Hyperactive mTOR Induces Neuroendocrine Differentiation in Prostate Cancer Cell with Concurrent Up-regulation of IRF1

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Abstract

BACKGROUND

Neuroendocrine-differentiated prostate cancer (NEPCa) is refractory to androgen deprivation therapy and shows a poor prognosis. The underlying mechanisms responsible for neuroendocrine differentiation (NED) are yet to be clarified. In this study, we investigated the role of mammalian target of rapamycin (mTOR) in NEPCa.

METHODS

We utilized a gain-of-function analysis by establishing a human PCa LNCaP stable line that expresses hyperactive mTOR (LNCaP-mTOR). Then, we employed a comprehensive mass spectrometric analysis to identify a key transcription factor in LNCaP-mTOR, followed by a loss-of-function analysis using CRISPR/Cas system.

RESULTS

The activation of mTOR induced NED. We observed significant cell growth arrest in NED of LNCaP-mTOR, which accompanied increased expression of $p21^{WAF1/CIP1}$. A comprehensive mass spectrometric analysis identified interferon regulatory factor 1 (IRF1) as a key transcription factor in growth arrest of LNCaP-mTOR. The disruption of *IRF1* gene in LNCaP-mTOR reversed cell growth arrest along with the suppression of its target $p21^{WAF1/CIP1}$. These results indicate that the growth arrest in NED is at least in part dependent on IRF1 through the induction of $p21^{WAF1/CIP1}$.

CONCLUSIONS

We identified active mTOR as a novel inducer of NED, and elucidated a mechanism underlying the malignant transformation of NEPCa by recapitulating NED *in vitro.*

Keywords: Hyperactive mTOR, Interferon Regulatory Factor 1, LNCaP, NED

1 INTRODUCTION

To date, several reports have suggested that neuroendocrine (NE) differentiation (NED) is responsible for progression of prostate cancer (PCa) to hormone-refractory state.[1-3] NE-differentiated PCa (NEPCa) is thought to accelerate PCa progression through several mechanisms.[2,4,5] Nevertheless, the underlying mechanisms responsible for NED development are yet to be fully clarified.

Meanwhile, the activation of the PI3K/Akt/mTOR pathway is a frequent event in many types of cancers including PCa, such as *PTEN* deletion and activating mutations in *PIK3CA*.[6] Interestingly, the activation of mTOR pathway has been reported in NE tumors of other tissues.[7,8] Thus, we hypothesized that activation of mTOR may induce NED in PCa as well. To prove this hypothesis and investigate the molecular mechanisms of NEPCa progression, we performed a gain-of-function analysis by establishing a PCa stable line that expresses hyperactive mTOR.

Here, we demonstrate that hyperactive mTOR induces NED in LNCaP with matching phenotypes reported earlier including the growth arrest,[9-16]and this growth arrest is at least in part dependent on interferon regulator factor 1 (IRF1) through the induction of $p21^{WAF1/CIP1}$.

In LNCaP stably expressing hyperactive mTOR (LNCaP-mTOR), we focused on IRF1 based on the results of a comprehensive proteomic analysis. Furthermore, *IRF1* knockout in LNCaP-mTOR by CRISPR/Cas system resulted in a partial recovery from growth arrest. Together, we elucidated the mechanism underlying the malignant transformation of NED by generating two types of NED models *in vitro* depending on *IRF1* gene status.

2 MATERIALS AND METHODS

2.1 Generation of a stable line expressing active mTOR with the Tet-On 3G system

The tetracycline-inducible (Tet-on) 3G bidirectional expression system was purchased from Clontech (Montain View, CA, USA). A stable line that expresses EGFP and active mTOR upon doxycycline (Dox, Sigma-Aldrich, St. Louis, MO, USA) administration (LNCaP-mTOR) was generated in accordance with the manufacturer's protocol.

2.2 Cell lines and cell culture

The human PCa cell line LNCaP was purchased from RIKEN BRC (Tsukuba, Japan) cell bank. LNCaP was maintained in the RPMI 1640 medium supplemented with 10% FBS and 1×Penicillin-Streptomycin-Glutamine (Gibco, Walthman, MA, USA). When antibiotics were used for selection or induction, they were added to the medium at the following concentrations: G418 at 500 μg/mL for selection and at 100 μg/mL for maintenance, puromycin at 0.25 μg/mL for both selection and maintenance, hygromycin at 100~125 μg/mL for both selection and maintenance, and Dox at 1 μg/mL for induction of the Tet-On system. For the inhibition of mTOR pathway, cells were incubated with an mTOR inhibitor, rapamycin (Cell Signaling Technology (CST), Danvers, MA, USA), for 7 days at concentrations of 100 nM, 10 nM, 1 nM, or 0.1 nM. For cell counting, 4.6×10^5 cells of LNCaP were seeded into one dish with or without Dox. The number of cells was counted manually with a hemocytometer.

2.3 Xenotransplantation of LNCaP-mTOR and immunohistochemical analysis

Experimental procedures were approved by the Institutional Animal Care and Use Committee of the University of Tokyo (Permit Number: M-P14-011). Eight NOD/SCID mice at 7 weeks of age were subcutaneously implanted with 1.0×10^7 LNCaP-mTOR suspended in Matrigel HC (Corning, New York, USA) at one site of each flank. Mice were given either 1 mg/mL Dox or pure water. After 4~6 months, when tumors became palpable (100 mg~1 g in wet weight), animals were euthanized and tumors were excised. Rapamycin was administrated at a dose of 2 mg/kg every other day by intraperitoneal injection for 1 month after tumors became palpable, during which oral Dox administration was continued. For a histological analysis, excised tumors were fixed with 4% formaldehyde, then, paraffin sections were made in accordance with standard protocols. Antibodies used for immunohistochemistry were anti-phospho-S6 ribosomal protein Ser235/236 (1:200; CST 2211), anti-NSE (1:200; a gift from Dr. Sakimura at Niigata University) and anti-chromogranin A (1:100; ab15160, from abcam, Cambridge, UK). The staining was developed with DAB substrate.

2.4 Analysis of cellular morphology

Phase-contrast images of cells were acquired with a light microscope (BZ 8000 KEYENCE, Osaka, Japan). For quantification of the length of cellular processes and the number of processes, phase-contrast images of LNCaP-mTOR cultured with or without Dox were taken on Day 7. For randomly chosen 20 cells, the sum of length of processes and branches stemming from one cell was calculated, and the number of processes per cell was counted, using image-J software. The results were compared by two-tail paired t-test. Also, in order to investigate the effects of Dox withdrawal from Dox-treated cells, LNCaP-mTOR was cultured with Dox for one week, followed by Dox withdrawal from the medium. GFP emission and cellular morphology were serially observed with a microscope.

For electron microscopic images, cells were fixed with 2.5% glutaraldehyde in 0.1 M PB for 1 h at 4℃, followed by incubation with 1% osmium in 0.1 M PB for 1 h at 4℃. After dehydration with ethanol, embedding in Epon (Epok 812, Okenshoji, Tokyo, Japan) was done in accordance with routine protocols. Thin sections (80 nm) were cut with glass or diamond knife and picked up on grid mesh. Sections were stained with uranyl acetate for 30 min at room temperature, followed by staining with lead citrate for 3 min. Images were captured with a scanning electron microscope (Hitachi HT 7700, Tokyo, Japan).

2.5 RNA extraction and RT-PCR analysis

Total RNA was isolated from cells with TRIzol reagent (Invitrogen, Walthman, MA, USA). Extracted RNA was converted to cDNA using RNA PCR Kit AMV Ver.3.0 (TaKaRa, Shiga, Japan). The equal amount of cDNA was PCR-amplified with TaKaRa Ex Taq. The primer sets used were as follows: the primer pair for *IRF1*: 5'-AATTCCAACCAAATCCCGGGG-3' and 5'-AGGCATCCTTGTTGATGTCCCAG-3', *IRF6*: 5'-GTGCCCATGAACCCAGTGAAG-3' and 5'-CTGATCCAGCTCATCTTCCTCATC-3', *interferon (IFN)-β*: 5'-AGCACTGG CTGGAATGAGACTATTG-3' and 5'-ACTGCTCATGAGTTTTCCCCTGG-3', *GAPDH*: 5'-AGCACCAGGTGGTCTCCTC-3' and 5'-CCCTGTTGCTGTAGCCAAATTC-3'. Fast SYBR Green Master Mix (ThermoFisher, Waltham, MA, USA) was used for real-time RT-PCR. The results were compared by two-tail paired t-test.

2.6 Western blot analysis

Extracted proteins were separated on SDS-polyacrylamide gels, and transferred to PVDF membrane (Millipore, Darmstadt, Germany). Antibodies used in a western blot analysis and dilution rates are as follows: anti-phospho-p70 S6 kinase Thr389 (1:2000; CST 9205), 4E-BP1 (1:2000; CST 9452), monoclonal anti-FLAG M2-peroxidase (1:1000; Sigma A8592), monoclonal anti-β-actin (1:2000; Sigma A2228), anti-p70 S6 kinase (1:3000; sc-230 from Santa Cruz Biotechnology, Dallas, TX, USA), anti-IRS1 (1:2000; CST 2382), anti-Akt (1:1000; CST 9272), anti-phospho-Akt Thr308 (1:1000; CST 9275), anti-phospho-Akt Ser473 (1:1000; CST 9271), anti-AR (1:2000; Santa Cruz sc-816), anti-p27^{Kip1} (1:2000; Santa Cruz sc-528), anti-p21$^{WAF1/CIP1}$ (1:1000; CST 2947), anti-phospho-STAT3 Ser727 (1:1000; CST 9134), anti-STAT3 (1:2000; CST 9139), anti-CDK1 (1:1000; CST 9116), anti-NKX3.1 (1:2000; Santa Cruz sc-15022), anti-IRF1 (1:1000; CST 8478), anti-IRF6 (1:200; Santa Cruz sc-377043), and anti-NSE (from Dr. K. Sakimura; 1:2500).

2.7 Mass spectrometric analysis

A total amount of 100 μg protein prepared from Dox (+) or Dox (-) LNCaP-mTOR were precipitated with 10% trichloroacetic acid and resuspended in 20 μL of 0.5 M triethylammonium bicarbonate, PH 8.5, containing 0.2% sodium dodecyl sulfate. Proteins were reduced by adding 2 μL of 50 mM tris-(2-carboxyethyl) phosphine and incubating at 60℃ for 1 h. Free sulfhydryl groups were alkylated with 1 μL of 20 mM methyl methanethiosulfonate by incubating at room temperature for 10 min. Five μg of trypsin (AB Sciex, Framingham, MA, USA) was added for digestion of proteins overnight at 37℃. Samples from Dox (+) LNCaP-mTOR and Dox (-) LNCaP-mTOR were labeled with the iTRAQ reagents (AB Sciex) resulting in MS/MS signals at 115 and 114 Da, respectively. After 1-hour incubation at room temperature, the two samples were mixed, diluted with 4 mL of SCX buffer (10 mM monobasic potassium phosphate, pH 2.65, 25% acetonitrile (ACN)), and acidified with 10% phosphoric acid. Separations of the labeled peptides were performed with an SCX column (AB Sciex). A total of 14 fractions were eluted with SCX buffer containing 20 mM, 40 mM, 60 mM, 80 mM, 100 mM, 120 mM, 140 mM, 160 mM, 180 mM, 200 mM, 225 mM, 250 mM, 300 mM and 360 mM of KCl, respectively. All samples were desalted with C18 Empore Disks (3M, St. Paul, Minnesota, USA) and subjected to LC-MS/MS analysis as described.[17,18] Peptides of each fraction were separated at a flow rate of 200 nl/min using the following gradient in a Dina AI system (KYA TECH, Tokyo, Japan): 0-50% solvent B (80% ACN, 0.1% formic acid) in solvent A from 0 to 315 min, 50-100% solvent B in solvent A from 315 to 320 min, and 100% solvent B from 320 to 330 min.

2.8 Cascade analysis of protein expression data with ExPlain

A cascade analysis is *in silico* computational approach to identify key transcription factors.[19,20] In the first step, proteins were extracted into two groups: those with large fold change (Yes-set), and those with small fold change (No-set). The transcription factors that are significantly enriched around transcription start sites of Yes-set were identified using ExPlain

3.1 (http://explain.biobase-international.com/) and TRANSFAC® database (BioBase GmbH, Wolfenbuettel, Germany). In the second step, based on the list of relevant transcription factors obtained in the first step, upstream analysis was initiated in search of proteins that influence changes in gene expressions.

2.9 Construction of Cas9-and-sgRNAs-expressing vector

For CRISPR/Cas-mediated *IRF1* gene disruption, the following two single guide RNA (sgRNA)-targeting sequences were selected: 5’-TTAATTCCAACCAAATCC CGGGG-3’ as T1 and 5’-ATTAATTCCAACCAAATCCCGGG-3’ as T4. Both target sequences were located in exon 2 of *IRF1* and harbored a SmaI recognition site to facilitate an RFLP analysis. These DNA oligonucleotides were ligated into BbsI-digested pX330-hSpCas9 to generate a bicistronic expression vector expressing Cas9 and sgRNA targeting exon 2 of *IRF1*.[21]

2.10 Generation of *IRF1*-knockout LNCaP-mTOR stable line

LNCaP-mTOR was co-transfected three times with pX330-hSpCas9pc harboring either T1 or T4 sgRNA (1.5 μg) and DNA4-TO-Hygromycin-mVenus-MAP (1.0 μg, from addgene, Cambridge, MA, USA), using Lipofectoamine 3000 (Invitrogen), followed by antibiotic selection with hygromycin. Each single colony was propagated to gain homogeneous clones. For gel-shift assay, a specific region including targeting sequences (exon 2 of *IRF1*) was PCR-amplified using the following primers: 5’-TGAAGCCATCACTTGCATGCC-3’ and 5’-CTGGAAACTGGAAGTGCCTTCAG-3’. PCR products were separated on 2% agarose gel to separate mutant heteroduplex bands with a different electric mobility from a WT band. For an RFLP analysis, PCR products were digested with SmaI and separated on 1.5% agarose gel to detect either SmaI-intact WT bands or SmaI-digested mutant bands. For detailed investigation of mutant alleles, the sequences of above PCR products were determined. To rule out off-target effects, homology search was done using CRISPR Design Tool (http://www.genome-engineering.org/crispr/? page_id=41).

3 RESULTS

3.1 Establishment of an active mTOR-expressing stable line

The FLAG-tagged hyperactive mutant of rat mTOR^{SL1+IT} harboring four point mutations (hereafter called active mTOR) was generated as previously reported.[22] We established an LNCaP stable line that expresses active mTOR and EGFP upon Dox administration (Fig. 1A). One selected clone, which is hereinafter referred to as LNCaP-mTOR, exhibited tightly controlled EGFP emission without visible leakage both *in vitro* and *in vivo* (Fig. 1B). Dox (+) LNCaP-mTOR collected on Day 7 showed increased phosphorylation of S6K1 at Thr389 and STAT3 at Ser727, both of which are direct targets of mTOR (Fig. 1C). Regarding 4E-BP1, 4E-BP1 comprises 4 isoforms and possesses multiple phosphorylation sites.[23] Dox (+) LNCaP-mTOR presented a slowly migrating band of 4E-BP1 because of phosphorylation (Fig. 1C). Phospho-S6 immunohistochemistry showed increased signal in xenografted LNCaP-mTOR from mice with Dox administration (Fig. 1D).

Next, we investigated the status of regulator proteins that act upstream of the PI3K/Akt/mTOR pathway. Active mTOR caused significant reduction in insulin receptor substrate 1 (IRS1), presumably due to the degradation of IRS1 by a rapamycin-sensitive pathway (Fig. 1C).[24] In accordance with IRS1 down-regulation, phosphorylation of Akt at both Thr308 and Ser473 decreased in Dox (+) LNCaP-mTOR (Fig. 1C). Given that mTOR complex 2 (mTORC2) phosphorylates Akt at Ser474, the effect of active mTOR appears to be limited to be the mTOR complex 1 (mTORC1) pathway, as reported previously.[22]

3.2 Active mTOR induces a morphological change and growth arrest characteristic of NED

After 7 days of Dox administration, LNCaP-mTOR started to show a morphological change typical of NED, which is characterized by a neuronal appearance and elongated cellular processes (Fig. 2A). Dox-treated LNCaP-mTOR developed significantly longer ($p = 3.2\times10^{-11}$)

and the larger number ($p = 1.3\times10^{-5}$) of processes, as compared with Dox-untreated cells (Fig. 2A). Also, consistent with the earlier report,[11] we observed that the neuronal morphological change was reversible in LNCaP-mTOR (Fig. S1).

This morphological change was further analyzed by transmission electron microscopy (Fig. 2B). Dox (+) LNCaP-mTOR developed numerous double membrane-bound dense-core granules in cytoplasm that are similar to those observed in adrenal chromaffin cells.[25] These dense core vesicles are a distinct feature of endocrine cells and are reportedly involved in the mechanism responsible for the storage and exocytosis of a variety of hormones and peptides.[25,26]

Corresponding to the morphological change, we observed growth arrest, which is congruous with the previously reported phenotype of NED.[9-11,13,14] The growth of LNCaP-mTOR came to a halt approximately 3 days after Dox administration (Fig. 2C). To rule out the cytotoxic effect of Dox,[27] we counted the cell number of a single stable line expressing only rtTA but not active mTOR. Although Dox (+) single stable line of rtTA showed slightly reduced cell number, the degree of growth suppression was much greater in Dox (+) LNCaP-mTOR, suggesting that the growth arrest of LNCaP-mTOR was indeed a repercussion of active mTOR. Accordingly, we confirmed up-regulation of cyclin-dependent kinase inhibitors, $\mathrm{p27^{Kip1}}$and $\mathrm{p21^{WAF1/CIP1}}$, and down-regulation of cyclin-dependent kinase 1 (CDK1) in Dox (+) LNCaP-mTOR (Fig. 2D).

3.3 Active mTOR augments NSE expression and down-regulates AR and its target NKX3.1

Since the features we observed matched some characteristics of NED reported earlier,[11,12,14,16] we further tested for the expression of NE cell markers by a western blot analysis and immunohistochemical analysis. Neuron specific enolase (NSE) expression was elevated in Dox (+) LNCaP-mTOR (Fig. 3A) as well as in Dox (+) xenografted tumor (Fig. 3B). Furthermore, we confirmed the increased expression of chromogranin A in Dox (+)

xenografted tumor (Fig. 3B). Dox (+) xenografted tumor presented enlarged cytoplasm containing small particles similar to endocrine tissues like pancreas. Since NE cells are known to be androgen receptor (AR) negative,[4] we tested LNCaP-mTOR for AR expression by a western blot analysis. AR expression decreased in a time-dependent manner after Dox administration. Notably, an androgen-regulated prostate-specific homeobox gene, *NKX3.1*, which is an alleged prostate-specific tumor suppressor gene,[28] was concurrently suppressed (Fig. 3C).

3.4 Rapamycin suppresses NED induced by active mTOR

To prove that phenotypes observed in LNCaP-mTOR are truly attributable to the expression of active mTOR, we confirmed that rapamycin suppressed phenotypes induced by active mTOR (Fig. 4A). Expectedly, rapamycin curbed the kinase activity of active mTOR as shown by suppressed phosphorylation of S6K1 at Thr389 and the suppression of phosphorylation-induced mobility shift of 4E-BP1 (Fig. 4B). Also, rapamycin suppressed NSE expression (Fig. 4B). In line with this, immunohistochemical analysis of xenografted tumors from Dox-treated mice with or without rapamycin administration showed that rapamycin suppressed mTOR activity (p-S6) and NED *in vivo* as well (Fig. 4C). By contrast, AR and NKX3.1 expressions were rescued by rapamycin (Fig. 4B). Regarding cell cycle regulators, rapamycin rescued CDK1 expression, and reduced $p27^{Kip1}$ and $p21^{WAF1/CIP1}$ expressions (Fig. 4B). Since mTORC2 has been reported to be rapamycin insensitive,[29] here again, it is highly likely that NED in our study was induced by mTORC1, rather than mTORC2.

3.5 Comprehensive mass spectrometric analysis and subsequent analysis suggest that members of IRF family are key transcription factors in NED of LNCaP-mTOR

Cell lysates of Dox (+) or Dox (-) LNCaP-mTOR were subjected to a mass spectrometric analysis for comprehensive protein expression profiling. Differences in protein expression were demonstrated as a fold change of Dox (+) to Dox (-) ratio (Table S1). In the following a cascade analysis, Yes-set (fold change＞1.8 in absolute value) comprised 144 proteins (Table S2), and No-set (fold change＜1.088 in absolute value) comprised 727 proteins (Table S3). ExPlain 3.1 and TRANSFAC® database identified 36 transcription factors (Table S4) that are significantly enriched around upstream of transcription start sites of Yes-set ($p < 0.05$, Yes/No ratio＞1.7). Based on these 36 transcription factors, Biobase upstream analysis suggested that 70 key node networks were likely to be involved in this model.

The members of interferon regulatory factor (IRF) family were frequently appearing transcription factors throughout all key node networks. Especially IRF1 was identified as the most frequently appearing transcription factor throughout multiple key node networks (Table S5). Then, we validated this result by a western blot analysis, and showed that IRF1 was indeed up-regulated in Dox (+) LNCaP-mTOR *in vitro* (Fig. 5A). Among other members of IRF family, IRF6 was also up-regulated (Fig. 5A). The expression of IRF1 and IRF6 augmented by active mTOR was suppressed by rapamycin (Fig. 5B). A real-time RT-PCR analysis showed that IRF1 and IRF6 were regulated by mTOR at transcription level (Fig. 5C). We proved that increased IRF1 was functioning as a transcription factor by showing the mRNA induction of IRF1-regulated gene, *interferon (IFN)-β* (Fig. 5D).[30]

3.6 Knockout of *IRF1* by CRISPR/Cas system rescues growth arrest via the suppression of *p21*

To further investigate the function of IRF1, we performed a loss-of-function analysis of IRF1 in LNCaP-mTOR. Given a marked induction of the IFN-mediated signaling pathway by siRNAs,[31] we generated *IRF1* knockout stable lines from LNCaP-mTOR using CRISPR/Cas system (Fig. S2A),[21] and screened for the gene disruption by gel-shift assay and an RFLP analysis (Fig. S2B). Two *IRF1* knockout stable lines, each derived from different single guide (sg) RNAs (T1 or T4), were chosen. Based on an RFLP analysis (Fig. S2B, right panel), both clones carried biallelic mutations in *IRF1* gene (hereafter called LNCaP-mTOR-*IRF1*$^{-/-}$). Sequencing data showed that clone 1 harbored biallelic mutations that consisted of 3-bp deletion in one allele and 161-bp deletion in the other allele, and clone 2 harbored biallelic mutations that consisted of 3-bp and 20-bp deletions (Fig. S2C). A western blot analysis of these two clones showed abrogated expression of IRF1 protein (Fig. 6A).

Next, we tested if this gene disruption affected the protein expression altered by active mTOR in LNCaP-mTOR, and found that the expression p21$^{\mathrm{WAF1/CIP1}}$ that is known to be IRF1 target [32] was down-regulated in both of two LNCaP-mTOR-*IRF1*$^{-/-}$ clones (Fig. 6A). *IRF1* knockout partially rescued active mTOR-induced growth arrest in both clones (Fig. 6B). Consistent with the earlier study reporting that the forced expression of IRF1 greatly reduces cell viability,[33] *IRF1* knockout possibly recovered active mTOR-induced growth arrest partially via the suppression of p21$^{\mathrm{WAF1/CIP1}}$ in our study. Meanwhile, AR, Nkx3.1, CDK1 and p27 expressions were not significantly different between LNCaP-mTOR-*IRF1*$^{-/-}$ and LNCaP-mTOR-*IRF1*$^{+/+}$. As for NSE, LNCaP-mTOR-*IRF1*$^{-/-}$ showed increased NSE expression for an unknown reason. Either way, the role of IRF1 appears to be specific to growth arrest, and unknown trans-differentiation pathway is allegedly responsible for other phenotypes, as schematically depicted in Fig. S3.

4 DISCUSSION

In this study, we conducted a gain-of-function analysis by establishing an LNCaP stable line that expresses active mTOR (LNCaP-mTOR), and found that active mTOR induces NED in LNCaP-mTOR, consistent with the activation of the mTOR pathway in the NE tumors of other tissues.[7,8] Also, in line with the earlier report,[11] we observed that the neuronal morphological change was reversible in LNCaP-mTOR. NED of LNCaP-mTOR presented the characteristics of NED described in previous studies.[9-16] Despite that the mTOR activation is well known to regulate cell growth positively,[34] we observed significant cell growth arrest in LNCaP-mTOR, which accompanied increased expression of $p27^{Kip1}$ and $p21^{WAF1/CIP1}$, and decreased expression of CDK1.

To date, several NED inducers of prostate cancer have been reported.[9-16] Our results were consistent with the findings of Wu et al.[15] showing that the activation of the PI3K/Akt/mTOR pathway is required for NED of LNCaP. Additionally, IL-6 is known to induce NED in LNCaP via STAT3 activation,[14] and increased phosphorylation of STAT3 at Ser727 by active mTOR was observed in our study as well. Although these findings support the notion that the activation of mTOR is important for cancer plasticity and differentiation, further investigation is required to identify specific factors responsible for NED.

Intriguingly, hyperactivation of mTOR led to the induction of the transcription factors, IRF1 and IRF6. Aside from their major roles in immune response,[32] IRF1 and IRF6 are known to possess a property of tumor suppressors both *in vitro* and *in vivo*.[33,35-37] The increased IRF1 was confirmed to be functioning as a transcription factor by showing the induction of IRF1-regulated gene, *IFN-β*.[30,38] Notably, the earlier studies reported the activation of IFN-inducible genes in androgen-independent LNCaP and other cancer cell lines with aggressive potential.[39,40] Their results together with our findings indicate that the activation of the IFN-mediated pathway may be some consensus event during PCa progression.

As for possible mechanisms of IRF1 induction by mTOR activation, the mTOR pathway is known to have multiple negative feedback regulatory loops. Consequently, mTORC1 activation suppresses the PI3K/Akt pathway axis,[41] which was also confirmed in our study by the down-regulation of IRS1 and decreased phosphorylation of Akt both at Thr308 and Ser473 in Dox-treated LNCaP-mTOR. Given that Akt suppression is known to promote IRF1 expression,[42] one of the possible mechanisms of IRF1 induction by mTOR activation might be the negative feedback regulatory loop of PI3K/Akt/mTOR signaling. As another possible mechanism of IRF1 induction by mTOR activation, the overexpression of EGFR located at the upstream of mTOR is reported to induce IRF1 expression via STAT1 and STAT3 activation, leading to growth arrest of other human cancer cells.[33] In our study, phosphorylation of STAT3 at Ser727 was augmented by active mTOR, and *IRF1* was up-regulated at transcriptional level. Taken together, it is plausible that IRF1 is induced at least in part by activation of STAT3 via increased phosphorylation at Ser727.

A knockout of *IRF1* by CRISPR/Cas system resulted in a partial recovery of active mTOR-induced growth arrest via suppression of IRF1 target, $p21^{WAF1/CIP1}$. Although the whole picture of NED mechanism remains to be elucidated, our results suggest that one of its signature traits, the growth arrest, is at least in part dependent on IRF1 through induction of $p21^{WAF1/CIP1}$ (Fig. S3).[32]

In summary, we identified active mTOR as a novel inducer of NED, and elucidated the mechanism underlying the malignant transformation of NEPCa by recapitulating NED with the different degree of malignancy; that is *IRF1* intact and *IRF1* disrupted. Our findings shed light on novel roles of mTOR and IRF1 in progression of NEPCa.

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FIGURE LEGENDS

FIGURE 1

The establishment of LNCaP-mTOR.

(A) A schematic diagram of LNCaP-mTOR that expresses active mTOR and EGFP mRNAs bidirectionally upon Dox administration.

(B) Dox (+) LNCaP-mTOR emitted EGFP upon Dox administration without any visible leakage both *in vitro* (upper panel) and *in vivo* (xenografted tumors, lower panel). Middle panel shows excised xenografted tumors from either Dox-treated or untreated NOD/SCID mice. Scale bars, 100 µm (upper panel), and 5 mm (middle and lower panels).

(C) Active mTOR increased phosphorylation of its downstream effectors. After 7 days of Dox administration LNCaP-mTOR showed increased phosphorylation of S6K1 at Thr389 and STAT3 at Ser727. 4E-BP1 showed phosphorylation-induced mobility shift. IRS1 and Akt that act upstream of mTOR were down-regulated.

(D) Phospho-S6 Ser235/236 immunohistochemistry showed increased signal in Dox (+) xenografted tumor (upper panel). Lower panel is hematoxylin and eosin (H&E) stain. Low-power field images of xenografted tumors resected from NOD/SCID mice with or without Dox administration are shown. Scale bars, 600 µm.

FIGURE 2

An NED-associated morphological change and growth arrest are induced by active mTOR.

(A) After 7 days of Dox administration, LNCaP-mTOR exhibited a neuronal appearance and elongated cellular processes (left panel). Scale bars, 100 µm. Phase-contrast images of LNCaP-mTOR cultured with or without Dox were taken on Day 7. For randomly chosen 20 cells, the sum of length of processes and branches stemming from one cell was calculated, and the number of processes per cell was counted, using image-J software. Values are means and error bars indicate SEM (*n* = 20). The results were compared by two-tail paired t-test. Dox (+) LNCaP-mTOR developed significantly longer ($p = 3.2 \times 10^{-11}$) and the larger number ($p = 1.3 \times 10^{-5}$) of processes than Dox (-) LNCaP-mTOR (right panel).

(B) The morphological change analyzed by transmission electron microscopy. Dox (+) LNCaP-mTOR developed numerous double membrane-bound dense-core granules in cytoplasm. Scale bars, 10 μm. The image in the box is magnified. Scale bar, 2 μm.

(C) Growth arrest of Dox (+) LNCaP-mTOR. As a control, the cell number of LNCaP expressing only rtTA (designated as LNCaP) was counted. Values are means and error bars indicate SEM (*n* = 5). The right bottom panel presents crystal violet staining of LNCaP-mTOR on Day 7.

(D) Growth arrest induced by active mTOR accompanied up-regulation of $p27^{Kip1}$ and $p21^{Waf1/Cip1}$, and down-regulation of CDK1.

FIGURE 3

Active mTOR augments NSE expression and down-regulates AR and its target NKX3.1.

(A) Active mTOR augmented NSE expression in LNCaP-mTOR. Shown is a western blot analysis of LNCaP-mTOR treated with or without Dox for 7 days.

(B) Immunohistochemical analysis of NSE and chromogranin A showed increased signal in Dox (+) xenografted tumors. Dox (+) tumor presented enlarged cytoplasm containing small particles (arrowheads) similar to endocrine tissues. Scale bars, 50 μm.

(C) Dox (+) LNCaP-mTOR showed increased expression of FLAG-tagged active mTOR, and decreased expression of AR and NKX3.1 in a time dependent manner.

FIGURE 4

Rapamycin suppresses NED induced by active mTOR.

(A) Rapamycin (Rapa) suppressed a morphological change induced by active mTOR. The concentration of rapamycin was 100 nM. Scale bars, 100 μm.

(B) Rapa curbed kinase activity of active mTOR *in vitro*. Rapa rescued AR, NKX3.1, and CDK1 expressions. Conversely, NSE, p27$^{\mathrm{Kip1}}$, and p21$^{\mathrm{Waf1/Cip1}}$ expressions were suppressed by Rapa.

(C) Xenografted tumor from Dox-treated mice with or without Rapa. Rapa suppressed mTOR activity (p-S6) and NED *in vivo* as well. Scale bars, 600 μm for upper and middle panel, and 50 μm for bottom panel.

FIGURE 5

IRF family members are up-regulated in NED induced by active mTOR.

(A) To validate the result of cascade analysis, Dox-treated or untreated LNCaP-mTOR for indicated time was subjected to a western blot analysis of IRF1 and IRF6. IRF1 and IRF6 expressions were augmented in Dox (+) LNCaP-mTOR *in vitro*.

(B) Rapa suppressed IRF1 and IRF6 expressions, showing that their expressions were induced by mTOR.

(C) A real-time RT-PCR analysis of mRNA from Dox-treated or untreated LNCaP-mTOR with or without Rapa (10 nM). *IRF1* and *IRF6* expressions were normalized by *GAPDH* expression. *IRF1* and *IRF6* were up-regulated at transcriptional level. Values are means and error bars indicate SEM (n = 4). (*IRF1*: p = 0.0001 for Dox (+)/Rapa (-) versus Dox (+)/Rapa (+), p = 0.0009 for Dox (+)/Rapa (-) versus Dox (-)/Rapa (-); *IRF6*: p = 0.003 for Dox (+)/Rapa (-) versus Dox (+)/Rapa (+), p = 0.0005 for Dox (+)/Rapa (-) versus Dox (-)/Rapa (-)).

(D) Increased mRNA expression of *interferon (IFN)-β*, IRF1 target gene, was confirmed by RT-PCR.

FIGURE 6

CRISPR/Cas-mediated *IRF1* gene disruption augments NED induced by active mTOR.

(A) Both LNCaP-mTOR-*IRF1*$^{-/-}$ clones showed abrogated IRF1 protein expression. *IRF1* knockout reduced p21$^{\mathrm{Waf1/Cip1}}$. Meanwhile, AR, Nkx3.1, CDK1 and p27 expressions were not significantly different between LNCaP-mTOR-*IRF1*$^{-/-}$ and LNCaP-mTOR-*IRF1*$^{+/+}$. LNCaP-mTOR-*IRF1*$^{-/-}$ showed increased NSE expression.

(B) The cell number of LNCaP-mTOR-*IRF1*$^{+/+}$ and 2 clones of LNCaP-mTOR-*IRF1*$^{-/-}$ treated with Dox on Day 7. *IRF1* knockout partially recovered active mTOR-induced growth arrest. Values are means and error bars indicate SEM (n = 5). P values were calculated using unpaired t-test ($p = 9.3\times10^{-5}$ for *IRF1*$^{-/-}$1 versus *IRF1*$^{+/+}$, $p = 0.00014$ for *IRF1*$^{-/-}$2 versus *IRF1*$^{+/+}$).

A list of supporting information

Supplementary Figure S1

Neuronal morphological change is reversible in LNCaP-mTOR

LNCaP-mTOR was treated with Dox for one week, followed by culturing in Dox (-) medium. Neuronal appearance gradually returned to normal. Scale bars, 100 μm.

Supplementary Figure S2

Generation of *IRF1*-disrupted LNCaP-mTOR

(A) The strategy of CRISPR/Cas-mediated *IRF1* gene disruption. The sgRNA sequences are designated as a blue (T1) or a brown (T4) arrow. The protospacer-adjacent motif (PAM) sequences are indicated as a blue (T1) or a brown (T4) box. The putative cleavage sites are designated as a blue (T1) or a brown (T4) arrowhead. The SmaI recognition site is indicated as a black box.

(B) Left panel: gel-shift assay of PCR products. Intact alleles yielded a single band of 590 bp, whereas mutant alleles yielded heteroduplex bands with different electrophoretic mobility. The experiment was triplicated. Right panel: An RFLP analysis of PCR products. SmaI-digested PCR products yielded either WT bands of 258+332 bp (SmaI site intact) or mutant bands of different length (SmaI site destroyed). Both T1 and T4 sgRNA-derived clones carried biallelic mutations in *IRF1* gene (LNCaP-mTOR-*IRF1*$^{-/-}$ 1 and 2).

(C) Sequencing of mutant *IRF1* alleles. Clone 1 harbored a 3-bp deletion resulting in one amino acid deletion of Isoleucine (I) 21 with amino acid replacement of Proline (P) 22 to Methionine (M) (c.63_65delCCC, p.Ile21_Pro22delinsMet), and a 161-bp deletion resulting in appearance of stop codon (X) (c.60_87+133del, p.Gln20X). Clone 2 harbored a 3-bp deletion resulting in one amino acid deletion of Isoleucine (I) 21 (c.61_63delATC, p.Ile21del), and a 20-bp deletion resulting in appearance of stop codon (X) (c.52_71del, p.Ser23HisfsX4).

Supplementary Figure S3

The role of IRF1 in NED

A schematic suggested by our results. Active mTOR induces NED, and the disruption of concurrently up-regulated IRF1 appears to accelerate proliferation via the suppression of an IRF1 target gene, *p21* $^{Waf1/Cip1}$. Trans-differentiation pathways responsible for other characteristics are yet to be identified.

Supplementary Table S1

Comprehensive protein expression profiling by mass spectrometric analysis

Supplementary Table S2

Fold change (absolute value)＞1.8 (Yes-set)

Supplementary Table S3

Fold change (absolute value)＜1.088 (No-set)

Supplementary Table S4

Thirty seven transcription factors that bind to Yes-set

Supplementary Table S5

Frequently appearing transcription factor throughout multiple key node networks.

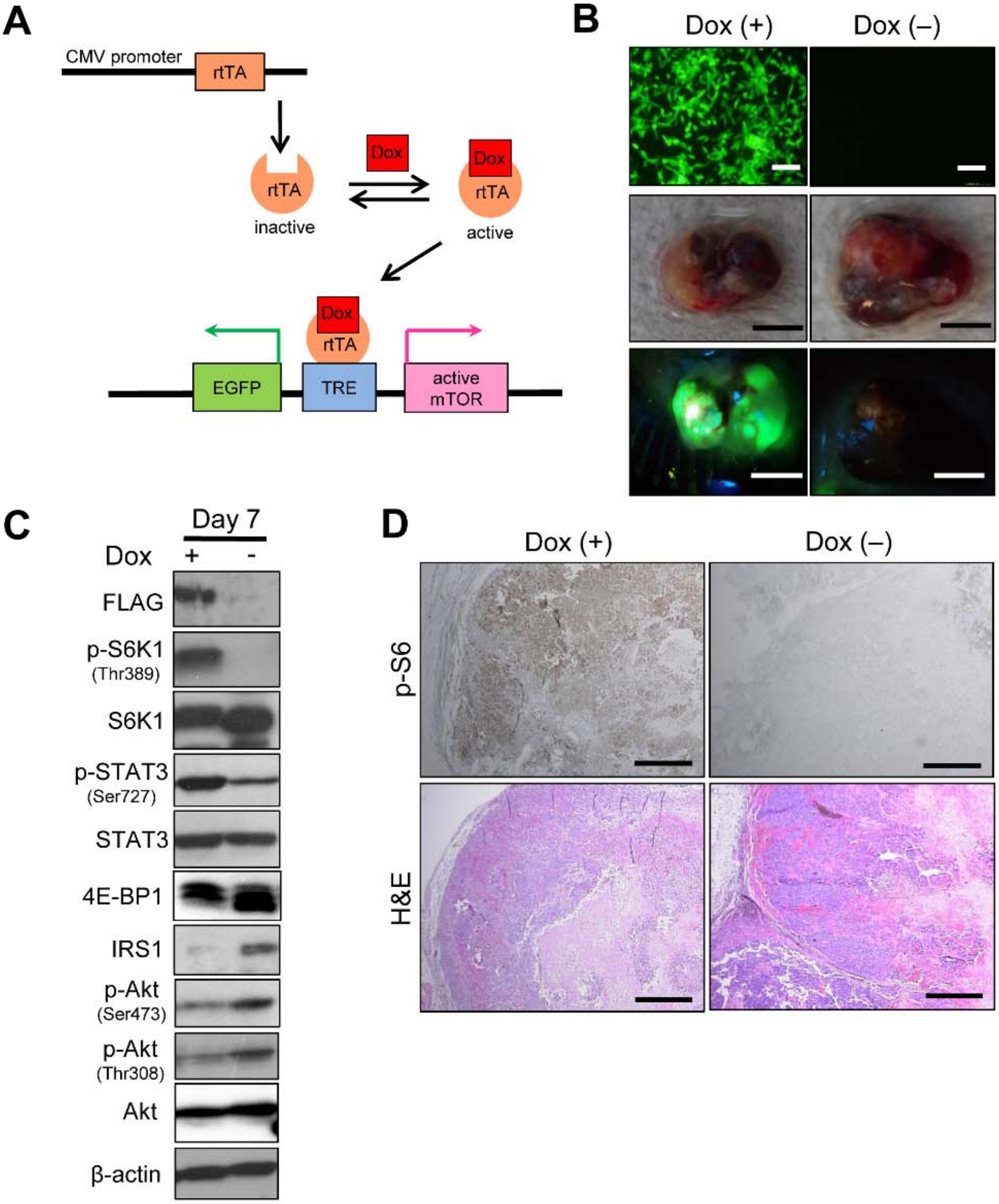

A
CMV promoter
rtTA
rtTA
inactive
Dox
Dox
rtTA
active
Dox
rtTA
EGFP
TRE
active mTOR
B
Dox (+)
Dox (–)
C
Day 7
Dox
+
-
FLAG
p-S6K1
(Thr389)
S6K1
p-STAT3
(Ser727)
STAT3
4E-BP1
IRS1
p-Akt
(Ser473)
p-Akt
(Thr308)
Akt
β-actin
D
Dox (+)
Dox (–)
p-S6
H&E

Figure 1

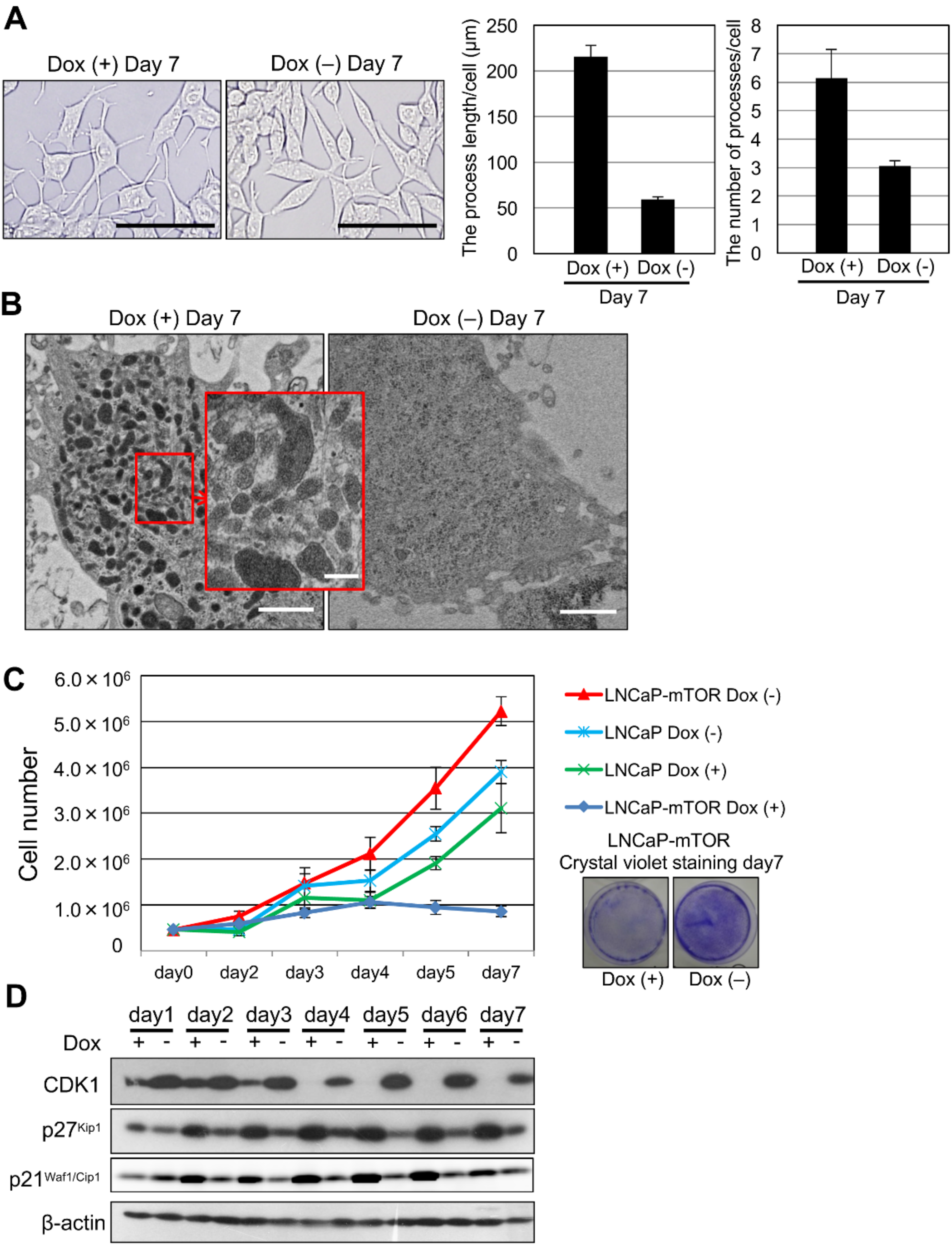

A
Dox (+) Day 7
Dox (–) Day 7
The process length/cell (μm)
250
200
150
100
50
0
Dox (+)
Dox (-)
Day 7
The number of processes/cell
8
7
6
5
4
3
2
1
0
Dox (+)
Dox (-)
Day 7
B
Dox (+) Day 7
Dox (–) Day 7
C
Cell number
6.0 × 10⁶
5.0 × 10⁶
4.0 × 10⁶
3.0 × 10⁶
2.0 × 10⁶
1.0 × 10⁶
0
day0
day2
day3
day4
day5
day7
LNCaP-mTOR Dox (-)
LNCaP Dox (-)
LNCaP Dox (+)
LNCaP-mTOR Dox (+)
LNCaP-mTOR
Crystal violet staining day7
Dox (+)
Dox (–)
D
day1
day2
day3
day4
day5
day6
day7
Dox
+ - + - + - + - + - + - + -
CDK1
p27Kip1
p21Waf1/Cip1
β-actin

Figure 2

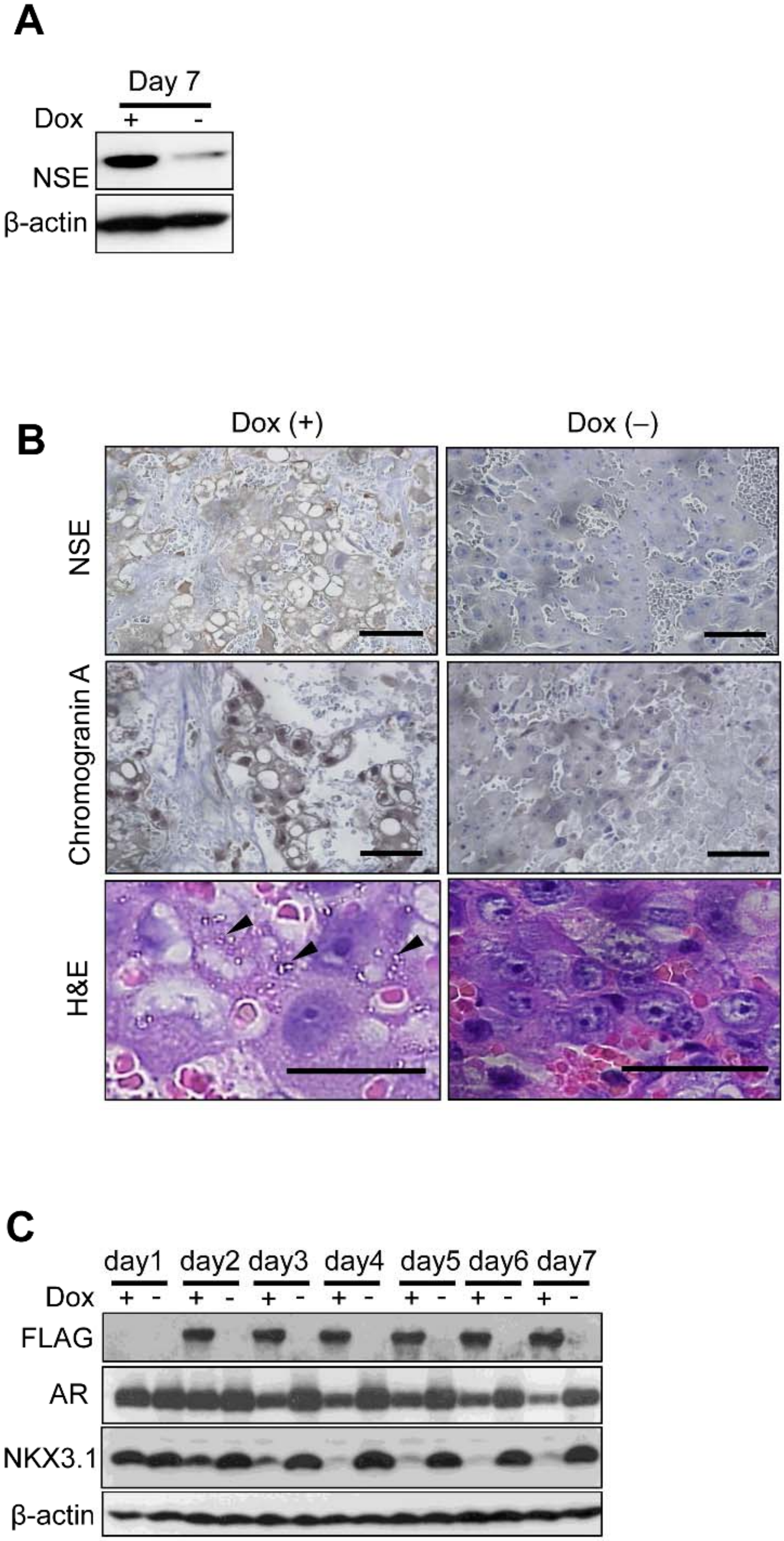

A
Day 7
Dox
+
-
NSE
β-actin
B
Dox (+)
Dox (–)
NSE
Chromogranin A
H&E
C
day1
day2
day3
day4
day5
day6
day7
Dox
+ - + - + - + - + - + - + -
FLAG
AR
NKX3.1
β-actin

Figure 3

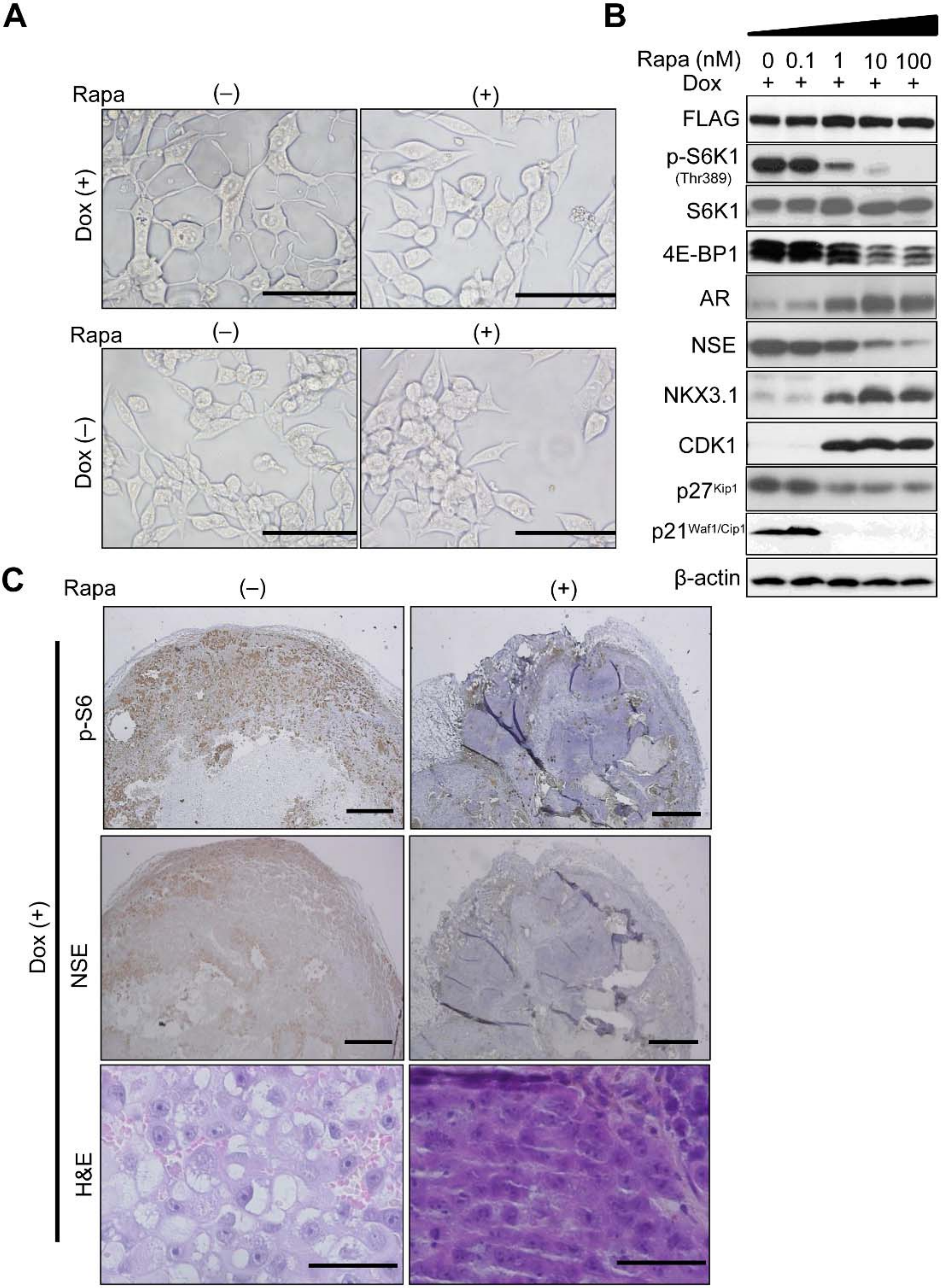

A
Rapa
(–)
(+)
Dox (+)
Rapa
(–)
(+)
Dox (–)
B
Rapa (nM)
0
0.1
1
10
100
Dox
+
+
+
+
+
FLAG
p-S6K1
(Thr389)
S6K1
4E-BP1
AR
NSE
NKX3.1
CDK1
p27^{Kip1}
p21$^{Waf1/Cip1}$
β-actin
C
Rapa
(–)
(+)
Dox (+)
p-S6
NSE
H&E

Figure 4

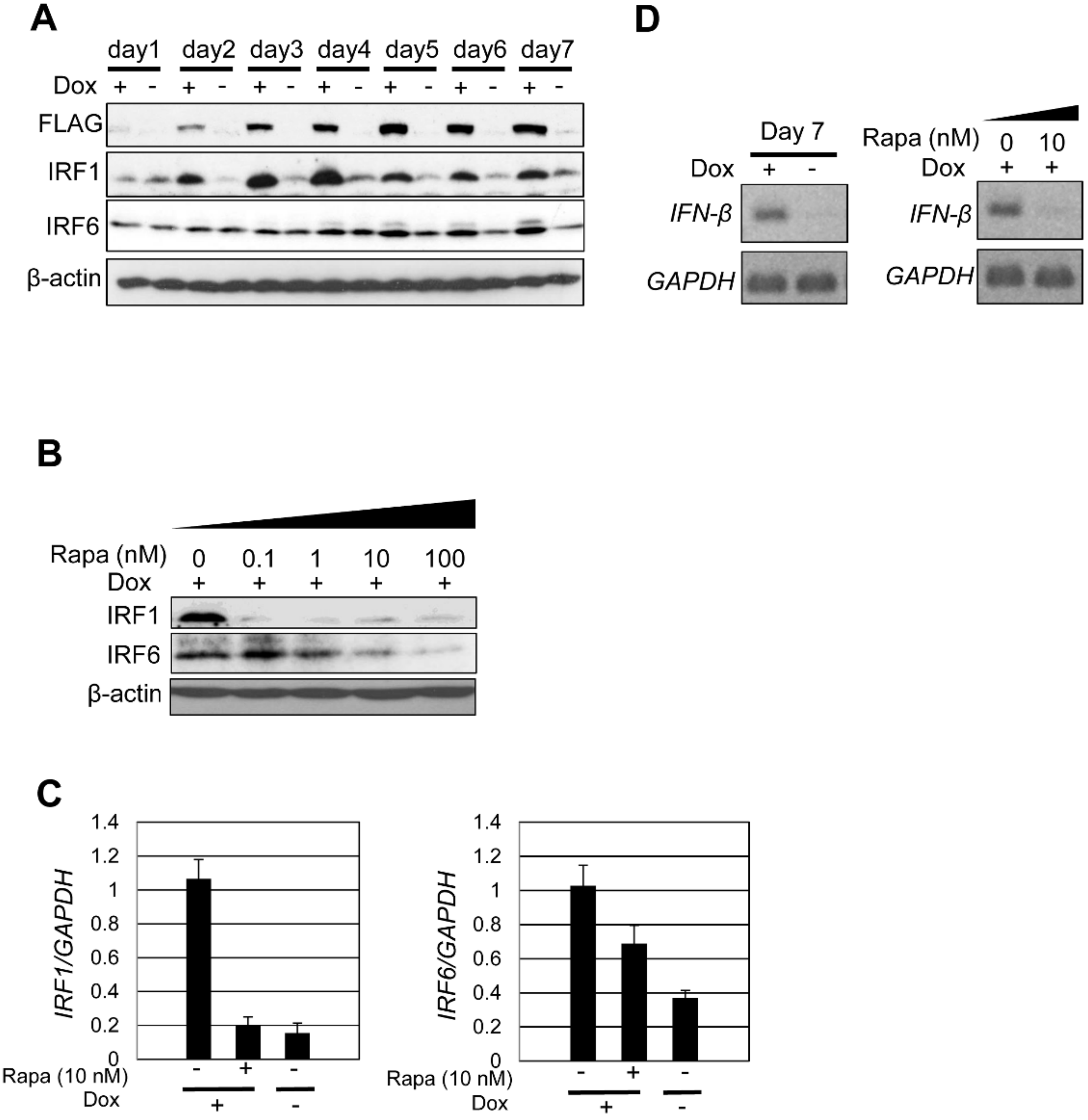

A
day1
day2
day3
day4
day5
day6
day7
Dox
+ - + - + - + - + - + - + -
FLAG
IRF1
IRF6
β-actin
B
Rapa (nM)
0
0.1
1
10
100
Dox
+ + + + +
IRF1
IRF6
β-actin
C
1.4
1.2
1
0.8
0.6
0.4
0.2
0
IRF1/GAPDH
Rapa (10 nM)
- + -
Dox
+ -
IRF6/GAPDH
Rapa (10 nM)
- + -
Dox
+ -
D
Day 7
Dox
+ -
IFN-β
GAPDH
Rapa (nM)
0
10
Dox
+ +
IFN-β
GAPDH

Figure 5

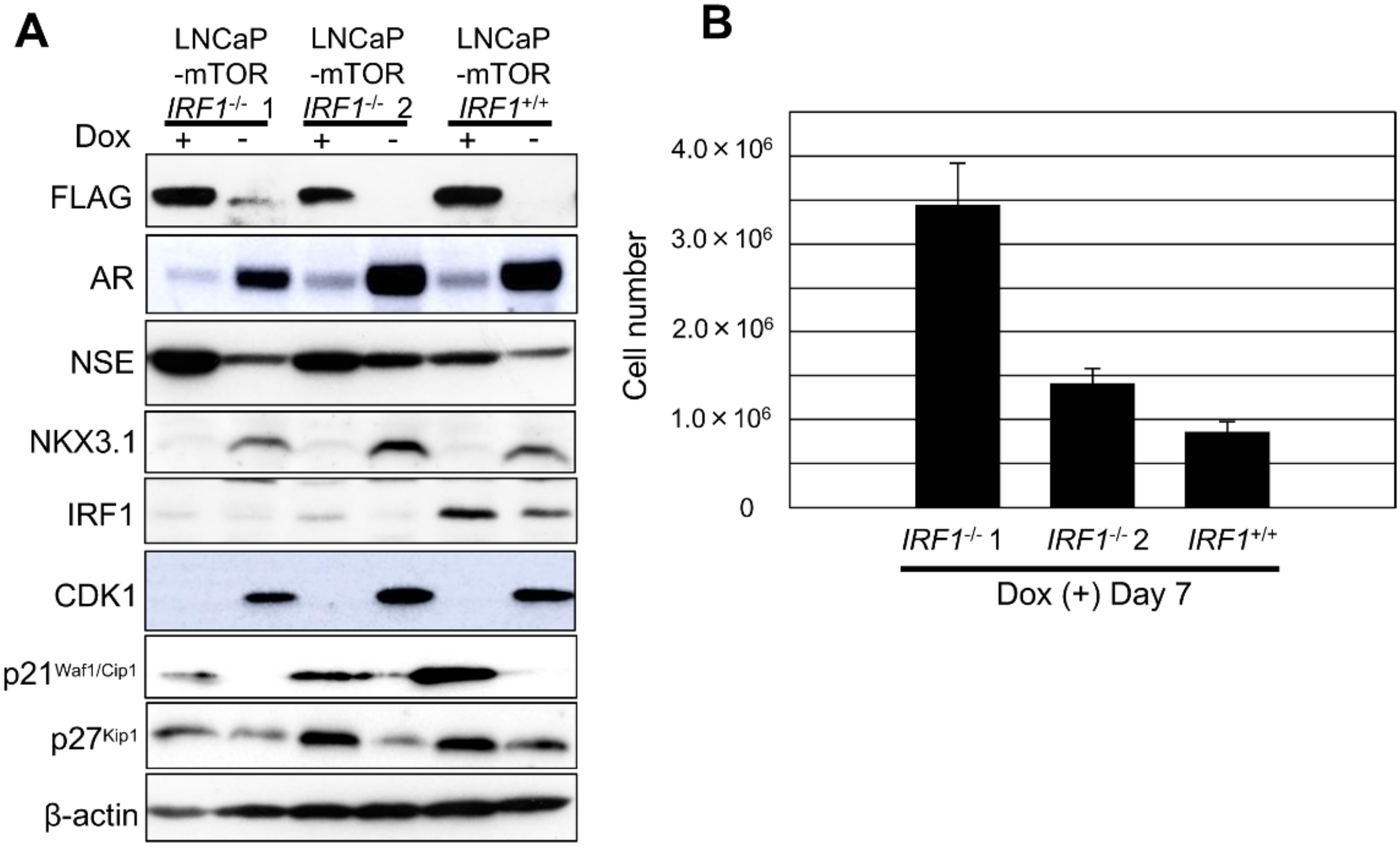
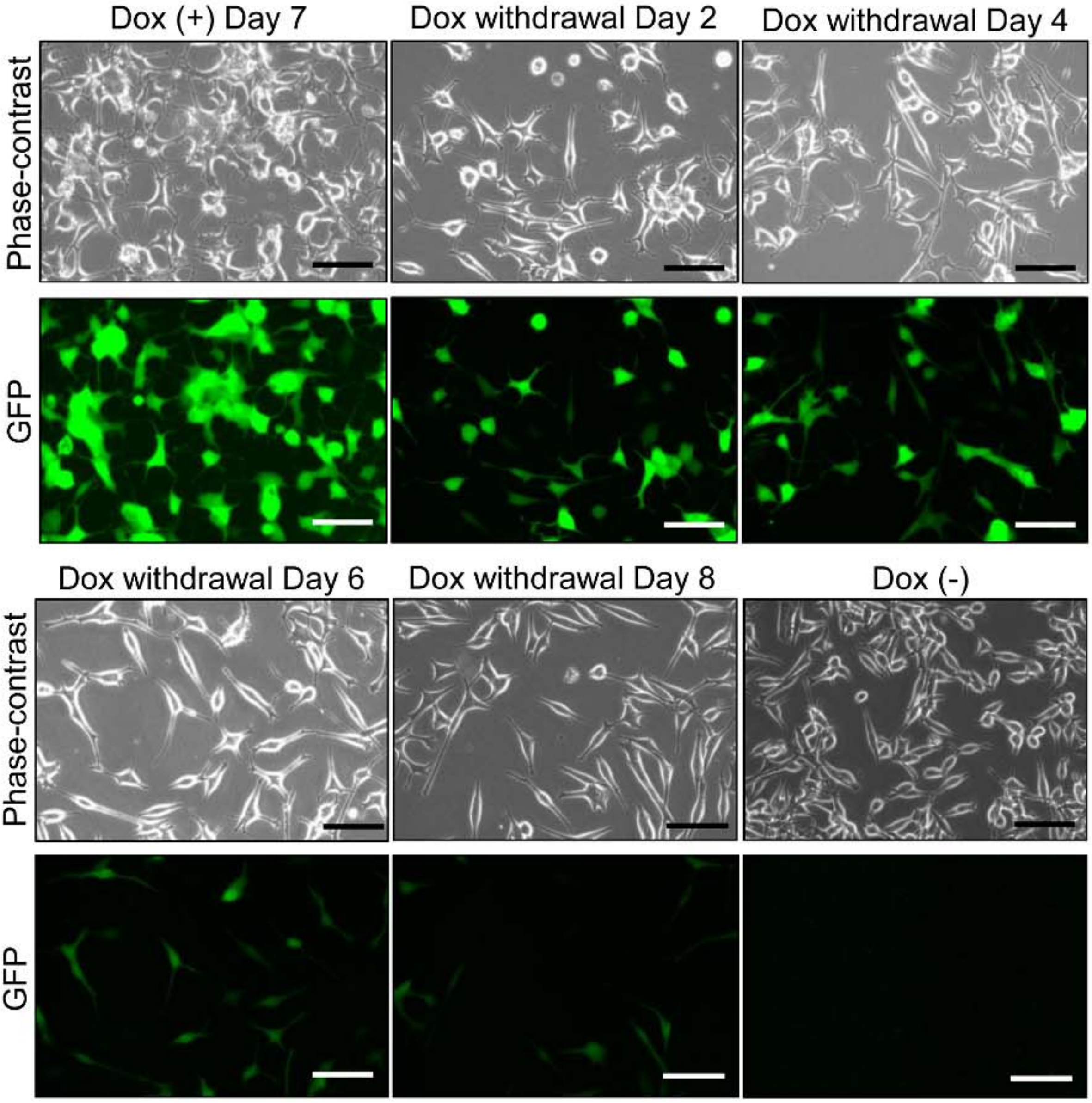
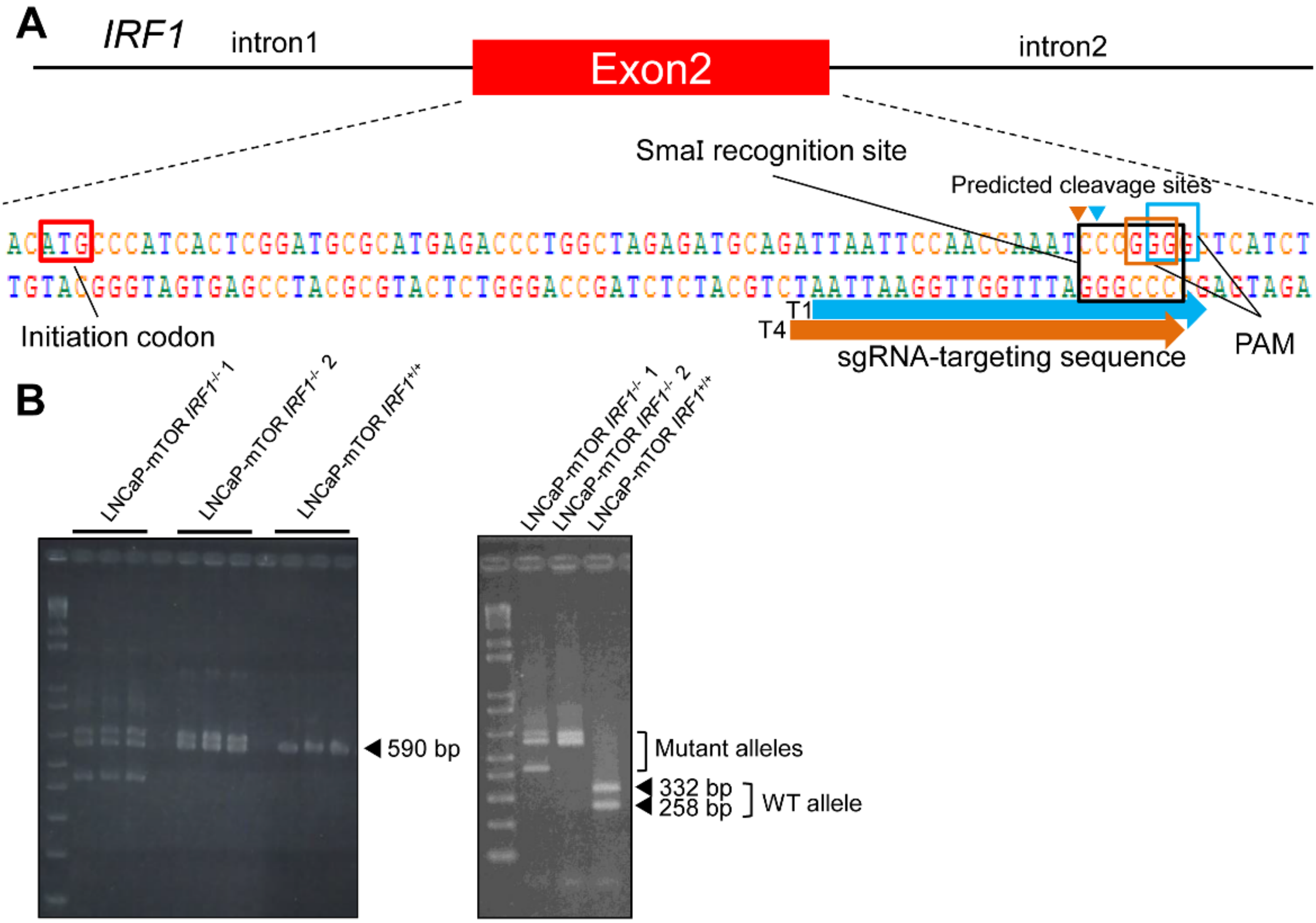

A
LNCaP -mTOR IRF1-/- 1
LNCaP -mTOR IRF1-/- 2
LNCaP -mTOR IRF1+/+
Dox
+ - + - + -
FLAG
AR
NSE
NKX3.1
IRF1
CDK1
p21Waf1/Cip1
p27Kip1
β-actin
B
Cell number
4.0×10⁶
3.0×10⁶
2.0×10⁶
1.0×10⁶
0
IRF1-/- 1
IRF1-/- 2
IRF1+/+
Dox (+) Day 7

Figure 6



Supplementary Figure S1 Neuronal morphological change is reversible in LNCaP-mTOR

LNCaP-mTOR was treated with Dox for one week, followed by culturing in Dox (-) medium. Neuronal appearance gradually returned to normal. Scale bars, 100 μm.



C

DNA sequence of LNCaP-mTOR *IRF1*$^{-/-}$ 1

```
      WT GATTAATTCCAACCAAATCCCGGGGCTCATCTGGATTAATAAAGTGAGTGTAACTCTTTGGGTTTTCCTGCCACTGTTTTAACCCATGT
mutant 1 GATTAATTCCAACCAAAT---GGGGCTCATCTGGATTAATAAAGTGAGTGTAACTCTTTGGGTTTTCCTGCCACTGTTTTAACCCATGT
mutant 2 GATTAATTCCAACCA--------------------------------------------------------------------------

      WT ACTTCTGGAGGGACCAAAGCTTCAGATGCAGCTCAAAAAGGGAAGTGATAACGGGACAAGCAGGTGTTTCTCCCAGTGGGTCCTGCATG
mutant 1 ACTTCTGGAGGGACCAAAGCTTCAGATGCAGCTCAAAAAGGGAAGTGATAACGGGACAAGCAGGTGTTTCTCCCAGTGGGTCCTGCATG
mutant 2 ---------------------------------------------------------------------------------------TG
```

Amino acid sequence of LNCaP-mTOR *IRF1*$^{-/-}$ 1

```
      WT MPITRMRMRPWLEMQINSNQIPGLIWINK
mutant 1 MPITRMRMRPWLEMQINSNQ-MGLIWINK
mutant 2 MPITRMRMRPWLEMQINSNX
```

DNA sequence of LNCaP-mTOR *IRF1*$^{-/-}$ 2

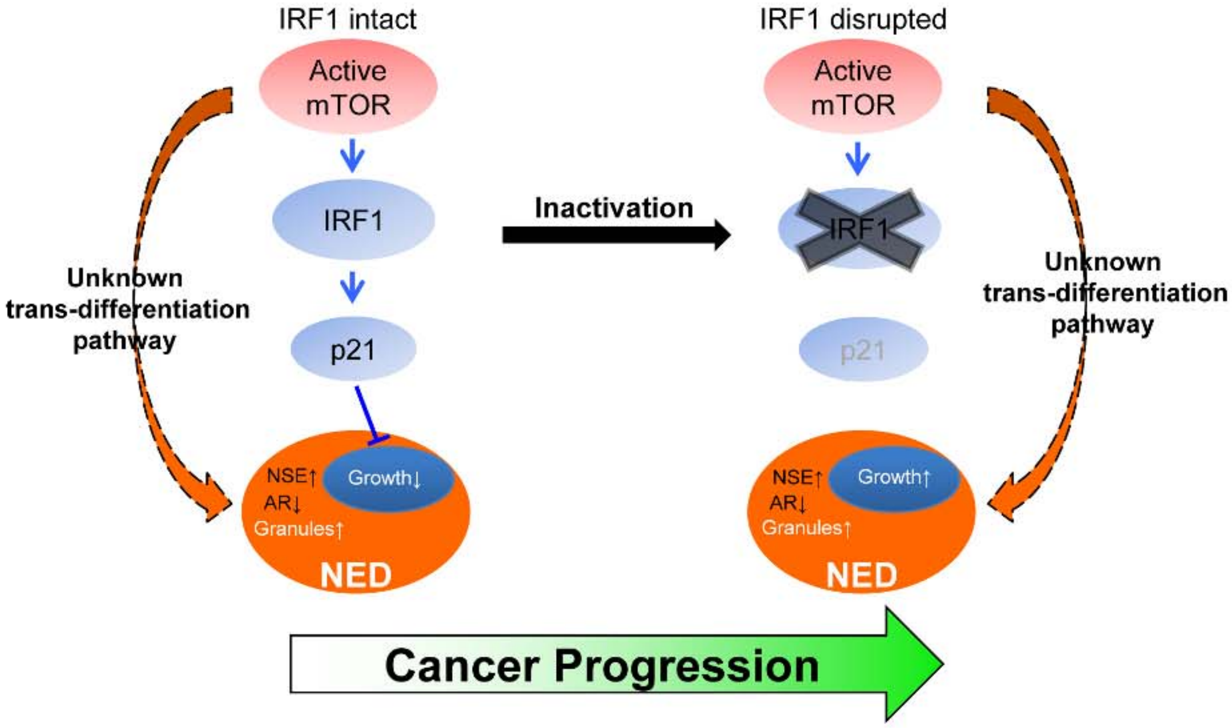
```
      WT GATTAATTCCAACCAAATCCCGGGGCTCATCTGGATTAATAAAG
mutant 1 GATTAATTCCAACCAA---CCGGGGCTCATCTGGATTAATAAAG
mutant 2 GATTAAT--------------------CATCTGGATTAATAAAG
```

Amino acid sequence of LNCaP-mTOR *IRF1*$^{-/-}$ 2

```
      WT MPITRMRMRPWLEMQINSNQIPGLIWINK
mutant 1 MPITRMRMRPWLEMQINSNQ-PGLIWINK
mutant 2 MPITRMRMRPWLEMQINHLDX
```

Supplementary Figure S2 Generation of *IRF1*-disrupted LNCaP-mTOR

(A) The strategy of CRISPR/Cas-mediated *IRF1* gene disruption. The sgRNA sequences are designated as a blue (T1) or a brown (T4) arrow. The protospacer-adjacent motif (PAM) sequences are indicated as a blue (T1) or a brown (T4) box. The putative cleavage sites are designated as a blue (T1) or a brown (T4) arrowhead. The SmaI recognition site is indicated as a black box. (B) Left panel: gel-shift assay of PCR products. Intact alleles yielded a single band of 590 bp, whereas mutant alleles yielded heteroduplex bands with different electric mobility. The experiment was triplicated. Right panel: A RFLP analysis of PCR products. SmaI-digested PCR products yielded either WT bands of 258+332 bp (SmaI site intact) or mutant bands of different length (SmaI site destroyed). Both T1 and T4 sgRNA-derived clones carried biallelic mutations in *IRF1* gene (LNCaP-mTOR-*IRF1*$^{-/-}$ 1 and 2). (C) Sequencing of mutant *IRF1* alleles. Clone 1 harbored a 3-bp deletion resulting in one amino acid deletion of Isoleucine (I) 21 with amino acid replacement of Proline (P) 22 to Methionine (M) (c.63_65delCCC, p.Ile21_Pro22delinsMet), and a 161-bp deletion resulting in appearance of stop codon (X) (c.60_87+133del, p.Gln20X). Clone 2 harbored a 3-bp deletion resulting in one amino acid deletion of Isoleucine (I) 21 (c.61_63delATC, p.Ile21del), and a 20-bp deletion resulting in appearance of stop codon (X) (c.52_71del, p.Ser23HisfsX4).



Supplementary Figure S3 The role of IRF1 in NED

A schematic suggested by our results. Active mTOR induces NED, and the disruption of concurrently up-regulated IRF1 appears to accelerate proliferation via the suppression of an IRF1 target gene, *p21* $^{Waf1/Cip1}$. Trans-differentiation pathways responsible for other characteristics are yet to be identified.

	Table S1. Comprehensive protein expression profiling by mass spectrometric analysis	
No	Accession	LNCaP-mTOR Dox+/Dox-
2514	Q99801|NKX31_HUMAN	0.271619797
1499	P06454|PTMA_HUMAN	0.313283414
2539	P40938|RFC3_HUMAN	0.314252317
782	P06493|CDC2_HUMAN	0.347577989
937	Q8WXX5|DNJC9_HUMAN	0.349164784
371	P26583|HMGB2_HUMAN	0.37759003
2807	Q96LA8|ANM6_HUMAN	0.38625282
1370	P00374|DYR_HUMAN	0.391479194
1460	P10275|ANDR_HUMAN	0.399355352
218	P49321|NASP_HUMAN	0.411442786
539	P16949|STMN1_HUMAN	0.415472895
634	P12004|PCNA_HUMAN	0.416661203
1422	Q96KB5|TOPK_HUMAN	0.417332441
1612	Q92769|HDAC2_HUMAN	0.424593419
391	P49736|MCM2_HUMAN	0.427071393
1763	Q96AT1|K1143_HUMAN	0.432348192
325	P33991|MCM4_HUMAN	0.436455786
368	P25205|MCM3_HUMAN	0.437654465
1468	Q16576|RBBP7_HUMAN	0.440932453
1596	P41223|BUD31_HUMAN	0.453352213
409	O75131|CPNE3_HUMAN	0.4615044
1322	P42166|LAP2A_HUMAN	0.466016889
2580	Q8N6N3|CA052_HUMAN	0.470680803
2469	P36639|8ODP_HUMAN	0.471518725
405	Q13451|FKBP5_HUMAN	0.472859621
717	Q9NTJ3|SMC4_HUMAN	0.475992084
2015	Q9BTT0|AN32E_HUMAN	0.482255369
2537	Q96EP0|RNF31_HUMAN	0.482343614

1644	Q96RR4|KKCC2_HUMAN	0.484797925
29	P09874|PARP1_HUMAN	0.490934014
1772	P05423|RPO3D_HUMAN	0.495705187
270	P33992|MCM5_HUMAN	0.49690339
830	P39748|FEN1_HUMAN	0.503371775
429	P07910|HNRPC_HUMAN	0.503982246
645	P37802|TAGL2_HUMAN	0.504403293
344	Q93009|UBP7_HUMAN	0.506201982
2039	Q9Y3B2|EXOS1_HUMAN	0.511736989
163	P09429|HMGB1_HUMAN	0.511871696
1465	P61956|SUMO2_HUMAN	0.513261974
2585	Q8IWD4|CC117_HUMAN	0.515225112
2835	Q9BZE2|PUS3_HUMAN	0.515978992
709	Q16222|UAP1_HUMAN	0.516243756
1354	P23443|KS6B1_HUMAN	0.517900467
302	Q53EL6|PDCD4_HUMAN	0.5227108
1110	Q9Y3Z3|SAMH1_HUMAN	0.523446739
2144	Q6P1R4|DUS1L_HUMAN	0.525165021
1902	Q12983|BNIP3_HUMAN	0.526655614
1300	Q9BTE3|CJ119_HUMAN	0.527639627
2005	Q6P6C2|ALKB5_HUMAN	0.529668212
2530	O00148|DDX39_HUMAN	0.536730587
1360	Q04726|TLE3_HUMAN	0.538777411
1862	P15927|RFA2_HUMAN	0.539572537
2365	P50750|CDK9_HUMAN	0.539680898
810	Q08945|SSRP1_HUMAN	0.540011764
1380	P11802|CDK4_HUMAN	0.540016353
2571	P31942|HNRH3_HUMAN	0.540223897
2811	Q02246|CNTN2_HUMAN	0.542729795
814	P23921|RIR1_HUMAN	0.545095503
2056	Q96A72|MGN2_HUMAN	0.545496345
2771	Q14527|SMRA3_HUMAN	0.548434138

1164	Q71UI9|H2AV_HUMAN	0.549024284
2268	O75940|SPF30_HUMAN	0.550459921
2711	Q14684|K0179_HUMAN	0.552808166
2721	Q8TB72|PUM2_HUMAN	0.553159237
2723	Q15291|RBBP5_HUMAN	0.553991497
1793	Q92688|AN32B_HUMAN	0.554967165
1287	Q14938|NFIX_HUMAN	0.555400014
2372	P28340|DPOD1_HUMAN	0.555864632
1625	P08651|NFIC_HUMAN	0.557395697
2651	Q15170|TCAL1_HUMAN	0.558537722
2863	O43169|CYB5B_HUMAN	0.558882594
1664	Q9Y5S9|RBM8A_HUMAN	0.565364301
469	Q01105|SET_HUMAN	0.567020595
1693	Q9UK45|LSM7_HUMAN	0.56840229
1666	Q92820|GGH_HUMAN	0.569293022
525	O95347|SMC2_HUMAN	0.571416795
2611	P49711|CTCF_HUMAN	0.572588563
864	P17480|UBF1_HUMAN	0.573897719
1896	O75362|ZN217_HUMAN	0.574170768
1094	P35249|RFC4_HUMAN	0.574235916
2179	Q01658|TBAP_HUMAN	0.575169384
1203	Q92597|NDRG1_HUMAN	0.577081501
1040	O15347|HMGB3_HUMAN	0.577174544
1023	Q09028|RBBP4_HUMAN	0.578880906
1046	Q9H1E3|NUCKS_HUMAN	0.579204679
2338	Q9UK59|DBR1_HUMAN	0.57946229
1966	P61244|MAX_HUMAN	0.580186963
350	P42167|LAP2B_HUMAN	0.581427693
515	Q9Y5B9|SPT16_HUMAN	0.582060993
2349	Q86YP4|P66A_HUMAN	0.582772076
918	Q99729|ROAA_HUMAN	0.582801044
1351	Q13572|ITPK1_HUMAN	0.583259702

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1056	Q8WWY3|PRP31_HUMAN	0.584954739
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2114	P21926|CD9_HUMAN	0.586080849
349	O15355|PP2CG_HUMAN	0.58626169
26	P19338|NUCL_HUMAN	0.587019503
2150	Q9H944|TRFP_HUMAN	0.587624848
2116	Q9Y6X9|MORC2_HUMAN	0.58900106
2521	Q9H4H8|FA83D_HUMAN	0.590695739
1509	Q9H814|RNUXA_HUMAN	0.590707779
372	P27694|RFA1_HUMAN	0.591824234
1373	Q9BPX3|CND3_HUMAN	0.592563272
1989	O15427|MOT4_HUMAN	0.592942536
1133	Q13185|CBX3_HUMAN	0.593439996
1073	P18754|RCC1_HUMAN	0.594245553
2689	Q15814|TBCC_HUMAN	0.595082462
2523	Q00613|HSF1_HUMAN	0.59561497
1346	Q96S55|WRIP1_HUMAN	0.59568423
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2381	P35250|RFC2_HUMAN	0.597257853
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748	Q8WW12|PCNP_HUMAN	0.599795878
740	P26358|DNMT1_HUMAN	0.599910975
1563	Q9BSV6|SEN34_HUMAN	0.600145757
2528	Q96DE0|NUD16_HUMAN	0.601656795
2321	P55854|SUMO3_HUMAN	0.602125585
1873	Q96LR5|UB2E2_HUMAN	0.606429636
2594	O75642|IF1AH_HUMAN	0.606901705
1912	Q9BX46|RBM24_HUMAN	0.607793629
648	Q14978|NOLC1_HUMAN	0.607836902
2159	O75586|MED6_HUMAN	0.608120978

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1480	O15119|TBX3_HUMAN	0.609839916
2517	Q6ICG6|CV009_HUMAN	0.609879851
2007	P51003|PAPOA_HUMAN	0.610603213
2309	P61964|WDR5_HUMAN	0.611013472
691	P52597|HNRPF_HUMAN	0.611388326
2688	Q13888|TF2H2_HUMAN	0.611857653
473	Q9UHD8|SEPT9_HUMAN	0.612178266
2831	Q14919|DRAP1_HUMAN	0.612811863
1905	P60763|RAC3_HUMAN	0.614019752
2853	Q9Y2S6|CCD72_HUMAN	0.614799678
1431	Q9P016|THYN1_HUMAN	0.617487848
1550	P35251|RFC1_HUMAN	0.617768228
1959	P31751|AKT2_HUMAN	0.619245529
542	Q16630|CPSF6_HUMAN	0.620042205
10	P78527|PRKDC_HUMAN	0.620303631
2862	Q96EK6|GNA1_HUMAN	0.621676803
2645	Q9H2J4|PDCL3_HUMAN	0.622107804
399	Q14566|MCM6_HUMAN	0.625510931
1507	Q8IWA5|CTL2_HUMAN	0.62571913
1167	Q8WUA2|PPIL4_HUMAN	0.62638092
2575	Q8IZL8|PELP1_HUMAN	0.627228022
903	Q9H0C8|ILKAP_HUMAN	0.627440453
2570	O00629|IMA4_HUMAN	0.627588212
644	Q15393|SF3B3_HUMAN	0.62765044
2464	Q9BZX2|UCK2_HUMAN	0.627694964
508	P53999|TCP4_HUMAN	0.62890029
2291	Q9Y4E8|UBP15_HUMAN	0.628998518
2091	O95453|PARN_HUMAN	0.629553556
2282	Q9NX58|LYAR_HUMAN	0.630499482
2132	O75792|RNH2A_HUMAN	0.631183803
1569	Q9Y2W2|WBP11_HUMAN	0.633032322

1399	O00584|RNT2_HUMAN	0.633456886
2254	Q06546|GABPA_HUMAN	0.633559644
2465	O75208|COQ9_HUMAN	0.63372153
2129	Q9BZQ6|EDEM3_HUMAN	0.635243893
1524	Q8IUE6|H2A2B_HUMAN	0.63527751
2082	Q6NYC1|PTDSR_HUMAN	0.636726081
502	Q9P258|RCC2_HUMAN	0.636854768
1710	Q9UBE0|SAE1_HUMAN	0.637588203
1522	P25490|TYY1_HUMAN	0.637812793
543	P16401|H15_HUMAN	0.638745129
52	P12956|KU70_HUMAN	0.638900459
849	Q8N684|CPSF7_HUMAN	0.638996661
240	P51858|HDGF_HUMAN	0.639302254
2130	Q96J01|THOC3_HUMAN	0.639771998
1145	P18615|NELFE_HUMAN	0.640950739
1807	Q9ULR0|ISY1_HUMAN	0.640994906
1700	Q9P287|BCCIP_HUMAN	0.642275929
1179	Q92733|PRCC_HUMAN	0.643545151
1938	Q13242|SFRS9_HUMAN	0.644278109
2488	O00220|TR10A_HUMAN	0.644517362
2775	Q09161|NCBP1_HUMAN	0.644845545
2603	Q9Y3D0|FA96B_HUMAN	0.646506608
1768	O96019|ACL6A_HUMAN	0.647290707
161	Q13435|SF3B2_HUMAN	0.647605956
2167	Q2TAY7|SMU1_HUMAN	0.647722304
1934	Q9BW71|HIRP3_HUMAN	0.647979975
241	Q9BQG0|MBB1A_HUMAN	0.6483832
1861	P52655|TF2AA_HUMAN	0.649017453
1820	Q9NXH9|TRM1_HUMAN	0.649262547
1378	P62316|SMD2_HUMAN	0.649330378
1887	Q8IXH7|NELFD_HUMAN	0.649445951
2057	Q9UNP9|PPIE_HUMAN	0.650469065

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393	P62826|RAN_HUMAN	0.65135783
142	P61978|HNRPK_HUMAN	0.651879787
113	Q00839|HNRPU_HUMAN	0.652045727
636	Q6P2Q9|PRP8_HUMAN	0.652562976
1788	P11908|PRPS2_HUMAN	0.652828693
1270	Q13573|SNW1_HUMAN	0.652857304
908	O95232|CROP_HUMAN	0.652926624
547	Q9NTZ6|RBM12_HUMAN	0.652942479
1743	Q96DI7|WDR57_HUMAN	0.653392553
139	P13010|KU86_HUMAN	0.653986335
201	Q15459|SF3A1_HUMAN	0.654118776
925	P45973|CBX5_HUMAN	0.654141009
1254	Q6P1J9|CDC73_HUMAN	0.654557467
2215	O60563|CCNT1_HUMAN	0.654852033
2738	Q6NW29|RWDD4_HUMAN	0.655246377
97	Q92945|FUBP2_HUMAN	0.65605253
2643	Q9NRG9|AAAS_HUMAN	0.657354712
1732	Q15050|RRS1_HUMAN	0.657393396
2613	Q9UET6|RRMJ1_HUMAN	0.657618344
180	Q96AE4|FUBP1_HUMAN	0.657940328
1572	O00193|SMAP_HUMAN	0.659407198
2279	Q96G25|MED8_HUMAN	0.659819663
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989	P35269|T2FA_HUMAN	0.660498917
623	P43487|RANG_HUMAN	0.660636365
485	P55060|XPO2_HUMAN	0.660670817
64	Q13263|TIF1B_HUMAN	0.660744131
2209	O15156|ZBT7B_HUMAN	0.662941635
1762	Q92879|CUGB1_HUMAN	0.663519561
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1424	Q8WXA9|SFR12_HUMAN	0.666572034
446	Q14683|SMC1A_HUMAN	0.667473257
1533	O43172|PRP4_HUMAN	0.667748094
504	P26599|PTBP1_HUMAN	0.667767584
2374	Q5TAP6|UT14C_HUMAN	0.667800844
581	P09661|RU2A_HUMAN	0.668190956
18	P12270|TPR_HUMAN	0.66914773
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1171	O43684|BUB3_HUMAN	0.673124731
620	Q9BZZ5|API5_HUMAN	0.673258424
2288	Q9C035|TRIM5_HUMAN	0.673746228
278	Q8N163|K1967_HUMAN	0.674022794
1806	P62979|RS27A_HUMAN	0.674025476
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789	Q9BWF3|RBM4_HUMAN	0.674673796
1786	O14802|RPC1_HUMAN	0.674714327
1636	Q9NVX2|NLE1_HUMAN	0.674744189
307	Q15029|U5S1_HUMAN	0.675067723
2866	Q6P2C8|CRSP8_HUMAN	0.675384283
1025	O43390|HNRPR_HUMAN	0.675425947
982	Q13148|TADBP_HUMAN	0.675469935
2234	Q05048|CSTF1_HUMAN	0.675605357
793	Q9UBT2|SAE2_HUMAN	0.675803483
1342	Q86WA6|BPHL_HUMAN	0.67659229
1317	Q14241|ELOA1_HUMAN	0.678906918
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880	P49006|MRP_HUMAN	0.67908591
313	Q9UQE7|SMC3_HUMAN	0.679551423
756	O43252|PAPS1_HUMAN	0.680786192
1761	O75937|DNJC8_HUMAN	0.681429863
1492	O95218|ZRAB2_HUMAN	0.681660354

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1067	Q13547|HDAC1_HUMAN	0.682494342
352	Q9BXP5|ARS2_HUMAN	0.684065759
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1446	P29083|T2EA_HUMAN	0.684251249
2518	O95684|FR1OP_HUMAN	0.68455255
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1118	P23634|AT2B4_HUMAN	0.6859833
1654	Q8WVJ2|NUDC2_HUMAN	0.686188757
1571	Q9GZU8|NIP30_HUMAN	0.686316371
2075	Q92599|SEPT8_HUMAN	0.686745167
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1366	Q8WVC0|LEO1_HUMAN	0.687975168
1885	P36873|PP1G_HUMAN	0.688357234
1456	Q5VTR2|BRE1A_HUMAN	0.688437581
2126	O15541|R113A_HUMAN	0.688978851
1217	Q01130|SFRS2_HUMAN	0.68945086
899	Q16762|THTR_HUMAN	0.690733075
1477	Q9NYL4|FKB11_HUMAN	0.690855145
2044	P54105|ICLN_HUMAN	0.690872729
2727	Q9NUU7|DD19A_HUMAN	0.691688895
2628	P62380|TBPL1_HUMAN	0.692240417
413	P60891|PRPS1_HUMAN	0.692382097
2731	O14662|STX16_HUMAN	0.692461371
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2451	P62308|RUXG_HUMAN	0.696819246
2278	O15393|TMPS2_HUMAN	0.69740212
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299	Q14103|HNRPD_HUMAN	0.698429465
412	P39687|AN32A_HUMAN	0.698705435
750	Q05519|SFR11_HUMAN	0.698875487
2109	O43766|LIAS_HUMAN	0.699344575
2128	O43818|U3IP2_HUMAN	0.69964844
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2196	Q96EI5|TCAL4_HUMAN	0.701700628
2474	Q6WCQ1|MRIP_HUMAN	0.701973319
1821	Q96PZ0|PUS7_HUMAN	0.702188969
1617	O60885|BRD4_HUMAN	0.702506781
1691	O43809|CPSF5_HUMAN	0.702578425
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762	Q99623|PHB2_HUMAN	0.703575015
2655	Q9BT73|CG048_HUMAN	0.70425117
2218	Q9NZW5|MPP6_HUMAN	0.70463717
466	Q96AY3|FKB10_HUMAN	0.704734683
2864	Q9NXR7|BRE_HUMAN	0.704760492
175	P49915|GUAA_HUMAN	0.70568949
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1692	Q9UQ88|CD2L2_HUMAN	0.70974189
2719	Q6P1M0|S27A4_HUMAN	0.710692108
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2171	Q96RT7|GCP6_HUMAN	0.711024761
1104	O60341|LSD1_HUMAN	0.711781383

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2559	Q86X55|CARM1_HUMAN	0.712407291
2481	Q9Y3B7|RM11_HUMAN	0.712692559
1092	P08579|RU2B_HUMAN	0.712745965
818	O75400|PRP40_HUMAN	0.712813318
1842	Q02083|ASAHL_HUMAN	0.713044703
2133	Q15427|SF3B4_HUMAN	0.713128448
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2578	P28702|RXRB_HUMAN	0.713383913
784	Q9UK76|HN1_HUMAN	0.713388383
2647	O00422|SAP18_HUMAN	0.71448195
781	Q15185|TEBP_HUMAN	0.714728117
219	P10412|H14_HUMAN	0.715119481
2172	P61619|S61A1_HUMAN	0.715401292
1152	Q9UMS4|PRP19_HUMAN	0.715578854
1962	Q9H9B4|SFXN1_HUMAN	0.716065466
1247	Q71UM5|RS27L_HUMAN	0.716157138
983	P26368|U2AF2_HUMAN	0.718357146
633	P49916|DNL3_HUMAN	0.718897641
1508	P63279|UBC9_HUMAN	0.71902585
310	P35527|K1C9_HUMAN	0.719732285
1717	Q6P9B9|INT5_HUMAN	0.721408784
1001	P82979|HCC1_HUMAN	0.721492767
1356	Q12972|PP1R8_HUMAN	0.72160399
1745	Q8NC60|CD014_HUMAN	0.721749246
2187	Q9GZT9|EGLN1_HUMAN	0.721847594
424	Q14839|CHD4_HUMAN	0.722994745
2385	O95140|MFN2_HUMAN	0.723102689
1334	Q9BV57|MTND_HUMAN	0.72337079
808	P19440|GGT1_HUMAN	0.72378701
1964	Q9UBL3|ASH2L_HUMAN	0.724102557

1213	Q05655|KPCD_HUMAN	0.72415328
2240	Q96PE7|MCEE_HUMAN	0.724799931
1299	P00492|HPRT_HUMAN	0.724904358
664	O60343|TBCD4_HUMAN	0.724991024
150	O75533|SF3B1_HUMAN	0.725320756
1010	O94906|PRP6_HUMAN	0.7264992
1264	Q9H3P2|NELFA_HUMAN	0.727132201
1141	Q9H857|NT5D2_HUMAN	0.72718668
1831	O14929|HAT1_HUMAN	0.727308333
2344	Q8TEM1|PO210_HUMAN	0.727646768
1000	O15160|RPA5_HUMAN	0.72862792
1714	O75607|NPM3_HUMAN	0.728983879
1808	O15381|NVL_HUMAN	0.729004622
923	Q9BXW7|CECR5_HUMAN	0.729433656
653	Q15020|SART3_HUMAN	0.729540527
1704	Q96GD0|PLPP_HUMAN	0.729546666
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152	Q15233|NONO_HUMAN	0.731070757
1541	P62318|SMD3_HUMAN	0.731305838
2859	Q8WYA6|CTBL1_HUMAN	0.731347859
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1984	Q9BVL2|NUPL1_HUMAN	0.731740415
2486	Q92785|REQU_HUMAN	0.731766164
2410	Q9P2N5|RBM27_HUMAN	0.731899917
2625	Q9UKD2|MRT4_HUMAN	0.732300222
2377	O14787|TNPO2_HUMAN	0.732609689
421	Q15637|SF01_HUMAN	0.732711196
1708	Q9BY42|CT043_HUMAN	0.733213007
2554	Q8TCC3|RM30_HUMAN	0.733257234
1566	Q13243|SFRS5_HUMAN	0.734279573
288	P23193|TCEA1_HUMAN	0.734914064
298	P22830|HEMH_HUMAN	0.734963715

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2247	P00813|ADA_HUMAN	0.851460099

1061	Q8N8N7|ZADH1_HUMAN	0.851476431
347	Q92841|DDX17_HUMAN	0.851739883
526	Q7Z4W1|DCXR_HUMAN	0.851970553
135	P54886|P5CS_HUMAN	0.851977289
996	Q99829|CPNE1_HUMAN	0.852343023
1852	Q9NRV9|HEBP1_HUMAN	0.852410376
520	P55209|NP1L1_HUMAN	0.85246563
2547	P46063|RECQ1_HUMAN	0.852538407
2269	Q9NPL8|CC001_HUMAN	0.852759302
2824	O75427|LRCH4_HUMAN	0.852801204
1530	Q9Y6E0|STK24_HUMAN	0.853036702
2239	O00217|NDUS8_HUMAN	0.853377819
465	P62701|RS4X_HUMAN	0.853519857
980	P41240|CSK_HUMAN	0.853605032
674	P49792|RBP2_HUMAN	0.853898644
2202	O60307|MAST3_HUMAN	0.853953063
551	Q10713|MPPA_HUMAN	0.854385018
233	P48735|IDHP_HUMAN	0.854408801
1198	Q15102|PA1B3_HUMAN	0.855040669
522	P25685|DNJB1_HUMAN	0.855386794
2607	Q9Y2Z9|COQ6_HUMAN	0.855555475
2224	Q9NQG5|CT077_HUMAN	0.855866313
2398	P42765|THIM_HUMAN	0.856462181
2555	Q9HAF1|CA149_HUMAN	0.856649458
713	Q16531|DDB1_HUMAN	0.85685122
1521	Q9Y276|BCS1_HUMAN	0.857774079
876	P62266|RS23_HUMAN	0.857894421
2720	Q96TA2|YMEL1_HUMAN	0.858175457
2354	Q8TBB5|KLDC4_HUMAN	0.858631492
1230	P37108|SRP14_HUMAN	0.858962238
1394	P62244|RS15A_HUMAN	0.859084308
1011	Q8TD19|NEK9_HUMAN	0.859181046

2574	Q96EE3|SEH1L_HUMAN	0.859250188
821	Q9Y295|DRG1_HUMAN	0.859636843
1102	Q9BPW8|NIPS1_HUMAN	0.859875739
2369	Q6NZY4|ZCHC8_HUMAN	0.859917641
238	Q9UQ80|PA2G4_HUMAN	0.860463619
1660	P09012|SNRPA_HUMAN	0.860951066
2520	O15254|ACOX3_HUMAN	0.861092687
2756	P14854|CX6B1_HUMAN	0.861387372
1223	O60282|KIF5C_HUMAN	0.861652493
2301	Q92793|CBP_HUMAN	0.861695707
1364	Q9HC35|EMAL4_HUMAN	0.861859262
217	Q9Y3I0|CV028_HUMAN	0.862098336
2632	Q9H4B7|TBB1_HUMAN	0.862353623
1489	P53985|MOT1_HUMAN	0.8624264
2253	P62995|TRA2B_HUMAN	0.862859488
2525	Q13951|PEBB_HUMAN	0.862871051
1613	O60220|TIM8A_HUMAN	0.863011599
1466	Q9UL18|I2C1_HUMAN	0.863369703
12	P58107|EPIPL_HUMAN	0.863492668
2053	Q9NPF4|GCP_HUMAN	0.863888025
1858	Q86WH2|RASF3_HUMAN	0.864312351
1669	Q9H3P7|GCP60_HUMAN	0.864707887
1396	Q9Y613|FHOD1_HUMAN	0.864751279
2059	Q8TAE8|G45IP_HUMAN	0.864982247
222	Q14008|CKAP5_HUMAN	0.865323365
2448	Q9H2P9|DPH5_HUMAN	0.865393579
2606	O75143|K0652_HUMAN	0.865614176
1686	O15235|RT12_HUMAN	0.865737557
468	Q9H0D6|XRN2_HUMAN	0.866040885
2798	Q9HD67|MYO10_HUMAN	0.866281033
1020	O95260|ATE1_HUMAN	0.866382718
1241	P21912|DHSB_HUMAN	0.866452992

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1119	O95071|EDD1_HUMAN	0.867393017
945	P08708|RS17_HUMAN	0.867427289
1402	P33527|MRP1_HUMAN	0.867684424
931	P82650|RT22_HUMAN	0.867775381
720	P27144|KAD4_HUMAN	0.867966712
764	P15880|RS2_HUMAN	0.868104935
921	P62993|GRB2_HUMAN	0.868149579
2652	O75380|NDUS6_HUMAN	0.86858654
1663	Q14240|IF4A2_HUMAN	0.868637919
1629	Q9NRF8|PYRG2_HUMAN	0.868754923
567	Q92900|RENT1_HUMAN	0.868988454
985	Q9BRT8|CBWD1_HUMAN	0.869068265
1916	Q9UBR2|CATZ_HUMAN	0.869325995
407	O75153|IF3X_HUMAN	0.869597137
440	Q07666|SAM68_HUMAN	0.869917631
2089	P02768|ALBU_HUMAN	0.869941771
2019	Q8TDX7|NEK7_HUMAN	0.870296836
1316	O75694|NU155_HUMAN	0.870620012
1747	Q9BQ39|DDX50_HUMAN	0.870666146
2696	P35749|MYH11_HUMAN	0.870670199
1736	P57772|SELB_HUMAN	0.87101388
2713	Q8N4Q0|ZADH2_HUMAN	0.871851623
1973	Q8WU79|SMP1L_HUMAN	0.871892333
1648	P51970|NDUA8_HUMAN	0.871980786
665	Q13428|TCOF_HUMAN	0.872107625
1591	Q13617|CUL2_HUMAN	0.872290611
1474	O95400|CD2B2_HUMAN	0.872920811
1645	Q9NQH7|XPP3_HUMAN	0.87316072
2020	Q14738|2A5D_HUMAN	0.873372257
2561	Q9NZL4|HPBP1_HUMAN	0.873387337

2327	Q8IZ69|HTF9C_HUMAN	0.873474896
2289	Q8WXD5|GEMI6_HUMAN	0.873865306
2685	O60264|SMCA5_HUMAN	0.874139786
919	O95202|LETM1_HUMAN	0.874434412
2340	O43933|PEX1_HUMAN	0.87478435
1391	Q9NUQ8|ABCF3_HUMAN	0.874794364
590	P52789|HXK2_HUMAN	0.875473142
43	P53396|ACLY_HUMAN	0.875587046
1926	Q9Y3D2|MSRB2_HUMAN	0.875593424
1853	Q92922|SMRC1_HUMAN	0.875619829
1127	O43395|PRPF3_HUMAN	0.875727654
797	P46783|RS10_HUMAN	0.875780046
729	O60502|NCOAT_HUMAN	0.876112759
878	Q15366|PCBP2_HUMAN	0.876342714
2085	P84085|ARF5_HUMAN	0.877041221
1725	Q13444|ADA15_HUMAN	0.877156079
1439	P49458|SRP09_HUMAN	0.877535701
101	P60174|TPIS_HUMAN	0.877877533
90	P68366|TBA1_HUMAN	0.878094912
1746	P29353|SHC1_HUMAN	0.878234625
704	Q9BSD7|U334_HUMAN	0.878580093
1812	P55769|NH2L1_HUMAN	0.879022717
2013	Q9H5Q4|TFB2M_HUMAN	0.879207373
2115	Q5TZA2|CROCC_HUMAN	0.879422009
2774	Q9UPN4|AZI1_HUMAN	0.879918635
2472	Q92526|TCPW_HUMAN	0.879991412
775	P16455|MGMT_HUMAN	0.880102038
1754	P16422|TACD1_HUMAN	0.880173624
1730	P08910|LBH2_HUMAN	0.880455792
1013	Q92506|DHB8_HUMAN	0.880545437
1974	P48739|PIPNB_HUMAN	0.880556464
2593	P07205|PGK2_HUMAN	0.880909324

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2563	Q8WZA0|LZIC_HUMAN	0.881350875
1408	Q92905|CSN5_HUMAN	0.881470203
1688	Q92796|DLG3_HUMAN	0.881825328
1976	Q99471|PFD5_HUMAN	0.881969035
902	P48634|BAT2_HUMAN	0.882060111
1620	P11172|PYR5_HUMAN	0.882207811
2318	Q96DP5|FMT_HUMAN	0.882221401
408	P62280|RS11_HUMAN	0.882317603
662	P09543|CN37_HUMAN	0.882384717
1757	O00506|STK25_HUMAN	0.882586062
2680	Q12756|KIF1A_HUMAN	0.882864714
2697	Q9H307|PININ_HUMAN	0.882963538
2587	Q9UHJ6|CARKL_HUMAN	0.883056283
1310	Q9NR56|MBNL_HUMAN	0.883069634
1433	Q9BZF9|UACA_HUMAN	0.883108079
2153	Q9Y5J9|TIM8B_HUMAN	0.88316077
2850	P12931|SRC_HUMAN	0.883224368
2847	Q92989|CLP1_HUMAN	0.883652866
1415	Q9HAT2|SIAE_HUMAN	0.884041548
474	P62269|RS18_HUMAN	0.884050369
944	P08559|ODPA_HUMAN	0.884503126
2772	Q9NYZ2|MFRN1_HUMAN	0.8857373
1012	O00330|ODPX_HUMAN	0.885852575
2427	P31327|CPSM_HUMAN	0.886044919
75	P40926|MDHM_HUMAN	0.886130929
1640	Q9HA64|KT3K_HUMAN	0.886175931
226	Q9UQ35|SRRM2_HUMAN	0.88680768
1082	P55265|DSRAD_HUMAN	0.886987925
2449	Q9Y676|RT18B_HUMAN	0.887410343
119	P06744|G6PI_HUMAN	0.887490094
966	O60884|DNJA2_HUMAN	0.887494504

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626	P27348|1433T_HUMAN	0.887964904
1760	Q9BV44|THUM3_HUMAN	0.888490438
40	P14625|ENPL_HUMAN	0.888499081
2762	P27986|P85A_HUMAN	0.8885113
511	P62241|RS8_HUMAN	0.888777614
1427	Q86VS8|HOOK3_HUMAN	0.888807356
1830	Q14141|SEPT6_HUMAN	0.88890487
1944	O95801|TTC4_HUMAN	0.888920128
997	P14174|MIF_HUMAN	0.889070034
1811	Q9UKX7|NUP50_HUMAN	0.889295459
2522	Q15390|MTFR1_HUMAN	0.8893857
809	P50897|PPT1_HUMAN	0.88985616
1470	Q9NPI6|DCP1A_HUMAN	0.889865696
901	Q9BQE3|TBA6_HUMAN	0.889889777
2468	Q9UNL2|SSRG_HUMAN	0.889907241
2567	Q8IXI2|MIRO1_HUMAN	0.89004457
15	P08238|HS90B_HUMAN	0.89009732
1234	Q08752|PPID_HUMAN	0.890173852
2287	P19474|RO52_HUMAN	0.890234768
926	P36551|HEM6_HUMAN	0.890269458
2453	P42338|PK3CB_HUMAN	0.890316188
2729	Q96D09|GASP2_HUMAN	0.890632391
1936	P82930|RT34_HUMAN	0.890840828
891	P23919|DTYMK_HUMAN	0.89086175
2856	Q8N806|CN130_HUMAN	0.89121604
1500	Q9NP92|RT30_HUMAN	0.891493559
381	Q6PKG0|LARP1_HUMAN	0.891825378
276	Q14157|UBP2L_HUMAN	0.891943455
1531	Q9H9P8|L2HDH_HUMAN	0.892362952
2648	Q86TS9|RM52_HUMAN	0.892397225
1713	Q14435|GALT3_HUMAN	0.892425299

2588	Q92485|ASM3B_HUMAN	0.892743766
1385	O95486|SC24A_HUMAN	0.892878652
2223	P51649|SSDH_HUMAN	0.893028498
977	O00154|BACH_HUMAN	0.893426657
227	P30084|ECHM_HUMAN	0.894297302
2843	Q13685|AAMP_HUMAN	0.89435941
1207	O95671|ASML_HUMAN	0.894504964
2760	Q13825|AUMH_HUMAN	0.894814789
1958	Q9UHG3|PCYOX_HUMAN	0.894847929
24	P00558|PGK1_HUMAN	0.894993603
266	Q14166|TTL12_HUMAN	0.894996941
1529	P04181|OAT_HUMAN	0.895001233
1920	O95999|BCL10_HUMAN	0.895056009
1047	P14324|FPPS_HUMAN	0.895110369
1393	P40123|CAP2_HUMAN	0.895122647
2243	Q8NFT2|STEA2_HUMAN	0.895278633
1707	Q9Y5L4|TIM13_HUMAN	0.895516276
2363	O00505|IMA3_HUMAN	0.895620108
1101	P08236|BGLR_HUMAN	0.895666599
960	Q9HA77|SYCM_HUMAN	0.896106601
1560	Q13363|CTBP1_HUMAN	0.896150231
1214	Q9BW83|RAYL_HUMAN	0.896156847
570	P62249|RS16_HUMAN	0.896704376
1045	P18583|SON_HUMAN	0.89681977
308	O76031|CLPX_HUMAN	0.897002161
476	P61221|ABCE1_HUMAN	0.897010684
1377	O43592|XPOT_HUMAN	0.897194266
2358	Q03426|KIME_HUMAN	0.897302806
2498	O15550|UTX_HUMAN	0.897352815
546	Q06203|PUR1_HUMAN	0.897495747
1917	Q8ND56|LS14A_HUMAN	0.897535324
1870	P62861|RS30_HUMAN	0.897582889

643	Q6FI81|CPIN1_HUMAN	0.897979915
660	P62277|RS13_HUMAN	0.898026526
2029	O00264|PGRC1_HUMAN	0.89823097
69	P42704|LPPRC_HUMAN	0.898879111
293	Q92499|DDX1_HUMAN	0.899059713
527	P51991|ROA3_HUMAN	0.899509251
1108	Q02809|PLOD1_HUMAN	0.900111139
2092	P08727|K1C19_HUMAN	0.900279999
2043	Q6P1L8|RM14_HUMAN	0.900473416
524	Q8TCS8|PNPT1_HUMAN	0.900555193
1306	Q86X29|LSR_HUMAN	0.900605738
777	Q8NBN7|RDH13_HUMAN	0.900684297
2246	Q8WVY7|UBCP1_HUMAN	0.900724649
647	P21397|AOFA_HUMAN	0.900757194
2568	Q8IWA4|MFN1_HUMAN	0.901251733
1676	P35658|NU214_HUMAN	0.901315629
635	O15067|PUR4_HUMAN	0.901380062
1472	Q99439|CNN2_HUMAN	0.901480913
1857	Q9H9S4|CB39L_HUMAN	0.901552498
2052	P24928|RPB1_HUMAN	0.901565731
2367	P18846|ATF1_HUMAN	0.901890755
2207	Q9Y6D9|MD1L1_HUMAN	0.901940048
1878	Q9NXG6|EGLX_HUMAN	0.902240932
510	Q13564|ULA1_HUMAN	0.90256238
2692	Q9H6E5|TUT1_HUMAN	0.902623534
1650	O43819|SCO2_HUMAN	0.902709186
1903	Q96BW9|MMP37_HUMAN	0.90294832
2134	Q9NWZ5|UCKL1_HUMAN	0.90318346
2787	P48380|RFX3_HUMAN	0.903316557
906	P62841|RS15_HUMAN	0.903511584
2357	O00161|SNP23_HUMAN	0.90374887
2249	P19784|CSK22_HUMAN	0.903987944

2100	Q8WW59|SPRY4_HUMAN	0.904049516
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1809	P49902|5NTC_HUMAN	0.905103743
1200	Q02338|BDH_HUMAN	0.905463219
2686	Q5H9R7|SAPS3_HUMAN	0.905664027
2235	Q96E09|F122A_HUMAN	0.906074464
1126	Q9UN36|NDRG2_HUMAN	0.906224012
1782	O00267|SPT5H_HUMAN	0.90627861
2657	Q9H3K6|BOLA2_HUMAN	0.906836629
2236	P42677|RS27_HUMAN	0.90704602
1150	Q5TFE4|NT5D1_HUMAN	0.907179415
1516	P62847|RS24_HUMAN	0.907417953
753	Q9H078|CLPB_HUMAN	0.907770276
1178	Q14289|FAK2_HUMAN	0.90787977
2687	P82932|RT06_HUMAN	0.908568501
2176	Q8N201|INT1_HUMAN	0.908677816
666	P05556|ITB1_HUMAN	0.908780098
1565	Q99717|SMAD5_HUMAN	0.908989549
1607	Q8IXI1|MIRO2_HUMAN	0.90937376
2726	Q5QJ74|TBCEL_HUMAN	0.909998
248	P23396|RS3_HUMAN	0.910407543
838	O00170|AIP_HUMAN	0.910477459
2216	O75347|TBCA_HUMAN	0.910568655
2383	Q9NP73|GT281_HUMAN	0.910708547
1097	Q86SF2|GALT7_HUMAN	0.910717666
297	P18669|PGAM1_HUMAN	0.911476672
2584	Q8IY67|RAVR1_HUMAN	0.911499023
2329	P62273|RS29_HUMAN	0.912484109
281	P61247|RS3A_HUMAN	0.91258055
493	P62081|RS7_HUMAN	0.912598491
698	Q9BRK5|CAB45_HUMAN	0.912753701
2629	Q8TDP1|RNH2C_HUMAN	0.912756205

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934	P34896|GLYC_HUMAN	0.913258135
2393	P84090|ERH_HUMAN	0.913390517
498	P49753|ACOT2_HUMAN	0.913765013
426	Q9P2R7|SUCB1_HUMAN	0.913878083
167	P07954|FUMH_HUMAN	0.914412022
1244	P82673|RT35_HUMAN	0.914474905
2049	Q9UKM7|MA1B1_HUMAN	0.91461128
2284	P78559|MAP1A_HUMAN	0.914871812
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1294	Q8TBC4|UBA3_HUMAN	0.914980471
2814	O95373|IPO7_HUMAN	0.915056527
1986	Q9P1Y5|K1543_HUMAN	0.915069997
2546	Q8WYA0|IFT81_HUMAN	0.915165246
817	P62136|PP1A_HUMAN	0.915207803
778	O75334|LIPA2_HUMAN	0.915500164
2384	Q86U38|CN021_HUMAN	0.915500343
406	Q07955|SFRS1_HUMAN	0.915517986
1655	Q9NVS2|RT18A_HUMAN	0.915853858
1906	O15439|MRP4_HUMAN	0.915933013
1510	Q9NR50|EI2BG_HUMAN	0.916096866
1751	Q96DH6|MSI2H_HUMAN	0.916160405
1261	Q15717|ELAV1_HUMAN	0.916332245
2238	Q9Y6R0|NUMBL_HUMAN	0.916340768
1227	Q96I59|SYNM_HUMAN	0.916523516
353	P30042|ES1_HUMAN	0.916784465
1540	Q01433|AMPD2_HUMAN	0.917024374
2490	Q8WWV3|RT4I1_HUMAN	0.917125583
2190	O43760|SNG2_HUMAN	0.917468369
491	P50213|IDH3A_HUMAN	0.917525113
1618	P45880|VDAC2_HUMAN	0.917624891
990	Q13620|CUL4B_HUMAN	0.917625725

1914	Q9UBQ0|VPS29_HUMAN	0.917747855
1335	P23258|TBG1_HUMAN	0.917991519
133	P22102|PUR2_HUMAN	0.918092906
1259	Q92665|RT31_HUMAN	0.918129861
425	Q14974|IMB1_HUMAN	0.918135524
1978	O95777|LSM8_HUMAN	0.918902814
1800	O43493|TGON2_HUMAN	0.919283986
1343	O15031|PLXB2_HUMAN	0.919312716
246	Q9Y230|RUVB2_HUMAN	0.919338942
1345	Q96ST3|SIN3A_HUMAN	0.919341743
842	Q7Z460|CLAP1_HUMAN	0.919500232
1128	Q9GZT3|SLIRP_HUMAN	0.919722795
746	Q13162|PRDX4_HUMAN	0.919759572
1880	Q8NFU3|KAT_HUMAN	0.919890821
1953	Q92783|STAM1_HUMAN	0.919943988
1606	Q13232|NDK3_HUMAN	0.920185924
1471	P61923|COPZ1_HUMAN	0.920309603
338	P30038|AL4A1_HUMAN	0.920432508
1598	Q92797|SYMPK_HUMAN	0.921098828
700	Q9Y5Z4|HEBP2_HUMAN	0.921112537
1931	Q7LBC6|JHD2B_HUMAN	0.921201646
2700	P49757|NUMB_HUMAN	0.921410739
1556	Q9Y5U2|TSSC4_HUMAN	0.922043741
2419	Q16637|SMN_HUMAN	0.92220962
223	Q08211|DHX9_HUMAN	0.922398746
215	Q16836|HCDH_HUMAN	0.922424257
950	Q15147|PLCB4_HUMAN	0.922490597
556	Q8TEX9|IPO4_HUMAN	0.922609448
856	Q9HB07|MYG1_HUMAN	0.922675669
1295	Q15165|PON2_HUMAN	0.922679782
292	Q13442|HAP28_HUMAN	0.922808468
2566	P20336|RAB3A_HUMAN	0.923653305

649	P09960|LKHA4_HUMAN	0.92394805
2735	Q5HYK3|COQ5_HUMAN	0.924265206
696	Q9Y2W1|TR150_HUMAN	0.924596667
2016	P36954|RPB9_HUMAN	0.925797641
2792	Q8WVM0|TFB1M_HUMAN	0.926139414
2783	Q9Y639|NPTN_HUMAN	0.926306665
860	P11177|ODPB_HUMAN	0.926332235
640	P61088|UBE2N_HUMAN	0.926453352
102	P00505|AATM_HUMAN	0.92660296
1582	Q9NRR5|UBQL4_HUMAN	0.92691505
907	Q96C36|P5CR2_HUMAN	0.927802265
2265	P63208|SKP1_HUMAN	0.92784375
2302	P46020|KPB1_HUMAN	0.927847624
1869	Q9H1E5|TXD13_HUMAN	0.927949667
1982	Q969Z0|TBRG4_HUMAN	0.928132832
492	P53597|SUCA_HUMAN	0.928256869
2193	P53384|NUBP1_HUMAN	0.928328097
549	Q13310|PABP4_HUMAN	0.928614795
1573	P54725|RD23A_HUMAN	0.928973436
1954	O60231|DHX16_HUMAN	0.929166317
358	O75821|IF34_HUMAN	0.929454267
718	Q15691|MARE1_HUMAN	0.929805815
2508	P22090|RS4Y1_HUMAN	0.930181205
759	P07108|ACBP_HUMAN	0.930235445
486	P31689|DNJA1_HUMAN	0.930709779
618	O14980|XPO1_HUMAN	0.930913389
1632	Q7RTV0|PHF5A_HUMAN	0.931233764
2360	P57678|GEMI4_HUMAN	0.931277871
2461	Q14739|LBR_HUMAN	0.931385815
2231	O95825|QORL_HUMAN	0.931537449
2759	P78362|SRPK2_HUMAN	0.932251751
370	P22392|NDKB_HUMAN	0.933148742

608	P35270|SPRE_HUMAN	0.933321416
2577	Q96BJ8|ELMO3_HUMAN	0.933373988
2509	Q9ULE0|WWC3_HUMAN	0.933430135
389	Q9HB71|CYBP_HUMAN	0.93347466
2573	Q9NRW7|VPS45_HUMAN	0.933546424
141	Q02252|MMSA_HUMAN	0.933878958
1891	P42771|CD2A1_HUMAN	0.933966696
973	P68371|TBB2C_HUMAN	0.934344471
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673	P49585|PCY1A_HUMAN	0.934577525
197	O95831|AIFM1_HUMAN	0.934750259
348	P07737|PROF1_HUMAN	0.934830129
1107	Q13057|COASY_HUMAN	0.934889317
1525	P49750|YLPM1_HUMAN	0.935105145
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305	Q15056|IF4H_HUMAN	0.935534537
1783	Q5JTZ9|SYAM_HUMAN	0.936201394
1665	P49406|RM19_HUMAN	0.936460912
1584	Q15599|NHRF2_HUMAN	0.936859012
641	P62263|RS14_HUMAN	0.937139511
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1090	Q9NYK5|RM39_HUMAN	0.938233614
1048	O00459|P85B_HUMAN	0.938399971
322	P62258|1433E_HUMAN	0.938408434
2558	Q9NWU5|RM22_HUMAN	0.938524425
336	P67809|YBOX1_HUMAN	0.9387483
2212	Q14687|GSE1_HUMAN	0.939067721
1051	Q8WTS6|SETD7_HUMAN	0.939116955
1549	P42285|SK2L2_HUMAN	0.939161897
1734	Q96A35|RM24_HUMAN	0.939204037

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414	Q9Y446|PKP3_HUMAN	0.93944943
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46	P22314|UBE1_HUMAN	0.940215826
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2341	P48730|KC1D_HUMAN	0.940590262
1034	P32969|RL9_HUMAN	0.941237569
661	P62829|RL23_HUMAN	0.941327095
976	Q969X5|ERGI1_HUMAN	0.941405833
594	Q12849|GRSF1_HUMAN	0.941761494
343	P62917|RL8_HUMAN	0.94201386
2744	O95630|STABP_HUMAN	0.942402303
2084	Q7KZI7|MARK2_HUMAN	0.942628026
1662	Q9Y3E2|BOLA1_HUMAN	0.942808628
827	O14744|ANM5_HUMAN	0.942872167
2411	O75879|GATB_HUMAN	0.943690836
1494	Q9BYD1|RM13_HUMAN	0.943783224
1286	Q9ULX3|NOB1_HUMAN	0.943901718
1963	Q96PK6|RBM14_HUMAN	0.943976879
1305	P36405|ARL3_HUMAN	0.945171416
450	P35237|SPB6_HUMAN	0.945201814
972	P82933|RT09_HUMAN	0.945297897
2669	Q9UBV8|PEF1_HUMAN	0.945492506
1930	Q9UL54|TAOK2_HUMAN	0.945820808
1336	O43264|ZW10_HUMAN	0.945821404
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2447	Q96S44|PRPK_HUMAN	0.946191907
824	P33240|CSTF2_HUMAN	0.946487427
905	Q7Z2W4|ZCC2_HUMAN	0.946585178
1997	P53365|ARFP2_HUMAN	0.946589887
2366	Q8NI27|THOC2_HUMAN	0.946837485
1694	Q6UXH1|CREL2_HUMAN	0.946932077

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2476	Q9NYY8|FAKD2_HUMAN	0.947149336
2854	Q7Z2W9|RM21_HUMAN	0.947912335
1864	P09417|DHPR_HUMAN	0.948409319
2668	O60783|RT14_HUMAN	0.948419213
2543	O43505|B3GN1_HUMAN	0.948673904
2684	Q9NZC9|SMAL1_HUMAN	0.948944867
1087	P62942|FKB1A_HUMAN	0.949497461
2478	P43307|SSRA_HUMAN	0.949779272
1975	P83436|COG7_HUMAN	0.949880421
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1255	Q99615|DNJC7_HUMAN	0.950290561
1379	Q9P0M9|RM27_HUMAN	0.950438917
2649	Q86V88|MGDP1_HUMAN	0.950499177
494	P35908|K22E_HUMAN	0.950617731
2513	O43633|CHM2A_HUMAN	0.950639844
209	Q8N1G4|LRC47_HUMAN	0.950828373
538	P11310|ACADM_HUMAN	0.951000333
2322	Q7Z4G4|CF075_HUMAN	0.951514542
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1687	Q96D71|REPS1_HUMAN	0.951749802
2142	Q13418|ILK_HUMAN	0.95187664
2244	P07305|H10_HUMAN	0.951988459
2143	Q9Y3B3|TMED7_HUMAN	0.952122152
815	P61081|UBC12_HUMAN	0.952634931
2156	O95302|FKBP9_HUMAN	0.952646554
2170	Q9NVT9|ARMC1_HUMAN	0.953713417
2634	Q08170|SFRS4_HUMAN	0.954240799
601	O00410|IMB3_HUMAN	0.954429328
1702	Q15843|NEDD8_HUMAN	0.954585552
1771	Q9NP79|CF055_HUMAN	0.95488894

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2694	Q8N6M0|OTU6B_HUMAN	0.955404997
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2595	Q66LE6|2ABD_HUMAN	0.955475807
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1327	Q8TC07|TBC15_HUMAN	0.955601037
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2390	Q8NF91|SYNE1_HUMAN	0.956087232
1940	O95239|KIF4A_HUMAN	0.956255972
2477	P50747|BPL1_HUMAN	0.95626688
88	Q86VP6|CAND1_HUMAN	0.956393361
896	Q9UJZ1|STML2_HUMAN	0.9565925
1532	Q96CW5|GCP3_HUMAN	0.956610739
434	Q86UE4|LYRIC_HUMAN	0.957464159
1059	P10636|TAU_HUMAN	0.958145201
2138	P54278|PMS2_HUMAN	0.958150744
1344	P37198|NUP62_HUMAN	0.958494246
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1341	Q6PD62|CTR9_HUMAN	0.958638489
1706	Q86SX6|GLRX5_HUMAN	0.958712161
1161	O43432|IF4G3_HUMAN	0.959746718
68	P27797|CALR_HUMAN	0.959963739
1731	Q9BZI7|REN3B_HUMAN	0.960192025
2306	Q13427|PPIG_HUMAN	0.960737467
2425	O75391|SPAG7_HUMAN	0.961088359
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2248	Q86Y79|PTH_HUMAN	0.961224973
1971	Q96EL3|RM53_HUMAN	0.961429417
2858	Q01484|ANK2_HUMAN	0.961490095
1799	Q969N2|PIGT_HUMAN	0.961647213
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1007	O95479|G6PE_HUMAN	0.962215185
560	Q06124|PTN11_HUMAN	0.962429225
2094	P49407|ARRB1_HUMAN	0.962721825
2714	O14734|ACOT8_HUMAN	0.962753177
2046	Q9HD15|SRA1_HUMAN	0.963043928
737	O14828|SCAM3_HUMAN	0.963114798
1028	Q13765|NACA_HUMAN	0.963153958
2220	Q99805|TM9S2_HUMAN	0.963278115
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1123	P62851|RS25_HUMAN	0.96382159
1921	O75351|VPS4B_HUMAN	0.963888645
1941	P61077|UB2D3_HUMAN	0.963920951
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657	Q9H1B7|CN004_HUMAN	0.964531004
2707	Q5T3U5|MRP7_HUMAN	0.964642286
85	O60313|OPA1_HUMAN	0.964857817
1661	Q9UKU7|ACAD8_HUMAN	0.964871585
364	Q9NSD9|SYFB_HUMAN	0.96505326
2725	O94910|LPHN1_HUMAN	0.96512115
1845	Q13424|SNTA1_HUMAN	0.965228915
1271	Q15819|UB2V2_HUMAN	0.966114938
2380	P15104|GLNA_HUMAN	0.96687603
239	O60664|M6PBP_HUMAN	0.967200279
261	P32119|PRDX2_HUMAN	0.967352748
112	P17858|K6PL_HUMAN	0.967499316
888	P61086|UBC1_HUMAN	0.967551351
889	P30405|PPIF_HUMAN	0.967732072
2219	P52815|RM12_HUMAN	0.96786654
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417	Q96RP9|EFG1_HUMAN	0.968613684
235	O60506|HNRPQ_HUMAN	0.968957782
146	P55809|SCOT_HUMAN	0.969017088
1913	Q99622|C10_HUMAN	0.96933651
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2763	Q9NYR9|KBRS2_HUMAN	0.970230639
795	Q96HC4|PDLI5_HUMAN	0.970536053
2503	Q8TEB1|WDR23_HUMAN	0.970669508
1495	P49366|DHYS_HUMAN	0.970705092
595	Q96EY8|MMAB_HUMAN	0.970717907
330	O14745|NHERF_HUMAN	0.970963776
1017	Q14318|FKBP8_HUMAN	0.971185744
1064	Q9BYD3|RM04_HUMAN	0.971229911
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2230	Q9Y2L1|RRP44_HUMAN	0.971548736
948	Q9BTZ2|DHRS4_HUMAN	0.971563935
467	O75439|MPPB_HUMAN	0.972150922
1682	P20936|RASA1_HUMAN	0.972325265
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603	Q9UHD9|UBQL2_HUMAN	0.972555935
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1851	Q9BQA1|MEP50_HUMAN	0.972975791
1994	O00139|KIF2A_HUMAN	0.97325778
1619	Q9UPT8|CS007_HUMAN	0.973538697
2200	Q9HCN8|SDF2L_HUMAN	0.973621011
1797	O60684|IMA7_HUMAN	0.9739663
1278	Q92805|GOGA1_HUMAN	0.974396288
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843	Q8WTW3|COG1_HUMAN	0.975138366

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1224	Q9BVP2|GNL3_HUMAN	0.975577116
2637	P20337|RAB3B_HUMAN	0.975687385
411	P20042|IF2B_HUMAN	0.975733936
1329	O00165|HAX1_HUMAN	0.976161659
1436	Q9NR28|DBLOH_HUMAN	0.976380825
611	Q5JTH9|K0690_HUMAN	0.976603329
2011	P47914|RL29_HUMAN	0.977173209
2125	Q12933|TRAF2_HUMAN	0.977207363
2021	O60547|GMDS_HUMAN	0.97734046
622	P61201|CSN2_HUMAN	0.97752583
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706	O14974|MYPT1_HUMAN	0.978082538
1504	O60476|MA1A2_HUMAN	0.978557825
326	Q9H4A4|AMPB_HUMAN	0.978595972
1191	Q9UBQ5|IF3C_HUMAN	0.979106307
2286	Q9NQ50|RM40_HUMAN	0.979233861
1562	Q71RC2|LARP4_HUMAN	0.979257286
2492	Q8WUR7|U235_HUMAN	0.979822755
1735	Q92747|ARC1A_HUMAN	0.979946315
295	O75390|CISY_HUMAN	0.980058968
1416	P63244|GBLP_HUMAN	0.98019433
103	P29401|TKT_HUMAN	0.980319083
2368	P11171|41_HUMAN	0.980398178
969	P30566|PUR8_HUMAN	0.980432272
506	Q9UIJ7|KAD3_HUMAN	0.980558336
2766	O75674|TM1L1_HUMAN	0.98056215
2305	O15116|LSM1_HUMAN	0.980872333
540	Q9BW92|SYTM_HUMAN	0.981395781

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719	P99999|CYC_HUMAN	0.98197937
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1289	O95571|ETHE1_HUMAN	0.982065678
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687	P34913|HYES_HUMAN	0.983175457
164	Q15084|PDIA6_HUMAN	0.983252347
533	P36957|ODO2_HUMAN	0.983257532
2834	Q13530|SERC3_HUMAN	0.983632445
2690	Q05823|RN5A_HUMAN	0.983679116
2702	Q13823|NOG2_HUMAN	0.984036207
1159	Q15031|SYLM_HUMAN	0.984173298
403	Q15181|IPYR_HUMAN	0.984465659
1999	Q8N5N7|RM50_HUMAN	0.984971106
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1369	P12694|ODBA_HUMAN	0.985621572
2004	P49840|GSK3A_HUMAN	0.985691905
2440	Q99707|METH_HUMAN	0.98584336
2065	P61927|RL37_HUMAN	0.985886395
1088	Q8WZ42|TITIN_HUMAN	0.985904634
2439	Q99567|NUP88_HUMAN	0.986090541
2017	Q96K17|BT3L4_HUMAN	0.986513436
2499	Q7LBR1|CHM1B_HUMAN	0.986531913
2857	P49116|TR4_HUMAN	0.986542165
2462	Q86YB8|ERO1B_HUMAN	0.986722052
300	Q15365|PCBP1_HUMAN	0.986835122
2833	Q8N5U6|RNF10_HUMAN	0.986913502
225	Q96G03|PGM2_HUMAN	0.987539113
1389	P62888|RL30_HUMAN	0.987566054
1021	Q96I24|FUBP3_HUMAN	0.988083184

875	P50336|PPOX_HUMAN	0.988238931
2232	Q9NZT2|OGFR_HUMAN	0.988275647
732	Q9BRA2|TXNL5_HUMAN	0.988310814
961	O00519|FAAH_HUMAN	0.988520026
1400	Q7L5N1|CSN6_HUMAN	0.988590002
2417	O60573|IF4E2_HUMAN	0.9885903
2770	Q15542|TAF5_HUMAN	0.988625705
1527	Q9H9A6|LRC40_HUMAN	0.988820732
2673	Q9UL03|INT6_HUMAN	0.989644051
678	Q9P015|RM15_HUMAN	0.989923
2107	O75044|FNBP2_HUMAN	0.990604579
900	P46779|RL28_HUMAN	0.990640283
870	P12236|ADT3_HUMAN	0.991043568
1226	Q9H488|OFUT1_HUMAN	0.991148412
251	P13674|P4HA1_HUMAN	0.9911533
2454	P55011|S12A2_HUMAN	0.991214097
1156	P16989|DBPA_HUMAN	0.991243601
701	Q9Y2Z4|SYYM_HUMAN	0.991359174
2024	Q6ZRP7|QSC6L_HUMAN	0.991449475
1580	Q9BYD2|RM09_HUMAN	0.991607368
173	Q99613|IF38_HUMAN	0.992352366
1576	Q7Z739|YTHD3_HUMAN	0.992370725
1432	Q9Y237|PIN4_HUMAN	0.992465317
833	Q15643|TRIPB_HUMAN	0.993019462
1621	P49593|PPM1F_HUMAN	0.99339211
1098	Q9NQX3|GEPH_HUMAN	0.993674695
1838	Q9BX40|LS14B_HUMAN	0.99383378
1855	Q9BUF5|TBB6_HUMAN	0.993942738
885	P43897|EFTS_HUMAN	0.993944287
2618	Q53H12|MULK_HUMAN	0.995069504
1426	P10515|ODP2_HUMAN	0.995395184
831	Q15139|KPCD1_HUMAN	0.995670199

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800	Q13813|SPTA2_HUMAN	0.996216536
2865	O15258|RER1_HUMAN	0.996842086
1748	Q9UNN5|FAF1_HUMAN	0.996981859
1319	Q9UIA9|XPO7_HUMAN	0.997112155
1502	O75340|PDCD6_HUMAN	0.997261941
1284	O95487|SC24B_HUMAN	0.99735415
66	Q7Z6Z7|HUWE1_HUMAN	0.997442245
2431	Q14139|UBE4A_HUMAN	0.998106837
329	Q9UNE7|STUB1_HUMAN	0.998213589
1979	Q7Z7H5|TMED4_HUMAN	0.998640299
2601	Q13043|STK4_HUMAN	0.998724997
1849	Q8IXM3|RM41_HUMAN	0.998780966
1109	Q9UBF2|COPG2_HUMAN	0.998854518
1564	Q99996|AKAP9_HUMAN	0.999032915
883	Q9Y6Y8|S23IP_HUMAN	0.999065459
156	Q08378|GOGA3_HUMAN	0.999491155
545	P31040|DHSA_HUMAN	1
2387	P18859|ATP5J_HUMAN	1.000502586
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627	Q92947|GCDH_HUMAN	1.000635266
2320	Q9Y6G3|RT32_HUMAN	1.000675559
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2389	O75717|WDHD1_HUMAN	1.001076937
1827	Q14696|MESD2_HUMAN	1.001167178
1843	Q9NTG7|SIRT3_HUMAN	1.001214385
2394	Q96JB2|COG3_HUMAN	1.001336813
2480	P06865|HEXA_HUMAN	1.001403809
2842	Q9H497|TOR3A_HUMAN	1.0014714
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2718	Q6P1M3|L2GL2_HUMAN	1.006451845
1308	O75323|NIPS2_HUMAN	1.006533623
2749	O95819|M4K4_HUMAN	1.007734895
2708	P62987|RL40_HUMAN	1.007806063
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2642	Q9UBN7|HDAC6_HUMAN	1.009921908
1291	Q9HBH1|DEFM_HUMAN	1.009948611
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2666	Q96A57|CT030_HUMAN	1.010196924
67	P12277|KCRB_HUMAN	1.010473609
614	P30050|RL12_HUMAN	1.010638237

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398	Q9UBQ7|GRHPR_HUMAN	1.011041164
2742	O00468|AGRIN_HUMAN	1.011113644
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1744	Q16539|MK14_HUMAN	1.011322737
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2351	Q13948|CASP_HUMAN	1.013541102
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2534	Q96C19|EFHD2_HUMAN	1.013796806
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2699	O60524|SDCG1_HUMAN	1.014926791
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89	P50990|TCPQ_HUMAN	1.016508222
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2717	Q99569|PKP4_HUMAN	1.017417431

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2335	O75251|NDUS7_HUMAN	1.018621206
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1375	Q9BZE1|RM37_HUMAN	1.018852949
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1348	P30876|RPB2_HUMAN	1.027052402
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94	Q15075|EEA1_HUMAN	1.028156877
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927	O43399|TPD54_HUMAN	1.03659451
2494	Q9NXW9|ALKB4_HUMAN	1.036793232
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2779	O75381|PEX14_HUMAN	1.039338708
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2018	Q7KZ85|SPT6H_HUMAN	1.052857995
83	P25705|ATPA_HUMAN	1.053008318
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1269	O60678|ANM3_HUMAN	1.054968834
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1006	Q13618|CUL3_HUMAN	1.059729576
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116	P49368|TCPG_HUMAN	1.062879562
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91	P23786|CPT2_HUMAN	1.063654304
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2062	Q9H2H8|PPIL3_HUMAN	1.069259048
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1135	P46778|RL21_HUMAN	1.070135474
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941	Q13526|PIN1_HUMAN	1.071815729
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273	Q02878|RL6_HUMAN	1.074799895
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1325	O75600|KBL_HUMAN	1.075628757
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2562	O15145|ARPC3_HUMAN	1.077777505
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439	P22033|MUTA_HUMAN	1.079396367
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587	Q96A33|CCD47_HUMAN	1.081368923
2140	P46527|CDN1B_HUMAN	1.081567407
1168	P51570|GALK1_HUMAN	1.082032442
123	P78371|TCPB_HUMAN	1.082916141

1683	O15511|ARPC5_HUMAN	1.082994342
435	Q15293|RCN1_HUMAN	1.083586454
483	Q9Y2B0|MSAP_HUMAN	1.084175825
2535	Q8IX18|DHX40_HUMAN	1.084523439
213	Q15046|SYK_HUMAN	1.085108042
898	Q96CW1|AP2M1_HUMAN	1.085221887
1117	Q9ULA0|DNPEP_HUMAN	1.085399747
2376	Q9UNS1|TIM_HUMAN	1.085456491
441	P18124|RL7_HUMAN	1.085747361
267	P78540|ARGI2_HUMAN	1.086161971
2375	Q96LD8|SENP8_HUMAN	1.086930394
484	P08473|NEP_HUMAN	1.087351322
794	O15372|IF33_HUMAN	1.087390184
1183	Q15750|TAB1_HUMAN	1.087433696
385	O75534|CSDE1_HUMAN	1.087809563
1337	Q86UK7|ZN598_HUMAN	1.088338494
631	Q8TD30|ALAT2_HUMAN	1.088511586
766	O00233|PSMD9_HUMAN	1.088528037
1656	Q9H444|CHM4B_HUMAN	1.088604331
2691	Q96DV4|RM38_HUMAN	1.088701248
2042	O00214|LEG8_HUMAN	1.088849902
2183	Q53GS9|SNUT2_HUMAN	1.088862896
1148	Q96CN9|GCC1_HUMAN	1.088970661
415	P23526|SAHH_HUMAN	1.089106321
639	Q9UNM6|PSD13_HUMAN	1.089317203
763	P06753|TPM3_HUMAN	1.089347124
462	P14923|PLAK_HUMAN	1.089593887
458	Q99714|HCD2_HUMAN	1.089662075
87	P51659|DHB4_HUMAN	1.089757681
2832	Q9BRK4|LZTS2_HUMAN	1.09003067
2736	P10620|MGST1_HUMAN	1.090421677
2371	O75376|NCOR1_HUMAN	1.090713978

416	P14550|AK1A1_HUMAN	1.091125965
92	P36578|RL4_HUMAN	1.091157436
1609	Q9Y5B0|CTDP1_HUMAN	1.091296792
2709	Q96JM3|K1802_HUMAN	1.091476679
1764	Q9UKS6|PACN3_HUMAN	1.091618538
928	P39656|OST48_HUMAN	1.091646552
155	P40227|TCPZ_HUMAN	1.091680646
2430	Q5JSH3|WDR44_HUMAN	1.092063665
1095	P39880|CUTL1_HUMAN	1.093242645
1987	Q9UPN6|RBM16_HUMAN	1.093476892
1513	Q92544|TM9S4_HUMAN	1.094288826
853	P09496|CLCA_HUMAN	1.095345497
2198	Q92614|MY18A_HUMAN	1.095659018
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395	P13798|ACPH_HUMAN	1.095961332
2416	Q7Z6J9|SEN54_HUMAN	1.096863151
2006	Q9BV19|CA050_HUMAN	1.096936107
2682	Q99715|COCA1_HUMAN	1.097307563
1778	P52824|DGKQ_HUMAN	1.097557783
478	P68036|UB2L3_HUMAN	1.098383427
63	P46939|UTRO_HUMAN	1.098889589
562	O43852|CALU_HUMAN	1.098968983
2008	P06132|DCUP_HUMAN	1.099140286
584	P11387|TOP1_HUMAN	1.09979856
2110	O43716|15E2_HUMAN	1.099901438
715	P40222|TXLNA_HUMAN	1.100658417
1304	Q13464|ROCK1_HUMAN	1.100709558
591	O43865|SAHH2_HUMAN	1.100820899
1461	O43237|DC1L2_HUMAN	1.101241469
311	P22570|ADRO_HUMAN	1.101282835
2192	Q7Z4S6|KI21A_HUMAN	1.101624727
1412	P00533|EGFR_HUMAN	1.102278113

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1215	Q14118|DAG1_HUMAN	1.102796674
1889	Q9UJW0|DCTN4_HUMAN	1.102818727
2442	Q8TEQ8|PIGO_HUMAN	1.103142023
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1998	Q9H3Z4|DNJC5_HUMAN	1.104557991
2533	Q8N442|GUF1_HUMAN	1.104999185
1985	Q15005|SPCS2_HUMAN	1.105193138
681	P55039|DRG2_HUMAN	1.105244875
2421	Q5VIR6|VPS53_HUMAN	1.105296254
2479	Q9BSR8|YIPF4_HUMAN	1.105321765
1511	P15735|PHKG2_HUMAN	1.105496407
1292	P68402|PA1B2_HUMAN	1.105664492
805	P50995|ANX11_HUMAN	1.105777979
1413	Q9Y3U8|RL36_HUMAN	1.106063962
1523	O75312|ZPR1_HUMAN	1.106145859
2755	P43304|GPDM_HUMAN	1.106290102
2743	Q16401|PSMD5_HUMAN	1.106325984
1357	P49590|SYHM_HUMAN	1.10661149
1204	P43155|CACP_HUMAN	1.106657863
1915	P14209|CD99_HUMAN	1.107843637
869	P61758|PFD3_HUMAN	1.108477116
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1773	Q9UP83|COG5_HUMAN	1.108679056
832	Q8NBJ7|SUMF2_HUMAN	1.109102488
2695	Q8N9U0|TAC2N_HUMAN	1.109326482
1129	Q9Y5Y2|NUBP2_HUMAN	1.109370947
1995	Q9Y6D6|BIG1_HUMAN	1.109531522
1605	Q9NQS1|AVEN_HUMAN	1.109973907
2796	Q9Y291|RT33_HUMAN	1.110165715
2507	Q5JU69|TOR2A_HUMAN	1.110293388

2524	P98170|BIRC4_HUMAN	1.110458493
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600	O94760|DDAH1_HUMAN	1.110836983
1186	Q13155|MCA2_HUMAN	1.11090064
2626	Q9BQC6|RT63_HUMAN	1.111053228
867	P48047|ATPO_HUMAN	1.112185001
2194	Q9Y2U8|MAN1_HUMAN	1.112280488
866	Q16512|PKN1_HUMAN	1.112568021
366	P50570|DYN2_HUMAN	1.112797976
2097	Q9UMY4|SNX12_HUMAN	1.113198876
2728	Q96AC1|PKHC1_HUMAN	1.113328815
2096	P62140|PP1B_HUMAN	1.113425136
1846	Q86X10|K1219_HUMAN	1.113439441
707	O00487|PSDE_HUMAN	1.11367619
2679	Q709C8|VP13C_HUMAN	1.114611149
1740	Q04206|TF65_HUMAN	1.11478734
1919	Q9BSJ2|GCP2_HUMAN	1.114919782
2681	O15083|ERC2_HUMAN	1.115033031
1194	Q9Y6I3|EPN1_HUMAN	1.115149736
2550	Q8N158|GPC2_HUMAN	1.115171313
1173	P49207|RL34_HUMAN	1.115472078
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1946	P06756|ITAV_HUMAN	1.115922332
2739	P46976|GLYG_HUMAN	1.116469622
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637	P05387|RLA2_HUMAN	1.116693258
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447	P61981|1433G_HUMAN	1.117733359
1169	P61254|RL26_HUMAN	1.118040442
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2208	O60832|DKC1_HUMAN	1.118228555

1543	Q9H7C9|CK067_HUMAN	1.118362546
2790	Q9Y5K8|VATD_HUMAN	1.11887002
187	Q96I99|SUCB2_HUMAN	1.119553685
1547	O43504|XIP_HUMAN	1.119927764
488	P26373|RL13_HUMAN	1.120128512
1293	P58546|MTPN_HUMAN	1.120188832
2160	Q9Y2E5|MA2B2_HUMAN	1.12042141
306	P13861|KAP2_HUMAN	1.120571613
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93	Q07065|CKAP4_HUMAN	1.120710373
72	Q9P2J5|SYLC_HUMAN	1.121082425
2178	Q9HD45|TM9S3_HUMAN	1.121148109
115	Q04609|FOLH1_HUMAN	1.121945381
386	Q9NTK5|GTPB9_HUMAN	1.121985555
2009	Q9Y2W6|TDRKH_HUMAN	1.122086525
760	Q9H845|ACAD9_HUMAN	1.122240901
2079	P38435|VKGC_HUMAN	1.122252822
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1157	Q9BT78|CSN4_HUMAN	1.122564793
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221	O43242|PSMD3_HUMAN	1.124075413
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2445	Q86TN4|TRPT1_HUMAN	1.124411583
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947	Q9BVK6|TMED9_HUMAN	1.124623179
2712	Q9BPZ7|SIN1_HUMAN	1.124754906
1201	Q8N0W3|FUK_HUMAN	1.124892116
80	Q12955|ANK3_HUMAN	1.124950767
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572	Q9UBS4|DNJBB_HUMAN	1.125512719

387	Q14258|TRI25_HUMAN	1.125884771
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2257	Q96P48|CEND2_HUMAN	1.126302719
384	P16152|DHCA_HUMAN	1.126314402
1155	Q9Y608|LRRF2_HUMAN	1.126691818
971	Q9BXK5|B2L13_HUMAN	1.126876235
1759	O14561|ACPM_HUMAN	1.12722218
1601	Q9NR09|BIRC6_HUMAN	1.127751589
1457	Q15813|TBCE_HUMAN	1.128507495
2614	O60613|SEP15_HUMAN	1.12933135
1739	O75116|ROCK2_HUMAN	1.129578352
214	O60701|UGDH_HUMAN	1.129770041
2788	Q8TCD5|NT5C_HUMAN	1.130138516
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585	Q9BWD1|THIC_HUMAN	1.130179644
598	P53992|SC24C_HUMAN	1.130500197
286	P23588|IF4B_HUMAN	1.130704284
2623	Q9Y316|MEMO_HUMAN	1.130781174
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2777	P56962|STX17_HUMAN	1.132860899
2352	P40692|MLH1_HUMAN	1.133613586
2135	Q96SZ6|CK5P1_HUMAN	1.133738756
2443	Q9H1K1|ISCU_HUMAN	1.134138227
1085	Q13439|GOGA4_HUMAN	1.134184241
1639	Q5U5X0|LYRM7_HUMAN	1.134192586
1491	Q96JJ7|TXD10_HUMAN	1.134599328
714	O43182|RHG06_HUMAN	1.134644032
2382	Q5VT25|MRCKA_HUMAN	1.134839058
1943	Q9Y666|S12A7_HUMAN	1.135481
519	P47756|CAPZB_HUMAN	1.13576138
114	Q14789|GOGB1_HUMAN	1.135797858
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1142	Q16186|ADRM1_HUMAN	1.13625741
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2860	P23229|ITA6_HUMAN	1.136895657
967	P62899|RL31_HUMAN	1.136999846
2767	O00469|PLOD2_HUMAN	1.137159824
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1589	Q9UBW8|CSN7A_HUMAN	1.137322545
2337	P52630|STAT2_HUMAN	1.138163567
376	Q02750|MP2K1_HUMAN	1.138674736
341	Q99961|SH3G1_HUMAN	1.139207959
1268	Q96FW1|OTUB1_HUMAN	1.139217377
1280	P29350|PTN6_HUMAN	1.139463902
2556	P15056|BRAF1_HUMAN	1.139507055
803	P63000|RAC1_HUMAN	1.139702559
1251	Q14444|GPIA1_HUMAN	1.13980782
195	Q9Y678|COPG_HUMAN	1.139950871
1882	Q92504|KE4_HUMAN	1.140298843
991	P61204|ARF3_HUMAN	1.140813828
282	Q9NYU2|UGGG1_HUMAN	1.141077518
2667	P62070|RRAS2_HUMAN	1.141132116
541	P43490|NAMPT_HUMAN	1.141135693
331	Q9UJU6|DBNL_HUMAN	1.141204715
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2813	P20674|COX5A_HUMAN	1.14169395
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194	P09972|ALDOC_HUMAN	1.142257452
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1856	Q9BXW6|OSBL1_HUMAN	1.1423347
2838	Q8TDJ6|DMXL2_HUMAN	1.142944932
1002	Q99627|CSN8_HUMAN	1.143105626
500	P62333|PRS10_HUMAN	1.143336892
1942	Q96IV0|NGLY1_HUMAN	1.143489242

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456	O76094|SRP72_HUMAN	1.143822312
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1493	Q7Z478|DHX29_HUMAN	1.144366264
857	Q16204|CCDC6_HUMAN	1.144415379
2635	P47755|CAZA2_HUMAN	1.144583941
2361	Q13443|ADAM9_HUMAN	1.144873857
1967	P55795|HNRH2_HUMAN	1.144902587
418	P51665|PSD7_HUMAN	1.14504981
1659	P05141|ADT2_HUMAN	1.145455599
2195	P06280|AGAL_HUMAN	1.14548254
2781	O43292|GPAA1_HUMAN	1.145533323
2730	P55789|ALR_HUMAN	1.145540833
605	Q9NZB2|F120A_HUMAN	1.145858288
2433	Q9H7D7|WDR26_HUMAN	1.146118641
530	P26038|MOES_HUMAN	1.146258354
964	P10768|ESTD_HUMAN	1.146974683
1233	P61457|PHS_HUMAN	1.147981763
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1134	Q9UI10|EI2BD_HUMAN	1.148465991
54	P35221|CTNA1_HUMAN	1.148991704
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1177	Q9UMX5|NENF_HUMAN	1.149742961
1671	Q5T6F2|UBAP2_HUMAN	1.150374293
2516	Q13627|DYR1A_HUMAN	1.150462389
1860	Q9C0E8|LNP_HUMAN	1.150624514
2705	Q9NUP1|CNO_HUMAN	1.150709271
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978	Q13425|SNTB2_HUMAN	1.151934266
935	P29144|TPP2_HUMAN	1.151966095
1933	Q96GX9|APIP_HUMAN	1.152038932
1539	Q9Y217|MTMR6_HUMAN	1.152288079

74	Q14697|GANAB_HUMAN	1.152474761
659	Q14677|EPN4_HUMAN	1.152516603
1552	P60953|CDC42_HUMAN	1.153110862
716	O14964|HGS_HUMAN	1.153353333
2274	Q9H7Z7|PGES2_HUMAN	1.153659821
2757	O00748|EST2_HUMAN	1.153910995
1948	Q9UHI6|DDX20_HUMAN	1.154110789
617	P61586|RHOA_HUMAN	1.154429674
1078	Q01415|GALK2_HUMAN	1.155009866
787	P25788|PSA3_HUMAN	1.155134201
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452	O00231|PSD11_HUMAN	1.155285954
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327	Q07157|ZO1_HUMAN	1.155736208
2072	P46977|STT3A_HUMAN	1.156713724
1781	P62873|GBB1_HUMAN	1.156864285
2434	Q969P0|IGSF8_HUMAN	1.156866074
1697	Q93008|USP9X_HUMAN	1.157016754
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33	P04406|G3P_HUMAN	1.157712698
703	O75822|IF31_HUMAN	1.158185244
2137	Q49B96|COX19_HUMAN	1.158346534
3	P49327|FAS_HUMAN	1.159167886
951	Q86WU2|LDHD_HUMAN	1.159294248
2048	Q93100|KPBB_HUMAN	1.159336567
668	Q96EY1|DNJA3_HUMAN	1.160185814
436	P05166|PCCB_HUMAN	1.160907149
334	Q9H2U2|IPYR2_HUMAN	1.160983205
1120	Q08257|QOR_HUMAN	1.161436081
1206	O95336|6PGL_HUMAN	1.161737561
2799	Q9NV88|INT9_HUMAN	1.161875725
881	Q8WZA9|IRGQ_HUMAN	1.16198647

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1670	Q9H0W9|CK054_HUMAN	1.163586974
1122	O00178|GTPB1_HUMAN	1.164234638
2747	Q6GQQ9|OTU7B_HUMAN	1.16466248
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2815	O95613|PCNT_HUMAN	1.166284442
1411	P31946|1433B_HUMAN	1.166304588
2188	Q96S52|PIGS_HUMAN	1.16636765
277	Q9UPN3|MACF1_HUMAN	1.167336583
1330	Q7Z417|NUFP2_HUMAN	1.16758287
2086	P51812|KS6A3_HUMAN	1.167734623
1062	O43768|ENSA_HUMAN	1.168370962
858	O14602|IF1AY_HUMAN	1.168437839
242	P48637|GSHB_HUMAN	1.169078231
212	P12081|SYHC_HUMAN	1.169231415
952	Q9Y5X3|SNX5_HUMAN	1.169504642
1901	Q96L92|SNX27_HUMAN	1.169885516
652	Q12907|LMAN2_HUMAN	1.170026541
340	P31937|3HIDH_HUMAN	1.170352817
2662	O75817|POP7_HUMAN	1.17128408
2184	P46108|CRK_HUMAN	1.171510458
1758	Q9Y2A7|NCKP1_HUMAN	1.171922207
2155	Q9H1I8|ASCC2_HUMAN	1.172290206
78	Q8WUM4|PDC6I_HUMAN	1.172383189
2095	P41743|KPCI_HUMAN	1.172875166
140	P04040|CATA_HUMAN	1.173318267
2036	Q96HD1|CREL1_HUMAN	1.17333293
2424	Q13017|RHG05_HUMAN	1.173744678
2397	Q8WXK8|BPAEB_HUMAN	1.174521327

2658	Q08722|CD47_HUMAN	1.174527049
1479	P56537|IF6_HUMAN	1.174922943
2151	P49770|EI2BB_HUMAN	1.175254107
2659	P56134|ATPK_HUMAN	1.175435424
2395	Q05397|FAK1_HUMAN	1.17609036
1220	Q05086|UBE3A_HUMAN	1.176200747
186	P23284|PPIB_HUMAN	1.176207781
988	P42126|D3D2_HUMAN	1.17644763
108	P63261|ACTG_HUMAN	1.176497579
2484	O15460|P4HA2_HUMAN	1.177172661
2698	P30626|SORCN_HUMAN	1.177535057
1052	O75976|CBPD_HUMAN	1.177651167
1253	Q13724|GCS1_HUMAN	1.177718163
1196	Q9HBH5|RDH14_HUMAN	1.177908659
1423	P63010|AP2B1_HUMAN	1.178041935
565	P55010|IF5_HUMAN	1.178255796
1512	Q12959|DLG1_HUMAN	1.178606868
1326	Q9Y305|ACOT9_HUMAN	1.17887044
2646	Q9BW60|ELOV1_HUMAN	1.179285407
1328	O15144|ARPC2_HUMAN	1.179759145
747	P30046|DOPD_HUMAN	1.17984283
2252	O00329|PK3CD_HUMAN	1.179876447
145	P56192|SYMC_HUMAN	1.179922462
397	P43686|PRS6B_HUMAN	1.180189013
1890	Q8NBX0|SCPDH_HUMAN	1.180447102
369	O94973|AP2A2_HUMAN	1.180505514
1116	Q16774|KGUA_HUMAN	1.181169271
1443	P11047|LAMC1_HUMAN	1.181361914
1004	P31150|GDIA_HUMAN	1.181524396
285	Q13011|ECH1_HUMAN	1.182079315
428	Q92598|HS105_HUMAN	1.182133317
2828	P31749|AKT1_HUMAN	1.183212161

2222	Q9HCD5|NCOA5_HUMAN	1.18339622
2817	P48382|RFX5_HUMAN	1.184900522
1405	Q9P2M7|CING_HUMAN	1.184914947
728	P16219|ACADS_HUMAN	1.185741186
663	P35813|PP2CA_HUMAN	1.185948968
1387	O15127|SCAM2_HUMAN	1.186561465
1053	P28066|PSA5_HUMAN	1.187113285
692	Q8TBA6|GOGA5_HUMAN	1.187386036
2511	Q9NXZ2|DDX43_HUMAN	1.187451839
936	Q6P1N0|CCD1A_HUMAN	1.187569261
1528	O94903|PROSC_HUMAN	1.187626839
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254	P62195|PRS8_HUMAN	1.187777638
887	Q93052|LPP_HUMAN	1.187927008
365	O14818|PSA7_HUMAN	1.188156962
27	P49588|SYAC_HUMAN	1.188243747
316	Q5VYK3|ECM29_HUMAN	1.188691139
825	P61160|ARP2_HUMAN	1.188946247
380	P22059|OSBP1_HUMAN	1.18971622
2123	O00401|WASL_HUMAN	1.190675259
96	Q9C0C2|TB182_HUMAN	1.191151619
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2624	Q7LG56|RIR2B_HUMAN	1.192689419
914	O00499|BIN1_HUMAN	1.192852855
2404	Q9NRX1|PNO1_HUMAN	1.192899466
1614	Q7Z2K6|K1815_HUMAN	1.193094969
2388	Q7RTP6|MICA3_HUMAN	1.193582892
2370	P42858|HD_HUMAN	1.193647027
339	P12830|CADH1_HUMAN	1.193744302
455	Q9HDC9|APMAP_HUMAN	1.194037557
1668	P63167|DYL1_HUMAN	1.194088221

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1181	P51148|RAB5C_HUMAN	1.19500494
1072	Q969S9|EFG2_HUMAN	1.19546628
1274	P08240|SRPR_HUMAN	1.195916057
162	Q5JRX3|PREP_HUMAN	1.19601202
2281	Q53GL7|PAR10_HUMAN	1.196317196
2356	Q96DA6|TIM14_HUMAN	1.197124839
1825	Q9NVE7|PANK4_HUMAN	1.197169065
694	Q9NQW7|XPP1_HUMAN	1.198268294
807	Q99700|ATX2_HUMAN	1.198460102
559	Q9Y266|NUDC_HUMAN	1.199178457
2093	P62910|RL32_HUMAN	1.199564457
2636	Q9BXS5|AP1M1_HUMAN	1.199661613
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1238	P28072|PSB6_HUMAN	1.203336477
2139	P04424|ARLY_HUMAN	1.20335865
916	P13489|RINI_HUMAN	1.203370571
1557	P68133|ACTS_HUMAN	1.203652978
296	P40925|MDHC_HUMAN	1.20418334
76	Q86UP2|KTN1_HUMAN	1.204805136
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1486	O75688|PP2CB_HUMAN	1.205256224
654	P50416|CPT1A_HUMAN	1.205462575
1833	P02765|FETUA_HUMAN	1.205684423
394	P21399|IREB1_HUMAN	1.206031561
1290	Q9NRX4|PHP14_HUMAN	1.206270218

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23	P38646|GRP75_HUMAN	1.210651398
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2640	Q8IY26|PPAC2_HUMAN	1.212104797
913	O00151|PDLI1_HUMAN	1.212865591
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2782	Q9NXW2|DNJBC_HUMAN	1.216125607
1455	Q8N6T3|ARFG1_HUMAN	1.216256618
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826	P48147|PPCE_HUMAN	1.217802286
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1281	Q9NT62|ATG3_HUMAN	1.220841408
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1209	Q92575|UBXD2_HUMAN	1.227516055
367	Q8NE71|ABCF1_HUMAN	1.227534294
579	Q9Y5S2|MRCKB_HUMAN	1.228609085
2660	Q7Z412|PEX26_HUMAN	1.228787184
2026	Q9HAB8|PPCS_HUMAN	1.228823543
1588	P48556|PSMD8_HUMAN	1.228993535
460	P35520|CBS_HUMAN	1.229128599
2553	Q92870|APBB2_HUMAN	1.229216456
1248	Q9Y6B6|SAR1B_HUMAN	1.229430437
1910	O75964|ATP5L_HUMAN	1.23198235
2120	Q6P587|FAHD1_HUMAN	1.232868671
1347	O75306|NDUS2_HUMAN	1.233309984
268	P25786|PSA1_HUMAN	1.23387897
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1381	Q14746|COG2_HUMAN	1.236099601
1481	Q7Z434|MAVS_HUMAN	1.236162066
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1174	O60271|JIP4_HUMAN	1.23662436
1130	O00442|RTC1_HUMAN	1.237234354
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933	P11766|ADHX_HUMAN	1.237947941
534	P20618|PSB1_HUMAN	1.238193393

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792	P02786|TFR1_HUMAN	1.238898277
2122	Q96G23|LASS2_HUMAN	1.239033461
1487	O00232|PSD12_HUMAN	1.239319563
1536	Q9NX05|F120C_HUMAN	1.239406586
2317	Q15276|RABE1_HUMAN	1.239639997
28	P35580|MYH10_HUMAN	1.239680648
1451	Q9UMX0|UBQL1_HUMAN	1.240850329
2066	Q96P11|NSUN5_HUMAN	1.241074324
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834	Q9Y263|PLAP_HUMAN	1.242236972
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1473	Q9GZZ9|UE1D1_HUMAN	1.243276358
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2716	P42696|RBM34_HUMAN	1.244140863
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158	Q13200|PSMD2_HUMAN	1.244821191
423	Q9NY33|DPP3_HUMAN	1.244834423
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1752	Q5VWZ2|LYPL1_HUMAN	1.24712348
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1302	Q9UJC3|HOOK1_HUMAN	1.248181701
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1352	Q9BQ70|TCF25_HUMAN	1.24952507

2519	Q8TCX5|RHPN1_HUMAN	1.249720216
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1981	Q9Y6I9|TX264_HUMAN	1.250144839
1245	Q96IU4|AB14B_HUMAN	1.250253797
118	P19367|HXK1_HUMAN	1.251522183
1099	P35080|PROF2_HUMAN	1.252274156
813	O00754|MA2B1_HUMAN	1.252988815
1172	P61106|RAB14_HUMAN	1.253397703
1701	P51688|SPHM_HUMAN	1.253473639
670	Q9BS26|TXND4_HUMAN	1.253503084
942	Q4V328|GRAP1_HUMAN	1.253873825
1918	P10586|PTPRF_HUMAN	1.253957391
2025	Q9UL46|PSME2_HUMAN	1.254789233
1501	P45985|MP2K4_HUMAN	1.255199075
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5	Q09666|AHNK_HUMAN	1.256169796
1084	P24534|EF1B_HUMAN	1.256739616
1677	P50552|VASP_HUMAN	1.256831169
2010	P31949|S10AB_HUMAN	1.257672668
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396	Q05639|EF1A2_HUMAN	1.258752942
73	P34932|HSP74_HUMAN	1.259001017
677	P22061|PIMT_HUMAN	1.259645104
1545	P59998|ARPC4_HUMAN	1.260905623
1276	O75368|SH3L1_HUMAN	1.261232376
1900	P04066|FUCO_HUMAN	1.262090683
2103	Q10471|GALT2_HUMAN	1.262095809
854	O00625|PIR_HUMAN	1.262327194
481	O60749|SNX2_HUMAN	1.262422442
249	Q06210|GFPT1_HUMAN	1.262665749
2638	P61225|RAP2B_HUMAN	1.262877107
953	Q9H6S3|ES8L2_HUMAN	1.262970805

2080	Q9UPY8|MARE3_HUMAN	1.263036251
1279	P07602|SAP_HUMAN	1.263051152
2087	O43815|STRN_HUMAN	1.263635039
1628	Q9BT22|ALG1_HUMAN	1.263656259
1031	Q96HY6|CT116_HUMAN	1.26426053
850	Q9UBC2|EP15R_HUMAN	1.264274836
1570	Q9H446|RWDD1_HUMAN	1.264412165
1435	P36507|MP2K2_HUMAN	1.264458656
689	P61011|SRP54_HUMAN	1.265224814
752	Q9NYL9|TMOD3_HUMAN	1.265620828
912	Q13492|PICAL_HUMAN	1.265754342
1727	Q9H173|SIL1_HUMAN	1.266359448
1219	O60493|SNX3_HUMAN	1.266629219
1350	P17612|KAPCA_HUMAN	1.267575145
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1265	Q13322|GRB10_HUMAN	1.26848948
699	P28482|MK01_HUMAN	1.269392967
2391	Q9Y3R5|CU005_HUMAN	1.269459248
477	P61158|ARP3_HUMAN	1.269753814
196	O60763|VDP_HUMAN	1.270117044
772	Q92538|GBF1_HUMAN	1.27053988
1296	Q9H3S7|PTN23_HUMAN	1.270843863
859	Q96QK1|VPS35_HUMAN	1.271509171
1774	P30519|HMOX2_HUMAN	1.272363544
179	Q99460|PSMD1_HUMAN	1.27243042
1410	P41236|IPP2_HUMAN	1.273143411
1208	Q14244|MAP7_HUMAN	1.273769736
582	O95359|TACC2_HUMAN	1.27532053
2396	O75363|BCAS1_HUMAN	1.275420189
328	Q12904|MCA1_HUMAN	1.275740147

1741	Q14165|K0152_HUMAN	1.275812507
955	Q6Y7W6|PERQ2_HUMAN	1.275830746
2332	P20339|RAB5A_HUMAN	1.276058555
1892	P16083|NQO2_HUMAN	1.276530504
360	Q9NP61|ARFG3_HUMAN	1.277438521
1956	P35914|HMGCL_HUMAN	1.277835488
1236	Q9Y6W5|WASF2_HUMAN	1.278442621
2734	P61018|RAB4B_HUMAN	1.278799534
2045	Q9UQM7|KCC2A_HUMAN	1.278815031
471	O95394|AGM1_HUMAN	1.278914213
667	P49773|HINT1_HUMAN	1.27910912
272	P46940|IQGA1_HUMAN	1.280665994
198	P20810|ICAL_HUMAN	1.281368136
658	P08195|4F2_HUMAN	1.281590104
2706	P53609|PGT1_HUMAN	1.282124639
2560	Q86Y82|STX12_HUMAN	1.282488108
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401	Q15435|PP1R7_HUMAN	1.284138441
2491	Q9NQ88|CL005_HUMAN	1.284186363
958	Q92520|FAM3C_HUMAN	1.28441155
35	Q00610|CLH1_HUMAN	1.284682393
2280	O95372|LYPA2_HUMAN	1.285153747
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1538	Q96CS3|UBXD8_HUMAN	1.285369396
2827	O43665|RGS10_HUMAN	1.285688996
1526	Q96ED9|HOOK2_HUMAN	1.285987139
1945	Q96KG9|NTKL_HUMAN	1.289149642
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628	O14841|OPLA_HUMAN	1.29051125
2590	Q9UBI1|COMD3_HUMAN	1.290757895
1886	O95155|UBE4B_HUMAN	1.290790319
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1949	Q12979|ABR_HUMAN	1.292391658
1303	O43681|ARSA1_HUMAN	1.292462945
550	Q9BX68|HINT2_HUMAN	1.292512417
822	Q9UNF1|MAGD2_HUMAN	1.292669177
125	P41252|SYIC_HUMAN	1.293156266
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705	P09525|ANXA4_HUMAN	1.293542743
767	Q9UQB8|BAIP2_HUMAN	1.294076085
45	P04075|ALDOA_HUMAN	1.294107318
16	P27816|MAP4_HUMAN	1.294766665
36	P18206|VINC_HUMAN	1.295235634
596	P62158|CALM_HUMAN	1.29541707
1362	Q92890|UFD1_HUMAN	1.296541095
2405	Q86XE5|DAPAL_HUMAN	1.296550393
946	Q8NBJ4|GP73_HUMAN	1.296741724
2324	P49427|UB2R1_HUMAN	1.297156215
2342	P36956|SRBP1_HUMAN	1.297237992
2441	O95470|SGPL1_HUMAN	1.297446728
1081	Q96QR8|PURB_HUMAN	1.298920631
207	P15311|EZRI_HUMAN	1.299764991
1042	P21291|CSRP1_HUMAN	1.300202608
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2786	Q9UGI6|KCNN3_HUMAN	1.300629854
2704	O14832|PAHX_HUMAN	1.301290274
552	Q99436|PSB7_HUMAN	1.301345468
1578	Q13107|UBP4_HUMAN	1.301733136
2426	Q9UJS0|CMC2_HUMAN	1.302376032
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269	P12814|ACTN1_HUMAN	1.30395484
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437	P42566|EP15_HUMAN	1.305409908

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58	P40939|ECHA_HUMAN	1.306794286
106	Q96KP4|CNDP2_HUMAN	1.307329655
304	P22307|NLTP_HUMAN	1.307361364
59	P05783|K1C18_HUMAN	1.30748868
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523	P00568|KAD1_HUMAN	1.310466766
1397	Q7Z3D6|CN159_HUMAN	1.310710311
130	P15924|DESP_HUMAN	1.310787678
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2392	Q9HCF4|ALO17_HUMAN	1.311735034
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861	Q9UMR2|DD19B_HUMAN	1.312871814
2450	P20933|ASPG_HUMAN	1.312907577
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1624	Q99538|LGMN_HUMAN	1.314420462
13	P11021|GRP78_HUMAN	1.315863729
758	P23368|MAOM_HUMAN	1.31980741
2844	P56749|CLD12_HUMAN	1.319976211
2225	P19838|NFKB1_HUMAN	1.320128679
742	Q04323|SAKS1_HUMAN	1.321359754
2852	Q05513|KPCZ_HUMAN	1.322200418
2805	Q8N2G8|GHDC_HUMAN	1.322715282
1301	O43708|MAAI_HUMAN	1.322951555
149	P47897|SYQ_HUMAN	1.323317289
231	P30153|2AAA_HUMAN	1.323575377
1791	Q15738|NSDHL_HUMAN	1.323909521
2467	P30039|MAWBP_HUMAN	1.324280977
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315	P27824|CALX_HUMAN	1.324693561
1035	Q12792|TWF1_HUMAN	1.325740814

2808	Q9Y3C0|CCD53_HUMAN	1.325809121
1008	Q9Y6G9|DC1L1_HUMAN	1.326527238
1151	P49023|PAXI_HUMAN	1.326615334
2088	Q96JQ2|CLMN_HUMAN	1.326967835
1742	O95816|BAG2_HUMAN	1.327798009
2536	Q9NPJ6|MED4_HUMAN	1.328051448
1520	Q9H0E2|TOLIP_HUMAN	1.328882217
1447	Q15437|SC23B_HUMAN	1.329003215
1256	Q9BW91|NUDT9_HUMAN	1.329651117
2829	Q6P158|DHX57_HUMAN	1.330101967
2459	Q9BVC6|TM109_HUMAN	1.330152512
799	Q9Y4E1|FA21C_HUMAN	1.33162725
865	P54802|ANAG_HUMAN	1.331775069
60	P36776|LONM_HUMAN	1.331901312
454	Q8NBS9|TXND5_HUMAN	1.335054636
2436	P37235|HPCL1_HUMAN	1.335158348
2557	O00308|WWP2_HUMAN	1.335423589
513	O75083|WDR1_HUMAN	1.335614324
1551	Q9NV70|EXOC1_HUMAN	1.335677743
1307	Q9Y371|SHLB1_HUMAN	1.336111784
2233	Q14376|GALE_HUMAN	1.336612582
228	P17174|AATC_HUMAN	1.337182403
1026	P61019|RAB2A_HUMAN	1.338016152
2206	Q92643|GPI8_HUMAN	1.338731647
1535	Q99653|CHP1_HUMAN	1.339279532
1658	Q96KC8|DNJC1_HUMAN	1.340532184
1332	P12955|PEPD_HUMAN	1.341394544
2031	P52594|NUPL_HUMAN	1.342619538
263	P55084|ECHB_HUMAN	1.342763186
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877	Q04837|SSB_HUMAN	1.343165278
41	P07237|PDIA1_HUMAN	1.344150782

2701	O95834|EMAL2_HUMAN	1.344966769
2	O75369|FLNB_HUMAN	1.345397592
2471	O75915|PRAF3_HUMAN	1.346372962
2069	Q9NZZ3|CHMP5_HUMAN	1.347092867
679	Q8ND30|LIPB2_HUMAN	1.348633766
1514	Q9UL25|RAB21_HUMAN	1.350431323
11	P07814|SYEP_HUMAN	1.350522995
86	P49748|ACADV_HUMAN	1.351574659
2379	Q99611|SPS2_HUMAN	1.351849079
290	Q96AG4|LRC59_HUMAN	1.354277253
2592	Q9Y3E0|GOT1B_HUMAN	1.354995131
81	P55786|PSA_HUMAN	1.355194092
134	Q7Z406|MYH14_HUMAN	1.355307817
143	P04843|RIB1_HUMAN	1.356544733
2213	Q6ZMG9|LASS6_HUMAN	1.356594086
1633	Q96LJ7|DHRS1_HUMAN	1.35695982
1972	Q8IZP0|ABI1_HUMAN	1.358770251
2541	P07738|PMGE_HUMAN	1.359214902
1643	Q96A49|SYAP1_HUMAN	1.35991776
183	Q32MZ4|LRRF1_HUMAN	1.359972
457	Q8TAT6|NPL4_HUMAN	1.360915542
743	Q07866|KLC1_HUMAN	1.361471415
1250	P61020|RAB5B_HUMAN	1.361921072
2177	Q9ULV4|COR1C_HUMAN	1.362040162
2199	Q9NUP9|LIN7C_HUMAN	1.362459421
553	Q9Y394|DHRS7_HUMAN	1.363727093
507	P63104|1433Z_HUMAN	1.364171982
882	O75396|SC22B_HUMAN	1.365068674
31	P05787|K2C8_HUMAN	1.365682125
2014	P18440|ARY1_HUMAN	1.365686774
82	Q14247|SRC8_HUMAN	1.365761518
280	Q9UHB9|SRP68_HUMAN	1.366067052

2670	P62891|RL39_HUMAN	1.36911571
929	O95865|DDAH2_HUMAN	1.36970067
986	P30533|AMRP_HUMAN	1.370511651
2422	Q9Y696|CLIC4_HUMAN	1.370912671
1077	P29218|IMPA1_HUMAN	1.371736884
190	Q02218|ODO1_HUMAN	1.372537971
144	Q13085|COA1_HUMAN	1.37261796
1170	Q12797|ASPH_HUMAN	1.374569297
2591	Q5RI15|FA36A_HUMAN	1.3749336
1775	P51452|DUS3_HUMAN	1.37579596
1176	P19971|TYPH_HUMAN	1.376085401
1478	P09132|SRP19_HUMAN	1.377792001
2001	Q8WU76|SCFD2_HUMAN	1.37852633
2489	Q9BXR0|TGT_HUMAN	1.378526807
2791	Q562E7|WDR81_HUMAN	1.380302668
2131	Q96AT9|RPE_HUMAN	1.38411665
1285	Q99442|SEC62_HUMAN	1.385449886
2722	Q8N9R8|CI126_HUMAN	1.386033893
2241	P51116|FXR2_HUMAN	1.386508465
771	P00387|NCB5R_HUMAN	1.387214184
968	P09497|CLCB_HUMAN	1.387724161
651	P46379|BAT3_HUMAN	1.388578892
274	Q13045|FLII_HUMAN	1.389719963
62	P33176|KINH_HUMAN	1.3899194
1594	P42574|CASP3_HUMAN	1.390270948
1805	Q9Y2Q3|GSTK1_HUMAN	1.39062798
1333	P60983|GMFB_HUMAN	1.392234087
886	P26885|FKBP2_HUMAN	1.392934203
2538	Q9H993|CF211_HUMAN	1.393285394
2308	Q9BZV1|UBXD1_HUMAN	1.39337492
2175	Q12846|STX4_HUMAN	1.393997073
1935	P11117|PPAL_HUMAN	1.394357562

801	O95292|VAPB_HUMAN	1.394461632
1418	Q11201|SIA4A_HUMAN	1.39446342
2161	O60825|F262_HUMAN	1.395976305
1262	Q9UNH7|SNX6_HUMAN	1.396460533
2406	Q9Y2I8|WDR37_HUMAN	1.39718914
578	P10644|KAP0_HUMAN	1.398447752
2180	Q9ULH7|MKL2_HUMAN	1.398886681
1037	P43034|LIS1_HUMAN	1.399245381
1816	Q14135|VGLL4_HUMAN	1.400548697
2035	P61960|UFM1_HUMAN	1.400887966
265	P16615|AT2A2_HUMAN	1.401093006
862	P53004|BIEA_HUMAN	1.402147532
9	Q14204|DYHC_HUMAN	1.402323604
2273	Q9UID3|CK002_HUMAN	1.403067708
1014	Q8WVM8|SCFD1_HUMAN	1.404337645
1574	P11279|LAMP1_HUMAN	1.404443383
2300	Q9UJC5|SH3L2_HUMAN	1.411014676
188	O43776|SYNC_HUMAN	1.417377949
20	P55072|TERA_HUMAN	1.417479157
2364	Q9BQ48|RM34_HUMAN	1.418377042
1611	O95166|GBRAP_HUMAN	1.421704173
1449	Q5T447|HECD3_HUMAN	1.423643112
2769	P50579|AMPM2_HUMAN	1.423929095
361	Q10567|AP1B1_HUMAN	1.424403548
1616	Q8NEU8|DP13B_HUMAN	1.424922943
2141	Q13217|DNJC3_HUMAN	1.425896406
47	O43175|SERA_HUMAN	1.428482533
1185	P48507|GSH0_HUMAN	1.430186391
846	Q99816|TS101_HUMAN	1.430439234
1716	P51580|TPMT_HUMAN	1.4307549
2415	Q9Y3B8|ORN_HUMAN	1.431737185
555	Q13596|SNX1_HUMAN	1.4321208

2221	Q9NZ32|ARP10_HUMAN	1.432177663
2400	Q69YQ0|CYTSA_HUMAN	1.434112191
890	Q9P0L0|VAPA_HUMAN	1.435554385
954	P62714|PP2AB_HUMAN	1.438583255
443	Q9NR46|SHLB2_HUMAN	1.439131856
1462	Q6WKZ4|RFIP1_HUMAN	1.441678166
1277	O14773|TPP1_HUMAN	1.444123864
1054	Q9Y6Q5|AP1M2_HUMAN	1.444636464
563	O94874|K0776_HUMAN	1.444725156
1131	Q15907|RB11B_HUMAN	1.445178032
301	Q01518|CAP1_HUMAN	1.445192218
2399	Q9NRD5|PICK1_HUMAN	1.447259426
320	P04792|HSPB1_HUMAN	1.447370648
383	P11216|PYGB_HUMAN	1.449540615
2633	P67775|PP2AA_HUMAN	1.449617028
2724	Q9BYJ1|LOXE3_HUMAN	1.450993061
790	O43396|TXNL1_HUMAN	1.453117371
137	P26639|SYTC_HUMAN	1.453781128
1703	O14976|GAK_HUMAN	1.454146624
2672	P20645|MPRD_HUMAN	1.45535779
2826	O95197|RTN3_HUMAN	1.455871344
2112	P48506|GSH1_HUMAN	1.45792222
2041	Q96JH7|VCIP1_HUMAN	1.459872007
939	P02794|FRIH_HUMAN	1.461563826
2693	Q96JP5|ZFP91_HUMAN	1.46186161
1192	P62820|RAB1A_HUMAN	1.463606596
224	P13796|PLSL_HUMAN	1.465319276
2299	O94905|SPFH2_HUMAN	1.465972781
2754	Q9BV36|MELPH_HUMAN	1.467172742
702	Q9BQS8|FYCO1_HUMAN	1.467383027
1313	P10109|ADX_HUMAN	1.467386365
390	P50502|F10A1_HUMAN	1.467581034

1553	P15374|UCHL3_HUMAN	1.468640685
1980	Q7Z6B0|CCD91_HUMAN	1.469524384
915	P80404|GABT_HUMAN	1.469737411
727	Q06323|PSME1_HUMAN	1.472327471
1789	O75165|DNJCD_HUMAN	1.472837567
199	P09110|THIK_HUMAN	1.472901344
1160	Q9P2T1|GMPR2_HUMAN	1.476459503
1485	Q6PIU2|ADCL1_HUMAN	1.476675153
2752	Q96BW5|PTER_HUMAN	1.478747487
1340	Q9NZ01|GPSN2_HUMAN	1.480421782
1623	Q9UKK9|NUDT5_HUMAN	1.480825543
1079	P61163|ACTZ_HUMAN	1.48383534
1070	P48449|ERG7_HUMAN	1.484548092
2083	P42766|RL35_HUMAN	1.48607409
283	P52209|6PGD_HUMAN	1.486838579
262	P08243|ASNS_HUMAN	1.488358021
1283	P13073|COX41_HUMAN	1.493389487
2710	O60232|SSA27_HUMAN	1.493925571
2037	Q9NRY4|GRLF1_HUMAN	1.496222258
2768	Q9BY49|PECR_HUMAN	1.496430278
695	Q9H2G2|SLK_HUMAN	1.496660709
2617	Q0VDG4|SCRN3_HUMAN	1.497545242
1960	Q8NI08|NCOA7_HUMAN	1.497565269
2616	Q8TB52|FBX30_HUMAN	1.497968078
998	Q14914|LTB4D_HUMAN	1.500914931
1103	Q13510|ASAH1_HUMAN	1.50499475
216	Q14203|DYNA_HUMAN	1.507050276
1440	P60520|GBRL2_HUMAN	1.512032986
229	Q9P2E9|RRBP1_HUMAN	1.519466043
7	P21333|FLNA_HUMAN	1.520896792
1312	P51572|BAP31_HUMAN	1.521778107
884	Q9BR76|COR1B_HUMAN	1.525610924

1136	P19105|MLRM_HUMAN	1.526266336
496	O94919|ENDD1_HUMAN	1.533500791
2028	O75436|VP26A_HUMAN	1.534386635
2185	Q8IYB5|SMAP1_HUMAN	1.535003662
48	Q9Y4L1|OXRP_HUMAN	1.540550828
924	P04062|GLCM_HUMAN	1.542895079
1724	Q14108|SCRB2_HUMAN	1.544039726
2205	Q9HB40|RISC_HUMAN	1.545340776
2251	Q9UJ83|HACL1_HUMAN	1.545393109
1417	P04080|CYTB_HUMAN	1.545913458
2732	Q969V6|MKL1_HUMAN	1.546463966
536	O76003|TXNL2_HUMAN	1.549265027
79	O75874|IDHC_HUMAN	1.55480516
2023	O15143|ARC1B_HUMAN	1.555979133
1111	Q96PU5|NED4L_HUMAN	1.556444645
1968	Q6IBS0|TWF2_HUMAN	1.557838798
2022	Q96CU9|FXRD1_HUMAN	1.564020514
1105	O43747|AP1G1_HUMAN	1.565433145
1425	Q13131|AAPK1_HUMAN	1.571828842
1776	Q96IZ0|PAWR_HUMAN	1.57707274
606	Q99988|GDF15_HUMAN	1.580296159
1867	Q9NQX5|NPDC1_HUMAN	1.583608031
335	P80303|NUCB2_HUMAN	1.588270545
1232	Q16851|UGPA2_HUMAN	1.588884711
55	P54577|SYYC_HUMAN	1.588974237
2544	Q8WYQ3|CV016_HUMAN	1.596207142
2512	Q15642|CIP4_HUMAN	1.596270442
1043	Q96JB5|CK5P3_HUMAN	1.598520637
2806	O75955|FLOT1_HUMAN	1.59875679
1879	Q8TCT9|HM13_HUMAN	1.60453999
2378	Q99570|PI3R4_HUMAN	1.611072183
597	P20020|AT2B1_HUMAN	1.61187005

181	P26641|EF1G_HUMAN	1.612153292
537	Q13561|DCTN2_HUMAN	1.614259601
2610	Q86YH6|DLP1_HUMAN	1.616511106
2136	P48729|KC1A_HUMAN	1.618238807
630	P30043|BLVRB_HUMAN	1.618495703
693	P60660|MYL6_HUMAN	1.6191535
1144	P13693|TCTP_HUMAN	1.61941123
1475	Q6IA17|SIGIR_HUMAN	1.620355964
624	O95817|BAG3_HUMAN	1.620689154
1577	P60981|DEST_HUMAN	1.620928526
2801	Q96EC8|YIPF6_HUMAN	1.624533772
354	P49591|SYSC_HUMAN	1.625178814
432	P29692|EF1D_HUMAN	1.628083825
2602	Q96BM9|ARL8A_HUMAN	1.62970376
1610	Q15833|STXB2_HUMAN	1.62977469
738	Q13409|DC1I2_HUMAN	1.632756352
1815	Q9UHR4|BI2L1_HUMAN	1.63317585
1246	P07858|CATB_HUMAN	1.638361096
2304	P17655|CAN2_HUMAN	1.641974688
2820	Q14409|GLPK3_HUMAN	1.643256307
404	P30044|PRDX5_HUMAN	1.644094706
377	Q9BSJ8|FA62A_HUMAN	1.644469023
359	P36871|PGM1_HUMAN	1.644691229
2061	Q9NZ08|ARTS1_HUMAN	1.646249294
1363	Q9NSK0|KLC4_HUMAN	1.648268104
2002	P05161|UCRP_HUMAN	1.649043202
2074	O75410|TACC1_HUMAN	1.649854541
53	P68104|EF1A1_HUMAN	1.651663423
2733	Q9NVJ2|ARL8B_HUMAN	1.654176235
1444	Q9HD20|AT131_HUMAN	1.654232979
49	Q16822|PPCKM_HUMAN	1.654616356
1854	P13473|LAMP2_HUMAN	1.657161832

205	P33121|ACSL1_HUMAN	1.661589861
2671	P61916|NPC2_HUMAN	1.661879301
166	P11717|MPRI_HUMAN	1.664426684
1355	Q08380|LG3BP_HUMAN	1.668028116
593	O43765|SGTA_HUMAN	1.668175817
690	Q9UGI8|TES_HUMAN	1.669370055
258	Q13228|SBP1_HUMAN	1.670034289
168	Q9Y617|SERC_HUMAN	1.670255065
1554	Q15011|HERPU_HUMAN	1.672672391
1419	Q9H223|EHD4_HUMAN	1.673418164
2793	O94864|ST65G_HUMAN	1.676403284
604	O15320|CTGE5_HUMAN	1.678491592
1690	Q8IXJ6|SIRT2_HUMAN	1.68137157
1188	O15173|PGRC2_HUMAN	1.683949351
374	P38606|VATA1_HUMAN	1.692122459
1358	Q9H2M9|RBGPR_HUMAN	1.698778749
840	Q16890|TPD53_HUMAN	1.704405665
337	P05091|ALDH2_HUMAN	1.708450079
798	Q8N8S7|ENAH_HUMAN	1.710017204
346	P49589|SYCC_HUMAN	1.715389132
1027	P04632|CPNS1_HUMAN	1.715527534
2182	O43741|AAKB2_HUMAN	1.720567822
836	P51149|RAB7_HUMAN	1.721827507
482	P15559|NQO1_HUMAN	1.723312736
379	Q16881|TRXR1_HUMAN	1.726307631
2650	Q9Y5X1|SNX9_HUMAN	1.72738409
1	P35579|MYH9_HUMAN	1.733729839
911	Q15042|RB3GP_HUMAN	1.736765623
932	P00966|ASSY_HUMAN	1.739515066
2214	O95721|SNP29_HUMAN	1.741406441
32	O43707|ACTN4_HUMAN	1.747684002
1143	P09104|ENOG_HUMAN	1.748849034

2118	P21266|GSTM3_HUMAN	1.749987125
2437	Q8TDY2|RBCC1_HUMAN	1.751492023
1928	O43278|SPIT1_HUMAN	1.751641273
1592	P51398|RT29_HUMAN	1.752251387
1721	P36543|VATE_HUMAN	1.753880143
1483	O15118|NPC1_HUMAN	1.755234122
2211	Q7L523|RRAGA_HUMAN	1.756533384
2797	P61224|RAP1B_HUMAN	1.757500768
2663	Q9UJ68|MSRA_HUMAN	1.759863734
1810	O95870|BAT5_HUMAN	1.769081116
1680	P42345|FRAP_HUMAN	1.776641846
2604	Q9NZ09|UBAP1_HUMAN	1.77883935
1331	Q13509|TBB3_HUMAN	1.780604839
1187	P11137|MAP2_HUMAN	1.783771873
2802	P30047|GFRP_HUMAN	1.785603762
2147	Q8TAA5|GRPE2_HUMAN	1.787631512
1361	P51151|RAB9_HUMAN	1.7895087
109	P35241|RADI_HUMAN	1.791903138
558	P07384|CAN1_HUMAN	1.792324781
2030	Q00765|REEP5_HUMAN	1.79811573
51	Q05682|CALD1_HUMAN	1.822292328
247	P21281|VATB2_HUMAN	1.835933685
785	P15586|GNS_HUMAN	1.837776542
1881	Q16625|OCLN_HUMAN	1.837862611
154	P46459|NSF_HUMAN	1.842655301
2330	O60437|PEPL_HUMAN	1.85085237
2154	Q96MW5|COG8_HUMAN	1.852891326
2583	Q8N357|CB018_HUMAN	1.871068358
303	P23381|SYWC_HUMAN	1.877939343
1595	P32929|CGL_HUMAN	1.888537645
1904	Q9UHA4|MK1I1_HUMAN	1.893025517
378	Q9Y6N5|SQRD_HUMAN	1.912019372

2531	Q14558|KPRA_HUMAN	1.913403034
1392	Q9UI12|VATH_HUMAN	1.913601637
735	Q16555|DPYL2_HUMAN	1.923000693
2579	Q9P2W9|STX18_HUMAN	1.930947065
2810	Q92574|TSC1_HUMAN	1.935617805
529	P07339|CATD_HUMAN	1.950637817
459	P63151|2ABA_HUMAN	1.961056709
1929	Q8N2K0|ABD12_HUMAN	1.962103844
943	Q15942|ZYX_HUMAN	1.965537071
444	P48163|MAOX_HUMAN	1.986655354
1804	O60784|TOM1_HUMAN	1.989610791
2612	Q9Y2T2|AP3M1_HUMAN	2.005886793
1158	O14967|CLGN_HUMAN	2.007550716
2639	Q8WWX9|SELM_HUMAN	2.010786533
1996	Q14689|DIP2A_HUMAN	2.017752886
796	P30040|ERP29_HUMAN	2.030169725
761	P30520|PURA2_HUMAN	2.038207293
2500	Q96EN8|MOCOS_HUMAN	2.0407691
1089	P46937|YAP1_HUMAN	2.043384075
2413	Q9HCS7|XAB2_HUMAN	2.082413673
77	P41250|SYG_HUMAN	2.094907522
1242	Q8NF37|PCAT1_HUMAN	2.098986387
1794	Q96HE7|ERO1A_HUMAN	2.103112698
1961	Q8IZ07|AN13A_HUMAN	2.110313416
1832	O76041|NEBL_HUMAN	2.119566441
930	Q53SF7|CBLL1_HUMAN	2.139914513
375	P30622|RSN_HUMAN	2.168561697
2174	Q9H299|SH3L3_HUMAN	2.207854748
1243	P47895|AL1A3_HUMAN	2.21714282
2355	O15533|TPSN_HUMAN	2.220907927
312	Q9UNF0|PACN2_HUMAN	2.272164106
2334	P26572|MGAT1_HUMAN	2.27447319

2641	P30419|NMT1_HUMAN	2.282536268
4	P46821|MAP1B_HUMAN	2.291236877
828	Q2M2I8|AAK1_HUMAN	2.292696476
683	P06396|GELS_HUMAN	2.316370726
260	Q13177|PAK2_HUMAN	2.330377579
1558	P61026|RAB10_HUMAN	2.338468075
204	P52888|MEPD_HUMAN	2.385234833
2169	Q9NP72|RAB18_HUMAN	2.407215595
2621	Q8TB40|ABHD4_HUMAN	2.418996096
351	P11413|G6PD_HUMAN	2.42952323
2403	Q969T9|WBP2_HUMAN	2.431432009
1877	Q9NQC3|RTN4_HUMAN	2.588263273
2003	Q9NZC3|GDE1_HUMAN	2.634101629
839	Q13501|SQSTM_HUMAN	2.722994089
2054	O14896|IRF6_HUMAN	2.758692265
844	Q99536|VAT1_HUMAN	2.802087307
1166	Q92974|ARHG2_HUMAN	2.832480192
829	Q14847|LASP1_HUMAN	2.905762672
583	P51648|AL3A2_HUMAN	2.943362474
1534	Q9BQE5|APOL2_HUMAN	2.959794044
1642	P62256|UBE2H_HUMAN	3.01350522
2505	P61769|B2MG_HUMAN	3.056506395
1506	P30460|1B08_HUMAN	3.111516714
2761	Q16526|CRY1_HUMAN	3.140068054
514	P07099|HYEP_HUMAN	3.169207096
2452	Q86XP1|DGKH_HUMAN	3.20305562
2551	O76024|WFS1_HUMAN	3.907998323
1673	P02511|CRYAB_HUMAN	4.513613701
2631	P25815|S100P_HUMAN	4.818594456
2267	O95429|BAG4_HUMAN	4.898168564
2630	P18510|IL1RA_HUMAN	5.193850994
2168	O60711|LPXN_HUMAN	5.847269058

2816	Q96CV9|OPTN_HUMAN	8.370360374

Table S2. Fold change (absolute value)＞1.8 (Yes-set)		
Gene symbol	**BKL description**	**Accession**
AAK1	AP2 associated kinase 1; a protein serine-threonine kinase that acts in protein amino acid phosphorylation and protein import; regulates receptor-mediated endocytosis	Q2M2I8
ABHD12	Abhydrolase domain containing 12; may function in endocannabinoid metabolism; gene mutation causes polyneuropathy; hearing loss; ataxia; retinitis pigmentosa; and cataract (PHARC)	Q8N2K0
ABHD4	Abhydrolase domain containing 4; a predicted lysophospholipase/phospholipase B that may play a role in biosynthesis of N-acyl ethanolamines including the endocannabinoid anandamide	Q8TB40
ADSS	Adenylosuccinate synthetase; catalyzes the first committed step in the conversion of IMP to AMP in the purine biosynthesis pathway; gene polymorphism is associated with schizophrenia	P30520
ALDH1A3	Aldehyde dehydrogenase 1 family member A3; acts in vitamin A metabolism; glucagon secretion; and sensory organ development; may play a role in cell proliferation and neurogenesis; upregulated in breast cancer; mRNA is upregulated psoriasis	P47895
ALDH3A2	Aldehyde dehydrogenase 3 family member A2; plays a role in leukotriene metabolism and fatty acid alpha-oxidation; involved in response to oxidative stress; gene mutation causes Sjogren Larsson syndrome; mRNA is downregulated in psoriasis	P51648
ALKBH5	AlkB alkylation repair homolog 5; a nuclear 2-oxoglutarate dependent oxygenase that catalyses decarboxylation of 2-oxoglutarate; cellular expression is induced by hypoxia	Q6P6C2
ANKRD13A	Member of the DUF3424 domain of unknown function family; has moderate similarity to human ANKRD13C; which is a prostaglandin D2 receptor binding protein that acts in GPCR signaling; regulates receptor biosynthesis and protein export from ER	Q8IZ07
ANP32B	Acidic nuclear phosphoprotein 32 family member B; a caspase inhibitor that acts in G1-S transition of mitotic cell cycle; cell proliferation; wound healing; and inhibition of apoptosis; may play a role in brain development and inflammatory response	Q92688
ANP32E	Protein with strong similarity to mouse Anp32e; which is a protein phosphatase inhibitor involved in synaptogenesis and protein amino acid dephosphorylation and interacts with the importin alpha proteins Rch1 and NPI-1; contains three leucine rich repeats	Q9BTT0
AP3M1	AP-3 adapter complex mu3A subunit; binds to GLUT4 and plays a role in protein targeting to lysosome and symbiosis encompassing mutualism through parasitism; mRNA expression is downregulated in cervical carcinomas	Q9Y2T2
APOL2	Apolipoprotein L 2; a putative lipid transporter that may play a role in cytokine-mediated signaling pathway and cholesterol biosynthesis; involved in response to cocaine; cannabis; and phencyclidine	Q9BQE5
AR	Androgen receptor; a transcription factor binding protein that regulates cell cycle; aberrant expression is associated with many cancers; trinucleotide repeat instability in the gene correlates with Kaposi sarcoma associated with HIV infections	P10275

ARHGEF2	Rho-Rac guanine nucleotide exchange factor 2; acts in Rho-Rac protein signal transduction and regulates cell proliferation; actin-mediated cell contraction; and apical junction assembly	Q92974
ATP6V1B2	V-ATPase B2 subunit; an H+-transporting ATPase that acts in maintenance of acid-base homeostasis and establishment of cell polarity; regulates bone resorption; may play a role in skeletal system development; mRNA is upregulated in spinal muscular atrophy	P21281
ATP6V1H	ATPase H+ transporting lysosomal 50-57kDa V1 subunit H; a component of vacuolar ATPase that plays a role in endocytosis; may be involved in endosome organization and lysosomal lumen acidification	Q9UI12
B2M	Beta 2-microglobulin; binds to CD82; regulates APKK activity and antigen processing and presentation; aberrant protein expression is associated with AIDS; Crohn Disease; Hemophilia A and B; nervous and digestive system diseases; and several neoplasms	P61769
BAG4	BCL2 associated athanogene 4; a cytoplasmic HSP70 inhibitor that plays a role in antiapoptosis and protein folding; mRNA is upregulated in multiple sclerosis; breast cancer; and pancreatic neoplasms	O95429
BNIP3	BCL2-adenovirus E1B 19kDa interacting protein 3; a luciferin monooxygenase that acts in chromatin remodeling; apoptosis; inflammation; and calcium ion homeostasis; aberrantly expressed in HELLP syndrome and lung; liver; and several other cancers	Q12983
BUD31	BUD31 homolog; induced by phorbol myristic acetate; may be involved in nuclear regulation of transcription; contains an N-terminal acidic domain and cysteine-rich C-terminal domain with a putative zinc-finger motif	P41223
C10orf119	Member of the DUF2044 domain of conserved membrane protein family; has low similarity to soybean Glyma04g39990; which is involved in cellular response to iron ion starvation	Q9BTE3
C1orf52	Protein of unknown function; has strong similarity to uncharacterized mouse 2410004B18Rik	Q8N6N3
C2orf18	Member of the plant triose-phosphate transporter; UAA transporter; EamA-like transporter; and nucleotide-sugar transporter families; has high similarity to C. elegans C29H12-2; which stimulates growth rate	Q8N357
CALD1	Caldesmon 1; a calmodulin binding protein that acts in actin cytoskeleton organization and biogenesis and cell growth; regulates cell shape and stress fiber formation; upregulated in glioma; gene polymorphism correlates with type I diabetes mellitus	Q05682
CAMKK2	Calcium-calmodulin dependent protein kinase kinase 2 beta; acts in calcium-mediated signaling; visual learning; and protein phosphorylation; upregulated in lateral sclerosis; mRNA upregulation correlates with tetraploid mantle cell lymphoma	Q96RR4
CBLL1	Cas-Br-M ecotropic retroviral transforming sequence-like 1; a ubiquitin ligase required for internalization of West Nile virus	Q53SF7
CCDC117	Protein of unknown function; has high similarity to uncharacterized mouse BC018601	Q8IWD4
CDK1	Cell division cycle 2; a cyclin-dependent protein kinase that acts in DNA damage checkpoint and regulation of neuron differentiation; aberrant protein expression is associated with Alzheimer disease; bullous lesions; HIV infection; and several neoplasms	P06493
CDK4	Cyclin-dependent kinase 4; acts in mitotic cell cycle; chromosome organization; induction of centriole replication; and Ras signaling; upregulated in Alzheimer disease; B-cell lymphocytic leukemia; glioma; and lung; bone and several other neoplasms	P11802

CDK9	Cyclin-dependent kinase 9; an RNA polymerase II transcription elongation factor that plays a role in apoptosis; histone methylation; stem cell differentiation; and skeletal muscle tissue development; stimulates cell growth and inhibits gene expression	P50750
CLGN	Calmegin; a putative testis specific chaperone that may play a role in male infertility; may cause protein folding	O14967
CLIP1	CAP-GLY domain containing linker protein 1; acts in microtubule stabilization; phagocytosis; protein transport; and antiapoptosis; upregulated in Hodgkin disease; autoimmune antibody correlates with idiopathic form of pleural effusion and scleroderma	P30622
CNTN2	Contactin 2; a receptor that plays a role in homophilic cell adhesion; cell migration; axonogenesis; learning; and memory; loss of protein expression is associated with T-cell leukemia; mRNA expression is upregulated in glioma	Q02246
COG8	Component of oligomeric Golgi complex 8; forms sub-complex with COG5-7 and COG1-4 and mediates the assembly of subcomplexes into complete COG complex; gene mutations are associated with type II congenital glycosylation disorder	Q96MW5, Q9HBH1
CPNE3	Copine III; a protein kinase that catalyzes protein amino acid phosphorylation; binds phosphorylated Tyr1248 of ErbB2 to enhance tumor cell migration; altered expression is associated with breast; prostate and ovarian tumors	O75131
CRY1	Cryptochrome 1; a transcription corepressor that mediates circadian regulation of heart rate and temperature homeostasis; acts in glucose metabolism and visual perception; methylation in the corresponding gene promoter correlates with endometrial cancers	Q16526
CRYAB	Crystallin alpha B; a chaperone that acts in antiapoptosis and platelet activation; involved in response oxidative stress and heat; upregulated in multiple sclerosis; gene mutation causes cataract and muscular diseases	P02511
CTH	Cystathionase; a cystathionine gamma-lyase that plays a role in activation of MAPK activity; cysteine metabolism; and transsulfuration; activity is downregulated in neuroblastoma and several neoplasms; gene mutations are associated with cystathioninuria	P32929
CTSD	Cathepsin D; a lysosomal aspartyl protease that acts in neuroprotection; tissue homeostasis; and apoptosis; upregulated in Alzheimer and digestive system diseases; and many cancers; gene mutation is associated with neuronal ceroid lipofuscinosis	P07339
DDX39	DEAD box polypeptide 39; a putative ATP-dependent RNA helicase that is involved in response to estrogen stimulus; may act in RNA splicing and mRNA export from nucleus	O00148
DGKH	Diacylglycerol kinase eta; a protein domain specific binding protein that mediates phosphorylation; acts as a regulatory component of the Ras; B-Raf; C-Raf; MEK; and ERK signaling cascade; regulated by glucocorticoids	Q86XP1
DHFR	Dihydrofolate reductase; an reductase that converts dihydrofolate into tetrahydrofolate; functions in methotrexate transport; gene amplification correlates with breast cancer and precursor cell lymphoblastic leukemia; upregulated in colorectal cancer	P00374
DHFRP1		P00374
DIP2A	Disco-interacting protein 2 homolog A; functions as a receptor for follistatin-like 1 (FSTL1) and mediates its cardiovascular protective effects	Q14689

DNAJC9	DnaJ (Hsp40) homolog subfamily C member 9; a type C DnaJ/HSP40 member; contains an N-terminal J domain; binds to and cochaperones HSP70; expression is induced following various forms of cellular stress and mitogenic stimulation	Q8WXX5
DPYSL2	Dihydropyrimidinase-like 2; a GTPase activator that induces microtubule polymerization; synaptic vesicle fusion; glutamate secretion; and neurite outgrowth; downregulated in Down syndrome; gene SNPs are associated with bipolar disorder and schizophrenia	Q16555
DUS1L	Member of the dihydrouridine synthase (Dus) family; has moderate similarity to S. cerevisiae Dus1p; which catalyzes dihydrouridine modification of tRNA	Q6P1R4
EPHX1	Epoxide hydroxylase 1 microsomal; a bile acid transporter that acts in xenobiotic metabolism; embryo development; and behavior; gene polymorphisms correlate with polycystic ovary syndrome; pre-eclampsia; COPD; bladder cancer; and several other neoplasms	P07099
ERO1L	ERO1-like; a protein disulfide oxidoreductase that regulates hormone secretion and protein transport; acts in cell redox homeostasis and protein thiol-disulfide exchange	Q96HE7
ERP29	Endoplasmic reticulum protein 29; plays a role in protein folding; protein secretion; protein transport; and sperm motility; may regulate fusion of sperm to egg plasma membrane	P30040
EXOSC1	Exosome component 1; a component of the exosome; interacts with other exosome subunits hRrp42p (KIAA0116) and hRrp46p (RRP46); has exoribonuclease activity; involved in RNA catabolism	Q9Y3B2
FEN1	Flap structure specific endonuclease 1; a 5'-flap endonuclease and a 5'-3' exonuclease that acts in DNA replication; telomere maintenance; DNA repair; and mRNA cleavage; upregulated in lung and various other cancers; mRNA is overexpressed in psoriasis	P39748
FKBP5	FK506 binding protein 5; a cis-trans prolyl isomerase involved in protein folding and short term recognition memory; regulates AR signaling; inhibits calcineurin activity and apoptosis; upregulated in prostate cancer	Q13451
G6PD	Glucose-6-phosphate dehydrogenase; catalyzes the formation of glucono-1-5-lactone 6-phosphate; aberrant expression correlates with Alzheimer disease; diabetes; thalassemia; and breast cancer; gene mutations are associated with spherocytosis and anemia	P11413
GARS	Glycyl-tRNA synthetase; a class II aminoacyl-tRNA synthetase; acts as an autoantigen in dermatomyositis; gene mutations are associated with Charcot Marie Tooth disease type 2D and distal spinal muscular atrophy type V	P41250
GDE1	Glycerophosphodiester phosphodiesterase 1; acts in GPCR pathway and phosphoinositide metabolism	Q9NZC3
GNS	Glucosamine-6-sulfatase; acts in the catabolism of heparan and keratan sulfates; enzyme deficiency causes Sanfilippo disease type D	P15586
GSN	Gelsolin; binds to phospholipids; acts in actin cytoskeleton reorganization; antiapoptosis; and regulation of deoxyribonuclease activity; aberrant expression is associated with lung and several neoplasms; gene mutation causes familial amyloidosis	P06396
HDAC2	Histone deacetylase 2; a histone deacetylase and a transcriptional corepressor that acts in chromatin remodeling; inflammatory response; and regulation of translation; aberrantly expressed in corticotroph adenomas; stomach; colorectal; and other neoplasms	Q92769
HLTF	Helicase-like transcription factor; a double-stranded DNA translocase and transcriptional activator that plays a role in protein polyubiquitination and promotes error-free replication of damaged DNA; gene methylation correlates with colon and many cancers	Q14527

HMGB1	High-mobility group box 1; a transcription regulator that acts in protein kinase cascade; inflammation; and DNA unwinding; upregulated in arteriosclerosis; HIV infection; arthritis; lung diseases; sepsis; and liver and various other cancers	P09429
HMGB2	High-mobility group box 2; a transcription factor that binds to and bends DNA; plays a role in DNA ligation; downregulated in osteoarthritis; acts as an autoantigen in juvenile idiopathic arthritis and autoimmune hepatitis	P26583
HNRNPC	Heterogeneous nuclear ribonucleoprotein C; binds to RNA; acts in cell differentiation; cell proliferation; and cellular ion homeostasis; involved in response to DNA damage stimulus; autoantibodies are associated with Sjogren's syndrome manifestations	P07910
HNRNPH3	Heterogeneous nuclear ribonucleoprotein H3 (2H9); a RNA binding protein that may play a role in RNA splicing and processing	P31942
IL1RN	Interleukin 1 receptor antagonist; a putative cytokine that functions in immune response; gene polymorphism correlates with alopecia areata; rheumatoid arthritis; type II diabetes; Alzheimer and coronary diseases; postmenopausal osteoporosis; and asthma	P18510
IRF6	Interferon regulatory factor 6; a transcription activator that regulates Notch signaling pathway; acts in organ development; gene mutations correlate with cleft lip; anodontia; popliteal pterygium syndrome; and skin and urogenital abnormalities	O14896
KIAA1143	Protein of unknown function; has strong similarity to uncharacterized mouse 1110059G10Rik	Q96AT1
LASP1	LIM and SH3 protein 1; binds to and regulates actin bundle formation; plays a role in mitotic cell cycle; cell proliferation; and cell migration; upregulated in breast cancers; gene translocation correlates with acute form of myeloid leukemia	Q14847
LPCAT1	Lysophosphatidylcholine acyltransferase 1; exhibits both lysophosphatidylcholine acyltransferase and lysophosphatidylglycerol acyltransferase activities; increased expression correlates with colorectal adenocarcinoma	Q8NF37
LPXN	Leupaxin; negatively regulates IL-2 production and BCR signaling; plays a role in MAPK and JNK cascades; mRNA expression is upregulated in splenic marginal zone lymphoma and genetic fusion with RUNX1 correlates with acute myeloid leukemia	O60711
MAGOHB	Protein with very strong similarity to mago-nashi homolog (human MAGOH); which may play a role in RNA localization and germ cell development; contains a mago nashi protein domain	Q96A72
MAP1B	Microtubule-associated protein 1B; a GPCR ligand that acts in neurogenesis; cytoskeleton organization; endocytosis; and apoptosis; aberrant phosphorylation correlates with Alzheimer disease	P46821
MAPKSP1	MAPK scaffold protein 1; exhibits protein homo and heterodimerization activity; plays a role in protein complex formation and activation of MAPK activity	Q9UHA4
MCM2	Minichromosome maintenance complex component 2; acts in DNA-dependent DNA replication initiation and mitotic cell cycle checkpoint; aberrant expression is associated with oral epithelial dysplasias; breast and various other neoplasms	P49736
MCM3	Minichromosome maintenance complex component 3; plays a role in DNA replication initiation; humoral immunity; and regulation of cell cycle; upregulation correlates with death associated with astrocytoma; mRNA is downregulated in CML	P25205
MCM4	Minichromosome maintenance complex component 4; an ATP-dependent DNA helicase that plays a role in the regulation of DNA replication	P33991

MCM5	Minichromosome maintenance complex component 5; a transcription coactivator and putative ATPase that acts in DNA replication and cell cycle; upregulated in ovarian; gastric; and thyroid cancers	P33992
ME1	Malic enzyme 1 NADP(+)-dependent cytosolic; catalyzes reversible oxidative decarboxylation of malate; plays a role in glucose-induced insulin secretion and citrate metabolism; mRNA aberrantly expressed in ductal and medullary breast cancers	P48163
MGAT1	Mannosyl (alpha-1; 3-)-glycoprotein beta-1; 2-N-acetylglucosaminyltransferase; catalyzes the transfer of N-acetylglucosaminyl residue to oligosaccharide; plays a role in N-glycan processing; nervous system development; and vasculogenesis	P26572
MOCOS	Molybdenum cofactor sulfurase; a putative pyridoxal phosphate binding protein that is involved in Xanthine metabolism; may play a role in cellular aldehyde and sulfur metabolic processes; gene mutation is associated with classical Xanthinuria type II	Q96EN8
NASP	Nuclear autoantigenic sperm protein; interacts with heat shock protein and histone; regulates ATPase activity; acts in S-phase of cell cycle; nucleosome assembly; embryo development; and protein transport to nucleus; may be involved in spermatogenesis	P49321
NEBL	Nebulette; a structural constituent of muscle that binds to actin; acts in actin filament organization; may play a role in sarcomere organization and muscle contraction; gene polymorphism is associated with nonfamilial idiopathic dilated cardiomyopathy	O76041
NFIX	Nuclear factor IX (CCAAT-binding transcription factor); an RNA polymerase III transcription factor that mediates endochondral ossification and mineralization	Q14938
NKX3-1	NK3 homeobox 1; a transcription factor that acts in androgen receptor and PKA cascades; cell proliferation; and prostate and skeleton development; downregulated in prostate and testicular cancers; loss of heterozygosity correlates with breast neoplasms	Q99801
NMT1	N-myristoyltransferase 1; an N-acyltransferase that acts in N-terminal protein myristoylation and multicellular organismal development; regulates cell death and monocyte differentiation; upregulated in colorectal and gallbladder neoplasms	P30419
NSF	N-ethylmaleimide-sensitive factor; an ATPase that plays a role in growth hormone secretion; membrane fusion; and acrosome reaction; regulates protein complex disassembly and exocytosis; decreased mRNA expression is associated with schizophrenia	P46459
NUDT1	Nudix-type motif 1; a 8-oxo-7 8-dihydroguanosine triphosphate pyrophosphatase that acts in DNA repair and oxidative stress induced apoptosis; upregulated in Parkinson disease; mRNA is aberrantly expressed in astrocytoma; breast; lung; and several cancers	P36639
OCLN	Occludin; a structural molecule that plays a role in acid secretion and cell-cell adhesion; aberrant expression is associated with colitis; Crohn disease; HIV infections; hydatidiform mole; psoriasis; endometrial and several neoplasms	Q16625
OPTN	Optineurin; a transcription coactivator that acts in the establishment of cell polarity; Golgi to plasma membrane transport; regulation of retinal cell apoptosis and neural retina layer; gene mutations are associated with primary open-angle glaucoma	Q96CV9
PACSIN2	Protein kinase C and casein kinase substrate in neurons 2; cytoplasmic adaptan SH2-SH3 er protein; interacts with FASLG; plays a role in microtubule polymerization; receptor recycling; microspike assembly; and regulation of endocytosis	Q9UNF0

PAK2	P21 protein activated kinase 2; a protein serine-threonine kinase that acts in GTPase mediated signaling; apoptosis; axon extension; spindle orientation; and regulation of cell cycle; gene mutation correlates with mental retardation	Q13177
PARP1	Poly ADP ribose polymerase family member 1; a transcription cofactor that acts in protein amino acid ADP-ribosylation; DNA repair; and apoptosis; aberrantly expressed in Alzheimer; Crohn disease; brain ischemia; ovary; prostate; and various neoplasms	P09874
PBK	PDZ binding kinase; binds to TP53; plays a role in histone phosphorylation; regulates DNA damage checkpoint and histone H3 modification; protein expression is upregulated in acute lymphocytic leukemia; myeloid leukemia; and mantle cell lymphoma	Q96KB5
PCNA	Proliferating cell nuclear antigen; a transcriptional regulator that acts in cell proliferation and DNA replication and repair; aberrantly expressed in glioblastoma; melanoma; asthma; psoriasis; arteriosclerosis; and liver; lung; and various other cancers	P12004
PDCD4	Programmed cell death 4; binds to DEAD-H-box RNA helicase; regulates cell cycle; apoptosis; transcription; and translation; downregulated in adenocarcinoma; upregulated in breast and urinary bladder neoplasms	Q53EL6
POLR3D	Polymerase III polypeptide D; a RNA polymerase III transcription factor that plays a role in ribosome biogenesis and regulation of cell cycle	P05423
PPL	Periplakin; an intermediate filament binding protein that plays a role in the assembly of the epidermal cornified envelope; regulates keratin bundling; epithelial cell migration; and wound healing; acts as an autoantigen in paraneoplastic pemphigus	O60437
PPP2R2A	Protein phosphatase 2 regulatory subunit B alpha; acts in the regulation of protein dephosphorylation; barrier function; and cell growth; expression is decreased in Alzheimer disease and lung cancer; gene fusion with CHEK2 is associated with teratoma	P63151
PRMT6	Protein arginine methyltransferase 6; acts in the regulation of histone H3-K4 methylation and protein binding; involved in response to virus	Q96LA8
PRPSAP1	Phosphoribosyl pyrophosphate synthetase-associated protein 1; a putative regulatory subunit of the phosphoribosylpyrophosphate (PRPP) synthetase complex; which catalyzes the formation of PRPP from ATP and ribose 5-phosphate	Q14558
PTMA	Prothymosin alpha; a transcriptional coactivator that acts in TLR cascade; lymphocyte activation; apoptosis; and immunity; upregulated in colon; prostate; and several other cancers	P06454
PUM2	Pumilio homolog 2; a cytoplasmic RNA binding protein that acts in protein complex assembly; may regulate translation; may play a role in in utero embryo and germ cell development	Q8TB72
PUS3	Protein with strong similarity to mouse Pus3; which is a ligand-dependent retinoic acid receptor transcription coactivator that pseudouridylates SRA1 and may play a role in tRNA processing; contains two type 1 tRNA pseudouridine synthase domain	Q9BZE2
RAB10	RAB10 member RAS oncogene family; a GTPase that activates JUN kinase and AKT; acts in early endosome to late endosome transport; induces protein transport form Golgi to plasma membrane; TLR4 signaling; and cytokine production	P61026
RAB18	RAB18 member RAS oncogene family; a putative GTPase that may play a role in vesicle-mediated transport and inflammatory response; localizes to lipid droplets	Q9NP72

RBBP5	Retinoblastoma binding protein 5; plays a role in regulation of estrogen receptor signaling pathway	Q15291
RBBP7	Retinoblastoma binding protein 7; a putative transcriptional repressor that inhibits cell growth; induces apoptosis; mediates protein localization; may play a role in methylation-dependent chromatin silencing and multicellular organismal development	Q16576
RFC3	Replication factor C 3; an ATPase that may play a role in DNA strand elongation during DNA replication	P40938
RNF31	Ring finger protein 31; an E3 ubiquitin ligase that binds; monoubiquitinates; and stabilizes the DAX1 (NR0B1) nuclear receptor to repress transcription and act as a coregulator of steroidogenic pathways	Q96EP0
RPA2	Replication protein A2 32kDa; binds to damaged DNA and mediates nucleotide-excision repair; acts in DNA unwinding during replication; regulates exit from mitosis; acts as an autoantigen in systemic lupus erythematosus and upregulated in breast neoplasms	P15927
RPS6KB1	Ribosomal protein S6 kinase 70kDa polypeptide 1; acts in GPCR pathway; regulates protein synthesis; cell cycle; and apoptosis; protein expression is increased in tuberous sclerosis and breast cancers	P23443
RRM1	Ribonucleotide reductase M1; catalyzes deoxyribonucleoside diphosphate and thioredoxin disulfide to ribonucleoside diphosphate and thioredoxin; involved in response to 5-fluorouracil; aberrant expression correlates with several neoplasms	P23921
RRP1B	Ribosomal RNA processing 1 homolog B; binds many nucleosome binding factors to potentially regulate transcription and chromatin structure; gene SNP correlates with metastasis susceptibility associated with breast cancer	Q14684
RTN4	Reticulon 4; a caspase activator that inhibits neurite outgrowth; acts in apoptosis; macrophage chemotaxis; neuron migration; neurotransmission; memory; and behavior; upregulated in lateral sclerosis; epilepsy; schizophrenia; and acute tubular necrosis	Q9NQC3
S100P	S100 calcium binding protein-P; binds to Ca2+; Zn2+; and Mg2+ ions; regulates endothelial cell migration and cell proliferation; upregulated in breast; lung; and several neoplasms; mRNA is increased in Crohn disease; ulcerative colitis; and skin neoplasm	P25815
SAMHD1	SAM domain and HD domain 1; a putative 3- 5-cyclic nucleotide phosphodiesterase that regulates innate immune response; gene mutations correlate with Aicardi-Goutieres syndrome; multiple myeloma; cerebral vasculopathy; and early onset of stroke	Q9Y3Z3
SELM	Selenoprotein M; a selenium binding putative oxidoreductase that is involved in response to biotic and endogenous stimulus; aberrant expression is associated with breast; fallopian; ovarian; lymphoma; uterine; and parotid tumors	Q8WWX9
SFTPD	Surfactant protein D; a lipid binding protein that acts in phagocytosis and inflammatory responses; upregulated in chronic periodontitis; psoriasis; respiratory distress syndrome; gene mutation correlates with ulcerative colitis and many infections	P30460
SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3; an antiapoptotic protein that inhibits TNF induced apoptosis; may act in retinoic acid receptor signaling and modulation of glutaredoxin activity	Q9H299
SMC4	Structural maintenance of chromosomes 4; a satellite DNA and rDNA binding protein; component of the condensin complex that associates with mitotic chromosomes and may play a role in mitotic chromosome condensation	Q9NTJ3

SMNDC1	Survival motor neuron domain containing 1; an RNA splicing factor that interacts with a wide variety of spliceosome complex proteins; functions in spliceosome assembly and induction of apoptosis	O75940
SQRDL	Protein containing a pyridine nucleotide-disulfide oxidoreductase domain; has moderate similarity to S. pombe Hmt2p; which is an oxidoreductase that is involved in sulfur compound metabolic process	Q9Y6N5
SQSTM1	Sequestosome 1; binds to ubiquitin and mediates proteasomal protein catabolism; regulates NF-kappaB activation and autophagy; upregulated in breast neoplasms; gene mutations are associated with Paget disease; mRNA is overexpressed in rheumatoid arthritis	Q13501
SSRP1	Structure specific recognition protein 1; a transcription elongation regulator that plays a role in antiapoptosis; cell growth; and embryonic development; upregulated in ovarian; breast; brain; and liver cancers	Q08945
STMN1	Stathmin 1; binds to microtubule; plays a role in axonogenesis; neuron migration; embryo implantation; and microtubule depolymerization; aberrant expression correlates with Alzheimer disease; multiple sclerosis; and in ovary and various other neoplasms	P16949
STX18	Syntaxin 18; an endoplasmic reticulum localized SNARE receptor that is involved in ER-mediated phagocytosis and endoplasmic reticulum to Golgi vesicle-mediated transport	Q9P2W9
SUMO2	SMT3 suppressor of mif two 3 homolog 2; a small conjugating protein ligase that acts as a protein modifier in the sentrinization pathway; plays a role in regulation of protein localization	P61956
TAGLN2	Transgelin 2; a putative actin binding protein; gene upregulation is associated with hepatocellular carcinoma	P37802
TAPBP	TAP binding protein; plays a role in MHC class I protein complex assembly; antigen processing and presentation; immunity; and retrograde vesicle-mediated transport; downregulated in kidney; maxillary; colon; and oral cancers	O15533
THOP1	Thimet oligopeptidase 1; a metalloendopeptidase that plays a role in antigen presentation exogenous antigen via MHC class I; may be involved in spermatogenesis; upregulated in Alzheimer disease	P52888
TLE3	Transducin-like enhancer of split 3 E(sp1) homolog; may play a role in Notch signaling pathway; keratinocyte differentiation; organ morphogenesis; and nervous system development; gene is upregulated in prostate tumor and malignant meningioma	Q04726
TMPO	Thymopoietin; a structural constituent of nuclear pore that acts in DNA replication; transcription; cell cycle; and cell proliferation; gene mutation is associated with dilated cardiomyopathy	P42166, P42167
TOM1	Target of myb1; binds to and recruits clathrin into endosome; plays a role in cell aging; receptor catabolism; and interleukin-8 production; SNP is associated with bipolar affective disorder	O60784
TSC1	Tuberous sclerosis 1; acts in TOR signaling; axonogenesis; and learning; loss of heterozygosity is associated with focal cortical dysplasia; gene mutations correlate with tuberous sclerosis; lymphangioleiomyomatosis; and urinary bladder cancer	Q92574
UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1; an enzyme that is involved in UDP-N-acetylglucosamine biosynthesis; may be involved in sperm motility	Q16222
UBE2H	Ubiquitin-conjugating enzyme E2H; a ubiquitin-protein ligase that binds and ubiquitinates histone H2A; upregulated in breast neoplasms	P62256
USP7	Ubiquitin specific peptidase 7; acts in protein stabilization and induction of apoptosis; regulates TLR signaling; protein deubiquitination; embryonic development; and innate immunity; upregulated in dilated cardiomyopathy	Q93009
VAT1	Vesicle amine transport protein 1 homolog; exhibits ATPase activity; plays a role in regulation of cell migration; may act in synaptic transmission and vesicle-mediated transport; expression is upregulated in glioblastoma	Q99536

WARS	Tryptophanyl-tRNA synthetase; exhibits protein homodimerization activity; plays a role in immune response; tryptophanyl-tRNA aminoacylation; and regulation of cytoskeleton organization; autoantibodies correlate with autoimmune diseases	P23381
WBP2	WW domain binding protein 2; interacts with Yes-associated protein 1; may play a role in signal transduction; contains two proline rich PY motifs	Q969T9
WFS1	Wolfram syndrome 1; an ATPase binding protein that regulates cell cycle; apoptosis; and insulin secretion; acts in female pregnancy; spermatid development; and ion homeostasis; gene mutations correlate with Wolfram syndrome; diabetes; and hearing loss	O76024
XAB2	XPA binding protein 2; forms a complex with RARA and HDAC3; inhibits all-trans retinoic acid-induced cellular differentiation and gene transcription; plays a role in transcription-coupled DNA repair	Q9HCS7
YAP1	Yes-associated protein 1; a onco-protein and transcription activator that regulates Notch signaling; acts in epithelial to mesenchymal transition and cell migration; upregulated in oral carcinoma and gastric cancer; downregulated in breast cancer	P46937
ZYX	Zyxin; a protein transporter that acts in actin cytoskeleton reorganization; focal adhesion assembly; cell adhesion; and cell proliferation; predominantly localizes to focal adhesion	Q15942

Table S3. Fold change (absolute value)＜1.088 (No-set)		
Gene symbol	**BKL description**	**Accession**
AARS2	Alanyl-tRNA synthetase 2 mitochondrial; a predicted mitochondrial Alanyl tRNA Synthetase; gene mutation causes perinatal or infantile cardiomyopathy with near total combined mitochondrial respiratory chain deficiency in the heart	Q5JTZ9
ABCB6	ATP-binding cassette subfamily-B member-6; an ATPase and transmembrane transporter that may play a role in heme biosynthesis; iron homeostasis; and cell proliferation; mRNA is upregulated in hepatocellular carcinoma	Q9NP58
ABCC10	ATP-binding cassette subfamily C member 10; a drug transmembrane transporter and an ATPase that acts in anion and hormone transport; regulates natural killer cell mediated cytotoxicity; increased mRNA expression correlates with acute myeloid leukemia	Q5T3U5
ABCF2	ATP-binding cassette subfamily F member 2; may play a role in mitochondrial transport; increased expression correlates with clear cell adenocarcinoma and ovarian neoplasms	Q9UG63
ACAD8	Acyl-Coenzyme A dehydrogenase family member 8; a mitochondrial acyl-CoA dehydrogenase that may play a role in lipid metabolic process; mutation in corresponding gene is associated with isobutyryl CoA dehydrogenase deficiency	Q9UKU7
ACADM	Acyl-Coenzyme A dehydrogenase C-4 to C-12 straight chain; an electron carrier that acts in fatty acid beta-oxidation; aberrant protein activity causes hepatomegaly; hypoglycemia; and sudden infant death associated with inborn errors lipid metabolism	P11310
ACCN2	Amiloride-sensitive cation channel 2 neuronal; a ligand-gated sodium channel that acts in calcium ion homeostasis; synaptic transmission; and visual learning; involved in inflammatory responses; behavioral fear response; and regulation of phosphorylation	P11171
ACF		Q9NQ94
ACO2	Aconitase 2 mitochondrial; a hydratase that catalyzes the interconversion of citrate to isocitrate via cis-aconitate in TCA cycle; acts in cell proliferation and iron homeostasis; downregulated in muscular diseases; gene is mutated in Parkinson disease	Q99798
ACOT13	Thioesterase superfamily member 2; a putative microtubule binding protein that	Q9NPJ3

	regulates cell proliferation	
ACOT8	Acyl-CoA thioesterase 8; cleaves thioester bonds mostly on medium chain acyl CoAs; increases peroxisome proliferation; may function in fatty acid oxidation and lipid metabolism; may mediate Nef-induced downregulation of CD4	O14734
ACOX1	Acyl-coenzyme A oxidase 1 palmitoyl; catalyzes the first step of very long chain fatty acid beta-oxidation by converting acyl-CoA to enoyl-CoA; mRNA is downregulated in Zellweger syndrome; gene mutation correlates with peroxisomal disorders	Q15067
ACP1	Acid phosphatase 1 soluble; a tyrosine phosphatase that acts in receptor-mediated signaling; overexpressed in breast and colon neoplasms; gene polymorphism is associated with diabetes; fetal macrosomia; and obesity; upregulated in neuroblastoma	P24666
ADD1	Adducin 1 alpha; plays a role in actin filament polymerization; angiogenesis; and ion transport; gene polymorphism is associated with stroke; hypertension; and kidney and cardiovascular diseases; gene map position correlates with Huntington disease	P35611
ADPGK	Member of the ADP-specific phosphofructokinase or glucokinase conserved region containing family; has strong similarity to uncharacterized mouse Adpgk	Q9BRR6
AGAP3	Protein with high similarity to human AGAP1; which is a GTPase that acts in MAPKKK cascade and actin cytoskeleton organization; and is associated with acute lymphoblastic leukemia; member of the miro-like protein family; contains a Ras family domain	Q96P47
AGK	Acylglycerol kinase; a ceramide kinase that mediates DNA replication; MAPK activation; lipid phosphorylation; and regulation of cell cycle; aberrant expression of the corresponding gene is associated with several cancers	Q53H12
AGRN	Agrin; an ATPase inhibitor that plays a role in placenta development; aberrant expression correlates with systemic lupus erythematosus and Alzheimer disease; increased mRNA expression correlates with cholangiocarcinoma and hepatocellular carcinoma	O00468
AIFM1	Apoptosis-inducing factor mitochondrion-associated 1; an apoptotic protease activator that plays a role in apoptosis; chromatin remodeling; mitochondrial genome maintenance; and stress granule assembly	O95831

AK2	Adenylate kinase 2; plays a role in adenine metabolic process and apoptotic mitochondrial changes; regulates energy homeostasis; adiponectin secretion; and fat cell differentiation; lack of protein expression correlates with reticular dysgenesis	P54819
AK3	Adenylate kinase 3; plays a role in nucleotide phosphorylation	Q9UIJ7
AKAP9	A kinase anchor protein 9; acts in microtubule nucleation; action potential propagation; stress granule formation; leukocyte migration; and heart contraction; gene translocation correlates with thyroid neoplasm; SNPs correlate with lung and breast cancers	Q99996
AKR7A2	Aldo keto reductase family 7 member A2; a dehydrogenase that plays a role in aldehyde metabolism and gamma hydroxybutyrate biosynthesis; upregulated in Alzheimer and Lewy body disease; rat Akr7a2 is associated with hepatocellular carcinoma	O43488
ALDH4A1	Aldehyde dehydrogenase 4 family member A1; an electron carrier that plays a role in proline metabolic process and is involved in response to cellular stress; gene mutation causes hyperprolinemia type II	P30038
ALDH6A1	Aldehyde dehydrogenase 6 family member A1; a putative methylmalonate-semialdehyde dehydrogenase that may play a role in valine metabolism	Q02252
ALDH9A1	Aldehyde dehydrogenase 9 family member A1; an electron carrier that plays a role in cellular aldehyde and carnitine metabolic process	P49189
ALKBH4	AlkB alkylation repair homolog 4; a Fe(II)/2-oxoglutarate-dependent decarboxylase that mediates decarboxylation of 2-oxoglutarate in absence of primary substrate	Q9NXW9
ANK2	Ankyrin 2 neuronal; a structural constituent of eye lens that acts in actin filament organization; posttranslational membrane targeting; and Ca2+ ion homeostasis; regulates heart rate; gene mutation causes cardiac arrhythmia and long QT syndrome	Q01484
ANKZF1	Protein containing two ankyrin repeats; which may mediate protein-protein interactions; has high similarity to uncharacterized rat RGD1359242	Q9H8Y5
ANXA6	Annexin A6; a calcium channel regulator that plays a role in lipoprotein catabolic process and receptor-mediated endocytosis; may act in cytoskeleton organization	P08133

	and endosome transport; upregulated in dilated cardiomyopathy and heart failure	
AP1G2	Adapter-related protein complex 1 subunit gamma-2; a member of the adaptin family; may play a role in intracellular protein transport and vesicle trafficking	O75843
AP2M1	Adaptor-related protein complex 2 mu 1 subunit; a putative transporter that plays a role in receptor-mediated endocytosis and embryonic development; may act in vesicle coating; gene upregulation correlates with squamous cell carcinoma of the lung	Q96CW1
AP3S2	Adaptor-related protein complex 3 sigma 2 subunit; a subunit of the AP-3 adaptor-like protein complex that plays a role in the recognition of tyrosine-based signals in sorting processes	P59780
APOO	Apolipoprotein O; a chondroitin sulfate chain containing apolipoprotein that promotes cholesterol efflux from macrophage cells; mRNA expression is upregulated in diabetic heart	Q9BUR5
APPL	Adaptor protein phosphotyrosine interaction PH domain and leucine zipper containing 1; acts in adiponectin; insulin; and Akt signaling pathways; neurite outgrowth; and apoptosis; regulates glucose uptake and protein translocation	Q9UKG1
ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2; a GTPase regulator that plays a role in protein targeting to membrane and exocytosis; regulates protein localization; secretion; and transport	Q9Y6D5
ARFIP2	ADP-ribosylation factor interacting protein 2; interacts with ARF1 and RAC1; acts in small GTPase mediated signaling and membrane ruffling; may play a role in cytoskeleton organization; upregulated in Huntington disease	P53365
ARG2	Arginase type-II; catalyzes the arginine hydrolysis to ornithine and urea; inhibits host immune response and nitric-oxide synthase activity; regulates macrophage apoptosis and citrulline synthesis; upregulated in hypertension; diabetes; and thyroid cancer	P78540
ARHGDIA	Rho GDP dissociation inhibitor alpha; binds to Rho GTPases; regulates protein stability and vascular permeability; acts in estrogen receptor signaling; spermatogenesis; and urogenital system development; upregulated in breast neoplasms	P52565
ARHGEF16	Rho guanine nucleotide exchange factor 16; a putative PDZ domain binding	Q5VV41

	protein that plays a role in activation of CDC42 GTPase activity	
ARHGEF6	Rac-Cdc42 guanine nucleotide exchange factor 6; binds to ARHGEF7; CDC42; and RAC1; involved in cell adhesion and migration; JNK cascade; PAK1 activation; and apoptosis; gene translocation and point mutation correlates with X-linked mental retardation	Q15052
ARL3	ADP-ribosylation factor like 3; a GTP binding protein that plays a role in kidney and photoreceptor development; mediates Golgi vesicle docking and transport; cytokinesis; and epithelial cell proliferation	P36405
ARMC1	Protein containing an armadillo or beta-catenin-like repeat; which mediate interactions with diverse binding partners; has very strong similarity to uncharacterized mouse Armc1	Q9NVT9
ARPC1A	Actin related protein 2-3 complex subunit 1A; may play a role in actin cytoskeleton organization; cell morphogenesis; and cell motion; increased mRNA expression is associated with pancreatic cancer	Q92747
ARPC3	Actin-related protein 2-3 complex subunit-3; regulates actin nucleation; trophoblast outgrowth; and actin assembly at the cell periphery of migrating cells; may be involved in lamellipodium biogenesis and cell motility	O15145
ARPC5	Actin related protein 2-3 complex subunit 5 16kDa; component of Arp2-3 complex; binds ARPC4 during Arp2-3 protein complex assembly; acts in actin cytoskeleton reorganization; may play a role in cell motility	O15511
ARRB1	Arrestin beta 1; a protein kinase regulator that activates transcription and ERK1/2 cascade; mediates ubiquitylation; endocytosis; and immune response; aberrantly expressed in multiple sclerosis; thyroid nodule; and major depressive disorder	P49407
ARSA	Arylsulfatase A; plays a role in myelination and sphingolipid metabolic process; aberrant expression causes metachromatic leukodystrophy and urologic neoplasms; gene deletion is associated with Lafora disease; vascular dementia; and Alzheimer disease	P15289
ARVCF	Armadillo repeat gene deletes in velocardiofacial syndrome; may play a role in cell adhesion and Wnt receptor signaling; gene polymorphism correlates with anorexia nervosa and schizophrenia	O00192
ASPSCR1	Alveolar soft part sarcoma chromosome region candidate 1; gene translocation with the gene encoding transcription factor TFE3 is associated with renal cell	Q9BZE9

	carcinoma and alveolar soft part sarcoma	
ATP5A1	ATP synthase H+ transporting mitochondrial F1 complex alpha subunit isoform 1 cardiac muscle; involved in ATP biosynthesis; may play a role in angiogenesis; mouse Atp5a1 is associated with intestinal polyposis	P25705
ATP5B	ATP synthase H+ transporting mitochondrial F1 complex beta polypeptide; functions in ATP synthesis during oxidative phosphorylation; downregulated in breast; colon; esophageal; kidney; lung; and stomach neoplasms	P06576
ATP5C1	Protein with strong similarity to rat Atp5c1; which is a component of the multisubunit enzyme that synthesizes ATP during oxidative phosphorylation; contains an ATP synthase domain	P36542
ATP5D	ATP synthase H(+) transporting mitochondrial F1 complex delta subunit; a putative hydrogen-exporting ATPase that may play a role in hydrogen transport; localizes to mitochondrial inner membrane	P30049
ATP5I	ATP synthase H+ transporting mitochondrial F0 complex subunit e; plays a role in MAPKKK cascade and negative regulation of cell proliferation; increased mRNA expression correlates with hepatocellular carcinoma	P56385
ATP5J	Mitochondrial ATPase coupling factor 6; binds to the beta subunit of ATP synthase and acts in ATP hydrolysis; regulates blood pressure and arachidonic acid secretion; increased expression correlates with ischemic heart disease in end-stage renal disease	P18859
ATPIF1	ATPase inhibitory factor 1; acts in mitochondrial hyperpolarization and glycolysis; upregulated in hepatoma; downregulated in mitochondrial myopathies; rat Atpif1 is downregulated in rat model of sepsis; mouse Atpif1 is elevated in experimental arthritis	Q9UII2
ATXN2L	Ataxin 2 like; binds to MPL thrombopoietin and EPOR erythropoietin receptors; may play a role in cytokine and chemokine mediated signaling pathway and visual perception	Q8WWM7
B3GNT1	UDP-GlcNAc-betaGal beta-1 3-N-acetylglucosaminyltransferase 1; acts in glycolipid metabolism; spermatogenesis; renal function; and neurotransmission; gene mutation is associated with adult i phenotype in congenital cataract	O43505
BCKDHA	Branched-chain alpha-keto acid dehydrogenase E1 alpha polypeptide; a	P12694

	carboxy-lyase that plays a role in branched chain family amino acid and leucine catabolism; gene mutation is associated with maple syrup urine disease	
BCKDK	Protein with strong similarity to rat Bckdk; which is a putative 3-methyl-2-oxobutanoate dehydrogenase that is involved in carbohydrate metabolism; branched chain family amino acid catabolism; and peptidyl-serine phosphorylation	O14874
BLMH	Bleomycin hydrolase; a cytosolic cysteine-type peptidase that protects bleomycin induced chromosome damage; mRNA is upregulated in Burkitt lymphoma and head and neck cancers; genetic polymorphisms are associated with Alzheimer disease	Q13867
BLOC1S3	Biogenesis of lysosomal organelles complex-1 subunit 3; plays a role in endosome and melanosome organization; platelet activation; and pigmentation during development; gene mutation is associated with Hermansky Pudlak syndrome	Q6QNY0
BOLA1	Member of the BolA-like protein family; which may control cell morphology; has strong similarity to uncharacterized mouse Bola1	Q9Y3E2
BRCC3	BRCA1-BRCA2 containing complex subunit 3; may be involved in regulation of transcription; gene translocation correlates with Ataxia telangiectasia leukemia and hemophilia A	P46736
BTF3L4	Protein with strong similarity to human BTF3; which is a general transcription factor that is required for transcriptional initiation by RNA polymerase II; member of the nascent polypeptide-associated complex (NAC) domain containing family	Q96K17
C12orf57	Protein of unknown function; has very strong similarity to uncharacterized mouse Grcc10	Q99622
C14orf156	Chromosome 14 open reading frame 156; a transcription corepressor involved in estrogen receptor signaling pathway; may play a role in lipid metabolism	Q9GZT3
C14orf4	Chromosome 14 open reading frame 4; a proline-rich protein that contains a C3HC4 RING finger domain and polyglutamine and polyalanine repeats; expressed primarily in the heart	Q9H1B7
C15orf38	Protein of unknown function; has strong similarity to uncharacterized mouse 2610034B18Rik	Q7Z6K5
C15orf40	Protein of unknown function	Q8WUR7

C17orf28	Chromosome 17 open reading frame 28 (downregulated in multiple cancer 1); member of a class of inside out membrane proteins; a putative integral membrane protein that is downregulated in many cancer cell lines	Q8IV36
C20orf30	Member of the DUF872 domain of unknown function family	Q96A57
C9orf64	Chromosome 9 open reading frame 64; may play a role in induced pluripotent stem cell generation and reprogramming; gene haploinsufficiency is associated with acute myeloid leukemia	Q5T6V5
CACYBP	Calcyclin binding protein; plays a role in DNA damage checkpoint; DNA recombination; and T-cell differentiation; inhibits apoptosis and fibroblast proliferation; upregulated in nasopharyngeal; osteogenic; and pancreatic cancers	Q9HB71
CALR	Calreticulin; a Ca2+ binding chaperone that acts in N-glycan processing; neutrophil activation; protein folding; and lactation; upregulated in pre-eclampsia; goiter; and several cancers; autoantibodies are associated with a variety of autoimmune diseases	P27797
CAND1	Cullin-associated and neddylation-dissociated 1; a transcription activator that acts in SCF complex assembly; cullin deneddylation; and regulation of ubiquitin-protein ligase activity; gene map position correlates with Emery-Dreifuss muscular dystrophy	Q86VP6
CCDC22	Member of the DUF812 domain of unknown function family; has strong similarity to uncharacterized mouse Ccdc22	O60826
CCDC47	Protein with very strong similarity to mouse Ccdc47; which plays a role in cellular calcium ion homeostasis and regulation of apoptosis	Q96A33
CCT2	Chaperonin containing TCP1 subunit 2; plays a role in folding of actin; tubulin; and other cytosolic proteins; may regulate cell cycle	P78371
CCT3	Chaperonin containing TCP-1 subunit 3; a putative unfolded protein binding protein; may play a role in the covalent and noncovalent assembly of single chain polypeptides or multisubunit complexes into the correct tertiary structure	P49368
CCT4	Chaperonin containing TCP1 subunit 4 (delta); a subunit of the cytosolic chaperonine-containing TCP-1 complex involved in ATP-dependent folding of actin and tubulin; rat Cct4 gene mutation causes early onset sensory neuropathy (mutilated foot)	P50991

CCT5	Chaperonin containing TCP1 subunit 5; a putative ATPase that is involved in tubulin complex assembly and response to stress; gene mutations cause autosomal recessive mutilating sensory neuropathy and spastic paraplegia	P48643
CCT7	Chaperonin containing TCP1 subunit 7 (eta); acts in protein folding; involved in response to stress and chemical stimulus; may play a role in oxidative stress induced neuronal apoptosis	Q99832
CCT8	Protein with high similarity to C. elegans Y55F3AR.3; which acts in reproduction; physiological processes; embryogenesis; and positive growth regulation; member of the tailless complex polypeptide (TCP-1) or chaperonin (cpn60) family	P50990
CD97	CD97 molecule; a chemoattractant receptor that promotes chemotaxis; angiogenesis; T-cell proliferation; and cytokine production; acts in integrin-mediated signaling; upregulated in multiple sclerosis and mouth; thyroid; and colorectal neoplasms	P48960
CDK5	Cyclin dependent kinase 5; a transcription regulator that acts in apoptosis and neuron differentiation; upregulated in brain disease; amyotrophic lateral sclerosis; inclusion body myositis; and nerve degeneration; mRNA is upregulated in lung neoplasms	Q00535
CDKN1B	Cyclin-dependent kinase inhibitor 1B; acts in GPCR pathway and cell cycle arrest; inhibits cell proliferation and induces apoptosis; downregulated in Alzheimer disease; multiple melanoma; and several cancers	P46527
CDKN2A	Cyclin dependent kinase inhibitor 2A; a transcription factor that acts in aging and cell cycle arrest; downregulated in adenocarcinoma and several neoplasms; upregulated in psoriasis and small cell carcinoma; gene mutation causes melanoma	P42771
CFL1	Cofilin 1 non-muscle; binds to actin monomer; plays a role in G protein-coupled receptor protein signaling pathway; in utero embryonic development; actin cytoskeleton organization; and neural tube formation	P23528
CHCHD5	Protein containing a coiled-coil-helix-coiled-coil-helix (CHCH) domain; has strong similarity to uncharacterized mouse Chchd5	Q9BSY4
CHMP1B	Chromatin modifying protein 1B; may play a role in endosome transport; multicellular organismal development; and protein localization; component of the ESCRT III complex	Q7LBR1

CHMP2A	Chromatin modifying protein 2A; plays a role in maintenance of centrosome and spindle organization; regulates chromosome segregation; cell division; and cell death; may play a role in protein targeting to vacuole	O43633
CIB1	Calcium and integrin binding 1; a kinase inhibitor and a transcriptional repressor that acts in integrin-mediated signaling; cell-matrix adhesion; and endothelial cell migration in sprouting angiogenesis; mRNA is upregulated in acute coronary syndrome	Q99828
CKB	Creatine kinase brain; plays a role in phosphorylation and regulation of cell proliferation; aberrant expression correlates with Alzheimer disease; lymphoblastic leukemia-lymphoma disease; and myocardial infarction	P12277
CLASP1	Cytoplasmic linker associated protein 1; a microtubule-associated protein that plays a role in chromosome segregation and organization of the bipolar mitotic spindle; regulates microtubule dynamics at the kinetochore	Q7Z460
CLASP2	Cytoplasmic linker associated protein 2; involved in chromosome segregation; mitotic metaphase plate congression; and spindle organization; inhibits microtubule depolymerization; decreased mRNA expression correlates with non-small-cell lung cancer	O75122
CMPK1	Cytidine monophosphate (UMP-CMP) kinase 1 cytosolic; phosphorylates nucleotide and deoxynucleotide monophosphates and chemotherapeutic deoxycytidine analogs; specificity for CMP versus dCMP is modulated by magnesium and ATP	P30085
CNPY2	Canopy 2 homolog (MIR interacting saposin like protein); a cytoplasmic protein that binds myosin regulatory light chain interacting protein (MYLIP) and promotes neurite outgrowth	Q9Y2B0
COASY	Coenzyme A synthase; a bifunctional enzyme catalyzing the last two steps in biosynthesis of CoA from pantothenate; interacts with p85alphaPI3K (PIK3R1) to regulate the PI3K signaling pathway; upregulated in some tumor cells	Q13057
COG1	Component of oligomeric Golgi complex 1; may play a role in ER to Golgi vesicle and Golgi to plasma membrane vesicle-mediated transport; mutation in the corresponding gene correlates with congenital disorder of glycosylation type II (CDG-II)	Q8WTW3
COG3	Component of oligomeric Golgi complex 3; plays a role in ER to Golgi	Q96JB2

	vesicle-mediated transport	
COG7	Component of oligomeric Golgi complex 7; plays a role in Golgi to plasma membrane transport; decreased expression correlates with inborn errors of metabolism	P83436
COL2A1	Collagen type II alpha 1; binds to integrin; acts in skeletal system development; transforming growth factor beta receptor signaling pathway; and collagen fibril organization; gene mutations cause chondrodysplasia; osteoarthritis; and Stickler syndrome	P02458
COPA	Coatomer protein complex subunit alpha; plays a role in pancreatic juice secretion; may be involved in ER to Golgi vesicle-mediated transport; mRNA expression is increased in hepatocellular carcinoma; gene map position correlates with neural tube defects	P53621
COPB1	Coatomer protein complex subunit beta 1; regulates the transport of CFTR protein from Golgi to plasma membrane and plays a role in establishment of protein localization; may regulate translation	P53618
COPB2	Coatomer protein complex subunit beta 2; may play a role in exocytosis; increased mRNA expression is associated with lung adenocarcinoma	P35606
COPD		P48444
COPG2	Coatomer protein complex subunit gamma 2; a putative transporter that may play a role in vesicle mediated transport; highly expressed in the brain	Q9UBF2
COPS6	COP9 constitutive photomorphogenic homolog subunit 6; a putative translation initiation factor that mediates p53 (TP53) degradation; may play a role in G2-M phase transition of cell cycle	Q7L5N1
COPZ1	Protein with high similarity to F59E10.3 (C. elegans F59E10.3); which is involved in reproduction; larval development; adult life span determination; embryogenesis; and osmoregulation	P61923
COQ5	Protein with high similarity to soybean Glyma08g22890; which is involved in response to fungus; contains a methyltransferase domain	Q5HYK3
COTL1	Coactosin-like 1 protein; binds to F-actin and lipoxygenase; may be involved in leukotriene metabolism; gene polymorphism is associated with rheumatoid arthritis and systemic lupus erythematosus	Q14019

COX17	COX17 cytochrome c oxidase assembly homolog; a putative copper ion transmembrane transporter that positively regulates cell proliferation; acts in aerobic respiration; mRNA expression is upregulated in non-small-cell lung neoplasms	Q14061
CPT2	Carnitine palmitoyltransferase 2; acts in fatty acid beta-oxidation; regulates mitochondrial membrane potential; gene mutations are associated with carnitine o-palmitoyltransferase deficiency; brain diseases; and muscular diseases	P23786
CREG1	Cellular repressor of E1A-stimulated genes 1; a transcription corepressor that regulates ERK and IGF receptor signaling; G0 to G1 transition; G2-M transition of mitosis; and smooth cell proliferation; acts in wound healing	O75629
CRELD2	Cysteine-rich with EGF-like domains 2; putative extracellular protein; member of a family of matricellular cysteine-rich proteins with EGF-like and WE domains; which may be important for interactions with other proteins	Q6UXH1
CRYL1	Crystallin lambda 1; a putative 3-hydroxyacyl-CoA dehydrogenase that may play a role in fatty acid metabolism	Q9Y2S2
CRYZL1	Protein containing an alcohol dehydrogenase GroES-like domain; which has catalytic activity; has weak similarity to human CRYZ; which is a NADPH-quinone reductase that is involved in response to toxin; may play a role in visual perception	O95825
CS	Citrate synthase; catalyzes the conversion of acetyl-CoA and oxaloacetate into citrate and CoA in the tricarboxylic acid cycle; altered enzyme activity correlates with Friedreich Ataxia; Huntington Disease; diabetes mellitus and pancreatic cancer	O75390
CSDA	Cold shock domain protein A; a transcriptional regulator that plays a role in RNA splicing; embryogenesis; antiapoptosis; and VEGF signaling; inhibits endothelial cell proliferation; upregulated in hepatocellular carcinoma	P16989
CSDE1	Cold shock domain containing E1 RNA-binding; a regulator of cell death that plays a role in nuclear-transcribed mRNA catabolic process deadenylation-dependent decay	O75534
CSN2	Casein beta; a cysteine-type endopeptidase inhibitor that may play a role in calcium ion transport and in defense response to bacteria and virus	P61201
CSN3	Casein kappa; a major constituent of milk casein content that plays a role in	Q9UNS2

	prevention of Helicobacter pylori adhesion to the gastric mucosa	
CSNK1D	Casein kinase 1 delta; plays a role in the regulation of protein complex assembly; and peptidyl-serine and threonine phosphorylation; mRNA is upregulated in Alzheimer disease	P48730
CSTF2	Cleavage stimulation factor 3' pre-RNA subunit 2; binds to RNA; acts in mRNA cleavage; polyadenylation; and processing	P33240
CTBS	Chitobiase di-N-acetyl; a chitinase that hydrolyzes 1; 4-beta-linkages in chitin and chitodextrins; involved in N-glycan processing	Q01459
CTNNB1	Catenin beta 1; a transcriptional activator that plays a role in antiapoptosis and cell differentiation; regulates G2-M transition of mitotic cell cycle and positive selection of thymocytes; aberrant expression is associated with several neoplasms	P35222
CTNND1	Catenin delta 1; a small GTPase activator that activates NF-kappaB; plays a role in focal adhesion assembly; cell cycle; cell proliferation; vasculogenesis; and inflammatory response; downregulated in lung; colon; and several other cancers	O60716
CTPS	CTP synthase; acts in Cytidine 5'-triphosphate biosynthetic process and nucleic acid and xenobiotic metabolism; phosphorylated and activated by GSK3 and protein kinase C	P17812
CTR9	Paf1-RNA polymerase II complex component homolog; a component of the Cdc73-Paf1 complex that binds CDC73; acts in transcription of IL6 responsive genes via regulating DNA association of STAT3 and modification of histone methylation	Q6PD62
CUL1	Cullin 1; a protein transmembrane transporter that plays a role in cell proliferation; embryonic development; endomitotic cell cycle; and cyclin catabolism; stimulates protein ubiquitination; may act in placenta development; upregulated in gastric cancer	Q13616
CUL3	Cullin 3; an ubiquitin-protein ligase that acts in organ growth; mitotic cell cycle; embryonic pattern specification; and in utero embryonic development; may play a role in cell proliferation and induction of apoptosis by intracellular signals	Q13618
CUX1	Cut-like homeobox 1; a transcription regulator that regulates cell cycle; immune response; macrophage and monocyte differentiation; lung development; epithelial cell differentiation; and post-embryonic morphogenesis	P39880, Q13948
CXorf26	Member of the DUF757 domain of unknown function family; has strong similarity	Q9BVG4

	to uncharacterized mouse 2610029G23Rik	
CYB5A	Cytochrome b5 type A; a hydroxylamine reductase that plays a role in hydrogen peroxide biosynthetic process and regulation of metabolic process; gene mutation is associated with congenital methemoglobinemia and pseudohermaphrodism	P00167
CYCS	Somatic cytochrome c; an electron carrier that plays a role in activation of caspase activity by cytochrome c; aerobic respiration; and induction of apoptosis; may act in generation of precursor metabolites and energy	P99999
DBI	Diazepam binding inhibitor; regulates cholesterol biosynthesis and fatty acid metabolism; aberrant expression correlates with astrocytoma; Alzheimer disease; and schizophrenia; upregulated in brain neoplasms; mouse DBI correlates with hyperplasia	P07108
DBT	Dihydrolipoamide branched chain transacylase E2; plays a role in the oxidative decarboxylation of the branched chain alpha keto acids derived from leucine; isoleucine; and valine; gene mutations cause maple syrup urine disease	P11182
DCAF11	Protein with moderate similarity to A. thaliana AT4G03020; which is involved in response to mannitol stimulus	Q8TEB1
DDX28	DEADH (Asp-Glu-Ala-AspHis) box polypeptide 28; an RNA-dependent ATPase and putative RNA helicase that may play a role in RNA processing or communication between the nucleus and mitochondria	Q9NUL7
DDX3X	DEAD box polypeptide 3 X-linked; an ATP-dependent RNA helicase that inhibits viral replication; acts in RNA export from nucleus; G1 to S checkpoint; and IFN-beta secretion; mRNA is downregulated in hepatoma and cutaneous squamous cell carcinoma	O00571
DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 Y-linked; plays a role in spermatogenesis; may be involved in spermatogonial cell division; decreased mRNA expression is associated with Sertoli cell-only syndrome and hypospermatogenesis	O15523
DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6; an ATP-dependent RNA helicase that plays a role in embryonic development; oogenesis; and spermatogenesis; upregulated in several neoplasms	P26196
DECR1	2-4-dienoyl CoA reductase 1 mitochondrial; a NADP binding protein; plays a role in fatty acid beta-oxidation and protein homotetramerization; protein expression is	Q16698

	downregulated in primary breast cancer	
DENND4C	DENNMADD domain containing 4C; plays a likely role in insulin-stimulated translocation of the GLUT4 glucose transporter to the cell surface in fat cells; gene mutation and translocation correlates with multiple myeloma	Q5VZ89
DHODH	Dihydroorotate dehydrogenase; a putative electron carrier that is involved in denovo pyrimidine base biosynthesis; oxidation-reduction process; and immunity; regulates apoptosis; may act in spermatogenesis; gene mutation is associated with Miller syndrome	Q02127
DHPS	Deoxyhypusine synthase; an homospermidine synthase that is involved in peptidyl-lysine modification to hypusine and spermidine catabolism; regulates neuronal outgrowth and its survival; induces cell proliferation	P49366
DHRS4	Dehydrogenase-reductase member 4; a 3-beta-hydroxysteroid dehydrogenase that is involved in xenobiotic metabolism and response to hormone stimulus	Q9BTZ2
DHX16	DEAH (Asp-Glu-Ala-His) box polypeptide 16; an ATP-dependent RNA helicase that binds GU at 5' splice site; may participate in the catalytic core of the spliceosome	O60231
DHX36	DEAH box polypeptide 36; binds to and resolves both DNA and RNA tetramolecular quadruplex structures; interacts with exosome components and AU binding proteins; may regulate both synthesis and degradation of mRNA in different subcellular compartments	Q9H2U1
DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40; a putative ATP-dependent RNA helicase; predicted to be involved in pre-mRNA splicing; ribosome biogenesis; and RNA processing; ubiquitously expressed	Q8IX18
DHX9	DEAH box polypeptide 9; an ATP-dependent 3'-5' DNA-RNA helicase and a transcription coactivator that is involved in EGFR signaling and retroviral mRNA nuclear export; autoantibodies are associated with systemic lupus erythematosus	Q08211
DIABLO	Diablo IAP-binding mitochondrial protein; activates caspase activity by release of cytochrome c; inhibits cell proliferation; may play a role in ovulation cycle; aberrantly expressed in ovarian; thyroid; and several other cancers	Q9NR28
DIS3	DIS3 mitotic control; a putative exoribonuclease and Ran guanyl-nucleotide exchange factor that binds Ran GTPase; may mediate rRNA processing	Q9Y2L1

DLAT	Dihydrolipoamide S-acetyltransferase; catalyzes the conversion of pyruvate to acetyl-CoA; acts as an autoantigen in biliary liver cirrhosis; gene mutation correlates with pyruvate dehydrogenase complex deficiency disease	P10515
DLD	Dihydrolipoamide dehydrogenase; an oxidoreductase that acts in energy derivation by oxidation of organic compounds and protein thiol-disulfide exchange; acts as an autoantigen in myocarditis; downregulated in acidosis; Alzheimer disease; and leigh disease	P09622
DLST	Dihydrolipoamide S-succinyltransferase; a mitochondrial alpha-ketoglutarate dehydrogenase complex component that acts in regulation of cell proliferation and response to toxin; decreased activity correlates with Alzheimer disease and Korsakoff syndrome	P36957
DNAJA1	DnaJ homolog subfamily A member 1; an ATPase activator and Hsp40 type 1 chaperones that acts in protein folding; protein complex assembly; androgen receptor signaling; and apoptosis; mouse Dnaja1 is downregulated in mouse model of Huntington disease	P31689
DNAJC7	DnaJ (Hsp40) homolog subfamily C member 7; a ligand-dependent nuclear receptor transcription coactivator that is involved in protein folding and cytoplasmic retention of transcription factor	Q99615
DNPEP	Aspartyl aminopeptidase; a putative metallopeptidase that plays a role in proteolysis and regulation of renal vasoactive peptide levels	Q9ULA0
DOCK7	Dedicator of cytokinesis 7; a Rac GTPase activator; binds the complex containing tuberous sclerosis complex 1 (TSC1) and 2 (TSC2); plays a role in axon formation and stathmin phosphorylation; regulates neuronal polarity	Q96N67
DSC3	Desmocollin 3; plays a role in cell-cell adhesion; ectodermal gut development; and epidermis development; downregulated in breast cancer; autoantigen is associated with pemphigus vulgaris	Q14574
DTWD2	Protein containing a DTW domain; has strong similarity to uncharacterized mouse Dtwd2	Q8NBA8
DYNLL2	Dynein light chain LC8-type 2; a myosin binding protein that plays a role in assembly of the coiled coil domains of myosin; may be involved in retrograde and anterograde axon cargo transport	Q96FJ2

DYNLRB1	Dynein light chain roadblock-type 1; interacts with dynein intermediate chain; acts in TGF-beta receptor signaling; folic acid transport; and inhibition of cell proliferation; mRNA expression is upregulated in hepatocellular carcinomas	Q9NP97
EEA1	Early endosome antigen 1; a putative effector of phosphatidylinositol-3-phosphate that plays a role in endosome organization and biogenesis; autoantigens are associated with subacute cutaneous systemic lupus erythematosus	Q15075
EEF2	Eukaryotic translation elongation factor 2; binds to ribonucleoprotein; acts in translation and G protein-coupled receptor protein signaling pathway; upregulated in ovarian neoplasms; increased phosphorylation correlates with Alzheimer disease	P13639
EFHD2	EF-hand domain family member D2; may play a role in calcium-mediated signaling and regulation of T cell mediated cytotoxicity	Q96C19
EHD1	EH-domain containing 1; binds to IGFR and mediates its endocytosis; acts in focal adhesion disassembly; cholesterol homeostasis; spermatogenesis; and male fertility; gene map position correlates with Bardet-Biedl syndrome	Q9H4M9
EIF2B5	Eukaryotic translation initiation factor 2B subunit 5; a guanyl-nucleotide exchange factor that plays a role in actin filament organization and translational initiation; gene mutations are associated with leukoencephalopathy and leukodystrophy	Q13144
EIF2S1	Eukaryotic translation initiation factor 2 subunit 1 alpha; mediates glucose homeostasis and apoptosis; upregulated in thyroid neoplasms and bronchiolo-alveolar adenocarcinoma; hyperphosphorylated in Alzheimer disease and Epstein-Barr virus infections	P05198
EIF2S2	Eukaryotic translation initiation factor 2 subunit 2 beta; involved in translational initiation and embryonic development; regulates cell proliferation and cell differentiation	P20042
EIF2S3	Eukaryotic translation initiation factor 2 subunit 3 gamma 52kDa; a putative translation factor; interacts with p67 (METAP2); inhibits eIF2alpha (EIF2S1) phosphorylation; regulates immune response and translational initiation	P41091
EIF3A	Eukaryotic translation initiation factor 3 subunit A; a putative translation initiation factor that inhibits epithelial cell differentiation; may maintain cell polarity and organismal growth; upregulated in colorectal; lung; and gastric cancers	Q14152
EIF3C	Eukaryotic translation initiation factor 3 subunit C; a cytosolic small ribosomal subunit that binds and recruits EIF1 to 40S ribosomes; negatively regulates cell	Q99613

	proliferation; mRNA is aberrantly expressed in systemic lupus erythematosus	
EIF3CL	Vacuolar basic amino acid transporter 2; mediates basic amino acid import into the vacuole in response to nutrient depravation	Q99613
EIF3D	Eukaryotic translation initiation factor 3 subunit D; may play a role in regulation of translational initiation	O15371
EIF3F	Eukaryotic translation initiation factor 3 subunit F; mediates muscle atrophy and translation initiation; acts in kinase-dependent mTOR signaling; mRNA processing; and protein transport; mRNA is downregulated in melanoma; pancreatic and other cancers	O00303
EIF3G	Eukaryotic translation initiation factor 3 subunit G; binds to mRNA and regulates the initiation of translation process	O75821
EIF3H	Eukaryotic translation initiation factor 3 subunit 3; plays a role in the regulation of translation and cell proliferation; mRNA expression is upregulated in prostatic and breast neoplasms; gene mutation correlates with Langer-Giedion Syndrome	O15372
EIF3I	Eukaryotic translation initiation factor-3 subunit-I; a transcription corepressor that acts in regulation of TGF-beta receptor signaling pathway; cell cycle; and cell proliferation	Q13347
EIF3K	Eukaryotic translation initiation factor 3 subunit k; a dynein intermediate chain binding protein that positively regulates apoptosis in epithelial cells by releasing caspase 3 from keratin-containing inclusions	Q9UBQ5
EIF4E2	Eukaryotic translation initiation factor 4E family member 2; binds to RNA; plays a role in the regulation of translation; may be involved in utero embryonic development	O60573
EIF4EBP3	Eukaryotic translation initiation factor 4E binding protein 3; a translation initiation factor that binds and represses eukaryotic translation initiation factor 4E (EIF4E) dependent translation	Q9HD15
EIF4G1	Eukaryotic translation initiation factor 4 gamma 1; acts in apoptosis and regulation of cell proliferation and autophagy; upregulated in squamous cell carcinoma; acts as a autoantigen in rheumatoid arthritis	Q04637
EIF4G2	Eukaryotic translation initiation factor 4 gamma 2; regulates cell cycle; cell proliferation; cell differentiation; and apoptosis; plays a role in gastrulation	P78344

EIF4G3	Eukaryotic translation initiation factor 4 gamma 3; part of eIF4F translation initiation complex; binds poly(A)-binding protein (PABPC1); may function in poly(A)-dependent translation; cleavage by viral proteins causes host protein shutoff and apoptosis	O43432
EIF4H	Eukaryotic translation initiation factor 4H; plays a role in mRNA catabolism and regulation of translational initiation; upregulated in colorectal neoplasms; gene mutation is associated with Williams syndrome	Q15056
EIF5B	Eukaryotic translation initiation factor 5B; a ribosome binding GTPase that plays a role in ribosomal subunit assembly; translation; and translational initiation	O60841
ELMO3	Protein with high similarity to human ELMO1; which is a translation regulator that acts in Rac protein signal transduction; actin filament organization; and regulation of catalytic activity; member of the DUF3361 domain of unknown function family	Q96BJ8
EMD	Emerin; a transcription regulator that acts in muscle development; cell cycle; and nuclear envelope reassemble; gene mutations are associated with dilated cardiomyopathy and Emery-Dreifuss muscular dystrophy	P50402
ENDOG	Endonuclease G; mediates class switch DNA recombination; acts in embryonic development and endonucleolytic DNA catabolism during apoptosis; may play a role in mitochondrial genome maintenance and cell proliferation	Q14249
ENO1	Enolase 1 alpha; a transcriptional repressor that is involved in inflammatory response; lipid metabolic process; and regulation of cell proliferation; aberrant expression correlates with Alzheimer disease; astrocytoma; meningioma; and glioblastoma	P06733
ENOPH1	Enolase-phosphatase 1; functions in the methionine salvage pathway to catalyze reactions of 2; 3-diketo-5-methylthio-1-phosphopentane to yield the acid-reductone metabolite	Q9UHY7
EPHX2	Epoxide hydrolase 2 cytoplasmic; a phosphoric ester hydrolase that acts in isoprenoid catabolsm and regulation of cholesterol level and blood pressure; gene polymorphisms are associated with cardiovascular diseases; type II diabetes; and leukemia	P34913
EPN2	Epsin 2; a putative SH2 SH3 adaptor that may play a role in endocytosis	O95208
ERGIC1	Endoplasmic reticulum-Golgi intermediate compartment 32 kDa protein; an ER-Golgi intermediate compartment protein; interacts with hErv46 (SDBCAG84)	Q969X5

	to stabilize an hErv46 (SDBCAG84) - hErv41 (PTX1) complex; may play a role in ER-to-Golgi transport	
ERO1LB	Endoplasmic reticulum oxidoreductin 1-L beta; a member of the endoplasmic reticulum oxidoreductin family; induced during the unfolded protein response; oxidizes protein disulfide isomerase (PDIP) promoting disulfide bond formation	Q86YB8
ETF1	Eukaryotic translation termination factor 1; binds to translation release factors; plays a role in selenocysteine incorporation; may be in involved in in utero embryonic development	P62495
ETFA	Electron-transfer-flavoprotein-alpha polypeptide; may act in fatty acid beta-oxidation and generation of precursor metabolites and energy; gene mutations are associated with type-II glutaric aciduria and inborn errors of amino acid and lipid metabolism	P13804
ETFB	Electron transfer flavoprotein beta polypeptide; transfers electrons from mitochondria; decreased activity causes inborn errors of metabolism; gene mutations are associated with glutaric acidemia and multiple acyl CoA dehydrogenase deficiency	P38117
ETFDH	Electron transferring flavoprotein (ETF) dehydrogenase; catalyzes the transfer of electrons from ETF to ubiquinone by ETF oxidoreductase; gene mutations are associated with glutaric acidemia type 2 and coenzyme Q10 deficiency	Q16134
ETHE1	Ethylmalonic encephalopathy 1; a transcriptional suppressor that interacts with histone deacetylase; acts in antiapoptosis; TP53 ubiquitylation and degradation; gene mutation causes ethylmalonic encephalopathy	O95571
EVI5L	Ecotropic viral integration site 5-like; exhibits RAB10 binding activity; and RAB2 and RAB10 GTPase activating protein activity	Q96CN4
EVPL	Envoplakin; a structural molecule that acts in protein hetero-oligomerization; may be involve in epidermis development and regulation of cell shape; autoantibodies are associated with paraneoplastic pemphigus	Q92817
EXOC4	Exocyst complex component 4; plays a role in exocytosis; gene translocation correlates with developmental disabilities	Q96A65
FAAH	Fatty acid amide hydrolase; regulates endocannabinoid signaling; serotonin secretion; and lipid biosynthesis; acts in antigen transport; immunity; and memory; aberrantly expressed in prostate cancer and Huntington and Alzheimer diseases	O00519

FAF1	Fas associated factor 1; induces apoptosis by inhibiting IKK complex formation and NF-kappaB cascade; acts in JUN kinase activation; glucocorticoid and steroid hormone receptor signaling; aberrantly expressed in Parkinson disease and gastric carcinoma	Q9UNN5
FAH	Fumarylacetoacetate hydrolase; catalyzes the cleavage of a carbon-carbon bond in fumarylacetoacetate forming fumarate and acetoacetate; involved in tyrosine catabolism; gene mutations are associated with Type 1 hereditary tyrosinemia	P16930
FAM160A2	Member of the retinoic acid induced 16-like protein family; has strong similarity to uncharacterized rat Fam160a2	Q8N612
FARSA	Phenylalanyl-tRNA synthetase alpha subunit; a phenylalanine-tRNA ligase that acts in phenylalanyl-tRNA aminoacylation	Q9Y285
FARSB	Phenylalanyl-tRNA synthetase beta-subunit; a regulatory subunit that heterodimerizes with the catalytic alpha subunit (FARSL); plays a role in phenylalanyl-tRNA aminoacylation and tumorigenic processes; expression is upregulated in various carcinomas	Q9NSD9
FASTKD2	FAST kinase domains 2; a mitochondrial inner compartment protein that plays a role in mitochondrial apoptosis; gene nonsense mutation causes infantile mitochondrial encephalomyopathy associated with cytochrome C oxidase deficiency	Q9NYY8
FDFT1	Farnesyl-diphosphate farnesyltransferase 1; acts in cholesterol biosynthesis and nervous system development; decreased activity correlates with sitosterolemia; mRNA is upregulated in esophageal adenocarcinomas; rat Fdft1 is associated with cataract	P37268
FKBP1A	FK506-binding protein 1A; a cis-trans isomerase that modulates the Ca2+-release activity of ryanodine receptors; expression is increased in the brain during HIV encephalitis; mouse Fkbp1a deficiency causes cardiomyopathy and ventricular septal defects	P62942
FKBP3	FK506 binding protein 3 25kDa; rapamycin-selective DNA-binding nuclear immunophilin with peptidylprolyl cis-trans-isomerase activity; forms complex with histone deacetylases HDAC1 and HDAC2; interacts with transcription regulator YY1; and casein kinase II	Q00688

FKBP8	FK506 binding protein 8; a protein phosphatase inhibitor that acts in protein folding and retinal pigment epithelium and neural tube development; regulates protein stability; hedgehog signaling; and apoptosis; mouse Fkbp8 is associated with microphthalmia	Q14318
FKBP9	FK506 binding protein 9; putative peptidyl prolyl isomerase and FK506 binding protein; contains a hydrophobic signal peptide and an endoplasmic reticulum retention motif	O95302
FUBP3	Far upstream element (FUSE) binding protein 3; a RNA polymerase II transcription factor that plays a role in regulation of gene expression; aberrantly expressed in prostate; renal; and urothelial cancers	Q96I24
G3BP2	GTPase activating protein SH3 domain binding protein 2; regulates p53 ubiquitylation and its activity; involved in transmembrane receptor protein tyrosine kinase signaling pathway; decreased mRNA expression correlates with 5q syndrome	Q9UN86
GALK1	Galactokinase 1; plays a role in galactose metabolism and visual perception; gene mutations correlate with galactosemia and autosomal recessive congenital cataract	P51570
GBAS	Glioblastoma amplified sequence; plays a role in oxidative phosphorylation; gene amplification is observed in some tumors that also exhibit amplification of the EGF receptor (EGFR) gene	O75323
GBE1	Glucan branching enzyme 1; plays a role in glycogen metabolism; gene mutation causes glycogen storage disease type IV and late onset form of nervous system diseases	Q04446
GCAT	Glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase); a putative transaminase that inhibits cell proliferation; may play a role in glycine and threonine metabolism	O75600
GCC2	GRIP and coiled-coil domain containing 2; a putative DNA binding protein that mediates protein targeting to Golgi and regulation of receptor recycling and transcription; antigen associated with chronic lymphocytic leukemia and cutaneous T-cell lymphoma	Q8IWJ2
GCDH	Glutaryl-CoA dehydrogenase; a mitochondrial enzyme that is involved in lysine and glutaryl-CoA catabolism; may act in neurotransmission; deficiency is associated with ketosis and glutaric aciduria; gene mutations correlate with nervous	Q92947

	system diseases	
GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1; associates with the histone kinase CDK8 subcomplex to perhaps regulate its cellular function	Q92616
GDI2	GDP dissociation inhibitor 2; involved in intracellular protein transport and localization; may play a role in vesicle-mediated transport; upregulated in pancreatic neoplasms	P50395
GEMIN4	Gem associated protein 4; a component of survival of motor neurons complex that plays a role in RNA splicing; may be involved in rRNA processing and spliceosome assembly; gene polymorphism is associated with bladder cancer and renal cell carcinoma	P57678
GFM1	G-elongation factor mitochondrial 1; a putative GTPase and translation elongation factor that acts in oxidative phosphorylation and mitochondrial translation; gene mutations correlate with encephalopathy; lactic acidosis; and early-onset Leigh syndrome	Q96RP9
GIPC1	GIPC PDZ domain containing family member 1; acts in maintenance of protein location; arteriogenesis; melanogenesis; and endosome transport; regulates cell adhesion; cell cycle; and apoptosis; upregulated in gastric and pancreatic ductal carcinoma	O14908
GLB1	Galactosidase beta 1; a lysosomal enzyme that hydrolyzes the terminal beta-galactose from ganglioside; acts in elastic fiber assembly and CNS development; gene mutations correlate with gangliosidoses; mucopolysaccharidosis; and Morquio-B syndrome	P16278
GLO1	Glyoxalase I; a lactoylglutathione lyase that plays a role in methylglyoxal metabolism; behavior; apoptosis; and cytolysis; upregulated in Alzheimer disease; diabetes; and colon and other cancers; gene polymorphism correlates with panic disorder	Q04760
GLRX5	Glutaredoxin 5; a putative protein disulfide oxidoreductase that acts in iron-sulfur cluster assembly and iron homeostasis; regulates erythropoiesis and heme biosynthesis; gene mutations correlate with iron overload associated with sideroblastic anemia	Q86SX6
GLS	Glutaminase; plays a role in glutamine metabolic process and synthesis of	O94925

	excitatory and inhibitory neurotransmitters; expressed in kidney; heart; and brain	
GLUL	Glutamate-ammonia ligase; catalyzes the synthesis of glutamine; plays a role in respiratory gaseous exchange; aberrant expression correlates with Alzheimer disease; hepatocellular carcinoma; multiple sclerosis; brain ischemia; and temporal lobe epilepsy	P15104
GMDS	GDP-mannose 4 6-dehydratase; plays a role in GDP-L-fucose biosynthetic process and immune response; activity is defective in leukocyte adhesion deficiency type II	O60547
GNAS	GNAS complex locus; a GTPase that induces adenylyl cyclase; acts in GPCR signaling and cell differentiation; upregulated in bipolar disorder; gene mutations correlate with hypertension; pseudohypoparathyroidism; Cushing syndrome; and many other neoplasms	Q5JWF2
GNB2L1	Guanine nucleotide binding protein beta polypeptide 2-like 1; a protein kinase activator that acts in antiapoptosis and cell cycle; mediates receptor signaling; downregulated in Alzheimer disease; mRNA expression is upregulated in hepatocellular carcinoma	P63244
GNL2	Guanine nucleotide binding protein-like 2; may exhibit GTPase activity	Q13823
GNL3	Guanine nucleotide binding protein-like 3; acts in G1-S checkpoint and cell cycle arrest; regulates telomerase activity and apoptosis; mRNA is upregulated in lung and esophageal cancers; gene polymorphisms correlate with bipolar disorder	Q9BVP2
GOLGA1	Golgi autoantigen golgin subfamily a 1; a Rab GTPase binding protein that mediates endosome to Golgi retrograde transport; involved in response to virus; may play a role in Golgi vesicle docking; autoantigen is associated with Sjogren syndrome	Q92805
GOLGA3	Golgi autoantigen golgin subfamily a 3; binds to GCP60; regulates apoptosis; may play a role in Golgi organization and biogenesis	Q08378
GOT2	Aspartate aminotransferase 2; an aspartate transaminase that plays a role in long-chain fatty acid transport; localizes to microvillus and sarcolemma; upregulation is associated with metastatic colorectal cancer	P00505
GPHN	Gephyrin; plays a role in regulation of glycine receptor diffusion; acts in molybdenum cofactor biosynthesis; nervous system development; and embryonic development; gene mutations correlate with hyperekplexia and acute monocytic leukemia	Q9NQX3

GRHPR	Glyoxylate reductase-hydroxypyruvate reductase; a glycerate dehydrogenase and electron carrier that mediates excretion and glyoxylate and pyruvate metabolism; gene mutation is associated with primary hyperoxaluria type II	Q9UBQ7
GRSF1	G-rich RNA sequence binding factor 1; a translation activator; binds to 5'-UTR of mRNA; may play a role in mRNA polyadenylation; associated with influenza viral infection	Q12849
GSK3A	Glycogen synthase kinase 3 alpha; a transcription activator that acts in protein amino acid phosphorylation; signal transduction; and keratinocyte migration; aberrant expression is associated with hepatocellular carcinoma and schizophrenic disorder	P49840
GSPT1	G1 to S phase transition 1; a translation release factor that positively regulates apoptosis and TOR signaling pathway; acts in protein ubiquitination and cell morphogenesis; increased mRNA expression is associated with stomach neoplasms	P15170
GSR	Glutathione reductase; a electron carrier that reduces glutathione disulfide; upregulated in Alzheimer disease; squamous cell carcinoma; and cervix neoplasms; gene overexpression correlates with lung neoplasms	P00390
H6PD	Hexose-6-phosphate dehydrogenase; a 6-phosphogluconolactonase that acts in pentose-phosphate pathway; lipid storage and transport; and skeletal muscle development; gene mutation correlates with polycystic ovary syndrome	O95479
HADH	Hydroxyacyl-Coenzyme A dehydrogenase; acts in fatty acid and glutamate metabolism; inhibits insulin secretion; decreased activity correlates with inborn errors of metabolism; gene mutations are associated with reye-like syndrome and hypoglycemia	Q16836
HAX1	HCLS1 associated protein X-1; interacts with vimentin; plays a role central nervous system maturation and myeloid cell differentiation; upregulated in lesional psoriasis; gene mutation causes autosomal recessive form of severe congenital neutropenia	O00165
HBS1L	HBS1-like; a GTPase that plays a role in protein complex assembly; may act in signal transduction and regulation of translational termination	Q9Y450
HDAC6	Histone deacetylase 6; deacetylates histones and thereby inhibits transcription; acts in cell proliferation; immunity; and redox homeostasis; upregulated in breast cancer and Alzheimer disease; gene mutation correlates with X-linked	Q9UBN7

	chondrodysplasia	
HDLBP	High density lipoprotein binding protein; a component of the ribonucleoprotein complex that is involved in tRNA export from nucleus and negatively regulates mRNA cleavage; may be involved in cholesterol metabolism	Q00341
HEATR2	Protein containing eight HEAT repeats; has high similarity to uncharacterized mouse Heatr2	Q86Y56
HEBP2	Heme binding protein 2; a putative heme-binding protein that localizes to extracellular space; may be involved in pregnancy and heme metabolism	Q9Y5Z4
HEXA	Hexosaminidase A (alpha polypeptide); a hydrolase that plays a role in ganglioside catabolic process; upregulated in myeloid leukemia; gene mutations causes gangliosidoses; muscular atrophy; and Tay-Sachs disease	P06865
HLCS	HLCS holocarboxylase synthetase; a biotin-protein ligase that catalyzes the biotinylation of histones; gene mutations are associated with holocarboxylase synthetase deficiency and inborn errors of biotin metabolism	P50747
HSP90AA1	Heat shock 90kDa protein 1 alpha; a chaperonin ATPase that acts in protein folding; cell migration; apoptosis; and sperm capacitation; aberrantly expressed in several neoplasms	P07900
HSPA1A	Heat shock 70 kDa protein 1A; acts in cytochrome c release from mitochondria and immunity; upregulated in osteosarcoma; cryptorchidism; myxedema; and diabetes; gene polymorphisms correlate with agranulocytosis; Celiac disease; spondylitis; and arthritis	P08107
HSPA1B	Heat shock 70kDa protein-1B; inhibits cytochrome-c release and caspase activity; acts in spermatogenesis; downregulated in male infertility; gene polymorphism correlates with breast cancer; celiac disease; non-Hodgkin lymphoma; and ankylosing spondylitis	P08107
HSPA4L	Heat shock 70kDa protein 4-like; a cytosolic protein that plays a role in heat shock response and may be involved in spermatogenesis	O95757
HSPA8	Heat shock 70kDa protein 8; a transcriptional cofactor that acts in protein folding and regulation of cell migration and differentiation; involved in response to oxidative stress and unfolded protein; upregulated in adenocarcinoma and Alzheimer disease	P11142

HSPD1	Heat shock 60kDa protein 1; a transcription activator; involved in immune response; acts as an autoantigen in abortion; arthritis; Alzheimer disease; cardiovascular diseases; diabetes; mouth diseases; multiple sclerosis; and nervous system diseases	P10809
HUWE1	HECT UBA and WWE domain containing 1; a ubiquitin-protein ligase that acts in protein destabilization; regulates transcription; upregulated in colorectal neoplasms; gene duplication causes mental retardation; mRNA is aberrantly expressed in breast cancer	Q7Z6Z7
IARS2	Member of the tRNA synthetases class I (M) family; contains an anticodon-binding domain; which binds to tRNA anticodon; has moderate similarity to A. thaliana OVA2; which plays a role in ovule development and hyperosmotic salinity response	Q9NSE4
IDH3B	Isocitrate dehydrogenase 3 beta; a putative regulatory subunit of mitochondrial isocitrate dehydrogenase that may regulate carbohydrate metabolic process	O43837
IGHMBP2	Immunoglobulin mu binding protein 2; an ATP-dependent 3'-5' DNA-RNA helicase that inhibits transcription; plays a role in immune response and muscle cell homeostasis; may acts in DNA repair; gene mutation correlates with childhood spinal muscular atrophy	P38935
ILK	Integrin-linked kinase; a serine-threonine kinase that regulates integrin-mediated signaling; apoptosis; cell cycle; ureteric bud morphogenesis; and bone formation; aberrantly expressed in prostate; colon; glioblastoma; and several other cancers	Q13418
IMMT	Inner membrane protein mitochondrial; plays a role in cristae formation; exists as a complex with SAM50; MTX1; MTX2; CHCHD6; CHCHD3 and DNAJC11; protein expression is downregulated in fetal down syndrome	Q16891
INTS6	Integrator complex subunit 6; a putative RNA helicase; suppresses tumor cell growth; downregulated in non small cell lung carcinomas; and is a candidate tumor suppressor for such carcinomas	Q9UL03
IPO13	Importin 13; involved in proteins nuclear import and export; acts in meiotic prophase I; may play a role in lung development and small GTPase mediated signal transduction	O94829
IPO4	Importin 4; binds CCAAT/enhancer binding protein delta (CEBPD) to function in FANCD2 nuclear import in the Fanconi anemia pathway of DNA repair	Q8TEX9

IPO5	Importin 5; a GTPase inhibitor that plays a role in ribosomal protein import into nucleus and symbiosis; may act in spermatogenesis; gene polymorphism is associated with schizophrenia	O00410
IPO8	Importin 8; a GTPase binding protein that plays a role in nuclear import of proteins	O15397
IPO9	Importin 9; a protein transporter that is involved in protein refolding and ribosome biogenesis	Q96P70
IVD	Isovaleryl Coenzyme A dehydrogenase; catalyzes the conversion of isovaleryl CoA to 3-methylcrotonyl CoA and plays a role in leucine metabolism; gene mutation causes isovaleric acidemia	P26440
KDM3B	Lysine specific demethylase 3B; a predicted nuclear protein that negatively regulates cell proliferation; upregulated in colorectal adenocarcinoma; gene mutation may be associated with acute myelocytic leukemia	Q7LBC6
KIAA0174	KIAA0174 (increased sodium tolerance-1); acts with CHMP1A to recruit and modulate specific VPS4A activities required during the final stages of cell division; may function in cytokinesis via interaction with spartin (SPG20)	P53990
KIF13B	Kinesin family member 13B; a microtubule motor protein that plays a role in regulation of myelination	Q9NQT8
KIF1C	Kinesin family member 1C; an ATPase and microtubule motor protein that regulates podosome dynamics; acts in Golgi to ER retrograde transport and cell migration; may play role in body fluid secretion	O43896
KIF2A	Kinesin heavy chain member 2A; a microtubule motor protein that acts in mitotic centrosome separation; chromosome organization; neuron migration; and axonogenesis; promotes microtubule depolymerization; gene polymorphism correlates with schizophrenia	O00139
KIF4A	Kinesin family member 4A; a microtubule-binding motor protein that acts in anterograde axon cargo transport; cytokinesis; metaphase plate congression; and spindle midzone assembly involved in mitosis; mRNA expression is upregulated in cervical cancer	O95239
KPNA6	Karyopherin alpha 6; plays a role in NLS-bearing substrate import into nucleus; may act in organ morphogenesis	O60684
KRT2	Keratin 2; a cytoskeletal protein that may play a role in epidermis development; mutations in the corresponding gene cause ichthyosis bullosa of Siemens	P35908

LAD1	Ladinin 1; a structural molecule that may play a role in cytoskeletal anchoring; acts as an autoantigen in linear IgA disease; expression is reduced in epidermolysis bullosa; presence of autoimmune antibody correlates with vesiculobullous	O00515
LAMB2	Laminin beta 2; a basement membrane protein that interacts with other laminin proteins; mediates cell-matrix adhesion and cell migration; decreased expression is associated with Walker Warburg Syndrome; gene mutation causes congenital nephrotic syndrome	P55268
LAP3	Protein containing a cytosol aminopeptidase family catalytic domain; has moderate similarity to S. pombe Spac13a11.05p; which is an aminopeptidase	P28838
LARP4	La ribonucleoprotein domain family member 4; binds poly(A) binding protein (PABPC1) and RACK1 (GNB2L1); binds poly(A) mRNA; positively regulates mRNA stability and translation	Q71RC2
LARS2	Mitochondrial leucyl-tRNA synthetase 2; a ligase that is involved in leucyl-tRNA aminoacylation; polymorphism in the corresponding gene is associated with higher risk for the development of type 2 diabetes	Q15031
LBR	Lamin B receptor; a delta14-sterol reductase that regulates granulocyte maturation and myelination; gene mutation causes Pelger-Huet anomaly and Greenberg skeletal dysplasia; mouse Lbr is associated with ichthyosis and hyperkeratinosis	Q14739
LLGL2	Lethal giant larvae homolog 2; binds LGN (GPSM2) during mitosis to regulate mitotic spindle organization; may act in cellular events associated with epithelial mesenchymal transition and metastasis; mRNA level is reduced in colorectal and breast cancers	Q6P1M3
LMAN1	Lectin mannose-binding 1; binds to calcium ion and monosaccharides; acts in ER to Golgi vesicle-mediated transport and blood coagulation; gene mutation causes hemophilia-A and factor-5 deficiency	P49257
LMNA	Lamin A-C; acts in nuclear envelope organization; myoblast differentiation; and axonogenesis; gene mutations are associated with progeria; Emery-Dreifuss muscular dystrophy; lipodystrophy; dilated cardiomyopathy; Werner syndrome; and diabetic nephropathy	P02545
LMNB2	Lamin B2; may regulate transcription; gene mutation correlates with lipoatrophic diabetes mellitus; increased level of autoantibodies correlates with rheumatoid arthritis; systemic lupus erythematosus; and chronic hepatitis	Q03252

LPHN1	Latrophilin 1; a latrotoxin receptor that plays a role in G protein-coupled receptor protein signaling pathway; exocytosis; and neurotransmitter secretion; regulates insulin secretion and ion transport	O94910
LRBA	Protein with high similarity to mouse Nbea; which binds protein kinase A type II regulatory subunits; member of the Beige or BEACH domain-containing family and the DUF1088 domain of unknown function family; contains five WD domain G-beta repeats	P50851
LRRC40	Protein containing sixteen leucine rich repeats; which mediate protein-protein interactions; has low similarity to A. thaliana AT3G15410; which is involved in response to ethylene and cytokinin stimulus; may be involved in signal transduction	Q9H9A6
LRRC47	Protein containing a B3-4 domain and a two leucine rich repeats; which mediate protein-protein interactions; has a region of low similarity to a region of C. elegans FRS-2 which plays a role in reproduction	Q8N1G4
LRSAM1	Leucine rich repeat and sterile alpha motif containing 1; an E3 ubiquitin ligase that binds and polyubiquitinates TSG101; and binds and regulates endocytic degradation of EGFR; regulates HIV-1 budding; a component of the antibacterial autophagic response	Q6UWE0
LSM1	LSM1 homolog U6 small nuclear RNA associated; regulates cell cycle and cell proliferation; aberrantly expressed in mesotheliomas and lung; breast; and prostate tumors	O15116
LSM14B	Protein with high similarity to human LSM14A; which may play a role in mRNA transport; contains an FFD and TFG box motifs motif and a DFDF motif	Q9BX40
LSM4	LSM4 homolog U6 small nuclear RNA associated; forms heteromer with other Sm-like proteins; binds to U6 snRNA; interacts with spinal muscular atrophy disease gene product (SMN1); acts as autoantigen in systemic lupus erythematosus	Q9Y4Z0
LTA4H	Leukotriene A4 hydrolase; an aminopeptidase that acts in leukotriene metabolism; may play a role in female pregnancy; upregulated in esophageal neoplasms; single nucleotide polymorphism is associated with asthma and allergy susceptibility	P09960
LYPLA1	Lysophospholipase I; a serine hydrolase and thioesterase that hydrolyzes lysophosphatidylcholine; may play a role in cell differentiation; downregulation of the corresponding mRNA may correlate with breast cancer	O75608

MAN1A2	Alpha 1;2-mannosidase IB (Golgi alpha 1;2 mannosidase IB); functions in maturation of complex and hybrid N-glycans; a member of the glycosyl hydrolase family 47	O60476
MANF	Mesencephalic astrocyte-derived neurotrophic factor; protects against ischemic brain injury in a rat stroke model; stimulates neuron proliferation; prevents tunicamycin-induced neuronal apoptosis; gene mutation is associated with a variety of cancers	P55145
MAP2K3	Mitogen-activated protein kinase kinase 3; involved in apoptosis; immune response; protein localization; and signal transduction; expression is upregulated in breast neoplasm; increased mRNA expression correlates with invasive form of glioma	P46734
MAP4K4	Mitogen-activated protein kinase kinase kinase kinase 4; a serine-threonine kinase that stimaultes JNK activity and T cell activation; regulates TNF alpha induced insulin resistance; increased expression correlates with pancreatic ductal adenocarcinoma	O95819
MAPK14	Mitogen activated protein kinase 14; a signal transducer; mediates apoptosis; mitotic G2-M transition; muscle development; and prostaglandin biosynthesis; increased activity is associated with psoriasis; gene upregulation is associated with colon cancers	Q16539
MAPRE1	Microtubule-associated protein RP-EB family member 1; plays a role in microtubule cytoskeleton organization; establishment of centrosome localization; myoblast differentiation; and axonogenesis	Q15691
MAPT	Microtubule-associated protein tau; a protein tyrosine kinase activator that inhibits microtubule depolymerization; aberrantly expressed in Alzheimer disease; gene mutation causes Parkinsonian disorders; dementia; tauopathies; and brain pick disease	P10636
MARK2	ELKL motif kinase 1; a protein serine-threonine kinase that plays a role in establishment of epithelial cell apical and basal polarity; and regulation of dendrite development through MAP2 phosphorylation	Q7KZI7
MARS2	Methionyl-tRNA synthetase 2 mitochondrial; a methionyl-tRNA synthetase that mediates methionyl-tRNA aminoacylation; involved in the metabolism of methionine to homocysteine thiolactone; which is possibly an editing mechanism	Q96GW9

	in tRNA aminoacylation	
MB	Myoglobin; a hemoprotein involved in oxidation of nitric oxide and fatty acid; acts in heart development; may play a role in muscle contraction; protein deficiency is associated with ischemic and idiopathic dilated cardiomyopathies	P02144
MBOAT2	Protein with high similarity to human MBOAT1; which is a O-acyltransferase that plays a role in phospholipid biosynthetic process and is associated with urothelial carcinoma; and brachydactyly syndactyly syndrome	Q6ZWT7
MDP1	Magnesium-dependent phosphatase 1; a protein-fructosamine-6-phosphatase potentially involved in glycation repair; member of the haloacid dehalogenase (HAD) superfamily of phosphatases	Q86V88
MECR	Mitochondrial trans-2-enoyl-CoA reductase; reduces trans-2-enoyl-CoA to acyl-CoA with chain length from C6 to C16 in an NADPH-dependent manner with preference to medium chain length substrate; plays a role in mitochondrial respiratory function	Q9BV79
MESDC2	Mesoderm development candidate 2; positively regulates secretion of LRP6; may play a role in multicellular organismal development and mesoderm development; gene disruption generates a fusion protein with SENP1 that causes infantile sacrococcygeal teratoma	Q14696
MICALL1	MICAL-like 1; binds EH-domain containing 1 (EHD1); the first of two Asn Pro Phe (NPF) motifs is required for binding to EHD1; with flanking residues affecting binding affinity	Q8N3F8
MLL2	Mixed-lineage leukemia 2; a ligand-dependent estrogen receptor transcription coactivator; plays a role in the regulation of estrogen receptor signaling pathway and cell growth; may regulate cell proliferation	O14686
MMAA	Methylmalonic aciduria cblA type; a GTPase that regulates methylmalonyl-CoA mutase activity; may play a role in cobalamin transport; gene mutation is associated with the cblA complementation group of vitamin B12-responsive methylmalonic acidemia	Q8IVH4
MMAB	Methylmalonic aciduria (cobalamin deficiency) cblB type; an adenosyltransferase that binds to ATP; plays a role in cobalamin metabolic process and cofactor biosynthesis; gene mutation is associated with methylmalonic acidemia and	Q96EY8

	metabolic ketoacidosis	
MME	Membrane metallo-endopeptidase; acts in beta-amyloid formation; neuroprotection; blood circulation; inflammatory response; and behavior; upregulated in multiple myeloma and downregulated in Alzheimer disease and prostate and several other cancers	P08473
MPST	Mercaptopyruvate sulfotransferase; catalyzes the transfer of a sulfur ion from 3-mercaptopyruvate to cyanide; plays a role in cell redox homeostasis; genetic polymorphism is associated with mercaptolactate-cysteine disulfiduria disorder	P25325
MRPL1	Mitochondrial ribosomal protein L1; a component of the mitochondrial ribosome large 39S subunit	Q9BYD6
MRPL12	Mitochondrial ribosomal protein L12; binds to POLRMT and stimulates transcription from the mitochondrial promoters; may play a role in protein biosynthesis	P52815
MRPL13	Mitochondrial ribosomal protein L13; a structural constituent of ribosome that may play a role in translation	Q9BYD1
MRPL15	Mitochondrial ribosomal protein L15; a component of the mitochondrial large ribosomal subunit that plays a role in translation	Q9P015
MRPL16	Mitochondrial ribosomal protein L16; a component of the 39S large subunit of the mitochondrial ribosome; abnormal mRNA expression correlate with tumorigenesis and tumor growth associated with sporadic colorectal cancer	Q9NX20
MRPL17	Mitochondrial ribosomal protein L17; putative component of the large ribosomal subunit	Q9NRX2
MRPL19	Mitochondrial ribosomal protein L19; a structural constituent of ribosome that plays a role in translation; may act in neurological system process	P49406
MRPL2	Mitochondrial ribosomal protein L2; a member of the ribosomal L2 family of proteins; a putative structural protein of the mitochondrial large 39S ribosomal subunit; may play a role in protein biosynthesis; splice variants are observed in malignant tissues	Q5T653
MRPL21	Member of the ribosomal prokaryotic L21 protein family; which are part of the large ribosomal subunit; has strong similarity to uncharacterized mouse BC028768	Q7Z2W9
MRPL22	Mitochondrial ribosomal protein L22; a component of the mitochondrial large 39S	Q9NWU5

	ribosomal subunit	
MRPL24	Mitochondrial ribosomal protein L24; a putative component of the mitochondrial large ribosomal subunit; may function in protein biosynthesis	Q96A35
MRPL27	Mitochondrial ribosomal protein L27; a component of the mitochondrial large ribosomal subunit	Q9P0M9
MRPL37	Mitochondrial ribosomal protein L37; putative component of the large subunit (39S) of the mitochondrial ribosome	Q9BZE1
MRPL39	Mitochondrial ribosomal protein L39; a putative subunit of the large subunit of the mitochondrial ribosome	Q9NYK5
MRPL4	Mitochondrial ribosomal protein L4; a predicted component of the mitochondrial ribosome large 39S subunit; gene SNP correlates with predisposition to atopy and allergic rhinitis	Q9BYD3
MRPL40	Mitochondrial ribosomal protein L40; a component of the mitochondrial large ribosomal subunit; corresponding gene is located in a chromosomal region deleted in Velo-cardio-facial syndrome	Q9NQ50
MRPL41	Mitochondrial ribosomal protein L41; a putative structural constituent of ribosomes that acts in TP53 and CDKN1B mediated inhibition of cell growth; induces cycle arrest at G1 phase and BCL2 mediated apoptosis; may activate caspases	Q8IXM3
MRPL42	Mitochondrial ribosomal protein L42; a component of the small mitochondrial ribosomal subunit	Q9Y6G3
MRPL45	Member of the mitochondrial import inner membrane; translocase subunit TIM44 family; has high similarity to uncharacterized mitochondrial ribosomal protein L45 (mouse Mrpl45)	Q9BRJ2
MRPL48	Mitochondrial ribosomal protein L48; component of the mitochondrial ribosome 39S large subunit; interacts with the C-terminal tail of mitochondrial inner membrane protein OXA1L	Q96GC5
MRPL50	Mitochondrial ribosomal protein L50; a component of the mitochondrial 39S ribosomal large subunit	Q8N5N7
MRPL53	Protein of unknown function; has strong similarity to mouse Mrpl53; which is the mitochondrial ribosomal protein L53	Q96EL3
MRPL9	Mitochondrial ribosomal protein L9; component of the large ribosomal subunit	Q9BYD2
MRPS14	Mitochondrial ribosomal protein S14; a component of the mitochondrial 28S small	O60783

	ribosomal subunit	
MRPS36	Mitochondrial ribosomal protein S36; a putative component of the small subunit of the mitochondrial ribosome; may play a role in translation	P82909
MRPS9	Member of the ribosomal protein S9 or S16 family; has low similarity to C. elegans F09G8.3; which is involved in embryogenesis and positive growth regulation	P82933
MT1X	Metallothionein 1X; a zinc ion binding protein that plays a role in cellular metal ion homeostasis; downregulated in advanced prostate cancer; increased mRNA expression correlates with bladder neoplasms	P80297
MTHFD2	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2 methenyltetrahydrofolate cyclohydrolase; an electron carrier that may act in utero embryonic development; mitochondrion organization; and translation; mRNA is upregulated in Friedreich ataxia	P13995
MTHFS	5 10-Methenyltetrahydrofolate synthetase; a cyclo ligase that plays a role in purine base biosynthesis; folic acid catabolism; and tetrahydrofolate metabolism; gene polymorphism is associated with lung cancer	P49914
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase; acts in methionine biosynthesis and blood circulation; gene mutations cause hyperhomocysteinemia; gene SNPs are associated with neural tube defects; Down syndrome; and colorectal cancer	Q99707
MTX1	Metaxin 1; an outer mitochondrial membrane protein that plays a role in protein transport; polymorphism in the corresponding gene is associated with Gaucher disease	Q13505
MUT	Methylmalonyl CoA mutase; catalyzes the isomerization of methylmalonyl-CoA to succinyl-CoA; regulates mitochondrial morphology; respiratory chain function; cytochrome c oxidase activity; and glutathione levels; gene mutations cause methylmalonic acidemia	P22033
MVD	Mevalonate pyrophosphate decarboxylase (diphosphomevalonate decarboxylase); catalyzes the decarboxylation of mevalonate pyrophosphate to isopentyl pyrophosphate in cholesterol biosynthesis	P53602
MYCBP2	MYC binding protein 2; an enzyme inhibitor that acts in synaptogenesis; axonogenesis; respiratory gaseous exchange; and neuron migration; negative regulates adenylyl cyclase activity	O75592

MYLK	Myosin light chain kinase; a transferase that acts in protein amino acid phosphorylation; calcium-mediated signaling; chemotaxis; and smooth muscle contraction; single nucleotide polymorphism in the gene is associated with sepsis and lung diseases	Q15746
MYO6	Myosin VI; an actin-dependent motor ATPase that acts in endocytosis; metaphase cell cycle; apoptosis; neurotransmission; inner ear hair cell maturation; and perception of sound; upregulated in ovarian and prostate cancers; gene mutation causes deafness	Q9UM54
NAA10	ARD1 homolog A N-acetyltransferase; regulates transcription; proteolysis; and amino acid acetylation; stimulates cell proliferation; upregulated in papillary carcinoma associated with thyroid neoplasms; mRNA downregulation correlates with anoxia	P41227
NAA15	NMDA receptor regulated 1; an acetyltransferase that acts in antiapoptosis; mRNA is upregulated in papillary thyroid carcinoma	Q9BXJ9
NACA	Nascent polypeptide-associated complex alpha subunit; binds to nucleic acids; plays a role in T cell proliferation and protein folding; increased expression correlates with osteosarcoma	Q13765
NANS	N-acetylneuraminic acid synthase; catalyzes the condensation of phosphoenolpyruvate and N acetylmannosamine 6 phosphate to synthesize N acetylneuraminic acid 9 phosphate; localizes to cytosol	Q9NR45
NAP1L4	Nucleosome assembly protein 1-like 4; binds to histone; mediates transfer of core and linker histones to DNA; involved in nucleosome assembly	Q99733
NCKIPSD	NCK interacting protein with SH3 domain; a putative SH3-SH2 adaptor that regulates cell adhesion; postsynaptic densities; and actin cytoskeleton organization; genetic translocation correlates with drug-induced acute monocytic leukemia	Q9NZQ3
NCLN	Nicalin homolog; regulates assembly and stability of the NOMO1; may play a role in the regulation of signal transduction and in-utero embryonic development	Q969V3
NDRG3	Protein with high similarity to human NDRG1; which likely acts in cellular differentiation and proliferation and is induced during colon carcinoma cell line differentiation; member of the Ndr family; contains an alpha or beta hydrolase fold domain	Q9UGV2

NDUFA4	NADH dehydrogenase 1 alpha subcomplex subunit 4; a putative NADH dehydrogenase that plays a role in T-cell differentiation; upregulated in renal cell carcinoma	O00483
NDUFA6	Member of the complex 1 protein (LYR) family; which may be components of NADH-ubiquinone oxidoreductase; has strong similarity to uncharacterized mouse Ndufa6	P56556
NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 10 (PDSW) 22kD; a putative subunit of NADH-ubiquinone oxidoreductase (complex I); which transports electrons from NADH to ubiquinone; upregulated in the heart of patients with hypertrophic cardiomyopathy	O96000
NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3 30kDa; a putative electron carrier that mediates IFN-B or RA-induced cell death by modulating ROS production and gene expression; gene mutation causes Leigh syndrome; optic atrophy; and complex I deficiency	O75489
NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7; involved in mitochondrial respiratory chain complex I assembly; gene mutations are associated with Leigh disease; gene polymorphisms correlates with multiple sclerosis	O75251
NEDD8	Neural precursor cell expressed developmentally downregulated 8; a transcription coactivator that acts in protein polyubiquitination and neddylation; regulates ubiquitin-protein ligase activity; decreased expression correlates with prostatic neoplasm	Q15843
NFS1	NFS1 nitrogen fixation 1 homolog; a cysteine desulfurase that promotes oxidoreductase activity and involved in sulfuration; acts in iron-sulfur cluster assembly; mitochondrial membrane organization; and cell growth; may play a role in iron ion homeostasis	Q9Y697
NIF3L1	NGG1 interacting factor 3-like 1; a cytoplasmic protein that homodimerizes and heterodimerizes with human NIF3L1BP1 through binding to the C-terminal region; binds the MLXIPL transcription factor	Q9GZT8
NKIRAS2	NFKB inhibitor interacting Ras-like 2; interacts with the PEST domains of IkappaB alpha (CHUK) and IkappaB beta (IKBKB) and decreases their rate of degradation; inhibits TNF-alpha-dependent activation of NF-kappaB	Q9NYR9

NME1-NME2	Protein containing two nucleoside diphosphate kinase domains; has a region of very strong similarity to human NME2; which is a transcription factor and endodeoxyribonuclease that binds to the MYC promoter and may function in DNA repair	P22392
NME2	Expressed in non-metastatic cells 2; a transcription factor that acts in nucleoside diphosphate phosphorylation and endocytosis; aberrantly expressed in Alzheimer Disease; ovarian; prostate; and various neoplasms	P22392
NME3	Protein expressed in non-metastatic cells 3; a nucleoside-diphosphate kinase that has tissue-specific effects on differentiation and cell adhesion; downregulated in pancreatic endocrine neoplasms	Q13232
NOB1	Protein containing an nin one binding (NOB1) Zn-ribbon like domain; has low similarity to C. elegans Y54E10BR-4; which plays a role in gamete generation and stimulation of growth	Q9ULX3
NOL3	Nucleolar protein 3; binds to enzymes; plays a role in activation of caspase activity and regulation of protein export from nucleus; aberrant expression is associated with Alzheimer disease and heart diseases	O60936
NPTN	Neuroplastin; involved in negative regulation of long-term neuronal synaptic plasticity; may play a role in synaptogenesis; neuron adhesion; and cognition; increased mRNA expression correlates with breast cancer	Q9Y639
NRD1	Nardilysin N-arginine dibasic convertase; a metalloendopeptidase that plays a role in peptide hormone processing; promotes membrane protein ectodomain proteolysis and metalloenzyme activity; regulates beta-amyloid formation and cell migration	O43847
NT5C3	5'-nucleotidase cytosolic III; hydrolyzes pyrimidine 5' monophosphate and 3' monophosphate; may play a role in erythrocyte differentiation and RNA catabolism; gene is upregulated in gastric cancer; gene mutation causes nonspherocytic hemolytic anemia	Q9H0P0
NUB1	Negative regulator of ubiquitin-like proteins 1; a proteasome binding protein that inhibits cell proliferation and formation of Lewy body-like inclusions; involved in proteasomal ubiquitin-dependent protein degradation; may function in eye development	Q9Y5A7
NUBP1	Nucleotide binding protein 1; a putative nucleotide binding protein that may play a	P53384

	role in cytokinesis	
NUDCD3	Protein containing a CS domain; has low similarity to rat Nudc; which plays a role in cell proliferation and nuclear migration	Q8IVD9
NUDT8	Vacuolar basic amino acid transporter 2; mediates basic amino acid import into the vacuole in response to nutrient depravation	Q8WV74
NUMA1	Nuclear mitotic apparatus protein 1; a structural molecule that acts in cytokinesis; expression is increased in colorectal cancers and promyelocytic leukemia; aberrant mRNA expression is associated with myeloid leukemia	Q14980
NUMB	Numb homolog; acts in notch signaling; cell fate commitment; adherens junction maintenance; neurogenesis; and apoptosis; aberrantly expressed in salivary gland neoplasms and non small cell lung carcinoma; mRNA is downregulated in breast cancer	P49757
NUP54	Protein with strong similarity to nucleoporin p54 (rat Nup54); which is a nucleocytoplasmic transporter that is involved in protein import into nucleus and binds to nuclear import factors p97 (Impnb) and NTF2 (Rn.7345)	Q7Z3B4
NUP62	Nucleoporin 62kDa; interacts with MUC1; plays a role in intracellular signaling cascade and nuclear import; gene mutation causes autosomal recessive infantile bilateral striatal necrosis	P37198
NUP88	Nucleoporin 88kDa; a putative transporter that mediates transcription; nuclear pore complex assembly; and spindle polarity formation and chromosome segregation in mitosis; upregulated in Hodgkin's disease; colon; skin; breast and several neoplasms	Q99567
NUP93	Nucleoporin 93kDa; a structural constituent of nuclear pore that may play a role in nuclear pore organization	Q8N1F7
OGFR	Opioid growth factor receptor; binds met-enkephalin; acts in the cell cycle; inhibiting growth of thyroid follicular cell-derived cancers; and cellular response to drugs; decreased expression correlates with squamous cell carcinoma of the head and neck	Q9NZT2
OPA1	Optic atrophy 1; a GTPase that acts in mitochondrion organization; antiapoptosis; and embryonic development; gene mutations correlate with autosomal dominant optic atrophy and glaucoma	O60313

OS9	Osteosarcoma amplified 9; a putative soluble acidic protein; may regulate cell growth and cell proliferation; may function in ER-to-Golgi transport; gene is amplified in sarcoma; gene mutation and antigen may correlate with melanoma	Q13438
OSTF1	Osteoclast stimulating factor 1; forms a complex with CBL and SRC and mediates bone mineralization; bone resorption; and cell proliferation	Q92882
OTUD6B	Member of the peptidase C65 Otubain family; which are involved in the regulation of protein stability; strong similarity to uncharacterized mouse Otud6b	Q8N6M0
OXCT1	3-oxoacid CoA transferase 1; catalyzes the reversible transfer of coenzyme A from succinyl-CoA to acetoacetate and regulates ketone catabolism; gene mutations are associated with SCOT deficiency and ketoacidosis	P55809
OXSR1	Oxidative-stress responsive 1; a serine-threonine kinase that regulates chloride co-transporter activity; activated in response to hypotonic stress	O95747
P4HA1	Prolyl 4-hydroxylase alpha polypeptide; involved in collagen synthesis and metabolism; plays a role in collagen fibril organization during embryonic development; aberrantly expressed in arteriosclerosis and osteoarthritis; mRNA is upregulated in anoxia	P13674
PABPC4	Poly(A)-binding protein cytoplasmic 4 (inducible form); binds to poly(A); poly(U) and AU-rich regions of mRNA; positively regulates interleukin-2 (IL2) mRNA translation; may play a role in blood coagulation and RNA catabolism	Q13310
PACS1	Phosphofurin acidic cluster sorting protein 1; regulates subcellular localization and function of polycystin-2; may act in Golgi to endosome transport	Q6VY07
PACS2	Phosphofurin acidic cluster sorting protein 2; an intracellular transporter that directs endoplasmic reticulum localization of PKD2; induces apoptosis; mediates ER folding and calcium homeostasis; maintains the mitochondria-endoplasmic reticulum axis	Q86VP3
PARD6G	Partitioning defective 6 homolog gamma; may function in cell polarization via interactions with the small GTPases RAC and CDC42 and atypical protein kinase C	Q9BYG4
PARK7	Parkinson disease 7; a transcription coactivator that mediates autophagy and mitochondrial membrane potential; aberrant expression correlates with Alzheimer disease; breast and lung carcinoma; and male infertility; gene mutation causes Parkinson disease	Q99497

PCBP1	Poly(rC) binding protein 1; a transcription activator and a translation regulator that regulates mRNA splicing and its stability; upregulated in aortic stenosis and cardiomyopathy; downregulated in uterine cervical neoplasms; mRNA is decreased in hepatoma	Q15365
PCCA	Propionyl CoA carboxylase alpha polypeptide; plays a role in fatty acid catabolism; may act in branched chain family amino acid catabolism; gene mutation causes propionic acidemia	P05165
PCM1	Pericentriolar material 1; acts in microtubule anchoring at centrosome; interkinetic nuclear migration; and cell cycle; decreased expression correlates with breast neoplasm and papillary thyroid carcinoma; gene fusion with JAK2 is associated with leukemia	Q15154
PCYT1A	Phosphate cytidylyltransferase 1 choline alpha; binds to cytoskeletal protein; acts in embryonic development; phosphatidylcholine biosynthetic process; and regulation of B cell proliferation; upregulated in colorectal tumor and Parkinson disease	P49585
PCYT2	Phosphate cytidylyltransferase 2 ethanolamine; a transferase that plays a role in embryonic development; may act in phospholipid homeostasis and lipid metabolism	Q99447
PDAP1	PDGFA associated protein 1; may play a role in cell proliferation and signal transduction	Q13442
PDCD6		O75340
PDF		Q9HBH1
PDHB	Pyruvate dehydrogenase (lipoamide)-beta; plays a role in pyruvate biosynthesis and tricarboxylic acid cycle; decreased protein activity is associated with pyruvate dehydrogenase deficiency	P11177
PDIA3	Protein disulfide isomerase family A member 3; an endopeptidase that is involved in protein complex assembly; aberrant mRNA expression correlates with several neoplasms; autoantibody correlates with male infertility; mouse Pdia3 is associated with scrapie	P30101
PDIA6	Protein disulfide isomerase family A member 6; plays a role in protein folding and refolding; regulates phosphoinositide 3-kinase cascade and alpha-granule secretion; upregulated in invasive breast cancer	Q15084

PDLIM5	PDZ and LIM domain 5; a calcium channel regulator that regulates actin cytoskeleton organization; aberrantly expressed in bipolar disorder; schizophrenia; and diabetes; abnormal splicing of the mouse Pdlim5 is associated with cardiac hypertrophy in mouse	Q96HC4
PECI	Peroxisomal D3-D2-enoyl-CoA isomerase; catalyzes the isomerization of 3-cis-octenoyl-CoA to 2-trans-octenoyl-CoA in the beta oxidation of fatty acids in peroxisomes; involved in cell-mediated immune response and immune pathophysiology of aplastic anemia	O75521
PEF1	Penta-EF-hand domain containing 1; a putative signal transducer that is involved in response to calcium ion; may play a role in calcium-mediated signaling	Q9UBV8
PELO	Pelota homolog; chromosomal location; frequency of anuploidy in cancer; and benign tumor formation in mice heterozygously deficient suggest a role in various human cancers; decreased mRNA expression is associated with acute myeloid leukemia	Q9BRX2
PET112L	PET112L; a putative translation factor; may play a role in regulating mitochondrial cytochrome c oxidase structure and function; corresponding gene is a candidate for Leigh disease	O75879
PEX14	Peroxisomal biogenesis factor 14; interacts with peroxisome receptor; functions in peroxisome organization and protein docking during peroxisome matrix protein import; aberrantly expressed in neuroblastoma; gene mutation correlates with Zellweger syndrome	O75381
PEX19	Peroxisomal biogenesis factor 19; involved in transport of protein; peroxisome membrane biogenesis; cell proliferation; and positive regulation of cell cycle; mRNA is downregulated in psoriasis; gene mutation correlates with Zellweger syndrome	P40855
PFDN2	Protein of unknown function; has very strong similarity to mouse Pfdn2; which may binds to unfolded protein and may be involved in protein folding	Q9UHV9
PFKL	Liver phosphofructokinase; plays a role in fructose metabolic process and phosphorylation; corresponding gene is upregulated in Down syndrome; gene map position correlates with Bipolar disorder	P17858
PFKM	Phosphofructokinase muscle; a transferase that acts in fructose 6-phosphate metabolism; ADP phosphorylation; aerobic respiration; and glucose and oxygen	P08237

	transport; downregulated in glycogen storage disease type VII	
PFKP	Platelet-type phosphofructokinase; a rate-limiting enzyme of glycolysis that catalyzes the formation of fructose 1; 6-bisphosphate from fructose 6-phosphate and ATP; increased mRNA expression may be associated with malignant form of neoplasms	Q01813
PFN1	Profilin I; plays a role in type I hypersensitivity; neurite development; actin filament organization in microspike biogenesis; and in the regulation of filopodia formation; downregulation of mRNA is associated with breast neoplasms	P07737
PGM2	Phosphoglucomutase 2; exhibits higher activity as a phosphopentomutase than as a phosphoglucomutase	Q96G03
PHF5A	Protein with very strong similarity to PHD finger protein 5A (rat Phf5a); which is a zinc finger protein that is a coactivator of estrogen-stimulated transcription; member of the PHF5-like protein family	Q7RTV0
PHKA1	Phosphorylase kinase alpha 1; plays a role in glucose and glycogen metabolic processes; may act in muscle contraction and generation of precursor metabolites and energy; gene mutations are associated with glycogen storage disease	P46020
PHKA2	Phosphorylase kinase alpha 2 (liver); the alpha subunit of liver phosphorylase kinase; a regulatory enzyme involved in glycogen breakdown; gene mutation causes several forms of glycogen storage diseases	P46019
PHLDB1	Pleckstrin homology-like domain family B member 1; a phosphatidylinositol binding protein that modulates AKT signaling and glucose transport in response to insulin; may act in cell death; map position correlates with neuroblastoma	Q86UU1
PIGT	Phosphatidylinositol glycan anchor biosynthesis class T; a component of the GPI-anchor transamidase complex that maintains the complex by stabilizing expression of GPAA1 and PIGK; overexpression is associated with breast cancer and perhaps cervical cancer	Q969N2
PIK3R2	Phosphoinositide-3-kinase regulatory subunit 2; an signal transducer that plays a role in actin cytoskeleton reorganization; cell motion; embryonic development; inositol phosphate-mediated signaling; and regulation of protein amino acid phosphorylation	O00459

PIN1	Peptidylprolyl cis-trans isomerase NIMA-interacting 1; catalyzes the phosphorylation dependent isomerization of several signaling molecules and transcription factors; aberrant expression is associated with Alzheimer disease and several neoplasms	Q13526
PIN4	Protein (peptidyl-prolyl cis-trans isomerase) NIMA-interacting 4; a double-stranded DNA binding protein that plays a role in protein folding; may act in mitochondrion organization and biogenesis and ribosome biogenesis and assembly	Q9Y237
PKM2	Pyruvate kinase muscle; involved in aerobic glycolysis and protein phosphorylation; regulates ATP biobsynthesis; T-cell chemotaxis and TNF-alpha production; upregulated in rheumatic disease and breast; colonic; lung; and several other neoplasms	P14618
PKP3	Plakophilin 3; a putative structural molecule that plays a role in RNA metabolic process and regulation of keratinocyte proliferation and apoptosis; aberrant expression is associated with lung and oropharyngeal cancers	Q9Y446
PKP4	Plakophilin 4; plays a role in the enhancement of adherens junction assembly and regulation of protein localization; inhibits cell migration	Q99569
PLCB4	Phospholipase C beta 4; a metabotropic glutamate receptor ligand that plays a role in multicellular organismal development and sensory perception to pain; may play a role in apoptosis; knockout of the mouse Plcb4 causes mouse model of absence seizures	Q15147
PLCG1	Phospholipase C gamma 1; binds to SLC22A3; mediates growth factor and T-cell receptor signaling; promotes keratinocyte differentiation; upregulated in adenomatous polyposis coli and various cancers; gene polymorphism correlates with bipolar disorder	P19174
PLEKHA3	Pleckstrin homology domain-containing family A member 3; binds to phosphatidylinositol-4-phosphate and ADP-ribosylation factor; plays a role in membrane tubulation; pelleting; and insertion	Q9HB20
PLIN3	Mannose-6-phosphate receptor binding protein 1; plays a role in endosome to Golgi trafficking of mannose-6-phosphate receptors; lipid droplet biogenesis; and apoptosis and differentiation of epithelial cells; upregulated in cervical carcinoma	O60664

PLOD3	Procollagen-lysine 2-oxoglutarate 5-dioxygenase 3; a galactosyltransferase that catalyzes the hydroxylation of lysyl residues in collagen during its biosynthesis; acts in embryo development; gene mutations correlate with connective tissue disorder	O60568
PLS3	Plastin 3; an actin binding protein that acts in comet organization and actin filament stabilization; may be involved in G2-M transition of mitotic cell cycle; aberrantly expressed in sezary syndrome; acts as an autoantigen in systemic lupus erythematosus	P13797
PLXNB2	Plexin B2; mediates neocortical development; neuron specification; differentiation; and migration; involved in regulation of vascular and endocrine system; mouse Plxnb2 is associated with neural tube closure defects	O15031
PMPCB	Peptidase (mitochondrial processing) beta; binds to metal ions; plays a role in mitochondrial protein processing during import and proteolysis	O75439
PMS2	PMS2 postmeiotic segregation increased 2; exhibits protein heterodimerization activity; plays a role in mismatch repair; spermatogenesis; synaptonemal complex assembly; and ATP catabolism; gene mutation correlates with various types of neoplasms	P54278
PNPO	Pyridoxamine 5-phosphate oxidase; an electron carrier that plays a role in pyridoxamine and pyridoxine metabolism; may regulates blood pressure; gene mutations are associated with neonatal epileptic encephalopathy and schizophrenia	Q9NVS9
POFUT1	Protein O-fucosyltransferase 1; plays a role in Notch signaling pathway; heart development; and neurogenesis; mRNA expression is upregulated in glioma; knockout of the mouse Pofut1 causes neonatal death	Q9H488
POGLUT1	Protein O-glucosyltransferase 1; a glycosyltransferase that catalyzes hydrolysis of UDP-Glc	Q8NBL1
POLDIP2	Polymerase delta interacting protein 2; binds PCNA; TFAM and mtSSB; inhibits POLD2 activity via direct binding; functions as a regulator of NADPH oxidase 4 (NOX4) and cytoskeletal integrity in vascular smooth muscle cells	Q9Y2S7
POLDIP3	Polymerase DNA-directed delta interacting protein 3; binds small DNA polymerase delta subunit (POLD2) and enhancer of rudimentary (ERH); a substrate of the RPS6KB1 kinase that regulates cell growth; may act as an autoantigen in atypical renal vasculitis	Q9BY77

POLR2B	Polymerase II (DNA directed) polypeptide B; plays a role in transcription from RNA polymerase II promoter	P30876
POLR2I	Polymerase (RNA) II (DNA directed) polypeptide I 14.5kDa; a putative DNA-directed RNA polymerase that binds to zinc ion; may play a role in transcription start site selection	P36954
PON2	Paraoxonase 2; an arylesterase that protects cells from oxidation; inhibits triglyceride synthesis; downregulated in atherosclerosis; gene polymorphism correlates with Alzheimer disease; amyotrophic lateral sclerosis; vascular dementia; and diabetes	Q15165
PPA1	Pyrophosphatase 1; a putative inorganic diphosphatase that may play a role in phosphate metabolism	Q15181
PPFIA1	Protein tyrosine phosphatase receptor type f polypeptide interacting protein alpha 1; interacts with ING4 and mediates cell migration; acts in cell morphogenesis and cell-matrix adhesion; upregulated in head and squamous cell carcinoma	Q13136
PPFIBP1	PTPRF interacting protein binding protein 1 (liprin beta 1); binds to alpha liprins and LAR family transmembrane protein tyrosine phosphatases; may play a role in cell adhesion; gene missense mutation correlates with multiple myeloma	Q86W92
PPIF	Peptidylprolyl isomerase F; induces mitochondrial membrane transition; neuron apoptosis; and neurotransmitter secretion; acts in necrosis and release of cytochrome c from mitochondria; reduces mitochondrial Ca2+ level; upregulated in Huntington disease	P30405
PPIG	Peptidyl-prolyl isomerase G (cyclophilin G); a cis-trans isomerase that may play a role in RNA splicing; mRNA processing; and protein transport	Q13427
PPIL3	Peptidylprolyl isomerase (cyclophilin)-like 3; putative peptidylprolyl isomerase that is ubiquitously expressed	Q9H2H8
PPM1F	Protein phosphatase 1F; a calcium-dependent protein kinase inhibitor that plays a role in the induction of apoptosis	P49593
PPOX	Protoporphyrinogen oxidase; catalyzes the oxidation of protoporphyrinogen IX to protoporphyrin IX in heme biosynthesis; inhibited by the tetrahydrophthalimide and diphenyl ether herbicides; mutation of corresponding gene causes variegate porphyria	P50336

PPP2R2D	Protein with very strong similarity to rat Ppp2r2d; which is a subunit of protein phosphatase 2A that may play a role in targeting the PP2A holoenzyme to the cytosol; contains five WD domain G-beta repeats	Q66LE6
PPP5C	Protein phosphatase 5 catalytic subunit; an serine - threonine phosphatase that acts in activation of JUN kinase activity and regulation of protein amino acid dephosphorylation; aberrant expression is associated with Alzheimer disease and breast cancer	P53041
PRDX1	Peroxiredoxin 1; regulates H2O2 homeostasis; apoptosis; and vasculature development; upregulated in Alzheimer disease and Down syndrome; aberrantly expressed in several cancers; autoimmune antibody correlates with vasculitis and lupus erythematosus	Q06830
PRDX2	Peroxiredoxin 2; a thioredoxin peroxidase that regulates inflammatory response; cell aging; and antiapoptosis; inhibits MAPK and JUN kinase activity; aberrantly expressed in Alzheimer disease; Down syndrome; Pick disease; and several cancers	P32119
PRDX4	Peroxiredoxin 4; an antioxidant that acts in IkappaB phosphorylation; spermatogenesis; and cell death; aberrantly expressed in many carcinomas; increased autoimmune antibody is associated with rheumatoid arthritis; Behcet syndrome; and lupus erythematosus	Q13162
PRDX6	Peroxiredoxin 6; an antioxidant that plays a role in glutathione catabolism; phospholipid metabolism; skin morphogenesis; and surfactant homeostasis; regulates apoptosis and epithelial cell proliferation involved in wound healing	P30041
PRKD1	Protein kinase D1; a serine-threonine kinase that induces cell proliferation and Golgi to plasma membrane protein transport; regulates cell migration and inflammatory response; aberrantly expressed in pancreatic and prostatic neoplasms	Q15139
PRMT3	Protein arginine methyltransferase 3; asymmetrically dimethylates arginine residues in a protein; regulates protein stability and dendritic spine morphogenesis	O60678
PRMT5	Protein arginine methyltransferase 5; a transcriptional repressor that acts in protein complex assembly; skeletal muscle tissue development; and spliceosomal snRNP biogenesis; protein expression is upregulated in stomach neoplasm and gastric cancer	O14744
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B; a kinetochore binding protein that plays a role in protein phosphorylation and localization; regulates mitosis;	Q13523

	transcription; and may be involved in mRNA splicing; signal transduction; chromatin remodeling	
PRPSAP2	Phosphoribosyl pyrophosphate synthetase-associated protein 2; a component of phosphoribosylpyrophosphate (PRPP) synthetase that is related to the other components of PRPP synthetase (PRPS1; PRPS2 and PRPSAP1)	O60256
PSMB5	Proteasome subunit beta type 5; a component of the proteasome core complex that acts in proteolysis and is involved in response to drug	P28074
PTCD1	Pentatricopeptide repeat domain 1; contains eight PPR domains; a mitochondrial matrix protein that associates with; and lowers cellular levels of; mitochondrial leucine tRNAs to perhaps regulate mithchondrial translation	O75127
PTH	Parathyroid hormone; a transcription activator that acts in GPCR mediated adenylyl cyclase activation; bone mineralization; and calcium ion homeostasis; upregulated in hyperparathyroidism; osteoporosis; and AIDS; mRNA is increased in Turner syndrome	Q86Y79
PTH2	Parathyroid hormone 2; a GPCR ligand that is involved in endocannabinoid signaling; adenylyl cyclase activation; cAMP biosynthesis; and calcium ion transport; regulates sensory perception of pain; may play a role in spermatogenesis	Q9Y3E5
PTPN11	Protein tyrosine phosphatase non-receptor type 11; acts in protein dephosphorylation; hemopoiesis; neurogenesis; and glucose homeostasis; activates NF-kappaB and MAPK activity; gene mutations are associated with Noonan syndrome and myeloid leukemia	Q06124
PYCR2	Protein with strong similarity to human PYCR1; which is a pyrroline-5-carboxylate reductase that plays a role in protein homooligomerization; member of the NADP oxidoreductase coenzyme F420-dependent family	Q96C36
QDPR	Quinoid dihydropteridine reductase; an electron carrier that catalyzes the NADH-dependent reduction of dihydrobiopterin; plays a role in pterin-dependent hydroxylating systems of aromatic amino acids; gene mutation causes phenylketonurias	P09417
QSOX2	Quiescin Q6 sulfhydryl oxidase 2; regulates the sensitivity of neuroblastoma cells to interferon-gamma (IFNG)-induced apoptosis; member of the sulfhydryl oxidase-Quiescin6 family; gene SNP may correlate with adult height	Q6ZRP7

RAB3A	Ras-related GTP-binding protein 3a; a GTPase that is involved in calcium-dependent exocytosis of synaptic vesicles; acts in acrosome reaction and insulin secretion; decreased protein expression is associated with Alzheimer disease	P20336
RAB3B	RAB3B member RAS oncogene family; a GTPase that binds to calmodulin; regulates dopamine uptake; synaptic transmission; and exocytosis	P20337
RAB3D	RAB3D member RAS oncogene family; a putative GTPase that regulates bone resorption and calcium ion-dependent exocytosis; acts in Golgi organization; mRNA is upregulated in glioblastoma; knockout of the mouse Rab3d causes osteopetrosis in experimental mice	O95716
RAB8A	RAB8A member RAS oncogene family; a putative GTPase that acts in intracellular protein transport; anterograde axonal transport; cell projection assembly; and nervous system development; inhibits cell-cell adhesion; upregulated in Alzheimer disease	P61006
RAD23A	RAD23 homolog A (S. cerevisiae); an enzyme activator that acts in G2-M transition of mitotic cell cycle; induction of apoptosis; nucleotide-excision repair; and regulation of transcription; mRNA is upregulated in nasopharyngeal neoplasm	P54725
RASA1	RAS p21 protein activator 1; involved in vasculogenesis and respiratory burst; regulates actin filament polymerization; apoptosis; cell adhesion; and transcription; downregulated in choriocarcinoma; gene mutation correlates with port-wine stain	P20936
RBM14	RNA binding motif protein 14; a transcription regulator that may act in RNA splicing	Q96PK6
RBM26	Member of the zinc finger C-x8-C-x5-C-x3-H type (and similar) family; which bind DNA or RNA; contains two RNA recognition motifs (RRM; RBD; or RNP); has low similarity to C. elegans B0336.3; which is involved in body morphogenesis and growth regulation	Q5T8P6
RBM3	RNA binding motif protein 3; a transcriptional activator that regulates mRNA stability; antiapoptosis and phosphorylation of initiation factors; promotes translation; inhibits mitotic catastrophe; mRNA is downregulated in oropharyngeal neoplasms	P98179
RBP1	Retinol binding protein 1 cellular; acts in retinoid metabolism and vitamin biosynthesis; may be involved in brain development; upregulated in skin	Q15311

	neoplasms and kidney diseases; aberrant mRNA expression is associated with breast and endometrial neoplasms	
RCN1	Reticulocalbin 1; binds to calcium ions; aberrant expression is associated with lung neoplasms and non small cell lung carcinoma	Q15293
RCN2	Reticulocalbin 2 EF-hand calcium binding domain; an endoplasmic reticulum protein that interacts with papillomavirus E6 oncoproteins; may play a role in tumorigenesis	Q14257
REPS1	RalBP1 associated Eps domain containing 1; forms a complex with ITSN1 and SGIP1 in clathrin coated pits to likely act in clathrin-mediated endocytosis	Q96D71
RER1	RER1 retention in endoplasmic reticulum 1 homolog; binds to acetylcholine receptor; involved in protein retention in ER lumen and skeletal muscle nicotinic acetylcholine receptor clustering; regulates synapse organization	O15258
RNASEL	Interferon-induced 2-5A-dependent RNase; binds to mitochondrial translation initiation factor and regulates mRNA stability; acts in release of cytochrome c from mitochondria; genetic variation is associated with breast and prostrate cancer	Q05823
RNF10	Ring finger protein 10; binds to transcription factor; may mediate protein-protein interactions	Q8N5U6
RNF114	Ring finger protein 114; binds ubiquitin via a ubiquitin interaction motif; may playa role in the regulation of immune responses; gene single nucleotide polymorphisms correlate with susceptibility to psoriasis	Q9Y508
RNPEP	Arginyl aminopeptidase (aminopeptidase B); a leukotriene-A4 hydrolase that binds to zinc; may play a role in T-cell activation; spermatid development; and protein secretion	Q9H4A4
RPL10	Ribosomal protein L10; a structural constituent of ribosome that inhibits phosphorylation and protein kinase activity; upregulation of the corresponding gene is associated with hepatocellular carcinomas	P27635
RPL10A	Ribosomal protein L10a; a structural constituent of ribosome that may play a role in regulation of translation and in-utero embryo development	P62906
RPL11	Ribosomal protein L11; binds to MDM2 and stabilizes TP53; negatively regulates ubiquitin protein ligase activity; may play a role in ribosomal subunit assembly; gene mutations correlate with Diamond-Blackfan anemia	P62913

RPL12	Ribosomal protein L12; a putative cytosolic large ribosomal subunit protein that binds to importin 11; may play a role in translation and ribosome biogenesis; expression of autoantibodies correlates with systemic lupus erythematosus	P30050
RPL13A	Ribosomal protein L13a; binds to mRNA 3'-UTR and inhibits translation; may play a role in cell proliferation; increased mRNA expression correlates with osteosarcoma	P40429
RPL14	Protein with strong similarity to rat Rpl14; which is a structural constituent of ribosome; member of the ribosomal L14e family; which are part of the large ribosomal subunit	P50914
RPL15	Ribosomal protein L15; a putative RNA binding protein; may play a role in translation; mRNA expression is upregulated in esophageal cancer	P61313
RPL17	Ribosomal protein L17; a cytosolic large ribosomal subunit protein that that may play a role in translation	P18621
RPL18	Ribosomal protein L18; involved in the regulation of translational initiation; protein kinase activity and eIF2 alpha phosphorylation by dsRNA; mRNA is upregulated in colon cancer	Q07020
RPL18A	Ribosomal protein L18a; a putative structural constituent of ribosome that is involved in response to ethanol and xenobiotic stimulus; may play a role in translation	Q02543
RPL19	Ribosomal protein L19; a putative structural constituent of ribosome that may play a role in translation; upregulated in breast tumors; increased mRNA expression is associated with prostate cancer	P84098
RPL21	Ribosomal protein L21; a component of large ribosomal subunit that may play a role in translation; altered expression in colorectal carcinogenesis	P46778
RPL23	Ribosomal protein L23; a putative structural constituent of ribosome that plays a role in the negative regulation of apoptosis; may be involved in translation and regulation of cell growth	P62829
RPL23A	Ribosomal protein L23a; a component of cytosolic large ribosomal subunit that may play a role in translation and cell proliferation inhibition; increased mRNA expression correlates with hepatocellular carcinoma	P62750
RPL24	Ribosomal protein L24; a putative structural constituent of 60S ribosomal subunit that may play a role in translation	P83731

RPL27	Ribosomal protein L27; a cytosolic large ribosomal subunit that may interact with RNA and plays a role in translation	P61353
RPL27A	Ribosomal protein L27a; component of the large 60S ribosomal subunit; may regulate macrophage proliferation and activation in response to bacteria; abnormally expressed in colorectal carcinomas and may be associated with atherosclerosis	P46776
RPL28	Ribosomal protein L28; a structural constituent of ribosome that may play a role in ribosome biogenesis and translation; mRNA is aberrantly expressed in colorectal carcinoma	P46779
RPL29	Ribosomal protein L29; a putative structural constituent of ribosome that acts in antiapoptosis and blood coagulation; may play a role in cell adhesion; upregulated in thyroid papillary carcinoma; gene mutation is associated with colorectal cancer	P47914
RPL3	Ribosomal protein L3; a RNA binding putative cytosolic large ribosomal subunit that may play a role in translation and nonsense mediated mRNA decay	P39023
RPL30	Ribosomal protein L30; a putative structural constituent of ribosome that may play a role in translation; mRNA expression is upregulated in liver neoplasms and hepatocellular carcinoma	P62888
RPL36A	Ribosomal protein L36a; a putative structural component of ribosome that may play a role in translation	P83881
RPL37	Ribosomal protein L37; a putative ribosomal protein that may bind to zinc ion and may play a role in translation; expression is upregulated in colon cancer	P61927
RPL5	Ribosomal protein L5; a structural constituent of ribosome that plays a role in translation and protein complex assembly; acts as an autoantigen in nephritis associated with systemic lupus erythematosus; mRNA expression is upregulated in several neoplasms	P46777
RPL6	Ribosomal protein L6; a putative RNA polymerase II transcription factor that functions in translation; may play a role in apoptosis and mammary gland development	Q02878
RPL7	Ribosomal protein L7; a nucleic acid binding protein that induces apoptosis; plays a role in ribosome binding to ER membrane; autoantigens are associated with coronary artery disease; autoantibodies are associated with systemic lupus erythematosus	P18124

RPL7A	Ribosomal protein L7a; a putative component of the 60S ribosomal subunit that binds thyroid hormone receptor; inhibits transcription by antagonizing nuclear receptors; upregulated in colorectal cancer and acts as trk-2h fusion oncogene in breast cancer	P62424
RPL8	Ribosomal protein L8; a structural constituent of ribosome that plays a role in translation; expression is downregulated in response to retinoic acid	P62917
RPL9	Ribosomal protein L9; may play a role in translation; mRNA expression is upregulated in hepatocellular carcinoma	P32969
RPLP0	Ribosomal protein P0; may play a role in apoptosis; acts as an autoantigen in systemic lupus erythematosus; mRNA is upregulated in several neoplasms	P05388
RPN2	Ribophorin II; an oligosaccharyl transferase that plays a role in protein amino acid N-linked glycosylation; protein retention in ER lumen; and protein modification process; mRNA is upregulated in colorectal neoplasms	P04844
RPS14	Ribosomal protein S14; a putative structural constituent of ribosome that may play a role in the chemical reactions and pathways resulting in the formation of a protein; gene haploinsufficiency correlates with myelodysplastic syndrome	P62263
RPS25	Ribosomal protein S25; a putative RNA-binding component of the small 40S ribosomal subunit that plays a role in induction of apoptosis and response to estrogen	P62851
RPS26	Ribosomal protein S26; a putative structural constituent of ribosome that binds mRNA; may play a role in translation; gene mutation is associated with Diamond-Blackfan anemia	P62854
RPS28	Protein with strong similarity to C. elegans Y41D4B.5; which is involved in reproduction; physiological processes; and positive regulation of growth; member of the ribosomal protein S28e family	P62857
RPS4Y1	Ribosomal protein S4 Y-linked 1; component of the small 40S ribosomal subunit; deficiency is proposed to play a role in Turner syndrome	P22090
RPS6	Ribosomal protein S6; involved in TOR; TCR; and PI3K cascades; plays a role in ribosome biogenesis; insulin secretion; glucose homeostasis; apoptosis; and gastrulation; mRNA is upregulated in colon cancer; knockout of the mouse Rps6 mimics hypoinsulinemia	P62753

RPS6KA1	Ribosomal protein S6 kinase 90kDa polypeptide 1; plays a role in protein amino acid phosphorylation; platelet activation; insulin receptor signaling pathway; neuron projection development; and antiapoptosis; upregulated in amyotrophic lateral sclerosis	Q15418
RRAS	Related RAS viral oncogene homolog; a Ral GTPase activator that regulates cell adhesion mediated by integrin; acts in GPCR signaling; antiapoptosis; cell proliferation; neurite growth; and endocytosis; mRNA is upregulated in glioblastoma	P10301
RRP12	Protein containing an NUC173 domain; has low similarity to A. thaliana AT2G34357	Q5JTH9
RSU1	Ras suppressor protein-1; plays a role in Ras protein signal transduction; MAPKK activation; and cell-matrix adhesion; inhibits cell proliferation	Q15404
RUVBL2	RuvB-like 2; an ATP-dependent DNA helicase that acts in protein oligomerization; ATP catabolism; and small nucleolar ribonucleoprotein complex assembly; may be involved in DNA recombination and repair; protein folding; and regulation of exit from mitosis	Q9Y230
SCAMP1	Secretory carrier membrane protein 1; a putative transporter that induces exocytosis; may play a role in post-Golgi vesicle-mediated transport; endocytosis; and clathrin coating of Golgi vesicle; decreased gene expression correlates with psychosis	O15126
SCAMP3	Secretory carrier membrane protein 3; may play a role in vesicular trafficking and recycling	O14828
SCO1	SCO cytochrome oxidase deficient homolog 1; a copper binding protein that acts in induction of apoptosis and aerobic respiration; may be involved in redox signal response; gene mutation causes cytochrome-c oxidase deficiency and neonatal ketoacidotic coma	O75880
SDCCAG1	Serologically defined colon cancer antigen 1; may regulate cell proliferation; mRNA expression is upregulated in response to methyl 4-methoxy-3-(3-methyl-2-butenoyl) benzoate treatment; high levels of autoimmune antibody correlates with colonic neoplasms	O60524
SDF2L1	Protein with strong similarity to mouse Sdf2l1; which is involved in response to antibiotic; calcium ion; heat; and unfolded protein; member of the protein	Q9HCN8

	mannosyltransferase IP3R and RyR (MIR) domain containing family	
SDHA	Succinate dehydrogenase complex subunit A flavoprotein; a mitochondrial electron carrier that acts in angiogenesis; downregulated in Huntington disease; gene mutation correlates with Leigh syndrome; paraganglioma; and cardiomyopathy	P31040
SEC13	SEC13 homolog; plays a role in ER to Golgi vesicle-mediated transport and genomic instability; mediates mitotic metaphase or anaphase transition; inhibits mitotic arrest	P55735
SEC16A	SEC16 homolog A; builds up endoplasmic reticulum exit sites in cooperation with p125 (SEC23IP) and acts in membrane traffic from the endoplasmic reticulum; plays a role in exit from mitosis	O15027
SEC23A	Sec23 homolog A; interacts with SEC24B and SEC24C; plays a role in intracellular protein transport; may function in exocytosis; gene mutation causes cranio lenticulo sutural dysplasia	Q15436
SEC23IP	Sec23-interacting protein; interacts with COPII components SEC24C and mouse Sec23a; regulates structures of ER exit sites; vesicular tubular clusters; and the cis-Golgi	Q9Y6Y8
SEC24B	SEC24 family member B; a component of COPII vesicle coat that is involved in protein transport and cochlea development; may act in endoplasmic reticulum to Golgi transport and cargo selection; mutant mice lacking murine Sec24b displays craniorachischisis	O95487
SEC63	SEC63 homolog; a putative transporter that interacts with Sec62 (TLOC1) and SEC61A1; may play a role in decidualization; gene mutations are associated with gastric tumors and polycystic liver disease	Q9UGP8
SENP8	SUMO-sentrin specific peptidase family member 8; a NEDD8-specific protease that is involved in protein deneddylation and neddylation	Q96LD8
SERF2	Small EDRK-rich factor 2; acts as a regulator of age-related proteotoxicity; may bind nucleic acids and function in pathogenesis	P84101
SERINC3	Serine incorporator 3; a putative membrane protein that plays a role in protection of cells from serum starvation and etoposide-induced apoptosis; mRNA is upregulated in lung tumor	Q13530
SERPINB6	Serpin peptidase inhibitor clade B member 6; acts in lysosome organization; may	P35237

	play a role in blood coagulation and keratinocyte differentiation; loss of function mutation causes autosomal-recessive nonsyndromic sensorineural hearing loss	
SETD7	SET domain containing 7; a histone H3 lysine 4-specific methyltransferase that acts in protein acetylation; promotes cell cycle arrest by p53-mediated DNA damage response; inhibits NF-kappaB activity; may play a role in chromatin silencing	Q8WTS6
SFRS4	Splicing factor arginine serine-rich 4; a RNA binding protein that acts in mRNA processing	Q08170
SHMT2	Serine hydroxymethyltransferase 2; involved in glycine biosynthesis and metabolism	P34897
SHOC2	Soc-2 suppressor of clear homolog; activates MAPK activity; regulates Ras protein signaling; epithelial to mesenchymal transition; embryonic atrioventricular development; and protein complex assembly; gene mutation is associated with Noonan like syndrome	Q9UQ13
SIN3A	SIN3 homolog A transcriptional regulator; a transcription corepressor that acts in histone deacetylation; cytotoxic T cell differentiation; apoptosis; and embryonic development; regulates cell cycle; mislocalization correlates with Huntington disease	Q96ST3
SIRT3	Sirtuin 3; an NAD-dependent histone deacetylase that acts in p53 mediated signal transduction; plays a role in neuroprotection; urea cycle; mitochondrial biogenesis; and brown fat cell differentiation; downregulated in breast cancer	Q9NTG7
SKIV2L2	Protein with high similarity to S. cerevisiae Mtr4p; which is a RNA-dependent ATPase that regulates translation; ribosomal large subunit export from nucleus; and snRNA processing; contains a DSHCT (NUC185) domain	P42285
SKP1	S-phase kinase-associated protein 1A; a ubiquitin-protein ligase that acts in cytokinesis; neuroprotection; and dopaminergic neuron differentiation; regulates inclusion body assembly and cyclin-dependent protein kinase activity; may act in RNA elongation	P63208
SLC12A2	Solute carrier family 12 member 2; regulates GABAergic synaptic transmission; Ca 2+ transport; and blood pressure; acts in neuron morphogenesis and inflammatory response; mRNA is upregulated in asthma; hemimegalencephaly; and ganglioglioma	P55011

SLC25A10	Solute carrier family 25 member 10; a putative dicarboxylic acid transporter that regulates malate transport; malate and citrate level; may be involved in gluconeogenesis; mouse Slc25a10 is associated with obesity	Q9UBX3
SLC25A6	Solute carrier family 25 member 6; a putative adenine transmembrane transporter that plays a role in TNF-alpha induced apoptosis; caspase activation; and cytochrome c release from mitochondria; regulates mitochondrial depolarization	P12236
SLC2A4	Solute carrier family 2 member 4; a glucose transmembrane transporter that acts in carbohydrate metabolism and regulation of transcription; aberrant expression is associated with obesity and type I diabetes mellitus	P14672
SLC35E1	Member of the UAA and EamA-like transporter family; has low similarity to rice Os09g0297400; which is involved in cellular response to sucrose starvation	Q96K37
SLC4A2	Solute carrier family 4 anion exchanger member 2; involved in bicarbonate transport; vacuolar acidification; ossification; enamel maturation; and spermatogenesis; regulates transcription; inhibits apoptosis; mouse Slc4a2 gene knockout causes osteopetrosis	P04920
SLC9A3R1	Solute carrier family 9 member 3 regulator 1; a cytoskeletal adaptor that plays a role in receptor-mediated regulation of Na+- H+ exchange; aberrantly expressed in breast cancer; glioblastoma; and inflammatory bowel diseases	O14745
SLC9A3R2	Solute carrier family 9 member 3 regulator 2; a ligand for various receptors that acts in GPCR pathway; elevation of cytosolic calcium ion concentration; and induction of apoptosis; regulates sodium-hydrogen antiporter activity	Q15599
SMARCAL1	SWI-SNF related matrix associated actin dependent regulator of chromatin subfamily a-like 1; an ATP-dependent DNA helicase that acts in regulation of transcription; gene mutation causes Schimke immuno osseous dysplasia and immunologic deficiency syndromes	Q9NZC9
SND1	Staphylococcal nuclease and tudor domain containing 1; a transcription coactivator that positively regulations cell proliferation; mRNA is upregulated and acts as a marker in prostate cancer	Q7KZF4
SNRPE	Small nuclear ribonucleoprotein polypeptide E; forms a 6S core particle with other snRNPs; may play a role in snRNP maturation; mRNA is upregulated in hormone-refractory prostate cancers	P62304

SNTA1	Syntrophin alpha 1; a water channel and structural constituent of muscle that acts in ephrin receptor signaling; regulates nitric oxide biosynthesis and vasoconstriction; upregulated in breast carcinoma; gene mutation correlates with long QT syndrome	Q13424
SOD1	Superoxide dismutase 1 soluble; acts in hydrogen peroxide production; aberrant expression correlates with Alzheimer disease; Parkinson disease; schizophrenic psychosis and arteriosclerosis; gene mutation causes amyotrophic lateral sclerosis	P00441
SOD2	Superoxide dismutase 2 mitochondrial; acts in superoxide metabolism; aging; antiapoptosis; and DNA double-strand break repair; aberrantly expressed in asthma; atherosclerosis; schizophrenia; pancreatitis; and colorectal and several neoplasms	P04179
SPAG7	Member of the R3H domain containing family; which may bind ssDNA; has very strong similarity to uncharacterized mouse Spag7	O75391
SPCS3	Protein with high similarity to C. elegans PHI-20; which is a putative subunit of the signal peptidase complex that has roles in reproduction; locomotory behavior and embryonic development; member of the signal peptidase subunit family	P61009
SPON2	Protein with strong similarity to rat Spon2; which plays a role in neuron cell-cell adhesion; neuron differentiation; and cell migration; may act in axon guidance and stimulation of axon regeneration; member of the spondin_N family	Q9BUD6
SPR	Sepiapterin reductase; acts in tetrahydrobiopterin and nitric oxide biosynthesis; gene mutation causes sepiapterin reductase deficiency disorder and dopa responsive dystonia; gene polymorphism is associated with Parkinson disease	P35270
SPTAN1	Non-erythrocytic alpha-spectrin 1; a calmodulin binding protein that binds to calcium ion; and is cleaved by CASP3 during apoptosis; may act as an autoantigen in the development of Sjogren syndrome	Q13813
SPTBN2	Spectrin beta non-erythrocytic 2; a putative structural constituent of cytoskeleton that regulates vesicle-mediated transport and synaptogenesis; may play a role in neurotransmitter secretion; gene mutation is associated with spinocerebellar ataxia type 5	O15020
SPTBN5	Spectrin beta non-erythrocytic 5; a putative structural protein of the rod and cone photoreceptor outer segments that may bind to actin	Q9NRC6
SRPK2	SFRS protein kinase 2; a serine-threonine kinase specific for SR splicing factors; enhances leukemia cell proliferation by phosphorylating acinus (ACIN1) and	P78362

	regulating cyclin A1 (CCNA1); increased expression may correlate with acute myelogenous leukemia	
SRPRB	Signal recognition particle receptor B subunit; inhibits cell growth; may play a role in apoptosis; expression is induced by retinoic acid	Q9Y5M8
SRR	Serine racemase; involved in peptidyl-serine racemization; D-serine production; and pyruvate metabolism; may play a role in synaptic transmission; gene polymorphism correlates with schizophrenia	Q9GZT4
SSR1	Signal sequence receptor alpha (translocon-associated protein alpha); a component of the signal sequence receptor complex that plays a role in the translocation of polypeptides across the endoplasmic reticulum membrane and may regulate cell proliferation	P43307
SSR4	Signal sequence receptor delta; interacts with an ubiquitin protein isopeptide ligase for dishevelled-1 (HECW1) to form a protein complex	P51571
STAM	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; negatively regulates EGF receptor activity; acts in antiapoptosis and thymocyte development; mRNA is upregulated in ependymomas	Q92783
STAMBP	STAM binding protein; a ubiquitin thioesterase that plays a role in protein stabilization; receptor degradation; and brain development; regulates apoptosis and growth; inhibits transcription	O95630
STAT1	Signal transducer and activator of transcription 1; mediates immune response; cell proliferation; and cell cycle regulation; induces apoptosis; aberrant expression is associated with HIV infection; Crohn disease; multiple sclerosis; and several neoplasms	P42224
STAT3	Signal transducer and activator of transcription 3; a transcriptional regulator that acts in antiapoptosis and angiogenesis; upregulated in rheumatoid arthritis and inflammatory bowel diseases; aberrant mRNA expression correlates with breast neoplasms	P40763
STAU1	Staufen RNA binding protein homolog 1; a tubulin binding protein that plays a role in intracellular mRNA localization; regulates dendrite morphogenesis; skeletal muscle development; and synaptogenesis	O95793
STIP1	Stress-induced phosphoprotein 1; a chaperone binding protein that plays a role in protein folding and refolding; ERK1-ERK2 cascade; neuron differentiation;	P31948

	neuroprotection; Ca ion import; and retina homeostasis; upregulated in colon cancer	
STK4	Serine-threonine kinase 4; regulates chromosome segregation; leukocyte migration; attachment of spindle microtubules to kinetochore; and protein stability; activates JUN kinase and caspase activity; inhibits T cell proliferation and cytokine production	Q13043
STOML2	Stomatin-like 2; a putative channel regulator that regulates mitochondrial membrane potential and protein stability; inhibits proteolysis; may mediate cytoskeletal anchoring at plasma membrane; aberrant gene expression is associated with several neoplasms	Q9UJZ1
STRAP	Serine-threonine kinase receptor associated protein; regulates TGF-beta receptor signaling; mediates cell cycle arrest and ubiquitin-dependent protein degradation; inhibits transcription and apoptosis; upregulated in colorectal; breast; and lung cancers	Q9Y3F4
STUB1	STIP1 homology and U-Box containing protein 1; an E3 ubiquitin protein ligase that acts in ubiquitin-dependent protein catabolism; protein targeting; protein folding; and Notch signaling; regulates transcription; antiapoptosis; and osteogenesis	Q9UNE7
STXBP3	Syntaxin binding protein 3; a glucose transporter that interacts with SNARE; plays a role in vesicle-mediated transport and regulation of exocytosis; may act in neurotransmitter release and vesicle docking; upregulated in type 2 diabetes	O00186
SUCLG1	Succinate-CoA ligase GDP-forming alpha subunit; catalyzes the conversion of succinyl CoA to succinate along with concomitant hydrolysis of GTP to GDP; gene mutations are associated with mitochondrial encephalomyopathies with methylmalonic aciduria	P53597
SUPT6H	Suppressor of Ty 6 homolog; a transcription elongation factor that mediates RNA elongation from RNA polymerase II promoter and chromatin remodeling	Q7KZ85
SYK	Spleen tyrosine kinase; a signal transducer that acts in Fc-receptor mediated signaling; B-cell activation; platelet activation; phagocytosis; and immunity; aberrantly expressed in systemic lupus erythematosus; lymphocytic leukemia; and breast cancer	Q15046

SYMPK	Symplekin; a transcription regulator that mediates mRNA polyadenylation; cell growth and proliferation and microtubule polymerization; mediates gene expression; phosphatase activity; establishment of cell polarity; and spindle assembly	Q92797
SYNCRIP	Synaptotagmin binding cytoplasmic RNA interacting protein; interacts with PRMT1; plays a role in cytidine to uridine editing; may be involved in establishment of RNA localization	O60506
SYNE1	Spectrin repeat containing nuclear envelope 1; a putative structural constituent of muscle that functions in nucleus organization and motor neuron innervation; gene mutation correlates with Emery-Dreifuss muscular dystrophy and cerebellar ataxia	Q8NF91
SYNE2	Spectrin repeat containing nuclear envelope 2; binds to emerin (EMD); lamin A/C (LMNA); and Sun1 (UNC84A); gene mutation may correlate with nuclear envelope abnormalities associated with Emery Dreifuss muscular dystrophy	Q8WXH0
SYNJ2BP	Synaptojanin 2 binding protein; promotes endocytosis; receptor internalization; and follicle-stimulating hormone secretion; mediates transcription; plays a role in hormone-mediated signaling and intracellular mitochondrial distribution	P57105
TAB1	TGF-beta activated kinase 1-MAP3K7 binding protein 1; regulates p38 MAPK and TGF-beta receptor pathways; acts in heart and lung development; apoptosis; IL production; and T-cell activation; may play a role in inflammatory response	Q15750
TAF15	TAF15 RNA polymerase II TATA box binding protein (TBP)-associated factor 68kDa; a RNA polymerase II transcription factor that stimulates transcription from RNA polymerase II promoter; gene translocation correlates with chondrosarcoma and acute leukemia	Q92804
TAF5	TAF5 RNA polymerase II; exhibits protein homodimerization activity; plays a role in histone acetylation and regulation of protein complex assembly	Q15542
TALDO1	Transaldolase 1; acts in pentose phosphate pathway; mitochondrial homoeostasis; and calcium ion fluxing; regulates cell proliferation and apoptosis; gene mutation is associated with hepatosplenomegaly; liver cirrhosis; and cardiomyopathy	P37837
TAOK1	TAO kinase 1; a protein kinase that acts in activation of MAPKK activity; chromosome segregation; protein amino acid phosphorylation; mitotic cell cycle spindle assembly checkpoint; and regulation of stress-activated MAPK cascade	Q7L7X3

TAOK2	TAO kinase 2; a MAP kinase kinase kinase that induces apoptosis; and muscarinic acetylcholine receptor and JNK signaling pathways; inhibits microtubule depolymerization; regulates cell shape; cell size; and protein catabolic process	Q9UL54
TAOK3	TAO kinase 3; interacts with IRE1a (ERN1); inhibits JNK (MAPK8)- SAPK (MAPK9) signaling	Q9H2K8
TARS2	Protein with high similarity to human TARS; which is a threonine-tRNA ligase; and is associated with connective tissue disorders and dermatomyositis; contains a threonyl and alanyl tRNA synthetase second additional domain	Q9BW92
TBC1D1	TBC1 domain family member 1; a Rab GTPase activator that regulates glucose import and fatty acid oxidation; may regulates cell cycle; mRNA is upregulated in gastric cancer; gene polymorphism is associated with obesity and male suicide	Q86TI0
TBC1D15	TBC1 domain family member 15; exhibits binding to RAB5A; RAB5B; and RAB5C; but does not exhibit GTPase activator protein activity towards RAB5A	Q8TC07
TBCD	Tubulin folding cofactor D; involved in response to arterial shear stress; may act in protein folding and protein stabilization	Q9BTW9
TBL2	Protein containing five WD domain G-beta repeats; has low similarity to A. thaliana AT4G00090; which acts in response to abscisic acid and virus	Q9Y4P3
TBRG4	Transforming growth factor beta regulator 4; interacts with DDEF2; involved in the regulation of cell proliferation; may play a role in cell cycle arrest	Q969Z0
TCEB1	Transcription elongation factor B SIII polypeptide 1; a ubiquitin-protein ligase that plays a role in RNA elongation from RNA polymerase II promoter; regulates proteolysis; forms a ternary complex with SOCS2 and TCEB2	Q15369
TCEB2	Transcription elongation factor B (SIII) polypeptide 2; a ubiquitin-protein ligase that plays a role in RNA elongation and protein stabilization; mouse Tceb2 is upregulated in cortical ischemia model	Q15370
TCHH	Trichohyalin; a structural protein of the hair follicle that acts in strengthening of the hair follicle; may play role in keratinocyte differentiation	Q07283
TCP1	T-complex 1; plays a role in protein hetero-oligomerization; protein folding; and maturation; may act in spermatogenesis; aberrant expression correlates with Down syndrome	P17987
TFB1M	Transcription factor B1 mitochondrial; catalyzes the transfer of a methyl group from S-adenosyl-L-methionine to a nucleoside residue in an rRNA molecule; may	Q8WVM0

	be involved in sensory perception of sound; gene polymorphism correlates with hearing loss	
TFG	TRK-fused gene; a signal transducer that plays a role in the negative regulation of SHP-1 phosphatase activity and dephosphorylation; gene translocation correlates with anaplastic large-cell lymphoma and thyroid neoplasms	Q92734
TGOLN2	Trans-Golgi network protein 2; may play a role in Golgi to endosome and Golgi to plasma membrane transport	O43493
THOC2	THO complex 2; a component of the TREX complex which may couple transcription to mRNA export; altered expression in brain may be associated with increased suicide in males	Q8NI27
THRAP3	Thyroid hormone receptor associated protein 3; a transcriptional coactivator that binds to spliced mRNA; activates pre-mRNA splicing and nuclear mRNA degradation	Q9Y2W1
TIMM44	Translocase of inner mitochondrial membrane 44; a putative P-P-bond-hydrolysis driven protein transmembrane transporter	O43615
TIMM50	Member of the NLI interacting factor family; has a region of low similarity to a region of S. cerevisiae Psr2p; which is a plasma membrane phosphatase required for sodium stress response	Q3ZCQ8
TJP2	Tight junction protein 2; involved in cell-cell adhesion; tight junction assembly; trophectodermal cell differentiation; and hippo signaling; mRNA is aberrantly expressed in breast and pancreatic neoplasms; gene mutation causes familial hypercholanemia	Q9UDY2
TKT	Transketolase; an enzyme that participates in the transfer of ketol groups; aberrant proteolysis correlates with Alzheimer disease; activity is decreased in Wernicke Korsakoff syndrome	P29401
TLK2	Tousled-like kinase 2; a protein serine-threonine kinase that may play a role in male meiosis; DNA replication-dependent nucleosome assembly; and transcription	Q86UE8
TM9SF2	Transmembrane 9 superfamily member 2; an endosomal protein that may play a role in ion transport	Q99805
TMED1	Transmembrane emp24 protein transport domain containing 1; binds to receptor; plays a role in cell maturation and is involved in response to antibiotic; may act in cell-cell signaling	Q13445

TMED10	Transmembrane emp24-like trafficking protein 10; involved in endoplasmic reticulum to Golgi vesicle-mediated protein transport and embryonic development; regulates protein targeting into nucleus and endopeptidase activity	P49755
TMED2	Transmembrane emp24 domain trafficking protein 2; plays a role in calcium sensing receptor maturation; plasma membrane targeting; and stabilization and embryonic placenta morphogenesis and heart looping	Q15363
TMED4	Member of the emp24 family; which are involved in protein transport; has low similarity to transmembrane protein p23 (mouse Tmed10); which is required for embryonic development and may be involved in secretory pathway	Q7Z7H5
TMED7	Transmembrane emp24 protein transport domain containing 7; member of the p24 family of small; abundant transmembrane proteins of the secretory pathway; forms a complex with other members of the p24 family; hp24alpha2; hp24beta1; and hp24delta1	Q9Y3B3
TMEM165	Member of the UPF0016 uncharacterized integral membrane protein family; has strong similarity to uncharacterized TPA regulated locus (rat Tparl); which may function in the negative regulation of cell proliferation	Q9HC07
TMEM30A	Transmembrane protein 30A; a potential beta subunit or chaperone for ATP8B1 plasma membrane trafficking and lipid flippase activity; increased mRNA expression may correlate with increased severity of disease progression associated with prostate neoplasm	Q9NV96
TMF1	TATA element modulatory factor 1; an androgen-enhanced transcriptional co-activator for the androgen receptor; expressed in testis	P82094
TMX4	Thioredoxin-related transmembrane protein 4; catalyzes oxidation-reduction (redox) reaction; may play a role in protein folding in endoplasmic reticulum	Q9H1E5
TOM1L1	Target of myb1(chicken)-like 1; a TOLLIP binding protein that promotes keratinocyte differentiation; regulates cell proliferation and transcription; involved in the recruitment of clathrin to endosomes; decreased expression correlates with skin neoplasm	O75674
TOMM70A	Translocase of outer mitochondrial membrane 70 homolog A; functions as a receptor of the preprotein import machinery of the mitochondrial outer membrane; interacts with heat shock proteins; expression in brain structures is inhibited by thyroid hormone	O94826

TOR3A	Torsin family 3 member A; a putative ATP-binding protein that is localized to endoplasmic reticulum	Q9H497
TP53RK	TP53 regulating kinase; a protein serine-threonine kinase that binds to and phosphorylates p53 (TP53) and regulates p53-mediated transcriptional activity; binds TPRKB and the GTPase RAB35; restrains apoptosis after mitotic stress	Q96S44
TPD52	Tumor protein D52; binds to annexin protein in calcium ion dependent manner; regulates cell proliferation; anchorage-independent cell growth; and apoptosis; increased expression is associated with breast; ovary; and prostate cancers	P55327
TPD52L2	Tumor protein D52-like 2; interacts with hD55 (TPD52L3); may play a role in cell proliferation and vesicle-mediated transport; increased mRNA expression correlates with breast carcinoma	O43399
TRADD	TNFRSF1A-associated via death domain; triggers NFKB1 activation and apoptosis; increased expression is associated with temporal lobe epilepsy; Alzheimer disease; and hepatitis B virus-induced liver cirrhosis and hepatocellular carcinoma	Q15628
TRAF2	TNF receptor-associated factor 2; regulates TNF-mediated signaling; NF-kappaB and JNK activation; antiapoptosis; B cell activation; and protein processing; upregulated in lung cancer; gene mutation is associated with chronic inflammatory disorders	Q12933
TRIM26	Member of the SPRY domain containing family; contains a B-box zinc finger domain and a C3HC4 type zinc finger; which may mediate protein-protein interactions; has moderate similarity to mouse Trim10; which plays a role in organ morphogenesis	Q12899
TRIP11	Thyroid hormone receptor interactor 11; a microtubule binding protein that interacts with ARNT; acts in Golgi ribbon formation; regulates transcription and gamma tubulin binding to Golgi membrane; gene translocation correlates with acute myeloid leukemia	Q15643
TRMT11	Protein containing a putative RNA methylase family UPF0020 domain; has moderate similarity to A. thaliana AT3G26410; which acts in tRNA modification and is involved in response to heat; abscisic and jasmonic acid; virus; nematode; and cytokinin	Q7Z4G4

TSC22D4	TSC22 domain family member 4; a transcriptional repressor that is involved in hyperosmotic response; may play a role in pituitary gland development; neuron fate specification; neuron development; and neuron maturation	Q9Y3Q8
TSFM	Ts translation elongation factor mitochondrial; a GTPase binding protein that may play a role in the regulation of translational elongation process	P43897
TSSC4	Tumor-suppressing subtransferable candidate 4; corresponding gene is located in a chromosomal region associated with tumor-suppressor activity	Q9Y5U2
TSTA3	Tissue specific transplantation antigen P35B; a GDP-L-fucose synthase that is involved in nucleotide-sugar metabolic process; protein amino acid glycosylation; and in utero embryonic development	Q13630
TSTD1		Q8NFU3
TTN	Titin; a structural constituent of muscle that acts in protein autoprocessing; acts as an autoantigen in melanoma associated retinopathy and myasthenia gravis; gene mutations are associated with dilated cardiomyopathy and muscular dystrophy	Q8WZ42
TUBB2B	Protein with very strong similarity to rat Tubb2b; which is a component of the microtubule that is involved in neuron migration; may play a role in axonogenesis and brain development	Q9BVA1
TUBB2C	Tubulin beta 2; an Notch binding protein that plays a role in protein complex assembly; regulates transcription from RNA polymerase II promoter and Notch signaling pathway; upregulated in prostatic neoplasms	P68371
TUBB6	Protein with strong similarity to beta-2 tubulin (rat Rgd1309427); which polymerizes to form microtubules and may act in axonal outgrowth and regeneration; contains a tubulin or FtsZ family GTPase domain and a tubulin or FtsZ family C-terminal domain	Q9BUF5
TUBGCP3	Tubulin gamma complex associated protein 3; a gamma tubulin binding protein that plays a role in microtubule nucleation	Q96CW5
TXN2	Thioredoxin 2; an antioxidant that acts in protein thiol-disulfide exchange and oxidative stress induced apoptosis; regulates angiogenesis; mRNA expression is associated with diabetic complications	Q99757
TXNDC17	Thioredoxin domain containing 17; a protein-disulfide reductase; negatively regulates NF-kappaB signaling pathway; regulates apoptosis by inhibiting caspase activation; regulates tumor necrosis factor-alpha (TNF) signaling pathway	Q9BRA2

TXNRD2	Thioredoxin reductase 2; acts in hydrogen peroxide catabolism; heart development; and hemopoiesis; regulates cell differentiation and cell proliferation; upregulated in hepatocellular carcinoma; SNPs are associated with susceptibility to breast cancer	Q9NNW7
UBA1	Ubiquitin-like modifier activating enzyme 1; required for estrogen receptor degradation and nucleotide excision repair upon macrophage differentiation; gene mutations are associated with X-linked infantile spinal muscular atrophy	P22314
UBE2D3	Ubiquitin-conjugating enzyme E2D 3; involved in ubiquitin-dependent protein catabolism; PML body organization; DNA damage checkpoint; and cell cycle arrest; inhibits transcription; increased mRNA expression correlates with meibomian cell carcinoma	P61077
UBE2K	Ubiquitin conjugating enzyme E2K; an ubiquitin ligase that activates JUN kinase; mediates proteasome mediated induction of apoptosis; involved in response to toxin; overexpressed in Alzheimer disease; upregulation is associated with psoriasis	P61086
UBE2M	Ubiquitin-conjugating enzyme E2M; an NEDD8 ligase that plays a role in induction of apoptosis; cell proliferation; and proteasomal ubiquitin-dependent protein catabolism	P61081
UBE2N	Ubiquitin-conjugating enzyme E2N; a ubiquitin-ligase that plays a role in regulation of DNA repair; MAPK and Wnt signaling; hemopoiesis; T cell development; and inflammatory response	P61088
UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2; exhibits protein heterodimerization and polyubiquitination; plays a role in DNA repair; cell cycle regulation; and cell proliferation	Q15819
UBE3C	Ubiquitin protein ligase E3C; interacts with 26 S proteasomes and catalyzes the assembly of Lys29- and Lys48-linked poly-ubiquitin chains	Q15386
UBE4A	Ubiquitination factor E4A; an ubiquitin-protein ligase that acts in apoptosis and protein polyubiquitination; may mediate ubiquitin-dependent protein catabolism; cell cycle; and cell differentiation; acts as an autoantigen in scleroderma	Q14139
UBL4A	Member of the ubiquitin-2 like Rad60 SUMO-like family; contains a ubiquitin family domain; has a region of moderate similarity to a region of S. cerevisiae Rol40p; which acts in ubiquitin-dependent protein catabolism and vesicle-mediated transport	P11441

UBQLN2	Ubiquilin 2; a proteasome binding protein that plays a role in ubiquitin-dependent protein catabolic process and may be involved in the G2-M transition of mitotic cell cycle	Q9UHD9
UBQLN4	Ubiquilin 4; an ataxin 1 interacting protein that may play a role in ubiquitin-dependent protein catabolic process and may link ataxin 1 (SCA1) to ubiquitin proteasome and chaperone pathways	Q9NRR5
UNC45A	Unc-45 homolog A; modulates progesterone receptor chaperoning by Hsp90; increased expression causes enhanced cell proliferation and metastasis in ovarian carcinoma	Q9H3U1
UPF3B	UPF3 regulator of nonsense transcripts homolog B; binds to spliced mRNA; plays a role in nuclear-transcribed mRNA catabolic process; gene mutation causes syndromic and nonsyndromic mental retardation	Q9BZI7
UQCRC1	Ubiquinol-cytochrome c reductase core protein I; a putative electron carrier that may play a role in aerobic respiration and oxidative phosphorylation; mRNA upregulation correlates with breast and ovarian neoplasms	P31930
UQCRC2	Ubiquinol-cytochrome c reductase core protein II; may act in aerobic respiration and oxidative phosphorylation	P22695
UQCRFS1	Protein with strong similarity to rat Uqcrfs1; which is involved in response to drug; member of the ubiquinol cytochrome reductase transmembrane region family; contains a rieske iron-sulfur protein 2Fe-2S domain	P47985
USP14	Ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase); acts in protein deubiquitination and spermatid differentiation; inhibits receptor degradtion; regulates synaptic transmission; cell chemotaxis; and ER associated degradation (ERAD) pathway	P54578
USP3	Ubiquitin specific protease 3; a chromatin binding protein that plays a role in acute-phase response; DNA damage checkpoint; histone dephosphorylation; and protein deubiquitination; regulates chromosome organization; S phase progression; and transcription	Q9Y6I4
USP47	Ubiquitin specific peptidase 47; binds E3 ubiquitin ligases; beta TRCP1 (BTRC) and beta TRCP2 (FBXW11); to regulate cell growth and survival; and cytotoxic effects of anticancer drugs	Q96K76
VARS	Valyl-tRNA synthetase; a putative tRNA ligase that may play a role in valyl tRNA	P26640

	aminoacylation	
VPS13A	Vacuolar protein sorting 13 homolog A; may play a role in protein targeting; gene mutation is associated with chorea-acanthocytosis	Q96RL7
VPS16	Vacuolar protein sorting 16 homolog; may function in vesicle docking and fusion between late endosomes and lysosomes	Q9H269
VPS18	Vacuolar protein sorting 18 homolog; a syntaxin binding ubiquitin ligase that plays a role in monoubiquitylation of GGA3; vesicle-mediated transport; and negative regulation of S phase cell cycle	Q9P253
VPS45	Vacuolar protein sorting 45 homolog; may play a role in inflammatory responses and post-Golgi vesicle-mediated transport	Q9NRW7
VPS4A	Vacuolar protein sorting 4 homolog A; an ATPase that plays a role in nucleus and centrosome organization; endosome transport; and protein-lysosome targeting; regulates spindle assembly and chromosome segregation	Q9UN37
VPS4B	Vacuolar protein sorting 4B; a component of the ESCRT III complex that plays a role in the proteolysis; formation of multivesicular bodies; endosome to lysosome transport; and lysosome organization; may act in meiosis and microtubule severing	O75351
VTA1	Vps20-associated 1 homolog; stimulates cell proliferation; may play a role in dopamine-induced cell growth	Q9NP79
WASH2P		Q6VEQ5
WASH3P		Q6VEQ5
WASH5P		Q6VEQ5
WDHD1	WD repeat and HMG-box DNA binding protein 1; a DNA replication initiation factor that links the MCM2-7 helicase and DNA pol alpha-primase complex; coordinates multiple cellular events in S phase and G2 phase	O75717
WDR77	WD repeat domain 77; binds to spliceosomal and histone proteins; mediates transcription repression; androgen receptor signaling; and cell differentiation; aberrantly localized in prostate cancer; mouse Wdr77 is associated with prostatic hyperplasia	Q9BQA1
WIPF2	WAS-WASL interacting protein family member 2; binds to Wiskott-Aldrich syndrome protein (WAS) in monocytes; functions in monocyte chemotaxis and actin polymerization	Q8TF74

WNK1	WNK lysine deficient protein kinase 1; a serine-threonine kinase that regulates protein autophosphorylation; MAPKK activation; K+ and Na+ transport; angiogenesis; and blood pressure; gene mutations correlate with pseudohypoaldosteronism and neuropathies	Q9H4A3
WWC3	Protein with moderate similarity to KIBRA protein (human KIBRA); which interacts with dendrin (human KIAA0749) and may be a structural protein	Q9ULE0
XPO1	Exportin 1; a nucleocytoplasmic transporter that plays a role in centrosome organization; antiapoptosis; and cytoplasmic NF-kappaB sequestration; increased mRNA expression correlates with cervical cancer	O14980
XPO7	Exportin 7 (RAN binding protein 16); a Ran GTPase that may play a role in nuclear export of proteins; binds the bHLH transcription factor E12 (TCF3) to likely enhance its activity	Q9UIA9
YARS2	Tyrosyl-tRNA synthetase 2 mitochondrial; a mitochondrial tyrosyl tRNA synthetase that forms homodimers; gene mutation causes causes myopathy; lactic acidosis; and sideroblastic anemia MLASA syndrome	Q9Y2Z4
YBX1	Y-box binding protein 1; a transcription factor that acts in DNA repair; spliceosome assembly; cell proliferation; and apoptosis; upregulated in anemia and breast and several other cancers; autoimmune antibody correlates with systemic scleroderma	P67809
YLPM1	YLP motif containing 1; a putative polynucleoside kinase that forms a complex with SAM68; CIA; NF110 or NF45; and HNRNP-G	P49750
YTHDF3	Protein with high similarity to human YTHDF2; which is an antigen reactive with autologous IgG from renal-cell carcinoma patients and determined to be a naturally occurring autoantigen; member of the YT521-B-like family	Q7Z739
YWHAE	Tyrosine 3-monooxygenase-tryptophan 5-monooxygenase activation protein epsilon polypeptide; acts in apoptosis; neuron migration; brain development; and memory; upregulated in Creutzfeldt-Jakob syndrome; lung cancer; and meningioma	P62258
ZC3H4	Member of the zinc finger C-x8-C-x5-C-x3-H type (and similar) family; has a region of moderate similarity to a region of human ZC3H8; which is a specific transcriptional repressor of GATA3 and may regulate thymocyte homeostasis and T-cell differentiation	Q9UPT8

ZC3HAV1	Zinc finger CCCH-type antiviral 1 (zinc finger antiviral protein); acts synergistically with an interferon-induced factor for maximal activity against alphaviruses	Q7Z2W4
ZNF622	Zinc finger-like protein 9; homodimeric transcription factor that binds human MYBL2 and enhances transcriptional activity; may enhance apoptosis induced by various extracellular signals; associates with human MELK and is a substrate of mouse Melk	Q969S3
ZW10	ZW10 kinetochore associated homolog; acts in mitotic sister chromatid segregation; mitotic metaphase-anaphase transition; and ER to Golgi vesicle-mediated transport; gene mutations are associated with colorectal neoplasms	O43264

Table S4. Thirty seven transcription factors that bind to Yes-set.		
Gene symbol	**BKL description**	**Molecule name**
ARNT	Aryl hydrocarbon receptor nuclear translocator; a transcriptional activator that acts in angiogenesis; cell fate determination; and placenta development; upregulates breast neoplasms; decreased mRNA expression correlates with type 2 diabetes and leiomyoma	arnt
DBP	D site albumin promoter binding protein; a transcription activator that plays a role in circadian rhythm; entrainment of circadian clock; and learning; involved in activation of MAPK activity and cellular response to starvation	DBP
E2F1	E2F transcription factor 1; binds to DNA; regulates neurogenesis; aberrant expression is associated with Alzheimer disease associated with Down syndrome; breast and several neoplasms; aberrant mRNA expression is associated with myelodysplastic syndromes	E2F-1
E2F2	E2F transcription factor 2; plays a role in T-helper cell differentiation; cell cycle arrest; and hemopoiesis; regulates apoptosis and arterial contraction; aberrant mRNA expression correlates with ovarian and prostate neoplasms and astrocytomas	E2F-2
E2F3	E2F transcription factor 3; a transcription activator that induces G1-S and G2-M phase transition in mitotic cell cycle; involved in DNA damage induced apoptosis and neuron migration; overexpressed in retinoblastoma; mRNA is upregulated in lung neoplasms	E2F-3a
E2F4	E2F transcription factor 4; a transcriptional regulator that regulate cell cycle; hemopoiesis; and eye pigmentation; involved in neuron differentiation and apoptosis; gene mutation correlates with T-cell leukemia and several cancers	E2F-4

E2F5	E2F transcription factor 5 p130-binding; a transcriptional activator that binds to RBL2; may regulate cell cycle; mRNA is aberrantly expressed in acute myelocytic leukemia and breast and ovarian neoplasms	E2F-5
E2F7	E2F transcription factor 7; a transcriptional repressor and putative tumor suppressor that acts in cell cycle progression by repressing a subset of E2F-responsive promoters; mRNA expression is induced in cutaneous squamous cell carcinomas	E2F-7-isoform1
FOXJ2	Fork head box J2; a transcriptional activator with dual DNA binding specificity; may play a role in spermatogenesis; erythropoiesis; and transcription; may be involved in the maintenance and survival of developing and adult neurons	Foxj2
GATA1	GATA binding protein 1; a transcriptional regulator that acts in erythropoiesis and platelet activation; gene mutation causes congenital erythropoietic porphyria; thrombocytopenia; and myeloproliferative disorders associated with Down syndrome	GATA-1
GATA2	GATA binding protein 2; a transcriptional activator that regulates megakaryocyte differentiation; apoptosis; and cell proliferation; involved in neurogenesis; angiogenesis; and cell fate determination; gene map position correlates with myeloid leukemia	GATA-2
GATA3	GATA-binding protein 3; a transcription regulator that acts in hair development and pigmentation; downregulated in Hodgkin lymphoma; gene mutaion causes hypoparathyroidism and deafness; mRNA is downregulated in psoriasis and atopic dermatitis	GATA-3
GATA4	GATA binding protein 4; a transcription factor that regulates cardiomyocyte differentiation; apoptosis; and organ development; aberrantly expressed in testis; ovary and various other cancers; gene mutations are associated with congenital heart defects	GATA-4

GATA5	GATA binding protein 5; a transcriptional activator that plays a role in endothelial cell differentiation and urogenital system development; mRNA expression is downregulated in colorectal and stomach neoplasms and upregulated in breast cancer	GATA-5
GATA6	GATA binding protein 6; a transcriptional activator that plays a role in cell cycle; antiapoptosis; and heart development; upregulated in ovarian; colorectal; and testicular carcinomas; gene mutation correlates with congenital heart diseases	GATA-6short
IRF1	Interferon regulatory factor 1; a transcription activator that acts in JAK-STAT cascade; immune response; and apoptosis; aberrantly expressed in psoriasis and multiple sclerosis; aberrant mRNA expression is associated with ovarian and several neoplasms	IRF-1
IRF2	Interferon regulatory factor 2; a transcription regulator; mediates G1-S transition of mitotic cell cycle and cell proliferation; mutations are associated with multiple sclerosis and atopic dermatitis; gene maps to a locus associated with psoriasis	IRF-2
IRF3	Interferon regulatory factor 3; a transcriptional coactivator that acts in innate immunity; and cytokine biosynthesis; negatively regulates DNA replication; plays a role in virus-induced apoptosis	IRF-3
IRF4	Interferon regulatory factor 4; a transcription factor that acts in TLR signaling and cell cycle; inhibits proinflammatory cytokine involved in immune response and apoptosis; aberrantly expressed in B-cell lymphocytic leukemia and multiple myeloma	IRF-4
IRF5	Interferon regulatory factor 5; a transcription factor that mediates cell growth; apoptosis; and immune response; gene polymorphisms are associated with inflammatory bowel disease; Wegener granulomatosis; ulcerative colitis; arthritis;	IRF-5, IRF-5-xbb3, IRF-5-xbb4

	and sclerosis	
IRF6	Interferon regulatory factor 6; a transcription activator that regulates Notch signaling pathway; acts in organ development; gene mutations correlate with cleft lip; anodontia; popliteal pterygium syndrome; and skin and urogenital abnormalities	IRF-6
IRF7	Interferon regulatory factor 7; a transcriptional regulator that mediates innate immune response via regulating type-I interferon production and monocyte and macrophage differentiation; increased expression correlates with lesional form of psoriasis	IRF-7A
IRF8	Interferon regulatory factor 8; a sequence-specific DNA binding transcription factor that acts in myeloid cell differentiation; cytokine biosynthesis; apoptosis; and T-cell mediated cytotoxicity; downregulated in chronic myeloid leukemia	IRF-8
ISGF3G	Interferon regulatory factor 9; binds to DNA; acts in JAK-STAT cascade and regulation of transcription; loss of protein is associated with chronic lymphocytic leukemia; mRNA is upregulated in tuberculosis and uterine neoplasms	IRF-9
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog; a transcription activator that acts in eye development and ossification; upregulated in T-cell lymphoma; gene mutations are associated with cataract; anterior segment dysgenesis; and microphthalmia	c-MAF-isoform2
NFIA	Nuclear factor I-A; a transcriptional regulator that acts in brain development; neuron differentiation; and redox signal response	NF-1A
NFIB	Nuclear factor 1-B; a transcription factor that binds and mediates activity of other NFI proteins; acts in dentate gyrus; lung epithelium; and chondrocyte development; downregulated in neuroblastoma; genetic translocation correlates with	NF-1B

	multiple myeloma	
NFIC	Nuclear factor I-C; induces RNA polymerase II mediated transcription; regulates hedgehog; Wnt; TGFB; and PDGFA signaling; S phase of cell cycle; anagen; odontogenesis; and wound healing; aberrantly expressed in breast cancer and lymph node metastases	CTF-1, CTF-2
NFIX	Nuclear factor IX (CCAAT-binding transcription factor); an RNA polymerase III transcription factor that mediates endochondral ossification and mineralization	NF-IX
RB1	Retinoblastoma 1; a transcription regulator that regulates Rac GTPase activity; acts in DNA damage checkpoint; apoptosis; cell proliferation; ossification; hemopoiesis; and organ development; downregulated in lung; breast; and several other cancers	pRb
STAT1	Signal transducer and activator of transcription 1; mediates immune response; cell proliferation; and cell cycle regulation; induces apoptosis; aberrant expression is associated with HIV infection; Crohn disease; multiple sclerosis; and several neoplasms	STAT1alpha, STAT1beta
STAT2	Signal transducer and activator of transcription 2; a transcription factor that plays a role in JAK-STAT cascade; immune response; and transmembrane receptor protein tyrosine phosphatase signaling pathway	STAT2-isoform1
TFDP1	Transcription factor Dp-1; a transcriptional coactivator that mediates cell cycle entry into S phase and apoptosis; regulates transcription of G1-S phase of mitotic cell cycle; gene amplification and mRNA overexpression correlates with breast cancer	DP-1

TFDP2	Transcription factor Dp-2 (E2F dimerization partner 2); a transcriptional activator that is involved in cell cycle regulation and induction of apoptosis; may be involved in cell proliferation	DP-2
USF1	Upstream stimulatory factor 1; a transcription activator; regulates cell proliferation; loss of activity is associated with breast neoplasms; mRNA is upregulated in vitiligo; gene polymorphisms are associated with cardiovascular disease and hyperlipidemia	usf1
USF2	Upstream transcription factor 2 c-fos interacting; a transcription activator that plays a role in central nervous system and utero embryonic development and lactose biosynthetic process; gene translocation correlates with hydronephrosis	USF2a, USF2b, USF2c

Table S5. Frequently appearing transcription factor throughout multiple key node networks.

key node name	the number of appearance in key node networks
IRF1	64
IRF4	54
IRF5	54
p53-isoform1	54
IRF8	53
ISGF3G	53
IKK-beta	50
IRF7	43
Src-isoform1	33
E2F-2	30
RB1	30
IRF2	29
Raf-1-isoform1	29
E2F-5: DP-1	28
c-Myc-isoform1	27
GATA3	27
brca1	26
STAT6-xbb1	25
p300	24
Jak2	23
RelA-p65	23
GATA6	22
CBP	20
ERK2	19
Bcl-3	18
MEKK1	18
AP-2alphaA	17
GSK3beta	17

IRF-6	17
TFAP2A	17
AhR: arnt	16
Ahr-xbb2	16
GATA4	16
c-Jun	15
NR0B2	15
SHP	15
IKK-alpha	14
SHP2-isoform2	14
TP53	14
MAF	13
NF-kappaB1-p50: RelA-p65	13
SHP-1L	13
Jak1	12
MYC	12
PKCdelta-xbb1	12
ATM	11
fakB	11
Jak3	11
SHP1-isoform1	11
FAS	10
GATA2	10
IkappaB-alpha	10
PKCdelta	10
VEGFR-2	10
ABL-1a	9
E2F1	9
GATA1	9
HIF-1alpha{p}	9
IKK-gamma{sumo}	9

NF-kappaB1-isoform 1	9
sumo1	9
APP695	8
DNA-PKcs-isoform1	8
ErbB2	8
LynA	8
MyoD	8
Sp1	8
STAT1	8
STAT4	8
AKT-1	7
IKK-i	7
PP2A	7
Bcl3	6
c-Kit	6
EGF: (ErbB1{pY})2: Src: STAT1alpha	6
ERK1	6
IKBKE	6
ILK	6
KIT	6
MITF-M1	6
NF-kappaB1-isoform 2	6
PDGFRbeta	6
STAT3-isoform1	6
Wip1	6
Cdk1-isoform1	5
Daxx	5
Hsp70-1	5
INS	5

insulin	5
NFIA	5
NFKB1	5
PTPN6	5
AT2	4
CDKN1A	4
cyclinD: Cdk4	4
ErbB1-p170	4
HIF-1alpha-isoform2	4
IFNGR2: Jak2: Tid-1: Hsp70-1	4
IKK-gamma	4
KDR	4
MKP-1	4
p21Cip1	4
p50	4
ABL-1b	3
AKT1	3
CASP6	3
HIF1A	3
IFNB1	3
IFNbeta	3
IFNG	3
IFNgamma	3
MEK1	3
MEK2	3
proCaspase-6	3
PTK2	3
SHP1-isoform2	3
STAT6-isoform1	3
Ubc9	3
angiotensin II	2

ATM{pS1981}	2
calcitriol: VDR{pS51}{pS208}: 9-cis-retinoic acid: RXR-alpha: SKIP: SRC-1: p300	2
CTLA-4	2
cyclinB: Cdk1	2
EKLF	2
Evi-1	2
IGF1R	2
IGF-1R	2
lepr-B	2
PIAS1	2
PIASy	2
RelA-p65: NF-kappaB1-p50	2
Roc1	2
SRC-1A	2
26S proteasome	1
A20	1
AGTR2	1
alpha-synuclein-isoform1	1
APC: axin: beta-catenin: CKI-epsilon: Dvl{p}: Frat1: GSK3beta	1
APC: axin: beta-catenin: GSK3beta	1

AT1A	1
ATF-2-xbb4	1
beta1A-integrin	1
beta1D-integrin	1
beta-catenin	1
beta-catenin{pS33} {pS45} {ub}: CKI-alpha; CKI-delta: axin{p}: APC{p}: GSK3beta: beta-TrCP1: Cul-1{nedd}: Skp1	1
BGPI-A	1
Cdc25A	1
Cdc25B3	1
Cdc25C-isoform1	1
Cdk2	1
cdk9	1
CEACAM1	1
CKI-delta-Isoform2	1
CREB	1
c-Rel	1
Csk	1
CSX	1
Cul-1	1
CUL4A-isoform2	1
cyclinD: Cdk6	1
EGR1	1
Egr-1	1
ER-alpha-L	1
FOXO3a	1
Frat1	1

GCN5-L	1
GCN5-S	1
GSK3B	1
HIF-1alpha{hydP}: p53: mdm2	1
HSF1-L	1
HSPA1A	1
huntingtin	1
IFNAR2-isoform1	1
InsR-A	1
IRF3	1
IRS-2	1
KSR	1
mdm2-isoform1	1
MSK1	1
NF-AT1B	1
NFIB	1
NF-kappaB	1
NIK	1
NKX2-5	1
p/CAF	1
p105{p} {ub}	1
p53beta	1
PDGFRB	1
PDGFRbeta{pY}	1
PDK1-isoform1	1
PIAS4	1
PIP3	1
PKCalpha	1
PKCgamma	1
PKCiota	1
RelA-p65delta	1

RSK2	1
SCF-beta-TrCP1	1
SHIP-110	1
Smad4	1
SOCS-1	1
SOCS3	1
SOCS-3	1
STAT1{pY701}	1
STAT2	1
TBK1	1
TC-PTPa	1
TC-PTPb	1
TGC	1
Tid-1L	1
TRAF6	1
TrkA-I	1
Tyk2	1
USF1	1
VEGF-145	1
VEGF-165	1
VEGF-D	1
VEGF-E	1
VRP	1