SUPPLEMENTAL INFORMATION TO

Combinatorial regulation of cytoplasmic signaling and nuclear transcriptional events by the OGT/REV-ERBα complex.

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www.pnas.org/cgi/doi/10.1073/pnas.1805397115

SUPPLEMENTAL FIGURES

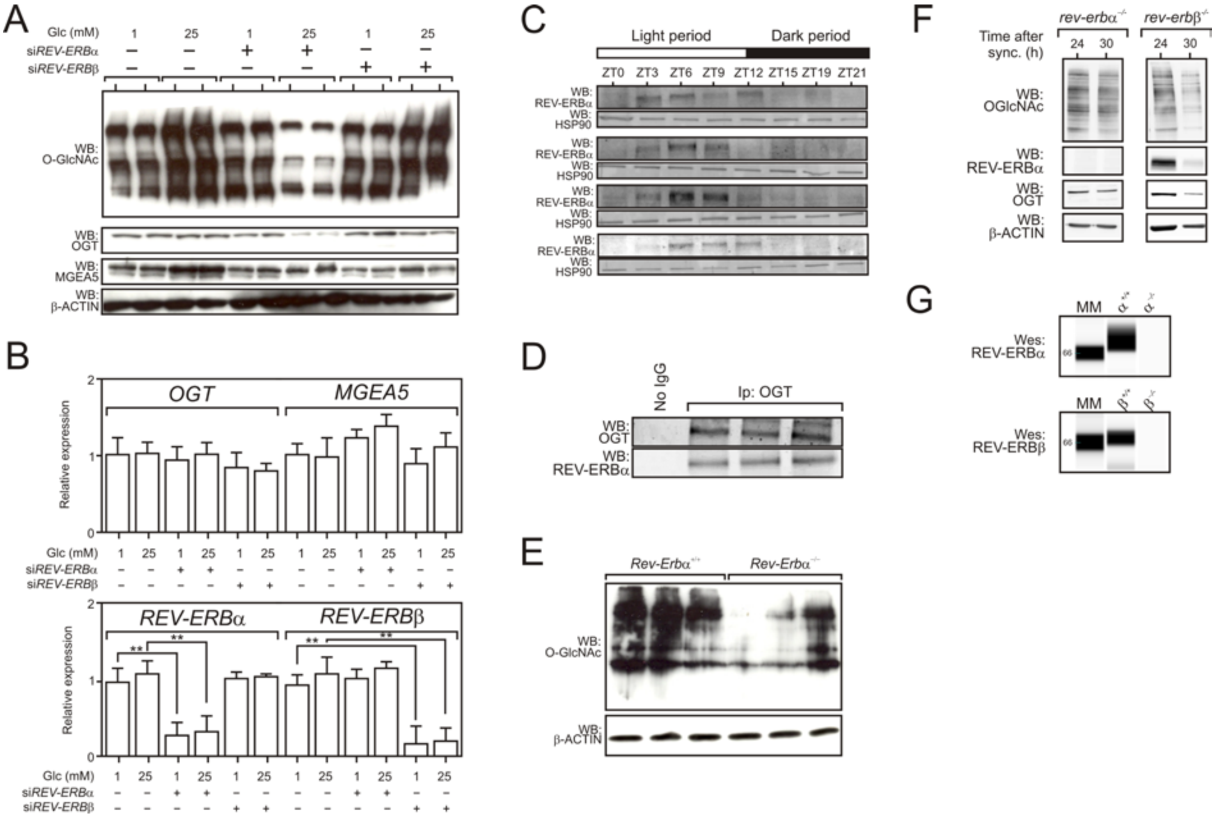

Fig. S1, related to Figure 1: OGT protein level and activity are stabilized by REV-ERBα but not by REV-ERBβ. A: Protein O-GlcNAcylation, OGT and OGA (MGEA5) protein levels were determined by western blotting (WB) of HepG2 whole cell extracts. HepG2 cells were transfected with siRNAs (targeting *REV-ERBα and REV-ERBβ*) and incubated for 24h at low (1 mM) or high (25 mM) glucose (Glc) concentration. B: Gene expression was determined by RT-qPCR analysis of total RNA extracted from siRNA-transfected HepG2 cells. Data are expressed relative to RNA amounts in siRNA control-transfected HepG2 cells incubated at 1 mM Glc. C: The hepatic REV-ERBα protein level in *ad libitum* fed mice was determined by western blot (WB) as a function of time. D: REV-ERBα interacts with OGT in mouse liver. Mouse liver extracts were immunoprecipitated with anti-OGT antibody and immunoprecipitates were analyzed by WB using anti-OGT and anti-REV-ERBα antibodies. E: O-GlcNAcylation level determined by WB for WT or *Rev-erbα* KO mouse liver at ZT6 (1). F: O-GlcNAcylation, REV-ERBα and OGT protein levels in *REV-ERBα* or *REV-ERBβ*-deficient U2OS cells 24 and 30 hours after synchronisation. G: CRISPR-generated *REV-ERBα* and *REV-ERBβ*-deficient U2OS clone validation by Simple Western (Wes). Statistical analysis: B: Histograms correspond to mean +/-SEM. The statistical significance was assessed by 2-way ANOVA followed by a Bonferroni post hoc test. **p<0.01.

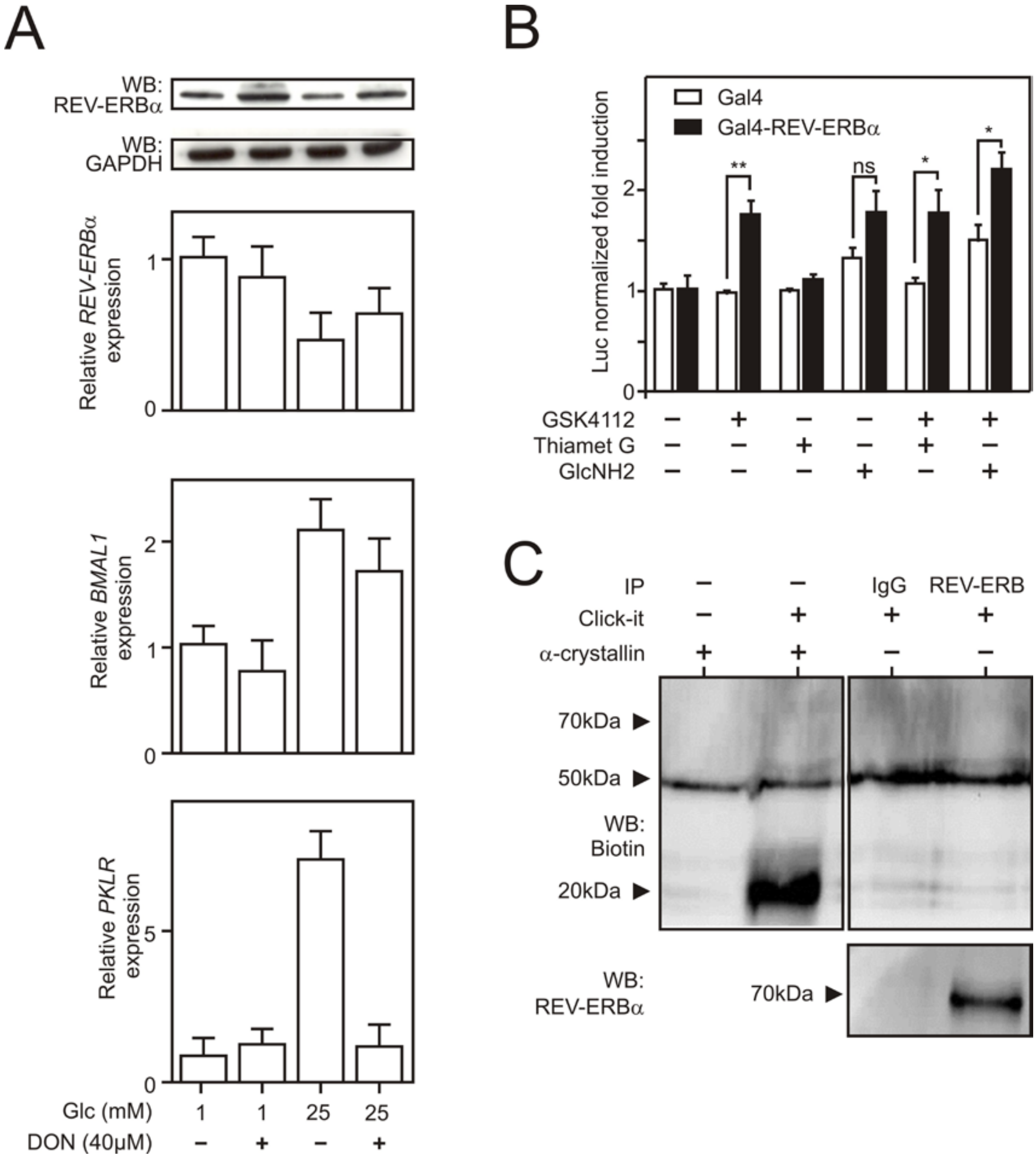

Fig. S2, related to Figure 1: REV-ERBα is not O-GlcNAcylated. A: HepG2 cells were cultured at 1 mM or 25 mM Glc and treated with 40 µM DON for 24 hours. REV-ERBα protein level was determined by western blot (WB) (top panel). *REV-ERBα*, *BMAL1* and *PKLR1* mRNAs were quantified using RT-qPCR (bottom panels). Data were expressed relative to mRNA amounts detected in control conditions (1mM Glc, no DON) arbitrarily set to 1. B: Mammalian 2-hybrid assay in HepG2 cells. After transfection with empty Gal4 or Gal4-REV-ERBα or VP16-NCOR expression vectors, Renilla normalization vector and luciferase-based reporter vector (pUAS-tk-Luc), cells were treated with 5 µM Thiamet G or 20 mM glucosamine in the presence or absence of 10 µM GSK 4112. Data were expressed relative to normalized RLU signals detected in control conditions (no treatment) arbitrarily set to 1. C: Click-it assay on immunoprecipitated REV-ERBα from HepG2 cell extracts or purified α-crystalin. Modified O-GlcNAcylated residues were detected using biotin western-blotting (WB). The presence of REV-ERBα was confirmed using WB (lower panel). Histograms represent mean +/-SEM.

The statistical significance of differences was assessed by a 2-way ANOVA followed by a Bonferroni post hoc test. *p<0.05, **p<0.01.

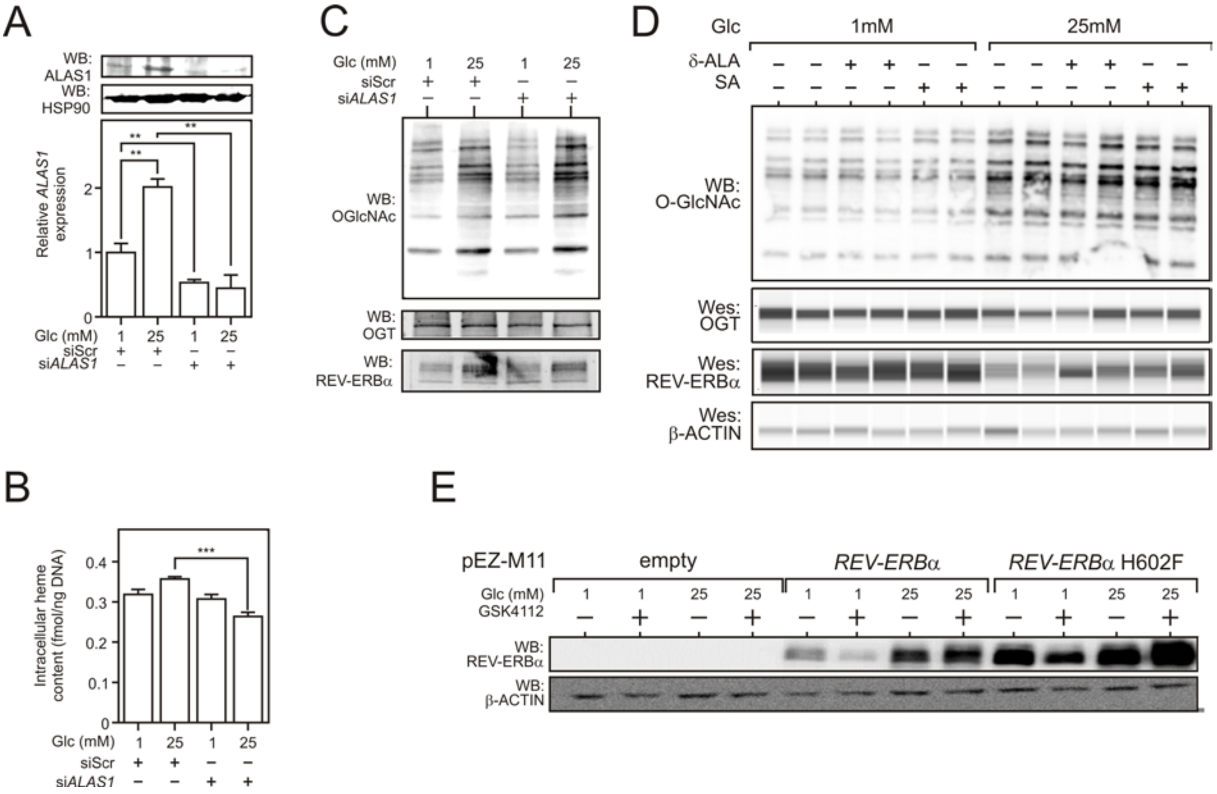

Fig. S3, related to Figure 2: Reduction of intracellular heme production increases O-GlcNAcylation. A: HepG2 cells were grown either in medium supplemented with 1 mM or 25 mM Glc and transfected either with a control siRNA (Scr) or with a siRNA targeting *ALAS1*. *ALAS1* knockdown was confirmed at the protein (top panel) and RNA (bottom panel) levels using western blot (WB) and RT-qPCR respectively. Data were expressed relative to RNA amount detected in siScr-transfected cells cultured in low Glc (1 mM) medium, which was arbitrarily set to 1. B: Determination of intracellular heme content after *ALAS1* knockdown. C: Protein O-GlcNAcylation, OGT and REV-ERBα protein levels in transfected HepG2 cells was determined by WB. D: O-GlcNAcylation, OGT and REV-ERBα protein levels after heme synthesis modulation in HepG2 cells treated with 0.1 mM δ-aminolevulinic acid (δ-ALA) or 0.5 mM succinylacetone (SA) at 1 mM or 25 mM Glc. E: REV-ERBα protein overexpression in HEK cells. REV-ERBα expression was assessed by WB. Cells were transfected with empty vector, *REV-ERBα* WT or *REV-ERBα* H602F mutant expression. Histograms represent mean +/-SEM. The statistical significance of differences was assessed by 2-way ANOVA followed by a Bonferroni post hoc test. **p<0.01, ***p<0.001.

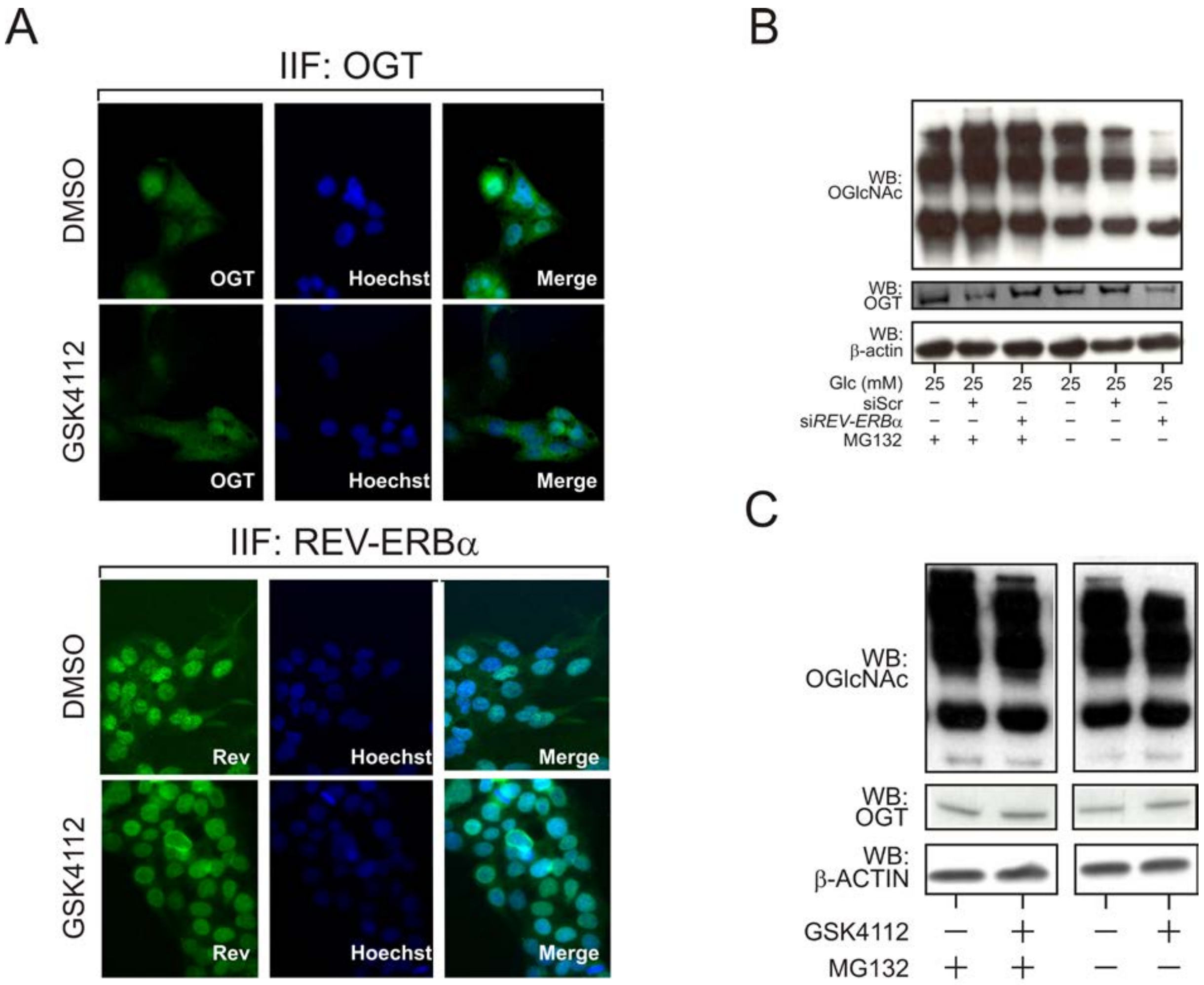

Fig. S4, related to Figure 3: GSK4112 favours REV-ERBα nuclear accumulation. A: Indirect immunofluorescence (IIF) detection of REV-ERBα and OGT in HepG2 cells cultured in 25 mM Glc and treated or not with 10 µM GSK4112. B: Protein O-GlcNAcylation and OGT protein level in HepG2 whole cell extracts. Cells were grown in medium supplemented with 25 mM Glc, transfected with the indicated siRNAs and treated with 10 µM GSK4112 in the presence or absence of 5 µM MG132. Protein O-GlcNAcylation, OGT and REV-ERBα were detected by western blot (WB). C: Protein O-GlcNAcylation and OGT protein level in HepG2 whole cell extracts. Cells were grown in medium supplemented with 25 mM Glc and treated as indicated with 10 µM GSK4112 in the presence or absence of 5 µM MG132.

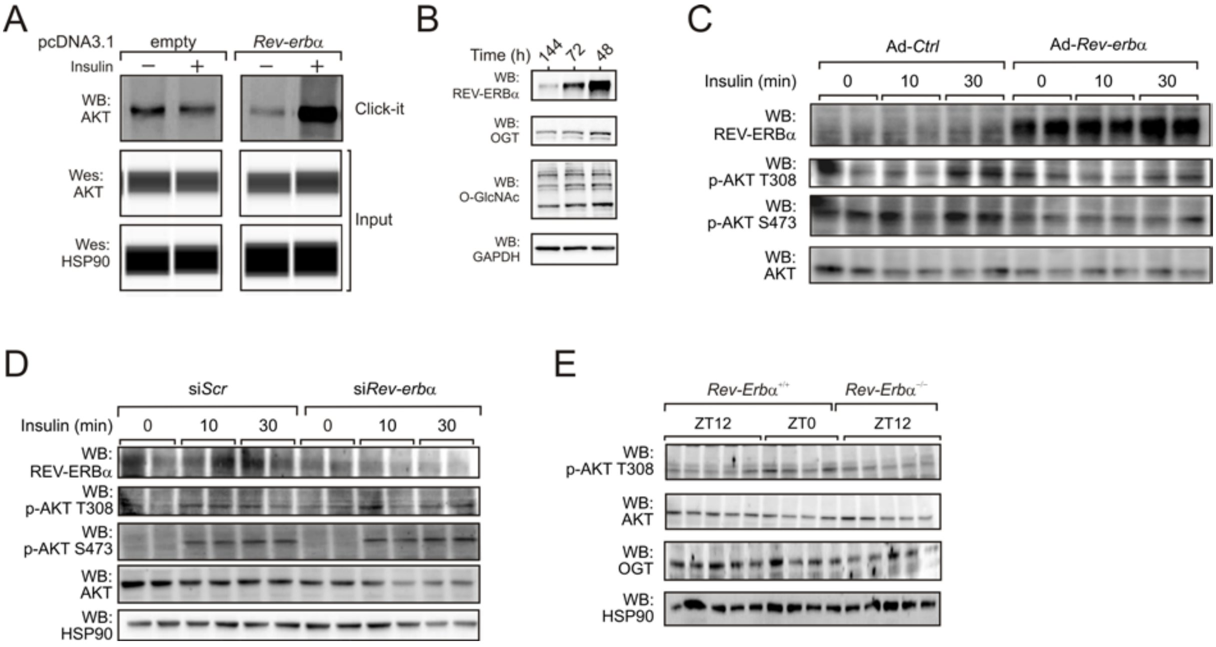

Fig. S5, related to Figure 5: *REV-ERBα* expression level affects both OGT protein level and AKT phosphorylation. A: AKT O-GlcNAcylation. HepG2 whole cell extracts were submitted to the Click-it chemical modification followed by streptavidin bead enrichment and AKT detection by western blotting (WB). Cells were co-transfected with AKT1 or REV-ERBα pcDNA3.1-based expression vectors. Twenty four hours after transfection, cells were maintained for 20 hours at 25 mM Glc without serum and treated for 10 min with 60 nM insulin. AKT and HSP90 (loading control) protein levels were determined by simple western (Wes). B: HepG2 cells were transduced with a *REV-ERBα*-encoding adenovirus and cultured for 48, 72 or 144h. REV-ERBα, OGT and O-GlcNAcylation content were determined by WB analysis. C: T308 and S473 AKT phosphorylation was determined by WB analysis of HepG2 cellular extracts after transduction with control or *REV-ERBα* adenoviruses and treatment with 60 nM insulin for the indicated durations. D: HepG2 cells were transfected with siRNA (Ctrl and *REV-ERBα*) and treated with 60 nM insulin for the indicated durations. REV-ERBα and AKT phosphorylation (T308 and S473) were determined by WB. E: Hepatic OGT protein level and AKT T308 phosphorylation were determined by WB from ad libitum fed *Rev-erbα*$^{+/+}$ (ZT12 and ZT0) and *Rev-erbα*$^{-/-}$ (ZT12) mice.

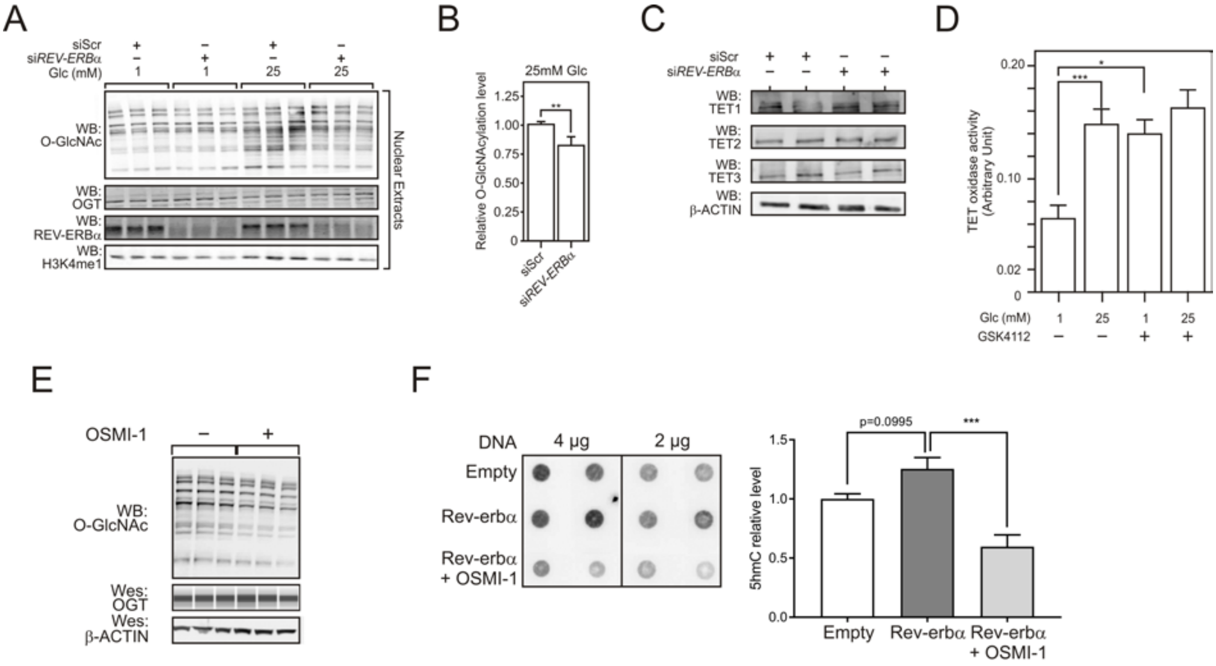

Fig. S6, related to Figure 6: REV-ERBα does not control TETs expression level but controls TET enzymatic activity. A: HepG2 nuclear protein O-GlcNAcylation, OGT and REV-ERBα protein levels were determined by western blotting (WB). Cells were transfected with siRNA [Scrambled (Scr) or targeting *REV-ERBα*] and incubated either at 1mM or 25mM Glc. A representative WB is shown. B: Densitometric quantification of nuclear protein O-GlcNacylation in control or REV-ERBα-depleted cells in 25mM Glc. The statistical significance was determined by a one-way t-test (n=5). C: HepG2 cells were transfected with siRNA (Scr or targeting *REV-ERBα*). TET1, TET2 and TET3 protein levels were determined by WB. D: HepG2 cells were grown in 1 mM or 25 mM Glc and treated with 10 µM GSK 4112. TET oxidase activities were determined in HepG2 nuclear extracts. E: Protein O-GlcNacylation and REV-ERBα expression were assayed by WB analysis in HepG2 cells grown at 1 mM Glc and treated or not overnight with the OGT inhibitor OSMI-1 (50 µM). F: HepG2 cells were transfected by control (empty) or *REV-ERBα*-encoding expression vectors. Cells were cultivated in 1 mM Glc and treated overnight with the OGT inhibitor OSMI-1 (50 µM) or vehicle (DMSO). DNA 5hmC content was assayed by dot blotting and quantified by densitometry. The statistical significance of differences was assessed by a 1-way ANOVA followed by a Bonferroni post hoc test *p<0.05, **p<0.01, ***p<0.001.

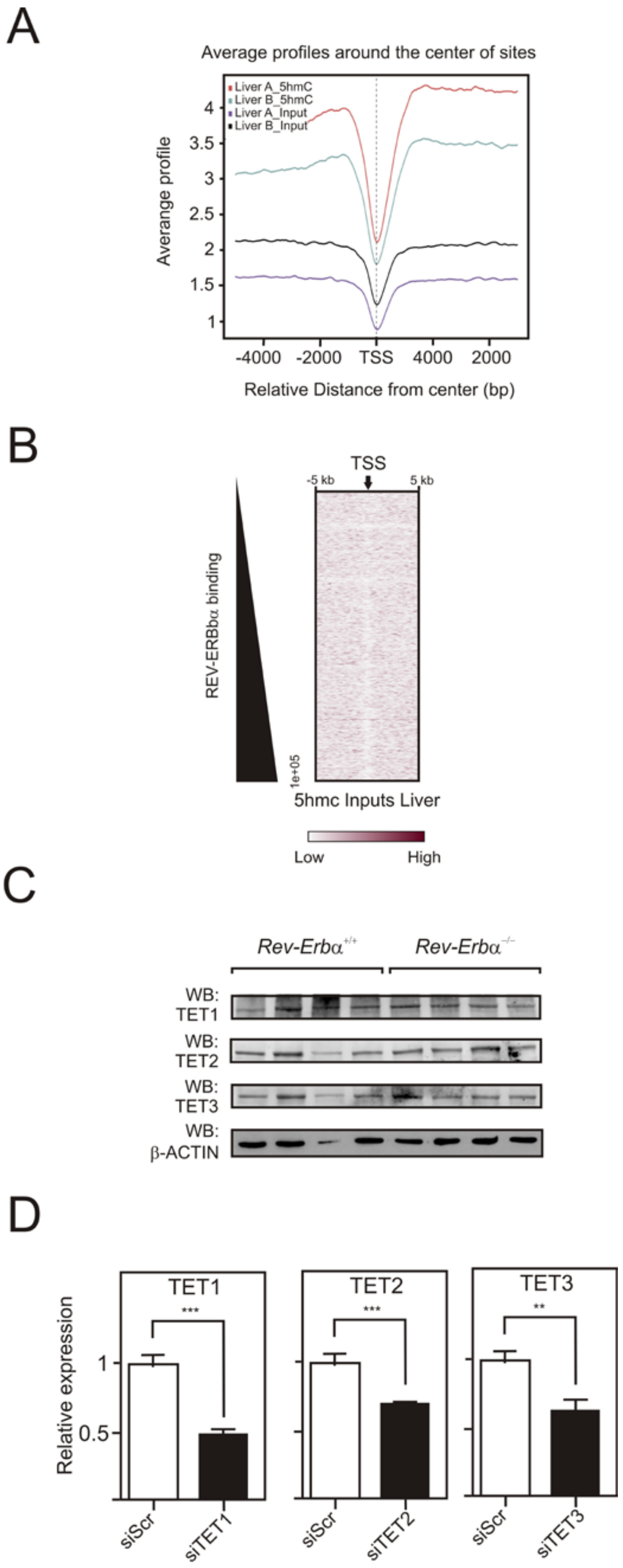

Fig. S7 Epigenomic features of mouse liver DNA and TET expression in HepG2 cells, related to Figure 6: A: Average 5hmC (red and green) and input (blue and black) ChIP-seq signal profiles on

Gencode Transcription Start Sites (TSS). TSS were aligned and regions extending 5 kb on each side were analyzed. B: Heatmaps represent input signal intensities in clusterized Gencode TSS. Gencode TSS (arrow) were aligned and extended 5 kb on each side. C: TET protein expression in Rev-erbα$^{-/-}$ and Reverbα$^{+/+}$ mouse livers. Whole tissue extracts were analyzed by WB. D: Relative expression of *TET1*, *TET2* and *TET3* were determined by qPCR on siRNA(Scr, *TET1*, *TET2* or *TET3*)-transfected HepG2 cells. Histogram represents mean +/-SEM. The statistical significance was assessed by 2-way ANOVA followed by a Bonferroni post hoc test. *p<0.05, ***p<0.001.

SUPPLEMENTARY MATERIAL AND METHODS

Rapid immunoprecipitation mass spectrometry of endogenous proteins (RIME)

RIME assay was performed as previously described (2). Briefly, 4 µg of rabbit monoclonal anti-REV-ERBα (#13418, Cell Signalling Technology), 10 µg of rabbit polyclonal anti-OGT (HPA030751, Sigma-Aldrich) or control rabbit IgG (sc-2027, Santa Cruz Biotechnology) were immobilized on SureBeads™ Protein A magnetic beads (Bio-Rad). HepG2 cells grown on P150 plates were cross-linked for 10 min with 1% formaldehyde at 37°C in DMEM. After quenching with 1.25 M glycine and nuclear protein extraction, samples were incubated overnight with immobilized antibodies at 4°C. Beads were washed with 1XRIPA buffer [50 mM HEPES (pH 7.6), 1 mM EDTA, 0.7% (v:v) sodium deoxycholate, 1% (v:v) NP-40 and 0.5 M LiCl] and then with 0.1 M ammonium hydrogen carbonate. Finally, beads were dried and flash frozen in liquid nitrogen, and LC-MS/MS analysis was performed to identify protein partners as follows. Tryptic digestion of bead-bound proteins was performed by adding 20 µL of trypsin (*Sus scrofa*, Promega) (10µg/mL in 50mM NH_4HCO_3) directly onto the washed beads. After brief vortexing, beads were incubated at 37°C overnight. Tubes were placed on a magnet to collect the supernatant which was directly placed into formic acid at a final concentration of 0.1%. Peptides were desalted with SPE (Ultra-Micro SpinColumn, Cole-Parmer, USA).

Tryptic digests were then analysed on a NanoAcquity (Waters) LC-system coupled to a Q-Exactive Plus orbitrap mass spectrometer (Thermo Fisher Scientific). The HPLC system consisted of a solvent degasser Nanoflow pump, a thermostated column oven kept at 60°C and a thermostated autosampler kept at 10°C. Mobile phase A (0.1% FA in water) and mobile phase B (0.1% FA in acetonitrile) were delivered at 450nL/min. Samples were loaded into a Symmetry C18 precolumn (0.18 x 20mm, 5 µm particle size, Waters) over 3 minutes in 1% B at a flow rate of 5µL/min. This step was followed by a reverse-phase separation using an ACQUITY UPLC® BEH130 C18 separation column (200 mm x 75 µm id, 1.7 µm particle size, Waters). Peptides were eluted using a gradient from 1 % to 8 % B over 2 minutes followed by an 8% to 25% B step in 88 minutes and finished by 25% to 90% B in 10 minutes. A 5 min plateau at 90% B was observed before column reconditioning at 1% B. The mass spectrometer was equipped with a nanospray ion source. The applied voltage was 1.8kV and the ion transfer tube temperature was set to 250°C. MS spectra were acquired at a resolution of 70,000 at 200m/z, an automatic gain control (AGC) was fixed at 3×10^6 ions and a max injection time was set at 50 msec under a full ratio fixed at 15%. Peptide fragmentation was performed via higher-energy collisional dissociation set at 27V of normalized collisional energy. The ten most intense peptide ions in each survey scan with a charge state ≥2 were selected for MS/MS in the mass range of 300 to 1800. MS/MS were performed at 17,500 resolution at 200m/z, AGC was fixed at 1×10^5 and the maximum injection time was set to 100 msec. Peaks selected for fragmentation were automatically put on a dynamic exclusion list for 10 s. MS data were saved in RAW file format (Thermo Fisher Scientific) using XCalibur and then converted into ".mgf" files using MSConvert (Proteowizard), which were then submitted to the Mascot search engine (version 2.5.1, Matrix Science, London, UK) installed on a local server. Searches were performed against an in-house generated protein database composed of protein sequences of *Homo sapiens* extracted from Uniprot database (May 2016) and common contaminants (human keratins, trypsin), and combined with reverse sequences for all entries (total 299,458 entries) using an in-house database generation toolbox [https://msda.unistra.fr (3)]. Searches were performed without any molecular mass, or isoelectric point restrictions, trypsin was selected as enzyme, carbamidomethylation of cysteine (+57 Da) and oxidation of methionine (+16 Da) were set as variable modifications and mass tolerances on precursor and fragment ions of 5 ppm and 0.05 Da were used, respectively. Mascot results were loaded into the in-house Proline software (4) and filtered in order to obtain a false discovery rate of less than 1%.

RNA extraction and RT-QPCR

Total RNA was isolated using Trizol (Life Technologies) according to the manufacturer's instructions. RNA quantity and purity were measured using a Nanodrop device (Thermo Fisher). Total RNA was treated with DNAse I (Thermo Scientific) and reverse-transcribed into cDNA with the High Capacity cDNA reverse transcription kit (Applied Biosystems). Quantitative PCR were performed using the Brillant III SYBR Green QPCR Master mix (Agilent) in a MX3005 qPCR system (Agilent). Settings were: step 1: 3 min at 95°C, step 2: 40 cycles of 5 sec at 95°C and 20 sec at 55°C.

Plasmid constructs and transient transfection experiments

Wild type human *REV-ERBα* cDNA (NM_021724) cloned into pEZ-M11 was purchased from GeneCopoeia. The pEZ-M11-REV-ERBα H602F construct was obtained by mutagenesis [QuickChange II Site-Directed Mutagenesis Kit (Agilent Technologies)] of the wild type vector following the supplier's recommendations to convert histidine 602 into a phenylalanine residue. The Gal4 DBD-REV-ERBα vector was built by cloning the sequence encoding the human ligand binding domain of REV-ERBα (from AA 216 to AA 614) into the pM backbone (Clontech). The Gal4-UAS tk Luc reporter gene and the pCMV NCoR RID-VP16 expression vector have been described elsewhere (5, 6). The Bmal-Luc vector was built by cloning the human Bmal1 promoter region (from -280 to +38) into pGL4 basic (Promega). The normalization vector pCMV-renilla was purchased from Promega. Detailed sequence information is available upon request. HepG2 cells ($5x10^5$) or HEK293 ($3x10^5$) were plated on 6-well plates and transfections were performed using JetPEI (Polyplus transfection). Twenty four hours after transfection, the medium was replaced by complete medium. Cells were treated or not with 10 µM GSK4112 or vehicle (DMSO) for 24 hours. Reporter assays were quantified using the Dual-Glo® luciferase assay system (Promega) following the supplier's recommendations.

Adenovirus transduction

Control and *REV-ERBα* adenovirus were purchased from Atlantic Gene Therapies. HepG2 cells were transduced in serum-free DMEM medium for 150 min. After a 48h incubation in complete DMEM medium, cells were washed with 1X PBS and incubated 24 hours in serum-free medium. Cells were then treated or not with 60 nM insulin for the indicated time.

Small interfering RNAs (siRNA)

HepG2 cells were transfected for 48 h with Interferin (Polyplus transfection) with 10 nM of siRNAs targeting either *MGEA5/OGA*, *OGT*, *REV-ERBα*, *REV-ERBβ* human transcripts or a scrambled control (siCtrl) sequence. SiRNAs were as follows: *REV-ERBα*: Nr1d1 Silencer Validated siRNA (Ambion, ID: 5940), *REV-ERBβ* : Nr1d2 Silencer Validated siRNA (Ambion, ID: 19380), *OGT*: On-target plus Smart pool siRNA (Dharmacon, ID: L-019111-00), *MGEA5*: On-target plus Smart pool siRNA (Dharmacon, ID: L-012805-00), *ALAS1*: On-target plus Smart pool siRNA (Dharmacon: ID: L-009276-01), Control: On-target plus Non-targeting pool (Dharmacon, ID: D-001810-10).

Western blot analysis

Proteins were resolved by 10% SDS-PAGE under reducing conditions and transferred to nitrocellulose (Amersham GE Healthcare). Equal loading and transfer efficiency were confirmed by Ponceau red staining. Membranes were blocked for 1h with 5% bovine serum albumin in TRIS-buffered saline (TBS)-0.1% Tween. Membranes were incubated overnight at 4°C with appropriate antibodies described below. Membranes were then washed 3 times with TBS-Tween for 10min. and incubated for 1 h with either an anti-rabbit or an anti-mouse horseradish peroxidase–labelled secondary antibody (1:10,000). Membranes were washed 3 times with TBS-Tween for 10 min and antigen-antibodies complexes were detected by enhanced chemiluminescence (Pierce-Thermo Scientific). The following antibodies were used: mouse monoclonal anti-O-GlcNAc (RL2, ab2739, Abcam), rabbit polyclonal anti-OGT (O6014, Sigma-Aldrich), rabbit monoclonal anti-REV-ERBα (#13418, Cell Signalling Technology), rabbit polyclonal anti-HSP90 (sc-7947, Santa Cruz Biotechnology), Rabbit polyclonal anti-H2B (#12364), anti AKT (#9272), anti-P-AKT T308 (#13038), anti-P-AKT S473(#4030) [Cell Signalling Technology], Rabbit polyclonal anti-TET2 (GTX124205) and TET3 (GTX121453), mouse monoclonal anti-TET1 (GTX627420) [Gentex] and mouse monoclonal anti-Actin (A5441, Sigma-Aldrich). As membrane stripping could potentially remove proteins bound to the membrane, each WB analysis was performed on separately processed membrane.

Simple Western immunoassays

Proteins were analysed by Simple Western® size-based assays using a Wes system as recommended by the manufacturer (ProteinSimple). Proteins (0.5 mg/mL) were detected with primary antibodies described above. Secondary antibodies were provided by the manufacturer (PS-MK14, ProteinSimple). Samples were processed according to manufacturer's recommendations. Data were analyzed using the Compass software (ProteinSimple).

Subcellular fractionation

HepG2 cells were harvested and washed twice with ice-cold 1x PBS. Cells were suspended into a hypotonic buffer [ca 10^7 cells/mL of 20 mM TRIS-HCl, pH 7.5, 10 mM NaCl, 3 mM $MgCl_2$, 0.2% NP40 with protease and phosphatase inhibitors(Roche)] and homogenized with 20 strokes of a Dounce grinder (pestle A). Homogenates were spun at 600g for 5 min. and the supernatant (cytosol) was collected and stored in 10% glycerol until use. Pellets were suspended in 500 µL of lysis buffer (25 mM Tris-HCl, pH 7.5, 500 mM NaCl, 2 mM EDTA, 0.5% NP-40, and protease inhibitors) for 30 min at 4°C then sonicated for 10 min with a Bioruptor device at high power mode (sonication cycle: 30 sec ON/30 sec OFF). Lysates were centrifuged at 12,000 rpm for 5 min at 4°C. The soluble fraction (nucleoplasm) was collected and stored in 10% glycerol until use.

Immunocytochemistry

Immunofluorescent detection of REV-ERBα and OGT was performed on paraformaldehyde-fixed HepG2 cells treated or not with 10 µM GSK4112 and cultured at high Glc concentration (25 mM). After a 24h-treatment, HepG2 cells were fixed with 4% formaldehyde and permeabilized with 0.1% Triton X100. Immuno-staining was processed with rabbit anti-REV-ERBα or mouse anti-OGT (ab184198, Abcam) monoclonal antibodies and FITC couple secondary antibodies. DNA was stained using the Hoechst 33,258 intercalating agent. Images were acquired using a Leica DMI6000B microscope.

TET enzyme activity assays

TET enzymatic activity was assayed in the nuclear fraction of treated cells as follows. Cells were grown on P150 plates and washed twice using ice-cold 1xPBS and harvested in 1 mL ice-cold PBS. Cells were centrifuged at 600g for 2 min. The pellet was suspended into 200 µL buffer A (10 mM HEPES pH 7.9, 10 mM KCl, 1.5 mM $MgCl_2$, 0.34 M sucrose, 10% glycerol) and incubated on ice for 10 min. After centrifugation at 1,300 rpm for 10 min, pellets were washed once with buffer A and suspended in 100 µL buffer B (10 mM HEPES pH 7.9, 10 mM KCl, 3 mM EDTA, 0.2 mM EGTA, 1 mM DTT) for 30 min. TET enzyme activity was measured with the Epigenase^{TM} 5mC Hydroxylase TET Activity/Inhibition Assay kit (Epigentek) according to manufacturer's instructions.

5-hmC assay

The 5hmC content was determined as follows. HepG2 and mouse liver genomic DNA were extracted using the phenol/chloroform method after proteinase K and RNase treatment (7). HepG2 5hmC levels were determined using the MethylFlash™ hydroxymethylated DNA quantification kit (Epigentek) according to manufacturer's instructions. Mouse liver 5hmC level was determined using a dot blot assay. Briefly, 200 ng DNA were denatured in 0.1 M NaOH at 99°C for 5 min followed by cooling down at 4°C and a neutralization step with 0.66 M ammonium acetate. DNA was blotted on Hybond™-N+ membrane (Amersham GE Healthcare) and UV crosslinked. Hydroxymethylated DNA was detected using an anti-5hmC-DNA rabbit polyclonal antibody (1/1000, C15310210, Diagenode). Immuno-stained DNA was detected by enhanced chemiluminescence (Pierce-Thermo Scientific).

Hydroxymethylated DNA immunoprecipitation (hMeDIP)

The hMeDIP assay was performed on mouse liver DNA using the hMeDIP kit (Diagenode) according to the manufacturer's instructions. Briefly, DNA was extracted with the phenol/chloroform method as above. Seven µg of purified DNA were sonicated for 4x10 min with a Bioruptor device at high power mode (sonication cycle: 30 sec ON/30 sec OFF) and heat-denaturated (10 min at 95°C). After 5 min incubation on ice, hydroxymethylated DNA was immunoprecipitated with an anti-5hmC-DNA mouse monoclonal antibody bound to magnetic beads. After an overnight incubation, beads were washed and DNA (IPed and input) was treated with proteinase K and purified. The *Srebf1* hydroxymethylated region enrichment were then quantified by qPCR and compared to input.

Immunoprecipitation assays

Immunoprecipitations were performed using the Crosslink Magnetic IP/Co-IP Kit (Pierce) according to manufacturer's instructions. Briefly, cells ($2x10^7$) were washed with 10 mL ice-cold 1x PBS then lysed on ice in 0.5 mL IP lysis buffer (25 mM TRIS-HCl pH7.4, 150 mM NaCl, 1 mM EDTA, 1% NP40 and 10% glycerol). Three µg of mouse monoclonal anti-FLAG antibody (M2; Sigma-Aldrich), rabbit monoclonal anti-REV-ERBα (#13418, Cell Signalling Technology) or rabbit polyclonal anti-OGT (HPA030751, Sigma-Aldrich) were crosslinked on magnetic beads. Immunoprecipitations were performed using 500 µg of protein samples. Bound proteins were eluted with elution buffer and analysed by WB as indicated.

Mass spectrometry analysis of the HepG2 O-GlcNAcylome

REV-ERBα–specific and control siRNA treatments were performed in HepG2 cells. HepG2 cell extracts were immunoprecipitated with the anti O-GlcNAc antibody RL2. An aliquot from immunoprecipitates was separated by SDS-PAGE, and each band was cut into small pieces to perform in-gel tryptic digestion. Briefly, chopped gel pieces were washed three times with 25 mM ammonium bicarbonate containing 50% (v/v) acetonitrile (ACN). Samples were dehydrated by ACN and dried for 10 min at 37°C. Reduction and alkylation of samples were performed by adding dithiothreitol and iodoacetamide, respectively. Then, gel pieces were rehydrated in a digestion buffer containing 50 mM ammonium bicarbonate and 10 ng/µL trypsin (Promega, sequencing grade). The rehydrated transparent gel pieces were placed into 50 mM ammonium bicarbonate, and then incubated overnight at 37°C. The digested products were extracted with 100 µL of 5% formic acid in 80% acetonitrile (v/v). The peptide solution was then dried completely by vacuum centrifugation.

In parallel, another aliquot of immunoprecipitated sample was used for label free quantification. The samples were treated with 0.5 M N-acetyl-D-glucosamine to elute bound proteins from beads. The supernatant was subjected to eFASP tryptic digestion. UF filters from Amicon® units (10 kDa cutoff limit; Millipore, Billerica, MA) were incubated overnight in 5% (v/v) TWEEN-20 (T20, Sigma-Aldrich). After incubation, the filter units were rinsed thoroughly by three immersions in MS-grade water. The eFASP digestion (8, 9) was as follows. Samples were mixed in 50 µL of reducing buffer [4% SDS, 0.2 % deoxycholic acid (DCA), 50 mM dithiothreitol (DTT), 200 mM NH_4HCO_3] overnight at 4°C, and then centrifuged at 13,000 g for 15 min at 20°C. Supernatants were mixed to 200 µL of SDS exchange buffer A (8 M urea, 0.2 % DCA, 100 mM NH_4HCO_3, pH 8), and transferred to Amicon® units and centrifuged at 13,000 g for 30 min. The filtrate was discarded, and 200 µL exchange buffer A were deposited on each filter unit which were centrifuged for 30 min. This wash/centrifugation step was repeated twice. Reduced proteins were then alkylated on the filter unit by addition of the alkylation buffer [8 M urea, 50 mM iodoacetamide (IAA), and 100 mM NH_4HCO_3, pH 8] and incubation at 37°C for 60 min with shaking in the dark. After centrifugation at 13,000 g for 30 min, the filtrate was discarded. To remove residual IAA, 200 µL of exchange buffer A was added to each filter unit and centrifuged. This buffer addition/centrifugation step was repeated once. Three washes with the eFASP digestion buffer (100 µL) (50 mM ABC, 0.2% DCA pH 8) were performed then 1 µg trypsin (1:50 w/w) was added. Digestion proceeded for 16 h at 37°C. Peptides were recovered by transferring the UF filter to a new collection tube and spinning at 13,000 g for 20 min. To achieve complete peptide recovery, filters were rinsed twice with 50 µL of 50 mM NH_4HCO_3. Ethyl acetate (200 µL) was added to the peptide-containing filtrate and was transferred to a 2 mL tube to which 2.5 µL TFA was added and quickly vortexed. White thread-like precipitates were visible for large quantities of peptides. Peptide precipitates were mixed with 800 µL of ethyl acetate and were centrifuged at 13,000 g for 10 min. The organic supernatant was discarded and this step was repeated twice. The aqueous phase was placed in a thermomixer at 60°C for 5 minutes to evaporate residual ethyl acetate and organic solvents and volatile salts were then removed by vacuum-drying. This step was repeated two times with 50% methanol. Samples were then diluted tenfold in buffer A of nano-HPLC (5% acetonitrile and 0.1% formic acid) and each sample (n = 4) was injected four times in HPLC instrument to be analyzed in triplicates.Peptides mixtures were analyzed using a nanoflow HPLC instrument (U3000 RSLC Thermo Fisher Scientific) coupled on-line to a quadrupole-Orbitrap mass spectrometer (Q Exactive Plus, Thermo Scientific) with a nano-electrospray ion source. One µL of peptide mixture (corresponding to 500 ng of proteins) was loaded onto the pre-concentration trap (Thermo Scientific, Acclaim PepMap100 C18, 5 µm, 300 µm i.d. × 5 mm) using partial loop injection, for 5 min at a 10 µL/min flow rate with buffer A. Peptides were separated on analytical column (Acclaim PepMap100 C18, 3 μm, 75 mm i.d. × 500 mm) with a linear gradient of 5–50% buffer B (75% acetonitrile and 0.1% formic acid) at a 250 nL/min flow rate and a 45 °C controlled temperature. The total time for a LC MS/MS run was about 180 min long. MS data were acquired in a top-20 data-dependent method dynamically choosing the most abundant precursor ions from the survey scan for HCD fragmentation. Dynamic exclusion duration was 60 s. Isolation of precursors was performed with a 1.6 m/z window and MS/MS scans were acquired with a starting mass of 80 m/z. Survey scans were acquired in the Orbitrap analyzer with mass range of 400–1600 m/z and 70,000 resolutions at m/z 400 (AGC set to 10^6 ions with a maximum fill time of 100 ms). Resolution for HCD spectra was set to 70,000 at m/z 200 (AGC set to 10^5 ions with a maximum fill time of 160 ms) and 28 eV normalized collision energy. The underfill ratio, which specifies the minimum percentage of the target value likely to be reached at maximum fill time, was defined as 0.4%. The instrument was run with peptide recognition mode (i.e. from 2 to 8 charges), exclusion of singly charged and of unassigned precursor ions enabled.

The acquired raw files were analysed with MaxQuant software (version 1.5.3.30) using the Andromeda search engine. Peptides and proteins were identified by using the mouse subset of the UniProt database (released 2017, 159.806 entries) supplemented with 517 contaminants sequences. The “target-decoy” search strategy was used for estimating the frequencies of incorrect protein identifications (FDR), based on a reverse database generated automatically in MaxQuant. The precursor mass and fragment mass were identified with an initial mass tolerance of 10 ppm and 20 ppm, respectively. The search included variable modifications of methionine oxidation, asparagine and glutamine deamidation, tyrosine, serine and threonine phosphorylation and N-terminal acetylation and glutamine to pyroglutamate conversion, and fixed modifications of carbamidomethyl cysteine and HexNAc serine and threonine. Minimal peptide length was set to six amino acids and a maximum of three mis-cleavages was allowed. The FDR was set to 0.01 for peptide and protein identifications. To maximize the number of quantification events across samples, MS runs from skeletal muscle were analysed with the “match between runs” option in the MaxQuant software, which allowed the quantification of high-resolution MS1 features that were not identified in each single measurement. This algorithm was enabled using a 60-sec retention time window for individual matching and a 20-min retention time window for complete alignment of the spectrum. In the case of identified peptides that are all shared between two proteins, these were combined and reported as one protein group. Moreover, proteins contaminants, proteins identified only based on variable modifications sites and proteins matching to the reverse decoy database were filtered out. LFQ intensities for respective protein groups were uploaded in Perseus (1.5.6.0) and analysed. Raw LFQ intensities were Log_2-transformed. At least four LFQ values per protein group needed to be present for the analysis. To replace non-quantified values with low intensities, data imputation was performed based on normal distribution of LFQ intensities. Significant interactors were determined using a two-sample analysis multiple sample test with Benjamini-Hochberg FDR at 0.05.

Click-it chemistry assay

REV-ERBα or IgG control immunoprecipitations from HepG2 whole cell extract were processed as follows. O-GlcNAcylation of bead-bound proteins or of α-crystalline (positive control) was detected using the Click-iT®/O-GlcNAc Enzymatic Labeling System (Thermo Fisher Scientific) according to manufacturer's instructions. Signal detection was performed using the Click-iT™ Biotin Protein Analysis Detection Kit (Thermo Fisher Scientific) according to manufacturer's instructions. For AKT O-GlcNAcylation detection, HepG2 cells were transfected with pEZ-M11 empty vector or pEZ-M11-REV-ERBα. Twenty four hours after transfection, cells were cultivated for 20 hours in 25 mM Glc-containing medium in absence of serum then treated for 10 min with 60 nM Insulin. O-GlcNAcylation detection was as previously described (10). Briefly, total proteins (200 µg) were labelled using the Click-iT®/O-GlcNAc Enzymatic Labelling System. Modified proteins were then resuspended in Tris-HCl 50 mM, pH 8, SDS 1% buffer and diluted in enrichment buffer (PBS 1 X, Triton X100 1%, SDS 0.1%) and incubated for 20h at 4°C with streptavidin-coupled magnetic beads (Life Technologies). After 4 washes with enrichment buffer, proteins were eluted in 2x Laemmli buffer and AKT was detected by western blotting.

ChIP seq data processing

Datasets corresponding to REV-ERBα ChIP-seq from ZT10 8/12-week-old C57BL/6 mouse liver [GSM647029(11)] and 5hmC-DNA ChIP-seq from 17-week-old C57BL/6 mouse liver [hMedIP_liver A (GSM1633770) and Input_liver A (GSM1633772)] (12) were downloaded from the GEO website. Gene transcription start site (TSS) coordinates (mm10, GENCODE VM4 basic) were downloaded from the UCSC Genome Browser (13). Analysis were performed using a customized local instance of Galaxy (14). The REV-ERBα ChIP-seq dataset was analysed as previously described (15). The wig files for 5hmC-DNA ChIP-seq data were converted to bigwig and lifted to mm10 using the liftOver tool from the UCSC Genome Browser web site. Functional regions of interest were defined as regions spanning 5kb in each direction around the center of TSS. The average ChIP-seq intensities were computed with SitePro (16) on these regions with a resolution of 50bp. The Heatmap tool (based on SitePro script) was used to cluster functional regions into 4 groups according the average signal intensity for all ChIP-seq data (setting « step » to 100bp and « saturation » to 0.01).

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SUPPLEMENTAL TABLES

Table S1, related to Figure 1A: REV-ERBα interacts with OGT. List of most relevant nuclear REV-ERBα-interacting proteins identified by RIME of HepG2 whole cell extracts.

		Protein set score				
Symbol	**Description**	**IP REV-ERBα**	**IP IgG**	**UniProt accession number**	**Protein Name**	**Gene name**
HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens (Human) GN=HNRNPC PE=1 SV=4	491	0	P07910	HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2
-	cDNA FLJ50838, highly similar to Apoptotic chromatin condensation inducer in thenucleus OS=Homo sapiens (Human) PE=2 SV=1	378	0	B4DQZ7	B4DQZ7_HUMAN	-
DDX46	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens (Human) GN=DDX46 PE=1 SV=2	202	0	Q7L014	DDX46_HUMAN	Probable ATP-dependent RNA helicase DDX46
NR1D1	Nuclear receptor subfamily 1 group D member 1 OS=Homo sapiens (Human) GN=NR1D1 PE=1 SV=1	120	0	P20393	NR1D1_HUMAN	Nuclear receptor subfamily 1 group D member 1
ROCK2	Rho-associated protein kinase 2 OS=Homo sapiens (Human) GN=ROCK2 PE=1 SV=4	94	0	O75116	ROCK2_HUMAN	Rho-associated protein kinase 2
RPS3	40S ribosomal protein S3 OS=Homo sapiens (Human) GN=RPS3 PE=1 SV=1	88	0	H0YF32	H0YF32_HUMAN	-
RDX	Radixin OS=Homo sapiens (Human) GN=RDX PE=1 SV=1	77	0	P35241	RADI_HUMAN	Radixin
-	cDNA FLJ54018, highly similar to PDZ and LIM domain protein 5 OS=Homo sapiens (Human) PE=2 SV=1	75	0	B7Z481	B7Z481_HUMAN	-
LAD1	Ladinin-1 OS=Homo sapiens (Human) GN=LAD1 PE=1 SV=2	72	0	O00515	LAD1_HUMAN	Ladinin-1
HSPA4	Heat shock 70 kDa protein 4 OS=Homo sapiens (Human) GN=HSPA4 PE=1 SV=4	70	0	P34932	HSP74_HUMAN	Heat shock 70 kDa protein 4
PSMC2	26S protease regulatory subunit 7 OS=Homo sapiens (Human) GN=PSMC2 PE=1 SV=3	69	0	P35998	PRS7_HUMAN	26S protease regulatory subunit 7
SUMO1	Small ubiquitin-related modifier 1 OS=Homo sapiens (Human) GN=SUMO1 PE=1	63	0	P63165	SUMO1_HUMAN	Small ubiquitin-related modifier 1

	SV=1					
NUP88	Nuclear pore complex protein Nup88 OS=Homo sapiens (Human) GN=NUP88 PE=1 SV=2	61	0	Q99567	NUP88_HUMAN	Nuclear pore complex protein Nup88
HDAC1	Histone deacetylase 1 OS=Homo sapiens (Human) GN=HDAC1 PE=1 SV=1	59	0	Q13547	HDAC1_HUMAN	Histone deacetylase 1
SEPT11	Septin-11 OS=Homo sapiens (Human) GN=SEPT11 PE=1 SV=3	57	0	Q9NVA2	SEP11_HUMAN	Septin-11
CCDC47	Coiled-coil domain-containing protein 47 OS=Homo sapiens (Human) GN=CCDC47 PE=1 SV=1	53	0	Q96A33	CCD47_HUMAN	Coiled-coil domain-containing protein 47
RPL30	60S ribosomal protein L30 OS=Homo sapiens (Human) GN=RPL30 PE=1 SV=2	52	0	P62888	RL30_HUMAN	60S ribosomal protein L30
LMAN1	Protein ERGIC-53 OS=Homo sapiens (Human) GN=LMAN1 PE=1 SV=2	52	0	P49257	LMAN1_HUMAN	Protein ERGIC-53
PPP1R12A	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens (Human) GN=PPP1R12A PE=1 SV=1	51	0	O14974	MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A
SCRIB	Protein scribble homolog OS=Homo sapiens (Human) GN=SCRIB PE=1 SV=4	50	0	Q14160	SCRIB_HUMAN	Protein scribble homolog
WHSC1	Histone-lysine N-methyltransferase NSD2 OS=Homo sapiens (Human) GN=WHSC1 PE=1 SV=1	50	0	O96028	NSD2_HUMAN	Histone-lysine N-methyltransferase NSD2
PTBP3	Polypyrimidine tract-binding protein 3 OS=Homo sapiens (Human) GN=PTBP3 PE=1 SV=2	49	0	O95758	PTBP3_HUMAN	Polypyrimidine tract-binding protein 3
ZC3H18	Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens (Human) GN=ZC3H18 PE=1 SV=2	48	0	Q86VM9	ZCH18_HUMAN	Zinc finger CCCH domain-containing protein 18
USP14	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens (Human) GN=USP14 PE=1 SV=3	48	0	P54578	UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14
SERPINH1	Serpin H1 OS=Homo sapiens (Human) GN=SERPINH1 PE=1 SV=2	48	0	P50454	SERPH_HUMAN	Serpin H1
CD3EAP	DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens (Human) GN=CD3EAP PE=1 SV=1	47	0	O15446	RPA34_HUMAN	DNA-directed RNA polymerase I subunit RPA34
EHMT2	Histone-lysine N-methyltransferase EHMT2 OS=Homo sapiens (Human) GN=EHMT2 PE=1 SV=3	47	0	Q96KQ7	EHMT2_HUMAN	Histone-lysine N-methyltransferase EHMT2

CFDP1	Craniofacial development protein 1 OS=Homo sapiens (Human) GN=CFDP1 PE=1 SV=1	46	0	Q9UEE9	CFDP1_HUMAN	Craniofacial development protein 1
PDXDC1	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens (Human) GN=PDXDC1 PE=1 SV=2	45	0	Q6P996	PDXD1_HUMAN	Pyridoxal-dependent decarboxylase domain-containing protein 1
SAMHD1	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens (Human) GN=SAMHD1 PE=1 SV=2	45	0	Q9Y3Z3	SAMH1_HUMAN	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1
IPO9	Importin-9 OS=Homo sapiens (Human) GN=IPO9 PE=1 SV=3	43	0	Q96P70	IPO9_HUMAN	Importin-9
UBB	Polyubiquitin-B OS=Homo sapiens (Human) GN=UBB PE=1 SV=1	42	0	P0CG47	UBB_HUMAN	Polyubiquitin-B
NAP1L4	Nucleosome assembly protein 1-like 4 OS=Homo sapiens (Human) GN=NAP1L4 PE=1 SV=1	42	0	Q99733	NP1L4_HUMAN	Nucleosome assembly protein 1-like 4
HIST1H3A	Histone H3.1 OS=Homo sapiens (Human) GN=HIST1H3A PE=1 SV=2	41	0	P68431	H31_HUMAN	Histone H3.1
SIN3A	Paired amphipathic helix protein Sin3a OS=Homo sapiens (Human) GN=SIN3A PE=1 SV=2	40	0	Q96ST3	SIN3A_HUMAN	Paired amphipathic helix protein Sin3a
SENP3	Sentrin-specific protease 3 OS=Homo sapiens (Human) GN=SENP3 PE=1 SV=2	40	0	Q9H4L4	SENP3_HUMAN	Sentrin-specific protease 3
CORO1B	Coronin-1B OS=Homo sapiens (Human) GN=CORO1B PE=1 SV=1	40	0	Q9BR76	COR1B_HUMAN	Coronin-1B
-	Adenylyl cyclase-associated protein OS=Homo sapiens (Human) PE=2 SV=1	40	0	B2RDY9	B2RDY9_HUMAN	-
TDP2	Tyrosyl-DNA phosphodiesterase 2 OS=Homo sapiens (Human) GN=TDP2 PE=1 SV=1	38	0	O95551	TYDP2_HUMAN	Tyrosyl-DNA phosphodiesterase 2
FARSB	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens (Human) GN=FARSB PE=1 SV=3	38	0	Q9NSD9	SYFB_HUMAN	Phenylalanine--tRNA ligase beta subunit
AP3D1	AP-3 complex subunit delta-1 OS=Homo sapiens (Human) GN=AP3D1 PE=1 SV=1	38	0	O14617	AP3D1_HUMAN	AP-3 complex subunit delta-1
PSMD14	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens (Human) GN=PSMD14 PE=1 SV=1	38	0	O00487	PSDE_HUMAN	26S proteasome non-ATPase regulatory subunit 14
IWS1	Protein IWS1 homolog OS=Homo sapiens (Human)	36	0	Q96ST2	IWS1_HUMAN	Protein IWS1 homolog

	GN=IWS1 PE=1 SV=2					
RPS27L	40S ribosomal protein S27-like OS=Homo sapiens (Human) GN=RPS27L PE=1 SV=3	36	0	Q71UM5	RS27L_HUMAN	40S ribosomal protein S27-like
TRMT1L	TRMT1-like protein OS=Homo sapiens (Human) GN=TRMT1L PE=1 SV=2	35	0	Q7Z2T5	TRM1L_HUMAN	TRMT1-like protein
SEC11A	Signal peptidase complex catalytic subunit SEC11A OS=Homo sapiens (Human) GN=SEC11A PE=1 SV=1	35	0	P67812	SC11A_HUMAN	Signal peptidase complex catalytic subunit SEC11A
SBDS	Ribosome maturation protein SBDS OS=Homo sapiens (Human) GN=SBDS PE=1 SV=4	35	0	Q9Y3A5	SBDS_HUMAN	Ribosome maturation protein SBDS
PINX1	PIN2/TERF1-interacting telomerase inhibitor 1 OS=Homo sapiens (Human) GN=PINX1 PE=1 SV=2	35	0	Q96BK5	PINX1_HUMAN	PIN2/TERF1-interacting telomerase inhibitor 1
SKP1	S-phase kinase-associated protein 1 OS=Homo sapiens (Human) GN=SKP1 PE=1 SV=2	34	0	P63208	SKP1_HUMAN	S-phase kinase-associated protein 1
PSMB6	Proteasome subunit beta type-6 OS=Homo sapiens (Human) GN=PSMB6 PE=1 SV=4	34	0	P28072	PSB6_HUMAN	Proteasome subunit beta type-6
NELFCD	Negative elongation factor C/D OS=Homo sapiens (Human) GN=NELFCD PE=1 SV=2	33	0	Q8IXH7	NELFD_HUMAN	Negative elongation factor C/D
CORO1A	Coronin-1A OS=Homo sapiens (Human) GN=CORO1A PE=1 SV=4	33	0	P31146	COR1A_HUMAN	Coronin-1A
CTR9	RNA polymerase-associated protein CTR9 homolog OS=Homo sapiens (Human) GN=CTR9 PE=1 SV=1	33	0	Q6PD62	CTR9_HUMAN	RNA polymerase-associated protein CTR9 homolog
PHIP	PH-interacting protein OS=Homo sapiens (Human) GN=PHIP PE=1 SV=2	32	0	Q8WWQ0	PHIP_HUMAN	PH-interacting protein
PRPF38A	Pre-mRNA-splicing factor 38A OS=Homo sapiens (Human) GN=PRPF38A PE=1 SV=1	32	0	Q8NAV1	PR38A_HUMAN	Pre-mRNA-splicing factor 38A
CBX5	Chromobox protein homolog 5 OS=Homo sapiens (Human) GN=CBX5 PE=1 SV=1	32	0	P45973	CBX5_HUMAN	Chromobox protein homolog 5
TRIM27	Zinc finger protein RFP OS=Homo sapiens (Human) GN=TRIM27 PE=1 SV=1	32	0	P14373	TRI27_HUMAN	Zinc finger protein RFP
PCIF1	Phosphorylated CTD-interacting factor 1 OS=Homo sapiens (Human) GN=PCIF1 PE=1 SV=1	31	0	Q9H4Z3	PCIF1_HUMAN	Phosphorylated CTD-interacting factor 1

ARAP1	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens (Human) GN=ARAP1 PE=1 SV=3	30	0	Q96P48	ARAP1_HUMAN	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1
GNL1	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens (Human) GN=GNL1 PE=1 SV=2	30	0	P36915	GNL1_HUMAN	Guanine nucleotide-binding protein-like 1
CWC22	Pre-mRNA-splicing factor CWC22 homolog OS=Homo sapiens (Human) GN=CWC22 PE=1 SV=3	30	0	Q9HCG8	CWC22_HUMAN	Pre-mRNA-splicing factor CWC22 homolog
KATNAL2	Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens (Human) GN=KATNAL2 PE=2 SV=3	30	0	Q8IYT4	KATL2_HUMAN	Katanin p60 ATPase-containing subunit A-like 2
GTF3C5	General transcription factor 3C polypeptide 5 OS=Homo sapiens (Human) GN=GTF3C5 PE=1 SV=2	29	0	Q9Y5Q8	TF3C5_HUMAN	General transcription factor 3C polypeptide 5
SETD1A	Histone-lysine N-methyltransferase SETD1A OS=Homo sapiens (Human) GN=SETD1A PE=1 SV=3	29	0	O15047	SET1A_HUMAN	Histone-lysine N-methyltransferase SETD1A
CLU	Clusterin OS=Homo sapiens (Human) GN=CLU PE=1 SV=1	28	0	P10909	CLUS_HUMAN	Clusterin
NCAPD2	Condensin complex subunit 1 OS=Homo sapiens (Human) GN=NCAPD2 PE=1 SV=3	28	0	Q15021	CND1_HUMAN	Condensin complex subunit 1
ZMYND8	Protein kinase C-binding protein 1 OS=Homo sapiens (Human) GN=ZMYND8 PE=1 SV=2	28	0	Q9ULU4	PKCB1_HUMAN	Protein kinase C-binding protein 1
GTF2H2	General transcription factor IIH subunit 2 OS=Homo sapiens (Human) GN=GTF2H2 PE=1 SV=1	28	0	Q13888	TF2H2_HUMAN	General transcription factor IIH subunit 2
CIT	Citron Rho-interacting kinase OS=Homo sapiens (Human) GN=CIT PE=1 SV=2	28	0	O14578	CTRO_HUMAN	Citron Rho-interacting kinase
IRF2BP1	Interferon regulatory factor 2-binding protein 1 OS=Homo sapiens (Human) GN=IRF2BP1 PE=1 SV=1	28	0	Q8IU81	I2BP1_HUMAN	Interferon regulatory factor 2-binding protein 1
ATRX	Transcriptional regulator ATRX OS=Homo sapiens (Human) GN=ATRX PE=1 SV=5	28	0	P46100	ATRX_HUMAN	Transcriptional regulator ATRX
PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens (Human) GN=PPP2R1A PE=1 SV=4	27	0	P30153	2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform
CORO1C	Coronin-1C OS=Homo sapiens (Human)	27	0	Q9ULV4	COR1C_HUMAN	Coronin-1C

	GN=CORO1C PE=1 SV=1					
UPF1	Regulator of nonsense transcripts 1 OS=Homo sapiens (Human) GN=UPF1 PE=1 SV=2	27	0	Q92900	RENT1_HUMAN	Regulator of nonsense transcripts 1
TLN2	Talin-2 OS=Homo sapiens (Human) GN=TLN2 PE=1 SV=4	27	0	Q9Y4G6	TLN2_HUMAN	Talin-2
ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens (Human) GN=ANP32A PE=1 SV=1	27	0	P39687	AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A
BPNT1	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens (Human) GN=BPNT1 PE=1 SV=1	27	0	O95861	BPNT1_HUMAN	3'(2'),5'-bisphosphate nucleotidase 1
CUL2	Cullin-2 OS=Homo sapiens (Human) GN=CUL2 PE=1 SV=2	26	0	Q13617	CUL2_HUMAN	Cullin-2
NMT1	Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens (Human) GN=NMT1 PE=1 SV=2	26	0	P30419	NMT1_HUMAN	Glycylpeptide N-tetradecanoyltransferase 1
GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens (Human) GN=GSPT1 PE=1 SV=1	26	0	P15170	ERF3A_HUMAN	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A
DUSP3	Dual specificity protein phosphatase 3 OS=Homo sapiens (Human) GN=DUSP3 PE=1 SV=1	26	0	P51452	DUS3_HUMAN	Dual specificity protein phosphatase 3
AP2B1	AP-2 complex subunit beta OS=Homo sapiens (Human) GN=AP2B1 PE=1 SV=1	25	0	P63010	AP2B1_HUMAN	AP-2 complex subunit beta
CAPNS1	Calpain small subunit 1 OS=Homo sapiens (Human) GN=CAPNS1 PE=1 SV=1	24	0	P04632	CPNS1_HUMAN	Calpain small subunit 1
CARM1	Histone-arginine methyltransferase CARM1 OS=Homo sapiens (Human) GN=CARM1 PE=1 SV=3	24	0	Q86X55	CARM1_HUMAN	Histone-arginine methyltransferase CARM1
OTUB1	Ubiquitin thioesterase OTUB1 OS=Homo sapiens (Human) GN=OTUB1 PE=1 SV=2	24	0	Q96FW1	OTUB1_HUMAN	Ubiquitin thioesterase OTUB1
RPP38	Ribonuclease P protein subunit p38 OS=Homo sapiens (Human) GN=RPP38 PE=1 SV=2	24	0	P78345	RPP38_HUMAN	Ribonuclease P protein subunit p38
KIF2A	Kinesin-like protein KIF2A OS=Homo sapiens (Human) GN=KIF2A PE=1 SV=3	24	0	O00139	KIF2A_HUMAN	Kinesin-like protein KIF2A
TBL1X	F-box-like/WD repeat-containing protein TBL1X OS=Homo sapiens (Human)	24	0	O60907	TBL1X_HUMAN	F-box-like/WD repeat-containing protein TBL1X

	GN=TBL1X PE=1 SV=3					
CKB	Creatine kinase B-type OS=Homo sapiens (Human) GN=CKB PE=1 SV=1	24	0	P12277	KCRB_HUMAN	Creatine kinase B-type
SNRPB2	U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens (Human) GN=SNRPB2 PE=1 SV=1	23	0	P08579	RU2B_HUMAN	U2 small nuclear ribonucleoprotein B''
RAE1	mRNA export factor OS=Homo sapiens (Human) GN=RAE1 PE=1 SV=1	23	0	P78406	RAE1L_HUMAN	mRNA export factor
AP2A2	AP-2 complex subunit alpha-2 OS=Homo sapiens (Human) GN=AP2A2 PE=1 SV=2	23	0	O94973	AP2A2_HUMAN	AP-2 complex subunit alpha-2
OGT	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens (Human) GN=OGT PE=1 SV=3	23	0	O15294	OGT1_HUMAN	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit
UMPS	Uridine 5'-monophosphate synthase OS=Homo sapiens (Human) GN=UMPS PE=1 SV=1	23	0	P11172	UMPS_HUMAN	Orotidine 5'-phosphate decarboxylase
BRD3	Bromodomain-containing protein 3 OS=Homo sapiens (Human) GN=BRD3 PE=1 SV=1	23	0	Q15059	BRD3_HUMAN	Bromodomain-containing protein 3
TXNL1	Thioredoxin-like protein 1 OS=Homo sapiens (Human) GN=TXNL1 PE=1 SV=3	22	0	O43396	TXNL1_HUMAN	Thioredoxin-like protein 1
PAF1	RNA polymerase II-associated factor 1 homolog OS=Homo sapiens (Human) GN=PAF1 PE=1 SV=2	22	0	Q8N7H5	PAF1_HUMAN	RNA polymerase II-associated factor 1 homolog
ACOT13	Acyl-coenzyme A thioesterase 13 OS=Homo sapiens (Human) GN=ACOT13 PE=1 SV=1	22	0	Q9NPJ3	ACO13_HUMAN	Acyl-coenzyme A thioesterase 13
P4HA1	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens (Human) GN=P4HA1 PE=1 SV=2	22	0	P13674	P4HA1_HUMAN	Prolyl 4-hydroxylase subunit alpha-1
ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens (Human) GN=ANP32B PE=1 SV=1	22	0	Q92688	AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B
MTDH	Protein LYRIC OS=Homo sapiens (Human) GN=MTDH PE=1 SV=1	22	0	H0YBE0	H0YBE0_HUMAN	-
SEC24A	Protein transport protein Sec24A OS=Homo sapiens (Human) GN=SEC24A PE=1 SV=2	21	0	O95486	SC24A_HUMAN	Protein transport protein Sec24A
UBA2	SUMO-activating enzyme subunit 2 OS=Homo sapiens	21	0	Q9UBT2	SAE2_HUMAN	SUMO-activating enzyme

	(Human) GN=UBA2 PE=1 SV=2					subunit 2
XPC	DNA repair protein complementing XP-C cells OS=Homo sapiens (Human) GN=XPC PE=1 SV=4	21	0	Q01831	XPC_HUMAN	DNA repair protein complementing XP-C cells
ORC3	Origin recognition complex subunit 3 OS=Homo sapiens (Human) GN=ORC3 PE=1 SV=1	21	0	Q9UBD5	ORC3_HUMAN	Origin recognition complex subunit 3
ZFP91	E3 ubiquitin-protein ligase ZFP91 OS=Homo sapiens (Human) GN=ZFP91 PE=1 SV=1	20	0	Q96JP5	ZFP91_HUMAN	E3 ubiquitin-protein ligase ZFP91
ZNF217	Zinc finger protein 217 OS=Homo sapiens (Human) GN=ZNF217 PE=1 SV=1	20	0	O75362	ZN217_HUMAN	Zinc finger protein 217
SNRPE	Small nuclear ribonucleoprotein E OS=Homo sapiens (Human) GN=SNRPE PE=1 SV=1	20	0	P62304	RUXE_HUMAN	Small nuclear ribonucleoprotein E
RPL31	60S ribosomal protein L31 OS=Homo sapiens (Human) GN=RPL31 PE=1 SV=1	59	8	P62899	RL31_HUMAN	60S ribosomal protein L31
DHX33	Putative ATP-dependent RNA helicase DHX33 OS=Homo sapiens (Human) GN=DHX33 PE=1 SV=2	33	10	Q9H6R0	DHX33_HUMAN	Putative ATP-dependent RNA helicase DHX33
SNRPD3	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens (Human) GN=SNRPD3 PE=1 SV=1	46	10	P62318	SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3
PTBP2	Polypyrimidine tract-binding protein 2 OS=Homo sapiens (Human) GN=PTBP2 PE=1 SV=1	21	11	Q9UKA9	PTBP2_HUMAN	Polypyrimidine tract-binding protein 2
PIN4	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Homo sapiens (Human) GN=PIN4 PE=1 SV=1	30	12	Q9Y237	PIN4_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
CTTN	Src substrate cortactin OS=Homo sapiens (Human) GN=CTTN PE=1 SV=2	111	12	Q14247	SRC8_HUMAN	Src substrate cortactin
RPS19	40S ribosomal protein S19 OS=Homo sapiens (Human) GN=RPS19 PE=1 SV=2	56	13	P39019	RS19_HUMAN	40S ribosomal protein S19
METTL16	Methyltransferase-like protein 16 OS=Homo sapiens (Human) GN=METTL16 PE=1 SV=2	28	14	Q86W50	MET16_HUMAN	Methyltransferase-like protein 16
PSMC5	26S protease regulatory subunit 8 OS=Homo sapiens (Human) GN=PSMC5 PE=1 SV=1	42	14	P62195	PRS8_HUMAN	26S protease regulatory subunit 8
PSMC1	26S protease regulatory subunit 4 OS=Homo sapiens (Human) GN=PSMC1 PE=1	30	14	P62191	PRS4_HUMAN	26S protease regulatory subunit 4

	SV=1					
HIC2	Hypermethylated in cancer 2 protein OS=Homo sapiens (Human) GN=HIC2 PE=1 SV=2	29	15	Q96JB3	HIC2_HUMAN	Hypermethylated in cancer 2 protein
BCCIP	BRCA2 and CDKN1A-interacting protein OS=Homo sapiens (Human) GN=BCCIP PE=1 SV=1	59	15	Q9P287	BCCIP_HUMAN	BRCA2 and CDKN1A-interacting protein
SMC6	Structural maintenance of chromosomes protein 6 OS=Homo sapiens (Human) GN=SMC6 PE=1 SV=2	21	15	Q96SB8	SMC6_HUMAN	Structural maintenance of chromosomes protein 6
CPVL	Probable serine carboxypeptidase CPVL OS=Homo sapiens (Human) GN=CPVL PE=1 SV=2	20	15	Q9H3G5	CPVL_HUMAN	Probable serine carboxypeptidase CPVL
RPL36	60S ribosomal protein L36 OS=Homo sapiens (Human) GN=RPL36 PE=1 SV=3	52	15	Q9Y3U8	RL36_HUMAN	60S ribosomal protein L36
PDCD5	Programmed cell death protein 5 OS=Homo sapiens (Human) GN=PDCD5 PE=1 SV=3	55	16	O14737	PDCD5_HUMAN	Programmed cell death protein 5
ZC3H11A	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens (Human) GN=ZC3H11A PE=1 SV=3	24	16	O75152	ZC11A_HUMAN	Zinc finger CCCH domain-containing protein 11A
EDC3	Enhancer of mRNA-decapping protein 3 OS=Homo sapiens (Human) GN=EDC3 PE=1 SV=1	42	16	Q96F86	EDC3_HUMAN	Enhancer of mRNA-decapping protein 3
ANXA4	Annexin A4 OS=Homo sapiens (Human) GN=ANXA4 PE=1 SV=4	94	16	P09525	ANXA4_HUMAN	Annexin A4
MRE11A	Double-strand break repair protein MRE11A OS=Homo sapiens (Human) GN=MRE11A PE=1 SV=3	56	16	P49959	MRE11_HUMAN	Double-strand break repair protein MRE11A
PRKAR1A	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens (Human) GN=PRKAR1A PE=1 SV=1	24	16	P10644	KAP0_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit
HELLS	Lymphoid-specific helicase OS=Homo sapiens (Human) GN=HELLS PE=1 SV=1	54	16	Q9NRZ9	HELLS_HUMAN	Lymphoid-specific helicase
PPP1R8	Nuclear inhibitor of protein phosphatase 1 OS=Homo sapiens (Human) GN=PPP1R8 PE=1 SV=2	40	16	Q12972	PP1R8_HUMAN	Activator of RNA decay
CMSS1	Protein CMSS1 OS=Homo sapiens (Human) GN=CMSS1 PE=1 SV=2	22	17	Q9BQ75	CMS1_HUMAN	Protein CMSS1
IQGAP2	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens (Human)	60	17	Q13576	IQGA2_HUMAN	Ras GTPase-activating-like protein IQGAP2

	GN=IQGAP2 PE=1 SV=4					
WDR12	Ribosome biogenesis protein WDR12 OS=Homo sapiens (Human) GN=WDR12 PE=1 SV=2	24	17	Q9GZL7	WDR12_HUMAN	Ribosome biogenesis protein WDR12
GBE1	1,4-alpha-glucan-branching enzyme OS=Homo sapiens (Human) GN=GBE1 PE=1 SV=3	32	18	Q04446	GLGB_HUMAN	1,4-alpha-glucan-branching enzyme
PARN	Poly(A)-specific ribonuclease PARN OS=Homo sapiens (Human) GN=PARN PE=1 SV=1	81	18	O95453	PARN_HUMAN	Poly(A)-specific ribonuclease PARN
UBE2N	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens (Human) GN=UBE2N PE=1 SV=1	22	18	P61088	UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N
IKBKAP	Elongator complex protein 1 OS=Homo sapiens (Human) GN=IKBKAP PE=1 SV=3	37	18	O95163	ELP1_HUMAN	Elongator complex protein 1
HMGN3	High mobility group nucleosome-binding domain-containing protein 3 OS=Homo sapiens (Human) GN=HMGN3 PE=1 SV=2	21	18	Q15651	HMGN3_HUMAN	High mobility group nucleosome-binding domain-containing protein 3
TP53BP1	Tumor suppressor p53-binding protein 1 OS=Homo sapiens (Human) GN=TP53BP1 PE=1 SV=2	31	18	Q12888	TP53B_HUMAN	Tumor suppressor p53-binding protein 1
NCBP2	Nuclear cap-binding protein subunit 2 OS=Homo sapiens (Human) GN=NCBP2 PE=1 SV=1	36	19	P52298	NCBP2_HUMAN	Nuclear cap-binding protein subunit 2
PPP2R4	Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens (Human) GN=PPP2R4 PE=1 SV=3	25	19	Q15257	PTPA_HUMAN	Serine/threonine-protein phosphatase 2A activator
CPSF2	Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens (Human) GN=CPSF2 PE=1 SV=2	63	19	Q9P2I0	CPSF2_HUMAN	Cleavage and polyadenylation specificity factor subunit 2
SRPK1	SRSF protein kinase 1 OS=Homo sapiens (Human) GN=SRPK1 PE=1 SV=2	44	20	Q96SB4	SRPK1_HUMAN	SRSF protein kinase 1
PDCD6	Programmed cell death protein 6 OS=Homo sapiens (Human) GN=PDCD6 PE=1 SV=1	22	20	O75340	PDCD6_HUMAN	Programmed cell death protein 6
PDIA6	Protein disulfide-isomerase A6 OS=Homo sapiens (Human) GN=PDIA6 PE=1 SV=1	66	20	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6
AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens (Human) GN=AHSA1 PE=1 SV=1	38	20	O95433	AHSA1_HUMAN	Activator of 90 kDa heat shock protein ATPase homolog 1

FKBP1A	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens (Human) GN=FKBP1A PE=1 SV=2	24	20	P62942	FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A
PSMA5	Proteasome subunit alpha type-5	27	21	P28066	PSA5_HUMAN	Proteasome subunit alpha type-5
WDR33	pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens (Human) GN=WDR33 PE=1 SV=2	38	21	Q9C0J8	WDR33_HUMAN	pre-mRNA 3' end processing protein WDR33
POP1	Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens (Human) GN=POP1 PE=1 SV=2	21	21	Q99575	POP1_HUMAN	Ribonucleases P/MRP protein subunit POP1
GPATCH4	G patch domain-containing protein 4 OS=Homo sapiens (Human) GN=GPATCH4 PE=1 SV=2	77	21	Q5T3I0	GPTC4_HUMAN	G patch domain-containing protein 4
OLA1	Obg-like ATPase 1 OS=Homo sapiens (Human) GN=OLA1 PE=1 SV=2	84	22	Q9NTK5	OLA1_HUMAN	Obg-like ATPase 1
APRT	Adenine phosphoribosyltransferase OS=Homo sapiens (Human) GN=APRT PE=1 SV=2	21	22	P07741	APT_HUMAN	Adenine phosphoribosyltransferase
CSNK2A2	Casein kinase II subunit alpha' OS=Homo sapiens (Human) GN=CSNK2A2 PE=1 SV=1	27	22	P19784	CSK22_HUMAN	Casein kinase II subunit alpha'
C14orf166	UPF0568 protein C14orf166 OS=Homo sapiens (Human) GN=C14orf166 PE=1 SV=1	80	22	Q9Y224	CN166_HUMAN	UPF0568 protein C14orf166
SPCS2	Signal peptidase complex subunit 2 OS=Homo sapiens (Human) GN=SPCS2 PE=1 SV=3	26	22	Q15005	SPCS2_HUMAN	Signal peptidase complex subunit 2
KARS	Lysine--tRNA ligase OS=Homo sapiens (Human) GN=KARS PE=1 SV=3	63	22	Q15046	SYK_HUMAN	Lysine--tRNA ligase
WTAP	Pre-mRNA-splicing regulator WTAP OS=Homo sapiens (Human) GN=WTAP PE=1 SV=2	62	22	Q15007	FL2D_HUMAN	Pre-mRNA-splicing regulator WTAP
POLD1	DNA polymerase delta catalytic subunit OS=Homo sapiens (Human) GN=POLD1 PE=1 SV=2	35	22	P28340	DPOD1_HUMAN	DNA polymerase delta catalytic subunit
SUZ12	Polycomb protein SUZ12 OS=Homo sapiens (Human) GN=SUZ12 PE=1 SV=3	39	23	Q15022	SUZ12_HUMAN	Polycomb protein SUZ12
SEC61A1	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens (Human) GN=SEC61A1 PE=1 SV=2	27	23	P61619	S61A1_HUMAN	Protein transport protein Sec61 subunit alpha isoform 1
BRD2	Bromodomain-containing protein 2 OS=Homo sapiens	37	23	P25440	BRD2_HUMAN	Bromodomain-containing

	(Human) GN=BRD2 PE=1 SV=2					protein 2
DAD1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens (Human) GN=DAD1 PE=1 SV=3	35	23	P61803	DAD1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1
ADSL	Adenylosuccinate lyase OS=Homo sapiens (Human) GN=ADSL PE=1 SV=2	25	23	P30566	PUR8_HUMAN	Adenylosuccinate lyase
NHP2	H/ACA ribonucleoprotein complex subunit 2 OS=Homo sapiens (Human) GN=NHP2 PE=1 SV=1	65	24	Q9NX24	NHP2_HUMAN	H/ACA ribonucleoprotein complex subunit 2
NUP62	Nuclear pore glycoprotein p62 OS=Homo sapiens (Human) GN=NUP62 PE=1 SV=3	27	24	P37198	NUP62_HUMAN	Nuclear pore glycoprotein p62
RPL35A	60S ribosomal protein L35a OS=Homo sapiens (Human) GN=RPL35A PE=1 SV=2	34	24	P18077	RL35A_HUMAN	60S ribosomal protein L35a
MPHOSPH8	M-phase phosphoprotein 8 OS=Homo sapiens (Human) GN=MPHOSPH8 PE=1 SV=2	22	24	Q99549	MPP8_HUMAN	M-phase phosphoprotein 8
COPB2	Coatomer subunit beta' OS=Homo sapiens (Human) GN=COPB2 PE=1 SV=2	45	24	P35606	COPB2_HUMAN	Coatomer subunit beta'
NAP1L1	Nucleosome assembly protein 1-like 1 OS=Homo sapiens (Human) GN=NAP1L1 PE=1 SV=1	47	24	P55209	NP1L1_HUMAN	Nucleosome assembly protein 1-like 1
TRMT61A	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens (Human) GN=TRMT61A PE=1 SV=1	21	24	Q96FX7	TRM61_HUMAN	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A
NELFB	Negative elongation factor B OS=Homo sapiens (Human) GN=NELFB PE=1 SV=1	29	25	Q8WX92	NELFB_HUMAN	Negative elongation factor B
SAR1A	GTP-binding protein SAR1a OS=Homo sapiens (Human) GN=SAR1A PE=1 SV=1	44	25	Q9NR31	SAR1A_HUMAN	GTP-binding protein SAR1a
COPB1	Coatomer subunit beta OS=Homo sapiens (Human) GN=COPB1 PE=1 SV=3	103	25	P53618	COPB_HUMAN	Coatomer subunit beta
ZYX	Zyxin OS=Homo sapiens (Human) GN=ZYX PE=1 SV=1	37	25	Q15942	ZYX_HUMAN	Zyxin
CHD1L	Chromodomain-helicase-DNA-binding protein 1-like OS=Homo sapiens (Human) GN=CHD1L PE=1 SV=2	25	25	Q86WJ1	CHD1L_HUMAN	Chromodomain-helicase-DNA-binding protein 1-like
SF3A2	Splicing factor 3A subunit 2 OS=Homo sapiens (Human) GN=SF3A2 PE=1 SV=2	24	25	Q15428	SF3A2_HUMAN	Splicing factor 3A subunit 2

PHF3	PHD finger protein 3 OS=Homo sapiens (Human) GN=PHF3 PE=1 SV=3	50	26	Q92576	PHF3_HUMAN	PHD finger protein 3
SP1	Transcription factor Sp1 OS=Homo sapiens (Human) GN=SP1 PE=1 SV=3	25	26	P08047	SP1_HUMAN	Transcription factor Sp1
SEPT7	Septin-7 OS=Homo sapiens (Human) GN=SEPT7 PE=1 SV=2	80	26	Q16181	SEPT7_HUMAN	Septin-7
EXOSC2	Exosome complex component RRP4 OS=Homo sapiens (Human) GN=EXOSC2 PE=1 SV=2	76	26	Q13868	EXOS2_HUMAN	Exosome complex component RRP4
NUP43	Nucleoporin Nup43 OS=Homo sapiens (Human) GN=NUP43 PE=1 SV=1	29	26	Q8NFH3	NUP43_HUMAN	Nucleoporin Nup43
API5	Apoptosis inhibitor 5 OS=Homo sapiens (Human) GN=API5 PE=1 SV=3	174	26	Q9BZZ5	API5_HUMAN	Apoptosis inhibitor 5
RBBP4	Histone-binding protein RBBP4 OS=Homo sapiens (Human) GN=RBBP4 PE=1 SV=3	95	27	Q09028	RBBP4_HUMAN	Histone-binding protein RBBP4
CHAMP1	Chromosome alignment-maintaining phosphoprotein 1 OS=Homo sapiens (Human) GN=CHAMP1 PE=1 SV=2	33	27	Q96JM3	CHAP1_HUMAN	Chromosome alignment-maintaining phosphoprotein 1
RBX1	E3 ubiquitin-protein ligase RBX1 OS=Homo sapiens (Human) GN=RBX1 PE=1 SV=1	34	27	P62877	RBX1_HUMAN	E3 ubiquitin-protein ligase RBX1
RAB11A	Ras-related protein Rab-11A OS=Homo sapiens (Human) GN=RAB11A PE=1 SV=3	31	27	P62491	RB11A_HUMAN	Ras-related protein Rab-11A
PSME1	Proteasome activator complex subunit 1 OS=Homo sapiens (Human) GN=PSME1 PE=1 SV=1	40	27	Q06323	PSME1_HUMAN	Proteasome activator complex subunit 1
KIF4A	Chromosome-associated kinesin KIF4A OS=Homo sapiens (Human) GN=KIF4A PE=1 SV=3	48	27	O95239	KIF4A_HUMAN	Chromosome-associated kinesin KIF4A
NXN	Nucleoredoxin OS=Homo sapiens (Human) GN=NXN PE=1 SV=2	33	27	Q6DKJ4	NXN_HUMAN	Nucleoredoxin
AURKB	Aurora kinase B OS=Homo sapiens (Human) GN=AURKB PE=1 SV=3	39	28	Q96GD4	AURKB_HUMAN	Aurora kinase B
EIF3E	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens (Human) GN=EIF3E PE=1 SV=1	38	28	P60228	EIF3E_HUMAN	Eukaryotic translation initiation factor 3 subunit E
RRP36	Ribosomal RNA processing protein 36 homolog OS=Homo sapiens (Human) GN=RRP36 PE=1 SV=1	27	29	Q96EU6	RRP36_HUMAN	Ribosomal RNA processing protein 36 homolog

CCDC59	Thyroid transcription factor 1-associated protein 26 OS=Homo sapiens (Human) GN=CCDC59 PE=1 SV=2	26	29	Q9P031	TAP26_HUMAN	Thyroid transcription factor 1-associated protein 26
ZCCHC3	Zinc finger CCHC domain-containing protein 3 OS=Homo sapiens (Human) GN=ZCCHC3 PE=1 SV=1	25	29	Q9NUD5	ZCHC3_HUMAN	Zinc finger CCHC domain-containing protein 3
NCOR1	Nuclear receptor corepressor 1 OS=Homo sapiens (Human) GN=NCOR1 PE=1 SV=2	39	29	O75376	NCOR1_HUMAN	Nuclear receptor corepressor 1
STAT1	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens (Human) GN=STAT1 PE=1 SV=2	85	29	P42224	STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta
NOL9	Polynucleotide 5'-hydroxyl-kinase NOL9 OS=Homo sapiens (Human) GN=NOL9 PE=1 SV=1	41	29	Q5SY16	NOL9_HUMAN	Polynucleotide 5'-hydroxyl-kinase NOL9
NOM1	Nucleolar MIF4G domain-containing protein 1 OS=Homo sapiens (Human) GN=NOM1 PE=1 SV=1	28	30	Q5C9Z4	NOM1_HUMAN	Nucleolar MIF4G domain-containing protein 1
VCL	Vinculin OS=Homo sapiens (Human) GN=VCL PE=1 SV=4	44	30	P18206	VINC_HUMAN	Vinculin
EIF3F	Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens (Human) GN=EIF3F PE=1 SV=1	65	30	O00303	EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F
GTF3C4	General transcription factor 3C polypeptide 4 OS=Homo sapiens (Human) GN=GTF3C4 PE=1 SV=2	27	30	Q9UKN8	TF3C4_HUMAN	General transcription factor 3C polypeptide 4
PTMA	Prothymosin alpha OS=Homo sapiens (Human) GN=PTMA PE=1 SV=2	23	30	P06454	PTMA_HUMAN	Prothymosin alpha
SEC13	Protein SEC13 homolog OS=Homo sapiens (Human) GN=SEC13 PE=1 SV=3	29	30	P55735	SEC13_HUMAN	Protein SEC13 homolog
RFC4	Replication factor C subunit 4 OS=Homo sapiens (Human) GN=RFC4 PE=1 SV=2	26	30	P35249	RFC4_HUMAN	Replication factor C subunit 4
BRD1	Bromodomain-containing protein 1 OS=Homo sapiens (Human) GN=BRD1 PE=1 SV=1	23	30	O95696	BRD1_HUMAN	Bromodomain-containing protein 1
BANF1	Barrier-to-autointegration factor OS=Homo sapiens (Human) GN=BANF1 PE=1 SV=1	54	31	O75531	BAF_HUMAN	Barrier-to-autointegration factor
YWHAB	14-3-3 protein beta/alpha OS=Homo sapiens (Human) GN=YWHAB PE=1 SV=3	95	31	P31946	1433B_HUMAN	14-3-3 protein beta/alpha

ARL6IP4	ADP-ribosylation factor-like protein 6-interacting protein 4 OS=Homo sapiens (Human) GN=ARL6IP4 PE=1 SV=2	72	31	Q66PJ3	AR6P4_HUMAN	ADP-ribosylation factor-like protein 6-interacting protein 4
CSTF2	Cleavage stimulation factor subunit 2 OS=Homo sapiens (Human) GN=CSTF2 PE=1 SV=1	125	31	P33240	CSTF2_HUMAN	Cleavage stimulation factor subunit 2
CMAS	N-acylneuraminate cytidylyltransferase OS=Homo sapiens (Human) GN=CMAS PE=1 SV=2	29	31	Q8NFW8	NEUA_HUMAN	N-acylneuraminate cytidylyltransferase
USP11	Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens (Human) GN=USP11 PE=1 SV=3	28	31	P51784	UBP11_HUMAN	Ubiquitin carboxyl-terminal hydrolase 11
MIF	Macrophage migration inhibitory factor OS=Homo sapiens (Human) GN=MIF PE=1 SV=4	53	31	P14174	MIF_HUMAN	Macrophage migration inhibitory factor
KPNA3	Importin subunit alpha-4 OS=Homo sapiens (Human) GN=KPNA3 PE=1 SV=2	51	32	O00505	IMA4_HUMAN	Importin subunit alpha-4
SMC2	Structural maintenance of chromosomes protein 2 OS=Homo sapiens (Human) GN=SMC2 PE=1 SV=2	28	32	O95347	SMC2_HUMAN	Structural maintenance of chromosomes protein 2
ANXA5	Annexin A5 OS=Homo sapiens (Human) GN=ANXA5 PE=1 SV=2	77	32	P08758	ANXA5_HUMAN	Annexin A5

Table S2, related to Figure 4B: REV-ERBα knockdown disturbs HepG2 cellular protein O-GlcNAcylation. List of identified O-GlcNAcylated protein identified by LC-MS/MS analysis after SDS-PAGE separation of enriched O-GlcNAcylated protein immunoprecipitated from HepG2 cells transfected by the indicated siRNA (Scr or targeting REV-ERBα).

siScr vs si NR1D1 HepG2		Score Sequest HT	
Accession	**Description**	**si Ctrl**	**si NR1D1**
A8K7Q2	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	5006,37	1697,81
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	4735,69	1953,91
A0A075B7D9	TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1	781,07	61,26
P55884	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	426,97	0
Q7Z3B4	Nucleoporin p54 OS=Homo sapiens GN=NUP54 PE=1 SV=2	1117,41	709,71
B4E227	Nuclear RNA export factor 1 OS=Homo sapiens GN=NXF1 PE=1 SV=1	602,67	229,74
V9HW22	Epididymis luminal protein 33 OS=Homo sapiens GN=HEL-S-72p PE=2 SV=1	493,49	129,89
O94855	Protein transport protein Sec24D OS=Homo sapiens GN=SEC24D PE=1 SV=2	564,3	205,07
Q53GZ6	Heat shock 70kDa protein 8 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	751,75	410,07
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	313,3	0
A6NEM2	Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2	2561,58	2257,76
Q59EJ3	Heat shock 70kDa protein 1A variant (Fragment) OS=Homo sapiens PE=2 SV=1	297,51	0
Q6IBQ5	FUS protein OS=Homo sapiens GN=FUS PE=2 SV=1	289,27	0
B3GQS7	Mitochondrial heat shock 60kD protein 1 variant 1 OS=Homo sapiens GN=HSPD1 PE=2 SV=1	419,17	130,7
Q53HF2	Heat shock 70kDa protein 8 isoform 2 variant (Fragment) OS=Homo sapiens PE=1 SV=1	630,16	358,1
O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3	361,79	105,11
A0A0D9SF53	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=1	748,17	492,07
P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	349,14	100,56
A0A0D9SEI3	Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=1 SV=1	345,38	98,5
P53992	Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3	496,9	257,06
B4DRT3	Pyruvate kinase OS=Homo sapiens PE=2 SV=1	1126,28	918,28
Q86X55	Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=3	712,68	516,06
H3BQK0	ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1	188,8	0
A8K3C3	T-complex protein 1 subunit delta OS=Homo sapiens PE=2 SV=1	305,47	117,48
P34931	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	408,34	221
P15924	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	645,88	459,82
I3L352	ATP-dependent RNA helicase DDX19A (Fragment) OS=Homo sapiens GN=DDX19A PE=1 SV=1	181,72	0
B0QY89	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	350,4	178,21
D6RIH9	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1	255,66	86,37
D6REX3	Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=1	362,77	203,55
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	321,56	163,08
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	276,47	122,41
Q59ET3	Chaperonin containing TCP1, subunit 6A isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	225,95	76,98

V9HWA9	Epididymis secretory sperm binding protein Li 62p OS=Homo sapiens GN=HEL-S-62p PE=2 SV=1	147,38	0
Q96RK0	Protein capicua homolog OS=Homo sapiens GN=CIC PE=1 SV=2	239,5	92,9
H7BXF5	Histone deacetylase complex subunit SAP130 OS=Homo sapiens GN=SAP130 PE=1 SV=1	143,4	0
Q6IRW3	Semenogelin II OS=Homo sapiens GN=SEMG2 PE=2 SV=1	143,02	0
G3V220	Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=1	283,12	140,53
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	322,43	181,15
A0A087WUL0	Protein TKFC OS=Homo sapiens GN=TKFC PE=1 SV=1	135,9	0
Q9UPQ9	Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	255,8	124,02
P0DMV9	Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1	340,78	209,56
Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2	235,29	104,32
Q9BVL2	Nucleoporin p58/p45 OS=Homo sapiens GN=NUPL1 PE=1 SV=1	443,79	316,17
O15027	Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=3	124,96	0
Q96KR1	Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2	151,44	26,82
Q8TBR3	Fusion (Involved in t(1216) in malignant liposarcoma) OS=Homo sapiens GN=FUS PE=2 SV=1	578,54	454,29
A0A024R1A3	Ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing), isoform CRA_a OS=Homo sapiens GN=UBE1 PE=3 SV=1	122,89	0
Q13835	Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	121,46	0
B7ZVY7	Cell division cycle 2-like 1 (PITSLRE proteins) OS=Homo sapiens GN=CDC2L1 PE=1 SV=1	180,12	62,34
A0A024RDH6	SEC31-like 1 (S. cerevisiae), isoform CRA_b OS=Homo sapiens GN=SEC31L1 PE=4 SV=1	250,56	134,7
A0A0C4DH82	SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1	416,68	303,67
Q59EA0	Ubiquitin associated protein 2 isoform 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1	122,52	10,26
B3KT93	Polyadenylate-binding protein OS=Homo sapiens PE=2 SV=1	287,56	176,12
E9PK59	N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=1 SV=1	105,37	0
B3KQT2	Protein disulfide-isomerase OS=Homo sapiens PE=2 SV=1	251,02	148,93
Q5CAQ4	TNF receptor-associated protein 1 OS=Homo sapiens GN=TRAP1 PE=2 SV=1	240,9	139,41
Q9HBB2	Aconitate hydratase OS=Homo sapiens GN=IRP1 PE=2 SV=1	124,36	23,35
E7EQR6	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	267,55	166,7
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2	140,64	41,97
B7ZAR1	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	96,98	0
Q3B7A7	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase OS=Homo sapiens GN=GART PE=2 SV=1	96,87	0
Q70T18	BBF2H7/FUS protein (Fragment) OS=Homo sapiens PE=2 SV=1	219,13	124,92
P54578	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3	93,66	0
Q92900	Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	134,02	40,75
A0A087WZS2	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1	188,83	99,28
B4DE36	Glucose-6-phosphate isomerase OS=Homo sapiens PE=2 SV=1	88,98	0
A0A024R9A4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked, isoform CRA_a OS=Homo sapiens GN=DDX3Y PE=3 SV=1	257,27	168,44

Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3	146,56	63,28
Q5QPR3	Cyclin-dependent kinase 11A OS=Homo sapiens GN=CDK11A PE=1 SV=1	123	40,82
Q86TG7	Retrotransposon-derived protein PEG10 OS=Homo sapiens GN=PEG10 PE=1 SV=2	133,16	51,44
H3BPE7	RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	289,27	211,47
Q13344	Fus-like protein (Fragment) OS=Homo sapiens PE=2 SV=1	289,27	211,47
Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	99,9	22,17
A0A087X078	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	136,75	59,95
Q53GR7	Solute carrier family 25, member 13 (Citrin) variant (Fragment) OS=Homo sapiens PE=2 SV=1	163,1	87,86
H0YM23	Ankyrin repeat domain-containing protein 17 (Fragment) OS=Homo sapiens GN=ANKRD17 PE=1 SV=1	74,48	0
Q5JYR4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Fragment) OS=Homo sapiens GN=RPN2 PE=1 SV=5	73,36	0
Q9BTC0	Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5	98,37	29,85
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	189,42	121,14
Q06AH7	Transferrin OS=Homo sapiens GN=TF PE=2 SV=1	68,2	0
E9PDF6	Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=1	66,9	0
I3L0K7	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=1	156,42	90,33
F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=1	201,78	136,26
H0Y6K5	Transcription factor Sp3 OS=Homo sapiens GN=SP3 PE=1 SV=1	170,5	106,56
Q05BK6	Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=1	251,14	189,67
J3KQ69	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=2	59,67	0
B0YIW6	Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=1 SV=1	56,57	0
F5H6E2	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=1	56,3	0
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2	55,08	0
P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	124,46	70,64
E9PK47	Alpha-1,4 glucan phosphorylase OS=Homo sapiens GN=PYGL PE=1 SV=1	207	153,49
A0A087WTE1	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=1	53,3	0
Q14119	Vascular endothelial zinc finger 1 OS=Homo sapiens GN=VEZF1 PE=1 SV=2	51,83	0
O60701	UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	85,27	34,29
A0A0A0MS59	Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=1	206,09	156,47
P28288	ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1	48,63	0
H7BZ94	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=2	47,97	0
P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	84,83	37,86
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	103,81	57,06
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	66,51	21,22
H0Y2W2	ATPase family AAA domain-containing protein 3A (Fragment) OS=Homo sapiens GN=ATAD3A PE=1 SV=1	44,6	0
Q5SYQ9	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=1	64,57	20,06
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	42,96	0

Q8IW76	EIF2AK2 protein (Fragment) OS=Homo sapiens GN=EIF2AK2 PE=2 SV=1	42,87	0
F8VQP2	Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=1	42	0
B5ME19	Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo sapiens GN=EIF3CL PE=3 SV=1	41,75	0
Q6IAP9	PRPF4 protein OS=Homo sapiens GN=PRPF4 PE=2 SV=1	41,1	0
A0A024R1V5	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila) translocated to, 6, isoform CRA_a OS=Homo sapiens GN=MLLT6 PE=4 SV=1	40,82	0
Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	175,62	135,32
O95782	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	39,88	0
A7XAK3	Capicua-like protein/double homeodomain 4 fusion protein OS=Homo sapiens GN=CIC/DUX4 fusion PE=2 SV=1	64,46	26,15
Q8NHX6	DNA helicase OS=Homo sapiens GN=HCC5 PE=2 SV=1	37,12	0
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	36,98	0
A0A087WY75	Nuclear envelope pore membrane protein POM 121C OS=Homo sapiens GN=POM121C PE=1 SV=1	472,89	435,94
B2RA56	Nicalin OS=Homo sapiens PE=2 SV=1	35,58	0
P05023	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	47,94	12,72
F8W108	AT-rich interactive domain-containing protein 2 OS=Homo sapiens GN=ARID2 PE=1 SV=1	34,78	0
A8MUD9	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	55,92	21,29
H3BUF6	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=1	34,33	0
P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4	92,07	58,56
C9JC84	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=1	33,36	0
O95399	Urotensin-2 OS=Homo sapiens GN=UTS2 PE=1 SV=1	32,94	0
P13674	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2	30,88	
O00425	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2	30,79	0
Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	30,6	0
V9HW37	Epididymis secretory protein Li 69 OS=Homo sapiens GN=HEL-S-69 PE=1 SV=1	30,57	0
P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	29,67	0
K7ER00	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=1	28,88	0
A8K8D9	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens PE=2 SV=1	391,32	362,48
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	28,8	0
A4D111	Similar to Chain , Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal) (E.C.3.6.1.3) Mutant With Asp 206 Replaced By Ser (D206s) OS=Homo sapiens GN=LOC401308 PE=3 SV=1	62,82	34,44
Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	120,67	92,3
A0A024R7U6	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=MCM4 PE=3 SV=1	27,24	0
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	26,15	0
Q53XL8	Proteasome (Prosome, macropain) 26S subunit, ATPase, 1 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	26,1	0
Q9Y678	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	56,56	31,12
Q53H53	Flavin containing monooxygenase 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1	25,3	0

P13637	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3	24,98	0
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	124,57	99,81
M0QXN5	Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=1	100,31	76,41
E9PP73	Coatomer subunit beta (Fragment) OS=Homo sapiens GN=COPB1 PE=1 SV=5	68,2	44,76
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	22	0
P14136	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	21,84	0
Q9BV61	TRAP1 protein (Fragment) OS=Homo sapiens GN=TRAP1 PE=2 SV=2	62,68	41,18
Q5JR04	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=MOV10 PE=1 SV=1	21,23	0
Q9P2N6	KAT8 regulatory NSL complex subunit 3 OS=Homo sapiens GN=KANSL3 PE=1 SV=2	77,43	56,42
A8K984	Structural maintenance of chromosomes protein OS=Homo sapiens PE=2 SV=1	21	0
Q13177	Serine/threonine-protein kinase PAK 2 OS=Homo sapiens GN=PAK2 PE=1 SV=3	18,51	0
P31749	RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2	18,13	0
O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	18	0
Q9UQC1	Heat shock protein 72 (Fragment) OS=Homo sapiens GN=HSP70-1 PE=3 SV=1	55,31	37,96
O15047	Histone-lysine N-methyltransferase SETD1A OS=Homo sapiens GN=SETD1A PE=1 SV=3	17	0
Q13884	Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3	16,95	0
Q86XN7	Proline and serine-rich protein 1 OS=Homo sapiens GN=PROSER1 PE=1 SV=2	16,32	0
P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	27,83	11,63
O95163	Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	15	0
Q76L82	Additional sex combs like 1 (Drosophila), isoform CRA_d OS=Homo sapiens GN=ASXH1 PE=1 SV=1	14,78	0
Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1	14,71	0
C9J9G2	PHD finger protein 12 OS=Homo sapiens GN=PHF12 PE=1 SV=2	100,64	86,28
Q96T67	TOB3 OS=Homo sapiens PE=2 SV=1	14,36	0
E9PF10	Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1	14	0
Q6P4R8	Nuclear factor related to kappa-B-binding protein OS=Homo sapiens GN=NFRKB PE=1 SV=2	14	0
O94925	Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1	13,78	0
A0A087WT27	Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1	13,74	0
Q7KZF4	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	84,2	70,76
P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	12,93	0
P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3	56,58	43,84
O95036	Similar to 60S ribosomal protein L7; similar to P18124 (PID:d133021) OS=Homo sapiens GN=WUGSC:H_RG054D04.1 PE=3 SV=1	12,62	0
P50570	Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2	12,54	0
P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2	12,52	0
A0A024R1N4	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_a OS=Homo sapiens GN=XRCC6 PE=4 SV=1	12,35	0
P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4	42,89	30,67
Q9UL79	Myosin-reactive immunoglobulin light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	11,9	0

P54577	Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	11,67	0
P55795	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	11,37	0
Q14683	Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2	11	0
Q8WY24	SNC66 protein OS=Homo sapiens PE=1 SV=1	10,86	0
O15371	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	10,64	0
Q5JRR6	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=1	10,51	0
E9KL44	Epididymis tissue sperm binding protein Li 14m OS=Homo sapiens PE=2 SV=1	10,35	0
Q2KHR3	Glutamine and serine-rich protein 1 OS=Homo sapiens GN=QSER1 PE=1 SV=3	10,33	0
O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP	30,96	20,64
Q14554	Protein disulfide-isomerase A5 OS=Homo sapiens GN=PDIA5 PE=1 SV=1	10,25	0
Q9UKI9	POU domain, class 2, transcription factor 3 OS=Homo sapiens GN=POU2F3 PE=2 SV=3	10,22	0
A0A0C4DGH5	Cullin-associated NEDD8-dissociated protein 1 (Fragment) OS=Homo sapiens GN=CAND1 PE=1 SV=1	47,67	37,62
Q9C0C2	182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	10	0
E9PRE7	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=1	122,86	113,09
B5BUE6	ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens GN=DDX5 PE=2 SV=1	49,49	41,39
Q05BV1	SMC2 protein (Fragment) OS=Homo sapiens GN=SMC2 PE=2 SV=1	7	0
Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1	7	0
V9HVX6	Epididymis luminal protein 9 OS=Homo sapiens GN=HEL-9 PE=2 SV=1	26,83	20,06
P56192	Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	30,79	24,21
Q6A165	HHa7 protein (Fragment) OS=Homo sapiens GN=KRTHA7 PE=2 SV=1	38,32	32,11
Q7Z3K3	Pogo transposable element with ZNF domain OS=Homo sapiens GN=POGZ PE=1 SV=2	6	0
Q2KQ72	Chromosome-associated protein E OS=Homo sapiens PE=2 SV=1	6	0
Q6IBN0	PSMD3 protein OS=Homo sapiens GN=PSMD3 PE=2 SV=1	33,03	27,24
A0A0B4J269	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=1	43,74	37,95
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	5	0
A0A024RDG1	Vesicle docking protein p115, isoform CRA_a OS=Homo sapiens GN=VDP PE=4 SV=1	14,03	10,31
O95429	BAG family molecular chaperone regulator 4 OS=Homo sapiens GN=BAG4 PE=1 SV=1	26,12	23,06
I6TRR8	SND1-BRAF fusion OS=Homo sapiens PE=2 SV=1	27,12	24,54
P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	36,17	33,89
Q13041	P67 OS=Homo sapiens PE=2 SV=1	11,33	10,61
Q1KSF8	XTP3TPA-transactivated protein 1 OS=Homo sapiens GN=XTP3TPATP1 PE=2 SV=1	15,16	14,7
Q9Y5X1	Sorting nexin-9 OS=Homo sapiens GN=SNX9 PE=1 SV=1	96,88	96,88
Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	51,88	51,88
K7EQ05	Granulins OS=Homo sapiens GN=GRN PE=1 SV=1	39,26	39,26
Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	37,62	37,62
Q7KYM9	ORF protein OS=Homo sapiens GN=ORF PE=2 SV=1	25,16	25,16
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2	18,86	18,86

Q71E78	Extraskeletal myxoid chondrosarcoma EWS/TEC/CHN fusion protein (Fragment) OS=Homo sapiens PE=2 SV=1	13,44	13,44
A9Z0R7	EWSR1/ZNF384 fusion protein (Fragment) OS=Homo sapiens GN=EWSR1/ZNF384 fusion PE=2 SV=1	13,44	13,44
Q14677	Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 PE=1 SV=1	12,61	12,61
Q59GL1	Synaptotagmin binding, cytoplasmic RNA interacting protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	10,32	10,32
P52948	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4	257,79	257,83
Q9Y3I0	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	36,83	37,31
P11217	Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6	11,68	12,59
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	54,79	57,27
Q96BA7	HNRPU protein OS=Homo sapiens PE=2 SV=1	12,65	15,95
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	29,26	32,94
Q00341	Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	40	43,98
Q86VP1	Tax1-binding protein 1 OS=Homo sapiens GN=TAX1BP1 PE=1 SV=2	21,06	25,04
P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	10,44	14,75
Q5SZU1	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=1	38,44	44,73
Q9Y520	Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=4	587,94	594,38
Q9HCJ0	Trinucleotide repeat-containing gene 6C protein OS=Homo sapiens GN=TNRC6C PE=1 SV=3	4	10,62
B7ZLC8	JMJD1C protein OS=Homo sapiens GN=JMJD1C PE=2 SV=1	9	16
P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2	19,85	27,83
B7Z795	Carboxylic ester hydrolase OS=Homo sapiens PE=2 SV=1	19,85	27,83
Q5CAQ5	Tumor rejection antigen (Gp96) 1 OS=Homo sapiens GN=TRA1 PE=2 SV=1	272,97	281,82
B3KRE9	POU domain protein OS=Homo sapiens PE=2 SV=1	80,77	90,3
Q6P452	Annexin OS=Homo sapiens GN=ANXA4 PE=1 SV=1	0	10,05
A0A024RCC4	Nucleoporin 98kDa, isoform CRA_a OS=Homo sapiens GN=NUP98 PE=4 SV=1	247,54	257,83
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	114,95	125,27
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	0	10,62
P49588	Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	17,55	28,49
Q6P2D7	HNRPM protein (Fragment) OS=Homo sapiens GN=HNRPM PE=2 SV=1	50,01	60,97
H9ZYJ2	Thioredoxin OS=Homo sapiens GN=TXN PE=2 SV=1	0	11,05
Q86UA1	Pre-mRNA-processing factor 39 OS=Homo sapiens GN=PRPF39 PE=1 SV=3	0	11,07
P0C7T5	Ataxin-1-like OS=Homo sapiens GN=ATXN1L PE=1 SV=1	0	11,16
A0A024R0E5	Capping protein (Actin filament) muscle Z-line, alpha 1, isoform CRA_a OS=Homo sapiens GN=CAPZA1 PE=4 SV=1	0	11,2
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	0	11,33
P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5	0	11,43
B2R4R0	Histone H4 OS=Homo sapiens GN=HIST1H4H PE=2 SV=1	0	11,55
F8W6N3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=BAP1 PE=1 SV=1	64,93	76,58

P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	10,68	22,48
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	0	11,92
M1VPF4	Tyrosine-protein kinase receptor OS=Homo sapiens GN=TPM3-ROS1 PE=2 SV=1	0	12,17
A8MX94	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=1	0	12,22
Q96J92	Serine/threonine-protein kinase WNK4 OS=Homo sapiens GN=WNK4 PE=1 SV=1	0	12,24
Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	0	12,34
Q8TDJ5	Tyrosine-protein kinase receptor OS=Homo sapiens GN=TFG/ALK fusion PE=2 SV=1	66,52	78,94
L0R5C4	Alternative protein POTEM OS=Homo sapiens GN=POTEM PE=3 SV=1	0	12,55
Q5K684	SCCA1/SCCA2 fusion protein OS=Homo sapiens GN=SERPINB3 PE=1 SV=1	0	12,71
A0A0A0MRN4	DBIRD complex subunit ZNF326 OS=Homo sapiens GN=ZNF326 PE=1 SV=1	55,01	67,91
V9HW69	Epididymis secretory protein Li 66 OS=Homo sapiens GN=HEL-S-66 PE=2 SV=1	0	12,98
P41252	Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	52	65,14
A0A024RCN6	Valyl-tRNA synthetase, isoform CRA_a OS=Homo sapiens GN=VARS PE=3 SV=1	16	29,18
F1JVV5	EWSR1/ATF1 fusion protein type 1 OS=Homo sapiens GN=EWSR1/ATF1 fusion PE=2 SV=1	51,85	65,31
Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	0	13,62
Q8N6B4	Myeloid/lymphoid or mixed-lineage leukemia/clathrin assembly protein fusion protein (Fragment) OS=Homo sapiens GN=MLL/CALM fusion PE=2 SV=1	0	13,84
O75342	Arachidonate 12-lipoxygenase, 12R-type OS=Homo sapiens GN=ALOX12B PE=1 SV=1	0	13,84
A6NIW5	Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=1 SV=2	0	13,86
Q58FF2	Heat shock protein 94c OS=Homo sapiens GN=GRP94c PE=2 SV=1	0	13,94
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	12,65	26,6
A0A024RAD8	Aldehyde dehydrogenase 4 family, member A1, isoform CRA_a OS=Homo sapiens GN=ALDH4A1 PE=3 SV=1	0	14,09
O75083	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	210,76	224,97
Q7Z589	Protein EMSY OS=Homo sapiens GN=EMSY PE=1 SV=2	216,13	230,41
P57740	Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1	0	14,97
A0A024R2A7	Lectin, mannose-binding, 1, isoform CRA_b OS=Homo sapiens GN=LMAN1 PE=4 SV=1	30,55	45,58
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	0	15,31
V9HWE9	Epididymis secretory protein Li 22 OS=Homo sapiens GN=HEL-S-22 PE=2 SV=1	0	16,01
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	0	16,33
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	0	16,37
Q6LC01	MRNA encoding beta-tubulin. (from clone D-beta-1) (Fragment) OS=Homo sapiens PE=2 SV=1	43,51	59,9
Q6GMX6	IGH@ protein OS=Homo sapiens GN=IGH@ PE=1 SV=1	0	17,29
V9HW68	Epididymis luminal protein 214 OS=Homo sapiens GN=HEL-214 PE=2 SV=1	0	17,29
Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2	110,05	127,7
Q14568	Heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2P PE=1 SV=2	0	17,89
Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2	12,82	30,8
A5A3E0	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	20,82	38,98

V9HWG3	Epididymis secretory protein Li 45 OS=Homo sapiens GN=HEL-S-45 PE=2 SV=1	0	18,52
Q8IW75	Serpin A12 OS=Homo sapiens GN=SERPINA12 PE=1 SV=1	0	18,74
F8WE04	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=1	0	18,92
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	146,56	165,5
O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	0	19,18
E9KL35	Epididymis tissue sperm binding protein Li 3a OS=Homo sapiens PE=1 SV=1	0	19,36
Q9UQM3	Alpha-tubulin (Fragment) OS=Homo sapiens PE=2 SV=1	11,01	31,05
B0QZ18	Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1	33,57	53,76
B7Z4L4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	201,67	222,99
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	0	21,62
Q96QA5	Gasdermin-A OS=Homo sapiens GN=GSDMA PE=1 SV=4	0	21,62
Q8N3Y7	Epidermal retinol dehydrogenase 2 OS=Homo sapiens GN=SDR16C5 PE=2 SV=2	0	22
H0Y4R1	Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=1 SV=1	0	22,1
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	10,8	33
A8MXP9	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1	0	22,22
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	0	22,25
V9HWK4	Epididymis luminal protein 162 OS=Homo sapiens GN=HEL162 PE=2 SV=1	42,4	64,71
P51812	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1	0	22,5
Q6S8J3	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	20,82	43,88
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	0	23,4
P08047	Transcription factor Sp1 OS=Homo sapiens GN=SP1 PE=1 SV=3	83,31	106,9
B2R5H0	Protein S100 OS=Homo sapiens PE=2 SV=1	0	24,2
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	0	24,57
B4DT28	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	48,6	73,96
O14841	5-oxoprolinase OS=Homo sapiens GN=OPLAH PE=1 SV=3	0	25,74
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	93,34	119,2
Q59F66	DEAD box polypeptide 17 isoform p82 variant (Fragment) OS=Homo sapiens PE=2 SV=1	61,12	87,23
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	0	26,59
A4FVC0	Protein argonaute (Fragment) OS=Homo sapiens GN=EIF2C2 PE=2 SV=1	0	26,7
Q9HCY8	Protein S100-A14 OS=Homo sapiens GN=S100A14 PE=1 SV=1	0	27,72
P36952	Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2	0	28,03
Q6ZVX7	F-box only protein 50 OS=Homo sapiens GN=NCCRP1 PE=1 SV=1	0	28,5
Q08188	Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	24,62	53,76
V9HW12	Epididymis secretory sperm binding protein Li 2a OS=Homo sapiens GN=HEL-S-2a PE=2 SV=1	0	29,22
Q53H37	Calmodulin-like skin protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	0	29,51
D3DQF6	POU domain, class 4, transcription factor 3, isoform CRA_a OS=Homo sapiens GN=POU4F3 PE=4	96,64	128,04

	SV=1		
O75400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2	51,75	83,21
Q9Y337	Kallikrein-5 OS=Homo sapiens GN=KLK5 PE=1 SV=2	0	32,01
Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3	16,25	48,28
P12036	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4	0	32,12
P49862	Kallikrein-7 OS=Homo sapiens GN=KLK7 PE=1 SV=1	0	32,26
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	14,54	47,07
B9EKV4	Aldehyde dehydrogenase 9 family, member A1 OS=Homo sapiens GN=ALDH9A1 PE=2 SV=1	0	32,58
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	11,23	43,91
P42357	Histidine ammonia-lyase OS=Homo sapiens GN=HAL PE=1 SV=1	0	32,82
Q5T8P6	RNA-binding protein 26 OS=Homo sapiens GN=RBM26 PE=1 SV=3	11	44,32
P20073	Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3	0	33,37
V9HW80	Epididymis luminal protein 220 OS=Homo sapiens GN=HEL-S-70 PE=1 SV=1	41,46	75,34
J3KPD9	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	0	33,97
C9J4V0	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	0	34,73
Q6UWP8	Suprabasin OS=Homo sapiens GN=SBSN PE=1 SV=2	13,84	48,7
P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	0	36,74
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	13,39	50,44
P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3	16,8	54,81
P0CG38	POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1	0	38,09
V9HW84	Epididymis secretory sperm binding protein Li 124m OS=Homo sapiens GN=HEL-S-124m PE=2 SV=1	135,51	174,64
V9HW26	ATP synthase subunit alpha OS=Homo sapiens GN=HEL-S-123m PE=1 SV=1	22,19	61,5
P06753	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2	0	39,33
A0A0A0MR02	Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=1	0	39,66
Q9H9G7	Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	0	39,97
Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0	40,65
Q96P63	Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	16,05	56,71
Q9BVA1	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	0	40,86
V9HW31	ATP synthase subunit beta OS=Homo sapiens GN=HEL-S-271 PE=1 SV=1	0	40,92
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	0	41,56
P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	10,85	53,05
Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	424,87	467,49
P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	0	43,48
O75322	Hsp89-alpha-delta-N OS=Homo sapiens PE=2 SV=1	32,6	77,81
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	18,75	66,12
B3KSI4	Transketolase OS=Homo sapiens PE=2 SV=1	89,08	136,91
V9HVZ7	Epididymis luminal protein 176 OS=Homo sapiens GN=HEL-176 PE=2 SV=1	12,3	61,05

Q9Y446	Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	0	48,76
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	0	49,38
B4DV12	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	0	49,38
P14735	Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	0	50,11
Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=1 SV=1	0	50,64
P27482	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2	0	50,68
B8ZZK2	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1	0	51,05
P47929	Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	0	51,33
V9HW43	Epididymis secretory protein Li 102 OS=Homo sapiens GN=HEL-S-102 PE=2 SV=1	0	51,74
P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	162,47	215,19
E5KNY5	Leucine-rich PPR-motif containing OS=Homo sapiens GN=LRPPRC PE=4 SV=1	24,19	76,94
Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2	0	52,84
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	0	53,13
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	0	54,02
Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1	0	57,48
Q8TA90	Similar to Elongation factor 2b (Fragment) OS=Homo sapiens PE=2 SV=1	133,3	191,38
Q5JQ13	Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=1 SV=1	0	58,45
O95486	Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2	0	60,63
A0A087WWI4	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	88	149,88
H0YMQ8	Protein-glutamine gamma-glutamyltransferase K (Fragment) OS=Homo sapiens GN=TGM1 PE=1 SV=1	0	62,09
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	253,54	317,53
B4DGU4	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1	41,58	105,81
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	0	64,58
F8VVB9	Tubulin alpha-1B chain (Fragment) OS=Homo sapiens GN=TUBA1B PE=1 SV=5	64,62	129,75
A0A024R8Y2	POU domain protein OS=Homo sapiens GN=POU2F1 PE=3 SV=1	202,16	270,2
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	0	68,14
F4ZW65	NF90b OS=Homo sapiens PE=2 SV=1	314,88	383,9
Q9P2N5	RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=1 SV=2	200,04	269,46
A8MT40	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2	0	69,91
F4ZW66	NF110b OS=Homo sapiens PE=2 SV=1	340,59	411,42
Q0P6H7	TRIM29 protein OS=Homo sapiens GN=TRIM29 PE=1 SV=2	0	72,97
Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	0	73,5
Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	30,9	105,25
Q9Y3S1	Serine/threonine-protein kinase WNK2 OS=Homo sapiens GN=WNK2 PE=1 SV=4	48,27	122,89
Q8WVV4	Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3	10,05	84,8
F8WD96	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	0	75,43
E9PLK3	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=1	53,82	129,41

C3UMV2	EWSR1/NFATC2 fusion protein OS=Homo sapiens PE=2 SV=1	119,14	195,93
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	0	77,5
P09086	POU domain, class 2, transcription factor 2 OS=Homo sapiens GN=POU2F2 PE=1 SV=3	0	78,41
A0A087X2G1	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=1	0	78,79
Q93009	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2	44,4	123,3
Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	31,42	110,37
B2CIS9	Caspase 14, apoptosis-related cysteine peptidase OS=Homo sapiens GN=CASP14 PE=2 SV=1	0	79,48
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	0	80,48
A7BI36	p180/ribosome receptor OS=Homo sapiens GN=RRBP1 PE=2 SV=2	0	80,94
F4ZW64	NF90a OS=Homo sapiens PE=2 SV=1	311,63	393,38
C9JGE3	EWS RNA-binding protein variant 6 OS=Homo sapiens GN=EWSR1 PE=1 SV=2	143,45	226,21
A0A024R1N1	Myosin, heavy polypeptide 9, non-muscle, isoform CRA_a OS=Homo sapiens GN=MYH9 PE=4 SV=1	0	84,56
A0A024R4H0	Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1, isoform CRA_a OS=Homo sapiens GN=PLOD1 PE=4 SV=1	0	84,78
B4DHB3	Phosphoglycerate kinase OS=Homo sapiens PE=2 SV=1	0	87,33
Q8IZ29	Tubulin, beta 2C OS=Homo sapiens GN=TUBB2C PE=2 SV=1	63,12	150,58
O43823	A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1	11,76	100,79
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	0	90,03
P52789	Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2	0	92,41
P05091	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2	0	93,96
B2R7L2	Annexin OS=Homo sapiens PE=2 SV=1	0	94,88
H0Y339	E3 ubiquitin-protein ligase RFWD2 (Fragment) OS=Homo sapiens GN=RFWD2 PE=1 SV=1	0	98,81
Q5JP53	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=1	141,84	241,58
Q08554	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	273,19	374,28
E7EVS6	Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens GN=ACTB PE=1 SV=5	10,25	111,61
B5BTZ6	Signal transducer and activator of transcription OS=Homo sapiens GN=STAT3 PE=2 SV=1	0	102,56
H3BVG0	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=1	0	102,81
O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	0	107,28
Q01212	Profilaggrin (Fragment) OS=Homo sapiens PE=4 SV=1	0	107,91
Q96IF9	VCP protein (Fragment) OS=Homo sapiens GN=VCP PE=2 SV=2	27,87	140,36
Q8NDV7	Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	21,17	135,52
E9PKU7	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=1	262,55	380,63
A0A0A0MS51	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	0	125,01
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	0	128,61
P47897	Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	0	128,93
Q96HA1	Nuclear envelope pore membrane protein POM 121 OS=Homo sapiens GN=POM121 PE=1 SV=2	0	129,74
D6RHH4	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=1	0	131,3
Q15437	Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	0	131,99

P63267	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1	42,96	176,65
O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	29,28	165,5
P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	0	137,45
A0A087WTA8	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=1	0	140,22
P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3	89,11	231,21
F8W726	Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	656,94	799,64
O95487	Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2	0	143,39
Q15436	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2	372,51	517,18
M0R1M6	Ubiquitin-60S ribosomal protein L40 (Fragment) OS=Homo sapiens GN=UBA52 PE=1 SV=1	0	155,26
V9GZ37	Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1	141,17	298,27
P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	57,83	216,15
A5GZ75	Beta-actin (Fragment) OS=Homo sapiens PE=2 SV=1	10,37	169,1
Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	10,59	177,19
P30876	DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1	0	167,1
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	0	167,44
Q92817	Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3	0	182,38
Q9UL18	Protein argonaute-1 OS=Homo sapiens GN=AGO1 PE=1 SV=3	0	183,88
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	0	185,65
F5H5D3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	142,52	330,32
Q59GA5	Insulysin variant (Fragment) OS=Homo sapiens PE=2 SV=1	0	187,95
Q99567	Nuclear pore complex protein Nup88 OS=Homo sapiens GN=NUP88 PE=1 SV=2	21,92	215,24
X5D7K9	Major vault protein isoform C (Fragment) OS=Homo sapiens GN=MVP PE=2 SV=1	251,09	449,41
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	0	204,49
B4DUI5	Triosephosphate isomerase OS=Homo sapiens PE=2 SV=1	0	213,36
I6L8B7	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=1	0	217,46
P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	94,68	318,32
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	35,65	261,85
V9HWB4	Epididymis secretory sperm binding protein Li 89n OS=Homo sapiens GN=HEL-S-89n PE=2 SV=1	0	237,58
A0A075B730	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	0	241,26
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	181,26	428,74
Q0EFA5	S protein OS=Homo sapiens GN=S PE=4 SV=1	0	262,14
A1XP52	Catecholamine-regulated protein 40 OS=Homo sapiens PE=2 SV=1	43,34	311,16
L8B196	Ubiquitin C OS=Homo sapiens GN=UbC PE=4 SV=1	168,39	455,94
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	230,76	560,94
Q02413	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	0	349,12
Q2TSD0	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens PE=2 SV=1	63,22	433,06
A0A087WYP0	Hepatocyte nuclear factor 1-alpha OS=Homo sapiens GN=HNF1A PE=1 SV=1	324,92	697,05

P02545	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	0	378,97
A0A0A0MRA5	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=1	674,39	1083,78
J3KT65	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	180,96	600,45
F5H2U4	Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBAP2 PE=1 SV=2	742,22	1169
A0A0D9SFL3	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1	620,53	1050,82
Q53G76	Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1	195,51	661,53
Q562L5	Actin-like protein (Fragment) OS=Homo sapiens GN=ACT PE=3 SV=1	0	497,85
H0YLV6	Annexin OS=Homo sapiens GN=ANXA2 PE=1 SV=1	0	591,3
Q9H4A3	Serine/threonine-protein kinase WNK1 OS=Homo sapiens GN=WNK1 PE=1 SV=2	911,75	1532,16
P20930	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	0	660,26
P49790	Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2	1951,66	2686,26
P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	526,78	1399,32
P35658	Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2	1292,99	2505,93
Q53G85	Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1	782,26	2309,22