCLE - (GSE62975)

SNAPIN		2.620119022	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
SNF8		0.747574778	NO	TFEB MUSCLE - (GSE62975)
SNRPB		1.798506296	NO	TFEB MUSCLE - (GSE62975)
SNRPB2		2.788074521	NO	TFEB MUSCLE - (GSE62975)
SNRPD1		1.585262917	NO	TFEB LIVER - (GSE35015)
SNRPF	-1.416871476	2.672164231	NO	NO
SNX14		1.386526288	NO	NO
SPATA18	-2.70199473	-1.356989533	NO	NO
SQSTM1	2.940783004	1.358516268	NO	NO
SREBF2	-0.97311099	1.725253147	NO	TFEB LIVER - (GSE35015)
STAM	0.812866667		NO	NO
STAM2		1.014632396	NO	TFEB MUSCLE - (GSE62975)
STK11		-0.844420371	NO	TFEB MUSCLE - (GSE62975)
STOM		-0.913877757	NO	TFEB Hela - (GSE16267) TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
STX17		-1.70432167	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
SUPT3H		1.1864235	NO	NO
TBC1D25		1.142821449	NO	NO
TBC1D5		-0.73817917	NO	NO
TFEB		-2.493901854	NO	TFEB Hela - (GSE16267) TFEB MUSCLE - (GSE62975) TFEB MUSCLE - KO(GSE62976)
TM9SF1		-1.637266958	NO	TFEB MUSCLE - (GSE62975)
TMBIM6		0.65522552	NO	NO
TMEM203	-1.688387327		NO	NO
TMEM208		0.864227583	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - KO(GSE62976)
TMEM39B	-1.489747779		NO	NO
TMEM59		2.485692846	NO	NO
TOLLIP		-1.944064216	NO	TFEB MUSCLE - KO(GSE62976)
TOMM20	-0.722652831		YES	TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
TOMM22	-1.046350342		NO	NO
TOMM40	-1.224150789	1.835390231	NO	NO
TOMM5		-2.434658521	NO	TFEB MUSCLE - (GSE62975)
TOMM7		2.591700883	NO	NO
TOMM70A		2.148704532	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
TP53INP1	0.699963736		YES	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB MUSCLE - KO(GSE62976)
TP53INP2	-1.288171788	-1.414366967	NO	TFEB MUSCLE - (GSE62975)
TRAPPC8	0.867418045	1.16680844	NO	NO
TRIM5	1.255085371		NO	TFEB MUSCLE - (GSE62975)
TXLNA		-2.205919804	NO	NO
U2AF1		2.063177239	NO	NO
UBB		2.203317304	NO	NO
UBC	0.768844925	2.728165062	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975) TFEB KIDNEY - KSP_P14 (GSE63376)
UBQLN1		3.995022287	NO	NO
UBQLN2		1.192569396	NO	TFEB MUSCLE - (GSE62975)
UCHL1	2.379741454	2.853948262	NO	TFEB MUSCLE - (GSE62975)
ULK1	0.919289577	3.324693815	NO	TFEB MUSCLE - (GSE62975)
ULK3		2.502937252	NO	NO
USP10		1.384602706	NO	TFEB MUSCLE - (GSE62975)
USP13	-1.751892005		NO	TFEB MUSCLE - (GSE62975)
USP30		1.339461497	NO	NO
VCP	1.116471208	0.977307752	NO	NO
VDAC1		-0.686391805	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
VMP1	0.623331091	1.618361606	NO	NO
VPS11		1.023044152	YES	TFEB Hela - (GSE16267)
VPS18	1.003122464	-1.60593021	YES	TFEB Hela - (GSE16267) TFEB LIVER - (GSE35015)
VPS25		2.10344121	NO	TFEB MUSCLE - (GSE62975) TFEB MUSCLE - KO(GSE62976) TFEB KIDNEY - KSP_P14 (GSE63376)
VPS26A		2.250928841	YES	TFEB LIVER - (GSE35015)
VPS33A		1.035254788	YES	NO

VPS37A		1.717926838	NO	TFEB MUSCLE - (GSE62975)
VPS37B	1.607711049		NO	NO
VPS37D		-3.374025602	NO	NO
VPS41		-1.374565964	NO	TFEB LIVER - (GSE35015) TFEB MUSCLE - (GSE62975)
VPS4B	0.773137518	1.597846534	NO	TFEB MUSCLE - KO(GSE62976)
VTA1		1.023009905	NO	NO
VTI1B	-0.703783794	-0.579065492	NO	TFEB MUSCLE - (GSE62975)
WBP11	0.831404756	0.736688597	NO	NO
WDR45		1.481997814	NO	NO
WIPI2		-0.843301852	NO	NO
YIPF1		2.347528243	NO	NO
ZBTB17		2.120352631	NO	NO
ZCCHC17	0.968142756		NO	NO
ZDHHC8		2.448513285	NO	TFEB MUSCLE - (GSE62975)
ZFYVE1		1.368890467	NO	NO

SUPPLEMENTARY TABLE 9

List of mitophagy-relevant genes, which were up-regulated in response to Cu.

The table shows Cu-sensitive genes with a known role in mitophagy and in mitochondria damage that were indeced in ATP7B-deficient HepG2 cells (ATP7B-KO+Cu vs ATP7B-KO) and in control HepG2 cells (WT+Cu vs WT). For each gene, the specific GO sub-category of mitophagy-relevant process is indicated. Among these genes 10 were up-regulated in both cell types, 11 only in control cells and 43 exclusively in ATP7B-KO cells.

Mitophagy genes	logFC (WT+Cu vs WT)	logFC (ATP7B-KO+Cu vs ATP7B-KO)	GO Category
MLLT11	5.321958261	5.335027834	Positive regulation of release of cytochrome c from mitochondria
MAP1A	2.819528308	5.133741995	MACROMITOPHAGY
NEFM	3.394813846	4.941871213	MACROMITOPHAGY
MAP1LC3B	1.32870735	3.462988691	REGULATION_OF_MITOPHAGY
ASB2	2.662655382	2.893258883	MACROMITOPHAGY
KCNK3	3.415669658	2.834592736	MACROMITOPHAGY
SNRPF		2.672164231	MACROMITOPHAGY
TOMM7		2.591700883	MACROMITOPHAGY
ZDHHC8		2.448513285	REGULATION_OF_MITOPHAGY
YIPF1		2.347528243	MACROMITOPHAGY
PI4K2A		2.341573516	MACROMITOPHAGY
ZBTB17		2.120352631	REGULATION_OF_MITOPHAGY
PFKP	1.437374509	2.0835823	MACROMITOPHAGY
U2AF1		2.063177239	REGULATION_OF_MITOPHAGY
COX8A		2.039100402	MACROMITOPHAGY
PDCD5		2.035216943	Positive regulation of release of cytochrome c from mitochondria
P2RX5		1.967088143	MACROMITOPHAGY
NUP93		1.949310999	MACROMITOPHAGY
BBC3		1.871835823	Positive regulation of release of cytochrome c from mitochondria
SNRPB		1.798506296	MACROMITOPHAGY
CD163L1		1.777355652	MACROMITOPHAGY
BNIP3L		1.76250051	REGULATION_OF_MITOPHAGY
PLAUR		1.740177813	Positive regulation of release of cytochrome c from mitochondria
SREBF2		1.725253147	REGULATION_OF_MITOPHAGY
NDUFB9		1.684881879	MACROMITOPHAGY
PPIF		1.651024929	Positive regulation of release of cytochrome c from mitochondria
SNRPD1		1.585262917	MACROMITOPHAGY
IST1		1.536157095	MACROMITOPHAGY
FAM162A		1.520186383	Positive regulation of release of cytochrome c from mitochondria
MAP2K1		1.510752336	MACROMITOPHAGY
BAK1		1.44459274	Positive regulation of release of cytochrome c from mitochondria
FAM13B	1.660615236	1.444574531	MACROMITOPHAGY
PLOD2		1.408550345	MACROMITOPHAGY
BID		1.408394824	Positive regulation of release of cytochrome c from mitochondria
SQSTM1	2.940783004	1.358516268	MACROMITOPHAGY
RFWD3		1.32958772	MACROMITOPHAGY
MOAP1		1.318074037	Positive regulation of release of cytochrome c from mitochondria
IPPK		1.250148296	MACROMITOPHAGY
CDC37		1.200532137	MACROMITOPHAGY
SUPT3H		1.1864235	MACROMITOPHAGY
PINK1		1.161312007	Positive regulation of release of cytochrome c from mitochondria
ANXA5		1.100929193	MACROMITOPHAGY
BLOC1S1		1.064596416	MACROMITOPHAGY
MDH1		1.053536946	MACROMITOPHAGY
MRPS2		1.03324963	MACROMITOPHAGY
ATG14		0.989595801	MACROMITOPHAGY
LARP1B		0.879709925	MACROMITOPHAGY
PIK3CA		0.875984307	MACROMITOPHAGY
RPL28		0.846470904	REGULATION_OF_MITOPHAGY
ATG5		0.810730323	REGULATION_OF_MITOPHAGY
WBP11	0.831404756	0.736688597	REGULATION_OF_MITOPHAGY
CSNK2A2		0.67345737	REGULATION_OF_MITOPHAGY
GSK3A		0.571046261	REGULATION_OF_MITOPHAGY
ACIN1	1.150634407		MACROMITOPHAGY
EIF2S1	0.664880571		MACROMITOPHAGY
FAS	1.373343015		Positive regulation of release of cytochrome c from mitochondria
FBXW7	0.6921135		REGULATION_OF_MITOPHAGY
HIF1A	0.987873664		REGULATION_OF_MITOPHAGY
MYH11	3.77605636		MACROMITOPHAGY
SLC1A4	1.424189018		MACROMITOPHAGY
SMURF1	1.318073771		MACROMITOPHAGY
USP36	1.037318957		REGULATION_OF_MITOPHAGY
WDR35	1.623745194		Positive regulation of release of cytochrome c from mitochondria
ZCCHC17	0.968142756		MACROMITOPHAGY