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**STUDY OF HYPOXIA DRIVEN PANCREATIC CANCER
DEVELOPMENT**

NIKHIL GUPTA

SCHOOL OF BIOLOGICAL SCIENCES

2019

**STUDY OF HYPOXIA DRIVEN PANCREATIC CANCER
DEVELOPMENT**

NIKHIL GUPTA

SCHOOL OF BIOLOGICAL SCIENCES

A thesis submitted to the Nanyang Technological University in partial
fulfillment of the requirement for the degree of Doctor of Philosophy

2019

Statement of Originality

I hereby certify that the work embodied in this thesis is the result of original research done by me except where otherwise stated in this thesis. The thesis work has not been submitted for a degree or professional qualification to any other university or institution. I declare that this thesis is written by myself and is free of plagiarism and sufficient grammatical clarity to be examined. I confirm that the investigations were conducted in accord with the ethics policies and integrity standards of Nanyang Technological University and that the research data are presented honestly and without prejudice.

18/05/2020

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.....

Newman Sze Siu Kwan

Authorship Attribution Statement

This thesis does contain materials from papers published in peer-reviewed journals or papers accepted at conferences in which I am listed as an author.

Chapter 3, 4 and 6 are published as **Gupta, N.**, Park, J. E., Tse, Wilford., Low, J. K., Kon, O, L., McCarthy, N., and Sze, S. K. (2019) ERO1 α promotes hypoxic tumor progression and is associated with poor prognosis in pancreatic cancer. *Oncotarget* 10(57): 5970–5982

The contributions of the co-authors are as follows:

- Associate/Prof Newman Sze provided the initial project direction, supervision, and edited the manuscript drafts.
- I prepared the manuscript drafts. The manuscript was revised by Dr. Wilford and Dr. Park.
- I co-designed the study with Associate/Prof Newman Sze and performed all the laboratory work at the School of Biological Sciences. I also analyzed the data.
- All microscopy, including sample preparation, was conducted by me in the Core instrument Facility.
- Dr. Park assisted in the interpretation of imaging and microscopy techniques.
- Dr. McCarthy, Dr. Low, and Dr. Kon provide reagents and guidance throughout the project.

18/05/2020

A handwritten signature in black ink, appearing to read 'Nikhil Gupta' with a stylized flourish at the end.

Nikhil Gupta

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TABLE OF CONTENTS

<u>Acknowledgments.....</u>	<u>I</u>
<u>Table of Contents.....</u>	<u>II</u>
<u>List of Figures.....</u>	<u>III</u>
<u>List of Tables.....</u>	<u>IV</u>
<u>Abbreviation.....</u>	<u>V</u>
<u>Abstract.....</u>	<u>VI</u>
Chapter 1 - Background and Literature Review.....	1
1.1 Pancreatic cancer: Current picture	2
1.2 Pancreatic cancer and hypoxia	6
1.3 Pancreatic cancer and Immunosuppression.....	11
1.4 Pancreatic cancer and exosome.....	13
1.5 Quantitative proteomics.....	15
1.6 Aims and objective of the project.....	20
1.6.1 Specific Aims.....	22
Chapter 2 – Material and Methods.....	27
2.1 Chemicals.....	28
2.2 Cell culture.....	28
2.3 Protein quantification assay	30
2.4 MTT assay.....	31

2.5 Western blot analysis	31
2.6 RNA Isolation and quantitative PCR (qPCR)	33
2.7 Cell Proteomics.....	34
2.7.1 pSILAC labeling (pulsed SILAC)	34
2.7.2 <i>In-solution</i> digestion	34
2.7.3 Reverse -Phase High-Performance Liquid chromatography.....	35
2.7.4 LC-MS/MS	37
2.7.5 Data Analysis	38
2.7.6 Bioinformatic Analysis.....	39
2.8 Exosome Proteomics (label-free).....	40
2.8.1 Exosome Isolation.....	40
2.8.2 Nanoparticle Tracking Analysis (NTA).....	41
2.8.3 Exosome digestion (Protein Isolation from exosome).....	41
2.8.4 One dimensional gel electrophoresis and <i>In-gel</i> digestion.....	42
2.8.5 LC-MS/MS.....	42
2.8.6 Data Analysis.....	43
2.8.7 Bioinformatic Analysis.....	46
2.9 CRISPR/Cas9 deletion of ERO1 α	46
2.10 Cell culture and Lentiviral Transduction.....	47
2.11 DNA sequencing.....	48
2.12 Colony Formation Assay (CFA).....	48
2.13 Transwell cell Invasion & Wound healing assay.....	48
2.14 Intracellular ROS detection.....	49

2.15 Xenograft tumor development assay.....	49
2.16 Cell Proteomics (TMT labeling).....	50
2.16.1 <i>In-solution</i> digestion	50
2.16.2 Reverse Phase HPLC Fractionation.....	51
2.16.3 Desalting peptide samples.....	51
2.16.4 LC-MS/MS.....	52
2.16.5 Data Analysis.....	53
2.16.6 Bioinformatic Analysis.....	54
2.17 Co-Immunoprecipitation (Co-IP).....	54
2.17.1 Protein assay.....	55
2.17.2 Protein Digestion.....	56
2.17.3 LC-MS/MS	56
2.17.4 Data Analysis	58
2.17.5 Bioinformatic Analysis	60
2.17.6 Western blot analysis	60
2.18 Statistical Analysis	61
2.19 Study Approval	61

Chapter 3 Developing of *in-vitro* hypoxic pancreatic cancer cell model (MIAPaCa-2)62

Establishment of a hypoxic pancreatic cancer cell model.....	63
3.1 Rationale	63
3.2 Results and discussion.....	64

Chapter 4 - Profiling of cellular proteomes of the PDAC cells under normoxia and hypoxia.....68

Profiling of *de-novo* protein synthesis of a pancreatic cancer cell line (MIAPaCa-2) under normoxia or hypoxia

4.1 Rationale69

4.2 Results and Discussion.....70

Chapter 5 - Profiling of exosomes secreted from PDAC cells under normoxia or hypoxia.....92

5.1 Rationale.....93

5.2 Results and Discussion.....94

Chapter 6 - Knockout, biochemical and functional studies of ERO1 α109

6.1 Rationale110

6.2 Results and discussion.....111

Chapter 7 - Quantitative proteomic profiling to identify the differentially expressed proteins (ERO1 α regulated proteins/pathways) using WT and ERO1 α KO PDAC cells.....123

7.1 Rationale124

7.2 Results and discussion.....124

Chapter 8 - Protein Interactomic analysis of highly expressed ERO1 α in PDAC cells.....134

8.1 Rationale	135
8.3 Results and discussion.....	136
 Chapter 9 - Conclusion and Future Direction.....	147
9.1 Concluding remarks and future perspective.....	148
 References	158
 Supplementary Data.....	175
 Appendix A – Publications.....	176
Appendix B – Conference presentation	178
Appendix C – Western Blot Images (Unadultered Version).....	181
Appendix D – Mass Spectrometry Data (New File in Landscape)	

LIST OF FIGURES

Chapter 1

Figure 1.1: (A) Five-year survival of pancreatic cancer in the world based on the CONCORD-3 study(22) (B) Progression model from a normal cell to metastatic pancreatic cancer in different stages..... 3

Figure 1.2: Hypoxia-induced factor, HIF-1 α , is a crucial mediator of tumor-related characteristics in pancreatic cancer..... 7

Figure 1.3: Hypoxia driven evolution of tumor progression and metastasis..... 10

Figure 1.4: Schematic diagram showing the experimental workflow of SILAC.....18

Figure 1.5: Illustration of the plausible hypothesis of hypoxia-driven pancreatic cancer development.....22

Chapter 3

Figure 3.1: Growth profile of PDAC cells (MIAPaCa-2) in (A) serum and (B) serum-free conditions under hypoxia as compared to normoxia.....65

Figure 3.2: RT-PCR assessment of fold change (Hx/Nx) in hypoxia markers (A) HK2 and (B) NDRG1 in serum and serum-free conditions at 24h (C) Western blot profile of HIF-1 α Western blot of HIF-1 α protein under normoxia or hypoxia in PDAC cells (MIAPaCa-2).....66

Chapter 4

Figure 4.1: Schematic representation of the experimental design to perform the quantitative global proteomics analysis of PDAC cells using pulsed SILAC.....71

Figure 4.2: (A) Venn diagram showing the total number of protein identified in 4 different conditions (NxS; NxSF; HxS; HxSF) of hypoxia-induced proteins identified as being newly synthesized under S or SF conditions (B) Analysis of protein distribution against log₂ H/L ratio for the S and SF culture conditions during normoxia/hypoxia revealed that most of these proteins are downregulated during hypoxia.....73

Figure 4.3: Volcano plot illustrates significantly differentially abundant proteins in serum and serum-free conditions under hypoxia.....	75
Figure 4.4: Gene ontology analysis of the proteins downregulated by hypoxic tumor cells in either serum-replete or serum-free conditions....	76
Figure 4.5: (A) Venn diagram showing the number of hypoxia-induced proteins identified as being newly synthesized under S or SF conditions (Calculated by Hx/Nx Ratio from proteomics data). (B) Functional classification of tumor proteins expressed de novo in response to hypoxia stress.....	78
Figure 4.6: Log ₂ fold change (Hx/Nx) in actively translating proteins detected in either S or SF culture conditions.....	79
Figure 4.7: Log ₂ fold change (Hx/Nx) in angiogenic factor expression comparing S and SF culture conditions.....	81
Figure 4.8: Schematic diagram of the pathway involved in pancreatic cancer.....	82
Figure 4.9: qPCR validation of key hypoxia-induced proteins as identified by pSILAC analysis.....	83
Figure 4.10: PREOCG analysis of genes associated with poor clinical prognosis in cancer patients and identified in our pSILAC dataset of hypoxia-induced proteins.....	85
Figure 4.11: Comparison and survival analysis of ERO1 α expression levels between healthy tissues and disease samples in relevant GEO datasets.....	87-88
Figure 4.12: ERO1 α mRNA and protein expression levels in PDAC cells.....	90

Chapter 5

Figure 5.1: Schematic diagram of the exosome-like vesicles (EVs) isolation protocol.....	95
Figure 5.2: Morphology and size distribution analysis of EVs derived from PDAC cells conditioned media depleted of cell debris and fractioned by differential centrifugation.....	97-98

Figure 5.3: Western blots of known exosome markers isolated from normoxic and hypoxic PDAC cells and negative control GM130.....	99
Figure 5.4: Vein diagram and analysis of differential protein expression in serum-free conditions under hypoxia.....	101
Figure 5.5: Gene ontology analysis of exosome proteome.....	105
Figure 5.6: Western blot profile of Immunecheckpoints in cell lysate and exosome under normoxia or hypoxia.....	108

Chapter 6

Figure 6.1: DNA sequencing analysis of wild type (WT) and ERO1 α KO.....	112
Figure 6.2: Cell growth analysis of WT and ERO1 α -KO clones under hypoxia.....	113-114
Figure 6.3: <i>Invitro</i> scratch assay performed by using the indicated cell clones and culture conditions.....	115
Figure 6.4: Transwell Migration assay performed by using the indicated cell clones and culture conditions.....	116
Figure 6.5: Western blot analysis of ERO1 α -regulated proteins comparing WT with ERO1 α -KO tumor cells.....	118
Figure 6.6: DCFDA assay with representative fluorescence images of WT and ERO1 α -KO PDAC cells.....	120
Figure 6.7: Representative images of xenografted mouse tumor experiment.....	122

Chapter 7

Figure 7.1: Schematic representation of the experimental design to perform the quantitative proteomics analysis of WT and KO ERO1 α by using TMT 6-plex isobaric tags.....	126
Figure 7.2: Comparison of protein count against the TMT Log ₂ ratio between different experimental conditions.....	128

Figure 7.3: GO analysis illustrates the classes of proteins with significantly reduced expression.....	133
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Chapter 8

Figure 8.1: Schematic representation of the experimental design of ERO1 α co-IP.....	137
---	-----

Figure 8.2: Comparison of the identified proteins between Nx, ERO1 α -co-IP, and Hx,ERO1 α -Co-IP.....	140
--	-----

Figure 8.3: The ERO1 α interacting proteins network diagram.....	142
---	-----

Figure 8.4: The ERO1 α interacting proteins network diagram ranked based on the clustering coefficient.....	144
--	-----

Figure 8.5: Gene ontology analysis of ERO1 α interacting partners.....	146
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List of Tables

Chapter 2

Table 2.1 Buffer composition for the 60-minute HPLC gradient.....37

Table 2.2 List of CRISPR guide RNA designed by CHOP CHOP V2.0...47

Chapter 4

Table 4.1 List of critical intrinsic hypoxia markers.....80

Table 4.2 List of gene expression microarray dataset used for ERO1 α expression analysis.....88

Chapter 5

Table 5.1 List of exosome markers identified.....102

Table 5.2 List of Cluster of differentiation (CDs) identified103

Chapter 7

Table 7.1 Top 20 proteins affected by ERO1 α Knockout129-130

Chapter 8

Table 8.1 List of ERO1 α interacting partners.....145

Supplementary Table

Supplementary Table 1: Primer sequences for quantitative PCR.....175

Abbreviations

ACN	Acetonitrile
ABB	Ammonium bicarbonate
BCA	Bicinchoninic acid protein assay
Co-IP	Co-immunoprecipitation
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
CTLs	Cytotoxic T lymphocytes
DMEM	Dulbecco's Modified Eagle Medium
DTT	Dithiothreitol
EMT	Epithelial to mesenchymal transition
emPAI	Exponentially modified protein abundance index
ERO1 α	Endoplasmic Reticulum Oxido-reductase Like 1 alpha
ESI	Electrospray Ionization
FBS	Fetal Bovine Serum
FDR	false discovery rate
gRNA	guide RNA
GEO	Gene Expression Omnibus
GO	Gene Ontology
H/L	Heavy to Light Ratio
HK2	Hexokinase 2
HRP	Horse Radish Peroxidase

HCD	High-energy collisional dissociation
HPLC	High-Performance Liquid Chromatography
HIF-1 α	Hypoxia-Inducible factor 1 alpha
IgG	Immunoglobulin G
KRAS	Kirsten rat sarcoma viral oncogene homolog
MS	Mass Spectrometry
MS/MS	HPLC coupled to tandem mass spectrometry
m/z	Mass to Charge Ratio
MDSCs	Myeloid-derived suppressor cells
PDAC	Pancreatic ductal adenocarcinoma
pSILAC	Pulse Stable Isotope Labelling of Amino acid in Cell Culture
PCR	Polymerase Chain Reaction
PRECOG	Prediction of clinical outcomes from genomics
ROS	reactive oxygen species
SDS	Sodium dodecyl sulfate
STRING	Search tool for the retrieval of interacting genes/proteins
VEGF	Vascular endothelial growth factor
TMT	Tandem mass tags

Abstract

Pancreatic cancer is one of the leading causes of death worldwide among all cancer types due to difficulty detecting in early-stages of disease. Poor understanding of the mediators that drive the progression of solid hypoxic tumors remains one of the significant challenges in treating pancreatic cancer. Hypoxia often correlates with poor survival of patients with pancreatic cancer. Pancreatic cancer cell adaptation to limited oxygen delivery promotes the induction of treatment-resistant and aggressive phenotype by triggering tumor evolution and metastasis at an early stage of tumor development. The hypoxic environment in tumor resists the infiltration of T-cells as compared to the normoxic area of the same tumor, suggesting its role in immunosuppression. Furthermore, hypoxia-induced exosomes also promote cancer development by enhancing migration, angiogenesis, and early metastasis in solid tumors. However, the precise mechanism of exosome-mediated tumor progression remains unclear.

We, therefore, used a heavy isotope 'pulse/trace' proteomic approach to determine how hypoxia alters pancreatic tumor expression of proteins that confer treatment resistance, promote metastasis, and suppress host immunity. Using this method, we identified that hypoxia stress stimulates pancreatic cancer cells to rapidly translate proteins that enhance metastasis (NOTCH2, NCS1, CD151, NUSAP1), treatment-resistance (ABCB6), immune suppression (NFIL3, WDR4), angiogenesis (ANGPT4, ERO1 α , FOS), alter cell metabolic activity (HK2, ENO2), and mediate

growth-promoting cytokine responses (CLK3, ANGPTL4). Proteome profiling of exosomes identified elevated expression of proteins that involved in metabolism, cytoskeleton assembly, signal transduction, and immune suppression. Hypoxia also regulates the expression of major immune checkpoint proteins (CTLA-4, TIM-3, GAL-9) in MIAPaCa-2 cells and exosomes, suggesting its role in immunosuppression. Database mining confirmed that the elevated gene expression of these hypoxia-induced mediators is significantly associated with poor patient survival in various stages of pancreatic cancer. Among these proteins, the oxidoreductase enzyme ERO1 α was highly sensitive to induction by hypoxia stress across a range of different pancreatic cancer cell lines and was associated with particularly poor prognosis in human patients. Consistent with these data, genetic deletion of ERO1 α substantially reduced growth rates and colony formation in pancreatic cancer cells when assessed in a series of functional assays *in vitro*. Accordingly, when transferred into a mouse xenograft model, ERO1 α -deficient tumor cells exhibited severe growth restriction and negligible disease progression *in vivo*. Tandem Mass Tags (TMT) proteomics and co-immunoprecipitation (Co-IP) approaches were used to identify the proteins regulated by ERO1 α and its interacting partners. TMT proteomic analysis showed a significant fraction of high confident proteins involved in VEGF signaling, protein folding, and metabolic process were severely suppressed in ERO1 α KO cell lines. Collectively, these data indicate that ERO1 α is a

potential prognostic biomarker and novel drug target for pancreatic cancer therapy.

Chapter 1: Background & Review of Literature

1.1 Pancreatic cancer: Current picture

Pancreatic cancer is associated with <10% patient survival within just 5-years of diagnosis, reflecting a mortality rate of approximately double that of other primary cancer types (Figure 1.1A) (1). Numerous studies predicted that pancreatic cancer would be the second leading cause of death after lung cancer by 2030(2, 3). Pancreatic Ductal Adenocarcinoma (PDAC) is the most common form of pancreatic malignancy and diagnosed at late-stage disease. Hence, both the incidence and deaths attributable to PDAC continue to increase(4). The death rate of pancreatic cancer patients has not improved despite various research efforts, conceivably due to its complex biological nature and poor prognosis(5-7). At present, there is no clinical procedure that can accurately detect early asymptomatic PDAC, primarily due to the lack of specific biomarkers of the disease(8).

KRAS is the most frequent mutated driver gene that accounts for more than 90% of all kinds of PDAC(9-11). KRAS is the first mutation that occurred in the early stages of pancreatic cancer(9, 11). Pancreatic intraepithelial neoplasia(10) (PanIN) (one of the most initial stages in pancreatic cancer) progresses to its more severe form with other signature mutations involving CDKNA2, TP53, and SMAD4(Figure 1.1B) (12, 13). Accumulation of these mutations leads to uncontrolled proliferation, rapid onset of metastasis, and PDAC(14-16). Single point

mutation of individual gene converges into the core molecular pathway involving cell cycle regulation, TGF- β signaling, cytoskeleton regulation, and chromatin regulation(17, 18). Targeting KRAS or other molecular signatures for therapy were not entirely successful so far due to its complexity(19-21).

Figure 1.1: Pancreatic cancer statistic and model (A) Five-year survival of pancreatic cancer in the world based on the CONCORD-3 study(22) (B) Progression model from a normal cell to metastatic pancreatic cancer in different stages(23, 24). (Adopted from an original illustration by Bona Kim)

An integrative study combining genomics, transcriptomics, and proteomics reveals the molecular landscape of 150 PDAC patients in a recent report conducted by TCGA(16). Deep sequencing of the KRAS gene reveals a biallelic mutation in a subset of cells, which possibly gives an additional advantage in harboring other oncogenic alterations(16). Furthermore, this study shows other oncogenic driver RREB1 besides other driver's genes, including KRAS and a potential role in the development of pancreatic cancer(16). Proteomics studies from high purity patient samples reveal four subsets exhibited significant differences in survival and could be explored therapeutically.

Our study relied on the fact that hypoxia plays a critical role in tumor development by regulating vital proteins/pathways to promote angiogenesis, rapid growth, drug resistance, and early metastasis, which clinically correlate with TCGA proteomic studies and could support our investigations.

The tumor microenvironment plays a very critical role in pancreatic cancer progression and metastasis. Researchers reported extensive fibrosis around the tumor, and that helps the tumor to migrate from its original place and metastasize to other body parts(25-27). One of the key characteristics of pancreatic cancer is the formation of dense stroma called desmoplastic reaction(27, 28). The pancreatic stellate cell plays a

very critical role in stroma formation by producing growth factors and cytokines like TGF- β , PDGF, FGF, etc(27, 29, 30). The production of these growth factors and cytokines alters ECM composition that promotes tumor progression and metastasis. Compared with the healthy pancreas, PDAC shows dense collagen 1 and 3 bundles associated with fibroblast and the loss of basement membrane integrity(26, 29, 30). Loss of basement membrane integrity results in the invasion of malignant cells through the interstitial matrix exposed to collagen(31). Tumor microenvironment also promotes metastasis via matrix metalloproteinase (MMP-3) and integrin by Rac1b and Rho signaling pathways, respectively, through rigid ECM (28, 32).

Metabolic reprogramming is one of the crucial hallmarks driven by KRAS mutation in pancreatic cancer as it shifts metabolic flux in cancer cells to provide more energy and nutrients, as well as increase uptake and metabolism of glucose(33). Intriguingly, high glucose uptake has shown to promote genomic alteration in pancreatic cancer cells(34).

In summary, despite extensive efforts in pancreatic cancer research over the last three decades, pancreatic cancer remains one of the challenges for oncologists and researchers to understand its complex biology and come up with a promising treatment. Hence there is an urgent need for

better predictors of pancreatic tumor progression and development in this patient group with abysmal prognosis.

1.2 Pancreatic cancer and hypoxia

Hypoxia (low oxygen availability) is one of the critical driving forces among solid tumors and pancreatic cancer progression(35-39). Solid tumors show critically low oxygen and acidic pH in their microenvironment compared to normal adjacent healthy tissues(40, 41). The acidic pH of the tumor microenvironment is mostly due to lactic acid production by anaerobic glycolysis under hypoxia(42).

Hypoxia frequently occurs in cancer and stromal cells when a tumor is proliferating and evolving rapidly(37, 38, 40). One of the studies has reported the average pO_2 (partial oxygen pressure) of a developing tumor is just 0-5.3 mmHg, whereas the pO_2 of adjacent healthy tissues ranges between 9.2 and 92.7 mmHg(43). These data indicate that oxygen level plays a crucial role in the fate of tumorigenesis.

Hypoxia activates many signaling and biological pathways (Figure 1.2) that affect the behaviors and characteristics of cancer and stromal cells. It also helps to maintain the aggressiveness of the tumor cells that favor the hypoxic microenvironment(44, 45). Furthermore, the hypoxic microenvironment contributes to chemotherapy resistance(46, 47) and

promotes invasiveness and metastasis through epithelial to mesenchymal transition (EMT), which is controlled by a network of transcription factors(37, 48).

Figure 1.2: HIF-1 α regulated pathways and characteristics: Hypoxia-induced factor, HIF-1 α , is a key mediator of tumor-related characteristics in pancreatic cancer (51)

Hypoxia-inducible factor (HIF-1 α) is a master regulator that controls the redox state and oxygen balance in response to intra-tumoral hypoxia and facilitates tumor progression (35, 49). The polymorphism (point mutation) in hypoxia-inducible factor (HIF-1 α) is associated with a variety of cancer, including PDAC (50) that indicates the critical role of HIF-1 α in tumorigenesis. Figure 1.2 describes the number of pathways that have been triggered by hypoxia with or without HIF-1 α regulation that helps the tumor to survive and proliferate under hypoxic microenvironment (51).

Furthermore, high expression of HIF-1 α and GM-CSF contributes to perineural invasion in PDAC(20). HIF-1 α expression in CD133+ (a stem cell marker) pancreatic cancer cells promotes epithelial to mesenchymal transition under hypoxia(52), which is one of the key hallmarks of pancreatic cancer in an advanced stage, reflecting the individual role of the heterogeneous cell population in the tumor microenvironment.

Angiogenesis is another key hallmark of tumor progression and the oncogenic pathway that is triggered by hypoxia(53-57). Hypoxia activates angiogenesis by inducing different pro-angiogenic and growth factors, which support tumor growth by forming new blood vessels to provide nutrients and oxygen for the proliferating tumors(54, 56, 58). Vascular endothelial growth factor (VEGF) plays a very important role in

angiogenesis(53-55), induced by HIF-1 α in a variety of tumors including PDAC(59) under hypoxic microenvironment(60).

Hypoxia reprogramming of cancer cells metabolism is an important driving factor in cancer progression including PDAC(61-64). Switching of metabolism routes helps tumors including PDAC to grow rapidly by getting unlimited nutrient supply. HIF-1 α had also shown to regulate microRNA to promote metastasis in(65-69). Furthermore, the hypoxic microenvironment also emerged as a barrier for immunotherapy by regulating the myeloid-derived suppressor's cells (MDSCs) and other immune checkpoints(70). Figure 1.3 shows the evolution and development model of hypoxia-driven invasion and metastasis(45).

Figure 1.3: Hypoxia-driven evolution of tumor progression and metastasis: Tumor starts from a single cell and grows exponentially after genetic alterations. When the tumor reaches 1 to 2 mm in diameter, there is insufficient oxygen and nutrient supply from surrounding blood vessels to support the growth of cancer cells. The cancer cells change their genome and epigenome through clonal evolution to produce a diversity of cancer cells to sustain and survive under hypoxic conditions. Cancer cells can spread to other parts of the body at this late stage and become resistant to radiotherapy and chemotherapy (45).

Research has been ongoing since the last few decades on hypoxia tumor biology, but current understanding does not give a clear picture of how environmental stress, such as hypoxia, governs the fate of tumors at later stages. Thus, a detailed understanding and research is needed to further explore the different aspects of hypoxia and shed light on how it contributes to tumor progression including PDAC.

1.3 Pancreatic cancer and Immunosuppression

Pancreatic cancer is one of the most dreadful cancers that kill thousands of people every year(71). Chemotherapy can only improve the extent of patient survival for a limited period but with lots of side-effects (72-74). Immunotherapy research to cure pancreatic cancer is in progress for the last two decades and is believed to be one of the effective cures in cancer research because it specifically kills cancer cells by using the patient's immune system.

Immune cells play a very important role in the tumor microenvironment, and often indicates the tumor-host interaction, as one of the unique kinds in pancreatic cancer(75). Generally, the solid tumor has high intra-tumoral infiltration of effector T cells (T_{reg} cells); however, PDAC has poor effector T cells infiltration and it may contribute to poor prognosis(75). Additionally, a high level of pan-macrophage, M2, CD4+ T-cell predicts poor survival of patients (75). It is very important to understand and examine the role of immune cells in pancreatic cancer, particularly in the development of immune response related to the prognosis of patients.

Immunotherapy drugs, especially immune checkpoint inhibitors anti-PD-1/PD-L1/CTLA-4 and CD19, have been approved by the FDA with extensive efforts from scientists for different cancer types(76-80). Nevertheless, acquired resistance from many cancer patients for these

drugs emphasizes the need for new immunotherapy and drug delivery approaches.

Natural killer cell plays a very important role in tumor elimination is found to be suppressed in most of the tumors including PDAC (81-87). CD8+ T-cell is believed to exert an anti-tumor effect and is found to be correlated with patient survival, though the nature of CD4+ T-cell is complex (Th1 induces Dendritic Cell, whereas Th2 has a role in tumor tolerance)(88, 89).

Furthermore, the myeloid-derived suppressor cell (MDSc) that is associated with cancer progression is highly elevated in the late-stage tumor (90). Immune-checkpoints which are often known as immune regulators are a diverse array of cytokines and co-stimulatory molecules (normally expressed in T-cell as receptors) are highly expressed in cancer, including PDAC(91). Inaccessibility of immune cells around the tumor environment due to fibrosis and extracellular matrix (ECM) remodeling is believed to be one of the important scenarios that lead to immunosuppression(92).

Accumulating evidence suggests that hypoxia may also help the tumor to evade immunity by modulating the immune cell's response (93). Recent research showed that crosstalk between exosomes and myeloid-derived suppressor cells plays a key role in immune suppression and metabolic

programming of tumor cells in tumorigenesis(94). Hypoxic dendritic cells (DC) induce allogeneic CD4+ naïve T-cell differentiation into Th2 helper cell, which promotes tumor progression by secretion of osteopontin and helps in tumor migration(95). Cancer immunotherapy (blockade of Immune-checkpoint inhibitors) has established itself as an important method of treating malignancies but still has some limitations(96, 97). Targeting these immunosuppressive (Treg, TAMs, MDSCs,) molecules with other methods could be an effective strategy to fight cancer(96-101).

1.4 Pancreatic cancer and exosome

Exosomes (30-200 nm in size) are endosome-derived vesicles released from different cell types, which are thought to play an important role in cell-cell communication for normal physiological functions(102-105). From the last decade, exosomes emerge as an important mediator for communications between tumor cells to promote growth, migration, angiogenesis, and ultimately progression, especially in pancreatic cancer (106-110). Numerous evidence suggests that exosomes produced by pancreatic stellate cells communicate with other tumor cells to promote fibrosis, ECM remodeling, and EMT(111-113).

Some recent reports emphasized that the presence of glypican-1 (GPC1+, a surface glycoprotein) on serum exosomes from cancer

patients is positively correlated with tumor progression in colorectal(114), prostate(115), glioma(116) and breast cancer cells(117) including PDAC(118-123). Increased level of GPC1+ exosomes in the serum of patients was detected in early PanIN, when the tumor was completely negative on MRI imaging, indicating exosomal GPC1+ could be a potential serum biomarker for early cancer diagnosis, especially for PDAC (124). On the contrary, few reports suggested that GPC1+ is not a good biomarker for PDAC(125, 126). Hence, large cohort studies are required to study the paradoxical role of GPC1+ as an early diagnostic marker for cancer patients.

Exosomes, produced by pancreatic cancer cells contain a genomic fragment of p53 and KRAS as confirmed by DNA sequencing, could be an informative tool to predict cancer progression, treatment efficiency, and therapy resistance(127). The emerging role of miRNA in exosome biogenesis, release, and uptake open a great understanding in the field of cancer biology(128-130). New evidence suggests that exosomes induce tumor growth, angiogenesis, EMT, metastasis, drug resistance primarily by miRNA in many cancers including PDAC(129, 131-133).

A recent study has reported that hypoxia-induced exosome can enhance tumor progression by modulating immune profiling(134). One preclinical data suggested that exosomes (exosome derived from Dendritic cell)

induce cytotoxic T-lymphocytes (CTLs) directed towards tumor cells (135). More research and study are required to understand the role of exosomes in cancer immunology (136).

Overall, exosomes play a very critical role in tumorigenesis, but the current understanding is far from getting a breakthrough for cancer treatment. More research and brainstorming are needed to understand the mechanism of intercellular communication played by tumor-derived exosomes.

1.5 Quantitative proteomics in cancer research

Mass spectrometry is a powerful technique to identify and quantify various molecules present in a complex sample by measuring the mass-to-charge (m/z) ratio(137-139). The art of mass spectrometry and its application-based techniques have been greatly valued for qualitative and quantitative analysis of complex proteome samples for discovery-driven research.

With the advancement in MS-based proteomics like Orbitrap, a novel mass analyzer with high resolution and high mass accuracy, many biological and biomedical questions have been challenged and answered(140). The shotgun/bottom-up approach to analyze enzymatically cleaved peptide is widely used to circumvent certain

technical limitations such as protein ionization and fragmentation during liquid chromatography-coupled tandem mass spectrometry (LC-MS/MS) analysis(141-144).

Raw data or spectra generated from MS mapped into protein database for protein identification and further analysis by using highly advanced quantitative software application such as Sequest, Mascot, MaxQuant, and Proteome Discoverer (145). To address critical biological and healthcare problems, both relative and absolute mass spectrometry-based quantitative proteomic profilings have been extensively used in cancer research.

Stable isotope labeling approach is often combined with MS-based shotgun proteomics to identify the differently regulated protein in different biological samples under certain conditions(139, 146). Several stable isotope labeling methods have been adopted, and each has its advantage and usefulness for the specific application (147). Our lab frequently uses these approaches to study key biological questions. Protein heavy isotope labeling can be performed in two ways:

(1) In-vivo labeling:

In-vivo labeling defined as an addition of isotopes to the growth media that can be metabolized by the cells and incorporated into proteins. In the present study, we utilized *in-vivo* pulsed stable isotope labeling of amino

acid in cell culture (pSILAC), an alternative of SILAC, and is commonly used for detecting *de-novo* protein synthesized upon a given treatment(148, 149). In pSILAC, heavy $^{13}\text{C}_6$ L-Arginine Hydrochloride and $^{13}\text{C}_6$ $^{15}\text{N}_2$ L-Lysine Hydrochloride (R6K8) are introduced into cell culture medium together with given treatment for a short period. Proteins regulated in that condition will incorporate these two heavy amino acids after translation, which can be further detected by MS (Figure 1.4). The amount of newly synthesized protein can be relatively quantified by using heavy to light isotope ratio (150).

Figure 1.4: Schematic presentation of SILAC Workflow: Schematic diagram showing the experimental workflow of SILAC. H/L = Heavy and Light Amino acid chain Ratio

(2) Post tryptic labeling:

Post tryptic labeling referred to the addition of chemical isotopes after protein extraction and digestion. TMT 6-plex based quantitative approach, a post tryptic labeling method was also used in this study to quantify six biological samples in different conditions(151). TMT 6-plex reagents are amine-reactive isobaric compounds and results in irreversible labeling of the peptide amino terminus and free amino termini of lysine residues.

1.6 Aims and objective of the project

Pancreatic cancer is one of the most lethal diseases among all kinds of tumors due to its poor prognosis(1, 152-157). New therapy and future biomarkers are required to predict cancer risks and earlier detection of the disease. Recently, immunotherapy has shown a great promising result, while other approaches failed in improving the survival of patients with pancreatic cancer(96-101, 158). Accumulating evidence suggests that hypoxia is a key player in driving tumor progression and metastasis (39, 159-162). Hypoxia modulates various biological pathways, resulting in an aggressive tumor phenotype(163, 164).

Hypoxia-inducible factor 1 α (HIF-1 α) is a key player that regulates many genes in response to hypoxia. A few examples of HIF-1 α regulated protein include Angiopoietin 4 (ANGPT 4), JUN, Nuclear Factor Kappa β (NF-kappa- β), Hexokinase 2(HK2). Additionally, some other HIF-1 α independent pathways also drive tumor progression(163, 165-167).

Targeting hypoxia pathway could be an effective and successful strategy to fight against pancreatic cancer(51). On the other hand, tumor-derived exosomes emerged as a key messenger that promotes growth, migration, angiogenesis, and metastasis(168-172). The interplay between exosomes and tumor cells under hypoxia could be a milestone for cancer

research especially for PDAC in terms of early diagnosis, therapy resistance, immunotherapy, and treatment(173).

While a great deal of research has been done in recent decades to study hypoxia-induced cancer, there is still no clear picture of how environmental stress, such as hypoxia, totally changes the tumor dynamics and leads to aggressive phenotype. Thus, the overall objective of this research is to study and understand the hypoxia-driven pancreatic cancer progression by using a combination of advanced proteomics, cellular, and molecular biology approaches. Figure 1.5 depicts the hypothesis of hypoxia-driven pancreatic cancer development.

Figure 1.5: Illustration of the plausible hypothesis of hypoxia-driven pancreatic cancer development (Adapted from Dutta *et al.*); Fast-growing cancer cells easily exhaust nutrient and oxygen and develop a microenvironmental state called hypoxia; To sustain growth and survival under these low-oxygen conditions, the cancer cells secrete exosomes(174, 175) and translate critical proteins to change the tumor dynamics to support aggressive phenotype and early metastasis.

1.6.1 Specific Aims

Through a combination of modern proteomics, cellular, and molecular techniques, we sought here to identify and explore the new molecular drivers of hypoxia-induced pancreatic cancer. We hypothesized that newly synthesized proteins under hypoxia are critical and give survival advantages to cancer cells. Therefore, it is a prerequisite to developing a hypoxic pancreatic cancer cell model for further and future studies.

Furthermore, we are interested to explore the role of critical proteins actively synthesized under hypoxia through biochemical and functional studies. We have previously found that B16 cancer cells secreted >7 times more exosomes under hypoxic conditions (data not published yet). Thus, we are also interested to understand the role of hypoxia-induced exosomes in tumor progression and metastasis. The overarching aim of my Ph.D. thesis is to explore the role of hypoxia and hypoxia-induced exosomes in pancreatic cancer development. To achieve this goal, our study is guided by the following specific aims:

Establish a hypoxic pancreatic cancer cell model

In our study, the most studied and relevant (molecular pattern similar to PDAC) pancreatic cancer cell line (MIAPaCa-2) (176), was used and originally derived from the epithelial cells of a 65-year-old Caucasian male(177). This cell line allows extensive genetic manipulation that can never have been possible in an animal study. Hence, we seek to develop a hypoxic pancreatic cancer cell model for further research analysis.

Profile the cellular proteomes and exosomes of the proposed hypoxic pancreatic cancer cell model

Through the usage of the pSILAC proteomic method, we aim to profile the newly synthesized proteins under hypoxic conditions. By profiling the proteome of the hypoxic pancreatic cancer cell line, we seek to understand the response of hypoxia on the pancreatic cancer cells and to detect the critical proteins which are newly synthesized by the cells under hypoxic stress. Next, we are interested to explore the actively translating hypoxia sensitive proteins to examine them in different biological pathways.

Moreover, we are also interested to isolate, characterize, and profile the exosomes from our hypoxia cell model (MIAPaCa-2). Exosomes are crucial for intercellular communication and play an important role in signaling and other biological functions(171, 172, 174). Here, we seek to explore the novel mechanism or pathway that is perturbed by hypoxia cancer cell-derived exosomes. We hypothesized that hypoxia-induced exosome is more crucial for intercellular communication between tumor cells, and how it affects their behaviors and characteristics which results in a more aggressive phenotype and leads to a rapid onset of metastasis.

Bioinformatics analysis and validation of key proteins synthesized under hypoxia

After analyzing the proteomes of cell lysate and exosome from our hypoxic pancreatic cancer cell model, we used different bioinformatics tools/approaches to shortlist the potential targets for further studies. We used different web tools such as the GEO(178) (Gene Expression Omnibus) database, FunRich V3.0(179) (Functional Enrichment analysis tool), and PRECOG(180) (PREdiction of Clinical Outcomes from Genomic Profiles) in our study. Furthermore, we will validate and correlate our key proteins through western blot and RT-qPCR, respectively.

Knockout, functional, biochemical and proteomics studies of potential target/s

After successful biochemical validation and correlation with clinical outcomes, we used, CRISPR/Cas9, a precise genome editing technology(181) to manipulate the target gene for further analysis. Knockout with CRISPR/Cas9 will help us understand the role of this protein in cell's behavior (growth pattern, rate, morphology) and how it affects the biological function under hypoxia through functional and biochemical techniques such as migration assay, proliferation assay, etc.

Furthermore, we are also interested to understand the role of a target protein by comparing the global proteome of its WT and KO pancreatic cancer cell lines. Additionally, we are also interested to explore the interacting partners of target protein through the Immunoprecipitation (IP) proteomics approach.

Chapter 2 Materials and Methods

Chapter 2 Materials and Methods

2.1 Chemicals

The highest quality reagents were used in experiments. All water used was prepared by using a Milli-Q system (Millipore, Bedford, MA). All chemicals and reagents were purchased from Sigma-Aldrich (St. Louis, MO, USA) unless otherwise stated. Protease inhibitor cocktail EDTA-free and phosSTOP were ordered from Roche Diagnostics (Indianapolis, IN, USA). Trypsin-EDTA, PBS, and penicillin-streptomycin for cell cultures were obtained from GIBCO-Invitrogen (Carlsbad, CA, USA), while FBS was purchased from Thermo Scientific HyClone (Waltham, MA, USA).

2.2 Cell Culture

Human pancreatic cancer cell line MIAPaCa-2 was obtained from American Type Culture Collection (ATCC, Manassas, VA) and cultured as recommended in Dulbecco's Modified Eagle medium (DMEM) (Biowest, France) supplemented with 1 % Penicillin/Streptomycin (Naclai-Teqsue, Japan) and 10% fetal bovine serum (FBS) (Gibco, USA) or 1 % Penicillin/Streptomycin (Naclai-Teqsue, Japan). MIAPaCa-2 cells were cultured in DMEM medium until 70 % confluency before sub-culturing. All cultures were maintained in a humidified atmosphere of 37 °C with 5 % CO₂ and 95 % air. For all the experiments 1×10⁶ PDAC cells were seeded on 10cm dishes unless otherwise stated. On reaching 40-50% confluency, the cells were washed 3 times with 1×PBS (Phosphate

Buffered Saline) and serum-free media before incubating in serum or serum-free media. They were subjected to normoxia (21% O₂/5% CO₂) or hypoxia (<0.1% O₂/5%CO₂) for 24 hours.

For exosome experiments, 2×10⁶ cells were seeded on 10 cm dishes in DMEM and kept in a humidified incubator at 37°C. On reaching 60% confluency, the cells were washed 3 times with 1×PBS and serum-free media before incubating in a serum-free medium to avoid any contamination from FBS. They were subjected to normoxia (21% O₂/ 5% CO₂) or hypoxia (<0.1% O₂/ 5% CO₂) in a hypoxia chamber for 48 hours. The conditioned media was collected after 48 hours. The cell lysate was obtained for protein and gene analysis.

For TMT proteomics experiments 2×10⁶ WT and KO cells were seeded on 10 cm dishes in DMEM and kept in a humidified incubator at 37°C and subjected to normoxia (21% O₂/ 5% CO₂) or hypoxia (<0.1% O₂/ 5% CO₂) in a hypoxia chamber for different time points(24,48 hours). The cell lysate was obtained for protein profiling and analysis.

2.3 Protein Quantification assay

Protein concentration was measured by using BCA (182) or Bradford (183) protein assay on a 96-well plate. Standard curve was made from standard bovine serum albumin solution of concentrations of 0.1, 0.2, 0.4, 0.6, 0.8, and 1 mg/ml, respectively.

For BCA, sample and working reagent (50 bicinchoninic acid solution: 1 $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ solution, v/v) were mixed in 96 well plates and incubated at 37 °C for 30 minutes. Thereafter, the optical density was measured at 562 nm with Infinite® M1000 Microplate Reader (Tecan, Switzerland) and exported to Microsoft Excel for calculations of protein concentration.

For Bradford (Brilliant Blue G in phosphoric acid and methanol), sample or blank mixed together with reagent (1:30) and vortex immediately. Assays are routinely performed at room temperature and color development begins immediately. The absorbance at 595 nm is recorded and the protein concentration is determined by comparison to a standard curve.

2.4 MTT Assay

The MTT assay was performed as described previously⁽¹⁸⁴⁾ to evaluate cell growth. Briefly, PDAC cells were seeded in 96-well plate (1×10^4 cells/well) in DMEM (10% FBS) and allowed to attach overnight. The cells were treated and analyzed for different time intervals (24, 48, and 72 hours). Subsequently, 200 μ l of DMSO (dimethyl sulphoxide) was added to each well to dissolve the formazan crystals. The OD (optical density) was measured at 570 nm by using a multimode reader Infinite F200 Pro (TECAN, Switzerland). The cell viability was calculated for each well as PDAC treated cells/PDAC control cells $\times$ 100%.

2.5 Western Blot analysis

The treated cell was washed with cold PBS twice, followed by the protein lysis with the RIPA buffer (0.1% SDS, 1% NP-40, 1% sodium deoxycholate, 150 mM NaCl, 1mM EDTA, and 50 mM Tris-HCl pH 7.4), and supplemented with Complete™ EASYpack protease and phosphatase inhibitors (Sigma-Aldrich, USA). The protein lysate was collected and sonicated, 3 round of 15 seconds pulses at 30% amplitude on ice. Thereafter, the protein lysate was centrifuged at 200,00 $\times$ g for 30 minutes at 4°C to remove cell debris and the supernatant was collected. Protein concentration was quantified by using the bicinchoninic acid (BCA) assay. 20-50 μ g of total protein was resolved in 10-13% SDS-PAGE and then transferred onto a 0.22 μ m nitrocellulose membrane.

Subsequently, the membrane was blocked with 5% skimmed milk powder dissolved in Tris-buffered saline with Tween 20 (TBS-T) (1 mM Tris, 0.15 M NaCl, pH 7.4, 0.1% Tween) for 1 hour at room temperature and probed with primary antibodies against HIF-1 α (1:1000) (Cell Signalling Technology), CTLA4 (1:2000) (Abcam), TIM-3 (1:2000) (Abcam) and Galectin- 9 (1:1000) (Abcam), Annexin V, GM 130, CD54 (Cell Signaling Technologies, Danvers, MA, United States), ERO1 α (CST), PDL1 (Abcam), NFIL3 (CST), PHD2 (CST) N-CAD (Santa Cruz), and E-CAD (BD Bioscience) overnight at 4°C. The loading control was β -actin (1:8000) (EMD Millipore, USA). The loading control for exosomal proteins was taken as ponceau staining of the membrane. The respective protein bands were incubated for 2 hours with either Horseradish Peroxidase (HRP) –conjugated anti-rabbit (Cell Signalling Technologies, USA), or anti-mouse (EMD Millipore, USA) or anti-goat (Cell Signalling Technologies, USA). The immunoreaction was detected with SuperSignal™ West Pico Chemiluminescent substrate (Thermo Fisher Scientific, USA) and visualized using Carestream Medical X-Ray Green/MXG film (Carestream Health, USA).

2.6 RNA Isolation and Quantitative PCR (qPCR)

Total RNA was isolated by using the Nucleospin RNA II Kit (Macherey-Nagel GmbH, Germany) with on-column DNase I digestion using the RNase-Free DNase Set (Macherey-Nagel). The RNA concentration was determined with the NanoDrop 200 spectrophotometer (Thermo Scientific, USA). DNase-treated total RNA was reverse transcribed to cDNA by RevertAid RT Reverse Transcription Kit (ThermoFisher Scientific, USA), with the following conditions: 70°C for 10 minutes, 42°C for 60 minutes and 70°C for 15 minutes. Quantitative PCR (qPCR) reactions were performed by using the CFX Connect™ Real-Time PCR Detection System (Bio-Rad Laboratories Incorporation, USA). Each sample was performed in triplicate and relative quantification was determined by using the comparative C_t method, and the results were normalized to PPIA mRNA. Calculation of normalized relative expression levels was done for β -actin. All primers were commercially obtained from Integrated DNA Technology (IDT, Singapore) and listed in Supplementary Table 1.

2.7 Cell Proteomics

2.7.1 pSILAC (pulsed SILAC) labeling

PDAC cells were cultured in a 10cm² petri dish following the condition mentioned in section 2.2. Upon reaching 85% confluency, cells were washed with phosphate-buffered saline (PBS) and serum-free (SF) media three times and kept for 24h in 'light' culture medium (containing unlabelled 146 mg/l ¹²C₆, ¹⁴N₂-L-Lysine, and 84mg/l ¹²C₆, ¹⁴N₂-L-Arginine), then switched onto 'heavy' medium (containing labeled 146 mg/l ¹³C₆, ¹⁵N₂-D-Lysine, and 84mg/l ¹³C₆, ¹⁵N₂-D-Arginine) and cultured for 24 hours under normoxic or hypoxic conditions in the presence or absence of FBS (n=2 independent biological replicates). Cells were then washed with cold PBS and lysed by using 8M Urea buffer containing cOmplete™ EASYpack protease inhibitor cocktail (Sigma Aldrich, USA). *In-solution* digestion was performed as described below in section 2.7.2.

2.7.2 In-solution digestion

Total protein was harvested in 8M Urea in 100mM Ammonium Bicarbonate (ABB) pH 8, supplemented with cOmplete™ EASYpack protease inhibitor (Sigma Aldrich, USA) and quantified by using the Bradford assay. The protein was reduced in 10mM dithiothreitol (DTT) (Sigma Aldrich, USA) for 1hour at 37°C followed by alkylation with 55mM Iodoacetamide (IAA) (Sigma Aldrich, USA) in the dark for 45 minutes. The protein lysate was diluted in 100mM ABB (solution) after the alkylation

step to reduce the concentration of Urea to less than 1M. This step is required for the trypsin to properly digest the proteins. The protein was digested with trypsin solution (1:50), (Sigma Aldrich, USA) for 18 hours at 37°C and the reaction was subsequently quenched with 0.5% acetic acid (Merck, USA). 500µg of the digested proteins were added into the Sep-Pak C18 1cc Vac Cartridge 50mg (Waters Corp, USA) for desalting under the following conditions.

1. Cartridge activation with 100% Acetonitrile (ACN), 4 times
2. Cartridge conditioning with 0.1% trifluoroacetic acid (TFA) to remove methanol, 5 times
3. Loading of peptides
4. Washing the column again with 0.1% trifluoroacetic acid, 5 times
5. Elution of peptide with 1.5 ml of 50% ACN(Aqueous)/0.1% formic acid (FA) The eluted peptides were dried in the Eppendorf Concentrator plus (Eppendorf, Germany) for 6-8 hours and kept in -20°C until further usage.

2.7.3 Reverse-phase High-Performance Liquid Chromatography

The dried peptides were reconstituted in 200µl of Buffer A (0.02% NH₄OH in HPLC water), vortex for 30 minutes, and centrifuged at 20,000× g for 30 minutes at 4°C. The supernatant was transferred into a 0.3 ml PP Short Thread Micro-Vial (Thermo Scientific, USA). High pH RO-HPLC was

performed on the 21st Prominence HPLC system (Shimadzu, Japan), using an XBridge™ BEH C18 column (130Å pore size, 4.6mm × 250mm, 5µm particle size). A 60-minute HPLC gradient was set at a flow rate of 1ml/minute of fractionation. The gradient comprises of Buffer A and Buffer B (0.02% NH₄OH in 80% ACN (Aqueous)) with the composition shown in Table 2.1. Fractions of the eluted peptide were collected and concatenated to 15 fractions by pooling fractions of different time intervals together (eg. 1, 16, 31, and 46). The samples were dried in the Eppendorf Concentrator plus (Eppendorf, Germany) and kept at -20°C until further usage.

Table 2.1 Buffer composition for the 60-minute HPLC gradient

Timepoint	Percentage Buffer A	Percentage of Buffer B
0th minute	97%	3%
3rd minute	97%	3%
5th minute	90%	10%
45th minute	65%	35%
50th minute	30%	70%
55th minute	0%	100%
60th minute	0%	100%
61st minute	97%	3%
65th minute	97%	3%

2.7.4 LC-MS/MS

The dried fractionated peptide was reconstituted in 0.1% formic acid (FA) and 3% ACN(Aqueous). LC-MS/MS analysis was performed on the Q-Exactive Hybrid Quadrupole Orbitrap Mass spectrometer, coupled with the ultimate 3000 RSLC nanosystem (Thermo Scientific Inc. Germany), by using in-house protocol(185). 2 µg of peptides from each fraction was injected for each run and all LC-MS/MS analyses were performed in duplicate. Peptides were separated and analyzed on a Dionex Ultimate 3000 RSLCnano system coupled to a Q-Exactive Hybrid Quadrupole-Orbitrap mass spectrometer (Thermo Fisher Scientific Inc, Germany). The separation was performed on a Dionex EASY-Spray 75µm×10 cm column packed with PepMap C18 3µm, 100 Å (ThermoFisher Scientific Inc. Germany) by using solvent A (0.1% formic acid in 99.9% water) and solvent B (0.1% formic acid in 90% ACN(Aqueous)) at a flow rate of 300nl/minute with a 60-minute gradient. Peptides were subsequently analyzed by using the Q-exactive MS with an EASY nanospray source (Thermo Fisher Scientific Inc, Germany) at an electrospray potential of 1.5kV. A full MS scan (350 – 1,600 m/z range) was acquired at a resolution of 70,000 at m/z 200 and a maximum ion accumulation time of 100 ms. Dynamic exclusion was set at 15 seconds. The resolution of high energy collisional dissociation (HCD) spectra was set to 17,500 at m/z 200. The automatic gain control settings of the full MS and MS2 scans

were 3E6 and 2E5, respectively. The 10 most intense ions above a 2,000-count threshold were selected for HCD fragmentation, with a maximum ion accumulation time of 100ms. An isolation width of 2 was used for MS2. Single and unassigned charged ions were excluded from MS/MS. For HCD, the normalized collision energy was set to 28%. The underfill ratio was defined as 0.2%.

2.7.5 Data Analysis

Protein identification and quantitation were performed by processing the raw data from two replicates using Protein Discoverer (PD) version 2.2 software (Thermo Scientific Inc. Germany). The MS/MS spectra were deisotoped and deconvoluted by using the MS2 spectrum processor node in PD. Mascot and Sequest HT were used in parallel and the data compared against a protein sequence file from the UniProt human database (downloaded on 06 Feb 2017, 1,586,248 sequences, 61,972,042 residues). For searches using both engines, maximum missed cleavage sites per protein were set at 2, with precursor and fragment ions mass tolerance set at 10ppm and 0.02Da respectively. Carbamidomethylation (C) was set as a fixed/static modification. SILAC_R6 (R)/13C(6), SILAC_K8 (K)/13C(6)15N(2), acetylation (Protein N-term), deamidation (NQ) and Oxidation (M) were set as dynamic/variable modifications in both searches. A protein group list was generated from Proteome Discoverer (PD) 2.2 software and the list was

filtered to exclude contaminating proteins. Only proteins with q-value <0.01 (<1% FDR) as determined by percolator and detected in both replicates were used for further analysis. The pSILAC H/L ratio was used as a basis for comparison between different conditions. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD014087.

2.7.6 Bioinformatic analysis

The pSILAC protocol allows newly synthesized proteins incorporating heavy (H) arginine and lysine to be distinguished from pre-existing proteins that include only light (L) arginine and lysine residues. Change in pSILAC H/L ratio under low-oxygen conditions can, therefore, be used to determine the impact of hypoxia on tumor cell protein expression activity. Proteins that were actively translated in response to hypoxia either in the presence of serum (HS/NS >1.5) or under serum-free conditions (HSF/NSF >1.5) ($p \leq 0.001$) were shortlisted for further analysis. Gene ontology and pathway analyses were performed by using Functional Annotation (FunRich)(179). Prediction of Clinical Outcomes from Genomic profiles (PRECOG)(186) and Gene Expression Omnibus (GEO)(187) web tools were used to correlate the pSILAC proteomic data with clinical pancreatic tumor gene expression profiles to identify hypoxia-inducible proteins associated with poor prognosis.

2.8 Exosome Proteomics (*label-free*)

2.8.1 Exosome Isolation

Exosomes were isolated from conditioned media through a combination of ultrafiltration and ultracentrifugation steps with some minor modification(188). The conditioned media was collected and centrifuged at 2500×g for 10 minutes to remove any cellular debris and supernatant was collected. To stop any protease activity, the conditioned media was supplemented with cOmplete EASYpack protease inhibitor (Sigma-Aldrich, USA) and concentrated with a VivaSpin 20 centrifugal concentrator, 1000 kDa MWCO (Sartorius AG, Germany) at 4000×g, 4°C, followed by 3 washes with PBS(1X). To remove the microvesicles, the concentrated media was centrifuged at 20,000 ×g for 30 minutes at 4°C and centrifugation was done to reduce the volume to 1ml. The supernatant was collected and diluted in 3ml of HPLC-grade water to reduce the viscosity. The diluted supernatant was poured into a 1 ml of 5.5% sucrose solution. The mixtures were then ultracentrifuged at 200,000×g for 18 hours, 4° in a Ti55 rotor (Beckman). The supernatant was removed carefully, and the pellet was reconstituted in PBS (supplemented with protease inhibitor) and kept at -20°C until further usage.

2.8.2 Nanoparticle Tracking Analysis (NTA)

Nanoparticle tracking analyses were performed by the NanoSight NS500 instruments. The instruments were equipped with a 488 nm laser, a high sensitivity sCMOS camera, and a syringe pump. The exosomes were mixed by vortexing, and subsequently diluted in particle-free PBS (0.02 μm filtered) to obtain a concentration within the recommended measurement range ($1\text{--}5 \times 10^6$ particles/mL), corresponding to dilutions from 1:100 to 1:100,000 depending on the initial sample concentration. Experiment videos were analyzed by using NTA 2.3 build 17 or NTA 3.1 build 54 software (Malvern) after capture in script control mode (3 videos of 60 s per measurement) by using syringe pump speed 20. A total of 1500 frames were examined per sample. Further settings, such as blur, minimum track length, and minimum expected size was set to “automatic” and viscosity to “water” (0.909–0.90 cP).

2.8.3 Exosome Digestion (Protein isolation from exosome)

1 % SDS was added in dissolved exosomes and heated at 100°C for 10 min to disrupt the lipid bilayer. The dissolved exosomes were then centrifuged at 20,000 $\times g$ for 30 minutes and the collected supernatant was quantified by BCA assay (Section 2.3).

2.8.4 One dimensional gel electrophoresis and *In-gel* digestion

The protein extracted from exosome was separated by SDS-PAGE at 100V for 90 min and bands were visualized with Coomassie brilliant blue. After a mild *de*-staining, each sample lane was cut nicely into small pieces approximately 1mm², then washed with 50% acetonitrile containing 100mM ammonium carbonate buffer (Sigma, USA) and subjected to complete de-staining. Gel pieces were reduced with dithiothreitol (DTT, 10mM) and then alkylated by using iodoacetamide (IAA, 55mM). The gel pieces were dehydrated with 100% acetonitrile and then subjected to overnight digestion with sequencing grade modified trypsin (Promega, Madison, WI) at 37°C. The peptides were extracted by using 50% ACN/5% acetic acid(Aqueous) and vacuum dried using a concentrator.

2.8.5 LC-MS/MS

The resultant peptides were dried with a vacuum concentrator and analyzed by LC-MS/MS. The dried peptides were firstly re-dissolved in LC-MS/MS-compatible buffer (3 % ACN(Aqueous), 0.1 % FA). Peptides were separated and analyzed on a Dionex Ultimate 3000 RSLC nano system coupled to a Q Exactive (Thermo Fisher, MA) as previously described with minor modification(189). Exosome samples were injected into an Acclaim peptide trap column (Thermo Fisher, MA) via the autosampler of the Dionex RSLC nano system. Peptides were separated

in a capillary column (75 μm x 10 cm) packed with C18 AQ (5 μm , 300 Å; Bruker-Michrom, Auburn, CA, USA) at room temperature. The flow rate was at 300 nl/minute. Mobile phase A (0.1 % formic acid in 5 % ACN(Aqueous)) and mobile phase B (0.1 % formic acid in 90 % ACN(Aqueous)) were used to establish a 60 minutes gradient: 30 minutes of 7-18 % B, 15 minutes of 18-30 % B, 4 minutes of 30-50 % B, 1 minute of 50-80 % B, 2 minutes of 80 % B, 5 minutes of 80-5 % B, followed by re-equilibration at 7 % for 3 minutes. Peptides were then analyzed on Q Exactive with a nanospray source 57 (Thermo Fisher, MA) at an electrospray potential of 1.5 kV. A full MS scan (350–1600 m/z range) was acquired at a resolution of 70,000 at m/z 200 and a maximum ion accumulation time of 100 ms. Dynamic exclusion was set at 30 s. The resolution for HCD spectra was set to 17,500 at m/z 200. The AGC settings of full MS scan and MS2 were set as 1E6 and 1E5, respectively. The 10 most intense ions above a 1000 counts threshold were selected for HCD fragmentation with a maximum ion accumulation time of 100 ms. Isolation width of 2 Th was used for MS2. Single and unassigned charged ions were excluded from MS/MS. For HCD, normalized collision energy was set to 28 %. The underfill ratio was defined as 0.1 %.

2.8.6 Data Analyses

The raw data files were converted into the dta format by using the extract_msn program (version 4.0) in Bioworks Browser 3.3 (Thermo

Electron, Bremen, Germany), and then the dta files were converted into Mascot generic file format by using Proteome Discoverer 1.4.1.14 (Thermo Electron, Bremen, Germany). Protein identification was performed by querying against the extracted Uniprot Homo sapiens database by using an in-house Mascot server (version 2.4.1, Matrix Science, Boston, MA) with peptide precursor mass tolerances of 10 ppm and fragment ions mass tolerance of 0.02 Da¹⁴⁷. Two missed cleavage sites of trypsin and # 13 C of 2 were allowed in the search. Carbamidomethylation of cysteine residues was set as a fixed modification, while oxidation of methionine, deamidation of asparagine and glutamine residues, and phosphorylation of serine, threonine and tyrosine residues were set as variable modifications.

EmPAI-based label-free quantification method was applied for the comparison of protein abundance in exosome experiments. emPAI values were calculated according to the stated equation 1 to 3, as shown below^(190, 191). The N_{obsd} and N_{obsbl} represented the number of observed peptides per protein and the number of observable tryptic peptides per protein, respectively. Only peptides with peptide scores equal to and/or higher than the homology threshold and identity threshold were collected and used for emPAI values calculation by the Mascot server during the database search procedure. The normalization of emPAI value was performed by dividing the emPAI value of each fraction with the sum of the respective fractions of each protein as stated in

Equation 3. After completion, peptide and protein lists were exported to CSV file format and further processed by using in-house scripts and Microsoft Excel for in-depth analysis. Further, label-free protein quantification was estimated by using emPAI values reported by the Mascot search engine which is based on the following equations: -

Equation 1,

$$PA1 = \frac{N_{obsd}}{N_{onsb1}}$$

Equation 2,

$$emPAI = 10^{PAI} - 1$$

Equation 3,

$$Normalized\ emPAI_i = \frac{emPAI_i}{\sum_{i=1}^x emPAI_i}$$

Where N_{obsd} and N_{onsb1} are the numbers of observe and observable tryptic peptides per protein respectively. False discovery rate of peptide identification was set to be less than 1 % [FDR = $2.0 \times (\text{decoy_hits}/\text{total_hits}) \times 100\%$]. Identified peptides were sorted from smallest to largest Mascot peptide expectation value, and largest to smallest ion score. Only peptides fulfilled these two requirements were selected for further analysis: (1) Peptides with ion scores greater than 20; and (2) Peptides with expectation value smaller than 0.001.

2.8.7 Bioinformatic Analysis

Several open-source online bioinformatics software tools, including Panther v14.0(192) and FunRich v3.1.3(179), were used to help to analyze and interpret the data.

2.9 CRISPR/Cas9 deletion of ERO1 α

All the CRISPR guide RNA (gRNA) were computationally designed to predict the Cas9 activity, using gRNA design software (Benchling, San Francisco, CA, USA) to determine a target score that predicts Cas9 cleavage efficiency by using different algorithms. We used CRISPR design software from CHOPCHOP v.2 (Harvard, USA)(193) to calculate an off-target score that denotes an inverse probability of cas9 off-target binding. Both scores are presented on a scale from 1 to 100, with a higher target score predicting higher cas9 activity. Three RNA were designed, and the target sequence was cloned into a lentiCRISPR v2.0 plasmid (Addgene plasmid # 52961) via BsmBI restriction enzyme sites upstream of the scaffold sequence of the U6-driven gRNA cassette. The single vector lentiviral system also includes SpCas9 expressed from an elongation factor1 alpha short promoter with FLAG octapeptide tag and a

puromycin resistance selection marker linked by a 2A self-cleaving peptide. Table 2.2 includes the list of CRISPR guide RNA.

Table 2.2 List of CRISPR guide RNA designed by CHOP CHOP

Exon 7_ CHOP CHOP (No mismatch)	
Name	Sequence
ERO1 α _Oligo1_LENTI_guide	CACCGGAGCGCTACACTGGTTACAA
ERO1 α _Oligo2_LENTI_guide	AAACTTGTAACCAGTGTAGCGCTAC
Exon 1_ CHOP CHOP (3 mismatches)	
ERO1 α _Oligo1_LENTI_guide	CACCGGCCGCGGCCCATTCAGCTC
ERO1 α _Oligo2_LENTI_guide	AAACGAGCTGCAATGGGCCGCGGCC
Exon 1_ CHOP CHOP (3 mismatches)	
ERO1 α _Oligo1_LENTI_guide	CACCGCGCGGCTGGGGATTCTTGTT
ERO1 α _Oligo2_LENTI_guide	AAACAACAAGAATCCCCAGCCGCGC

2.10 Lentiviral Transduction

PDAC cells were cultured in DMEM (Biowest, France) supplemented with 10% FBS (Gibco, USA) and 1% penicillin /streptomycin (Naclai Tesque, Japan) in a humidified incubator with 5% CO₂ at 37°C. Cells were grown to 70% confluence and infected with lipofectamine coated lentiviral vector for efficient transduction. The media was changed 1 day after viral transduction and incubated for 2 days before selection with 2-5 μ g/ml puromycin for 7 days. Genomic DNA and total mRNA were collected 14 days after viral transduction.

2.11 DNA sequencing

Sanger sequencing of PCR products amplified from genomic DNA, using sequencing primers approximately 200-250bp upstream from predicted cut sites, were performed by the 1st Base Asia sequencing facility in Singapore.

2.12 Colony formation assay

Colony formation assays were performed as previously described⁽¹⁹⁴⁾ by using a total of 200 cells/chamber seeded into six-well plates and cultured in DMEM.

2.13 Transwell cell Invasion & Wound healing assay

Transwell cell invasion assay was performed by using BD Falcon Cell Culture Inserts, 2×10^5 cells were seeded in the Matrigel-coated inserts and allowed to invade for 36 h. The outer chamber was filled with 500 μ l of medium containing 10% FBS. After incubation, non-invasive & migratory cells on the upper surface of the insert were removed with a cotton swab. Migrated & Invasive cells were fixed and stained with crystal violet, and then eluted with 10% acetic acid. Absorbance was measured at 595 nm by using a microplate reader and analyzed by using an optical microscope⁽¹⁹⁵⁾.

To quantify migratory potential, cells were spread and cultured until confluence, then scratched by using a 200 μ l pipette tip before washing and incubating in a fresh serum-free medium. After 24h culture, scratch dimensions were analyzed by using an optical microscope(196). The cell migration was established by measuring the width of the scratched area at each time point in the scratched area at a magnification of $\times 200$.

2.14 Intracellular ROS (Reactive Oxygen Species) detection

Intracellular ROS analysis was performed as previously described(197). Briefly, cells were incubated with 10 μ M DCFDA (2',7' –dichlorofluorescein diacetate) reagent in culture media for 1h at 30°C before harvesting, then washed twice in ice-cold PBS and examined under a fluorescent microscope (λ_{ex} = 495 nm λ_{em} = 530nm) to identify green fluorescence generated by ROS production.

2.15 Xenograft tumor development assay

All animal studies were approved and conducted in compliance with the guidelines of the Institutional Animal Care and Use Committee (IACUC) of Nanyang Technological University. Ncr-nude mice (males aged 7 weeks) were obtained from InVivos Pte, Ltd (Singapore). For tumor formation studies, mice were administered 3×10^6 PDAC-Control cells (n=6) or PDAC-ERO1 $\alpha^{-/-}$ (KO) cells injected subcutaneously into the neck

area and tumor size was monitored by caliper measurement. Mice were euthanized when tumor size exceeded 2000 mm³.

2.16 Cell Proteomics (TMT Labeling)

2.16.1 *In-solution* digestion

Protein concentrations were measured by using Bradford protein assay before digestion. TMT Kit (Pierce, Idaho, ID, USA) was used in quantitative proteomic profiling of PDAC cells proteome in different conditions. One hundred micrograms (100 µg) of each sample were reconstituted in 100 µL 8 M urea, and 100 mM Tetraethylammonium bromide buffer (TEAB) (pH 8.5). Then, each sample was reduced by 10 mM Tris (2- carboxyethyl) phosphine hydrochloride solution (TCEP) for 2 hours at 30 °C and alkylated by 20 mM IAA for 1 hour at room temperature in the dark. Six samples were digested with 2.5 µg of sequencing grade modified trypsin for overnight at 37 °C. TMT reagents were reconstituted according to the manufacturer's instructions. Briefly, each tube containing the different isobaric chemical tags (0.8 mg each) was added with 41 µl of anhydrous acetonitrile at room temperature. Reagents were dissolved by vortexing for 5 minutes and then spun down to concentrate the labeling reagents. All the 41 µl of TMT isobaric tag was added into each sample and incubated at room temperature for 1 hour. Then, the labeling reaction was quenched with 8 µl of 5 % hydroxylamine at room temperature for 15

min. Finally, six samples were pooled together and subsequently vacuum-dried. The dried TMT sample would be fractionated by using HPLC before mass spectrometry analysis.

2.16.2 Reverse-phase HPLC fractionation

The pooled TMT-labelled peptides were fractionated by using a high pH reverse phase C18 column (4.6 × 200 mm; 5 µm, 300 Å; Waters XBridge) on a Prominence HPLC system (Shimadzu, Kyoto, Japan). The UV detection was monitored at a wavelength of 280 nm. Mobile phase A [0.02 % ammonia hydroxide (NH₄OH) in HPLC water] and mobile phase B (0.02 % NH₄OH in 80 % ACN) were used to establish a 65-minutes gradient at a flow rate of 1 ml/min. Briefly, 3 % buffer B for 5 minutes, 3 - 35 % buffer B for 40 minutes, 35 – 70 % buffer B for 5 minutes, 70 – 100 % buffer B for 5 minutes, 100 % buffer B for 5 minutes, and finally re-equilibrated the column with 0 % buffer B for 5 minutes. A total of 60 fractions were collected. Then the fractions were pooled in the concatenated way into 15 fractions and dried in a vacuum concentrator.

2.16.3 Desalting peptide samples

Pre-equilibrated SEP-PAK C18 cartridges 50 mg with 1 ml of ACN followed by 3 ml of 0.1 % trifluoroacetic acid (TFA). Resuspended

vacuum-dried samples in 1mL of 0.4 % TFA and loaded the suspension onto pre-equilibrated C18 cartridges. Washed the cartridges with 4 mL of 0.1 % TFA and eluted peptides with 1mL of 50 % ACN, 0.1 % FA. Eluate was subsequently vacuum-dried.

2.16.4 LC-MS/MS

The resultant peptides were dried with a vacuum concentrator and analyzed by LC-MS/MS. The dried peptides were firstly re-dissolved in LC-MS/MS-compatible buffer (3 % ACN, 0.1 % FA). Peptides were separated and analyzed on a Dionex Ultimate 3000 RSLC nano system coupled to Q Exactive (Thermo Fisher, MA) as previously described with minor modification(189). Approximately 1.5 µg of peptides from each sample was injected into an Acclaim peptide trap column (Thermo Fisher, MA) via the autosampler of the Dionex RSLC nano system. Peptides were separated in a capillary column (75 µm x 10 cm) packed with C18 AQ (5 µm, 300 Å; Bruker-Michrom, Auburn, CA, USA) at room temperature. The flow rate was at 300 nl/min. Mobile phase A (0.1 % formic acid in 5 % ACN) and mobile phase B (0.1 % formic acid in 90 % ACN) were used to establish a 60 minutes gradient: 30 minutes of 7-18 % B, 15 minutes of 18-30 % B, 4 minutes of 30-50 % B, 1 minute of 50-80 % B, 2 minutes of 80 % B, 5 minutes of 80-5 % B, followed by re-equilibration at 7 % for 3 minutes. Peptides were then analyzed on Q Exactive with a nanospray

source 57 (Thermo Fisher, MA) at an electrospray potential of 1.5 kV. A full MS scan (350–1600 m/z range) was acquired at a resolution of 70,000 at m/z 200 and a maximum ion accumulation time of 100 ms. Dynamic exclusion was set at 30 s. The resolution for HCD spectra was set to 17,500 at m/z 200. The AGC setting of full MS scan and MS2 was set as 1E6 and 1E5, respectively. The 10 most intense ions above a 1000 counts threshold were selected for HCD fragmentation with a maximum ion accumulation time of 100 ms. Isolation width of 2 Th was used for MS2. Single and unassigned charged ions were excluded from MS/MS. For HCD, normalized collision energy was set to 28 %. The underfill ratio was defined as 0.1 %.

2.16.5 Data Analyses

Protein identification and quantitation were performed by processing the raw data from three replicates using Protein Discoverer (PD) version 2.2 software (Thermo Scientific Inc. Germany). The MS/MS spectra were deisotoped and deconvoluted by using the MS2 spectrum processor node in PD. Mascot and Sequest HT were used in parallel and the data compared against a protein sequence file from the UniProt human database (downloaded on 06 Feb 2017, 1,586,248 sequences, 61,972,042 residues). For searches using both engines, maximum missed cleavage sites per protein were set at 2, with precursor and

fragment ions mass tolerance set at 10ppm and 0.02Da respectively. Carbamidomethylation (C) was set as a fixed/static modification. TMT 6-plex modification of lysine residues and peptide N terminals was set as the additional variable and fixed modification, respectively. A protein group list was generated from PD 2.2 software and the list was filtered to exclude contaminating proteins. Only proteins with q-value <0.01 (<1% FDR) as determined by percolator and detected in both replicates were used for further analysis.

2.16.6 Bioinformatic Analysis

Several open-source online bioinformatics software tools, including Panther v14.0(192) and FunRich v3.1.3(179), were used to help to analyze and interpret the data.

2.17 Co-Immunoprecipitation (Co-IP)

Co-IP of ERO1 α protein complexes from PDAC cells was performed according to the Bonifacino et al.'s protocol with some modification under normoxia or hypoxia. To extract ERO1 α -related proteins, PDAC cells were mixed with 500 μ l of lysis buffer (1X PBS, 0.5 % NP-40) for 30 minutes on ice. To remove the nonspecific binding of the protein, 50 μ l of the protein G-Sepharose 4FF beads (GE Healthcare) was added to the

sample at 4°C for 60 minutes. After centrifugation (5000 rpm, 5 minutes, 4°C), the sample supernatant was retained, co-IP of ERO1 α complex was performed with 10 μ g of anti- ERO1 α mouse monoclonal antibody (target, Santa Cruz Biotechnology), and 10 μ g of normal mouse IgG (control, Santa Cruz Biotechnology) by using the classic magnetic co-IP kit (Pierce, Thermo Scientific) according to the manufacturer's protocol. To estimate the efficiency of immunoprecipitation, the samples were tested by SDS-PAGE. Protein extracts were *in-gel* digested and analyzed by using mass spectrometry as described below.

2.17.1 Protein assay

Protein concentration was measured by using BCA protein assay on a 96-well plate. Standard curve was made from standard bovine serum albumin solution of concentrations of 0.1, 0.2, 0.4, 0.6, 0.8, and 1 mg/ml, respectively. The plate was incubated at 37 °C for 30 minutes after the sample/standard and working reagent (50 bicinchoninic acid solution: 1 CuSO₄.5H₂O solution, v/v) were mixed. Thereafter, the optical density was measured at 562 nm with Infinite® M1000 Microplate Reader (Tecan, Switzerland) and exported to Microsoft Excel for calculation of protein concentration.

2.17.2 Protein Digestion

Protein concentrations were measured by using BCA protein assay before SDS-PAGE. Co-IP ERO1 α complex was separated by SDS-PAGE at 100 V for 90 min and bands were visualized with Coomassie brilliant blue following the manufacturer's protocol. Gel bands were excised and diced into 1 mm $\times$ 1 mm, followed by reduction with 10 mM DTT at 56 °C for 1 hour, and then alkylation with 55 mM IAA at room temperature in the dark for 1 hour. Proteins were digested with 10 ng/ μ l of sequencing grade modified trypsin for 4 hours at 37 °C. The same amount of trypsin was added for a second time tryptic digestion overnight at 37 °C. Peptides were extracted from gel pieces with 50 % isopropanol, 5 % HOAc followed by 50 % ACN(Aqueous), 5 % FA. Peptide extracts from each band were vacuum-dried with an SPD 2010 SpeedVac system (Thermo Electron, Waltham, MA, USA) and desalted with SEP-PAK C18 cartridges 50 mg (Water Corp., Milford, MA, USA). Desalted peptides were subsequently vacuum-dried again.

2.17.3 LC-MS/MS

The resultant peptides were dried with a vacuum concentrator and analyzed by LC-MS/MS. The dried peptides were re-dissolved in LC-MS/MS-compatible buffer (3 % ACN(Aqueous), 0.1 % FA). Peptides were separated and analyzed on a Dionex Ultimate 3000 RSLC nano system

coupled to Q Exactive (Thermo Fisher, MA) as previously described with minor modification(189). Co-IP samples were injected into an Acclaim peptide trap column (Thermo Fisher, MA) via the autosampler of the Dionex RSLC nano system. Peptides were separated in a capillary column (75 μm x 10 cm) packed with C18 AQ (5 μm , 300 Å; Bruker-Michrom, Auburn, CA, USA) at room temperature. The flow rate was set at 300 nL/min. Mobile phase A (0.1 % formic acid in 5 % ACN(Aqueous)) and mobile phase B (0.1 % formic acid in 90 % ACN(Aqueous)) were used to establish a 60 minutes gradient: 30 minutes of 7-18 % B, 15 minutes of 18-30 % B, 4 minutes of 30-50 % B, 1 minute of 50-80 % B, 2 minutes of 80 % B, 5 minutes of 80-5 % B, followed by re-equilibration at 7 % for 3 minutes. Peptides were then analyzed on Q Exactive with a nanospray source 57 (Thermo Fisher, MA) at an electrospray potential of 1.5 kV. A full MS scan (350–1600 m/z range) was acquired at a resolution of 70,000 at m/z 200 and a maximum ion accumulation time of 100 ms. Dynamic exclusion was set at 30 seconds. The resolution for HCD spectra was set to 17,500 at m/z 200. The AGC setting of full MS scan and MS2 was set as 1E6 and 1E5, respectively. The 10 most intense ions above a 1000 counts threshold were selected for HCD fragmentation with a maximum ion accumulation time of 100 ms. Isolation width of 2 Th was used for MS2. Single and unassigned charged ions were excluded from MS/MS. For HCD, normalized collision energy was set to 28 %. The underfill ratio was defined as 0.1 %.

2.17.4 Data Analyses

The raw data files were converted into the dta format by using the extract_msn program (version 4.0) in Bioworks Browser 3.3 (Thermo Electron, Bremen, Germany), and the dta files were then converted into Mascot generic file format by using Proteome Discoverer 1.4.1.14 (Thermo Electron, Bremen, Germany). Protein identification was performed by querying against the extracted Uniprot Homo sapiens database by using an in-house Mascot server (version 2.4.1, Matrix Science, Boston, MA) with peptide precursor mass tolerances of 10 ppm and fragment ions mass tolerance of 0.02 Da¹⁴⁷. Two missed cleavage sites of trypsin and # 13 C of 2 were allowed in the search. Carbamidomethylation of cysteine residues was set as a fixed modification, while oxidation of methionine, deamidation of asparagine and glutamine residues, and phosphorylation of serine, threonine and tyrosine residues were set as variable modifications.

EmPAI-based label-free quantification method was applied for the comparison of protein abundance in co-IP experiments. emPAI values were calculated according to the stated equation 1 to 3, as shown below (190, 191). The Nobsd and Nobsbl represented the number of observed peptides per protein and the number of observable tryptic peptides per protein, respectively. Only peptides with peptide scores equal to and/or higher than the homology threshold and identity threshold were collected

and used for emPAI values calculation by the Mascot server during the database search procedure. The normalization of emPAI value was performed by dividing the emPAI value of each fraction with the sum of the respective fractions of each protein as stated in Equation 3. After completion, peptide and protein lists were exported to CSV file format and further processed by using in-house scripts and Microsoft Excel for in-depth analysis. Further, label-free protein quantification was estimated by using emPAI values reported by the Mascot search engine which is based on the following equations:

Equation 1,

$$PA1 = \frac{N_{obsd}}{N_{obsb1}}$$

Equation 2,

$$emPAI = 10^{PAI} - 1$$

Equation 3,

$$Normalized\ emPAI_i = \frac{emPAI_i}{\sum_{i=1}^x emPAI_i}$$

Where N_{obsd} and N_{onsb1} are the numbers of observed peptides per protein and observable tryptic peptides per protein respectively. False discovery rate of peptide identification was set to be less than 1 % [FDR = $2.0 \times (\text{decoy_hits}/\text{total_hits}) \times 100$ %]. Identified peptides were sorted from smallest to largest Mascot peptide expectation value, and largest to

smallest ion score. Only peptides fulfilled these two requirements were selected for further analysis: (1) Peptides with ion scores greater than 20; and (2) Peptides with expectation value smaller than 0.001.

2.17.5 Bioinformatic Analysis

To map the interaction network, the gene list of ERO1 α , and the proteins that interact with it were analyzed by the open-source software STRING (*version 11*)(198). The interaction network was further processed by Cytoscape(3.7.1)(199) and Cytohubba plugin. Network analysis was set at high confidence (STRING score = 0.7). The biological process and molecular function of the ERO1 α -interacting proteins were performed by topological and ontological analysis, which was carried out with STRING, Cytoscape and bingo plugin.

2.17.6 Western Blot analysis

Western blot analysis was used to validate the expression level of ERO1 α in various cells. The total protein from PDAC cells was precipitated in an appropriate lysis buffer containing the ERO1 α antibody. The purified proteins were further analyzed by western blot to ensure that the samples contained ERO1 α . Mouse IgG antibodies replaced the ERO1 α antibodies.

2.18 Statistical analysis

Data are presented as means $\pm$ standard error of the mean (sem) GraphPad Prism 6.0 software (GraphPad Softwares Inc., La Jolla, CA, USA). Statistical significance was determined by the Student's paired t-test, and p values <0.05 were considered significant.

2.19 Study Approval

All mouse studies were performed under the approval of the Institutional Animal Care and Use Committee (IACUC) of the ASTAR BRC, in accordance to the guidelines of the Agri-Food Veterinary Authority (AVA) and the National Advisory Committee for Laboratory Animal Research (NACLAR) of Singapore (IACUC protocol # ARF-SBS/NIE-A0242).

Chapter 3 Developing of in-vitro hypoxic pancreatic cancer cell model (MIAPaCa-2)

Chapter 3 Developing of in-vitro hypoxic pancreatic cancer cell model (MIAPaCa-2)

Establishment of a hypoxic pancreatic cancer cell model

3.1 Rationale

Solid tumors such as pancreatic tumors have been reported severely hypoxic in patients (43, 200). Studies have shown the role of hypoxia in pancreatic cancer including other solid tumors (39) but so far the current understanding remains poorly understood. Thus, we need to understand the role of hypoxia through extensive research and create a platform that will create a unique opportunities to treat cancer patients. To understand and study the role of hypoxia in pancreatic cancer, we first established a suitable hypoxia model, which closely resembles the *in-vivo* environment of cancer patients.

To create a hypoxia model, a pancreatic cancer cell line (MIAPaCa-2), was treated with hypoxic gas (0.1% O₂, 5% CO₂), along with normoxia (21% O₂, 5% CO₂) as an experimental control and kept in a humidified incubator at 37°C for a different time interval. The hypoxia model is confirmed by determining the growth pattern of the pancreatic cancer cell line under normoxia and hypoxia using MTT assay (201). The hypoxia model is further validated by determining the gene expression level of well-studied hypoxia-induced proteins (HIF-1 α , Hexokinase 2, NDRG1).

3.2 Results and discussion

To mimic tumor hypoxia *in vivo*, we first cultured pancreatic ductal adenocarcinoma (PDAC) cells under low-oxygen conditions *in vitro*, either in the presence or absence of serum, and then compared viability with cells maintained on normal oxygenation (normoxia) throughout. When assessed in MTT assays, PDAC cells displayed stable growth rates over a 24-hour culture period irrespective of serum supplementation, and cell viability remained essentially unchanged thereafter. In contrast, PDAC cells subjected to low-oxygen conditions displayed reduced proliferation after just a 24-hour culture (Figure 3.1), while substantially upregulating the characteristic hypoxia markers HIF-1 α , hexokinase 2 (HK2) and N-Myc Downregulated protein1 (NDRG1) (Figure 3.2).

Figure 3.1: Growth profile of PDAC cells (MIAPaCa-2) in (A) serum and (B) serum-free conditions under hypoxia as compared to normoxia (experimental control) (n= 3 independent experiments) Data represented the means $\pm$ SEM, *p <0.05; **p<0.01; *p<0.001. Nx; Normoxia, Hx; Hypoxia**

Figure 3.2: RT-PCR assessment of fold change (Hx/Nx) in hypoxia markers (A) HK2 and (B) NDRG1 in serum and serum-free conditions at 24 hour (C) Western blot profile of HIF-1α protein under normoxia or hypoxia in PDAC cells (MIAPaCa-2); HIF-1α (93-110 kDa), Actin(35-38 kDa); (n= 3 independent experiments) Nx, normoxia; Hx, hypoxia Data represented the means $\pm$ SEM, *p <0.05; **p<0.01; *p<0.001**

The results showed a reduction in growth reflects the state of hypoxia (202). Although hypoxia leads to a cessation of growth in both cancer and normal cells, through genetic and adaptive changes, cancer cells allow themselves to survive and even proliferate in that environment (203). The severity and nature of the effect mainly depend on the types of hypoxia (acute, chronic, or cyclic) and the percentage of O₂ (204). Nonetheless, MTT results indicate the effect of hypoxia on cell proliferation rate which possibly reflects the hypoxic state of the pancreatic cancer cell model. These data confirmed that our model system reproduces the oxygen-deprived state encountered by solid pancreatic tumors *in vivo* and replicates their associated cellular responses *in vitro*.

Chapter 4 Profiling of cellular proteomes of PDAC cells under hypoxia in serum and serum-free condition

Chapter 4 Profiling of *de-novo* protein synthesis from PDAC cells under hypoxia in serum and serum-free conditions

4.1 Rationale

Prolonged exposure of low oxygen encourages tumor to adopt certain genetic changes and activates new pathways that are required for the tumor to sustain in a hypoxic environment(160-163). The molecular mechanisms by which hypoxia favors pancreatic cancer progression and therapy resistance remain poorly understood. We hypothesized that hypoxic cancer cells co-opt normal metabolic pathways to force the translation of proteins that support growth in unfavorable local conditions. Studies also show the critically low or no serum in the vicinity of cancer tissue compared to adjacent normal tissue in cancer patients (205-208), indicating the importance of serum level in cancer progression. Our rationale is to identify the proteins which are *de novo* (newly synthesized) or highly upregulated under hypoxia either in presence or absence of serum by using advanced proteomics coupled with labeling method such as pSILAC in this experiment.

4.2 Results and discussion

Identification and quantification of differentially regulated proteins under hypoxia by pSILAC quantitative proteomics

We used a pSILAC proteomic approach to investigate how the pancreatic tumor cell proteome is modified in response to a hypoxic microenvironment. Human pancreatic cancer cell line MIAPaCa-2 was used in this study. PDAC cells were incubated under normoxia (experimental control) and hypoxia for 24h with special media before lysis (Figure 4.1). The pSILAC protocol allows newly synthesized proteins incorporating heavy (H) arginine and lysine to be distinguished from pre-existing proteins that include only light (L) arginine and lysine residues. Change in pSILAC H/L ratio under low-oxygen conditions can, therefore, be used to determine the impact of hypoxia on tumor cell protein expression activity.

Figure 4.1: Schematic representation of the experimental design to perform the quantitative global proteomics analysis of PDAC cells using pulsed SILAC: PDAC cells grown in “light-medium” (R0K0) were switched to “heavy medium” (R6K8, Arginine 6 Lysine 8) and cultured for 24 hr under either normoxia or hypoxia with serum or serum-free conditions. Pre-existing protein was fully labeled R0K0 and newly synthesized protein was labeled R6K8. Protein quantified using BCA assay. The protein synthesis ratio was determined by a heavy/light labeled peptide. Nx, normoxia; Hx, hypoxia; S, serum; SF, serum-free; H/L, heavy/light chain ratio

Proteins that were actively translated in response to hypoxia either in the presence of serum (HS/NS >1.5) or under serum-free conditions (HSF/NSF >1.5) ($p \leq 0.001$) were shortlisted for further analysis ($n=2$ biological replicates). Adjusted p values were generated from PD 2.2 software for pSILAC analysis. We observed that PDAC cells expressed a wide range of different proteins after culture, whether conducted in normoxia under serum replete (5684) or serum-free conditions (5944), followed by hypoxia with serum provided (5932), or withheld for the duration (5677) (Figure 4.2A). Unsurprisingly, most of these proteins were derived from a common pool of shared molecules ($n=5010$), but a substantial fraction was specifically modulated in response to changing microenvironmental conditions (threshold $>0.6 \log_2$ Fold Change in H/L ratio) (Figure 4.2B).

Figure 4.2: (A) Venn diagram showing the total number of protein identified in 4 different conditions (NxS; NxSF; HxS; HxSF) of hypoxia-induced proteins identified as being newly synthesized under S or SF conditions **(B)** Analysis of protein distribution against log₂ H/L ratio for the S and SF culture conditions during normoxia/hypoxia revealed that most of these proteins are downregulated during hypoxia. Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free; H/L, heavy/light chain ratio

To graphically represent these t-test data, volcano plot – $\log_{10}(\text{P-value})$ vs. $\log_2(\text{fold change of Heavy/Light chain ratio})$ was constructed to graphically display the quantitative data in serum and serum-free conditions under hypoxia (Figure 4.3). Points above the non-axial horizontal line represent proteins with significantly different abundances ($p < 0.001$). Points to the left of the left-most non-axial vertical line denote protein fold changes of Heavy /Light chain less than -3 , while points to the right of the right-most non-axial vertical line denote protein fold changes of Heavy /Light chain greater than 3 .

Figure 4.3: Volcano plot showing proteomics data. Volcano plot illustrates significantly differentially abundant proteins (Analyzed by Proteome Discoverer 2.2). The $-\log_{10}$ (Benjamini–Hochberg corrected p -value) is plotted against the $\log_2$ (fold change: Heavy/Light chain ratio) in **(A)** serum and **(B)** in the serum-free condition under hypoxia. The green circle denotes a significant increase in fold change (H/L) while the red circle denotes significant decrease. Grey circles represent proteins without any significant fold change. The area below the shaded (colored) region is the p -value cutoff ($p=0.001$)

Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free; H/L, heavy/light chain ratio

Hypoxia induces dynamic changes in pancreatic cancer cell translational activity

Distribution analyses revealed that most of these proteins were substantially downregulated during hypoxia stress, regardless of serum provision, including several key mediators of cell translation, metabolism, and mRNA maturation processes (Figure 4.4).

Figure 4.4: Classification of the downregulated proteins by hypoxic tumor cells in either (A) serum or (B) serum-free conditions (Analyzed by FunRich). Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free;

Among the proteins induced by pancreatic tumor hypoxia (high Hx/Nx ratios), we observed that 206 were actively synthesized under serum-free conditions, 138 were translated in the presence of serum, and 20 were actively expressed in both conditions (Figure 4.5A). Comparisons between these groups based on functional classification revealed that the majority of hypoxia-sensitive proteins as mediators of signaling pathways/communication and cell growth, but we also detected marked hypoxia effects on key regulators of protein and nucleic acid metabolism (Figure 4.5B).

Figure 4.5: Proteomic analysis of pSILAC data: (A) Venn diagram showing the number of hypoxia-induced proteins identified as being newly synthesized under S or SF conditions (Calculated by Hx/Nx Ratio from proteomics data). (B) Functional classification of tumor proteins expressed *de novo* in response to hypoxia stress. Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free;

Some of the well-known cancer-promoting proteins are upregulated under hypoxia (Table 4.1), and they served as positive control and intrinsic markers, supporting the model of hypoxia(209-218) (Table 4.1). Angiogenic potential of PDAC cells increased synergistically under Hx and serum-free conditions by increasing angiogenic factors such as NOTCH2, FOSL2, JUN (Figure 4.6).

Figure 4.6: Hypoxia induces angiogenic factors: Log₂ fold change (Hx/Nx) in angiogenic factor expression comparing S and SF culture conditions. Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free;

Table 4.1 Hypoxia intrinsic and extrinsic markers(219-221) List of Intrinsic and extrinsic hypoxia markers identified in the proteomic dataset S, serum/serum replete; SF, serum-free; Hx/Nx, Hypoxia/Normoxia Fold Ratio #DIV/0!, Fold Ratio cannot be calculated due to no or very low detection under hypoxia		
Gene	SF (Hx/Nx)	Serum (Hx/Nx)
SLC2A1	2.504203	1.401008
ANGPTL4	43.6944	#DIV/0!
LOXL2	2.190801	2.005373
HK2	8.534743	4.502235
BNIP3L	7.975452	4.901043
JUN	6.62331	9.215521

Furthermore, proteins (NOTCH2, NCS1, CD151) that are known to promote metastasis(222-225) increased more than 10 times under hypoxia (Figure 4.7). Additionally, some of the proteins confer to drug resistance (ABCB6)(227) also increased under hypoxia and might contribute to the poor survival of PDAC patients(Figure 4.7). Several critical mediators of cellular transport and metabolic activity were more potently induced by hypoxia under serum-free conditions (Figure 4.7), indicating the role of serum in determining how oxygen restriction modifies pancreatic tumor biology. Among the 20 proteins induced by hypoxia irrespective of serum were several well-established mediators of cancer progression, including key oncogenic transcription factors FOS and JUN,

as well as the pro-angiogenic factor, ANGPTL4 which was directly involved in neo-vascularization events (Figure 4.7). Several other proteins in this group also displayed greater induction under serum-free conditions (NOL3, NCS1, CD151), suggesting synergistic effects of hypoxia and nutrient deprivation on pancreatic cancer cell development and angiogenic activity (Figure 4.7).

Figure 4.7: Log₂ fold change (Hx/Nx) in actively translating proteins detected in either S or SF culture conditions. Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free;

KEGG Pathway analysis (228) revealed hypoxia-induced genes were involved in angiogenesis, cell cycle progression, ECM remodeling, cell migration (Figure 4.8).

Figure 4.8 Schematic diagram of the pathway involved in (A) cancer and (B) pancreatic cancer. Proteins highlighted by the red box are found to be upregulated under hypoxia in pSILAC proteomics data (Data retrieved from DAVID)

Bioinformatic Analysis

Some important candidate mediators of the tumor response to hypoxia stress were subsequently screened and cross-validated by RT-qPCR to verify the pSILAC data (Figure 4.9). Having identified a range of hypoxia-induced proteins that were expressed by pancreatic cancer cells *in vitro*, it remained unclear which of these mediators exerted the greatest impact on malignant disease progression *in vivo*. We, therefore, proceeded to investigate whether hypoxia-induced changes in pancreatic cancer cell proteome has an impact on disease progression and modify patient outcome by using real-world clinical data.

Figure 4.9 PCR Validation: qPCR validation of key hypoxia-induced proteins as identified by pSILAC analysis (expressed as Hx/Nx fold-change in gene expression, n=3, $p > 0.001$). Nx, normoxia; Hx, hypoxia;

Oxygen restriction induces pancreatic cancer cell expression of key mediators that predict poor clinical outcome

Hypoxia-induced proteins that also displayed upregulated gene expression in cancer cells as reported in the GEO database were identified as potential targets. These targets were then further analyzed by using 'PREdiction of clinical outcome from genomic profiles' (PRECOG) tool to query associations between gene expression profiles and real-world patient outcomes. Potential targets associated with poor prognosis were identified by the PRECOG meta z score.

ERO1 α displayed one of the highest meta z scores in the dataset and was therefore followed-up in subsequent functional studies (Figure 4.10A). Using this approach, we observed that several proteins associated with poor prognosis were more strongly induced by hypoxia during serum-free/starvation (Figure 4.10B), and meta z scores for the pancreatic cancer dataset were generally higher in serum-free relative to serum/serum replete conditions. Among these were several proteins (ERO1 α , ANGPTL4, HK2, etc.) (Figure 4.10A) for which high gene expression levels were strongly associated with poor patient prognosis⁽¹⁸⁶⁾, suggesting a likely role in hypoxia driven PDAC progression.

Figure 4.10: PRECOG analysis of pSILAC data (A) Top 20 genes associated with poor clinical prognosis in cancer patients and identified in our pSILAC dataset of hypoxia-induced proteins (high meta z values indicating proteins most strongly associated with adverse [red] or favorable [green] survival data) **(B)** Protein count in serum (S) and serum-free (SF) conditions, indicating that markers associated with poor prognosis are more strongly induced by hypoxia (meta z value >3) during SF culture. Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free;

*The data were obtained from the PREdiction of Clinical Outcomes from Genomic Profiles (PRECOG) database(186) (precog.stanford.edu)

*Hypoxia-induced proteins were first integrated into the PRECOG tool/server and meta z scores were calculated to determine the confidence level of associations with adverse or favorable clinical outcomes.

Further analysis of ERO1 α expression patterns in relevant GEO databases, enabled us to confirm that a range of different pancreatic cancer cell lines strongly upregulates ERO1 α under hypoxic conditions (Figure 4.11D). Mining of additional publicly available datasets (Table 4.2) revealed that this enzyme is also expressed at significantly higher levels in pancreatic tumor samples compared with adjacent healthy tissue (Figure 4.11A & 4.11B), in clear association with adverse patient outcomes (Figure 4.11C& E).

Figure 4.11: (A) Comparison of ERO1 α expression levels between healthy tissues and disease samples in relevant GEO datasets: GSE28735; 45 pancreatic tumor samples and 45 matching normal samples (B) GSE15471; 78 pancreatic cancer and normal tissue samples (C) GSE78229; 50 pancreatic tissue samples grouped by survival duration, and (D) GSE67549; n=9 pancreatic cancer cell lines either cultured in Nx or subjected to Hx (E) Kaplan Meier-plot (KM) of ERO1 α in PDAC with high and low expression.

*Database selection criteria are displayed together with an overview of the 4 studies selected in Table 4.2

*Datasets GSE15471, GSE78229, GSE67549, and GSE28735 reporting the results of pancreatic cancer microarrays in the NCBI GEO database (<http://www.ncbi.nlm.nih.gov/geo/>) were analyzed to confirm differential ERO1 α expression.

Table 4.2 List of gene expression microarray dataset (GEO Database) used for ERO1 α expression analysis

* S.No. = Serial number

S.NO.	GEO accession	Platform	Sample	Cancer Type
1	GSE28735 (Figure 4.12A)	GPL6244	Pancreatic tissue and adjacent normal tissue	Pancreatic Cancer(229, 230)
2	GSE15471 (Figure 4.12B)	GPL570	Whole-tissue pancreatic ductal adenocarcinoma	Pancreatic Cancer(231)
3	GSE78229 (Figure 4.12C)	GPL6244	Pancreatic tumours tissue	Pancreatic Cancer(232)
4	GSE67549 (Figure 4.12D)	GPL15207	Cancer cell line	Pancreatic Cancer

Together, these data indicate that under hypoxic conditions, pancreatic tumor cells significantly upregulate the enzyme ERO1 α , which is a critical determinant of pancreatic cancer patient survival. While ERO1 α plays a well-established role mediating disulfide bond formation in a range of different secreted and membrane proteins(233, 234), the survival advantages this confers on PDAC cells and the mechanisms involved remain unknown. These data were then verified by qRT-PCR and western blot analyses, which confirmed that PDAC cells express ERO1 α under hypoxia at levels consistent with our proteomic results (Figure 4.12A & 4.12B).

Figure 4.12: Validation of ERO1 α (A) ERO1 α mRNA expression levels were assessed by using qPCR (See Appendix for primers) (B) Western blot confirming that ERO1 α (50-60kda) protein is highly expressed during tumor hypoxia in both S and SF conditions (TGP47- Mouse Pancreatic Cancer cells, MIAPaCa-2-Human pancreatic cancer cell line) consistent with the pSILAC data and patient gene expression profiles in the PRECOG and GEO datasets. (n= 3 independent experiments) Nx, normoxia; Hx, hypoxia Data represented the means $\pm$ SEM, *p <0.05; **p<0.01; ***p<0.001

*Protein Loading amount = 50 μ g

Exploration of potential target/s

ERO1 α , one of the highly upregulated proteins under hypoxia found in our dataset and an oxide-reductase enzyme involved in disulfide bond formation of secreted and membrane proteins, seems to play a very interesting role in cancer progression. ERO1 α has been reported to express in a variety of cancer (235, 236). Current evidence suggests that high expression of ERO1 α promotes cancer cell invasion, chemoresistance (237), and angiogenesis (by oxidative protein folding) (238). One recent report also suggested its role in immune regulation by producing tumor-promoting myeloid-derived suppressor cells via oxidative protein folding (239). Accumulated evidence reveals the importance of ERO1 α in cancer progression, but clear mechanisms and regulations have yet to be explored.

Chapter 5 Profiling of exosomes secreted from PDAC cells under normoxia and hypoxia

Profiling of exosomes secreted from PDAC cells under normoxia and hypoxia

5.1 Rationale

Exosomes are protein and lipid-rich vesicles derived from endosomes (103, 105, 133, 172, 174, 175, 240). Exosome contains protein, messenger RNA, and microRNA, and it has been demonstrated to change the disease state of the affected organ, representing the novel reservoir for biomarker discovery (133, 174, 241). Currently, the role of exosome in cancer has been shown to promote metastasis, angiogenesis, and immune suppression (242). Furthermore, current evidence strongly suggests that radiotherapy frequently changes the composition of exosomes thus modulate tumor microenvironment (243). Exosomes from different cell lines had distinct cytokine profiles, with exosomes from HTLV-1 infected cells having increased levels of GM-CSF and IL-6 as compared to non-infected HTLV-1 cells(244). These data suggest that exosomes may play a role in cytokine signaling. In one study, some key proteins found in exosomes have known to play an important role in cancer progression and some other diseases (245). Additionally, exosomes secreted by pancreatic cancer cells promote the recruitment of cancer-associated fibroblasts (CAFs)(113). Exosomes initiate the pre-metastatic niche in the liver, suggesting the role of exosome in metastasis(246). Recent studies suggested that PDAC derived exosomes may carry a PD-L1, an important immune-checkpoint inhibitor (247), and

could be explored therapeutically. Exosomes emerged as a strong key player in tumor communication and could be the milestone for future research. Further Research and brainstorming are required to understand the role of hypoxia-induced exosomes in tumor progression and early metastasis. Thus, here our objective is to explore and profile the composition of exosomes derived from a pancreatic cancer cell line (MIAPaCa-2) using quantitative mass spectrometry (label-free) under hypoxia.

5.2 Results and Discussion

Isolation and characterization of exosomes like vesicles

Exosomes were purified from cell culture supernatants of PDAC cells by a combination of ultracentrifugation and filtration (molecular cut-off), which were kept under normoxia or hypoxia (see Figure 5.1 & section 2.3 in Material and Methods) and supplemented with serum-free media to avoid any contamination from FBS derived exosomes/microvesicles. The vesicles obtained with this method (Figure 5.1) displayed physical features characteristic of exosomes, with a mean particle size 130 and 210 nm diameter for Nx and Hx respectively.

Figure 5.1: Schematic diagram of the exosome-like vesicles (EVs) isolation protocol (A) Schematic diagram illustrating the workflow of isolation of exosomes from PDAC cells for quantitative proteomics study (See Section 2.8 for more details) Nx, normoxia; Hx, hypoxia; S, serum/serum replete; SF, serum-free;

To verify the presence of intact exosomes, the preparations were analyzed by Nanoparticle Tracking Analysis (See Section 2.8.2 for M&M). The images suggested that the preparations contained vesicles of various sizes (Figure 5.2 A&B). Nanoparticle Tracking analysis reveals exosomes produced under hypoxia show a more homogenous population as compared to normoxic cultures (Figure 5.2B). Nanoparticle tracking analysis showed that the majority of the isolated particles to be within 200nm and have a mean size of 126 and 210 nm for Nx and Hx respectively, which are the characteristic size of EVs isolated from ultracentrifugation(248). Hypoxia-induced a ~4-fold increase in the absolute quantity of particles released by pancreatic cancer cells (Figure 5.2C), thus could exert potent effects on tumor exosome production.

A Nano-Particle Tracking Analysis (Video Frames)

B

C

Figure 5.2 Morphology and size distribution analysis of EVs derived from PDAC cells conditioned media depleted of cell debris and fractioned by differential centrifugation (A): Representative NTA (Nanoparticle Tracking analysis) images of Evs (Extracellular Vesicles) isolated from PDAC cells under normoxia and hypoxia; Frames from a video captured by Nanosight; each bright spot represents one nanoparticle in liquid. **(B)** Physical characteristics of the vesicles isolated from PDAC cells under (B) Nx and Hx were assessed by Nanoparticle Tracking Analysis using Nanosight Instrument **(C)** Nanosight quantification of EVs output per 10^9 tumor cells during culture in either normoxic or Hypoxic conditions for 48h (bars indicate mean $\pm$ S.E.M. of $n=3$ independent batches) Nx, normoxia; Hx, hypoxia;

*All images indicate the presence of intact vesicles of various sizes

The presence of exosome-like vesicles was confirmed by the detection of known markers such CD54, Annexin V, and there was minimal or no cellular as indicated by the absence of GM130 (endoplasmic reticulum marker) protein (Figure 5.3).

Figure 5.3: Western blots of known exosome markers isolated from normoxic and hypoxic PDAC cells and negative control GM130 (Molecular weight GM130, 112 kDa; CD54, 56-90 kDa; Annexin V, 36 kDa;) Nx, normoxia; Hx, hypoxia.

*Red colored gel is ponceau staining used as a loading control for exosomal western blot.

*Protein Loading amount: Exosome (30µg)

Identification and quantification of exosomes

The proteomic analysis (label-free approach) of exosomes identified 2480 and 2193 proteins under normoxia and hypoxia, respectively, by at least 2 peptides (Figure 5.4A). Proteins were further categorized based on their fold change (Hypoxia/normoxia ratio) (Figure 5.4B). Further analysis showed that 425 proteins were upregulated under hypoxia and 531 proteins were found exclusively (newly synthesized) under hypoxia. Figure 5.4A depicts the number of proteins found in normoxia or hypoxia.

All the markers of exosome have been identified (Table 5.1), and cross-validated with ExoCarta (online database of an exosome), support the enrichment of exosomes (249). Apart from exosome markers (CD9, CD81, Hsp70, TSG101, and CD63), some other cell surface glycoproteins (CDs, Cluster of differentiation) have also been identified (Table 5.2). Some of the CDs (CD44, CD10, CD147, CD164) have been reported to play a role in cancer progression and metastasis(250-253).

LC-MS/MS analysis identified several proteins (Appendix D) involved in the endosomal pathway, exosome biogenesis (ESCRT complex, Rab proteins), signal transduction (Rab GTPase, Kinases, EGFR, etc.), metabolism and key cytoskeleton proteins (Actin, Ezrin, Myosin, Coffillin).

Figure 5.4 Identification and quantification of exosomes: **(A)** Venn diagram (Analysed by FunRich V3.0, MS/MS Data in Appendix D): represent the number of exosome proteins found in normoxia or hypoxia **(B)** Analysis of differential protein expression in serum-free conditions under hypoxia, based on log₂ fold change. A threshold is determining at ≥ 2 fold for upregulated protein expression and ≤ 0.5 fold for downregulated protein Nx, normoxia; Hx, hypoxia; Hx/Nx, Hypoxia/normoxia Ratio;

Table 5.1 List of exosome markers identified cross-validated with Exocarta(249) (online database for exosome)

*Nx- Normoxia; Hx – Hypoxia emPAI – Quantification value (Data Analysed by MasCot; see section 2.8.6 for more description in material and methods)

Gene	Nx_Score	Hx_Score	Nx_emPAI	Hx_emPAI
GAPDH	27898	27383	248.7	2658.96
ALDOA	34386	41522	163.67	1308.52
PKM	37186	48909	62.98	179.94
LDHA	15712	19557	115.63	202.21
CD81	1704	1323	0.87	1.41
ENO1	52558	40509	299.81	419.8
EEF2	39620	41383	20.72	27.39
HSPA8	26176	24679	37.84	47.69
PGK1	11840	9081	33.59	38.86
CD9	3062	1868	1.76	1.76
YWHAЕ	4361	3990	21.64	21.64
HSP90AA1	37989	45349	31.87	30.82
HSP90AB1	42304	50709	53.66	49.61
MSN	13435	11779	30.4	27.57
CFL1	3150	2640	92.78	77.21
PDCD6IP	9383	7070	5.47	3.96
ACTB	47675	33755	392.38	268.52
ANXA2	7054	2716	15.73	8.67
YWHAZ	2564	2839	7.55	3.86
CD63	261	281	0.45	0.21
ALB	8942	7267	2.53	1.06
ANXA5	654	193	1.41	0.55
EEF1A1	28634	15050	56.18	19.79

SDCBP	0	5560		6.34
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**Table 5.2 List of Cluster of differentiation (CDs) identified
(Proteomic Analysis from MasCot)**

*Nx- Normoxia; Hx – Hypoxia (Data Analysed by MasCot; see section 2.8.6 for more description in materials and methods)

Gene	Nx_Score	Hx_Score	Nx_emPAI	Hx_emPAI
CD9	3062	1868	1.76	1.76
CD109	40159	29477	5.49	3.72
CD59	84	54	1.05	0.61
CD63	261	281	0.45	0.21
CD97	275	97	0.12	0.04
CD44	5372	0	2.05	0
CD44	0	3761	0	4.08
CD276	263	0	0.2	0
CD151	47	0	0.12	0

Gene ontology analysis

Gene ontology analysis has been performed by using FunRich v3.0 (Functional enrichment analysis tool) (179), which reveals most of the proteins found to be located in the cytoplasm, nucleus, and exosomes of profiled exosome proteome data (Figure 5.5A). During exosome formation, most of the cytosolic proteins are included in the vesicles, containing a lot of metabolic enzymes which is true in this case (254). The phenomenon of increased expression of glycolytic and other metabolic enzymes in exosomes could reflect an ongoing tumoral process (254). After comparing our data to other protein databases like ExoCarta, we noticed that exosomes have a comparable abundance of nuclear proteins, a higher abundance of cytosolic protein and substantially, less abundance of exosomal proteins, supporting the current theory of exosome biogenesis (255).

Proteins associated with molecular function and biological process belong to the transporter, catalytic activity, protein metabolism, cell growth (exosome, vesicles), and energy pathways (Figure 5.5B & D). This could indicate their role in tumor progression or metastasis especially under hypoxia which is a well-known factor to modulate tumor dynamics. One possible way in which exosome can modulate the tumor dynamics is by frequent conversion of glucose using ATP to provide energy to tumor cells(256).

Exosome-derived proteins were then categorized by transcription factor as percentages of the total number of identified proteins using the FunRich database (Figure 5.5C). SP1 is a basal transcription factor that regulates many genes involved in cell proliferation, signal transduction, metabolism and immunity. High expression of SP1 strongly correlates with cancer cell proliferation and metastasis during tumorigenesis (257). The FunRich analysis revealed that SP1 is associated with more than 30% of the protein, and is the highest in the hypoxia-induced proteins. Other key transcription factors associated with exosome-derived proteins are KLF7, SP4, GABPA, and EGR1.

Figure 5.5 Exosome proteome analysis (Analysed by FunRich V3.0): Gene ontology analysis of identified proteins (A) at the cellular location (B) molecular function (C) regulated by transcription factors and (D) biological process $p \leq 0.05$ considered significant; $- \log_{10}(p\text{-value})$

Hypoxia-induced immunosuppressive markers in the pancreatic cancer cell and EVs (extracellular vesicles)

Since the last decade, numerous researches have been carried out in the field of tumor immunology and the results are very promising, but still, a lot of understanding and research are needed in terms of hypoxia-related immunosuppression. Hypoxia suppresses immunity by multiple mechanisms. Hypoxia induces Nanog, a stemness associated transcription factor, which supports the infiltration of regulatory T-cell and macrophage in tumor microenvironment via TGF-beta signaling(258). Interestingly, hypoxia also induces adenosine production which binds with adenosine receptors found on different immune cells and suppresses pro-inflammatory cytokine, thus leads to immunosuppression(259).

Recent evidence suggested that hypoxia also induces the expression of immune-checkpoints receptors and their ligands such as TIM-3 and Galectin-9, respectively, but how hypoxia changes the expression of immune-checkpoints is still not fully understood. Exosomes are small vesicles that are very important for cell communication and potentially can play a role in immune suppression secreted by the hypoxia-induced tumor. Preliminary experiments have been performed on exosome and cell lysate of PDAC cells to check the expression of important immune checkpoints regulators such as CTLA4, TIM-3, and their ligand Galectin-9 at the protein level through western blot.

Preliminary results (Figure 5.6) showed a significantly high expression of TIM-3, and CTLA-4 under hypoxia in PDAC cells (Cell lysate). Furthermore, Galectin-9 induced under hypoxia in PDAC exosomes (Figure 5.6A). These preliminary results indicate that perhaps hypoxia regulates the expression of these immune-checkpoints and modulate tumor dynamics. Further research and understanding are needed to explore the pathway or mechanism involved in exosome-mediated immunosuppression.

A**MiaPaCa-2 Cell Line** **B**

Figure 5.6 Upregulation of Immune-checkpoint inhibitors in PDAC cells: Western blot profile of (A) TIM-3 (30-33 kDa non-glycosylated; 45-50 kDa non-glycosylated variant)(260-262); its ligand Galectin 9 (different isoform and variants from 10-40kda)(263-266); and (B) CTLA-4 (variants; Glycosylated form 43-45kda)(267) in cell lysate and exosome under normoxia or hypoxia. Nx, normoxia; Hx, hypoxia.

*Red colored gel is ponceau staining used as a loading control for exosomal western blot.

*Protein Loading amount: Cell lysate (50µg) Exosome (20µg)

*Protein Ladder(Bio-Rad, USA) Precision Plus Protein™ Dual Color Standards, #1610374

Chapter 6: Knockout, biochemical and functional studies of ERO1 α

6.1 Rationale

Validation of ERO1 α has been done through qRT-PCR and western blot (Figure 4.12) that significantly showed a much higher expression of ERO1 α in both serum and serum-free conditions under hypoxia as compared to normoxia (experimental control) and is also one of the poor prognosis proteins in cancer patients (Analyzed through different bioinformatic tools). ERO1 α , an oxidoreductase enzyme involved in disulfide bond formation of secreted and membrane proteins, seems to play a very interesting role in cancer progression. ERO1 α has been reported to express in a variety of cancer(235, 236). Current evidence suggests that high expression of ERO1 α promotes cancer cell invasion, chemoresistance(237), and angiogenesis(238). One recent report also suggested its role in immune regulation by producing tumor-promoting myeloid-derived suppressor cells via oxidative protein folding(239). Accumulated evidence reveals the importance of ERO1 α in cancer progression, but clear mechanisms and regulations have yet to be explored. We are specifically interested to study the effect of ERO1 α in pancreatic cancer. To do that, we used, CRISPR/Cas9, a precise genome editing technology to knock out those genes to study the function of proteins on cancer cell behavior by using the functional and biochemical assay.

6.2 Result and discussion

Knockout of ERO1 α by programmed CRISPR/cas9

ERO1 α , an oxide-reductase enzyme involved in disulfide bond formation of secreted and membrane proteins. It has 16 exons and 11 transcript variants. To better understand the role of ERO1 α in pancreatic cancer progression, we next deleted the corresponding gene by using CRISPR/Cas9 genome editing technology and assessed the impact on tumor cell function both *in vitro* and *in vivo*. For this, we selected a sgRNA with the highest 'on target' score, which was directed against exon 7 of human ERO1 α and predicted to induce a frameshift mutation that generates non-functional/truncated gene products.

We then transfected human PDAC cells with Cas9-expressing lentiviral vectors to disrupt the ERO1 α gene and used Sanger sequencing to verify mutation at the predicted site. Sanger sequencing confirmed the indel formation occurs at a predicted site (Figure 6.1B). To determine if genomic disruption of the ERO1 α gene resulted in changes in protein levels, we performed western blot on transfected cells. Accordingly, western blot analysis of ERO1 α expression in the treated cells confirmed that our gene disruption strategy achieved a complete knockout of ERO1 α protein (Figure 6.1A). Two clones were confirmed by Sanger sequencing and both showed no expression of the protein (Figure 6.1A).

Figure 6.1: (A) Western blot profile of WT and ERO1α KO (molecular weight; 50-60Kda) PDAC cells confirmed the ERO1α deletion **(B)** Sequence alignment of WT and ERO1α KO DNA sequence; PCR products from Colonies 1 and 2 were further analyzed via Sanger Sequencing. Two different mutant sequences were detected in selected colonies likely to indicate biallelic mutation. The 20-bp target sequence of sgRNA no. 1 is indicated in the red box, adjacent to the NGG protospacer adjacent motif (PAM) sequence in the green box.

C1, C2; KO clones, Nx, normoxia; Hx, hypoxia; Hx/Nx,

*Protein Loading Amount; 50μg

ERO1 α mediates pancreatic cancer cell growth, ROS production, and tumorigenicity in vivo

Next, we proceeded to test whether pancreatic tumor cell proliferation rates differed between WT and ERO1 α -KO clones. Unlike their WT counterparts, ERO1 α -KO tumors displayed little to no growth over a 24-72h culture period (Figure 6.2A), and colony formation was reduced by as much as 50% (Figure 6.2B), suggesting that ERO1 α deletion significantly reduces the replicative capacity of pancreatic cancer cells.

Figure 6.2: Cell growth assay: (A) MTT assay performed to check the growth of WT and ERO1 α -KO clone under hypoxia (B) Colony formation potential of PDAC cells comparing WT and ERO1 α -KO clones WT; wild Type, KO; Knockout ERO1 α (n= 3 independent experiments) Data represented the means $\pm$ SEM, *p <0.05; **p<0.01; ***p<0.001

*One of the Selected clones (C1) used to perform an *in-vitro* assay.

Furthermore, when assessed in a series of wound healing assays, we observed that ERO1 α -KO tumor cells displayed impaired ability to close the injury due to migration rates being reduced by almost 2 folds relative to ERO1 α -competent tumor cells (Figure 6.3).

Figure 6.3: In vitro scratch assay: PDAC cells using the indicated clone (C1) and culture conditions, demonstrating the reduced migratory potential of ERO1 α -KO tumor cells. WT; wild Type, KO; Knockout ERO1 α (n= 3 independent experiments) Data represented the means $\pm$ SEM, *p <0.05; **p<0.01; ***p<0.001

Next, we performed a matrigel invasion assay in PDAC cells to check the reduced invasion in ERO1 α -KO tumor cells compared to WT cells. Indeed, WT tumor cells but ERO1 α -KO tumor cells showed enhanced cell invasion (Figure 6.4A). Given these marked defects in cell motility, we next assessed tumor cell expression of cadherins, which play a central role in restricting cancer cell migration and tissue invasion. When

analyzed by western blot, key EMT suppressor E-cadherin was found to be highly expressed in ERO1 α -KO tumor cells, perhaps explaining their reduced migratory potential in our functional assays (Figure 6.4B).

Figure 6.4 (A) Transwell Migration assay performed by using the indicated cell clones (WT and KO) and culture conditions, demonstrating the reduced migratory potential of ERO1 α -KO tumor cells. After a 48-h treatment, cells that migrated from the upper chamber to the lower chamber were stained with Crystal Violet and counted. Photomicrographs represent migrated cells. (B) Western blot analysis of the archetypal EMT suppressor protein E-cadherin & inducer N-cadherin in ERO1 α -KO PDAC cells. WT; wild Type, KO; Knockout ERO1 α (n= 3 independent experiments). Data represented the means $\pm$ SEM, *p <0.05; **p<0.01; ***p<0.001

Having detected a clear impact of ERO1 α deletion on PDAC cell expression of a key protein regulator of tumor development, we next investigated whether ERO1 α was also required to induce other critical mediators of disease progression. HIF-1 α is a key regulator of many oncogenic pathways known to be triggered by hypoxia, and our western blot analyses revealed a significant deficit in expression of this transcription factor in ERO1 α -KO cells (Figure 6.5). Furthermore, in the absence of ERO1 α , we observed that PDAC cells also displayed substantially reduced expression of the immune inhibitory molecule PD-L1, which is typically upregulated in many different cancer types. (Figure 6.5).

Figure 6.5: Western blot analysis of ERO1 α -regulated proteins comparing WT with ERO1 α -KO tumor cells: HIF-1 α (93-110 Kda); PHD2 (different variants 45-60 kda); PDL1 (variants; 33,45-70kda); NFIL3 (60 kda); and PDI (55-60 kda) in cell lysate. Nx; Normoxia; Hx; Hypoxia, KO; Knockout cells under normoxia, HxKO; KO cells under hypoxia (n= 3 independent experiments)

*Protein Loading amount: Cell lysate (50 μ g)

*Protein Ladder(Bio-Rad, USA) Precision Plus Protein™ Dual Color Standards, #1610374

Given that HIF-1 α expression is known to be controlled by reactive oxygen species (ROS), we next assessed whether the generation of these mediators might represent a critical mechanism by which ERO1 α influences pancreatic cancer progression. Indeed, previous work has identified that ERO1 α oxidizes PDI which in-turn catalyzes the formation of disulfide bonds in folding proteins, which simultaneously generates intracellular hydrogen peroxide (H₂O₂) that can mutate DNA and trigger oncogenic events. When assessed in fluorescence-based DCDFA assays, we observed that PDAC cells lacking ERO1 α displayed substantially reduced ability to generate ROS, exhibiting only 66% of the ROS capacity detected in WT tumor cells (Figure 6.6).

A **B**

Figure 6.6: ROS Analysis: (A) Representative fluorescent microscopic images of WT and ERO1 α -KO PDAC cells showing a significant reduction in ROS generation in ERO1 α -deficient cells. (B) Fluorescence intensity was measured by microplate reader confirming significant ROS impairment in ERO1 α -KO clones (Analyzed by DCFDA assay); *Scale bar - 100 μ m, WT (Wild Type Cells) KO (ERO1 α Knockout cells) (n= 3 independent experiments) Data represented the means $\pm$ SEM, *p <0.05; **p<0.01; ***p<0.001

Together, these data confirmed that ERO1 α -deficient PDAC cells exhibit impaired tumor development *in vitro*, so we next performed xenograft experiments in Ncr-nude mice to determine whether these cells also displayed reduced oncogenic potential *in vivo*. When administered by subcutaneous (s.c) injection, ERO1 α -competent tumors developed after 28 days, whereas ERO1 α -deficient cancer cells failed to drive tumor formation in recipient animals (n= 6 per group). Indeed, when the skin was excised from the injection sites we were unable to detect significant tumor development in any mice that had received ERO1 α -KO PDAC cells (Figure 6.7). These data confirm that in the absence of ERO1 α , pancreatic tumor cells undergo regression rather than progression *in vivo*.

Figure 6.7 Xenograft Studies: (A) Representative images of xenografted mouse tumor injection sites before and 28 days after inoculation with the indicated cancer cells. (B) Tumors were excised and weighed; mean values are shown (n=6). ***P<.001 (student t-test). WT; Wild type group KO; Knockout group

*Skin excised to show the tumor inoculation site in KO group

Chapter 7 Quantitative proteomic profiling to identify the differentially expressed proteins (ERO1 α regulated proteins/pathways) using WT and ERO1 α KO PDAC cells

7.1 Rationale

ERO1 α has been frequently found dysregulated in many cancers (236, 238, 268). Recent studies showed ERO1 α promotes neo-vascularisation by increasing VEGF expression through disulfide formation(238). Overexpression of ERO1 α under hypoxia could relate to rapid tumor proliferation, angiogenesis, invasiveness, metastasis, and protection from apoptosis in cancer cells. Further, we were interested to know the effect of ERO1 α deletion on the whole protein expression level. This might give us a broad picture of crucial proteins involved in pancreatic cancer development under hypoxia. We adopted TMT based high throughput quantitative proteomics approach to identify differentially regulated proteins in WT and KO ERO1 α PDAC cells treated with/ without hypoxia for 24 or 48 hours, respectively.

7.2 Results and Discussion

Identification and quantification of proteins

Quantitative proteomic profiling of WT and ERO1 α deficient PDAC cells treated with hypoxia was performed by using differentially labeled tags TMT coupled with multidimensional liquid chromatography and tandem mass spectrometry. The workflow of the experiment is shown below (Figure 7.1). Briefly, six PDAC samples were reduced with TCEP, alkylated with IAA, digested with trypsin, differentially labeled at peptide level with TMT 6-plex reagents, pooled together, fractionated by using

RP-HPLC and finally subjected to analyses by LC-MS/MS by Q Exactive instrument (Figure 7.1). Of these, one sample WT (control) was labeled with TMT6 -126 (TMT with reporter ions at $m/z = 126$); two samples treated with hypoxia for 24 h and 48h were labeled with TMT6 -127 and TMT6 -130, respectively; one sample KO ERO1 α cells was labeled with TMT6-128; two samples KO ERO1 α cells treated with hypoxia for 24h and 48h were labeled with TMT6 -129 and TMT6 -131, respectively. Technical replicate analyses of the samples were performed on the high mass resolution Q Exactive instrument. The raw data files obtained after LCMS/MS analyses were processed in Proteome Discoverer version 2.2. After searching against the Uniprot Homo sapiens database and filtering with a 1 % FDR, proteins were identified and quantified according to the intensity of reporter ions and normalized on the protein median. Ratios of protein abundance were calculated for each sample by comparing it with that of the control sample (TMT6 -126). By combining all the data, a total of 5285 proteins, which have quantitative information and detected in both technical replicates were obtained (MS/MS Data in Appendix D).

Figure 7.1: Schematic representation of the experimental design to perform the quantitative proteomics analysis of WT and KO ERO1α MIAPaCa-2 proteome by using TMT 6-plex isobaric tags. WT and KO ERO1α MIAPaCa-2 cells were treated with hypoxia for different durations before protein extraction and TMT labeling.

Figure 7.2 describes the protein count against the TMT Log_2 ratio suggests that ERO1 α KO cells have reduced translation as compared to WT, treated with or without hypoxia. Since ERO1 α increases the active translation by inducing the correct disulfide bond formation and its deletion might contribute to the reduced expression of proteins and reflect the significance of ERO1 α deletion on the whole proteome level (Figure 7.2).

Figure 7.2: Comparison of protein count against the TMT Log₂ ratio between different experimental condition Control; normoxia, Hx; hypoxia; ERO1α KO; ERO1α Knockout group.

Table 7.1 summarize the top 20 proteins affected by ERO1 α deletion.

Table 7.1 Top 20 proteins affected by ERO1 α Knockout

*Control- Normoxia; Hx – Hypoxia, KO; ERO1 α KO cells, HxKO; KO cells under hypoxia (Data Analysed by PD2.2)

Name	Gene	#	Hx	KO	HxKO	Hx	HxKO48/Con
		Uniqu e Peptid es	24/Cont rol	24/Control	24/Co ntrol	48/Cont rol	trol
PODXL protein	PODXL	11	2.54	0.79	0.68	1.76	0.66
Creatine kinase brain isoform 2 (Fragment)	CKB	7	2.62	0.72	0.73	1.47	0.78
Reticulon-1	RTN1	6	2.54	0.75	0.73	1.93	0.75
Homeobox protein Hox-B8	HOXB8	4	2.65	1.83	0.86	1.27	0.62
Xylosyltransfera se 2	XYLT2	2	2.17	1.96	0.79	1.83	1.02
Formin-binding protein 1-like	FNBP1L	5	3.14	1.28	1.16	2.02	1.21
Integrin alpha-6	ITGA6	12	2.77	1.16	1.04	2.08	0.95
Serpin B6	SERPIN B6	12	2.50	0.89	0.96	1.93	0.74
Adipogenesis regulatory factor	ADIRF	7	1.98	0.83	0.77	1.47	0.69

Basal adhesion molecule (Lutheran blood group)	cell	BCAM	4	1.98	0.89	0.76	2.75	0.79
Isoform 2 of Gelsolin	2	of GSN	25	2.22	0.84	0.86	2.03	0.98
Calmin		CLMN	4	1.61	0.59	0.62	1.45	0.74
Isoform 2 of Integrin alpha-3	2	of ITGA3	12	2.66	1.27	1.05	2.14	1.06
ATR-interacting protein		ATRIP	1	2.05	0.85	0.81	0.94	0.86
Dedicator of cytokinesis protein 11	of	DOCK1 1	49	2.76	1.17	1.11	1.79	1.00
Transformation-related protein 14		TRG14	3	2.14	0.73	0.88	2.29	1.34
Peptidyl-prolyl isomerase		cis-trans	1	1.39	0.74	0.57	0.84	0.48
Calretinin		CALB2	17	3.02	1.41	1.29	1.81	1.10
C-type domain family 2 member B	lectin	CLEC2B	1	2.01	0.78	0.92	1.90	1.05

Bioinformatic analysis

The cut-off for defining perturbed and unperturbed protein expression in TMT experiments depends on the characteristics of biological samples as well as MS instruments. To avoid setting the cut-offs arbitrarily, we examined the distribution of the expression levels of the 5285 proteins. Most of the relative expression levels of proteins were all normally distributed, indicating modulation of a small percentage of ERO1 α KO cells proteome. We thus focused on the top 10% of proteins whose expression was most perturbed by ERO1 α deletion. With this criterion, protein ratios 1.5 and 0.8 were considered over and under-expressed, thereby narrowing the reliable differentially expressed proteins to a small number, which reflected significant effects of ERO1 α deletion on the global proteome in PDAC cells. Proteins with significant TMT ratio change under the effect of ERO1 α deletion were selected for further analysis. However, we noticed that ERO1 α deletion results in reduced expression of the proteins as compared to other conditions.

Proteins were further analyzed with FunRich V3.0. Although only 593 of the 765 confidently identified proteins were available in GO annotation, we found that major fraction of the identified proteins involved in the catalytic activity (43 %, Figure 7.3B), oxidoreductase and transporter activity (13.5 % and 10.5 %, Figure 7.3B) in the classification of molecular function. ERO1 α deletion affected VEGF signaling as well as

oxidoreductase activity, which might affect the angiogenesis by reducing active VEGF expression in pancreatic cancer under hypoxia (Figure 7.3 B & C) and requires further research and understanding. The biological process includes metabolism, energy pathway, protein folding, and antiapoptotic process, suggesting these roles can change the tumor dynamics under the effect of ERO1 α deletion (Figure 7.3E). Further analysis shows that most of the genes regulated by SP1, JUNB, FOSB, SP4 transcription factors have been reduced in ERO1 α KO cells (Figure 7.3D). Together, these results suggested that ERO1 α deletion plays a critical role in catalytic activity, metabolic energy pathways, and protein folding which will contribute to pancreatic cancer oncogenesis.

Figure 7.3 GO (Gene Ontology) analysis illustrates the classes of proteins with significantly reduced expression. Proteins with significant decreased fold change at least in one condition of ERO1 α KO cells were subjected to GO classification in terms of **(A)** Cellular Location **(B)** molecular function **(C)** Biological pathway **(D)** Transcription factor **(E)** Biological process

Chapter 8 Protein Interactomic analysis of highly expressed ERO1 α in PDAC cells

8.1 Rationale

ERO1 α belongs to the oxidoreductase family involved in disulfide formation in the endoplasmic reticulum(233, 234, 269, 270). ERO1 α reoxidizes the P4HB, an enzyme catalyzing the disulfide formation, to allow an additional round of disulfide formation(271, 272). Overexpression of ERO1 α is associated with many cancers(236, 238, 268) but the molecular mechanism underlying this process remains elusive. ERO1 α is one of the highly expressed proteins found under hypoxia in PDAC cells (Figure 4.12). Current studies show high expression of ERO1 α is associated with increased angiogenesis and migration, but clear understanding remains unknown(238, 273). Thus, in-depth understanding is required to explore the role of hypoxia-induced ERO1 α in cancer progression. Recently, co-immunoprecipitation (Co-IP) coupled with proteomics analysis based on Mass spectrometry is a comprehensive and effective way to study the bait protein and its interacting protein(274-277).

The aim of this study to use ERO1 α , as a target protein and applied co-immunoprecipitation combined with mass spectrometry to purify and analyze the ERO1 α -interacting proteins, can help us further understand the molecular mechanism of ERO1 α regulation of pancreatic cancer invasion and metastasis, and provide accurate targeting to develop new drugs for specific treatment.

8.2 Results and discussion

Purification of ERO1 α interacting proteins

After purification by co-immunoprecipitation, ERO1 α interacting proteins were separated by SDS-PAGE (10% acrylamide gel) for further analysis. To verify that ERO1 α can be purified and enriched by co-immunoprecipitation, we used western blot to examine the expression of ERO1 α in protein samples to assess enrichment efficiency. The results demonstrated that ERO1 α was purified by a specific monoclonal antibody in the experimental group compared with the IgG control antibody (Figure 8.1). These experiments were repeated three times respectively with the same conditions.

Figure 6.1: (A) Schematic representation of the experimental design of ERO1α co-IP. ERO1α and associated proteins were isolated according to the workflow, and protein extracts were eventually subjected to LCMS analysis (B) Western blot to test ERO1α in the experimental group (Nx-IP and Hx-IP) and control group (NxC-IgG and HxC-IgG) of protein samples. Nx, normoxia; Hx, hypoxia.

Identification of ERO1 α interacting proteins

In the study we would like to identify the candidate protein associated with ERO1 α , aiming to discover the potential substrate of ERO1 α and its role in pancreatic cancer development. Since ERO1 α is initially known as an oxidoreductase enzyme that executes its functions from and locates on endoplasmic reticulum (ER) lumen, the putative substrate of ERO1 α may be an ER or cytoplasmic protein. We approached this by combining the selective co-IP of ERO1 α with a label-free, quantitative proteomics method.

As described in Figure 8.1A, ERO1 α and associated proteins were co-immunoprecipitated by using an anti- ERO1 α mouse monoclonal antibody or a normal mouse IgG. Protein extracts pulled down by the anti- ERO1 α antibody (target) were analyzed by gel electrophoresis and mass spectrometry, and then we subsequently compared the result to that of protein extracts pulled down by the normal mouse IgG (control). The proteins in the gel were digested by trypsin. The tryptic peptides were analyzed with LC-MS/MS. The raw MS/MS data were searched by using the MASCOT engine against the UniProt Human database and UniProt cricetus Griseus database. To ensure the accuracy and reliability of the proteome detected by the LC-MS/MS, the biological replicates of co-IP were performed, and protein extracts were pooled together to minimize sample-to-sample variation. Then technical replicates of the protein

extracts from both control and target were analyzed in triplicate on a high mass resolution Q *Exactive* instrument.

Stringent inclusion criterion was employed to filter the qualitative proteomics dataset, i.e. only proteins quantified from at least two unique peptides, and having ion scores $\geq$ identity/homology scores were considered as confident protein hits and advanced to the next phase of analysis (Full data shown in the appendix). In total, 151 and 112 candidate proteins were identified under Nx and Hx, respectively (Figure 8.2A). Of them, the number of uniquely identified proteins under Nx and Hx was 84 and 45 respectively, whereas 67 shared in both conditions. In contrast to previous pSILAC results, we finally screened 62 and 38 overlapping proteins under Nx and Hx respectively (Figure 8.2B), that could bind to ERO1 α . Among them, we observed 55 proteins upregulated and 16 proteins downregulated under Hx in pSILAC data. These proteins were further analyzed by using a bioinformatic tool (FunRich) in terms of molecular functions and biological processes.

Figure 8.2 Proteomic analysis of Co-IP proteins: Comparison of the identified proteins between (A) Nx, ERO1 α -co-IP and Hx, ERO1 α -co-IP (B) Comparison of the Overlapped proteins between co-IP and pSILAC data (Analysed by FunRich 3.1.3). Nx; Normoxia, Hx; Hypoxia

Functional analysis of ERO1 α interacting proteins in pancreatic cancer

To reveal the molecular function and biological process, we used a gene ontology analysis (FunRich V3) to identify the functional group of proteins. The analysis showed that ERO1 α interacting proteins may participate in diverse biological processes, such as protein folding, cellular localization, and intracellular transport. The molecular function includes protein binding and dimerization activity (Figure 8.3).

Figure 8.3 Gene ontology analysis: FunRich (V 3.1) analysis of ERO1 α interacting partners **(A)** Biological process **(B)** Molecular function

To map the enriched protein interaction pattern, the list of candidate proteins was submitted to the online biological database, STRING database, to disclose the known and predicted protein-protein interactions in our dataset. High confidence (score 0.70) cut-off threshold was set to connect the ERO1 α with any proteins pulled down in our study based on previously published works. A highly complex protein-protein interactions network as shown in Figure 8.4. Table 8.1 summarized the proteins that have been shown interacting or connecting to ERO1 α in previous works through data and text mining.

Figure 8.4 The ERO1 α interacting proteins network diagram. Each protein interaction is derived from the STRING database and is visualized using Cytoscape. The **cyan** color represents the direct partners of ERO1 α and **yellow** color indicates the second node of interaction (Table 8.1).

Table 8.1 List of ERO1 α interacting partners

*TXNDC5; (Thioredoxin Domain Containing 5), HSPA5; (Heat Shock Protein Family A (Hsp70) Member 5), PRDX4; (Peroxiredoxin-5), P4HB; (Protein disulfide-isomerase). (Data Analysed by Cytoscape)

Node1	Node2	Neighborhood	Experimental	Database	Textmining	Score
ERO1 α	TXNDC5	--	0.095	0.6	0.428	0.78
ERO1 α	HSPA5	--	0.082	--	0.732	0.778
ERO1 α	PRDX4	--	--	--	0.477	0.489
ERO1 α	P4HB	--	0.472	0.9	0.714	0.984

The results of database analysis showed that 67 of the 71 identified proteins were able to interact with at least one another protein. ERO1 α was found interacting with P4HB (Protein disulfide-isomerase), PRDX4(Peroxiredoxin-4), TXNDC5(Thioredoxin Domain Containing 5), and HSPA5(Heat Shock Protein Family A (Hsp70) Member 5) protein through data mining in previous experimental data, computational prediction and public text collections (Table 8.1). As shown in Figure 8.4, P4HB, PRDX4, TXNDC5, and HSPA5 were identified as the direct neighbors of ERO1 α and upregulated under hypoxia in MIAPaCa-2 pancreatic cancer cells. Although the above 4 proteins considered to be the direct neighbors of ERO1 α , only the interaction of ERO1 α with P4HB, HSPA5 and TXNDC5 have been experimentally verified. We also

reconstructed a network model to identify central genes among the shared targets, which showed ERO1 α was a central protein with a high clustering coefficient (Figure 8.5). This result suggests that there is a great possibility that ERO1 α interacting proteins may also affect the occurrence and development of pancreatic cancer.

Figure 8.5 The ERO1 α interacting proteins network diagram ranked based on cluster coefficient (Analyzed by Cytohubba plugin, Cytoscape)

Chapter 9: Conclusion and Future Direction

9.1 Concluding remarks and future perspectives

Low oxygen availability in solid tumors is now well established as a crucial factor in driving malignant progression, promoting treatment resistance, and conferring poor clinical outcome in pancreatic cancer(37). Since the molecular basis of these effects remains poorly defined, we used a pSILAC proteomic approach to identify hypoxia-sensitive proteins expressed by pancreatic cancer cells when subjected to oxygen restriction *in vitro* either in the presence or absence of serum supplementation (mimicking restricted blood/nutrient supply *in vivo*). Using this model, we detected a rapid induction of several established biomarkers of tumor hypoxia and observed that active protein translation was broadly downregulated in the oxygen-deprived microenvironment.

Hypoxia is known to impede the growth of both tumors and healthy cell types, but variable severity and duration of hypoxia can induce a range of different effects that have been shown to increase cancer cell viability, therapy resistance, and metastatic potential(38, 39, 134, 160, 161, 278). While tumor translational activity was generally downregulated during low-oxygen stress in our assays, we also detected a group of proteins that was instead selectively induced by hypoxia (206 in serum-free cultures, 138 under serum-replete conditions, and 20 that were actively synthesized in both settings). The relatively high number of tumor proteins upregulated in serum-free culture might indicate the translation of

molecules that support cancer cell survival under adverse conditions. In support of this concept, the profile of proteins induced in the presence/absence of serum displayed divergent functional profiles, with serum/serum-replete culture favoring mediators of cell communication and signal transduction, whereas serum-free conditions induced regulators of cellular transport and metabolic processes. Hypoxia-induced several proteins have shown to increase metastasis, immune suppression, and treatment-resistance in different cancers. One such highly upregulated (Hx/Nx >10) protein in our dataset NCS1 (neuronal calcium sensor 1) a calcium-binding protein involved in many cellular processes, has shown to promote metastasis in breast cancers(222). Furthermore, our data indicated that hypoxic tumors subjected to serum starvation displayed greater induction of the anti-apoptotic protein NOL3, a key mediator of tumor migration/invasion CD151, and angiogenic factor ANGPTL4 which supports tumor neovascularization. Together, these data indicate that hypoxia effects on pancreatic tumor development are strongly influenced by the nutrient status of the constituent cancer cells, which subsequently upregulate key mediators of cell survival, dissemination, and angiogenic processes.

In a previous study, the proteomic analysis of 45 high purity PDAC samples reveals 4 different prognostic subtypes (16), whereas our study relied on hypoxia-induced individual target/s and are poor prognosis for

cancer patients. We used a targeted approach to explore and identify the hypoxia-induced proteins that are clinically correlated with poor prognosis.

To determine the clinical relevance of hypoxia-induced protein translational activity in pancreatic cancer cells, we integrated our data with cancer patient survival statistics available via public gene expression databases. Using the 'PRECOG' tool to identify associations between gene expression levels and clinical outcomes, we were able to identify which hypoxia-triggered proteins exert the greatest influence on cancer patient prognosis. Intriguingly, proteins associated with poor prognosis were more actively translated by hypoxic tumors in serum-free cultures than in serum-replete conditions, further indicating that nutrient availability is a major determinant of how hypoxia impacts cancer progression.

Further screening of these proteins revealed that ERO1 α was associated with a particularly poor prognosis and displayed a high meta z score irrespective of serum availability. We, therefore, analyzed the expression of ERO1 α in relevant GEO datasets which confirmed that ERO1 α is induced by hypoxia stress across a range of pancreatic cell lines. These analyses also indicated that ERO1 α is expressed at elevated levels in pancreatic cancers relative to adjacent healthy tissues from the same

patient and that high tumor expression of this enzyme is significantly correlated with short survival duration.

We are also interested to isolate, characterize, and identify the exosomal proteome under hypoxia. We found several proteins are induced under hypoxia (CD44, MIF, etc). CD44, a surface glycoprotein, found exclusively in Hx has been shown to express in a variety of cancer and one of the markers of cancer stem cell and many malignancies (279). Current evidence suggests that this protein involved in cancer progression and metastasis through extracellular and intracellular signaling (280). Macrophage migration inhibitory factor (MIF), a pro-inflammatory cytokine initially described as a key component of innate immunity (281) has recently been found to be upregulated in many cancers, including PDAC (282). Provided evidence suggests the role of MIF in cancer. MIF expression increased more than four times under hypoxia in our dataset, indicating the potential role of MIF in hypoxia-driven tumor progression. Further studies are needed to understand the role and mechanism of exosome driven pancreatic tumor progression produced under hypoxia.

ERO1 α , an oxidoreductase enzyme, was found highly upregulated in both cell lysate and exosomes under hypoxia in our proteomics study. However, we also identified that hypoxic stress induces pancreatic tumor cell expression of the oxidoreductase protein ERO1 α , which displayed a clear association with poor survival statistics mined from patient gene

expression databases by using different tools such as PRECOG and GEO datasets. Previous studies have implicated ERO1 α in a range of different cancer types, with current evidence suggesting potential roles in cancer cell invasion of healthy tissues, acquisition of chemoresistant properties, and promotion of angiogenesis (236, 238, 268, 273). Recent data have also suggested that ERO1 α -mediated protein folding is required for the generation of myeloid-derived suppressor cells that protect tumors against immune destruction(268).

To test the function of ERO1 α in pancreatic cancer cells, we used a CRISPR/Cas9 approach to delete the corresponding gene and assessed the impact on the oncogenic potential in a range of different assays. While ERO1 α -KO pancreatic cancer cells were morphologically indistinguishable from their wild-type counterparts, tumor proliferation and colony-forming potential were significantly reduced in the absence of this enzyme. Similarly, when we assessed the motility of ERO1 α -KO tumor cells using in vitro wound healing assays, we observed a marked reduction in migratory potential compared with WT clones. Since ERO1 α enzyme activity is known to generate reactive oxygen species (ROS) (283) which directly regulates the hypoxic response through transcription factor HIF-1 α , we next assessed whether ROS generation might underpin the influence of ERO1 α on pancreatic cancer progression. Using DCFDA assays to quantify ROS levels in hypoxic tumor cells, we observed that

ERO1 α -KO clones displayed a significant reduction in ROS generation relative to WT clones. Hypoxia-induced ERO1 α might regulate the HIF-1 α through disulfide bond formation and require further research and understanding. Accordingly, when WT or ERO1 α -KO cancer cells were injected into BALB/c nu/nu mice, the enzyme-deficient tumors failed to develop whereas wild-type cells were highly tumorigenic in vivo.

Then we applied the proteomic method to study the differentially regulated proteins between WT and ERO1 α deficient cells to understand the effect of ERO1 α deletion on the global proteome in PDAC cells under hypoxia and to identify the key regulator for a potential drug target in oncogenesis for future cancer treatment. To identify the potential interacting partner of ERO1 α , we employed co-immunoprecipitation to pull down the associated protein complex of ERO1 α , then identified the proteins by LC-MS/MS-based proteomic approach, and finally quantified them with emPAI based label-free quantification technique. According to the co-IP results, ERO1 α is involved in the maintenance of protein folding and ER stress in pancreatic oncogenesis. According to the common understanding, ERO1 α has an unusually high expression in breast cancer(268), lung cancer,(284) gastric cancer,(236), and other tumors. No studies has shown the definite relationship between the abnormal expression of ERO1 α and pancreatic cancer invasion and metastasis behaviors, and the mechanism of how ERO1 α regulates the invasion and

metastasis of pancreatic is still elusive. Therefore, we conducted a proteomic analysis of the immunoprecipitates of ERO1 α . Combined with pSILAC proteomics data, we identified 71 proteins interacting with ERO1 α in MIAPaCa-2 cells. The bioinformatic analysis shows that these ERO1 α interacting proteins are involved in a variety of biological processes such as protein folding and intracellular transport. Among the ERO1 α interacting proteins, we have identified previously recognized interacting partners, such as P4HB (Protein disulfide-isomerase), HSPA5 (Heat Shock Protein Family A (Hsp70) Member 5), and TXNDC5 (Thioredoxin Domain Containing 5) (285). This also demonstrates that we have identified the confidence of ERO1 α interacting proteins. Previous studies showed that ERO1 α serves as one of the important components of the folding process by supplying disulfide bond to protein disulfide isomerase (PDI or P4HB) and receiving electrons that are passed onto the terminal electron acceptor molecular oxygen and producing reactive oxygen species as a by-product (284). High expression of ERO1 α under hypoxia may, in turn, increase the expression of critical proteins involved in the pancreatic cancer development by inducing the disulfide bond formation through protein disulfide isomerase (P4HB). Studies reported that targeting the critical interaction between ERO1 α -P4HB can help in suppressing the progression of cervical cancer (269). HSPA5 belongs to the heat shock protein 70 (HSP70) family and localizes in the lumen of the endoplasmic reticulum (ER). HSPA5 might play a key role in the

regulation of protein folding and transport through the cell and may assist in the function of ERO1 α to promote pancreatic cancer progression. This study has some limitations. First, we cannot determine whether these identified proteins interact with the activated ERO1 α or the inactivated form of ERO1 α . Second, we cannot tell whether these identified ERO1 α interacting proteins are directly or indirectly bound to ERO1 α . This requires us to verify by yeast two-hybrid system. Nonetheless, we can analyze our results through a bioinformatic database which will help us identify some of the interaction that has been proven. Also, the precipitates used in this trial were derived from the whole cell lysate, which includes cell membrane proteins, cytoplasmic proteins, and nuclear proteins. Therefore, some weak interaction may be interrupted, and some of the original non-existent interaction may be identified. If we can extract the ERO1 α interacting proteins from each part of the cell separately, we may exclude these disturbances. In conclusion, by analyzing the ERO1 α interacting proteins, we have gained new insights into the mechanism of pancreatic cancer invasion and metastasis. This provides a new idea for the development of novel anti-pancreatic cancer molecular targeted drugs with tumor-specific and fewer side effects. Further study and analysis are required to study the interacting partners of ERO1 α .

Taken together, these data indicate that a combination of microenvironmental hypoxia and restricted blood/nutrient supply trigger

pancreatic cancer cell translation of a range of different proteins that act to increase malignancy and are associated with poor clinical outcome. In particular, the oxidizing enzyme ERO1 α is predominantly activated only under abnormal conditions such as hypoxia, which perhaps explains the marked induction of this protein in oxygen-starved tumors. Consistent with this concept, our data confirmed that ERO1 α -deficient pancreatic cancer cells displayed a negligible ability to form tumors in vivo, thus implicating ERO1 α as a potential novel target for cancer therapy in human patients. Given that ERO1 α function appears less critical under steady-state conditions, it is also possible that therapeutic disruption of this enzyme may succeed in limiting tumor growth and metastasis without significantly damaging nearby healthy cells and tissues. Further investigations will now be required to assess this possibility. Collectively, the findings of this systematic study using pSILAC-based quantitative proteomics reveal that tumor hypoxia induces active translation of a range of critical proteins that are associated with poor prognosis in human cancer patients. Specifically, our data reveal that the oxidoreductase enzyme ERO1 α is a major proliferation regulator in pancreatic cancer cells both in vitro and in vivo, hence this protein may constitute a useful diagnostic marker of tumor progression and possible new therapeutic target in pancreatic malignancy.

Data availability

1. LC-MS/MS raw data from the pulsed-SILAC experiments and results for protein and peptide identification and quantification from PD2.2 have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD014087. The raw data and search results can be accessed using the following login to the PRIDE data depository.

Project Name: Proteomics analysis of pancreatic cancer cell line (MiaPaCa-2)

Project accession: PXD014087

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Supplementary Data

Supplementary Table 1 : Primer sequences for quantitative PCR

Primer	5' - 3'
ERO1 α _FW	ATGACATCAGCCAGTGTGGA
ERO1 α _RV	CATGCTTGGTCCACTGAAGA
NFIL3_FW	AATGCAGACCGTCAAAAAGG
NFIL3_RV	TTGTTCTTCCCCACACTTCC
HBEGF_FW	GGTGGTGCTGAAGCTCTTTC
HBEGF_RV	GCTTGTGGCTTGGAGGATAA
VEGFA_FW	AAGGAGGAGGGCAGAATCAT
VEGFA_RV	ATCTGCATGGTGATGTTGGA
FGF1_FW	TGCCTCCAGGGAATTACAAG
FGF1_RV	TATAAAAGCCCGTCGGTGTC
ACTIN_FW	GGACTTCGAGCAAGAGATGG
ACTIN_RV	AGCACTGTGTTGGCGTACAG
SLC2A3_FW	ACCGGCTTCCTCATTACCTT
SLC2A3_RV	AGGCTCGATGCTGTTTCATCT
ANGPTL4_FW	GCCTATAGCCTGCAGCTCAC
ANGPTL4_RV	AGTACTGGCCGTTGAGGTTG
JUNB_FW	AATGGAGGACACGGACTTTG
JUNB_RV	ATGTCTCTGGCATCCCTACG
FOS_FW	AGAATCCGAAGGGAAAGGAA
FOS_RV	CTTCTCCTTCAGCAGGTTGG
NDRG1_FW	ACAACCCTGAGATGGTGGAG
NDRG1_RV	TGTGGACCACTTCCACGTTA
HK2_FW	TCTATGCCATCCCTGAGGAC
HK2_RV	TCTCTGCCTTCCACTCCACT

Appendix A

Publications

1. **Gupta, N.**, Park, J. E., Tse, Wilford., Low, J. K., Kon, O. L., McCarthy, N., and Sze, S. K. (2019) ERO1 α promotes hypoxic tumor progression and is associated with poor prognosis in pancreatic cancer. *Oncotarget* 10(57): 5970–5982
2. Park, J. E., Dutta, B., Tse, Wilford., **Gupta, N.**, Tan, C. F., Low, J. K., Yeoh, K. W. Kon, O. L., Tam, J. P., and Sze, S. K. (2019) Hypoxia-induced tumor exosomes promote M2-like macrophage polarization of infiltrating myeloid cells and microRNA-mediated metabolic shift. *Oncogene* 38(26), 5158-5173
3. Tse, Wilford., Tan, C. F., Park, J. E., **Gupta, N.**, Tay, C. Y., McCarthy, N., Lim, S. K., and Sze, S. K. (2019) Microenvironmental Hypoxia Induces Dynamic Changes in Lung Cancer Synthesis and Secretion of extracellular vesicles. *Journal of Extracellular Vesicles* (Final Revision)

4. **Gupta, N.**, Manikandan, N. A., and Pakshirajan, K. (2017) Real-time lipid production and dairy wastewater treatment using *Rhodococcus opacus* in a bioreactor under fed-batch, continuous and continuous cell recycling modes for potential biodiesel application. *Biofuels*, Pages 239-245
5. Kumar, S., **Gupta, N.**, and Pakshirajan, K. (2015) Simultaneous lipid production and dairy wastewater treatment using *Rhodococcus opacus* in a batch bioreactor for potential biodiesel application. *Journal of Environmental Chemical Engineering* 3, 1630–1636

Appendix B

Conference Presentation

1. Conference: American Society for Cell Biology (ASCB) 2018 ASCB
| EMBO Meeting, from December 8th– 12th 2018.

Venue: San Diego Convention Center, San Diego, California,
United States of America.

Title: pSILAC proteome profiling reveals ERO1 α as a hypoxia-sensitive protein and drug target that is associated with poor pancreatic cancer prognosis

2. Conference: 2nd PEPTIDES AND PROTEINS SYMPOSIUM
SINGAPORE 2016, from December 8th– 9th 2016.

Venue: Nanyang Technological University, School of Biological
Science.

Title: Study of hypoxia driven pancreatic cancer development

3. Conference: 3rd PEPTIDES AND PROTEINS SYMPOSIUM
SINGAPORE 2017, from December 4th– 5th 2017.

Venue: Nanyang Technological University, School of Biological Science.

Title: Study of hypoxia driven pancreatic cancer development

4. Conference: International Conference on Energy Research and Environmental Technology organized by Krishi Sanskriti, from April 4th– 5th 2015.

Venue: Jawahar Lal Nehru University, New Delhi, India.

Title: Simultaneous lipid production and dairy wastewater treatment using *Rhodococcus opacus* in a batch bioreactor for potential biodiesel application

Awards

1. NTU Graduate Research Scholarship, International Ph.D. Programme.
2. Graduate Aptitude Test in Engineering (GATE 2013) Scholarship in Life Science conducted by world-renowned institutes like the Indian Institute of Sciences (IISc) and IITs with 98.44 Percentile, All India Rank(AIR-201).
3. Council of Scientific and Industrial Research (CSIR) Government of India Award National Eligibility Test (NET-LS) All India Rank-31 (2013 December); CSIR (NET-LS) All India Rank 45 (2014 June).

Appendix C (Western blot Images unadulterated):

Chapter 3 Figure 3.1

Chapter 4 Figure 4.12

Chapter 5 Figure 5.3

Chapter 5 Figure 5.5

Chapter 6 Figure 6.1

Chapter 6 Figure 6.4

Chapter 6 Figure 6.5

Chapter 8 Figure 8.1

Appendix-D (Mass Spectrometry Data)

Chapter 5 (Exosome Proteomics Data)

GENE	Name	Normo xia _emPAI	Hypoxia_em PAI	Normo xia _Peptid e	Hypoxia_Pep tide
CELSR3	Isoform 2 of Cadherin EGF LAG seven-pass G-type receptor 3	0	0.01	0	2
ACAN	Aggrecan core protein	0	0.01	0	2
AHCTF1	Isoform 2 of Protein ELYS	0	0.01	0	2
DOCK7	Dedicator of cytokinesis protein 7 (Fragment)	0	0.02	0	2
CCDC180	Isoform 2 of Coiled-coil domain-containing protein 180	0	0.02	0	2
DMBT1	Isoform 9 of Deleted in malignant brain tumors 1 protein	0	0.03	0	2
ZW10	Isoform 2 of Centromere/kinetochore protein zw10 homolog	0	0.04	0	2
ATG7	Isoform 2 of Ubiquitin-like modifier-activating enzyme ATG7	0	0.04	0	2
GYS2	Glycogen [starch] synthase, liver	0	0.04	0	2

PLOD2	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	0	0.04	0	2
TMEM132A	Isoform 4 of Transmembrane protein 132A	0	0.04	0	2
MTIF2	Translation initiation factor IF-2, mitochondrial	0	0.04	0	2
TXLNA	Alpha-taxilin	0	0.05	0	2
DLAT	Acetyltransferase component of pyruvate dehydrogenase complex (Fragment)	0	0.06	0	2
CHURC1-FNTB	Protein CHURC1-FNTB	0	0.06	0	2
ESRP1	Epithelial-splicing regulatory protein 1 (Fragment)	0	0.06	0	2
PWP1	Periodic tryptophan protein 1 homolog	0	0.07	0	2
GRSF1	G-rich sequence factor 1 (Fragment)	0	0.07	0	2
PLIN3	Isoform 3 of Perilipin-3	0	0.07	0	2
KRT78	Isoform 2 of Keratin, type II cytoskeletal 78	0	0.07	0	2
PRRC1	Isoform 2 of Protein PRRC1	0	0.07	0	2
HPDL	4-hydroxyphenylpyruvate dioxygenase-like protein	0	0.08	0	2
FAM45B	Protein FAM45B	0	0.08	0	2
TOR2A	Torsin-2A	0	0.09	0	2

XRCC4	Isoform 2 of DNA repair protein XRCC4	0	0.09	0	2
CIRH1A	Cirhin (Fragment)	0	0.09	0	2
PTRF	Isoform 2 of Polymerase I and transcript release factor	0	0.1	0	2
PPIE	Isoform B of Peptidyl-prolyl cis-trans isomerase E	0	0.1	0	2
QPCT	Glutaminyl-peptide cyclotransferase (Fragment)	0	0.1	0	2
SDHB	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	0	0.1	0	2
CRYL1	Isoform 2 of Lambda-crystallin homolog	0	0.1	0	2
SUMF1	Isoform 2 of Sulfatase-modifying factor 1	0	0.1	0	2
PDE12	Isoform 2 of 2~,5~-phosphodiesterase 12	0	0.11	0	2
NHEJ1	HCG2043685, isoform CRA_b	0	0.12	0	2
VPS28	Isoform 2 of Vacuolar protein sorting-associated protein 28 homolog	0	0.12	0	2
ECI1	Enoyl-CoA delta isomerase 1, mitochondrial (Fragment)	0	0.13	0	2

COL6A2	Collagen alpha-2(VI) chain (Fragment)	0	0.13	0	2
APCS	Serum amyloid P-component	0	0.13	0	2
SLC25A23	Calcium-binding mitochondrial carrier protein SCaMC-3 (Fragment)	0	0.13	0	2
HTRA1	Serine protease HTRA1 (Fragment)	0	0.14	0	2
PRTG	Protogenin (Fragment)	0	0.14	0	2
HEATR2	HEAT repeat-containing protein 2 (Fragment)	0	0.15	0	2
EXOSC1	Exosome complex component CSL4	0	0.18	0	2
WDR54	WD repeat-containing protein 54	0	0.19	0	2
CHCHD2P9	Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9, mitochondrial	0	0.22	0	2
UBE2Z	Ubiquitin-conjugating enzyme E2 Z (Fragment)	0	0.23	0	2
tr A0A087WSV2 A0A087WSV2_H UMAN	Uncharacterized protein (Fragment)	0	0.26	0	2
PHF5A	PHD finger-like domain-containing protein 5A	0	0.26	0	2
TRAPPC6B	Trafficking protein particle complex subunit 6B (Fragment)	0	0.29	0	2
RNF7	Isoform 4 of RING-box protein 2	0	0.3	0	2
LAMTOR4	Regulator complex protein LAMTOR4	0	0.32	0	2

PPIH	Peptidyl-prolyl cis-trans isomerase H (Fragment)	0	0.33	0	2
NUDT3	Diphosphoinositol polyphosphate phosphohydrolase 1	0	0.37	0	2
CBFB	Core-binding factor subunit beta (Fragment)	0	0.48	0	2
ATP1B3	Sodium/potassium-transporting ATPase subunit beta-3 (Fragment)	0	0.75	0	2
MDN1	Midasin	0	0.01	0	3
LPHN2	Latrophilin-2 (Fragment)	0	0.02	0	3
LTN1	Isoform 3 of E3 ubiquitin-protein ligase listerin	0	0.02	0	3
FANCA	Isoform 3 of Fanconi anemia group A protein	0	0.02	0	3
RAPGEF6	Rap guanine nucleotide exchange factor 6	0	0.02	0	3
SMARCC2	Isoform 2 of SWI/SNF complex subunit SMARCC2	0	0.03	0	3
TM9SF4	Transmembrane 9 superfamily member 4	0	0.04	0	3
PREPL	Isoform 2 of Prolyl endopeptidase-like	0	0.04	0	3
TM9SF1	Transmembrane 9 superfamily member 1	0	0.04	0	3

ATF6	Cyclic AMP-dependent transcription factor ATF-6 alpha	0	0.04	0	3
CCDC93	Coiled-coil domain-containing protein 93	0	0.04	0	3
CAMK2G	Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma, isoform CRA_a	0	0.05	0	3
MSH2	DNA mismatch repair protein Msh2	0	0.05	0	3
TRMT1	Isoform 2 of tRNA (guanine(26)-N(2))-dimethyltransferase	0	0.05	0	3
PROS1	Protein S (Alpha), isoform CRA_b	0	0.05	0	3
WDR6	WD repeat-containing protein 6	0	0.05	0	3
SLCO4A1	Solute carrier organic anion transporter family member 4A1	0	0.05	0	3
C18orf8	Uncharacterized protein C18orf8	0	0.05	0	3
MMS19	Isoform 4 of MMS19 nucleotide excision repair protein homolog	0	0.06	0	3
MATR3	Matrin-3	0	0.06	0	3
MCCC2	Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	0	0.06	0	3
ITPRIPL2	Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2	0	0.06	0	3
MATN2	Isoform 2 of Matrilin-2	0	0.06	0	3

CEP55	Isoform 2 of Centrosomal protein of 55 kDa	0	0.07	0	3
VLDLR	Isoform Short of Very low-density lipoprotein receptor	0	0.07	0	3
NAB2	Isoform 3 of NGFI-A-binding protein 2	0	0.07	0	3
F8A1	Factor VIII intron 22 protein	0	0.08	0	3
DEDD	Death effector domain containing, isoform CRA_b	0	0.08	0	3
GTPBP1	GTP-binding protein 1	0	0.09	0	3
PUF60	Poly(U)-binding-splicing factor PUF60 (Fragment)	0	0.09	0	3
L3HYPDH	Trans-L-3-hydroxyproline dehydratase	0	0.09	0	3
CASP6	Caspase-6	0	0.1	0	3
SLC25A51	Solute carrier family 25 member 51	0	0.1	0	3
DNM2	Dynamin-2 (Fragment)	0	0.1	0	3
FBXO21	F-box only protein 21 (Fragment)	0	0.11	0	3
PRKAG1	5~-AMP-activated protein kinase subunit gamma0 (Fragment)	0	0.11	0	3
KPNA1	Importin subunit alpha-5	0	0.11	0	3
PRPSAP1	Phosphoribosyl pyrophosphate synthase-associated protein 1	0	0.11	0	3
TSTA3	GDP-L-fucose synthase (Fragment)	0	0.11	0	3

BID	Isoform 2 of BH3-interacting domain death agonist	0	0.12	0	3
ATP6V0D1	V-type proton ATPase subunit d 1 (Fragment)	0	0.12	0	3
FUT11	Isoform 2 of Alpha-(1,3)-fucosyltransferase 11	0	0.13	0	3
ABI1	Abl interactor 1	0	0.13	0	3
COMMD4	COMM domain-containing protein 4 (Fragment)	0	0.14	0	3
PCID2	Isoform 2 of PCI domain-containing protein 2	0	0.15	0	3
TRMT61A	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A (Fragment)	0	0.16	0	3
VPS37B	Vacuolar protein sorting-associated protein 37B (Fragment)	0	0.16	0	3
NUP43	Nucleoporin Nup43	0	0.16	0	3
KCNAB2	Isoform 5 of Voltage-gated potassium channel subunit beta-2	0	0.16	0	3
DCAF7	DDB1- and CUL4-associated factor 7	0	0.17	0	3
SNRNP40	U5 small nuclear ribonucleoprotein 40 kDa protein	0	0.17	0	3
AIP	AH receptor-interacting protein	0	0.18	0	3
MAN2B1	Lysosomal alpha-mannosidase (Fragment)	0	0.18	0	3

FEN1	Isoform FENMIT of Flap endonuclease 1	0	0.19	0	3
RPL24	60S ribosomal protein L24	0	0.19	0	3
CDC2	Cell division cycle 2, G1 to S and G2 to M, isoform CRA_a	0	0.2	0	3
ANP32E	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E	0	0.2	0	3
RAD23B	Isoform 2 of UV excision repair protein RAD23 homolog B	0	0.2	0	3
VSTM2L	Isoform 2 of V-set and transmembrane domain-containing protein 2-like protein	0	0.2	0	3
GMFB	Glia maturation factor beta	0	0.2	0	3
RPS10-NUDT3	Protein RPS10-NUDT3 (Fragment)	0	0.21	0	3
FAM175B	BRISC complex subunit Abro1	0	0.23	0	3
TRPT1	tRNA 2~-phosphotransferase 1 (Fragment)	0	0.27	0	3
FBXO22	F-box only protein 22	0	0.32	0	3
CTBP1	C-terminal-binding protein 1 (Fragment)	0	0.35	0	3
SLC39A14	Zinc transporter ZIP14 (Fragment)	0	0.36	0	3
IFITM2	Interferon-induced transmembrane protein 2 (Fragment)	0	0.43	0	3
SMYD5	SET and MYND domain-containing protein 5	0	0.45	0	3

METTL1	tRNA (guanine-N(7)-)-methyltransferase (Fragment)	0	0.49	0	3
POLR2K	DNA-directed RNA polymerases I, II, and III subunit RPABC4	0	0.49	0	3
NIP7	60S ribosome subunit biogenesis protein NIP7 homolog	0	0.61	0	3
ACACB	Isoform 3 of Acetyl-CoA carboxylase 2	0	0.01	0	4
BIRC6	Baculoviral IAP repeat-containing protein 6	0	0.01	0	4
LPHN3	Latrophilin-3	0	0.02	0	4
ABCC11	Isoform 2 of ATP-binding cassette sub-family C member 11	0	0.02	0	4
TRIM33	E3 ubiquitin-protein ligase TRIM33 (Fragment)	0	0.03	0	4
PCNXL4	Pecanex-like protein 4	0	0.03	0	4
UBE3A	Isoform I of Ubiquitin-protein ligase E3A	0	0.03	0	4
ZYG11B	Protein zyg01 homolog B	0	0.04	0	4
UTP15	U3 small nucleolar RNA-associated protein 15 homolog (Fragment)	0	0.05	0	4
TYRP1	5,6-dihydroxyindole-2-carboxylic acid oxidase	0	0.05	0	4
SLC12A2	Solute carrier family 12 (Sodium/potassium/chloride	0	0.05	0	4

	transporters), member 2, isoform CRA_a				
NPLOC4	Isoform 2 of Nuclear protein localization protein 4 homolog	0	0.05	0	4
NCAPD2	Condensin complex subunit 1	0	0.06	0	4
SHCBP1	SHC SH2 domain-binding protein 1	0	0.09	0	4
RQCD1	Isoform 2 of Cell differentiation protein RCD1 homolog	0	0.09	0	4
LRRC14	Leucine-rich repeat-containing protein 14 (Fragment)	0	0.1	0	4
ECM1	Isoform 4 of Extracellular matrix protein 1	0	0.1	0	4
TCEA2	Transcription elongation factor A protein 2 (Fragment)	0	0.11	0	4
SEMA4D	Semaphorin-4D	0	0.11	0	4
ARRDC1	Arrestin domain-containing protein 1 (Fragment)	0	0.11	0	4
ANAPC5	Anaphase-promoting complex subunit 5	0	0.12	0	4
PSPC1	Paraspeckle component 1 (Fragment)	0	0.12	0	4
PPT2	Lysosomal thioesterase PPT2 (Fragment)	0	0.16	0	4

PRPSAP1	Isoform 2 of Phosphoribosyl pyrophosphate synthase-associated protein 1	0	0.16	0	4
GMPPB	Isoform 2 of Mannose0-phosphate guanyltransferase beta	0	0.16	0	4
APOH	Beta-2-glycoprotein 1	0	0.17	0	4
DIABLO	Diablo homolog, mitochondrial	0	0.18	0	4
MFGE8	Lactadherin short form	0	0.18	0	4
PRKAG2	Isoform B of 5~-AMP-activated protein kinase subunit gamma-2	0	0.18	0	4
ANG	Angiogenin	0	0.2	0	4
FAM76A	Protein FAM76A (Fragment)	0	0.24	0	4
WBP2	WW domain-binding protein 2	0	0.27	0	4
PRKCG	Protein kinase C gamma type (Fragment)	0	0.3	0	4
CXCL8	C-X-C motif chemokine	0	0.31	0	4
CMPK1	UMP-CMP kinase	0	0.38	0	4
CANX	Calnexin (Fragment)	0	0.39	0	4
PSMG4	Isoform 2 of Proteasome assembly chaperone 4	0	0.41	0	4
SUPT4H1	Suppressor of Ty 4 homolog 1 (S. cerevisiae), isoform CRA_b	0	0.41	0	4
EPS8	Epidermal growth factor receptor kinase substrate 8 (Fragment)	0	0.5	0	4
HEBP1	Heme-binding protein 1	0	0.51	0	4

NUDT16L1	Protein syndesmos (Fragment)	0	0.53	0	4
RPS15	40S ribosomal protein S15 (Fragment)	0	1.08	0	4
DNAH9	Dynein heavy chain 9, axonemal	0	0.01	0	5
PTPRD	PTPRD protein	0	0.02	0	5
KIF1B	Isoform 3 of Kinesin-like protein KIF1B	0	0.02	0	5
EFTUD1	Elongation factor Tu GTP-binding domain-containing protein 1	0	0.03	0	5
EXOC3L4	Exocyst complex component 3-like protein 4	0	0.04	0	5
CFHR5	Complement factor H-related protein 5	0	0.05	0	5
SEC24D	Isoform 2 of Protein transport protein Sec24D	0	0.06	0	5
DDX46	Probable ATP-dependent RNA helicase DDX46	0	0.06	0	5
SEMA3B	Semaphorin-3B	0	0.06	0	5
PRAME	Melanoma antigen preferentially expressed in tumors	0	0.06	0	5
SEC31A	Protein transport protein Sec31A	0	0.07	0	5
LSS	Isoform 2 of Lanosterol synthase	0	0.09	0	5
STXBP1	Isoform 2 of Syntaxin-binding protein 1	0	0.1	0	5
CCNH	Cyclin-H	0	0.11	0	5

ELP3	Elongator complex protein 3	0	0.11	0	5
FBXW11	Isoform A of F-box/WD repeat-containing protein 11	0	0.11	0	5
VPS53	Vacuolar protein sorting-associated protein 53 homolog (Fragment)	0	0.12	0	5
NDFIP2	NEDD4 family-interacting protein 2	0	0.13	0	5
MAP4	Microtubule-associated protein (Fragment)	0	0.14	0	5
RPL18	60S ribosomal protein L18 (Fragment)	0	0.15	0	5
AGA	N(4)-(beta-N-acetylglucosaminy)-L-asparaginase	0	0.18	0	5
DCTN3	Isoform 3 of Dynactin subunit 3	0	0.19	0	5
USP13	Ubiquitin carboxyl-terminal hydrolase 13 (Fragment)	0	0.2	0	5
DBI	Acyl-CoA-binding protein	0	0.21	0	5
PCYT1A	Choline-phosphate cytidylyltransferase A (Fragment)	0	0.22	0	5
NCAPG	Condensin complex subunit 3 (Fragment)	0	0.23	0	5
KCNAB2	Isoform 3 of Voltage-gated potassium channel subunit beta-2	0	0.23	0	5
MVD	Diphosphomevalonate decarboxylase (Fragment)	0	0.24	0	5

EIF3J	Isoform 2 of Eukaryotic translation initiation factor 3 subunit J	0	0.31	0	5
KLK13	Kallikrein 13 splice variant 7	0	0.31	0	5
UCHL3	Ubiquitin carboxyl-terminal hydrolase	0	0.33	0	5
ADI1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	0	0.34	0	5
NADSYN1	Glutamine-dependent NAD(+) synthetase (Fragment)	0	0.37	0	5
PSMG4	Proteasome assembly chaperone 4	0	0.37	0	5
DCUN1D1	DCN1-like protein	0	0.39	0	5
GSTM3	Glutathione S-transferase Mu 3	0	0.42	0	5
MTPN	Myotrophin	0	0.59	0	5
RAB5B	Ras-related protein Rab-5B (Fragment)	0	0.6	0	5
RPS9	40S ribosomal protein S9	0	0.74	0	5
RPS15	40S ribosomal protein S15	0	0.8	0	5
KDM5C	Isoform 2 of Lysine-specific demethylase 5C	0	0.02	0	6
MAGI2	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2	0	0.02	0	6
NDST1	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	0	0.03	0	6
HECTD3	E3 ubiquitin-protein ligase HECTD3	0	0.03	0	6

SRCIN1	SRC kinase-signaling inhibitor 1 (Fragment)	0	0.03	0	6
WDR48	Isoform 3 of WD repeat-containing protein 48	0	0.04	0	6
LEKR1	Leucine-, glutamate- and lysine-rich protein 1	0	0.04	0	6
F13A1	Coagulation factor XIII A chain	0	0.04	0	6
COL4A1	Isoform 2 of Collagen alpha0(IV) chain	0	0.05	0	6
RAP1GDS1	Isoform 4 of Rap1 GTPase-GDP dissociation stimulator 1	0	0.05	0	6
SERINC1	Serine incorporator 1	0	0.06	0	6
DHX16	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	0	0.06	0	6
MASTL	Serine/threonine-protein kinase greatwall (Fragment)	0	0.06	0	6
KRT39	Keratin, type I cytoskeletal 39	0	0.06	0	6
NPC1	Niemann-Pick C1 protein	0	0.07	0	6
NBPF7	Putative neuroblastoma breakpoint family member 7	0	0.07	0	6
RANBP10	Ran-binding protein 10	0	0.09	0	6
MOV10	Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a	0	0.09	0	6
VEGFA	Vascular endothelial growth factor A	0	0.09	0	6
XYLT2	Xylosyltransferase 2	0	0.13	0	6

RANBP9	Ran-binding protein 9	0	0.13	0	6
SERPINI1	Neuroserpin	0	0.15	0	6
PVR	Poliovirus receptor	0	0.16	0	6
DTD2	Probable D-tyrosyl-tRNA(Tyr) deacylase 2	0	0.18	0	6
ERI2	ERI1 exoribonuclease 2	0	0.19	0	6
AIDA	Axin interactor, dorsalization- associated protein	0	0.2	0	6
tr F2Z2F3 F2Z2F3_HUMAN	Uncharacterized protein	0	0.21	0	6
FBXO2	F-box only protein 2	0	0.21	0	6
SCARB1	Isoform 2 of Scavenger receptor class B member 1	0	0.23	0	6
RRAGB	Isoform 2 of Ras-related GTP-binding protein B	0	0.26	0	6
MAPK14	Mitogen-activated protein kinase 14	0	0.26	0	6
EPDR1	Mammalian ependymin-related protein 1	0	0.27	0	6
UFD1L	Isoform Long of Ubiquitin fusion degradation protein 1 homolog	0	0.28	0	6
THOC6	Isoform 2 of THO complex subunit 6 homolog	0	0.31	0	6
ARMC8	Armadillo repeat-containing protein 8 (Fragment)	0	0.35	0	6
NPC2	Epididymal secretory protein E1 (Fragment)	0	0.37	0	6

HSPA9	Stress-70 protein, mitochondrial (Fragment)	0	0.4	0	6
GSTT2B	Glutathione S-transferase theta-2B	0	0.41	0	6
ECHDC1	Isoform 4 of Ethylmalonyl-CoA decarboxylase	0	0.45	0	6
ATP6V1F	Isoform 2 of V-type proton ATPase subunit F	0	0.75	0	6
PFN2	Profilin-2	0	0.83	0	6
MAP1LC3B	Microtubule-associated protein 1 light chain 3 beta, isoform CRA_f	0	1.68	0	6
ATP6V1G3	Isoform 3 of V-type proton ATPase subunit G 3	0	2.43	0	6
DNAH17	Dynein heavy chain 17, axonemal	0	0.01	0	7
SETX	Isoform 4 of Probable helicase senataxin	0	0.01	0	7
BLM	Bloom syndrome protein	0	0.02	0	7
LOC728763	Protein LOC728763	0	0.02	0	7
FYCO1	Isoform 4 of FYVE and coiled-coil domain-containing protein 1	0	0.02	0	7
NBEA	Neurobeachin	0	0.02	0	7
AGAP2	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2 (Fragment)	0	0.03	0	7
TTLL6	Isoform 2 of Tubulin polyglutamylase TTLL6	0	0.05	0	7

ADCY7	Adenylate cyclase type 7	0	0.07	0	7
MGEA5	Isoform 4 of Protein O-GlcNAcase	0	0.07	0	7
DNAJB4	DnaJ homolog subfamily B member 4	0	0.09	0	7
ASPSCR1	Isoform 2 of Tether containing UBX domain for GLUT4	0	0.1	0	7
CCDC65	Isoform 2 of Coiled-coil domain-containing protein 65	0	0.11	0	7
PAK1IP1	p21-activated protein kinase-interacting protein 1	0	0.15	0	7
SMEK1	Serine/threonine-protein phosphatase 4 regulatory subunit 3A (Fragment)	0	0.17	0	7
GYS1	Isoform 2 of Glycogen [starch] synthase, muscle	0	0.18	0	7
PPP2R5D	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	0	0.2	0	7
SFXN4	Isoform 2 of Sideroflexin-4	0	0.2	0	7
ADAMTSL1	Isoform 1 of ADAMTS-like protein 1	0	0.24	0	7
PPME1	Isoform 4 of Protein phosphatase methylesterase 1	0	0.24	0	7
SCARB1	Scavenger receptor class B member 1	0	0.26	0	7

TRMT6	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	0	0.26	0	7
MBD3	Methyl-CpG binding domain protein 3, isoform CRA_b	0	0.27	0	7
MPST	Isoform 2 of 3-mercaptopyruvate sulfurtransferase	0	0.31	0	7
RAB18	Ras-related protein Rab08	0	0.35	0	7
RCN1	Isoform 2 of Reticulocalbin0	0	0.47	0	7
C12orf10	UPF0160 protein MYG1, mitochondrial	0	0.47	0	7
ENTPD6	Ectonucleoside triphosphate diphosphohydrolase 6 (Fragment)	0	0.47	0	7
LIN7A	Protein lin-7 homolog A (Fragment)	0	0.53	0	7
PDE4DIP	Myomegalin	0	0.01	0	8
KNTC1	Kinetochore-associated protein 1	0	0.04	0	8
ABCF1	Isoform 2 of ATP-binding cassette sub-family F member 1	0	0.07	0	8
JMJD4	JmjC domain-containing protein 4	0	0.07	0	8
EPHB2	Ephrin type-B receptor 2	0	0.08	0	8
NEK9	Serine/threonine-protein kinase Nek9	0	0.09	0	8
tr Q6ZNX1 Q6ZNX1_HUMAN	CDNA FLJ26957 fis, clone SLV00486	0	0.11	0	8
ELAC2	Isoform 2 of Zinc phosphodiesterase ELAC protein 2	0	0.12	0	8

RPL7L1	60S ribosomal protein L7-like 1	0	0.12	0	8
DECR1	2,4-dienoyl-CoA reductase, mitochondrial (Fragment)	0	0.15	0	8
CRLF1	Cytokine receptor-like factor 1 (Fragment)	0	0.17	0	8
DCPS	m7GpppX diphosphatase	0	0.18	0	8
MEMO1	Isoform 3 of Protein MEMO1	0	0.2	0	8
GRB2	Growth factor receptor-bound protein 2	0	0.28	0	8
OSGEP	Probable tRNA N6-adenosine threonylcarbamoyltransferase	0	0.29	0	8
RHOBTB3	Rho-related BTB domain-containing protein 3 (Fragment)	0	0.3	0	8
DCTD	Deoxycytidylate deaminase (Fragment)	0	0.38	0	8
ASNA1	ATPase ASNA1	0	0.4	0	8
CDK7	Cyclin-dependent kinase 7	0	0.44	0	8
RPL10	60S ribosomal protein L10 (Fragment)	0	0.49	0	8
AP3S1	AP-3 complex subunit sigma0	0	0.53	0	8
CSRP1	Cysteine and glycine-rich protein 1	0	0.55	0	8
PSMD10	26S proteasome non-ATPase regulatory subunit 10	0	0.58	0	8
NUDT16	U8 snoRNA-decapping enzyme	0	0.8	0	8

EIF6	Eukaryotic translation initiation factor 6 (Fragment)	0	1.12	0	8
SWAP70	Switch-associated protein 70	0	0.05	0	9
DNAJC3	DnaJ homolog subfamily C member 3	0	0.06	0	9
ETNPPL	Ethanolamine-phosphate phospho-lyase	0	0.06	0	9
SYMPK	Symplekin	0	0.07	0	9
OPLAH	5-oxoprolinase	0	0.07	0	9
MAPK8IP3	C-Jun-amino-terminal kinase-interacting protein 3	0	0.07	0	9
DEPDC1	DEP domain-containing protein 1A (Fragment)	0	0.09	0	9
PPP2R2C	Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B gamma isoform	0	0.13	0	9
THOC2	THO complex subunit 2 (Fragment)	0	0.16	0	9
C9orf135	Uncharacterized protein C9orf135 (Fragment)	0	0.2	0	9
ACY1	Aminoacylase0	0	0.23	0	9
TXNRD2	Thioredoxin reductase 2, mitochondrial	0	0.26	0	9
RPP40	Ribonuclease P 40kDa subunit, isoform CRA_c	0	0.29	0	9
RAB43	Ras-related protein Rab-43 (Fragment)	0	0.36	0	9

TPT1	Translationally-controlled tumor protein	0	0.67	0	9
NQO2	Ribosyldihyronicotinamide dehydrogenase [quinone]	0	0.78	0	9
GMPR2	GMP reductase 2 (Fragment)	0	2.07	0	9
DST	Isoform 3 of Dystonin	0	0.01	0	10
STRN3	Isoform Alpha of Striatin-3	0	0.04	0	10
THOC2	THO complex subunit 2	0	0.07	0	10
RRBP1	Ribosome-binding protein 1	0	0.08	0	10
MRPS30	28S ribosomal protein S30, mitochondrial	0	0.08	0	10
SMARCA1	Probable global transcription activator SNF2L1	0	0.11	0	10
EPHB4	EPH receptor B4, isoform CRA_b	0	0.13	0	10
CAND2	Cullin-associated NEDD8-dissociated protein 2	0	0.28	0	10
RPS2	40S ribosomal protein S2	0	0.28	0	10
BCCIP	Isoform 2 of BRCA2 and CDKN1A-interacting protein	0	0.3	0	10
NMNAT1	Nicotinamide mononucleotide adenylyltransferase 1	0	0.34	0	10
CSTF1	Cleavage stimulation factor subunit 1 (Fragment)	0	0.5	0	10
SKP1	S-phase kinase-associated protein 1	0	0.64	0	10

PTPN12	Tyrosine-protein phosphatase non-receptor type 12 (Fragment)	0	0.72	0	10
LONP2	Lon protease homolog 2, peroxisomal	0	0.03	0	11
TBR1	T-box brain protein 1	0	0.04	0	11
ANK1	Isoform Br21 of Ankyrin0	0	0.05	0	11
GAPVD1	GTPase-activating protein and VPS9 domain-containing protein 1	0	0.06	0	11
HUWE1	E3 ubiquitin-protein ligase HUWE1 (Fragment)	0	0.07	0	11
MAN2A2	Alpha-mannosidase (Fragment)	0	0.07	0	11
KIAA1429	Isoform 3 of Protein virilizer homolog	0	0.1	0	11
POFUT2	GDP-fucose protein O-fucosyltransferase 2	0	0.14	0	11
AP3D1	Isoform 4 of AP-3 complex subunit delta0	0	0.15	0	11
UBQLN4	Ubiquilin-4	0	0.16	0	11
HZGJ	HZGJ	0	0.16	0	11
AGO3	Isoform 2 of Protein argonaute-3	0	0.19	0	11
CTNNA1	Catenin (Cadherin-associated protein), alpha 1, 102kDa, isoform CRA_a	0	0.19	0	11
ITPRIP	Inositol 1,4,5-trisphosphate receptor-interacting protein (Fragment)	0	0.25	0	11

BPNT1	3~(2~),5~-biphosphate nucleotidase 1	0	0.34	0	11
TYMS	Isoform 2 of Thymidylate synthase	0	0.35	0	11
TIA1	Nucleolysin TIA0 isoform p40	0	0.41	0	11
HIBCH	Isoform 2 of 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	0	0.51	0	11
DCXR	L-xylulose reductase (Fragment)	0	0.91	0	11
TCHH	Trichohyalin	0	0.01	0	12
LRBA	Lipopolysaccharide-responsive and beige-like anchor protein	0	0.02	0	12
PRMT3	Protein arginine N-methyltransferase 3	0	0.06	0	12
NOL11	Nucleolar protein 11	0	0.08	0	12
IDH2	Isoform 2 of Isocitrate dehydrogenase [NADP], mitochondrial	0	0.23	0	12
NT5C2	Cytosolic purine 5~-nucleotidase (Fragment)	0	0.35	0	12
FNTA	Protein farnesyltransferase/geranylgeranyltransferase type0 subunit alpha	0	0.43	0	12
PPP6C	Isoform 2 of Serine/threonine-protein phosphatase 6 catalytic subunit	0	0.46	0	12

POLDIP2	Polymerase delta-interacting protein 2	0	0.57	0	12
GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (Fragment)	0	0.62	0	12
GHRH	Isoform 2 of Somatoliberin	0	0.63	0	12
RPL26	60S ribosomal protein L26 (Fragment)	0	1.18	0	12
RPS5	40S ribosomal protein S5	0	1.28	0	12
CAND2	Isoform 2 of Cullin-associated NEDD8-dissociated protein 2	0	0.03	0	13
ITGAV	Isoform 2 of Integrin alpha-V	0	0.15	0	13
CYR61	Protein CYR61	0	0.24	0	13
TRMT61B	tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial (Fragment)	0	0.29	0	13
RAE1	mRNA export factor	0	0.47	0	13
CAD	CAD protein (Fragment)	0	0.5	0	13
ANXA4	Isoform 2 of Annexin A4	0	0.59	0	13
DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	0	0.65	0	13
tr A0A087WWQ2 A0A087WWQ2_HUMAN	Uncharacterized protein (Fragment)	0	0.66	0	13
NAPA	Alpha-soluble NSF attachment protein	0	0.71	0	13

PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit (Fragment)	0	0.8	0	13
CC2D2A	Isoform 2 of Coiled-coil and C2 domain-containing protein 2A	0	0.02	0	14
RAB40C	Ras-related protein Rab-40C (Fragment)	0	0.12	0	14
HNRNPM	Heterogeneous nuclear ribonucleoprotein M	0	0.18	0	14
SCFD1	Sec1 family domain-containing protein 1	0	0.19	0	14
PPP1R7	Protein phosphatase 1 regulatory subunit 7 (Fragment)	0	0.39	0	14
RPS8	40S ribosomal protein S8	0	0.53	0	14
CAPNS2	Calpain small subunit 2	0	0.57	0	14
HSPE1-MOB4	Protein HSPE1-MOB4	0	0.69	0	14
Sep 09	Septin-9 (Fragment)	0	1.18	0	14
EEF1E1	Eukaryotic translation elongation factor 1 epsilon0 (Fragment)	0	2.3	0	14
U2SURP	U2 snRNP-associated SURP motif-containing protein (Fragment)	0	0.07	0	15
MAN2B2	Alpha-mannosidase (Fragment)	0	0.23	0	15
DCTN2	Dynactin subunit 2 (Fragment)	0	0.24	0	15
PRKACA	cAMP-dependent protein kinase catalytic subunit alpha	0	0.37	0	15

SAE1	SUMO-activating enzyme subunit 1	0	0.38	0	15
NAGK	Isoform 2 of N-acetyl-D-glucosamine kinase	0	0.96	0	15
YKT6	Synaptobrevin homolog YKT6	0	1	0	15
PFDN5	Prefoldin subunit 5	0	1.9	0	15
FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed	0	3.52	0	15
RPL22	60S ribosomal protein L22 (Fragment)	0	4.58	0	15
GBF1	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	0	0.02	0	16
PAM	Isoform 2 of Peptidyl-glycine alpha-amidating monooxygenase	0	0.14	0	16
DIS3	Exosome complex exonuclease RRP44	0	0.15	0	16
PTPN11	Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11	0	0.21	0	16
TRIP10	Isoform 2 of Cdc42-interacting protein 4	0	0.23	0	16
TFPI	Tissue factor pathway inhibitor (Fragment)	0	0.32	0	16
STK24	Serine/threonine-protein kinase 24 12 kDa subunit (Fragment)	0	0.47	0	16
LANCL1	LanC-like protein 1	0	0.52	0	16

RAB11B	Isoform 2 of Ras-related protein Rab01B	0	1.18	0	16
MYO18A	Isoform 3 of Unconventional myosin-XVIIIa	0	0.07	0	17
UBQLN1	Isoform 2 of Ubiquilin0	0	0.31	0	17
GNB1	Isoform 2 of Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta0	0	0.41	0	17
GMPR2	GMP reductase	0	0.71	0	17
MRI1	Methylthioribose0-phosphate isomerase	0	0.9	0	17
ATP2B4	Isoform ZA of Plasma membrane calcium-transporting ATPase 4	0	0.08	0	18
TRIP12	Isoform 4 of E3 ubiquitin-protein ligase TRIP12	0	0.09	0	18
MTA1	Metastasis-associated protein MTA1 (Fragment)	0	0.25	0	18
MRI1	Isoform 2 of Methylthioribose0-phosphate isomerase	0	0.9	0	18
SMC4	Isoform 2 of Structural maintenance of chromosomes protein 4	0	0.1	0	19
POLR2A	DNA-directed RNA polymerase II subunit RPB1	0	0.11	0	19
GYG1	Glycogenin0 (Fragment)	0	0.37	0	19
CUL4A	Cullin-4A	0	0.45	0	19

HTRA2	Isoform 3 of Serine protease HTRA2, mitochondrial	0	0.51	0	19
LMNB1	Lamin-B1	0	0.9	0	19
EML4	Echinoderm microtubule-associated protein-like 4	0	0.26	0	20
H2AFZ	Histone H2A.Z	0	0.96	0	20
LYPLA1	Acyl-protein thioesterase 1	0	1.34	0	20
MCTS1	Isoform 2 of Malignant T-cell-amplified sequence 1	0	2.06	0	20
CYFIP2	Cytoplasmic FMR1-interacting protein 2	0	0.09	0	21
HKDC1	Putative hexokinase HKDC1	0	0.13	0	21
EGFR	Epidermal growth factor receptor	0	0.16	0	22
DNM1L	Dynamin0-like protein (Fragment)	0	0.92	0	22
MAST4	Isoform 3 of Microtubule-associated serine/threonine-protein kinase 4	0	0.01	0	23
CTH	Cystathionine gamma-lyase	0	0.76	0	23
RAC1	Isoform B of Ras-related C3 botulinum toxin substrate 1	0	2.26	0	23
MAST1	Microtubule-associated serine/threonine-protein kinase 1	0	0.02	0	24
KRT17	Keratin, type I cytoskeletal 17 (Fragment)	0	0.31	0	25
SCPEP1	Isoform 2 of Retinoid-inducible serine carboxypeptidase	0	0.47	0	25

ARCN1	Coatomer subunit delta	0	0.48	0	25
CRK	Adapter molecule crk	0	0.92	0	25
ATP6V1D	V-type proton ATPase subunit D	0	0.95	0	25
ALDH1A3	Aldehyde dehydrogenase 1 family, member A3, isoform CRA_b	0	0.15	0	26
ADAMTS4	A disintegrin and metalloproteinase with thrombospondin motifs 4	0	0.32	0	26
RRM2	Isoform 2 of Ribonucleoside-diphosphate reductase subunit M2	0	0.86	0	26
KRT72	Keratin, type II cytoskeletal 72 (Fragment)	0	0.23	0	27
CAPRIN1	Caprin0	0	0.14	0	28
COPS8	COP9 signalosome complex subunit 8	0	3.38	0	28
ERAP2	Endoplasmic reticulum aminopeptidase 2	0	0.3	0	29
RPL5	60S ribosomal protein L5 (Fragment)	0	2.6	0	29
LDHB	L-lactate dehydrogenase B chain (Fragment)	0	2.97	0	29
USP39	U4/U6.U5 tri-snRNP-associated protein 2	0	0.4	0	31
GSPT1	Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	0	0.38	0	32
STAT3	Signal transducer and activator of transcription	0	0.52	0	32

TRAP1	Heat shock protein 75 kDa, mitochondrial	0	0.12	0	35
USP9Y	Probable ubiquitin carboxyl-terminal hydrolase FAF-Y	0	0.12	0	35
HLA-A	HLA class I histocompatibility antigen, A-2 alpha chain	0	0.47	0	35
NPEPL1	Probable aminopeptidase NPEPL1	0	1.08	0	35
ATP6AP2	Renin receptor (Fragment)	0	1.67	0	35
SNRPD2	Isoform 2 of Small nuclear ribonucleoprotein Sm D2	0	10.2	0	35
EIF3K	Eukaryotic translation initiation factor 3 subunit K	0	3.43	0	36
TPM1	Tropomyosin alpha0 chain (Fragment)	0	3.48	0	36
ARPC4	Isoform 2 of Actin-related protein 2/3 complex subunit 4	0	0.63	0	37
MCM5	DNA replication licensing factor MCM5	0	0.47	0	38
TSN	Translin (Fragment)	0	4.04	0	39
TLN2	Talin-2	0	0.09	0	40
MDH1	Malate dehydrogenase, cytoplasmic (Fragment)	0	10.42	0	40
IKBKAP	Elongator complex protein 1	0	0.29	0	42
API5	Apoptosis inhibitor 5	0	0.56	0	42
LDHC	L-lactate dehydrogenase	0	0.13	0	43

ATP6V1E1	V-type proton ATPase subunit E 1	0	2.32	0	43
TAGLN2	Isoform 2 of Transgelin-2	0	6.65	0	43
DPYD	Dihydropyrimidine dehydrogenase [NADP(+)]	0	0.72	0	51
EIF4A1	Eukaryotic initiation factor 4A-I (Fragment)	0	5.46	0	51
TNPO3	Isoform 3 of Transportin-3	0	0.64	0	53
ERO1LB	ERO1-like protein beta (Fragment)	0	1.17	0	53
HSPH1	Heat shock protein 105 kDa	0	3.26	0	54
Sep 07	Septin-7	0	1.12	0	59
LDLR	Low-density lipoprotein receptor (Fragment)	0	1.62	0	59
QARS	Glutamine--tRNA ligase	0	0.6	0	60
HNRNPR	Heterogeneous nuclear ribonucleoprotein R	0	0.31	0	61
HNRNPCL1	Heterogeneous nuclear ribonucleoprotein C-like 1	0	1.42	0	61
YBX1	Nuclease-sensitive element-binding protein 1	0	1.31	0	62
EIF3S3	Eukaryotic translation initiation factor 3 subunit H	0	2.94	0	63
KRT72	Isoform 2 of Keratin, type II cytoskeletal 72	0	0.19	0	64
RBBP4	Isoform 2 of Histone-binding protein RBBP4	0	1.08	0	64

RBBP7	Histone-binding protein RBBP7	0	1.1	0	65
IGFBP6	Insulin-like growth factor-binding protein 6	0	2.33	0	65
CARM1	Histone-arginine methyltransferase CARM1 (Fragment)	0	1.26	0	66
HIST1H2BJ	Histone H2B type 1-J	0	2.74	0	66
ACAT2	Isoform 2 of Acetyl-CoA acetyltransferase, cytosolic	0	3.72	0	68
ETF1	Eukaryotic peptide chain release factor subunit 1	0	3.07	0	70
XPNPEP1	Isoform 3 of Xaa-Pro aminopeptidase 1	0	1.66	0	71
XRN2	Isoform 2 of 5~-3~ exoribonuclease 2	0	1.02	0	74
ISYNA1	Inositol-3-phosphate synthase 1	0	0.77	0	76
AMPD2	Isoform Ex1A-3 of AMP deaminase 2	0	0.49	0	77
PGK2	Phosphoglycerate kinase 2	0	1.33	0	77
TPM3	Isoform 2 of Tropomyosin alpha-3 chain	0	9.76	0	77
AMPD2	Isoform Ex1A-2-3 of AMP deaminase 2	0	0.52	0	79
CLTCL1	Isoform 2 of Clathrin heavy chain 2	0	0.26	0	83
NRD1	Nardilysin	0	0.48	0	83
MACF1	Isoform 2 of Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	0	0.13	0	84
TPP2	Tripeptidyl-peptidase 2	0	0.65	0	87

TRIM28	Isoform 2 of Transcription intermediary factor 1-beta	0	0.82	0	88
MACF1	Isoform 4 of Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	0	0.11	0	90
DIAPH1	Protein diaphanous homolog 1	0	0.61	0	90
MYH11	Isoform 2 of Myosin01	0	0.17	0	92
PSMD13	26S proteasome non-ATPase regulatory subunit 13	0	5.8	0	92
KRT13	Keratin, type I cytoskeletal 13	0	0.88	0	93
MYOF	Isoform 6 of Myoferlin	0	0.53	0	94
GNS	N-acetylglucosamine-6-sulfatase	0	0.7	0	100
SEC24C	Protein transport protein Sec24C	0	0.62	0	104
MACF1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	0	0.1	0	107
CD44	CD44 antigen	0	4.08	0	112
NAP1L1	Nucleosome assembly protein 1-like 1	0	1.48	0	116
HEXA	Beta-hexosaminidase	0	1.79	0	122
PLAU	Urokinase-type plasminogen activator chain B	0	2.51	0	129
SDCBP	Syndecan binding protein (Syntenin), isoform CRA_a	0	6.34	0	146
AP1B1	Isoform B of AP0 complex subunit beta0	0	1.16	0	170

SYNCRIP	Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	0	1.65	0	177
AP2A2	AP-2 complex subunit alpha-2	0	1.29	0	197
PTPRS	Isoform PTPS-MEA of Receptor-type tyrosine-protein phosphatase S	0	0.71	0	203
ENO3	Beta-enolase	0	1.94	0	209
POTEI	POTE ankyrin domain family member I	0	0.37	0	232
PABPC1	Polyadenylate-binding protein 1	0	2.25	0	234
SPTBN1	Spectrin beta chain, non-erythrocytic 1	0	1.33	0	277
AARS	Alanine--tRNA ligase, cytoplasmic	0	2.32	0	287
EZR	Ezrin	0	17.34	0	503
PLEC	Isoform 6 of Plectin	0	1.48	0	576
UGP2	UTP--glucose0-phosphate uridylyltransferase	0	12.95	0	581
EEF1A1	Isoform 2 of Elongation factor 1-alpha 1	0	20.04	0	628
GSN	Gelsolin	0	22.68	0	784
GAPDH	Isoform 2 of Glyceraldehyde-3-phosphate dehydrogenase	0	3503.72	0	921
ERO1L	ERO1-like protein alpha	0.26	19.37	17	553
FTH1	Ferritin	1.39	31.51	16	100
USP24	Ubiquitin carboxyl-terminal hydrolase 24	0.01	0.19	3	37

GPRC5A	Retinoic acid-induced protein 3	0.08	1.02	8	44
SNRPG	Small nuclear ribonucleoprotein G	0.46	5.66	3	11
CRKL	Crk-like protein	0.1	1.11	7	18
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	248.7	2658.96	957	1012
TOR1A	Torsin0A	0.09	0.95	3	28
PRDX4	Peroxiredoxin-4	12.03	123.68	128	588
ALDOC	Fructose-bisphosphate aldolase C	1.22	10.85	214	394
PSMB5	Isoform 3 of Proteasome subunit beta type-5	12.2	103.06	89	224
ALDOA	Fructose-bisphosphate aldolase A	163.67	1308.52	1074	1458
PSMB2	Proteasome subunit beta type-2	29.02	230.07	117	303
NIPSNAP1	Protein NipSnap homolog 1	0.1	0.77	4	13
RPS17L	40S ribosomal protein S17-like	0.22	1.67	7	12
CDK6	Cyclin-dependent kinase 6	0.09	0.67	3	14
DNPEP	Aspartyl aminopeptidase	0.5	3.27	37	120
H6PD	GDH/6PGL endoplasmic bifunctional protein	0.33	2.11	22	191
WTAP	Pre-mRNA-splicing regulator WTAP	0.07	0.43	6	14
ACP2	Lysosomal acid phosphatase	0.07	0.43	1	19
HTT	Huntingtin	0.01	0.06	2	16
LAP3	Isoform 2 of Cytosol aminopeptidase	0.52	2.98	21	109
PPAT	Amidophosphoribosyltransferase	0.06	0.32	9	19
FTL	Ferritin light chain	6.48	34.15	34	103
RBM3	Putative RNA-binding protein 3	0.2	1.05	5	11

FDPS	Isoform 2 of Farnesyl pyrophosphate synthase	0.48	2.47	21	42
NANS	Sialic acid synthase	0.17	0.87	13	20
HK2	Hexokinase-2	0.17	0.86	11	77
DNAJC13	DnaJ homolog subfamily C member 13	0.03	0.15	3	28
POLR1A	DNA-directed RNA polymerase	0.05	0.25	12	31
PSMA7	Proteasome subunit alpha type-7	19.63	98.13	172	332
PSMB5	Proteasome subunit beta type-5	11.55	57.56	126	303
NADSYN1	Glutamine-dependent NAD(+) synthetase	0.08	0.38	6	18
ACTR2	Actin-related protein 2	1.69	7.95	60	91
TFRC	Transferrin receptor protein 1	7.27	33.69	592	1031
COPS5	COP9 signalosome complex subunit 5	1.32	5.92	31	59
UBQLN2	Ubiquilin-2	0.05	0.22	8	12
NAA20	N-acetyltransferase 5 (ARD1 homolog, <i>S. cerevisiae</i>), isoform CRA_a	0.39	1.68	6	17
PM20D2	Peptidase M20 domain-containing protein 2	0.07	0.3	1	10
ERAP1	Isoform 2 of Endoplasmic reticulum aminopeptidase 1	0.23	0.98	18	105
TBCD	Tubulin-specific chaperone D	0.05	0.21	10	39
DOCK11	Dedicator of cytokinesis protein 11	0.11	0.46	28	82

MIF	Macrophage migration inhibitory factor	1.05	4.35	16	37
PTER	Isoform 2 of Phosphotriesterase-related protein	0.32	1.32	10	21
GCN1L1	Translational activator GCN1	0.03	0.12	11	20
IST1	IST1 homolog (Fragment)	0.49	1.9	14	22
LGALS1	Galectin0	5.22	20.03	24	43
SNRPD3	Isoform 2 of Small nuclear ribonucleoprotein Sm D3	2.9	11.09	17	29
OSBP	Oxysterol-binding protein 1	0.04	0.15	11	9
PSMA7	Isoform 2 of Proteasome subunit alpha type-7	7.63	28.57	112	205
CHID1	Isoform 2 of Chitinase domain-containing protein 1	0.82	3.04	45	56
YBX3	Isoform 2 of Y-box-binding protein 3	0.22	0.81	10	30
COPS7A	COP9 signalosome complex subunit 7a	0.68	2.47	22	58
TPM1	Tropomyosin alpha0 chain	0.39	1.41	12	34
SNRPD2	Small nuclear ribonucleoprotein Sm D2	3.77	13.56	24	43
GUSB	Beta-glucuronidase	1.56	5.58	57	168
CPOX	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	0.28	0.99	13	35

PLCG1	Isoform 2 of 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma0	0.02	0.07	3	7
OAT	Ornithine aminotransferase, mitochondrial	0.3	1.05	13	31
PSMB3	Proteasome subunit beta type-3	18.41	64.32	98	223
SAR1A	GTP-binding protein SAR1a	0.15	0.52	6	7
NEU1	Sialidase0	0.15	0.52	5	17
ADPRHL2	Poly(ADP-ribose) glycohydrolase ARH3	0.18	0.62	9	13
MVP	Major vault protein	0.18	0.62	12	35
TCEB1	Transcription elongation factor B polypeptide 1 (Fragment)	1.42	4.88	9	16
NPM1	Isoform 2 of Nucleophosmin	11.86	40.44	356	366
PRMT5	Protein arginine N-methyltransferase 5	0.85	2.88	56	138
TPM3	Isoform 3 of Tropomyosin alpha-3 chain	2.29	7.74	39	75
CDA	Cytidine deaminase	0.45	1.52	4	12
H2AFY	Isoform 1 of Core histone macro-H2A.1	0.08	0.27	6	6
GMDS	Isoform 2 of GDP-mannose 4,6 dehydratase	0.08	0.27	6	8
SRI	Sorcin	1.38	4.64	17	27

ATP6V1H	ATPase, H ⁺ transporting, lysosomal 50/57kDa, V1 subunit H, isoform CRA_c	0.06	0.2	3	4
LDHB	L-lactate dehydrogenase B chain	0.41	1.36	39	85
DPYSL2	Dihydropyrimidinase-related protein 2	4.98	16.48	307	588
NAGA	Alpha-N-acetylgalactosaminidase	0.07	0.23	5	7
ACAT2	Acetyl-CoA acetyltransferase, cytosolic	1.9	6.22	68	80
EXOSC8	Exosome complex component RRP43	0.11	0.36	3	7
SERPINB6	Serpin B6	0.55	1.8	31	39
CSNK2A2	Casein kinase II subunit alpha~	0.59	1.93	16	37
PRPSAP2	Phosphoribosyl pyrophosphate synthase-associated protein 2	0.26	0.85	13	23
EIF2B2	Translation initiation factor eIF-2B subunit beta	0.28	0.91	15	22
MAT2B	Methionine adenosyltransferase 2 subunit beta	0.8	2.52	46	63
SPAG9	C-Jun-amino-terminal kinase-interacting protein 4	0.07	0.22	28	39
SORD	Sorbitol dehydrogenase	2.13	6.68	49	67
CAPNS1	Calpain small subunit 1	4.27	13.3	46	85
PSMD7	26S proteasome non-ATPase regulatory subunit 7	1.79	5.57	73	69

VPS26A	Vacuolar protein sorting-associated protein 26A	1.11	3.45	55	50
ENO2	Gamma-enolase	1.09	3.36	213	203
PSMA5	Proteasome subunit alpha type-5	11.03	33.94	108	245
PRDX1	Peroxiredoxin0	233.83	718.53	321	385
GPS1	COP9 signalosome complex subunit 1	0.34	1.04	26	55
ASL	Isoform 2 of Argininosuccinate lyase	1.03	3.11	29	53
HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	0.04	0.12	2	5
EIF2B4	Translation initiation factor eIF-2B subunit delta	0.06	0.18	2	14
MARS	Methionine--tRNA ligase, cytoplasmic (Fragment)	0.42	1.26	12	24
PURB	Transcriptional activator protein Pur-beta	0.61	1.83	23	25
NLN	Neurolysin, mitochondrial	0.32	0.96	18	49
PPWD1	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	0.05	0.15	5	12
GOT2	Aspartate aminotransferase, mitochondrial	6.39	19.09	188	216
TWF2	Twinfilin-2	0.17	0.49	6	13
PGM2	Phosphoglucomutase-2	0.67	1.93	40	67
CAPZA2	F-actin-capping protein subunit alpha-2	1.59	4.56	57	88

MARS	Methionine--tRNA ligase, cytoplasmic	0.37	1.06	42	91
ATP6V1A	Isoform 2 of V-type proton ATPase catalytic subunit A	1.43	4.09	51	135
RRM2B	Ribonucleoside-diphosphate reductase subunit M2 B (Fragment)	0.14	0.4	7	12
PKM	Isoform M1 of Pyruvate kinase PKM	62.98	179.94	1084	1453
PSMB6	Proteasome subunit beta type-6	2.87	8.14	52	165
FARSA	Phenylalanine--tRNA ligase alpha subunit (Fragment)	0.16	0.45	6	26
TRIM25	E3 ubiquitin/ISG15 ligase TRIM25	0.05	0.14	2	14
PAPSS1	Bifunctional 3~-phosphoadenosine 5~-phosphosulfate synthase 1	0.05	0.14	1	15
CUL5	Cullin-5	0.15	0.42	18	26
NUP37	Nucleoporin Nup37	0.19	0.53	14	12
PPP2R4	Serine/threonine-protein phosphatase 2A activator	0.77	2.14	30	38
OGDH	2-oxoglutarate dehydrogenase, mitochondrial	0.09	0.25	17	34
PSMA2	Proteasome subunit alpha type-2	11.67	32.32	133	213
AHCY	Adenosylhomocysteinase	6.26	17.31	344	415
GNE	Isoform 2 of Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	0.21	0.58	11	31

TBL1XR1	F-box-like/WD repeat-containing protein TBL1XR1	0.12	0.33	9	13
SLC38A2	Sodium-coupled neutral amino acid transporter 2	0.12	0.33	14	19
BTF3	Isoform 2 of Transcription factor BTF3	1.4	3.84	18	28
MYL1	Isoform MLC3 of Myosin light chain 1/3, skeletal muscle isoform	0.74	2.01	8	11
GNPDA2	Isoform 3 of Glucosamine-6-phosphate isomerase 2	1.92	5.19	34	87
PLBD2	Putative phospholipase B-like 2	0.48	1.29	43	80
UBR4	Isoform 2 of E3 ubiquitin-protein ligase UBR4	0.12	0.32	75	156
IPO11	Isoform 2 of Importin01	0.09	0.24	10	24
ACACA	Isoform 2 of Acetyl-CoA carboxylase 1	0.05	0.13	9	25
PSMB1	Proteasome subunit beta type0	67.73	174.96	192	315
PSMA6	Proteasome subunit alpha type-6	14.05	36.16	164	286
CCT7	T-complex protein 1 subunit eta	6.24	16.05	283	370
NCDN	Isoform 2 of Neurochondrin	0.09	0.23	8	12
KIF5C	Kinesin heavy chain isoform 5C	0.09	0.23	34	51
PKM	Pyruvate kinase PKM	98.11	250.25	1228	1631
NIPSNAP3A	Protein NipSnap homolog 3A	0.56	1.42	9	17
AP2M1	AP-2 complex subunit mu	0.53	1.34	23	29

COPS2	Isoform 2 of COP9 signalosome complex subunit 2	0.53	1.34	26	48
PYGB	Glycogen phosphorylase, brain form	17.38	43.91	778	1007
PAICS	Multifunctional protein ADE2	4.3	10.79	186	238
CPSF1	Cleavage and polyadenylation specificity factor subunit 1	0.1	0.25	23	63
AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1	0.78	1.93	42	48
CAPZA1	F-actin-capping protein subunit alpha0	1.86	4.59	79	100
BTF3L4	Transcription factor BTF3 homolog 4	0.48	1.18	6	13
UROD	Uroporphyrinogen decarboxylase	1.01	2.45	47	42
PSMD5	26S proteasome non-ATPase regulatory subunit 5	0.43	1.04	8	6
ALDH1A1	Retinal dehydrogenase 1	36.73	88.54	725	905
NME1-NME2	Nucleoside diphosphate kinase	56	134.56	228	347
PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	1.31	3.14	43	61
SSBP1	Single-stranded DNA-binding protein, mitochondrial	1.05	2.51	13	22
CDKN2AIPNL	Isoform 2 of CDKN2AIP N-terminal-like protein	0.36	0.86	4	4
USO1	Isoform 2 of General vesicular transport factor p115	0.16	0.38	25	43

ADH5	Alcohol dehydrogenase class-3	1.19	2.8	40	43
AP1S1	AP0 complex subunit sigma0A (Fragment)	0.32	0.75	7	10
PSMA1	Isoform Long of Proteasome subunit alpha type0	23.67	55.41	181	390
PRPF8	Pre-mRNA-processing-splicing factor 8	0.44	1.03	90	171
PPP1R10	Serine/threonine-protein phosphatase 1 regulatory subunit 10	0.03	0.07	4	6
HEATR1	HEAT repeat-containing protein 1	0.03	0.07	6	12
XPO5	Exportin-5	0.21	0.49	47	62
PYCRL	Pyrroline-5-carboxylate reductase 3	0.37	0.86	5	9
GOT1	Aspartate aminotransferase, cytoplasmic	5.85	13.58	190	221
PSMB4	Proteasome subunit beta type-4	5.98	13.87	86	139
TIMM13	Mitochondrial import inner membrane translocase subunit Tim13	0.32	0.74	3	6
HIST1H1B	Histone H1.5	0.32	0.74	8	10
MYADM	Myeloid-associated differentiation marker (Fragment)	0.26	0.6	12	17
CCT3	T-complex protein 1 subunit gamma	4.95	11.41	337	474
SMS	Spermine synthase	3.26	7.45	91	138
PFDN1	Prefoldin subunit 1	0.25	0.57	2	5
ACTR1B	Beta-centractin	0.25	0.57	18	26

ATP6V1B2	V-type proton ATPase subunit B, brain isoform	0.25	0.57	22	30
DLD	Isoform 3 of Dihydrolipoyl dehydrogenase, mitochondrial	1.61	3.65	68	122
BLMH	Bleomycin hydrolase	1.32	2.98	61	78
CUL2	Cullin-2	0.24	0.54	19	30
GDI1	Rab GDP dissociation inhibitor alpha	3.76	8.46	198	212
VPS26B	Vacuolar protein sorting-associated protein 26B	0.08	0.18	5	3
THOC5	THO complex subunit 5 homolog	0.08	0.18	10	13
ARPC5	Actin-related protein 2/3 complex subunit 5	1.57	3.52	17	28
RPS23	40S ribosomal protein S23	0.21	0.47	5	6
PFKM	Isoform 2 of ATP-dependent 6-phosphofructokinase, muscle type	0.42	0.94	34	49
EIF3K	Eukaryotic translation initiation factor 3 subunit K (Fragment)	1.54	3.44	15	29
COPB2	Isoform 2 of Coatamer subunit beta~	0.73	1.63	105	161
CHMP4B	Charged multivesicular body protein 4b	0.13	0.29	3	5
ACLY	ATP-citrate synthase	3.3	7.35	371	719
B4GALT7	Beta0,4-galactosyltransferase 7	0.18	0.4	14	8
EXOSC4	Exosome complex component RRP41	0.27	0.6	6	14
SNAPIN	SNARE-associated protein Snapin	0.23	0.51	3	5
RPL19	Ribosomal protein L19	0.14	0.31	9	10

ANGPTL4	Angiopoietin-related protein 4	0.75	1.66	48	97
STRAP	Isoform 2 of Serine-threonine kinase receptor-associated protein	1.04	2.29	62	66
PIR	Pirin	0.1	0.22	2	4
PDXP	Pyridoxal phosphate phosphatase	0.1	0.22	3	5
UBE4A	Isoform 2 of Ubiquitin conjugation factor E4 A	0.05	0.11	6	6
SEC13	Isoform 2 of Protein SEC13 homolog	0.2	0.44	5	12
POLR1B	Isoform 2 of DNA-directed RNA polymerase I subunit RPA2	0.05	0.11	11	14
VBP1	Prefoldin subunit 3	0.73	1.6	19	20
MAT2A	S-adenosylmethionine synthase isoform type-2	1.96	4.29	87	116
REEP6	Receptor expression-enhancing protein 6	0.16	0.35	2	6
GPHN	Gephyrin	0.16	0.35	9	29
SARS	Serine--tRNA ligase, cytoplasmic	0.59	1.29	39	84
AP2M1	Isoform 2 of AP-2 complex subunit mu	0.67	1.46	23	30
RPS10	40S ribosomal protein S10	0.18	0.39	2	5
STX7	Isoform 2 of Syntaxin-7	0.12	0.26	4	11
POLR1C	Isoform 2 of DNA-directed RNA polymerases I and III subunit RPAC1	0.18	0.39	9	11
CACHD1	VWFA and cache domain-containing protein 1	0.12	0.26	21	25

HUWE1	Isoform 2 of E3 ubiquitin-protein ligase HUWE1	0.06	0.13	18	48
USP9X	Isoform 2 of Probable ubiquitin carboxyl-terminal hydrolase FAF-X	0.12	0.26	33	74
DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	0.6	1.3	218	390
NIF3L1	Isoform 2 of Putative GTP cyclohydrolase 1 type 2 NIF3L1	0.76	1.64	26	36
MOB1B	Isoform 2 of MOB kinase activator 1B	0.13	0.28	10	4
SF3B5	Splicing factor 3B subunit 5	2.22	4.77	9	15
ARMC8	Armadillo repeat containing 8, isoform CRA_e	0.07	0.15	3	2
AAR2	Protein AAR2 homolog	0.07	0.15	1	3
AGO1	Protein argonaute	0.07	0.15	6	14
DLST	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	0.14	0.3	13	22
RPIA	Ribose-5-phosphate isomerase	1.13	2.41	28	49
DYNLL1	Dynein light chain 1, cytoplasmic	2.11	4.49	15	17
POLR2E	DNA-directed RNA polymerases I, II, and III subunit RPABC1	0.16	0.34	3	6
NUTF2	Nuclear transport factor 2	0.87	1.84	8	11
PFDN6	Prefoldin subunit 6	0.88	1.86	8	12
HMBS	Porphobilinogen deaminase	0.09	0.19	7	5
ACTN4	Alpha-actinin-4 (Fragment)	26.96	56.67	189	219

EIF3M	Eukaryotic translation initiation factor 3 subunit M	1.62	3.4	50	50
SEH1L	Nucleoporin SEH1 (Fragment)	0.11	0.23	3	5
SAAL1	Protein SAAL1 (Fragment)	0.11	0.23	1	5
CAD	CAD protein	0.7	1.46	175	259
BCAT2	Branched-chain-amino-acid aminotransferase (Fragment)	0.14	0.29	5	8
FLNA	Filamin A	1.76	3.64	608	1010
PLBD1	Phospholipase B-like 1	0.5	1.03	29	76
SNRNP200	U5 small nuclear ribonucleoprotein 200 kDa helicase	0.56	1.15	150	258
MYL6	Myosin light polypeptide 6 (Fragment)	5.58	11.34	18	15
PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	1.71	3.47	52	72
PSAT1	Phosphoserine aminotransferase	5.48	11.07	178	143
ACADVL	Isoform 2 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	0.05	0.1	2	3
SEC14L2	SEC14-like 2 (<i>S. cerevisiae</i>), isoform CRA_c	0.09	0.18	4	3
LIMA1	LIM domain and actin-binding protein 1	0.05	0.1	3	6

PBK	Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase	0.09	0.18	7	6
PTPN23	Tyrosine-protein phosphatase non-receptor type 23	0.02	0.04	4	8
ANKRD28	Isoform 3 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	0.03	0.06	1	9
EXOSC9	Exosome complex component RRP45	0.07	0.14	8	9
TMEM106B	Transmembrane protein 106B	0.11	0.22	2	11
SMG1	Serine/threonine-protein kinase SMG1 (Fragment)	0.01	0.02	7	17
PICALM	Isoform 2 of Phosphatidylinositol-binding clathrin assembly protein	0.1	0.2	17	20
EPPK1	Epiplakin	0.01	0.02	9	21
NAA25	Isoform 2 of N-alpha-acetyltransferase 25, NatB auxiliary subunit	0.17	0.34	10	33
VTN	Vitronectin	0.06	0.12	25	38
DST	Dystonin	0.09	0.18	90	141
AIMP1	Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	2.01	4.01	49	65
SEC23A	Protein transport protein Sec23A	2.15	4.28	95	161
TPM3	Tropomyosin alpha-3 chain	1.58	3.14	31	55
ACTR1A	Alpha-centractin	0.56	1.11	36	49

DPP3	Dipeptidyl peptidase 3	0.46	0.91	23	42
Sep 02	Isoform 2 of Septin-2	1.15	2.27	47	58
PSMC2	26S protease regulatory subunit 7	2.45	4.81	115	113
PLAA	Phospholipase A-2-activating protein	0.2	0.39	17	27
PTGR1	Prostaglandin reductase 1	1.41	2.74	28	41
PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	1.4	2.72	31	40
KIF5B	Kinesin0 heavy chain	0.96	1.86	139	232
MAN2B1	Isoform 2 of Lysosomal alpha-mannosidase	0.62	1.2	53	118
FASN	Fatty acid synthase	2.91	5.63	883	1264
COPS4	COP9 signalosome complex subunit 4	1.99	3.84	82	120
NCKAP1	Isoform 2 of Nck-associated protein 1	0.13	0.25	20	18
PLD3	Phospholipase D3	0.26	0.5	25	52
VCP	Transitional endoplasmic reticulum ATPase	10	19.22	556	952
SEC23B	Protein transport protein Sec23B	0.61	1.17	28	55
TXN	Thioredoxin	2.52	4.83	14	11
SNRPB	Small nuclear ribonucleoprotein-associated proteins B and B~	1.29	2.47	35	57
PSMD12	26S proteasome non-ATPase regulatory subunit 12	2.13	4.05	111	81

FKBP9	Isoform 3 of Peptidyl-prolyl cis-trans isomerase FKBP9	0.2	0.38	12	16
PPP1CC	Serine/threonine-protein phosphatase	1.66	3.15	49	59
FLNB	Isoform 2 of Filamin-B	3.15	5.94	651	910
NME1	Isoform 2 of Nucleoside diphosphate kinase A	67.26	126.6	171	243
GDI2	Rab GDP dissociation inhibitor beta	69.33	130.45	518	368
FN1	Isoform 10 of Fibronectin	0.24	0.45	45	87
ELP2	Isoform 2 of Elongator complex protein 2	0.16	0.3	7	22
TPM2	Tropomyosin beta chain	0.62	1.16	16	34
AKR1A1	Alcohol dehydrogenase [NADP(+)]	0.29	0.54	9	13
COPG2	Coatamer subunit gamma-2	0.14	0.26	21	25
PFKL	ATP-dependent 6-phosphofructokinase, liver type	0.89	1.65	63	90
ALAD	Delta-aminolevulinic acid dehydratase	0.54	1	11	25
PFN1	Profilin0	45.13	83.46	86	69
RUVBL2	RuvB-like 2	7.84	14.49	203	195
AIMP2	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	1.04	1.91	29	41
PRDX2	Peroxiredoxin-2	10.05	18.45	85	111
GIPC1	PDZ domain-containing protein GIPC1	0.3	0.55	8	11
AASDHPPT	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0.3	0.55	8	14

LRP1	Prolow-density lipoprotein receptor-related protein 1	0.12	0.22	57	105
CUL4B	Cullin 4B, isoform CRA_e	0.41	0.75	44	48
LNPEP	Isoform 2 of Leucyl-cystinyl aminopeptidase	1.37	2.49	123	237
TLN1	Talin0	1.14	2.07	350	470
CALR	Calreticulin	0.59	1.07	47	58
CALM2	Calmodulin (Fragment)	2.3	4.16	30	45
EIF5B	Eukaryotic translation initiation factor 5B	0.35	0.63	50	65
OSBP2	Oxysterol-binding protein 2	0.05	0.09	7	10
PACSN2	Isoform 2 of Protein kinase C and casein kinase substrate in neurons protein 2	0.2	0.36	15	22
VASN	Vasorin	0.14	0.25	11	21
DCTN1	Uncharacterized protein	0.18	0.32	29	55
CBX3	Chromobox protein homolog 3	0.81	1.44	13	18
GNPNAT1	Glucosamine 6-phosphate N-acetyltransferase	0.81	1.43	9	16
IGF2R	Cation-independent mannose-6-phosphate receptor	1.43	2.51	454	847
APEH	Acylamino-acid-releasing enzyme	1.26	2.21	59	141
HSPBP1	Isoform 3 of Hsp70-binding protein 1	0.24	0.42	13	18
WDR5	WD repeat-containing protein 5	1.16	2.03	41	41
LDHA	Isoform 3 of L-lactate dehydrogenase A chain	115.63	202.21	536	687
DPY30	Protein dpy-30 homolog	0.71	1.24	5	5

MYL6	Myosin light polypeptide 6	8	13.95	36	32
FAT1	Protocadherin Fat 1	0.54	0.94	222	333
LSM2	U6 snRNA-associated Sm-like protein LSm2	0.73	1.27	8	5
PYGL	Isoform 2 of Glycogen phosphorylase, liver form	3.25	5.65	312	433
REXO2	Oligoribonuclease, mitochondrial (Fragment)	0.72	1.25	15	11
CORO1B	Coronin0B	0.34	0.59	11	14
TOP1	DNA topoisomerase 1	0.11	0.19	5	13
PLRG1	Isoform 2 of Pleiotropic regulator 1	0.33	0.57	22	22
GBE1	1,4-alpha-glucan-branching enzyme	1.49	2.57	71	117
XPO7	Exportin-7	0.47	0.81	72	97
ARPC1A	Actin-related protein 2/3 complex subunit 1A	0.57	0.98	29	26
HIST1H4A	Histone H4	40.24	69.16	68	76
ERH	Enhancer of rudimentary homolog	0.63	1.08	9	11
PSMD1	26S proteasome non-ATPase regulatory subunit 1	1.26	2.15	132	174
COPG1	Coatomer subunit gamma0	0.74	1.26	88	114
HINT1	Histidine triad nucleotide-binding protein 1	3.66	6.23	15	25
TKT	Isoform 2 of Transketolase	21.06	35.66	635	905
PRPF19	Pre-mRNA-processing factor 19	2.54	4.3	124	192
RNPEP	Aminopeptidase B	0.55	0.93	22	42
RPS26	40S ribosomal protein S26	0.58	0.98	7	9

TXNDC17	Thioredoxin domain-containing protein 17	0.54	0.91	10	9
ECHDC1	Isoform 2 of Ethylmalonyl-CoA decarboxylase	0.46	0.77	10	20
PFDN4	Prefoldin subunit 4	0.49	0.82	4	12
RPL7A	60S ribosomal protein L7a	0.52	0.87	17	10
PSMC6	26S protease regulatory subunit 10B	1.63	2.72	99	124
RABGAP1	Rab GTPase-activating protein 1	0.03	0.05	11	7
MACF1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	0.06	0.1	75	109
GLRX3	Glutaredoxin-3	1.52	2.53	54	51
RNASE4	Ribonuclease 4	0.43	0.71	8	10
ARPC4-TTLL3	Protein ARPC4-TTLL3	5.76	9.51	44	50
TARS	Threonine--tRNA ligase, cytoplasmic	2.52	4.16	135	230
AP1G1	AP0 complex subunit gamma0	0.57	0.94	57	104
NPM3	Nucleoplasmin-3	0.37	0.61	5	8
NCBP1	Nuclear cap-binding protein subunit 1	0.74	1.22	36	55
ESYT1	Isoform 2 of Extended synaptotagmin0	0.14	0.23	12	19
FARSA	Phenylalanine--tRNA ligase alpha subunit	0.36	0.59	23	31
PURA	Transcriptional activator protein Pur-alpha	0.44	0.72	14	20
RPS12	40S ribosomal protein S12	4.19	6.84	15	22
POLR2G	DNA-directed RNA polymerase II subunit RPB7	0.38	0.62	5	7
NME3	Nucleoside diphosphate kinase 3	0.38	0.62	6	11

FH	Isoform Cytoplasmic of Fumarate hydratase, mitochondrial	1.43	2.33	70	67
NIP7	60S ribosome subunit biogenesis protein NIP7 homolog	0.35	0.57	4	4
SLC5A3	Sodium/myo-inositol cotransporter	0.08	0.13	8	5
C1QTNF3	Isoform 2 of Complement C1q tumor necrosis factor-related protein 3	0.32	0.52	13	25
CAPN1	Calpain0 catalytic subunit	1.45	2.35	89	116
CD81	Tetraspanin (Fragment)	0.87	1.41	62	49
ME2	NAD-dependent malic enzyme, mitochondrial	0.79	1.28	33	64
NT5C2	Cytosolic purine 5~-nucleotidase	0.55	0.89	33	63
GGCT	Gamma-glutamylcyclotransferase	0.34	0.55	5	9
GARS	Glycine--tRNA ligase	5.81	9.39	323	428
HARS2	Isoform 2 of Probable histidine--tRNA ligase, mitochondrial	0.26	0.42	34	32
GNAI2	Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2	0.7	1.13	32	20
PYGM	Glycogen phosphorylase, muscle form	0.75	1.21	173	240
AKR1D1	3-oxo-5-beta-steroid 4-dehydrogenase	0.18	0.29	14	15
CBS	Isoform 2 of Cystathionine beta-synthase	0.59	0.95	25	32
IPO9	Importin-9	0.69	1.11	93	150
ALDH9A1	4-trimethylaminobutyraldehyde dehydrogenase	0.79	1.27	57	36
ACOT7	Isoform 4 of Cytosolic acyl coenzyme A thioester hydrolase	1.98	3.18	96	91

C1orf50	Uncharacterized protein C1orf50	0.33	0.53	5	9
HIST1H1E	Histone H1.4	0.33	0.53	5	9
ASMTL	Isoform 2 of N-acetylserotonin O-methyltransferase-like protein	0.33	0.53	36	24
DERA	Deoxyribose-phosphate aldolase	1.04	1.67	24	47
CUL1	Cullin0	1.62	2.6	76	126
AKR1C1	Aldo-keto reductase family 1 member C1	7.44	11.93	179	97
THOP1	Thimet oligopeptidase	0.83	1.33	42	50
CDC37	Hsp90 co-chaperone Cdc37	0.15	0.24	19	13
BAG2	BAG family molecular chaperone regulator 2	0.3	0.48	10	14
PRMT7	Protein arginine N-methyltransferase 7	0.1	0.16	3	4
CTPS2	CTP synthase 2	0.1	0.16	3	6
tr H3BN98 H3BN98_HUMAN	Uncharacterized protein (Fragment)	0.77	1.23	15	16
SOD1	Superoxide dismutase [Cu-Zn]	3.57	5.68	25	25
RPS3A	40S ribosomal protein S3a	0.83	1.32	21	25
PAIP1	Uncharacterized protein	0.17	0.27	12	11
SEC24A	Protein transport protein Sec24A	0.17	0.27	15	21
WDR77	Methylosome protein 50	0.97	1.54	27	41
SEC22B	Vesicle-trafficking protein SEC22b	0.29	0.46	7	8
PDCD5	Programmed cell death protein 5	1.45	2.3	9	8
SCARB2	Lysosome membrane protein 2	0.12	0.19	6	9
EIF6	Eukaryotic translation initiation factor 6	0.79	1.25	15	17
HSD17B4	Peroxisomal multifunctional enzyme type 2	0.43	0.68	25	27

KIAA0368	Proteasome-associated protein ECM29 homolog	0.54	0.85	113	186
ERP44	Endoplasmic reticulum resident protein 44	0.14	0.22	12	8
DDB2	DNA damage-binding protein 2	0.14	0.22	5	8
CS	Citrate synthase	0.56	0.88	29	60
FLNC	Isoform 2 of Filamin-C	0.07	0.11	48	71
GAA	Lysosomal alpha-glucosidase	2.37	3.71	278	354
KLC1	Kinesin light chain 1	0.23	0.36	11	22
GBAS	Protein NipSnap homolog 2	0.59	0.92	15	17
WDR26	Isoform 2 of WD repeat-containing protein 26	0.09	0.14	10	13
FAM129B	Isoform 2 of Niban-like protein 1	0.65	1.01	79	108
ACTN1	Alpha-actinin0 (Fragment)	20.64	32.07	326	339
TP53I3	Quinone oxidoreductase PIG3	1.23	1.91	34	29
COPS3	COP9 signalosome complex subunit 3	0.69	1.07	28	28
RPL12	60S ribosomal protein L12	2.96	4.59	24	34
AKR7A2	Aflatoxin B1 aldehyde reductase member 2 (Fragment)	0.2	0.31	13	12
EPRS	Bifunctional glutamate/proline--tRNA ligase	1.24	1.92	310	493
DARS	Aspartate--tRNA ligase, cytoplasmic	2.6	4.02	150	220
CPNE3	Copine-3	0.11	0.17	5	4
GNPDA1	Glucosamine-6-phosphate isomerase 1	6.55	10.1	86	152
IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	0.72	1.11	48	41

FKBP1A	Peptidyl-prolyl cis-trans isomerase FKBP1A	1.13	1.74	10	9
VIM	Vimentin	23.85	36.69	432	523
PSMC6	26S protease regulatory subunit 10B (Fragment)	5.5	8.45	29	28
HIBADH	3-hydroxyisobutyrate dehydrogenase, mitochondrial	0.56	0.86	13	26
FAH	Fumarylacetoacetase	0.15	0.23	13	10
LAMP2	Isoform LAMP-2B of Lysosome- associated membrane glycoprotein 2	0.15	0.23	13	19
MAPK1	Mitogen-activated protein kinase 1	2.14	3.26	66	53
ME1	NADP-dependent malic enzyme	1.97	3	61	130
RPS25	40S ribosomal protein S25	0.94	1.43	13	10
CTSA	Carboxypeptidase	1.02	1.55	67	54
IMPDH2	Inosine-5~-monophosphate dehydrogenase 2	1.78	2.7	131	207
CCT8	T-complex protein 1 subunit theta	6.97	10.57	306	407
RPA3	Replication protein A 14 kDa subunit	0.95	1.44	6	11
AP1M1	AP0 complex subunit mu0	0.95	1.44	42	33
TCP1	T-complex protein 1 subunit alpha	6.79	10.27	329	521
CUL3	Isoform 2 of Cullin-3	0.45	0.68	44	56
CCT2	T-complex protein 1 subunit beta	14.05	21.17	303	446
HECTD1	E3 ubiquitin-protein ligase HECTD1	0.02	0.03	10	7
TTLL12	Tubulin--tyrosine ligase-like protein 12	0.6	0.9	37	50
EIF3A	Eukaryotic translation initiation factor 3 subunit A	0.9	1.35	261	318

SETD3	Histone-lysine N-methyltransferase setd3	0.1	0.15	5	8
MST4	Serine/threonine-protein kinase 26	0.14	0.21	10	9
NUP93	Nuclear pore complex protein Nup93	0.14	0.21	13	16
NHP2L1	NHP2-like protein 1	0.89	1.33	15	10
ARPC5L	Actin-related protein 2/3 complex subunit 5-like protein	0.72	1.07	8	10
COPB1	Coatomer subunit beta	0.66	0.98	83	121
LSM4	U6 snRNA-associated Sm-like protein LSm4	0.81	1.2	5	11
PFKP	ATP-dependent 6-phosphofructokinase, platelet type	1.63	2.41	81	137
GGH	Gamma-glutamyl hydrolase	7.14	10.54	201	125
GEMIN5	Gem-associated protein 5	0.61	0.9	86	146
ARPC3	Actin-related protein 2/3 complex subunit 3	2.86	4.21	19	28
PSMC4	26S protease regulatory subunit 6B	1.93	2.84	106	99
CAPN2	Calpain-2 catalytic subunit	2.17	3.19	187	223
ARSK	Arylsulfatase K	0.3	0.44	13	22
PSMD2	26S proteasome non-ATPase regulatory subunit 2	4.26	6.24	364	363
NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	0.41	0.6	67	55
IPO5	Isoform 3 of Importin-5	1.69	2.47	241	381
NSFL1C	Isoform 3 of NSFL1 cofactor p47	0.6	0.87	26	35
ACO2	Aconitate hydratase, mitochondrial	0.2	0.29	15	36

CPD	Carboxypeptidase D	0.18	0.26	24	50
SF3B3	Splicing factor 3B subunit 3	2.85	4.11	368	518
VPS35	Vacuolar protein sorting-associated protein 35	2.63	3.79	200	242
COPA	Isoform 2 of Coatomer subunit alpha	0.82	1.18	115	163
SNRPA1	U2 small nuclear ribonucleoprotein A~	0.39	0.56	11	12
PSMB7	Proteasome subunit beta type-7	5.52	7.91	79	160
PDCD6	Programmed cell death protein 6	3.17	4.54	27	40
PALD1	Paladin	0.07	0.1	4	5
PPP6R3	Isoform 2 of Serine/threonine-protein phosphatase 6 regulatory subunit 3	0.07	0.1	6	7
VTA1	Chromosome 6 open reading frame 55, isoform CRA_b	0.35	0.5	9	10
EIF3E	Eukaryotic translation initiation factor 3 subunit E	1.81	2.58	92	69
TPI1	Isoform 2 of Triosephosphate isomerase	73.67	104.94	312	222
SNRPE	Small nuclear ribonucleoprotein E	2.97	4.23	13	19
UCHL5	Ubiquitin carboxyl-terminal hydrolase	0.26	0.37	8	10
AP2B1	Isoform 2 of AP-2 complex subunit beta	1.8	2.56	160	234
TPM4	Tropomyosin alpha-4 chain	1.41	2	22	42
PSMC5	Isoform 2 of 26S protease regulatory subunit 8	1.34	1.9	56	64
EIF3L	Eukaryotic translation initiation factor 3 subunit L	1.58	2.24	117	168
NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	2.78	3.93	96	126

ACO1	Cytoplasmic aconitate hydratase	0.34	0.48	27	40
PGM1	Phosphoglucomutase0	0.68	0.96	24	50
RPS6	40S ribosomal protein S6	0.39	0.55	18	18
CAP2	Adenylyl cyclase-associated protein 2	0.44	0.62	35	41
ANKFY1	Isoform 2 of Rabankyrin-5	0.22	0.31	24	56
TBCA	Tubulin-specific chaperone A	1.25	1.76	9	10
PPIA	Peptidyl-prolyl cis-trans isomerase A	193.65	272.5	146	151
ENO1	Alpha-enolase	299.81	419.8	1343	1129
ABCE1	ATP-binding cassette sub-family E member 1	0.6	0.84	28	63
TROVE2	Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein	0.81	1.13	38	51
HIST2H3PS2	Histone H3	1.22	1.7	18	15
CALU	Isoform 3 of Calumenin	0.28	0.39	15	12
VCL	Isoform 1 of Vinculin	9.09	12.66	590	764
GOLGA7	Golgin subfamily A member 7	1.15	1.6	9	5
IARS	Isoleucine--tRNA ligase, cytoplasmic	1.32	1.83	198	294
RPL10A	60S ribosomal protein L10a	2.98	4.12	35	36
DUT	Isoform 2 of Deoxyuridine 5~-triphosphate nucleotidohydrolase, mitochondrial	1	1.38	14	16
UPF1	Isoform 2 of Regulator of nonsense transcripts 1	0.4	0.55	43	52
HDAC1	Histone deacetylase 1	0.19	0.26	32	27
ITIH3	Isoform 2 of Inter-alpha-trypsin inhibitor heavy chain H3	0.38	0.52	77	85

DUSP3	Dual specificity protein phosphatase 3	0.83	1.13	11	7
IDE	Insulin-degrading enzyme	0.5	0.68	57	63
UBB	Ubiquitin (Fragment)	12.17	16.54	234	192
FERMT2	Fermitin family homolog 2 (Fragment)	0.14	0.19	7	10
HSPE1	10 kDa heat shock protein, mitochondrial	8.07	10.95	31	26
KRT8	Isoform 2 of Keratin, type II cytoskeletal 8	2.47	3.35	157	121
UBA3	Isoform 2 of NEDD8-activating enzyme E1 catalytic subunit	0.65	0.88	31	18
PSPH	Phosphoserine phosphatase (Fragment)	0.82	1.11	11	10
CCT5	T-complex protein 1 subunit epsilon	7.44	10.02	237	345
NAP1L4	Isoform 2 of Nucleosome assembly protein 1-like 4	0.78	1.05	42	63
MAPK3	Isoform 2 of Mitogen-activated protein kinase 3	1.1	1.48	40	37
EFTUD2	Isoform 2 of 116 kDa U5 small nuclear ribonucleoprotein component	1.34	1.8	142	241
RAB6A	Isoform 2 of Ras-related protein Rab-6A	0.7	0.94	25	21
BLVRA	Biliverdin reductase A	1.55	2.08	43	32
DDB1	DNA damage-binding protein 1	3	4.02	315	434
DNPH1	2~-deoxynucleoside 5~-phosphate N-hydrolase 1 (Fragment)	0.62	0.83	5	11
ARPC1B	Actin-related protein 2/3 complex subunit 1B	3.26	4.35	111	88
DIP2B	Disco-interacting protein 2 homolog B	0.06	0.08	10	11
FUBP1	Far upstream element-binding protein 1	0.15	0.2	28	45

MCMBP	Isoform 2 of Mini-chromosome maintenance complex-binding protein	0.36	0.48	26	18
MTA2	Metastasis-associated protein MTA2	0.18	0.24	24	32
KRT18	Keratin, type I cytoskeletal 18	2.71	3.61	106	97
CSNK2A1	CSNK2A1 protein	0.86	1.14	26	34
RARS	Arginine--tRNA ligase, cytoplasmic	2.55	3.38	139	221
NUDT21	Cleavage and polyadenylation specificity factor subunit 5	5	6.62	49	49
CAP1	Isoform 2 of Adenylyl cyclase-associated protein 1	6.07	8.03	259	314
CAP1	Adenylyl cyclase-associated protein 1	6.07	8.03	269	329
EEF2	Elongation factor 2	20.72	27.39	1392	1474
UBA1	Isoform 2 of Ubiquitin-like modifier-activating enzyme 1	8.74	11.54	848	1023
S100A4	Protein S100-A4	8.66	11.42	48	43
PSME2	Proteasome activator complex subunit 2	3.05	4.02	69	76
RPLP2	60S acidic ribosomal protein P2	16.2	21.28	26	34
EIF5	Eukaryotic translation initiation factor 5	0.29	0.38	23	22
EIF3I	Eukaryotic translation initiation factor 3 subunit I	1.58	2.06	47	49
PABPC1L	Polyadenylate-binding protein 1-like	0.2	0.26	51	57
USP14	Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 14	1.97	2.56	100	102
GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha	1.34	1.74	43	29
CCT6A	T-complex protein 1 subunit zeta	4.76	6.17	237	293

ATP6V1C1	V-type proton ATPase subunit C 1	0.34	0.44	9	13
SNRPD1	Small nuclear ribonucleoprotein Sm D1	6.81	8.81	26	41
CSE1L	Exportin-2	3.39	4.38	359	388
CAT	Catalase	0.24	0.31	9	13
PTPRF	Isoform 2 of Receptor-type tyrosine-protein phosphatase F	0.53	0.68	125	177
COPS6	COP9 signalosome complex subunit 6	2.09	2.68	34	79
NUDT5	ADP-sugar pyrophosphatase	0.82	1.05	13	28
NQO1	Isoform 2 of NAD(P)H dehydrogenase [quinone] 1	13.15	16.81	137	170
DNM1L	Dynamin0-like protein	0.83	1.06	62	90
RPS16	40S ribosomal protein S16	5.64	7.19	25	25
RPS18	40S ribosomal protein S18	2.38	3.03	25	20
RANBP6	Ran-binding protein 6	0.11	0.14	27	40
NPEPPS	Puromycin-sensitive aminopeptidase	1.62	2.06	193	225
EXOSC7	Exosome complex component RRP42	0.63	0.8	17	18
PSMA3	Isoform 2 of Proteasome subunit alpha type-3	15.85	20.12	128	289
IMPDH1	Inosine-5~-monophosphate dehydrogenase	0.26	0.33	15	18
PPP5C	Serine/threonine-protein phosphatase (Fragment)	0.26	0.33	26	23
PPP4C	Serine/threonine-protein phosphatase 4 catalytic subunit	0.56	0.71	20	23
NACA	Nascent polypeptide-associated complex subunit alpha, muscle-specific form (Fragment)	1.26	1.59	49	59

CLTC	Clathrin heavy chain	1.72	2.17	364	464
UBE2K	Ubiquitin-conjugating enzyme E2 K	1.3	1.64	20	21
TSNAX	Translin-associated protein X	4.06	5.12	56	91
HSPA8	Heat shock cognate 71 kDa protein	37.84	47.69	1017	987
AP2A1	Isoform B of AP-2 complex subunit alpha0	0.62	0.78	62	94
HSPA13	Heat shock 70 kDa protein 13	0.97	1.22	51	67
CRYZ	Quinone oxidoreductase	3.19	4.01	45	46
NMT1	Isoform Short of Glycylpeptide N-tetradecanoyltransferase 1	0.39	0.49	13	14
PSMA4	Proteasome subunit alpha type-4	13.16	16.51	150	318
COLGALT1	Procollagen galactosyltransferase 1	0.63	0.79	32	32
SERPINB8	Serpin B8	0.44	0.55	18	17
ACTL6A	Isoform 2 of Actin-like protein 6A	0.44	0.55	35	20
DRG1	Developmentally-regulated GTP-binding protein 1	0.48	0.6	31	24
CSDE1	Isoform 2 of Cold shock domain-containing protein E1	0.2	0.25	14	27
GSR	Isoform Cytoplasmic of Glutathione reductase, mitochondrial	1.08	1.35	50	70
MYH14	Isoform 2 of Myosin04	0.12	0.15	67	84
AP2A2	Isoform 2 of AP-2 complex subunit alpha-2	1.09	1.36	111	196
ALDH16A1	Aldehyde dehydrogenase family 16 member A1	0.89	1.11	63	98
CAB39	Calcium-binding protein 39	0.49	0.61	13	12

PSMC3	26S protease regulatory subunit 6A	1.39	1.73	81	61
ACTN4	Alpha-actinin-4	43.6	54.26	1148	1360
SMC3	Structural maintenance of chromosomes protein 3	0.41	0.51	34	59
RAB1A	Ras-related protein Rab0A	1.6	1.99	39	39
HIST1H2BN	Histone H2B	2.75	3.42	75	71
CARS	Isoform 3 of Cysteine--tRNA ligase, cytoplasmic	1.41	1.75	86	113
LARS	Leucine--tRNA ligase, cytoplasmic	0.46	0.57	74	86
PSMD14	26S proteasome non-ATPase regulatory subunit 14	5.19	6.43	59	67
NARS	Asparagine--tRNA ligase, cytoplasmic	2.18	2.7	143	172
LAMP1	Lysosome-associated membrane glycoprotein 1	0.42	0.52	39	41
DHX9	ATP-dependent RNA helicase A	0.72	0.89	122	152
MAGOHB	Protein mago nashi homolog 2	4.95	6.11	29	35
U2AF2	Splicing factor U2AF 65 kDa subunit	0.74	0.91	39	35
CNDP2	Cytosolic non-specific dipeptidase	1.32	1.62	56	75
USP5	Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5	0.98	1.2	73	85
PSMD2	26S proteasome non-ATPase regulatory subunit 2 (Fragment)	10.09	12.35	71	62
RAB1B	Ras-related protein Rab0B	2.06	2.52	41	40
CFL2	Isoform 3 of Cofilin-2	9.6	11.72	54	52
CARM1	Isoform 1 of Histone-arginine methyltransferase CARM1	0.92	1.12	62	99

CDC42	Cell division control protein 42 homolog	2.68	3.26	25	25
TALDO1	Transaldolase	5.92	7.19	139	117
KPNB1	Importin subunit beta0	4.85	5.89	470	481
SOD2	Isoform 4 of Superoxide dismutase [Mn], mitochondrial	3.78	4.59	24	35
RAB14	Ras-related protein Rab04	1.83	2.22	35	33
HADH	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0.57	0.69	17	21
XPO1	Exportin0	1.97	2.38	209	267
ACTN3	Alpha-actinin-3	0.92	1.11	203	229
LTA4H	Leukotriene A-4 hydrolase	2.62	3.16	104	147
SMC2	Structural maintenance of chromosomes protein 2	0.15	0.18	21	18
FLII	Isoform 2 of Protein flightless0 homolog	0.15	0.18	18	27
OGFOD1	Prolyl 3-hydroxylase OGFOD1	0.35	0.42	31	31
AGL	Isoform 5 of Glycogen debranching enzyme	0.1	0.12	16	35
NUDC	Nuclear migration protein nudC	0.79	0.94	37	28
CAND1	Cullin-associated NEDD8-dissociated protein 1	1.16	1.38	157	248
PSMD6	26S proteasome non-ATPase regulatory subunit 6	3.97	4.71	85	65
VAT1	Synaptic vesicle membrane protein VAT0 homolog	0.7	0.83	29	24
PRKCSH	Glucosidase 2 subunit beta	0.44	0.52	38	34
CHORDC1	Cysteine and histidine-rich domain-containing protein 1	0.94	1.11	48	26

RDX	Radixin	5.8	6.83	300	253
PRMT1	Protein arginine N-methyltransferase 1	8.89	10.46	246	256
PSMA4	Isoform 2 of Proteasome subunit alpha type-4	7.78	9.15	92	195
MTHFD1	C0-tetrahydrofolate synthase, cytoplasmic	1.42	1.66	137	136
ACTR3	Actin-related protein 3	5.47	6.39	142	100
IPO7	Importin-7	2.15	2.51	266	328
RANGAP1	Ran GTPase-activating protein 1	0.42	0.49	39	37
HSPA2	Heat shock-related 70 kDa protein 2	1.28	1.49	340	344
GPI	Glucose-6-phosphate isomerase (Fragment)	35.52	41.34	675	853
RTN4	Reticulon	1.16	1.35	80	68
PGK1	Phosphoglycerate kinase 1	33.59	38.86	389	334
PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	2.46	2.84	48	39
AGO2	Protein argonaute-2	0.26	0.3	17	23
RPA1	Replication protein A 70 kDa DNA-binding subunit	0.52	0.6	43	60
SPTAN1	Isoform 3 of Spectrin alpha chain, non-erythrocytic 1	1.11	1.28	233	322
PSMD5	26S proteasome non-ATPase regulatory subunit 5	0.66	0.76	35	23
RPS3	40S ribosomal protein S3	5.51	6.31	82	84
GLUD1	Glutamate dehydrogenase 1, mitochondrial	3.51	4	188	226
TPR	Nucleoprotein TPR	0.51	0.58	158	158

SMC1A	Structural maintenance of chromosomes protein 1A	0.22	0.25	48	72
MYH10	Isoform 2 of Myosin00	0.44	0.5	131	138
PSAP	Saposin-D	4.55	5.13	325	357
CAPZB	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a	8.42	9.48	104	138
SUPT6H	Transcription elongation factor SPT6	0.16	0.18	31	44
HSP90AB4P	Putative heat shock protein HSP 90-beta 4	0.92	1.03	123	166
FKBP10	Peptidyl-prolyl cis-trans isomerase FKBP10	0.9	1	40	36
G6PD	Isoform Long of Glucose-6-phosphate 1-dehydrogenase	0.91	1.01	45	56
ACTN2	Isoform 2 of Alpha-actinin-2	1.45	1.6	289	329
PDIA4	Protein disulfide-isomerase A4	8.35	9.2	239	226
MDH2	Malate dehydrogenase, mitochondrial	10.8	11.89	224	211
ROCK2	Rho-associated protein kinase 2	0.2	0.22	23	29
PAFAH1B1	Platelet-activating factor acetylhydrolase IB subunit alpha	2.61	2.87	95	79
HSPA5	78 kDa glucose-regulated protein	15.36	16.87	383	465
DDX39B	Spliceosome RNA helicase DDX39B	2.88	3.14	108	84
GSS	Glutathione synthetase	2.38	2.59	97	69
DHX15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	0.69	0.75	58	57
EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	2.67	2.9	163	128

PTBP1	Polypyrimidine tract binding protein 1, isoform CRA_b	2.1	2.28	171	151
GFPT1	Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	0.94	1.02	55	57
COL6A3	Isoform 2 of Collagen alpha-3(VI) chain	0.98	1.06	283	239
AIFM1	Isoform 3 of Apoptosis-inducing factor 1, mitochondrial	1.62	1.75	68	72
C4A	Isoform 2 of Complement C4-A	0.25	0.27	70	86
PREP	Prolyl endopeptidase	1.29	1.38	64	72
HARS	Isoform 4 of Histidine--tRNA ligase, cytoplasmic	6.15	6.57	212	143
PSAP	Isoform Sap-mu-9 of Prosaposin	4.77	5.09	307	338
ATIC	Bifunctional purine biosynthesis protein PURH	8.19	8.65	222	324
NAGLU	Alpha-N-acetylglucosaminidase	2.34	2.47	222	238
IQGAP1	Ras GTPase-activating-like protein IQGAP1	2.84	2.98	442	518
ANKRD30A	Ankyrin repeat domain-containing protein 30A	0.02	0.02	8	1
IFIT5	Isoform 2 of Interferon-induced protein with tetratricopeptide repeats 5	0.06	0.06	4	1
HAPLN3	Hyaluronan and proteoglycan link protein 3	0.07	0.07	6	1
DPP8	Dipeptidyl peptidase 8 (Fragment)	0.08	0.08	6	1
APOA1	Truncated apolipoprotein A-I	0.12	0.12	6	1
GTF2F2	General transcription factor IIF subunit 2	0.12	0.12	2	1

SERPINA5	Plasma serine protease inhibitor (Fragment)	0.13	0.13	3	1
TMBIM1	Protein lifeguard 3	0.14	0.14	3	1
MGMT	Methylated-DNA--protein-cysteine methyltransferase	0.15	0.15	3	1
RAB22A	Ras-related protein Rab-22A	0.15	0.15	2	1
GCSAM	Isoform 2 of Germinal center-associated signaling and motility protein	0.16	0.16	8	1
PTMS	Parathymosin	0.28	0.28	2	1
CLASP1	Isoform 2 of CLIP-associating protein 1	0.02	0.02	3	2
PWP2	Periodic tryptophan protein 2 homolog	0.03	0.03	4	2
GAS6	Isoform 2 of Growth arrest-specific protein 6	0.04	0.04	2	2
PSIP1	PC4 and SFRS1-interacting protein	0.05	0.05	3	2
PMPCA	Mitochondrial-processing peptidase subunit alpha	0.06	0.06	1	2
DYNC1LI1	Cytoplasmic dynein 1 light intermediate chain 1	0.06	0.06	4	2
FAM98A	Isoform 2 of Protein FAM98A	0.06	0.06	2	2
RGMA	Repulsive guidance molecule A	0.06	0.06	3	2
SERPING1	Plasma protease C1 inhibitor	0.06	0.06	3	2
PTBP2	Isoform 2 of Polypyrimidine tract-binding protein 2	0.06	0.06	2	2
DBNL	Drebrin-like protein (Fragment)	0.08	0.08	6	2
C6orf211	UPF0364 protein C6orf211	0.09	0.09	4	2
FN3K	Fructosamine-3-kinase	0.09	0.09	2	2

OR5AC2	Olfactory receptor 5AC2	0.09	0.09	3	2
C9	Complement component C9	0.1	0.1	14	2
YARS2	Tyrosine--tRNA ligase (Fragment)	0.1	0.1	4	2
C11orf68	Isoform 2 of UPF0696 protein C11orf68	0.11	0.11	4	2
ASB7	Isoform 2 of Ankyrin repeat and SOCS box protein 7	0.11	0.11	8	2
PLAUR	Urokinase plasminogen activator surface receptor (Fragment)	0.13	0.13	2	2
BCAS2	Pre-mRNA-splicing factor SPF27	0.13	0.13	1	2
NGLY1	Peptide-N(4)-(N-acetyl-beta-glucosaminy)asparagine amidase (Fragment)	0.13	0.13	5	2
SPP2	Secreted phosphoprotein 24	0.14	0.14	2	2
CLNS1A	Methylosome subunit pICln	0.15	0.15	3	2
CHMP1B	Charged multivesicular body protein 1b	0.15	0.15	4	2
PRTFDC1	Isoform 2 of Phosphoribosyltransferase domain-containing protein 1	0.16	0.16	4	2
CASP16	Putative caspase06	0.16	0.16	2	2
WDR43	WD repeat-containing protein 43 (Fragment)	0.16	0.16	2	2
MARCKSL1	MARCKS-related protein	0.17	0.17	6	2
LOC102724023	Protein LOC102724023	0.17	0.17	3	2
ZC3H15	Isoform 2 of Zinc finger CCCH domain-containing protein 15	0.18	0.18	5	2
C1orf123	UPF0587 protein C1orf123	0.18	0.18	3	2
MSRA	Isoform 2 of Mitochondrial peptide methionine sulfoxide reductase	0.18	0.18	2	2

ASF1B	Histone chaperone ASF1B	0.18	0.18	1	2
TM4SF18	Transmembrane 4 L6 family member 18 (Fragment)	0.19	0.19	4	2
FIS1	Mitochondrial fission 1 protein	0.2	0.2	4	2
COMMD2	COMM domain-containing protein 2	0.22	0.22	1	2
RPL31	60S ribosomal protein L31	0.22	0.22	1	2
NT5DC3	5~-nucleotidase domain-containing protein 3 (Fragment)	0.23	0.23	2	2
APOM	Apolipoprotein M	0.24	0.24	3	2
HSPB11	Chromosome 1 open reading frame 41, isoform CRA_b	0.26	0.26	3	2
C11orf73	Protein Hikeshi	0.34	0.34	3	2
OTOA	Isoform 4 of Otoancorin	0.03	0.03	3	3
PCDHA8	Isoform 2 of Protocadherin alpha-8	0.04	0.04	5	3
NHLRC2	NHL repeat-containing protein 2	0.04	0.04	2	3
HGFAC	Hepatocyte growth factor activator	0.04	0.04	2	3
CLINT1	Isoform 2 of Clathrin interactor 1	0.05	0.05	4	3
TH1L	Negative elongation factor C/D	0.05	0.05	5	3
DET1	Isoform 2 of DET1 homolog	0.05	0.05	3	3
HRG	Histidine-rich glycoprotein	0.05	0.05	4	3
GNA12	Guanine nucleotide-binding protein subunit alpha02	0.07	0.07	12	3
WDR4	Isoform 2 of tRNA (guanine-N(7))-methyltransferase non-catalytic subunit WDR4	0.07	0.07	2	3

GTF2F1	General transcription factor IIF subunit 1 (Fragment)	0.07	0.07	3	3
SLC16A3	Monocarboxylate transporter 4	0.07	0.07	1	3
WNT16	Protein Wnt06	0.08	0.08	3	3
RNMT	mRNA cap guanine-N7 methyltransferase	0.09	0.09	3	3
ARG2	Arginase-2, mitochondrial	0.09	0.09	1	3
SCAMP3	Isoform 2 of Secretory carrier-associated membrane protein 3	0.09	0.09	4	3
ATG3	Ubiquitin-like-conjugating enzyme ATG3	0.09	0.09	1	3
FKRP	Fukutin-related protein	0.12	0.12	6	3
PLIN3	Isoform 2 of Perilipin-3	0.12	0.12	10	3
ALYREF	THO complex subunit 4	0.12	0.12	3	3
KCTD5	BTB/POZ domain-containing protein KCTD5	0.12	0.12	2	3
AKR1E2	1,5-anhydro-D-fructose reductase	0.14	0.14	6	3
SH3BGRL3	SH3 domain-binding glutamic acid-rich-like protein 3	0.14	0.14	2	3
DRAP1	Dr1-associated corepressor	0.14	0.14	3	3
THOC7	THO complex subunit 7 homolog	0.14	0.14	2	3
RBP4	Retinol binding protein 4, plasma, isoform CRA_b	0.14	0.14	1	3
FLOT1	Isoform 2 of Flotillin0	0.16	0.16	9	3
CNPY2	Protein canopy homolog 2 (Fragment)	0.17	0.17	3	3
TXNDC12	Thioredoxin domain-containing protein 12	0.17	0.17	3	3

POMP	Proteasome maturation protein	0.21	0.21	1	3
RPS24	40S ribosomal protein S24	0.22	0.22	2	3
BANF1	Barrier-to-autointegration factor	0.34	0.34	4	3
RPS28	40S ribosomal protein S28	0.45	0.45	3	3
LAYN	Layilin (Fragment)	0.47	0.47	8	3
CHRA1	Chromatin accessibility complex protein 1	0.58	0.58	3	3
CNTNAP4	Contactin-associated protein-like 4	0.02	0.02	1	4
STON2	Isoform 2 of Stonin-2	0.03	0.03	2	4
HDLBP	High density lipoprotein binding protein (Vigilin), isoform CRA_a	0.05	0.05	12	4
NLE1	Notchless protein homolog 1	0.06	0.06	1	4
ATG16L1	Isoform 3 of Autophagy-related protein 160	0.06	0.06	3	4
ARSA	Isoform 2 of Arylsulfatase A	0.07	0.07	3	4
RPS6KA3	Ribosomal protein S6 kinase alpha-3	0.08	0.08	5	4
PRKACG	cAMP-dependent protein kinase catalytic subunit gamma	0.08	0.08	1	4
NELFB	Negative elongation factor B	0.1	0.1	4	4
NUP85	Nuclear pore complex protein Nup85	0.11	0.11	4	4
LRRC47	Leucine-rich repeat-containing protein 47	0.11	0.11	5	4
SLC2A14	Isoform 2 of Solute carrier family 2, facilitated glucose transporter member 14	0.12	0.12	4	4
Sep 15	15 kDa selenoprotein	0.18	0.18	3	4

CHMP2A	Charged multivesicular body protein 2a (Fragment)	0.18	0.18	5	4
EIF2S2	Eukaryotic translation initiation factor 2 subunit 2	0.18	0.18	6	4
PAFAH1B2	Isoform 2 of Platelet-activating factor acetylhydrolase IB subunit beta	0.19	0.19	4	4
SUMO4	Small ubiquitin-related modifier 4	0.32	0.32	8	4
NCALD	Neurocalcin-delta	0.32	0.32	4	4
RPL11	Isoform 2 of 60S ribosomal protein L11	0.36	0.36	5	4
AK3	Isoform 2 of GTP:AMP phosphotransferase AK3, mitochondrial	0.41	0.41	6	4
RPL27A	60S ribosomal protein L27a	0.79	0.79	4	4
LSM6	U6 snRNA-associated Sm-like protein LSM6	0.9	0.9	4	4
MYO15A	Unconventional myosin-XV	0.01	0.01	5	5
AQR	Intron-binding protein aquarius	0.02	0.02	5	5
INADL	InaD-like protein	0.02	0.02	6	5
DKC1	Isoform 3 of H/ACA ribonucleoprotein complex subunit 4	0.07	0.07	6	5
ZPR1	Zinc finger protein ZPR1 (Fragment)	0.08	0.08	2	5
ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment)	0.1	0.1	6	5
MAPK15	Isoform 2 of Mitogen-activated protein kinase 15	0.11	0.11	5	5
HOOK3	Protein Hook homolog 3	0.12	0.12	6	5
ASAH1	Acid ceramidase	0.16	0.16	5	5
DAZAP1	DAZ-associated protein 1	0.16	0.16	9	5

GIN54	DNA replication complex GINS protein SLD5	0.32	0.32	8	5
TIGAR	Fructose-2,6-bisphosphatase TIGAR	0.37	0.37	6	5
ARRB1	Beta-arrestin0 (Fragment)	0.38	0.38	10	5
AP1S2	AP0 complex subunit sigma-2	0.39	0.39	4	5
ETFB	Isoform 2 of Electron transfer flavoprotein subunit beta	0.4	0.4	9	5
VAMP3	Vesicle-associated membrane protein 3	0.7	0.7	5	5
C19orf10	UPF0556 protein C19orf10 (Fragment)	0.84	0.84	7	5
SNRPF	Small nuclear ribonucleoprotein F	0.84	0.84	4	5
RPL35A	60S ribosomal protein L35a	1.06	1.06	7	5
RPL38	60S ribosomal protein L38	1.13	1.13	5	5
KPNA6	Importin subunit alpha-7	0.05	0.05	8	6
MKLN1	Isoform 2 of Muskelin	0.05	0.05	3	6
RANBP3	Ran-binding protein 3	0.06	0.06	8	6
CFI	Complement factor I	0.07	0.07	6	6
SLC7A5	Large neutral amino acids transporter small subunit 1	0.12	0.12	9	6
MGAT4B	Alpha0,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B (Fragment)	0.14	0.14	9	6
SLC35A2	UDP-galactose translocator	0.14	0.14	12	6
CANX	Calnexin (Fragment)	0.15	0.15	2	6
FBXO6	F-box only protein 6	0.2	0.2	4	6
WDR82	WD repeat-containing protein 82	0.2	0.2	4	6

POLR2C	DNA-directed RNA polymerase II subunit RPB3	0.22	0.22	5	6
GSTM2	Glutathione S-transferase Mu 2	0.27	0.27	6	6
FAHD1	Isoform 2 of Acylpyruvase FAHD1, mitochondrial	0.28	0.28	7	6
RPL9	60S ribosomal protein L9 (Fragment)	0.35	0.35	8	6
IGF2	Isoform 2 of Insulin-like growth factor II	0.35	0.35	5	6
CBX1	Chromobox protein homolog 1 (Fragment)	0.36	0.36	3	6
AP3S1	AP-3 complex subunit sigma0	0.39	0.39	6	6
LAGE3	EKC/KEOPS complex subunit LAGE3	0.51	0.51	4	6
SF3B6	Splicing factor 3B subunit 6	0.52	0.52	8	6
YPEL5	Protein yippee-like 5	0.54	0.54	5	6
REEP5	Receptor expression-enhancing protein 5	0.54	0.54	9	6
TRMT112	Multifunctional methyltransferase subunit TRM112-like protein	0.65	0.65	5	6
LSM7	U6 snRNA-associated Sm-like protein LSM7	0.68	0.68	6	6
tr B4E1Z4 B4E1Z4_HUMAN	Uncharacterized protein	0.02	0.02	9	7
CUX2	Homeobox protein cut-like 2	0.02	0.02	11	7
LONRF1	Isoform 2 of LON peptidase N-terminal domain and RING finger protein 1	0.04	0.04	10	7
EWSR1	RNA-binding protein EWS	0.05	0.05	5	7
FARS2	Phenylalanine--tRNA ligase, mitochondrial	0.06	0.06	5	7
PLG	Plasminogen	0.07	0.07	6	7

CKM	Creatine kinase M-type	0.08	0.08	8	7
RAB33B	Ras-related protein Rab-33B	0.13	0.13	12	7
PITRM1	Presequence protease, mitochondrial (Fragment)	0.17	0.17	5	7
F10	Coagulation factor X	0.19	0.19	15	7
GSTM5	Glutathione S-transferase M5, isoform CRA_a	0.3	0.3	6	7
RPE	Isoform 2 of Ribulose-phosphate 3-epimerase	0.3	0.3	4	7
GIN51	DNA replication complex GINS protein PSF1	0.31	0.31	6	7
TBCB	Tubulin-folding cofactor B	0.34	0.34	8	7
HSD3B1	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1 (Fragment)	0.37	0.37	5	7
UFC1	Ubiquitin-fold modifier-conjugating enzyme 1	0.61	0.61	6	7
RPL21	60S ribosomal protein L21 (Fragment)	0.91	0.91	7	7
POLD1	DNA polymerase	0.03	0.03	4	8
JPH3	Junctophilin-3	0.04	0.04	5	8
LMOD3	Leiomodin-3	0.05	0.05	8	8
SEC24B	Isoform 2 of Protein transport protein Sec24B	0.07	0.07	6	8
KNG1	Isoform LMW of Kininogen0	0.07	0.07	5	8
SNX2	Isoform 2 of Sorting nexin-2	0.07	0.07	6	8
APOE	Apolipoprotein E	0.09	0.09	6	8
CALB1	Calbindin	0.11	0.11	9	8

HNRNPH3	Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3	0.2	0.2	3	8
GNA11	Guanine nucleotide-binding protein subunit alpha01	0.35	0.35	12	8
CNBP	Isoform 2 of Cellular nucleic acid-binding protein	0.37	0.37	4	8
CFAP20	Cilia- and flagella-associated protein 20	0.5	0.5	9	8
UBE2E3	Ubiquitin-conjugating enzyme E2 E3	0.5	0.5	13	8
CLEC3B	Tetranectin	0.67	0.67	9	8
VPS29	Vacuolar protein sorting-associated protein 29	1.17	1.17	13	8
SRSF3	Serine/arginine-rich-splicing factor 3	1.34	1.34	8	8
CPSF2	Cleavage and polyadenylation specificity factor subunit 2	0.04	0.04	10	9
SHBG	Sex hormone-binding globulin	0.09	0.09	14	9
DKFZp686H13261	Putative uncharacterized protein DKFZp686H13261	0.09	0.09	5	9
DDX23	Probable ATP-dependent RNA helicase DDX23	0.11	0.11	16	9
C11orf65	Isoform 2 of Uncharacterized protein C11orf65	0.11	0.11	6	9
KLC2	Isoform 2 of Kinesin light chain 2	0.11	0.11	12	9
HAS1	Hyaluronan synthase 1	0.14	0.14	8	9
SLC9A3R1	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	0.28	0.28	11	9
UBLCP1	Ubiquitin-like domain-containing CTD phosphatase 1	0.54	0.54	16	9

RAB4B	HCG1995540, isoform CRA_b	0.56	0.56	15	9
ACP1	Low molecular weight phosphotyrosine protein phosphatase	0.65	0.65	9	9
POLR2H	DNA-directed RNA polymerases I, II, and III subunit RPABC3 (Fragment)	0.72	0.72	3	9
COPZ1	Coatomer subunit zeta0	0.75	0.75	9	9
PSMD10	26S proteasome non-ATPase regulatory subunit 10	0.81	0.81	14	9
ROCK1	Rho-associated protein kinase 1	0.06	0.06	5	10
RBM6	RNA-binding protein 6	0.06	0.06	12	10
SEMA4F	Semaphorin-4F	0.08	0.08	18	10
SLC2A1	Solute carrier family 2, facilitated glucose transporter member 1	0.19	0.19	10	10
UTS2	Urotensin-2	0.21	0.21	7	10
CREG1	Protein CREG1	0.3	0.3	8	10
TWF1	Isoform 4 of Twinfilin0	0.55	0.55	14	10
CNTRL	Isoform 5 of Centriolin	0.01	0.01	10	11
TERT	Isoform 3 of Telomerase reverse transcriptase	0.03	0.03	4	11
SERPINF2	Alpha-2-antiplasmin (Fragment)	0.12	0.12	10	11
GCLM	Glutamate--cysteine ligase regulatory subunit	0.23	0.23	8	11
MPPE1	Metallophosphoesterase 1	1.27	1.27	4	11
UBE2D1	Ubiquitin-conjugating enzyme E2 D1	1.63	1.63	11	11
ADAR	Double-stranded RNA-specific adenosine deaminase (Fragment)	0.02	0.02	15	12

SLC29A1	Isoform 2 of Equilibrative nucleoside transporter 1	0.11	0.11	21	12
AXL	Isoform Short of Tyrosine-protein kinase receptor UFO	0.14	0.14	17	12
LUM	Lumican	0.18	0.18	9	12
NRBP1	Nuclear receptor-binding protein	0.23	0.23	13	12
IMPA1	Inositol monophosphatase 1 (Fragment)	0.24	0.24	5	12
PFDN2	Prefoldin subunit 2	1.1	1.1	10	12
ELAC2	Isoform 4 of Zinc phosphodiesterase ELAC protein 2	0.2	0.2	16	13
DYNC1I2	Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2	0.2	0.2	8	13
NASP	Isoform 2 of Nuclear autoantigenic sperm protein	0.3	0.3	9	13
LAMTOR1	Ragulator complex protein LAMTOR1	0.41	0.41	12	13
SEPHS1	Selenide, water dikinase 1	0.67	0.67	29	13
ABHD14B	Alpha/beta hydrolase domain-containing protein 14B	0.86	0.86	11	13
LZTS1	Isoform 2 of Leucine zipper putative tumor suppressor 1	0.05	0.05	17	14
SCFD1	Isoform 2 of Sec1 family domain-containing protein 1	0.17	0.17	6	14
SGTA	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	0.45	0.45	12	14
GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	0.69	0.69	18	14
CUTA	Isoform A of Protein CutA	1.09	1.09	13	14

PCBD1	Pterin-4-alpha-carbinolamine dehydratase	3.48	3.48	14	14
RAB15	Isoform 2 of Ras-related protein Rab05	0.3	0.3	27	15
AKR1D1	Isoform 2 of 3-oxo-5-beta-steroid 4-dehydrogenase	0.33	0.33	25	15
EIF4E	Eukaryotic translation initiation factor 4E	0.39	0.39	10	15
LRGUK	Leucine-rich repeat and guanylate kinase domain-containing protein	0.03	0.03	10	16
PPP2R2B	Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform	0.13	0.13	14	16
TIAL1	Nucleolysin TIAR	0.26	0.26	12	16
NACA2	Nascent polypeptide-associated complex subunit alpha-2	0.31	0.31	18	16
RAB8A	Ras-related protein Rab-8A	0.48	0.48	31	16
RAB10	Ras-related protein Rab00	0.51	0.51	32	16
CRIP2	Cysteine-rich protein 2 (Fragment)	0.55	0.55	15	16
SNRNPB2	U2 small nuclear ribonucleoprotein B~~	0.45	0.45	9	17
CACNG6	Voltage-dependent calcium channel gamma-6 subunit	0.12	0.12	10	18
CDO1	Cysteine dioxygenase type 1	0.14	0.14	11	18
CCNI	Cyclin-I (Fragment)	0.17	0.17	11	18
ADK	Isoform 2 of Adenosine kinase	0.28	0.28	16	18
ANXA6	Isoform 2 of Annexin A6	0.3	0.3	13	18
DNAJB1	DnaJ homolog subfamily B member 1	0.52	0.52	21	18

EIF2B1	Translation initiation factor eIF-2B subunit alpha	0.59	0.59	13	18
S100A6	Protein S100 (Fragment)	2.38	2.38	10	18
H3F3B	Histone H3 (Fragment)	3.18	3.18	24	18
POSTN	Periostin	0.24	0.24	12	19
PRPH	Peripherin (Fragment)	0.14	0.14	15	20
ADIG	Adipogenin (Fragment)	0.17	0.17	17	20
TFG	Protein TFG	0.35	0.35	21	20
HBD	Hemoglobin subunit delta	0.81	0.81	15	20
RPS11	40S ribosomal protein S11	2.67	2.67	21	20
KIAA1279	KIF1-binding protein	0.49	0.49	24	21
EEF1E1	Eukaryotic translation elongation factor 1 epsilon0	3.78	3.78	24	21
CROCC	Isoform 2 of Rootletin	0.02	0.02	19	22
PTK2	Focal adhesion kinase 1 (Fragment)	0.06	0.06	17	22
GFPT2	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2	0.23	0.23	31	22
TRIM6-TRIM34	Protein TRIM6-TRIM34	0.03	0.03	22	23
XPNPEP3	Isoform 2 of Probable Xaa-Pro aminopeptidase 3	0.07	0.07	26	23
KATNAL2	Katanin p60 ATPase-containing subunit A-like 2 (Fragment)	0.09	0.09	16	23
CCAR2	Isoform 2 of Cell cycle and apoptosis regulator protein 2	0.13	0.13	21	23
RAB28	RAB28 protein	0.33	0.33	19	23

IQGAP2	Ras GTPase-activating-like protein IQGAP2	0.06	0.06	23	24
STRBP	Isoform 2 of Spermatid perinuclear RNA- binding protein	0.36	0.36	38	25
UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2	2.08	2.08	24	25
HIST1H3A	Histone H3.1	3.86	3.86	28	25
HIST2H3A	Histone H3.2	3.91	3.91	27	25
CSTF3	Cleavage stimulation factor subunit 3	0.31	0.31	23	26
GLOD4	Glyoxalase domain-containing protein 4	0.41	0.41	21	26
PLS1	Plastin0	0.31	0.31	24	27
DDX3X	Isoform 2 of ATP-dependent RNA helicase DDX3X	0.43	0.43	33	27
PDXK	Pyridoxal kinase	1.24	1.24	23	27
PPIF	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	2.5	2.5	30	27
PPFIA3	Liprin-alpha-3	0.04	0.04	24	28
PITRM1	Isoform 2 of Presequence protease, mitochondrial	0.21	0.21	24	28
TARSL2	Isoform 2 of Probable threonine--tRNA ligase 2, cytoplasmic	0.26	0.26	20	28
ALDH1L1	Isoform 2 of Cytosolic 10- formyltetrahydrofolate dehydrogenase	0.04	0.04	22	29
IGSF8	Isoform 3 of Immunoglobulin superfamily member 8	0.87	0.87	52	30
UBE2N	Ubiquitin-conjugating enzyme E2 N	5.01	5.01	32	30
H2AFX	Histone H2AX	2.38	2.38	23	31

ST13	Hsc70-interacting protein	0.56	0.56	27	32
Sep 06	Septin 6, isoform CRA_b	0.57	0.57	51	32
PGLS	6-phosphogluconolactonase	1.76	1.76	28	32
HBA1	Hemoglobin subunit alpha	3.06	3.06	26	33
TNPO2	Isoform 2 of Transportin-2	0.1	0.1	33	34
IGHG4	Ig gamma-4 chain C region	0.19	0.19	29	34
PRMT8	Isoform 2 of Protein arginine N-methyltransferase 8	0.43	0.43	39	37
RSU1	Ras suppressor protein 1	1.46	1.46	33	37
PDIA3	Protein disulfide-isomerase A3 (Fragment)	2.78	2.78	47	38
GLO1	Isoform 2 of Lactoylglutathione lyase	2.62	2.62	36	41
APOA1BP	Isoform 2 of NAD(P)H-hydrate epimerase	3.52	3.52	30	42
S100A11	Protein S100-A11	4.92	4.92	41	42
THBS1	Thrombospondin0	0.21	0.21	33	43
HIST3H2A	Histone H2A type 3	4.65	4.65	36	43
ADSS	Adenylosuccinate synthetase isozyme 2	1.42	1.42	69	44
TRAJ56	Protein TRAJ56 (Fragment)	1.81	1.81	49	44
CYFIP1	Cytoplasmic FMR1-interacting protein 1	0.25	0.25	34	45
tr M0QYT0 M0QYT0_HUMAN	Uncharacterized protein (Fragment)	0.84	0.84	52	46
ASAP2	Isoform 2 of Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	0.03	0.03	52	48
TUBA4B	Putative tubulin-like protein alpha-4B	0.4	0.4	67	49

YWHAB	Isoform Short of 14-3-3 protein beta/alpha	2.45	2.45	43	49
SGSH	N-sulphoglucosamine sulphohydrolase	0.65	0.65	24	50
LDHAL6B	L-lactate dehydrogenase A-like 6B	0.16	0.16	49	51
HIST1H2AG	Histone H2A type 1	7.72	7.72	42	51
CCT6B	T-complex protein 1 subunit zeta-2	0.55	0.55	56	53
HSPA4L	Heat shock 70 kDa protein 4L	0.23	0.23	54	54
IPO4	Isoform 2 of Importin-4	0.46	0.46	70	54
KPNA4	Importin subunit alpha-3	0.73	0.73	74	55
SYNE2	Nesprin-2	0.01	0.01	52	56
DDX39A	ATP-dependent RNA helicase DDX39A	1.16	1.16	62	56
KRT84	Keratin, type II cuticular Hb4	0.16	0.16	59	57
CTPS1	CTP synthase 1	0.95	0.95	47	57
KRT82	Keratin, type II cuticular Hb2	0.18	0.18	58	59
HSPA9	Stress-70 protein, mitochondrial	1.49	1.49	104	59
COPE	Coatomer subunit epsilon	3.71	3.71	52	60
CD9	Tetraspanin	1.76	1.76	104	61
DES	Desmin	0.27	0.27	46	64
TSN	Translin	8.06	8.06	61	64
RCC2	Protein RCC2	1.91	1.91	110	69
PCBP2	Poly(rC)-binding protein 2 (Fragment)	1.2	1.2	84	72
USP7	Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 7	0.43	0.43	69	75
PDIA6	Isoform 2 of Protein disulfide-isomerase A6	1.15	1.15	98	84

DARS	Aspartate--tRNA ligase, cytoplasmic (Fragment)	3.84	3.84	69	93
HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	2.62	2.62	127	99
PSMD11	Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11	2.55	2.55	93	100
RAN	GTP-binding nuclear protein Ran (Fragment)	4.75	4.75	105	103
PCBP1	Poly(rC)-binding protein 1	0.95	0.95	97	105
PSMC1	26S protease regulatory subunit 4	2.01	2.01	90	110
RNH1	Ribonuclease inhibitor	2.44	2.44	106	113
MCM6	DNA replication licensing factor MCM6	0.99	0.99	146	123
YWHAQ	14-3-3 protein theta	6.52	6.52	104	125
UBBP4	Protein UBBP4	1.07	1.07	187	141
PLS3	Plastin-3	3.62	3.62	139	154
SET	Protein SET	3.98	3.98	160	165
WDR1	WD repeat-containing protein 1	3.22	3.22	135	170
HSPA6	Heat shock 70 kDa protein 6	1.05	1.05	186	179
PGD	Isoform 2 of 6-phosphogluconate dehydrogenase, decarboxylating	6.04	6.04	239	192
HSPA1A	Heat shock 70 kDa protein 1A/1B	2.76	2.76	188	202
HSP90AA4P	Putative heat shock protein HSP 90-alpha A4	0.49	0.49	185	203
YWHAE	14-3-3 protein epsilon	21.64	21.64	194	203
PZP	Pregnancy zone protein	0.34	0.34	222	235
TPP1	Tripeptidyl-peptidase 1	3.06	3.06	183	243

HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	12.77	12.77	278	244
HSP90AB2P	Putative heat shock protein HSP 90-beta 2	3.18	3.18	190	279
ACTBL2	Beta-actin-like protein 2	3.5	3.5	330	282
C3	Complement C3	0.48	0.48	483	287
ACTN1	Alpha-actinin0	25.23	25.23	817	961
HSP90AA1	Isoform 2 of Heat shock protein HSP 90-alpha	31.87	30.82	1358	1625
PFAS	Phosphoribosylformylglycinamidine synthase	0.86	0.82	120	135
EIF3B	Isoform 2 of Eukaryotic translation initiation factor 3 subunit B	2.1	2	253	275
LMNA	Prelamin-A/C	5.98	5.69	350	365
GART	Trifunctional purine biosynthetic protein adenosine-3	1.82	1.73	242	241
GGACT	Gamma-glutamylaminecyclotransferase	0.2	0.19	12	14
EIF4G1	Eukaryotic translation initiation factor 4 gamma 1	0.36	0.34	58	52
KARS	Lysine--tRNA ligase	4.4	4.15	235	272
TXNRD1	Thioredoxin reductase 1, cytoplasmic	6.02	5.66	238	234
CCT4	T-complex protein 1 subunit delta	5.1	4.78	264	306
PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	2.21	2.05	146	164
CLUH	Clustered mitochondria protein homolog (Fragment)	0.41	0.38	61	72

HSP90AB1	Heat shock protein HSP 90-beta	53.66	49.61	1393	1763
PSMD3	26S proteasome non-ATPase regulatory subunit 3	1.71	1.57	107	131
SF3B1	Splicing factor 3B subunit 1	0.36	0.33	41	42
MSN	Moesin	30.4	27.57	508	437
HNRNPK	Heterogeneous nuclear ribonucleoprotein K (Fragment)	2.92	2.63	210	160
EIF3F	Eukaryotic translation initiation factor 3 subunit F	2.86	2.54	110	79
POTEE	POTE ankyrin domain family member E	0.88	0.78	643	496
EEF1D	Elongation factor 1-delta	0.51	0.45	53	74
HEXB	Beta-hexosaminidase subunit beta	4.29	3.78	179	255
EIF3D	Isoform 2 of Eukaryotic translation initiation factor 3 subunit D	0.82	0.72	69	58
PDIA3	Protein disulfide-isomerase A3	6.09	5.34	235	173
PSME3	Proteasome activator complex subunit 3	3.93	3.44	75	78
F5	Coagulation factor V	0.08	0.07	19	16
GLB1	Isoform 3 of Beta-galactosidase	0.48	0.42	32	37
TXNL1	Thioredoxin-like protein 1	2.52	2.2	38	35
NRD1	Nardilysin	0.55	0.48	85	84
MANBA	Beta-mannosidase	1.01	0.88	93	76
LGALS3	Galectin-3	6.68	5.81	135	124
HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	7.61	6.59	79	71
PARP1	Poly [ADP-ribose] polymerase 1	1.55	1.34	197	169
PCNA	Proliferating cell nuclear antigen	3.09	2.67	50	70

HK1	Isoform 2 of Hexokinase0	0.87	0.75	68	108
SHMT1	Isoform 2 of Serine hydroxymethyltransferase, cytosolic	0.78	0.67	34	25
BAG6	Isoform 2 of Large proline-rich protein BAG6	0.21	0.18	21	23
PRKDC	Isoform 2 of DNA-dependent protein kinase catalytic subunit	0.07	0.06	30	23
CTSL	Cathepsin L1	1.31	1.12	51	35
MYH9	Myosin-9	1.31	1.12	307	327
ILF3	Isoform 2 of Interleukin enhancer-binding factor 3	4.6	3.93	316	266
ADSL	Adenylosuccinate lyase	0.68	0.58	33	36
UBE2L3	Isoform 3 of Ubiquitin-conjugating enzyme E2 L3	4.38	3.73	37	29
ECH1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	1.2	1.02	35	44
GMPS	GMP synthase [glutamine-hydrolyzing]	3.65	3.1	170	230
DDX6	Probable ATP-dependent RNA helicase DDX6	0.59	0.5	36	17
HSPA1L	Heat shock 70 kDa protein 1-like	1.37	1.16	196	206
TNPO1	Isoform 2 of Transportin0	0.65	0.55	89	93
ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2	0.52	0.44	175	180
RAB2A	Ras-related protein Rab-2A	3.86	3.26	39	40
RECQL	ATP-dependent DNA helicase Q1	1.08	0.91	58	72
C14orf166	UPF0568 protein C14orf166	2.06	1.73	25	22
LGMN	Legumain	3.11	2.61	144	118

PSME1	Proteasome activator complex subunit 1	1.67	1.4	39	43
EIF4A2	Isoform 2 of Eukaryotic initiation factor 4A-II	3.19	2.66	141	108
CFL1	Cofilin 1 (Non-muscle), isoform CRA_a	92.78	77.21	109	101
MDH1	Isoform 3 of Malate dehydrogenase, cytoplasmic	8.87	7.38	146	159
EIF3CL	Eukaryotic translation initiation factor 3 subunit C-like protein	1.07	0.89	132	120
KPNA3	Importin subunit alpha-4	0.47	0.39	35	25
KRT8	Keratin, type II cytoskeletal 8 (Fragment)	1.17	0.97	79	65
ELAVL1	Isoform 2 of ELAV-like protein 1	0.76	0.63	29	29
B4GALT4	N-acetyllactosamine synthase	1.05	0.87	47	20
HNRNPK	Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	2.27	1.88	215	160
TGM2	Protein-glutamine gamma-glutamyltransferase 2	6.16	5.08	310	347
XRCC6	X-ray repair cross-complementing protein 6	2.78	2.29	157	170
SERPINB1	Leukocyte elastase inhibitor	0.68	0.56	24	11
TMEM189-UBE2V1	HCG2044781	0.68	0.56	23	24
EEF1D	Isoform 3 of Elongation factor 1-delta	1.41	1.16	38	54
PEPD	Xaa-Pro dipeptidase	1.52	1.25	70	68
SRM	Spermidine synthase	0.9	0.74	17	20
CTSB	Cathepsin B	5.59	4.59	151	106
MYL12A	Myosin regulatory light chain 12A	3.55	2.91	23	20
LMNB2	Lamin B2, isoform CRA_a	0.99	0.81	41	35

HDAC2	Isoform 2 of Histone deacetylase 2	0.44	0.36	53	43
RHOA	Transforming protein RhoA	2.57	2.1	29	21
GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1	8.31	6.78	129	139
NAE1	Isoform 2 of NEDD8-activating enzyme E1 regulatory subunit	0.38	0.31	25	22
SHMT2	Isoform 3 of Serine hydroxymethyltransferase, mitochondrial	0.43	0.35	19	14
TIPRL	TIP41-like protein	1.01	0.82	16	20
MCTS1	Malignant T-cell-amplified sequence 1	2.86	2.32	27	21
AHCYL1	Isoform 2 of Putative adenosylhomocysteinase 2	0.42	0.34	18	22
BRCC3	Isoform 1 of Lys-63-specific deubiquitinase BRCC36	0.94	0.76	33	34
XRCC5	X-ray repair cross-complementing protein 5	2.86	2.31	136	204
APOB	Apolipoprotein B000	0.05	0.04	24	28
FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	4.57	3.64	126	127
SIL1	Nucleotide exchange factor SIL1	0.44	0.35	20	15
FARSB	Phenylalanine--tRNA ligase beta subunit	0.78	0.62	26	48
OTUB1	Ubiquitin thioesterase OTUB1	0.82	0.65	18	23
RBMX	RNA-binding motif protein, X chromosome, N-terminally processed (Fragment)	0.81	0.64	14	11

NOP2	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	0.19	0.15	15	11
EPHA7	Isoform 4 of Ephrin type-A receptor 7	0.19	0.15	16	14
ANXA7	Isoform 2 of Annexin A7	0.37	0.29	18	15
G3BP2	Isoform B of Ras GTPase-activating protein-binding protein 2	0.37	0.29	24	19
UBE2D3	Isoform 2 of Ubiquitin-conjugating enzyme E2 D3	3.28	2.57	18	20
APIP	Methylthioribulose0-phosphate dehydratase	0.97	0.76	19	33
TUBB8	Tubulin beta-8 chain	1.14	0.89	156	118
EIF4A3	Eukaryotic initiation factor 4A-III	1.41	1.1	86	56
EEF1B2	Elongation factor 1-beta	1.13	0.88	24	34
COL5A2	Collagen alpha-2(V) chain	7.98	6.19	1085	591
SLC1A5	Amino acid transporter	0.49	0.38	25	10
SF3A3	Splicing factor 3A subunit 3	0.31	0.24	22	13
C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial	3.92	3.03	63	51
OLA1	Obg-like ATPase 1	4.07	3.14	167	88
CLIC1	Chloride intracellular channel protein 1	9.1	7.02	99	108
HNRNPL	Heterogeneous nuclear ribonucleoprotein L (Fragment)	1.95	1.5	134	118
PRDX6	Peroxiredoxin-6	21.78	16.74	107	89
EHD1	EH domain-containing protein 1	0.3	0.23	8	15
HPCAL1	Hippocalcin-like protein 1	1.49	1.14	13	10

CORO1C	Isoform 2 of Coronin0C	2.03	1.55	139	155
P4HB	Protein disulfide-isomerase	5.27	4.02	192	147
DNASE2	Isoform 2 of Deoxyribonuclease-2-alpha	0.59	0.45	41	11
RPS20	Isoform 2 of 40S ribosomal protein S20	2.78	2.12	21	17
WARS	Tryptophan--tRNA ligase, cytoplasmic	8.12	6.18	216	263
RPRD1B	Regulation of nuclear pre-mRNA domain-containing protein 1B	0.54	0.41	17	9
LDLR	Low-density lipoprotein receptor	0.87	0.66	175	144
UAP1	Isoform AGX1 of UDP-N-acetylhexosamine pyrophosphorylase	4.96	3.76	269	238
KPNA2	Importin subunit alpha0	1.69	1.28	103	71
RTN3	Isoform 2 of Reticulon-3	0.12	0.09	16	11
SPTBN4	Spectrin beta chain, non-erythrocytic 4	0.04	0.03	30	32
KHSRP	Far upstream element-binding protein 2	0.48	0.36	53	79
NAA10	N-alpha-acetyltransferase 10	0.8	0.6	16	8
COPS7B	COP9 signalosome complex subunit 7b	0.8	0.6	20	18
GC	Vitamin D-binding protein	0.8	0.6	91	84
TUBA8	Isoform 2 of Tubulin alpha-8 chain	3.67	2.75	207	189
GSTP1	Glutathione S-transferase P	11.51	8.59	102	77
PUS7	Pseudouridylate synthase 7 homolog	0.47	0.35	30	23
SEMA4B	Semaphorin-4B	0.31	0.23	30	21
FUS	RNA-binding protein FUS	0.27	0.2	20	8
RPS15A	40S ribosomal protein S15a	2.41	1.78	18	17
AP2S1	AP-2 complex subunit sigma	1.25	0.92	11	12
PNP	Purine nucleoside phosphorylase	24.27	17.84	125	154

SND1	Staphylococcal nuclease domain-containing protein 1	2.86	2.1	275	235
UBE2M	NEDD8-conjugating enzyme Ubc12	1.09	0.8	13	11
ACTC1	Actin, alpha cardiac muscle 1	42.04	30.85	666	516
DDX42	ATP-dependent RNA helicase DDX42	0.45	0.33	24	28
MCM7	DNA replication licensing factor MCM7	1.19	0.87	74	58
PGM3	Isoform 3 of Phosphoacetylglucosamine mutase	0.22	0.16	8	9
PTX3	Pentraxin-related protein PTX3	17.53	12.74	686	424
HSP90B1	Endoplasmic	2.26	1.64	246	266
Sep 08	Septin-8	0.29	0.21	34	21
PDCD6IP	Programmed cell death 6-interacting protein	5.47	3.96	347	301
SDC4	Isoform 2 of Syndecan-4	1.54	1.11	45	25
PPT1	Palmitoyl-protein thioesterase 1	1.5	1.08	32	37
SLC3A2	4F2 cell-surface antigen heavy chain	1.56	1.12	149	102
EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	4.23	3.03	74	74
COL2A1	Isoform 1 of Collagen alpha0(I) chain	0.07	0.05	7	5
PITPNA	Phosphatidylinositol transfer protein alpha isoform	0.49	0.35	11	12
OPA1	Dynamin-like 120 kDa protein, mitochondrial	0.21	0.15	18	13
EEF1G	Isoform 2 of Elongation factor 1-gamma	6.26	4.47	328	274
SRP14	Signal recognition particle 14 kDa protein	1.84	1.31	15	14

SERPINH1	Serpin H1	1.8	1.28	81	44
PRDX3	Isoform 2 of Thioredoxin-dependent peroxide reductase, mitochondrial	2.76	1.96	38	36
KDM1A	Isoform 2 of Lysine-specific histone demethylase 1A	0.31	0.22	29	18
CYCS	Cytochrome c (Fragment)	3.85	2.73	40	10
CASP3	Caspase-3	0.48	0.34	11	7
DNAJA1	Isoform 2 of DnaJ homolog subfamily A member 1	1.13	0.8	42	22
PEF1	Peflin	0.51	0.36	12	9
BZW2	Basic leucine zipper and W2 domain-containing protein 2 (Fragment)	1.58	1.11	62	28
SERPINB9	Serpin B9	2.04	1.43	60	50
SLK	Isoform 2 of STE20-like serine/threonine-protein kinase	0.1	0.07	9	15
PSMG2	Isoform 2 of Proteasome assembly chaperone 2	0.6	0.42	14	9
PA2G4	Proliferation-associated protein 2G4	5.09	3.56	127	89
HSPH1	Isoform Beta of Heat shock protein 105 kDa	4.09	2.86	311	255
DNAJA2	DnaJ homolog subfamily A member 2	0.73	0.51	38	19
CUTC	Copper homeostasis protein cutC homolog	0.53	0.37	9	11
RPL30	60S ribosomal protein L30 (Fragment)	2.28	1.59	17	9
LIN7C	Protein lin-7 homolog C	0.76	0.53	8	14
ARF3	ADP-ribosylation factor 3	6.1	4.25	29	30
MCM4	DNA replication licensing factor MCM4	1.45	1.01	113	97

RAB7A	Ras-related protein Rab-7a	3.26	2.27	49	39
ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	0.82	0.57	29	18
CSNK2B	Casein kinase 2, beta polypeptide, isoform CRA_d	0.59	0.41	12	6
THBS4	Thrombospondin-4	0.26	0.18	46	30
BUB3	Mitotic checkpoint protein BUB3 (Fragment)	1.43	0.99	51	47
CALB2	Calretinin	1.46	1.01	28	22
QPCTL	Glutaminyl-peptide cyclotransferase-like protein	0.81	0.56	25	27
TXNDC5	Thioredoxin domain-containing protein 5	1.36	0.94	64	27
ACTB	Actin, cytoplasmic 1	392.38	268.52	1418	1160
BPI	Bactericidal permeability-increasing protein	0.19	0.13	8	2
RUVBL1	RuvB-like 1	6.1	4.17	174	224
NONO	Isoform 2 of Non-POU domain-containing octamer-binding protein	0.79	0.54	52	24
VAR5	Valine--tRNA ligase	0.85	0.58	120	80
HNRNPH1	Heterogeneous nuclear ribonucleoprotein H	1.1	0.75	100	94
DCTPP1	dCTP pyrophosphatase 1	0.94	0.64	9	9
XPOT	Exportin-T	0.5	0.34	34	43
ARPC2	Actin-related protein 2/3 complex subunit 2	21.85	14.81	140	137
CD109	CD109 antigen	5.49	3.72	1220	1034
ACTA1	Actin, alpha skeletal muscle	28.29	19.12	604	478

DSTN	Destrin	6.1	4.12	34	30
EPHA4	Ephrin type-A receptor 4	0.77	0.52	104	59
CLTC	Clathrin heavy chain 1 (Fragment)	1.17	0.79	16	16
FABP5	Fatty acid-binding protein, epidermal	1.2	0.81	16	9
TK1	Thymidine kinase, cytosolic	1.96	1.32	24	16
ALDH7A1	Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase	0.49	0.33	36	30
ACOT9	Isoform 2 of Acyl-coenzyme A thioesterase 9, mitochondrial	0.61	0.41	31	14
COTL1	Coactosin-like protein	1.15	0.77	10	3
SUB1	Activated RNA polymerase II transcriptional coactivator p15	1.33	0.89	6	7
ESD	S-formylglutathione hydrolase	3.41	2.28	48	47
FXR1	Fragile X mental retardation syndrome-related protein 1	0.15	0.1	16	5
TUFM	Elongation factor Tu, mitochondrial	0.21	0.14	12	5
SF3A2	Splicing factor 3A subunit 2	0.21	0.14	11	8
LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	0.06	0.04	13	10
SERPIND1	Heparin cofactor 2	0.18	0.12	9	7
NUMA1	Nuclear mitotic apparatus protein 1	0.18	0.12	32	25
COL1A1	Collagen alpha0(I) chain	0.18	0.12	29	27
TUBA1C	Tubulin alpha0C chain	5.06	3.37	324	301
FSCN1	Fascin	0.89	0.59	53	29
NAMPT	Nicotinamide phosphoribosyltransferase	2.74	1.81	108	113
TUBB6	Tubulin beta-6 chain	1.94	1.28	181	133

APRT	Adenine phosphoribosyltransferase	3.82	2.52	24	24
SF3A1	Splicing factor 3A subunit 1	0.44	0.29	70	36
RHOC	Rho-related GTP-binding protein RhoC (Fragment)	2.61	1.72	29	18
RAB5C	Isoform 2 of Ras-related protein Rab-5C	1.52	1	28	18
Sep 11	Septin 11, isoform CRA_b	2.01	1.32	93	62
QDPR	Dihydropteridine reductase	1.63	1.07	19	14
tr A0A087X1E9 A0A087X1E9_HUMAN	Uncharacterized protein	0.29	0.19	13	9
TUBB3	Tubulin beta-3 chain	3.52	2.3	247	194
TCEB2	Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b	1.61	1.05	13	11
RCC1	Isoform 2 of Regulator of chromosome condensation	1.06	0.69	63	31
SFPQ	Splicing factor, proline- and glutamine-rich	1.23	0.8	177	102
MAN2A1	Alpha-mannosidase 2	7.03	4.56	679	448
SUMF2	Sulfatase-modifying factor 2	0.85	0.55	18	11
C5	Complement C5	0.17	0.11	58	24
RPLP1	60S acidic ribosomal protein P1	1.81	1.17	9	10
CSTB	Cystatin-B	1.92	1.24	10	8
EXOSC2	Exosome complex component RRP4	0.96	0.62	26	39
LIPA	Lysosomal acid lipase/cholesteryl ester hydrolase	9.08	5.86	230	212
RPLP0	60S acidic ribosomal protein P0	6.57	4.24	119	138

BSG	Basigin (Fragment)	1.83	1.18	37	20
KIAA0319L	Dyslexia-associated protein KIAA0319-like protein	0.28	0.18	12	4
HEATR2	HEAT repeat-containing protein 2 (Fragment)	0.14	0.09	8	5
ATP5B	ATP synthase subunit beta, mitochondrial	4.17	2.68	152	113
SSRP1	FACT complex subunit SSRP1	0.67	0.43	89	44
EXOSC6	Exosome complex component MTR3	0.39	0.25	9	9
PSMG1	Isoform 2 of Proteasome assembly chaperone 1	0.36	0.23	11	10
ARF5	ADP-ribosylation factor 5 (Fragment)	5.01	3.2	23	19
UBA2	SUMO-activating enzyme subunit 2	1.24	0.79	78	64
PSMD8	26S proteasome non-ATPase regulatory subunit 8	2.19	1.39	39	41
PRNP	Major prion protein (Fragment)	0.41	0.26	22	9
PLOD3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	13.03	8.26	690	530
HAT1	Histone acetyltransferase type B catalytic subunit	0.9	0.57	54	21
UBE2I	SUMO-conjugating enzyme UBC9	3.62	2.29	27	17
ITGB1	Isoform 2 of Integrin beta0	0.38	0.24	45	17
ARHGDIA	Rho GDP-dissociation inhibitor 1 (Fragment)	2.17	1.37	23	25
DYNLT1	Dynein light chain Tctex-type 1	2.22	1.4	7	7
PIN1	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (Fragment)	2.3	1.45	10	7

PBDC1	Protein PBDC1	0.43	0.27	8	4
B3GAT3	Beta0,3-glucuronyltransferase 3 (Glucuronosyltransferase I), isoform CRA_a	1.69	1.06	47	24
ZC3HAV1L	Zinc finger CCCH-type antiviral protein 1-like	0.32	0.2	4	5
PDLIM5	PDZ and LIM domain protein 5	0.16	0.1	18	9
PHGDH	D-3-phosphoglycerate dehydrogenase	0.4	0.25	21	13
TUBA1A	Isoform 2 of Tubulin alpha0A chain	8.5	5.31	299	288
EEF1A2	Elongation factor 1-alpha 2	5.21	3.25	584	341
RPS7	40S ribosomal protein S7	0.53	0.33	10	6
LSM8	U6 snRNA-associated Sm-like protein LSM8	6.19	3.85	9	8
GLA	Alpha-galactosidase A	2.63	1.63	113	54
PAFAH1B3	Platelet-activating factor acetylhydrolase IB subunit gamma	1.34	0.83	14	15
GID8	Glucose-induced degradation protein 8 homolog	0.42	0.26	16	13
DNAJB11	DnaJ homolog subfamily B member 11	1.18	0.73	68	23
TRAPPC3	Trafficking protein particle complex subunit 3	0.55	0.34	7	4
RPL6	60S ribosomal protein L6	0.34	0.21	16	11
HMGA1	Isoform HMG-R of High mobility group protein HMG-I/HMG-Y	0.6	0.37	7	4
GINS3	Isoform 3 of DNA replication complex GINS protein PSF3	0.39	0.24	9	6
CAPG	Macrophage-capping protein	1.27	0.78	48	24

YARS	Tyrosine--tRNA ligase, cytoplasmic	1.01	0.62	80	40
CBR1	Carbonyl reductase [NADPH] 1	6.85	4.2	73	77
PTGES3	Prostaglandin E synthase 3	0.62	0.38	9	8
PPM1G	Protein phosphatase 1G	0.62	0.38	37	24
PDCL3	Phosducin-like protein 3	0.41	0.25	7	7
KRT79	Keratin, type II cytoskeletal 79	1.05	0.64	124	90
STIP1	Isoform 2 of Stress-induced-phosphoprotein 1	3.89	2.37	169	133
ARL2	ADP-ribosylation factor-like protein 2	0.56	0.34	6	9
MANF	Mesencephalic astrocyte-derived neurotrophic factor	1.81	1.09	18	13
TUBA1B	Tubulin alpha0B chain	8.01	4.81	363	343
SMARCA5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	0.05	0.03	5	5
EIF1AX	Eukaryotic translation initiation factor 1A, X-chromosomal	3.44	2.06	20	15
HNRNPF	Heterogeneous nuclear ribonucleoprotein F	0.87	0.52	66	63
TF	Serotransferrin (Fragment)	0.77	0.46	14	15
PARK7	Protein DJ0	10.9	6.48	59	45
GTF2I	Isoform 2 of General transcription factor II-I	0.27	0.16	33	22
ATP6V1G1	V-type proton ATPase subunit G 1	0.93	0.55	4	4
HRSP12	Ribonuclease UK114	0.88	0.52	9	6
SMPD1	Isoform 4 of Sphingomyelin phosphodiesterase	0.44	0.26	24	15

EIF4A1	Eukaryotic initiation factor 4A-I	12.61	7.41	267	161
SNX3	Sorting nexin-3	2.18	1.28	15	14
ERP29	Endoplasmic reticulum resident protein 29	0.92	0.54	10	4
NT5E	5~-nucleotidase (Fragment)	2.76	1.62	74	56
AK2	Adenylate kinase 2, mitochondrial	2.8	1.64	35	29
GANAB	Neutral alpha-glucosidase AB	6.96	4.07	588	505
RRM1	Ribonucleoside-diphosphate reductase large subunit	1.1	0.64	48	66
CD59	CD59 glycoprotein	1.05	0.61	10	10
CTSC	Dipeptidyl peptidase 1	1.64	0.95	118	58
CDCP1	CUB domain-containing protein 1	0.19	0.11	26	6
S100A16	Protein S100-A16	1.14	0.66	11	6
TXNDC16	Thioredoxin domain-containing protein 16	0.19	0.11	17	8
G3BP1	Ras GTPase-activating protein-binding protein 1	1.66	0.96	72	46
YWHAG	14-3-3 protein gamma	5.58	3.22	89	115
PLCB3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3	0.26	0.15	38	19
YWHAH	14-3-3 protein eta	2.03	1.17	51	49
RTCB	tRNA-splicing ligase RtcB homolog	0.33	0.19	13	7
EPHA2	Ephrin type-A receptor 2	0.47	0.27	55	35
PLOD1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	11.5	6.6	671	557

PPP2R2A	Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	0.35	0.2	36	18
HMGB3	High mobility group protein B3 (Fragment)	1.33	0.76	25	18
FAM49B	Protein FAM49B	2.05	1.17	39	32
ILF2	Interleukin enhancer-binding factor 2	8.74	4.98	159	107
APEX1	DNA-(apurinic or apyrimidinic site) lyase	4.83	2.75	120	65
SSB	Lupus La protein	1.96	1.11	103	59
NCSTN	Isoform 2 of Nicastrin	0.23	0.13	20	5
SORT1	Isoform 2 of Sortilin	0.23	0.13	18	6
CBR3	Carbonyl reductase [NADPH] 3	1.49	0.84	41	43
ARF4	ADP-ribosylation factor 4	5.11	2.88	29	21
HSPA4	Heat shock 70 kDa protein 4	10.06	5.66	477	468
GNAS	Isoform XLas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	0.16	0.09	19	8
ARHGAP1	Rho GTPase-activating protein 1	0.66	0.37	33	14
SKIV2L2	Superkiller viralicidic activity 2-like 2	0.5	0.28	45	31
NCL	Nucleolin	2.52	1.41	397	248
HNRNPU	Isoform Short of Heterogeneous nuclear ribonucleoprotein U	0.59	0.33	113	72
MGAT1	Alpha0,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	0.99	0.55	57	22
F2	Thrombin light chain	0.27	0.15	29	22
ANXA2	Isoform 2 of Annexin A2	15.73	8.67	219	113

DDX17	Probable ATP-dependent RNA helicase DDX17	0.49	0.27	61	43
MAN1B1	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	0.69	0.38	49	35
GABARAPL2	Gamma-aminobutyric acid receptor-associated protein-like 2	3.71	2.03	18	12
HNRNPA3	Isoform 2 of Heterogeneous nuclear ribonucleoprotein A3	0.53	0.29	44	29
DDX1	ATP-dependent RNA helicase DDX1	1.43	0.78	61	48
ARIH2	E3 ubiquitin-protein ligase ARIH2	0.11	0.06	8	5
COMP	Cartilage oligomeric matrix protein	0.22	0.12	21	21
RPS13	40S ribosomal protein S13	1.93	1.05	12	8
EXTL2	Exostosin-like 2	0.96	0.52	57	14
ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1	0.13	0.07	21	22
KRT77	Keratin, type II cytoskeletal 1b	0.67	0.36	155	141
EIF3G	Eukaryotic translation initiation factor 3 subunit G	0.56	0.3	12	11
HYOU1	Hypoxia up-regulated protein 1	1.29	0.69	146	99
SART3	Squamous cell carcinoma antigen recognized by T-cells 3	0.3	0.16	21	20
HNRNPAB	Heterogeneous nuclear ribonucleoprotein A/B	3	1.59	106	79
COL18A1	Isoform 2 of Collagen alpha0(XVIII) chain	0.34	0.18	73	24
BTD	Isoform 2 of Biotinidase	1.27	0.67	104	33
HDGF	Hepatoma-derived growth factor	0.8	0.42	29	9

BZW1	Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1	0.86	0.45	56	21
FAM3C	Protein FAM3C	4.8	2.51	50	44
AK1	Adenylate kinase isoenzyme 1	0.94	0.49	14	13
B2M	Beta-2-microglobulin	2.67	1.38	19	8
PLA2G15	Group XV phospholipase A2	0.97	0.5	44	14
CPSF7	Cleavage and polyadenylation-specificity factor subunit 7 (Fragment)	0.99	0.51	11	6
RAB5A	Isoform 2 of Ras-related protein Rab-5A	1.01	0.52	13	6
YWHAZ	14-3-3 protein zeta/delta	7.55	3.86	103	110
RAB35	Ras-related protein Rab-35 (Fragment)	1.06	0.54	33	17
WDR12	Ribosome biogenesis protein WDR12	0.59	0.3	24	12
BROX	BRO1 domain-containing protein BROX	0.61	0.31	25	11
RPA2	Replication protein A 32 kDa subunit (Fragment)	1.22	0.62	20	14
HSPG2	Basement membrane-specific heparan sulfate proteoglycan core protein	1.74	0.88	589	334
IL27RA	Interleukin-27 receptor subunit alpha	0.1	0.05	6	1
AAMP	Angio-associated migratory cell protein	0.14	0.07	6	1
SERINC5	Serine incorporator 5	0.14	0.07	4	2
USP11	Ubiquitin carboxyl-terminal hydrolase	0.06	0.03	5	3
VNN1	Pantetheinase	0.12	0.06	5	3
PTPN1	Tyrosine-protein phosphatase non-receptor type	0.16	0.08	8	3
PUS1	tRNA pseudouridine synthase	0.16	0.08	7	4
STAG2	Isoform 2 of Cohesin subunit SA-2	0.04	0.02	8	5

SNX9	Sorting nexin	0.1	0.05	7	5
RPL17	60S ribosomal protein L17 (Fragment)	1.2	0.6	9	8
ZFR	Zinc finger RNA-binding protein	0.06	0.03	11	9
IARS2	Isoleucine--tRNA ligase, mitochondrial	0.18	0.09	17	9
CA11	Carbonic anhydrase-related protein 11	0.84	0.42	44	12
SPTB	Isoform 2 of Spectrin beta chain, erythrocytic	0.04	0.02	22	21
RPSA	40S ribosomal protein SA (Fragment)	2.22	1.11	67	63
UGGT1	Isoform 2 of UDP-glucose:glycoprotein glucosyltransferase 1	0.64	0.32	85	68
METAP2	Isoform 3 of Methionine aminopeptidase 2	1.11	0.55	35	26
GLG1	Isoform 2 of Golgi apparatus protein 1	3.05	1.5	469	300
ADAM10	Disintegrin and metalloproteinase domain-containing protein 10	0.82	0.4	157	72
TUBB4B	Tubulin beta-4B chain	10.9	5.31	394	313
LOXL2	Lysyl oxidase homolog 2 (Fragment)	25.6	12.43	399	207
MCM2	DNA replication licensing factor MCM2	1.57	0.76	145	137
RFNG	Beta0,3-N-acetylglucosaminyltransferase radical fringe	0.31	0.15	4	1
ASF1A	Histone chaperone ASF1A	0.31	0.15	5	3
EXT1	Exostosin0	0.62	0.3	32	20
GRWD1	Glutamate-rich WD repeat-containing protein 1	0.29	0.14	11	12
CLIC4	Chloride intracellular channel protein 4	1.14	0.55	27	14

FUCA1	Tissue alpha-L-fucosidase	0.27	0.13	7	2
RGMB	RGM domain family member B	0.27	0.13	17	4
ATXN10	Ataxin00	0.27	0.13	20	7
PAK2	Serine/threonine-protein kinase PAK 2	0.25	0.12	9	11
DNAJC9	DnaJ homolog subfamily C member 9	0.23	0.11	3	2
HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	0.23	0.11	17	14
ARF6	ADP-ribosylation factor 6	2.43	1.16	22	16
NT5E	5~-nucleotidase	4.23	2.01	232	159
AFP	Alpha-fetoprotein	0.19	0.09	49	40
EXT2	Isoform 3 of Exostosin-2	0.74	0.35	43	19
CHST14	Carbohydrate sulfotransferase 14	0.94	0.44	89	17
LUC7L2	Isoform 2 of Putative RNA-binding protein Luc7-like 2	0.15	0.07	3	1
SF3B4	Splicing factor 3B subunit 4	0.15	0.07	11	4
RRAS	Ras-related protein R-Ras	0.3	0.14	9	4
CD63	CD63 antigen	0.45	0.21	18	13
EXOSC5	Exosome complex component RRP46	1.35	0.63	16	15
GRN	Granulins	1.44	0.67	130	48
RACGAP1	Rac GTPase-activating protein 1 (Fragment)	0.43	0.2	33	17
A2M	Alpha-2-macroglobulin	4.31	2	952	613
CPSF6	Cleavage and polyadenylation-specificity factor subunit 6	0.13	0.06	9	2
SHPK	Sedoheptulokinase	0.13	0.06	10	7

GNB4	Guanine nucleotide-binding protein subunit beta-4	0.39	0.18	15	7
KDEL2	KDEL motif-containing protein 2	0.39	0.18	12	9
KRT9	Keratin, type I cytoskeletal 9	19.81	9.13	755	640
PGAM1	Phosphoglycerate mutase 1	108.38	49.94	199	155
TNC	Tenascin	0.48	0.22	82	30
TUBB4A	Tubulin beta-4A chain	6.7	3.07	329	259
PPIL3	Peptidyl-prolyl cis-trans isomerase (Fragment)	0.35	0.16	4	3
NUDT19	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	0.35	0.16	14	7
Sep 10	Septin 10, isoform CRA_c	0.35	0.16	19	8
RANBP1	Ran-specific GTPase-activating protein	0.22	0.1	6	1
CCDC58	Coiled-coil domain-containing protein 58	0.44	0.2	6	2
PLP2	Proteolipid protein 2	0.44	0.2	7	5
BRE	BRCA1-A complex subunit BRE (Fragment)	0.22	0.1	7	6
RACGAP1	Rac GTPase-activating protein 1	0.31	0.14	19	8
TOMM34	Mitochondrial import receptor subunit TOM34	0.2	0.09	6	2
RALA	Ras-related protein Ral-A (Fragment)	0.4	0.18	5	3
PSMG3	Proteasome assembly chaperone 3	0.58	0.26	6	2
RPL23	60S ribosomal protein L23	0.58	0.26	4	3
IDI1	Isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1	0.47	0.21	8	5

CMBL	Carboxymethylenebutenolidase homolog	0.56	0.25	11	7
DPP9	Isoform 2 of Dipeptidyl peptidase 9	0.65	0.29	53	32
DYNLRB1	Dynein light chain roadblock-type 1	0.45	0.2	3	1
HLA-G	HLA class I histocompatibility antigen, alpha chain G	0.18	0.08	20	14
UBE2A	Ubiquitin-conjugating enzyme E2 A	0.43	0.19	5	4
TSG101	Tumor susceptibility gene 101 protein	0.59	0.26	21	4
PRPS1	Ribose-phosphate pyrophosphokinase 1	5.02	2.21	64	53
SNRPA	U1 small nuclear ribonucleoprotein A	0.5	0.22	12	13
TIMM50	Mitochondrial import inner membrane translocase subunit TIM50 (Fragment)	0.66	0.29	9	2
LYAR	Cell growth-regulating nucleolar protein	0.16	0.07	3	1
FBLN1	Fibulin0	1.12	0.49	116	38
tr E5RI56 E5RI56_HUMAN	Uncharacterized protein (Fragment)	0.78	0.34	5	4
HSD17B10	Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2	0.62	0.27	12	5
RPL7	60S ribosomal protein L7	0.67	0.29	18	7
RPL13	60S ribosomal protein L13	0.67	0.29	17	9
HMGB1	High mobility group protein B1	12.81	5.52	89	88
SRP9	Signal recognition particle 9 kDa protein	0.79	0.34	6	3
TOR1B	Torsin0B	2.19	0.94	63	21
S100A10	Protein S100-A10	0.7	0.3	5	2
ESYT2	Isoform 2 of Extended synaptotagmin-2	0.07	0.03	7	4
TUBB2A	Tubulin beta-2A chain	13.39	5.72	382	289
TUBB2B	Tubulin beta-2B chain	12.43	5.28	371	280

LASP1	LIM and SH3 domain protein 1 (Fragment)	0.92	0.39	8	6
EIF2A	Isoform 3 of Eukaryotic translation initiation factor 2A	0.85	0.36	36	16
GALNS	N-acetylgalactosamine-6-sulfatase	2.72	1.15	151	70
GALC	Galactocerebrosidase	2.07	0.87	102	49
RPS21	40S ribosomal protein S21	0.93	0.39	5	5
ALB	Serum albumin	2.53	1.06	543	454
GPR126	Isoform 2 of G-protein coupled receptor 126	0.65	0.27	212	70
STAT1	Signal transducer and activator of transcription	0.41	0.17	29	15
RPL23A	60S ribosomal protein L23a (Fragment)	1	0.41	7	5
THBS3	Thrombospondin-3	2.44	1	583	165
GBA	Isoform Short of Glucosylceramidase	4.26	1.71	155	120
PDCD10	Programmed cell death protein 10	1.15	0.46	21	9
ATP1A2	Sodium/potassium-transporting ATPase subunit alpha-2	0.15	0.06	34	24
MCM3	Isoform 2 of DNA replication licensing factor MCM3	0.65	0.26	53	31
SPTBN2	Isoform 2 of Spectrin beta chain, non-erythrocytic 2	0.05	0.02	23	21
RHOG	Rho-related GTP-binding protein RhoG	1.36	0.54	13	5
TUBB	Tubulin beta chain	12.66	4.96	374	300
CKAP5	Isoform 2 of Cytoskeleton-associated protein 5	0.23	0.09	49	26
GM2A	Ganglioside GM2 activator	1.41	0.55	26	10

ANXA5	Annexin A5	1.41	0.55	28	15
CTSD	Cathepsin D	14.76	5.75	373	193
VASP	Vasodilator-stimulated phosphoprotein	2.3	0.89	78	36
CTSZ	Cathepsin Z	1.5	0.58	63	22
HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	14.73	5.69	184	150
KRT2	Keratin, type II cytoskeletal 2 epidermal	19.6	7.56	616	506
PLXNB2	Plexin-B2	0.26	0.1	52	26
COL6A1	Collagen alpha0(VI) chain	5.41	2.07	650	211
MYO1C	Unconventional myosin-Ic	0.21	0.08	31	6
PRCP	Lysosomal Pro-X carboxypeptidase	3.91	1.48	169	82
RAP1B	Isoform 3 of Ras-related protein Rap0b	3.35	1.26	22	13
SERPINE1	Plasminogen activator inhibitor 1	23.08	8.61	420	223
KHDRBS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	0.59	0.22	37	18
SERPINC1	Antithrombin-III	0.35	0.13	49	23
KTN1	Isoform 2 of Kinectin	0.19	0.07	26	9
RAP2B	Ras-related protein Rap-2b	5.05	1.86	27	20
RRP9	U3 small nucleolar RNA-interacting protein 2	0.36	0.13	14	4
IGHG1	Ig gamma0 chain C region	0.36	0.13	35	34
CYB5B	Cytochrome b5 type B	2.2	0.79	16	4
B4GALT1	Isoform Short of Beta0,4-galactosyltransferase 1	0.45	0.16	26	3
HSPD1	60 kDa heat shock protein, mitochondrial	5.25	1.85	217	155

EEF1A1	Elongation factor 1-alpha 1	56.18	19.79	1098	685
S100A13	Protein S100-A13	5.32	1.87	18	10
POFUT1	GDP-fucose protein O-fucosyltransferase 1	0.43	0.15	18	7
MAPRE1	Microtubule-associated protein RP/EB family member 1	2.5	0.87	53	22
PRPS2	Isoform 2 of Ribose-phosphate pyrophosphokinase 2	5.55	1.93	70	51
ASNS	Isoform 2 of Asparagine synthetase [glutamine-hydrolyzing]	0.67	0.23	28	16
HNRNPD	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	3.88	1.33	126	80
PITPNB	Phosphatidylinositol transfer protein beta isoform	1.44	0.49	22	15
MBTPS1	Membrane-bound transcription factor site0 protease	2.41	0.82	300	101
LOXL2	Lysyl oxidase homolog 2	26.04	8.8	1593	736
NAA50	N-alpha-acetyltransferase 50	4.75	1.6	31	15
ALB	Serum albumin	2.2	0.74	315	253
QSOX1	Sulfhydryl oxidase 1	36.56	12.26	1154	583
CD97	Isoform 2 of CD97 antigen	0.12	0.04	8	1
TOMM70A	Mitochondrial import receptor subunit TOM70	0.15	0.05	8	3
ATP1A3	Sodium/potassium-transporting ATPase subunit alpha-3	0.15	0.05	29	18
SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0.18	0.06	11	15

COCH	Cochlin	3.69	1.23	233	76
LMAN2	Vesicular integral-membrane protein VIP36	2.07	0.68	45	13
KRT75	Keratin, type II cytoskeletal 75	1.62	0.53	138	90
GSTO1	Glutathione S-transferase omega0	7.55	2.46	80	61
DDT	D-dopachrome decarboxylase	9.77	3.16	32	20
PPA1	Inorganic pyrophosphatase	5.77	1.86	82	56
ATRN	Isoform 2 of Attractin	0.78	0.25	126	31
PRKAR2A	Isoform 2 of cAMP-dependent protein kinase type II-alpha regulatory subunit	0.25	0.08	6	4
TTYH3	Isoform 2 of Protein tweety homolog 3	0.19	0.06	18	1
PEBP1	Phosphatidylethanolamine-binding protein 1	15.33	4.84	63	59
PFN2	Profilin	1.08	0.34	12	6
NUDCD1	Isoform 2 of NudC domain-containing protein 1	0.16	0.05	4	5
ANXA11	Isoform 2 of Annexin A11	0.64	0.2	27	14
TSPAN4	Tetraspanin	0.39	0.12	21	8
CLSTN1	Isoform 2 of Calsyntenin0	6.37	1.96	893	346
CLU	Isoform 4 of Clusterin	8.6	2.64	395	140
HSPB1	Heat shock protein beta0	7.91	2.42	71	35
RPL3	60S ribosomal protein L3	0.23	0.07	5	3
SEMA4C	Semaphorin-4C	0.23	0.07	29	6
UNC45A	Isoform 2 of Protein unc-45 homolog A	0.33	0.1	22	17
FBLN1	Fibulin0	0.87	0.26	102	23
BAX	Isoform Beta of Apoptosis regulator BAX	0.47	0.14	3	2

GRPEL1	GrpE protein homolog 1, mitochondrial	0.47	0.14	10	3
FUCA2	Plasma alpha-L-fucosidase	8.9	2.64	354	177
MOGS	Isoform 2 of Mannosyl-oligosaccharide glucosidase	0.27	0.08	16	8
RPS19	40S ribosomal protein S19	1.6	0.47	10	4
COASY	Bifunctional coenzyme A synthase (Fragment)	0.48	0.14	12	6
ECHS1	Enoyl-CoA hydratase, mitochondrial	1.21	0.35	18	10
BLVRB	Flavin reductase (NADPH)	0.52	0.15	14	2
COL3A1	Collagen alpha0(III) chain	6.82	1.96	1097	238
POLR2B	DNA-directed RNA polymerase	0.07	0.02	4	2
CCDC80	Isoform 2 of Coiled-coil domain-containing protein 80	0.42	0.12	50	10
NIT2	Omega-amidase NIT2	1.26	0.36	29	20
SUPT16H	FACT complex subunit SPT16	0.95	0.27	84	36
RBM8A	Isoform 2 of RNA-binding protein 8A	0.6	0.17	8	8
EFNA5	Ephrin-A5	0.53	0.15	20	2
C20orf27	Isoform 2 of UPF0687 protein C20orf27	0.53	0.15	11	4
HIST2H2BC	Putative histone H2B type 2-C	0.53	0.15	12	11
ICAM5	Intercellular adhesion molecule 5	0.92	0.26	138	26
ARL3	ADP-ribosylation factor-like protein 3	0.57	0.16	5	2
RPL15	Ribosomal protein L15 (Fragment)	0.57	0.16	7	2
ACE	Angiotensin-converting enzyme	0.61	0.17	109	27
FKBP2	Peptidyl-prolyl cis-trans isomerase FKBP2	0.79	0.22	7	3
CACYBP	Isoform 3 of Calcyclin-binding protein	20.57	5.7	90	89

NT5C	5~(3~)-deoxyribonucleotidase, cytosolic type	0.58	0.16	5	2
C7	Complement component C7	0.11	0.03	15	3
ATP1A1	Isoform 3 of Sodium/potassium-transporting ATPase subunit alpha0	0.59	0.16	64	22
KRT3	Keratin, type II cytoskeletal 3	1.57	0.42	131	74
PNPT1	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	0.45	0.12	19	8
PPIB	Peptidyl-prolyl cis-trans isomerase B	636.36	169.63	289	137
GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	2.09	0.55	158	53
CANT1	Isoform 3 of Soluble calcium-activated nucleotidase 1	2.4	0.63	67	15
TGFB1	Transforming growth factor-beta-induced protein ig-h3	11.94	3.09	502	200
SBDS	Ribosome maturation protein SBDS	3.56	0.92	50	28
ANP32B	Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B	9.68	2.5	90	46
MRC2	C-type mannose receptor 2	0.31	0.08	59	14
COL4A2	Collagen alpha-2(IV) chain	0.47	0.12	117	17
GSN	Gelsolin	148.98	38.03	2590	1364
PLTP	Phospholipid transfer protein	11.94	3.04	396	136
GPC1	Glypican0	2.97	0.75	164	70
S100A7	Protein S100-A7	1.19	0.3	13	1
SRC	Isoform 2 of Proto-oncogene tyrosine-protein kinase Src	0.44	0.11	22	2
SF1	Isoform 2 of Splicing factor 1	0.2	0.05	5	3

CELSR1	Cadherin EGF LAG seven-pass G-type receptor 1	0.08	0.02	15	4
TGFB1	Transforming growth factor beta0	2.58	0.64	84	25
CST3	Cystatin-C	55.82	13.78	113	41
PPIC	Peptidyl-prolyl cis-trans isomerase C	1.27	0.31	23	9
GOLM1	Isoform 2 of Golgi membrane protein 1	1.37	0.33	58	26
ISOC1	Isochorismatase domain-containing protein 1	3.3	0.79	39	31
EIF5A	Isoform 2 of Eukaryotic translation initiation factor 5A0	51.51	12.33	71	46
SEMA3A	Semaphorin-3A	14.74	3.5	1022	460
KIF23	Kinesin-like protein	0.38	0.09	56	23
GSN	Isoform 2 of Gelsolin	154.26	36.15	2474	1301
DPP7	Dipeptidyl peptidase 2	0.26	0.06	17	7
NUCB1	Nucleobindin0	8.55	1.91	277	101
AHNAK	Neuroblast differentiation-associated protein AHNAK	0.09	0.02	56	6
LTBP3	Latent-transforming growth factor beta-binding protein 3 (Fragment)	0.45	0.1	74	28
APLP2	Amyloid-like protein 2	6.76	1.5	535	208
ITM2B	Integral membrane protein 2B	0.51	0.11	9	4
DAG1	Dystroglycan	1.21	0.26	132	28
SPR	Sepiapterin reductase	0.56	0.12	8	3
NIT1	Isoform 1 of Nitrilase homolog 1	0.47	0.1	9	3
MITD1	MIT domain-containing protein 1 (Fragment)	0.57	0.12	9	3

MATN3	Isoform 2 of Matrilin-3	0.67	0.14	32	4
SERPINF1	Pigment epithelium-derived factor	25.85	5.37	773	137
UBE2S	Ubiquitin-conjugating enzyme E2 S (Fragment)	0.74	0.15	11	3
GSTM3	Glutathione S-transferase Mu 3	1.39	0.28	19	3
ALDH18A1	Isoform Short of Delta0-pyrroline-5-carboxylate synthase	0.2	0.04	8	2
HMGB2	High mobility group protein B2	5.97	1.17	47	23
SEMA3C	Semaphorin-3C	11.09	2.17	766	249
LAMC1	Laminin subunit gamma0	0.58	0.11	116	31
DDX21	Isoform 2 of Nucleolar RNA helicase 2	0.43	0.08	32	5
VGF	Neurosecretory protein VGF	0.27	0.05	22	4
GALNT10	Polypeptide N-acetylgalactosaminyltransferase 10	0.82	0.15	40	5
PGP	Phosphoglycolate phosphatase	1.75	0.32	28	8
MF12	Melanotransferrin	1.78	0.32	147	18
PROSC	Proline synthase co-transcribed bacterial homolog protein	1.28	0.23	31	3
ANXA1	Annexin A1	14.99	2.69	249	73
S100A8	Protein S100-A8	4.23	0.74	13	5
MANEA	Glycoprotein endo-alpha0,2-mannosidase	0.35	0.06	17	4
MINPP1	Multiple inositol polyphosphate phosphatase 1	1.11	0.19	63	21
CNP	Isoform CNPI of 2~,3~-cyclic-nucleotide 3~-phosphodiesterase	0.88	0.15	29	4

KRT4	Keratin, type II cytoskeletal 4	1.06	0.18	74	51
ECE1	Endothelin-converting enzyme 1	0.71	0.12	60	9
RAB27B	Ras-related protein Rab-27B	1.74	0.29	21	8
GALNT4	Polypeptide N-acetylgalactosaminyltransferase 4	0.61	0.1	44	3
KRT15	Keratin, type I cytoskeletal 15	2.88	0.47	232	115
LEPRE1	Isoform 3 of Prolyl 3-hydroxylase 1	1.41	0.23	179	40
RAB21	Ras-related protein Rab-21	0.88	0.14	8	2
PAM	Isoform 3 of Peptidyl-glycine alpha-amidating monooxygenase	1.07	0.17	144	17
SIAE	Sialate O-acetylesterase	1.96	0.31	84	40
LRRC59	Leucine-rich repeat-containing protein 59	0.57	0.09	34	7
DKK1	Dickkopf-related protein 1	0.7	0.11	20	4
LAMB1	Laminin subunit beta0	0.13	0.02	19	3
KRT19	Keratin, type I cytoskeletal 19	5.09	0.78	192	91
QSOX2	Sulfhydryl oxidase 2	1.18	0.18	92	9
LGALS3BP	Galectin-3-binding protein	1.77	0.27	126	30
VEGFC	Vascular endothelial growth factor C	2.02	0.3	85	12
EEA1	Early endosome antigen 1	0.27	0.04	45	13
GALNT1	Polypeptide N-acetylgalactosaminyltransferase 1	1.09	0.16	34	11
SAP18	Histone deacetylase complex subunit SAP18	1.21	0.17	12	3
RNASET2	Ribonuclease T2	2	0.28	40	6
AGRN	Isoform 6 of Agrin	1.22	0.17	315	28

MEGF8	Multiple epidermal growth factor-like domains protein 8	0.36	0.05	122	13
PRDX5	Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial	1.45	0.2	8	4
CHST3	Carbohydrate sulfotransferase 3	0.89	0.12	37	2
ACAT1	Acetyl-CoA acetyltransferase, mitochondrial	0.52	0.07	23	7
HLA-A	HLA class I histocompatibility antigen, A-24 alpha chain	5.44	0.72	147	38
DDX5	Probable ATP-dependent RNA helicase DDX5	0.38	0.05	37	13
TNFRSF6B	Tumor necrosis factor receptor superfamily member 6B	3.46	0.45	187	11
B3GNT1	Beta0,4-glucuronyltransferase 1	3.1	0.4	159	17
KRT5	Keratin, type II cytoskeletal 5	9	1.15	304	144
NOG	Noggin	1.05	0.13	26	1
SRGN	Serglycin	31.51	3.79	171	34
ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A	12.89	1.53	82	31
APP	Isoform 11 of Amyloid beta A4 protein	14.02	1.66	894	209
RTN4R	Reticulon-4 receptor (Fragment)	0.51	0.06	20	2
DTD1	D-tyrosyl-tRNA(Tyr) deacylase 1	1.22	0.14	22	3
NT5DC1	5~-nucleotidase domain-containing protein 1	0.53	0.06	19	5
FSTL5	Isoform 3 of Follistatin-related protein 5	36.73	4.02	1115	327
CTBS	Di-N-acetylchitobiase	0.65	0.07	30	2
KRT6B	Keratin, type II cytoskeletal 6B	11.81	1.22	371	150

KRT17	Keratin, type I cytoskeletal 17	7.25	0.69	253	103
TGFB3	Isoform 2 of Transforming growth factor beta receptor type 3	1.19	0.11	119	8
JUP	Junction plakoglobin	0.87	0.08	53	3
S100A9	Protein S100-A9	2.94	0.26	30	2
KLK6	Kallikrein-6	2.94	0.26	43	4
FLG2	Filaggrin-2	0.12	0.01	26	3
TMEM256-PLSCR3	Protein TMEM256-PLSCR3	1.34	0.11	27	8
LTF	Lactotransferrin (Fragment)	2.86	0.23	188	95
CTSV	Cathepsin L2	6.48	0.52	157	13
KRT6A	Keratin, type II cytoskeletal 6A	18.59	1.47	382	143
HAPLN1	Hyaluronan and proteoglycan link protein 1	1.02	0.08	51	2
HNRNPDL	Heterogeneous nuclear ribonucleoprotein D-like	1.04	0.08	47	26
PRSS23	Isoform 2 of Serine protease 23	1.05	0.08	26	1
TCN1	Transcobalamin0	0.92	0.07	23	4
KRT1	Keratin, type II cytoskeletal 1	161.27	11.43	1395	802
PCOLCE2	Procollagen C-endopeptidase enhancer 2	4.55	0.32	129	11
B3GNT2	Isoform 2 of N-acetyllactosaminide beta0,3-N-acetylglucosaminyltransferase 2	1	0.07	38	7
BMP1	Isoform BMP10 of Bone morphogenetic protein 1	0.58	0.04	47	5
KRT10	Keratin, type I cytoskeletal 10	312.05	20.98	1329	739

KRT16	Keratin, type I cytoskeletal 16	31	2.05	433	148
CRISPLD2	Cysteine-rich secretory protein LCCL domain-containing 2	0.95	0.06	46	1
MGAT5	Alpha0,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A	2.09	0.12	132	10
TIMP1	Metalloproteinase inhibitor 1	165.75	8.3	737	221
COL1A2	Collagen alpha-2(I) chain	404.72	15.71	5613	1042
TIMP2	Metalloproteinase inhibitor 2	586.92	19.1	523	109
DSP	Desmoplakin	0.31	0.01	71	2
KRT14	Keratin, type I cytoskeletal 14	100.69	2.43	578	199
POLR2A	DNA-directed RNA polymerase	0.01	0	2	0
MAP4	Microtubule-associated protein	0.01	0	5	0
SPEN	Msx2-interacting protein	0.01	0	8	0
MYO10	Unconventional myosin-X	0.01	0	4	0
LAMA3	Laminin subunit alpha-3	0.01	0	5	0
PTPRZ1	Isoform 2 of Receptor-type tyrosine-protein phosphatase zeta	0.01	0	2	0
sp H7BZ55 CROL3_HUMAN	Putative ciliary rootlet coiled-coil protein-like 3 protein	0.01	0	4	0
KMT2D	Isoform 3 of Histone-lysine N-methyltransferase 2D	0.01	0	4	0
GVINP1	Interferon-induced very large GTPase 1	0.01	0	4	0
MYH8	Myosin-8	0.01	0	19	0
MYH7	Myosin-7	0.01	0	19	0
MYH3	Myosin-3	0.01	0	19	0
SETX	Isoform 3 of Probable helicase senataxin	0.01	0	13	0

ANKRD31	Putative ankyrin repeat domain-containing protein 31	0.01	0	3	0
VPS13D	Vacuolar protein sorting-associated protein 13D (Fragment)	0.01	0	9	0
CENPF	Centromere protein F	0.01	0	4	0
MYO9A	Isoform 2 of Unconventional myosin-IXa	0.01	0	2	0
NACAD	NAC-alpha domain-containing protein 1	0.02	0	6	0
PPL	Periplakin	0.02	0	2	0
CUBN	Cubilin	0.02	0	7	0
COL4A5	Isoform 2 of Collagen alpha-5(IV) chain	0.02	0	52	0
FLG	Filaggrin	0.02	0	7	0
PRG4	Isoform B of Proteoglycan 4	0.02	0	3	0
VWA5B1	Isoform 2 of von Willebrand factor A domain-containing protein 5B1	0.02	0	4	0
RAPGEF2	Rap guanine nucleotide exchange factor 2	0.02	0	2	0
SEC31A	Protein transport protein Sec31A	0.02	0	2	0
XPO4	Exportin-4	0.02	0	3	0
RANBP2	E3 SUMO-protein ligase RanBP2	0.02	0	8	0
COL5A3	Collagen alpha-3(V) chain	0.02	0	2	0
DMXL2	DmX-like protein 2 (Fragment)	0.02	0	19	0
HRNR	Hornerin	0.03	0	6	0
HCFC1	HCF N-terminal chain 5	0.03	0	12	0
MUC5B	Mucin-5B	0.03	0	15	0
EVPL	Envoplakin	0.03	0	16	0
MGEA5	Isoform 2 of Protein O-GlcNAcase	0.03	0	6	0

ANK1	Ankyrin0 (Fragment)	0.03	0	4	0
EPHA10	EPH receptor A10, isoform CRA_b	0.03	0	4	0
CELSR2	Cadherin EGF LAG seven-pass G-type receptor 2	0.03	0	5	0
SORCS2	VPS10 domain-containing receptor SorCS2	0.03	0	5	0
SUPT5H	Transcription elongation factor SPT5	0.03	0	3	0
NUP133	Nuclear pore complex protein Nup133	0.03	0	2	0
ZC3HAV1	Zinc finger CCCH-type antiviral protein 1	0.03	0	2	0
PCDHAC2	Isoform Short of Protocadherin alpha-C2	0.03	0	6	0
HIP1	Huntingtin interacting protein 1 variant	0.03	0	3	0
MDC1	Isoform 2 of Mediator of DNA damage checkpoint protein 1	0.03	0	5	0
KCNH5	Potassium voltage-gated channel subfamily H member 5	0.03	0	19	0
AP3B1	Isoform 2 of AP-3 complex subunit beta0	0.03	0	3	0
RBM15	Putative RNA-binding protein 15	0.03	0	4	0
LARP1	Isoform 2 of La-related protein 1	0.03	0	2	0
PCDHA3	Isoform 2 of Protocadherin alpha-3	0.04	0	4	0
CPSF3	Cleavage and polyadenylation specific factor 3, 73kDa, isoform CRA_b	0.04	0	3	0
EIF4G3	Eukaryotic translation initiation factor 4 gamma 3	0.04	0	5	0
PKP3	Isoform PKP3b of Plakophilin-3	0.04	0	3	0
CAPN7	Calpain-7	0.04	0	3	0

CEACAM5	Carcinoembryonic antigen-related cell adhesion molecule 5	0.04	0	3	0
ATP5J2-PTCD1	Protein ATP5J2-PTCD1	0.04	0	3	0
GFM2	Isoform 2 of Ribosome-releasing factor 2, mitochondrial	0.04	0	8	0
SMCHD1	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 (Fragment)	0.04	0	5	0
MTA1	Metastasis-associated protein MTA1	0.04	0	4	0
RAD54B	DNA repair and recombination protein RAD54B	0.04	0	6	0
NSF	Vesicle-fusing ATPase	0.04	0	3	0
LRRFIP1	Isoform 4 of Leucine-rich repeat flightless-interacting protein 1	0.04	0	7	0
PDS5A	Sister chromatid cohesion protein PDS5 homolog A	0.04	0	4	0
TBC1D23	Isoform 2 of TBC1 domain family member 23	0.04	0	2	0
ACSL6	Long-chain-fatty-acid--CoA ligase 6	0.04	0	5	0
SH3D19	Isoform 2 of SH3 domain-containing protein 19	0.04	0	4	0
EXOC8	Exocyst complex component 8	0.04	0	5	0
P4HA1	Isoform 2 of Prolyl 4-hydroxylase subunit alpha0	0.05	0	9	0
CTNNA2	Catenin alpha-2	0.05	0	5	0
CHD4	Chromodomain-helicase-DNA-binding protein 4	0.05	0	12	0

STXBP3	Syntaxin-binding protein 3	0.05	0	6	0
PGLYRP2	Isoform 2 of N-acetylmuramoyl-L-alanine amidase	0.05	0	3	0
COL10A1	Collagen alpha0(X) chain	0.05	0	4	0
ATP2B3	Isoform XA of Plasma membrane calcium-transporting ATPase 3	0.05	0	10	0
LRRC40	Leucine-rich repeat-containing protein 40	0.05	0	2	0
CTNNBL1	Beta-catenin-like protein 1	0.05	0	6	0
EXTL3	Exostosin-like 3	0.05	0	2	0
PRPF4B	Serine/threonine-protein kinase PRP4 homolog (Fragment)	0.05	0	2	0
AP3D1	Isoform 2 of AP-3 complex subunit delta0	0.05	0	5	0
KIF4A	Isoform 2 of Chromosome-associated kinesin KIF4A	0.05	0	5	0
ENG	Isoform Short of Endoglin	0.05	0	3	0
HAL	Isoform 2 of Histidine ammonia-lyase	0.05	0	2	0
DNAJC2	Isoform 2 of DnaJ homolog subfamily C member 2	0.05	0	2	0
FRMPD1	Isoform 2 of FERM and PDZ domain-containing protein 1	0.05	0	9	0
ITPRIP	Inositol 1,4,5-trisphosphate receptor-interacting protein	0.05	0	13	0
CHAF1B	Chromatin assembly factor 1 subunit B	0.05	0	6	0
PDS5A	Isoform 2 of Sister chromatid cohesion protein PDS5 homolog A	0.05	0	3	0

TRIM23	Isoform Beta of E3 ubiquitin-protein ligase TRIM23	0.05	0	2	0
YES1	Tyrosine-protein kinase Yes	0.05	0	4	0
PRMT3	Protein arginine N-methyltransferase 3	0.05	0	14	0
ARHGAP18	Isoform 2 of Rho GTPase-activating protein 18	0.05	0	3	0
ERAP2	Isoform 2 of Endoplasmic reticulum aminopeptidase 2	0.05	0	2	0
CCDC63	Coiled-coil domain-containing protein 63	0.05	0	11	0
SLC22A6	Isoform 2 of Solute carrier family 22 member 6	0.05	0	5	0
AFM	Afamin	0.05	0	4	0
ASNSD1	Asparagine synthetase domain-containing protein 1	0.05	0	2	0
IQGAP3	Ras GTPase-activating-like protein IQGAP3	0.06	0	16	0
NEO1	Isoform 2 of Neogenin	0.06	0	9	0
SMU1	WD40 repeat-containing protein SMU1	0.06	0	12	0
KIAA1429	Isoform 2 of Protein virilizer homolog	0.06	0	13	0
UQCRC1	Cytochrome b-c1 complex subunit 1, mitochondrial	0.06	0	6	0
NCAPD2	Condensin complex subunit 1 (Fragment)	0.06	0	5	0
TAPBP	Tapasin	0.06	0	6	0
LTBP4	Isoform 2 of Latent-transforming growth factor beta-binding protein 4	0.06	0	7	0

EPHB2	Ephrin type-B receptor 2	0.06	0	5	0
TOR1AIP2	Torsin0A-interacting protein 2	0.06	0	3	0
NOL6	Nucleolar protein 6	0.06	0	3	0
JMJD4	Isoform 2 of JmjC domain-containing protein 4	0.06	0	13	0
TOR1AIP1	Torsin0A-interacting protein 1	0.06	0	2	0
IKBKAP	Elongator complex protein 1	0.06	0	4	0
NLK	Mitogen-activated protein kinase (Fragment)	0.06	0	6	0
EPHA5	EPH receptor A5	0.06	0	15	0
HMGCS1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	0.06	0	3	0
LYN	Isoform 2 of Tyrosine-protein kinase Lyn	0.06	0	2	0
KPNA7	Importin subunit alpha-8	0.06	0	5	0
OGT	Isoform 2 of UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	0.06	0	8	0
NUP107	Isoform 2 of Nuclear pore complex protein Nup107	0.06	0	2	0
CORO1A	Coronin0A	0.06	0	2	0
EMILIN2	EMILIN-2	0.06	0	10	0
SRSF4	Serine/arginine-rich splicing factor 4	0.06	0	3	0
ADPGK	Isoform 2 of ADP-dependent glucokinase	0.06	0	2	0
SPTLC1	Serine palmitoyltransferase 1	0.06	0	2	0
PTK7	Inactive tyrosine-protein kinase 7	0.06	0	2	0

PPP2R5D	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform (Fragment)	0.06	0	3	0
TRIP12	Isoform 2 of E3 ubiquitin-protein ligase TRIP12	0.07	0	19	0
PLXND1	Isoform 2 of Plexin-D1	0.07	0	9	0
IPO8	Isoform 2 of Importin-8	0.07	0	7	0
SNX6	Sorting nexin 6, isoform CRA_b	0.07	0	6	0
TRIP13	Pachytene checkpoint protein 2 homolog	0.07	0	3	0
CHST4	Carbohydrate sulfotransferase 4	0.07	0	5	0
COL26A1	Isoform 2 of Collagen alpha0(XXVI) chain	0.07	0	5	0
KRT35	Keratin, type I cuticular Ha5	0.07	0	11	0
PPM1F	Protein phosphatase 1F	0.07	0	5	0
tr I3L4J1 I3L4J1_HUMAN	Uncharacterized protein (Fragment)	0.07	0	12	0
BRAT1	BRCA1-associated ATM activator 1	0.07	0	2	0
FAM98B	Isoform 2 of Protein FAM98B	0.07	0	2	0
SYT1	Synaptotagmin I, isoform CRA_b	0.07	0	6	0
CPNE2	Isoform 2 of Copine-2	0.07	0	3	0
CDC5L	Cell division cycle 5-like protein	0.07	0	19	0
MCM8	Isoform 3 of DNA helicase MCM8	0.07	0	4	0
CPE	Isoform 2 of Carboxypeptidase E	0.07	0	2	0
BMP8A	Bone morphogenetic protein 8A	0.07	0	4	0
B4GALT5	Beta0,4-galactosyltransferase 5	0.07	0	4	0
SP9	Transcription factor Sp9	0.07	0	2	0

PHKG1	Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform	0.07	0	2	0
F9	Isoform 2 of Coagulation factor IX	0.07	0	3	0
LAMB2	Laminin subunit beta-2	0.08	0	23	0
PTRF	Polymerase I and transcript release factor	0.08	0	12	0
PRTG	Protogenin	0.08	0	15	0
A2ML1	Alpha-2-macroglobulin-like protein 1	0.08	0	13	0
HLA-C	HLA class I histocompatibility antigen, Cw-3 alpha chain	0.08	0	14	0
KIF11	Kinesin-like protein KIF11	0.08	0	10	0
TLL1	Metalloendopeptidase	0.08	0	12	0
LRP6	Low-density lipoprotein receptor-related protein 6 (Fragment)	0.08	0	7	0
NRP1	Neuropilin0	0.08	0	8	0
SH3GL2	Endophilin-A1	0.08	0	8	0
DEK	Protein DEK	0.08	0	5	0
VN1R5	Vomeroneasal type0 receptor 5	0.08	0	14	0
SERPINA1	Isoform 2 of Alpha0-antitrypsin	0.08	0	2	0
TBCC	Tubulin-specific chaperone C	0.08	0	2	0
TPST2	Protein-tyrosine sulfotransferase 2	0.08	0	4	0
ANTXR1	Isoform 2 of Anthrax toxin receptor 1	0.08	0	4	0
TP53	Cellular tumor antigen p53	0.08	0	3	0
TLN2	Talin-2 (Fragment)	0.09	0	30	0
CANX	Isoform 2 of Calnexin	0.09	0	10	0
WDR48	WD repeat-containing protein 48	0.09	0	5	0

WDR45B	WD repeat domain phosphoinositide-interacting protein 3	0.09	0	2	0
ASPRV1	Retroviral-like aspartic protease 1	0.09	0	3	0
SLC44A1	Isoform 2 of Choline transporter-like protein 1	0.09	0	7	0
C6orf58	UPF0762 protein C6orf58	0.09	0	3	0
SLC25A3	Phosphate carrier protein, mitochondrial	0.09	0	4	0
B3GALT6	Beta0,3-galactosyltransferase 6	0.09	0	2	0
TSKU	Tsukushin	0.09	0	4	0
GLB1L	Beta-galactosidase0-like protein	0.09	0	3	0
EFNB1	Ephrin-B1	0.09	0	2	0
FAHD2A	Fumarylacetoacetate hydrolase domain-containing protein 2A	0.09	0	3	0
SRSF6	Isoform SRP55-3 of Serine/arginine-rich splicing factor 6	0.09	0	3	0
OXCT1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	0.09	0	2	0
PIM1	Isoform 2 of Serine/threonine-protein kinase pim0	0.09	0	5	0
NF2	Isoform 2 of Merlin	0.09	0	4	0
RPL4	60S ribosomal protein L4	0.09	0	3	0
MSH2	DNA mismatch repair protein Msh2	0.1	0	9	0
ABCF1	ATP-binding cassette sub-family F member 1 (Fragment)	0.1	0	6	0
MCCC2	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (Fragment)	0.1	0	7	0

AMPD2	AMP deaminase 2 (Fragment)	0.1	0	20	0
SEZ6L2	Seizure 6-like protein 2	0.1	0	7	0
NOP56	Nucleolar protein 56	0.1	0	10	0
UBA6	Isoform 2 of Ubiquitin-like modifier-activating enzyme 6	0.1	0	9	0
PPM1B	Protein phosphatase 1B (Fragment)	0.1	0	4	0
POF1B	Isoform 1 of Protein POF1B	0.1	0	4	0
TBCE	Isoform 2 of Tubulin-specific chaperone E	0.1	0	3	0
RMDN1	Isoform 2 of Regulator of microtubule dynamics protein 1	0.1	0	4	0
NAA16	N-alpha-acetyltransferase 16, NatA auxiliary subunit	0.1	0	8	0
HSD17B12	Estradiol 17-beta-dehydrogenase 12	0.1	0	5	0
STOML2	Isoform 2 of Stomatin-like protein 2, mitochondrial	0.1	0	3	0
CYB5R3	Isoform 2 of NADH-cytochrome b5 reductase 3	0.1	0	3	0
KPRP	Keratinocyte proline-rich protein	0.1	0	7	0
ABHD11	Alpha/beta hydrolase domain-containing protein 11	0.1	0	6	0
CAB39L	Calcium-binding protein 39-like (Fragment)	0.1	0	4	0
RPRD1A	Isoform 2 of Regulation of nuclear pre-mRNA domain-containing protein 1A	0.1	0	3	0
MAP2K2	Dual-specificity mitogen-activated protein kinase kinase 2	0.1	0	6	0

KCTD15	BTB/POZ domain-containing protein KCTD15	0.1	0	2	0
PHOX2B	Paired mesoderm homeobox protein 2B	0.1	0	18	0
RNF212	Isoform 4 of Probable E3 SUMO-protein ligase RNF212	0.1	0	9	0
TGM1	Protein-glutamine gamma-glutamyltransferase K	0.11	0	8	0
GLCE	D-glucuronyl C5-epimerase	0.11	0	5	0
ITFG3	Protein ITFG3	0.11	0	7	0
DSG2	Desmoglein-2	0.11	0	12	0
RAP1GDS1	Isoform 2 of Rap1 GTPase-GDP dissociation stimulator 1	0.11	0	3	0
CHMP4A	Isoform 2 of Charged multivesicular body protein 4a	0.11	0	2	0
TSPAN9	Tetraspanin	0.11	0	6	0
tr H0YHG0 H0YHG0_HUMAN	Uncharacterized protein (Fragment)	0.11	0	7	0
ADAMTS13	A disintegrin and metalloproteinase with thrombospondin motifs 13	0.11	0	3	0
WDR18	WD repeat-containing protein 18 (Fragment)	0.11	0	4	0
GET4	Isoform 2 of Golgi to ER traffic protein 4 homolog	0.11	0	3	0
ARFGAP1	ADP-ribosylation factor GTPase-activating protein 1 (Fragment)	0.11	0	3	0
BAG3	BAG family molecular chaperone regulator 3	0.11	0	4	0

SRSF5	Isoform SRP40-4 of Serine/arginine-rich splicing factor 5	0.11	0	3	0
SRPRB	Signal recognition particle receptor subunit beta	0.11	0	3	0
KCTD21	BTB/POZ domain-containing protein KCTD21	0.11	0	4	0
UBE3B	Ubiquitin-protein ligase E3B	0.11	0	6	0
TCP11L2	T-complex 11 (Mouse) like 2, isoform CRA_c	0.11	0	6	0
KRT80	Isoform 3 of Keratin, type II cytoskeletal 80	0.12	0	28	0
L1CAM	Isoform 2 of Neural cell adhesion molecule L1	0.12	0	14	0
LPHN3	Latrophilin-3	0.12	0	18	0
CXCL16	C-X-C motif chemokine 16	0.12	0	11	0
SEMA3G	Semaphorin-3G	0.12	0	17	0
DIS3	Exosome complex exonuclease RRP44	0.12	0	18	0
THSD4	Thrombospondin type0 domain-containing protein 4	0.12	0	8	0
PUF60	Isoform 2 of Poly(U)-binding-splicing factor PUF60	0.12	0	7	0
UFL1	Isoform 2 of E3 UFM1-protein ligase 1	0.12	0	7	0
FURIN	Furin	0.12	0	8	0
FAM3A	Family with sequence similarity 3, member A, isoform CRA_c	0.12	0	3	0
SRRT	Serrate RNA effector molecule homolog (Fragment)	0.12	0	8	0

HSD17B11	Estradiol 17-beta-dehydrogenase 11	0.12	0	3	0
LUC7L3	Cisplatin resistance-associated overexpressed protein, isoform CRA_b	0.12	0	18	0
GLMN	Glomulin (Fragment)	0.12	0	3	0
FBXO22	F-box only protein 22 (Fragment)	0.12	0	2	0
CD151	Tetraspanin	0.12	0	4	0
GGPS1	Isoform 2 of Geranylgeranyl pyrophosphate synthase	0.12	0	3	0
RBBP5	Isoform 2 of Retinoblastoma-binding protein 5	0.12	0	7	0
TMED9	Transmembrane emp24 domain-containing protein 9	0.12	0	6	0
TMA16	Translation machinery-associated protein 16 (Fragment)	0.12	0	3	0
EIF2B5	Translation initiation factor eIF-2B subunit epsilon	0.13	0	11	0
TGM3	Protein-glutamine gamma-glutamyltransferase E	0.13	0	6	0
ATP2B4	Isoform XA of Plasma membrane calcium-transporting ATPase 4	0.13	0	13	0
MANEAL	Glycoprotein endo-alpha0,2-mannosidase-like protein	0.13	0	10	0
KRT37	Keratin, type I cuticular Ha7	0.13	0	11	0
VPS45	Vacuolar protein sorting-associated protein 45	0.13	0	4	0
TMEM33	Transmembrane protein 33 (Fragment)	0.13	0	2	0

B4GALNT1	Isoform 2 of Beta0,4 N-acetylgalactosaminyltransferase 1	0.13	0	4	0
PPA2	Inorganic pyrophosphatase 2, mitochondrial (Fragment)	0.13	0	3	0
ADAM9	ADAM9 protein	0.13	0	13	0
PYCR1	Pyrroline-5-carboxylate reductase (Fragment)	0.13	0	4	0
UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	0.13	0	2	0
VWA9	von Willebrand factor A domain-containing protein 9	0.13	0	2	0
MT-CO2	Cytochrome c oxidase subunit 2	0.13	0	4	0
SYPL1	Synaptophysin-like protein 1	0.13	0	6	0
GSTK1	Glutathione S-transferase kappa 1	0.13	0	5	0
LONP2	Lon protease homolog 2, peroxisomal (Fragment)	0.13	0	7	0
RABL3	Rab-like protein 3	0.13	0	4	0
DLG1	Isoform 2 of Disks large homolog 1	0.13	0	5	0
LYPLAL1	Lysophospholipase-like protein 1	0.13	0	4	0
CYFIP2	Cytoplasmic FMR1-interacting protein 2	0.14	0	20	0
CSTF1	Cleavage stimulation factor subunit 1	0.14	0	8	0
SMYD5	SET and MYND domain-containing protein 5	0.14	0	9	0
LIPG	Endothelial lipase	0.14	0	12	0
ATP6V1E1	V-type proton ATPase subunit E 1 (Fragment)	0.14	0	3	0
CLDN1	Claudin0	0.14	0	2	0

SDF2L1	Stromal cell-derived factor 2-like protein 1	0.14	0	2	0
POMGNT1	Protein O-linked-mannose beta0,2-N-acetylglucosaminyltransferase 1	0.14	0	10	0
PDGFA	Platelet-derived growth factor subunit A (Fragment)	0.14	0	2	0
AP3M1	AP-3 complex subunit mu0	0.14	0	6	0
BPIFB2	BPI fold-containing family B member 2	0.14	0	5	0
PACSN3	Protein kinase C and casein kinase substrate in neurons protein 3	0.14	0	4	0
WDR18	WD repeat-containing protein 18 (Fragment)	0.14	0	5	0
PRSS21	Testisin (Fragment)	0.14	0	5	0
PITHD1	Isoform 2 of PITH domain-containing protein 1	0.14	0	2	0
RAE1	mRNA export factor	0.14	0	3	0
GLMN	Isoform 2 of Glomulin	0.14	0	4	0
NBL1	Neuroblastoma suppressor of tumorigenicity 1	0.14	0	3	0
MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	0.14	0	3	0
AACS	Acetoacetyl-CoA synthetase	0.14	0	2	0
IL6ST	IL6ST nirs variant 3	0.14	0	3	0
PPP3CC	Serine/threonine-protein phosphatase (Fragment)	0.14	0	4	0
UBAC2	Ubiquitin-associated domain-containing protein 2 (Fragment)	0.14	0	9	0

MYH11	Myosin heavy chain 11 smooth muscle isoform	0.15	0	71	0
TLL2	Tolloid-like protein 2	0.15	0	33	0
RAB13	Ras-related protein Rab03	0.15	0	17	0
STK24	Serine/threonine-protein kinase 24	0.15	0	11	0
NCAPG	Condensin complex subunit 3	0.15	0	12	0
EIF2B3	Isoform 2 of Translation initiation factor eIF-2B subunit gamma	0.15	0	13	0
GNA13	Guanine nucleotide-binding protein subunit alpha03	0.15	0	8	0
PARVA	Alpha-parvin	0.15	0	6	0
RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	0.15	0	8	0
KLK5	Kallikrein-5 (Fragment)	0.15	0	3	0
LIF	Leukemia inhibitory factor	0.15	0	6	0
PLIN3	Isoform 4 of Perilipin-3	0.15	0	8	0
SLC7A1	High affinity cationic amino acid transporter 1	0.15	0	7	0
GYG1	Glycogenin 1, isoform CRA_e	0.15	0	9	0
SNRNP40	Isoform 2 of U5 small nuclear ribonucleoprotein 40 kDa protein	0.15	0	5	0
UFD1L	Ubiquitin fusion degradation protein 1 homolog (Fragment)	0.15	0	7	0
SERBP1	Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein	0.15	0	11	0
NSMF	NMDA receptor synaptonuclear-signaling and neuronal migration factor	0.15	0	15	0

CASP6	Isoform Beta of Caspase-6	0.15	0	2	0
KRT72	Keratin, type II cytoskeletal 72 (Fragment)	0.15	0	7	0
RAB9B	Ras-related protein Rab-9B	0.15	0	3	0
EFNA4	Isoform 2 of Ephrin-A4	0.15	0	2	0
ANK2	Ankyrin-2 (Fragment)	0.15	0	5	0
MGAT4B	Isoform 2 of Alpha0,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B	0.16	0	13	0
RAD50	Isoform 2 of DNA repair protein RAD50	0.16	0	19	0
CHST15	Carbohydrate sulfotransferase 15	0.16	0	12	0
MVD	Diphosphomevalonate decarboxylase	0.16	0	9	0
HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	0.16	0	13	0
PCYT1A	Choline-phosphate cytidyltransferase A	0.16	0	8	0
ACY1	Isoform 4 of Aminoacylase0	0.16	0	10	0
B3GNT9	UDP-GlcNAc:betaGal beta0,3-N-acetylglucosaminyltransferase 9	0.16	0	8	0
NLGN2	Neuroigin-2 (Fragment)	0.16	0	4	0
LCN15	Lipocalin05	0.16	0	3	0
ZNF207	BUB3-interacting and GLEBS motif-containing protein ZNF207 (Fragment)	0.16	0	2	0
EFNA1	Isoform 2 of Ephrin-A1	0.16	0	6	0
FCHO2	Isoform 2 of FCH domain only protein 2	0.16	0	5	0
ARMCX3	Armadillo repeat-containing X-linked protein 3	0.16	0	4	0

CAV1	Caveolin0	0.16	0	3	0
GDF11	Growth/differentiation factor 11 (Fragment)	0.16	0	3	0
C6orf120	UPF0669 protein C6orf120	0.16	0	2	0
PTGES2	Prostaglandin E synthase 2	0.16	0	3	0
NDEL1	Nuclear distribution protein nudE-like 1 (Fragment)	0.16	0	7	0
SMC4	Structural maintenance of chromosomes protein 4	0.17	0	21	0
PKP1	Plakophilin0	0.17	0	12	0
RTCA	Isoform 2 of RNA 3~-terminal phosphate cyclase	0.17	0	9	0
EML4	Isoform 2 of Echinoderm microtubule-associated protein-like 4	0.17	0	12	0
tr M0QYV0 M0QYV0_HUMAN	Uncharacterized protein (Fragment)	0.17	0	6	0
SEMA3B	Isoform 2 of Semaphorin-3B	0.17	0	16	0
MEGF8	Multiple epidermal growth factor-like domains protein 8 (Fragment)	0.17	0	3	0
FAM50A	Protein FAM50A	0.17	0	3	0
RP2	Protein XRP2	0.17	0	9	0
ARL2BP	ADP-ribosylation factor-like protein 2-binding protein (Fragment)	0.17	0	2	0
NCS1	Isoform 2 of Neuronal calcium sensor 1	0.17	0	3	0
CDC73	Parafibromin	0.17	0	9	0
PPOX	Protoporphyrinogen oxidase	0.17	0	3	0
CAPRIN1	Isoform 2 of Caprin0	0.18	0	41	0

ITGA3	Isoform 2 of Integrin alpha-3	0.18	0	19	0
DSG1	Desmoglein0	0.18	0	15	0
SYMPK	Symplekin	0.18	0	15	0
DNAJC3	DnaJ homolog subfamily C member 3	0.18	0	12	0
LMAN1	Protein ERGIC-53	0.18	0	8	0
MYOF	Isoform 3 of Myoferlin	0.18	0	27	0
TF	Serotransferrin	0.18	0	15	0
ZYX	Zyxin (Fragment)	0.18	0	8	0
ABHD14A-ACY1	Protein ABHD14A-ACY1	0.18	0	11	0
SEMA7A	Semaphorin-7A	0.18	0	8	0
ST3GAL4	Isoform 2 of CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 4	0.18	0	8	0
FAM198B	Isoform 2 of Protein FAM198B	0.18	0	11	0
DAK	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	0.18	0	7	0
TOR3A	Isoform 2 of Torsin-3A	0.18	0	7	0
RABGGTB	Geranylgeranyl transferase type-2 subunit beta	0.18	0	4	0
EVA1B	Protein eva0 homolog B	0.18	0	2	0
GPD1L	Glycerol-3-phosphate dehydrogenase 1-like protein	0.18	0	3	0
GMPR2	GMP reductase	0.18	0	6	0
GIT1	ARF GTPase-activating protein GIT1 (Fragment)	0.18	0	10	0

TRAP1	Isoform 2 of Heat shock protein 75 kDa, mitochondrial	0.19	0	28	0
ADAMTS7	A disintegrin and metalloproteinase with thrombospondin motifs 7	0.19	0	24	0
ARG1	Isoform 2 of Arginase0	0.19	0	13	0
ITGAV	Isoform 3 of Integrin alpha-V	0.19	0	17	0
HSPA14	Heat shock 70 kDa protein 14	0.19	0	7	0
CEP55	Centrosomal protein of 55 kDa	0.19	0	12	0
LCN1P1	Putative lipocalin 1-like protein 1	0.19	0	3	0
PWP1	Periodic tryptophan protein 1 homolog	0.19	0	7	0
TRMT6	Isoform 4 of tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	0.19	0	9	0
DCTN3	Dynactin subunit 3 (Fragment)	0.19	0	3	0
RAB34	Ras-related protein Rab-34, isoform NARR (Fragment)	0.19	0	2	0
PTP4A1	Protein tyrosine phosphatase type IVA 1	0.19	0	2	0
SMARCA1	Probable global transcription activator SNF2L1	0.2	0	19	0
NTN1	Netrin0	0.2	0	9	0
CD276	Isoform 3 of CD276 antigen	0.2	0	7	0
POSTN	Isoform 2 of Periostin	0.2	0	11	0
NUP88	Nuclear pore complex protein Nup88 (Fragment)	0.2	0	5	0
GOLPH3	Golgi phosphoprotein 3	0.2	0	5	0
AGA	N(4)-(beta-N-acetylglucosaminy)-L-asparaginase (Fragment)	0.2	0	3	0

UPP1	Uridine phosphorylase 1	0.2	0	3	0
STX4	Isoform 2 of Syntaxin-4	0.2	0	6	0
SLC44A2	Choline transporter-like protein 2 (Fragment)	0.2	0	2	0
POLR2J3	DNA-directed RNA polymerase II subunit RPB11-b2	0.2	0	3	0
ATP6AP1	V-type proton ATPase subunit S1	0.2	0	6	0
CALML3	Calmodulin-like protein 3	0.2	0	2	0
RRM2	Ribonucleoside-diphosphate reductase subunit M2 (Fragment)	0.2	0	10	0
SRSF1	Serine/arginine-rich-splicing factor 1 (Fragment)	0.2	0	4	0
AOC3	Membrane primary amine oxidase (Fragment)	0.2	0	4	0
PIN4	Isoform 2 of Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	0.2	0	3	0
SCPEP1	Retinoid-inducible serine carboxypeptidase	0.21	0	20	0
CARHSP1	Calcium-regulated heat stable protein 1	0.21	0	3	0
NDST2	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 2	0.21	0	9	0
MMS19	MMS19 nucleotide excision repair protein homolog (Fragment)	0.21	0	6	0
ATP5C1	Isoform Heart of ATP synthase subunit gamma, mitochondrial	0.21	0	3	0
NUCB2	Nucleobindin 2, isoform CRA_b	0.21	0	7	0
LACTB2	Beta-lactamase-like protein 2	0.21	0	6	0

FBL	rRNA 2~-O-methyltransferase fibrillar	0.21	0	4	0
UBE2C	Isoform 2 of Ubiquitin-conjugating enzyme E2 C	0.21	0	4	0
SECTM1	Secreted and transmembrane protein 1 (Fragment)	0.21	0	2	0
UBQLN1	Ubiquilin0 (Fragment)	0.21	0	2	0
CLTCL1	Clathrin heavy chain 2	0.22	0	61	0
MAN2A2	Isoform 1 of Alpha-mannosidase 2x	0.22	0	40	0
CPNE8	Copine-8	0.22	0	14	0
SEMA4D	Semaphorin-4D	0.22	0	21	0
NHP2	H/ACA ribonucleoprotein complex subunit 2 (Fragment)	0.22	0	4	0
SMAP1	Isoform 2 of Stromal membrane-associated protein 1	0.22	0	11	0
EDF1	Isoform 2 of Endothelial differentiation-related factor 1	0.22	0	2	0
POP7	Ribonuclease P protein subunit p20 (Fragment)	0.22	0	2	0
JAG1	Protein jagged0	0.23	0	51	0
DMBT1	Isoform 4 of Deleted in malignant brain tumors 1 protein	0.23	0	34	0
SLC39A10	Zinc transporter ZIP10	0.23	0	35	0
GPLD1	Phosphatidylinositol-glycan-specific phospholipase D	0.23	0	15	0
GCNT2	N-acetylglucosaminide beta0,6-N-acetylglucosaminyl-transferase, isoform C	0.23	0	15	0

FAM20B	Glycosaminoglycan xylosylkinase	0.23	0	8	0
XPNPEP1	Xaa-Pro aminopeptidase 1	0.23	0	21	0
MRPL49	39S ribosomal protein L49, mitochondrial (Fragment)	0.23	0	2	0
KLK10	Kallikrein00	0.23	0	4	0
FUOM	Isoform 2 of Fucose mutarotase	0.23	0	3	0
CHRD	Chordin	0.24	0	21	0
ADAM15	Isoform 12 of Disintegrin and metalloproteinase domain-containing protein 15	0.24	0	19	0
MPZL1	Isoform 2 of Myelin protein zero-like protein 1	0.24	0	13	0
BAP18	Isoform 2 of Chromatin complexes subunit BAP18	0.24	0	2	0
B4GALT2	Isoform 3 of Beta0,4-galactosyltransferase 2	0.24	0	6	0
GALNT7	N-acetylgalactosaminyltransferase 7	0.24	0	12	0
FBLN7	Isoform 2 of Fibulin-7	0.24	0	7	0
DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	0.24	0	4	0
CASP14	Caspase04	0.25	0	6	0
SERPINI1	Neuroserpin (Fragment)	0.25	0	5	0
MAN1A2	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB	0.25	0	10	0
RAD23B	UV excision repair protein RAD23 homolog B	0.25	0	5	0
DYNLRB2	Dynein light chain roadblock-type 2	0.25	0	2	0

sp P01768 HV307_HUMAN	Ig heavy chain V-III region CAM	0.25	0	7	0
PCBD2	Pterin-4-alpha-carbinolamine dehydratase 2 (Fragment)	0.25	0	3	0
ADTRP	Androgen-dependent TFPI-regulating protein (Fragment)	0.25	0	2	0
ADAMTSL1	ADAMTS-like protein 1	0.26	0	93	0
TMEM132A	Isoform 2 of Transmembrane protein 132A	0.26	0	24	0
IQCA1	IQ and AAA domain-containing protein 1	0.26	0	23	0
HP	Haptoglobin (Fragment)	0.26	0	10	0
CHMP6	Charged multivesicular body protein 6 (Fragment)	0.26	0	2	0
IGKV2D-28	Protein IGKV2-28 (Fragment)	0.26	0	3	0
SLC16A1	Monocarboxylate transporter 1	0.26	0	6	0
PPID	Peptidyl-prolyl cis-trans isomerase D	0.26	0	8	0
FGF5	Isoform Short of Fibroblast growth factor 5	0.26	0	18	0
EIF4E2	Eukaryotic translation initiation factor 4E type 2	0.26	0	3	0
FNTA	Farnesyltransferase, CAAX box, alpha, isoform CRA_c	0.26	0	5	0
COPB2	Coatomer subunit beta~ (Fragment)	0.26	0	4	0
GSTT1	Glutathione S-transferase theta0	0.26	0	5	0
PCDHGC3	Isoform 2 of Protocadherin gamma-C3	0.27	0	14	0
TRIP10	Cdc42-interacting protein 4	0.27	0	11	0
C1RL	Complement C1r subcomponent-like protein	0.27	0	14	0

SDF4	Isoform 6 of 45 kDa calcium-binding protein	0.27	0	11	0
BTC	Probetacellulin (Fragment)	0.27	0	3	0
sp P01625 KV402_HUMAN	Ig kappa chain V-IV region Len	0.27	0	3	0
ADI1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (Fragment)	0.27	0	3	0
ENAH	Isoform 2 of Protein enabled homolog	0.28	0	12	0
RAB32	Ras-related protein Rab-32	0.28	0	5	0
APOH	Beta-2-glycoprotein 1 (Fragment)	0.28	0	5	0
AK4	Adenylate kinase 4, mitochondrial	0.28	0	4	0
COMT	Catechol O-methyltransferase (Fragment)	0.28	0	2	0
sp P01767 HV306_HUMAN	Ig heavy chain V-III region BUT	0.28	0	2	0
CUL4A	Cullin-4A	0.29	0	24	0
PSMD9	26S proteasome non-ATPase regulatory subunit 9	0.29	0	9	0
OVCA2	Ovarian cancer-associated gene 2 protein	0.29	0	4	0
RPL13A	60S ribosomal protein L13a (Fragment)	0.29	0	7	0
LAMA5	Laminin subunit alpha-5	0.3	0	110	0
FJX1	Four-jointed box protein 1	0.3	0	17	0
HS6ST1	Heparan-sulfate 6-O-sulfotransferase 1	0.3	0	10	0
TPD52L2	Tumor protein D54	0.3	0	4	0
TMEM14C	Transmembrane protein 14C	0.3	0	2	0

TMED4	Isoform 2 of Transmembrane emp24 domain-containing protein 4	0.3	0	9	0
KRT73	Keratin, type II cytoskeletal 73	0.31	0	52	0
CFH	Complement factor H	0.31	0	28	0
TOR4A	Torsin-4A	0.31	0	8	0
LRP11	Low-density lipoprotein receptor-related protein 11	0.31	0	8	0
TATDN1	Putative deoxyribonuclease TATDN1 (Fragment)	0.31	0	5	0
SERPINA3	Alpha0-antichymotrypsin	0.31	0	8	0
SLC35A4	Alternative protein SLC35A4	0.31	0	2	0
TMPO	Thymopentin	0.32	0	21	0
EPHB4	Isoform 2 of Ephrin type-B receptor 4	0.32	0	20	0
GNPTG	N-acetylglucosamine0-phosphotransferase subunit gamma	0.32	0	12	0
CBFB	Isoform 2 of Core-binding factor subunit beta	0.32	0	4	0
ZG16B	Zymogen granule protein 16 homolog B	0.32	0	8	0
HPCA	Neuron-specific calcium-binding protein hippocalcin	0.32	0	5	0
PPME1	Isoform 2 of Protein phosphatase methylesterase 1	0.32	0	7	0
PRKAG1	5~-AMP-activated protein kinase subunit gamma0 (Fragment)	0.32	0	3	0
BTF3L4	Isoform 2 of Transcription factor BTF3 homolog 4	0.32	0	2	0

sp P01621 KV303_HUMAN	Ig kappa chain V-III region NG9 (Fragment)	0.32	0	3	0
KTN1	Kinectin (Fragment)	0.32	0	2	0
EGFR	Epidermal growth factor receptor	0.33	0	58	0
FAM20C	Extracellular serine/threonine protein kinase FAM20C	0.33	0	9	0
DCTN2	Isoform 2 of Dynactin subunit 2	0.33	0	15	0
KRAS	Isoform 2B of GTPase KRas	0.33	0	6	0
SDC1	Syndecan0 (Fragment)	0.33	0	5	0
HSPG2	Endorepellin (Fragment)	0.33	0	5	0
RPL9	60S ribosomal protein L9 (Fragment)	0.33	0	2	0
DDX19B	ATP-dependent RNA helicase DDX19B	0.34	0	15	0
SCARB1	SCARB1 protein	0.34	0	10	0
EPDR1	Isoform 2 of Mammalian ependymin-related protein 1	0.34	0	4	0
TWSG1	Twisted gastrulation protein homolog 1	0.34	0	6	0
SCGB1D2	Secretoglobin family 1D member 2	0.34	0	3	0
GSTZ1	Maleylacetoacetate isomerase	0.34	0	3	0
APMAP	Isoform 2 of Adipocyte plasma membrane-associated protein	0.34	0	4	0
Sep 09	Isoform 2 of Septin-9	0.35	0	25	0
NPEPL1	Isoform 4 of Probable aminopeptidase NPEPL1	0.35	0	11	0
PTPN11	Isoform 3 of Tyrosine-protein phosphatase non-receptor type 11	0.35	0	11	0

COMMD3	COMM domain-containing protein 3 (Fragment)	0.35	0	5	0
CDV3	Protein CDV3 homolog (Fragment)	0.35	0	8	0
VPS25	Vacuolar protein-sorting-associated protein 25	0.35	0	3	0
UBL4A	Ubiquitin-like protein 4A	0.35	0	4	0
C1R	Complement C1r subcomponent	0.36	0	21	0
HLA-C	HLA class I histocompatibility antigen, Cw07 alpha chain	0.36	0	31	0
NCCRP1	F-box only protein 50	0.36	0	8	0
PDLIM7	PDZ and LIM domain protein 7 (Fragment)	0.36	0	4	0
VDAC3	Isoform 2 of Voltage-dependent anion-selective channel protein 3	0.36	0	9	0
SFPQ	Splicing factor, proline- and glutamine-rich (Fragment)	0.36	0	3	0
CTH	Isoform 2 of Cystathionine gamma-lyase	0.37	0	25	0
ABHD14A	Alpha/beta hydrolase domain-containing protein 14A	0.37	0	9	0
LIN7A	Protein lin-7 homolog A (Fragment)	0.37	0	6	0
HS6ST1	Isoform 2 of Heparan-sulfate 6-O-sulfotransferase 1	0.37	0	7	0
HTATIP2	Isoform 3 of Oxidoreductase HTATIP2	0.37	0	6	0
CNN2	Calponin (Fragment)	0.37	0	5	0
RFC2	Replication factor C subunit 2 (Fragment)	0.37	0	4	0

PSMD9	26S proteasome non-ATPase regulatory subunit 9	0.37	0	3	0
SHH	Sonic hedgehog protein	0.38	0	12	0
VPS4B	Vacuolar protein sorting-associated protein 4B	0.38	0	17	0
DNAJC7	DnaJ homolog subfamily C member 7	0.38	0	6	0
SSR4	Translocon-associated protein subunit delta	0.38	0	3	0
ARCN1	Coatomer subunit delta	0.38	0	3	0
MCM5	DNA replication licensing factor MCM5	0.39	0	29	0
SAE1	SUMO-activating enzyme subunit 1	0.39	0	14	0
UGDH	Isoform 2 of UDP-glucose 6-dehydrogenase	0.39	0	20	0
LGALS8	Galectin (Fragment)	0.39	0	7	0
KRT72	Keratin, type II cytoskeletal 72	0.4	0	57	0
IGJ	Immunoglobulin J chain (Fragment)	0.4	0	11	0
CCNH	Cyclin-H	0.4	0	11	0
ULBP2	NKG2D ligand 2	0.4	0	8	0
UXT	Protein UXT	0.4	0	4	0
CFD	Complement factor D	0.4	0	8	0
RHEB	GTP-binding protein Rheb	0.4	0	2	0
RPL8	60S ribosomal protein L8	0.4	0	5	0
TPP2	Tripeptidyl-peptidase 2	0.41	0	45	0
MENT	Protein MENT	0.41	0	12	0
ARRDC1	Arrestin domain-containing protein 1	0.41	0	27	0
NAGK	N-acetyl-D-glucosamine kinase	0.41	0	8	0

CDV3	Protein CDV3 homolog	0.41	0	10	0
MTIF2	Translation initiation factor IF-2, mitochondrial (Fragment)	0.41	0	2	0
RWDD1	RWD domain-containing protein 1 (Fragment)	0.41	0	2	0
EMG1	Ribosomal RNA small subunit methyltransferase NEP1	0.42	0	20	0
IGFBP2	Insulin-like growth factor-binding protein 2	0.42	0	9	0
USP39	U4/U6.U5 tri-snRNP-associated protein 2	0.43	0	48	0
ARCN1	Archain 1, isoform CRA_a	0.43	0	21	0
ERAP1	Endoplasmic reticulum aminopeptidase 1 (Fragment)	0.43	0	10	0
GOLT1B	Golgi transport 1 homolog B (S. cerevisiae), isoform CRA_c	0.43	0	2	0
PRR4	Proline-rich protein 4	0.44	0	6	0
PIP	Prolactin-inducible protein	0.44	0	10	0
AZGP1	Zinc-alpha-2-glycoprotein	0.45	0	10	0
CRIM1	Processed cysteine-rich motor neuron 1 protein (Fragment)	0.45	0	13	0
EIF4H	Isoform Short of Eukaryotic translation initiation factor 4H	0.45	0	7	0
RPS14	40S ribosomal protein S14	0.45	0	5	0
AIDA	Isoform 2 of Axin interactor, dorsalization-associated protein	0.45	0	4	0

PABPC4	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e	0.46	0	77	0
LTBP3	Latent-transforming growth factor beta-binding protein 3	0.46	0	121	0
SEC24C	Protein transport protein Sec24C	0.46	0	76	0
BCCIP	Isoform 3 of BRCA2 and CDKN1A-interacting protein	0.46	0	22	0
MVB12A	Isoform 2 of Multivesicular body subunit 12A	0.46	0	9	0
TPRKB	Isoform 2 of EKC/KEOPS complex subunit TPRKB	0.46	0	3	0
VAPA	Isoform 2 of Vesicle-associated membrane protein-associated protein A	0.47	0	8	0
GALNT11	Polypeptide N-acetylgalactosaminyltransferase 11 (Fragment)	0.47	0	3	0
C12orf49	UPF0454 protein C12orf49	0.47	0	9	0
LTBP3	Isoform 2 of Latent-transforming growth factor beta-binding protein 3	0.48	0	117	0
PVR	Isoform Beta of Poliovirus receptor	0.48	0	18	0
MTHFD2	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	0.48	0	7	0
ISG15	Ubiquitin-like protein ISG15 (Fragment)	0.48	0	4	0
S100A2	Protein S100-A2	0.48	0	2	0
ISYNA1	Isoform 2 of Inositol-3-phosphate synthase 1	0.49	0	44	0

CSF1	Macrophage colony-stimulating factor 1 (Fragment)	0.49	0	17	0
APLP1	Amyloid-like protein 1	0.49	0	32	0
PABPC4	Polyadenylate-binding protein 4 (Fragment)	0.49	0	7	0
LFNG	Isoform 3 of Beta0,3-N-acetylglucosaminyltransferase lunatic fringe	0.49	0	15	0
RPS2	40S ribosomal protein S2	0.49	0	14	0
TRMT61A	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	0.49	0	6	0
GALNT7	N-acetylgalactosaminyltransferase 7 (Fragment)	0.49	0	9	0
SCP2	Isoform SCP2 of Non-specific lipid-transfer protein	0.49	0	3	0
CRLF1	Cytokine receptor-like factor 1	0.5	0	42	0
RCN1	Reticulocalbin0	0.5	0	27	0
OAF	Out at first protein homolog	0.5	0	22	0
PPP1R7	Protein phosphatase 1 regulatory subunit 7	0.5	0	12	0
ST6GAL1	Beta-galactoside alpha-2,6-sialyltransferase 1	0.5	0	24	0
RAB18	Ras-related protein Rab08	0.5	0	8	0
PVRL2	Nectin-2 (Fragment)	0.5	0	4	0
GFAP	Glial fibrillary acidic protein (Fragment)	0.5	0	2	0
TNPO3	Isoform 1 of Transportin-3	0.51	0	52	0

VDAC2	Voltage-dependent anion-selective channel protein 2 (Fragment)	0.51	0	9	0
TOLLIP	Toll-interacting protein	0.51	0	9	0
TAGLN	Transgelin	0.51	0	7	0
OLFML2A	Isoform 2 of Olfactomedin-like protein 2A	0.52	0	56	0
GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment)	0.52	0	31	0
ADAM17	ADAM17 protein	0.52	0	12	0
TNC	Tenascin	0.54	0	83	0
B4GALT3	Beta0,4-galactosyltransferase 3	0.54	0	21	0
BPNT1	Isoform 4 of 3~(2~),5~-bisphosphate nucleotidase 1	0.54	0	14	0
DCTD	Isoform 2 of Deoxycytidylate deaminase	0.54	0	8	0
NRAS	GTPase NRas	0.54	0	9	0
RRAGA	Ras-related GTP-binding protein A	0.54	0	12	0
CHP1	Calcineurin B homologous protein 1	0.54	0	4	0
QARS	Isoform 2 of Glutamine--tRNA ligase	0.55	0	44	0
TYMS	Thymidylate synthase	0.55	0	10	0
RPP14	Ribonuclease P protein subunit p14	0.55	0	3	0
LSM4	U6 snRNA-associated Sm-like protein LSM4	0.55	0	5	0
ARL2BP	ADP-ribosylation factor-like protein 2-binding protein	0.55	0	3	0
YBX1	Nuclease-sensitive element-binding protein 1	0.56	0	32	0

RPP30	Isoform 2 of Ribonuclease P protein subunit p30	0.56	0	15	0
HNRNPR	Isoform 2 of Heterogeneous nuclear ribonucleoprotein R	0.57	0	104	0
PDAP1	28 kDa heat- and acid-stable phosphoprotein	0.57	0	8	0
SERPINB12	Isoform 2 of Serpin B12	0.58	0	18	0
QPCT	Glutaminy-peptide cyclotransferase	0.59	0	26	0
PPCS	Phosphopantothenate--cysteine ligase	0.59	0	12	0
SNX12	Sorting nexin02	0.59	0	13	0
IGHV3OR1603	Protein IGHV3OR1603 (Fragment)	0.59	0	6	0
STAT3	Isoform Del-701 of Signal transducer and activator of transcription 3	0.6	0	35	0
ST3GAL2	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 2	0.6	0	18	0
EFHD2	EF-hand domain-containing protein D2	0.6	0	12	0
HNRNPM	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	0.61	0	52	0
PDGFC	Platelet-derived growth factor C	0.61	0	15	0
AP1B1	AP0 complex subunit beta0 (Fragment)	0.61	0	20	0
NOMO1	Nodal modulator 1	0.62	0	80	0
GCNT2	N-acetyllactosaminide beta0,6-N-acetylglucosaminyl-transferase, isoform A	0.62	0	42	0
CDK2	Cyclin-dependent kinase 2	0.62	0	15	0

MGAT2	Alpha0,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	0.63	0	34	0
VPS28	Vacuolar protein sorting-associated protein 28 homolog	0.63	0	11	0
RPL18	60S ribosomal protein L18 (Fragment)	0.63	0	12	0
IGLV1-47	Protein IGLV1-47 (Fragment)	0.63	0	6	0
MTPN	Myotrophin	0.63	0	3	0
ACOT13	Isoform 2 of Acyl-coenzyme A thioesterase 13	0.63	0	3	0
C1S	Complement C1s subcomponent	0.64	0	42	0
NOMO2	Isoform 2 of Nodal modulator 2	0.65	0	84	0
DIAPH1	Protein diaphanous homolog 1	0.65	0	82	0
XRN2	5~-3~ exoribonuclease 2	0.65	0	81	0
KRT78	Keratin, type II cytoskeletal 78	0.65	0	30	0
MEMO1	Isoform 2 of Protein MEMO1	0.65	0	10	0
CYR61	Protein CYR61	0.66	0	33	0
NDST1	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	0.66	0	42	0
sp P80748 LV302_HUMAN	Ig lambda chain V-III region LOI	0.66	0	6	0
S100A14	Protein S100-A14	0.66	0	6	0
RRAS2	Isoform 4 of Ras-related protein R-Ras2	0.67	0	12	0
FEN1	Flap endonuclease 1	0.68	0	26	0
MMP11	Stromelysin-3	0.69	0	56	0
TPST1	Protein-tyrosine sulfotransferase 1	0.69	0	17	0
RPL26	60S ribosomal protein L26 (Fragment)	0.69	0	9	0
XYLT2	Xylosyltransferase 2	0.7	0	83	0

IGHM	Ig mu chain C region	0.7	0	29	0
RTCA	RNA 3~-terminal phosphate cyclase	0.7	0	4	0
OSGEP	O-sialoglycoprotein endopeptidase, isoform CRA_b	0.7	0	4	0
SLC39A14	Zinc transporter ZIP14 (Fragment)	0.71	0	10	0
SDF2	Stromal cell-derived factor 2	0.71	0	10	0
IGHM	Ig mu chain C region	0.72	0	28	0
PLEC	Isoform 8 of Plectin	0.73	0	341	0
RPL18A	60S ribosomal protein L18a (Fragment)	0.73	0	10	0
CYSTM1	Cysteine-rich and transmembrane domain-containing protein 1	0.73	0	5	0
PRKACA	Isoform 2 of cAMP-dependent protein kinase catalytic subunit alpha	0.74	0	14	0
IFI30	Gamma-interferon-inducible lysosomal thiol reductase	0.74	0	15	0
DCUN1D1	DCN1-like protein (Fragment)	0.75	0	5	0
TRIM28	Transcription intermediary factor 1-beta	0.77	0	88	0
ADAMTSL1	Isoform 2 of ADAMTS-like protein 1	0.77	0	58	0
GSTT2	Glutathione S-transferase theta-2	0.77	0	9	0
IGKV1-27	Protein IGKV1-27	0.77	0	5	0
ECI1	Enoyl-CoA delta isomerase 1, mitochondrial	0.78	0	15	0
ECHDC1	Isoform 5 of Ethylmalonyl-CoA decarboxylase	0.78	0	11	0
PPIH	Peptidyl-prolyl cis-trans isomerase (Fragment)	0.78	0	5	0

SCG2	Secretogranin-2	0.8	0	67	0
HEBP1	Heme-binding protein 1	0.8	0	13	0
LYPLA1	Acyl-protein thioesterase 1 (Fragment)	0.8	0	14	0
CSNK1A1	Isoform 3 of Casein kinase I isoform alpha	0.8	0	18	0
DTYMK	Isoform 2 of Thymidylate kinase	0.8	0	13	0
UXS1	Isoform 2 of UDP-glucuronic acid decarboxylase 1	0.81	0	69	0
SPTBN1	Spectrin beta chain, non-erythrocytic 1	0.82	0	219	0
METAP2	Methionine aminopeptidase 2	0.82	0	31	0
CTSH	Pro-cathepsin H	0.83	0	36	0
C1GALT1C1	C1GALT1-specific chaperone 1	0.83	0	30	0
GRB2	Isoform 2 of Growth factor receptor-bound protein 2	0.83	0	11	0
PFAS	Phosphoribosylformylglycinamide synthase (Fragment)	0.84	0	31	0
DCXR	L-xylulose reductase (Fragment)	0.84	0	11	0
NUDT1	Isoform p22 of 7,8-dihydro-8-oxoguanine triphosphatase	0.84	0	8	0
API5	Isoform 2 of Apoptosis inhibitor 5	0.85	0	66	0
IGKC	Ig kappa chain C region	0.85	0	37	0
RPL14	60S ribosomal protein L14	0.87	0	9	0
DNAJC8	DnaJ homolog subfamily C member 8	0.88	0	16	0
RPS4X	40S ribosomal protein S4, X isoform	0.88	0	20	0
Sep 07	Septin 7, isoform CRA_a	0.89	0	72	0

VPS37B	Vacuolar protein sorting-associated protein 37B (Fragment)	0.89	0	17	0
METRNL	Meteorin-like protein	0.89	0	13	0
COPS8	COP9 signalosome complex subunit 8	0.9	0	15	0
METTL1	tRNA (guanine-N(7)-)-methyltransferase (Fragment)	0.9	0	4	0
SNAP23	Synaptosomal-associated protein (Fragment)	0.91	0	6	0
CLSTN3	Isoform 2 of Calsyntenin-3	0.92	0	116	0
SETSIP	Protein SETSIP	0.93	0	88	0
NAPA	Alpha-soluble NSF attachment protein	0.93	0	20	0
RAB5B	Ras-related protein Rab-5B	0.93	0	13	0
SKP1	S-phase kinase-associated protein 1	0.93	0	12	0
GNS	N-acetylglucosamine-6-sulfatase	0.94	0	90	0
GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta0	0.94	0	29	0
ATP5O	ATP synthase subunit O, mitochondrial	0.95	0	12	0
SLC25A6	ADP/ATP translocase 3	0.95	0	30	0
MATN2	Isoform 3 of Matrilin-2	0.96	0	125	0
COL6A2	Collagen alpha-2(VI) chain	0.97	0	147	0
KRT76	Keratin, type II cytoskeletal 2 oral	0.97	0	113	0
CRTAP	Cartilage-associated protein	0.97	0	53	0
RPL18A	60S ribosomal protein L18a	0.97	0	11	0
SUPT4H1	Transcription elongation factor SPT4	0.97	0	7	0
PPIL1	Peptidyl-prolyl cis-trans isomerase-like 1	0.97	0	5	0

ATP1B3	Sodium/potassium-transporting ATPase subunit beta-3	1	0	28	0
RPS5	40S ribosomal protein S5 (Fragment)	1	0	11	0
VSTM2L	V-set and transmembrane domain-containing protein 2-like protein	1	0	15	0
LANCL1	LanC-like protein 1 (Fragment)	1.01	0	15	0
NUDT16	Isoform 3 of U8 snoRNA-decapping enzyme	1.01	0	7	0
CMPK1	UMP-CMP kinase	1.01	0	11	0
AP1B1	Isoform C of AP0 complex subunit beta0	1.03	0	113	0
PPP6C	Serine/threonine-protein phosphatase 6 catalytic subunit	1.03	0	23	0
PFDN5	Prefoldin subunit 5 (Fragment)	1.04	0	8	0
ENO3	Isoform 2 of Beta-enolase	1.05	0	241	0
EIF3H	Eukaryotic translation initiation factor 3 subunit H	1.05	0	49	0
PIGR	Polymeric immunoglobulin receptor	1.06	0	68	0
CHST12	Carbohydrate sulfotransferase 12	1.06	0	41	0
ECM1	Extracellular matrix protein 1	1.06	0	56	0
IGKV1-8	Protein IGKV1-8	1.07	0	37	0
IGKV301	Protein IGKV301	1.07	0	37	0
PTPRS	Isoform 2 of Receptor-type tyrosine-protein phosphatase S	1.1	0	318	0
CDK1	Cyclin-dependent kinase 1	1.1	0	22	0
BPIFA1	Isoform 2 of BPI fold-containing family A member 1	1.1	0	21	0

C1QL4	Complement C1q-like protein 4	1.12	0	20	0
CHST7	Carbohydrate sulfotransferase 7	1.13	0	75	0
AARS	Isoform 2 of Alanine--tRNA ligase, cytoplasmic	1.14	0	179	0
PHB2	Prohibitin-2	1.14	0	17	0
sp P01623 KV305_HUMAN	Ig kappa chain V-III region WOL	1.14	0	8	0
SLC25A5	ADP/ATP translocase 2	1.15	0	31	0
RAB11B	Ras-related protein Rab01B	1.15	0	28	0
RPS8	40S ribosomal protein S8	1.16	0	26	0
GM2A	Ganglioside GM2 activator (Fragment)	1.17	0	16	0
NTS	Neurotensin/neuromedin N	1.18	0	11	0
HNRNPCL4	Heterogeneous nuclear ribonucleoprotein C-like 4	1.19	0	72	0
PLEC	Plectin (Fragment)	1.2	0	15	0
ANXA4	Annexin A4	1.21	0	24	0
PPP2CB	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	1.21	0	29	0
MRT04	mRNA turnover protein 4 homolog	1.22	0	23	0
ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family member E	1.27	0	36	0
LMNB1	Lamin-B1	1.27	0	48	0
CRK	Isoform Crk-I of Adapter molecule crk	1.27	0	24	0
RPL5	60S ribosomal protein L5	1.28	0	37	0
HTRA1	Serine protease HTRA1	1.36	0	60	0
FKBP3	Peptidyl-prolyl cis-trans isomerase FKBP3	1.39	0	36	0

GLUD2	Glutamate dehydrogenase 2, mitochondrial	1.42	0	129	0
EIF3K	Isoform 2 of Eukaryotic translation initiation factor 3 subunit K	1.43	0	19	0
LYZ	Lysozyme C	1.48	0	48	0
GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	1.5	0	42	0
PABPC1	Polyadenylate-binding protein 1	1.53	0	174	0
ENTPD6	Isoform 2 of Ectonucleoside triphosphate diphosphohydrolase 6	1.54	0	77	0
IGHA2	Ig alpha-2 chain C region	1.55	0	52	0
MFGE8	Lactadherin	1.57	0	56	0
EIF3J	Isoform 3 of Eukaryotic translation initiation factor 3 subunit J	1.58	0	23	0
PROS1	Vitamin K-dependent protein S	1.61	0	100	0
MAN2B2	Epididymis-specific alpha-mannosidase	1.61	0	122	0
CALML5	Calmodulin-like protein 5	1.63	0	14	0
YKT6	Isoform 2 of Synaptobrevin homolog YKT6	1.7	0	13	0
HLA-A	HLA class I histocompatibility antigen, A-69 alpha chain	1.73	0	96	0
ATP5A1	ATP synthase subunit alpha, mitochondrial	1.76	0	55	0
VDAC1	Voltage-dependent anion-selective channel protein 1	1.78	0	22	0
RBBP7	Isoform 2 of Histone-binding protein RBBP7	1.8	0	102	0

RBBP4	Isoform 3 of Histone-binding protein RBBP4	1.8	0	100	0
GABARAP	GABARAP-a	1.81	0	7	0
PHB	Prohibitin (Fragment)	1.86	0	33	0
PSMA8	Isoform 2 of Proteasome subunit alpha type-7-like	1.87	0	71	0
IGHA1	Ig alpha0 chain C region	1.92	0	68	0
HEXA	Beta-hexosaminidase subunit alpha	2	0	102	0
RPS9	40S ribosomal protein S9	2.02	0	19	0
CD44	Isoform 12 of CD44 antigen	2.05	0	138	0
SERPINB4	Serpin B4 (Fragment)	2.06	0	48	0
NPC2	Epididymal secretory protein E1 (Fragment)	2.13	0	23	0
TPT1	Translationally-controlled tumor protein	2.17	0	19	0
RPS27	40S ribosomal protein S27	2.17	0	6	0
RBBP7	Histone-binding protein RBBP7	2.29	0	104	0
IGFBP4	Isoform 2 of Insulin-like growth factor-binding protein 4	2.31	0	33	0
LGALS7	Galectin-7	2.38	0	16	0
APRT	Adenine phosphoribosyltransferase (Fragment)	2.41	0	20	0
TFPI	Tissue factor pathway inhibitor	2.42	0	152	0
PSMD13	Isoform 2 of 26S proteasome non-ATPase regulatory subunit 13	2.49	0	84	0
IGKC	Ig kappa chain C region (Fragment)	2.56	0	24	0

UGP2	UTP--glucose0-phosphate uridylyltransferase	2.63	0	117	0
RPL22	60S ribosomal protein L22 (Fragment)	2.66	0	11	0
IGLC1	Ig lambda0 chain C regions	2.69	0	19	0
IGLC2	Ig lambda-2 chain C regions	2.73	0	31	0
RAP1A	Ras-related protein Rap0A	2.73	0	21	0
SYNCRIP	Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q	2.77	0	258	0
ATP6AP2	Isoform 2 of Renin receptor	2.8	0	59	0
BPIFB1	BPI fold-containing family B member 1	2.8	0	72	0
CSTA	Cystatin-A	2.92	0	18	0
ESD	S-formylglutathione hydrolase (Fragment)	2.94	0	19	0
TPM3	Tropomyosin alpha-3 chain	3.64	0	41	0
ETF1	Eukaryotic peptide chain release factor subunit 1	4.07	0	125	0
CLSTN1	Calsyntenin0 (Fragment)	4.47	0	620	0
RAC1	Ras-related C3 botulinum toxin substrate 1	4.54	0	28	0
CTSD	Cathepsin D light chain (Fragment)	4.59	0	117	0
PSAP	Isoform Sap-mu-6 of Prosaposin	4.79	0	306	0
HIST3H2BB	Histone H2B type 3-B	4.8	0	71	0
KRT13	Keratin, type I cytoskeletal 13	4.99	0	232	0
TAGLN2	Transgelin-2 (Fragment)	5.76	0	31	0
SERPINB3	Serpin B3	5.87	0	89	0
CLSTN1	Calsyntenin0	6.21	0	862	0

GANAB	Isoform 2 of Neutral alpha-glucosidase AB	6.37	0	563	0
IGFBP6	Insulin-like growth factor-binding protein 6	8.76	0	144	0
PLOD1	Isoform 2 of Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	10.3	0	673	0
ANXA1	Annexin (Fragment)	12.59	0	163	0
PLAU	Urokinase-type plasminogen activator	14.61	0	442	0
KRT6C	Keratin, type II cytoskeletal 6C	15.71	0	380	0
EZR	Ezrin	21.06	0	651	0
KRT19	Keratin, type I cytoskeletal 19 (Fragment)	21.97	0	172	0
NME2P1	Putative nucleoside diphosphate kinase	22.1	0	105	0
SDCBP	Syntenin0	25.97	0	181	0
MDH1	Malate dehydrogenase, cytoplasmic (Fragment)	30.58	0	74	0

Chapter 6 (TMT Proteomics Data)

Name	Gene	# Unique Peptides	Control Nx 24	Hx 24	KO 24	HxKO 24	Hx 48	HxKO48
ERO1-like protein alpha	ERO1A	23	4376.9	15222.3	3886.23 3	3607.26 7	19920.6 3	3751.13 3
PODXL protein	PODXL	11	4229.4	10755.6 7	3323.03 3	2861.83 3	7454	2778.93 3

Creatine kinase brain isoform 2 (Fragment)	CKB	7	1440.366667	3766.9	1041.767	1052.133	2117.633	1123.933
Reticulon-1	RTN1	6	919.4	2334.967	692.9667	670.9	1775.667	690.6667
Lipase		1	227.7	1016	557.0333	305.0333	414.7333	266.4667
Homeobox protein Hox-B8	HOXB8	4	751.9333333	1993.1	1374.8	643	954.2	464.4333
Xylosyltransferase 2	XYLT2	2	35.76666667	77.66667	70.26667	28.36667	65.3	36.36667
Formin-binding protein 1-like	FNBP1L	5	640.4333333	2013.033	818.9333	744.7333	1290.933	771.8
Integrin alpha-6	ITGA6	12	854.3333333	2367.333	995.2	889.4	1779.5	807.7667
Tumor necrosis factor receptor superfamily, member 6 isoform 1 variant (Fragment)		1	126.4	583.9667	284.2667	221.3	311.5667	177.2
Keratin, type I cytoskeletal 19	KRT19	17	8554.533333	16878.97	6705.567	6419.167	14641.97	6432.2
Serpin B6	SERPINB6	12	3304.2	8265.167	2949.267	3165.533	6366.867	2449.167
Adipogenesis regulatory factor	ADIRF	7	3354.2	6654.833	2793.933	2568.633	4930.333	2318.967
Basal cell adhesion molecule (Lutheran blood group)	BCAM	4	571.4	1130.333	509.1667	436.3667	1573.667	454.2333
Isoform 2 of Gelsolin	GSN	25	7021.533333	15562.9	5929.6	6046.9	14282.27	6852.2

Calmin	CLMN	4	453.8	729.1	265.5	283.3	660.1	335.233 3
Isoform 2 of Integrin alpha-3	ITGA3	12	2535.63333 3	6753.13 3	3226	2653.5	5417.06 7	2675.9
Torsin-1B	TOR1B	2	247.4	845.066 7	943.933 3	332.4	484.033 3	289.966 7
ATR-interacting protein	ATRIP	1	148.433333 3	304.8	126.366 7	120.566 7	139.9	128.133 3
Uncharacterized protein (Fragment)		5	787.9	2090.1	1396	827.566 7	1501.93 3	715.6
Torsin-1A-interacting protein 2	TOR1AIP2	6	557.566666 7	1898.2	1719.86 7	751.7	1001.83 3	622.233 3
Dedicator of cytokinesis protein 11	DOCK11	49	8835.16666 7	24373.6 3	10317.6 7	9801.56 7	15835.2 3	8796.26 7
Transformation-related protein 14	TRG14	3	486.866666 7	1041.3	355.633 3	426.466 7	1115.23 3	653.6
Peptidyl-prolyl cis-trans isomerase		1	50.1666666 7	69.5	37.2666 7	28.5333 3	42.2666 7	24.1
Dynein light chain Tctex-type 1	DYNLT1	2	372.4	833.3	368.766 7	344.666 7	350.766 7	295.033 3
cDNA, FLJ94534, highly similar to Homo sapiens capping protein (actin filament), gelsolin-like(CAPG), mRNA		14	3083.4	7361.56 7	3122.36 7	3059.06 7	5238.56 7	3095.3
15 kDa selenoprotein	Sep 15	4	624.933333 3	1710.46 7	1519.43 3	721.166 7	1341.23 3	464.2
Calretinin	CALB2	17	5888.93333 3	17795.8 3	8319.7	7596.46 7	10667.4 3	6484.9

Kinectin	KTN1	3	25541.4666 7	54819.2	24337.1 7	23608.3 7	47341.3 3	23061.5 3
Isoform 4 of Kinectin	KTN1	1	26162.6666 7	54168.4 7	24063.8 3	23337.6 7	46849.5	22837.8 3
cDNA FLJ35730 fis, clone TESTI2003131, highly similar to ALPHA-1-ANTICHYMOTRYPSIN		2	205.833333 3	402.533 3	183.8	180.1	288.4	181.6
Torsin-4A	TOR4A	7	1257.8	2724.46 7	2685.36 7	1219.4	2252.83 3	1084.93 3
GDP-fucose protein O-fucosyltransferase 1	POFUT1	5	967.633333 3	1555.8	1404.8	703.066 7	1147.43 3	647.666 7
Isoform 2 of Keratin, type II cytoskeletal 8	KRT8	42	55450.8666 7	95344.7 3	43184.6	43326.3	93043.4 3	44588.7 3
RNA-binding protein 8A	RBM8A	3	498.633333 3	1136.63 3	651.133 3	517.566 7	455.866 7	449.566 7
Coactosin-like protein	COTL1	19	5040.63333 3	14810.6 3	7162.26 7	6768.7	9508.93 3	6549.56 7
C-type lectin domain family 2 member B	CLEC2B	1	210.166666 7	421.6	163.3	193.7	400.2	221.666 7
HCG23833, isoform CRA_b	hCG_23833	8	1942.53333 3	3203.53 3	2843.63 3	1475.56 7	1470.93 3	1048.4
Ectonucleoside triphosphate diphosphohydrolase 6	ENTPD6	2	87.9666666 7	344.633 3	314.266 7	159.066 7	169.333 3	130.066 7
Tapasin	TAPBP	2	76.2666666 7	73.3	64.3	33.8666 7	74.5666 7	38.6666 7
Histone RNA hairpin-binding protein	SLBP	3	321.1	485.5	533.7	224.9	322.2	261.366 7
Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	34	12551	27955.1 3	13063	12979.8	26348.4 3	12900.2 3

Histamine N-methyltransferase	HNMT	1	448.8	762.633 3	392.833 3	354.633 3	560.166 7	323.033 3
Lysophospholipid acyltransferase 5	LPCAT3	1	183	753	515	351.366 7	442.066 7	369.866 7
Isoform 2 of Mucin-1	MUC1	3	420.6	1445.7	745.333 3	684.933 3	2023.06 7	813.7
Uncharacterized protein C7orf26	C7orf26	1	74.3333333 3	137.9	86.0666 7	65.6	63.0666 7	61.2
Rho GTPase-activating protein 5	ARHGAP5	27	2983.6	8624.36 7	4907.26 7	4117.7	5734.46 7	3928.86 7
Signal transducer and activator of transcription 3	STAT3	24	4475.96666 7	10715.6	5676.1	5154.1	6520.16 7	4378.03 3
Prolyl 4-hydroxylase subunit alpha-2	P4HA2	1	3521.5	11618.1	5418.93 3	5611.63 3	13794.0 7	7500.06 7
Desmoglein-2	DSG2	3	136.133333 3	637.4	354.666 7	310.266 7	502.933 3	284.4
Disintegrin and metalloproteinase domain-containing protein 10	ADAM10	12	1618.76666 7	4154.36 7	4112.23 3	2023.2	3036.03 3	2018.16 7
PDZ and LIM domain protein 1	PDLIM1	4	261.166666 7	232.733 3	113.166 7	113.7	129	106.666 7
Keratin, type I cytoskeletal 18	KRT18	6	33419.6333 3	40000.8	19848.2	19560.4	36941.2 3	19563.1 7
Isoform IIa of Prolyl 4-hydroxylase subunit alpha-2	P4HA2	1	3601.5	11909.2 3	5640.6	5841.43 3	14357.0 7	7880.53 3
Carboxymethylenebutenolidase homolog	CMBL	7	1442.86666 7	2972.26 7	1750.63 3	1466.03 3	1968.66 7	1486.33 3

Ras and Rab interactor 1	RIN1	10	1010.66666 7	1620.76 7	807.933 3	802.566 7	1101.53 3	790.133 3
Succinate dehydrogenase assembly factor 2, mitochondrial	SDHAF2	3	387.266666 7	1144.93 3	917.833 3	568	961.566 7	523.366 7
Keratin, type I cytoskeletal 16	KRT16	5	1707.26666 7	2984.63 3	2122.26 7	1495.76 7	3126.63 3	1584.43 3
Endoplasmic reticulum metalloproteinase 1	ERMP1	5	763.866666 7	1693	899.1	848.866 7	1507.33 3	870.033 3
Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	17	3830.53333 3	8929.53 3	6314.16 7	4492.3	8156.73 3	5107.6
Protein S100-A2	S100A2	3	595.1	2030.1	1201.6	1022.63 3	2669.3	807.433 3
Kidney ankyrin repeat-containing protein 4	Kank4	7	1309.5	1941.13 3	1111.36 7	978.666 7	1492.36 7	924.033 3
Acylphosphatase	ACYP1	3	571.833333 3	1901.33 3	1141.3	965	1068.26 7	827.3
TMSB4X protein (Fragment)	TMSB4X	6	6513.43333 3	34284	21096.8 7	17633.7 3	17124.4 3	15238.3
Keratin, type I cytoskeletal 18	KRT18	1	19990.8666 7	28922.7 7	14827.6	14938.5	27316.9 3	14742.4
cDNA, FLJ93389, highly similar to Homo sapiens multiple inositol polyphosphate histidine phosphatase, 1 (MINPP1), mRNA		2	362.633333 3	707.266 7	668.6	366.166 7	595.066 7	391.1
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	ALDH6A1	11	2307.6	5346.66 7	2535.83 3	2776.26 7	5087.16 7	3585.13 3

Stathmin-3 (Fragment)	STMN3	3	543.7	1402.53 3	1027.2	730.266 7	714.166 7	657.933 3
Protein THEM6	THEM6	2	126.9	299.3	194.633 3	156.3	227.766 7	145.833 3
cDNA FLJ55809		2	486.033333 3	611.433 3	533.633 3	319.466 7	555.7	327.466 7
Oral-facial-digital syndrome 1 protein	OFD1	2	69.4	413	355.566 7	216.2	177.833 3	139.133 3
Transcription factor AP-2 alpha (Activating enhancer binding protein 2 alpha), isoform CRA_c	TFAP2A	5	728.766666 7	943.166 7	701.433 3	494	712.3	433.233 3
HCG2044836, isoform CRA_a	hCG_2044836	6	953.566666 7	2132.33 3	993.133 3	1118.16 7	1097.46 7	1041.4
Acyl-CoA desaturase	SCD	3	366.866666 7	1414.96 7	962.1	742.133 3	723.433 3	695.8
Cathepsin Z		5	1385.96666 7	4204.33 3	3159.1	2209	3317	1799.53 3
Isoform 2 of AMSH-like protease	STAMBPL1	4	236.6	645.966 7	323.566 7	340.633 3	409.8	330.133 3
Prolyl 3-hydroxylase 3	P3H3	10	1209.83333 3	2669.43 3	2032.53 3	1409.33 3	1924.63 3	1189.93 3
Nuclear pore membrane glycoprotein 210	NUP210	5	498.5	1371.93 3	970.633 3	726.4	927.533 3	660.6
Apolipoprotein B (Including Ag(X) antigen)	APOB	5	423.933333 3	892.466 7	682.7	472.566 7	719.366 7	496.266 7
Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	20	2408.4	5398.36 7	3135.9	2873.43 3	4191.9	2752.73 3

Isoform 2 of Creatine kinase U-type, mitochondrial	CKMT1A	5	635.433333 3	827.866 7	453.266 7	441.4	818.266 7	412.5
ER lumen protein-retaining receptor 1 (Fragment)	KDEL1	1	168.033333 3	810.866 7	826.5	432.733 3	410.666 7	329.433 3
Ectopic P granules protein 5 homolog	EPG5	2	153.133333 3	172.7	137.266 7	92.5333 3	116.833 3	101.1
L-xylulose reductase	DCXR	8	1516.73333 3	2431.63 3	1346.26 7	1303.96 7	1521.8	1233.53 3
3'-5' exoribonuclease 1	ERI1	7	1141.46666 7	2748.76 7	1844.86 7	1474.93 3	1520.2	1222.63 3
Serine/arginine repetitive matrix 1 isoform 2 (Fragment)	SRRM1	8	1739.73333 3	3506.7	2217.76 7	1884.16 7	1937.33 3	1630.13 3
Vinculin	VCL	69	19203.7666 7	40084	23720.5	21539.5 3	27503.9 3	20296.5 7
Four and a half LIM domains protein 2	FHL2	12	2052.53333 3	3915	1958.43 3	2104.63 3	2408.76 7	1609.73 3
D-dopachrome decarboxylase	DDT	8	1562	4151.76 7	2394.96 7	2234.8	2988.63 3	2113.56 7
Isoform 2 of Prolyl 4-hydroxylase subunit alpha-1	P4HA1	24	6085.13333 3	16480.3	10035.6 7	8886.13 3	20122.7 7	10995.8 3
Beta-2-microglobulin		1	107.333333 3	312.433 3	234.933 3	168.466 7	204	157.766 7
Peptidase M20 domain-containing protein 2	PM20D2	8	633.766666 7	1525.56 7	916.066 7	825.6	1029.6	828.533 3
cDNA, FLJ92217, highly similar to Homo sapiens ubiquitin-conjugating enzyme E2C (UBE2C), mRNA		6	1922.16666 7	3200.03 3	3460.43 3	1737.16 7	1361.16 7	1168.63 3
Arylsulfatase A, isoform CRA_a	ARSA	2	182.766666 7	318.6	234.566 7	173.333 3	335.133 3	224.566 7

Filamin-B	FLNB	1	50353.9	99309.0	55071.8	54036.2	70762.7	51334.4
				7	7		3	3
Isoform 8 of Filamin-B	FLNB	1	50428.1333	99374.9	55160.3	54116.4	70853.0	51402.1
			3	7	3	3	3	7
Isoform Er13 of Ankyrin-1	ANK1	18	2884.46666	5766.76	3416.73	3143.73	4375.36	3203.63
			7	7	3	3	7	3
Niban-like protein 1	FAM129B	24	5831.26666	13016.7	6686.73	7099.9	9257.83	7621.76
			7		3		3	7
Hereditary hemochromatosis protein	HFE	2	136.133333	348.633	225.966	190.233	234.866	192.1
			3	3	7	3	7	
Keratin, type II cytoskeletal 6B	KRT6B	3	9074.56666	18423.1	10233.1	10062.8	17596.9	9765.1
			7	3	7			
Isoform 2 of Nesprin-2	SYNE2	31	2616.66666	5085.43	3602.5	2780.66	3631.3	2584.3
			7	3		7		
Isoform 2 of Fatty aldehyde dehydrogenase	ALDH3A2	11	1727.43333	4836.96	3243.96	2646.96	3028.16	2165.73
			3	7	7	7	7	3
Isoform 2 of Myc-associated zinc finger protein	MAZ	2	172.1	194.433	135.533	106.566	175.7	89.5333
				3	3	7		3
Hippocalcin-like protein 1	HPCAL1	11	1379.86666	4063.93	2774.2	2228	2449.36	2046.23
			7	3			7	3
Proteasome activator complex subunit 1	PSME1	14	3540.76666	8138.96	4702.63	4493.43	6079.43	4917.33
			7	7	3	3	3	3
Leukocyte elastase inhibitor	SERPINB1	7	2099.2	4751.33	2685.73	2633.03	3974.6	2590.83
				3	3	3		3
Kunitz-type protease inhibitor 2	SPINT2	1	341.3	1075.86	451.933	596.566	800.2	664.866
				7	3	7		7
Integrin beta-1	ITGB1	21	7930.16666	17878.5	15155.8	9947.76	14271.3	9163.96
			7	3	3	7	3	7

Isoform 2 of Ras-related protein Ral-B	RALB	5	984.233333 3	2195.3	1228.86 7	1222.13 3	1882.73 3	1258.56 7
CUE domain-containing protein 1	CUEDC1	1	42.9333333 3	55.2	39.5333 3	30.7333 3	43.2	28.5666 7
cDNA FLJ53399, highly similar to Monocarboxylate transporter 1		2	1612.8	4494.8	2580.6	2504.9	4177.86 7	2317.5
Aldehyde dehydrogenase family 1 member A3	ALDH1A3	24	3519.76666 7	9262.86 7	5192.16 7	5171.06 7	6344.4	5128.43 3
Endothelin-converting enzyme 1	ECE1	11	1332.5	3169.4	2912.06 7	1769.5	2681.03 3	1689.13 3
Peptidyl-prolyl cis-trans isomerase	LOC105371242	1	1284.66666 7	5397.26 7	3288.2	3013.36 7	2722.96 7	2809.33 3
Glutathione S-transferase Mu 1	GSTM1	12	1260.3	3814.46 7	2492.96 7	2135.96 7	2550.06 7	1931.86 7
Aspartyl/asparaginyl beta-hydroxylase	ASPH	14	1626.5	3633.6	1900.06 7	2036.8	3819.46 7	2218.23 3
Tetraspanin (Fragment)	CD9	3	573.2	1109.73 3	584.033 3	623.6	1007.73 3	563.933 3
Isoform 6 of Inactive tyrosine-protein kinase 7	PTK7	5	606.8	1137.36 7	766	640.4	1038.5	625.066 7
Protein FAM134C	FAM134C	1	126.866666 7	167.466 7	129.6	94.4	115.6	107.233 3
Protein S100-A11	S100A11	7	6164.96666 7	14807.4 7	10536.8 7	8351.7	8627.56 7	7599.73 3
Carboxypeptidase	CTSA	6	1387.03333 3	4627.16 7	3346.06 7	2609.86 7	3198.2	1933.76 7
cDNA FLJ10554 fis, clone NT2RP2002385, highly similar to Synaptic glycoprotein SC2		9	1658.5	3628.2	2389.63 3	2047.23 3	2315.76 7	1770.9

Plasma membrane citrate carrier	SLC25A1	7	1502.13333 3	4128.16 7	2658.8	2333.43 3	3190.5	2138.66 7
Isoform 4 of Centrosomal protein of 85 kDa-like	CEP85L	1	257.566666 7	1677.03 3	1428.93 3	948	1182.33 3	703.066 7
Isoform Alpha-2 of Glucocorticoid receptor	NR3C1	5	324.1	735.9	476.866 7	416.133 3	581.733 3	413.7
Amyloid beta A4 protein	APP	12	1234.83333 3	3027.76 7	2479.46 7	1712.3	2860.56 7	1773.03 3
Gamma-glutamyl carboxylase	GGCX	6	1377.3	3441.4	2644.03 3	1946.46 7	2665.3	1638.33 3
Destrin	DSTN	13	8357.73333 3	11885.4 7	6831.26 7	6727.56 7	7637.7	6272.06 7
Monocarboxylate transporter 1	SLC16A1	2	1577.06666 7	4404.9	2545.46 7	2497.2	4143.53 3	2308.93 3
DTGCU2	DTGCU2	16	2473.1	6305.53 3	3792.86 7	3581.56 7	3752.96 7	3254.03 3
Vitamin K epoxide reductase complex subunit 1	VKORC1	2	432.5	1501.6	854.433 3	854.3	1132.3	783.933 3
GPI-anchor transamidase	PIGK	4	548.5	1466.76 7	1183.9	835.633 3	1022.1	662.4
Isoform 2 of Protein BRICK1	BRK1	4	48.7	83.4	62	47.6333 3	36.9333 3	45.2333 3
Reactive oxygen species modulator 1	ROMO1	1	136.566666 7	194.066 7	221.566 7	110.866 7	106.066 7	73.0666 7
SH3 domain-containing kinase-binding protein 1	SH3KBP1	14	2447.06666 7	4614.93 3	2865.53 3	2637.56 7	2927.36 7	2476.73 3
Retinol dehydrogenase 11	RDH11	7	894.066666 7	2696.6	1854.76 7	1544.3	2173.7	1404.23 3

Glutathione S-transferase Mu 3	GSTM3	10	1217.1	4880.76 7	3091.66 7	2800.43 3	3512.5	2644.9
Nuclear fragile X mental retardation-interacting protein 1	NUFIP1	2	143.3	232.666 7	201.166 7	133.5	90.6666 7	100.966 7
Proteasome activator complex subunit 2	PSME2	11	1991.7	5387.23 3	3406	3094.66 7	3666.73 3	2838.03 3
Peptidyl-prolyl cis-trans isomerase		1	2972.2	6628.26 7	4103.63 3	3811.23 3	3689.23 3	3562.16 7
DNA dC->dU-editing enzyme APOBEC-3B	APOBEC3B	4	467.2	1491.53 3	1357.03 3	858.033 3	835.833 3	762.7
Enoyl-CoA hydratase, mitochondrial	ECHS1	18	5424.3	12693.9 3	7996.4	7303.66 7	9380.86 7	6683.63 3
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	ALDH4A1	11	3056.86666 7	5349.5	3059.86 7	3082.13 3	4802.53 3	3138.56 7
Isoform 2 of Cerebral cavernous malformations 2 protein	CCM2	5	113.9	444.566 7	272.033 3	256.766 7	223.433 3	257.933 3
cDNA, FLJ96514		2	173.133333 3	182.933 3	152.6	105.8	113.966 7	78.2
Sn1-specific diacylglycerol lipase beta	DAGLB	3	491.166666 7	809.1	584.566 7	468.133 3	463.8	389.933 3
Isoform 3 of Keratin, type II cytoskeletal 80	KRT80	5	379.666666 7	533.466 7	341.433 3	309.1	428.266 7	272.366 7
DENN domain-containing protein 5B	DENND5B	3	403.5	1030.63 3	719.666 7	597.7	617.3	545.066 7
Integrin beta	ITGB4	26	4452.46666 7	8575.9	4867.4	4981.96 7	7530.03 3	5291.43 3

Rap guanine nucleotide exchange factor 2	RAPGEF2	1	65.36666667	377.7	302.9667	219.6333	216.3333	225.8667
UDP-glucose 4-epimerase	GALE	6	447.5	1094.1	711.6667	637.4	632.1	612
Cdc42 effector protein 1	CDC42EP1	5	496.0333333	983.9667	637.1	573.3333	778.2	544.5333
Trans-2-enoyl-CoA reductase, mitochondrial	MECR	2	371.0333333	793.6667	485.4	463.0667	499.3667	441.7333
Transcription factor AP-1	JUN	2	915.5	3123.233	1640.467	1823.667	2459.5	2067.267
Uncharacterized protein (Fragment)		2	434.2	1077	667.3	628.9667	754.4	626.7
Transcription factor jun-B	JUNB	2	700.5666667	2452.533	1289.567	1433.733	1930.367	1494.133
Sepiapterin reductase	SPR	14	2125.5	5376.5	3841.9	3146.4	3014.533	2787
Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	5	925.3333333	2238.2	1489.7	1311.633	1639.633	1274.1
cDNA FLJ57619, highly similar to Delta 3,5-delta 2,4-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)		1	156.0666667	368.6	224.1667	216.0333	339.2333	223.5
cDNA FLJ78516		12	2644.1	4762.7	3104.033	2793.7	2783.7	2110.033
cDNA FLJ76725, highly similar to Homo sapiens L-2-hydroxyglutarate dehydrogenase (L2HGDH), mRNA		9	1889.433333	5324.1	3338.233	3123.333	3755.6	3152.667
Copper transport protein ATOX1	ATOX1	3	465.9666667	1339.8	1008.567	786.4	752.2667	703.9667
Adenylate kinase isoenzyme 1	AK1	16	3609.1	6853.233	4488.267	4031.5	4423.767	3652.567

Protein NipSnap homolog 1	NIPSNAP1	8	1400.53333 3	3904.36 7	2255.7	2297.43 3	3039.8	2160.9
Mitochondrial ribosomal protein S2, isoform CRA_a	MRPS2	6	479.8	1225	1149.63 3	722.366 7	647.966 7	609.7
Isoform 2 of Serine/threonine-protein kinase N1	PKN1	8	1524.03333 3	3127.5	2037.26 7	1844.93 3	1976.2	1653.3
Basigin	BSG	9	2543.73333 3	7664.23 3	4779.83 3	4521.6	5578.73 3	3774.43 3
Isoform 2 of Mitochondrial dicarboxylate carrier	SLC25A10	8	1612.16666 7	3077.66 7	2065.8	1817.16 7	2018.7	1691.33 3
Protein S100-A13	S100A13	9	882.566666 7	2210.46 7	1565.26 7	1306.46 7	1453.13 3	1133.36 7
Caprin-2	CAPRIN2	6	900.666666 7	2379.23 3	1594.7	1408.53 3	1257.03 3	1077.4
Tyrosine-protein phosphatase non-receptor type 12	PTPN12	15	2892.7	5624.13 3	3445.56 7	3332.13 3	3908.53 3	3186.86 7
Mannosyl-oligosaccharide glucosidase	MOGS	11	1055.46666 7	2838.8	1778.5	1685.6	1783.56 7	1644.36 7
Protein S100-A4	S100A4	11	6187.2	11546.8 7	6815.26 7	6858.36 7	9596.23 3	6485.33 3
Delta(24)-sterol reductase	DHCR24	5	606.566666 7	1272.2	1114.3	757.666 7	852.466 7	660.6
Prostaglandin reductase 2	PTGR2	4	607.3	1366.6	913.5	814.833 3	921.166 7	808.133 3
Isoform 2 of Rho guanine nucleotide exchange factor 12	ARHGEF12	6	721.2	1186.1	787.7	708.966 7	1071.13 3	706.633 3
Isoform 4 of Tumor necrosis factor alpha-induced protein 8	TNFAIP8	1	733.066666 7	1011.36 7	599.8	604.633 3	782.1	678.933 3

Calmodulin	CALM1	1	1996.23333 3	10431.6 7	8795.8	6236.76 7	5273.43 3	4809.9
Isoform 3 of Regulator of G-protein signaling 4	RGS4	6	407.266666 7	783.266 7	366.433 3	468.5	603.5	442.466 7
cDNA, FLJ95265, highly similar to Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (ACAA2), nuclear gene encoding mitochondrial protein, mRNA		25	5870.03333 3	11507.8 7	7078.2	6884.56 7	9430.76 7	6590.5
TOM1-like protein 2	TOM1L2	5	478.833333 3	1118.4	812.833 3	670.966 7	657.833 3	613.966 7
Platelet-activating factor acetylhydrolase IB subunit gamma	PAFAH1B3	6	1106.53333 3	2283.3	1489	1370.46 7	1402.23 3	1348.8
Ribosomal protein S6 kinase alpha-4	RPS6KA4	13	2699.1	6339.3	4573.43 3	3805.36 7	3689.4	3176.16 7
Tyrosine-protein kinase Sgk223	SGK223	6	527	787.7	500.233 3	472.866 7	656	508.166 7
Uracil-DNA glycosylase	UNG	2	270	665.1	548.266 7	399.3	508.7	361.133 3
Isoform 3 of Adhesion G-protein coupled receptor G6	ADGRG6	7	1577.66666 7	3233.36 7	2478.06 7	1942.6	2429	1645.53 3
CD109 antigen	CD109	10	929.033333 3	1627.63 3	1235.43 3	978.666 7	3848.66 7	1114.76 7
Isoform 3 of Mitochondrial Rho GTPase 1	RHOT1	5	711.366666 7	1844.66 7	1370.53 3	1111	1221.76 7	913.066 7
AP-2 complex subunit sigma	AP2S1	2	133.733333 3	226.3	177.6	136.3	214.4	127.633 3

Plexin-A1	PLXNA1	3	493.566666 7	973.733 3	921.633 3	587.633 3	516.8	545.333 3
Ribonucleoside-diphosphate reductase large subunit	RRM1	20	3488.1	8431.86 7	7120.93 3	5097.53 3	4467.66 7	3513.76 7
Retinoblastoma-associated protein variant (Fragment)		13	1846.76666 7	4530.13 3	3841.1	2738.9	2926.7	2251.26 7
cDNA FLJ59211, highly similar to Glucosidase 2 subunit beta		26	7867.8	14736.6 7	10444.0 3	8916.23 3	11618.6	7640.66 7
Bcl-2-like protein 11	BCL2L11	1	36.2333333 3	80.5666 7	64.0666 7	48.8	69.5333 3	63.6
Collagen alpha-2(I) chain	COL1A2	10	1230.56666 7	2718.23 3	2536.46 7	1648.8	1762.56 7	1354.26 7
Serpin B9	SERPINB9	17	3733.8	10324.0 7	6229.8	6263.13 3	6739.13 3	5643.4
TBC1 domain family, member 9B	TBC1D9B	16	1345.93333 3	3678.96 7	2087.5	2232	2870.6	2346.46 7
Sulfatase-modifying factor 2	SUMF2	11	1539.56666 7	3316.06 7	2382.06 7	2014.2	2526.5	1883.26 7
Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	18	2922.6	7224.2	4559.4	4390.7	6531.23 3	4460.9
Myeloid differentiation primary response protein MyD88	MYD88	2	113.066666 7	358.566 7	229.4	218	264.266 7	199.3
Transforming growth factor-beta-induced protein ig-h3	TGFB1	1	169.633333 3	805.066 7	511.533 3	489.8	516	499.166 7
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	12	1409.63333 3	5300.66 7	4233.76 7	3227.73 3	3303.53 3	2244.83 3

cDNA FLJ76883, highly similar to Homo sapiens FKSG44 gene (FKSG44), mRNA		3	115.333333 3	151.633 3	102.933 3	92.3666 7	101.166 7	80.2
Annexin (Fragment)	ANXA4	18	4259.56666 7	9817.23 3	5866.23 3	5983.1	6504.5	6182.4
Transmembrane emp24 domain-containing protein 5	TMED5	3	287.333333 3	701.533 3	575.566 7	427.666 7	416	396.533 3
Keratin, type I cytoskeletal 10	KRT10	12	2516.53333 3	5328.46 7	2697.8	3248.6	7291.23 3	2512.76 7
Isoform 2 of Ribosomal protein S6 kinase alpha-1	RPS6KA1	9	1250.7	3266.26 7	2319.93 3	1993.76 7	2032.76 7	1654.8
Beta-hexosaminidase		7	595.266666 7	1391	990.766 7	849.8	979.1	715.833 3
Isoform 2 of Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	GNE	17	3057.13333 3	5553.1	3595.86 7	3392.56 7	3528.26 7	3179.86 7
Transmembrane protein 41A	TMEM41A	1	114.2	239.633 3	201.1	146.5	170.766 7	140.966 7
Keratin, type II cytoskeletal 5	KRT5	2	7889.3	14138.8 3	8526.7	8646.86 7	14395.3 7	8360.76 7
cDNA FLJ38470 fis, clone FEBRA2022013, highly similar to CCR4-NOT transcription complex subunit 2 (Fragment)		4	623.566666 7	2122.8	1442.3	1298.5	1308.7	1078.13 3
Exportin-7	XPO7	22	2379.16666 7	6644.4	5040.46 7	4067.63 3	4058.03 3	3787.56 7
Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	5	1000.1	2584.6	1748.23 3	1583.46 7	1573.46 7	1392.5

Major vault protein	MVP	24	3830.1	7090.43 3	4839.8	4352.46 7	5746.26 7	4278.9
WD repeat-containing protein 26	WDR26	8	738	2136.5	1443.3	1311.8	1622.43 3	1164.73 3
Receptor expression-enhancing protein 6	REEP6	2	553.433333 3	931.7	623.166 7	572.433 3	936.8	615.866 7
Isoform 2 of Inorganic pyrophosphatase 2, mitochondrial	PPA2	12	1872.1	5281.06 7	3545.8	3247.46 7	3855.63 3	3012.1
Ubiquitin-conjugating enzyme E2 E3	UBE2E3	2	411.133333 3	966.3	793.566 7	594.5	565.433 3	489.566 7
Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	DHTKD1	7	357.966666 7	920.3	665.966 7	566.366 7	738.8	550.333 3
Protein AHNAK2	AHNAK2	114	19231.9333 3	44756.4 3	28013.3 3	27543.9 7	37647.6 3	28295.3 3
Regulator of microtubule dynamics protein 3	RMDN3	6	629.333333 3	1499.03 3	1093.36 7	922.966 7	897.3	832.866 7
COMM domain-containing protein 3	COMMD3	4	107.1	76.5666 7	68.8333 3	47.1666 7	57.5333 3	55.2333 3
Transcription factor SOX-9	SOX9	5	805.133333 3	2092.8	1798.23 3	1289.93 3	1279.76 7	1096.5
EH domain-binding protein 1-like protein 1	EHBP1L1	6	375.933333 3	800.4	537.9	493.466 7	611.666 7	479.233 3
Histone H2AX	H2AFX	4	4917.23333 3	10027.9 3	7193.33 3	6184.86 7	6123.53 3	6831.7
55 kDa erythrocyte membrane protein	MPP1	2	176.566666 7	281.066 7	248.133 3	173.366 7	166.6	141.233 3

Isoform 3 of Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	1	218.9666667	776.1333	594.2	478.8667	427.5667	405.2
Cytochrome b-c1 complex subunit 9	UQCR10	2	303.7333333	1136.9	835.7	702	604.6667	500.4
SPRY domain-containing protein 4	SPRYD4	3	325.7	935.2	699.9333	577.7667	681.3667	593.7667
Inositol monophosphatase 3	IMPAD1	3	390.8333333	1369.433	946.8	846.0667	1154.367	731.3
Nucleolar protein 9	NOP9	4	347.3333333	538.1333	412.6333	332.6333	345.5667	326.6667
FAST kinase domain-containing protein 1, mitochondrial	FASTKD1	2	134.2	254.4	197.9667	157.2667	169.7667	143.6
Isoform 3 of Peptidyl-prolyl cis-trans isomerase FKBP9	FKBP9	9	1171.633333	2423.033	2297.367	1498.133	2418.333	1725.267
Prenylcysteine oxidase 1	PCYOX1	10	1000.7	2988.5	2039.133	1848.533	2543.167	2023.8
Collagen alpha-1(VI) chain	COL6A1	3	409.4	886.1667	711.0667	548.7333	908.7667	571.8
Cytochrome b5 type B	CYB5B	3	159.6	368.9667	289.2	228.5667	227.7	203.5
Centrosomal protein of 170 kDa protein B	CEP170B	7	1118.7	1787.533	1261.633	1107.6	1185.867	997.8667
Anthrax toxin receptor 2	ANTXR2	3	373.9333333	906.8667	772.3333	562.4	633.3333	456.2
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	NDUFB6	2	297	633.4667	533.9667	392.9	455.0333	361.8667

Ubiquitin-conjugating enzyme E2 E1	UBE2E1	3	1185.133333	2416.967	1718.833	1499.7	1239.033	1197.333
Transmembrane 4 L6 family member 18	TM4SF18	1	300.3333333	644.9667	560.5667	400.3333	393.6333	350.3667
Non-homologous end-joining factor 1	NHEJ1	1	170.0666667	591.8	465.6	367.4667	343.2333	309.3667
Histone-lysine N-methyltransferase SUV39H1	SUV39H1	4	480.2	1011.1	1466.9	628.0667	461.8	435.9
Myotubularin-related protein 1	MTMR1	4	273.5333333	921.4667	728.6	573.1	697	544.1667
cDNA FLJ16549 fis, clone PLACE7003657, highly similar to RAC-alpha serine/threonine-protein kinase (EC 2.7.11.1)		6	1132.366667	3611.7	2652.433	2246.6	2539.567	2147.033
Glycolipid transfer protein	GLTP	3	609.5666667	1455.567	884.9667	906.3	827.4333	734.9333
cDNA FLJ60744, moderately similar to B-cell lymphoma 9 protein		1	99.23333333	372.3667	260.7	231.8667	232.7333	202.4
Putative RNA-binding protein 15B	RBM15B	6	474.9333333	720.6	505.2667	448.8	425.2333	403.5
Fructose-bisphosphate aldolase C	ALDOC	17	11354.36667	21640.7	11937.4	13478.43	17736.27	15801.77
GDH/6PGL endoplasmic bifunctional protein	H6PD	15	1517.5	3275.833	2283.533	2040.7	3116.4	2017.4
Protein O-glucosyltransferase 1	POGLUT1	3	203.0333333	338.1667	321.2	210.7	232.8	251.7
CUB domain containing protein 1 (Fragment)		9	589.9666667	2069.233	1282.167	1293.8	1173.967	948.2667

Trinucleotide repeat containing 5, isoform CRA_c	TNRC5	9	1537.36666 7	3662	2543.46 7	2290.06 7	3818.23 3	2493.63 3
Transmembrane protein 120A	TMEM120A	3	698.666666 7	1461.66 7	895.7	914.1	1437.53 3	934.233 3
Synaptonemal complex protein SC65	P3H4	3	839.033333 3	1816.3	1477.93 3	1136.2	1412.9	1264.26 7
Calcium/calmodulin-dependent protein kinase I	CAMK1	4	285.333333 3	856.933 3	568.766 7	536.2	520.966 7	489.066 7
Ribonuclease T2		2	211.466666 7	436.2	221.666 7	273	527.4	490.166 7
cDNA FLJ78235		8	2267.63333 3	4925.73 3	3320.1	3086.1	4181.9	2448.43 3
Isoform Heart of ATP synthase subunit gamma, mitochondrial	ATP5C1	1	3041.33333 3	8584.46 7	6664.6	5378.9	5626.43 3	4852.06 7
ATP synthase subunit gamma, mitochondrial	ATP5C1	1	3070.46666 7	8608.1	6686.13 3	5395.5	5643.7	4862
Glucosamine-6-phosphate isomerase		7	2003.23333 3	6649.4	4796.86 7	4169.66 7	3734.93 3	4175.96 7
Probable ergosterol biosynthetic protein 28	C14orf1	1	309.233333 3	1303.43 3	993.033 3	817.533 3	987.133 3	752.266 7
Polyadenylate-binding protein-interacting protein 1	PAIP1	4	744.1	862.733 3	688.766 7	541.3	507.266 7	548.4
Prelamin-A/C	LMNA	69	31420.8	71348.7	47550.1 7	44792.6 3	53298.4	42466.6 3
Melanoma inhibitory activity protein 3	MIA3	14	2046.56666 7	3330.16 7	2682.7	2090.96 7	2479.2	2087.76 7

Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	9	1285.766667	2653.533	1709.233	1666.733	2166.833	1663.133
MHC class I antigen (Fragment)	HLA-Cw	2	411.5	1147.967	708.8667	721.4333	1110.9	716.2
MHC class I antigen (Fragment)	HLA-Cw	2	411.5	1147.967	708.8667	721.4333	1110.9	716.2
FLYWCH family member 2	FLYWCH2	6	784.5	1935.467	1153.467	1216.367	1432.767	1229.4
Translation initiation factor eIF-2B subunit alpha	EIF2B1	9	1069.9	2752.367	2046.133	1729.933	1461.6	1367.5
Carnitine O-acetyltransferase	CRAT	7	618.3333333	2296.5	1436.7	1443.8	1844.267	1113.8
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1, isoform CRA_b	RAPH1	9	949.1333333	2171.233	1324.567	1366.8	1433.233	1252.267
Adenylate kinase 4, mitochondrial	AK4	8	2841.733333	5066.067	2835.9	3189.633	3989.5	3396.633
Myoferlin	MYOF	90	14799.1	35696.03	23636.53	22478.63	23362.13	22839.97
Uridine phosphorylase 1	UPP1	4	440.4666667	1165	615.9	733.9333	853.3	604.5
Flotillin-1	FLOT1	15	1892.433333	4119.2	2825.4	2595.267	2874.967	2540.133
Ral GTPase-activating protein subunit alpha-1	RALGAPA1	2	162.7333333	216.8	156.4	136.6	164.5333	122.6667
WD repeat-containing protein 76	WDR76	1	247.8333333	398.3667	701.0333	251.3333	265.3667	212.9333

Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1	4	631.933333 3	1909.5	1656.8	1205.3	1009.9	1095.53 3
Inhibitor of growth protein	ING1	1	156.7	618.7	448.566 7	390.633 3	399.266 7	355.633 3
cDNA FLJ77748		5	360.3	779.5	590.533 3	492.6	530.033 3	421.533 3
Isoform 4 of Neuropathy target esterase	PNPLA6	10	973.733333 3	1696.76 7	1080.6	1072.4	1482.03 3	1105.26 7
Activated RNA polymerase II transcription cofactor 4 (Fragment)		1	671.066666 7	1922.6	1353.26 7	1215.2	979.066 7	946.766 7
cDNA FLJ77740, highly similar to Homo sapiens 7-dehydrocholesterol reductase, mRNA		3	723.266666 7	1515.1	1141.36 7	957.7	1185.83 3	925.433 3
Alternative protein EDARADD	EDARADD	2	5975.3	21416.5 7	13949.9 7	13546.1	13407.2 3	12816.8 3
Protein TSSC1	TSSC1	4	886.433333 3	2871.36 7	1928.3	1816.46 7	1355.03 3	2473.36 7
Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1	15	3567.36666 7	8490.43 3	5584.3	5372.56 7	5420.76 7	5461.6
Homeobox protein SIX5	SIX5	1	66.7333333 3	283.4	140.633 3	179.433 3	266.533 3	183.8
Isoform PKP3b of Plakophilin-3	PKP3	12	2736.83333 3	4627.86 7	3292.13 3	2930.76 7	3456.6	2611.83 3
Homeobox protein Hox-B9	HOXB9	3	511.433333 3	1319.46 7	782.233 3	836.033 3	756.5	618.133 3
Protein ECT2	ECT2	12	2228.1	3930.16 7	4589.4	2490.23 3	2204.1	2178

Lipase maturation factor 2	LMF2	3	330.533333 3	469.633 3	382.833 3	297.766 7	326.166 7	269.133 3
Isoform 3 of Protein phosphatase 1A	PPM1A	2	419.933333 3	1391.7	1022.03 3	883.133 3	968.966 7	873.233 3
3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	OXSM	3	136.033333 3	375.4	250.766 7	238.333 3	261.2	240.533 3
Keratin, type II cytoskeletal 2 epidermal	KRT2	8	4762.36666 7	6761.3	3452.2	4293.43 3	9167.56 7	3493.73 3
Ran-binding protein 6	RANBP6	4	1131.63333 3	2423.43 3	1931.93 3	1539.26 7	1337.5	1417.66 7
G2/mitotic-specific cyclin-B1	CCNB1	9	1755.7	2968.06 7	5293.6	1886.76 7	1434.53 3	1326.03 3
Glutathione peroxidase	GPX4	4	384.666666 7	972.166 7	888.733 3	618	758.6	603.833 3
cDNA FLJ41463 fis, clone BRSTN2017237		1	313.7	1158.36 7	1089.8	736.633 3	527.233 3	544.733 3
Torsin-1A-interacting protein 1	TOR1AIP1	1	2958.7	7361.2	5553	4681.86 7	4915.6	4420.36 7
cDNA FLJ55158, highly similar to Thioredoxin, mitochondrial		3	217.7	512.8	404.9	326.166 7	347.133 3	289.6
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	25	4167.56666 7	9835.83 3	7543.1	6260.66 7	7692.33 3	5725.8
Isoform 2 of Reticulocalbin-2	RCN2	6	1042.5	1798.43 3	1434.2	1144.73 3	1362.23 3	1042.26 7
Sin3 histone deacetylase corepressor complex component SDS3	SUDS3	1	177.166666 7	504.133 3	402.433 3	321.066 7	302.566 7	279.233 3

Nuclear autoantigen Sp-100	SP100	7	3212.33333 3	7392.7	4766.33 3	4708.86 7	4732.73 3	4313
cDNA FLJ12857 fis, clone NT2RP2003513, highly similar to Homo sapiens paralemmin (PALM), transcript variant 2, mRNA		2	577.5	1518.3	1054.73 3	967.6	1265.83 3	922.5
E3 ubiquitin-protein ligase ZFP91	ZFP91	4	512.933333 3	976.333 3	946.966 7	622.233 3	514.566 7	542.833 3
Isoform 2 of Phosphofurin acidic cluster sorting protein 2	PACS2	2	149.766666 7	244.366 7	188.533 3	155.766 7	238.7	174.633 3
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	ADI1	13	3589.86666 7	8430.43 3	5133.66 7	5373.86 7	5618.03 3	5875.36 7
BCKDHB protein	BCKDHB	7	780	1917.2	1228.96 7	1222.46 7	2002.43 3	1314.63 3
Maleylacetoacetate isomerase	GSTZ1	3	217.466666 7	381.266 7	275.6	243.133 3	274.533 3	256.566 7
Histone deacetylase complex subunit SAP30	SAP30	5	608.833333 3	1273.06 7	855.066 7	812.1	1012.76 7	803.333 3
Isoform 2 of Golgi apparatus protein 1	GLG1	24	4232.56666 7	9814.83 3	9069.86 7	6268.06 7	8065.86 7	4884.3
Mitogen-activated protein kinase (Fragment)		2	400.3	615.4	380.933 3	393.066 7	521.366 7	319.233 3
Protein zyg-11 homolog B	ZYG11B	3	339.766666 7	1093.03 3	910.933 3	698.466 7	608.666 7	539.8
Cytosolic 5'-nucleotidase 3A	NT5C3A	5	467.3	1742.86 7	1543.16 7	1114.2	987.866 7	872.6
Enhancer of polycomb homolog 1	EPC1	1	74.6333333 3	34.4	31.4666 7	22	27.9333 3	20.5333 3

RAB31, member RAS oncogene family variant (Fragment)		4	600.666666 7	1235.7	916.233 3	790.633 3	810.633 3	758.966 7
Collagen alpha-2(V) chain	COL5A2	5	447.766666 7	678.866 7	663.966 7	434.8	524.766 7	361.933 3
PRA1 family protein		3	647.266666 7	1400.46 7	1014.76 7	897.233 3	1165	826.366 7
Gamma-glutamylcyclotransferase	GGCT	9	2777.73333 3	5692.53 3	4396.26 7	3647.96 7	3512.8	3473.76 7
ADP-ribosylation factor 6	ARF6	8	804.6	2768.56 7	1867.2	1774.23 3	1907.36 7	1706.16 7
tRNA-dihydrouridine(16/17) synthase [NAD(P)(+)]-like	DUS1L	4	442.5	1108.03 3	887.4	710.166 7	643.866 7	651.266 7
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	3	5262.13333 3	9768.46 7	7126.4	6265.5	6314.03 3	5478.06 7
Glucose-6-phosphate isomerase (Fragment)	GPI	31	14985.1666 7	32679.4 3	17696.1	20978.5 7	29261.9 7	22394.3 7
Isoform 5 of Acyl-CoA-binding protein	DBI	6	1963.26666 7	4971.5	3594.66 7	3192.46 7	2923.5	3000.16 7
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	10	2006.96666 7	4258.46 7	2816.9	2735.73 3	3698.46 7	2625.73 3
D-beta-hydroxybutyrate dehydrogenase, mitochondrial	BDH1	3	585.733333 3	1126.7	791.933 3	723.933 3	832.766 7	752.066 7
Lambda-crystallin homolog	CRYL1	2	268.233333 3	564.433 3	355	362.733 3	442.866 7	316.666 7
Cation-dependent mannose-6-phosphate receptor	M6PR	7	1225.3	2928.13 3	2845.9	1881.8	1728.36 7	1505.3

cDNA FLJ60317, highly similar to Aminoacylase-1 (EC 3.5.1.14)		8	945.866666 7	2172.56 7	1274.9	1396.36 7	1799.13 3	1449.2
Isoform 2 of Acetyl-coenzyme A synthetase, cytoplasmic	ACSS2	3	465.433333 3	892.6	631.866 7	573.7	707.066 7	585.166 7
cDNA, FLJ92320, highly similar to Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA		6	913.366666 7	2366.16 7	1675.6	1522.6	1955.16 7	1542.03 3
Translation initiation factor IF-2, mitochondrial	MTIF2	6	383.4	905.633 3	798.2	582.866 7	616.3	576.166 7
Beta-hexosaminidase subunit beta	HEXB	11	2952.83333 3	7129.26 7	5740.3	4588.6	5605.86 7	3466.73 3
Isoform 2 of AP-2 complex subunit mu	AP2M1	14	2661.76666 7	6135.6	4487.8	3950.76 7	4332.13 3	3578.66 7
Phosphopantothenate--cysteine ligase	PPCS	7	675.5	2060.5	1489.9	1327.43 3	1394.66 7	1181.3
60S ribosome subunit biogenesis protein NIP7 homolog	NIP7	6	712.733333 3	3535.23 3	3076.56 7	2277.8	1692	1752.26 7
Glucan, branching enzyme 1 variant (Fragment)		24	4976.53333 3	12882.5	6108.7	8301.46 7	11177.3	9074.63 3
Protein JTB	JTB	1	129.766666 7	251.633 3	279.966 7	162.166 7	158.633 3	114.733 3
Glutathione S-transferase kappa 1	GSTK1	8	1995.76666 7	4380.23 3	3074.83 3	2823.23 3	3757.03 3	2695.23 3
Calpain 2, large [catalytic] subunit variant (Fragment)		26	6820.13333 3	15184.2	10005.0 7	9801.46 7	9713.43 3	8785.16 7
Thymidine kinase	TK1	8	1358.73333 3	1919.06 7	1644.9	1238.86 7	1251.83 3	1257.73 3

CUE domain-containing protein 2	CUEDC2	1	194.266666 7	425.966 7	473.266 7	275	219.566 7	181.4
Mutant hemoglobin alpha 2 globin chain	HBA2	2	803.966666 7	2021.43 3	1574.63 3	1305.03 3	2794.43 3	1858.56 7
ATPase inhibitor, mitochondrial	ATPIF1	3	384.866666 7	735.733 3	487.066 7	475.4	648.9	463.166 7
Poly(A) RNA polymerase, mitochondrial	MTPAP	7	907.133333 3	2201.73 3	1931.56 7	1423.86 7	1272.56 7	1153.5
Valacyclovir hydrolase	BPHL	5	119.4	304.266 7	203.366 7	196.8	277.066 7	219.8
Selenocysteine-specific elongation factor	EEFSEC	6	806.033333 3	2352.83 3	1925.23 3	1522.03 3	1479.16 7	1322.53 3
HCG2010666, isoform CRA_a	hCG_2010666	3	446.066666 7	787.433 3	616.5	509.533 3	685.666 7	473.5
Receptor-type tyrosine-protein phosphatase F	PTPRF	10	1241.86666 7	2354.1	1184.2	1525	2885.83 3	1647.03 3
cDNA FLJ78441, highly similar to Homo sapiens nucleolar and spindle associated protein 1 (NUSAP1),mRNA		5	1004.4	1685.4	1638.36 7	1091.83 3	1632.43 3	1351.33 3
Protein NipSnap homolog 2	GBAS	11	2323.53333 3	5499.5	3543.73 3	3565.9	4561.86 7	3307.9
Isoform 4 of Protein lunapark	LNP	6	859.2	1532.06 7	985.333 3	993.433 3	1586.46 7	1158.33 3
UPF0600 protein C5orf51	C5orf51	4	353.833333 3	916.966 7	664.233 3	594.6	384.9	371.166 7
Sulfatase-modifying factor 1	SUMF1	2	226.366666 7	690.833 3	546.533 3	447.966 7	564.1	486.666 7

Uroporphyrinogen decarboxylase	UROD	7	1484.1	2460.3	1754.5	1596.03 3	1739.6	1583.36 7
MHC class I antigen	HLA-A	4	1336.96666 7	2949.9	1949.63 3	1914.1	2836.46 7	1992.03 3
Protein MB21D2	MB21D2	3	394.633333 3	755.866 7	527.566 7	490.5	545.266 7	468.233 3
cDNA FLJ46277 fis, clone TEST14029731		1	639.033333 3	1416.26 7	1026.4	919.366 7	918.8	824.7
Protein SAAL1	SAAL1	2	456.033333 3	1477.3	1391.13 3	959.366 7	698.833 3	726.766 7
Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 2	CMTR2	2	182.5	437.866 7	385.366 7	284.4	228.5	243.833 3
Nicotinamide phosphoribosyltransferase	NAMPT	26	6199.46666 7	16918.5	9768.93 3	10989.2 7	12342.9	10729.5 3
Isoform 3 of Torsin-1A-interacting protein 1	TOR1AIP1	1	3440.46666 7	7994.7	6092.7	5196.23 3	5439	4918.3
cDNA FLJ75401, highly similar to Homo sapiens endoglin (Osler-Rendu-Weber syndrome 1), mRNA		1	201.2	396.2	363.033 3	257.533 3	281.533 3	246.133 3
Cyclin-dependent-like kinase 5	CDK5	7	613.1	1087.56 7	795.033 3	707.1	714.233 3	630.933 3
Spermatid perinuclear RNA-binding protein	STRBP	8	1332.16666 7	4693.63 3	3509.46 7	3051.9	2602.7	2435.16 7
Mixed lineage kinase domain-like protein	MLKL	1	213.033333 3	560.966 7	474.4	364.8	328.1	332.8
Serine/threonine-protein phosphatase 2A activator	PPP2R4	1	1279.9	3095.93 3	2191.93 3	2013.4	2069.63 3	1812.86 7

Mycophenolic acid acyl-glucuronide esterase, mitochondrial	ABHD10	9	1489.133333	2981.967	2278.733	1939.467	2198.533	1806.033
Citrate synthase, mitochondrial	CS	13	2280.3	7352.667	5650.7	4782.4	4611.433	4357.767
MHC class I antigen (Fragment)	HLA-A	2	1222.266667	2635	1797.2	1713.967	2561.367	1790.967
Insulin receptor substrate 1	IRS1	6	372.5333333	530.9333	396.7	345.3667	380.7333	330.1333
Mitochondrial amidoxime reducing component 2	Mar 02	2	144.2	405.0333	267.5333	263.6333	332.8333	292.9667
NAD(P)H dehydrogenase, quinone 2, isoform CRA_a	NQO2	6	693.3666667	1313.967	841	855.4	921.5333	735.7667
Serine/threonine-protein phosphatase 2A activator	PTPA	1	1576.133333	4212.567	2964.433	2744.333	2738.467	2489
Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	5	618.3666667	1818.533	1514.6	1184.767	1179.4	943.5
STAG1 variant protein (Fragment)	STAG1variantprotein	5	272.1666667	529.5	478.6333	345.2667	317.2	285.8
Pleckstrin homology domain-containing family A member 2	PLEKHA2	5	510.7666667	1359.7	764.0333	886.7	1016	899.6
Enolase-phosphatase E1	ENOPH1	4	684.9333333	1187.067	978.7667	774.5	663.1	664.3667
2-oxoglutarate dehydrogenase, mitochondrial	OGDH	37	5349.2	11757	9074.7	7671.4	8584.4	7144.4
DnaJ homolog subfamily C member 10	DNAJC10	7	504.7	897.9333	697.3333	585.9	679.4	604.0667

Peptide-N(4)-(N-acetyl-beta-glucosaminy)asparagine amidase	NGLY1	10	1010.5	2496.6	1340.23 3	1630.66 7	2052.8	1651.2
Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	5	1275.16666 7	2209	1645.66 7	1442.9	1653.43 3	1207.36 7
Actin-related protein 2/3 complex subunit 2	ARPC2	10	1624.5	4875.3	3884.63 3	3186.3	2781.76 7	2798.8
MHC class I antigen	HLA-A	2	1299	2880.96 7	1975.43 3	1883.5	2776.4	1967.56 7
Inositol-tetrakisphosphate 1-kinase	ITPK1	2	566.566666 7	809.5	648.933 3	529.233 3	586.566 7	523.8
Isoform 6 of Unconventional myosin-VI	MYO6	16	2110.13333 3	4361.96 7	2976.66 7	2852.33 3	3269.86 7	2694
Isoform 2 of Protocadherin-1	PCDH1	10	1329.8	2722.8	1832.86 7	1780.7	4879.93 3	1963.23 3
KDEL motif-containing protein 2	KDELC2	10	1195.86666 7	3042.6	2691.23 3	1989.9	2438.9	1710.76 7
Peroxiredoxin-6	PRDX6	17	4197.8	11335.3	8613.03 3	7413.56 7	6687.23 3	6433.4
Nucleotide triphosphate diphosphatase NUDT15	NUDT15	1	262.2	481.733 3	420.466 7	315.066 7	315.833 3	307.8
Hsp70-binding protein 1	HSPBP1	9	1423.73333 3	3429.03 3	2758.43 3	2243.43 3	1752.7	1913.96 7
RAC-beta serine/threonine-protein kinase	AKT2	4	580.3	1457.2	1077.86 7	954.2	1023.4	907.133 3
Isoform 2 of Rhomboid domain-containing protein 2	RHBDD2	1	65.8333333 3	53.6	58.0333 3	35.1	44.4333 3	33.7333 3

Ribosomal protein S6 kinase alpha-5	RPS6KA5	4	274.7	884.066 7	643.966 7	579.133 3	641.866 7	552.633 3
E3 ubiquitin-protein ligase MGRN1 (Fragment)	MGRN1	1	102.733333 3	275.333 3	230.466 7	180.4	169.833 3	193.766 7
Alpha-centractin	ACTR1A	5	1700.66666 7	4729.23 3	3761.43 3	3101.33 3	2857.83 3	2622.6
14-3-3 protein theta	YWHAQ	20	16178.9	36102.1 3	25121.2 7	23691.8	22936.7 7	21537.7 3
Zinc finger protein 553, isoform CRA_a	ZNF553	1	323.766666 7	857.766 7	669.5	562.933 3	638.233 3	533.533 3
Translation factor GUF1, mitochondrial	GUF1	4	90.1333333 3	184.633 3	157.3	121.2	120.966 7	120.633 3
cDNA, FLJ93132, highly similar to Homo sapiens CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), mRNA		2	167.166666 7	231.6	307.7	152.033 3	145.366 7	117.266 7
Ras GTPase-activating protein 2	RASA2	2	101	275.233 3	204.066 7	180.766 7	187.5	168.6
Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB	4	490.733333 3	707.266 7	502.066 7	464.633 3	559.8	463.366 7
Cathepsin D	CTSD	17	5330.56666 7	10094.3 3	10163.9 7	6634.7	6593.8	5513.6
Transcription factor jun-D	JUND	3	1015.6	3037.06 7	1845.46 7	1996.7	2410.23 3	2339.1
Isoform 2 of ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	7	1104.16666 7	2162.96 7	1639.23 3	1422.23 3	1644.9	1437.4
Kinesin-like protein KIF22	KIF22	3	632.766666 7	1127.13 3	1222.56 7	741.633 3	713.566 7	630.766 7

DNA mismatch repair protein Msh3	MSH3	7	928.566666 7	1975.43 3	1698.66 7	1299.9	1242.53 3	1142.6
Zinc finger protein 217, isoform CRA_b	ZNF217	15	2503.06666 7	5197.3	4400.86 7	3420.83 3	3589.03 3	3049.66 7
cDNA FLJ77346, highly similar to Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (DDX49), mRNA		3	395.866666 7	467.966 7	451.9	308.133 3	284.7	295.3
Tubulin--tyrosine ligase-like protein 12	TTLL12	22	3548.1	7024.86 7	4876.73 3	4628.56 7	4489.6	4182.06 7
Isoform 4 of Cyclin-K	CCNK	7	700.766666 7	1683	1359.83 3	1109.26 7	1122.03 3	1012.43 3
Probable methyltransferase TARBP1	TARBP1	4	135.2	400.933 3	300.7	264.266 7	244.6	239.266 7
Isoform 4 of DNA topoisomerase 2-alpha	TOP2A	44	10824.8333 3	21586.9	25808.1 7	14237.0 3	13051.5 7	10775.7 3
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	26	6387.73333 3	14090.5	9346.7	9293.53 3	10625.4 3	8841.13 3
Hepatoma-derived growth factor	HDGF	18	5445.13333 3	12261.2 7	8299.73 3	8088.6	8221.43 3	7379.96 7
Glycerol kinase	GK	8	1215.9	1960.46 7	1446	1293.33 3	1449.96 7	1306.63 3
cDNA, FLJ93596, highly similar to Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA		8	1771.6	3537.43 3	2502.93 3	2333.96 7	2989	2523
cDNA FLJ10398 fis, clone NT2RM4000349, highly similar to Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), mRNA		13	3085.5	7355.76 7	6791.23 3	4853.7	3773.53 3	3839.36 7

Isoform 2 of Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	13	3266.966667	7803.2	6156.1	5149.6	5485.567	4726.667
Flotillin-2	FLOT2	15	3168.633333	6466.033	4584.033	4267.6	5286.933	4196.7
Thioredoxin reductase 2 isoform 1 variant (Fragment)		6	1619.966667	3820.033	2640.333	2521.3	2807.267	2079.433
Acyl-CoA dehydrogenase family member 10	ACAD10	8	576.3333333	1513.8	972.5333	999.3667	1275.867	1123.233
Isoform 4 of Leucine-rich repeat flightless-interacting protein 2	LRRFIP2	6	759.6333333	1641.4	1073.5	1083.7	1120.6	945.3667
Leukotriene A-4 hydrolase	LTA4H	28	6917.933333	15182.83	10809.13	10026.57	11147.77	9877.5
cDNA, FLJ92992, highly similar to Homo sapiens methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA		6	786.0666667	2128.267	1449.867	1405.667	1858.333	1615.933
Ubiquitin-conjugating enzyme E2 G1	UBE2G1	3	120.7	434.8667	358.8667	287.2667	279.8	242.5
Deoxyhypusine synthase	DHPS	6	770.8	1229.067	804.2667	811.9333	768.3333	778.1667
3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	EBP	1	329.2333333	754.7	687.5667	498.5667	511.2333	476.8667
Puromycin-sensitive aminopeptidase	NPEPPS	42	10862.5	27311.6	17800.97	18042.97	20371.7	18630.53
Disks large homolog 5	DLG5	2	63.26666667	70.83333	57.43333	46.8	60.23333	38.43333

Tripeptidyl peptidase I, isoform CRA_a	TPP1	4	332.7	567.9	424.6667	375.6	481.9667	397.0333
Cytochrome c	CYCS	5	1712	4032.267	4147.9	2667.667	2294.3	2319.467
1-acyl-sn-glycerol-3-phosphate acyltransferase	AGPAT2	2	209.4	504.8333	395.7667	334	335.2667	304.9
Glucosamine-6-phosphate isomerase 2	GNPDA2	1	872.6	2672.2	1988.633	1768	1426.8	1686.233
Coiled-coil domain-containing protein 51	CCDC51	4	406.7666667	1166.8	889.6333	772	823.1333	706.1667
V-type proton ATPase catalytic subunit A	ATP6V1A	22	3762.2	9527.1	7126.2	6304.533	6154.9	5802.9
Isoform 2 of Nucleoside diphosphate kinase A	NME1	1	7335.166667	19345.33	14613.53	12801.73	10719.67	11158.6
Isoform 3 of Ethanolamine-phosphate cytidyltransferase	PCYT2	5	551.3666667	1265.733	965.6	837.9667	915.5	868.7
Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	29	3579.6	7031.367	4996.4	4657.133	4988	4587.333
Isoform 8 of RNA binding protein fox-1 homolog 2	RBFOX2	4	661.6	1609.867	1279.833	1066.3	1028.8	901.3
Rab-like protein 3	RABL3	4	889.7	1557.133	1114.067	1031.567	1068.267	997.6333
Cullin-4A	CUL4A	6	1984.7	5832.4	4271	3864.533	3783.433	3435.733
Histone H2A.Z	H2AFZ	3	3250.233333	6516.233	4598.833	4318.667	4115.6	4621.067
Paraspeckle component 1	PSPC1	14	3979.1	7400.467	6021.733	4906.867	5849.8	4060.467

6-phosphogluconate dehydrogenase, decarboxylating		6	4663.83333 3	11636.6	9135.8	7717.7	7275.93 3	6776.8
Non-histone chromosomal protein HMG-17	HMGN2	8	5569.56666 7	13623.1	9995.63 3	9036.63 3	10799.2	7967.53 3
Mitochondrial ribosome-associated GTPase 1	MTG1	1	352.4	709.666 7	594.866 7	470.8	516.366 7	470.3
Isoform 2 of Transcription elongation factor A protein-like 1	TCEAL1	4	190.666666 7	554.766 7	432	368.233 3	419	345.2
Low-density lipoprotein receptor	LDLR	2	267.366666 7	588.566 7	484.566 7	390.7	426.366 7	524.966 7
ATP synthase subunit d, mitochondrial	ATP5H	13	4304.1	8819.8	6688.73 3	5854.76 7	6059.33 3	5239.3
DNA polymerase	POLD1	19	2308.3	5302.56 7	4251.63 3	3521.26 7	3324.56 7	2941.93 3
Cullin-4B	CUL4B	20	3866.1	11872.2 7	8602.8	7886.63 3	8456.23 3	7258.46 7
G patch domain-containing protein 8	GPATCH8	11	1657.03333 3	4104.83 3	2993.23 3	2727.46 7	3061.4	2748.4
Tetratricopeptide repeat protein 9C	TTC9C	3	402.166666 7	688.933 3	465.766 7	457.766 7	359.933 3	427.566 7
Mitochondrial fission 1 protein	FIS1	3	467.033333 3	936.1	790.333 3	622.3	610	552.6
cDNA FLJ51495, highly similar to ADP-ribosylation factor 5		4	1667.06666 7	3890.8	3225.33 3	2587	2298.93 3	2289.2
Rab-like protein 6	RABL6	5	1287.96666 7	2229.73 3	1703.83 3	1482.8	1492.03 3	1387.86 7

Isoform 3 of L-lactate dehydrogenase A chain	LDHA	25	13263	38545.3	24362.9 7	25640.0 3	26301.3 7	25036.7 7
cDNA FLJ12766 fis, clone NT2RP2001520, highly similar to Calcium-binding mitochondrial carrier protein Aralar1		8	2326	5123.46 7	4092.53 3	3408.43 3	3713.26 7	3230.96 7
Isoform 2 of C-terminal-binding protein 2	CTBP2	3	1461.76666 7	3169.5	2166.33 3	2109.13 3	2415.7	2006.56 7
Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2	7	874.9	2458.83 3	1815.06 7	1636.3	1572.6	1239.23 3
Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A	MGAT5	3	210.833333 3	489.933 3	556.366 7	326.066 7	396	302.1
Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	1	4952.06666 7	8629.23 3	6346.03 3	5744.93 3	5771.83 3	5057.13 3
F-box only protein 22 isoform a variant (Fragment)		5	376.933333 3	508.833 3	445.133 3	338.833 3	274.433 3	311.433 3
Splicing factor U2AF 26 kDa subunit	U2AF1L4	1	332.466666 7	1654.43 3	1461.06 7	1101.96 7	756.566 7	828.133 3
Forkhead box protein J3	FOXJ3	1	109.3	130.133 3	133.4	86.7	95.2333 3	73.3333 3
Protein SCAF11	SCAF11	10	1401.13333 3	2713.3	2006.1	1807.86 7	2275.3	1639.43 3
Coiled-coil domain containing 6, isoform CRA_a	CCDC6	10	1674.96666 7	3051.4	2249.33 3	2033.26 7	2071.93 3	1843.76 7

Elongation factor-like GTPase 1	EFL1	6	315.766666 7	497.733 3	344.5	331.666 7	378.2	372.533 3
cDNA FLJ76043, highly similar to Homo sapiens cyclin T1 (CCNT1), mRNA		6	618.333333 3	1652.1	1241.83 3	1101.36 7	1065.1	975.333 3
DBIRD complex subunit ZNF326	ZNF326	11	2391.86666 7	3701.3	2626.56 7	2467.46 7	3049.16 7	2222.4
Protein MON2 homolog	MON2	11	917.566666 7	2160	1662.06 7	1440.03 3	1375.86 7	1508.4
Phospholipase B-like 1	PLBD1	5	127.633333 3	452.533 3	508.366 7	301.7	259.966 7	236.966 7
Mitochondrial inner membrane protein OXA1L	OXA1L	9	1411.4	3525.9	2924.33 3	2351.53 3	2292.93 3	1837.23 3
Cytoplasmic dynein 1 light intermediate chain 2	DYNC1LI2	15	3704.23333 3	6756.43 3	5080.63 3	4506.7	4446.23 3	4534.93 3
Protein FAM162A	FAM162A	8	1450.06666 7	4261.73 3	2066.43 3	2843.03 3	4618.26 7	3093.66 7
HCG2044781	TMEM189-UBE2V1	5	2528.76666 7	6341.93 3	4963.6	4230.93 3	3737.13 3	3848.83 3
3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH	11	1707.66666 7	3497.43 3	2315.76 7	2333.5	2792.36 7	2124.1
cDNA FLJ13636 fis, clone PLACE1011160, highly similar to RING finger protein 14		3	371.533333 3	1136.2	975.633 3	758.2	722.866 7	663.733 3
Procollagen galactosyltransferase 1	COLGALT1	16	3010.16666 7	6536.43 3	5188.13 3	4362.63 3	5189.83 3	4163.5
Isoform 6 of Extended synaptotagmin-2	ESYT2	23	3917.96666 7	8280.46 7	5445.73 3	5528.43 3	6034.3	5281.3

Phosphoinositide-3-kinase, regulatory subunit 2 (P85 beta), isoform CRA_a	PIK3R2	7	605.5	704.6333	484.2333	470.5667	504	449.2667
Huntingtin	HTT	8	839.3	1393	1032.333	930.3	1131.067	992.1667
Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	11	3441.633333	9864.667	7261.967	6592.967	7365.367	6205.167
Protein Hikeshi	HIKESHI	1	277	922.6667	825	616.7	558.6	574.6333
Centromere protein C	CENPC	4	338.0333333	699.9667	574.0333	467.9667	589.7	465.8
Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	186	32398.36667	82842.67	56577.4	55410.27	53917.33	52924.97
Protein arginine N-methyltransferase 1	PRMT1	16	3817.033333	11796.53	11170.53	7891.6	5916.067	6171.9
Redox-regulatory protein FAM213A	FAM213A	2	220.9666666	416.5	299.7333	278.7667	345.4333	289.2333
Amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferaseprovided	AGL	17	1329.233333	2839.167	2071.133	1900.433	2242.6	1934.133
Isoform 4 of Sphingomyelin phosphodiesterase 4	SMPD4	8	830.3333333	2321.767	1922.933	1554.4	1455.2	1350.067
Neuroblast differentiation-associated protein AHNAK	AHNAK	387	134234.9333	294625.5	193754.9	197324.9	223353.8	182132.5
cDNA FLJ75085, highly similar to Homo sapiens glutamyl-tRNA synthetase (QARS), mRNA		3	4006.6	10861.07	8852.133	7274.367	6325.467	6343.467

Mitochondrial ribonuclease P protein 1	TRMT10C	14	2851.9	6223.63 3	5040.4	4168.5	4316.06 7	3994.36 7
NAD(P)H-hydrate epimerase	APOA1BP	13	1998.23333 3	3680.4	2555.33 3	2465.23 3	2644.36 7	2280.8
Glutamine--tRNA ligase (Fragment)	QARS	1	3431.23333 3	9453.06 7	7710.16 7	6334.46 7	5456.1	5586.13 3
Isoform 2 of Interferon-related developmental regulator 2	IFRD2	3	245.633333 3	503.6	382.766 7	337.5	215.266 7	280.033 3
DNA mismatch repair protein Msh2	MSH2	26	5594.03333 3	12297.0 7	10871.7 3	8244.16 7	7806.03 3	7041.83 3
Lysophospholipid acyltransferase 7	MBOAT7	4	1239.53333 3	2577.9	1695.7	1728.36 7	1959.8	1686.06 7
Aminopeptidase B	RNPEP	24	3453.86666 7	8037.6	5512.43 3	5389.13 3	5692.73 3	4980.5
HCG20123, isoform CRA_b	hCG_20123	4	280.633333 3	777.733 3	594.166 7	521.5	579.9	517.3
Pyruvate carboxylase, mitochondrial	PC	17	2757.03333 3	4861.06 7	3417.8	3260.93 3	4106.53 3	3438.46 7
Protein ABHD11	ABHD11	7	848.066666 7	1444	1055.5	968.766 7	1186.13 3	905.733 3
Phosphatidylethanolamine-binding protein 1	PEBP1	5	5721.46666 7	12344.8	9082.86 7	8283.33 3	8625.76 7	7716.46 7
FAST kinase domain-containing protein 3, mitochondrial	FASTKD3	1	60.6333333 3	145.233 3	84.8666 7	97.4666 7	58.7666 7	83.8
Isoform 9 of Caspase-8	CASP8	20	2233.86666 7	6514.1	4289.9	4371.96 7	4002.43 3	4057.4
Heterogeneous nuclear ribonucleoprotein F	HNRNPF	9	4122.5	9898.3	8121.93 3	6645	6365.3	5579.13 3

Diablo homolog, mitochondrial	DIABLO	3	454.6	994.766 7	767.066 7	668	683.4	588.166 7
Beta-catenin-like protein 1	CTNNBL1	12	1481.6	4646.36 7	4052.13 3	3122.43 3	2676.3	2525
60S ribosomal protein L18a	RPL18A	12	4453.33333 3	9536.46 7	8131.63 3	6408.96 7	5211	6200.93 3
cDNA FLJ55484, highly similar to ATP-dependent RNA helicase DDX39 (EC 3.6.1.-)	5	4842.5	11248.17	9196	7559.83 3	6985.63 3	6880.73 3	
Cytoskeleton-associated protein 2	CKAP2	6	1077.33333 3	1116.8	1409.8	750.666 7	683.966 7	574.966 7
Fatty acid synthase	FASN	80	23679.4	44051.3	36407.6	29609.7	28982.0 7	26418.7 3
Actin-binding LIM protein 1	ABLIM1	2	79.1	174.6	118.966 7	117.366 7	140.9	120.766 7
HIV Tat-specific factor 1	HTATSF1	16	1074.86666 7	2512.2	2040.43 3	1689.16 7	1761.33 3	1446.23 3
Unc-84 homolog A (C. elegans)	UNC84A	17	2698.96666 7	4791.3	3553.3	3221.9	2645.3	2722.76 7
Polynucleotide 5'-hydroxyl-kinase NOL9	NOL9	8	678.933333 3	1978.66 7	1635.33 3	1331.4	1248	1110.23 3
Centromere protein F	CENPF	30	3763.53333 3	6404.76 7	6290.1	4311.9	4195.96 7	3651.43 3
Sec1 family domain-containing protein 2	SCFD2	4	179.766666 7	445.433 3	380.033 3	299.9	265.933 3	326.633 3
DNA ligase 1	LIG1	11	1653.76666 7	2364.03 3	2081.4	1591.73 3	1798.5	1368.7

Guanine nucleotide exchange factor VAV2	VAV2	9	1241.76666 7	2490.83 3	1867.3	1677.76 7	1824.5	1605.93 3
Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1	BZW1	14	3235.76666 7	10381.9	7783.8	6993.73 3	6113.56 7	5930.2
Very-long-chain 3-oxoacyl-CoA reductase	HSD17B12	8	1035.73333 3	3381.16 7	2308.8	2277.8	2193.6	1882.73 3
Integrin beta-5	ITGB5	2	95.9333333 3	172.866 7	173.6	116.466 7	127.666 7	96.6333 3
Codanin-1	CDAN1	3	214.1	987.733 3	818.233 3	665.533 3	720.666 7	569.833 3
Isoform 4 of Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	2	1175	2301.3	1522.63 3	1550.63 3	1472.7	1415.7
Oxysterol-binding protein	DKFZp686C0249	16	1682	4468	3344.26 7	3011.23 3	3062.9	2871.13 3
Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2	17	2710.1	6445.1	4546.5	4343.86 7	4347.63 3	4065.63 3
MHC class I antigen (Fragment)	HLA-B	1	558.566666 7	1361.56 7	889.233 3	917.7	1517.23 3	965.7
ATP synthase-coupling factor 6, mitochondrial	ATP5J	8	2140.5	4887.06 7	3646.9	3294.1	3518.03 3	2796.53 3
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	13	1209.1	2791.36 7	2223.23 3	1881.56 7	1923.6	1651.53 3
Isoform 2 of Transgelin-2	TAGLN2	18	10143.2333 3	15671.6	10755.5 3	10565.7 7	10516.5 7	9351.56 7
Epididymis luminal protein 210	HEL-210	1	3059.9	6757.83 3	4824.96 7	4556.2	4521.1	4089.1

Calpain small subunit 1	CAPNS1	12	3013.46666 7	5390.76 7	3706.63 3	3634.63 3	3728.3	3402.5
WD repeat domain phosphoinositide-interacting protein 3	WDR45B	3	805.466666 7	2519.4	1665.76 7	1699.6	1980.96 7	1640.43 3
EH domain-containing protein 2	EHD2	3	462.633333 3	1134.4	777.2	765.4	668.533 3	664.9
TRPM8 channel-associated factor 1	TCAF1	1	95.7666666 7	116.366 7	151.6	78.5333 3	72.6	68.1
6-phosphogluconate dehydrogenase, decarboxylating		8	5953.03333 3	14187.63	11079.7 7	9576.23 3	9050.26 7	8470.6
Centrosomal protein of 170 kDa	CEP170	2	8553.2	17256.0 7	11686.1	11649.6	11031.4	10252.8 7
Nuclear pore glycoprotein p62	NUP62	8	1009.23333 3	2218.86 7	1796.96 7	1497.96 7	1512.66 7	1504.33 3
7,8-dihydro-8-oxoguanine triphosphatase	NUDT1	3	1206.03333 3	1845.83 3	1512.33 3	1246.13 3	976.033 3	1025.7
cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA		37	6573.86666 7	17177.17	13896.7 3	11597	10835.4 3	10518.7 7
HEAT repeat containing 1	HEATR1	33	3474.23333 3	9634.66 7	8000.86 7	6505.8	5355.6	5242.1
Bcl-2-like protein 13	BCL2L13	7	1102.66666 7	2872.5	2306.9	1939.76 7	2167.23 3	1743.23 3
Fos-related antigen 2	FOSL2	3	451.766666 7	1371.73 3	821.533 3	926.733 3	964.366 7	934.9

Endoplasmic reticulum-Golgi intermediate compartment protein 3 (Fragment)	ERGIC3	3	387.9	710.2	582.733 3	480.1	614.433 3	425.9
CD97 antigen	CD97	8	1218.66666 7	2133.13 3	1688.96 7	1442.3	1331.23 3	1129.03 3
TraB domain-containing protein	TRABD	5	270.066666 7	766	678.866 7	517.933 3	521.466 7	400.366 7
DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	5	970.966666 7	2699.9	1957.43 3	1826.13 3	1607.1	1562.26 7
S100 calcium binding protein A10 (Annexin II ligand, calpactin I, light polypeptide (P11)), isoform CRA_b (Fragment)	S100A10	9	3447.4	11535.7	7343.53 3	7803.03 3	9539.73 3	7336.83 3
Up-regulated during skeletal muscle growth protein 5	USMG5	3	1184.2	3140.46 7	2697.7	2124.36 7	2231.33 3	2003.36 7
Ras-related protein Rab-3D	RAB3D	4	2194.43333 3	4454.76 7	3186.56 7	3013.93 3	2877.86 7	2915.03 3
Dr1-associated corepressor	DRAP1	2	423.166666 7	1389.3	1229.96 7	940.2	821.033 3	711.866 7
Transmembrane protein 126A	TMEM126A	3	132.166666 7	361.633 3	318.4	244.733 3	206.266 7	216.7
Histone deacetylase complex subunit SAP18	SAP18	9	2398.66666 7	6322.2	5025.1	4278.83 3	4019.36 7	3434.33 3
Insulin-degrading enzyme	IDE	20	1846.46666 7	4985.8	3976.46 7	3375.03 3	3016.83 3	2941.1
DNA-dependent protein kinase catalytic subunit	PRKDC	155	28212.2666 7	72826.0 3	54183.3 3	49324.2	50203.7 7	45541.7

Phospholipase D3	PLD3	4	878.433333 3	913.433 3	733.7	618.666 7	652.333 3	558.233 3
Isoform 3 of NADH-cytochrome b5 reductase 3	CYB5R3	8	938.633333 3	1766.4	1340.03 3	1196.86 7	1430.76 7	1146.6
cDNA FLJ56092, highly similar to Pentatricopeptide repeat protein 1	5	1042	1938.733	1646.46 7	1313.83 3	1184.63 3	1162.1	
Microsomal glutathione S-transferase 1	MGST1	5	946.666666 7	1743.4	1552.86 7	1181.63 3	1136.6	1089.13 3
BRO1 domain-containing protein BROX	BROX	4	1127.03333 3	3629.46 7	3401.13 3	2460.33 3	2282.13 3	2259.56 7
Ubiquitin-conjugating enzyme E2 N	UBE2N	8	2555.33333 3	7205.23 3	6006.16 7	4884.46 7	4398.36 7	4396.4
Superoxide dismutase [Cu-Zn]	SOD1	8	1129.46666 7	3461.93 3	1966.23 3	2347.26 7	2456.26 7	1900.66 7
Mothers against decapentaplegic homolog 3	SMAD3	2	818.133333 3	1241.83 3	915.3	842.033 3	954.6	842.333 3
Ras-related protein Rab-23	RAB23	3	163.066666 7	276.533 3	258.1	187.566 7	184.666 7	166.133 3
cDNA, FLJ96923, highly similar to Homo sapiens ribophorin II (RPN2), mRNA	18	3983.36666 7	9501.533	7525.7	6445.13 3	6272.4	6127.23 3	
ADP-ribosylation factor 3	ARF3	2	2270.13333 3	6581.2	5322.2	4465.4	3674.53 3	3907.6
S-phase kinase-associated protein 1	SKP1	11	2764.26666 7	7426.76 7	6175.06 7	5039.26 7	4171.46 7	3564

Receptor-interacting serine/threonine-protein kinase 1	RIPK1	6	617.5	1225.86 7	1010.53 3	831.833 3	776.133 3	720.366 7
DNA mismatch repair protein Msh6	MSH6	45	8537.46666 7	17200.4 7	15335.4 7	11675.3 3	11570.5 7	10403.6 3
Centrosomal protein 170kDa	CEP170	1	8511.66666 7	16952.5 7	11511.6 7	11508.7	10886.4 7	10136.5 7
DnaJ homolog subfamily B member 1	DNAJB1	20	5724.63333 3	11818.6	9162	8027.73 3	8012.73 3	7036.33 3
Peroxiredoxin-2	PRDX2	14	6589.7	13943.1	9436.2	9472.3	11482.6 3	9814.6
Migration and invasion enhancer 1	MIEN1	3	381.2	860.466 7	667.133 3	584.566 7	555.766 7	561.933 3
Glutathione S-transferase theta-1	GSTT1	1	469.7	689.8	463.4	468.8	650.466 7	477.3
H/ACA ribonucleoprotein complex non-core subunit NAF1	NAF1	1	158.9	363.366 7	417.233 3	246.966 7	162.766 7	135.5
Forkhead box protein K1	FOXK1	5	1764.96666 7	3190.13 3	2632.96 7	2168.63 3	2357.7	2148.36 7
Alcohol dehydrogenase class-3	ADH5	16	4397.5	10468.6	7659.8	7119.63 3	6852.1	6839.4
14-3-3 protein epsilon	YWHAE	25	11964.9666 7	31409.8	23841.4 3	21362.8	20334.3 7	19773.8 3
Probable Xaa-Pro aminopeptidase 3	XPNPEP3	3	945.4	1675.8	1307.46 7	1139.76 7	1014.53 3	1090.8
Dematin variant (Fragment)		1	228.1	462.2	288.533 3	314.4	409.133 3	325.9

U1 small nuclear ribonucleoprotein C	SNRPC	5	1129.466667	3780.033	2905.267	2571.8	2393.667	2338.967
Isoform 2 of Testis-expressed sequence 2 protein	TEX2	5	459.5	607.2	492.5667	413.1333	488.5667	402.2
Forkhead box protein K2	FO XK2	4	804.4666667	1954.1	1651.367	1329.867	1316.867	1201.967
Beta-centractin	ACTR1B	2	897	2523.733	2021.8	1717.6	1691.4	1582.867
RB-associated KRAB zinc finger protein	RBAK	1	183.1333333	436.4667	266	297.1	325	209.6333
Cytosolic purine 5'-nucleotidase (Fragment)	NT5C2	1	713.8666667	2171.067	1739.433	1477.867	1213.6	1297.967
Isoleucine--tRNA ligase, mitochondrial	IARS2	29	6454.066667	15051.83	10475.47	10246.4	11867.27	9805.5
GRHPR protein (Fragment)	GRHPR	6	2322.633333	4608.333	3298.933	3137.7	3497.367	3209.1
Phosphatidylinositol transfer protein alpha isoform	PITPNA	9	1726.4	4356.9	3618.433	2967.667	2633.767	2639.233
Adenosylhomocysteinase	AHCY	24	10840.9	24916.97	19118.23	16980.33	15329.47	15259.8
S-formylglutathione hydrolase	ESD	12	3726.866667	7935.067	5887.333	5408.3	5086.167	5296.6
cDNA FLJ76102, highly similar to Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum		7	970.9	1919.867	1564.133	1308.733	1304.767	1161.633

group B complementing) (ERCC3), mRNA								
Nucleus accumbens-associated protein 1	NACC1	5	236.033333 3	823.366 7	761.066 7	561.433 3	586.666 7	453.766 7
Core histone macro-H2A.1	H2AFY	13	4104.83333 3	7721.66 7	5457.03 3	5266.03 3	5784.7	5157.06 7
Electron transfer flavoprotein subunit beta	ETFB	18	5681.23333 3	9288.6	6393.4	6337.7	7737.16 7	5934.9
Putative ribonuclease	YBEY	3	166.533333 3	307.433 3	232.3	209.766 7	204.1	189.533 3
Isoform 2 of Procollagen- lysine,2-oxoglutarate 5- dioxygenase 1	PLOD1	24	4584.7	10261.9 3	6555.3	7002.53 3	9310.26 7	7455.1
5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	2	372.066666 7	1176.23 3	1036.83 3	802.766 7	498.9	481.7
N6-adenosine- methyltransferase 70 kDa subunit	METTL3	12	1530.23333 3	3905.23 3	3303	2666.23 3	2426.63 3	2299.1
Rho GTPase-activating protein 35	ARHGAP35	11	1437.3	3231.63 3	2519.5	2206.4	2385.56 7	2173.6
Exportin-4	XPO4	4	427.166666 7	1215.56 7	981.166 7	829.933 3	750.533 3	724.9
Isoform 2 of NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	NDUFB11	4	515.933333 3	621.833 3	563.6	424.566 7	411.933 3	364.2
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	18	6141.06666 7	9875.83 3	6738	6743.3	8298.66 7	6586.06 7

Programmed cell death protein 6	PDCD6	6	593.866666 7	1308.43 3	908.9	893.633 3	745.566 7	722.933 3
Unconventional myosin-XVIIIa	MYO18A	51	8633.56666 7	16083.6 3	12240.4	10984.9	12056.4	10477.5
E3 ubiquitin-protein ligase UHRF2	UHRF2	7	1339.06666 7	2417	1954.33 3	1651.23 3	1825.26 7	1367.23 3
Translocator protein	TSPO	3	635.933333 3	1435.13 3	1133.76 7	980.466 7	862.433 3	1021.53 3
NIMA (Never in mitosis gene a)-related kinase 9, isoform CRA_a	NEK9	10	1398.3	2638.8	2170.76 7	1802.8	1793.4	1668.83 3
Isoform 2 of Butyrophilin subfamily 2 member A1	BTN2A1	1	207.2	921.966 7	773.066 7	629.966 7	441.166 7	507.966 7
DDX11 protein	DDX11	3	410.1	737.833 3	609.833 3	504.166 7	497.3	432.633 3
Transforming acidic coiled-coil-containing protein 3	TACC3	6	343.233333 3	404.4	458.2	276.333 3	258.8	228.533 3
Isoform 2 of Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	9	1468.13333 3	3168.46 7	2469.2	2165.06 7	1914.86 7	1912.3
V-type proton ATPase subunit S1	ATP6AP1	3	325.433333 3	262.8	256.466 7	179.6	167.433 3	177
WD repeat-containing protein 3	WDR3	17	1139.73333 3	3160.53 3	2433.9	2160.1	2055.63 3	1972.3
Methyltransferase-like protein 16	METTL16	5	811.5	1636.16 7	1325.6	1118.33 3	944.266 7	1013.73 3
Carnitine O-palmitoyltransferase II,		1	1182.7	3633.467	2826.4	2483.6	2694.63 3	2213.96 7

mitochondrial variant (Fragment)								
cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB	2	6204.266667	16251.67	12027.53	11112.3	13041.6	10680.33	
Mannose-6-phosphate isomerase	MPI	7	1444.566667	2955.233	1507.267	2021.067	2536.5	1995.167
Calcium uniporter protein, mitochondrial	MCU	6	355.8333333	529.2667	386.4667	361.9667	385.5667	340.3667
cDNA, FLJ79026, highly similar to Dual specificity protein kinase CLK1 (EC2.7.12.1)	1	211.6666667	397.9	340.1333	272.1333	290.9667	286.1333	
Protein Smaug homolog 2	SAMD4B	2	421.4666667	466.2	382.3	318.9333	328.2667	329.8
Sorting nexin-12	SNX12	4	668.0666667	1771.3	1491.533	1212.4	1051.9	1064.233
Isoform 2 of EH domain-binding protein 1	EHBP1	9	1288.1	2009.033	1581.867	1375.133	1391.567	1144.633
Tetraspanin	CD81	2	279.6333333	369.3667	280.9667	252.8333	249.4667	224.8667
Interleukin-1 receptor-associated kinase 1	IRAK1	3	261.5666667	454.7	370.7	311.2667	291.0333	255.1
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	ETFDH	6	510.4666667	858.0667	599.0333	587.5667	768.6667	595.5333
Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	11	1652.066667	3050.933	2084.033	2089.2	2102.533	2219.533

Transcription elongation factor A protein-like 3	TCEAL3	2	120.166666 7	386.933 3	174.666 7	264.966 7	474.766 7	352.866 7
MAP kinase-activating death domain protein	MADD	4	248.4	603.833 3	457.233 3	413.7	409.366 7	374.166 7
Kinetochore-associated protein 1	KNTC1	7	793.666666 7	2269.76 7	2115.63 3	1555.4	1304.7	1295.36 7
Protein NDRG2	NDRG2	1	322	998.666 7	725.733 3	684.433 3	728.766 7	671.033 3
THO complex subunit 3	THOC3	12	1851.36666 7	5149.6	4004.86 7	3529.7	3481.46 7	3039
Molybdopterin synthase catalytic subunit	MOCS2	2	220.966666 7	420.7	306.966 7	288.366 7	323.566 7	271.8
Calmodulin (Fragment)	CALM2	8	6773.3	25303.6 7	21395.8 3	17344.3	14012.1	14708.3 3
Inverted formin-2	INF2	37	5533.23333 3	8269.33 3	6132.4	5668.3	6197.83 3	5301.96 7
All-trans-retinol 13,14-reductase	RETSAT	6	817.333333 3	1443.1	1076.46 7	989.233 3	1109.46 7	1007.43 3
Isoform 6 of PR domain zinc finger protein 10	PRDM10	3	319.6	745.366 7	586.533 3	511.033 3	522.4	435.966 7
Fumarate hydratase, mitochondrial	FH	19	5294.8	10416.7	7909.26 7	7142.26 7	7433.3	6860.9
Acetyl-coenzyme A synthetase 2-like, mitochondrial	ACSS1	4	386.166666 7	668.633 3	448.166 7	458.533 3	520.066 7	492.4
GrpE protein homolog 1, mitochondrial	GRPEL1	12	2593	8142.06 7	6089.36 7	5585.66 7	5928.5	5129.86 7
Serine/threonine-protein phosphatase 2A 65 kDa	PPP2R1A	22	7536.66666 7	17167.5 7	13726.6 3	11781.1 3	10039.0 3	10163.8 7

regulatory subunit A alpha isoform								
Proteasome subunit beta type-2	PSMB2	11	2413.56666 7	6159.96 7	5071.93 3	4228.5	3874.66 7	3747.9
Hermansky-Pudlak syndrome 5 protein	HPS5	2	120.133333 3	127.8	96.4	87.7333 3	103.233 3	92.2
cDNA, FLJ95005, highly similar to Homo sapiens kinesin family member 11 (KIF11), mRNA	24	3817	7256.667	8237.7	4982.3	3997.06 7	3638.63 3	
Protein FAM127A	FAM127A	2	284.266666 7	652.333 3	529.533 3	448	469	438.3
Voltage-dependent anion-selective channel protein 3	VDAC3	12	3892.23333 3	13475	11153.7	9255.56 7	8716.7	7664.33 3
Twinfilin-2	TWF2	11	2568.93333 3	4770.5	3324.5	3277.06 7	3339.46 7	3047.13 3
LEM domain-containing protein 2	LEMD2	4	480.066666 7	610.233 3	571.166 7	419.2	500.966 7	408.266 7
14-3-3 protein gamma	YWHAG	13	12725.1	27662.6 7	19911.9	19005.3 7	20707.8	18660.0 7
Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	2	300.433333 3	523.133 3	478.6	359.5	345.933 3	319.733 3
Histone deacetylase	HDAC1	10	2832.6	6683.46 7	5554.13 3	4593.66 7	4321.1	3871.66 7
Isoform 2 of Nuclear receptor 2C2-associated protein	NR2C2AP	4	503.466666 7	513.166 7	398.1	352.733 3	360.666 7	326.566 7
Isoform 3 of REST corepressor 3	RCOR3	4	723.6	1194.76 7	1071.93 3	821.3	905.266 7	710.766 7

Persulfide dioxygenase ETHE1, mitochondrial	ETHE1	6	1674.83333 3	2703.33 3	1933.96 7	1858.36 7	2289.2	1789.23 3
Trifunctional enzyme subunit beta, mitochondrial	HADHB	26	4357.06666 7	10125.5	7706.63 3	6961.13 3	8182.83 3	6714.7
Peptidyl-tRNA hydrolase 2, mitochondrial	PTRH2	7	1008.13333 3	1547.4	1054.43 3	1063.9	1092.76 7	947.7
Peroxiredoxin-4	PRDX4	8	4665.7	14264.7	10510.2 3	9809.43 3	9912.3	9118.3
DNA-directed RNA polymerase II subunit RPB7	POLR2G	4	805.666666 7	1750.03 3	1594.83 3	1203.6	1157.46 7	1058.9
Bromodomain and WD repeat-containing protein 1	BRWD1	2	423.866666 7	1060.1	994.2	729.1	666.933 3	569.133 3
Neudesin	NENF	7	1713.9	3830.5	2865.46 7	2634.7	3254.53 3	2548.56 7
Prostaglandin E synthase 2	PTGES2	12	1432.8	2712.56 7	2047.53 3	1865.8	2062	1810.7
cDNA FLJ12979 fis, clone NT2RP2006334, highly similar to WD repeat domain phosphoinositide-interacting protein 2		2	462.133333 3	1392.3	941.366 7	958.166 7	1007.63 3	866.933 3
cDNA FLJ78417, highly similar to Homo sapiens low density lipoprotein receptor-related protein associated protein 1 (LRPAP1), mRNA		14	1921.9	2500.667	2556.4	1721.13 3	2267.16 7	1733.3

cDNA FLJ75441, highly similar to Homo sapiens vaccinia related kinase 1 (VRK1), mRNA		7	1771.83333 3	3079.833	3039.5	2120.6	1678.63 3	1531.43 3	
DCN1-like protein 1	DCUN1D1		6	1276.16666 7	3418	2752.86 7	2354.1	2165.76 7	2146.13 3
Pancreatic progenitor cell differentiation and proliferation factor	PPDPF		1	336.5	227.266 7	185.766 7	156.566 7	152.7	128.933 3
CTP synthase 2	CTPS2		11	1653	3919.56 7	3038.2	2700.96 7	2469.1	2444
Dystroglycan 1 (Dystrophin-associated glycoprotein 1), isoform CRA_a	DAG1		6	758.133333 3	1119.33 3	1005.3	771.433 3	1488.33 3	721.566 7
Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT		4	337.466666 7	805.266 7	670.4	555.033 3	566.733 3	510.033 3
GTP:AMP phosphotransferase AK3, mitochondrial	AK3		12	1927.9	4385.93 3	3356.36 7	3023.3	3228.36 7	2769.03 3
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1		6	2118.83333 3	4304.73 3	2792.36 7	2967.46 7	4848.3	3119.36 7
Isoform 3 of Nuclear factor 1 X-type	NFIX		5	1145.3	2128.93 3	1640.23 3	1468.16 7	1727.46 7	1442.1
Microtubule cross-linking factor 1	MTCL1		9	1015.86666 7	1887.56 7	1468.43 3	1301.76 7	1452.1	1287.63 3
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	PPP3CA		1	645.366666 7	1157.13 3	773.433 3	798.1	951.4	828.433 3

Proliferating cell nuclear antigen	PCNA	18	12437.6333 3	18933.3	16145.5 7	13062	10617.9 3	10533.1
Uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	39	6828.73333 3	14794.6	10706.9 3	10207.7	11717.9 7	9795.43 3
CWF19-like protein 1	CWF19L1	12	1351.7	3354.2	2649.3	2314.46 7	1948.06 7	2213.66 7
Isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	1	1676.3	3810.33 3	3385.96 7	2629.8	2378.83 3	2278.56 7
YEATS domain-containing protein 2	YEATS2	9	1056.56666 7	2205.73 3	1851.5	1522.43 3	1534.23 3	1400.56 7
Dehydrogenase/reductase SDR family member 4	DHRS4	11	1775.1	4447.6	3615.2	3069.83 3	3371	2889.2
Epididymal secretory protein E1 (Fragment)	NPC2	7	2238.93333 3	2779.26 7	2600.86 7	1918.43 3	2377.96 7	1824.46 7
cDNA FLJ34919 fis, clone NT2RP7002779, highly similar to Leucine-rich repeat-containing protein 8D		4	360.866666 7	562.7667	445.333 3	388.5	443.566 7	374.6
cDNA, FLJ92955, highly similar to Homo sapiens transportin-SR (TRN-SR), mRNA		15	2223.73333 3	4517.433	4003.56 7	3118.6	2962.86 7	2715.9
Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate	MTHFD1	59	20498.1666 7	38259.6 7	28829.8 7	26414.4 7	26188.3 3	24467.7 3

cyclohydrolase, formyltetrahydrofolate synthetase, isoform CRA_a								
Fanconi anemia, complementation group I	FANCI	7	730.666666 7	1447.43 3	1544.23 3	999.366 7	810.6	687.133 3
Arginase-2, mitochondrial	ARG2	5	449.066666 7	1286.3	762.066 7	888.3	982.4	1146.03 3
Mediator of RNA polymerase II transcription subunit 15	MED15	9	817.966666 7	1204.06 7	1052.83 3	831.733 3	772.766 7	744.866 7
Chromodomain-helicase-DNA- binding protein 1-like	CHD1L	14	1420.3	2751	2195.3	1901.06 7	2021.33 3	1773.5
Tetratricopeptide repeat protein 38	TTC38	6	361.233333 3	1097.96 7	556.433 3	758.8	572.333 3	591.333 3
Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	7	4438.1	12466.3 7	9969.03 3	8618.9	7354.2	7367.2
Isoform 2 of Actin filament- associated protein 1	AFAP1	5	569.333333 3	823.666 7	644.833 3	569.466 7	576.266 7	412.533 3
Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	33	9341.2	19306.4	12934.5 3	13349.7	17270.6 3	13467
Isoform 2 of Amino-terminal enhancer of split	AES	2	127.866666 7	204.433 3	163.9	141.4	155.633 3	131.533 3
Nuclear cap-binding protein subunit 1	NCBP1	17	2487.83333 3	5843.9	4941.33 3	4042.4	3756.86 7	3583.16 7
Proteasome subunit alpha type-4	PSMA4	14	2757.06666 7	6420.26 7	5040.9	4441.13 3	3914.7	3850.5

Isoform 2 of 3-mercaptopyruvate sulfurtransferase	MPST	8	1741.66666 7	2985.13 3	2187.66 7	2065.16 7	2246.23 3	2082.6
Pre-mRNA-splicing factor SYF1	XAB2	12	1072.36666 7	1943.56 7	1663.5	1344.73 3	1193.73 3	1082.1
DNA-(apurinic or apyrimidinic site) lyase	APEX1	18	5103.53333 3	9511.43 3	7193.46 7	6581.1	6049.63 3	6249.66 7
DNA replication complex GINS protein PSF2	GINS2	3	502.666666 7	1659.46 7	1854.2	1148.4	961.666 7	858.133 3
Isoform 2 of Neutral alpha-glucosidase AB	GANAB	1	5916.53333 3	15174.3 7	11313.2 7	10502.4 7	12247.5 7	10129.0 7
Adenylyl cyclase-associated protein 2	CAP2	13	1782.7	3675.93 3	2677.86 7	2544.56 7	2358.26 7	2284.26 7
U4/U6.U5 tri-snRNP-associated protein 2	USP39	17	2751.03333 3	7428.73 3	6226.96 7	5143.66 7	4580.96 7	4226.16 7
cDNA FLJ10772 fis, clone NT2RP4000243, highly similar to Cartilage-associated protein		4	1038.53333 3	2765.733	2716.5	1915.7	2142.03 3	1215.36 7
cDNA FLJ61705, highly similar to Symplekin		19	3237.06666 7	6376.8	5237.43 3	4417.13 3	4335.63 3	3803.5
CAD protein	CAD	60	13378.5333 3	23532.0 3	17791.6	16303.1	14943	14633.7
cDNA, FLJ95164, highly similar to Homo sapiens SEC14-like 2 (S. cerevisiae) (SEC14L2), mRNA		4	570.866666 7	1323.5	842.466 7	917.033 3	1072.73 3	978.6
Echinoderm microtubule-associated protein-like 4	EML4	3	5092.33333 3	10424.9 7	7813.2	7224.53 3	7270.73 3	6629.3

Inner centromere protein	INCENP	4	865.366666 7	1316.66 7	1318.2	912.466 7	795	794.1
Isoform 2 of Ras-responsive element-binding protein 1	RREB1	8	817.2	1548.46 7	1033.2	1073.4	1292.3	1061.73 3
cDNA FLJ51426, highly similar to Adapter-related protein complex 3 beta-1 subunit	1	2320.33333 3	6343.6	4859.83 3	4397.6	4270.66 7	4081.8	
Isoform 3 of Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B	MGAT4B	1	152.966666 7	226.666 7	178.833 3	157.133 3	174.4	156.5
NHS-like protein 1 (Fragment)	NHSL1	1	373.833333 3	812.533 3	594.566 7	563.566 7	633	509.733 3
Isoform 5 of MMS19 nucleotide excision repair protein homolog	MMS19	13	1362.76666 7	3466.06 7	2590.83 3	2404.5	2138.56 7	2133.6
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	14	1588.76666 7	5098.66 7	3058.26 7	3537.2	3821.73 3	3244.73 3
Plexin-B2	PLXNB2	14	1523.86666 7	3421.66 7	2595.46 7	2373.86 7	2940.76 7	2208.5
Trafficking protein particle complex subunit 3	TRAPPC3	6	732.933333 3	2484.76 7	2154.7	1724.2	1357.66 7	1375.7
Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	11	7418.53333 3	19627.3 3	14672.1	13620.8 7	12742.3	11672.8 3
Uncharacterized protein		2	240.633333 3	700.866 7	552.5	486.466 7	446.7	471.233 3

Gem-associated protein 5	GEMIN5	38	5743.2	14975.2	12837.4 7	10395.6 7	8202.7	8482.96 7
Manganese-transporting ATPase 13A1	ATP13A1	16	2010	3348.36 7	2536.33 3	2324.43 3	2930.7	2279.56 7
Zinc transporter ZIP10	SLC39A10	4	484.666666 7	1469.6	1207.63 3	1020.33 3	1206.9	744.266 7
Cat eye syndrome critical region protein 5	CECR5	6	676.466666 7	1275.26 7	938.466 7	885.466 7	897.733 3	759.533 3
Activated RNA polymerase II transcription cofactor 4 variant (Fragment)	8	3529.4	5753.4	4269.5	3995.06 7	3788.56 7	3462.93 3	
Replication protein A 70 kDa DNA-binding subunit	RPA1	24	4590.16666 7	11161.7 3	9030.3	7753.36 7	7500.96 7	6793.46 7
S-adenosylmethionine synthase isoform type-2	MAT2A	19	4972.2	9494.43 3	8627.16 7	6596.5	5914.53 3	5317.96 7
UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	30	4552.93333 3	8939.2	7015.23 3	6210.8	7427.2	6473.2
Melanotransferrin	MELTF	6	640.833333 3	794.9	659.7	552.333 3	777.533 3	564.933 3
HEAT repeat containing 5B	HEATR5B	3	174.066666 7	401.3	311.6	278.9	240.633 3	301.633 3
Echinoderm microtubule-associated protein-like 4	EML4	1	4638.16666 7	9099.7	6803.43 3	6325.2	6351.9	5830.76 7
Aldehyde dehydrogenase 1 family, member L1 variant (Fragment)	1	232.766666 7	515.5667	458.1	358.466 7	334.733 3	331.966 7	
cDNA FLJ32418 fis, clone SKMUS2000863, weakly similar	2	142.033333 3	648.2333	580.266 7	450.833 3	399	407.533 3	

to PROBABLE ASPARAGINYL- TRNA SYNTHETASE (EC 6.1.1.22)								
Nuclear receptor coactivator 5	NCOA5	10	939.9	2023.4	1806.1	1407.26 7	1354.8	1262.76 7
Lamin-B2	LMNB2	41	14042.8333 3	24448.9	17971.9 3	17004.7	18415.3 7	16338.2 3
Isoform 3 of Metastasis- associated protein MTA1	MTA1	20	3672.53333 3	7763.03 3	6678.46 7	5399.8	5395.33 3	4279.5
Rho GTPase-activating protein 12	ARHGAP12	5	980.466666 7	1864.76 7	1405.43 3	1297.2	1262.06 7	1155.86 7
cDNA FLJ55760, highly similar to Squalene synthetase (EC 2.5.1.21)	4	604.366666 7	1085.7	1355.8	755.333 3	649.433 3	661.833 3	
Mevalonate kinase (Fragment)		2	570.466666 7	809.433 3	682	563.133 3	573.333 3	568.666 7
Upstream stimulatory factor 2	USF2	1	1050.9	2588.26 7	2191.76 7	1800.83 3	1727.76 7	1663.3
BRCA1-associated ATM activator 1	BRAT1	7	833.166666 7	1114.86 7	1117.9	775.866 7	714.3	706.466 7
Isoform 2 of Cytochrome c oxidase protein 20 homolog	COX20	4	1102.06666 7	2550.2	1960.46 7	1774.76 7	1991.86 7	1535.46 7
Kynurenine--oxoglutarate transaminase 3	KYAT3	7	687.166666 7	1295.3	915.133 3	901.5	916.966 7	847.1
Protein ELOB (Fragment)	ELOB	7	1644.93333 3	3246.46 7	2633.03 3	2260.26 7	2033.7	1773.16 7
Acyl-CoA-binding domain- containing protein 7	ACBD7	2	426.366666 7	872.1	633.2	607.233 3	728.066 7	593.766 7

cDNA, FLJ94852, highly similar to Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA	4	289.9	1071.6	836.533 3	746.166 7	708.3	732	
Methylthioribose-1-phosphate isomerase	MRI1	8	941.566666 7	1949.8	1401.83 3	1357.9	1395.83 3	1373.86 7
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	7	702.666666 7	1899.2	1735.93 3	1322.76 7	1261.3	1119
Polyadenylate-binding protein 2	PABPN1	9	1578.96666 7	4394.6	3534.03 3	3060.83 3	2951.1	2810.1
Translin-associated protein X	TSNAX	15	1328.8	4125.3	3367.23 3	2873.66 7	2440.03 3	2460.03 3
Isoform 3 of Malate dehydrogenase, cytoplasmic	MDH1	18	9764.96666 7	20014.1 7	14795.5	13942.3 7	13488.4 7	13308.2 3
39S ribosomal protein L22, mitochondrial	MRPL22	5	1175.16666 7	3254.4	2556.96 7	2267.43 3	2217.7	2112.86 7
Exportin-1	XPO1	30	5477.06666 7	14642.7 3	11577.4 7	10202.1 7	8588.8	9558.5
Negative elongation factor B	NELFB	13	1712.76666 7	4204.26 7	3621.4	2930.13 3	2516.26 7	2430.9
Protein LSM14 homolog A	LSM14A	9	1405.93333 3	2524.9	2003.3	1759.83 3	1676.23 3	1549.46 7
NAD-dependent protein deacetylase sirtuin-6	SIRT6	1	55.6666666 7	69.2	77.2333 3	48.2333 3	47.8666 7	43.3666 7
cDNA FLJ58659, highly similar to Homo sapiens pre-B-cell leukemia transcription factor		11	1044.93333 3	2168.667	1463.3	1511.73 3	1753.43 3	1871.63 3

interacting protein 1 (PBXIP1), mRNA								
cDNA, FLJ96143, highly similar to Homo sapiens paralemmmin (PALM), mRNA	3	699.0666667	1836.967	1248.4	1280.533	1879.467	1294.7	
Elongation factor Ts, mitochondrial	TSFM	10	2337.6	3971.1	2937.333	2768.3	2636.2	2446.333
Mitochondrial antiviral-signaling protein	MAVS	4	778.8333333	1511.267	1143.3	1053.567	1177.1	957.0333
Dystonin	DST	3	23228.7	49828.33	37425.23	34743.63	32531.47	31361.47
Polymerase delta-interacting protein 2	POLDIP2	9	2081.6666667	4903.133	4382.2	3419.1	3202.833	2842.3
Macrophage migration inhibitory factor	MIF	4	3360.8	3965.6	2788.833	2765.6	3877.7	2971.333
Isoform 2 of Uncharacterized protein KIAA2013	KIAA2013	8	221.6	521.3	400.4667	363.5667	443.2667	334.9333
Isoform 2 of Nuclear factor NF-kappa-B p105 subunit	NFKB1	9	1446.733333	3332.867	2606.8	2324.667	2292.767	2222.5
Syndetin	VPS50	5	162.56666667	601.5	490.4	419.6	363.1667	350.8667
Ephrin type-B receptor 2	EPHB2	3	562.6	1035.9	889.2667	722.6667	563.6333	443.2333
Protein DEK	DEK	19	5364.3	12124.47	9575.6	8459.6	8501.833	7444.8
Importin-9	IPO9	14	2980.333333	7419.067	5612.5	5176.867	4690.433	4758.3

Glucosidase, alpha acid (Pompe disease, glycogen storage disease type II), isoform CRA_a	GAA	7	1037.2	2485.93 3	1912.86 7	1734.73 3	2517.5	1408.3
PEST proteolytic signal-containing nuclear protein	PCNP	10	2568.5	4538.56 7	3500.3	3167.9	2959.5	2784.7
cDNA FLJ43948 fis, clone TESTI4014924, highly similar to Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1), transcript variant 1, mRNA	18	2020.9	6362.533	5068.26 7	4441.03 3	4200.16 7	4064.96 7	
28S ribosomal protein S25, mitochondrial	MRPS25	2	363.8	432.533 3	341.433 3	301.933 3	301.866 7	280.9
Protein FPGT-TNNI3K	FPGT-TNNI3K	1	179.966666 7	377.7	250.6	263.7	270.366 7	244.233 3
Farnesyltransferase, CAAX box, alpha, isoform CRA_a	FNTA	4	520.8	1753.7	1249.83 3	1224.56 7	1282.36 7	1151.73 3
Dystonin	DST	4	23861.9333 3	50687.1	38141.6	35394.8 3	33133.1	31949.9
Anamorsin	CIAPIN1	12	3110.3	7151.53 3	6091.8	4994.7	4171.33 3	4166.2
PIK4CA variant protein (Fragment)	PIK4CAvariantprotein	4	466.033333 3	1395.66 7	1185.7	974.766 7	859.933 3	871
Prostaglandin reductase 3	ZADH2	3	311.8	681.066 7	498.333 3	475.733 3	530.1	421.266 7
Nucleoside diphosphate kinase	NME1-NME2	1	9984.56666 7	22373.4 3	17049.3	15630.1	12982.3 3	13375.6 7

RNA polymerase I-specific transcription initiation factor RRN3	RRN3	3	620.4	1170.6	1112.06 7	817.9	843.733 3	752.566 7
Histone deacetylase 2	HDAC2	4	2482.73333 3	5192.63 3	4577.86 7	3628.36 7	3344.7	2938.46 7
cDNA, FLJ93313, highly similar to Homo sapiens lectin, mannose-binding, 1 (LMAN1), mRNA	15	2042.46666 7	4444.867	3648.13 3	3106.36 7	3199	2660.66 7	
Isoform 2 of DNA-directed RNA polymerase I subunit RPA49	POLR1E	11	2408.3	5251.93 3	4612.46 7	3671.33 3	3384.66 7	3148.53 3
cDNA FLJ41718 fis, clone HLUNG2013097, highly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 2	1	309	1460.333	1188.63 3	1021	959.4	969.933 3	
Beta-enolase	ENO3	2	8777.36666 7	17063.8 7	11060.7 7	11933.0 3	12247.3 7	12359.9 3
14-3-3 protein sigma	SFN	2	5036.76666 7	11373.7 7	8368.73 3	7954.53 3	8744.83 3	7807.9
Deoxyribose-phosphate aldolase	DERA	7	754.6	1615.8	1225.83 3	1130.1	1170.4	1061.73 3
Hermansky-Pudlak syndrome 3 protein	HPS3	4	141.933333 3	289.533 3	231.366 7	202.533 3	180.066 7	198.066 7
Dihydropyrimidine dehydrogenase [NADP(+)]	DPYD	26	3040.2	7672.03 3	3963.33 3	5366.73 3	6001.83 3	5423.3
Ancient ubiquitous protein 1	AUP1	10	1456.4	2458.83 3	2087.96 7	1720.4	1654.76 7	1490.7

Protein flightless-1 homolog	FLII	32	5668.66666 7	12102.1 7	8816.53 3	8468.06 7	7682.93 3	8524.8
Transmembrane and ubiquitin-like domain-containing protein 1	TMUB1	2	149.133333 3	200.033 3	154.333 3	139.966 7	152.033 3	162.066 7
Mothers against decapentaplegic homolog 4	SMAD4	8	709.5	2100.23 3	1795.1	1469.6	1293.46 7	1351.93 3
Immunity-related GTPase family Q protein	IRGQ	10	1098.76666 7	1922.16 7	1616.3	1345.23 3	1149.06 7	1176.33 3
28S ribosomal protein S23, mitochondrial	MRPS23	6	1401.8	2652.5	2424.2	1856.66 7	1728.76 7	1531.06 7
Short-chain acyl-CoA dehydrogenase	ACADS	5	595.533333 3	1329	922.2	930.3	1237.13 3	901.366 7
Isoform 2 of Caspase recruitment domain-containing protein 19	CARD19	4	93.2666666 7	30.2333 3	24.6333 3	21.1666 7	24.4	21.0333 3
Serine hydroxymethyltransferase, cytosolic	SHMT1	12	2341.16666 7	4176.53 3	2984.33 3	2924.23 3	3302.23 3	2604.83 3
Isoform 3 of Replication protein A 32 kDa subunit	RPA2	7	1404.46666 7	2573.36 7	2074.5	1802.06 7	1690.33 3	1476.4
Putative peptidyl-tRNA hydrolase PTRHD1	PTRHD1	7	895.466666 7	1648.4	1432.83 3	1154.46 7	1123.3	1051.26 7
Nardilysin	NRDC	17	2242.8	6106.23 3	5551.4	4276.66 7	3438.53 3	3339.7
Coatomer subunit gamma-2	COPG2	9	722.466666 7	1588.66 7	1133.3	1112.7	1032.16 7	1015.8

Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	22	3208.36666 7	6657.93 3	4991.2	4663.5	5330.5	4362.83 3
[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial	BCKDK	5	850.733333 3	1721.43 3	1046.6	1206.16 7	1828.23 3	1239.3
Isoform 3 of Histone deacetylase 5	HDAC5	1	263.466666 7	1028.8	804	721.266 7	623.933 3	555.8
Dolichol-phosphate mannosyltransferase subunit 1 (Fragment)	DPM1	6	913.333333 3	2266.93 3	1898.03 3	1589.4	1619.7	1513.26 7
Isoform 2 of Fas apoptotic inhibitory molecule 1	FAIM	2	156.4	557.366 7	524.233 3	390.8	363.733 3	363.7
Glomulin	GLMN	6	931	1781.06 7	1517.9	1248.93 3	1082.43 3	1162.6
N-acetyltransferase ESCO1	ESCO1	2	363.1	1060.36 7	811.3	743.9	743.633 3	1204.06 7
General transcription factor II-I	GTF2I	55	18400.3333 3	31758.5 3	26038.5 3	22285	22999.3	20027.2 7
Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1	10	2204.53333 3	4340.4	3051.93 3	3045.86 7	3009.86 7	2572.6
ATP synthase subunit epsilon, mitochondrial	ATP5E	4	1247.6	2693.36 7	2155.63 3	1890.3	2131.3	1710.06 7
Ornithine aminotransferase, mitochondrial	OAT	28	5264	13717.0 7	10254.2 3	9627.26 7	10379.4	9906.9
Isoform 2 of Cohesin subunit SA-2	STAG2	12	1791.4	4742.93 3	4055.23 3	3328.83 3	3337.16 7	3110.66 7

Peroxisomal biogenesis factor 19	PEX19	2	325.433333 3	961.733 3	767.9	675.2	622.966 7	570.066 7
Isoform 3 of Protein MEMO1	MEMO1	6	833.3	1991.33 3	1687.06 7	1398.1	1160.56 7	1196.36 7
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	13	3075	6148.73 3	4371.83 3	4317.86 7	4881.93 3	4236.83 3
Glycosaminoglycan xylosylkinase	FAM20B	1	127.933333 3	239.233 3	261.066 7	168	190.4	137.433 3
Pachytene checkpoint protein 2 homolog	TRIP13	14	2537.93333 3	6409.66 7	5172.2	4501.23 3	3736.06 7	3882.16 7
Signal peptidase complex subunit 3 homolog (S. cerevisiae), isoform CRA_a	SPCS3	4	398.033333 3	1454.63 3	1198.26 7	1021.6	853.9	915.5
Telomere-associated protein RIF1	RIF1	37	3638.63333 3	6912.53 3	6281.13 3	4855.86 7	4630.43 3	4146.56 7
Cytochrome c oxidase copper chaperone	COX17	4	764.6	1335.16 7	1356.03 3	938	904.366 7	742.033 3
Isoform 2 of Protein TANC2	TANC2	3	354.5	688.5	542.733 3	483.733 3	607	483.166 7
Tubulin beta-3 chain	TUBB3	6	28782.6	54396.0 7	41746.7	38218.2 7	35305.3 7	34179.6 7
Ephrin type-A receptor 2	EPHA2	30	4424.83333 3	14115.5	12803.3 3	9918.8	9939.16 7	7277.66 7
REST corepressor 1	RCOR1	11	2036.8	4402.96 7	3521.53 3	3094.2	3371.46 7	2721.16 7

Isoform Tau-C of Microtubule-associated protein tau	MAPT	5	709.366666 7	1775.73 3	1189.86 7	1248.5	1609.6	1314.66 7
FAD synthase	FLAD1	5	235.366666 7	537.733 3	423.366 7	378.133 3	408.2	394.633 3
Isoform 3 of Phosphatidylinositol transfer protein beta isoform	PITPNB	2	2241.43333 3	5457.93 3	4659.33 3	3838.1	3105.86 7	3216.23 3
Isoform 2 of Dipeptidyl peptidase 9	DPP9	16	1964.63333 3	5227.13 3	3555.36 7	3675.83 3	3228.2	3485.83 3
Enolase 1 (Fragment)		1	16565.8	33161.4 3	22853.8 3	23321.8	23195.9	23086.7 3
NFATC2-interacting protein	NFATC2IP	6	1185.83333 3	1308.33 3	1013.4	920.266 7	798.233 3	751.533 3
Peptidyl-prolyl cis-trans isomerase A	PPIA	14	31368.5333 3	55713.0 3	39731.6 3	39193.6	37364.8	38047.7 7
Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	8	756.6	2102.96 7	1395.93 3	1479.5	1723.06 7	1457.86 7
Kinesin-like protein KIFC1	KIFC1	14	1990.53333 3	2724.63 3	2705.76 7	1916.93 3	1902.93 3	1778
Retinol dehydrogenase 14	RDH14	6	500.633333 3	932.766 7	704.8	656.366 7	688.766 7	651.533 3
CDGSH iron-sulfur domain-containing protein 1	CISD1	4	566.3	997.366 7	626.633 3	702.066 7	790.033 3	662.633 3
F-box-like/WD repeat-containing protein TBL1X	TBL1X	1	221.133333 3	832.033 3	663	585.766 7	533.633 3	483.166 7
Serine palmitoyltransferase 2	SPTLC2	8	1222.73333 3	2185.2	1625.56 7	1538.93 3	1430.7	1413.1

Isoform 2 of BAG family molecular chaperone regulator 5	BAG5	5	648.866666 7	1624.06 7	1306.13 3	1144.03 3	1109.43 3	1010.26 7
Nuclear receptor-binding protein	NRBP1	5	732.966666 7	1478.73 3	1257.5	1041.7	957.266 7	913.8
cDNA FLJ76156, highly similar to Homo sapiens aspartyl-tRNA synthetase 2 (DARS2), mRNA	16	3439.63333 3	6533.033	4997.56 7	4602.43 3	4742.36 7	4273.43 3	
Fructose-bisphosphate aldolase (Fragment)	1	6471.7	11907.17	7742.6	8389.5	9274.63 3	9091.3	
Cytochrome b5	CYB5A	4	190.833333 3	640.733 3	581.1	451.533 3	371.233 3	367.866 7
rRNA adenine N(6)-methyltransferase		7	673.233333 3	1852.23 3	1468.36 7	1305.3	1288.8	1151.46 7
Aflatoxin B1 aldehyde reductase member 2	AKR7A2	7	2212.3	5112.16 7	3436.7	3602.7	4119.26 7	3605.36 7
Vesicle-associated membrane protein-associated protein B/C	VAPB	10	2881.16666 7	6448.46 7	4571.5	4545.5	5189.26 7	4349.5
Histone H2A		3	13975	28179.3 3	22178.1 7	19864.2 7	19989.5 3	21836.4 3
cDNA FLJ75337		7	765.033333 3	1888.73 3	1783.56 7	1331.46 7	1324.46 7	1256.2
Plasma membrane calcium-transporting ATPase 1	ATP2B1	2	1821.9	3026.8	2312.96 7	2133.8	3115.53 3	2047.33 3
Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	4	2128.3	5136.13 3	4530.03 3	3621.4	3336.9	3143.23 3

NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3	2	343.033333 3	804.7	793.7	567.4	573.466 7	428.533 3
ATPase WRNIP1	WRNIP1	16	2988.63333 3	5054.06 7	3450.8	3564.03 3	4042.06 7	3217.86 7
1-phosphatidylinositol 4,5- bisphosphate phosphodiesterase beta-3	PLCB3	23	3346.86666 7	6704.8	4862.86 7	4728.13 3	4794.9	4264.76 7
Transcription initiation factor TFIID subunit 4	TAF4	4	677.8	1146.03 3	987.533 3	808.2	843.3	705.9
Prosaposin variant (Fragment)		14	3805.73333 3	7954.4	5426.96 7	5610.03 3	7604.06 7	5860.76 7
Isoform 2 of RAF proto- oncogene serine/threonine- protein kinase	RAF1	2	459	1076.8	995.533 3	759.466 7	727.733 3	668.433 3
Isoform 3 of Collagen type IV alpha-3-binding protein	COL4A3BP	11	1691.66666 7	3967.9	3147.63 3	2798.93 3	2733.53 3	2705
3-keto-steroid reductase	HSD17B7	4	951.066666 7	1995.2	1324.6	1407.5	1437.93 3	1251.13 3
V-type proton ATPase subunit E 1	ATP6V1E1	9	1584.7	3248.46 7	2604.16 7	2291.93 3	2290.86 7	2244.4
Zinc finger CCHC-type and RNA- binding motif-containing protein 1	ZCRB1	1	175.4	727.633 3	607.233 3	513.4	473.7	453.133 3
Isoform 3 of Calmodulin- regulated spectrin-associated protein 1	CAMSAP1	6	347.366666 7	854.633 3	698.666 7	603.333 3	543.9	502.966 7

Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	PHKA1	6	438.9	1346.53 3	1029.16 7	950.766 7	985.7	949.666 7
Receptor tyrosine-protein kinase erbB-2	ERBB2	2	652.366666 7	1050.23 3	877	741.733 3	813.366 7	624.866 7
COBW domain-containing protein 2	CBWD2	11	1056.66666 7	1399.2	1028.76 7	988.2	1017.26 7	982.8
Isoform 2 of COP9 signalosome complex subunit 1	GPS1	10	1998.9	3762.2	3206.03 3	2657.1	2367.26 7	2421.16 7
Isoform 2 of STE20-like serine/threonine-protein kinase	SLK	49	10201.9	22144	15684.1 3	15642.8	15201.3	13900.9 7
Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	11	1797.9	3966.76 7	2881.46 7	2803.33 3	3067.2	2576.13 3
Isoform 2 of HBS1-like protein	HBS1L	2	937.533333 3	1914.63 3	1571.5	1353.53 3	1230.93 3	1155.2
Perilipin-3	PLIN3	28	13325.1666 7	20042.2	13265.7 3	14169.9	14549.7 7	13477.1 7
Ubiquitin-conjugating enzyme E2 L3	UBE2L3	13	3602.6	6115.53 3	4838.5	4323.8	3534.2	3799.33 3
Thymidylate kinase	DTYMK	13	1991.96666 7	4512.3	3644.4	3190.73 3	2867.66 7	2846.36 7
Copine-3	CPNE3	14	3211.3	7449.26 7	5822.86 7	5268.46 7	5365.6	5082.1
RNA pseudouridylate synthase domain-containing protein 2	RPUSD2	4	905.9	1782.83 3	1460	1260.93 3	1038.56 7	1170.46 7

Reticulon-4	RTN4	9	2622.26666 7	4315.23 3	3657.5	3052.5	2950.2	2576.4
STIM1L	STIM1	7	292.3	599.066 7	524.966 7	423.8	380.433 3	374.533 3
(E3-independent) E2 ubiquitin-conjugating enzyme	UBE2O	20	2700.46666 7	6010.23 3	4245.3	4253.3	4147.33 3	4163.5
Probable aminopeptidase NPEPL1	NPEPL1	8	715.3	2017.13 3	1285.43 3	1427.56 7	1549.43 3	1415.56 7
Receptor-type tyrosine-protein phosphatase S	PTPRS	2	610.266666 7	1213.5	609.266 7	858.9	1203.6	943.766 7
DNA-directed RNA polymerase, mitochondrial	POLRMT	9	1001	1916.2	1631.96 7	1356.33 3	1372	1261.36 7
Nucleoporin 54kDa variant (Fragment)		14	2517.3	4302.8	3538.86 7	3045.73 3	2895.1	2873.73 3
Lysocardiolipin acyltransferase 1	LCLAT1	7	896.866666 7	2905.46 7	2505.86 7	2056.7	1966.33 3	1896.96 7
Golgi phosphoprotein 3	GOLPH3	4	921.1	2545.16 7	2356.76 7	1801.76 7	1591.73 3	1705
Choline-phosphate cytidyltransferase A	PCYT1A	17	4956.4	8666.96 7	6535.63 3	6135.86 7	5792.76 7	5952.86 7
Cytochrome b-c1 complex subunit 6, mitochondrial	UQCRH	4	1659.86666 7	3019.66 7	2480.3	2138.06 7	2227.13 3	1849.63 3
KIAA0415 gene product	KIAA0415	4	1775.13333 3	3260.73 3	2734.23 3	2309.2	2355.2	2296.26 7
Glycogen phosphorylase, brain form	PYGB	2	19888.7333 3	45402.5 7	32311.1	32154.5	33149.5	32646.4 7
Matrin-3	MATR3	36	9843.7	19928.3 3	15924.1 7	14114.1	14510.5 3	12802.2 7

Alpha-1,4 glucan phosphorylase (Fragment)		2	19831.9333 3	45300.07	32248	32090.1	33076.1 7	32584.1 3	
Copine-7	CPNE7		4	1011.96666 7	1788.2	1407.7	1266.76 7	1469.1	1230.26 7
Intersectin-1	ITSN1		5	1163.43333 3	2280.86 7	1711.86 7	1615.86 7	1750.3	1581.76 7
cDNA, FLJ94599, highly similar to Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA		9	2260.13333 3	4993.533	3658.66 7	3537.76 7	3575.9	3220.86 7	
cDNA FLJ53353, highly similar to ATP-binding cassette sub-family D member 3		8	1313.23333 3	3756.2	3049.86 7	2661.33 3	2779	2676.66 7	
B-cell CLL/lymphoma 9-like protein	BCL9L		3	341.733333 3	844.833 3	864.8	598.733 3	522.633 3	511.3
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB		9	2351.4	4348.9	3098.76 7	3082.1	3499.33 3	3192.53 3
Tubulin beta-6 chain	TUBB6		10	19295	40355.8 7	30613.4 7	28600.5 7	25743.9	25751.4
Isoform 2 of Leucine-rich repeat flightless-interacting protein 1	LRRFIP1		1	6702.4	14063.8 3	9147.16 7	9967.7	9470.13 3	8782.23 3
RNA-binding protein 47	RBM47		2	213.9	436.966 7	316.166 7	309.7	336.633 3	286.233 3
Borealin	CDCA8		6	743.9	1021.53 3	1243.13 3	724.033 3	691.433 3	628.066 7

RNA-binding protein Musashi homolog 2	MSI2	7	767.166666 7	1276.8	904.9	905	885.633 3	842.9
3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	14	4267.43333 3	6947.06 7	5261.83 3	4924.16 7	4902.86 7	4538.76 7
Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	29	10008.9	22228.6 7	15063.6	15756.4 7	16298.9 3	15221.6
Mitochondrial-processing peptidase subunit beta	PMPCB	15	2926.93333 3	5342.9	4307.96 7	3788.76 7	3606.73 3	3296.66 7
Isoform 6 of SHC-transforming protein 1	SHC1	12	1975.23333 3	3430.46 7	2257.1	2432.8	2552.13 3	2458.33 3
Transforming growth factor beta receptor type 3	TGFBR3	2	286.266666 7	263.4	205.7	186.8	192.433 3	223.133 3
Carnitine O-palmitoyltransferase 2, mitochondrial	CPT2	4	1399.86666 7	4534.9	3524.7	3216.3	3564.56 7	2968.96 7
cDNA, FLJ96812, highly similar to Homo sapiens threonyl-tRNA synthetase (TARS), mRNA		37	8082.86666 7	19041.7	14750.6 3	13505.0 7	11043.9 7	12379.3
Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	18	2474.46666 7	4351.3	3775.26 7	3086.63 3	2918.33 3	2707.8
Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 2	HACD2	2	575.133333 3	743.9	637.866 7	527.8	530.233 3	394.433 3
Isoform 2 of Galactokinase	GALK1	13	2278.33333 3	4008.63 3	3021.9	2844.53 3	3105.93 3	2828.3
Similar to AFG3 ATPase family gene 3-like 2 (Yeast) (Fragment)		30	6099.16666 7	14467.07	10863.6 7	10265.9	11182.4	9889.4

Isoform 3 of Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma	PIP5K1C	2	136.766666 7	175.633 3	184.133 3	124.633 3	173.933 3	96.6666 7
GC-rich sequence DNA-binding factor 2	GCFC2	6	530.8	1208.06 7	1115.43 3	857.366 7	584.266 7	663.5
MHC class I antigen (Fragment)	HLA-B	2	425.2	844.933 3	570.366 7	599.7	1013.36 7	675.366 7
High mobility group protein B1	HMGB1	17	18693.1666 7	33111	21576.6 3	23501.4	21914.6 3	20338.7 7
cDNA FLJ10711 fis, clone NT2RP3000917, highly similar to 5'-3' exoribonuclease 2 (EC 3.1.11.-)		33	6018.6	12420.6	10768.8	8816	8149.3	7527.7
Presenilins-associated rhomboid-like protein, mitochondrial	PARL	4	355.033333 3	659.266 7	570.266 7	468.066 7	492.766 7	427.233 3
Signal transducer and activator of transcription (Fragment)		8	1045.23333 3	2168.633	1842.23 3	1539.86 7	1418.53 3	1421.76 7
Putative uncharacterized protein (Fragment)		21	3729.8	9032.6	7271.56 7	6414.7	6436.26 7	6422.63 3
ATP synthase subunit alpha, mitochondrial	ATP5A1	37	16952.0666 7	31564.2 3	24108.1 7	22416.4	23752.9	21814.3
von Willebrand factor A domain-containing protein 8	VWA8	6	217.7	416.266 7	345.1	295.633 3	337.666 7	246.9
Phosphatidylinositol transfer protein beta isoform	PITPNB	1	2397.86666 7	5834.96 7	5090.16 7	4144.03 3	3447.03 3	3521.36 7

Torsin family 3, member A, isoform CRA_b	TOR3A	2	214	556.333 3	686.4	395.133 3	383.166 7	382
AP-2 complex subunit alpha-2	AP2A2	1	6345.3	12379.0 3	9622.76 7	8792.53 3	9552.23 3	8286.7
Heterogeneous nuclear ribonucleoprotein L-like	HNRPLL	14	2133.43333 3	4954.26 7	4010.66 7	3519.3	3512.53 3	2963.1
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	1	12998.1	27551.6 7	20856.3 3	19572.0 7	18746.7 3	16867.7 7
Isoform 2 of Iron-sulfur cluster assembly 1 homolog, mitochondrial	ISCA1	3	807.066666 7	2121.6	1683.1	1507.26 7	1496.5	1288.73 3
Isoform 2 of CXXC-type zinc finger protein 1	CXXC1	6	488.6	925.833 3	782.2	657.766 7	715.6	564.866 7
ADP-ribosylation factor-like protein 3	ARL3	9	1497.66666 7	2986.1	2201.83 3	2121.56 7	1797.23 3	1938.53 3
Breast cancer anti-estrogen resistance 2	BCAR2	2	271.666666 7	473.633 3	425.4	336.633 3	382.966 7	318.366 7
Gem-associated protein 2	GEMIN2	4	571.266666 7	1602.06 7	1413.86 7	1138.9	997.033 3	892.866 7
Isoform Beta-1 of DNA topoisomerase 2-beta	TOP2B	30	5337.06666 7	12104.5	10866.5	8606.9	8559.66 7	7679.8
cDNA FLJ77678, highly similar to Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 23, mRNA		23	4035.63333 3	8261.267	6460.43 3	5874.56 7	6423.86 7	5554.73 3
Isoform 2 of AP-2 complex subunit alpha-2	AP2A2	1	6286.66666 7	12210.0 7	9496.83 3	8684.73 3	9435.6	8177.43 3

Alpha-enolase	ENO1	27	56255.3666 7	106290. 5	72439.6 7	75620.0 7	76409.2 3	77358.1
Sister chromatid cohesion protein PDS5 homolog A	PDS5A	33	5098.6	9153	7869.06 7	6511.96 7	6074.16 7	5531.56 7
Multiple endocrine neoplasia I, isoform CRA_a	MEN1	3	152.5	330.333 3	303.1	235.033 3	199	188.466 7
cDNA, FLJ93435, highly similar to Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA	6	739.7	1319.8	1034.33 3	939.266 7	953.433 3	914.366 7	
Metalloendopeptidase OMA1, mitochondrial	OMA1	3	224.8	484.733 3	385.833 3	345	304.3	295.5
Elongation factor Tu, mitochondrial	TUFM	30	8637.2	20770.1 7	15322.1 3	14783.5 3	15998.5 3	13669.7
cDNA PSEC0207 fis, clone HEMBA1002981, highly similar to Homo sapiens nurim (nuclear envelope membrane protein) (NRM), mRNA	1	274.733333 3	550.8333	457.9	392.066 7	445.266 7	360.866 7	
ATPase ASNA1	ASNA1	10	868.833333 3	2340.63 3	1739.56 7	1666.1	1612.86 7	1492.36 7
Mitochondrial carrier homolog 2	MTCH2	2	1593.43333 3	3311.4	2674.43 3	2357.16 7	2436.6	2035.46 7
Isoform 3 of Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	3	387.733333 3	617.633 3	460.3	439.666 7	494.3	430.766 7

C-terminal-binding protein 1	CTBP1	5	2039.66666 7	4322.13 3	3161.76 7	3076.76 7	3285.06 7	2927.03 3
Spermatogenesis-associated serine-rich protein 2	SPATS2	4	622.766666 7	1060.43 3	882.966 7	755	747.033 3	673.6
BUB3-interacting and GLEBS motif-containing protein ZNF207	ZNF207	4	553.333333 3	1018.36 7	918.633 3	725.166 7	616.4	856.333 3
Coiled-coil domain-containing protein 58	CCDC58	7	2046.53333 3	4694.7	3862.5	3343.36 7	3125.6	2995.9
X-ray repair cross-complementing protein 5	XRCC5	42	11710.6333 3	28614.3	21782.9 3	20378.4 3	19006.4	18352.5 7
14-3-3 protein eta	YWHAH	12	8141.63333 3	19688.8 7	15504.1 3	14022.2	13527.0 7	13129.2
Isoform 2 of Ribose-phosphate pyrophosphokinase 2	PRPS2	11	3929.53333 3	9774.6	8269.23 3	6962.8	5908.46 7	6085.23 3
BTB/POZ domain-containing protein KCTD9	KCTD9	7	1177.7	2769.56 7	2373.73 3	1972.86 7	1763.86 7	1662.03 3
Metallothionein		2	6674.66666 7	10833.3 7	9792.3	7717.26 7	7186.23 3	6387.6
Hepatoma-derived growth factor-related protein 2	HDGFRP2	13	2804.76666 7	5727.26 7	4636.73 3	4079.93 3	4423.26 7	3908.5
Cancer-related nucleoside-triphosphatase	NTPCR	8	1924.16666 7	3242.76 7	2565.96 7	2310.1	2116.23 3	2177.4
Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	3	461.066666 7	1321.83 3	1146.43 3	941.666 7	790.033 3	841.766 7
cDNA FLJ90373 fis, clone NT2RP2004606, highly similar	3	1038.96666 7	1314.533	1095.13 3	936.6	1113.5	917	

to Metalloproteinase inhibitor 1								
Protein arginine methyltransferase NDUF7, mitochondrial	NDUF7	7	527.133333 3	1300.16 7	1039.3	926.466 7	1002.63 3	934.166 7
Beta-adrenergic receptor kinase 1	GRK2	4	840.8	1729.26 7	1312.36 7	1232.3	1394.23 3	1208.43 3
Lamin-B1	LMNB1	46	17775.3333 3	33889.4 7	25563.8	24150.5	27117.4	22851.5 3
DNA replication licensing factor MCM6	MCM6	32	5814.3	13001.2	12516.0 3	9265.33 3	7541.16 7	6863.6
26S proteasome non-ATPase regulatory subunit 8	PSMD8	10	1393.4	4395.83 3	4094.3	3132.83 3	2506.3	2435.96 7
Transcription initiation factor TFIID subunit 12	TAF12	2	65.0333333 3	145.4	145.566 7	103.633 3	91.9	85.9666 7
Glutaminyl-peptide cyclotransferase-like protein	QPCTL	3	217.833333 3	620.633 3	477.633 3	442.366 7	574.733 3	493.133 3
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	IDH3B	9	1279.46666 7	3469.93 3	2920.26 7	2473.33 3	2240.66 7	2300.2
ATP synthase subunit beta, mitochondrial (Fragment)	ATP5B	1	4288.4	7633.96 7	5786.6	5441.73 3	5748.16 7	5323.56 7
Eukaryotic translation initiation factor 2D	EIF2D	15	1977.5	3355.23 3	2678.53 3	2392.53 3	2321.7	2247.06 7
Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	BAIAP2L1	3	318.7	661.533 3	529.166 7	471.733 3	596.533 3	512.4
Glutamate--cysteine ligase catalytic subunit	GCLC	5	778.633333 3	1566.93 3	1144.53 3	1117.4	1273.43 3	1137.06 7

V-type proton ATPase subunit G 1	ATP6V1G1	4	582.566666 7	1588.56 7	1335.46 7	1132.9	1061.66 7	959.933 3
Protein arginine N-methyltransferase 5	PRMT5	15	3249.26666 7	6673.76 7	5319.06 7	4760.23 3	3739.1	4239.66 7
Archaeometzincins-2, isoform CRA_d	AMZ2	1	77.8	186.7	160.333 3	133.2	125.1	118.266 7
Protein UXT	UXT	4	361.233333 3	590.633 3	538.133 3	421.466 7	402.6	390.333 3
Epoxide hydrolase 1	EPHX1	7	887.833333 3	1319.66 7	1086.26 7	941.8	962.766 7	956.2
Polymerase I and transcript release factor	PTRF	18	5243.23333 3	10495.2 3	7696.8	7490.1	7396	5951.53 3
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	PPP2R5E	11	2336.06666 7	4859.93 3	4137.16 7	3468.76 7	3047.5	2894.33 3
Isoform Non-brain of Clathrin light chain B	CLTB	10	2664.8	5232.56 7	3960	3735	3814.46 7	3350.96 7
Ubiquitin-fold modifier-conjugating enzyme 1	UFC1	3	360.833333 3	968.133 3	779	691.066 7	698.433 3	689.133 3
Ubiquitin-protein ligase E3C	UBE3C	15	1113.3	2794.36 7	2288.5	1994.7	1732.1	1766.76 7
Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	17	2819.16666 7	6621	4870.5	4726.96 7	5202.46 7	4494.7
HEAT repeat-containing protein 3	HEATR3	11	1450.8	2959	2783.76 7	2112.56 7	1797.16 7	1738.66 7
cDNA FLJ10347 fis, clone NT2RM2001035, highly similar		2	471.366666 7	715.7333	588.466 7	511	480.133 3	459.4

to CCR4-NOT transcription complex subunit 7								
Serine/threonine-protein kinase MARK2	MARK2	3	378.6	637.166 7	614.433 3	455.066 7	377.066 7	403.6
Chromobox protein homolog 1	CBX1	11	4143.1	8813.53 3	6736.53 3	6295.33 3	6756.96 7	5626.73 3
Myosin-10	MYH10	92	21970.6666 7	45224.5 7	31683.7	32304.9	37972.2 3	33046.3 7
Eukaryotic peptide chain release factor subunit 1	ETF1	18	2532.1	7057.43 3	6811	5041.8	3568.26 7	3827.03 3
Glycogen phosphorylase, liver form	PYGL	46	11327.8666 7	30515.9	20940.7 7	21805.6	25733.6 3	22443.3
Cytochrome c1, heme protein, mitochondrial	CYC1	4	2385.2	4420.66 7	3619.66 7	3159	3246.03 3	2782
Glutamine-rich protein 1	QRICH1	5	872.766666 7	2233	1838.36 7	1595.83 3	1330.7	1111.26 7
2'-deoxynucleoside 5'-phosphate N-hydrolase 1 (Fragment)	DNPH1	5	623.633333 3	814.933 3	604.933 3	582.4	656.166 7	554.1
Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase (Fragment)	B3GAT3	3	500.2	735.766 7	647.266 7	525.833 3	646.033 3	489.633 3
Glutamate dehydrogenase 1, mitochondrial	GLUD1	26	5896	12774.5 3	9645.66 7	9135.66 7	9948.46 7	8895.63 3
39S ribosomal protein L35, mitochondrial	MRPL35	2	316.133333 3	928.2	817.9	663.866 7	400.833 3	451.133 3

Sister chromatid cohesion protein PDS5 homolog B	PDS5B	18	4519.5	8686.13 3	6879.9	6213.53 3	6368.76 7	5664.16 7
OTU domain containing 6B, isoform CRA_b	OTUD6B	4	401.766666 7	803.333 3	567.5	574.666 7	483.133 3	557.666 7
Lysine-specific demethylase 3B	KDM3B	32	4517.03333 3	8158.06 7	5965.7	5836.4	6183.7	5195.93 3
Isoform 3 of Acyl-CoA-binding domain-containing protein 5	ACBD5	5	499.8	1006.3	658.6	719.933 3	769.666 7	611.2
Cyclin-dependent kinase 2-associated protein 1	CDK2AP1	3	722.633333 3	1132.63 3	1124.43 3	810.366 7	726.833 3	621.5
Beta-galactosidase		10	1495.6	3479.16 7	2515.8	2489.4	3007.46 7	2441.3
39S ribosomal protein L41, mitochondrial	MRPL41	4	674.033333 3	1926.13 3	1830.36 7	1378.3	1016.7	1211
Protein kinase C and casein kinase substrate in neurons 3, isoform CRA_b	PACSIN3	12	2510.73333 3	4852.9	3977.1	3473.43 3	3089.7	2914.96 7
Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	8	1005.46666 7	2059.6	1693.2	1474.23 3	1326.73 3	1336.33 3
Serine/arginine-rich splicing factor 2	SRSF2	1	390.366666 7	1378.13 3	1149.26 7	986.5	913.9	897.066 7
DNA damage-binding protein 1	DDB1	40	6938.5	14892.3	12229.9 3	10663.3 3	10114.1	9664.26 7
Isoform 4 of Ubiquitin-associated protein 1	UBAP1	3	241	511.966 7	402.366 7	366.6	380.533 3	354.833 3
Alpha-soluble NSF attachment protein	NAPA	13	3801.4	6508.66 7	5372.9	4660.73 3	4017	4515.9

Protein CIP2A	KIAA1524	18	2668.63333 3	5910.6	5484.86 7	4232.83 3	3475.66 7	3309.33 3
ERI1 exoribonuclease 3	ERI3	2	718.933333 3	1413.06 7	1114.83 3	1011.96 7	1001.03 3	1042.6
Metastasis-associated protein MTA3	MTA3	2	818.5	2130.66 7	1994.13 3	1525.93 3	1381.03 3	1119.86 7
Kinesin-like protein KIF1C	KIF1C	5	1051.06666 7	2080.16 7	1712.93 3	1489.76 7	1490.06 7	1275.03 3
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Fragment)	MACF1	0	917.2	1897.16 7	1353.6	1358.93 3	1330.46 7	1247.83 3
Long-chain-fatty-acid--CoA ligase 4	ACSL4	12	3433.46666 7	5980.8	5121.13 3	4285	4226.4	4140.1
Syntaxin-12	STX12	8	1153.8	2362.2	2051.36 7	1692.5	1420.3	1475.3
m-AAA protease-interacting protein 1, mitochondrial	C2orf47	5	710.166666 7	1878.6	1483.96 7	1346.1	1373.46 7	1225.96 7
Flavin reductase (NADPH)	BLVRB	7	1143.63333 3	2294.6	1669.76 7	1644.6	1809.46 7	1695.13 3
BRCA2 and CDKN1A-interacting protein	BCCIP	10	2026.36666 7	4116.63 3	3394.36 7	2950.63 3	2699.96 7	2486
Tubulin-specific chaperone A	TBCA	17	12852.8	14770.7 7	11176.7	10587.4 7	9978.56 7	9502.36 7
Isoform 2 of V-type proton ATPase subunit F	ATP6V1F	2	240.8	529.866 7	508.2	379.833 3	324.6	321.433 3
WD repeat-containing protein 44	WDR44	13	1571.96666 7	3158.13 3	2475.6	2264.03 3	2149.7	2244.66 7

COP9 signalosome complex subunit 3	COPS3	5	1501.86666 7	2462.06 7	2249.43 3	1765.03 3	1631.4	1632.83 3
Transmembrane protein 43	TMEM43	7	494.966666 7	1759.76 7	1844.23 3	1261.56 7	1065.23 3	1109.9
U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	65	10590.6	27364.5	23168.2 3	19619.0 7	16826.2	16600.4 3
Importin subunit alpha-4	KPNA3	7	2744.5	6710.06 7	5848.33 3	4811	4029.83 3	3995.53 3
Isoform 4 of tRNA 2'-phosphotransferase 1	TRPT1	2	138.733333 3	275.133 3	216.833 3	197.266 7	228.033 3	201.766 7
Ribosomal protein S6 kinase alpha-3	RPS6KA3	10	1006.43333 3	2173.83 3	1803.13 3	1558.63 3	1328.6	1317.2
Negative elongation factor C/D	TH1L	3	492.533333 3	880.133 3	739.3	631.1	558.6	597.2
Protein diaphanous homolog 1	DIAPH1	36	6399.13333 3	14799.8 7	11860.8 3	10612.3 3	9029.76 7	9368.5
Ras-related protein Rab-27B	RAB27B	12	3732.33333 3	7456.43 3	5459.86 7	5347.2	5547.83 3	4904.33 3
Rab5 GDP/GTP exchange factor	RABGEF1	5	626.2	1621.5	1194.03 3	1162.9	950.766 7	1186.33 3
Crk-like protein	CRKL	15	2601.93333 3	4816.16 7	3469.56 7	3454.43 3	3530.9	3605.16 7
Thioredoxin-related transmembrane protein 1	TMX1	8	2541.3	7251.33 3	6188.2	5202.06 7	4394.96 7	4002.23 3
Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	9	3888.83333 3	7975.03 3	6089.16 7	5721.56 7	5654.03 3	5573.3

Syntaxin-8	STX8	3	278.8	386.066 7	381.866 7	277	239.733 3	235.766 7
Plastin-1	PLS1	6	2064	4028.3	3141.2	2890.66 7	2803.83 3	2806.06 7
F-actin-capping protein subunit alpha-2	CAPZA2	12	3078.13333 3	6451.23 3	5021.13 3	4629.53 3	4018.16 7	4172
Transcription initiation factor IIE subunit beta	GTF2E2	7	1376.8	3506.16 7	2896.2	2516.13 3	2058.96 7	1941.43 3
Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A	17	2546.4	5023.73 3	5583.23 3	3605.2	3339.26 7	2834.16 7
cDNA, FLJ92106, highly similar to Homo sapiens adaptor-related protein complex 3, sigma 1 subunit(AP3S1), mRNA	4	794.233333 3	1645.667	1292.23 3	1181.1	1133	1159.43 3	
Adenine phosphoribosyltransferase	APRT	10	1629.36666 7	3487.13 3	2593.13 3	2503.26 7	2505	2325.7
L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT	10	2044	4272.83 3	3944.26 7	3067.3	2275.8	2590.86 7
Putative uncharacterized protein DKFZp451F173	DKFZp451F173	1	525.8	1418.83 3	1148.03 3	1018.56 7	1073.4	889.933 3
Dihydrofolate reductase	DHFR	10	3175.66666 7	4815.3	4782.1	3457.7	2792.4	2341.66 7
Histone H2A type 1-B/E	HIST1H2AB	2	10439.7666 7	19867.3 3	13895.5 3	14268.5 3	12034.5 3	13540.9 7
cDNA, FLJ93192, highly similar to Homo sapiens	6	721.2	1072.367	1646.93 3	770.166 7	588.6	571.6	

serine/threonine kinase 6 (STK6), mRNA								
Twinfilin-1	TWF1	9	1375.13333 3	3384.6	2659.86 7	2431.03 3	2191.7	2058.26 7
Mitogen-activated protein kinase 3	MAPK3	7	2018.5	4886.56 7	3972.46 7	3510.16 7	3373.06 7	3075.26 7
cDNA, FLJ95817, highly similar to Homo sapiens ZYG homolog (ZYG), mRNA	1	97.7666666 7	202.9667	158.166 7	145.8	151.5	143.1	
Structural maintenance of chromosomes protein	SMC3	51	9795.26666 7	21973.4	17396.3	15785.1 7	15896.8	14979.2 7
Zinc finger protein 184	ZNF184	1	424.733333 3	1275	1146.4	916	995.033 3	831.933 3
Huntingtin-interacting protein K	HYPK	3	536.633333 3	708.466 7	538.466 7	509.033 3	538.966 7	500.566 7
Endonuclease G, mitochondrial	ENDOG	8	1317.73333 3	2299.96 7	1706.93 3	1652.53 3	1593.93 3	1433.06 7
Histone-binding protein RBBP4	RBBP4	5	2668.83333 3	4775.33 3	4699.06 7	3431.26 7	2766.3	2537.6
Protein scribble homolog	SCRIB	23	2533.7	4445.56 7	3633	3194.4	3502.63 3	2925.96 7
Kinesin-like protein KIF20A	KIF20A	8	1518.13333 3	2364.5	2528.96 7	1699.2	1543	1452.26 7
Isoform 2 of [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	PDK3	3	809.733333 3	1551.43 3	1055.8	1115.1	1396	1144.03 3

UPF0565 protein C2orf69	C2orf69	1	206.633333 3	377.566 7	334.5	271.4	261.633 3	230.866 7
HAUS augmin-like complex subunit 8	HAUS8	5	510	655.266 7	641	471.033 3	405.566 7	372.866 7
Protein LSM14 homolog B	LSM14B	2	1145.83333 3	1562.16 7	1351.93 3	1123.06 7	1116.86 7	970.133 3
Protein mago nashi homolog 2	MAGOHB	10	2504.26666 7	7266.13 3	5910.2	5224.23 3	4182.4	4443.76 7
AT-rich interactive domain-containing protein 2	ARID2	6	759.3	1436.4	1211.83 3	1032.76 7	908.566 7	772.333 3
Poly(A) polymerase alpha	PAPOLA	17	2363.23333 3	5269.8	4197.2	3789.73 3	3490.1	3504.43 3
Isoform 2 of Phosphofurin acidic cluster sorting protein 1	PACS1	5	360.3	650.966 7	522.333 3	468.166 7	500.466 7	404.033 3
Mitogen-activated protein kinase (Fragment)	MAPK9	3	690.9	1157.2	988	832.266 7	867.033 3	762.233 3
Phosphoglycerate kinase 2	PGK2	4	3701.26666 7	12216.7	5961.9	8787.26 7	11127.6	10545.6 3
ATP-dependent 6-phosphofructokinase, liver type	PFKL	21	6206.56666 7	12113.4 3	8310.56 7	8714.56 7	9328.33 3	8247.96 7
Protein-S-isoprenylcysteine O-methyltransferase	ICMT	2	153.866666 7	362.6	326.933 3	260.866 7	297.566 7	244.933 3
Serine/threonine-protein kinase MRCK beta	CDC42BPB	17	2843.76666 7	5371.23 3	3853.86 7	3864.6	3997.46 7	3600.2
Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	3	235.9	910.933 3	719.666 7	655.433 3	690.1	660.4

Metallothionein-2	MT2A	2	11884.9666 7	18252.2	15769.0 7	13133.2 3	13151.5 3	12059.1 3
OTU domain-containing protein 7B	OTUD7B	5	597.466666 7	851.4	712.6	612.766 7	560.133 3	563.533 3
General transcription factor 3C polypeptide 6	GTF3C6	1	202.6	857.266 7	793.166 7	617.033 3	516.933 3	562.6
G protein-regulated inducer of neurite outgrowth 1	GPRIN1	22	2585.8	4864.66 7	4245.23 3	3501.56 7	3539.33 3	3187.16 7
Dynein light chain 1, cytoplasmic	DYNLL1	5	1783.5	5550	4601.66 7	3994.9	3715.4	3406.83 3
cDNA FLJ78476, highly similar to Homo sapiens WD repeat and HMG-box DNA binding protein 1 (WDHD1), transcript variant 1, mRNA	26	4486.4	8012.233	7157.7	5767.33 3	4687.86 7	4318.56 7	
14-3-3 protein beta/alpha	YWHAB	9	10703.3333 3	22182.6 7	16532.4 3	15970.6 3	16064.1	15162.1
AP-3 complex subunit beta		13	4038.36666 7	11241.8 7	8935.16 7	8093.76 7	7447.83 3	7635.43 3
cDNA FLJ39996 fis, clone STOMA2002166, highly similar to Splicing factor 3B subunit 4	4	1113.46666 7	2959.633	2627.1	2131.06 7	1918.33 3	1910.6	
KIAA0528, isoform CRA_b	KIAA0528	6	869.366666 7	1772.86 7	1484.46 7	1276.6	1257.26 7	1155.56 7
Fructose-bisphosphate aldolase A	ALDOA	31	41145.6333 3	67330.2 7	42507.3	48490.1	56327.7 7	54324.1 3
Phosphoglycerate mutase 1	PGAM1	16	11531.1666 7	20636.5	13850.7 7	14862.4 3	14834.6 7	14795.9 7

Mitochondrial Rho GTPase 2	RHOT2	9	1405.56666 7	2809.13 3	2170.73 3	2023.2	2102.46 7	1889.53 3
DnaJ homolog subfamily C member 9	DNAJC9	11	1722.6	3232.93 3	2980.96 7	2328.46 7	1809.26 7	2054.03 3
Zinc finger FYVE domain-containing protein 1	ZFYVE1	3	179.5	409.033 3	291.6	294.633 3	299.033 3	332.966 7
Acyl-protein thioesterase 2	LYPLA2	2	543.1	1666.33 3	1228.23 3	1200.3	1270.76 7	1305.06 7
Male-specific lethal 1 homolog	MSL1	4	137.933333 3	274.733 3	219.666 7	197.9	193.933 3	212.2
RUS1 family protein C16orf58	C16orf58	3	355.8	1147.9	858.333 3	826.933 3	803.1	941.933 3
Isoform 2 of Lysine-specific histone demethylase 1A	KDM1A	24	4019.03333 3	7812.2	6323.6	5628.46 7	5979.3	4932.53 3
Ubinuclein-2	UBN2	3	81.6	91.4666 7	86.6	65.9	74.1	75.6666 7
Small nuclear ribonucleoprotein Sm D2	SNRPD2	12	4369.6	9403.03 3	7853.7	6774.93 3	6063.63 3	5906
Isoform 3 of Actin-related protein 2/3 complex subunit 4	ARPC4	8	1020.23333 3	2471.66 7	2006.13 3	1781.06 7	1487.2	1634.36 7
Uncharacterized protein (Fragment)		13	3817.6	7052.83 3	4918.6	5082.26 7	6395.16 7	5348.93 3
Tubulin-specific chaperone D	TBCD	20	2382.4	3840.5	3027.4	2767.56 7	2477.43 3	2392.7
Protein prune homolog	PRUNE	5	895.933333 3	1508.3	1154.4	1086.93 3	1118	1133.8
cDNA, FLJ93285, highly similar to Homo sapiens cell division		4	532.733333 3	1150.267	1150.16 7	828.933 3	609	1206.6

cycle associated 3 (CDCA3), mRNA								
cDNA, FLJ95508, highly similar to Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA	25	8653.7	16624	13734.17	11980	12623.3	9970.2	
Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2	6	261.8	577.4667	501.4	416.2	438.9667	387.3
Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	8	839.5	1525.933	1185.8	1099.833	1079.967	1092.267
Ubiquitin thioesterase otulin	OTULIN	5	682.1666667	2125.533	1733.967	1532.233	1387.333	1492.1
Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	16	1524.233333	2965.1	2241.7	2137.467	2286.5	2208.633
NADH-cytochrome b5 reductase 1	CYB5R1	4	562.36666667	1298.567	1069.633	936.1333	1104.9	848.7
Putative uncharacterized protein DKFZp686E1899	DKFZp686E1899	18	3934.8	7318.033	5284.367	5276.2	5146.333	4840.7
Zinc finger CCCH-type antiviral protein 1-like	ZC3HAV1L	7	1476.8	3460	2373.067	2494.867	2965.767	2473.467
Proteasome subunit beta type-5	PSMB5	10	3042	7118.367	5590.233	5132.933	4231.433	4137.5
Cullin-1	CUL1	20	3500.333333	9319.3	7697.167	6720.667	6003.3	6259.567
Calponin-3	CNN3	1	403.3	1104.833	1068.433	796.7667	642.7667	596.3333

cDNA, FLJ96156, highly similar to Homo sapiens leucyl-tRNA synthetase (LARS), mRNA		45	8116.63333 3	18525.27	13709.2 3	13360.6	11833.5 7	13076.4	
Beta-1,3-glucosyltransferase	B3GLCT		3	634.9	1342.16 7	1061	968.033 3	1314.43 3	1228.16 7
28S ribosomal protein S16, mitochondrial	MRPS16		3	397.9	782	722.333 3	564.033 3	491.833 3	476.866 7
Atlastin-2	ATL2		8	1143.8	2540.4	2193.33 3	1832.83 3	1419.63 3	1334.16 7
28S ribosomal protein S34, mitochondrial	MRPS34		6	372.133333 3	720.866 7	683.2	520.1	424.4	404.7
Isoform ATE1-2 of Arginyl-tRNA--protein transferase 1	ATE1		5	505.366666 7	914.9	721.766 7	660.133 3	647.966 7	651.566 7
Histone-arginine methyltransferase CARM1	CARM1		12	2806.46666 7	5426.8	4382.2	3915.9	3563.23 3	3456.56 7
Dihydropteridine reductase	QDPR		5	646.033333 3	1301.73 3	1062	939.4	905.3	876.766 7
Oxysterol-binding protein	OSBPL7		2	87.5666666 7	271.266 7	258.4	195.766 7	224.2	200.066 7
Isoform 2 of Importin-11	IPO11		6	408.966666 7	1084.33 3	893.533 3	782.6	529.866 7	626.2
NDRG family member 3, isoform CRA_c	NDRG3		2	1163.76666 7	2556.7	1956.73 3	1845.43 3	1785.43 3	1770.9
Isoform 2 of Dynamin-like 120 kDa protein, mitochondrial	OPA1		50	8783.4	18071.2 7	13927.6 7	13044.2 3	13830.1	11333.0 3
IQ motif containing GTPase activating protein 3	IQGAP3		17	2147.8	5348.2	4338.23 3	3860.8	3658.83 3	3544.1

cDNA FLJ55764, highly similar to Apolipoprotein-L2	5	773.466666 7	1822.067	1347.5	1315.33 3	1333.06 7	1368.66 7	
Ubiquinol-cytochrome-c reductase complex assembly factor 2	UQCC2	3	720.966666 7	1205.83 3	1016.93 3	870.533 3	863.8	782.766 7
AT-rich interactive domain-containing protein 4B	ARID4B	5	550.5	1624.1	1337.56 7	1172.5	1160.56 7	1108.96 7
Calcium-binding protein 39-like	CAB39L	1	154.633333 3	320.3	320.966 7	231.266 7	186.4	218.666 7
39S ribosomal protein L21, mitochondrial	MRPL21	2	166.533333 3	240.7	188.833 3	173.9	147.033 3	160.233 3
Arsenite methyltransferase	AS3MT	5	909.133333 3	1476.93 3	1204.96 7	1067.13 3	1038.13 3	1045.63 3
cDNA FLJ59248, highly similar to Homo sapiens cytochrome P450, family 20, subfamily A, polypeptide 1, transcript variant 1, mRNA		2	276.366666 7	534.2333	449.266 7	386.033 3	350.3	391.433 3
Bcl-2-like protein 1	BCL2L1	1	222.966666 7	436.033 3	411.566 7	315.1	320.666 7	316.3
Secretory carrier-associated membrane protein		4	625.533333 3	1644.933	1341	1188.8	1210.3	1058.66 7
DNA polymerase epsilon catalytic subunit protein isoform a	POLE1	13	1234.33333 3	1730.26 7	1694.16 7	1250.5	1058.93 3	969.333 3
Paraneoplastic antigen MA2	PNMA2	4	313.533333 3	1072.63 3	641.9	775.266 7	676.433 3	561.733 3

Double-strand-break repair protein rad21 homolog	RAD21	14	1308.66666 7	2175.36 7	1681.66 7	1572.3	1393.53 3	1449.43 3
Chromobox protein homolog 3	CBX3	12	8245.76666 7	13340	11126.2	9641.86 7	9701.96 7	7982.13 3
General transcription factor 3C polypeptide 4	GTF3C4	15	1938.13333 3	4060.46 7	3772.9	2935.56 7	2636.36 7	2389.53 3
Isoform 3 of UPF0696 protein C11orf68	C11orf68	5	1019.36666 7	1869.56 7	1451.9	1351.8	1212.03 3	1179.43 3
Focal adhesion kinase 1	PTK2	5	606.9	1312.93 3	999.4	949.4	1005.5	848.4
cDNA FLJ90758 fis, clone SKNMC1000082, highly similar to Mitochondrial deoxynucleotide carrier	6	375.9	840.9	726.8	608.066 7	596.466 7	542.233 3	
Ribose-phosphate pyrophosphokinase 1	PRPS1	10	4696.6	10160.8	8521.1	7347.43 3	6128.9	6581.56 7
Surfeit locus protein 4	SURF4	3	507.033333 3	947.733 3	798.833 3	685.333 3	696.8	598.9
Neurabin-2	PPP1R9B	11	2242.96666 7	4328.6	3472.6	3130.3	3282.7	2806.53 3
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	14	2965.9	6703.13 3	5187.5	4848.46 7	4915.4	4589.86 7
Protein FAM136A	FAM136A	12	4112.06666 7	6439.96 7	4792.7	4658.3	5467.5	4328.5
Splicing factor U2AF 65 kDa subunit	U2AF2	9	2191.2	3866.2	3346.76 7	2796.76 7	2589.2	2534.63 3

Isoform 2 of 39S ribosomal protein L10, mitochondrial	MRPL10	2	341.9	385.7	356.733 3	279.133 3	296.933 3	283
Isoform 2 of Anoctamin-6	ANO6	5	385.4	924.466 7	649.9	669.066 7	820.9	631.9
Lon protease homolog, mitochondrial	LONP1	40	9170.8	19508.2 7	12651.1 7	14118.8 3	17307.2	15535.1 3
Protein arginine N-methyltransferase 7	PRMT7	5	233.366666 7	573.1	522.333 3	414.833 3	357.133 3	377.466 7
CCR4-NOT transcription complex subunit 1	CNOT1	30	3244.46666 7	7061.96 7	6038.13 3	5111.93 3	4576.23 3	4336.66 7
Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	11	4923.03333 3	12643.6 7	9834.26 7	9152.56 7	8243.03 3	8039.8
Isoform 2 of Protein LZIC	LZIC	6	954.1	2789	2316.26 7	2018.93 3	1920.16 7	1976.03 3
Nuclear pore complex protein Nup205	NUP205	25	4264.76666 7	10044.9	9283.83 3	7271.83 3	6200.36 7	5830.66 7
DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	5	507.733333 3	891.966 7	731.4	645.733 3	538.9	533.966 7
Glyceronephosphate O-acyltransferase variant (Fragment)		7	493.833333 3	904.9333	743.5	655.2	608.833 3	565.4
Isoform 2 of SPATS2-like protein	SPATS2L	1	4140.93333 3	6675.4	5195.5	4833.2	4721.5	3970.6
Isoform 3 of Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	3	7662.8	15398.4	9983.76 7	11149.0 7	10750.8 7	9961.26 7

Eukaryotic translation initiation factor 5A-1	EIF5A	13	8151	17246.67	14158.43	12488.5	10035.8	11006.23
Isoform 2 of Ribonuclease P protein subunit p30	RPP30	6	617.5	1215.8	1056.2	880.5	858.2	786.5
Uncharacterized protein		1	4888.4	6758.833	4526.233	4895	5138	5005.2
Isoform 2 of Bifunctional coenzyme A synthase	COASY	10	992.2	1537.167	1218.1	1113.433	1040.467	1043.533
Serine/arginine-rich splicing factor 5	SRSF5	11	1832.5	3086.2	2510.3	2235.5	2096.633	1791.867
CD320 antigen	CD320	4	365.5333333	744.1333	643.1	539.0667	657.0667	536.8
Thimet oligopeptidase	THOP1	27	4411.733333	8962.7	7184.167	6496.033	5559.367	5886.767
Purine nucleoside phosphorylase		14	3093.166667	6670.6	5167.467	4835	4254.167	4542.3
cDNA FLJ34494 fis, clone HLUNG2005030, highly similar to VIMENTIN		1	104676.6333	179868.8	135087.5	130374.7	147050.5	125166.6
Homeobox protein TGIF1	TGIF1	1	140.1	510.0333	328.1	369.7	355.3667	361.2
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	PTPMT1	4	484.0666667	620.3667	523.5	449.7333	478.2333	360.2333
1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	AGPAT1	3	439.1	650.6	516.3667	471.7	507.4	479.2667
Isoform 3 of Importin-5	IPO5	29	5057.2	11267.73	10157.8	8169.367	6184.767	6937.833

Proline synthetase co-transcribed homolog (Bacterial), isoform CRA_b	PROSC	12	1744.33333 3	2741	2032.7	1987.4	1822.53 3	1983.96 7
Dolichyl-phosphate beta-glucosyltransferase		4	512.033333 3	1102.233	828.533 3	799.2	825.7	747.833 3
Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	1	13595.2666 7	28964.2 3	21781.3	21002.0 7	20175.9	18165.3 7
Probable ATP-dependent RNA helicase DDX41 (Fragment)	DDX41	17	2278.83333 3	6665.8	3732.23 3	4834.43 3	4628.33 3	4263.03 3
Threonine--tRNA ligase, mitochondrial	TARS2	14	1356.46666 7	2393.43 3	1832.3	1735.86 7	1945.13 3	1798.63 3
Aspartate aminotransferase	GOT2	20	5256	10197.8	8539.3	7396.36 7	7670.03 3	7231.53 3
Clathrin heavy chain 1	CLTC	84	18202.3666 7	39738.5 7	30123.9 3	28822.0 7	27850.5	26475.8 3
cDNA FLJ27420 fis, clone WMC07143		1	1305.1	1983.13 3	1834.93 3	1438.36 7	1170.43 3	1338.2
cDNA FLJ43389 fis, clone OCBBF2007068, highly similar to Ankyrin repeat domain-containing protein 52		2	323.133333 3	605.4	671.466 7	439.1	377.5	337.9
Phosphoribosylformylglycinamide synthase (FGAR amidotransferase), isoform CRA_b	PFAS	21	3712.66666 7	5296.63 3	4105.06 7	3841.7	3654.96 7	3864.46 7

NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10	5	1065.96666 7	1903.63 3	1941.83 3	1380.83 3	1228.9	1143.03 3
Early endosome antigen 1	EEA1	56	10779.2666 7	20458.5 3	15863.7 7	14842.0 3	16125.6 7	14900.2
Zinc finger matrin-type protein 2	ZMAT2	6	1781.5	3424.8	2874.23 3	2484.76 7	2299.03 3	2166.6
E3 ubiquitin-protein ligase ARIH2	ARIH2	8	1102.33333 3	2416.06 7	2009.96 7	1752.93 3	1614.7	1560.03 3
cDNA, FLJ93299, highly similar to Homo sapiens sterol carrier protein 2 (SCP2), mRNA	20	4821.1	10062.1	7079.46 7	7300.4	8634.2	7260	
DNA helicase		31	8255.36666 7	14537	12800	10547.9 3	8742.83 3	9014.1
39S ribosomal protein L11, mitochondrial	MRPL11	12	1507.96666 7	3170.13 3	2706.4	2300.4	2394.9	2030.53 3
Isoform 2 of Importin-4	IPO4	25	3399.2	6067.73 3	5157.56 7	4403.5	3854	3909.2
Myosin regulatory light chain 12A	MYL12A	10	3678.3	6240.96 7	4457.4	4529.46 7	4910.16 7	4462.03 3
ATP-dependent RNA helicase DHX29	DHX29	27	4750.5	7807.76 7	6613.33 3	5666.63 3	4852.03 3	5063.63 3
Adenosine kinase	ADK	16	1578	4559.86 7	3588.13 3	3309.53 3	2859.06 7	2917.6
Thioredoxin reductase 3	TXNRD3	4	316.933333 3	674.466 7	538.7	489.6	542.7	503.633 3
3-ketodihydrosphingosine reductase	KDSR	5	951.2	2111.23 3	1470.73 3	1532.63 3	1673.23 3	1535.7

Xyloside xylosyltransferase 1	XXYLT1	2	296.433333 3	586.666 7	625.3	425.933 3	460.7	328.533 3
cDNA FLJ57190, highly similar to Actin-binding protein anillin		1	9646.83333 3	15843.77	19516.6 7	11505.3 7	9418.8	8761.5
Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP	2	215.5	528.7	407.666 7	383.933 3	430.033 3	407.033 3
Isoform 2 of Cullin-2	CUL2	10	1728.6	3988.23 3	3065.5	2896.33 3	2582.16 7	2444.8
Adipocyte plasma membrane-associated protein	APMAP	13	4453.36666 7	9268.73 3	8096.36 7	6731.43 3	7486.16 7	6111.63 3
Transcription intermediary factor 1-alpha	TRIM24	11	791.633333 3	1716.7	1634.26 7	1246.76 7	1272.86 7	1063.86 7
Zinc finger MYM-type protein 3	ZMYM3	16	1729.2	3323.86 7	2681.73 3	2414	2582.4	2141.26 7
SH3 domain binding glutamic acid-rich protein like 3, isoform CRA_a (Fragment)	SH3BGRL3	3	1089.46666 7	2249.8	1555.1	1634.23 3	2025.13 3	1721.26 7
Vimentin	VIM	9	120918.8	206131. 7	154986. 1	149738. 8	169551. 8	144037. 2
Adenosylhomocysteinase 2	AHCYL1	16	4069.86666 7	8868.73 3	7694.33 3	6442.6	5966.8	5708.13 3
Processing of 1, ribonuclease P/MRP subunit (S. cerevisiae)	POP1	18	2963.1	5123.43 3	4267.03 3	3721.96 7	3638.53 3	3291.7
Plasma membrane calcium-transporting ATPase 4	ATP2B4	15	3757.3	6712.3	5233.1	4876.33 3	6493.96 7	4585.73 3
cDNA FLJ30079 fis, clone BGGI12000544, highly similar		2	584.3	1713.9	1424.6	1245.23 3	1054.23 3	984.033 3

to Snurportin-1 (RNA U transporter 1)								
TFIIH basal transcription factor complex helicase XPD subunit	ERCC2	7	712.933333 3	1860.8	1709.33 3	1352.76 7	1252.33 3	1043.53 3
Tryptophan--tRNA ligase, mitochondrial	WARS2	4	417.266666 7	901.466 7	766.233 3	655.366 7	682.8	669.366 7
cDNA FLJ75444, highly similar to Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, alpha (PRKAR2A), mRNA	12	2748.8	7043.367	5462.13 3	5121.16 7	5610.93 3	4892.8	
Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	3	2018.76666 7	5558.13 3	4415.6	4041.73 3	3518.03 3	3635.8
Prothymosin alpha (Fragment)	PTMA	5	5796.46666 7	16320.0 3	12046.3	11868.1 7	10957	10593.1 3
Exosome complex component RRP4	EXOSC2	8	1672.16666 7	3246.3	2851.63 3	2360.76 7	2036.76 7	2019.16 7
Nuclear pore complex protein Nup88	NUP88	14	2448.3	5859.5	5028.86 7	4261.26 7	4189.16 7	3998.8
Tubulin alpha chain	TUBA1C	6	32884.4666 7	64675.8	51763	47039.2 7	39265.2	40893.7 3
Antigen peptide transporter 1	TAP1	3	227.766666 7	333.466 7	267.733 3	242.566 7	305.666 7	266.2
Chloride channel protein	CLCN7	2	337.466666 7	647.133 3	631.166 7	470.733 3	426.3	507.933 3
3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	7	1102.4	1739.33 3	1283.06 7	1265.46 7	1551.73 3	1312.63 3

Hydroxyacylglutathione hydrolase, mitochondrial	HAGH	4	243.466666 7	695.7	551.566 7	506.2	455.733 3	850.433 3
Glycogen [starch] synthase, muscle	GYS1	18	3416.13333 3	8078.03 3	5043.56 7	5877.96 7	6748.83 3	5474.83 3
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	2	178.666666 7	566.066 7	514.766 7	411.9	378.733 3	387.633 3
E3 SUMO-protein ligase ZNF451	ZNF451	8	1033.63333 3	1879.76 7	1541.06 7	1367.93 3	1418.26 7	1429.36 7
Origin recognition complex subunit 4		4	286.933333 3	505.533 3	436.2	367.966 7	357.2	333.366 7
Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	21	6586.73333 3	12458.6 7	9343.73 3	9069.4	10822.1 3	8755.86 7
Uncharacterized protein		1	1379.2	4077.63 3	3357.36 7	2968.7	2462.9	2606.13 3
Serrate RNA effector molecule homolog	SRRT	41	6770.53333 3	16473.5 7	13741.8 7	11995.1 3	10865.6	10396.9
Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	OXCT1	8	1455.36666 7	2436.96 7	1853.86 7	1774.8	1897.1	1678.2
Methylosome protein 50	WDR77	6	1228.23333 3	1947.1	1592.63 3	1418.3	1242.63 3	1302.83 3
Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	24	2508.63333 3	5824.5	4616.86 7	4242.93 3	3889.86 7	3880.16 7
39S ribosomal protein L20, mitochondrial	MRPL20	2	572.433333 3	1051.96 7	972.733 3	766.333 3	708.466 7	718.366 7

Isoform 2 of Nck-associated protein 1	NCKAP1	15	1993.53333 3	3761.6	3223.7	2740.4	2465.56 7	2456.73 3
Chromodomain Y-like protein	CDYL	6	1138.96666 7	1666.46 7	1441.8	1214.1	1233.3	937.233 3
Poly(rC)-binding protein 4	PCBP4	2	731.733333 3	1488.06 7	1253.96 7	1084.13 3	1133.03 3	1023.73 3
cDNA, FLJ94267, highly similar to Homo sapiens glutathione S-transferase omega 1 (GSTO1), mRNA		19	6250.66666 7	13574.73	10484.3	9889.9	9350.16 7	9502.96 7
General transcription factor IIH subunit 3	GTF2H3	3	375.1	754.833 3	660.666 7	550	604.5	543.733 3
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	3	702.366666 7	1274.36 7	1123.26 7	928.6	938.4	805.133 3
Anillin	ANLN	5	9947.93333 3	16430.9 7	20292.3	11974.8 7	9769.7	9096.93 3
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	13	5889.03333 3	12054.6	10187.0 3	8785.43 3	8475.96 7	7417.3
Protein BORCS7-ASMT	BORCS7-ASMT	2	451.166666 7	590.6	470.633 3	430.433 3	448.4	384.5
Putative GTP-binding protein 6	GTPBP6	10	1011.7	2673	2208.4	1948.13 3	1875.46 7	1871.4
cDNA FLJ75144, highly similar to Homo sapiens ash2 (absent, small, or homeotic)-like (ASH2L), mRNA		13	758.366666 7	1412.3	1046.8	1029.36 7	1103.26 7	1013.26 7

Glutathione peroxidase 1	GPX1	4	379.633333 3	824.066 7	764.166 7	600.7	729.866 7	593.1
Actin-like protein 6A	ACTL6A	14	2634.3	6041.9	5339.23 3	4404.33 3	3597.5	3344
cDNA FLJ55972, highly similar to Methyl-CpG-binding domain protein 1	5	553.1	1051.633	921.933 3	766.633 3	709.366 7	722.933 3	
General transcription factor IIF subunit 1	GTF2F1	15	1704.56666 7	3590.33 3	3111.33 3	2617.46 7	2170.7	2156.63 3
SLC25A5 protein (Fragment)	SLC25A5	8	6915.43333 3	17416.9 7	14566.7 7	12697.5 7	12080.0 3	10333.9
Nucleus accumbens-associated protein 2	NACC2	3	245.433333 3	677.533 3	653	493.966 7	496.9	435.833 3
General transcription factor IIH subunit 2	GTF2H2	6	1012.36666 7	1993.3	1836.86 7	1453.33 3	1465.73 3	1339.06 7
Ribosome biogenesis protein WDR12	WDR12	13	2023.03333 3	5695.03 3	5546.66 7	4152.73 3	3208.1	3372.33 3
Thioredoxin domain-containing protein 5	TXNDC5	21	8797.3	13740.1	10638.8	10019.2	10211.5	8841.6
39S ribosomal protein L54, mitochondrial	MRPL54	2	221.3	706.733 3	658.966 7	515.466 7	477.533 3	516.233 3
Leucine zipper protein 1, isoform CRA_a	LUZP1	5	411.233333 3	839.9	711.433 3	612.6	600.766 7	551.733 3
Prothymosin a14		5	5848.83333 3	16571.4 3	12262.4 3	12087.3	11179.0 7	10792.7
Atrophin 1	ATN1	5	928.5	1083.73 3	931.233 3	790.5	835	687.8

Phosphatidylinositol 3-kinase catalytic subunit type 3	PIK3C3	8	1152.76666 7	2613.83 3	2149.03 3	1906.66 7	1408.86 7	1785.23 3
Isoform 2 of Probable glutamate--tRNA ligase, mitochondrial	EARS2	3	195.666666 7	391.133 3	328.266 7	285.333 3	274.033 3	269.466 7
Tubulin alpha chain		7	35564.0333 3	67585.4	53747.2	49309.5 7	41583.0 7	43614.9 3
Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	CMTR1	13	1201.16666 7	2882.46 7	2444.1	2103.46 7	1818.53 3	1848.56 7
Mitochondrial import receptor subunit TOM5 homolog	TOMM5	3	414.366666 7	1212.1	1069.2	884.566 7	907.833 3	730.8
Guanine nucleotide-binding protein-like 3-like protein	GNL3L	5	1264.76666 7	1837.06 7	1991.23 3	1340.66 7	1171.26 7	1183.63 3
Serine/threonine-protein phosphatase 4 regulatory subunit 1	PPP4R1	8	902.933333 3	1201.06 7	1049.2	876.533 3	693.633 3	768.7
Protein 4.1	EPB41	8	1094.83333 3	2247.16 7	1838.06 7	1640.1	1529.8	1636
Ankyrin repeat domain-containing protein 16	ANKRD16	1	172.433333 3	195.7	135	142.833 3	173.6	160.1
cDNA, FLJ96486, highly similar to Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 32 (DHX32), mRNA		2	402.466666 7	1103.267	831.733 3	805.233 3	696	725
Isoform 2 of Presequence protease, mitochondrial	PITRM1	29	4500.73333 3	10656.6	8150.83 3	7778.3	8103.16 7	7428.66 7

N6-adenosine-methyltransferase subunit METTL14	METTL14	4	542	1470.26 7	1246.16 7	1073.2	1092.23 3	1015.3
Mini-chromosome maintenance complex-binding protein	MCMBP	12	1760.03333 3	2745.96 7	2541.1	2004.63 3	1671.2	1619.96 7
TBC1 domain family member 2A	TBC1D2	13	1160.6	2280.8	1892.73 3	1665.23 3	1452.1	1493.43 3
cDNA FLJ38699 fis, clone KIDNE2002168, highly similar to Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial (EC 1.1.1.35)	11	2611.5	4036.367	2855.73 3	2947.16 7	3715.93 3	3032.4	
Isoform 3 of Chromodomain-helicase-DNA-binding protein 3	CHD3	1	516.9	2164.43 3	1939.26 7	1580.46 7	1339.7	1222.93 3
Peroxisomal membrane protein PEX14	PEX14	6	682.533333 3	1461.26 7	1195.33 3	1067.03 3	1037.83 3	997.1
60S ribosomal protein L37	RPL37	4	2290.96666 7	4801.66 7	3931	3506.46 7	2613.23 3	2867.2
Pentatricopeptide repeat-containing protein 2, mitochondrial	PTCD2	3	99.7	129.3	121.166 7	94.4333 3	86.7666 7	94.4333 3
Isoform B of Nucleoporin SEH1	SEH1L	8	1299.46666 7	2649	2441.6	1934.73 3	1685.4	1537.13 3
SUMO-activating enzyme subunit 1	SAE1	20	5144.33333 3	11246.0 3	9598.16 7	8213.9	7220.43 3	7206.26 7

V-raf murine sarcoma 3611 viral oncogene-like protein isoform 2 (Fragment)	ARAF	4	500.533333 3	1529.66 7	1381.53 3	1117.33 3	1186.63 3	944.766 7
Guanylate kinase 1, isoform CRA_b	GUK1	5	798.766666 7	1559.6	1159.8	1139.3	1346.63 3	1210.73 3
Protein PML	PML	7	1003.93333 3	1704.33 3	1243.06 7	1245.03 3	1336.4	1287.9
Calcium homeostasis endoplasmic reticulum protein	CHERP	17	3140.6	5790.6	5149.13 3	4230.46 7	4298.93 3	3674.56 7
Scaffold attachment factor B2	SAFB2	17	5089.43333 3	10409.8 3	8753.83 3	7606.3	6907.73 3	6770.03 3
Exportin-6	XPO6	4	525.5	1625	1431.83 3	1187.4	1249.56 7	1066.3
Rho guanine nucleotide exchange factor 18	ARHGEF18	3	710.966666 7	1737.3	1240.66 7	1269.5	1326.03 3	1136.1
cDNA, FLJ93437, highly similar to Homo sapiens histidyl-tRNA synthetase-like (HARSL), mRNA		3	1556.8	4191.433	3412.43 3	3062.93 3	2786.7	2742.33 3
Stomatin-like protein 2, mitochondrial	STOML2	18	4993.43333 3	7721.7	5949.1	5643.73 3	6393.43 3	5811.43 3
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	43	10205.4333 3	19170.9 7	14446.6	14012.4 7	15972.8	13778.6 3
Kinesin light chain 1	KLC1	18	5827.66666 7	11765.7 7	9759.16 7	8600.43 3	7220.7	7084.3
Nuclear transport factor 2	NUTF2	5	1645.3	1912.16 7	1449.5	1397.9	1306.76 7	1349.33 3
cDNA FLJ78452, highly similar to Homo sapiens legumain		3	390.966666 7	905.6	779.333 3	662.1	505.933 3	441.866 7

(LGMN), transcript variant 2, mRNA								
ATP synthase subunit delta, mitochondrial	ATP5D	3	662.066666 7	1481.2	1181.36 7	1082.93 3	1142.26 7	1039.56 7
Isoform C of AP-1 complex subunit beta-1	AP1B1	1	6789.86666 7	14843.5 7	12206.9 3	10853.3 3	10325.1	9656.93 3
A-kinase anchor protein 1, mitochondrial	AKAP1	10	1999.6	2934.2	2362.53 3	2145.43 3	2321.66 7	1985.5
Transmembrane protein 248	TMEM248	1	116.3	195.633 3	170	143.066 7	142.7	152.666 7
E3 ubiquitin-protein ligase UBR1	UBR1	3	147.366666 7	314.9	285.166 7	230.3	239.833 3	232.633 3
U3 small nucleolar RNA-associated protein 15 homolog	UTP15	16	2257.73333 3	4869.03 3	4098.53 3	3561.03 3	3021.1	3128.86 7
Charged multivesicular body protein 2a	CHMP2A	8	2222.4	3960.83 3	2595.43 3	2897.03 3	3489.8	2873.73 3
Sorting nexin-27	SNX27	8	719.966666 7	1203.76 7	938.633 3	880.533 3	966.166 7	886.466 7
E3 ubiquitin-protein ligase HECTD3	HECTD3	6	304.433333 3	682.033 3	556.033 3	498.9	488.966 7	462.233 3
Serologically defined colon cancer antigen 3	SDCCAG3	1	309.333333 3	693.8	643.166 7	507.566 7	512.733 3	429.633 3
Mitochondrial glutamate carrier 1	SLC25A22	7	1436.46666 7	2479.7	2107.5	1814.1	1722.3	1640.23 3
Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	51	17053.4	34962.2 3	31187.9 7	25581.5 3	20293.8 3	21255.9 7

Isoform 4 of WD repeat-containing protein 62	WDR62	7	1148.36666 7	1856.36 7	1663.66 7	1358.33 3	1199.3	1113.8
Zinc finger protein 716	ZNF716	1	430.966666 7	1287.76 7	1156.8	942.433 3	998.566 7	848.866 7
39S ribosomal protein L16, mitochondrial	MRPL16	7	768	1599.83 3	1442.83 3	1170.9	1154.2	1128.43 3
2',5'-phosphodiesterase 12	PDE12	12	1706.2	3059.53 3	2459.1	2239.33 3	2050.63 3	1994.76 7
Chromosome 6 open reading frame 139, isoform CRA_a	C6orf139	1	117.666666 7	201.433 3	193.733 3	147.466 7	144.033 3	128.9
28S ribosomal protein S15, mitochondrial	MRPS15	2	449.966666 7	932.9	986	683	721.866 7	654.4
Interferon regulatory factor 3	IRF3	1	324.5	584.866 7	466.933 3	428.233 3	393.566 7	407.833 3
WD repeat-containing protein 5	WDR5	9	2405.1	5653.03 3	4959.46 7	4139.16 7	3498.53 3	3390.63 3
Lysine-specific demethylase 5C	KDM5C	11	1469.1	2516.6	1606.8	1842.9	2106.73 3	2081.3
ATP synthase subunit O, mitochondrial	ATP5O	14	7897.1	12709.0 3	9637.96 7	9306.9	9392.33 3	8819.93 3
Periodic tryptophan protein 2 homolog	PWP2	13	1743.4	3682.73 3	3134.36 7	2696.93 3	2534.03 3	2469.16 7
Nuclear pore complex protein Nup107	NUP107	11	1885.93333 3	4350.5	3838.53 3	3186.1	2965.2	2825.93 3
Insulin-like growth factor 1 receptor	IGF1R	2	262.866666 7	576.6	513.066 7	422.3	462.433 3	457.4
Transmembrane emp24 domain-containing protein 4	TMED4	4	751.433333 3	1798.56 7	1475.16 7	1317.26 7	1333.83 3	1192

LanC lantibiotic synthetase component C-like 1 (Bacterial), isoform CRA_b	LANCL1	6	1363.43333 3	2529.33 3	1799.43 3	1852.6	1644.76 7	1707.4
Homer homolog 1 (Drosophila)	HOMER1	3	470.866666 7	1189.86 7	881.1	871.633 3	1121	883.033 3
Eukaryotic translation initiation factor 4 gamma, 3 variant (Fragment)	17	3928.3	9680.933	8652.2	7091.76 7	6305.16 7	6575.76 7	
Quinone oxidoreductase PIG3	TP53I3	5	853.366666 7	1741.7	1235.53 3	1275.9	1224.06 7	1111.56 7
Survival of motor neuron-related-splicing factor 30	SMNDC1	6	1093.4	2916.16 7	2539.6	2136.36 7	1522.26 7	1473.6
Isoform 2 of DNA replication licensing factor MCM3	MCM3	27	6641.36666 7	12745.3	10982.4	9337.2	7457.76 7	7653.76 7
Ubiquitin-conjugating enzyme E2 D2	UBE2D2	2	320.066666 7	738.233 3	662.1	540.833 3	412.433 3	454.3
Splicing factor 45	RBM17	14	2371.46666 7	4669.23 3	3990.7	3420.9	3109.8	2693.86 7
Thioredoxin domain-containing protein 17	TXNDC17	5	1861.4	2696.53 3	1791.33 3	1975.66 7	2047.23 3	2082.23 3
Peroxisome proliferator activated receptor interacting complex protein	PRIC295	77	12304.7666 7	26035.1 7	21383.3	19075.7 7	16514.0 3	17015.4 7
Transcription initiation factor TFIID subunit 7	TAF7	8	736.1	1261.06 7	1206.76 7	924.033 3	956.5	933.466 7
Isoform 3 of Nucleolar and coiled-body phosphoprotein 1	NOLC1	1	19449.4333 3	28319.0 3	23737.9 3	20752.1 7	18969.4 3	15860.6 3

Serine/threonine-protein kinase PRP4 homolog	PRPF4B	17	2368.36666 7	4880.06 7	4191.43 3	3576.46 7	3615.3	3177.93 3
Actin-related protein 2/3 complex subunit 1A	ARPC1A	6	594	1527.7	1308.76 7	1119.63 3	1015.5	1101.8
Structural maintenance of chromosomes protein 1A	SMC1A	50	9609.83333 3	22670	17973.0 7	16614.6 7	17048.0 7	15196.6 3
Neutral cholesterol ester hydrolase 1	NCEH1	10	3005.36666 7	6019.56 7	4831.93 3	4411.7	4357.56 7	4131.76 7
Choline dehydrogenase, isoform CRA_a	CHDH	3	238.133333 3	405.566 7	322.2	297.266 7	359.033 3	289.8
39S ribosomal protein L37, mitochondrial	MRPL37	13	1358.3	2992.1	2597.1	2193.13 3	2229.46 7	1927.73 3
Ephrin type-A receptor 4	EPHA4	17	3484.93333 3	6306.13 3	5555.86 7	4622.43 3	6004.83 3	4107.93 3
cDNA FLJ76790		6	982.766666 7	1567.63 3	1352.1	1149.1	1167.43 3	1111.46 7
Nucleoporin NUP188 homolog	NUP188	17	1388.4	2536	2421.83 3	1858.96 7	1670.53 3	1743.83 3
N-lysine methyltransferase SMYD2	SMYD2	4	1153.6	1508.5	1174.66 7	1106.03 3	1173.36 7	993.833 3
ATP-binding cassette sub-family B member 6, mitochondrial	ABCB6	3	353.133333 3	790.266 7	569.633 3	579.433 3	641.566 7	570.733 3
cDNA FLJ75449, highly similar to Homo sapiens aquarius homolog (mouse) (AQR), mRNA		25	2464.23333 3	5710.633	4916.13 3	4187.13 3	4014.03 3	4012.03 3
Isoform 4 of YLP motif-containing protein 1	YLPM1	25	2959.56666 7	5606.16 7	4534.3	4110.8	4078.4	3520.3

DNA polymerase delta subunit 2	POLD2	7	1887.3	2577.4	2211.06 7	1890.2	1635.96 7	1685.13 3
TBC1 domain family member 10B	TBC1D10B	7	426.9	926.033 3	780.833 3	679.133 3	633.866 7	587.2
AP-1 complex subunit beta-1	AP1B1	1	6858.23333 3	14817.3 7	12211.7 7	10867.6 7	10351.1 3	9731.66 7
Myosin-9	MYH9	129	43201.8666 7	80860.2	61021.7 3	59307.3 3	62915.5	56871.3 3
Isoform 3 of Phosphorylase b kinase regulatory subunit beta	PHKB	10	1250.03333 3	2823.63 3	2290.6	2071.06 7	2038.43 3	2042.5
Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	4	1071.1	2044.53 3	1775.53 3	1499.73 3	1481.4	1272.5
Isoform Beta of Nucleolar and coiled-body phosphoprotein 1	NOLC1	2	19527.6333 3	28461.6 7	23863.8 3	20880.4 7	19107.4 7	15964.7 7
Serine racemase	SRR	4	699.166666 7	1082.63 3	1085.06 7	794.3	745.733 3	683.5
Isoform 2 of ATP-binding cassette sub-family F member 2	ABCF2	18	3419.93333 3	6312.53 3	6237	4631.4	3822.26 7	3918.16 7
H/ACA ribonucleoprotein complex subunit 1	GAR1	4	637.366666 7	1153.5	895.833 3	846.4	759.633 3	822.133 3
Vacuolar protein sorting-associated protein 26B	VPS26B	3	379.066666 7	818.3	665.433 3	600.466 7	633.833 3	555.6
THO complex subunit 2	THOC2	34	4166.56666 7	9923.8	8293	7283.7	6806.16 7	6586.26 7
DNA repair protein XRCC4	XRCC4	13	1774.06666 7	3186.53 3	2558.23 3	2339.23 3	1990.5	1948.2

Mitochondrial import receptor subunit TOM34	TOMM34	20	4340.4	9576.3	7579.33 3	7030.16 7	6386.63 3	6160.43 3
Hsp70-binding protein 1 (Fragment)	HSPBP1	1	343.466666 7	528.7	426.766 7	388.133 3	314.733 3	359.566 7
Methylthioribulose-1-phosphate dehydratase	APIP	5	624.166666 7	1226.3	939.866 7	900.4	817.8	926.033 3
Zinc finger MYM-type protein 2	ZMYM2	7	604.833333 3	1383.26 7	1049.76 7	1015.76 7	1117.86 7	883.6
Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	23	11631.0666 7	24744.8 7	20233.0 3	18173.1 7	16445.4 3	13963.4 7
Tripartite motif-containing 33, isoform CRA_a	TRIM33	12	1121.1	2095.36 7	1682.1	1538.96 7	1423.56 7	1120.1
Pleckstrin homology-like domain family B member 1	PHLDB1	3	384.8	846.633 3	684.533 3	621.833 3	522.2	571.866 7
Rho GTPase-activating protein 17	ARHGAP17	11	1345.96666 7	4180.73 3	3357.63 3	3070.7	2888.13 3	3046.9
RNA-binding protein 33	RBM33	7	1059.9	1904.7	1554.53 3	1399.06 7	1485.26 7	1441.7
Histone cluster 1, H1t	HIST1H1T	1	5298.36666 7	9256.6	7578.03 3	6799.73 3	6555.43 3	5968.93 3
39S ribosomal protein L1, mitochondrial	MRPL1	16	2591.73333 3	6000.36 7	5063.3	4407.96 7	4156.16 7	3952.6
Nuclear factor 1		6	1755.83333 3	3274.16 7	3010.83 3	2405.3	2220.2	2047.13 3
Eukaryotic translation initiation factor 4E type 2	EIF4E2	4	719.5	1826.56 7	1505.06 7	1341.86 7	1077.93 3	1156.96 7

Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	2	4998.86666 7	7554.83 3	5953.56 7	5550.93 3	5615.56 7	5159.8
Pyrroline-5-carboxylate reductase	PYCRL	6	902.7	1473.13 3	1233.5	1082.43 3	988.5	1064.3
Peptidylprolyl isomerase		8	1408.03333 3	2248.73 3	1770.06 7	1652.43 3	1741.2	1429.73 3
Protein regulator of cytokinesis 1, isoform CRA_e	PRC1	6	690.666666 7	1230.13 3	1427.53 3	903.966 7	766.533 3	801
Isoform 4 of Citron Rho-interacting kinase	CIT	19	1934.63333 3	3418.93 3	3356.03 3	2512.43 3	2524.1	2272.8
EF-hand domain-containing protein D2	EFHD2	11	1573.96666 7	3543.73 3	3010.76 7	2604.16 7	2138.56 7	2313.86 7
ATP synthase subunit beta, mitochondrial	ATP5B	17	14927.3666 7	24257.7 3	18300.0 3	17827.2 3	18684.1 7	17081.4 7
tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4	WDR4	8	880.3	2637.96 7	2280.33 3	1938.66 7	1522.9	1570.26 7
Isoform 2 of 28S ribosomal protein S18a, mitochondrial	MRPS18A	5	763	1949.63 3	1651.9	1432.83 3	1496.8	1379.46 7
cDNA FLJ10425 fis, clone NT2RP1000326, highly similar to Metaxin-2		5	1042.13333 3	1946.6	1592.13 3	1430.73 3	1374.53 3	1319.3
Inosine triphosphate pyrophosphatase	ITPA	7	1758.73333 3	3129.46 7	2544.5	2300.6	2097.2	2084.2
DNA-directed RNA polymerase II subunit RPB1	POLR2A	35	5013.7	9909.76 7	7916.73 3	7285.2	7228.7	6601.26 7

LYR motif-containing protein 4	LYRM4	1	463.433333 3	843.133 3	716	619.833 3	475.9	585.3
Metallothionein-1X	MT1X	3	8281.6	15718.4 7	13098.5 3	11557.5 7	12098.3 7	11211.6 7
Isoform 3 of 60S ribosomal protein L17	RPL17	14	5614.3	12232.3 7	11104.5 7	8994.9	7501.9	7252.2
Probable leucine--tRNA ligase, mitochondrial	LARS2	8	740.533333 3	1516.26 7	1306.23 3	1115	1140.86 7	1025.16 7
39S ribosomal protein L47, mitochondrial	MRPL47	6	1068.96666 7	2111.73 3	1975.13 3	1552.9	1380.3	1398.16 7
Poly(rC)-binding protein 1	PCBP1	11	9498.26666 7	12968.5 3	10466.1	9536.86 7	8425.36 7	8995
Glutaredoxin-3	GLRX3	18	3797	9979.7	7831.8	7338.93 3	5429.53 3	6183.3
Sister chromatid cohesion protein PDS5 homolog B (Fragment)	PDS5B	1	1922.13333 3	3545.8	2816.2	2607.56 7	2729.6	2500.26 7
Glutaredoxin-related protein 5, mitochondrial	GLRX5	7	1716.93333 3	2843.4	2145.5	2091.03 3	2208.33 3	1995.26 7
Isoform 2 of Ferrochelatase, mitochondrial	FECH	13	1514.4	2981.73 3	2221.96 7	2192.96 7	2403.2	2175.46 7
Exocyst complex component 5	EXOC5	8	997.933333 3	2466.36 7	2090.8	1814.5	1789.6	1803
Isoform D of Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	1	4430.63333 3	6846.16 7	5324.06 7	5036.73 3	5145.2	4712
Transforming acidic coiled-coil-containing protein 2	TACC2	6	1365.23333 3	2313.4	1936.3	1702.06 7	1644.8	1648.16 7

Interferon regulatory factor 3, isoform CRA_a	IRF3	1	336.966666 7	677.833 3	540.833 3	498.766 7	465.2	473.6
UV excision repair protein RAD23 homolog A	RAD23A	4	797.466666 7	677.5	591.466 7	498.6	481.966 7	479.366 7
Extended synaptotagmin-1	ESYT1	37	6380.83333 3	11689.9 7	8382.36 7	8603.7	9513.46 7	8884.8
Regulator of nonsense transcripts 3B	UPF3B	16	2057.43333 3	4646.26 7	3562.66 7	3420.2	2914.5	2976.33 3
Carbonic anhydrase 5B, mitochondrial	CA5B	2	317.6	396.4	246.633 3	291.8	493	394.4
Poly [ADP-ribose] polymerase 4	PARP4	6	931.033333 3	1654.83 3	1562.33 3	1218.23 3	1222.73 3	1248.53 3
Targeting protein for Xklp2	TPX2	24	4983.8	6624.5	7636.26 7	4876.83 3	4725.6	4100.36 7
Neurogenic locus notch homolog protein 3	NOTCH3	1	432.6	695.066 7	654.233 3	511.7	1036.53 3	496.266 7
Probable dimethyladenosine transferase	DIMT1	10	1263.46666 7	3075.53 3	2885.26 7	2264.4	1824.96 7	1826.2
Argininosuccinate lyase	ASL	12	1044.36666 7	3380.1	2425.76 7	2488.96 7	2547.93 3	2231.23 3
39S ribosomal protein L50, mitochondrial	MRPL50	6	1080.7	1462.23 3	1203	1077.26 7	997.133 3	967.833 3
CDKN2A-interacting protein	CDKN2AIP	10	1661.36666 7	2131.73 3	1718.8	1570.53 3	1678.73 3	1493.5
Spindle and kinetochore-associated protein 3	SKA3	6	955.866666 7	1237.26 7	1329.03 3	911.566 7	681.8	688.3
Centrosome and spindle pole-associated protein 1	CSPP1	1	53.1333333 3	66.5	62.8333 3	49	58.1	51.8

cDNA FLJ76282, highly similar to Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (PSMD5), mRNA	17	3934.5	7498.333	6035.6	5525.9	5243.66 7	5343.16 7	
Chromodomain-helicase-DNA-binding protein 2	CHD2	9	1321.3	2928.6	2187.76 7	2158.23 3	2350.86 7	2336.9
Elongator complex protein 3	ELP3	11	1600.76666 7	4058.06 7	3028.96 7	2990.8	2589	2696.86 7
Protein ARL2-SNX15	ARL2-SNX15	1	648.566666 7	1260.2	1054.66 7	928.8	790.433 3	857.1
Ubiquitin domain-containing protein UBFD1	UBFD1	8	1371.33333 3	2346.8	1943.13 3	1729.66 7	1529.03 3	1677.36 7
Gem (Nuclear organelle) associated protein 4	GEMIN4	9	1001.53333 3	2650.23 3	2329.36 7	1953.33 3	1746.93 3	1782.43 3
Cyclin-G-associated kinase	GAK	12	1517.83333 3	2680.3	2202.03 3	1975.7	1803.96 7	1851.93 3
HCLS1-binding protein 3	HS1BP3	6	662.733333 3	1300.16 7	862.966 7	958.533 3	910.833 3	1191.83 3
Isoform 9 of Serine/threonine-protein kinase Chk2	CHEK2	9	853.966666 7	1521.03 3	1273.23 3	1121.36 7	1208.2	1063.8
Transcription initiation factor TFIID subunit 10	TAF10	2	395.166666 7	448.2	383.633 3	330.466 7	283.633 3	259.2
NK-tumor recognition protein	NKTR	4	300.4	438.9	394.3	323.633 3	350.133 3	336.433 3
UBX domain-containing protein 7	UBXN7	12	1499.9	3878.86 7	2960.33 3	2860.26 7	2904.16 7	2767.53 3

IKBKAP variant protein (Fragment)	IKBKAPvariantprote in	27	3459.96666 7	6776.2	5394.16 7	4996.83 3	4201.83 3	4203.56 7
CD2-associated protein	CD2AP	20	3444.5	7935.4	6214.23 3	5851.93 3	5571.66 7	5543.7
Elongation of very long chain fatty acids protein 1	ELOVL1	1	1449.53333 3	2442.93 3	2018.36 7	1801.63 3	1822.1	1372.36 7
cDNA FLJ34950 fis, clone NT2RP7017284, highly similar to Casein kinase I isoform epsilon (EC 2.7.11.1)		1	186.233333 3	315.5	270.2	232.7	241	179.6
MICOS complex subunit	CHCHD3	14	4963.83333 3	8651.2	7225.46 7	6383.36 7	6595.9	5660.53 3
Protein FAM234A	FAM234A	3	337.833333 3	571.866 7	521.8	421.966 7	429.066 7	362.666 7
Actin-related protein 6	ACTR6	2	330.766666 7	374.9	348.933 3	276.633 3	279.8	268.433 3
FH1/FH2 domain-containing protein 1 variant	FHOD1	10	1078.43333 3	1962.8	1642.86 7	1448.46 7	1332.96 7	1372.83 3
GTP-binding protein SAR1a	SAR1A	8	1721.96666 7	4276.46 7	4249.76 7	3156.26 7	2380.43 3	2489.1
Centrosomal protein of 170 kDa	CEP170	1	1585.13333 3	3291.16 7	2429.3	2429.06 7	2235.96 7	2286.93 3
Transmembrane protein 165	TMEM165	4	1004.9	1194.56 7	1152.43 3	881.733 3	941.533 3	836.966 7
Putative uncharacterized protein DKFZp686B04128	DKFZp686B04128	9	2755.63333 3	4950.53 3	4081.43 3	3654.33 3	3498.73 3	3299.9
Inorganic pyrophosphatase	PPA1	24	8002.33333 3	18776.5 7	15625.8	13860.9 3	11194.4	11703.7 3

Glutamate-rich protein 1 (Fragment)	ERICH1	3	167.766666 7	575.7	506.366 7	425.066 7	344.866 7	324.666 7
rRNA methyltransferase 3, mitochondrial	MRM3	6	1196.33333 3	2046.93 3	1700.03 3	1511.5	1408.6	1400.6
Isoform 2 of Kin of IRRE-like protein 1	KIRREL	7	1219.86666 7	1983.06 7	1629.53 3	1464.46 7	1495	1219.26 7
Ubiquitin-conjugating enzyme E2 G2	UBE2G2	3	346.3	1185	1088.93 3	875.166 7	859.7	821.9
ADP-ribosylation factor-like protein 2	ARL2	4	1113.56666 7	2438.23 3	2057	1801.06 7	1543.83 3	1636.16 7
Eukaryotic translation initiation factor 3 subunit K	EIF3K	7	1652.93333 3	3649.56 7	3285.7	2695.86 7	2147.53 3	2184.06 7
Uncharacterized protein		4	511.4	1007.86 7	888.766 7	744.533 3	619.266 7	616.966 7
Glyceraldehyde-3-phosphate dehydrogenase		1 58864.5333 3	109269.7	77519.5 7	80727.2 7	87360.9	79421.3 7	
Hermansky-Pudlak syndrome 6 protein	HPS6	5	395.733333 3	493.966 7	401.7	364.966 7	384.7	368.366 7
Isoform 7 of LETM1 domain-containing protein 1	LETMD1	1	208.833333 3	536.9	461.2	396.7	391.6	372.066 7
cDNA FLJ77896, highly similar to Homo sapiens Ras homolog enriched in brain (RHEB), mRNA		7 1081.73333 3	3100.933	2977.43 3	2291.46 7	1645.46 7	1638.4	
Cyclin-dependent kinase 2	CDK2	6	1052.46666 7	1691.06 7	1643.3	1249.7	1056.6	1022.8
Receptor protein-tyrosine kinase		28	5137.26666 7	8454.7	7430.4	6249.23 3	5720.43 3	5171.46 7

60S acidic ribosomal protein P0		20	8488.83333 3	15497.8 3	13920.3 3	11455.5 7	8948.63 3	10129.5 3
Isoform 8 of Plectin	PLEC	2	61667.0666 7	111674. 3	91088.2 3	82552.8	87446.4	76275.5 3
Elongation protein 4 homolog (S. cerevisiae), isoform CRA_b	ELP4	5	683.366666 7	906.966 7	762.2	670.533 3	634.933 3	612.866 7
Isoform 2 of Cysteine-rich with EGF-like domain protein 1	CRELD1	1	44.5333333 3	29.6666 7	21.6333 3	21.9333 3	31.4666 7	22.4666 7
Actin-related protein 2/3 complex subunit 3		8	1707.8	4608.567	3369.36 7	3407.26 7	2948	2746.53 3
MURR1 variant (Fragment)		3	326.433333 3	738.966 7	749.366 7	546.366 7	439.566 7	428.966 7
ADP-ribosylation factor 4	ARF4	5	1178.06666 7	3370	2833.66 7	2491.86 7	1823.86 7	2267.53 3
U3 small nucleolar RNA-interacting protein 2	RRP9	10	1559.1	3187.03 3	2625.63 3	2356.6	1866.96 7	1847.33 3
Isoform 3 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	29	7735.86666 7	14648.1 7	10718.0 7	10831.4	14799.5 7	10561.4 7
Disco-interacting protein 2 homolog A	DIP2A	4	710.366666 7	1566.13 3	1427.03 3	1158.16 7	1112.93 3	1042.7
Ribosomal protein L7, isoform CRA_a	RPL7	23	8519.43333 3	19947.1	18588.1	14751.2 7	11864.2	13015.1
Isoform 2 of Kinesin-like protein KIF1B	KIF1B	6	1629.46666 7	2672.8	2119.03 3	1976.7	1994.5	1904.3
Condensin complex subunit 3	NCAPG	17	2814.36666 7	4629.4	4321.53 3	3423.93 3	2860.13 3	2827.93 3

Mediator of RNA polymerase II transcription subunit 10	MED10	2	179.5	257.333 3	262.433 3	190.333 3	172.133 3	171
TATA box-binding protein-like protein 1	TBPL1	2	217.433333 3	407.033 3	369.166 7	301.1	220.833 3	220.866 7
Serine/threonine-protein kinase N2	PKN2	23	4158.33333 3	6677.9	5329.33 3	4940.03 3	5125.23 3	4978.93 3
Receptor of activated protein C kinase 1	RACK1	22	8537.3	20330.5	19308.8 3	15042.4	10677.6	12546.6 7
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	0	13100.8	27511.3 7	21029.8 3	20356.4 3	19965.2 3	18938.9 7
Isoform 2 of Apoptosis inhibitor 5	API5	27	5789.96666 7	12335	10248.9 3	9128.16 7	8189.16 7	8188.53 3
Protein polybromo-1	PBRM1	11	889.666666 7	1924.23 3	1580.4	1424.03 3	1277.56 7	1024.5
cDNA FLJ76434, highly similar to Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform (PPP2R1B), transcript variant 2, mRNA		2	1956.2	3063.1	2982.53 3	2266.86 7	1780.26 7	1831.26 7
28S ribosomal protein S26, mitochondrial	MRPS26	4	688.5	1203.9	1113.06 7	890.966 7	803	788.966 7
Tubulin beta-4A chain (Fragment)	TUBB4A	1	9381.83333 3	17046.9 3	14123.5	12616.4 3	10408.4	10877.5 3
cDNA, FLJ94999, highly similar to Homo sapiens calpain 7 (CAPN7), mRNA		5	658.433333 3	1554.433	1358.43 3	1150.46 7	1118.9	1106.43 3

Transport and Golgi organization protein 6 homolog	TANGO6	7	794.6	1288.9	1210.46 7	953.966 7	828.8	821.466 7
Serine protease HTRA2, mitochondrial	HTRA2	6	1156.66666 7	1568.83 3	1134.56 7	1161.2	1330.9	1104.2
Acetyltransferase component of pyruvate dehydrogenase complex	DLAT	16	2236.13333 3	4528.96 7	3704.4	3352.4	3329.56 7	3309.86 7
Ephrin type-B receptor 4	EPHB4	5	723.733333 3	1362.86 7	1246.76 7	1008.83 3	869.533 3	689.6
ATP-dependent DNA helicase Q4	RECQL4	3	143.033333 3	372	325.833 3	275.366 7	237	233.766 7
Zinc finger, FYVE domain containing 16, isoform CRA_a	ZFYVE16	14	1372.43333 3	2725.26 7	2493.4	2017.56 7	1839.3	1816.23 3
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	4	66757.4333 3	122037. 9	86317.5	90352.8 7	97043.3 3	88496.4 3
Replication factor C subunit 3	RFC3	9	1272.8	1900.9	1804.3	1407.5	1255.9	1196.7
Egl nine homolog 1	EGLN1	15	2596.13333 3	5903.4	3262	4371.26 7	4994.53 3	4895.06 7
cDNA FLJ56414, highly similar to Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), mRNA		11	2202.13333 3	3476.567	2806.6	2574.4	2430.96 7	2465.76 7
Tyrosine-protein phosphatase non-receptor type 1	PTPN1	11	1327.96666 7	3423.73 3	3001.6	2535.53 3	2205.8	2243.1
Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	13	2864.56666 7	6198.7	5219.23 3	4590.93 3	4500.53 3	3976.46 7
Mitogen-activated protein kinase kinase kinase MLT	ZAK	4	225.6	368.333 3	328.433 3	272.8	270.933 3	248.5

Isoform 3 of Plectin	PLEC	2	61208.6	110509. 9	90200.5 7	81847.9 7	86493.6 7	75515.5 3
Eyes absent homolog 3	EYA3	1	347.3	562.066 7	586.5	416.333 3	334.5	323.133 3
PECI protein	PECI	15	3096.83333 3	5193.76 7	3437.43 3	3847.26 7	4234.6	3806.93 3
Alternative protein SLC35A4	SLC35A4	4	230.333333 3	748.766 7	744	554.666 7	540.666 7	442.233 3
Complex I assembly factor TIMMDC1, mitochondrial	TIMMDC1	10	2459.9	4545.4	3835.9	3368.1	3258.7	2925.7
Succinate-CoA ligase subunit beta (Fragment)	DKFZp686D0880	13	3160.66666 7	6625.16 7	5425.5	4909.3	4627.36 7	4506.73 3
cDNA, FLJ94921, highly similar to Homo sapiens prolyl endopeptidase (PREP), mRNA	22	3298.6	6210.833	4830.6	4602.4	4631.9	3968.36 7	
Ubiquilin-4	UBQLN4	3	602.933333 3	953.5	790.4	706.666 7	650.733 3	619.066 7
40S ribosomal protein S16	RPS16	16	4525.33333 3	11312.4	10320.3 3	8385.53 3	6082.93 3	6383.93 3
Plectin	PLEC	5	61761.3	111664. 2	91237.4 7	82782.7 7	87298.6	76414.7
G protein-coupled receptor kinase interactor 1 variant (Fragment)	14	2471.4	4694.433	3937.96 7	3480.8	3218.86 7	3074.8	
Mitochondrial ribosome recycling factor, isoform CRA_a	MRRF	8	1417.2	2477.13 3	2049.03 3	1836.8	1767.5	1628.1
Spermidine synthase	SRM	10	1851.9	3139.66 7	2472.53 3	2328.26 7	2511.2	2378.93 3

FAS-associated death domain protein	FADD	4	108.5	300.7	275	223.033 3	202.366 7	209.266 7
Girdin	CCDC88A	16	3541.03333 3	6076.36 7	5078.2	4506.93 3	4463.96 7	4313.73 3
tRNA:m(4)X modification enzyme TRM13 homolog	TRMT13	2	236.3	374.366 7	340.966 7	277.7	294.566 7	278.866 7
ATP-binding cassette sub-family E member 1	ABCE1	24	5909.9	13398.8 3	11453.0 3	9939.36 7	8326.06 7	8854.6
39S ribosomal protein L39, mitochondrial	MRPL39	10	1731.66666 7	3893.26 7	3717.1	2888.26 7	2682.86 7	2520.4
Renin receptor (Fragment)	ATP6AP2	5	336.966666 7	484.9	503.133 3	359.766 7	378.2	327.166 7
Oxysterol-binding protein-related protein 11	OSBPL11	6	722.433333 3	1306.46 7	1190.23 3	969.333 3	779.666 7	799.6
cAMP-dependent protein kinase type II-beta regulatory subunit	PRKAR2B	4	799.066666 7	2220.56 7	1678.9	1647.56 7	1811.46 7	1578.33 3
Coiled-coil domain-containing protein 25	CCDC25	7	1403.4	2227.1	1786.63 3	1652.43 3	1754.33 3	1586.8
Tumor protein 63	TP63	9	1219	2721.76 7	2163.1	2019.46 7	1956.26 7	1824.56 7
HAUS augmin-like complex subunit 3	HAUS3	4	659.633333 3	1771.03 3	1481.5	1314.06 7	1181.9	1169.23 3
Protein arginine N-methyltransferase 3	PRMT3	12	1282.93333 3	2963.36 7	2752.4	2199.13 3	1696.2	1790.03 3
BRCA1-A complex subunit RAP80	UIMC1	8	1710.1	3448.63 3	2664.23 3	2559.56 7	2272.6	2492.66 7

Transcription factor 3 variant 3	TCF3	4	667.866666 7	645.5	801.233 3	479.166 7	403	356.2
Transcriptional repressor protein YY1	YY1	11	2013.73333 3	3549.73 3	2802.66 7	2635.06 7	2929.7	2430.06 7
Transcription elongation regulator 1	TCERG1	17	3042.26666 7	7331.7	5960.33 3	5442.66 7	5203.53 3	4621.43 3
Acetoacetyl-CoA synthetase	AACS	10	1499.3	4298.03 3	3302	3190.7	2909.03 3	3145.06 7
Isoform 3 of DNA-directed RNA polymerase I subunit RPA2	POLR1B	9	1103.46666 7	2868.8	2572.2	2129.73 3	1794.4	1856.23 3
cDNA, FLJ92996, highly similar to Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA		5	1685.16666 7	4050.733	3262.96 7	3007.33 3	2680.53 3	2696
RNA polymerase II subunit A C-terminal domain phosphatase	CTDP1	10	1893.4	4074.63 3	3055.7	3025.46 7	3050.26 7	2829
F-box/LRR-repeat protein 18	FBXL18	6	334.333333 3	867.133 3	753.3	643.933 3	431.166 7	492.6
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	5	2855.7	7372.43 3	5930.26 7	5474.86 7	5222.43 3	4860.93 3
Isoform 4 of Acetyl-CoA carboxylase 1	ACACA	33	5011.33333 3	9153.93 3	7973.53 3	6797.86 7	6186.7	6275.46 7
Chromatin assembly factor 1, subunit A (P150), isoform CRA_a	CHAF1A	7	1019.96666 7	1389.43 3	1544.23 3	1031.83 3	876.1	702

Ran-specific GTPase-activating protein	RANBP1	14	4325.66666 7	8060.5	6531.66 7	5986.86 7	5255.26 7	5338.2
La-related protein 4B (Fragment)	LARP4B	1	2144.2	3535.73 3	2947.36 7	2626.16 7	2191.06 7	2218.63 3
Ribosomal protein S6 kinase beta-1	RPS6KB1	5	835	1255.43 3	1023.73 3	932.5	1058.36 7	1040
Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	37	12932.2	28219.7	22482.8	20960.9 7	18068.0 3	17974.7
Isoform 2 of Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	2	13051.3	26820.1 7	20453.6 7	19921.4 7	19435.7	18615.6 3
Isoform 2 of Kinesin-like protein KIF1A	KIF1A	3	896.5	1723.66 7	1365.36 7	1280.4	1371.26 7	1290.76 7
ATPase family AAA domain-containing protein 3B	ATAD3B	5	5529.8	12027.1 3	10108.3 7	8934.26 7	8225.26 7	8092.83 3
Rho GTPase-activating protein SYDE1	SYDE1	7	520.866666 7	1156.9	821.133 3	859.433 3	899.833 3	790.2
Isoform 4 of Vacuolar protein sorting-associated protein 53 homolog	VPS53	7	785.666666 7	1810.63 3	1625.8	1345.2	1156.4	1202.53 3
Palmitoyl-protein thioesterase 1	PPT1	6	746.033333 3	1451.46 7	1458.5	1078.36 7	965.266 7	924.466 7
Nuclear RNA export factor 1	NXF1	13	1210.36666 7	2344.83 3	2023.26 7	1742.13 3	1612.63 3	1572.23 3
cDNA FLJ75392, highly similar to Homo sapiens hexokinase II (HKII) mRNA		43	8904.93333 3	25355.67	11794.5	18840.6	21439.5 7	21744

Poly [ADP-ribose] polymerase 1	PARP1	60	20317.9666 7	37582.0 3	28540.1	27927.4 3	29091.4 7	26555.4 7
Protein deglycase DJ-1	PARK7	21	6936.76666 7	12998.5	10051.6	9659.46 7	8573.16 7	8715.96 7
Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	4	463.166666 7	1034.1	771.066 7	768.5	752.533 3	708.8
NAD kinase 2, mitochondrial	NADK2	9	580.3	1390.83 3	1109.1	1033.86 7	1140.36 7	1048.9
Polyribonucleotide 5'-hydroxyl-kinase Clp1	CLP1	2	37.3333333 3	90.1666 7	77.6333 3	67.0333 3	57.2	60.3666 7
cDNA FLJ77588, highly similar to Homo sapiens MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae) (MAK10), mRNA		6	964.533333 3	2195.267	1992.1	1632.16 7	1243.7	1254.16 7
14-3-3 protein zeta/delta	YWHAZ	19	13744.2	23037.2	17828.6 3	17130.0 3	16339.9 3	16461.8
Acyl-coenzyme A thioesterase 8	ACOT8	3	442.766666 7	866.2	683.1	644.1	646.5	620.5
Proteasome maturation protein	POMP	3	688.633333 3	1051.36 7	782.466 7	781.8	716.666 7	718.566 7
Cell division cycle protein 16 homolog	CDC16	4	182.2	275.266 7	245.066 7	204.7	202.1	193.566 7
tRNA-splicing endonuclease subunit Sen34	TSEN34	5	673.366666 7	1058.63 3	1048.83 3	787.333 3	648.733 3	683.6
Annexin (Fragment)	ANXA2	2	10904.1	24548.7	17765.1 3	18260.2	18532.6 3	17605.1 7

39S ribosomal protein L40, mitochondrial	MRPL40	7	1123.16666 7	2561.4	2280.33 3	1905.4	1750.33 3	1774.8
Active breakpoint cluster region-related protein	ABR	3	535.866666 7	715.466 7	530.666 7	532.233 3	519.633 3	624.566 7
PHP14 protein	PHP14	3	1800.26666 7	593.233 3	420.666 7	441.333 3	465.5	499.8
Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	14	2353.36666 7	3563.83 3	2928.33 3	2651.36 7	2184.13 3	2375
E3 ubiquitin-protein ligase RNF213	RNF213	30	3330.66666 7	6592.2	5206.9	4904.5	4783.66 7	4758.66 7
RAB13 protein (Fragment)	RAB13	5	1925	4023.23 3	3353.43 3	2993.3	2683.3	2514.66 7
Splicing factor 3B subunit 1	SF3B1	48	10878.2666 7	23008.1 3	19755.7 3	17118.4 7	16004.0 3	15130.8 7
Abl interactor 1	ABI1	4	604.833333 3	1278.96 7	1091.53 3	951.633 3	869	865.933 3
Ubiquitin-conjugating enzyme E2 Z	UBE2Z	3	655.833333 3	1608.6	1355.03 3	1197.1	1128.43 3	1093.46 7
TATA-binding protein-associated factor 2N	TAF15	6	1435.76666 7	3378.33 3	2933.76 7	2514.16 7	2172.73 3	2089.93 3
Catenin delta-1	CTNND1	27	4027.63333 3	6262.16 7	5184.43 3	4660.8	4161.63 3	4248.96 7
Ragulator complex protein LAMTOR3	LAMTOR3	3	315.866666 7	467.466 7	353.9	347.933 3	339.6	316.366 7
BLOC-1-related complex subunit 6	BORCS6	2	78.7666666 7	165.433 3	114.266 7	123.133 3	113.066 7	97.9
UDP-N-acetylglucosamine--peptide N-	OGT	13	1793.56666 7	3275.46 7	3089.66 7	2438.4	2057.56 7	1947.43 3

acetylglucosaminyltransferase 110 kDa subunit								
CREB-binding protein	CREBBP	4	612.266666 7	728.733 3	735.066 7	542.533 3	700.4	707.566 7
Glycerol-3-phosphate phosphatase	PGP	7	981.166666 7	1323.06 7	1082.83 3	985.166 7	968.966 7	911.633 3
cDNA, FLJ96345, Homo sapiens SET translocation (myeloid leukemia-associated) (SET),mRNA	1	4757.83333 3	8424.633	6791.96 7	6273.36 7	5121.06 7	4839.5	
Protein SYNJ2BP-COX16 (Fragment)	SYNJ2BP-COX16	6	1162.86666 7	2574.33 3	2152.3	1916.96 7	2030.23 3	1681.86 7
5'-AMP-activated protein kinase subunit gamma-2	PRKAG2	4	595.933333 3	1983.53 3	1964.06 7	1477.13 3	1164.43 3	1263.1
cDNA FLJ55508, highly similar to Sad1/unc-84-like protein 2	5	301.833333 3	633.9667	566.133 3	472.166 7	458.066 7	402.4	
cDNA FLJ78635, highly similar to Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), transcript variant 1, mRNA	8	1832.36666 7	4490.933	3576.96 7	3345.2	3171.7	2732.66 7	
Calpastatin isoform a variant (Fragment)		3	11990.5333 3	24152.8 3	17516.3 7	17991.2 7	18724.7 3	17216.6 7
Protein phosphatase 1 regulatory subunit 3D	PPP1R3D	2	149.3	232.2	198.166 7	172.966 7	157.6	182.233 3
Trafficking protein particle complex subunit 2-like protein	TRAPPC2L	2	328.6	894	931.7	665.966 7	553.7	585.233 3

F-box-like/WD repeat-containing protein TBL1XR1	TBL1XR1	7	790.366666 7	2029.5	1616.9	1511.86 7	1474.1	1375.96 7
FACT complex subunit SSRP1	SSRP1	26	3902.8	10558.9	8887.13 3	7866.9	6484.53 3	6245.56 7
Aldehyde dehydrogenase 9 family, member A1	ALDH9A1	19	5571.9	9957.2	7888.56 7	7418.8	7238.1	6918.16 7
mRNA-decapping enzyme 1B	DCP1B	7	780.6	1516.7	1261.1	1130.06 7	1060.8	1026.76 7
Cleavage and polyadenylation specificity factor subunit 1	CPSF1	22	2236.86666 7	4730.36 7	3987.23 3	3524.83 3	3448.26 7	3156.96 7
Neurobeachin	NBEA	2	1016.1	1394.06 7	1006.03 3	1038.83 3	1031.43 3	1122.76 7
RNA-binding protein 39	RBM39	22	4874.63333 3	7469.5	6123.2	5566.3	4661.16 7	4751.46 7
Cleavage stimulation factor subunit 1	CSTF1	8	1589.2	4019.5	3397.8	2995.36 7	3041.8	2748.36 7
Dehydrogenase/reductase SDR family member 7B	DHRS7B	3	302.466666 7	394.466 7	361.5	293.966 7	286.7	250.933 3
Kallikrein-6	KLK6	1	208.5	247.1	275.266 7	184.166 7	173.533 3	147.633 3
Krueppel-like factor 16	KLF16	4	420.6	820.3	992.9	611.433 3	570.033 3	513.466 7
Tubulin-specific chaperone C	TBCC	7	965.433333 3	1710	1522.6	1274.6	1212.7	1295.7
Protein Wiz	WIZ	9	1776.93333 3	3056	2533.36 7	2278.2	2376.8	1880.36 7
COP9 signalosome complex subunit 5	COPS5	9	1066.1	2346.53 3	1908.83 3	1749.33 3	1499.06 7	1568.36 7

RNA demethylase ALKBH5	ALKBH5	12	1716	3821.13 3	2396.6	2848.73 3	3290.76 7	3051.9
Ras-related protein Rab-5B	RAB5B	3	1012.4	2010.66 7	1643.53 3	1499.13 3	1256.03 3	1393.86 7
Probable global transcription activator SNF2L1	SMARCA1	18	3813.63333 3	8875.6	8833	6617.56 7	5837.6	5467.4
Metallothionein		1	3676.7	7498.6	6214.7	5591.63 3	5974.73 3	5698.06 7
Replication protein A 14 kDa subunit	RPA3	5	1572.96666 7	3380.93 3	2814.46 7	2521.2	2543.56 7	2347.26 7
cDNA FLJ10286 fis, clone HEMBB1001384, highly similar to COP9 signalosome complex subunit 4	17	3867.03333 3	7326.767	6045.96 7	5463.86 7	4851.9	4927.86 7	
Synemin	SYNM	4	296.1	276.966 7	201.766 7	206.566 7	268.766 7	217.533 3
ADP/ATP translocase 1	SLC25A4	2	4741.53333 3	11319.2 7	9751.8	8442.23 3	8319.2	6572.9
Heme oxygenase 2	HMOX2	11	1524.6	4631.3	3552.36 7	3454.33 3	3326.06 7	3624.6
Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	GNG5	3	662.4	1354.56 7	1058.53 3	1010.36 7	1013.9	830.333 3
N-alpha-acetyltransferase 30	NAA30	5	839.133333 3	1740.13 3	1456.5	1297.96 7	1145.93 3	1087.53 3
Isoform Long of Glucose-6-phosphate 1-dehydrogenase	G6PD	22	3522.96666 7	8999.7	7116.3	6713.1	5797.76 7	5638.7

Protein SCO1 homolog, mitochondrial	SCO1	3	885.233333 3	2266.16 7	1827.5	1690.66 7	1676.4	1400.36 7
cDNA FLJ55296, highly similar to Homo sapiens WD repeat domain 42A (WDR42A), mRNA		7	892.833333 3	2005.933	1637.7	1496.53 3	1384.73 3	1294.43 3
cDNA, FLJ93645, highly similar to Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B),mRNA		7	1031.86666 7	1561.5	1667.13 3	1164.96 7	1027.33 3	913.6
Glyceraldehyde 3-phosphate dehydrogenase (Fragment)	GAPD	1	5433.73333 3	9916.16 7	6795.76 7	7398.3	7547.23 3	7006.43 3
Dynactin subunit 3	DCTN3	6	683	2034.3	1597.26 7	1518	1341.4	1378.33 3
Transcription factor E2F4	E2F4	3	313.4	635.033 3	642.433 3	473.866 7	446	373.2
cDNA FLJ78586, highly similar to Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA		13	3704.83333 3	8561.633	6504.73 3	6389.23 3	6532.83 3	5815.93 3
Translocase of inner mitochondrial membrane 50 homolog (<i>S. cerevisiae</i>)	TIMM50	12	2663.33333 3	5293.8	4682.93 3	3950.7	3365.7	3251.4
Parkinson disease 7 domain-containing protein 1	PDDC1	6	443.366666 7	1212.7	1056.43 3	905.066 7	943.666 7	889.566 7
Golgi to ER traffic protein 4 homolog	GET4	2	330.566666 7	759.433 3	735.433 3	566.833 3	460.133 3	483.5

cDNA FLJ78370, highly similar to Homo sapiens bromodomain containing 8 (BRD8), transcript variant 1, mRNA		8 3	1143.73333 3	1357.633 7	1280.76 7	1013.36 7	886.1	923.866 7	
NAD-dependent malic enzyme, mitochondrial	ME2	18	3535.63333 3	5881.5	4899.06 7	4390.26 7	4407.56 7	4313.23 3	
Staufen isoform b variant (Fragment)		29	6483.43333 3	12250.6 7	10222.2 3	9144.73 3	7549.66 7	7033.63 3	
Small nuclear ribonucleoprotein Sm D3	SNRPD3	4	967.533333 3	1806.8	1484.8	1348.73 3	1266.36 7	1268.4	
Dynein light chain roadblock-type 1	DYNLRB1	3	1083.36666 7	1797.63 3	1333.66 7	1341.93 3	1223.73 3	1465.06 7	
Dedicator of cytokinesis protein 7	DOCK7	25	3161.46666 7	7916.13 3	5935.8	5909.53 3	4849.5	5097.16 7	
Isoform 6 of Calpastatin	CAST	0	11415.9666 7	23321.6 3	16978.3 7	17410.5	17995.6 7	16625.1 3	
DNA polymerase epsilon subunit 4	POLE4	4	788.133333 3	1110	1049.16 7	828.666 7	764.766 7	666.433 3	
UMP-CMP kinase	CMPK1	8	2614.96666 7	4680.86 7	3474.6	3494.83 3	3398.76 7	3263.13 3	
39S ribosomal protein L44, mitochondrial	MRPL44	7	1292.76666 7	1742.16 7	1461.8	1300.76 7	1279.8	1288.7	
FACT complex subunit SPT16	SUPT16H	45	9349.93333 3	22282.9 7	18149.6 3	16637.6 7	14870.0 7	14689	
Isoform 2 of Regulator of chromosome condensation	RCC1	15	4588.2	8521.8	6835.33 3	6363.96 7	5722.13 3	5668.73 3	

Isoform IIB of Myc box-dependent-interacting protein 1	BIN1	18	5646.83333 3	9434.2	7384.93 3	7045.8	7199.76 7	6341.26 7
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	7	670.733333 3	1851.13 3	1610.06 7	1382.53 3	1351.8	1244.7
Beta-actin-like protein 2	ACTBL2	5	19959.7	40277.8	29913.4	30090.3 7	28805.6	29622
CTD small phosphatase-like protein 2	CTDSPL2	5	390.5	661.466 7	581.666 7	494.166 7	469.866 7	400.933 3
Lamin B receptor, isoform CRA_a	LBR	12	2533.66666 7	5389.53 3	4432.43 3	4026.46 7	4182.4	3644.06 7
Membrane-associated progesterone receptor component 1	PGRMC1	10	1379	2187.43 3	1730.03 3	1634.26 7	1938.03 3	1790.23 3
WD repeat-containing protein 61	WDR61	6	679.133333 3	1501.63 3	1168.36 7	1121.9	982.9	967.633 3
Annexin (Fragment)		23	4351.03333 3	8417.3	6586	6289.23 3	6168.16 7	6164.16 7
Lysosome membrane protein 2	SCARB2	8	1233.33333 3	2855.36 7	2409.13 3	2133.53 3	2263.56 7	1948.23 3
m7GpppX diphosphatase	DCPS	10	872.766666 7	1762.26 7	1392.8	1316.8	1379	1283.86 7
cDNA FLJ39696 fis, clone SMINT2011033, highly similar to Sorting and assembly machinery component 50 homolog		1	338.566666 7	600.9333 3	526.333 3	449.033 3	408.2	412.033 3

Heterogeneous nuclear ribonucleoprotein K, isoform CRA_d	HNRPK	0	16428.3333 3	25609.3	20198.1 7	19136.2 7	16736.1	17004.3 7
Nuclear pore complex protein Nup155	NUP155	24	4777.76666 7	9271.4	8080.1	6928.06 7	6340.36 7	6201.63 3
Stathmin	STMN1	21	12528.7333 3	20850.3	15426.4	15581.2	14779.8 7	14216
Tubulin beta chain		3	40357.4333 3	71339.4 7	58578.8	53313.7	45438.8 3	48186.8 3
Vesicle transport protein SEC20	BNIP1	5	577.433333 3	1443.33 3	1217.9	1078.73 3	1114.26 7	997.4
Discoidin domain-containing receptor 2	DDR2	3	227	385.866 7	285.666 7	288.4	261.833 3	232.233 3
Periphrin-1	PPHLN1	1	563.066666 7	1274.13 3	1141.16 7	952.3	819.733 3	784.7
cDNA, FLJ96603, highly similar to Homo sapiens actin-related protein 10 homolog (S. cerevisiae) (ACTR10), mRNA		6	697.3	1304.4	1124.26 7	975.1	955.866 7	966.733 3
Isoform 4 of Rabankyrin-5	ANKFY1	18	2260.2	4449.23 3	3614.23 3	3326.33 3	3309.9	3081.5
Poly(ADP-ribose) glycohydrolase ARH3	ADPRHL2	3	531.466666 7	1180.4	799.333 3	882.533 3	894.966 7	786.833 3
Isoform 3 of Anaphase-promoting complex subunit 4	ANAPC4	4	304.9	971.6	801.2	726.533 3	685.3	725.133 3
Isoform 2 of MOB kinase activator 1B	MOB1B	4	1122.8	2130.36 7	2040.7	1593.06 7	1333.56 7	1357.9

NF110b		1	11436.4666 7	27616.8 3	21989.7 7	20657.0 7	18682.3 3	18060.1 7
Protein phosphatase 1 regulatory subunit 35	PPP1R35	3	525.233333 3	757.866 7	673.266 7	566.9	455.2	404.366 7
Gem-associated protein 6	GEMIN6	4	318	1232.53 3	1124.7	921.966 7	816.6	836.233 3
Proteasome subunit beta type	PSMB7	13	6430.1	12698.8 3	10077.0 3	9499.06 7	8348.63 3	8298.23 3
Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	5	2346.63333 3	5082.7	4222.36 7	3802.13 3	3588.76 7	3799.2
General transcription factor IIF subunit 2	GTF2F2	9	1515.3	3464.73 3	3010.63 3	2591.86 7	2167.5	2153.93 3
Isoform 4 of PCI domain-containing protein 2	PCID2	4	567.9	1612.66 7	1449.46 7	1206.4	886.733 3	848.866 7
Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	13	3259.8	7519.2	6100.23 3	5625	4628.5	4899.9
28S ribosomal protein S36, mitochondrial	MRPS36	4	848.8	1390	1208.56 7	1039.9	1060.33 3	958.1
Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	HNRNPK	1	16563.9666 7	25801.6	20372.8 3	19303.1	16879.1 7	17135.9
Cytosolic carboxypeptidase 1	AGTPBP1	2	95.4333333 3	173.533 3	144.766 7	129.833 3	132.466 7	120.733 3
Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	15	2518.56666 7	6477.9	6009.83 3	4846.66 7	3824.6	4067.33 3
pre-mRNA 3' end processing protein WDR33	WDR33	12	1448.56666 7	3081.83 3	2589.96 7	2306.13 3	2160	2132.56 7

Leucine-rich repeat-containing protein 59	LRRC59	24	9184.5	16614.6 3	15142.8 3	12433.2 3	11057.0 7	8024.2
Cytochrome c oxidase subunit 5A, mitochondrial	COX5A	7	2775.43333 3	5445.73 3	4597.33 3	4075.33 3	4025.86 7	3192.7
Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	10	1126.53333 3	3036.5	2692.06 7	2272.43 3	1971.2	1920.53 3
DnaJ homolog subfamily C member 11	DNAJC11	10	2293.7	5520.23 3	4557.16 7	4131.2	3795.56 7	3677.63 3
Lysine-specific demethylase 4A	KDM4A	7	400.966666 7	1569.8	904.2	1174.9	1068.93 3	957.266 7
Transcription initiation factor TFIID subunit 9	TAF9	3	1192.3	2010.3	1895.96 7	1504.63 3	1487.8	1289.76 7
Endoribonuclease Dicer	DICER1	2	154.066666 7	353.1	308.533 3	264.3	250.7	222.966 7
Isoform 7 of Interleukin enhancer-binding factor 3	ILF3	2	12587.5333 3	29635.5 7	23614.7	22183.4 7	20154.3	19590.3 3
Protein NOXP20	FAM114A1	12	1504.53333 3	2885.26 7	1987.5	2160.03 3	2041.96 7	2465.03 3
Prohibitin-2	PHB2	20	7391.26666 7	16054.0 3	12489.3	12018.8	11363.4 7	11119.2 7
Isoform 2 of Origin recognition complex subunit 3	ORC3	6	1191.93333 3	1602.4	1428.56 7	1199.63 3	1071.8	993.533 3
N-alpha-acetyltransferase 10	NAA10	10	1631.13333 3	3470.06 7	3192.53 3	2598.83 3	2054.96 7	2259.8
DNA primase large subunit	PRIM2	11	1617.53333 3	3356.46 7	3164.46 7	2513.86 7	1912.86 7	1882.66 7

cDNA FLJ76472, highly similar to Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1, mRNA	16	2131.73333 3	4167.7	3510.13 3	3121.73 3	2681.76 7	2752.23 3	
Thioredoxin domain-containing protein 12	TXNDC12	8	1968.13333 3	3155.96 7	2106.33 3	2363.96 7	2764	2338.16 7
Ubiquitin carboxyl-terminal hydrolase 24	USP24	22	1779.66666 7	3107.13 3	2443.83 3	2327.43 3	2285.2	2590.06 7
cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K	2	16868.8333 3	26387.43	20887.9 3	19768.8 7	17315.8 7	17609.9 7	
cDNA, FLJ95791, highly similar to Homo sapiens aurora kinase B (AURKB), mRNA	3	890.733333 3	938.5	1125.83 3	703.133 3	653.333 3	729.833 3	
40S ribosomal protein S9	RPS9	23	8338.03333 3	15742.6 3	14574.4 3	11794.7	8965.46 7	9244.13 3
cDNA FLJ12440 fis, clone NT2RM1000131, highly similar to Homo sapiens transmembrane protein 63A (TMEM63A), mRNA	2	217.933333 3	422.2	317.333 3	316.333 3	308.233 3	310.8	
Isoform 2 of Tubulin-specific chaperone E	TBCE	12	1738.4	4367.83 3	3511.16 7	3272.86 7	2955.86 7	3144.8
Ubiquitin carboxyl-terminal hydrolase 4	USP4	6	1063.16666 7	2082.23 3	1694.56 7	1560.26 7	1459.93 3	1434.93 3
Dihydropyrimidinase-related protein 5	DPYSL5	4	766.7	1245.76 7	1062.93 3	933.5	872.133 3	837

Rab GDP dissociation inhibitor		13	14538.0333 3	26246.1 7	20841.7	19667.9 7	17084.8	18023.7 3
Dihydroxyacetone kinase 2 homolog (Yeast), isoform CRA_a	DAK	15	2612.03333 3	4065.73 3	2981.66 7	3047.06 7	3125.3	3023.4
IQ motif containing GTPase activating protein 1	IQGAP1	73	18612.6666 7	40465.2 3	29194.1	30326.9	31666.0 7	30945.2
Histone acetyltransferase KAT7	KAT7	2	170.933333 3	402.066 7	314.9	301.333 3	284.5	290.433 3
Cyclin-dependent kinase 7	CDK7	7	965.266666 7	2398.9	2126	1798.03 3	1576.6	1530.9
MICOS complex subunit MIC13	C19orf70	3	402.833333 3	685.4	471.633 3	513.766 7	604.7	487.666 7
Chromodomain-helicase-DNA-binding protein 5	CHD5	1	1131.56666 7	2751.4	2502.93 3	2062.8	1868.5	1721.43 3
cDNA FLJ16452 fis, clone BRAWH3002467, highly similar to RAB GDP DISSOCIATION INHIBITOR BETA		1	7998.7	14975.13	12088.6 3	11227.8	9759.93 3	10692.0 7
Nuclear pore complex protein Nup85	NUP85	7	912.366666 7	2323.93 3	2069.2	1742.4	1338.53 3	1516.9
Isoform 2 of Lymphokine-activated killer T-cell-originated protein kinase	PBK	14	2894.36666 7	5537.83 3	5776.7	4152.16 7	3328.93 3	3188.06 7
Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	24	8203.33333 3	15199.9	12871.9	11397.2	10008.9	9847.06 7
Heat shock 70 kDa protein 14	HSPA14	14	2511.06666 7	4121.76 7	3444.33 3	3090.73 3	2528.96 7	2719.03 3

U2 small nuclear ribonucleoprotein B''	SNRPB2	5	1627.96666 7	2965.33 3	2464.13 3	2223.73 3	2225.16 7	1967.56 7
HAUS augmin-like complex subunit 6	HAUS6	10	1714.16666 7	2490.33 3	2125.46 7	1867.6	1674.46 7	1688
Isoform 3 of Scaffold attachment factor B1	SAFB	17	6576.26666 7	12070.5	10091.4	9052.63 3	8741.46 7	8203.66 7
Isoform B of Phosphate carrier protein, mitochondrial	SLC25A3	16	5222.83333 3	11857.0 7	10157.2 7	8893	9384.8	7846.9
Probable cysteine--tRNA ligase, mitochondrial	CARS2	8	1171.73333 3	3292.76 7	2532.13 3	2469.73 3	2760.06 7	2442.3
HELZ protein	HELZ	11	895.9	1572.46 7	1200.1	1179.46 7	1176.56 7	1139.53 3
40S ribosomal protein S3	RPS3	28	11640.7	21096.1 3	18693.3 3	15823.7	12284.3	13949.8 7
Acetolactate synthase-like protein	ILVBL	10	1536.33333 3	2221.4	1654.3	1666.23 3	1811.53 3	1565.2
E3 ubiquitin-protein ligase UHRF1	UHRF1	14	3388.23333 3	3646.76 7	5286.73 3	2735.9	2430.53 3	1987.53 3
Obg-like ATPase 1	OLA1	19	4951.23333 3	10835.5	9409.86 7	8129.16 7	6354.03 3	6848.4
Centrosome-associated protein CEP250	CEP250	21	1707.1	3642.46 7	2661.7	2733.13 3	2680.26 7	2493.43 3
Transcriptional regulator Kaiso	ZBTB33	1	240.833333 3	382.8	366.266 7	287.266 7	326.966 7	311.6
Phenylalanine--tRNA ligase beta subunit	FARSB	30	6277.3	14714.2 3	12333.5 7	11044.1 3	9422.7	9908.56 7

NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	14	1338.1	3700.36 7	2662.36 7	2777.83 3	2528.63 3	2304.16 7
Voltage-dependent anion-selective channel protein 1	VDAC1	22	9295.7	22612.9 7	18301.0 7	16975.6 3	16924.1	15706.9 3
LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	28	5733.16666 7	10781.7	8453.86 7	8095.33 3	8368.5	7737.6
Calcium signal-modulating cyclophilin ligand	CAMLG	3	165	166.7	137.733 3	125.166 7	121.933 3	118.633 3
Isoform 2 of Zinc finger FYVE domain-containing protein 21	ZFYVE21	3	290.7	442.833 3	362.7	332.566 7	341.3	316.566 7
Isoform 2 of Polycomb protein EED	EED	5	352.7	659.033 3	642.033 3	494.966 7	475.9	426.533 3
Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	7	652.3	937.433 3	841.666 7	704.066 7	635.566 7	655.3
Galectin (Fragment)		10	3551.86666 7	5733.43 3	3713.9	4306.46 7	5436	5111.6
cDNA FLJ76823, highly similar to Homo sapiens splicing factor, arginine/serine-rich 6 (SFRS6), mRNA		7	3835.86666 7	7394.9	6597.26 7	5554.7	4866.9	4808.73 3
Ribonuclease UK114	HRSP12	5	1312.16666 7	1697.03 3	1451.33 3	1274.86 7	1292.83 3	1206.9
TATA box-binding protein-like protein 2	TBPL2	2	366	971.666 7	900.333 3	729.966 7	445.366 7	441.333 3

Brefeldin A-inhibited guanine nucleotide-exchange protein 1	ARFGEF1	1	926.866666 7	2069.56 7	1818.43 3	1554.76 7	1400.33 3	1558.83 3
Ubiquinone biosynthesis O-methyltransferase, mitochondrial	COQ3	3	453.433333 3	683	531.233 3	513.133 3	533.866 7	501.5
GMP synthase [glutamine-hydrolyzing]	GMPS	43	10109.8666 7	21833.6 3	20893.9	16404.7	12757.7 7	13124.8 7
Epidermal growth factor receptor substrate 15	EPS15	20	2363.13333 3	4655.6	3689.63 3	3498.23 3	3389.16 7	3318.9
Polymerase (RNA) III (DNA directed) polypeptide E variant (Fragment)		2 44.4333333 3	190.7	179.233 3	143.3	113	118.1	
Tubulin beta-2B chain	TUBB2B	2	41091	71572.1	58807.8 7	53783.4 7	45882.7 7	48703.1 3
Ras-related protein Rab-10	RAB10	8	4027.7	9214.1	7614.6	6924.8	5836.06 7	6005.1
DCC-interacting protein 13-alpha	APPL1	12	1774.36666 7	3066.76 7	2372.93 3	2304.96 7	2485.26 7	2249.06 7
Protein KIAA0196 variant (Fragment)		10	763.633333 3	1906.76 7	1476.2	1433.16 7	1407.56 7	1371.73 3
Putative heat shock protein HSP 90-alpha A4	HSP90AA4P	1	5580.93333 3	12998.7	9974.86 7	9770.66 7	8116.33 3	8452.4
MICOS complex subunit MIC60		1	10451.2333 3	18270.8 7	13930.3	13734.1 3	13627.8 3	12331.0 7
RNA-binding protein with serine-rich domain 1	RNPS1	3	1045.16666 7	1384.96 7	1127.06 7	1041.1	1049.43 3	931.066 7
Tubulin beta-1 chain	TUBB1	2	6186.16666 7	12286.2	9934.1	9235.86 7	7989.83 3	8261.1

Deoxynucleotidyltransferase terminal-interacting protein 1	DNTTIP1	5	630.366666 7	1288.53 3	983.4	968.666 7	1005	816.766 7
cDNA, FLJ96431		2	174.6	415.866 7	367.566 7	312.633 3	240.1	273.966 7
Up-regulator of cell proliferation	URGCP	4	231.066666 7	316.933 3	331.533 3	238.266 7	200.6	229.633 3
DNA topoisomerase		3	136.833333 3	461.2	377.166 7	346.733 3	317.633 3	348.933 3
Interferon regulatory factor 2-binding protein-like	IRF2BPL	8	2005.43333 3	3177.16 7	2645.4	2388.7	2456.86 7	2363.33 3
Transmembrane protein 205	TMEM205	1	153.566666 7	364.466 7	285.9	274.033 3	298.566 7	245.733 3
cDNA, FLJ93032, highly similar to Homo sapiens zinc finger, A20 domain containing 3 (ZA20D3), mRNA		1	354.533333 3	558.0667	570.933 3	419.6	382.066 7	353.333 3
Male-enhanced antigen 1	MEA1	1	345.433333 3	593.633 3	513.9	446.366 7	381.3	460.633 3
Ral guanine nucleotide dissociation stimulator-like 2	RGL2	1	96.9666666 7	179.533 3	148.533 3	135	146.166 7	141.6
cDNA FLJ13562 fis, clone PLACE1008080, highly similar to Homo sapiens hexamethylene bis-acetamide inducible 1 (HEXIM1), mRNA		9	1713.1	3359.433	3044	2526.2	2359.46 7	2123.6
cDNA, FLJ92597, highly similar to Homo sapiens NFS1 nitrogen		5	770.533333 3	1297.6	1116.43 3	975.766 7	961.633 3	889.366 7

fixation 1 (<i>S. cerevisiae</i>) (NFS1), mRNA								
cDNA, FLJ95309, highly similar to Homo sapiens adenosine monophosphate deaminase 2 (isoform L)(AMPD2), mRNA	23	2752.46666 7	5044.667	3787.63 3	3793.83 3	3908.9	3775.43 3	
THO complex subunit 7 homolog	THOC7	7	1089.2	2071.23 3	1812.2	1557.73 3	1654.6	1514.5
Mitochondrial genome maintenance exonuclease 1	MGME1	5	1159.63333 3	1863.33 3	1804	1401.56 7	1451.36 7	1357.4
Protein sprouty homolog 4	SPRY4	8	783.7	1354.23 3	992.366 7	1018.7	969.533 3	1025.3
Interferon regulatory factor 2-binding protein 2	IRF2BP2	1	2465.93333 3	4106.46 7	3549.83 3	3089.13 3	2889.56 7	3008.26 7
DnaJ homolog subfamily B member 11	DNAJB11	9	1900.36666 7	3868.16 7	3118.43 3	2910.06 7	2381.83 3	2441.76 7
Mediator of RNA polymerase II transcription subunit 22	MED22	1	153.833333 3	211.966 7	170.366 7	159.466 7	153.133 3	150.433 3
Nectin-2	NECTIN2	4	363.8	1128.26 7	1085.2	848.833 3	781.066 7	619.9
Thiosulfate sulfurtransferase	TST	6	522.533333 3	952.7	744.833 3	716.833 3	843.4	702.966 7
Isoform 2 of Ras-related protein Rab-4B	RAB4B	1	1234.1	2362.56 7	1815.36 7	1777.76 7	1601.96 7	1747.26 7
Isoform 2 of Spliceosome RNA helicase DDX39B	DDX39B	11	8457.83333 3	14549.3 7	11731.0 7	10948.1	10611.7	10798.2 7
Selenoprotein N	SEPN1	2	13.6	29.5	24.0666 7	22.2	40.6	29.8

Testis-expressed sequence 10 protein	TEX10	11	1190.53333 3	2301.56 7	1924.3	1732.1	1653.46 7	1581.8
cDNA FLJ33691 fis, clone BRAWH2002976, highly similar to GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2		7	3258.2	7845.9	6324.1	5905.03 3	5417.43 3	5617.03 3
Lethal(2) giant larvae protein homolog 1	LLGL1	4	828.133333 3	1331.86 7	1073.76 7	1002.43 3	1140.53 3	1005.7
ATP-dependent RNA helicase A	DHX9	44	8753.46666 7	17865.6 7	15025	13449.5	13064.9 7	11695.4
Adaptor-related protein complex 1, mu 1 subunit variant (Fragment)		18	2560.23333 3	5367.767	4313.96 7	4040.96 7	3547.9	3834.5
Condensin complex subunit 1	NCAPD2	36	5402.96666 7	10070.8	10842.4 7	7581.63 3	5911.16 7	5980.06 7
Isoform 2 of Probable hydrolase PNKD	PNKD	1	342.933333 3	725.5	679.566 7	546.2	441.1	372.7
Nuclear migration protein nudC	NUDC	28	7937.5	17343.6 3	16888.2	13058.8 3	9040.33 3	10283.3 3
Spermine synthase	SMS	18	3564.33333 3	8686.8	5742.5	6541.9	6435.93 3	7064.8
Protein HSPE1-MOB4	HSPE1-MOB4	7	12033.2333 3	13807.6 7	11411.5 7	10398.5	9912.96 7	9778.93 3
Isoform 2 of UPF0687 protein C20orf27	C20orf27	2	513.866666 7	1085.66 7	997.033 3	817.7	665.766 7	669.666 7
Cell division cycle protein 20 homolog	CDC20	6	1162.23333 3	1178.63 3	2964.43 3	887.8	748.8	660.533 3

Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	3	1008.36666 7	2078.06 7	1844.13 3	1565.43 3	1389.1	1566.16 7
Isoform 2 of Calnexin	CANX	37	7583.8	20447.9	15418.4 7	15403.8 7	15133.2 3	15363.0 7
28S ribosomal protein S22, mitochondrial	MRPS22	9	1432.3	3065.66 7	2999.43 3	2309.5	2081.33 3	1994.2
NAD(P) transhydrogenase, mitochondrial	NNT	3	599.4	941.233 3	737.1	709.1	749.2	754.033 3
Putative uncharacterized protein DKFZp686C1054	DKFZp686C1054	7	896.566666 7	2401.46 7	2252.66 7	1809.7	1532.23 3	1550.53 3
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	HIBCH	9	1184.1	2799.56 7	2025.36 7	2109.9	2399.83 3	2265.76 7
Separin	ESPL1	1	206.7	304.4	350	229.433 3	182.633 3	159.6
cAMP-dependent protein kinase catalytic subunit beta	PRKACB	1	451.4	870.433 3	801.5	656.1	620.166 7	564.8
Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	22	10012.4	16929.8	15052.4 7	12761.6 3	10431.6 7	10652.8
Proteasome 26S non-ATPase subunit 2 variant (Fragment)		37	7841.3	19848.53	17981.8 3	14964.2	10701.5	11380.1 7
Golgin subfamily A member 7	GOLGA7	4	442.033333 3	1000.46 7	923.933 3	754.3	632.9	605.5
Malate dehydrogenase, mitochondrial	MDH2	30	24946	39009.5 3	30069.3	29411.1 7	32109.5	28431.0 3
Nuclear pore complex protein Nup133	NUP133	22	2067.23333 3	4863.3	4320.6	3666.73 3	3458.8	3339.8

Calpain-1 catalytic subunit	CAPN1	20	2885.06666 7	6212.1	4488.56 7	4683.73 3	4782.93 3	4769.36 7
Acylglycerol kinase, mitochondrial	AGK	15	2961.06666 7	6939.26 7	6386.53 3	5232.26 7	5122.23 3	4683.73 3
cDNA FLJ77826, highly similar to Homo sapiens BCS1-like (yeast), mRNA		7	800.566666 7	1555.733 7	1344.46 7	1173.16 7	1069.2	1076.06 7
Isoform 2 of NHS-like protein 1	NHSL1	10	560.8	806.133 3	598.433 3	607.9	647.533 3	563.733 3
Required for meiotic nuclear division protein 1 homolog	RMND1	5	207.666666 7	509.833 3	427.666 7	384.466 7	391.366 7	357.133 3
cDNA, FLJ92661, highly similar to Homo sapiens microtubule- associated protein, RP/EB family, member 3 (MAPRE3), mRNA		1	275.433333 3	627.5667 7	619.766 7	473.3	388.633 3	399.4
Isoform 2 of Epsin-1	EPN1	8	1689.76666 7	1809.1	1403.73 3	1364.46 7	1416.36 7	1362.53 3
Isoform 2 of Interferon regulatory factor 2-binding protein 2	IRF2BP2	1	2326.86666 7	3868.73 3	3362.9	2918.03 3	2724.43 3	2851.56 7
Ufm1-specific protease 2	UFSP2	5	393.8	846.9	637.5	638.8	672.8	630.8
cDNA FLJ77957, highly similar to Homo sapiens HBS1-like (S. cerevisiae) (HBS1L), mRNA		17	4132.73333 3	8182.633	6752.93 3	6172.76 7	5615.36 7	5324.56 7
cDNA, FLJ96655, highly similar to Homo sapiens stromal		4	664.033333 3	1886.767	1535.46 7	1423.4	1311.3	1215.63 3

membrane-associated protein 1 (SMAP1), mRNA								
Glycine cleavage system H protein, mitochondrial	GCSH	2	900.566666 7	1661.03 3	1178.03 3	1253.13 3	1240.96 7	1060.26 7
cDNA FLJ55391		2	247.866666 7	353.433 3	284.1	266.666 7	305.2	221.566 7
SUMO-activating enzyme subunit 2	UBA2	25	5027.66666 7	9786.56 7	8293.7	7384	6800.46 7	6657.2
Elongation factor 2	EEF2	68	41089.0666 7	79796.3 3	72310.8 3	60207.4	48627.8 3	51496.6
F-box and leucine-rich repeat protein 20, isoform CRA_a	FBXL20	2	245.866666 7	411.533 3	293.233 3	310.533 3	325.866 7	344.8
Myosin light chain 6B	MYL6B	3	2735.83333 3	4057.96 7	3024	3062.06 7	3424.13 3	3026.7
Isoform 2 of Heat shock protein HSP 90-alpha	HSP90AA1	51	72937.9	137432. 5	113202. 7	103711. 2	84642.3	88242.2
Alcohol dehydrogenase [NADP(+)]	AKR1A1	14	2278.56666 7	5026.43 3	3394.46 7	3793.5	3912.3	4165.43 3
Ankyrin repeat domain-containing protein SOWAHC	SOWAHC	6	426.9	978	766.8	738.166 7	699.266 7	696.9
Isoform 2 of Centromere protein S	APITD1	2	611.166666 7	1004.03 3	885.466 7	757.833 3	758.433 3	699.466 7
Glycerol-3-phosphate acyltransferase 3	GPAT3	5	1317.9	2601.96 7	2452.96 7	1963.96 7	1653	1532.93 3
Aldehyde dehydrogenase family 16 member A1	ALDH16A1	13	1733.03333 3	2453.86 7	1915.83 3	1852.2	1856.86 7	1772.16 7
Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	5	1167.03333 3	4017.33 3	3457.1	3032.96 7	2156.03 3	3025.36 7

USP6 N-terminal-like protein	USP6NL	2	105.366666 7	163.933 3	140.166 7	123.766 7	112.233 3	121.533 3
Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial	PRDX5	10	3118.7	4558.5	3186.9	3441.86 7	4172.26 7	3895.56 7
Lysophospholipid acyltransferase LPCAT4	LPCAT4	4	354.166666 7	625.566 7	512.366 7	472.433 3	487.533 3	413.933 3
Exportin-2	CSE1L	35	8979.9	17498.0 3	14892.5	13215.5 7	10831.2	11795.6
Acyl-coenzyme A oxidase	ACOX1	11	889.133333 3	1721.93 3	1088.23 3	1300.53 3	1466.16 7	1295.16 7
Ubiquitin carboxyl-terminal hydrolase 34	USP34	8	848.866666 7	1420.93 3	1235.83 3	1073.26 7	961.3	973.766 7
Serine arginine-rich pre-mRNA splicing factor SR-A1, isoform CRA_a	SR-A1	15	1888.56666 7	3222.96 7	2531.9	2434.4	2840.2	2255.53 3
Isoform 3 of Acylpyruvase FAHD1, mitochondrial	FAHD1	4	867.866666 7	1206.2	901.8	911.1	919.633 3	902
Dynein light chain 2, cytoplasmic	DYNLL2	3	954.233333 3	2418.66 7	2080.73 3	1827.06 7	1718.83 3	1601.66 7
V-type proton ATPase subunit C 1	ATP6V1C1	13	1391.33333 3	4568.7	3929.26 7	3451.56 7	3183.8	3421
Arginine/serine-rich protein PNISR	PNISR	3	335.3	846.3	764.766 7	639.4	626.366 7	574.8
Protein archease	ZBTB8OS	1	110.066666 7	343.866 7	337.066 7	259.833 3	239.533 3	249.733 3
cDNA FLJ75877, highly similar to Homo sapiens 5'-	3	930.9	2626.833	1932.66 7	1984.9	1591.56 7	1833.76 7	

nucleotidase, cytosolic II (NT5C2), mRNA								
Probable ATP-dependent RNA helicase DDX6	DDX6	14	2422.33333 3	4745.96 7	3905.76 7	3586.33 3	3189.56 7	3177.36 7
1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	AGPAT5	3	532.7	1104.33 3	909.4	834.533 3	827.733 3	743.5
RNA polymerase II subunit A C-terminal domain phosphatase SSU72	SSU72	3	458.266666 7	872.666 7	835.9	659.5	587.666 7	562.733 3
Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain, isoform CRA_a	ACADM	13	2069.33333 3	3598.53 3	2856.56 7	2719.63 3	3304.8	2699.7
TATA-binding protein-associated factor 172	BTAF1	12	881.533333 3	1617.13 3	1245.76 7	1222.23 3	1150	1128.9
Isoform 5 of Cysteine-rich with EGF-like domain protein 2	CRELD2	4	611.066666 7	1339.1	893.133 3	1012.16 7	1001.26 7	954.5
Acylamino-acid-releasing enzyme	APEH	16	2720.56666 7	4735.66 7	3471.03 3	3580.1	3885.43 3	3780.96 7
Protein RCC2	RCC2	28	5666.46666 7	10174.6 3	8857.1	7692.03 3	6424.36 7	6544.76 7
Isoform 4 of Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform	PPP3CB	3	597.133333 3	820	618.3	619.933 3	635.8	626.966 7
CAP-GLY domain containing linker protein 2	CLIP2	15	2030.6	3444.13 3	2875.63 3	2603.93 3	3014.83 3	2717.43 3
Mitogen-activated protein kinase 1	MAPK1	8	2418.5	5438.36 7	4740.96 7	4112.73 3	3542.16 7	3480.56 7

Kinesin-like protein	KIF3A	6	776.766666 7	1723.13 3	1543.9	1303.13 3	1070.63 3	1094.66 7
Isoform 7 of Breast cancer type 1 susceptibility protein	BRCA1	3	237.3	318.566 7	339.6	240.933 3	218.7	209.4
Mothers against decapentaplegic homolog 2	SMAD2	4	774.833333 3	1112.2	930.8	841.233 3	747.9	801.5
Ubiquitin-conjugating enzyme E2 H	UBE2H	3	229.266666 7	1077.2	855.966 7	814.8	560.966 7	506.2
Nucleoporin NDC1	NDC1	8	1952.83333 3	4511.33 3	3928.03 3	3412.5	3460.46 7	3290.8
RuvB-like 2	RUVBL2	29	9761.8	20239.5	15926.7 7	15310.2 3	11982.5 3	13756.2
Uncharacterized protein NCBP2-AS2	NCBP2-AS2	2	151.4	202.766 7	169.033 3	153.4	164.3	141.166 7
Isoform 3 of Alanyl-tRNA editing protein Aarsd1	AARSD1	6	846.066666 7	1666.16 7	1290.6	1260.56 7	885.533 3	1133
Bleomycin hydrolase	BLMH	6	772.366666 7	1663.76 7	1493.4	1258.8	1106.73 3	1151.63 3
Signal recognition particle 9 kDa protein	SRP9	7	2138.36666 7	4779.2	3830.96 7	3615.96 7	3406.7	3305.46 7
TSC22 domain family protein 1	TSC22D1	2	646.9	1229.8	981.7	930.566 7	940.533 3	832
cDNA FLJ13319 fis, clone OVARC1001610, highly similar to Homo sapiens choline/ethanolamine phosphotransferase 1 (CEPT1), transcript variant 1, mRNA		1	307.766666 7	430.8	346.833 3	326	325.933 3	316.466 7

G protein-coupled receptor 89B isoform B (Fragment)	GPR89B	1	232.366666 7	373	331.233 3	282.266 7	306.5	258.233 3
Breakpoint cluster region protein	BCR	3	538.366666 7	953.666 7	840.533 3	721.8	691	684.766 7
cDNA FLJ78647, highly similar to Homo sapiens zinc finger, FYVE domain containing 20 (ZFYVE20), mRNA	2	201	262.2	219	198.466 7	187.833 3	191.266 7	
Aryl hydrocarbon receptor nuclear translocator	ARNT	3	321.033333 3	526.733 3	402.4	398.7	432.733 3	364.8
PR domain containing 2, with ZNF domain, isoform CRA_b	PRDM2	3	448.4	1385.1	1236.96 7	1048.43 3	801.166 7	903.866 7
Protein SET	SET	5	5902.06666 7	10957.3	8930.96 7	8294	7048.66 7	6886.7
Chromodomain-helicase-DNA-binding protein 1	CHD1	16	2327.5	3904.3	3542.1	2955.43 3	2777.63 3	2573.53 3
Methionine--tRNA ligase, mitochondrial	MARS2	9	818.533333 3	1124.8	889.6	851.466 7	882.066 7	802.666 7
cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA	31	9421	19023.4	16012.6 3	14403	12229.3 3	13376.6 3	
Protein S100-A6	S100A6	9	5144.3	12590.8 7	9607.43 3	9534.43 3	8950.66 7	8466.76 7
3'(2'),5'-bisphosphate nucleotidase 1	BPNT1	12	2511.26666 7	3778.36 7	2971.2	2861.4	2779.83 3	2868.36 7

EGF domain-specific O-linked N-acetylglucosamine transferase	EOGT	2	504.833333 3	1067	1201.33 3	808.1	741.866 7	589.633 3
Origin recognition complex subunit 2	ORC2	7	1629.43333 3	2728.96 7	2296.3	2066.9	1839.66 7	1813.13 3
cDNA FLJ11884 fis, clone HEMBA1007194, highly similar to Origin recognition complex subunit 6		2	517.433333 3	591.8667	833.933 3	448.3	343.533 3	334.7
Isoform B of Ras-related C3 botulinum toxin substrate 1	RAC1	3	2946.96666 7	6775.96 7	6000.2	5132.5	4402.66 7	4544.43 3
Ras-related protein Rab-4A	RAB4A	3	1645.56666 7	3287.23 3	2596.4	2490.2	2263.73 3	2379.53 3
COP9 signalosome complex subunit 6	COPS6	8	1659.63333 3	2897.03 3	2415.43 3	2194.66 7	1898.76 7	2000.8
Coronin-1B	CORO1B	10	5149.63333 3	5059.2	3771.76 7	3832.96 7	4284.43 3	3779.63 3
RUN and FYVE domain-containing protein 1	RUFY1	18	3164.33333 3	7252.83 3	6000.1	5495.1	5187.03 3	5037.6
Uroporphyrinogen-III synthase	UROS	5	652.733333 3	1053.66 7	790.633 3	798.333 3	914.533 3	798.233 3
Proteasome subunit alpha type-7	PSMA7	18	5837.9	10158.9 7	8481.7	7697.3	6894.13 3	7016.53 3
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	COX4I1	7	2078.06666 7	4087.96 7	3833.93 3	3097.4	2883.13 3	2690.8
Threonylcarbamoyladenosine tRNA methyltransferase	CDKAL1	7	1223.86666 7	2267.76 7	2020.53 3	1718.3	1511.13 3	1490

Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2	RPAP2	2	244.433333 3	384.8	338.366 7	291.566 7	239.766 7	245.2
V-type proton ATPase subunit B, brain isoform	ATP6V1B2	15	4250.93333 3	6961.06 7	5488.96 7	5274.5	4822.36 7	4729.2
cDNA FLJ52742, highly similar to Periphilin-1	1	517	1351.867	1222.5	1024.36 7	869.766 7	906	
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	7	1878.5	3726.86 7	2911.8	2824.16 7	2643.83 3	2753.56 7
ER degradation-enhancing alpha-mannosidase-like protein 3	EDEM3	1	95.4	208.433 3	186.766 7	157.966 7	162.666 7	176.133 3
39S ribosomal protein L27, mitochondrial	MRPL27	4	574.233333 3	1469.36 7	1240.7	1113.66 7	1178.73 3	1063.13 3
RuvB-like helicase (Fragment)	RUVBL1	31	10017.7333 3	19189.9 7	15780.9 3	14545.0 7	11652.6 3	12858.2 3
ATP synthase subunit e, mitochondrial	ATP5I	6	2996.16666 7	4911.26 7	4189.3	3722.66 7	3827	3448.5
Myosin light polypeptide 6	MYL6	7	7177.23333 3	11208	8128.06 7	8496.13 3	9073	8508.4
cDNA FLJ46199 fis, clone TESTI4007965, highly similar to AP-1 complex subunit gamma-1	12	2358.06666 7	4146.4	3561.83 3	3143.46 7	2462.83 3	2740.2	
Protein-glutamate O-methyltransferase	ARMT1	9	751.766666 7	2172.43 3	1808.26 7	1646.96 7	1382.33 3	1588.86 7

Isoform 6 of 39S ribosomal protein L43, mitochondrial	MRPL43	2	543.933333 3	1008.06 7	908.033 3	764.333 3	651.8	681.366 7
cDNA FLJ76072, highly similar to Homo sapiens GIPC PDZ domain containing family, member 1 (GIPC1), transcript variant 1, mRNA	8	942.9	2568.767	2382.1	1947.7	1320.2	1335.06 7	
cDNA FLJ10153 fis, clone HEMBA1003417, highly similar to BAG family molecular chaperone regulator 2	9	1780.9	3265.733	2805.86 7	2476.33 3	2142.8	2289.86 7	
V-type proton ATPase subunit d 1	ATP6V0D1	12	1859.5	4248.4	4287.03 3	3221.53 3	2727.3	2984.66 7
DAZAP1/MEF2D fusion protein	DAZAP1/MEF2Dfusion	1	2210.16666 7	3745.46 7	3582.56 7	2840.3	2575.46 7	2543.4
Ethylmalonyl-CoA decarboxylase	ECHDC1	6	1378.53333 3	2174.73 3	1980.56 7	1649.2	1117.5	1305.5
SLIT-ROBO Rho GTPase-activating protein 1	SRGAP1	4	1249.4	2699.5	2135.1	2047.16 7	1896.6	1913.1
Peptidylprolyl isomerase domain and WD repeat-containing protein 1	PPWD1	16	2382.8	6099.76 7	5103.1	4625.8	4089.4	4329.66 7
TELO2-interacting protein 1 homolog	TTI1	2	94.7666666 7	369.2	360.9	280	213.266 7	224.8
Mitochondrial transcription factor A		16	5310.36666 7	9946.8	7565.33 3	7544.06 7	8350.8	7627.06 7
RNA-binding protein 25	RBM25	26	4855.03333 3	8716.56 7	6864.86 7	6611.36 7	6488.66 7	6123.4

Kinetochore protein Spc24 (Fragment)	SPC24	6	1583.46666 7	2307	2442.76 7	1750.13 3	1303	1306.6
Probable ATP-dependent RNA helicase DDX46	DDX46	1	8651.56666 7	17896.0 7	14571.2 7	13577.4	12361.9 7	12144.3
rRNA 2'-O-methyltransferase fibrillarin	FBL	18	5710.1	10355.4	8528.86 7	7856.7	7429.9	7437.96 7
WD repeat-containing protein 82	WDR82	10	1108.56666 7	3090.76 7	2683.6	2345	2085.9	2180.66 7
Probable ATP-dependent RNA helicase DDX46	DDX46	1	8603.06666 7	17842.8	14523.6 3	13537.7 3	12326.9 7	12104.5 3
cDNA FLJ46788 fis, clone TRACH3028855, highly similar to Pseudouridylate synthase 7 homolog (EC 5.4.99.-)		21	3239.86666 7	7016.7	5512.5	5324.26 7	4661.46 7	4668.46 7
Isoform 3 of Xaa-Pro aminopeptidase 1	XPNPEP1	13	2246.8	4239.6	3085.9	3218	3165.63 3	3125.5
Isoform 2 of Tether containing UBX domain for GLUT4	ASPSCR1	13	1585.13333 3	2298.13 3	1759.7	1744.43 3	1609.4	1606.76 7
Glucosamine 6-phosphate N-acetyltransferase	GNPNAT1	5	826.1	1533.46 7	1139.13 3	1164.03 3	1067.73 3	1152.83 3
Actin-related protein 3	ACTR3	19	6216.26666 7	14608.1	12238.5	11088.9 7	9657.16 7	9769.6
Adenosine 3'-phospho 5'-phosphosulfate transporter 1	SLC35B2	6	936	2107.36 7	1962.26 7	1599.7	1544.26 7	1353.3
Armadillo repeat-containing protein 8	ARMC8	8	1220.76666 7	2149.43 3	1914.86 7	1631.66 7	1468.56 7	1452.56 7
Dysbindin	DTNBP1	3	514.2	1066.53 3	999.1	809.666 7	569.133 3	777.966 7

B-cell lymphoma/leukemia 10	BCL10	5	741.833333 3	1412.13 3	867.533 3	1072.03 3	1001.76 7	960.1
39S ribosomal protein L23, mitochondrial	MRPL23	2	279.533333 3	445.8	395	338.433 3	327.633 3	296.6
Mitochondrial GTPase 1		1	458.966666 7	826.033 3	723.033 3	627.1	672.366 7	596.4
PEPD protein	PEPD	7	1245.03333 3	2834.83 3	2160.66 7	2152.16 7	1711.73 3	1871.6
Serine/threonine-protein phosphatase 4 catalytic subunit	PPP4C	6	1715.86666 7	3356.23 3	3020.63 3	2548.46 7	2233.06 7	2136.43 3
Estradiol 17-beta-dehydrogenase 11	HSD17B11	9	1090.33333 3	2206.63 3	2043.56 7	1675.6	1471.33 3	1418.96 7
Integrator complex subunit 11	CPSF3L	4	458.666666 7	875.033 3	868.7	664.5	560.466 7	572.2
39S ribosomal protein L19, mitochondrial	MRPL19	9	1580.73333 3	3287.16 7	3276.7	2496.53 3	2243.93 3	2253.7
Heterogeneous nuclear ribonucleoprotein M (Fragment)	HNRNPM	1	3773.66666 7	7426.46 7	6158.16 7	5641.76 7	5127.53 3	5001.96 7
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	4	297.233333 3	500.066 7	337.4	379.9	486.2	434.566 7
Calcineurin B homologous protein 1	CHP1	12	2073.43333 3	4063.83 3	3859.06 7	3087.43 3	2580.56 7	2480.53 3
Mitochondrial intermediate peptidase	MIPEP	11	1479.8	2898.9	2353.16 7	2202.46 7	2273.53 3	2079.7

F-BAR domain only protein 2	FCHO2	10	960.1	2227.46 7	1624.23 3	1692.6	1873.56 7	1742.63 3
Ankyrin repeat domain-containing protein 50	ANKRD50	12	2314.26666 7	4306.6	3645.3	3272.56 7	2973.7	3037.13 3
KIAA1033 protein	KIAA1033	12	1383.9	3943.73 3	3346.76 7	2997.13 3	2571.8	2806.96 7
Histone-binding protein RBBP7	RBBP7	8	3660.76666 7	6052.7	5629.26 7	4599.96 7	3587.9	3414.46 7
Polycomb protein SUZ12	SUZ12	7	1008.73333 3	1532.96 7	1555.76 7	1165.03 3	1031	985.2
Leucine-rich repeat and WD repeat-containing protein 1	LRWD1	16	1787.73333 3	2678.83 3	2411.2	2036.2	2040.66 7	1838.86 7
Zinc finger and BTB domain-containing protein 7A	ZBTB7A	5	455.1	859.033 3	749.366 7	652.966 7	669.533 3	601.933 3
Signal transducer and activator of transcription		5	324.733333 3	741.8667	653.066 7	563.933 3	498.033 3	457.533 3
Pre-mRNA-processing factor 6	PRPF6	29	5385.36666 7	10366.1	9054.46 7	7880.2	6927.8	6831.53 3
NF-kappa-B inhibitor-interacting Ras-like protein 1	NKIRAS1	2	517.5	875.666 7	901.833 3	665.766 7	620.966 7	637.866 7
Melanoma inhibitory activity protein 2	MIA2	3	271.366666 7	624.1	546.033 3	474.533 3	505.333 3	436.933 3
U6 snRNA-associated Sm-like protein LSM7	LSM7	3	401.833333 3	1257.66 7	1033.8	956.266 7	933.8	891
Threonine synthase-like 1	THNSL1	4	509.666666 7	803.133 3	657.1	610.666 7	620.266 7	575.6
Serine/threonine-protein kinase 38-like	STK38L	3	394.166666 7	638.033 3	579.4	485.166 7	580.5	443.1

Transcription initiation factor TFIID subunit 6	TAF6	12	1258.2	2042.9	1764.93 3	1553.5	1571.36 7	1526.4
Aconitate hydratase, mitochondrial	ACO2	31	4862.56666 7	9998.23 3	7413.73 3	7603.16 7	8328.13 3	7753.7
WAS protein family homolog 2	WASH2P	1	1072.73333 3	1615.9	1358.43 3	1229	1181.9	1221.2
Constitutive coactivator of PPAR-gamma-like protein 2	FAM120C	2	618.666666 7	1043.86 7	853.1	793.966 7	820.6	821.4
HCG2039996	PPAN-P2RY11	8	1254.8	3024.36 7	2753.3	2300.63 3	1924.33 3	2002.06 7
Actin, cytoplasmic 2 (Fragment)	ACTG1	2	27875.8333 3	49725.5	38572.0 7	37826.2	35236.9 3	35925.6
Small EDRK-rich factor 2	SERF2	3	1044	1750.03 3	1331.33 3	1331.3	1150.63 3	1139.83 3
Isoform 6 of Elongator complex protein 2	ELP2	13	831.766666 7	2358.46 7	1817.46 7	1794.26 7	1441.83 3	1638.2
Arf-GAP with coiled-coil, ANK repeat and PH domain- containing protein 2	ACAP2	10	2660.36666 7	4830.43 3	3749.9	3674.9	3585.96 7	3584.3
Protein ENL	MLLT1	5	688.633333 3	1023.73 3	1032.33 3	778.9	786.733 3	677.9
Translationally-controlled tumor protein	TPT1	10	3336.2	6728.03 3	6481.2	5119.03 3	4240.73 3	4350.66 7
Glycerol-3-phosphate dehydrogenase		19	3272.9	7379.2	6033.66 7	5614.56 7	5340.7	5007.36 7
Prolyl 3-hydroxylase 1	P3H1	18	2410.93333 3	5085.36 7	4702.43 3	3869.6	3853.03 3	3264.56 7

Solute carrier family 30 (Zinc transporter), member 9, isoform CRA_b	SLC30A9	4	434.2	1099.33 3	842.7	836.633 3	953.766 7	863.833 3
Tyrosine-protein kinase		11	1354.96666 7	3681.16 7	3119.93 3	2801.63 3	2449.4	2323.63 3
Polymerase (RNA) III (DNA directed) polypeptide C (62kD) variant (Fragment)		4	106.366666 7	285.9	274.133 3	217.6	242.066 7	215.833 3
NudC domain-containing protein 3	NUDCD3	17	2460.56666 7	5919.36 7	5056.5	4505.46 7	3654.16 7	3664.33 3
Isoform 2 of UPF0449 protein C19orf25	C19orf25	1	73.4	98.6666 7	100.3	75.1	111.133 3	109.233 3
Periphrin-1	PPHLN1	0	613.566666 7	1486.43 3	1335.76 7	1131.5	963.633 3	1000.13 3
Mitogen-activated protein kinase kinase kinase 7 interacting protein 1 isoform alpha variant (Fragment)		5	588.766666 7	1420.7	1242.26 7	1081.53 3	939.366 7	989.133 3
Protein TASOR	FAM208A	12	1333.63333 3	2008.13 3	1727.26 7	1528.73 3	1603.63 3	1556.26 7
Zinc phosphodiesterase ELAC protein 2	ELAC2	23	4632.4	7446.13 3	7365.2	5669.5	4665.03 3	4810.13 3
Zinc finger MYM-type protein 1	ZMYM1	3	792.566666 7	1162.63 3	1099.73 3	885.233 3	893.133 3	816.233 3
cDNA FLJ77113		6	564.566666 7	815.833 3	724.066 7	621.2	617.233 3	559.666 7
THO complex subunit 5 homolog	THOC5	9	1307.56666 7	3875.23 3	3242.46 7	2950.73 3	2934.2	2769.46 7

2,4-dienoyl-CoA reductase, mitochondrial	DECR1	15	3162.8	6175.1	5037.9	4702	4692.66 7	4352.8
Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	6	729.766666 7	1494.16 7	1130.2	1137.76 7	1361.16 7	1160.13 3
DNA topoisomerase 2-binding protein 1	TOPBP1	2	277.433333 3	257.3	260.933 3	195.933 3	203.833 3	187.033 3
Fructosamine-3-kinase	FN3K	5	861.233333 3	1845.86 7	1199.96 7	1405.63 3	1356.5	1390.56 7
cDNA FLJ42347 fis, clone UTERU2003399, highly similar to Actin, gamma-enteric smooth muscle		4	34537.0666 7	65983.5	50209.7 7	50248.8	49420.9	50766.7
Hepatitis B virus x interacting protein	LAMTOR5	3	231.2	305.3	286.833 3	232.5	156.1	209.066 7
Protein Dr1	DR1	4	710.166666 7	1826.56 7	1548.8	1391.03 3	1267.9	1136.96 7
Metallothionein-1E	MT1E	2	6158.13333 3	10285.3	8980.36 7	7832.96 7	7720.96 7	7683.06 7
Formin-binding protein 1	FNBP1	9	1438.66666 7	2727.66 7	2111.4	2077.43 3	1804.23 3	1662.36 7
39S ribosomal protein L13, mitochondrial	MRPL13	3	307.633333 3	604.066 7	511.7	460.066 7	433.2	434.566 7
Phosphomevalonate kinase	PMVK	5	972.666666 7	1924.86 7	1615.4	1466.26 7	1340.83 3	1387.86 7
cDNA FLJ34980 fis, clone OCBBF2000522, highly similar to Rab GTPase-binding effector protein 2		9	1271.56666 7	2468.5	1959.1	1880.56 7	1846.93 3	1779.33 3

Dipeptidyl peptidase 1	CTSC	5	540.4	704.666 7	565.733 3	536.866 7	644.366 7	562.033 3
Poly(rC)-binding protein 2	PCBP2	2	6807.46666 7	8993.4	7623.13 3	6852	5889.73 3	6137.2
YTH domain-containing family protein 3	YTHDF3	7	3384.1	6495.16 7	6173.63 3	4950.2	4303.66 7	4253.7
Apoptosis-inducing factor 1, mitochondrial	AIFM1	25	6349.43333 3	11176.6 3	8606.43 3	8518.63 3	8656.03 3	7764.66 7
Polypeptide N-acetylgalactosaminyltransferase 2	GALNT2	6	560.133333 3	1331.23 3	1577.43 3	1014.66 7	1036.9	728.5
Nucleoporin p58/p45	NUP58	6	647.7	1132.66 7	897.166 7	863.366 7	870.433 3	827.666 7
COMM domain-containing protein 10	COMMD10	3	240.133333 3	249.433 3	215.3	190.133 3	201.1	186.533 3
E3 ubiquitin-protein ligase ARIH1	ARIH1	5	219.3	1038.43 3	1045.96 7	791.566 7	664.066 7	683.433 3
Cofilin-2	CFL2	11	9932.6	13208.9 7	10458.5	10068.8 7	8541.26 7	9269.96 7
Atypical kinase COQ8A, mitochondrial	COQ8A	5	746.7	1835.43 3	1354.16 7	1399.2	1388.33 3	1558.93 3
Isoform 2 of ATPase family AAA domain-containing protein 3A	ATAD3A	6	5792.3	12111.4 3	10174.7 3	9233.83 3	8359.2	8348.46 7
Oxysterol-binding protein	OSBPL9	11	2066.06666 7	4247.63 3	3581.9	3239.13 3	2754.33 3	2946.7
Coiled-coil domain-containing protein 90B, mitochondrial	CCDC90B	1	339.3	465.233 3	608.266 7	354.833 3	329.566 7	286.466 7

Dihydrolipoyl dehydrogenase, mitochondrial	DLD	20	7165	10231.5	10874.5	7803.96 7	7322.7	6704.46 7
Cleavage and polyadenylation specific factor 3, 73kDa variant (Fragment)	13	1145.23333 3	2211.767	2110.73 3	1687.2	1582.2	1576.46 7	
Ribonucleoprotein PTB-binding 1	RAVER1	25	4460.43333 3	5746.7	4433.5	4383.93 3	4178.13 3	4157.03 3
Tensin-3	TNS3	13	2381.46666 7	3435.33 3	3120.73 3	2620.76 7	2505.66 7	2295.4
SHINC3	SHINC3	5	646.8	2038.16 7	2186.23 3	1555.03 3	1237.9	1268.36 7
Cilia- and flagella-associated protein 20	CFAP20	3	639.2	1862.43 3	1799.03 3	1421.13 3	1012.3	1025.93 3
Dehydrogenase/reductase SDR family member 11	DHRS11	5	1744.96666 7	2342.06 7	1776	1787.16 7	1835.5	1735.4
Protein unc-45 homolog A	UNC45A	17	2920.03333 3	5530.7	4791.06 7	4220.33 3	3636.3	3620.83 3
Ubiquitin-conjugating enzyme E2 A	UBE2A	2	378.366666 7	936.566 7	1008.66 7	714.7	586.2	617.033 3
Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	76	17480.7666 7	36399.7 3	35337.2 3	27778.0 3	21733.7	21271.1 3
cDNA FLJ78615, highly similar to Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 1, mRNA	7	1071.6	2143.233	1903.53 3	1635.7	1500.5	1447.53 3	

Isoform 2 of Delta-aminolevulinic acid dehydratase	ALAD	3	334	562.3	429.5	429.1667	423.1	404.5
cDNA, FLJ95462, highly similar to Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 3 (FACL3),mRNA	18	4774.433333	8931.7	7583.9	6817.133	6325	6260.567	
Splicing factor, arginine/serine-rich 4, isoform CRA_b	SFRS4	12	3113.366667	6257.3	5372.267	4776.1	4614.233	4227.033
Sentrin-specific protease 3	SENP3	4	339.5666667	488.6333	390.8667	372.9667	375.9667	346.9
Protein LLP homolog	LLPH	1	273.1666667	689.1	635.7333	526	419.4667	439.0667
CCR4-NOT transcription complex subunit 3	CNOT3	9	1238.9	2591.733	2009.367	1978.667	1752.133	1733.267
CDK5 regulatory subunit-associated protein 1	CDK5RAP1	6	804.2333333	1468.1	1265.933	1120.833	914.7333	858.8
cDNA FLJ77256, highly similar to Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA	2	116.7	99.43333	89.56667	75.93333	71.16667	66.2	
Terpene cyclase/mutase family member		17	3016.3	7060.667	5882.8	5392.1	5521.533	5577.433
39S ribosomal protein L2, mitochondrial	MRPL2	7	1051.433333	2374.967	1890.467	1813.8	1813.433	1720.633
Armadillo repeat-containing protein 10	ARMC10	9	1455.066667	2247.533	1763.1	1716.567	2018	1733.467

SWI/SNF complex subunit SMARCC2	SMARCC2	9	2147.93333 3	3320.16 7	2759.26 7	2535.86 7	2723.2	2288.53 3
Histone-lysine N-methyltransferase NSD2	WHSC1	10	1486.63333 3	2561.33 3	2359.46 7	1956.3	1832.23 3	1592.06 7
Actin-like protein (Fragment)	ACT	2	5676	9328.63 3	7267.63 3	7125.13 3	7099.9	6957.4
Interleukin enhancer-binding factor 2	ILF2	18	6622.43333 3	12872.5 3	11047.4	9832.06 7	8717.46 7	9126.76 7
Serine/threonine-protein phosphatase 4 regulatory subunit 3B	PPP4R3B	5	1425.53333 3	3561.93 3	3205.36 7	2720.7	2421.1	2175.13 3
Isoform 2 of Eukaryotic translation initiation factor 4E	EIF4E	5	1160.13333 3	2102.43 3	1652.33 3	1605.9	1455.93 3	1472.4
Gamma-enolase	ENO2	16	6453.73333 3	12547.2 3	6968.66 7	9584.06 7	10945.3 3	11073.7 7
Tubulin beta-4A chain	TUBB4A	3	39377.8333 3	67890.6 7	56248.3 7	51859.2 3	43379.2	46828.1
Ras-related protein Rab-39A	RAB39A	2	1501.53333 3	3624.8	2876.96 7	2768.86 7	2229.66 7	3301.36 7
DNA-directed RNA polymerase subunit beta	DKFZp686D10173	2	82.8333333 3	233.633 3	257.566 7	178.466 7	153.4	137.733 3
Isoform 3 of Cleavage and polyadenylation specificity factor subunit 7	CPSF7	11	1852.5	3927.5	3616.1	3000.56 7	2815.16 7	2722.7
Phostensin	PPP1R18	15	1461.2	2471.7	1944.36 7	1888.46 7	1930.8	1703.3
Zinc finger protein 329	ZNF329	1	487.866666 7	1072.86 7	1103.7	819.733 3	738.5	743.566 7

Isoform 3 of La-related protein 7	LARP7	10	1706.43333 3	3627.73 3	3067.53 3	2772.23 3	2819.96 7	2629.06 7
Vacuolar protein sorting-associated protein 35	VPS35	28	4625.83333 3	9357.63 3	8331.96 7	7151.16 7	5981.83 3	6610.56 7
Tudor and KH domain-containing protein	TDRKH	4	509.3	960.9	781.233 3	734.433 3	694.933 3	721.6
Phosducin-like protein 3	PDCL3	7	719.2	1263.8	1159.06 7	966	833.966 7	821.066 7
RNA polymerase-associated protein RTF1 homolog	RTF1	19	3281.23333 3	6800.33 3	5884.66 7	5197.93 3	4927.6	4741.3
DAZ-associated protein 1	DAZAP1	0	2902	3529	2861.76 7	2697.46 7	2573.03 3	2555.4
Isoform 3 of Fermitin family homolog 2	FERMT2	8	1258.53333 3	3746.2	3305.2	2863.53 3	2992.03 3	2949.6
Isoform 2 of Myosin-14	MYH14	3	4348.33333 3	8887.33 3	6506.56 7	6793.46 7	7660.9	6786.96 7
U2 snRNP-associated SURP motif-containing protein	U2SURP	26	4414.66666 7	9611.76 7	8389.73 3	7347.76 7	6586.66 7	5813.76 7
Flap endonuclease 1	FEN1	14	2391.2	4347.73 3	4029	3323.66 7	2866.6	2908.86 7
Hsc70-interacting protein	ST13	18	7915.8	16820.6	14298.8 7	12859.4 7	11951.5 3	11618.3 3
Hexokinase 1 isoform HKI variant (Fragment)	32	6722.8	14945.93	10244.6 3	11426.9 3	13883.5	11709.5 3	
NAD-dependent protein deacetylase sirtuin-2	SIRT2	4	880.6	1575.63 3	1198.26 7	1204.86 7	1215.83 3	1296.4
Inactive ubiquitin carboxyl-terminal hydrolase 54	USP54	2	238	356.066 7	273.566 7	272.333 3	283.666 7	261

Isoform 2 of Casein kinase I isoform gamma-3	CSNK1G3	2	124.033333 3	238.733 3	184.366 7	182.6	176.8	184.5
39S ribosomal protein L38, mitochondrial	MRPL38	6	490.3	927.866 7	827.9	709.7	680.4	617.466 7
Importin subunit alpha-3	KPNA4	9	2967.43333 3	6219.13 3	5638.83 3	4756.96 7	3890.7	4014.76 7
Phosphomannomutase		4	497	764.4	635.633 3	584.7	538.566 7	570.266 7
DNA (cytosine-5)-methyltransferase	DNMT1	4	13544.7	17639.6 3	19949.1 7	13492.8	10224.9 3	9392.93 3
THO complex subunit 1	THOC1	11	1961.46666 7	5069.73 3	4414.26 7	3878.03 3	3693.5	3500.66 7
TELO2-interacting protein 2	TTI2	4	292.866666 7	551.866 7	512.7	422.166 7	323.133 3	331.966 7
Myosin phosphatase Rho interacting protein	MPRIP	11	1663.2	3076.46 7	2632.73 3	2353.46 7	2487.56 7	1984.6
Isoform 6 of Serine/threonine-protein kinase MRCK alpha	CDC42BPA	7	931.3	1472.03 3	1137.13 3	1126.1	1206.26 7	1094.6
Sorting nexin-4	SNX4	7	1205.2	1905.16 7	1626.4	1457.6	1487.53 3	1328.26 7
Acyl-CoA dehydrogenase family member 11	ACAD11	10	886.866666 7	2332.5	1870.63 3	1784.56 7	2146.5	1869.43 3
Isoform 3 of SPATS2-like protein	SPATS2L	3	3842.86666 7	6383.7	5152.9	4884.16 7	4554.36 7	4053.1
NIF3-like protein 1	NIF3L1	5	846.766666 7	1886.36 7	1614.66 7	1443.26 7	1211.2	1265.26 7
Isoform 3 of Poly(rC)-binding protein 2	PCBP2	1	7351.23333 3	9975.46 7	8520.8	7632.66 7	6586.6	6802.63 3

Actin nucleation promoting factor (Fragment)	WASH	2	1165.8	1723	1442.13 3	1318.46 7	1264.26 7	1308.83 3
Integrin, alpha 5 (Fibronectin receptor, alpha polypeptide), isoform CRA_b	ITGA5	4	192.633333 3	463.733 3	440	354.866 7	335.3	292.4
DNA excision repair protein ERCC-6-like	ERCC6L	21	3644.36666 7	6229.73 3	5795.46 7	4767.5	3763.83 3	3818.6
FAD-dependent oxidoreductase domain-containing protein 1	FOXRED1	5	310.366666 7	384.166 7	294.466 7	294	309.266 7	337.866 7
WD repeat, sterile alpha motif and U-box domain containing 1, isoform CRA_a	WDSUB1	3	175.3	429.066 7	322.566 7	328.366 7	337.366 7	389.366 7
Cation-independent mannose-6-phosphate receptor	IGF2R	37	4668.43333 3	10203.5 7	10624.2 7	7809.36 7	8440.3	7427.33 3
COP9 constitutive photomorphogenic homolog subunit 7B variant (Fragment)	6	865.6	1684.533	1422.53 3	1289.53 3	1188.36 7	1215.53 3	
Alpha-ketoglutarate-dependent dioxygenase alkB homolog 4	ALKBH4	4	858.9	796.6	637.5	609.833 3	634.4	594.9
Isoform 6 of CCR4-NOT transcription complex subunit 10	CNOT10	8	222.933333 3	424.466 7	361.6	324.966 7	349.133 3	345.233 3
Ras suppressor protein 1	RSU1	10	2392.2	5476.76 7	4581.6	4193.5	3322.16 7	3560.6
Thyroid adenoma-associated protein	THADA	9	543.333333 3	893.066 7	835.8	683.866 7	514.233 3	548.866 7

Actin-like protein (Fragment)	ACT	1	5275.53333 3	8290.56 7	6424.63 3	6348.53 3	6314.16 7	6174
NADPH:adrenodoxin oxidoreductase, mitochondrial	FDXR	16	3563.73333 3	5014.16 7	3843.9	3840.06 7	4434.1	3833.8
Oxysterol-binding protein		4	381.2	704.166 7	628.266 7	539.366 7	522.533 3	568.866 7
Isoform 3 of WD repeat domain phosphoinositide-interacting protein 4	WDR45	2	313.566666 7	731.7	636.8	560.533 3	479.766 7	512.566 7
Protein DGCR14	DGCR14	4	274.733333 3	278.6	312.933 3	213.433 3	168.4	162.466 7
Protein numb homolog	NUMB	4	2278.86666 7	3828.5	2983.53 3	2933.13 3	3080.26 7	2882.16 7
Beta actin variant (Fragment)		6	65738	114421. 1	88292.9 3	87665.5 3	82992.3 7	84359.0 7
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex		11	1709.56666 7	2489.433	1854.56 7	1907.4	2080.5	2058.96 7
Ubiquitin-like modifier-activating enzyme 1	UBA1	52	24296.4666 7	41332.4 3	30769.1	31671.2	29732.6 7	30487.8 7
Trafficking protein particle complex subunit 5	TRAPPC5	3	692.533333 3	1769.66 7	1751.2	1356.1	871.533 3	879.733 3
Serine/threonine-protein phosphatase 4 regulatory subunit 3A	PPP4R3A	6	2261.86666 7	4306.66 7	3790	3300.83 3	3273.5	2988.43 3
cDNA, FLJ95615, highly similar to Homo sapiens ubiquitin-		17	2282.96666 7	4367.033	3556.43 3	3347.13 3	3012	3049.46 7

activating enzyme E1C (UBA3 homolog, yeast)(UBE1C), mRNA								
ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	10	1465.36666 7	2739.73 3	2393.4	2100	2124.56 7	1969.53 3
Quinone oxidoreductase	CRYZ	16	3098.2	7234.63 3	5677.06 7	5545.86 7	5311.56 7	5492.8
Vacuolar protein-sorting-associated protein 25	VPS25	6	934.5	1577.83 3	1371.86 7	1209.83 3	1138.66 7	1163.36 7
SAFB-like, transcription modulator, isoform CRA_b	SLTM	23	4271.83333 3	8870.03 3	6886.5	6802.13 3	5966.23 3	5672.66 7
Alternative protein MKKS	MKKS	1	380.6	700.033 3	642.3	536.833 3	447.733 3	566
Histidine--tRNA ligase, cytoplasmic	HARS	25	6545.4	15084.9 7	12911.0 3	11568.5 3	9444.26 7	10182.3 7
Dynamin-2	DNM2	31	3956.5	7556.6	5976.26 7	5795.13 3	5117.4	5400.46 7
Chromosome 20 open reading frame 129	FAM83D	3	287.533333 3	497.2	612.866 7	381.366 7	326.5	320.066 7
Ribonuclease P protein subunit p25	RPP25	1	178.6	310	293	237.8	233.4	246.1
Rho-associated protein kinase 2	ROCK2	36	6391.16666 7	12417.3	10478.0 7	9525.6	9271.4	9306.5
Paired amphipathic helix protein Sin3a	SIN3A	14	1998.83333 3	4361.66 7	3600.6	3346.06 7	3262.83 3	3102.63 3
Isoform Beta of Apoptosis regulator BAX	BAX	5	1246.06666 7	2051.86 7	1555.23 3	1574.16 7	1485.9	1522.56 7

Dynamin 1-like, isoform CRA_c	DNM1L	1	7555.06666 7	15075.5 7	12961.2	11568.7 3	8965.3	10042.5 7
cDNA FLJ78246, highly similar to Homo sapiens splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA		14	4315.33333 3	8105.333	7081.66 7	6220.2	5938.9	5787.8
Isoform 2 of Casein kinase I isoform alpha	CSNK1A1	7	1137.4	2269.56 7	2260.43 3	1741.73 3	1568.43 3	1502
Phosphoglycerate kinase 1	PGK1	41	32232.5666 7	75151.2	37814.1	57675.3 7	75815.5 7	77167.2
Dynein assembly factor 5, axonemal	DNAAF5	23	2374.06666 7	4234.73 3	3621.06 7	3250.3	2692.26 7	2953
40S ribosomal protein S2	RPS2	19	12103.4333 3	16682.5 3	14890.4 3	12805.6	9906.93 3	11865.3
Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	12	1416.56666 7	2517.63 3	2198.96 7	1932.86 7	1791.23 3	1731.6
Transcription factor p65	RELA	8	958.9	2399.73 3	1926.16 7	1842.43 3	1696.66 7	1681.96 7
Mitochondrial import receptor subunit TOM40 homolog	TOMM40	10	1638.63333 3	4767.3	4661.16 7	3660.2	2767.43 3	2945.03 3
Calpastatin, isoform CRA_a	CAST	2	9845.9	19080.6	14091.2 7	14649.8 3	14864.0 3	14124.3 7
Cisplatin resistance-associated overexpressed protein, isoform CRA_b	LUC7L3	15	3490.36666 7	6219.63 3	5695.6	4775.56 7	4059.13 3	4247
DNA polymerase subunit gamma-1		6	463.833333 3	1065.6	910.6	818.333 3	849.533 3	755.566 7

Isoleucyl-tRNA synthetase, cytoplasmic variant (Fragment)		46	8851.066667	20194	15709.33	15509	13258.13	15066.8	
Tyrosine--tRNA ligase, mitochondrial	YARS2		16	2465	4964.867	4611.033	3813.1	3217.367	3358.7
Apoptotic protease-activating factor 1	APAF1		7	508.3666667	1798.767	1360.567	1381.5	1297.567	1312.4
Putative E3 ubiquitin-protein ligase UBR7	UBR7		3	241.2	547.2	488.8	420.2667	419	356.9333
Vacuolar protein sorting-associated protein 18 homolog	VPS18		2	240.7333333	525.8	481.3667	403.9	386.8667	422.1333
Dynamin 1-like, isoform CRA_a	DNM1L		2	7181.333333	14456.27	12397.63	11107.57	8610.767	9672.567
39S ribosomal protein L4, mitochondrial	MRPL4		5	647.4666667	826.0333	719.7	634.7	646.5333	636.5667
Kinesin-like protein KIF15	KIF15		12	2115.8	2785.8	2596.233	2140.7	1815.967	1755.767
Developmentally-regulated GTP-binding protein 2	DRG2		11	1296.433333	3461.233	3069.833	2659.733	2334.3	2463.4
Syntaxin-10	STX10		3	1007.2	1247.167	998.3667	958.5333	1028.467	1035.667
F-box only protein 42	FBXO42		3	401.4	495.1667	414.7333	380.6333	410.1667	377.7
Vacuolar protein sorting 11 (Yeast), isoform CRA_a	VPS11		6	507.7333333	781.4	655.9	600.7	586.6667	635.2667
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2		6	1034.266667	1899.267	1434.567	1460.133	1401.2	1288.667

Ran GTPase-activating protein 1	RANGAP1	29	8668.43333 3	14112.6 7	14013.2	10850.0 7	8872	8985.56 7
Trimeric intracellular cation channel type B	TMEM38B	1	360.133333 3	512.133 3	470	393.8	398.366 7	360.4
DNA excision repair protein ERCC-1	ERCC1	5	226.566666 7	379.3	321.9	291.666 7	272.5	251.366 7
Nuclear-interacting partner of ALK	ZC3HC1	7	611.166666 7	1625.5	1348.13 3	1249.96 7	1163.06 7	1128.26 7
Cold-inducible RNA-binding protein	CIRBP	5	920.866666 7	1651.33 3	1633	1270.03 3	1082.9	995.266 7
Small nuclear ribonucleoprotein Sm D1	SNRPD1	3	767.166666 7	1626.76 7	1470.5	1251.2	1244.23 3	1315.66 7
Vacuolar protein sorting-associated protein 16 homolog	VPS16	2	27.2333333 3	119.433 3	117.033 3	91.8666 7	80.5	101.6
N-terminal kinase-like protein	SCYL1	4	718.233333 3	1022.63 3	944.9	786.6	706.5	773.633 3
Colipase	CLPS	1	344.9	524.7	485.766 7	403.633 3	207.733 3	526.6
Vacuolar protein sorting-associated protein 45	VPS45	6	861.166666 7	1838.36 7	1618.46 7	1414.3	1257.63 3	1296.36 7
DNA polymerase epsilon subunit 3	POLE3	5	1200.66666 7	2043.3	1940.36 7	1571.96 7	1335.5	1215.3
Leucine-rich repeat-containing protein 41	LRRC41	8	1129.4	1372.53 3	1345.2	1056.06 7	1101.3	913.033 3
Lysosomal Pro-X carboxypeptidase	PRCP	2	129.2	305.666 7	286.8	235.2	242.133 3	199.666 7

Disintegrin and metalloproteinase domain-containing protein 17	ADAM17	9	594.033333 3	1512.33 3	1187.4	1163.73 3	1106.8	1239.36 7
Translocation protein SEC62	SEC62	6	1869.63333 3	3043.7	2634.1	2342.2	2410.9	2376.96 7
cDNA FLJ54316, highly similar to DNA polymerase subunit delta 3	11	2543.03333 3	3932.6	3730.03 3	3026.23 3	2746.56 7	2429.93 3	
Isoform 11 of Partitioning defective 3 homolog	PARD3	9	1355.4	2031.03 3	1727.83 3	1562.93 3	1560.1	1569.03 3
Nuclear transcription factor Y subunit beta	NFYB	1	194.133333 3	415.9	342.833 3	320.1	293.766 7	276.8
Notchless protein homolog 1	NLE1	11	1832.4	4836.5	4463.8	3723.06 7	2755.2	3069.73 3
La-related protein 4B	LARP4B	5	3515.4	5912	4987.86 7	4551.2	3884.66 7	3860.5
Nucleolar protein 56	NOP56	28	6539.06666 7	11152.5 3	8930.5	8586.26 7	8188.13 3	8460.8
Protein enabled homolog	ENAH	14	2061.8	4184.3	3646.96 7	3221.56 7	3025.66 7	2855.46 7
Tubulin beta-4B chain	TUBB4B	1	48756.5666 7	80721.7	66480.4	62149.6 3	52067.0 3	55780
Isocitrate dehydrogenase [NADP]		23	4470.86666 7	11545.6 7	8438.36 7	8889.66 7	8397.1	9447.23 3
Splicing factor 3B subunit 5	SF3B5	5	756.933333 3	1262.93 3	1170.5	972.466 7	720.133 3	948.933 3
Polypyrimidine tract-binding protein 1	PTBP1	14	5952.26666 7	8076.3	6674.3	6219.06 7	5718.13 3	5701.5

Acyl-CoA:lysophosphatidylglycerol acyltransferase 1	LPGAT1	3	130.166666 7	350.066 7	295.933 3	269.566 7	290.933 3	261.966 7
Arginine-hydroxylase NDUFAF5, mitochondrial	NDUFAF5	2	301.166666 7	684.7	603.4	527.266 7	498.1	492.833 3
Parafibromin	CDC73	21	3343.56666 7	6687.3	5702.66 7	5150.96 7	4898.86 7	4382.36 7
FAST kinase domain-containing protein 5, mitochondrial	FASTKD5	5	246.166666 7	314.433 3	290.133 3	242.233 3	217.366 7	211.766 7
Isoform 2 of Vesicle-associated membrane protein 7	VAMP7	3	531.933333 3	1340.9	1192.3	1033.06 7	936.6	854.366 7
cDNA FLJ40986 fis, clone UTERU2014898, highly similar to Vacuolar ATP synthase subunit H (EC 3.6.3.14)	6	756.3	1070.833	987.2	825.033 3	743.866 7	760.7	
Aldose reductase	AKR1B1	7	1083.56666 7	2215.96 7	1705.53 3	1707.33 3	1808.13 3	1835.8
Fus-like protein (Fragment)		13	6025.9	15411.7	13035.6 3	11874.4 7	10083.9 7	9927.96 7
Transmembrane protein 209	TMEM209	6	572.5	1527.73 3	1360.23 3	1177.1	1064.36 7	1072.06 7
CSNK2A1 protein	CSNK2A1	14	2342.26666 7	4780.26 7	4455.03 3	3683.6	2759.33 3	2745.66 7
ACLY variant protein (Fragment)	ACLYvariantprotein	1	17359.5	33638.7 7	26774.9 3	25921.5 3	24716.0 3	24596.4 3
Density-regulated protein	DENR	8	1480.83333 3	4096.66 7	3225.66 7	3156.83 3	2512.76 7	2987.1

Isoform 2 of Cell division cycle protein 27 homolog	CDC27	14	1950.2	3707.23 3	3551.63 3	2857.03 3	2420.83 3	2360.73 3
U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	12	2534.16666 7	4752.76 7	4124	3662.83 3	3463.9	3428.46 7
GTP-binding nuclear protein Ran (Fragment)	RAN	17	8293.96666 7	20019.6 3	16507.6	15428.9	12446.1	13266.1 7
Isoform 3 of Transcriptional repressor p66-alpha	GATAD2A	9	2083.73333 3	3282.53 3	3131.26 7	2529.83 3	2225.4	1944.1
GrpE protein homolog (Fragment)	DKFZp451C205	3	369.166666 7	824.333 3	609.9	635.333 3	518.466 7	535.6
DENN domain-containing protein 4C	DENND4C	8	1446.1	2618.6	2119.93 3	2018.3	2071.4	2262.9
TAR DNA-binding protein 43	TARDBP	9	2146.43333 3	2993.16 7	2528.4	2307.06 7	2330.7	2120.93 3
N-alpha-acetyltransferase 50	NAA50	13	2392.4	5355.23 3	4682.73 3	4127.7	2721.36 7	3086.3
Eukaryotic translation initiation factor 3 subunit M	EIF3M	12	1446.53333 3	2661.13 3	2685.1	2051.36 7	1509	1810.76 7
Hydroxysteroid dehydrogenase-like protein 2	HSDL2	15	3710.4	7772.8	6064.86 7	5992.46 7	6928.26 7	5794.06 7
Tonsoku-like protein	TONSL	6	394.966666 7	555.033 3	561.2	427.933 3	394.433 3	380.533 3
ATP-binding cassette sub-family D member 1	ABCD1	1	168.666666 7	289.733 3	237.233 3	223.433 3	253.566 7	223.3
Protein O-GlcNAcase	MGEA5	19	4405.76666 7	8355.16 7	6111.6	6445.3	6257	6305.9
Isoform 2 of MICOS complex subunit MIC60	IMMT	8	12285.3333 3	20308.4	15532.1	15667.5 3	15612.7	14159

cDNA FLJ75839, highly similar to Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA	4	320.8	1012.233	744.466 7	780.933 3	901.566 7	799.8	
Intraflagellar transport protein 74 homolog	IFT74	5	427.433333 3	605.966 7	524.1	467.566 7	437.966 7	459.3
Integrator complex subunit 9	INTS9	5	164	442.8	384.7	341.666 7	310.4	326.433 3
Isoform 2 of Proteasome activator complex subunit 3	PSME3	14	3276.3	6978.4	7120.8	5384.6	3827.43 3	3861
Clustered mitochondria protein homolog (Fragment)	CLUH	3	5139.5	9520.73 3	9439.46 7	7346.3	5490.5	5537.73 3
CAAX prenyl protease 1 homolog	ZMPSTE24	10	2192.13333 3	4515.06 7	3901.76 7	3484	3253.86 7	3094.46 7
Round spermatid basic protein 1	RSBN1	7	716.033333 3	2019.13 3	1520.3	1558.16 7	1653.03 3	1460.73 3
Pre-mRNA-processing-splicing factor 8	PRPF8	75	12132.7666 7	25302.9	22396.0 3	19527.7 7	16699.7	16338.7
Lysosome-associated membrane glycoprotein 1	LAMP1	6	1838.6	2215.36 7	2201.96 7	1710.06 7	1463.6	1599.2
UHRF1-binding protein 1	UHRF1BP1	5	462.4	858.866 7	723.7	663	583.233 3	579.733 3
Isoform 2 of ATP-citrate synthase	ACLY	1	16772.8333 3	32453.8	25901.5 3	25052.7 7	23899.2	23821.4 7
Isoform 7 of Protein OS-9	OS9	1	734.933333 3	1322.26 7	1174.7	1020.8	1111	1575.63 3
Isoform 1 of BRCA1-A complex subunit BRE	BRE	5	627.033333 3	1167.26 7	962.366 7	901.3	761.133 3	805.133 3

Isoform 2 of Ras-related protein Rab-5C	RAB5C	10	3991.3	5687.6	4622.83 3	4392.16 7	5075.3	3963.2
X-ray repair cross-complementing protein 6	XRCC6	48	17665.2	33570.2	26819.7 7	25925.1	24339.6	23704.0 3
4-hydroxyphenylpyruvate dioxygenase-like protein	HPDL	8	1117.73333 3	1306.73 3	1076.46 7	1009.16 7	883.966 7	1066.23 3
Cytochrome c oxidase assembly factor 7	COA7	5	545.7	776.4	827.366 7	599.7	485.133 3	439
Septin-9	Sep 09	32	6640.93333 3	12041.7 3	9830.76 7	9301.2	9107.6	8518.86 7
Isoform 2 of Eukaryotic translation initiation factor 3 subunit B	EIF3B	25	6310.7	14964.5 3	14549.4 7	11559.4 7	8136.33 3	8799.03 3
Zinc finger protein 629	ZNF629	4	1210.1	2964.63 3	2587.73 3	2290.2	2295.83 3	2117.96 7
60S ribosomal protein L9	RPL9	13	5764.36666 7	8244.83 3	7222.4	6369.56 7	4978.2	5882.1
DNA replication complex GINS protein PSF1	GIN51	3	487.2	1041.83 3	1013.86 7	804.9	696.133 3	746.066 7
FBRNP	D10S102	1	3258.6	6985.23 3	5236.3	5396.83 3	4800.23 3	4635.33 3
Cytochrome b-245 light chain	CYBA	3	491.166666 7	1701.76 7	1624.26 7	1314.8	1132.1	898.366 7
Host cell factor 1	HCFC1	1	6747.73333 3	11812.6 3	9917.1	9127.13 3	8845.66 7	8238.43 3
SNARE-associated protein Snapin	SNAPIN	4	376.466666 7	695.933 3	608.966 7	537.766 7	508.533 3	494.966 7

DNA polymerase	POLA1	16	2585.8	5191.13 3	4905	4012.5	3316.9	3253.66 7
Protein RMD5 homolog A	RMND5A	3	482.6	1330.6	1193.06 7	1028.6	931.066 7	849.4
Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	2	607.7	755.633 3	708.233 3	584.233 3	576.9	545.366 7
Zinc finger CCCH domain-containing protein 8	ZC3H8	3	703.066666 7	747.733 3	623.766 7	578.133 3	509.933 3	499.4
Leucine-rich repeat-containing protein 40	LRRC40	17	2925.5	5496.96 7	4328.33 3	4250.63 3	4049.33 3	4058.16 7
Histone acetyltransferase type B catalytic subunit	HAT1	12	2089.23333 3	3857.1	4098.7	2982.6	2309.23 3	2202.86 7
Dynactin subunit 1	DCTN1	34	6538.63333 3	10565.6	8908.33 3	8170.53 3	7142.46 7	6937.13 3
Protein VPRBP	VPRBP	5	379.4	760.633 3	741.966 7	588.3	541.6	567.066 7
cDNA FLJ56153, highly similar to Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 1, mRNA	16	2619.46666 7	6159.733	5564.9	4764.33 3	4101.86 7	3841.86 7	
cDNA FLJ77640, highly similar to Homo sapiens copine II (CPNE2), mRNA	5	728.7	1471.633	1301.63 3	1138.26 7	1120.3	1126.13 3	
Leucine-rich repeat-containing protein 47	LRRC47	22	5040.73333 3	7032.1	5868.1	5439.33 3	4589.46 7	4834.66 7

Ras-related protein Rab-22A	RAB22A	3	484.233333 3	964.466 7	754.266 7	746.033 3	696	734.366 7
DNA (Cytosine-5-)-methyltransferase 1 variant (Fragment)	1	12111.3333 3	15949.43	18176.1 7	12337.3	9276.7	8528.96 7	
cDNA FLJ76620, highly similar to Homo sapiens C2f protein (C2F), mRNA	11	2007.53333 3	3954.267	3636.9	3059.06 7	2400.4	2397.36 7	
Cell cycle and apoptosis regulator protein 2	CCAR2	35	7938.83333 3	14030.2	11390.5 3	10854.4	10899.5 7	9942.86 7
cDNA, FLJ95691, highly similar to Homo sapiens PRP18 pre-mRNA processing factor 18 homolog (yeast) (PRPF18), mRNA	3	138.866666 7	397.8333	369.033 3	307.8	264.6	289.4	
Neurogenic locus notch homolog protein 1	NOTCH1	2	276.366666 7	599.333 3	536.733 3	463.7	627.833 3	453.266 7
Histone-lysine N-methyltransferase SETD1A	SETD1A	8	854.7	1153.96 7	941	892.933 3	948.433 3	873.966 7
TNPO2 variant protein (Fragment)	TNPO2variantprotein	3	718.7	1426	1256.76 7	1103.56 7	881.533 3	994.266 7
AP complex subunit beta		19	9921.73333 3	20342.6 7	17233.5 3	15743.6	15062.8 3	13896.8 3
40S ribosomal protein S5	RPS5	10	4577.6	6450.1	6018.1	4992.03 3	4042.76 7	3881.13 3
Isoform 2 of Cullin-7	CUL7	3	135.766666 7	251.433 3	199.833 3	194.6	211.6	222.8

cDNA FLJ55996, highly similar to Conserved oligomeric Golgi complex component 8	8	174.4	855.6	709.333 3	662.233 3	653.233 3	643.333 3	
Ran-binding protein 3	RANBP3	7	1135.3	1795.2	1586.9	1389.6	1175.86 7	1053.23 3
Uncharacterized protein		9	2678.46666 7	4018.66 7	2824.63 3	3110.73 3	3624.16 7	3072.86 7
Importin subunit alpha		10	3355.76666 7	6392.26 7	5790.73 3	4948.1	4256.73 3	4323.86 7
SURP and G-patch domain-containing protein 2	SUGP2	26	4835.4	7066.63 3	6568	5470.13 3	5470.5	4988.6
Full-length cDNA clone CS0DC015YK16 of Neuroblastoma of Homo sapiens (human) (Fragment)	2	294.5	453.3	338.833 3	350.9	381.766 7	345.966 7	
[F-actin]-methionine sulfoxide oxidase MICAL3	MICAL3	10	1651.23333 3	2740.26 7	2525.5	2121.33 3	2123.26 7	1936.96 7
UPF0598 protein C8orf82 (Fragment)	C8orf82	1	182.933333 3	218.566 7	164.7	169.2	170.3	146.7
Proteasome subunit beta type-3	PSMB3	8	1932.3	3294	2665.63 3	2550	2295.1	2454.96 7
G patch domain-containing protein 11	GPATCH11	3	429.966666 7	659.933 3	640.566 7	510.966 7	457.933 3	444.666 7
FAS-associated factor 2	FAF2	18	2985.43333 3	5393.7	4347.53 3	4176.23 3	4104.53 3	3841.43 3
Ras-related protein Rab-12	RAB12	6	2002.93333 3	3640.33 3	3204.83 3	2818.7	2449.6	2620.43 3

Dynamin 1-like, isoform CRA_f	DNM1L	2	7492	15093.9 3	13064.2 3	11687.2 3	8951.43 3	10212.7 7
Histidine triad nucleotide-binding protein 1	HINT1	8	4392.86666 7	5122.53 3	4194.7	3966.46 7	3591.43 3	3760.1
Vacuolar protein sorting-associated protein 52 homolog	VPS52	3	495	791.866 7	733.633 3	613.2	565.566 7	586.033 3
Proteasome assembly chaperone 2	PSMG2	5	917.4	2092.83 3	1892.73 3	1620.8	1260.16 7	1398.06 7
Eukaryotic initiation factor 4A-III	EIF4A3	21	7216.63333 3	15549.2 3	13938.1	12043.0 7	9914.63 3	10394.7 3
cAMP-dependent protein kinase catalytic subunit alpha	PRKACA	8	1708.13333 3	2824.36 7	2518.3	2187.53 3	2157.73 3	2049.1
Sperm-associated antigen 7	SPAG7	6	425.3	732.933 3	628.833 3	567.7	564.466 7	502.7
Programmed cell death protein 2	PDCD2	2	582.666666 7	831	973.133 3	643.666 7	508.9	481.366 7
Baculoviral IAP repeat-containing protein 5	BIRC5	1	130.566666 7	194.5	237.5	150.666 7	138.5	131.166 7
Vesicle-fusing ATPase	NSF	29	6276.86666 7	12615.7 3	10295.1 7	9772.7	9412.46 7	9095.76 7
DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	DDX20	9	1232.2	2304.4	2171.5	1785.4	1502.6	1405.73 3
Serine-protein kinase ATM	ATM	7	590.333333 3	1051.4	841.6	814.633 3	838.033 3	844.766 7
Probable tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial	OSGEPL1	2	320.033333 3	717.3	652.366 7	555.866 7	592.466 7	658.133 3

Protein phosphatase 1F	PPM1F	10	1785.43333 3	3175.7	2563.43 3	2461.06 7	2475.36 7	2284.66 7
Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	SMARCAD1	3	542.066666 7	872.4	856.933 3	676.1	647.266 7	608.6
Ubiquitin carboxyl-terminal hydrolase BAP1	BAP1	2	370.933333 3	755.4	720.4	585.5	539.4	531
Transcription elongation factor B polypeptide 1	TCEB1	6	1811.4	2664.3	2109.33 3	2065.13 3	1777.96 7	1960.46 7
2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	22	4677.86666 7	8571.16 7	7530.56 7	6644.1	6313.3	5917.13 3
Microtubule-associated protein 4	MAP4	1	23505.4	44288.0 3	34789.1 3	34330.8 3	31446.7 3	33150.6 3
cDNA FLJ51188, highly similar to N-acetylglucosamine-6-sulfatase (EC3.1.6.14)	5	1352.8	2676.367	2307.06 7	2074.66 7	2061.36 7	1941.63 3	
ZZ-type zinc finger-containing protein 3	ZZZ3	5	715.566666 7	1033.8	969.733 3	801.7	775.166 7	709.033 3
40S ribosomal protein SA	RPSA	15	6135.13333 3	9338.03 3	8319.33 3	7243.56 7	5739.2	6438.26 7
TRAF-type zinc finger domain-containing protein 1	TRAFD1	3	512.3	537.266 7	603.933 3	416.766 7	380.666 7	322.7
AGTRAP-BRAF fusion protein		1	501.633333 3	565.8	461.433 3	438.933 3	434.966 7	409.566 7
cDNA FLJ76879, highly similar to Homo sapiens DEAH (Asp-	9	2686.3	4872.5	4422.03 3	3780.1	3729.1	3525.8	

Glu-Ala-His) box polypeptide 8 (DHX8), mRNA								
cDNA FLJ56323, highly similar to Methylated-DNA--protein-cysteinemethyltransferase (EC 2.1.1.63)	7	1436.2	2277.733	2104.73 3	1767.16 7	1345.4	1335.63 3	
Receptor expression-enhancing protein 5	REEP5	5	1639.8	3612.8	2890.66 7	2803.1	2844.06 7	2684.43 3
Transmembrane protein 135	TMEM135	2	157.2	275.6	222.833 3	213.833 3	246.166 7	246.9
H/ACA ribonucleoprotein complex subunit 4	DKC1	22	5714.16666 7	9419.93 3	8064.36 7	7309	7415.53 3	7031.5
Solute carrier family 12 member 4	SLC12A4	5	885.4	2700.16 7	2564.46 7	2095.1	1746.36 7	1804.63 3
Paraplegin	SPG7	10	1078.4	2305.13 3	1862.7	1788.6	1606	1555.83 3
Ras-related C3 botulinum toxin substrate 3	RAC3	1	899.066666 7	1923.63 3	1749.33 3	1492.6	1274.43 3	1372.6
Importin subunit alpha-5	KPNA1	9	3530.2	6146	5682.66 7	4769.16 7	3958.16 7	4014.63 3
Isoform 3 of Protein transport protein Sec24B	SEC24B	3	468.033333 3	896.7	769.666 7	695.833 3	669.533 3	708.633 3
cDNA FLJ55475	VWA9	5	227.8	654.1	523.066 7	507.6	503.066 7	470.5
RNA polymerase II-associated factor 1 homolog	PAF1	13	1696.63333 3	4493.3	3674.7	3486.96 7	3211.4	3093.36 7
Dynamin-binding protein	DNMBP	11	1047.16666 7	2452.86 7	2057.86 7	1903.8	1562.1	1639.23 3

General transcription factor 3C polypeptide 1	GTF3C1	19	2119.16666 7	3520	3314.56 7	2732.06 7	2623.53 3	2457.5
RER1 protein	RER1	3	511.833333 3	1059.56 7	989.866 7	822.4	591.866 7	493.6
Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3	ALKBH3	2	312.333333 3	621.6	517.866 7	482.5	486.2	518.833 3
U2 small nuclear ribonucleoprotein A'	SNRPA1	21	2767.1	5960.13 3	5079.43 3	4626.73 3	4451.5	4341.93 3
Isoform 2 of Translation initiation factor eIF-2B subunit delta	EIF2B4	1	1799.93333 3	2414.13 3	1828.66 7	1874.16 7	1554.03 3	1649
Serine/threonine-protein phosphatase 6 regulatory subunit 2	PPP6R2	6	531.6	894.3	730.866 7	694.333 3	638.533 3	654.066 7
ER membrane protein complex subunit 4	EMC4	3	364.5	700.266 7	565.4	543.733 3	412.8	445.733 3
Laminin subunit gamma-1	LAMC1	4	350.733333 3	341.866 7	335.966 7	265.466 7	315.066 7	316.133 3
cDNA FLJ61700, highly similar to ATP-dependent DNA helicase Q5 (EC 3.6.1.-)	1	295.666666 7	509.2	422.133 3	395.433 3	397.366 7	383.6	
Isoform 3 of Nucleolar protein 3	NOL3	4	845.666666 7	1444.46 7	880.533 3	1121.76 7	1286.86 7	1391.63 3
Isoform 7 of Calcium-transporting ATPase type 2C member 1	ATP2C1	8	936.233333 3	1529.7	1309.93 3	1187.96 7	1331.83 3	1073.3

Host cell factor 1	HCFC1	2	7056.43333 3	12144.4 7	10238.4	9432.83 3	9085.86 7	8585.06 7
TRAP1 protein (Fragment)	TRAP1	26	9251.5	18413.8	15657.6 3	14302.7 7	12616.8 3	12705.3
DNA replication complex GINS protein PSF3	GIN3	9	1051	1995.9	2065.13 3	1550.4	1000	1109.23 3
26S proteasome non-ATPase regulatory subunit 10	PSMD10	7	1345.4	2493.1	1808.46 7	1936.63 3	1580.6	1637.33 3
Ras-related protein Rab-9A	RAB9A	5	466.466666 7	1018.83 3	831.433 3	791.566 7	732.3	702.766 7
cDNA FLJ76207, highly similar to Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA	1	146.133333 3	171.4	130.4	133.166 7	179.6	133.5	
28S ribosomal protein S9, mitochondrial	MRPS9	10	1448.86666 7	2578.4	2360.9	2003.26 7	1938.56 7	1868.33 3
Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1	10	1970.03333 3	3417.9	2612.26 7	2655.56 7	2559.93 3	2446.83 3
Putative RNA-binding protein 15	RBM15	18	2388.93333 3	3804.23 3	3147.86 7	2955.73 3	3004.7	2745.16 7
KIAA1012, isoform CRA_b	KIAA1012	10	1056.6	2018.66 7	1726.46 7	1568.53 3	1444.36 7	1547.6
Pre-mRNA-splicing factor CWC22 homolog	CWC22	7	493.7	1222.66 7	1220.36 7	950.066 7	638.4	604.966 7
Protein phosphatase 1 regulatory subunit 21	PPP1R21	11	1269.46666 7	2697	2008.26 7	2095.7	2174.73 3	2158.6

Vacuolar protein sorting-associated protein 51 homolog	VPS51	3	344.3	504.766 7	450.2	392.266 7	354.266 7	360.166 7
Protein asunder homolog	ASUN	11	1350.4	3346.03 3	2654.76 7	2600.3	2623.93 3	2362.13 3
ACTA2 protein (Fragment)	ACTA2	5	31864.5333 3	58965.0 7	45435.8	45823.8	44375.0 3	44276.8 7
Pre-mRNA-splicing factor 38B	PRPF38B	4	657.433333 3	1741	1603.53 3	1353.06 7	1225.56 7	1228.2
Transcription factor IIIB 90 kDa subunit	BRF1	2	554.9	547.2	499.633 3	425.333 3	412.733 3	409.833 3
Non-histone chromosomal protein (Fragment)		4	1140.73333 3	3241.867	2406.56 7	2520.03 3	2168.6	2375.13 3
Serine/threonine-protein kinase ATR	ATR	5	145.733333 3	301.733 3	286.533 3	234.566 7	205.266 7	202.833 3
Isoform 2 of Cyclin-dependent kinase 13	CDK13	1	1085.9	2184.66 7	1731.63 3	1698.4	1376.3	1532.73 3
Hypoxia-inducible lipid droplet-associated protein	HILPDA	1	181.033333 3	602.766 7	277.433 3	468.7	477.266 7	609.266 7
Isoform 2 of Transketolase	TKT	34	12279.0333 3	19212.4 3	15611	14939.4	12877.7	14551.4
Dopamine receptor interacting protein 4	DRIP4	55	12591.9666 7	27840.5 3	20980.6 3	21649.3	20533.7 3	21406.1 7
Phosphatidylserine decarboxylase proenzyme, mitochondrial	PISD	4	37.8666666 7	180.933 3	157.066 7	140.7	142.333 3	168.466 7
Translation machinery-associated protein 16 (Fragment)	TMA16	7	1437.76666 7	3132.9	2625.93 3	2436.53 3	2361.43 3	2156.73 3

Striatin, calmodulin binding protein 3	STRN3	1	1369.96666 7	2488.36 7	2106.46 7	1935.33 3	1847.33 3	1804.8
Isoform 2 of Glycogen synthase kinase-3 beta	GSK3B	8	1097.26666 7	2452.16 7	1967	1907.36 7	1779.13 3	1822.56 7
Methionine adenosyltransferase 2 subunit beta	MAT2B	9	1836.2	3469.66 7	2835.73 3	2699.03 3	2452.13 3	2625.3
Zinc finger protein 598	ZNF598	10	1168.6	2099.2	1989.56 7	1632.96 7	1338.23 3	1268.26 7
cDNA, FLJ93988, highly similar to Homo sapiens baculoviral IAP repeat-containing 2 (BIRC2), mRNA		4	601.533333 3	1099.633	985.133 3	855.466 7	692.566 7	752.466 7
Tetratricopeptide repeat protein 27	TTC27	6	1032.83333 3	2102.3	1834.23 3	1635.5	1258.9	1472.1
Translation initiation factor eIF-2B subunit delta	EIF2B4	1	1901.86666 7	2434.6	1844.5	1894.1	1571.1	1675.06 7
Isoform 2 of Leukocyte receptor cluster member 8	LENG8	6	728.2	1236.56 7	1049.76 7	962.2	935.833 3	909.033 3
Kinesin-like protein KIF13B	KIF13B	3	625.333333 3	1125	886.566 7	875.466 7	880.266 7	862.333 3
Isoform 6 of Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	2	294.3	698.133 3	629.5	543.333 3	470.4	530.533 3
Oxysterol-binding protein-related protein 3	OSBPL3	23	3818.93333 3	7733.53 3	6654.06 7	6019.13 3	5227.06 7	5491.66 7
Glucosylceramidase		2	117.333333 3	155.333 3	153.7	120.9	124.833 3	136.733 3

Nuclear pore complex protein Nup160	NUP160	15	1168.9	3180.3	2844.5	2475.36 7	2227.9	2210.6
Isoform 2 of Mediator of RNA polymerase II transcription subunit 12	MED12	8	783	1441.2	1212.7	1121.76 7	1168.36 7	1108.83 3
Phosphorylase b kinase gamma catalytic chain, liver/testis isoform	PHKG2	2	326.266666 7	443.4	368.5	345.133 3	360.233 3	330.433 3
Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	7	827.4	1106.3	916.333 3	861.133 3	886	775.4
cDNA FLJ61141, highly similar to Ras-related protein Rab-34		2	392.266666 7	956.4333	857.7	744.5	662.533 3	611.366 7
RNA-binding protein 5	RBM5	8	1573.7	2682.16 7	2555	2087.86 7	1996.7	1981.4
cDNA FLJ55400, highly similar to Protein OS-9		2	476.666666 7	1086.2	911.3	845.533 3	910.733 3	1264.43 3
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	PFKFB4	8	462.866666 7	1176.83 3	615.666 7	916.133 3	887.266 7	962.933 3
Actin-related protein 2	ACTR2	13	4103.13333 3	9270.03 3	7960.6	7216.53 3	6163.16 7	6193.53 3
UPF0587 protein C1orf123	C1orf123	5	1340.1	2316.76 7	1803.7	1803.7	1929.33 3	1810.83 3
Isoform B of Membrane cofactor protein	CD46	2	284.566666 7	812	813.666 7	632.2	659.333 3	586.3
Isoform 5 of Microtubule-associated protein 4	MAP4	1	13715.8666 7	27100.4 3	21593.5 3	21099.7	18973.5	19899.1 7

Phosphatidylinositol 5-phosphate 4-kinase type-2 beta	PIP4K2B	2	567.5	897.433 3	764.7	698.733 3	794.833 3	678.533 3
WD repeat-containing protein 48	WDR48	5	778.3	1769.3	1461.73 3	1377.56 7	1326.9	1317.96 7
Nucleoporin NUP53		7	2041.83333 3	3236.83 3	2882.6	2520.2	2416.43 3	2335
Spermatogenesis-associated protein 5-like protein 1	SPATA5L1	9	948	1182.6	1125.83 3	920.8	567.166 7	594.766 7
52 kDa repressor of the inhibitor of the protein kinase	THAP12	3	236.7	493.033 3	413.533 3	383.9	367.8	310.266 7
DnaJ homolog subfamily C member 8	DNAJC8	18	4916.73333 3	8958.66 7	7670.16 7	6975.93 3	6306.96 7	6400.03 3
Cysteine and glycine-rich protein 2	CSRP2	5	407.466666 7	811.566 7	533.533 3	631.966 7	719.6	641.333 3
Histone-lysine N-methyltransferase EHMT1	EHMT1	8	810.266666 7	1410.46 7	1416.66 7	1098.36 7	962.866 7	877.466 7
Helicase with zinc finger domain 2	HELZ2	8	625.566666 7	925.7	793.566 7	720.9	651.366 7	717.433 3
Isoform 2 of Cyclin-dependent kinase 9	CDK9	5	520.7	1327.23 3	1190.96 7	1033.63 3	925.6	991.433 3
Acyl-CoA thioesterase 1	ACOT1	10	1472.3	2266.96 7	1871.36 7	1765.53 3	1941.9	1701.73 3
ER membrane protein complex subunit 3	EMC3	2	239.066666 7	244.166 7	212.8	190.166 7	172.933 3	183.4
Mitochondrial tRNA-specific 2-thiouridylase 1	TRMU	1	166.033333 3	384.733 3	331.966 7	299.666 7	289.866 7	273.066 7
Peroxisomal targeting signal 1 receptor	PEX5	4	149.466666 7	305.466 7	300.966 7	237.933 3	221.233 3	220.7

Histone H1.0	H1F0	11	3519.46666 7	6819.56 7	4397.3	5311.96 7	7357.63 3	6719.63 3
Serine/threonine-protein kinase	PRKD2	2	160.8	245.666 7	200.666 7	191.366 7	184.1	173.066 7
RNA binding motif protein 7, isoform CRA_c	RBM7	3	447.566666 7	757.833 3	660.4	590.366 7	606.466 7	528.766 7
cDNA FLJ76690, highly similar to Homo sapiens neuronal protein isoform a mRNA	1	379.233333 3	1450.233	1278.83 3	1129.8	781.466 7	1042.86 7	
Transmembrane protein 161A	TMEM161A	1	161.566666 7	645.633 3	542.733 3	503.033 3	447.266 7	389.566 7
Piezo-type mechanosensitive ion channel component 1	PIEZO1	5	747.5	1151.9	976.166 7	897.533 3	1147.53 3	817.466 7
RNA-binding protein 14	RBM14	22	4458.06666 7	9171.4	7699.36 7	7146.23 3	7067.1	6150.2
Adenylate kinase 2, mitochondrial	AK2	13	6361.13333 3	10658.9 7	7522.4	8306.13 3	9649.66 7	8688.53 3
Actin-related protein 5	ACTR5	5	219.433333 3	371.066 7	355.566 7	289.166 7	257.5	236.366 7
Cytokine-like nuclear factor n-pac, isoform CRA_c	N-PAC	7	829.2	1229	1123	957.766 7	764.933 3	889.666 7
Isoform 2 of RNA 3'-terminal phosphate cyclase	RTCA	6	826.033333 3	1827.13 3	1604.8	1423.96 7	1122.93 3	1321.56 7
Cysteine and glycine-rich protein 1	CSRP1	7	1590.06666 7	3317.43 3	2841.4	2585.53 3	2445.13 3	2477.96 7
ATP synthase subunit g, mitochondrial	ATP5L	7	1566.26666 7	2807.06 7	2502.3	2187.9	2158.53 3	1949.7

Coiled-coil domain-containing protein 134	CCDC134	6	633.633333 3	1353	1009.1	1054.7	926.266 7	961.833 3
Sorting nexin	SNX6	16	3216.7	5914.56 7	4642.96 7	4610.8	4326.23 3	4491.3
Protein DENND6A	DENND6A	1	162.2	204.666 7	183.133 3	159.566 7	164.3	187.366 7
Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	13	9187.63333 3	13628.8	10997.5	10626.1	9842.86 7	9286.46 7
Isoform 2 of ELAV-like protein 1	ELAVL1	18	4477.3	8247.93 3	6757.86 7	6431.3	5886.73 3	5549.36 7
E3 ubiquitin-protein ligase UBR2	UBR2	10	1347.16666 7	2353.36 7	1932.33 3	1835.13 3	1738.53 3	1776.03 3
Isoform 2 of Annexin A2	ANXA2	21	23211.3666 7	47917.4 7	34810.9 7	37366.6 7	37179.9 3	35611.0 3
Ras-related protein Rab-8B	RAB8B	2	2916	6645	5331.33 3	5181.86 7	4198.8	4834.73 3
Bromodomain adjacent to zinc finger domain protein 2B	BAZ2B	2	267.433333 3	399.366 7	263.133 3	311.433 3	343.3	308.9
Beta-actin (Fragment)		1	21948.7333 3	37174.3 3	29467.4 7	28990.2 7	28848.6 7	29112.0 7
Protein FAM50A	FAM50A	10	2430.86666 7	4539.93 3	3982.8	3540.93 3	3386.9	3219.5
Isoform Short of Eukaryotic translation initiation factor 4H	EIF4H	15	7416.93333 3	12642.9	10282.6 3	9860.93 3	8387.16 7	8572.56 7
cDNA, FLJ94965, highly similar to Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA		10	1185.26666 7	2600.933	2018.2	2028.63 3	1619.5	1819.6

Anaphase-promoting complex subunit 7	ANAPC7	11	1550.5	2952.2	3237.1	2302.63 3	1986.9	1979.7
LPP protein	LPP	12	1703.73333 3	3353.1	2625.96 7	2615.43 3	2837.96 7	2566.36 7
Spermatogenesis-defective protein 39 homolog	VIPAS39	6	684.433333 3	1155.33 3	939.8	901.4	776.2	783.966 7
Isoform 5 of Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	10	1176.56666 7	2547.43 3	2303.23 3	1987.53 3	1579.96 7	1764.33 3
Isoform 2 of Putative ATP-dependent RNA helicase DHX30	DHX30	19	2639.7	3953.13 3	4293.8	3084.53 3	2687.13 3	2572.43 3
RNA polymerase-associated protein LEO1	LEO1	4	766.3	1358.96 7	1041.2	1060.46 7	1070.13 3	1033.53 3
Ubiquitin-conjugating enzyme E2 variant 3	UEVLD	4	347.366666 7	603.4	547.5	470.866 7	432.3	440.133 3
Mitochondrial import inner membrane translocase subunit Tim8 B	TIMM8B	3	656.366666 7	867.466 7	1136.33 3	677	394.1	334.466 7
Telomere length regulation protein TEL2 homolog	TELO2	3	46.0333333 3	71.3666 7	85.1333 3	55.7	41.0666 7	46.6333 3
Nucleoporin 214kDa, isoform CRA_b	NUP214	28	6008.83333 3	10046.1 3	8270.6	7841.06 7	7851.96 7	7582.9
Cytochrome c-type heme lyase	HCCS	12	1265.66666 7	3161.53 3	3011.03 3	2468.03 3	2092.63 3	1879.4
Heterogeneous nuclear ribonucleoprotein U	HNRNPU	6	25290.3	51633.3 3	42102.1 7	40315.6 3	39428.4	37004.3 3

Sodium/potassium-transporting ATPase subunit alpha		1	3670.1	6585.333	6008.3	5142.33 3	5506	4642.33 3	
Integrator complex subunit 6	INTS6	4	704.733333 3	1105.76 7	1003.33 3	863.5	810.666 7	825.8	
Uncharacterized protein C6orf203	C6orf203	3	380.633333 3	898.633 3	717.2	701.8	762.133 3	696.3	
Pre-mRNA-splicing regulator WTAP	WTAP	15	3349.26666 7	5915.6	5263.1	4620.4	4269.66 7	4068.83 3	
39S ribosomal protein L46, mitochondrial	MRPL46	4	437.133333 3	1359.6	1196.56 7	1061.96 7	987.633 3	989.6	
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	35	4701.73333 3	11020.9	8559.86 7	8608.4	7763.46 7	8685.86 7	
Major facilitator superfamily domain-containing protein 10	MFSD10	2	161	482.866 7	359.533 3	377.166 7	509.933 3	350.733 3	
Spastin	SPAST	6	645.566666 7	996.3	830.066 7	778.266 7	698.633 3	721.866 7	
Isoform 1 of Transmembrane protein 230	TMEM230	2	417.633333 3	638.7	552.4	498.933 3	506.233 3	488.8	
Elongation factor G, mitochondrial	GFM1	19	3160.43333 3	5738.46 7	5582.26 7	4482.9	3806.7	3468.93 3	
Eukaryotic elongation factor 2 kinase	EEF2K	5	772.6	1983.26 7	1595.2	1549.36 7	1264.83 3	1244.4	
Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	8	2896.23333 3	6811.5	4807.9	5321.3	4884.16 7	5252.63 3	
Actin-like protein (Fragment)	ACT	1	7369.06666 7	10377.9 7	8066.1	8107.96 7	7921.36 7	7920.56 7	

Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	6	1186.1	1969.83 3	1541.23 3	1538.96 7	1661.13 3	1488.06 7
Nuclear receptor corepressor 1	NCOR1	14	1738.33333 3	2384.23 3	1935.23 3	1862.73 3	1666.33 3	1664.43 3
Sorbitol dehydrogenase	SORD	13	3022.63333 3	5696.23 3	4490.73 3	4450.73 3	3838.83 3	4152.73 3
Uridine kinase (Fragment)		7	338.2	657.333 3	519.5	513.666 7	542.066 7	522.866 7
39S ribosomal protein L49, mitochondrial	MRPL49	5	1310.23333 3	2184.53 3	1956.4	1707.1	1543.5	1495.26 7
SHC SH2-domain binding protein 1, isoform CRA_a	SHCBP1	15	1197.46666 7	1754	2491.06 7	1370.73 3	825.4	839.033 3
28 kDa heat- and acid-stable phosphoprotein	PDAP1	18	9363.13333 3	14425.6 7	11473.6 7	11274.4 7	9596.73 3	9995.93 3
Peroxisomal trans-2-enoyl-CoA reductase	PECR	3	188.166666 7	275.6	212.5	215.433 3	304.5	238.633 3
MHC class II regulatory factor RFX1	RFX1	4	913.466666 7	1623.66 7	1360.66 7	1269.3	1314.23 3	1230.56 7
Vam6/Vps39-like protein	VPS39	4	422.266666 7	769.1	603.366 7	601.333 3	518.866 7	508.433 3
Isoform 2 of Proteasome assembly chaperone 4	PSMG4	2	849	1195.96 7	984.833 3	935.1	853.666 7	848
Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	38	8067.03333 3	16063.5	12388.5	12559.8 7	13388.7	12777.5

cDNA FLJ78655, highly similar to Homo sapiens exportin 5 (XPO5), mRNA		23	4520.93333 3	8122.967	7265.23 3	6351.26 7	5161.86 7	5234.16 7	
RING finger protein 219	RNF219		2	350.333333 3	656.166 7	732.866 7	513.133 3	464.266 7	397.633 3
cDNA, FLJ94931, highly similar to Homo sapiens zinc finger protein 148 (pHZ-52) (ZNF148), mRNA		7	763.633333 3	1308.233	1124.6	1023.1	978.633 3	990.133 3	
Isoform 2 of WD repeat-containing protein 37	WDR37		1	55.2666666 7	81.3666 7	58.8333 3	63.6333 3	64.7666 7	62.6333 3
Acyl-CoA synthetase family member 3, mitochondrial	ACSF3		11	1046.66666 7	2057.9	1603.6	1609.43 3	1765.7	1544.4
Nucleolar protein 11	NOL11		18	2855.33333 3	5796.1	5556.23 3	4533.73 3	3837.43 3	3877.5
Centrosomal protein of 131 kDa	CEP131		6	567.066666 7	631.266 7	614.1	493.8	454.1	393.7
WD40 repeat-containing protein SMU1	SMU1		15	2784.8	5784.03 3	4729.86 7	4525	4136.76 7	4065.1
Mothers against decapentaplegic homolog 1	SMAD1		4	779.8	1400.56 7	1320.13 3	1095.73 3	966.166 7	1069.1
PAX-interacting protein 1	PAXIP1		4	325.2	482.166 7	453.1	377.233 3	379.5	381.666 7
Death-inducer obliterator 1	DIDO1		25	2526.7	4105.16 7	3473.2	3212	3306.63 3	3027.7
Isoform Short of Heterogeneous nuclear ribonucleoprotein U	HNRNPU		2	25643.6	51755.8 7	42117.9 7	40496.5	39605.3 3	37080

E3 SUMO-protein ligase RanBP2	RANBP2	89	22051	43676.3	38181	34175.2 3	31678.7 7	30342.8 7
Proteasome subunit alpha type-3	PSMA3	13	3485.03333 3	8005.96 7	6221.46 7	6265.13 3	5583.8	6081.63 3
Cleavage and polyadenylation specificity factor subunit 2	CPSF2	13	2714.86666 7	4615.33 3	4247.2	3611.83 3	3260.6	3272.73 3
Ankyrin repeat and SOCS box protein 9	ASB9	2	118.433333 3	126.033 3	105.066 7	98.6333 3	99.9333 3	97.5
Zinc finger and BTB domain- containing protein 11	ZBTB11	5	383	320.3	349.933 3	250.666 7	222.966 7	190.5
cDNA FLJ13198 fis, clone NT2RP3004454, highly similar to Heparan sulfate 2-O- sulfotransferase 1 (EC 2.8.2.-)	4	220.6	311.2667	298.933 3	243.6	259.7	213.5	
Far upstream element-binding protein 2	KHSRP	15	18193.5333 3	22613.5	18457.5	17699.1	17281.4 7	16211.7
Mitotic spindle assembly checkpoint protein MAD1	MAD1L1	16	3171.46666 7	5598.56 7	5265.1	4381.93 3	3953.76 7	3907.96 7
Zinc finger protein 687	ZNF687	8	834.8	1799.33 3	1526.66 7	1408.36 7	1466.93 3	1424.8
Protein disulfide-isomerase A5	PDIA5	13	1583.63333 3	3669.63 3	2565.36 7	2872.3	3215.46 7	3222.76 7
Protein FAM114A2	FAM114A2	10	1231.73333 3	2470.6	2002.2	1933.96 7	1581.7	2085.73 3
DnaJ (Hsp40) homolog, subfamily B, member 4 variant (Fragment)	5	1382.36666 7	2693.333	2247.6	2108.43 3	1684.3	1910.13 3	

Putative uncharacterized protein DKFZp667H197 (Fragment)	DKFZp667H197	20	3906.13333 3	7105.16 7	5930.63 3	5562.5	5551.5	5198.66 7
Malectin	MLEC	12	1792.4	3917.7	3114.73 3	3067.16 7	2812.33 3	3039.16 7
Signal recognition particle 14 kDa protein	SRP14	7	3248.43333 3	7616.23 3	6045.83 3	5962.83 3	5482.53 3	5378.9
ETS domain-containing transcription factor ERF	ERF	2	132.2	203.966 7	178.933 3	159.7	169.033 3	138.433 3
Structural maintenance of chromosomes protein	SMC2	52	10414.1	20889.6 3	17903.4	16356.5	13347.5	13376.5 3
Lysosomal acid phosphatase	ACP2	5	489.433333 3	892.166 7	822.533 3	698.6	697.1	588.4
cDNA FLJ10527 fis, clone NT2RP2000932, highly similar to Ankyrin repeat and MYND domain-containing protein 2	1	250.1	571.5	484.566 7	447.533 3	326.533 3	393.933 3	
Isoform 3 of Tumor protein D52	TPD52	15	3094.23333 3	4963.13 3	3526.8	3887.06 7	4844.66 7	4095.83 3
Ribonucleoprotein PTB-binding 2	RAVER2	5	551.766666 7	666.066 7	634.866 7	521.666 7	512.6	497.066 7
Isoform 5 of AP-3 complex subunit delta-1	AP3D1	16	2264.53333 3	4407.46 7	3817.06 7	3452	2644.56 7	2854.26 7
5'-3' exoribonuclease 1	XRN1	9	984.233333 3	2111.4	1717.43 3	1653.86 7	1444.83 3	1575.9
U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	21	5544.06666 7	11205.8 3	9441.33 3	8777.6	8209.5	7664.96 7

Transcriptional regulator ATRX	ATRX	23	4058.06666 7	7204.76 7	6118.46 7	5644.76 7	5425.23 3	5071.06 7
NAD-dependent protein deacylase sirtuin-5, mitochondrial	SIRT5	5	335.766666 7	516.333 3	447.833 3	404.566 7	386.3	412.7
cDNA FLJ77327, highly similar to Homo sapiens cyclin H (CCNH), mRNA		5	384.466666 7	873.6333	843.033 3	684.533 3	605.4	582.433 3
Transforming growth factor-beta receptor-associated protein 1	TGFBRAP1	2	96.5666666 7	234.1	184.266 7	183.433 3	210.933 3	185.966 7
cDNA FLJ14389 fis, clone HEMBA1002876		5	332	857.1	731.7	671.6	595.766 7	666.366 7
Microphthalmia-associated transcription factor	MITF	2	286.666666 7	1238.3	993.466 7	970.366 7	964.133 3	986.333 3
Baculoviral IAP repeat-containing protein 6	BIRC6	23	1634.5	3014.6	2480.36 7	2362.56 7	2305.43 3	2217.8
DNA replication licensing factor MCM5	MCM5	28	8518.9	12922.7 3	10968.2 7	10128.5 7	8939	9246.43 3
Vacuolar-sorting protein SNF8	SNF8	3	742.133333 3	1396.66 7	1236.9	1094.8	761.8	773.266 7
RANBP2-like and GRIP domain-containing protein 5/6	RGPD5	1	5502.46666 7	11105.0 7	9737.56 7	8705.1	8148.9	7656.23 3
Isoform 4 of MAX gene-associated protein	MGA	9	918.366666 7	1120.73 3	1132.7	878.566 7	837.5	818.2
Replication factor C 2 isoform 1 (Fragment)	RFC2	5	953.766666 7	1447.16 7	1390.2	1134.5	1045.2	1011.73 3

GMP reductase	GMPR2	6	557.4	1365.7	1113.56 7	1070.66 7	915.366 7	979.7
cDNA FLJ76830, highly similar to Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), transcript variant 1, mRNA	16	1480.9	2764.167	2690.33 3	2167.03 3	1917.63 3	2002.16 7	
Spindle and kinetochore-associated protein 1	SKA1	3	890.5	1702.33 3	2180.43 3	1334.63 3	1000.26 7	1005.06 7
Isoform 6 of Serine/threonine-protein kinase WNK1	WNK1	17	4061.86666 7	8032.6	6972.83 3	6297.76 7	5786.2	5696.73 3
Multiple myeloma tumor-associated protein 2	MMTAG2	8	948.4	1840.26 7	1542.96 7	1442.83 3	1463.63 3	1360.1
Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	6	4254.6	7122.46 7	5572.73 3	5584.36 7	5141.8	4878.26 7
Cleavage stimulation factor subunit 3	CSTF3	16	2699.26666 7	5685.13 3	4958.93 3	4457.46 7	3713.96 7	3595.93 3
Sorting and assembly machinery component 50 homolog	SAMM50	7	1187.4	2580.7	2509.3	2023.53 3	1833.7	1921.56 7
Merlin	NF2	10	1163.53333 3	2278.76 7	2043.9	1787	1889.53 3	1466.93 3
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PPP2CA	3	2890.2	5935.36 7	5544.23 3	4655.3	3565.33 3	3755.2

Isoform 2 of Splicing regulatory glutamine/lysine-rich protein 1	SREK1	12	2385.1	4328.2	3500.63 3	3395.06 7	3149.63 3	3161.03 3
Phosphoinositide-3-kinase, regulatory subunit 4	PIK3R4	11	1584.16666 7	2793.03 3	2505.13 3	2191.4	1966.63 3	2066.16 7
PR371 c-K-ras oncogene (Fragment)		2	788.9	1684.16 7	1256.4	1321.46 7	1306.06 7	1162.4
General transcription factor IIH, polypeptide 4, 52kDa variant (Fragment)	5	603.8	1588.6	1371.56 7	1246.5	1207.8	1168.76 7	
ADP/ATP translocase 3	SLC25A6	7	7588.16666 7	19665.6 7	17657.3 3	15431.6 3	14078.2 3	12811.7 7
Hematological and neurological expressed 1 protein	HN1	8	2872.5	4405.23 3	3588.7	3457.33 3	3218.2	3027.66 7
Isoform 2 of Chromosome transmission fidelity protein 18 homolog	CHTF18	5	464.466666 7	616.866 7	533.366 7	484.133 3	469.633 3	501.033 3
Transcription intermediary factor 1-beta	TRIM28	36	12629.6	18107.0 7	16649.3 7	14210.9 3	13497.3	12392.0 7
Isoform 2 of Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	ASAP2	7	742.8	1351.73 3	1092.63 3	1060.9	1107.7	1051.7
cDNA FLJ61052, highly similar to Homo sapiens myosin head domain containing 1 (MYOHD1), transcript variant 2, mRNA	6	645.366666 7	1223.933	1132.83 3	960.6	1007.5	988.633 3	
Serine/arginine-rich splicing factor 11	SRSF11	7	2987.8	5442	4471.06 7	4271.16 7	4092.16 7	3884.43 3

Uncharacterized protein (Fragment)		1	1281.96666 7	2292.36 7	2024.1	1799.2	1528.33 3	1539
Deoxyribonuclease II (Fragment)		6	951.833333 3	1666.36 7	1461.6	1307.93 3	1057.93 3	1204.26 7
Importin-8	IPO8	5	301.766666 7	638.8	812.633 3	501.433 3	363.133 3	393.8
cDNA FLJ77630, highly similar to Homo sapiens BPY2 interacting protein 1, mRNA		13	1913.66666 7	3839.733	3148.36 7	3014.1	2855.53 3	3021.46 7
Zinc finger protein 768	ZNF768	2	912.6	1450.6	1283.13 3	1138.73 3	1152.16 7	998.8
Uncharacterized protein C18orf8	C18orf8	2	136.733333 3	227	216.4	178.2	141.966 7	165
Ubiquitin-conjugating enzyme E2 S	UBE2S	7	793.5	1433.3	2750.7	1125.23 3	953.2	911.5
Histone H1.4	HIST1H1E	8	29596.9666 7	26592.2	21123.8 7	20879.5 7	21167.8	20535.4 3
39S ribosomal protein L18, mitochondrial	MRPL18	3	798.233333 3	1837.66 7	1681.93 3	1442.96 7	1302	1357.83 3
Trifunctional purine biosynthetic protein adenosine-3 (Fragment)		43	11963.2666 7	22483.2	18697.4 7	17654.3	13118.2 7	15528.6 3
Metallothionein-1F	MT1F	2	2954.86666 7	5992.36 7	5035.46 7	4705.46 7	4186.03 3	4387.06 7
DNA helicase	MCM4	38	9979.13333 3	16615.7 3	16809.6 7	13047.9	10754.9 3	10877.3 3
Zinc finger protein 12	ZNF12	2	249.166666 7	445.933 3	383.3	350.2	326.466 7	378.633 3

Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1	30	4382.6	10023.0 3	9010.86 7	7871.36 7	7333.53 3	7308.4
Diphosphoinositol polyphosphate phosphohydrolase 1	NUDT3	4	1145.1	1610.06 7	1208.6	1264.5	1265.06 7	1294.96 7
Metallothionein-1L	MT1L	3	2013.83333 3	3394.23 3	2789.56 7	2665.76 7	2389.43 3	2634.93 3
Microtubule-associated protein	MAP4	14	24846.5333 3	46941.1	37604.6 7	36868.7 3	33515.2 3	35729.6 3
MICOS complex subunit MIC26	APOO	3	279.4	618.6	549.9	485.866 7	528.366 7	436.666 7
cDNA, FLJ93125, highly similar to Homo sapiens cleavage and polyadenylation specific factor 5, 25 kDa(CPSF5), mRNA		11	1749.23333 3	4300.1	4134.33 3	3377.43 3	2552.3	2340.46 7
GTPase Era, mitochondrial	ERAL1	7	344.4	776.9	856.233 3	610.233 3	529.866 7	506.533 3
Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	4	1553.26666 7	3558.73 3	3121.86 7	2795.36 7	2385.2	2381.33 3
Probable ATP-dependent RNA helicase DDX47	DDX47	13	2576.56666 7	5580.1	5753.63 3	4383.7	3408.93 3	3868
HZGJ	HZGJ	6	680.7	1554.06 7	1295.96 7	1220.9	1023.7	1091.2
N-terminal Xaa-Pro-Lys N-methyltransferase 1	NTMT1	4	777.433333 3	791	664.166 7	621.533 3	477.033 3	488.866 7

cDNA FLJ77615, highly similar to Homo sapiens nucleolar complex associated 3 homolog (S. cerevisiae) (NOC3L), mRNA	16	2084.066667	4743.033	3845.1	3727	3331.8	3313.5	
Nuclear receptor coactivator 6	NCOA6	3	343.9333333	540.3	307.9	424.5667	266.9	232.8
Transcription elongation factor B polypeptide 3	TCEB3	13	2050.033333	3880.7	3384.433	3049.467	3036.567	2739.467
Myotubularin-related protein 12	MTMR12	4	307.6666667	580.9667	531.7333	456.5333	417.0667	411.4
PHD finger protein 6	PHF6	11	2470.833333	4178.6	3646.3	3283.633	3376.867	3023.1
Bromodomain-containing protein 4	BRD4	7	684.1666667	1798.7	1544.567	1413.533	1396.3	1283.267
Isoform 2 of Transcription elongation factor A protein-like 4	TCEAL4	8	915.0333333	2256.6	1663.8	1773.433	1778.233	1651.467
cDNA FLJ34373 fis, clone FEBRA2017333, highly similar to Dual specificity protein kinase CLK3 (EC 2.7.12.1)		3	502.1666667	908.5	692.7667	714	636.3667	657.1
Alpha-parvin	PARVA	7	983.8666667	2168.3	2011.767	1704.167	1317.767	1472.467
39S ribosomal protein L28, mitochondrial	MRPL28	7	1316.8	2962.9	2808.133	2328.733	2141.9	2190.8
Aspartate--tRNA ligase, cytoplasmic	DARS	37	7688.4	20206.93	16095.7	15882.7	13510.33	15197.9

Isoform 3 of Apoptosis-stimulating of p53 protein 2	TP53BP2	2	535.433333 3	739.666 7	698.233 3	581.4	675.433 3	610.966 7
Heterogeneous nuclear ribonucleoprotein M	HNRNPM	30	14608.0333 3	25929.2	21458.7	20381.5 3	19021.6 3	18492.9
RNA-binding protein 45	RBM45	5	942.166666 7	1365.1	1174.93 3	1073.06 7	942.033 3	994.566 7
Centrosomal protein 55kDa, isoform CRA_a	CEP55	15	2569.36666 7	3421.8	3379.16 7	2689.96 7	2649.76 7	2263.6
Serine/threonine-protein phosphatase		1	2511.3	5284.76 7	4829.53 3	4154.63 3	3112.13 3	3336.13 3
Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	7	1569.16666 7	2499.53 3	2040.33 3	1965.23 3	1915.63 3	1868.9
Isoform 2 of NF-kappa-B-repressing factor	NKRF	18	3178.4	6768.36 7	6434.3	5321.6	4514	4594.13 3
Putative nucleoside diphosphate kinase	NME2P1	1	5999.86666 7	10389.0 3	8134.2	8168.5	6697.83 3	7157.1
Isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1	IDI1	7	883.1	1757.2	1526.7	1381.63 3	1117.56 7	1405.46 7
H/ACA ribonucleoprotein complex subunit 3	NOP10	4	549.766666 7	1169.23 3	911.766 7	919.466 7	846.8	889.166 7
Heat shock 70 kDa protein 4L	HSPA4L	24	5978.86666 7	10111.3	9010.46 7	7952.23 3	6923.7	7014.43 3
cDNA, FLJ94417, highly similar to Homo sapiens WD repeat domain 57 (U5 snRNP specific) (WDR57), mRNA		11	1665.26666 7	3392.8	2999.03 3	2668.66 7	2457.63 3	2317.96 7

Regulator of nonsense transcripts 1	UPF1	39	8037.3	16505.1 7	15071.7 7	12982.5	10643.8	11229.1 7
cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial	6	1473.2	3123.867	3108.66 7	2457.16 7	2329	2230.03 3	
Tubulin beta chain	TUBB	3	49336.1333 3	79530.9 3	67778.3	62557.9	51289.2 3	56371.2 7
UHRF1-binding protein 1-like	UHRF1BP1L	8	678.166666 7	1237.83 3	1118.76 7	973.833 3	871.4	839
cDNA, FLJ94105, highly similar to Homo sapiens GA binding protein transcription factor, alpha subunit 60kDa (GABPA), mRNA	5	771	1241.767	1083.4	976.933 3	936.033 3	892.066 7	
Poly(rC)-binding protein 2 (Fragment)	PCBP2	2	2059	3190.56 7	2792.36 7	2510.2	2117.06 7	2251.96 7
Isoform 2 of Multifunctional protein ADE2	PAICS	28	8865.73333 3	15620.5 3	11892.8 7	12290.1 7	11316.9 3	11804.7
Isoform 3 of E3 ubiquitin-protein ligase listerin	LTN1	5	508.333333 3	879.2	798.466 7	691.766 7	544.133 3	584.066 7
Calcium uniporter regulatory subunit MCUB, mitochondrial	MCUB	3	543.766666 7	650.666 7	528.3	512.033 3	519.3	473.466 7
182 kDa tankyrase-1-binding protein	TNKS1BP1	38	6384.43333 3	11321.9 3	8609.96 7	8909.76 7	9194.9	8394.96 7
Stromal membrane-associated protein 2	SMAP2	8	1062.16666 7	2209.53 3	1478.36 7	1738.93 3	1777.46 7	1496.66 7
Liprin-beta-2	PPFIBP2	4	693.4	1145.56 7	1027.9	901.6	872	837.1

Isoform 2 of Y-box-binding protein 3	YBX3	7	2814.9	4838.13 3	4424.8	3807.96 7	2833.36 7	3100.33 3
Clustered mitochondria protein homolog (Fragment)	CLUH	4	5963.93333 3	10123.1 7	10009.4 7	7967.76 7	5996.4	6057.96 7
Protein AAR2 homolog	AAR2	4	719.7	1042.83 3	953.9	820.8	601.8	748.233 3
Uncharacterized protein C19orf43	C19orf43	9	1765.66666 7	2753.33 3	2521.93 3	2167.13 3	1850.63 3	1816.6
Putative heat shock protein HSP 90-beta 4	HSP90AB4P	2	6818.76666 7	13287.2 7	11995.9 7	10458.9 3	7663.7	8986.46 7
SLC9A3R2 protein (Fragment)	SLC9A3R2	4	720.966666 7	1098.53 3	1096.6	864.7	837.8	812.766 7
Transducin beta-like protein 3	TBL3	18	3336.3	4789.56 7	3942.7	3770.2	3554.66 7	3553.96 7
Ras-related protein Rab-2B	RAB2B	2	1882.66666 7	3746.9	3141.9	2949.46 7	2322.1	2788.93 3
Nucleolar complex protein 2 homolog	NOC2L	16	3240.4	7384.26 7	6087.46 7	5812.83 3	5124.9	5459.63 3
Alpha-endosulfine	ENSA	7	2606.5	4975.8	3729.93 3	3916.96 7	3464.46 7	3355.43 3
Heterogeneous nuclear ribonucleoprotein R	HNRNPR	3	11529.8666 7	20568.2 3	16604.0 7	16192.6 3	14735.4 7	14694.2 3
E3 ubiquitin-protein ligase HERC2	HERC2	10	878.033333 3	1767.86 7	1562.83 3	1391.8	1116.83 3	1261.63 3
BRISC complex subunit Abro1	FAM175B	6	1484.46666 7	2706.63 3	2268.73 3	2131.3	1810.4	1866
Ran-binding protein 9	RANBP9	5	747.466666 7	913.266 7	803.033 3	719.166 7	657.766 7	650.033 3

Exosome complex component RRP43	EXOSC8	4	1009.53333 3	1699.66 7	1604.96 7	1338.43 3	1093.73 3	1136.7
Chromobox protein homolog 8	CBX8	9	1026.13333 3	2277	1618.53 3	1793.1	1853.9	1549.23 3
Prolow-density lipoprotein receptor-related protein 1	LRP1	13	778.333333 3	1501.03 3	1027.43 3	1182.06 7	1729.7	1729.13 3
COP9 constitutive photomorphogenic homolog subunit 2 variant (Fragment)		14	3567.9	8375.933	7375.06 7	6596.36 7	5456.76 7	5755.06 7
Kinesin-like protein KIF2C	KIF2C	15	2989.06666 7	5104.8	6016.13 3	4020.33 3	2589.7	2640.63 3
Isoform 4 of Polypyrimidine tract-binding protein 3	PTBP3	5	1492.73333 3	3306.7	2917.26 7	2604.53 3	2192.96 7	2278.63 3
Helicase SRCAP	SRCAP	7	766.3	1713.2	1403.4	1349.5	1350.8	1165.1
Ras-related protein Rab-8A	RAB8A	5	4056.53333 3	8587.8	7051.8	6764.93 3	5385.6	6110.16 7
DNA helicase		8	7894.73333 3	13521.5 3	13791.5	10651.5 7	8914.56 7	8834.4
Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN	PTEN	1	238.566666 7	459.466 7	380.033 3	361.966 7	355.566 7	365.6
cDNA FLJ75071, highly similar to Homo sapiens pinin, desmosome associated protein (PNN), mRNA		20	6230.43333 3	10890.43	9865.93 3	8579.53 3	8120.6	7638.2
Caseinolytic peptidase B protein homolog (Fragment)	CLPB	7	1044.43333 3	1699.73 3	1185.5	1339.06 7	1115.86 7	959.366 7

Heterogeneous nuclear ribonucleoprotein L	HNRNPL	23	11584.3666 7	21184.8 3	16635.4	16689.7 3	15464.4 3	14312.8
E3 ubiquitin-protein ligase UBR5	UBR5	19	2249.5	3774.23 3	3116.83 3	2973.53 3	2720.3	2558.4
Isoform 3 of Centrosomal protein of 192 kDa	CEP192	9	265.133333 3	718.7	724.6	566.233 3	504.366 7	484.333 3
Nuclear pore complex protein Nup98-Nup96	NUP98	25	5043.76666 7	9014.06 7	8169.86 7	7102.16 7	6399.73 3	6312.96 7
Phosphatidylinositol phosphatase SAC2	INPP5F	3	442.766666 7	714.433 3	613.2	563	589.733 3	575.1
Isoform 3 of Gamma-tubulin complex component 2	TUBGCP2	8	1192.23333 3	2357.33 3	2234.16 7	1857.66 7	1530.93 3	1525.66 7
Neurogenic locus notch homolog protein 2	NOTCH2	5	790.433333 3	1233.4	1134.03 3	971.966 7	1447.43 3	965.766 7
Protein PBDC1	PBDC1	19	3371.03333 3	8297.5	7149.8	6538.83 3	5189.93 3	5440.33 3
Transportin-1	TNPO1	14	3659.26666 7	7214.03 3	6493.83 3	5685.86 7	4507.76 7	4887.3
Cyclic AMP-dependent transcription factor ATF-2	ATF2	2	344.133333 3	450.2	356.566 7	354.833 3	379.733 3	345.5
26S proteasome non-ATPase regulatory subunit 6	PSMD6	19	3419.33333 3	9185.96 7	8274.93 3	7240.43 3	6331.66 7	6772.7
tRNA (guanine(10)-N2)-methyltransferase homolog	TRMT11	2	346.666666 7	641.366 7	580.766 7	505.533 3	502.333 3	490.066 7
RNA polymerase II-associated protein 3	RPAP3	23	3103.5	7400.03 3	6429.96 7	5832.86 7	4662	5010.4
cDNA FLJ34106 fis, clone FCBBF3008073, highly similar	1	2188.53333 3	5943.5	5193.76 7	4684.8	4136.16 7	4154.2	

to SPLICING FACTOR, ARGININE/SERINE-RICH 7								
CD44 antigen	CD44	14	6663.9	14060.1 7	12396.3 7	11083.3	11003.7	8666.76 7
Isoform 2 of M-phase phosphoprotein 8	MPHOSPH8	5	884.4	1488.63 3	1224.86 7	1173.53 3	1089.66 7	978.166 7
Zinc finger protein 638	ZNF638	34	5126.13333 3	9148.96 7	7551.3	7212.4	7367.73 3	7121.83 3
Small kinetochore-associated protein	KNSTRN	6	1164.46666 7	1895.73 3	2680.83 3	1494.56 7	1013.6	962.2
Cdc42 effector protein 4	CDC42EP4	2	551.366666 7	703.333 3	645.366 7	554.533 3	518	461.966 7
ATPase family AAA domain- containing protein 2	ATAD2	5	623.366666 7	668.166 7	965.1	526.833 3	527.033 3	565.766 7
Meiotic nuclear division protein 1 homolog	MND1	2	208.733333 3	306.733 3	325.166 7	241.866 7	205.933 3	204.1
SH3 and PX domain-containing protein 2B	SH3PXD2B	6	833.066666 7	1210.2	1061.86 7	954.3	892.266 7	912.3
Inhibitor of nuclear factor kappa-B kinase subunit beta	IKBKB	3	616.5	891.066 7	765.966 7	702.666 7	649.333 3	701.4
Isoform 2 of Protein bicaudal D homolog 2	BICD2	12	2372.9	4224.7	4210	3331.9	2862.86 7	2742.33 3
Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	1	4109.56666 7	7481.86 7	7135.83 3	5901.3	4713.46 7	4702.66 7
Gamma-tubulin complex component 3	TUBGCP3	9	1016.16666 7	2307.36 7	2018.3	1819.93 3	1567.43 3	1647.46 7
Centromere protein H	CENPH	4	610.033333 3	687.066 7	755.8	541.966 7	480.633 3	421.5

Transcription elongation factor SPT6	SUPT6H	35	4407.9	8408.7	7996.16 7	6633.1	5770.56 7	5348.26 7
Mutant methyl CpG binding protein 2 variant 1	MECP2	11	1820.6	3255.8	2619.53 3	2568.43 3	3230.36 7	2786.7
Copine-8	CPNE8	2	488.133333 3	827.833 3	696.8	653.1	646.666 7	617.266 7
cDNA, FLJ96850		6	746.266666 7	1504.7	1368.1	1187.1	1042.9	1045
Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	ANKRD28	17	1909.6	3507.8	2992.36 7	2767.83 3	2468.26 7	2669.83 3
Phenylalanine--tRNA ligase alpha subunit	FARSA	15	2487.73333 3	4762.96 7	3817.2	3758.26 7	3357.46 7	3248.56 7
WD repeat-containing protein 18	WDR18	8	2067.3	3727.5	3088.03 3	2941.3	2771.2	2672.4
Transmembrane 9 superfamily member 3	TM9SF3	5	1017.1	2637.1	2464.43 3	2080.9	1829.03 3	1645.06 7
Tumor necrosis factor receptor superfamily member 10D	TNFRSF10D	5	297.533333 3	912.2	559.2	719.866 7	703.9	697.8
Isoform 2 of Cleavage and polyadenylation specificity factor subunit 6	CPSF6	12	3290.46666 7	5663.23 3	4670.5	4469.16 7	4197.16 7	3960.6
Charged multivesicular body protein 4b	CHMP4B	9	2739.2	5044.23 3	4117.4	3981.03 3	3803.13 3	3809.4
Developmentally regulated GTP-binding protein 1	DRG1	19	3244.36666 7	6203	5705.8	4896.23 3	3996.06 7	4276.36 7
Dimethyladenosine transferase 2, mitochondrial	TFB2M	8	806.9	1937.56 7	1849.53 3	1529.4	1293.63 3	1280.6

cDNA, FLJ92810, highly similar to Homo sapiens protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (PPM1G), mRNA	23	7076.36666 7	11660.43	11411.8	9204.9	7444.5	6948.56 7	
Prolyl endopeptidase-like	PREPL	10	529.9	1403.63 3	1124.23 3	1108.2	948.3	895.366 7
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	20	4864.6	11144.5	10932.9 7	8799.4	7222	7379.56 7
High-mobility group nucleosome binding domain 1	HMGN1	3	3714.7	5404.66 7	4363.1	4267.43 3	4697.6	3525.66 7
Eukaryotic translation initiation factor 5B	EIF5B	63	13440.7	27007.9 3	22563.7	21325.5	17442.5	18660.2 7
TBC1 domain family, member 4, isoform CRA_b	TBC1D4	2	308.6	361.9	330.166 7	285.766 7	307.4	278.366 7
Ubiquinone biosynthesis protein COQ9, mitochondrial	COQ9	7	876.3	1627.96 7	1306.1	1285.5	1257.23 3	1414.76 7
cDNA FLJ39640 fis, clone SMINT2003386, highly similar to DNA REPLICATION LICENSING FACTOR MCM7		2	6374.9	11499.7	11538.5	9080.66 7	7530.4	7533.96 7
Protein phosphatase 1 regulatory subunit 7	PPP1R7	16	3097.56666 7	6051.1	5114.8	4778.36 7	4530.26 7	4835.93 3
Pre-rRNA-processing protein TSR1 homolog	TSR1	19	2426.06666 7	5122.2	4685.4	4045.43 3	3142.6	3302.03 3

Phosphoglucomutase-1	PGM1	17	1896.86666 7	5765	4054.43 3	4553.2	5197.33 3	4566.83 3
cDNA FLJ39883 fis, clone SPLEN2016268, highly similar to Protein CHMP7	13	1160.66666 7	2710.767	2468.46 7	2141.06 7	1736.23 3	1817.16 7	
cDNA FLJ10442 fis, clone NT2RP1000738, highly similar to Negative elongation factor A	1	1130.86666 7	1677.867	1372.4	1325.36 7	1263.13 3	1166.96 7	
Tyrosine-protein kinase BAZ1B	BAZ1B	44	7819.83333 3	13688.8 3	14494.3 3	10813.3 7	9075.56 7	9026.6
Cell differentiation protein RCD1 homolog	RQCD1	4	522.933333 3	807.566 7	723.733 3	637.966 7	638.8	612.166 7
Transcription initiation factor IIB	GTF2B	6	1169.26666 7	2046.56 7	1990.73 3	1616.83 3	1307.93 3	1474.86 7
Serine/arginine-rich splicing factor 7	SRSF7	2	3005.06666 7	7221.26 7	6301.06 7	5705.46 7	5021.23 3	5071.06 7
Uncharacterized protein		5	336.366666 7	438.633 3	351.6	346.566 7	312.233 3	349.233 3
USP19 protein (Fragment)	USP19	4	309.6	351.3	315	277.566 7	248.6	258.766 7
Protein FAM98A	FAM98A	8	1622.63333 3	3494.13 3	3285.86 7	2761.3	2146.26 7	2327.06 7
Putative glutathione-specific gamma- glutamylcyclotransferase 2	CHAC2	4	747.6	1877.8	1974	1484.13 3	1163.93 3	1194.93 3
cDNA FLJ77656, highly similar to Homo sapiens UV radiation	5	496.466666 7	1159.567	1054.16 7	916.5	782	858.8	

resistance associated gene (UVRAG), mRNA								
Cytosolic endo-beta-N-acetylglucosaminidase	ENGASE	1	47.1	59.96667	50.4	47.4	42.63333	47.33333
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	8	1121.966667	3113.033	2371.8	2460.7	2209.4	2380.667
WD repeat-containing protein 91	WDR91	3	331.2	563.3	465.8	445.2667	462.8667	456.8333
RNA-binding protein 12B	RBM12B	8	448.3	1347.367	1127.133	1065.1	1023.767	1031.1
Surfeit locus protein 2	SURF2	4	607.6666667	1002.033	920.9667	792.1333	684.4333	701.2333
Actin-related protein 2/3 complex subunit 5		5	962.7666667	1593.833	1348.1	1260.1	1027.3	1115.567
Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	9	1312.366667	2868.667	2047.533	2268	2721.167	2507.767
Negative elongation factor A	NELFA	1	1187.5	1693.667	1389.167	1339.467	1273.4	1179.633
Protein PRRC2B	PRRC2B	8	693.9666667	1218.7	1321	963.9667	854.8	815.5
Vacuolar protein sorting-associated protein 4A	VPS4A	6	1990.2	3423.633	3184.033	2708.033	2307.167	2348.7
Mitogen-activated protein kinase kinase kinase 4	MAP3K4	5	452.8666667	852.6	758.7	674.5	656.1333	647.7333
E3 ubiquitin-protein ligase HECTD1	HECTD1	15	2660.7	4157.533	4613.7	3289.6	2758.167	2704.467

ATP-dependent RNA helicase DDX51	DDX51	16	2362.23333 3	3877.13 3	3524.93 3	3067.9	2659.1	2598.63 3
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	5	2670.83333 3	3954.93 3	3252.7	3129.5	2633.86 7	2632.83 3
U3 small nucleolar ribonucleoprotein protein IMP4	IMP4	6	692.6	1458.76 7	1348.73 3	1154.33 3	1048.46 7	1043.8
Gamma-taxilin	TXLNG	19	3445.66666 7	5648.56 7	5541.53 3	4469.76 7	3603.66 7	3718.4
Cytidine 5'-monophosphate N-acetylneuraminic acid synthetase variant (Fragment)		8	1326.56666 7	2195.667	1673.83 3	1737.5	1680.46 7	1648.86 7
Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	1	4507.23333 3	7912.93 3	7563.8	6261.86 7	5007.36 7	5006.23 3
Activating signal cointegrator 1 complex subunit 3	ASCC3	12	1347.9	3586.4	3478.8	2838.26 7	2166.3	2372.66 7
Cytoplasmic aconitate hydratase	ACO1	21	2981.26666 7	7329.93 3	5469.8	5800.96 7	5257	5474.3
Mitofusin-1	MFN1	2	385.9	566.566 7	621.766 7	448.4	453.933 3	371.266 7
Proteasome subunit beta type-1	PSMB1	10	2788	5201.13 3	4458.76 7	4116.46 7	3645.66 7	3930.66 7
RNA cytidine acetyltransferase	NAT10	34	6679.4	13592	11088.9 3	10757.4 7	9694.13 3	9906.6
Heterochromatin protein 1-binding protein 3	HP1BP3	17	5703.53333 3	9859.8	7334.6	7803.93 3	8780.96 7	6857.03 3

Vesicle transport-related protein isoform a variant (Fragment)		14	1967.1	3803.533	3093.567	3010.7	2535.833	3137.6	
TIP41-like protein	TIPRL	9	2008.666667	4901.2	4168.733	3879.567	3341.3	3698.267	
Transaldolase	TALDO1	25	7913.633333	15535.37	12943.03	12297.5	10779.67	11350.07	
Rho-related GTP-binding protein RhoB	RHOB	1	727.2666667	1384.833	1055.9	1096.233	1089.367	970.8	
Tyrosine-protein kinase (Fragment)	LYN	1	466.0666667	1190.4	1103.867	942.3333	844.7333	765.3667	
OCIA domain-containing protein 1	OCIAD1	7	1055.2	2318.067	2095.933	1835.033	1509.933	1313.533	
Bifunctional polynucleotide phosphatase/kinase	PNKP	9	1931.8	1745.267	1378.233	1381.6	1611.4	1452.967	
Uridine 5'-monophosphate synthase	UMPS	25	4023.066667	6996.7	6357.867	5538.867	4620.967	4996.933	
HAUS augmin-like complex subunit 5	HAUS5	3	439.3666667	507.2333	469.4333	401.5667	342.9667	389.1333	
Histone PARylation factor 1	HPF1	6	241.9666667	522.6333	459.5	413.7667	350.8333	367.6	
Exosome component 10	EXOSC10	28	4139.766667	8594.133	7933.933	6804.3	6110.8	5681.3	
Vacuolar protein sorting-associated protein 29	VPS29	9	1151.566667	3013.767	2754.633	2386.167	1676.533	2092.033	
ATP-dependent RNA helicase DDX1	DDX1	34	6983.4	15496.1	14201.83	12269.27	9822.1	10553.87	

Alpha-globin transcription factor CP2	TFCP2	6	943.033333 3	2012.9	1729.23 3	1593.83 3	1396.76 7	1332.03 3
Isoform 2 of Poly(U)-binding-splicing factor PUF60	PUF60	22	6878.03333 3	10998.9	9737.2	8709.26 7	7705.5	7461.83 3
Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	QRSL1	8	1011.4	1716.23 3	1710.13 3	1358.96 7	1012.53 3	1239.5
Nitrilase homolog 1	NIT1	5	1152.03333 3	2426.53 3	1899.66 7	1921.56 7	1784.43 3	1951.16 7
Paraoxonase 2, isoform CRA_a	PON2	3	310.933333 3	777.2	719.5	615.5	675.366 7	546.3
Phosphorylated adapter RNA export protein	PHAX	8	1447.2	2694.63 3	2531.93 3	2134.06 7	1836	1534.96 7
THRAP3 protein (Fragment)	THRAP3	5	2200.43333 3	4095.46 7	3361.33 3	3244.06 7	2902.73 3	2617.7
Splicing factor 3A subunit 1	SF3A1	30	9106.9	15868.8 3	13390.9 7	12570.2 3	11552.1	11479.7 3
Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11	PSMD11	23	3678.46666 7	8640.06 7	8517.46 7	6844.16 7	5250.33 3	5837.3
NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	NFU1	3	1541.7	2194.66 7	2108.3	1738.5	1583.5	1525.16 7
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform	PPP2R2D	2	1149.5	2821.66 7	2407.2	2235.46 7	1767.26 7	1955.36 7

Isoform 2 of Monoacylglycerol lipase ABHD12	ABHD12	7	1032.76666 7	1831.23 3	1606.33 3	1450.8	1628.3	1427.3
Dystonin (Fragment)	DST	0	285.133333 3	553.3	455.9	438.4	408.133 3	418.7
Prohibitin	PHB	21	9406.8	13851.4	11080.5 3	10975.9 7	11379.2 7	11132.8 3
Spermatogenesis-associated protein 5	SPATA5	9	2462.66666 7	4697.3	4282.76 7	3722.36 7	3026.5	3272.6
Nicalin	NCLN	8	1146.63333 3	1921	1765.6	1522.33 3	1394.06 7	1323.26 7
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	PPP2R5A	6	707.533333 3	1023.56 7	829	811.166 7	716.4	706.633 3
Germinal-center associated nuclear protein	MCM3AP	11	1271.76666 7	1687.06 7	1499.93 3	1337	1467.7	1418.63 3
Pescadillo homolog	PES1	28	5979.3	12672.3 7	11723.7	10042.9 3	7381.33 3	7767.93 3
AP1 gamma subunit binding protein 1, isoform CRA_d	AP1GBP1	7	877.1	2007.06 7	1652.3	1590.66 7	1420.96 7	1573.43 3
Isoform 2 of Formin-binding protein 4	FNBP4	8	1107.6	2348.53 3	1970.46 7	1861.33 3	1664.23 3	1719.26 7
28S ribosomal protein S18b, mitochondrial	MRPS18B	4	546.666666 7	1005.83 3	1215.1	797.2	627	721.166 7
Embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein	HMCES	12	2310.76666 7	3161.66 7	4158.03 3	2505.86 7	1879.5	1801.96 7

Peptidyl-prolyl cis-trans isomerase H	PPIH	11	2188.33333 3	4771.6	4103.13 3	3781.9	3102.2	3263.66 7
Proteasome activator complex subunit 4	PSME4	8	791.433333 3	1837.23 3	1734.6	1456.16 7	1106.9	1119.43 3
PH and SEC7 domain-containing protein 3	PSD3	21	2551.33333 3	4137.6	3078.93 3	3279.63 3	3250.13 3	3292.06 7
Lanosterol 14-alpha demethylase	CYP51A1	5	1076.1	1387.16 7	2266.06 7	1099.53 3	1186.46 7	1081.7
Isoform 9 of Transcriptional coactivator YAP1	YAP1	1	983.733333 3	1821.86 7	1442.93 3	1444.1	1291.13 3	1334.23 3
Sperm surface protein Sp17	SPA17	2	162.566666 7	190.7	212.933 3	151.166 7	149.7	146.666 7
Isoform 5 of Double-stranded RNA-specific editase 1	ADARB1	3	617.7	1101.3	954.8	873.033 3	1027.86 7	867.866 7
Exocyst complex component 6B	EXOC6B	6	457.133333 3	707.2	580.466 7	560.633 3	414.266 7	394.366 7
Isoform 2 of Centrosomal protein of 97 kDa	CEP97	4	694.5	1370.9	1391.96 7	1086.83 3	911.7	902.333 3
Lysine-specific demethylase 2A	KDM2A	6	344.1	635.766 7	555.2	504.033 3	521.866 7	498.9
G-protein-signaling modulator 2	GPSM2	2	425.4	724.133 3	675.733 3	574.1	499.166 7	538.033 3
GTP-binding protein 10	GTPBP10	7	1262.66666 7	2053.36 7	2232.36 7	1627.93 3	1414.86 7	2991
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	11	1331.3	3638.3	3049.96 7	2884.86 7	2392.43 3	2765.13 3

Solute carrier family 12 member 9	SLC12A9	6	334.466666 7	216.566 7	202.966 7	171.733 3	166.266 7	168.9
ELM2 and SANT domain-containing protein 1	ELMSAN1	7	488.3	857.233 3	651.166 7	679.8	785.333 3	792.2
Ribosomal biogenesis protein LAS1L	LAS1L	17	1634.9	3514.6	3043.3	2787.16 7	2661.9	2378.5
Isoform 2 of Cytochrome c oxidase assembly factor 6 homolog	COA6	7	1978.26666 7	3689.56 7	3070.56 7	2926.1	2968.4	2595.9
Nucleoporin GLE1	GLE1	2	234.2	368.266 7	335.466 7	292.066 7	269.7	254.633 3
Cofilin-1	CFL1	18	15435.9	23760.9 3	19174.0 3	18845.1 3	15440	17300
Protein strawberry notch homolog 1	SBNO1	25	4118.7	7563.3	7312.3	5998.6	5233	5356.5
Calcium uptake protein 1, mitochondrial	MICU1	6	555.033333 3	945.3	848.466 7	749.766 7	715.166 7	669.066 7
Desmoplakin	DSP	11	718.9	1883.06 7	1496.8	1493.8	1666.3	1433.63 3
Sodium/potassium-transporting ATPase subunit alpha-3	ATP1A3	2	4685.93333 3	7906.3	7204.5	6272	6517.8	5662.4
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	11	1492	3803.9	3637.4	3017.66 7	2588.9	2773.5
CCAAT/enhancer-binding protein zeta	CEBPZ	21	2637.6	4616.4	4039.16 7	3662.26 7	3526.1	3545.7
Protein Hook homolog 3	HOOK3	25	3571.23333 3	6573.5	5415.03 3	5214.93 3	4863.26 7	5194.9

10 kDa heat shock protein, mitochondrial	HSPE1	9	18912.6	22720.5	18553.7 3	18025.2	17997.9 7	18062.5 3
Coilin	COIL	12	1435.76666 7	2105.4	1893.93 3	1670.36 7	1538.93 3	1478.66 7
Phosphoinositide phospholipase C (Fragment)	PLCG1variantprotei n	5	1714.63333 3	3602.1	3096.56 7	2857.96 7	2364.03 3	2565.86 7
Caspase-3	CASP3	4	366.833333 3	943.7	808.966 7	748.8	613.833 3	636.466 7
E3 ubiquitin-protein ligase TRIM4	TRIM4	2	185.4	276.566 7	245.166 7	219.5	234.066 7	213.233 3
Mitofusin-2	MFN2	8	596.166666 7	1078.13 3	1101.36 7	855.733 3	781.633 3	744.133 3
Zinc finger and BTB domain-containing protein 41	ZBTB41	1	215.4	299.766 7	272.1	237.933 3	221.4	209
PH-interacting protein	PHIP	13	2374.76666 7	4570.16 7	4361.16 7	3627.53 3	3194.06 7	3059.86 7
Isoform 2 of Coatomer subunit alpha	COPA	57	9925.96666 7	23339.9 7	18735.2 3	18526.0 3	13881.9 3	17132.3 7
Phosphoglucomutase-2	PGM2	16	2540.83333 3	7081.96 7	5585.3	5622.36 7	5339.16 7	5283.26 7
Valine--tRNA ligase	VARS	48	8603.33333 3	15382.1	12940.3	12212.1	10146.5 3	10940.8 3
Isoform 4 of LIM domain and actin-binding protein 1	LIMA1	2	13415.2333 3	22457.8	19840	17830.4 7	17043.3 3	13648.4 7
Carboxypeptidase D	CPD	15	1490.7	2939.06 7	2641.2	2333.5	2228.16 7	1968.53 3
Pre-mRNA-processing factor 19	PRPF19	14	3676.53333 3	6761.3	5921.56 7	5368.63 3	4980.3	4765.8

Ras-related protein Rab-18	RAB18	9	1701.9	2601.33 3	2371.26 7	2065.53 3	1751.3	1857.43 3
Nucleoprotein TPR	TPR	106	24867.9666 7	44963.5	36578.4 3	35706.3	34981.1 7	34739.4 7
Protein FAM83G	FAM83G	4	388.333333 3	1019.83 3	841.566 7	809.9	719.633 3	713.1
Eukaryotic translation initiation factor 3 subunit D	EIF3D	15	4289.66666 7	6732.06 7	6065.96 7	5346.33 3	4140.13 3	4732.4
Isoform 6 of Inosine-5'-monophosphate dehydrogenase 1	IMPDH1	12	3521.06666 7	7205.6	6072.8	5722.7	4314.33 3	4620.33 3
Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	22	9455.06666 7	16234.3 3	14623.9 3	12894.9 7	14234.5 7	12016.2 7
ATP-dependent RNA helicase DDX18	DDX18	28	5115.46666 7	11596.2 3	9604.76 7	9211.83 3	7885.6	7503.13 3
BTB/POZ domain-containing protein KCTD5	KCTD5	2	349.266666 7	690.666 7	766.633 3	548.733 3	491	468.2
Midasin	MDN1	47	4963.9	9532.6	8574.16 7	7574.06 7	6615.36 7	7168.33 3
Mitochondrial-processing peptidase subunit alpha	PMPCA	15	2558.3	4487.6	3920.2	3565.6	3203.56 7	3120.36 7
Cerebellar degeneration-related protein 2-like	CDR2L	2	496.866666 7	849.866 7	766.833 3	675.333 3	637.866 7	630.8
Epithelial protein lost in neoplasm beta variant (Fragment)	1	13674.7	22937.63	20297.7 7	18227.7 7	17409.6 7	13938.7 3	

Nodal modulator 1	NOMO1	1	3839.43333 3	6732	5852.2	5349.7	5364.66 7	4939.7
UV excision repair protein RAD23 homolog B	RAD23B	14	3512.8	7512.3	6431.46 7	5970.2	5384.06 7	5383.6
Sex comb on midleg-like protein 2	SCML2	9	988.4	1786.76 7	1704.63 3	1420.03 3	1297.93 3	1206.26 7
MICAL-like protein 2	MICALL2	2	137.966666 7	231.3	237	183.833 3	204.133 3	207.8
Isoform 2 of Chromodomain- helicase-DNA-binding protein 4	CHD4	27	4788	10741.5 7	9879.96 7	8537.66 7	7538.53 3	7085.5
28S ribosomal protein S31, mitochondrial	MRPS31	7	1103.96666 7	2058.03 3	1861.86 7	1635.83 3	1380.83 3	1382.4
Protein TMED8	TMED8	3	432.5	523.866 7	444.766 7	416.4	395.9	390.366 7
Pogo transposable element with KRAB domain	POGK	2	313.9	754	730.4	599.333 3	552.366 7	488.733 3
60S acidic ribosomal protein P2 (Fragment)	RPLP2	1	2586.03333 3	4010.96 7	3893.73 3	3188.53 3	2615	2724.4
Ribosomal protein 63, mitochondrial	MRPL57	3	474.5	1021.86 7	950.633 3	812.433 3	652.9	830.1
Isoform 2 of Eukaryotic initiation factor 4A-II	EIF4A2	10	8544.06666 7	19064.6	18262.6 7	15158.7 7	11270.8 7	12344.5
116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	42	9652.5	16019.6 3	14575.8 3	12737.8	11220.7 3	11002.3 7
28S ribosomal protein S11, mitochondrial	MRPS11	4	562.166666 7	797.666 7	847.866 7	634.266 7	603.3	551.333 3
Nucleoplasmin-3	NPM3	2	338.233333 3	441.9	389.7	351.4	258	269.7

Tetratricopeptide repeat domain 1 variant (Fragment)		15	3097.96666 7	7029.567	6239.33 3	5589.96 7	3889.5	4835.06 7	
Quinone oxidoreductase-like protein 1	CRYZL1		8	1213.73333 3	2726.96 7	2308.96 7	2168.53 3	1985.06 7	2111.3
Zinc finger protein 281	ZNF281		3	433.366666 7	487.766 7	476.4	387.9	357.166 7	343.166 7
Putative RNA helicase Ski2w	SKI2W		3	144.233333 3	232.666 7	187.666 7	185.033 3	200.6	191.733 3
GO2-q chimeric G-protein			1	568.766666 7	1649.36 7	1475	1311.9	1176.96 7	1148.66 7
39S ribosomal protein L53, mitochondrial	MRPL53		4	1482.06666 7	2318.03 3	2089.4	1843.93 3	1672.46 7	1622.33 3
DnaJ homolog subfamily C member 13	DNAJC13		36	3931.6	8545.76 7	7335.36 7	6798.7	6353.43 3	6541.23 3
Zinc finger CCCH domain-containing protein 14	ZC3H14		16	3075.7	4927.13 3	4548.63 3	3920.06 7	3769.2	3592.26 7
DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C		7	1301.63333 3	1780.43 3	1595.7	1416.53 3	1203.83 3	1272.6
WD repeat-containing protein 43	WDR43		17	2638.63333 3	5142.7	4921.96 7	4091.93 3	3350.36 7	3368.8
Vacuolar protein-sorting-associated protein 36	VPS36		5	304.3	626.633 3	498.533 3	498.666 7	434.8	485.3
Diacylglycerol kinase zeta	DGKZ		2	258.033333 3	600.633 3	522.733 3	478	465.866 7	501.366 7
Isoform 2 of DNA-directed RNA polymerase I subunit RPA34	CD3EAP		10	2737.46666 7	3813.16 7	3455.36 7	3034.76 7	2999.6	2764.93 3

cDNA FLJ56198, highly similar to Serine/threonine-protein kinase PCTAIRE-1 (EC 2.7.11.22)	10	838.466666 7	1237.167	1090.73 3	984.633 3	890.166 7	930.3	
Isoform 3 of Wings apart-like protein homolog	WAPL	18	3171.23333 3	5229.06 7	4486.73 3	4161.96 7	3349.86 7	5324.56 7
Nodal modulator 2	NOMO2	2	3417.8	6056.3	5249.7	4820.46 7	4763.56 7	4516.46 7
SUMO-conjugating enzyme	UBE2I	5	1668.53333 3	3731.23 3	3070.7	2970.13 3	2507.66 7	2793.73 3
GDP-L-fucose synthase	TSTA3	3	843.6	977.033 3	799.366 7	777.766 7	664.233 3	662.9
Isoform 2 of Myb-binding protein 1A	MYBBP1A	46	9204.56666 7	17221.6 7	15059.2	13710.8 3	11704.0 7	11828.1 7
Poly(A)-specific ribonuclease PARN	PARN	8	864.466666 7	1745	1478.8	1389.26 7	1457.23 3	1312.63 3
Transformer-2 protein homolog alpha	TRA2A	10	1809.33333 3	3788.6	3190.16 7	3016.3	2843.86 7	2739.03 3
Geranylgeranyl pyrophosphate synthase	GGPS1	3	540.9	1221.56 7	1106.86 7	972.566 7	911.266 7	1213.76 7
Nucleoporin Nup37	NUP37	9	1040.36666 7	2574.8	2516.43 3	2049.96 7	1463.16 7	1483.03 3
cDNA FLJ75774, highly similar to Homo sapiens lectin, mannose-binding 2 (LMAN2), mRNA		8	1600.2	3181.733	2787.23 3	2533.23 3	2573.1	2341.76 7
Glutamine and serine-rich protein 1	QSER1	8	617.033333 3	1319.83 3	1373.56 7	1051	909.466 7	832.7

cDNA FLJ51330, highly similar to Far upstream element-binding protein 2	2	13314.9	13610.27	11011.7 7	10838.5 3	10903.0 7	10343.2	
Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	PIP4K2C	2	380.733333 3	918.166 7	865.1	731.233 3	732.4	725.733 3
cDNA FLJ54836		3	234.133333 3	513.166 7	430	408.733 3	383.966 7	371.2
Achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A) variant (Fragment)		9	711.733333 3	1857.733	1507.2	1479.7	1411.6	1406.1
Ubiquitin carboxyl-terminal hydrolase (Fragment)	UCHL5	12	1959.9	4665.63 3	4112.73 3	3716.3	3060	3247.46 7
Adenosine deaminase, RNA-specific isoform ADAR-a variant (Fragment)		2	8769.1	16382.7	13687.2 7	13049.3 7	12459.5	12497.7
Pleckstrin homology-like domain family A member 2	PHLDA2	2	117.433333 3	158	199.366 7	125.866 7	228.766 7	122.533 3
Neuroblastoma-amplified sequence	NBAS	16	1475.8	3756.63 3	3096.56 7	2992.7	2873.33 3	2874.13 3
Histone H3	HIST2H3PS2	5	5386.73333 3	9843.33 3	9815.23 3	7841.66 7	7003.56 7	8412.13 3
cDNA FLJ60436, highly similar to Homo sapiens dolichyl-phosphate mannosyltransferase		2	490.333333 3	808.9667	694.766 7	644.5	573.633 3	658.333 3

polypeptide 3, transcript variant 1, mRNA								
Syntaxin-binding protein 3	STXBP3	20	3581.43333 3	7208.63 3	6004.86 7	5743.13 3	6049.43 3	5695.93 3
Isoform 7 of BRCA2-interacting transcriptional repressor EMSY	EMSY	5	746.733333 3	1084.63 3	895.533 3	864.133 3	860.166 7	802.366 7
ATP synthase mitochondrial F1 complex assembly factor 1	ATPAF1	9	1395.1	2710.36 7	2312.33 3	2159.4	2108.9	2036.66 7
Histone-lysine N-methyltransferase SMYD3	SMYD3	3	478.633333 3	764.3	637.3	608.966 7	585.933 3	554
Haloacid dehalogenase-like hydrolase domain-containing protein 2	HDHD2	3	430.866666 7	731.033 3	601.4	582.5	584.433 3	599.2
cDNA FLJ34689 fis, clone MESAN2000815, highly similar to Homo sapiens leucine zipper protein 5 (LUZP5), mRNA		2	56.1666666 7	52.66667	52.1666 7	41.9666 7	43.8666 7	38.4
Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	25	4864.73333 3	11343.4 7	9396.53 3	9039.2	8154.2	8144.13 3
THO complex subunit 6 homolog	THOC6	7	1386.56666 7	2371.73 3	1817.36 7	1890.03 3	1868.46 7	1872.16 7
Protein AATF	AATF	12	1420.53333 3	3067.06 7	2572.96 7	2444.3	2173.96 7	2221.6
Nucleoside diphosphate-linked moiety X motif 19	NUDT19	8	1086.86666 7	1485.46 7	1270.03 3	1183.86 7	1051	1042.73 3
Transmembrane protein 192	TMEM192	3	310.2	576.866 7	547.166 7	459.766 7	382.2	424

Isoform 4 of Apoptotic chromatin condensation inducer in the nucleus	ACIN1	1	5832.96666 7	8907.43 3	7275.76 7	7099.36 7	7548.13 3	6626.43 3
Splicing factor 3B subunit 3	SF3B3	36	8212.2	16290.1 7	16090.7 3	12983.5 3	10879	10713.2 3
Metaxin 1, isoform CRA_b	MTX1	8	1111.93333 3	2756.5	2263.6	2197.16 7	2160.96 7	2028.36 7
Isoform 2 of Membrane-associated progesterone receptor component 2	PGRMC2	6	996.533333 3	2261	1569.73 3	1802.5	1705.33 3	1964.83 3
eIF-2-alpha kinase GCN2	EIF2AK4	6	562.766666 7	1207.6	1084.93 3	962.766 7	897.933 3	1007.7
Vesicle-associated membrane protein 3	VAMP3	1	1973.73333 3	2963.06 7	2600.2	2362.33 3	2004.83 3	2091.1
Isoform 4 of Double-stranded RNA-specific adenosine deaminase	ADAR	1	8504.3	16057.5 7	13426.9 7	12802.0 7	12169.8 3	12237
Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	4	255.666666 7	339.7	281.8	270.833 3	259.266 7	255.366 7
Ribonuclease H2 subunit B	RNASEH2B	6	863.3	1668.2	1569.1	1330.03 3	874.866 7	971.5
Ubiquitin carboxyl-terminal hydrolase 15	USP15	14	1176.76666 7	2872.16 7	2526.5	2289.96 7	1854.63 3	1991.4
Cyclin-dependent kinase 12	CDK12	12	1818.06666 7	2608.33 3	2292.7	2079.83 3	1976.23 3	1960.2
RCC1-like G exchanging factor-like protein	RCC1L	3	460.6	793.233 3	768.133 3	632.566 7	607.933 3	516.566 7

Tropomyosin beta chain	TPM2	4	13062.9333 3	23882.4	20103.9 3	19045.2	15450.6 7	16489.6
Anion exchange protein (Fragment)		5	1125.76666 7	1836.03 3	1575.7	1464.16 7	1620.1	1492.5
Isoform 3 of Echinoderm microtubule-associated protein-like 2	EML2	6	882.933333 3	1846.13 3	1353.3	1472.23 3	1672.86 7	1492.66 7
NEDD4-binding protein 1	N4BP1	9	951.366666 7	1857.2	1766.53 3	1481.13 3	1265.6	1502.26 7
ELKS/Rab6-interacting/CAST family member 1	ERC1	22	2739.36666 7	3929.26 7	3413.3	3133.93 3	3001.33 3	3035
Isoform 4 of UDP-galactose translocator	SLC35A2	1	90.0666666 7	146.433 3	140.266 7	116.8	117	115.533 3
Abl interactor 2	ABI2	6	918.366666 7	1771.46 7	1531.43 3	1413	1316.96 7	1246.56 7
Vacuolar protein sorting-associated protein 33B	VPS33B	1	78.4	116	116.366 7	92.5333 3	92.9333 3	99.1333 3
E3 SUMO-protein ligase NSE2	NSMCE2	3	135.533333 3	248	244.366 7	197.833 3	157.2	155.4
cAMP-dependent protein kinase type I-alpha regulatory subunit	PRKAR1A	9	2451.43333 3	4162.23 3	5488.86 7	3320.33 3	2744.46 7	2807
Putative protein FAM45B	FAM45BP	3	328.9	547.3	453.2	436.6	357.033 3	383.166 7
Pre-mRNA-processing factor 40 homolog A	PRPF40A	25	4474.26666 7	10063.5	8549.56 7	8028.33 3	7356.9	6899.03 3
Synaptojanin-1	SYNJ1	6	907.833333 3	1563.66 7	1509.4	1247.46 7	1325.46 7	1212.9

Histone deacetylase complex subunit SAP130	SAP130	3	812.3	1129.5	912	901.1	926	842.933 3
Mediator of RNA polymerase II transcription subunit 23	MED23	5	691.266666 7	1777.33 3	1695.73 3	1417.93 3	1106.96 7	1218.93 3
Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1	22	4280.23333 3	11504.3 3	10100.7	9178.56 7	7490.73 3	7908.76 7
YTH domain-containing protein 1	YTHDC1	9	1459.86666 7	2670.16 7	2089.4	2130.4	2102.33 3	2030.16 7
cDNA, FLJ96764, highly similar to Homo sapiens sorting nexin 8 (SNX8), mRNA		4	239.066666 7	277.4	284.333 3	221.333 3	162.566 7	226.733 3
Target of EGR1 protein 1	TOE1	5	518.333333 3	756.466 7	712.433 3	603.6	490.9	485.6
Complex III assembly factor LYRM7	LYRM7	5	844.466666 7	1373.16 7	1115.4	1095.73 3	1101.53 3	1092.1
RNA-binding protein 4B	RBM4B	1	2081.46666 7	4419.36 7	4050.03 3	3526.56 7	2902.1	3002.63 3
Nucleosome-remodeling factor subunit BPTF	BPTF	13	1886.9	4126.7	3851.83 3	3293.23 3	2975.46 7	2759.16 7
Isoform 3 of Hematological and neurological expressed 1-like protein	HN1L	11	2490.66666 7	3323.4	2757.56 7	2652.5	2226.36 7	2298.2
Kinetochore protein Spc25	SPC25	6	816	1756.63 3	1853.66 7	1402.03 3	1170.93 3	1046.83 3
F-actin-capping protein subunit alpha-1	CAPZA1	14	4006.6	7144.9	5959.6	5702.73 3	4779.86 7	5203.13 3

Phospholipase DDHD1	DDHD1	1	42.8333333 3	54.8333 3	47.5333 3	43.7666 7	46.6666 7	35.7666 7
Transcription initiation factor TFIID subunit 5	TAF5	3	378.366666 7	585	492.466 7	466.933 3	454.933 3	448.9
Serine/threonine kinase 4 variant (Fragment)	7	1382.6	3022.3	2760.13 3	2412.33 3	1988.6	2171.53 3	
Pericentriolar material 1, isoform CRA_a	PCM1	12	1848	3597.03 3	3402.76 7	2871.16 7	2615.76 7	2400.33 3
Ubiquitin carboxyl-terminal hydrolase 32	USP32	4	132.133333 3	371.5	339.3	296.533 3	271.233 3	265.8
Ribonuclease H2 subunit C	RNASEH2C	3	417.333333 3	892.633 3	820.933 3	712.533 3	591.2	569.9
SCY1-like protein 2	SCYL2	7	1004.63333 3	2672.26 7	2355.56 7	2133.2	1757.4	1795.4
cDNA, FLJ93570, highly similar to Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA	8	1349.46666 7	2418.467	1942.73 3	1930.63 3	1678.76 7	1721.36 7	
Acyl-coenzyme A oxidase		3	109.933333 3	166.1	146.166 7	132.6	129.2	133.766 7
Histone-lysine N- methyltransferase setd3	SETD3	13	2167.66666 7	3468.83 3	3072.76 7	2769.23 3	2171.63 3	2170.9
Ras-related protein Rab-43	RAB43	5	1946.03333 3	4350.03 3	3381.26 7	3472.93 3	2815.1	3254.06 7
Endoplasmic reticulum resident protein 29	ERP29	16	4026.6	8697.66 7	6641.53 3	6944.66 7	7536.86 7	6502.66 7

Serpin H1	SERPINH1	20	5809.43333 3	11675.5	9396.96 7	9322.4	9159.56 7	9406.06 7
Galactosamine (N-acetyl)-6-sulfatase	GALNS	4	226.933333 3	339.9	324.666 7	271.4	292.333 3	269.666 7
Caspase activity and apoptosis inhibitor 1	CAAP1	3	609.266666 7	1370.13 3	1121.9	1094.03 3	970.466 7	1107.73 3
Histone-lysine N-methyltransferase EHMT2	EHMT2	6	518.8	731.5	694.5	584.166 7	567.766 7	516.633 3
Structural maintenance of chromosomes protein 5	SMC5	11	1104.53333 3	2029.33 3	1719.66 7	1620.76 7	1465.5	1492.36 7
Mitochondrial import inner membrane translocase subunit Tim9	TIMM9	5	1005.8	1752.2	1525.5	1399.43 3	1175.2	1163.6
Spectrin, alpha, non-erythrocytic 1 (Alpha-fodrin), isoform CRA_g	SPTAN1	1	15614.1	31096.9 3	26248.3 7	24837.0 7	22486.7 3	22825.6 3
Ubiquitin carboxyl-terminal hydrolase 5	USP5	23	4838.23333 3	8871.2	7026.4	7085.9	6250.5	6677.43 3
26S proteasome non-ATPase regulatory subunit 4	PSMD4	1	3937.8	6656.83 3	5747.66 7	5318.23 3	4427.43 3	5064.53 3
Isoform 8 of Transcriptional coactivator YAP1	YAP1	1	754.133333 3	1591.7	1243.06 7	1271.63 3	1121.5	1172.7
Translation initiation factor eIF-2B subunit epsilon	EIF2B5	10	1097.86666 7	1934.8	1702.76 7	1545.8	1402.9	1504.63 3
cAMP-regulated phosphoprotein 19	ARPP19	1	993.366666 7	2618.96 7	1988.53 3	2092.5	1473.56 7	1645.53 3
Signal recognition particle subunit SRP72	SRP72	29	5049.43333 3	11560.1 3	9649.13 3	9236.33 3	7157.43 3	7807.4

Numb-like protein	NUMBL	6	2447.1	4668.63 3	3428.56 7	3730.16 7	4061.9	3806.1
Mth938 domain-containing protein	AAMDC	4	923.666666 7	1057.4	757.333 3	844.966 7	813.033 3	885.2
Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	12	4649.46666 7	7690.63 3	6451.4	6145.73 3	5116.1	5309.1
Pygopus homolog 2	PYGO2	2	185.733333 3	225.266 7	195.266 7	180.033 3	169.066 7	173.233 3
Ubiquitin thioesterase		11	2240.96666 7	4449.03 3	3880.23 3	3555.73 3	3202.36 7	3375.76 7
Uncharacterized protein KIAA1671	KIAA1671	3	988.733333 3	1683.6	1355.33 3	1345.63 3	1376.9	1207.73 3
Tyrosine-protein kinase		1	574.5	1366.73 3	1262.23 3	1092.4	1003.73 3	912.8
E3 ubiquitin-protein ligase makorin-1	MKRN1	1	41.6	92.5666 7	75.3666 7	74	67.9	72.1666 7
U6 snRNA-associated Sm-like protein LSM6	LSM6	5	550.033333 3	1290.96 7	1077.03 3	1032.13 3	832.766 7	902.266 7
Isoform 2 of NF-kappa-B essential modulator	IKBKG	5	633.1	809.366 7	722.166 7	647.133 3	612.733 3	626.333 3
cDNA, FLJ95468, highly similar to Homo sapiens transcriptional coactivator tubedown-100 (TBDN100), transcript variant 1, mRNA		1 3	6997.33333 3	16419.53	15031.3 7	13129.1 3	10146.8 3	11195.8 3

Telomeric repeat-binding factor 2	TERF2	7	1236.9	2080.16 7	1988.46 7	1663.33 3	1475.56 7	1384.16 7
Ubiquitin-like modifier-activating enzyme 6	UBA6	26	3517.7	9412.13 3	7142	7526.23 3	6796.3	7466.53 3
Cyclin-dependent kinase 13	CDK13	1	1041.83333 3	1955.96 7	1541.06 7	1564.06 7	1264.96 7	1426.9
Isoform C15orf38-AP3S2 of Arpin	ARPIN	3	226.966666 7	301.333 3	262.1	240.966 7	198.933 3	217.9
Translation initiation factor eIF-2B subunit beta	EIF2B2	8	970.066666 7	1889.4	1691.56 7	1511	1276.3	1564
60 kDa SS-A/Ro ribonucleoprotein	TROVE2	18	2133.93333 3	4838.4	3766.83 3	3869.7	3525.7	3699
Endophilin-B2	SH3GLB2	10	1632.23333 3	2760.06 7	2243.26 7	2207.53 3	2112.1	2025.63 3
Tubulin gamma-1 chain	TUBG1	7	1116	1402.66 7	1324	1121.9	1064.23 3	1043.96 7
tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	TRMT61A	4	371.5	839.433 3	750.266 7	671.433 3	583.333 3	547.8
Isoform 2 of Replication initiator 1	REPIN1	3	1101.93333 3	1183.3	1011.1	946.533 3	960.233 3	811.666 7
cDNA FLJ14631 fis, clone NT2RP2000660, highly similar to Homo sapiens fidgetin-like 1 (FIGNL1), mRNA		2	493.433333 3	788.7333	746.3	630.933 3	524.766 7	630.933 3
UBX domain-containing protein 6	UBXN6	10	786.633333 3	2048.03 3	1424.5	1638.3	1711.56 7	1730.8

Isoform 3 of Coronin-7	CORO7	15	3490.03333 3	5319.4	4219.43 3	4255.33 3	3960.66 7	3812.13 3
Protein bicaudal D homolog 1	BICD1	1	854.8	1211.13 3	1225.56 7	968.866 7	893.866 7	787.066 7
Mitochondrial DNA polymerase subunit gamma-2		2	341.666666 7	623.6	504.7	498.866 7	563.7	507.5
Coiled-coil and C2 domain-containing protein 1B (Fragment)	CC2D1B	7	703	1163.23 3	1063.13 3	930.666 7	890.566 7	908.833 3
RNA-binding protein PNO1	PNO1	6	1255.56666 7	2467.66 7	2502.8	1974.33 3	1536.46 7	1724.86 7
Protein virilizer homolog	KIAA1429	9	1153.03333 3	1771.5	1494.96 7	1417.4	1317.86 7	1337.7
Prostate cancer upregulated protein 1		7	1113.56666 7	2673.56 7	2432.13 3	2139.26 7	1670.2	1724.96 7
Isoform 4 of Beta-arrestin-2	ARRB2	3	345.9	503.066 7	481.933 3	402.533 3	330.833 3	358.466 7
Ring finger protein 40, isoform CRA_a	RNF40	20	3203.33333 3	4949.63 3	4979.3	3960.96 7	3968.9	3425.06 7
Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GSPT1	17	9230.66666 7	16879.1 3	14889.4 7	13508.9	10973.0 3	12008.5 3
AP-2 complex subunit alpha-1	AP2A1	16	6878.96666 7	11478.4	9408.16 7	9187.13 3	9564.63 3	8843.33 3
Catalase	CAT	10	1056.83333 3	1824.13 3	1722.33 3	1460.2	1260.73 3	1218.06 7
Calcium load-activated calcium channel	TMCO1	4	1297.96666 7	2115.23 3	1750.3	1693.26 7	1556.8	1574.1

Isoform A of Syntaxin-16	STX16	5	434.5	844.5	701.9	676.1	607.933 3	612.066 7
Cleft lip and palate transmembrane protein 1-like protein	CLPTM1L	3	220.066666 7	664.866 7	547.5	532.3	556.6	511.433 3
ADP-sugar pyrophosphatase	NUDT5	10	2863.73333 3	4803.06 7	3763.03 3	3846.33 3	3356.93 3	3622.4
Axin interactor, dorsalization-associated protein	AIDA	9	777.033333 3	1388.46 7	1163.33 3	1111.93 3	1065.96 7	1008.43 3
45 kDa calcium-binding protein	SDF4	12	1746.66666 7	4217.96 7	3278.06 7	3377.96 7	3282.76 7	3458.86 7
Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	PIP4K2A	3	744.533333 3	1278.73 3	1113.46 7	1024.16 7	1083.33 3	991.533 3
Cysteine protease		6	1707.16666 7	3388.46 7	3440.7	2713.93 3	2075.13 3	2027.33 3
Peptidyl-prolyl cis-trans isomerase FKBP5	FKBP5	15	2223.16666 7	5623.86 7	5349.83 3	4504.6	3288.16 7	3853.73 3
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	INPPL1	6	1363	1886.9	1720.8	1511.53 3	1466.53 3	1516.1
DNA-directed RNA polymerase I subunit RPA1	POLR1A	26	3492.53333 3	5539.86 7	4946.8	4438.26 7	3786.86 7	3985.8
DNA-directed RNA polymerase II subunit RPB3	POLR2C	9	1292.63333 3	2612.33 3	2634.63 3	2092.93 3	1947.33 3	1957.13 3
Eukaryotic translation initiation factor 3 subunit L	EIF3L	23	6131.63333 3	13462.0 7	12774.9	10785.7 7	7998.1	8693.96 7
Endophilin-A2	SH3GL1	20	5447.4	9804	8497.33 3	7855.13 3	6857.2	7192

Isoform 2 of Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1	11006.1	19242.5 7	15691.9 7	15418.2	13964.6 3	13920.9 7
Histone-lysine N-methyltransferase ASH1L	ASH1L	3	96.7666666 7	112.433 3	101.966 7	90.1	94.8666 7	86.3
Vacuolar protein sorting-associated protein 26A	VPS26A	7	1666.43333 3	4592.36 7	4300	3680.3	2789.76 7	3072.5
Transforming protein RhoA	RHOA	3	5001.43333 3	9129	7258.73 3	7316	5372.4	5993.5
cDNA FLJ60834, highly similar to Engulfment and cell motility protein 2 (CED-12 homolog A)	6	180.1	314.8667	296.266 7	252.366 7	236.633 3	247.566 7	
Holliday junction recognition protein	HJURP	8	1116.83333 3	2495.86 7	2420.46 7	2000.46 7	1733.46 7	1356.5
DNA-directed RNA polymerase II subunit RPB4	POLR2D	5	633.866666 7	975.6	881.633 3	781.966 7	791.366 7	704.7
Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	29	6401.36666 7	13627.6 3	11751.2 7	10923.8	8976.2	9998.03 3
Ras-related protein Rab-7a	RAB7A	17	5551.5	10954.7 7	9848.86 7	8781.43 3	6902.2	7940.1
GTP-binding protein 1	GTPBP1	11	1530.6	2601.63 3	2314.96 7	2085.5	1762.23 3	1910.73 3
Isoform 2 of Tropomyosin beta chain	TPM2	2	12446.9333 3	22370.9 7	18836.6 3	17932.9	15028.7 3	15848.1 3
Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial	COQ6	3	184	324.033 3	264.4	259.8	249.4	246.033 3
Nuclear inhibitor of protein phosphatase 1	PPP1R8	6	359.4	1057.93 3	879.9	848.3	793.1	835.7

39S ribosomal protein L34, mitochondrial	MRPL34	2	471.6	836.6	766.833 3	670.833 3	667.366 7	598.466 7
Actin-like protein (Fragment)	ACT	3	7915.46666 7	11868.8	9271.5	9517.16 7	8893.26 7	9005.03 3
Nuclear export mediator factor NEMF	NEMF	19	4902.83333 3	9409.03 3	8316.13 3	7545.46 7	5961.13 3	6649.53 3
ATP-dependent zinc metalloprotease YME1L1	YME1L1	13	2791.83333 3	4185	4093.76 7	3356.26 7	2845.53 3	2790.5
Rho-related GTP-binding protein RhoC	RHOC	3	3099.9	6143.46 7	5111.63 3	4927	3828.03 3	4115.73 3
DnaJ homolog subfamily C member 2	DNAJC2	24	4659	8260.26 7	7351.93 3	6624.8	5461.46 7	6040.56 7
Heat shock protein beta-1	HSPB1	16	13766.4666 7	21992.9	17794.9 7	17639.3	14534.2 3	15515.4
DDR GK domain-containing protein 1	DDR GK1	8	1077.56666 7	1485.7	1342.96 7	1191.63 3	1153.26 7	1185.4
Probable tRNA pseudouridine synthase 1	TRUB1	7	1444	2465.36 7	2097.4	1977.5	1531.23 3	1523.23 3
Transformation/transcription domain-associated protein	TRRAP	14	2210.23333 3	3599.9	3581.4	2887.53 3	2761.3	2530.76 7
Nuclear distribution protein nudE homolog 1	NDE1	7	2276.83333 3	3291.1	2735	2640.3	2516.1	2349.76 7
Syntaxin-binding protein 5	STXBP5	3	422.733333 3	607.233 3	460.5	487.166 7	489.466 7	495.466 7
Kelch-like protein 11	KLHL11	2	191.833333 3	486.7	440.366 7	390.466 7	338.966 7	328.266 7
Ras-related protein Rab-11B	RAB11B	11	2192.6	4243.4	3595.33 3	3404.66 7	2823.7	3026.13 3

RNA-binding motif protein, X-linked 2	RBMX2	3	694.766666 7	1292.56 7	1323.46 7	1037.16 7	945.666 7	883.066 7
Alpha-ketoglutarate-dependent dioxygenase FTO	FTO	7	1224.43333 3	2479.93 3	2198.36 7	1989.96 7	1522.2	1659.4
Spectrin alpha chain, non-erythrocytic 1	SPTAN1	2	15885.9666 7	30833.8 3	26104.5	24744.1 7	22334.8	22749.5 7
WD repeat-containing protein 70	WDR70	9	2205.66666 7	3318.16 7	3016.43 3	2663	2624.63 3	2426.86 7
Peptidylprolyl isomerase	AIP	12	2653.8	5125.5	4381.93 3	4113.5	3811.73 3	3828.9
cDNA, FLJ92896, highly similar to Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), mRNA		34	7340.46666 7	13211.47	11295.0 7	10603.2 7	8135.5	9079.1
Glia maturation factor beta	GMFB	5	1323.93333 3	3132.86 7	2765	2514.5	2092.13 3	2221.73 3
Isoform Long of Proteasome subunit alpha type-1	PSMA1	20	6209.26666 7	11877.5	10230.2 7	9533.23 3	7842	8426.33 3
Vesicle-associated membrane protein 4	VAMP4	1	199.3	348.833 3	271.233 3	280	264.166 7	251.1
Serine/arginine repetitive matrix protein 2	SRRM2	32	6683.76666 7	12398.0 3	11378.2 7	9951.63 3	9344.66 7	8967.36 7
Esterase OVCA2	OVCA2	3	280.266666 7	313.066 7	277.266 7	251.3	215.566 7	227.966 7
Cyclic AMP-responsive element-binding protein 1	CREB1	1	644.9	1652.8	1384.3	1326.86 7	1288.46 7	1215.03 3

Active regulator of SIRT1	RPS19BP1	5	663.5	1463.56 7	1263.3	1175.06 7	1043.6	1074.03 3
60S ribosomal protein L27a	RPL27A	12	4317.6	7260.33 3	7061.26 7	5829.33 3	4896.36 7	4858.5
cDNA FLJ60607, highly similar to Acyl-protein thioesterase 1 (EC 3.1.2.-)	5	1272.76666 7	2051.133	1567.16 7	1647.1	1529.16 7	1686.46 7	
Chromatin accessibility complex protein 1	CHRA1	2	837.9	1193.56 7	992.933 3	958.466 7	943.6	926
NGFI-A-binding protein 2	NAB2	3	347.6	823.366 7	639.666 7	661.2	607.633 3	667.2
Isoform 3 of Zinc finger protein 691	ZNF691	1	377.666666 7	621.066 7	627.133 3	498.766 7	506.166 7	442.3
Protein FAM172A	FAM172A	1	326.866666 7	530.1	459.3	425.733 3	448.766 7	419.1
Angiogenic factor with G patch and FHA domains 1	AGGF1	3	721.3	1302.93 3	1307.33 3	1046.43 3	916.2	860.433 3
2-hydroxyacyl-CoA lyase 1	HACL1	4	477.566666 7	746.966 7	595.033 3	599.933 3	541.8	523.066 7
Conserved oligomeric Golgi complex subunit 3	COG3	3	130.3	214.4	169.466 7	172.2	153.366 7	180.9
Pantothenate kinase 2, mitochondrial	PANK2	2	591.766666 7	919.766 7	840.266 7	738.733 3	654.166 7	714
DNA ligase 3	LIG3	31	5499.16666 7	9034.26 7	7098.36 7	7256.7	7051.16 7	6559.23 3
Isoform 2 of Nucleolysin TIAR	TIAL1	7	2465.56666 7	4316.3	3517.06 7	3467.13 3	2926.8	3189.43 3

Rho-associated protein kinase	ROCK1	24	4459.23333 3	8402.06 7	6955.63 3	6749.36 7	6111.4	6820.73 3
NEDD8-conjugating enzyme Ubc12	UBE2M	10	2923.13333 3	6183.66 7	5221.23 3	4967.7	4352.23 3	4766.7
Mitochondrial carrier homolog 2 (Fragment)	MTCH2	1	1145.86666 7	2157.26 7	1771.83 3	1733.1	1645.36 7	1606.8
AP-4 complex subunit epsilon-1	AP4E1	2	470.7	398.133 3	364.366 7	319.866 7	314.966 7	321.2
E3 ubiquitin-protein ligase BRE1A	RNF20	21	3137.4	5905.96 7	5973.86 7	4745.26 7	3986.3	3721
Peripheral plasma membrane protein CASK	CASK	5	711.2	1298.2	1056.7	1043.16 7	1159.53 3	1047.36 7
Methionine aminopeptidase 1	METAP1	7	1621.06666 7	2866.86 7	2464.8	2303.9	2014.96 7	2044.5
Nucleolar protein 58	NOP58	27	6731.43333 3	14156.6	12267.6 3	11376.9	10446.0 7	10578.0 7
Tubulin-specific chaperone cofactor E-like protein	TBCEL	5	457.2	1480.16 7	1169.6	1189.6	1053.16 7	1288.8
Growth factor receptor-bound protein 2	GRB2	1	1934.43333 3	3600.43 3	2850.26 7	2893.7	2713.93 3	2767.83 3
Phosphatidylinositide phosphatase SAC1	SACM1L	9	2416.1	3427.16 7	3287.2	2754.5	2416.4	2481.3
AF4/FMR2 family member 4	AFF4	10	1010.63333 3	1766.93 3	1485.26 7	1420.33 3	1431.36 7	1454.23 3
Peroxisome biogenesis factor 1	PEX1	8	629.166666 7	775.5	653.4	623.433 3	629.8	604.4
40S ribosomal protein S14	RPS14	11	5413.3	7992.3	7194.76 7	6425.2	5516.73 3	5863.46 7

Heme-binding protein 1	HEBP1	9	1634.83333 3	3207.56 7	2882.9	2579.23 3	2325.63 3	2333.13 3
Nucleosome assembly protein 1-like 1	NAP1L1	11	5239.73333 3	7110.56 7	6942.36 7	5717.9	4359.26 7	4811.9
Trafficking protein particle complex subunit 4	TRAPPC4	5	594.233333 3	928.533 3	891.333 3	746.733 3	695.633 3	697.866 7
Microtubule-associated serine/threonine-protein kinase 2	MAST2	3	107.433333 3	96.0333 3	77.9333 3	77.2333 3	86.5666 7	77.0666 7
Tubulin beta chain	TUB4q	1	9339.2	14598.7 3	11866.7 3	11741.3 7	9268.8	10418.9 7
Dystrophia myotonica WD repeat-containing protein	DMWD	1	90.3	147.333 3	157.8	118.5	93.3666 7	70.7333 3
Zinc finger protein 22	ZNF22	1	246.366666 7	507.433 3	521.333 3	408.133 3	408.7	344.766 7
Isoform 6 of Breast cancer anti-estrogen resistance protein 1	BCAR1	18	2734.26666 7	5202.96 7	4776.16 7	4185.13 3	3481.66 7	3625.53 3
SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	9	2644.2	3869.5	3785.83 3	3112.56 7	2424.26 7	2503.9
Canalicular multispecific organic anion transporter 1	ABCC2	2	157.5	173.533 3	148.633 3	139.6	136.566 7	125.133 3
Cell cycle checkpoint protein RAD17	RAD17	3	123.266666 7	188.366 7	160.033 3	151.533 3	135.8	144.666 7
Heat shock factor-binding protein 1	HSBP1	4	396.866666 7	537	534.933 3	432.066 7	387.966 7	367.666 7
UPF0235 protein C15orf40	C15orf40	3	472.9	786.266 7	627.666 7	632.633 3	659.333 3	650.7

Ubiquitin-specific protease 7 isoform (Fragment)		21	2465.8	5666.167	4760.26 7	4559.1	4014.83 3	4218.43 3	
SEC23-interacting protein	SEC23IP		21	3452.86666 7	6268.63 3	5242.36 7	5044.8	4247.96 7	4932
Protein IWS1 homolog	IWS1		8	1032.83333 3	1969.2	1769.96 7	1584.76 7	1486.56 7	1448.53 3
cDNA FLJ56105, highly similar to Nuclear valosin-containing protein-like		9	1427.46666 7	2334.833	2245.03 3	1879.23 3	1670.3	1707.3	
Nuclear cap-binding protein subunit 3	NCBP3		9	1478.36666 7	2602.36 7	2265.1	2094.56 7	2098.96 7	1777.46 7
ATP-dependent RNA helicase SUPV3L1, mitochondrial	SUPV3L1		14	1946.73333 3	3564.03 3	3004.1	2868.8	2766.46 7	3115.93 3
MTHFD1L protein	MTHFD1L		21	3124.9	6345.26 7	6115.93 3	5107.86 7	4147.23 3	4281.8
Heat shock cognate 71 kDa protein	HSPA8		20	50292.1666 7	85419.4 7	80497.3 3	68762.9 7	56176.9 7	64619.9 3
Dedicator of cytokinesis 1	DOCK1		4	575.766666 7	812.666 7	677.5	654.2	620.8	612.2
MIF4G domain-containing protein	MIF4GD		3	173	473.366 7	398.566 7	381.066 7	369.6	399.533 3
Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1		6	1018.4	2187.03 3	2054.4	1760.6	1310	1521.23 3
Eukaryotic translation initiation factor 3 subunit G	EIF3G		11	5582.93333 3	10951.9	10095.6 3	8817.03 3	6269.03 3	6948.56 7
dCTP pyrophosphatase 1	DCTPP1		7	1249.06666 7	1771.03 3	1721.26 7	1425.9	1182.13 3	1223.06 7

Protein furry homolog-like	FRYL	14	1025.6	2325.93 3	2097.13 3	1872.7	1619.76 7	1398.6
Adenylyl cyclase-associated protein		31	13869.1	27552.5	21504	22186.1	17615.3 3	19914.7 7
Phosphoinositide phospholipase C		1	1340.43333 3	3044.16 7	2615.13 3	2451.36 7	1974.83 3	2136.06 7
Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	20	4574.7	8948.56 7	6998.73 3	7206	6574.56 7	6400.06 7
Nucleobindin-1	NUCB1	11	1206.33333 3	1638.66 7	1344.63 3	1319.6	1467.43 3	1345.4
39S ribosomal protein L12, mitochondrial	MRPL12	10	6582.46666 7	6962.2	5667.73 3	5606.7	5645.03 3	5585.6
Tyrosine-protein phosphatase non-receptor type 9	PTPN9	2	293.6	580.4	565.633 3	467.4	311.466 7	335.133 3
Uncharacterized protein	FLJ20643	6	1355.93333 3	2627.83 3	2271.4	2116.23 3	1654.3	1828.06 7
WAS/WASL-interacting protein family member 2	WIPF2	12	1854.8	2995.9	2168.2	2412.83 3	2118.4	2038.7
tRNA nucleotidyl transferase, CCA-adding, 1, isoform CRA_b	TRNT1	13	1489.56666 7	2593.43 3	2202.86 7	2088.73 3	1950.2	2029.16 7
Carbonyl reductase [NADPH] 3	CBR3	7	3039.46666 7	3912.93 3	3014.66 7	3151.56 7	3220.6	3158.46 7
40S ribosomal protein S4, X isoform	RPS4X	25	9948.26666 7	15092.6 7	14161.1 7	12156.3 7	9444.46 7	10549.3
Transmembrane 9 superfamily member		8	971.366666 7	2573.66 7	2091.73 3	2073.06 7	1948.93 3	1913.76 7
rRNA methyltransferase 1, mitochondrial	MRM1	3	781.833333 3	955.666 7	834.5	769.9	659.233 3	732.566 7

Tubulin beta-8 chain	TUBB8	1	19985.5666 7	31230.9 3	26677.6	25164.4 7	20609.3	23014.2
Dual specificity phosphatase 3 (Fragment)	DUSP3	4	1072.46666 7	1674.8	1321.6	1349.56 7	1519.23 3	1420.86 7
cDNA, FLJ93089, highly similar to Homo sapiens NCK adaptor protein 1 (NCK1), mRNA	14	2425.73333 3	5270.533	4278.46 7	4247.1	3664.86 7	4010.9	
Pleckstrin homology-like domain family B member 2	PHLDB2	1	2780.36666 7	6026.33 3	5536.53 3	4856.4	3680.26 7	3361.9
WD repeat-containing protein 55	WDR55	3	482.733333 3	930.8	754.3	750.166 7	750.966 7	755.3
Striatin-3	STRN3	1	1626.9	2974.7	2574.86 7	2397.53 3	2309.73 3	2299.76 7
Chromodomain-helicase-DNA-binding protein 8	CHD8	13	1796.2	2782.93 3	2661.36 7	2243.03 3	1957.23 3	1909.2
Heat shock 70 kDa protein 4	HSPA4	67	26846.0666 7	49523.8	42571.9 7	39916.5	34301.6 3	35762.5
Splicing factor 3B subunit 2	SF3B2	27	6061.46666 7	13095.3 7	10671.1 7	10555.0 3	9904.03 3	9301.63 3
OCIA domain-containing protein 2	OCIAD2	2	41.7	255.3	244.033 3	205.8	12.9	14.4
CD276 antigen	CD276	2	182.533333 3	421.766 7	362.5	340.033 3	333.566 7	314.166 7
Amidophosphoribosyltransferase	PPAT	15	2275.86666 7	3778.1	2848.3	3046.03 3	2618.63 3	2738.3
Protein PRRC2A	PRRC2A	28	4385.93333 3	7425.4	6516.96 7	5986.86 7	5439.83 3	5362.4

Protein unc-119 homolog B	UNC119B	3	397.633333 3	983.233 3	792.933 3	792.8	711.066 7	713.8
Prefoldin subunit 1	PFDN1	7	3007.3	4695.73 3	3935.26 7	3786.53 3	2978.63 3	3499.16 7
TMEM106B protein (Fragment)	TMEM106B	3	331.766666 7	867.2	772.7	699.3	636.933 3	629.966 7
Proteasome subunit alpha type-5	PSMA5	14	4886.6	8071.46 7	6838.56 7	6509	5365.63 3	6043.83 3
Isoform 3 of Eukaryotic translation initiation factor 4E transporter	EIF4ENIF1	2	576.7	835.5	758.066 7	673.766 7	590.7	538.933 3
Atherin	SAMD1	5	535.933333 3	649.033 3	501.366 7	523.4	491.966 7	456.466 7
Eukaryotic translation initiation factor 3 subunit F	EIF3F	12	3020.13333 3	4908.96 7	4653.1	3958.96 7	3024.86 7	3468.66 7
Splicing factor 3B subunit 6	SF3B6	4	1899.2	2939.86 7	2552.36 7	2371	2119.03 3	2104.03 3
Insulin-like growth factor-binding protein 6	IGFBP6	3	129.733333 3	305.033 3	258.2	246.033 3	246.133 3	236.033 3
Metallo-beta-lactamase domain-containing protein 2	MBLAC2	2	184.833333 3	218.7	188.133 3	176.4	175.7	184.066 7
60 kDa heat shock protein, mitochondrial	HSPD1	40	62775.0333 3	79897.2 3	62449.4 3	64445.1 7	65816.2	64888.1 7
Histone H4	HIST1H4A	18	9136.8	16584.7 3	16729.7	13377.7 7	11776.9	13139.2
Importin-7	IPO7	20	2088.66666 7	4324.4	4584.63 3	3488.26 7	2422.26 7	2821

Anaphase-promoting complex subunit 1	ANAPC1	8	759.033333 3	1821.4	1626.5	1469.3	1299.93 3	1303.4
NUMA1 variant protein (Fragment)	NUMA1variantprot ein	4	17401.5	28459.3 3	23276.3	22959.7 3	23912.5 3	22676.0 7
Coiled-coil domain-containing protein 47	CCDC47	10	2084.76666 7	4944.2	3777.4	3988.76 7	3416.3	3593
CTP synthase 1	CTPS1	22	4545.7	9968.3	9529.16 7	8042.2	6180.06 7	6784
Putative uncharacterized protein DKFZp686L20222	DKFZp686L20222	12	3618.1	5158.03 3	5200.83 3	4161.6	3268.66 7	3436.56 7
Histone deacetylase 4	HDAC4	1	387.166666 7	595.3	569.3	480.3	446.5	451.1
Rab GTPase-activating protein 1	RABGAP1	17	2707.1	4956.4	4288.86 7	3999.13 3	3625.13 3	3921.86 7
Uncharacterized protein C1orf131	C1orf131	6	500.133333 3	857.6	711.866 7	691.966 7	730.6	605.7
Parathymosin	PTMS	6	5157.1	2762.9	2272.2	2229.3	2586.96 7	2293.43 3
Isoform 3 of Alpha-actinin-1	ACTN1	31	17816.5	34807	28686.8 3	28085.4 3	23197.1 3	25647.9
Unconventional myosin-IXb	MYO9B	24	3027.6	6266.8	5131.6	5056.86 7	4742.4	4684.06 7
Isoform 3 of Disks large-associated protein 5	DLGAP5	19	3473.63333 3	3926.86 7	4522.73 3	3169.2	2537.26 7	2554.7
Zinc finger CCH domain-containing protein 15	ZC3H15	16	3828.16666 7	6461.13 3	6102.66 7	5214.73 3	3881.86 7	4209.6
WD repeat-containing protein 75	WDR75	12	1314.4	3439.53 3	3075.06 7	2776.2	2349.33 3	2420.7

28S ribosomal protein S35, mitochondrial	MRPS35	7	331.933333 3	420.933 3	431.833 3	339.766 7	284.9	289.733 3
Tumor necrosis factor alpha-induced protein 2	TNFAIP2	6	189.5	338.2	255.8	273	273.066 7	278.666 7
Exosome complex component RRP40	EXOSC3	4	471.833333 3	908.366 7	855.4	733.266 7	703.266 7	660.733 3
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	SMARCC1	3	481.533333 3	757.6	659.433 3	611.566 7	598.633 3	572.066 7
cDNA FLJ38476 fis, clone FEBRA2022504, highly similar to YTH domain protein 1		3	1058.96666 7	2378.1	2389.06 7	1919.73 3	1504.53 3	1719.56 7
Sorting nexin-1	SNX1	15	3684.03333 3	8056	6159.1	6503.86 7	5610.86 7	5857.83 3
Peptidyl-prolyl cis-trans isomerase FKBP3	FKBP3	25	9487.2	14817.2 7	10699.2 3	11962.6 3	12055.4	11761.2 7
Isoform 3 of Synembryn-A	RIC8A	4	781.166666 7	1944.76 7	1837.06 7	1570.13 3	1295.83 3	1429.03 3
E3 ubiquitin-protein ligase CHIP	STUB1	11	1833.76666 7	3234.26 7	2923.3	2611.26 7	2362.36 7	2371.4
Pleckstrin homology-like domain family B member 2	PHLDB2	1	3029.03333 3	6275.63 3	5806.06 7	5066.93 3	3924.66 7	3629.1
G-protein-signaling modulator 1	GPSM1	12	1137.56666 7	2090.96 7	1846.33 3	1688.26 7	1543.5	1571.1
Putative transferase CAF17, mitochondrial	IBA57	3	530.4	809.2	673.366 7	653.366 7	619.366 7	669.966 7

Bifunctional lysine-specific demethylase and histidyl-hydroxylase MINA	MINA	7	1566.93333 3	2722.4	3163.63 3	2198.33 3	1411.13 3	1443.3
Programmed cell death protein 5	PDCD5	9	4423.43333 3	6526.1	5718.2	5270.96 7	4391.2	4663.8
Rab GDP dissociation inhibitor alpha	GDI1	8	4565.46666 7	8239.06 7	6701.36 7	6655	5701	6390.56 7
Pre-mRNA-splicing factor 38A	PRPF38A	4	412.733333 3	988.633 3	828.466 7	798.566 7	790.9	746.933 3
Ubiquitin carboxyl-terminal hydrolase 13	USP13	8	1421.33333 3	2292.03 3	2156.93 3	1851.43 3	1528.76 7	1608.36 7
Isoform 2 of Rho guanine nucleotide exchange factor 11	ARHGEF11	4	341.133333 3	575.433 3	500.033 3	464.833 3	471.466 7	473.733 3
Caspase-2	CASP2	3	224.366666 7	228.233 3	238.633 3	184.366 7	174.233 3	180.766 7
Dystrobrevin alpha	DTNA	1	368.7	573.566 7	476.166 7	463.366 7	467.5	443.7
Peroxisomal 2,4-dienoyl-CoA reductase	DECR2	4	159.066666 7	470.166 7	393	379.833 3	389.4	364.466 7
Bromodomain-containing protein 3	BRD3	7	771.966666 7	1299.46 7	1124.26 7	1049.8	968.333 3	942.066 7
26S proteasome non-ATPase regulatory subunit 4	PSMD4	2	4786.23333 3	7423.96 7	6465.06 7	5997.93 3	4963.9	5672
cDNA, FLJ92036, highly similar to Homo sapiens ribosomal protein L31 (RPL31), mRNA	11	4054.73333 3	7200.667	6645.73 3	5817.73 3	4614.53 3	4807.4	
Ubiquitin-conjugating enzyme E2 K	UBE2K	13	2464.16666 7	6136.96 7	5667.2	4958.4	3891.73 3	4358.43 3

Ras-related protein Rab-35	RAB35	11	3316.26666 7	6295.26 7	5575.53 3	5086.33 3	4206.83 3	4719.3
Protein lin-9 homolog (Fragment)	LIN9	2	286.533333 3	315.7	297.1	255.1	245.366 7	230.9
Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	3	731.6	1405.06 7	1144.4	1135.46 7	964.3	1110.26 7
cDNA FLJ39748 fis, clone SMINT2017436, highly similar to Homo sapiens haloacid dehalogenase-like hydrolase domain containing 3 (HDHD3), mRNA		3	378.033333 3	653.1	497.533 3	527.8	515.666 7	504.6
Isoform 3 of Drebrin-like protein	DBNL	18	4421.23333 3	6189.8	5128.4	5002.26 7	4779.23 3	4682.16 7
NUP98/NSD1 fusion protein	NUP98	3	976.466666 7	1937.56 7	1855.33 3	1565.93 3	1391.63 3	1380
Isoform 3 of Chromatin complexes subunit BAP18	BAP18	5	1332.36666 7	1844.23 3	1206.43 3	1490.6	1626.96 7	1395.9
PRSS3 protein	PRSS3	2	839.1	1250.06 7	1078.96 7	1010.36 7	856.766 7	1304.36 7
N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	1	6934.26666 7	15885.7 3	14588.0 7	12841.5 3	9943.86 7	10972.5
Metal transporter CNNM4	CNNM4	2	191.266666 7	280.6	276.366 7	226.833 3	216.433 3	187.366 7
Isoform 3 of Coronin-1C	CORO1C	23	8021	18340.9	15648.4	14829	14111.8	13543.7 3

Isoform 2 of Structural maintenance of chromosomes protein 6	SMC6	7	592.333333 3	1180.96 7	1049	954.933 3	863.366 7	851.066 7
Isoform 3 of G patch domain-containing protein 4	GPATCH4	6	628.866666 7	1459.5	1546.7	1180.2	667.9	664.033 3
Regulator of nonsense transcripts 2	UPF2	13	1750	4292.26 7	3599.06 7	3471.2	2903.53 3	3396.13 3
mRNA turnover protein 4 homolog	MRT04	10	1427.13333 3	4090.3	3841.63 3	3308.26 7	2681.13 3	2765.1
cDNA FLJ76308, highly similar to Homo sapiens origin recognition complex, subunit 1-like (yeast) (ORC1L), mRNA	4	219.4	290.3667	241.9	234.866 7	294.533 3	223.566 7	
Polymerase delta-interacting protein 3	POLDIP3	14	3445.76666 7	4593.1	3927.26 7	3715.43 3	3350.36 7	3115.46 7
Retinol dehydrogenase 13	RDH13	6	1317.76666 7	1624.5	1313.03 3	1314.23 3	1344.63 3	1311.6
Arrestin domain-containing protein 1	ARRDC1	1	156.1	289.4	239.733 3	234.133 3	201.033 3	213.033 3
Ribosome biogenesis protein BOP1	BOP1	14	2974.53333 3	4245.9	3990.7	3435.33 3	2493.43 3	2616.8
Proteasome subunit alpha type	PSMA6	18	5810.83333 3	11169.8 3	9204.76 7	9039.83 3	7711.83 3	8208.8
cDNA FLJ38830 fis, clone MESAN1000080, highly similar to ERBB receptor feedback inhibitor 1	11	1283.5	2564.4	1778.9	2075.5	1750.8	1913.73 3	

DDB1- and CUL4-associated factor 13	DCAF13	14	2320.13333 3	4429.36 7	4113.6	3585.03 3	3152.76 7	3231.66 7
Isoform 2 of Dynactin subunit 2	DCTN2	25	5062.03333 3	9288.63 3	7497.83 3	7518.26 7	6578.56 7	6661.66 7
WD repeat-containing protein 54	WDR54	2	255.266666 7	479.733 3	356.8	388.433 3	325.433 3	313.7
cDNA FLJ76467, highly similar to Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA	10	1373.5	3195.933	2899.3	2587.76 7	2358.5	2364.23 3	
Protein argonaute-2	AGO2	6	632.433333 3	1703.23 3	1538.2	1379.26 7	1114.63 3	1230.7
DET1- and DDB1-associated protein 1	DDA1	4	935.933333 3	1706.33 3	1821.26 7	1381.83 3	1150.53 3	1290.13 3
Exocyst complex component 1	EXOC1	8	889	2127.76 7	1857.7	1723.26 7	1481.63 3	1727.6
Probable proline--tRNA ligase, mitochondrial	PARS2	4	483.433333 3	873.8	754.333 3	707.7	726.833 3	660.866 7
Biliverdin reductase A	BLVRA	14	2941.56666 7	7263.93 3	6004.6	5883.26 7	4824.5	5163.4
Isoform 4 of Protein tweety homolog 3	TTYH3	1	50.5666666 7	30.7	32.6333 3	24.8666 7	22.5333 3	22.6333 3
Putative monooxygenase p33MONOX	KIAA1191	3	214.4	247.9	174.766 7	200.8	216.5	184.233 3
KIF1-binding protein	KIF1BP	8	1888.66666 7	2985.4	2890.06 7	2418.2	2076.56 7	2096.3
Macrophage erythroblast attacher	MAEA	4	791.033333 3	1613.56 7	1547.16 7	1307.03 3	1050.73 3	1238.66 7

Ras-related protein Rab-14	RAB14	13	4236.76666 7	7839.8	6754.63 3	6350.63 3	5156.76 7	6118.43 3
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	16	1954.5	4131.13 3	3458.26 7	3346.56 7	3553.16 7	3179.46 7
Zinc finger CCCH domain-containing protein 7B	ZC3H7B	4	374.533333 3	459.166 7	375.666 7	371.966 7	275.233 3	304.7
Platelet-activating factor acetylhydrolase IB subunit beta	PAFAH1B2	3	787.3	1280.33 3	1012.76 7	1037.26 7	1054.56 7	993.266 7
Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1	51	7785.5	16385.0 3	14205.1	13274.6	12513.6	11841.7 7
40S ribosomal protein S15	RPS15	4	1557.26666 7	2802.73 3	2441.46 7	2270.7	1788.13 3	2047.76 7
MO25-like protein		8	1025.23333 3	4032.43 3	3904.73 3	3267	2594.8	2675.76 7
39S ribosomal protein L15, mitochondrial	MRPL15	12	2744.76666 7	4870.66 7	4422.66 7	3946.6	3809.73 3	3428.13 3
Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	PIK3C2A	10	1197.4	2399.16 7	1967.63 3	1944.13 3	1888.2	2078.7
Isoform 2 of Nuclear mitotic apparatus protein 1	NUMA1	1	16427.8666 7	26852.4 3	22152.5	21759.7 3	22215.0 7	21331.4
cDNA FLJ51028, highly similar to 60 kDa heat shock protein, mitochondrial		1	22479.2666 7	28639.67	21919.0 7	23208.3 7	22777.3	23020.1

Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	10	3817	7440.26 7	7844.43 3	6029.33 3	4517.3	4631.9
Synembryn-B	RIC8B	1	321.733333 3	733.066 7	698.533 3	594.066 7	509.366 7	509.9
Exocyst complex component 7	EXOC7	11	1157.86666 7	1943.36 7	1690.06 7	1575	1471	1510.4
cDNA FLJ38538 fis, clone HCHON2001407, highly similar to LanC-like protein 2		5	513.166666 7	980.8	958.333 3	794.9	696.9	747.233 3
tRNA (uracil-5-)-methyltransferase homolog A	TRMT2A	5	246.966666 7	380.533 3	327.033 3	308.433 3	286.133 3	294.1
RNA-binding protein 4	RBM4	2	2239.73333 3	4728.36 7	4370.13 3	3832.56 7	3161	3273.26 7
Wiskott-Aldrich syndrome protein family member 2	WASF2	9	2118.66666 7	3360.4	2733.9	2723.76 7	2779.33 3	2587.16 7
Trinucleotide repeat-containing gene 6B protein	TNRC6B	8	881.366666 7	1826.86 7	1638.8	1480.86 7	1297.16 7	1403.3
Protein transport protein Sec24A	SEC24A	9	1647.73333 3	2747.6	2024.7	2227.23 3	2088.8	2232.13 3
Coiled-coil and C2 domain-containing protein 1A	CC2D1A	15	2127.6	3510.93 3	3021.23 3	2846.43 3	2531.76 7	2711.5
Putative RNA-binding protein Luc7-like 1	LUC7L	9	3275.83333 3	5784.96 7	5488.93 3	4690.16 7	3992.36 7	4476.1
Structural maintenance of chromosomes protein 4	SMC4	49	8478.56666 7	14648.6 3	15903.9	11877.2 3	9126.2	9419.7
Charged multivesicular body protein 2b	CHMP2B	6	1060.86666 7	2085.83 3	1833.1	1691.23 3	1464.46 7	1777.96 7

Trafficking protein particle complex subunit 12	TRAPPC12	5	744.666666 7	1398.86 7	1286.13 3	1134.23 3	1026.33 3	999.4
ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP	2	159.5	448.466 7	358.433 3	363.733 3	366.833 3	333.033 3
Transcription initiation factor IIA subunit 1	GTF2A1	1	126.666666 7	293	267.2	237.666 7	167.566 7	195.666 7
Isoform 2 of Cytochrome c oxidase assembly factor 4 homolog, mitochondrial	COA4	3	573.733333 3	1115.3	982.3	904.7	844.866 7	778.4
Lysophospholipase-like protein 1	LYPLAL1	4	602.1	1175.33 3	1004.03 3	953.433 3	715.6	970.533 3
40S ribosomal protein S13	RPS13	17	5225.43333 3	10323.0 7	9326.9	8374.33 3	6197.43 3	5905.16 7
Autoantigen La (Fragment)	SSB	42	14030.4666 7	25405.3 7	20181.9	20612.5	18115.5 3	18646.4
Reticulon		4	343.366666 7	335.933 3	297.1	272.566 7	246.766 7	277.2
39S ribosomal protein L24, mitochondrial	MRPL24	3	114.066666 7	447.833 3	388.6	363.366 7	333.733 3	314.7
Serine hydroxymethyltransferase, mitochondrial	SHMT2	24	6274.93333 3	12977.5 3	11112.1 3	10530.9	9339.6	9879.46 7
Isoform 2 of Small integral membrane protein 20	SMIM20	1	460.9	600.133 3	537.7	487.033 3	377	379.066 7
Ras-related protein Rab-1B	RAB1B	8	6392.86666 7	13167.8 7	11041.2	10686.6 3	8506.43 3	9710.86 7

Methyl-CpG-binding domain protein 3	MBD3	8	1746.23333 3	2986.8	2644.1	2424	1956.2	1939.96 7
DNA topoisomerase 3-alpha	TOP3A	5	684.033333 3	933.833 3	936.333 3	757.933 3	692.266 7	653.7
DIS3-like exonuclease 2	DIS3L2	10	861.1	2314.5	2108.9	1878.7	1674.66 7	1697.03 3
Craniofacial development protein 1	CFDP1	10	2332.8	3758.03 3	2919.66 7	3050.43 3	2838.7	2934.63 3
Cystatin-B	CSTB	3	1057.9	2154.56 7	1924.06 7	1748.9	1761.9	1791.76 7
Protein FAM91A1	FAM91A1	5	204.166666 7	557.833 3	469.3	452.833 3	430.033 3	424.033 3
Isoform 3 of CLIP-associating protein 2	CLASP2	12	3061.03333 3	5407.03 3	4796.4	4389.3	3903.93 3	3975.16 7
Pyruvate kinase (Fragment)		1	2599.56666 7	2443.96 7	1994.1	1984	2143.63 3	2128.56 7
40S ribosomal protein S26	RPS26	4	2965.53333 3	5071.73 3	4438.83 3	4117.63 3	3437.03 3	3668.26 7
Carnosine N-methyltransferase	CARNMT1	2	127.8	163.066 7	142.9	132.4	116.533 3	142.566 7
PCNA-associated factor	KIAA0101	3	628.9	233.833 3	743.966 7	189.866 7	180.8	171.4
SPFH domain family, member 1, isoform CRA_a	SPFH1	13	3205.93333 3	6795.83 3	6371.13 3	5518.1	5370.83 3	5258.7
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	2	624.3	859.933 3	972.766 7	698.266 7	663.833 3	539.166 7
Tetratricopeptide repeat protein 28	TTC28	3	192.8	543.266 7	478.766 7	441.133 3	407.4	392.3

Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	10	1307.53333 3	3894.53 3	3341.26 7	3162.43 3	2880.46 7	3192.56 7
Coiled-coil domain-containing protein 124	CCDC124	12	4047.56666 7	5637.76 7	4788.16 7	4578.2	3925.23 3	4219.26 7
Rho GTPase activating protein		8	729.1	1377.2	1296.93 3	1118.5	1145.3	1114.43 3
Uncharacterized protein C1orf50	C1orf50	5	384.766666 7	531.5	481	431.666 7	388.3	387.666 7
GPALPP motifs-containing protein 1	GPALPP1	5	585.366666 7	1176.3	948.566 7	955.4	974.766 7	846.433 3
Isoform D of Caspase-10	CASP10	3	65.3	100.133 3	69.7333 3	81.3333 3	71.6333 3	71.9
39S ribosomal protein L9, mitochondrial	MRPL9	8	1116.2	1567.36 7	1484.3	1273.13 3	1090.1	1076.2
Ubiquitin-conjugating enzyme E2 Q1	UBE2Q1	6	1107.06666 7	2871.3	2590.56 7	2332.5	2003.86 7	2032.3
Heat shock cognate 71 kDa protein (Fragment)	HSPA8	1	31069.5333 3	43916.3 7	40298.4 7	35675.8	30935.9	31424.3
Non-specific serine/threonine protein kinase	MARK3	2	638.966666 7	599.733 3	536.566 7	487.2	468.666 7	501.5
cDNA, FLJ95596, highly similar to Homo sapiens activity-dependent neuroprotector (ADNP), mRNA		16	2337.86666 7	4294.333	3736.5	3488.56 7	3420.26 7	3196.73 3
Cullin-5	CUL5	11	1085.63333 3	1817.36 7	1543.63 3	1476.4	1214.43 3	1382.93 3

EWSR1/ATF1 fusion protein type 1	EWSR1/ATF1fusion	1	515.633333 3	1306.9	1082.56 7	1061.8	1017.23 3	973.4
Apoptosis regulatory protein Siva	SIVA1	1	121.233333 3	143.9	154.6	116.933 3	130.633 3	112.666 7
CLIP-associating protein 1	CLASP1	23	3744.2	7873.63 3	6460.33 3	6398.33 3	5772.3	5763.93 3
Nuclear nucleic acid-binding protein C1D	C1D	5	395.766666 7	1160.33 3	1120.93 3	943	805.066 7	820.5
Transcriptional regulator	NIPBL	17	2208.76666 7	3849.33 3	3403.83 3	3128.5	2948.13 3	2814.73 3
PRKR-interacting protein 1	PRKRIP1	2	323.3	1172.2	1128.1	952.8	676.666 7	714.366 7
Nucleic acid dioxygenase ALKBH1	ALKBH1	2	130.666666 7	260.766 7	210.4	211.966 7	201.666 7	204.433 3
60S ribosomal protein L12	RPL12	13	6533.13333 3	9524.86 7	8829.26 7	7743.33 3	6125.9	6756.26 7
Oxidoreductase-like domain-containing protein 1	OXLD1	1	417.666666 7	499.266 7	355.1	405.9	407.233 3	412.666 7
Isoform 3 of V-type proton ATPase 116 kDa subunit a isoform 1	ATP6V0A1	8	749.066666 7	1704.73 3	1487.9	1386	1225.06 7	1278.76 7
Full-length cDNA 5-PRIME end of clone CS0DF013YM24 of Fetal brain of Homo sapiens (Human) variant (Fragment)		9	1664.63333 3	4453.533	3855.63 3	3621.06 7	3434.13 3	3250.83 3
Thymosin beta-10	TMSB10	8	7344.43333 3	24932.5 3	17826.5 3	20274.7 3	20778.8 3	21179.1

Translation initiation factor eIF-2B subunit gamma	EIF2B3	14	2570.96666 7	4575.16 7	4183.6	3720.66 7	3042.03 3	3526.36 7
U6 snRNA-associated Sm-like protein LSM1	LSM1	2	227.9	315.233 3	261.166 7	256.366 7	202.466 7	191.533 3
Proteasome subunit alpha type-2	PSMA2	11	5191.03333 3	8932.16 7	7209.53 3	7264.56 7	5981.93 3	6559.66 7
Echinoderm microtubule associated protein like 3, isoform CRA_e	EML3	6	337.233333 3	662.633 3	554.2	539.033 3	516.3	516.766 7
Glutathione S-transferase pi (Fragment)	GSTP1	1	3040.23333 3	7077.86 7	5695.56 7	5757.76 7	4872.6	5431.46 7
Uridine-cytidine kinase 2	UCK2	7	1125.1	1415.23 3	1904.93 3	1151.3	954.333 3	978.066 7
cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA		1	690.366666 7	1274.7	1240	1037	1009.8	956.133 3
Multifunctional methyltransferase subunit TRM112-like protein	TRMT112	4	521.466666 7	861.033 3	789.833 3	700.5	631.533 3	629
Fumarylacetoacetase	FAH	3	1076.9	1769.8	1480.4	1439.86 7	1472.06 7	1451
Rho guanine nucleotide exchange factor 1	ARHGEF1	19	2378.2	3892.43 3	3176.56 7	3167.16 7	2561	3072.36 7
Muskelin	MKLN1	7	962.2	1284.46 7	1684.63 3	1045.26 7	972.166 7	961.433 3

40S ribosomal protein S18	RPS18	17	7549.36666 7	16613.3	15493.2 7	13520.9 7	10389.2 7	11417.9
BAG family molecular chaperone regulator 3 (Fragment)	BAG3	1	502.266666 7	722.8	665.633 3	588.266 7	528.1	504.233 3
Isoform E of Protein SON	SON	2	4127.56666 7	7316.16 7	6883.13 3	5954.53 3	5335.7	5566.1
Isoform 3 of ATP-dependent 6-phosphofructokinase, muscle type	PFKM	14	2993.36666 7	5370.1	4434.93 3	4370.9	3815.13 3	4221.1
cDNA, FLJ93452, highly similar to Homo sapiens nucleoporin like 2 (NUPL2), mRNA	4	305.766666 7	498.2667	492.033 3	405.566 7	475.566 7	397.066 7	
Ankyrin repeat domain-containing protein 17	ANKRD17	14	3089.23333 3	4860.4	4769.23 3	3956.23 3	3161.86 7	3372.06 7
Spectrin beta chain, non-erythrocytic 1	SPTBN1	7	14366.5666 7	27192.0 7	22856.1	22133.8	19332.3 7	19486.9 7
RNA 3'-terminal phosphate cyclase-like protein	RCL1	6	1195.2	2081.93 3	1839.43 3	1694.73 3	1636.26 7	1592.33 3
Pre-mRNA-splicing factor RBM22	RBM22	13	2559.8	4563.06 7	4095.03 3	3714.7	3376.96 7	3326.16 7
DNA primase		6	527.066666 7	625.966 7	660.666 7	509.666 7	458.733 3	449.833 3
Ras-related protein Rap-2b	RAP2B	12	2383.6	6608.36 7	4958.7	5380.76 7	5631.26 7	5493.16 7
Speckle targeted PIP5K1A-regulated poly(A) polymerase	TUT1	3	182.333333 3	397.1	448.2	323.333 3	285.533 3	281.066 7

X-ray repair cross complementing protein 1 variant (Fragment)		18	3170.43333 3	6159.067	5113.33 3	5015	4907.03 3	4718.4	
WD repeat-containing protein 1 isoform 1 variant (Fragment)		31	7995.43333 3	17550.87	14744.5 7	14291.8 3	12175.3 7	12630.3	
DDB1- and CUL4-associated factor 7	DCAF7		5	586.566666 7	1163.43 3	1153.7	947.466 7	758.866 7	778.366 7
Importin subunit alpha			17	6516.53333 3	7525.9	12847.6	6129.23 3	4739.03 3	4611.96 7
Disco-interacting protein 2 homolog B	DIP2B		8	951.033333 3	1951.9	1845.96 7	1589.96 7	1474.93 3	1344.7
Treacle protein	TCOF1		2	20589.2666 7	31975.8 3	24750.4	26046.7 3	24953.5 7	25112.7 7
AP-3 complex subunit mu-1	AP3M1		9	1526.13333 3	3096.16 7	2657.26 7	2522.1	2115.66 7	2386.8
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	NDUFAF3		4	378.666666 7	727.8	647.633 3	592.966 7	511.133 3	551.3
Zinc finger protein 273	ZNF273		1	384.366666 7	867.466 7	852.166 7	706.766 7	686.8	623.9
Cysteine-rich protein 2	CRIP2		3	658.633333 3	1088.2	919.333 3	886.633 3	941.833 3	810.266 7
Proline-rich protein PRCC	PRCC		7	1188.4	1873.33 3	1632.73 3	1526.4	1568.66 7	1316.83 3
Protein PAT1 homolog 1	PATL1		9	1232.63333 3	2011.96 7	1725.46 7	1639.5	1496.93 3	1629.23 3
Isoform 4 of Mitogen-activated protein kinase 8	MAPK8		4	705.266666 7	1079	1001.7	879.366 7	689.133 3	774.2

Isoform 2 of RNA-binding protein 26	RBM26	17	2669.9	4659.7	3911.86 7	3797.6	3510.46 7	3507.1
Isoform 3 of Cell adhesion molecule 2	CADM2	1	101.1	74.0666 7	69.2666 7	60.3666 7	59.5	58.9
Isoform 2 of 40S ribosomal protein S20	RPS20	8	4394	3988.1	3744.2	3250.43 3	2519.26 7	2795.73 3
Ubiquitin-protein ligase E3A	UBE3A	16	2007.56666 7	5008.53 3	4528.2	4082.66 7	3211.86 7	3423.3
Dual specificity tyrosine-phosphorylation-regulated kinase 1A	DYRK1A	6	644.833333 3	1365.9	1245	1113.43 3	1055.03 3	1089.46 7
ADP-ribosylation factor-binding protein GGA2	GGA2	5	1360.63333 3	1500.2	1229.93 3	1222.93 3	1307.63 3	1177.3
Coiled-coil domain-containing protein 22	CCDC22	9	1412.83333 3	1804.83 3	1563.93 3	1471.33 3	1369.53 3	1427.3
Isoform 5 of Uncharacterized protein C20orf24	C20orf24	1	639.9	808.7	693.233 3	659.3	569.466 7	585.433 3
Isoform A of Arfaptin-1	ARFIP1	1	1322.66666 7	2788.03 3	2413.06 7	2273.03 3	1891.16 7	2152.9
cDNA FLJ78244, highly similar to Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA	14	12837.4666 7	26622.63	26396.6 3	21705.3	14907.9 7	17429.3 3	
26S protease regulatory subunit 6A	PSMC3	26	6902.93333 3	12393.2 7	10943.5 7	10105.1 7	8257.9	9123.36 7
cDNA FLJ55943, highly similar to Death domain-associated protein 6	5	890.266666 7	1184.767	965.266 7	966.033 3	925.666 7	813.4	

Mitochondrial dynamics protein MID51	MIEF1	2	165.033333 3	415.2	363.633 3	338.6	306.633 3	316.266 7
Ribosomal RNA-processing protein 7 homolog A	RRP7A	7	1302.03333 3	2236	2236.66 7	1823.5	1637.83 3	1578.63 3
Apoptotic chromatin condensation inducer in the nucleus	ACIN1	3	7528.4	11708.5	9556.23 3	9548.53 3	9993.23 3	8763.3
Leucine-rich repeat protein SHOC-2	SHOC2	4	550.166666 7	1023.1	866.4	834.433 3	799.366 7	845.966 7
Isoform 4 of Ubiquitin conjugation factor E4 B	UBE4B	8	1007.46666 7	1395.6	1182.83 3	1138.3	1052.63 3	1128.93 3
ATP-binding cassette sub-family F member 3	ABCF3	14	1993.2	4195.6	4089.16 7	3422.16 7	2420.13 3	2819.7
Vezatin	VEZT	3	193.466666 7	444.866 7	358.533 3	362.866 7	380.333 3	337.3
Isoform E of Nuclear factor of activated T-cells 5	NFAT5	6	820.9	2069.6	1933.8	1688.16 7	1557.7	1755.3
Isoform 5 of IST1 homolog	IST1	7	1350.5	2621.56 7	2255.5	2138.7	2097.06 7	2225.06 7
Gem-associated protein 8	GEMIN8	2	506.666666 7	1035.9	950.433 3	845.166 7	742.733 3	834.166 7
Serine/threonine-protein kinase OSR1	OXR1	7	1032.2	2200.56 7	1591.46 7	1795.4	1692.66 7	1779.13 3
Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 4	MAP2K4	6	533.133333 3	1211.83 3	1070.4	988.766 7	1005.43 3	954.433 3
Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 10	USP10	22	4092.76666 7	6698.06 7	6546.7	5465.53 3	4522.03 3	4487.7

cDNA FLJ60094, highly similar to F-actin capping protein subunit beta		25	9392.23333 3	20653.47	17020.0 7	16853.7	14403.4	15243.3 3	
cDNA FLJ75478, highly similar to Homo sapiens splicing factor 4 (SF4), transcript variant a, mRNA		15	2102.93333 3	3378.267	3166.43 3	2756.8	2462.96 7	2436.5	
Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP		11	1981.76666 7	3223.06 7	3166.16 7	2630.43 3	2081.2	2292.3
UPF0461 protein C5orf24	C5orf24		1	142.5	178.566 7	146.933 3	145.733 3	141.866 7	121.633 3
Serine/threonine-protein phosphatase 5	PPP5C		16	3819.16666 7	7599.4	6499.33 3	6202.43 3	5586.16 7	5644.63 3
Pyruvate kinase PKM	PKM		7	50932.5	78832.4 7	63651.1 3	64342.7 7	57277.8	61416.7 7
E1A-binding protein p400	EP400		17	2165.43333 3	2390.9	2143.2	1951.5	1687.13 3	1670.66 7
Isoform 2 of UPF0488 protein C8orf33	C8orf33		6	1440	2117.86 7	1816.13 3	1728.76 7	1540	1633.36 7
Zinc finger protein 280C	ZNF280C		12	1453.03333 3	2689.73 3	2630.2	2195.83 3	1857.33 3	1825.4
Isoform 4 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	PPP2R5C		1	877	2012	2029.63 3	1642.76 7	1257.8	1236.63 3
Isoform 2 of Transcription elongation factor SPT5	SUPT5H		21	3395.3	6193.26 7	5523.3	5056.83 3	4586.46 7	4698.96 7

Eukaryotic translation initiation factor 3 subunit J	EIF3J	14	3031.96666 7	4835.46 7	4225.66 7	3948.23 3	3086.63 3	3450.16 7
p21-activated protein kinase-interacting protein 1	PAK1IP1	9	1133.06666 7	2681.5	2488.56 7	2189.5	1812.36 7	1914.86 7
26S protease regulatory subunit 8	PSMC5	25	6769.93333 3	12810.2 3	11642.9 7	10460.1	8904.7	9586.16 7
BUD13 homolog	BUD13	6	706.5	1370.93 3	1255.33 3	1119.46 7	1053.13 3	1107.56 7
Isoform 3 of Histone-lysine N-methyltransferase 2A	KMT2A	11	868.333333 3	1619.5	1605.76 7	1322.5	1278.96 7	1306.7
Vacuolar protein sorting-associated protein 8 homolog	VPS8	2	178.766666 7	256.333 3	209.866 7	209.333 3	209.4	204.833 3
Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	26	6248.7	12486.6	11354.5 3	10197.3 7	7690.93 3	8953.06 7
Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	21	3392.1	6399.26 7	5804.9	5226.1	4241.43 3	4695.4
Sorting nexin-18	SNX18	3	699.5	994.566 7	861.7	812.3	763.1	794.333 3
CLE		14	3832.26666 7	8409.16 7	8101.53 3	6868.5	5378.36 7	5626.13 3
Annexin		12	2400.03333 3	4660.46 7	3950.3	3806.8	2771.03 3	3573.53 3
Homer homolog 3 (Drosophila), isoform CRA_b	HOMER3	7	753.966666 7	2085.3	1966.26 7	1703.36 7	1326.7	1207.33 3
DNA-directed RNA polymerases I and III subunit RPAC2	POLR1D	1	99.6333333 3	169.266 7	158.533 3	138.266 7	127.6	149.366 7
Bridging integrator 3 variant (Fragment)		4	854.7	1188.73 3	948.2	971.133 3	904.033 3	894.1

Signal peptidase complex subunit 1	SPCS1	1	151.133333 3	663.533 3	573.533 3	542.1	409.566 7	467.5
Iron-sulfur cluster assembly 2 homolog, mitochondrial	ISCA2	3	479.766666 7	567.566 7	465.533 3	463.7	436.333 3	454.366 7
Protein SCAF8	SCAF8	12	1584.53333 3	2772.1	2619.6	2264.86 7	2139.23 3	2005.66 7
Serine/threonine-protein phosphatase 4 regulatory subunit 2	PPP4R2	9	975.533333 3	1309.7	1268.1	1070.13 3	974.733 3	897.666 7
Isoform 2 of TBC1 domain family member 5	TBC1D5	9	1250.96666 7	2523.4	2437.3	2061.96 7	1622.7	1872.5
ATPase family AAA domain-containing protein 1	ATAD1	9	1186.96666 7	2349.93 3	1973.26 7	1920.23 3	1726.06 7	1773.43 3
ATP-dependent RNA helicase DDX3X	DDX3X	37	10678.3666 7	19060.2	18413.9 3	15576.5 3	11854.7 7	12570.1 3
Protein HGH1 homolog	HGH1	7	1229.03333 3	1781.3	1772.76 7	1455.8	1372.3	1317.1
LisH domain-containing protein ARMC9	ARMC9	4	224.166666 7	561.7	481.733 3	459.1	368.633 3	438.9
E3 SUMO-protein ligase PIAS2	PIAS2	5	434.9	854.833 3	675.2	698.733 3	603.8	605.733 3
Isoform 4 of Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	AGAP3	1	696.6	1273.2	1150.86 7	1040.73 3	909.033 3	931.933 3
Thyroid hormone receptor-associated protein 3	THRAP3	25	7623.9	13869.9	11351.6 7	11338.3	10714.6 3	10130.1 7
Chromosome-associated kinesin KIF4A	KIF4A	41	7427.8	11501.1 3	13398.0 7	9402.13 3	7216.13 3	6577.2

cDNA FLJ54776, highly similar to Cell division control protein 42 homolog		11	3779.86666 7	6385.267	6219.16 7	5220	4108.9	4499.1	
cDNA FLJ56420, highly similar to Aspartyl aminopeptidase (EC 3.4.11.21)		12	1470.43333 3	2814	2160.86 7	2300.56 7	2167.73 3	2202.2	
cDNA FLJ75097, highly similar to Homo sapiens upstream binding protein 1 (LBP-1a) (UBP1), mRNA		3	608.766666 7	1082.233	877.3	884.8	745	799.766 7	
Methionine synthase reductase	MTRR		7	584.333333 3	1564.6	1474.5	1279.2	1026.6	1112.73 3
PHD and RING finger domain-containing protein 1	PHRF1		3	539.066666 7	1190.36 7	1070.1	973.233 3	976.533 3	904.5
Kinetochore protein NDC80 homolog	NDC80		18	3005.23333 3	4587.66 7	5885.23 3	3750.86 7	2774.16 7	2823.83 3
Isoform Gamma-1 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	PPP2R5C		1	590.066666 7	1550.26 7	1455.3	1267.53 3	973.933 3	1012.66 7
Syntaxin-4	STX4		3	384.7	736.966 7	607.2	602.6	697.433 3	621.3
Sideroflexin-1	SFXN1		12	2929.6	5071.56 7	4169.3	4147.03 3	4214.23 3	3987.16 7
Uncharacterized protein C1orf198	C1orf198		3	851.066666 7	1335.06 7	1138.26 7	1091.7	1170.13 3	1103.7

Isoform Crk-I of Adapter molecule crk	CRK	1	2831.5	5437.36 7	4681	4446.4	3790.66 7	4203.63 3
Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	15	2213.5	4870.1	4221.03 3	3982.66 7	3682.36 7	3592.36 7
Pogo transposable element with ZNF domain	POGZ	15	2042.46666 7	3811.66 7	3216.36 7	3117.23 3	2598.53 3	2734.93 3
HEBP2 protein (Fragment)	HEBP2	5	440.833333 3	1903.7	1735.5	1556.9	1200.93 3	1327.63 3
General transcription factor 3C polypeptide 5	GTF3C5	6	536.8	1037.86 7	953.7	848.8	695.766 7	653.866 7
Serine--tRNA ligase, mitochondrial	SARS2	10	1859.96666 7	3440.13 3	2956.8	2813.6	2811.1	2775.43 3
Wolframin	WFS1	3	479.133333 3	914.766 7	894.133 3	748.166 7	731.266 7	647.433 3
Ribosomal protein S6 kinase	RPS6KB2	3	783.033333 3	1082.06 7	879.733 3	885.033 3	837.6	853.7
DEAD box polypeptide 17 isoform p82 variant (Fragment)		29	10646.6333 3	19984.53	18989.0 7	16346.7 7	15347.0 7	14642.9 7
Serine/threonine-protein kinase TAO1	TAOK1	11	1149.46666 7	2386.7	2053.23 3	1952.33 3	1825.4	1998.43 3
RcNSEP1 (Fragment)		1	4280.5	6996.96 7	6583.43 3	5723.76 7	3932.03 3	5070.26 7
ARF GTPase-activating protein GIT2	GIT2	3	1347.26666 7	2322.7	2138.96 7	1900.23 3	1576.86 7	1680.06 7
Cyclin-dependent kinase 11B	CDK11B	20	2750.53333 3	6508.93 3	6039.9	5325.83 3	4410.06 7	4011.16 7

DNA polymerase alpha subunit B	POLA2	8	1445.73333 3	2581.46 7	2619.03 3	2112.43 3	1764.2	1803.4
POTE ankyrin domain family member F	POTEF	2	14715.9	25654.8	20200.4 3	20994.5 7	19083.7 7	19290.1 7
T-complex protein 1 subunit delta	CCT4	34	16040.4	26243.7 3	23960.6 7	21477.4 7	16661.7 3	19531.0 7
DNA-directed RNA polymerase III subunit RPC4	POLR3D	1	146.766666 7	349.5	399.033 3	286.033 3	233.9	208.766 7
Protein ABHD14B	ABHD14B	4	263.6	336.133 3	267.8	275.1	286.7	276.833 3
Protein odr-4 homolog	ODR4	4	320.833333 3	459.5	343.066 7	376.066 7	318.266 7	320.966 7
cDNA FLJ76940, highly similar to Homo sapiens ubiquitin specific peptidase 8 (USP8), mRNA	17	1608.4	3805.2	3461.46 7	3114.36 7	2487.76 7	2827.56 7	
Eukaryotic translation initiation factor 3 subunit H	EIF3H	16	3746.9	5544.6	5292.93 3	4538.03 3	3426.03 3	3824
cDNA FLJ76176, highly similar to Homo sapiens carnitine deficiency-associated, expressed in ventricle 1 (CDV1), transcript variant 1, mRNA	4	478.066666 7	798.3667	694.3	653.466 7	632.233 3	680.233 3	
Isoform 2 of Spectrin beta chain, non-erythrocytic 1	SPTBN1	1	13633.9	25795.5 3	21653.0 3	21116.5	18470.3 3	18610.0 3
Protein phosphatase inhibitor 2	PPP1R2	7	1162.53333 3	1989.86 7	1577.26 7	1628.93 3	1610.16 7	1658.13 3

Rab11 family-interacting protein 5	RAB11FIP5	5	192.9	384.3	310.566 7	314.6	369.766 7	322.133 3
THO complex subunit 4	ALYREF	8	2590.63333 3	3300.5	2736.8	2701.96 7	2431.83 3	2520.56 7
Transmembrane 9 superfamily member 2	TM9SF2	4	317.233333 3	868.466 7	825.8	711	497.833 3	431.866 7
COMM domain-containing protein 8	COMMD8	3	243	634.533 3	612.366 7	519.5	434.133 3	453.966 7
Sodium/myo-inositol cotransporter	SLC5A3	4	564.866666 7	1111.63 3	1209.56 7	910.233 3	711.866 7	915
MIP18 family protein FAM96A	FAM96A	2	302.933333 3	415.033 3	353.3	339.9	302.866 7	296.5
Exonuclease 3'-5' domain-containing protein 2	EXD2	1	1033.76666 7	1697.76 7	1394.7	1390.5	1360.13 3	1410.56 7
Serine palmitoyltransferase 1	SPTLC1	12	1833.9	3800.7	3507.53 3	3112.93 3	2990.83 3	2801.8
cDNA FLJ75279, highly similar to Homo sapiens elongation factor RNA polymerase II (ELL), mRNA		3	175.033333 3	311.3333	303.666 7	255	259.3	246.766 7
Isoform b of Ataxin-7	ATXN7	2	151.7	215.2	192.466 7	176.266 7	213.233 3	232.933 3
Peroxiredoxin-1	PRDX1	22	26290.4333 3	60512.9 3	43766.7 3	49565.8 7	43120.6	49071.1 7
Omega-amidase NIT2	NIT2	14	2969.83333 3	5617.1	4405.06 7	4601.06 7	4099.73 3	4366.9
cDNA FLJ78528, highly similar to Homo sapiens vacuolar		9	1558.6	2592.1	2269.23 3	2123.43 3	1764.16 7	1938.9

protein sorting 4B (yeast) (VPS4B), mRNA								
Probable ATP-dependent RNA helicase DHX34	DHX34	2	109.7	289.1	333.1	236.833 3	174.466 7	205.033 3
Isoform 2 of Epidermal growth factor receptor substrate 15-like 1	EPS15L1	19	3377.7	5025.63 3	4278.7	4117.16 7	3812.16 7	3972.1
cDNA, FLJ93976, highly similar to Homo sapiens COP9 homolog (COP9), mRNA	5	1019.76666 7	1546.967	1345.53 3	1267.33 3	1074.06 7	1171.26 7	
Eukaryotic translation initiation factor 3 subunit E	EIF3E	15	3496.2	8934.73 3	8529.16 7	7320.03 3	5328.23 3	5912.36 7
DNA-directed RNA polymerase II subunit RPB2	POLR2B	22	4146.03333 3	8656.86 7	7857.13 3	7092.46 7	6648.73 3	6556.13 3
UPF0489 protein C5orf22	C5orf22	5	309.333333 3	633	620.633 3	518.666 7	464.733 3	516.866 7
Condensin complex subunit 2		11	2512.43333 3	4956.1	4680.16 7	4061.23 3	3267.6	3296.36 7
tRNA-dihydrouridine(20) synthase [NAD(P)+]-like	DUS2	6	1012.2	1789.03 3	1745.03 3	1466.13 3	1148.33 3	1168
OTU domain-containing protein 4	OTUD4	6	674.4	970.333 3	830.1	795.2	760.066 7	813.966 7
40S ribosomal protein S3a	RPS3A	28	13651.4666 7	28903.5 3	26969.3	23687.3 3	18151.7	19685
Heat shock protein 105 kDa	HSPH1	54	23458.4333 3	38344.5 7	33894.6	31430.8 3	24779.7	25549.7 7
Nucleolar transcription factor 1	UBTF	22	3598.03333 3	6999.6	6868.96 7	5737.9	5151.2	4948.5

26S protease regulatory subunit 4	PSMC1	30	10061.5	18573.4	17243	15226.9 3	11255.7	12354
E3 ubiquitin-protein ligase RNF25	RNF25	4	266.633333 3	371.066 7	340.933 3	304.233 3	265.5	271.233 3
Signal recognition particle subunit SRP68	SRP68	22	4892.16666 7	10912.0 7	9452.4	8947.26 7	7034.26 7	7897.2
Sterile alpha and TIR motif-containing protein 1	SARM1	2	105.433333 3	164.833 3	148.866 7	135.166 7	138.066 7	139.166 7
Nuclear pore complex protein Nup50	NUP50	20	3910.46666 7	5764.6	5546.36 7	4727.4	4105.93 3	3842
Pumilio homolog 1	PUM1	11	2703.16666 7	4627.7	4465.46 7	3795.3	3092.1	3251.03 3
ATP synthase subunit a	ATP6	1	400.266666 7	717	819.966 7	588.033 3	587.366 7	544.4
ADP-ribosylation factor-like protein 1	ARL1	4	315.066666 7	898.066 7	766.166 7	736.566 7	555.833 3	744
Replication factor C subunit 1	RFC1	18	3237.56666 7	4829.7	4739.23 3	3961.26 7	3535.06 7	3252.83 3
cDNA, FLJ96709, highly similar to Homo sapiens glutamate rich WD repeat protein GRWD (GRWD), mRNA	8	1771.8	3256.3	3165.46 7	2671	1927.83 3	2083.76 7	
Isoform 3 of Drebrin	DBN1	26	6071.23333 3	11329.5 7	9820.3	9293.8	7997.6	7570.2
cDNA FLJ78298		1	1007	1653.96 7	1362.63 3	1356.9	1320	1364.7
High-mobility group box 2		1	10933.7333 3	19157.5 3	14266.8 3	15716.7 3	14253.2	14202.1

Cell division cycle protein 23 homolog	CDC23	5	679.6	1104.83 3	1046.66 7	906.466 7	816.1	878.166 7
Ubiquitin carboxyl-terminal hydrolase 47	USP47	18	3114.9	5199.53 3	4768.2	4266.16 7	3905.7	4064.73 3
Transmembrane and TPR repeat-containing protein 3	TMTC3	5	415.3	778.933 3	726.2	639.133 3	611.666 7	602.6
Bifunctional glutamate/proline-tRNA ligase	EPRS	91	21930.9333 3	45658.4	35886.9	37464.6	30764.7	36583.1
Transcriptional activator protein Pur-alpha	PURA	5	1040.53333 3	1803.56 7	1680.96 7	1480	1441.76 7	1529.96 7
cDNA FLJ13654 fis, clone PLACE1011477, highly similar to Sorting nexin-2		15	4521.96666 7	10574.8	8493.9	8677.7	7449.06 7	8347.73 3
Profilin-1	PFN1	18	22919.4333 3	39662.8	30755.0 7	32550.0 3	26544.1 7	30920.9 3
Isoform 2 of Ubiquitin conjugation factor E4 A	UBE4A	7	723.133333 3	1716.96 7	1535.5	1409.06 7	1093.96 7	1262.43 3
Protein MAK16 homolog	MAK16	8	1405.1	2932.33 3	2703.03 3	2406.6	1963.63 3	1937.43 3
Hamartin	TSC1	2	154.9	180.366 7	130.833 3	148.033 3	147.7	151.466 7
High mobility group protein B2	HMGB2	1	10995.3333 3	19193.6 3	14330.2 7	15754.2	14260.4 7	14212.2 7
Ankyrin repeat and zinc finger domain-containing protein 1	ANKZF1	20	2394.36666 7	4428.46 7	2879.6	3635.03 3	3421.93 3	3581.03 3
Emerin	EMD	9	1693.66666 7	3281.43 3	2577.96 7	2693.53 3	2565.3	2597.66 7

Isoform 2 of Protein SOGA1	SOGA1	17	1742.36666 7	1991.96 7	2241.9	1635.16 7	1313.5	1415.26 7
Cellular tumor antigen p53 (Fragment)	TP53	1	312.233333 3	1097.43 3	893.533 3	900.933 3	612.833 3	886.366 7
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	2	360.5	770.633 3	713.566 7	632.7	512.933 3	483.066 7
cDNA FLJ76436		15	5270.7	9711.53 3	7787.3	7974.16 7	6951.1	7862.7
cDNA FLJ77502		2	463.433333 3	719.533 3	569.2	590.833 3	558.933 3	571.066 7
Isoform 2 of Serine/threonine-protein kinase 3	STK3	7	1596.13333 3	2863.06 7	2786.5	2351.03 3	1998.56 7	2098.8
Proliferation-associated protein 2G4	PA2G4	23	8607.73333 3	20526.1	18552.7 7	16855.2 7	12717.8 7	14744.8 7
Minor histocompatibility antigen H13	HM13	8	1282.63333 3	3737.23 3	3398.66 7	3068.9	2594.26 7	2817.36 7
TSC22 domain family protein 2	TSC22D2	3	382.1	864.8	723.4	710.166 7	645.2	594.166 7
Small nuclear ribonucleoprotein F	SNRPF	3	1127.73333 3	1707.5	1479.43 3	1402.2	1215	1249.7
Spindlin-1	SPIN1	3	515.933333 3	1054.3	927.533 3	865.866 7	835.3	758.766 7
cDNA, FLJ96179, highly similar to Homo sapiens glucocorticoid modulatory element binding protein 1 (GMEB1), transcript variant 1, mRNA		2	469.8	738.1	647.066 7	606.2	633.1	544.666 7

Histone deacetylase 8	HDAC8	2	115.733333 3	211.733 3	174	173.9	138.433 3	170.7
Isoform 2 of Protein FAM98B	FAM98B	8	1496.46666 7	2564.43 3	2360.9	2106.3	1889.56 7	1959.66 7
FERM, RhoGEF and pleckstrin domain-containing protein 2	FARP2	2	450.533333 3	771.433 3	693.366 7	633.633 3	604.166 7	550.133 3
E3 ubiquitin-protein ligase RBBP6	RBBP6	31	3055.26666 7	6401.2	5570.23 3	5258.76 7	5291.5	5128.1
Anaphase-promoting complex subunit 5	ANAPC5	6	966.033333 3	1428.4	1285.56 7	1173.56 7	1028.33 3	1039.16 7
26S protease regulatory subunit 6B	PSMC4	22	4880.66666 7	10079.1	9077.4	8281.46 7	6547.36 7	7181.66 7
ArfGAP with FG repeats 1 isoform 2 (Fragment)	AGFG1	6	641.966666 7	1732.1	1622.1	1423.2	1128.96 7	1205.9
Isoform 4 of Treacle protein	TCOF1	8	22991.7666 7	35434.7	27920.8	29120.9 7	27597.1 3	27828.7
TOM1-like protein 1	TOM1L1	1	169.333333 3	202.8	188.533 3	166.666 7	100.933 3	159.766 7
Isoform 4 of Kinesin-like protein KIF2A	KIF2A	9	1491.2	2719.43 3	2442.13 3	2235.06 7	1859.7	1783.4
Splicing factor U2AF 35 kDa subunit-like protein	U2AF1L5	6	2150.43333 3	4162.76 7	3799.1	3421.36 7	2870.7	2976.9
Mitochondrial fission factor	MFF	4	522.633333 3	878.6	728.6	722.133 3	606.833 3	628.066 7
Glutathione S-transferase P	GSTP1	11	8776.06666 7	16718.9 7	13697.6 7	13742.1 3	12209.2	12916
Isoform 6 of POU domain, class 2, transcription factor 1	POU2F1	3	680.733333 3	1478.03 3	1276.1	1214.93 3	1159.66 7	1119.33 3

Histone H1.2	HIST1H1C	11	33003.6	30681.1 7	26039.2	25219.8 3	24226.1	25056.0 3
Isoform 2 of Nuclear protein localization protein 4 homolog	NPLOC4	16	3416.46666 7	6630.23 3	6366.83 3	5450.16 7	4440.56 7	4860.3
Putative RNA-binding protein Luc7-like 2	LUC7L2	16	7347	12882.0 7	11701.1 3	10589.6 7	8556.16 7	9615.13 3
Zinc finger protein 732	ZNF732	1	375.533333 3	744.3	767.266 7	611.866 7	568.933 3	513.466 7
CGG triplet repeat-binding protein 1	CGGBP1	5	990	1603.46 7	1514.66 7	1318.2	1132.66 7	1187.8
Helicase, lymphoid-specific, isoform CRA_b	HELLS	8	1915.86666 7	1812.2	3120.5	1489.9	1022.26 7	1094.83 3
rRNA-processing protein FCF1 homolog	FCF1	4	598.366666 7	1657.23 3	1410.13 3	1362.5	1258.73 3	1415.13 3
High mobility group protein 20A	HMG20A	4	306.866666 7	398.533 3	325.166 7	327.666 7	319.666 7	357.1
Autophagy-related protein 16-1	ATG16L1	9	1052.96666 7	1647.26 7	1478.3	1354.36 7	1200.93 3	1260.13 3
Charged multivesicular body protein 3	CHMP3	5	385.333333 3	1225.2	1106.8	1007.36 7	850.5	863
DKFZP586J0619 protein	DKFZP586J0619	16	1754.63333 3	2381.8	2209.06 7	1958.36 7	1868.33 3	1877.3
Ubiquitin-fold modifier 1	UFM1	4	509.833333 3	788.066 7	572.066 7	648	490.7	734.3
cDNA FLJ39026 fis, clone NT2RP7005675	6	520.3	1106.067	927.1	909.5	720.433 3	715.3	
H/ACA ribonucleoprotein complex subunit 2	NHP2	7	2169.66666 7	3504.63 3	3130	2882.1	2754.86 7	2626.3

Zinc finger, UBR1 type 1, isoform CRA_c	ZUBR1	1	3367	8499.83 3	7178.9	6990.13 3	5426.5	6456.03 3
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	11	1945.26666 7	3451.5	3160.1	2838.7	2275.33 3	2284.76 7
Nucleolar pre-ribosomal-associated protein 1	URB1	13	1583.86666 7	2137.06 7	2110.86 7	1757.7	1486.7	1543.63 3
60S ribosomal protein L3	RPL3	27	11297.7666 7	26482.1	22626.3 7	21784.3	14974.1 3	17850.0 7
Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	6	816.066666 7	1166.23 3	981.133 3	959.4	926.366 7	948.533 3
CDK-activating kinase assembly factor MAT1	MNAT1	9	845.433333 3	1657.06 7	1508.33 3	1363.2	1274.56 7	1246.4
Pyruvate kinase (Fragment)	PKM	3	43868.5666 7	67228.4 3	54257.6 3	55308.6 7	49759.5 3	52902.5 3
Eukaryotic translation initiation factor 3 subunit C	EIF3C	28	6193.56666 7	13557	13168.9 3	11153.6	7647.03 3	8885.53 3
DNA-3-methyladenine glycosylase	MPG	8	1561.56666 7	3141.73 3	2695.7	2584.76 7	2071.76 7	2101.26 7
BCR/ABL fusion protein isoform X3	BCR/ABLfusion	4	689	1072.2	911.3	882.133 3	812.1	859.366 7
Isoform 4 of Breast carcinoma-amplified sequence 3	BCAS3	4	586.433333 3	1010.83 3	907.3	831.766 7	827.166 7	839.133 3
Talin-1	TLN1	94	25184.0666 7	40104.2	30504.1 3	32999.9	30551.2 7	34613.9
Mitogen-activated protein kinase 14	MAPK14	7	376.266666 7	507.466 7	474.9	417.7	347.833 3	355.966 7

40S ribosomal protein S17	RPS17	12	5632.2	8348.53 3	7657.16 7	6871.9	5459.3	5799.06 7
cDNA FLJ77796, highly similar to Homo sapiens evolutionarily conserved G-patch domain containing protein mRNA	6	316.366666 7	776.2667	691.2	638.966 7	604.366 7	575.2	
Isoform 2 of FTS and Hook-interacting protein	FAM160A2	2	175.7	212.8	171.166 7	175.166 7	184.6	175.6
Activating signal cointegrator 1 complex subunit 2	ASCC2	3	157.333333 3	335.233 3	307.533 3	275.966 7	239.4	252.066 7
cDNA, FLJ96406, highly similar to Homo sapiens NOL1/NOP2/Sun domain family, member 5 (NSUN5), transcript variant 1, mRNA	22	2682.56666 7	4421.433	4327.7	3640.1	2765.33 3	3027.5	
Heat shock factor protein 1	HSF1	4	295.1	420.366 7	356.666 7	346.1	334.233 3	328.5
Sarcolemmal membrane-associated protein	SLMAP	10	1662.2	3056.9	2653.06 7	2516.96 7	2519.46 7	2450.96 7
Isoform 5 of Cell growth regulator with EF hand domain protein 1	CGREF1	3	98.4	316.9	247.366 7	260.966 7	225.5	232.133 3
Probable threonine--tRNA ligase 2, cytoplasmic	TARSL2	2	688.066666 7	1011.53 3	842.466 7	833.1	838.7	887.066 7
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	9	1172.96666 7	2279.5	1920.56 7	1877.5	1729.86 7	1710.7

cDNA FLJ16777 fis, clone BRHIP2029567, highly similar to Cell division cycle 5-like protein		32	6138.7	10392.63	9107.63 3	8560.96 7	8089.4	7740.06 7	
ADP-ribosylation factor-like protein 8A	ARL8A	1	627.766666 7	1570.23 3	1410.46 7	1293.53 3	1167.33 3	1107.1	
G-rich sequence factor 1	GRSF1	11	1846.06666 7	2449	2544.43 3	2017.46 7	1636.33 3	1541.66 7	
Mediator of RNA polymerase II transcription subunit 27	MED27	3	451.666666 7	1161.7	1250.06 7	957	814.4	758.9	
Kinesin-1 heavy chain	KIF5B	52	13099.1333 3	20093.3	18485.8 3	16555.9	13278.1 3	13504.8 3	
Mitotic checkpoint protein BUB3	BUB3	12	4008.06666 7	6409.33 3	6092	5281.03 3	4553.93 3	4481.33 3	
Small subunit processome component 20 homolog	UTP20	33	4319.66666 7	7834.6	7408.73 3	6455.73 3	5441.26 7	5923.06 7	
Transcription activator BRG1	SMARCA4	8	1861.73333 3	2953.9	2784.26 7	2434.16 7	2278.96 7	2142.1	
Mitogen-activated protein kinase kinase kinase	MAP4K5	7	1046.2	1930.83 3	1628.26 7	1591.13 3	1359.73 3	1274.13 3	
Superkiller viralicidic activity 2-like 2	SKIV2L2	28	4092.86666 7	8151	8556.33 3	6717.3	5174.93 3	5410.23 3	
tRNA (guanine(37)-N1)-methyltransferase	TRMT5	7	1034.8	1751.23 3	1482.86 7	1443.3	1393.73 3	1401.16 7	
Sulfhydryl oxidase 2	QSOX2	8	702.4	2076.9	2286.26 7	1711.73 3	1597.83 3	1440.86 7	
DNA/RNA-binding protein KIN17	KIN	4	462.866666 7	1043.1	1042.46 7	859.7	669.033 3	696.566 7	

Vasodilator-stimulated phosphoprotein isoform 4 (Fragment)	VASP	1	3483.4	7933.2	6523.93 3	6539.43 3	5652.33 3	5835.5
Coiled-coil domain-containing protein 9	CCDC9	3	543.733333 3	1740.66 7	1396.56 7	1434.96 7	1197.33 3	1285.46 7
Arginine--tRNA ligase, cytoplasmic	RARS	44	7841.16666 7	17010.4	15079.2	14023.1 7	11908.9 7	13225.0 7
Isoform 3 of Exocyst complex component 3	EXOC3	8	998.666666 7	2163.53 3	1916.23 3	1783.6	1520.56 7	1680.1
von Hippel-Lindau binding protein 1, isoform CRA_b	VBP1	10	3185.56666 7	5865.93 3	5175.56 7	4836.1	3910.2	4405.83 3
cDNA FLJ77399, highly similar to Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 2, 150kDa (CRSP2), mRNA		4	650.333333 3	1332	1332.76 7	1098.16 7	937.566 7	960.833 3
Mitochondrial import receptor subunit TOM70	TOMM70	24	4194.33333 3	9170.73 3	8170.7	7561.3	6716.13 3	7019.76 7
Golgi autoantigen, golgin subfamily a, 1, isoform CRA_a	GOLGA1	11	559.533333 3	1402.6	1133.76 7	1156.5	1399.96 7	1046.93 3
Bystin	BYSL	10	1443.5	2586.23 3	2562	2132.46 7	1586.7	1685.4
Histone H2B type 2-E	HIST2H2BE	0	16121.6666 7	17067.6	13256.6	14074.8 7	15230.6 3	11581.0 3
Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	12	1230.5	2267.4	1982.86 7	1869.86 7	1640.4	1974.66 7

Tyrosine-protein kinase JAK1	JAK1	1	210.866666 7	288.833 3	273.4	238.2	236.833 3	242.9
Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	8	1404.3	3846.23 3	3162.63 3	3172	2940.7	3080.3
60S ribosomal protein L36	RPL36	8	2497.36666 7	4714.36 7	4235.03 3	3888.03 3	3166.1	3423.16 7
MAP kinase-activated protein kinase 2	MAPKAPK2	6	609.233333 3	850.266 7	779.633 3	701.233 3	693.433 3	710
Zinc finger protein 24 (KOX 17), isoform CRA_b	ZNF24	1	294.233333 3	433.833 3	400.166 7	357.8	308.933 3	295.8
cDNA, FLJ92910, highly similar to Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 1, mRNA		12	1046.3	2505.033	1432.23 3	2066.16 7	1847.66 7	2317.76 7
Isoform 2 of Gephyrin	GPHN	8	1860.76666 7	3614.56 7	3404.86 7	2981.83 3	2401.33 3	2706.7
cDNA FLJ76216, highly similar to Homo sapiens xeroderma pigmentosum, complementation group C (XPC), mRNA		5	468.133333 3	955.0333	787.933 3	787.866 7	735.833 3	769
Pumilio homolog 2	PUM2	3	1214.73333 3	2144.53 3	2085.4	1769.3	1425.4	1509.8
ATP-dependent DNA helicase Q1	RECQL	30	6613.43333 3	15315	13499.3	12636	9903.8	11126.8

Histone H2B type 1-B	HIST1H2BB	1	15501.9	17248.8 7	13441.5 3	14232.1 7	15434.4 3	11848
Zinc finger protein 330 variant (Fragment)		2	1387.16666 7	1284.1	1245.6	1059.6	865.1	900.133 3
Isoform 2 of Protein ELYS	AHCTF1	35	6894.03333 3	11199.6	10950.5 7	9242.43 3	8568.56 7	8555.36 7
ATP-dependent RNA helicase DHX36	DHX36	16	2455.7	4437.66 7	4421.56 7	3662.2	2892.7	3119.46 7
DCN1-like protein 5	DCUN1D5	4	1588.6	2877.23 3	2635.3	2374.63 3	1798.2	1896.46 7
Serine/threonine-protein kinase 25 (Fragment)	STK25	2	2156.23333 3	3655.03 3	3376.3	3016.56 7	2407.36 7	2554.3
Exocyst complex component 8	EXOC8	10	1498.63333 3	2865.73 3	2436.56 7	2365.2	2169.46 7	2327.73 3
Adenylosuccinate synthetase isozyme 2	ADSS	14	3283.46666 7	5089.13 3	4904.93 3	4200.6	3216.6	3404.83 3
Diphosphomevalonate decarboxylase	MVD	5	750.4	1622.46 7	1486.7	1339.33 3	1165.96 7	1363.7
Isoform USP25m of Ubiquitin carboxyl-terminal hydrolase 25	USP25	3	98.3333333 3	193.333 3	157.966 7	159.6	140.266 7	146.966 7
Cx9C motif-containing protein 4	CMC4	4	717.266666 7	1157.76 7	986.2	955.766 7	1142.83 3	1033.46 7
cDNA, FLJ96901, highly similar to Homo sapiens Rac GTPase activating protein 1 (RACGAP1), mRNA		8	1626.56666 7	2188.033	2812.46 7	1806.43 3	1356.56 7	1328.8
E3 ubiquitin-protein ligase HUWE1	HUWE1	46	5962.06666 7	12024.2 3	10034.7 3	9928.16 7	8267.2	9588.1

Tumor necrosis factor receptor type 1-associated DEATH domain protein	TRADD	5	555.633333 3	1163.93 3	881.633 3	961.166 7	955.5	1068.93 3
Isoform 13 of Protein kinase C-binding protein 1	ZMYND8	13	1397.86666 7	2097.76 7	1704.66 7	1732.33 3	1541.56 7	1473
p53 and DNA damage-regulated protein 1	PDRG1	2	291.2	533.666 7	457.833 3	440.733 3	368.866 7	360.333 3
Isoform 2 of N-acetyl-D-glucosamine kinase	NAGK	3	571.3	683.166 7	646.366 7	564.2	519.2	588.266 7
Eukaryotic translation initiation factor 3 subunit A	eIF3a	64	13884.5333 3	28904.8 3	27743.9 3	23871.8 7	17544.3 3	20292.1 7
Isoform 5 of Rho guanine nucleotide exchange factor 7	ARHGEF7	11	1220.63333 3	3065.7	2492.13 3	2532.13 3	2244.2	2347.5
cDNA, FLJ92044, highly similar to Homo sapiens death-associated protein (DAP), mRNA	1	69	241.2667	160.133 3	199.3	185.533 3	206.9	
Isoform 2 of Mediator of RNA polymerase II transcription subunit 8	MED8	5	57.6	313.633 3	289.466 7	259.1	229	237.2
Geranylgeranyl transferase type-2 subunit beta	RABGGTB	3	276.9	867	1000.8	716.3	467.666 7	538.4
Mitochondrial import receptor subunit TOM22 homolog	TOMM22	4	1362.2	1904	1563.7	1573.2	1448.26 7	1616.96 7
Hsp90 co-chaperone Cdc37	CDC37	25	8557.73333 3	17804.7	15338.2	14712	11905.6 7	13271.6 3
Lysine-specific demethylase 5A	KDM5A	6	649.4	1506.93 3	1463.56 7	1245.2	1015.7	1001.96 7

Zinc finger protein 701	ZNF701	1	447.133333 3	880.633 3	868	727.733 3	700.266 7	615.1
Isoform 2 of Histone H2B type 2-F	HIST2H2BF	1	14093	16298.4	12612.5 3	13468.8	14542.8 7	11219.4
Methenyltetrahydrofolate synthase domain-containing protein	MTHFSD	2	264.033333 3	660.333 3	610.6	545.7	596.4	544.9
Lysine-specific demethylase 3A	KDM3A	35	3910.86666 7	9304.9	5281.56 7	7690.56 7	8258.4	9626.36 7
DNA-binding protein SMUBP-2	IGHMBP2	5	315.266666 7	552.8	538.3	456.9	384.566 7	406.633 3
Ras-related protein Rab-24	RAB24	5	654.166666 7	1600.63 3	1279.53 3	1322.96 7	1334.36 7	1320.96 7
Transcription termination factor 2	TTF2	11	1448.5	2485.73 3	2281.26 7	2054.53 3	1809.46 7	1809.53 3
cDNA FLJ59722, highly similar to Retinoblastoma-binding protein 5	11	1564.66666 7	2200.633	2044.7	1819.03 3	1854.5	1646	
Eukaryotic translation initiation factor 3 subunit G	EIF3G	1	2651.06666 7	4287.5	3953.36 7	3544.06 7	2643.4	2981.3
Translin	TSN	14	2690.13333 3	6651.56 7	5718.96 7	5498.36 7	4597.53 3	5191.66 7
cDNA FLJ75056, highly similar to Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA	10	2427.26666 7	4906.6	3781.1	4056.03 3	3741.73 3	3965.46 7	

Leucine-rich repeat and calponin homology domain-containing protein 3	LRCH3	6	1299.96666 7	3174.83 3	2778.83 3	2624.5	2077.23 3	2418.16 7
Histidine triad nucleotide-binding protein 3	HINT3	3	338.633333 3	469.566 7	414.2	388.2	379	372.933 3
Isoform D of Protein SON	SON	9	5256.7	9770.46 7	9271.46 7	8078.23 3	7188.93 3	7382.56 7
Isoform 2 of TNF receptor-associated factor 2	TRAF2	4	728.933333 3	1292.5	1217.6	1068.66 7	922.8	934.2
Isoform 4 of Queuine tRNA-ribosyltransferase accessory subunit 2	QTRT2	5	870.933333 3	1910.06 7	1819.83 3	1579.53 3	1341.56 7	1290.76 7
Serine/threonine-protein kinase SMG1	SMG1	11	810.5	2007.83 3	1569.73 3	1660.63 3	1333.1	1512.23 3
Conserved oligomeric Golgi complex subunit 7	COG7	7	523.333333 3	710.933 3	600.966 7	588.033 3	551.1	645
cDNA, FLJ96012, highly similar to Homo sapiens interferon regulatory factor 2 binding protein 1 (IRF2BP1), mRNA		6	558.433333 3	841.4333	759.766 7	696	698.633 3	667.2
T-complex protein 1 subunit zeta	CCT6A	30	11689.4333 3	22065.9 3	20523.2	18253.9	13808.1 3	16198.4 3
Isoform SM-B1 of Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	8	2590.43333 3	4150.2	3792.36 7	3433.46 7	3088.96 7	3055.03 3
Isoform 3 of Mediator of RNA polymerase II transcription subunit 25	MED25	2	345.7	404	379.933 3	334.266 7	307	298.166 7

N-acetylserotonin O-methyltransferase-like protein	ASMTL	22	3190.9	6157.3	5260.13 3	5094.83 3	4890.83 3	4918.5
U3 small nucleolar ribonucleoprotein protein IMP3	IMP3	7	622.6	1052.6	945.266 7	871.033 3	798.733 3	857.9
Isoform 3 of Striatin-4	STRN4	8	806.666666 7	1805.23 3	1595	1493.93 3	1273.16 7	1289.36 7
28S ribosomal protein S5, mitochondrial	MRPS5	4	768.333333 3	1154.63 3	1185.7	955.566 7	877.5	878.5
Prefoldin subunit 2	PFDN2	9	4726	6194.73 3	5593.76 7	5126.76 7	4015.16 7	4623.06 7
Enhancer of rudimentary homolog	ERH	7	3447.66666 7	6241.1	5232.66 7	5165.2	4466.43 3	4785.9
Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	13	5292.63333 3	10483.2 7	9155.6	8676.23 3	6576.7	7564.7
Putative small nuclear ribonucleoprotein G-like protein 15	SNRPGP15	4	1792.13333 3	2909.33 3	2560.16 7	2407.86 7	2271.93 3	2359.9
Protein FAM199X	FAM199X	1	128.566666 7	159.2	197.2	131.766 7	105.3	119.6
WW domain-containing adapter protein with coiled-coil	WAC	4	283.1	346.466 7	319.8	286.766 7	268	296.933 3
Histone H1.5	HIST1H1B	19	30435.1333 3	28998.9	24726.7	24002.7	24032.9	24766.1 7
5-aminolevulinate synthase, nonspecific, mitochondrial	ALAS1	8	869.066666 7	1841.93 3	810.266 7	1524.6	1551.8	1218.63 3
NAD(P)H dehydrogenase [quinone] 1	NQO1	19	7817.86666 7	14571.7	11984.7 3	12061.5	11329.8 3	11262.4

Poly (ADP-ribose) glycohydrolase	PARG	8	221.666666 7	574.033 3	506.6	475.166 7	433.233 3	466.7
Diphthamide biosynthesis protein 2	DPH2	7	352.533333 3	514.366 7	437.466 7	425.8	380.633 3	387.366 7
Zinc finger MYM-type protein 4	ZMYM4	7	1269.66666 7	2807.56 7	2509	2324.5	2346.93 3	2219.26 7
COUP transcription factor 2	NR2F2	4	355.5	1571.36 7	1566.1	1301	942.966 7	1057.83 3
cDNA FLJ52663, highly similar to SET and MYND domain-containing protein 5	4	337	1099.8	948.333 3	910.666 7	758.733 3	806.433 3	
WW domain-binding protein 11	WBP11	17	5042.8	9422.46 7	8686.5	7802.53 3	6735.86 7	6740.03 3
Kelch domain-containing protein 4	KLHDC4	2	295.933333 3	575.933 3	542.8	476.933 3	375.1	406.7
Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	23	9462.9	15208.3 7	13463.4 3	12594.5 3	10835.3	11038.3 7
Myotubularin-related protein 6	MTMR6	7	508.966666 7	1222	1105.46 7	1012.06 7	848.6	898.433 3
Isoform 3 of Cytoskeleton-associated protein 5	CKAP5	68	14342.7666 7	27348.0 3	28022.0 7	22652.2	15796.1 7	17960.9 7
Zinc finger protein 664	ZNF664	1	157.8	260.433 3	231.8	215.8	203.666 7	194.666 7
Thioredoxin domain-containing protein 9	TXNDC9	10	2160.6	3552.9	3902.96 7	2944.2	1980.5	2159.96 7
cDNA, FLJ94435		9	1307.46666 7	2239.36 7	2466.2	1855.73 3	1504.83 3	1512.76 7

Fukutin-related protein	FKRP	2	34.2666666 7	203.033 3	189.7	168.266 7	14.3	19.8
Isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	21	11577.8333 3	20407.2 7	18347.1 3	16912.9 3	14780.8	14439.2
Fasciculation and elongation protein zeta 2 (Zygin II)	FEZ2	4	605.933333 3	585.733 3	506.233 3	485.466 7	446.6	457.1
Signal transducer and activator of transcription 2	STAT2	4	122.166666 7	309.033 3	220.233 3	256.166 7	218.7	295.766 7
40S ribosomal protein S27	RPS27	3	2444.8	4390.36 7	3801.16 7	3639.53 3	2806	3018.56 7
Protection of telomeres protein 1	POT1	2	197.066666 7	361.966 7	332.733 3	300.066 7	258.733 3	256.333 3
NudC domain-containing protein 2	NUDCD2	6	1884.16666 7	2510.33 3	1899.66 7	2081.06 7	2032	2029.43 3
Protein KTI12 homolog	KTI12	4	418.033333 3	363.566 7	337.866 7	301.4	285.933 3	286.9
cDNA FLJ37346 fis, clone BRAMY2021310, highly similar to Transcriptional repressor p66 beta		5	1851.33333 3	2462.9	2266.03 3	2042	1651.36 7	1721.16 7
Transcription factor BTF3 homolog 4	BTF3L4	7	1378.6	2182.56 7	1776.5	1809.7	1685.66 7	1798.46 7
HEAT repeat-containing protein 6	HEATR6	4	394.633333 3	496.766 7	339.333 3	411.9	314.466 7	325.3
Peptidylprolyl isomerase (Fragment)	FKBP15	16	2594.96666 7	3974.03 3	3431.83 3	3295.13 3	3069.53 3	3050.3
Polyadenylate-binding protein		11	14699.0666 7	25885.5 7	24925.7 7	21464.9 7	16067.7	18054.0 7

SAR1a gene homolog 2 variant (Fragment)	2	326.233333 3	935.6333	966.633 3	775.9	550	559	
Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	8	2636	5211.56 7	4666.06 7	4321.93 3	3738.06 7	3862.9
cDNA, FLJ96618, highly similar to Homo sapiens tyrosyl-DNA phosphodiesterase 1 (TDP1), mRNA	1	220.1	278.5	236.4	230.966 7	219.5	189.266 7	
RNA pseudouridylate synthase domain-containing protein 3	RPUSD3	2	83.1	391.133 3	355.466 7	324.4	302.766 7	300
cDNA, FLJ92988, highly similar to Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1), mRNA	5	550.466666 7	1067.9	979.533 3	885.8	729.9	826.1	
Chloride intracellular channel protein 4	CLIC4	12	1451.93333 3	2708.2	2296.56 7	2246.43 3	1827.03 3	1986.2
Isoform 2 of NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	21	3031.33333 3	5991.73 3	4638.33 3	4970.33 3	4876.7	4532.53 3
Isoform 3 of Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	6	2187.96666 7	4042.53 3	2819.4	3353.73 3	3220.4	3640.06 7
Survival motor neuron protein	SMN1	8	2920.16666 7	4908.1	4474.26 7	4071.96 7	3224.56 7	3612.43 3
Cytochrome b-c1 complex subunit 8	UQCRCQ	4	452.233333 3	1437.56 7	1509.26 7	1192.7	1286.96 7	1088.6

SLIT-ROBO Rho GTPase-activating protein 3	SRGAP3	1	589.833333 3	941.366 7	774.133 3	781.033 3	716.633 3	770.366 7
Adenylosuccinate lyase	ADSL	8	1512.43333 3	3044.1	2633.76 7	2525.63 3	1908.7	2078.5
E3 ubiquitin-protein ligase RNF185	RNF185	1	20.1333333 3	32.1	27.8	26.6333 3	22.8666 7	23.6666 7
Tryptophan--tRNA ligase, cytoplasmic	WARS	29	10629.8333 3	23422.8	16398.1 7	19434.4	17339.5	19828.1 3
Exosome complex exonuclease RRP44	DIS3	24	2898.86666 7	5230.86 7	4688.9	4340.36 7	3524.66 7	4122.46 7
Nucleolar protein 8, isoform CRA_a	NOL8	16	1833.46666 7	3766.1	3425.73 3	3125.03 3	2743.83 3	2731.1
Isoform 2 of Kinesin-like protein KIF23	KIF23	12	1397.1	2070.73 3	2742.86 7	1718.3	1310.73 3	1257.13 3
Antigen MU-RMS-40.16A (Fragment)		1	1147.86666 7	1994.76 7	1780.23 3	1655.4	1548.63 3	1708.63 3
Casein kinase II subunit beta	CSNK2B	5	1178.43333 3	2681.53 3	2440.06 7	2225.96 7	1694.76 7	1936.26 7
cDNA FLJ76427, highly similar to Homo sapiens SH2 domain binding protein 1 (tetratricopeptide repeat containing) (SH2BP1), mRNA		15	3128.16666 7	6083.667	5314.5	5050.16 7	4776.36 7	4842.43 3
Integrator complex subunit 7	INTS7	6	1066.4	1611.5	1391.43 3	1337.76 7	1275.96 7	1275.2
Polycomb group RING finger protein 2	PCGF2	4	290.4	839.933 3	856.6	697.266 7	684.4	624.966 7

Queuine tRNA-ribosyltransferase catalytic subunit 1	QTRT1	7	1459.66666 7	2545.13 3	2321.13 3	2112.86 7	1593.06 7	1691.63 3
Malignant T-cell-amplified sequence 1	MCTS1	13	3037.86666 7	6629.4	5890.5	5503.53 3	4268.86 7	4533.36 7
Rho GDP-dissociation inhibitor 1	ARHGDI1	10	4752.86666 7	9516.6	8352.4	7902.96 7	5720.03 3	7055.93 3
E3 ubiquitin-protein ligase TRIM56	TRIM56	12	1797.4	3255.96 7	2644.33 3	2703.9	2552.96 7	2814.33 3
Double-stranded RNA-binding protein Stau60 homolog 2	STAU2	6	1135.33333 3	2049.63 3	1879.6	1702.2	1504.76 7	1558.23 3
Zinc finger protein 292	ZNF292	12	1251.53333 3	2257.93 3	1623.46 7	1875.53 3	1836.03 3	1941.5
HCG1818442, isoform CRA_a	MCRIP1	5	838.966666 7	1423.4	1401.73 3	1182.43 3	885.433 3	881.366 7
cDNA, FLJ92583, highly similar to Homo sapiens glycogenin (GYG), mRNA		2	514.766666 7	330.3	1030.13 3	274.466 7	254.6	272.6
Ataxin-2-like protein	ATXN2L	28	5345.83333 3	10721	10144.5	8908.86 7	6872.5	7155
Protein RRP5 homolog	PDCD11	43	7018.63333 3	13480.2	12304.7 7	11202.4 3	9689.43 3	10293.4
Ferritin light chain	FTL	3	474.1	728.5	783.266 7	605.433 3	666.6	723.3
cDNA FLJ12434 fis, clone NT2RM1000037, highly similar to Homo sapiens KIAA0690 protein		14	2693.83333 3	4406.733	3640.63 3	3662.86 7	3030.1	2965.33 3

Proteasome-associated protein ECM29 homolog	KIAA0368	40	5344.33333 3	10322.2	9338.5	8580.46 7	6304.7	7441.7
Uncharacterized protein (Fragment)		2	343.966666 7	376.133 3	411.266 7	312.666 7	265.466 7	252.466 7
60S acidic ribosomal protein P2	RPLP2	10	6796.26666 7	12278.0 3	12311.7	10206.7 3	7546.86 7	8600.96 7
Core histone macro-H2A.2	H2AFY2	9	1771.36666 7	3362.83 3	3088.26 7	2795.76 7	2543.5	2881
ATP-dependent RNA helicase DDX42	DDX42	20	4869.26666 7	8837.8	8106.26 7	7347.53 3	6669.63 3	6719.06 7
Lamina-associated polypeptide 2, isoforms beta/gamma	TMPO	11	8658.46666 7	13131.5 7	11898.8	10918.1 3	10289.9 3	10338.5 7
DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	8	1071.9	1577.5	1479.53 3	1311.66 7	1218.06 7	1252.03 3
Unconventional prefoldin RPB5 interactor 1	URI1	11	1598.06666 7	3812.9	3167.23 3	3170.5	2828.3	2969.06 7
DNA polymerase beta	POLB	3	264.933333 3	585.533 3	479.966 7	486.9	505.933 3	517.633 3
Cytosolic non-specific dipeptidase	CNDP2	17	3638.16666 7	6415.03 3	4843.16 7	5334.7	4809.4	5439.53 3
cDNA FLJ78223		9	537.4	1036.03 3	956.9	861.6	870.666 7	974.466 7
NLR family member X1	NLRX1	3	379.5	581.766 7	469.933 3	483.833 3	522.833 3	485.433 3
Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A	9	679.866666 7	1324.03 3	1227.73 3	1101.3	1128.6	1045.83 3

Sphingosine-1-phosphate lyase 1	SGPL1	4	514.366666 7	1095.8	1021.33 3	911.466 7	754.7	794.633 3
Nucleolar complex protein 4 homolog	NOC4L	8	677.733333 3	916.033 3	818.966 7	762	663.233 3	651.433 3
Barrier-to-autointegration factor	BANF1	8	1890.76666 7	3896.93 3	3543.23 3	3241.7	2207.03 3	2867.43 3
cDNA FLJ77959, highly similar to Homo sapiens protein kinase, cAMP-dependent, regulatory, type I, beta (PRKAR1B), mRNA		4	534.966666 7	572.9667	816.233 3	476.633 3	399.1	426.7
Phospholipase A-2-activating protein	PLAA	23	4401.43333 3	9351.56 7	8693.23 3	7779.4	6501	7067.4
cDNA FLJ14522 fis, clone NT2RM1000883, highly similar to Homo sapiens nischarin (NISCH), mRNA		8	685.666666 7	576.6	472.433 3	479.666 7	504.7	566.933 3
U6 snRNA-associated Sm-like protein LSM8	LSM8	3	248.533333 3	261.8	248.6	217.8	216.966 7	234
Proteasome subunit beta type-4	PSMB4	8	3179.76666 7	5177.03 3	4378.13 3	4307.03 3	3911.1	4190.96 7
Centromere protein U	CENPU	5	278.333333 3	308.3	323	256.5	215.066 7	224.233 3
AP-1 complex subunit sigma-1A	AP1S1	3	759.633333 3	915.233 3	805.966 7	761.533 3	807.666 7	733.366 7
Poly [ADP-ribose] polymerase 2	PARP2	6	769.2	1120.03 3	1047.36 7	931.966 7	648.833 3	734.833 3

Liprin-beta-1	PPFIBP1	1	470.466666 7	910.8	800.033 3	758.033 3	733.966 7	757.5
Isoform 4 of Elongator complex protein 5	ELP5	2	146.933333 3	354.066 7	307.566 7	294.7	251.3	237.933 3
A-kinase anchor protein 8-like	AKAP8L	5	1017.06666 7	1469.13 3	1343.26 7	1222.96 7	1011.53 3	1182.03 3
Alpha-taxilin	TXLNA	28	7447.16666 7	9458.2	9415.2	7873.4	6283.63 3	6366.2
Histone H2B type 1-K	HIST1H2BK	1	16514.2666 7	15972.4	12359.0 3	13296.3 3	14314.3	11056.3 3
SNW domain-containing protein 1	SNW1	19	3669.4	5282.26 7	4575.93 3	4397.5	4029.76 7	3835.03 3
Serine/arginine-rich splicing factor 9	SRSF9	12	4062.6	7938.4	6495.96 7	6608.93 3	6479.56 7	5952.56 7
Uncharacterized protein C9orf78	C9orf78	8	841.966666 7	1897.8	1996.46 7	1580.1	1211.1	1180.26 7
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	19	2627.8	3713.6	2968.13 3	3092	2491.5	2814.86 7
Isoform 2 of HAUS augmin-like complex subunit 7	HAUS7	5	726.466666 7	1203.66 7	1119.76 7	1002.2	947.6	1032.7
cDNA, FLJ92019, highly similar to Homo sapiens mitochondrial ribosomal protein S14 (MRPS14), nuclear gene encoding mitochondrial protein, mRNA		1	318.066666 7	233.4333	209.4	194.366 7	163.233 3	164.466 7

N-acetylgalactosamine kinase	GALK2	2	351.233333 3	570.733 3	406.2	475.233 3	403.966 7	530.366 7
E3 ubiquitin-protein ligase RNF31	RNF31	3	552.8	784.3	662.4	653.066 7	592.633 3	594.6
Eukaryotic translation elongation factor 1 alpha 1 variant (Fragment)	1	23239.8	36461.2	40765.1 3	30360.8 7	22455.5 7	25907.6 7	
Histone H2B (Fragment)	HIST1H2BM	1	14331.4333 3	16201.2	12599.6 7	13492.2	14487.2 7	11284.0 3
Isoform Non-brain of Clathrin light chain A	CLTA	13	6242.4	9221.1	7368.3	7679.36 7	7452.16 7	7320.93 3
Isoform 3 of Activating transcription factor 7-interacting protein 1	ATF7IP	2	467.1	512.333 3	529.3	426.7	404.533 3	413.066 7
cDNA, FLJ92932, highly similar to Homo sapiens serine/threonine kinase 38 (STK38), mRNA	3	770.9	1323.567	1337	1102.53 3	930.366 7	976.166 7	
Serine/threonine-protein kinase tousled-like 2	TLK2	2	478.966666 7	1503.4	1411.3	1252.4	1096.9	1118.36 7
Mitochondrial import inner membrane translocase subunit Tim8 A	TIMM8A	6	2299.23333 3	2703.16 7	2351.66 7	2252.16 7	2235.13 3	2100.83 3
Isoform 2 of Serine-threonine kinase receptor-associated protein	STRAP	20	8296.06666 7	16507.4 3	16193.3	13754.5 3	9088.36 7	10284.5 3
Protein VAC14 homolog	VAC14	9	1476.33333 3	2731.86 7	2444.3	2276.53 3	2021.9	2203.46 7

Synapse-associated protein 1	SYAP1	21	3947.9	7656.33 3	6768.4	6380.3	5209.73 3	5481.66 7
Isochorismatase domain-containing protein 1	ISOC1	7	1167.26666 7	2005.86 7	1781.5	1671.66 7	1443.06 7	1528.43 3
Serine/Arginine-related protein 53	RSRC1	5	555.233333 3	1227.83 3	1074.46 7	1023.3	855.3	904.133 3
Isoform 2 of CREB-regulated transcription coactivator 1	CRTC1	1	109.4	143.1	118.166 7	119.266 7	101.833 3	116.533 3
Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	GSPT2	3	6310.26666 7	10590.6	9482.26 7	8828.5	7078	8084.9
E3 ubiquitin-protein ligase LRSAM1	LRSAM1	8	376.133333 3	614.066 7	602.7	511.9	464.1	449
Transcriptional repressor CTCF	CTCF	11	1788.66666 7	2684.83 3	2394.26 7	2238.4	2008.16 7	2010.33 3
Proteasome inhibitor PI31 subunit	PSMF1	7	1867.03333 3	3656	2689.83 3	3048.23 3	1985.16 7	2219.76 7
Sorting nexin		14	1772.36666 7	3360.3	2715.13 3	2801.83 3	2581.2	2663.9
Rho GTPase-activating protein 1	ARHGAP1	10	2066.56666 7	3501.86 7	3014.26 7	2920.06 7	2619.5	2741.03 3
Component of oligomeric golgi complex 4, isoform CRA_d	COG4	7	739.6	989.9	925.366 7	825.633 3	727.5	825.666 7
Thioredoxin	TXN	8	6374.93333 3	14099.0 3	10927.7	11759.9	10475.5	11237.0 3
Mediator complex subunit 4 (Fragment)	MED4	3	309.5	957.4	908.833 3	798.566 7	739.933 3	757.533 3

Heat shock protein 90Bf	HSP90Bf	2	5992.66666 7	12517.0 7	11507.8 3	10441.0 7	7730.13 3	8693.26 7
Huntingtin-interacting protein 1-related protein	HIP1R	5	1224.4	3243.93 3	2956.03 3	2705.93 3	2191.66 7	2381.16 7
Trans-Golgi network integral membrane protein 2	TGOLN2	1	1928.76666 7	2785.83 3	3064.16 7	2324.06 7	2469.9	2115.5
Eukaryotic translation initiation factor 2 subunit 2	EIF2S2	23	7842.3	16070.4	14104.8 3	13407.5	10014.4 7	11221.9
Nuclear pore complex protein Nup93	NUP93	38	7975.53333 3	15898.4	15443.0 3	13265.4	10388.0 7	11024.8 3
KRR1 small subunit processome component homolog	KRR1	18	3115.33333 3	6482.7	5443.73 3	5409.5	4192	4371.9
WD repeat-containing protein 36	WDR36	20	2800.06666 7	5803.56 7	5050.66 7	4843.4	4219.33 3	4458.73 3
28S ribosomal protein S6, mitochondrial	MRPS6	7	923.4	1435	1603.23 3	1197.66 7	981.2	1270.23 3
M-phase phosphoprotein 6	MPHOSPH6	4	452.966666 7	847.266 7	794.766 7	707.166 7	616.066 7	605.233 3
40S ribosomal protein S28	RPS28	8	4272.53333 3	6548.46 7	6144.66 7	5465.66 7	4439.33 3	4985.76 7
Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	32	24979.4666 7	40977.0 7	33750.8 7	34201.7 7	29841.8 3	29602.1
Adenylyltransferase and sulfurtransferase MOCS3	MOCS3	2	333.233333 3	664.333 3	605.166 7	554.5	525.033 3	537.5
NTF2-related export protein 1	NXT1	3	621.666666 7	1027.1	772.5	857.5	789.166 7	777.8
MORC family CW-type zinc finger protein 3	MORC3	13	1658.23333 3	3169.96 7	2671.03 3	2646.66 7	2365.1	2413.63 3

Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	1	1650.76666 7	2270.83 3	2472.4	1896.13 3	1253.13 3	1289.56 7
Myelin expression factor 2	MYEF2	6	1200.16666 7	1727.66 7	1470.93 3	1442.73 3	1640.3	1507.16 7
Sorting nexin-17	SNX17	5	407.3	417	513.333 3	348.266 7	287.466 7	299.933 3
NF-kappa-B-activating protein	NKAP	6	523.466666 7	724.466 7	632.466 7	605.1	529.2	541.066 7
Isoform Long of Ubiquitin fusion degradation protein 1 homolog	UFD1L	10	1952.6	3567.4	3479.03 3	2979.73 3	2067.63 3	2442.1
Nuclease-sensitive element-binding protein 1	YBX1	3	7531.43333 3	10492	9953.8	8765.06 7	6115.6	7509.46 7
Proliferation marker protein Ki-67	MKI67	119	27820.8	32931.9 3	40339.5 7	27512.4 7	24724.0 7	19746.2
T-complex protein 1 subunit theta	CCT8	44	24387.0333 3	45065.3	40822.8	37649.9 3	28105.1 7	33301.6
tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6	13	1629.16666 7	3348.33 3	2979.93 3	2797.43 3	2631.96 7	2586.73 3
cDNA, FLJ95321, highly similar to Homo sapiens ATG7 autophagy related 7 homolog (S. cerevisiae) (ATG7), mRNA		6	480.566666 7	1169.9	1039.86 7	977.433 3	823.166 7	903
60S ribosomal protein L36a-like	RPL36AL	2	4551.33333 3	7682.93 3	6813.23 3	6419.96 7	5200.2	5425.96 7

DNA replication complex GINS protein SLD5	GIN54	5	498.633333 3	703.266 7	685.433 3	587.666 7	503.466 7	507.633 3
Transmembrane protein 231	TMEM231	2	71.2666666 7	263.533 3	240.833 3	220.233 3	201.666 7	197
26S protease regulatory subunit 7	PSMC2	35	10106.4666 7	16511.2 7	15725.5 7	13799.3	10249.3 3	12030.8
Protein transport protein Sec24C	SEC24C	16	2604.46666 7	4877.8	4166.66 7	4076.83 3	3575.66 7	3719.76 7
Glutathione synthetase	GSS	11	1985.86666 7	3842.7	3352.53 3	3212.06 7	2796.26 7	3081.06 7
Abnormal spindle-like microcephaly-associated protein	ASPM	2	474.733333 3	541.1	856.5	452.3	408.3	414.966 7
cDNA FLJ76065		13	1861.53333 3	3605.2	3297.03 3	3013.73 3	2570.26 7	2555.26 7
Histone H1.3	HIST1H1D	4	26027.2666 7	21995.6	18833.5 3	18388.8	17891.2 3	17654.7 7
Serine/arginine-rich splicing factor 3	SRSF3	10	8690.43333 3	14443.6	12831.4 7	12077.5	11115.7 7	11023.1
DnaJ homolog subfamily C member 7	DNAJC7	25	4851.7	10116.1 3	10133.8 3	8465.2	5516.53 3	6995.36 7
Dipeptidyl peptidase 3	DPP3	15	2660.7	6275.96 7	5744.4	5251.83 3	4440.26 7	4592.4
Tetratricopeptide repeat protein 4	TTC4	10	1442.8	2100	2047.83 3	1757.53 3	1431.7	1570.23 3
Isoform 2 of LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468	9	677.8	866.2	730.333 3	724.966 7	650.1	712.4

Apoptosis-inducing factor 2	AIFM2	5	425.566666 7	1068.46 7	1049.7	894.333 3	726.3	767.533 3
Transmembrane protein 214	TMEM214	13	1632.13333 3	3629.83 3	2828.13 3	3038.3	2581.53 3	2624.6
Selenide, water dikinase 1	SEPHS1	7	1971.53333 3	3384.36 7	2766.16 7	2832.93 3	2603.13 3	2605.76 7
U3 small nucleolar RNA-associated protein 4 homolog	UTP4	15	1718.96666 7	3322.83 3	3394.13 3	2781.43 3	2327.46 7	2451.46 7
cDNA FLJ56474, highly similar to Histone deacetylase 6	4	231.966666 7	507	457.433 3	424.433 3	412.3	440.833 3	
cDNA FLJ30880 fis, clone FEBRA2004767, highly similar to Breast cancer anti-estrogen resistance protein 3	12	1584.33333 3	2755.9	2600.06 7	2307.23 3	1999.2	2056.73 3	
TBC1 domain family member 13	TBC1D13	6	641.233333 3	1509.93 3	1325.36 7	1264.16 7	1157.23 3	1169.43 3
Isoform 3 of LIM and senescent cell antigen-like-containing domain protein 1	LIMS1	12	1945.7	4281.6	4132.7	3585.33 3	3210.36 7	3350.63 3
cDNA, FLJ95184, highly similar to Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA	7	955	1474.6	1345.13 3	1234.9	992.5	1042.06 7	
U4/U6.U5 tri-snRNP-associated protein 1	SART1	29	5836.4	10007.3 7	9224.6	8380.93 3	7193.73 3	7030.56 7
La-related protein 1	LARP1	33	6098.23333 3	8866.7	7812.96 7	7426.66 7	6217.4	6947

Protein LSM14 homolog B (Fragment)	LSM14B	1	1320.33333 3	1821.56 7	1661.63 3	1525.86 7	1470.63 3	1295.33 3
cDNA FLJ61387, highly similar to Homo sapiens conserved nuclear protein NHN1 (NHN1), mRNA	21	4428.83333 3	7173.1	6696.66 7	6008.93 3	5501.76 7	5205.1	
Signal recognition particle 54 kDa protein	SRP54	20	4056.83333 3	8244.1	6633.9	6906.23 3	5106.03 3	5991.86 7
Transcription factor Sp3	SP3	3	567.166666 7	801	769.633 3	671.2	605.3	607.366 7
cDNA FLJ61383, highly similar to Serine/threonine-protein kinase 24 (EC 2.7.11.1)	8	2921.43333 3	6380.367	5961.1	5346.5	4403.7	4694.43 3	
Dihydropyrimidinase-like 2		3	8365.36666 7	14584.3	12089.6	12221.9 7	10528.5	11454.1 3
FERM, RhoGEF and pleckstrin domain-containing protein 2 (Fragment)	FARP2	1	352.466666 7	560.766 7	561.333 3	469.966 7	465.6	403.733 3
40S ribosomal protein S10	RPS10	12	7438.5	13571.8 7	12725.3	11374.6 3	8971.13 3	9561.93 3
Cytoplasmic tRNA 2-thiolation protein 2	CTU2	2	168.533333 3	281.5	256.766 7	235.933 3	202.266 7	217.166 7
Nucleoredoxin	NXN	6	1009.8	1820.13 3	1751.13 3	1525.53 3	1357.2	1349.7
28S ribosomal protein S7, mitochondrial	MRPS7	6	1222.03333 3	1998.16 7	2332.46 7	1674.8	1348.53 3	1321.2
Ski oncogene	SKI	6	721.7	878.766 7	803.533 3	736.566 7	693.033 3	724.833 3

DNA-directed RNA polymerase I subunit RPA43	TWISTNB	5	571.3	1322.5	1430.53 3	1108.53 3	968.933 3	922.833 3
Probable E3 ubiquitin-protein ligase HERC4	HERC4	15	1495.33333 3	2900.13 3	2610.96 7	2431	1977.03 3	2221.7
Putative helicase MOV-10	MOV10	10	1609.9	3490.46 7	2898.13 3	2926.23 3	2832.23 3	3019.33 3
Serine/arginine-rich-splicing factor 1	SRSF1	18	8095.56666 7	11786.8	10023.6	9884.06 7	9413.66 7	9502.36 7
RNA binding motif protein 10, isoform CRA_d	RBM10	15	3658.13333 3	6556.16 7	5809.3	5498	5035.73 3	4839.53 3
ATP-dependent RNA helicase DDX50	DDX50	18	4487.03333 3	9621.66 7	8148.53 3	8069.6	7235.73 3	6497.46 7
Nuclear envelope pore membrane protein POM 121C	POM121C	9	936	1110.3	1152.63 3	931.3	873.9	839.033 3
Adapter molecule crk	CRK	5	3498.03333 3	6599.56 7	5818.96 7	5535.6	4587.2	5189.1
YTH domain-containing family protein 2	YTHDF2	8	2178.03333 3	4888.8	4882.16 7	4100.83 3	3227.9	3289.96 7
cDNA, FLJ93657, highly similar to Homo sapiens ribosomal protein L3-like (RPL3L), mRNA	1	1440.43333 3	2962.133	2796.2	2484.76 7	1825.13 3	2205.4	
60S ribosomal protein L13a (Fragment)	RPL13A	16	9871.56666 7	17156.7	16037.5 3	14392.4 7	11257.6	12000.5 3
Isoform 4 of Trans-Golgi network integral membrane protein 2	TGOLN2	1	1793.1	2552.26 7	2821.5	2141.33 3	2285.86 7	1963.73 3
Chromosome 12 open reading frame 43, isoform CRA_a	C12orf43	6	558.2	982.466 7	896	824.4	774.933 3	792.266 7

Protein transport protein Sec16A	SEC16A	2	3027.16666 7	5158.13 3	4305.6	4328.33 3	3370.93 3	4177.83 3
Transcription factor MafF	MAFF	1	309.7	593.333 3	433.3	497.9	489.933 3	492.2
cDNA, FLJ92803, highly similar to Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA	29	4864	8445.4	6171.96 7	7088.23 3	7087.86 7	8008.06 7	
Biogenesis of lysosome-related organelles complex 1 subunit 4	BLOC1S4	4	203.1	349.933 3	285.066 7	293.733 3	276.1	281.466 7
Isoform 5 of RNA-binding protein EWS	EWSR1	7	2840.23333 3	5397.33 3	4684.66 7	4530.76 7	3840	4097.4
Nucleotide exchange factor SIL1	SIL1	2	541.4	833.433 3	735.6	699.633 3	690.333 3	806.8
40S ribosomal protein S6	RPS6	5	11905.1333 3	18687.2 3	16867.8 7	15687.2 3	13138.9	12985.1 3
Fragile X mental retardation syndrome-related protein 2	FXR2	8	2042.56666 7	4189.3	3909.06 7	3516.86 7	2834.16 7	3048.13 3
60S ribosomal protein L21	RPL21	11	4614.46666 7	7773.43 3	6961.4	6526.33 3	5237.16 7	5769.33 3
Isoform 2 of Protein SMG8	SMG8	7	1114.53333 3	1241.7	1088.23 3	1042.6	902.866 7	929.5
Isoform 2 of TIR domain-containing adapter molecule 2	TICAM2	5	549.266666 7	1513.63 3	1141.9	1270.93 3	1039	1200.4
Crooked neck-like protein 1	CRNKL1	16	2630.7	5894.36 7	5762.8	4950.06 7	4265.3	4283.16 7

cDNA FLJ75454, highly similar to Homo sapiens arrestin, beta 1 (ARRB1), transcript variant 1, mRNA	6	1142.766667	2212.867	2068.733	1858.467	1794.833	1764.9	
POTE ankyrin domain family member I	POTEI	1	8115.766667	14956.2	11634.5	12560.97	10704.93	11161.3
Isoform 2 of Nucleophosmin	NPM1	15	33510.5	33232.17	27703.67	27912.6	24373.3	25343.33
Glycerol-3-phosphate acyltransferase 4	GPAT4	2	433.9666667	435.2333	394.1	365.5667	356.9333	357.8667
Protein FAM83H	FAM83H	4	375.3	464.2	410.1667	389.9	360.1	385.8333
Isoform 2 of Gamma-aminobutyric acid receptor-associated protein-like 1	GABARAPL1	1	277.1	793.1333	818.6667	666.2	505.1333	679.2333
Centrosomal protein 350kDa, isoform CRA_a	CEP350	7	971.7666667	1305.767	1174.9	1096.8	957.8	996.3333
Stress-70 protein, mitochondrial	HSPA9	51	36173.56667	58829.47	49875.47	49421.2	43235.07	49294.23
cDNA FLJ76440, highly similar to Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 1, mRNA		2	176.2333333	402.1	418.4667	337.8	293.5	341.5667
cDNA FLJ54492, highly similar to Eukaryotic translation initiation factor 4B		22	6902.766667	9755.067	8936	8195.533	6092.7	6842.067
Isoform 2 of mRNA cap guanine-N7 methyltransferase	RNMT	19	3453.333333	7581.3	5077.833	6369.433	5888.567	6354.967

A-kinase anchor protein 8	AKAP8	7	871.7	1282.2	1198.56 7	1077.26 7	1010.73 3	956.233 3
KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	14	5996.76666 7	8817.56 7	7436.23 3	7408.26 7	7703.66 7	7045.1
RNA-binding protein 27	RBM27	16	3073.73333 3	5419.9	5041.23 3	4553.76 7	4160.86 7	4035.83 3
26S proteasome non-ATPase regulatory subunit 12	PSMD12	21	4308.63333 3	9260.5	8637.83 3	7780.83 3	5753.73 3	6556.83 3
Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	6	2306.93333 3	4904.23 3	4359.83 3	4121.23 3	3353	3418.6
cDNA, FLJ95513, highly similar to Homo sapiens cyclin fold protein 1 (CFP1), mRNA	1	106.9	138.4667	109.266 7	116.366 7	120.033 3	102.1	
Nucleolar protein 10	NOL10	14	3234.16666 7	5795.6	5184.9	4871.43 3	4431.1	4644.86 7
cDNA FLJ51883, highly similar to Mitochondrial 39S ribosomal protein L3	7	1211.4	2042.767	2175.2	1717.13 3	1487.5	1404.06 7	
cDNA FLJ75831, highly similar to Homo sapiens exportin, tRNA (nuclear export receptor for tRNAs) (XPOT), mRNA	9	1053.26666 7	2296.033	1939.76 7	1930.03 3	1646.73 3	1898.6	
DnaJ homolog subfamily B member 14	DNAJB14	2	424.566666 7	458	828.6	385	460	269.966 7
Leydig cell tumor 10 kDa protein homolog	C19orf53	5	1108.76666 7	890.8	816.6	748.833 3	670.366 7	723.133 3

Ubiquitin-like domain-containing CTD phosphatase 1	UBLCP1	9	885.4	2274.03 3	2290.76 7	1911.83 3	1379.6	1568.33 3
pre-rRNA processing protein FTSJ3	FTSJ3	17	4738.2	7965.13 3	7054.1	6696.73 3	5923.03 3	5843.26 7
Inner nuclear membrane protein Man1	LEMD3	10	1434.13333 3	2008.73 3	1837.53 3	1688.93 3	1576.46 7	1659.53 3
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13, isoform CRA_a	PSMD13	19	5879.03333 3	8378.03 3	8124.3	7044.26 7	5355.6	5872.06 7
cDNA FLJ76106, highly similar to Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA		14	2478.96666 7	6057.467	5346.56 7	5093.4	4451	4997.7
High mobility group protein B3	HMGB3	13	8547.73333 3	13223.6 7	10603.3	11120.1	10524.5	10722.5 7
Nuclear protein localization protein 4 homolog	NPLOC4	1	799.166666 7	1379.56 7	1386.13 3	1160.26 7	898.466 7	1018.36 7
40S ribosomal protein S7	RPS7	14	4816.73333 3	8340.66 7	8356.53 3	7014.9	5338.23 3	5583.66 7
Integrator complex subunit 12	INTS12	6	847	1054.23 3	984.333 3	886.666 7	954.3	750.566 7
Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	3	16246.1	27720.7 3	23030.5 7	23315.6	19390.3 3	21015.8 3
ADNP homeobox protein 2	ADNP2	2	147.766666 7	182.2	185.566 7	153.266 7	153.2	145.8
cDNA FLJ44463 fis, clone UTERU2024969, highly similar		6	865.933333 3	1495.6	1434.66 7	1258.1	1115.2	1113.33 3

to Mortality factor 4-like protein 2								
PC4 and SFRS1-interacting protein	PSIP1	30	6612.7	12479.1	10700.7 3	10498.6	9188.7	9351.43 3
MARCKS-related protein	MARCKSL1	13	2906.96666 7	3847.3	3495.4	3236.73 3	3106.16 7	2526.33 3
Galectin-1	LGALS1	13	10182.7666 7	19543.4 3	15323.5 7	16443.0 7	15117.6 3	16988
Isoform 6 of CCR4-NOT transcription complex subunit 4	CNOT4	7	1011.63333 3	1723.83 3	1453.6	1450.36 7	1216.06 7	1353.56 7
Neuroguidin	NGDN	5	855.8	1663.93 3	1467.33 3	1400.36 7	1241.2	1445.16 7
Lysine-specific demethylase PHF2	PHF2	4	462.666666 7	621.066 7	566.766 7	522.733 3	497.133 3	415.866 7
Isoform 2 of tRNA pseudouridine synthase A, mitochondrial	PUS1	12	1626.23333 3	3117.06 7	2862.56 7	2623.83 3	2203.43 3	2342.23 3
Nuclear factor of-activated T-cells 5 (Fragment)	NFAT5	1	637.366666 7	1494.6	1519	1258.13 3	1138.03 3	1276.5
cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA		35	14017.2666 7	21231.1	19526.8 7	17872.5 3	16817.7	16961.9 7
tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	32	6193.66666 7	12901.4 3	11475.5 3	10860.5 7	9002.76 7	9286.7
39S ribosomal protein L48, mitochondrial	MRPL48	4	738.466666 7	1706.96 7	1549.9	1436.96 7	1332.36 7	1334.9

Cytokine receptor-like factor 3	CRLF3	5	407.666666 7	837.966 7	727.533 3	705.433 3	639.266 7	649.833 3
Ran-binding protein 10	RANBP10	3	1040.63333 3	1395.86 7	1348.96 7	1175.16 7	1009.13 3	1023.8
NHL repeat-containing protein 2	NHLRC2	12	1450.73333 3	2275.03 3	1921.2	1915.5	1681	1881.13 3
Calcyclin-binding protein	CACYBP	23	8597.06666 7	17017.1 7	14948.6	14328.3 7	10479.7 7	12195.9
Protein transport protein Sec16A	SEC16A	1	3109.53333 3	5175.86 7	4286.33 3	4358.2	3388.93 3	4202.06 7
Epithelial membrane protein 2	EMP2	1	146.033333 3	346.466 7	371.433 3	291.733 3	264.3	253.5
Protein FAM208B	FAM208B	7	749.433333 3	1211.16 7	1112.4	1019.83 3	922.133 3	953.066 7
Isoform 3 of Polyadenylate-binding protein 4	PABPC4	23	10058.6666 7	18383.6 3	17578.4 7	15479.6 3	11667.6 3	13625.1 7
RUN and FYVE domain-containing protein 2	RUFY2	5	747.166666 7	1302.83 3	1134.83 3	1097.03 3	971.133 3	1099.56 7
60S ribosomal protein L30	RPL30	9	4683.03333 3	9005.46 7	8070.66 7	7583.23 3	5882.53 3	6489.33 3
Methylosome subunit pICln	CLNS1A	4	3144.6	4290.46 7	4452	3612.9	2957.96 7	3176.33 3
Serine/threonine-protein kinase Chk1	CHEK1	5	995.566666 7	1163.06 7	1453.33 3	979.4	765.066 7	922.2
cDNA FLJ76924, highly similar to Homo sapiens brix domain containing 1 (BXDC1), mRNA		6	808.733333 3	1586.967	1590	1336.36 7	1134.6	1004.26 7

POTE ankyrin domain family member J	POTEJ	2	8493.53333 3	15235.6 3	11893.4 3	12830.6	10924.8 3	11413
Gem-associated protein 7	GEMIN7	2	376.3	614.066 7	586.566 7	517.133 3	387.133 3	473.6
Isoform 4 of Cold shock domain-containing protein E1	CSDE1	33	7867.76666 7	13306.0 7	14355.5 3	11206.7 3	7921.03 3	8192.8
JMJD2B protein	JMJD2B	4	434.1	1004.83 3	383.066 7	846.4	726.9	662.5
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	7	1753.7	3411.13 3	3424.83 3	2873.73 3	2399.56 7	2627
Lys-63-specific deubiquitinase BRCC36	BRCC3	5	433.866666 7	855.6	708.766 7	720.866 7	649.6	696.066 7
Isoform 2 of Tumor suppressor p53-binding protein 1	TP53BP1	32	3960.66666 7	6589.56 7	5477.3	5552.76 7	5537.23 3	5429.63 3
Isoform 4 of Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	17	3496.26666 7	8316.46 7	6819.43 3	7008.06 7	6798	6885.93 3
Dual specificity protein kinase TTK	TTK	4	596.433333 3	863.433 3	1179.1	727.666 7	550.166 7	487.666 7
cDNA FLJ78252, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1), transcript variant 1, mRNA	26	5680.26666 7	9871.967	8794.96 7	8319.96 7	8577.46 7	7928.23 3	
BCL2-associated athanogene 3 variant (Fragment)	10	2636.23333 3	4093.233	3773.7	3449.83 3	3146.03 3	3013.3	

Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	ISCU	5	1074.23333 3	2532.53 3	2148.33 3	2134.7	2029.36 7	2202.66 7
Keratin 1	KRT1	17	4533.1	10665.7 3	5982.13 3	8990.26 7	10743.8	5345.63 3
cDNA FLJ32002 fis, clone NT2RP7009394, highly similar to Exocyst complex component 2	10	1340.03333 3	2337.967	2115.23 3	1970.73 3	1790.83 3	1897.36 7	
PNAS-106		1	457.166666 7	517.733 3	475.2	436.5	423.3	423.8
Isoform 2 of 28S ribosomal protein S27, mitochondrial	MRPS27	7	1725.4	3045.3	3186.1	2567.6	2101.63 3	2069.06 7
Serine/threonine-protein kinase PAK 2	PAK2	16	12720.1666 7	16870.4 3	13700.7 3	14226.1	12655.0 7	13099.3 7
ITGAV protein	ITGAV	7	1042.23333 3	1750.23 3	1739.9	1475.96 7	1201.53 3	1231.13 3
Transferrin receptor protein 1	TFRC	41	11280.3666 7	22132.5 7	24432.6 7	18666.8	12537.5	13033.1 3
Mediator of RNA polymerase II transcription subunit 6	MED6	6	510.466666 7	1301.76 7	1267.3	1098	946.366 7	1031.6
Dual specificity protein phosphatase 12	DUSP12	3	187.3	381.433 3	350.2	321.733 3	264	340.2
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	13	4970.9	7793.43 3	6697.43 3	6573.93 3	5250.13 3	5337.56 7
Tripeptidyl-peptidase 2	TPP2	32	4551.56666 7	8699.1	7599.5	7338.23 3	5893.2	7304

Transmembrane protein 201	TMEM201	2	567.733333 3	833.233 3	780.6	702.933 3	669.633 3	709.3
Tetratricopeptide repeat protein 21B	TTC21B	2	192.266666 7	328.066 7	327.533 3	276.766 7	248.933 3	253.733 3
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	4	564.6	1587.8	1288.8	1339.53 3	1263.36 7	1269.13 3
NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2	2	482.833333 3	1386.53 3	1515.46 7	1169.83 3	1087.7	1022.86 7
Chromosome 15 open reading frame 24, isoform CRA_b	C15orf24	2	317.9	904.166 7	917.866 7	762.866 7	440.566 7	544.033 3
Proteasome subunit beta type-6	PSMB6	5	1676.06666 7	2495.13 3	2082.9	2105.3	1805	1870.53 3
Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	19	5932.36666 7	8592.93 3	7792.86 7	7250.46 7	5928.5	6456.83 3
Isoform 2B of GTPase KRas	KRAS	1	1120.63333 3	2051.6	1554.73 3	1731.26 7	1777	1543.73 3
cDNA FLJ56631		7	556.5	738.6	676.233 3	623.3	561.733 3	558.6
PRPF4 protein variant (Fragment)		21	4127.63333 3	6954.26 7	6705.16 7	5868.66 7	4834.7	5133.53 3
Myeloid-derived growth factor	MYDGF	5	1970.9	4658.46 7	3253.03 3	3931.3	3608.9	3671.23 3
Sorting nexin-3	SNX3	10	2198.63333 3	3447	3180.56 7	2909.36 7	2531.06 7	2569.56 7
Vesicle-trafficking protein SEC22b	SEC22B	8	1747.86666 7	3904.8	3413.86 7	3296	2828.7	3253.5
Ras-related protein Rab-6B	RAB6B	1	2318.6	3931.8	2917.73 3	3318.9	3111.7	3571.73 3

AP-3 complex subunit mu-2	AP3M2	1	476.5	1172.6	1042.23 3	989.833 3	798.933 3	961.766 7
Isoform 2 of Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	3	1119.2	1383.66 7	1063.86 7	1168.03 3	1155.23 3	1211.33 3
TBC1 domain family member 24	TBC1D24	3	365.533333 3	633.9	577.933 3	535.133 3	489.533 3	487.366 7
Bola-like protein 2	BOLA2	5	1852.56666 7	3313.8	2821.06 7	2797.53 3	2216.73 3	2546.36 7
Paxillin	PXN	18	4975.03333 3	9337.93 3	7725.96 7	7883.56 7	6317.23 3	6306.8
Autophagy protein 5		4	510.333333 3	1062.3	950.7	896.866 7	761.3	804.033 3
cDNA, FLJ95432, highly similar to Homo sapiens Alport syndrome, mental retardation, midfacehypoplasia and elliptocytosis chromosomal region, gene 1 (AMMECR1),mRNA		1	534.033333 3	1163.5	1381.56 7	982.366 7	723.666 7	764.733 3
Cancer susceptibility candidate 3, isoform CRA_a	CASC3	6	438.466666 7	934.6	878	789.2	742.666 7	780.9
BRCA1 associated protein variant (Fragment)		3	293.333333 3	456.1667	388.466 7	385.2	363.633 3	375.766 7
Coiled-coil domain-containing protein 127	CCDC127	2	330.366666 7	452.366 7	390.133 3	382.066 7	399.666 7	353.833 3

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUFA2	6	1174.13333 3	2220.93 3	1680.93 3	1875.83 3	1781.6	1760.53 3
RNA polymerase II-associated protein 1	RPAP1	6	272.166666 7	658.733 3	599.4	556.466 7	433.9	539.8
Proteasome assembly chaperone 1		7	985.266666 7	1697.13 3	1594.2	1433.8	1050.46 7	1156.83 3
UTP--glucose-1-phosphate uridylyltransferase	UGP2	24	3674.66666 7	8367.93 3	6069.76 7	7069.6	5781.4	6799.5
Zinc finger and BTB domain-containing protein 21	ZBTB21	7	626.933333 3	748.033 3	626.366 7	632	624.766 7	591.166 7
Glutamate--cysteine ligase regulatory subunit	GCLM	5	1391.1	2068.73 3	1793.03 3	1748.1	1311.13 3	1526.03 3
cDNA, FLJ92684, highly similar to Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA		15	2609.03333 3	4133.3	3305.13 3	3492.76 7	3021.83 3	2800.16 7
Isoform 2 of PDZ domain-containing protein 11	PDZD11	3	452.133333 3	542.266 7	537.5	458.233 3	416.666 7	374.666 7
Arfaptin-1	ARFIP1	2	1376.8	2615.3	2305.43 3	2210.43 3	1824.13 3	2138.53 3
Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	AGAP1	1	501.6	972.8	858.666 7	822.233 3	730.433 3	745.1
Isoform 2 of B-cell receptor-associated protein 31	BCAP31	20	5868.2	11680	9056.96 7	9872.46 7	10443.5	9803.33 3
Isoform 2 of Ubiquitin-associated protein 2-like	UBAP2L	1	6929.76666 7	10277.9 7	9149.76 7	8687.93 3	6964.4	7262.03 3

Isoform 2 of Rab3 GTPase-activating protein catalytic subunit	RAB3GAP1	17	1646.2	3547.46 7	3280.46 7	2998.7	2526.56 7	2827.33 3
Isoform 2 of Lysine-specific demethylase 5B	KDM5B	5	216.333333 3	667.9	453.633 3	564.633 3	513.933 3	469.533 3
Isoform 2 of SRSF protein kinase 2	SRPK2	7	1710.13333 3	2159.66 7	2042.86 7	1825.93 3	1517.86 7	1522
Coiled-coil domain-containing protein 85C	CCDC85C	3	272.933333 3	601.066 7	642.666 7	508.2	414	425.9
Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	4	494.733333 3	689.333 3	595.3	582.833 3	531.166 7	528.8
Protein C10	C12orf57	5	1619.83333 3	1869.93 3	1603.73 3	1581.16 7	1078.43 3	1121.1
Phosphatidylinositol 4-kinase type 2-alpha	PI4K2A	5	445.9	784.6	696.8	663.466 7	593.9	640.333 3
cDNA FLJ60863, highly similar to High mobility group protein 2-like 1	2	161.566666 7	214.8667	172.333 3	181.7	161.966 7	171.166 7	
cDNA FLJ78740, highly similar to Homo sapiens sperm associated antigen 5 (SPAG5), mRNA	13	1716.6	2309.8	2637	1953.46 7	1605.03 3	1566.13 3	
SLAIN motif-containing protein 2	SLAIN2	7	1166.26666 7	1794.16 7	1665.4	1517.43 3	1148.93 3	1151.46 7
Ribosomal RNA processing protein 1 homolog B	RRP1B	29	4978	7344.06 7	6811.3	6212.03 3	5127.6	4947.26 7
Acetyl-CoA acetyltransferase, cytosolic	ACAT2	11	1637.93333 3	1302.53 3	1103.06 7	1101.76 7	1146.5	1207.46 7

Isoform 2 of Syntaxin-binding protein 1	STXBP1	8	348.333333 3	676.533 3	578.733 3	572.266 7	502.766 7	539.066 7
Serine/threonine-protein kinase mTOR	MTOR	15	1299.76666 7	2452.36 7	2377.56 7	2074.43 3	1701.33 3	1769.4
E3 ubiquitin-protein ligase TRIM32	TRIM32	7	175.333333 3	449.433 3	431.2	380.233 3	358.6	360.133 3
Mortality factor 4-like protein 1	MORF4L1	4	639.8	887.033 3	1239.76 7	750.5	604.2	585.433 3
Exosome complex component MTR3	EXOSC6	8	2284.13333 3	3277.4	3206.7	2773.2	2356.2	2567.13 3
Protein SGT1 homolog	SUGT1	17	4359.8	8024.23 3	7371.26 7	6790.36 7	5395.56 7	5947.13 3
WD repeat-containing protein 89	WDR89	2	342.9	504.5	423.766 7	426.933 3	447.233 3	451.466 7
Arf-GAP domain and FG repeat-containing protein 2	AGFG2	2	332.133333 3	925.666 7	934.066 7	783.4	636.366 7	658.5
Protein Mis18-alpha	MIS18A	3	105.4	261.033 3	359.433 3	220.933 3	130.966 7	129.1
SYNCRIP protein (Fragment)	SYNCRIP	1	14659.1666 7	24891.0 3	20661.8 3	21069.8	17276.8	19135.3 3
Mitotic-spindle organizing protein 1	MZT1	1	204.666666 7	219.166 7	212.666 7	185.566 7	160.066 7	141.466 7
Ras-related protein Rab-1A	RAB1A	12	6686.9	15250.2	12774.8 7	12915.6	9663.63 3	11819.6 7
Isoform 3 of Double-strand break repair protein MRE11A	MRE11A	21	3147.36666 7	6145.93 3	5510.4	5205.46 7	4403.16 7	4659.46 7
CTTNBP2 N-terminal-like protein	CTTNBP2NL	7	1537.5	2278.2	2033.86 7	1929.86 7	1802.06 7	1882

Isoform 2 of Protein FAM177A1	FAM177A1	3	386	698.1	613.066 7	591.366 7	511.6	516.6
Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase	MAN1B1	3	282.766666 7	749.366 7	696.933 3	634.8	401.566 7	598.6
Carbonyl reductase [NADPH] 1	CBR1	17	7189.7	9450.66 7	8021.33 3	8005.83 3	7508.33 3	7917.93 3
60S ribosomal protein L23	RPL23	13	4325.7	6758.03 3	6336.66 7	5725	4526.7	5006.13 3
Actin-related protein 2/3 complex subunit 5	ARPC5	7	2038.66666 7	2931.4	2414.13 3	2483.36 7	2270.96 7	2415.5
SAP domain-containing ribonucleoprotein	SARNP	11	4549.83333 3	7064.4	5647.23 3	5985.06 7	6173.9	6219.26 7
Bcl-2-associated transcription factor 1	BCLAF1	1	4797.46666 7	11319.4 3	9800.76 7	9590.83 3	8536.83 3	8231.3
60S ribosomal protein L23a	RPL23A	17	7632.9	13530.2	12804.7 7	11466.7 3	8931.36 7	9760.16 7
ATP-binding cassette sub-family F member 1 (Fragment)	ABCF1	3	2178.16666 7	4617.8	4335.46 7	3913.66 7	2909.66 7	3462.06 7
CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2	6	1696.76666 7	2062.43 3	2068.86 7	1748.13 3	1429.76 7	1348.93 3
Nucleosome-remodeling factor subunit BPTF (Fragment)	BPTF	1	561.133333 3	1054.23 3	1028.56 7	893.7	828.9	693.2
ATP-dependent RNA helicase DDX24	DDX24	27	3747.53333 3	5117.86 7	4976.6	4338.56 7	3727.8	3635.16 7
Microfibrillar-associated protein 1	MFAP1	10	1922.6	3844.13 3	3403.5	3259.06 7	2890.83 3	2879.4

cDNA FLJ77548, highly similar to Homo sapiens bin3, bicoid-interacting 3, homolog (Drosophila) (BCDIN3), mRNA	14	1780.63333 3	2761.5	2559.7	2341.43 3	2130.6	2026.26 7	
Isoform 4 of Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	1	13770.8	24266.7 3	20943.5	20576.6 7	18319.7	18729.5 3
Isoform 2 of E3 ubiquitin-protein ligase UBR4	UBR4	33	8357.2	19028.4 3	16303.7 7	16135.0 7	12319.9 3	15151.7 7
Mitochondrial import inner membrane translocase subunit Tim23	TIMM23	2	598.033333 3	840.066 7	972.466 7	712.366 7	548.366 7	536.366 7
Eukaryotic translation elongation factor 1 alpha (Fragment)		2	6744.66666 7	18783.67	24183.9	15929.8 7	11431.0 3	12785.1 7
Isoform 2 of Ras-related protein Rab-6A	RAB6A	6	3560.83333 3	5341.16 7	3912.33 3	4530.26 7	4169.16 7	4954.36 7
Ubiquitin carboxyl-terminal hydrolase 28	USP28	10	812.2	1863.96 7	1362.16 7	1581.06 7	1482.36 7	1525.36 7
RILP-like protein 1	RILPL1	5	535.666666 7	926.9	919.1	786.233 3	650.6	718.5
Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	2	14315.1333 3	25237.4 7	21618.9 7	21407.5 3	18771.2	19223.8
E3 ubiquitin-protein ligase RBX1	RBX1	1	625.166666 7	1171.26 7	949.1	993.6	1022.06 7	962.533 3
Isoform 2 of Equilibrative nucleoside transporter 1	SLC29A1	3	488.666666 7	1530.33 3	2007.86 7	1298.26 7	823.733 3	843.233 3
Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A	9	1206.2	2558.33 3	2076.43 3	2170.46 7	1959.23 3	2004.46 7

F-box only protein 2	FBXO2	5	892.433333 3	1550.43 3	1244.03 3	1315.4	1563.83 3	1417.53 3
Alpha-tubulin N-acetyltransferase 1	ATAT1	1	187.433333 3	305.966 7	240.833 3	259.6	215.666 7	244.7
cDNA FLJ78532, highly similar to Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 2 (DNAJB2), mRNA	1	255.533333 3	921.4333	986.7	781.866 7	525.2	713.833 3	
Actin-related protein 2/3 complex subunit 1B	ARPC1B	16	3966.9	7081.53 3	5940.66 7	6009	5454.4	5857.53 3
Actin-related protein 3B	ACTR3B	2	611.833333 3	698.833 3	620.433 3	593.166 7	565.6	593.1
5-methyltetrahydrofolate-homocysteine methyltransferase	MTR	17	2179.36666 7	3787.13 3	2746.3	3215.26 7	2616.86 7	2804.73 3
Dedicator of cytokinesis protein 6	DOCK6	5	412.733333 3	741.066 7	634.333 3	629.2	669.133 3	608.733 3
Immunoglobulin-binding protein 1	IGBP1	9	1724.86666 7	2559.23 3	2394.46 7	2173.06 7	1538.66 7	1734.3
Cell division cycle and apoptosis regulator protein 1	CCAR1	16	2665.8	4884	4139.93 3	4147.2	4067.06 7	4012.4
cDNA, FLJ96533, highly similar to Homo sapiens golgi coiled-coil 1 (GCC1), mRNA	4	389.933333 3	1107.567	1009.43 3	940.566 7	861.966 7	926.8	
Isoform 2 of Integrator complex subunit 3	INTS3	6	1054.43333 3	1365.93 3	1336.23 3	1160.06 7	944.066 7	978.9
Rab9 effector protein with kelch motifs	RABEPK	4	352.733333 3	662.166 7	613.7	562.4	469.1	552.533 3

Retinoic acid-induced protein 1	RAI1	8	456.833333 3	742.1	653.966 7	630.3	708.633 3	579.333 3
E3 ubiquitin-protein ligase RNF114	RNF114	6	511.533333 3	793.366 7	819.566 7	673.866 7	494.733 3	582.566 7
cDNA, FLJ96494, highly similar to Homo sapiens ubiquitin specific peptidase 14 (tRNA- guanine transglycosylase) (USP14), mRNA	26	5045.43333 3	11263.5	10582.8 3	9568.2	6979.96 7	8498.6	
Isoform 4 of Probable 28S rRNA (cytosine(4447)-C(5))- methyltransferase	NOP2	2	11974.2333 3	18203.0 3	16190.9	15465	13125.2 3	13116.4 7
Isoform 5 of DNA-directed RNA polymerase II subunit GRINL1A, isoforms 4/5	POLR2M	3	650.5	824.666 7	685.666 7	700.7	656.266 7	713.433 3
Isoform 2 of Probable 28S rRNA (cytosine(4447)-C(5))- methyltransferase	NOP2	1	11413.8333 3	17473.6	15518.9 7	14847.8 3	12556.5	12703.6
Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	5	1671.2	2353.83 3	1866.8	2000.13 3	2039.43 3	2089.13 3
Isoform 2 of Deoxyuridine 5'- triphosphate nucleotidohydrolase, mitochondrial	DUT	1	1900.03333 3	2800.56 7	2832.03 3	2379.76 7	1477.16 7	1560.76 7
THUMP domain-containing protein 3	THUMPD3	5	1001.53333 3	1716.73 3	1590.8	1458.9	1308.23 3	1362.1
Adrenodoxin, mitochondrial	FDX1	5	1173.46666 7	1501.6	1385.5	1276.1	1267.4	1114.56 7

Coiled-coil domain-containing protein 115	CCDC115	2	335.5	431.066 7	411.666 7	366.366 7	320.6	321.266 7
RNA-binding protein 42	RBM42	6	956.033333 3	2052.7	1990.43 3	1744.8	1378.16 7	1307.33 3
Isoform 3 of Large proline-rich protein BAG6	BAG6	19	2417.7	4525.26 7	4161.76 7	3846.6	3010.66 7	3478.53 3
cDNA FLJ16308 fis, clone PUAEN2006335	1	1893.8	4248.733	3135.33 3	3611.73 3	3316.2	3589.86 7	
Mitochondrial peptide methionine sulfoxide reductase	MSRA	3	253.333333 3	706.2	683.3	600.366 7	475.033 3	533.266 7
Ras-related C3 botulinum toxin substrate 2	RAC2	1	1487.53333 3	3462.2	3515.9	2943.46 7	2071.66 7	2617.56 7
60S ribosomal protein L37a	RPL37A	6	2388.66666 7	4501.53 3	4168.1	3827.26 7	2957.9	3148.73 3
MORC family CW-type zinc finger protein 2	MORC2	8	1071.8	1686.66 7	1633.7	1434.06 7	1224.66 7	1352.4
Ataxin-10	ATXN10	12	3057.8	5002.16 7	5116.33 3	4253.06 7	3048.26 7	3377.63 3
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	2	563.733333 3	1025.06 7	1064.33 3	871.566 7	582.366 7	625.933 3
Cleavage and polyadenylation specificity factor subunit 4	CPSF4	5	1136.1	1654.13 3	1383.1	1406.56 7	1401.73 3	1358.76 7
Elongation factor 1-alpha 1	PTI-1	2	17599.5666 7	26603.8 3	31604.6 3	22628.5	16529.3 3	19110.6 7
Peptidyl-prolyl cis-trans isomerase B	PPIB	18	7736.83333 3	17760.6 7	12923.3 7	15107.8 7	14043.2 7	15132.3 3

Isoform 3 of Nuclear autoantigenic sperm protein	NASP	34	9551.53333 3	17682.7	17128.6	15042.6 3	12158.5 7	12406.4 7
Probable ATP-dependent RNA helicase DDX5	DDX5	30	14095.3666 7	21370.5	25580.5 7	18182.3	13671.5 7	13182.2 7
Isoform 4 of E3 ubiquitin-protein ligase UBR3	UBR3	6	440.3	558.433 3	493.6	475.166 7	415.166 7	437.6
Acid phosphatase 1 isoform c variant (Fragment)		9	2598.83333 3	4286.633	3558.46 7	3647.63 3	3032.06 7	3459.56 7
Nucleosome-remodeling factor subunit BPTF (Fragment)	BPTF	1	454.233333 3	891.666 7	894.633 3	758.8	693.533 3	565.666 7
Serine/threonine-protein kinase PLK		12	1379.06666 7	2162.73 3	3241.26 7	1840.5	1548.76 7	1586.23 3
NUP98/PHF23 fusion 2 protein (Fragment)		3	1620.63333 3	2865.333	2756.7	2438.46 7	2219.8	2158.06 7
6-phosphogluconolactonase	PGLS	11	3441.06666 7	4980.93 3	4102.7	4238.96 7	3774.06 7	4229.06 7
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, isoform CRA_c	SMARCB1	3	567.6	1077.83 3	1170	917.3	656.533 3	723.933 3
cDNA FLJ55582, highly similar to Homo sapiens DPH1 homolog (DPH1), mRNA		3	257.966666 7	293.9	240.666 7	250.133 3	209.3	229.7
Isoform 2 of Formin-like protein 2	FMNL2	8	2538	6204.33 3	4820.16 7	5282	4997.5	5533.93 3
Cell growth-regulating nucleolar protein	LYAR	26	5099.26666 7	8881.1	7861.33 3	7561.13 3	6816.16 7	6520.8

Adaptin ear-binding coat-associated protein 1	NECAP1	3	754.233333 3	1405.33 3	1290.06 7	1196.5	862	1169.7
Secretory carrier-associated membrane protein		2	299.533333 3	365.8667	327.833 3	311.5	270.133 3	270.3
Beta-4 tubulin (Fragment)		2	5350.33333 3	7138.3	6095.56 7	6077.7	5555.8	5540
Beclin-1	BECN1	6	686.533333 3	1365.3	1288.43 3	1162.6	861	880.366 7
Misshapen-like kinase 1	MINK1	4	595.866666 7	701.666 7	616.133 3	597.5	616.766 7	560.7
DNA-directed RNA polymerase II subunit RPB9	POLR2I	3	793.733333 3	988.833 3	932.466 7	842.1	829.066 7	790.6
Major centromere autoantigen B	CENPB	4	308.1	545.966 7	561.533 3	465.033 3	421.033 3	449.266 7
Isoform 2 of Voltage-dependent anion-selective channel protein 2	VDAC2	20	6272.26666 7	15627.3 3	15381	13311.2 7	10559.8 7	11499.6 7
MAP7 domain-containing protein 1	MAP7D1	16	2508.43333 3	3088.8	3418.76 7	2631.03 3	2301.13 3	2198.4
tRNA-splicing ligase RtcB homolog	RTCB	25	5402.33333 3	10307.9 7	9524.76 7	8780.43 3	7031.7	8166.33 3
Isoform 5 of Muscleblind-like protein 1	MBNL1	1	1322.8	2359.3	1836.53 3	2009.86 7	1864.53 3	2122
cDNA FLJ32640 fis, clone SYNOV2001033, highly similar to U3 small nucleolar RNA-associated protein 6 homolog		9	1035.36666 7	1805.267	1625.96 7	1537.9	1297	1340.13 3

Protein phosphatase 1B	PPM1B	7	645.966666 7	1563.2	1290.5	1331.7	1184.16 7	1196.43 3
Ubiquilin-2	UBQLN2	4	1139.03333 3	1442	1250.36 7	1228.5	1179.2	1276.03 3
CYTSA protein	CYTSA	7	1174.53333 3	1677.3	1735.23 3	1429.3	1283.56 7	1230.4
LIM domain-containing protein 1	LIMD1	6	848.833333 3	1141.06 7	1002.33 3	972.366 7	820.133 3	921.7
Nitric oxide synthase-interacting protein		11	2422.1	3324.06 7	3606.53 3	2832.7	1895.83 3	1988.6
General transcription factor IIE subunit 1	GTF2E1	4	292.633333 3	444.7	396.566 7	379	332.6	328.6
CLK4-associating serine/arginine-rich protein	CLASRP	3	442.666666 7	576.4	510.033 3	491.3	468.333 3	519.566 7
Kinesin-like protein	KIF3C	1	315.033333 3	618.433 3	578.666 7	527.133 3	427.266 7	465.466 7
cDNA FLJ13037 fis, clone NT2RP3001268, highly similar to Zinc finger protein 228	1	281	440.8667	392.933 3	375.8	345.4	325.533 3	
Transmembrane 9 superfamily member 4	TM9SF4	7	997.366666 7	2237.26 7	2137.93 3	1907.6	1902.1	1692.96 7
cDNA, FLJ94609		10	2592.5	4447.86 7	4556.7	3792.5	2809.5	3133.8
Isoform 5 of Non-canonical poly(A) RNA polymerase PAPD5	PAPD5	7	383.666666 7	466.7	460.966 7	397.966 7	336	356.966 7
CCR4-NOT transcription complex subunit 11	CNOT11	5	587.3	1288.96 7	1187.66 7	1099.23 3	939.133 3	957.733 3

Isoform 3 of Homeobox protein cut-like 1	CUX1	10	963.366666 7	1505.03 3	1395.86 7	1283.56 7	1305.7	1208.53 3
Ras-related protein Rab-21	RAB21	6	769.533333 3	1576.7	1490.03 3	1344.7	1111.5	1230.1
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	12	2189.63333 3	4335.06 7	3951.63 3	3697.23 3	3153.86 7	3083.36 7
Zinc finger RNA-binding protein	ZFR	2	5639.36666 7	10253.0 7	9057.13 3	8744.7	7545.53 3	7832.43 3
Tyrosine-protein phosphatase non-receptor type 23	PTPN23	13	1739.1	3263.9	2882.43 3	2783.9	2386.8	2551.86 7
cDNA FLJ60912, highly similar to Vinexin		10	1477.1	2701.6	2134.73 3	2304.33 3	2014.16 7	2286.33 3
T-complex protein 1 subunit gamma (Fragment)		46	17147.3333 3	31284.03	29779.5 7	26684.5 3	19292.9 3	23008.7 7
Plastin-3	PLS3	22	7337.33333 3	14911.9	12951.0 7	12720.7	10842.1	12035.1 3
Putative zinc finger protein 876	ZNF876P	2	433.733333 3	811	702.233 3	691.866 7	773.366 7	714.5
Isoform 8 of Calcium/calmodulin-dependent protein kinase type II subunit gamma	CAMK2G	7	1731.96666 7	3149.8	3164.43 3	2687.53 3	2530.33 3	2607.16 7
Histone H3.3	H3F3A	7	5641.06666 7	9996.06 7	9555.1	8529.13 3	7297.16 7	8732.76 7
Probable 18S rRNA (guanine-N(7))-methyltransferase	WBSCR22	4	749.933333 3	1209.73 3	1171.3	1032.23 3	827.5	733.9

RNA binding protein (Autoantigenic, hnRNP- associated with lethal yellow) long isoform variant (Fragment)	RALY	18	6148.03333 3	11984.3	10237.2 3	10226.0 3	9151.93 3	9011.46 7
Deubiquitinating protein VCIP135	VCIP1	7	1037.56666 7	1711.4	1419.96 7	1460.33 3	1258.4	1404.76 7
Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1AX	8	6250.96666 7	12917.3 3	11993.6 7	11022.5 7	8142.13 3	9182.06 7
Centromere-associated protein E	CENPE	2	244.666666 7	313.766 7	471.866 7	267.766 7	209.9	214.666 7
ATP-dependent 6- phosphofructokinase, platelet type	PFKP	31	9177.73333 3	18687.4 7	13595.5	15958.6 3	15969.1	16336.5
Cullin-3	CUL3	13	1762.36666 7	3019.03 3	3244.53 3	2578.2	2030.03 3	2172.66 7
Ataxin 3 variant ref (Fragment)	ATXN3	3	162.666666 7	196.333 3	167.7	167.666 7	169.766 7	176.233 3
Mitogen-activated protein kinase kinase kinase 2	MAP3K2	5	487.866666 7	1156.7	1030.2	987.833 3	731.866 7	829.066 7
Isoform 4 of Protein phosphatase methylesterase 1	PPME1	12	3489.96666 7	6592.96 7	4995.3	5630.76 7	4657.73 3	4935.03 3
Anaphase-promoting complex subunit CDC26	CDC26	3	1091.36666 7	1469.13 3	1353.9	1254.93 3	1058.46 7	1140.6
Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	21	2142.86666 7	4757.13 3	4166.56 7	4063.7	3351.43 3	3864.76 7
Mediator of RNA polymerase II transcription subunit 20	MED20	3	166.133333 3	194.333 3	162.533 3	166.033 3	162.2	172.9

Nucleolin (Fragment)	NCL	1	24765.7333 3	40442.7 7	33533.5 7	34558.0 7	32092.0 3	31166.6
Non-structural maintenance of chromosomes element 3 homolog	NSMCE3	2	449.466666 7	960.533 3	918.3	820.8	743.266 7	767.233 3
Thymocyte nuclear protein 1	THYN1	10	1469.96666 7	4104.4	3668.73 3	3507.4	2876.96 7	3242.16 7
cDNA, FLJ93681, highly similar to Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA	5	987.933333 3	2010.3	1537.4	1718.1	1675.46 7	1646.66 7	
Protein diaphanous homolog 3	DIAPH3	6	799.2	1388.7	1489.4	1186.93 3	889.3	847.6
TIMELESS-interacting protein	TIPIN	2	387.233333 3	564.966 7	617.7	482.9	405.933 3	422.366 7
Microtubule-associated protein RP/EB family member 1	MAPRE1	17	5404.26666 7	8590	7887.26 7	7342.3	6187.5	6248.23 3
Translation machinery- associated protein 7	TMA7	5	2398.63333 3	3340.8	2878.7	2855.6	2536.7	2574.06 7
Exocyst complex component 4	EXOC4	10	885.266666 7	1484.43 3	1323.03 3	1268.93 3	1070.13 3	1197.86 7
CCDC24 protein	CCDC24	1	80.8	133.133 3	140.3	113.833 3	82.5333 3	90.9
Protein kinase C iota type	PRKCI	5	292.6	342.5	298.666 7	292.866 7	245.166 7	262.5
Isoform 1 of Synaptic functional regulator FMR1	FMR1	1	2400.16666 7	4056.06 7	3664.06 7	3468.3	3130.36 7	3365.43 3

Protein SMG9	SMG9	5	418.433333 3	472.4	420.5	403.966 7	366.166 7	368.3
Peptidyl-prolyl cis-trans isomerase-like 4	PPIL4	11	1790.6	3413.3	3208.86 7	2918.86 7	2264.13 3	2393.56 7
RNA exonuclease 4	REXO4	7	1132.86666 7	2003.96 7	1954.66 7	1713.86 7	1495.23 3	1410.5
Ribonuclease H2 subunit A	RNASEH2A	8	1906	2290.46 7	2249.63 3	1958.9	1624.86 7	1718
Transcription elongation factor 1 homolog	ELOF1	1	429.4	506.333 3	456.5	433.066 7	478.566 7	430.133 3
Peroxisomal NADH pyrophosphatase NUDT12	NUDT12	5	1141	1544.33 3	1367.23 3	1320.9	1284.2	1251.83 3
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	16	4329.93333 3	7322.16 7	6365.06 7	6262.8	5273.8	4914
Phytanoyl-CoA dioxygenase, peroxisomal	PHYH	5	921.766666 7	1704.2	1229.33 3	1457.7	1707.3	1428.26 7
60S acidic ribosomal protein P1	RPLP1	3	2594.96666 7	2484.36 7	2400.93 3	2125.03 3	1645.5	1987.6
Tyrosine--tRNA ligase, cytoplasmic	YARS	46	11539.6666 7	24659.8 3	20863.5 7	21093.2 7	16102.2	19362.4 3
RING finger and SPRY domain-containing protein 1	RSPRY1	3	203	238.566 7	214.3	204.066 7	171.666 7	188.6
cDNA, FLJ93224		7	840.9	1482.16 7	1376.66 7	1267.83 3	991	1090.16 7
Rhophilin-2	RHPN2	4	154.633333 3	321.2	273.433 3	274.766 7	260.033 3	259.133 3

39S ribosomal protein L51, mitochondrial	MRPL51	3	144.866666 7	184.633 3	161.333 3	157.966 7	160.733 3	164.966 7
YEATS domain-containing protein 4	YEATS4	3	568.1	685.5	645.1	586.5	595.6	569.5
Eukaryotic translation initiation factor 3 subunit I	EIF3I	13	3756.13333 3	6001.06 7	5772.73 3	5134.5	3754.9	4301.96 7
Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	29	6154.8	11280.9 7	10129.8 3	9653.36 7	8402.2	9198.3
Guanine nucleotide-binding protein subunit alpha-11	GNA11	5	1248.1	2865.4	2643.16 7	2452.16 7	2380.53 3	2287.7
Ubiquitin-like 7 (Bone marrow stromal cell-derived), isoform CRA_a	UBL7	2	484.666666 7	862.066 7	771.2	737.8	689	1039.86 7
Isoform 3 of Phosphatidate cytidyltransferase, mitochondrial	TAMM41	4	496.9	750.533 3	660.533 3	642.533 3	571.2	606.1
Influenza virus NS1A-binding protein	IVNS1ABP	5	524.533333 3	1166.03 3	1118.96 7	998.266 7	871.233 3	959.2
Nucleoporin 153kDa, isoform CRA_a	NUP153	37	8641.16666 7	12841.5	11550.6 3	10994.4 3	10531.8	9995.8
mRNA export factor	RAE1	15	3010	5512.06 7	4916.83 3	4719.4	4140.26 7	4481.7
Msx2-interacting protein	SPEN	9	904.833333 3	1228.5	1126.66 7	1051.86 7	973	989.4
60S ribosomal protein L15	RPL15	9	3309.1	7179.03 3	6787.6	6147.56 7	4441.2	4538.7

Tyrosine-protein phosphatase non-receptor type 11	PTPN11	25	3508.03333 3	7413.06 7	6858.3	6348.5	4792.53 3	5732.9
YKT6 v-SNARE protein	YKT6	12	2051	6166.9	5909.1	5281.43 3	3886.06 7	4579.26 7
Myosin IC, isoform CRA_a	MYO1C	1	5428.6	12428.7	10404.2 7	10644.8 3	9799.66 7	9733.06 7
Polyadenylate-binding protein	PABPC3	6	9465.6	16588.7	16155.6 7	14210.7 7	10439.4	11878.6 3
CDK2-associated and cullin domain-containing protein 1	CACUL1	3	626.2	657.666 7	586.266 7	563.4	503.133 3	552.066 7
Guanine nucleotide-binding protein-like 1	GNL1	14	2854.9	4918.4	4416.36 7	4213.73 3	3764.7	4003.73 3
Aldo-keto reductase family 1 member C1	AKR1C1	15	4924.86666 7	9724.46 7	8757.86 7	8331.63 3	6506.9	7551.6
Ras-related protein Rab-2A	RAB2A	8	5820.93333 3	9594.63 3	8351.73 3	8220.76 7	6532.96 7	8109.63 3
Transcription factor Sp4	SP4	2	459.066666 7	664.5	586.933 3	569.366 7	541.2	539.866 7
Long-chain fatty acid transport protein 4	SLC27A4	6	824.766666 7	1535.86 7	1424.53 3	1316	1127.1	1177.83 3
IQ and AAA domain-containing protein 1	IQCA1	6	928.9	1988.36 7	1719.66 7	1703.86 7	1332.63 3	1635.16 7
60S ribosomal protein L39	RPL39	2	1136.46666 7	1631.43 3	1489.1	1398.4	1213.96 7	1327.9
Kinesin light chain 2	KLC2	17	4076.83333 3	7209.76 7	7364.23 3	6180.4	4670.26 7	5025.76 7

IQ motif containing GTPase activating protein 2, isoform CRA_b	IQGAP2	14	2220.76666 7	5159.36 7	4439.9	4423.1	3918.33 3	4428.4
Isoform 3 of Chromatin modification-related protein MEAF6	MEAF6	6	727.433333 3	933.7	900.8	800.466 7	724.133 3	707.3
Isoform 9 of Multidrug resistance-associated protein 1	ABCC1	10	775.166666 7	1020.1	856.766 7	874.566 7	992.533 3	846.2
Zinc finger protein 787	ZNF787	3	551.766666 7	726.7	620.966 7	623.033 3	567.433 3	569.133 3
Splicing factor, arginine/serine-rich 15	SCAF4	8	1912.6	2860.23 3	2619.8	2452.3	2343.4	2200.3
U3 small nucleolar RNA-associated protein 18 homolog	UTP18	12	2540.16666 7	5013.73 3	4920.33 3	4298.8	3560.73 3	3499.76 7
Isoform 4 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS	1	1963.16666 7	3770.66 7	3253	3233.06 7	3113.2	3191.96 7
AMMECR1-like protein	AMMECR1L	1	527.8	1123.03 3	1363.4	962.933 3	733.166 7	761.866 7
Chromosome transmission fidelity protein 8 homolog isoform 2	CHTF8	1	492.466666 7	887.6	778.666 7	761.066 7	599.666 7	722.866 7
Erlin-2	ERLIN2	11	3932.16666 7	5636.93 3	5024	4833.8	5225	4714.66 7
NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	NDUFV3	2	259.933333 3	411.666 7	311.833 3	353.033 3	316.4	280.4

Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	13	3365.73333 3	5870.76 7	6343.76 7	5035.06 7	5086.03 3	4672.13 3
Integrator complex subunit 5	INTS5	3	250.266666 7	362.066 7	336.066 7	310.533 3	277.633 3	323.466 7
Negative elongation factor E	NELFE	11	1920.8	2709.63 3	2419.4	2324.03 3	2201.13 3	2123.9
Uncharacterized protein C7orf50	C7orf50	8	3001.36666 7	4472.26 7	4264.8	3835.83 3	2832.56 7	3410.8
Isoform 2 of Serine/threonine-protein kinase Sgk1	SGK1	1	139.533333 3	232.166 7	198.766 7	199.133 3	189.466 7	178.6
Isoform 2 of 39S ribosomal protein L30, mitochondrial	MRPL30	2	586.933333 3	732.933 3	657.266 7	628.7	568.066 7	587.566 7
Ribosomal protein L10 isoform A (Fragment)	RPL10	16	8394.96666 7	10135	9316.36 7	8693.86 7	6717.13 3	8007.8
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	6	1753.06666 7	2853.8	2642.76 7	2448.13 3	2117.26 7	2118.9
Terminal uridylyltransferase 7	ZCCHC6	3	236.133333 3	442.033 3	408.8	379.233 3	332.166 7	365.3
cDNA FLJ16146 fis, clone BRAMY2040159, highly similar to Homo sapiens MRIP-1 mRNA		1	152.633333 3	258.4333	245.8	221.733 3	186.833 3	194.266 7
Golgi membrane protein 1	GOLM1	5	1216.8	2786.46 7	3117.16 7	2390.93 3	1895.7	2262.06 7
GTPase HRas	HRAS	2	846.966666 7	1325.86 7	1124.36 7	1137.83 3	974.333 3	892.933 3
Niemann-Pick disease, type C1 variant (Fragment)		4	221.2	584.8333	685.6	501.933 3	475.633 3	443.233 3

Protein SDA1 homolog	SDAD1	12	1904.33333 3	4030.46 7	4501.03 3	3459.2	2450.33 3	2770.8
Nuclear receptor corepressor 2	NCOR2	3	221.966666 7	313.066 7	279.166 7	268.733 3	252.933 3	256.4
Isoform 2 of Histone-lysine N-methyltransferase EZH2	EZH2	6	1150.3	1697.6	1771.2	1457.23 3	1314.76 7	1271.56 7
40S ribosomal protein S21	RPS21	7	1407.16666 7	2048.2	1915.56 7	1758.23 3	1521.26 7	1744.2
Coiled-coil domain-containing protein 93	CCDC93	4	464.433333 3	892.4	736.2	766.066 7	687	689.933 3
cDNA FLJ57476		1	350.8	457.4	382.133 3	392.666 7	344.266 7	400.433 3
E3 ubiquitin-protein ligase RING1	RING1	3	403.666666 7	361.1	330.9	310	278	290.966 7
TOX high mobility group box family member 4	TOX4	5	1672.76666 7	2209.1	2103.16 7	1896.5	1568.3	1734.16 7
Isoform 6 of Ankyrin repeat and KH domain-containing protein 1	ANKHD1	20	4461.9	6055.13 3	5342.56 7	5198.83 3	4390.83 3	4830.83 3
Impact homolog (Mouse), isoform CRA_c	IMPACT	4	203.133333 3	639.433 3	561.033 3	549.066 7	478.2	499.5
Zinc finger RNA binding protein	ZFR	1	5218	8914.96 7	8097.43 3	7655.56 7	6505.83 3	6861.06 7
Isoform 7 of Protein MTO1 homolog, mitochondrial	MTO1	5	805.9	1110.76 7	1107.83 3	953.866 7	798.9	845.533 3
Synaptosomal-associated protein 23	SNAP23	12	2578.43333 3	4548.16 7	4258.26 7	3905.9	3191.86 7	3457.26 7

EEF1A1 protein (Fragment)	EEF1A1	1	14594.1	14879.2 7	13732.6 3	12778.2 7	9581.5	11749.3 3
Unconventional myosin-Ic	MYO1C	7	6950.66666 7	14614.7 7	12152.0 3	12551.1 7	11548.6 3	11264.6 3
Peroxisomal bifunctional enzyme	EHHADH	9	1044	1999.66 7	1597.26 7	1717.36 7	1685.33 3	1783.63 3
TBC1 domain family member 15	TBC1D15	13	1414.2	2708.23 3	2481.2	2326.13 3	1837.03 3	2407.3
ATPase family AAA domain-containing protein 5	ATAD5	2	174.266666 7	152.9	211.233 3	131.333 3	111.466 7	91.3333 3
Coatomer subunit beta	COPB1	30	4369.4	9092.93 3	8225.83 3	7810.83 3	5999.53 3	7254.2
60S ribosomal protein L32	RPL32	9	4920.33333 3	9988.93 3	8928.2	8580.6	6366.66 7	7035.86 7
Programmed cell death protein 10	PDCD10	3	493.433333 3	1049.2	971.1	901.3	683.7	739
ATP-dependent RNA helicase DDX55	DDX55	7	531.866666 7	1266.4	1284.8	1087.96 7	853.6	964.866 7
Kinesin-like protein KIF3B	KIF3B	5	1148.8	1964.16 7	1809.9	1687.5	1415.63 3	1617.16 7
Huntingtin-interacting protein 1	HIP1	11	1631.3	2806.36 7	2572.46 7	2411.4	2325.06 7	2241.96 7
SNX5 protein (Fragment)	SNX5	14	1869.76666 7	3600.8	3341.26 7	3094.16 7	2217.4	2758.13 3
Nucleolar MIF4G domain-containing protein 1	NOM1	8	1831.43333 3	3447.16 7	3215.5	2962.6	2470.33 3	2518.43 3
Zinc finger C3H1 domain-containing protein	ZFC3H1	4	409.5	884.3	663.666 7	760	771.566 7	768.6

Glycogen synthase kinase-3 alpha	GSK3A	9	2093.63333 3	3959.26 7	3288.86 7	3402.83 3	2686.33 3	2815.46 7
T-complex protein 1 subunit epsilon	CCT5	36	12252.4666 7	26141.2	24174.8 3	22473.4 3	17188.4 3	19985
Pre-mRNA-processing factor 39	PRPF39	7	886.633333 3	1780.93 3	1588.6	1531.1	1275.8	1395.6
cDNA, FLJ94330		2	152.966666 7	166.266 7	140.933 3	142.966 7	130.933 3	145.233 3
Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	9	1781.36666 7	3602.36 7	3220.8	3097.7	2508.66 7	2682.3
SLIT-ROBO Rho GTPase activating protein 2	SRGAP2	7	1461.06666 7	2859.2	2566.73 3	2458.83 3	2092.43 3	2284.46 7
Protein FAM76B	FAM76B	3	381	592.6	530.2	509.733 3	438.8	501.3
Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	14	2139.33333 3	4151.3	4302.9	3571.1	3433.7	3224.7
Isoform 6 of GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	22	3248.6	5650.8	5160.33 3	4861.56 7	3885.2	4381
PAX3- and PAX7-binding protein 1	PAXBP1	6	1118.8	1437.7	1420.86 7	1236.93 3	1119.66 7	1210.1
Peflin	PEF1	3	499.866666 7	572.9	498.833 3	492.9	429.9	470.3
Serine/threonine-protein kinase greatwall	MASTL	2	242.966666 7	255.366 7	282.333 3	219.733 3	192.7	178.866 7

cDNA FLJ56439, highly similar to Pantothenate kinase 4 (EC 2.7.1.33)		12	1977.23333 3	4579.633	4312.4	3940.73 3	3167.53 3	3771.63 3	
Soluble calcium-activated nucleotidase 1	CANT1	7	545.666666 7	1295.86 7	1325.3	1115.13 3	872.3	960.633 3	
Small nuclear ribonucleoprotein E	SNRPE	3	1114.7	1562.5	1298.73 3	1344.66 7	1205.6	1329.36 7	
Isoform 2 of Cdc42-interacting protein 4	TRIP10	24	4098.33333 3	8029.43 3	7207.46 7	6910.4	6342.83 3	6524.96 7	
Tuftelin-interacting protein 11	TFIP11	6	906.4	1204.26 7	1194.16 7	1036.6	888.733 3	976.566 7	
Nucleoside diphosphate-linked moiety X motif 22	NUDT22	1	107.6	52.2	50.4666 7	44.9333 3	54.3333 3	52.3333 3	
40S ribosomal protein S8	RPS8	19	11334.7666 7	16599.7	15516.0 7	14291.4 7	12086.8	12465.1	
General transcription factor 3C polypeptide 3	GTF3C3	6	849.9	815.266 7	824.833 3	701.966 7	634.066 7	624.7	
DNA methyltransferase 1-associated protein 1	DMAP1	7	322.533333 3	450.633 3	420.766 7	388.066 7	425.3	320.2	
Retinal dehydrogenase 1	ALDH1A1	29	23220.7	43643.0 7	36961.2 7	37583.9 3	32533.5	34799.6	
Lactoylglutathione lyase	GLO1	10	4357.33333 3	6928.3	6061.83 3	5967	5030.46 7	5374.93 3	
Lin-7 homolog C variant (Fragment)		4	1002.6	1644.96 7	1578.7	1416.73 3	1351.56 7	1319.93 3	
Isoform 1 of Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	ASAP1	10	922.266666 7	1366.36 7	1180.63 3	1176.8	1146.53 3	1142.4	

Zinc finger CCCH domain-containing protein 13	ZC3H13	11	739.2	1410.7	1254.33 3	1215	1057.26 7	1089.26 7
RWD domain-containing protein 1	RWDD1	4	500.1	732.533 3	697.766 7	630.933 3	513.666 7	540.7
U4/U6 small nuclear ribonucleoprotein Prp3	PRPF3	23	5941.06666 7	8972.5	8313	7729.16 7	6547	6894.76 7
Transcriptional activator protein Pur-beta	PURB	11	2503.33333 3	3969.83 3	3431.56 7	3419.9	3045.5	3292.2
Muscleblind-like protein 1	MBNL1	2	1412.93333 3	2439.13 3	1929.83 3	2101.3	1930.16 7	2211.1
Prolyl 3-hydroxylase OGFOD1	OGFOD1	10	691.8	1857.5	1970.33 3	1600.6	1126.66 7	1230
Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS	1	1616.6	3332.73 3	2843.36 7	2871.93 3	2779.7	2804.96 7
Isoform 5 of Ubiquitin-associated protein 2-like	UBAP2L	2	6967.93333 3	10061.3 3	9094.7	8671.23 3	6954.33 3	7251.96 7
Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	13	4088.93333 3	8766.43 3	7666.23 3	7555.9	6238.2	6888.96 7
E3 ubiquitin-protein ligase RING2	RNF2	3	302.4	344.066 7	317.5	296.566 7	265.266 7	279.066 7
Atlastin-3	ATL3	11	1122.23333 3	1919.3	1898.1	1654.36 7	1337.03 3	1502.86 7
SWI/SNF-related matrix-associated actin-dependent	SMARCAL1	7	328	1082.9	944.133 3	933.466 7	846.166 7	1045.26 7

regulator of chromatin subfamily A-like protein 1								
Clathrin interactor 1	CLINT1	18	3586.73333 3	7125.93 3	6155.16 7	6143.2	4961.23 3	5491.33 3
Partner of Y14 and mago	PYM1	9	2874.73333 3	4034.96 7	3197.6	3478.7	3375.16 7	3434.5
40S ribosomal protein S6	RPS6	1	8503.43333 3	13169.1 7	12015.5 3	11354.1 7	9559.73 3	9114.9
cDNA FLJ76871, highly similar to Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA		22	2106.66666 7	4727.067	4640.36 7	4075.6	3412.43 3	3588.16 7
Secretory carrier-associated membrane protein 3	SCAMP3	2	2796.36666 7	4220.26 7	3913.46 7	3638.73 3	3162.46 7	3340.56 7
Isoform 4 of 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	PFKFB3	6	760.866666 7	1532.03 3	1181.43 3	1321	1133.13 3	1148.96 7
Isoform 4 of Transcription initiation factor TFIID subunit 1	TAF1	5	515.233333 3	658.466 7	655.333 3	567.766 7	545.366 7	531.8
Isoform 7 of Synaptic functional regulator FMR1	FMR1	1	2585.13333 3	4255.4	3875.66 7	3669.43 3	3277.6	3546.7
Biogenesis of lysosome-related organelles complex 1 subunit 3	BLOC1S3	2	694.3	1455.73 3	1177.3	1255.53 3	1097.5	1204.46 7
Bcl-2-associated transcription factor 1	BCLAF1	3	5475.53333 3	12460.3 3	10783.0 7	10748.2	9596.13 3	9220.76 7
Vesicle transport protein USE1	USE1	2	493.366666 7	870.7	818.866 7	751.133 3	708.8	782.566 7

Zinc finger protein 551 (Fragment)	ZNF551	2	123.666666 7	420.166 7	349.466 7	362.5	302.066 7	307.333 3
Striatin	STRN	15	1850.23333 3	3500.4	3264.43 3	3020	2758.93 3	2776.26 7
U6 snRNA-associated Sm-like protein LSM5	LSM5	2	238.366666 7	222.333 3	197.9	191.833 3	193.933 3	209.2
LIM domain-containing protein ajuba	AJUBA	1	147.166666 7	277.633 3	225.466 7	239.566 7	204.933 3	192.8
Isoform 2 of Serine/threonine- protein kinase tousled-like 1	TLK1	4	629.7	1276.46 7	1207.5	1101.56 7	876.7	940.5
UPF0690 protein C1orf52	C1orf52	4	193	687.633 3	682.233 3	593.5	474.566 7	462.133 3
Intersectin-2	ITSN2	5	497.533333 3	661.233 3	599.266 7	570.733 3	539.7	584.633 3
Signal recognition particle 19 kDa protein	SRP19	12	2759.8	4222.66 7	3765.8	3645.16 7	3085.43 3	3540.96 7
60S ribosomal protein L22	RPL22	9	4059.83333 3	5140.1	4812.63 3	4437.53 3	3562.6	4008.33 3
Zinc finger protein 609	ZNF609	6	1205.63333 3	1339.9	1152.23 3	1156.76 7	1071.36 7	1056.03 3
Isoform 2 of Pre-mRNA-splicing factor ISY1 homolog	ISY1	12	2979.66666 7	3865.96 7	3707.4	3337.63 3	2804.1	2720.06 7
Uncharacterized protein KIAA1143	KIAA1143	7	687.433333 3	1139.43 3	1046.23 3	983.8	855.566 7	934.466 7
Rootletin	CROCC	12	1766.43333 3	2687.46 7	2475.9	2320.66 7	1925.3	2059.16 7
Myeloid leukemia factor 2	MLF2	5	564.2	1019.96 7	862.866 7	880.766 7	795.333 3	973.933 3

Dihydropyrimidinase-related protein 2	DPYSL2	16	13214.2	23916.6	19737.1 7	20653.0 7	17713.4 7	19304.3 3
Isoform 2 of Type-1 angiotensin II receptor-associated protein	AGTRAP	1	517.833333 3	409.966 7	379.3	354.066 7	316.6	316.933 3
39S ribosomal protein L32, mitochondrial	MRPL32	4	464.4	540	514.7	466.4	431.666 7	388.9
T-complex protein 1 subunit eta	CCT7	2	16710.2	27326.7 7	25618.9 7	23609.4 7	18172.7 3	20741.6 7
Retinal dehydrogenase 1 (Fragment)	ALDH1A1	1	7218.43333 3	13403.4 3	11549.7 3	11581.1	10192.1	10991.3 3
Ribosomal RNA-processing protein 8	RRP8	9	1229.3	1844.8	1601.96 7	1594.06 7	1504.4	1426.1
ADP-ribosylation factor-like protein 2-binding protein	ARL2BP	3	331.133333 3	400.866 7	376.266 7	346.4	279.633 3	255.333 3
Isoform 2 of Splicing factor, suppressor of white-apricot homolog	SFSWAP	8	720.133333 3	2093.73 3	1931	1809.26 7	1727.83 3	1663.06 7
Ragulator complex protein LAMTOR1	LAMTOR1	4	757.566666 7	995.933 3	998.733 3	860.7	660.4	786.6
Eukaryotic translation initiation factor 6	EIF6	9	2808.66666 7	3797.46 7	3415.66 7	3281.96 7	2732.56 7	3259.53 3
Protein LYRIC	MTDH	20	4387.3	6215.36 7	4642.76 7	5372.26 7	4818.43 3	5723.7
60S ribosomal protein L27	RPL27	12	5948.16666 7	10142.8	9386.23 3	8767.03 3	7164	6407.1
Protein-L-isoaspartate O-methyltransferase	PCMT1	10	2584.6	4386.56 7	3656.6	3791.66 7	3137.76 7	3767.03 3

cDNA, FLJ93510, highly similar to Homo sapiens JTV1 gene (JTV1), mRNA		8	2372.4	4288.7	4012.93 3	3707.43 3	2883.6	3516.73 3	
WD repeat-containing protein 6	WDR6		4	468	585.266 7	570.233 3	506	378.8	462.166 7
Cytochrome c oxidase assembly protein COX19	COX19		2	519.066666 7	736.9	654.733 3	637.1	577.2	576.533 3
cDNA, FLJ96114, highly similar to Homo sapiens bromodomain and WD repeat domain containing 2 (BRWD2), mRNA		9	732.933333 3	1175.133	971.166 7	1016.06 7	915.933 3	981.3	
Putative ATP-dependent RNA helicase DHX57	DHX57		5	1031	1692.1	1534.1	1463.13 3	1306.3	1447.56 7
40S ribosomal protein S19	RPS19		16	11795.4666 7	15576.6 3	14574.2 3	13469.4 3	10062.7 3	12309.3 7
Serine dehydratase-like	SDSL		2	346.733333 3	324.233 3	306.466 7	280.4	277.666 7	281.666 7
Biotin--protein ligase	HLCS		2	237.866666 7	280.3	260.4	242.433 3	214.166 7	233.4
SAP30-binding protein (Fragment)	SAP30BP		5	656.8	921.733 3	887.866 7	797.233 3	694.5	702.166 7
ER membrane protein complex subunit 1	EMC1		12	983.066666 7	1672.63 3	1656.5	1446.73 3	1201.53 3	1435.96 7
Mediator of RNA polymerase II transcription subunit 1	MED1		14	1604.5	2304.16 7	2236.8	1993.06 7	1804.96 7	1786.8
Protein FRG1	FRG1		5	1125.8	1651.6	1615.23 3	1428.63 3	1072.46 7	1213.13 3

RISC-loading complex subunit TARBP2	TARBP2	2	207.433333 3	241.766 7	206.2	209.133 3	199.966 7	187.166 7
Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	NDUFV3	13	2393.3	3996.76 7	3402.86 7	3457.63 3	3522.76 7	3402.6
Pyrroline-5-carboxylate reductase 2	PYCR2	8	3333.06666 7	5533.96 7	4645.26 7	4787.53 3	4635.26 7	4780.9
Segment polarity protein dishevelled homolog DVL-3	DVL3	1	280.133333 3	365.333 3	298.233 3	316.066 7	308.133 3	307.166 7
Ribosomal L1 domain-containing protein 1	RSL1D1	45	13963.7333 3	25607.8	22259.5 7	22154.8 7	18847.8 3	19677.9
Glycylpeptide N-tetradecanoyltransferase 1	NMT1	9	1826.6	3215.6	2923.66 7	2782.13 3	2228.93 3	2544.23 3
Maternal embryonic leucine zipper kinase	MELK	2	61.5333333 3	68.5	90.9333 3	59.2666 7	46.8666 7	50.9
Ankyrin repeat and LEM domain-containing protein 2	ANKLE2	12	2003.3	3531.1	3569.8	3055.5	2836.06 7	2807.8
Uncharacterized protein	MGC20255	5	815.1	1227.8	1168.46 7	1062.5	855.666 7	813.466 7
DNA ligase		2	247.366666 7	447.466 7	431.3	387.233 3	323.933 3	352.433 3
Proteolipid protein 2	PLP2	1	780.133333 3	840.733 3	803.033 3	727.566 7	675.1	705.533 3
Erythroid differentiation-related factor 1	EDRF1	3	448	672.4	572.866 7	581.9	606.3	551.233 3
Mitotic-spindle organizing protein 2A	MZT2A	3	620.033333 3	678.133 3	633.3	586.866 7	515	521.133 3

Nuclear cap-binding protein subunit 2	NCBP2	6	988	2220.43 3	1961.8	1921.86 7	1722.1	1661.63 3
Mitochondrial import receptor subunit TOM6 homolog	TOMM6	3	575.966666 7	974.066 7	903.866 7	843.133 3	780.733 3	829.266 7
Probable RNA-binding protein 19	RBM19	17	2149.3	4317.6	4298.83 3	3737.3	2936.6	3100.96 7
Zinc finger Ran-binding domain-containing protein 2	ZRANB2	7	1288.76666 7	2658.96 7	2496.6	2301.6	2110.46 7	2159
Nuclear receptor coactivator 3 isoform a variant (Fragment)	2	229.5	218.1	211.4	188.8	165.733 3	164.033 3	
Ubiquitin-conjugating enzyme E2 R1	CDC34	5	686.833333 3	1177.2	1307.23 3	1019.06 7	836.966 7	848.433 3
Isoform 5 of Caldesmon	CALD1	1	7490.93333 3	14085.6 7	10546.7	12193.7 3	12575.9 7	12308.6 3
Enhancer of mRNA-decapping protein 4	EDC4	27	4254.46666 7	6716.26 7	6034.76 7	5814.83 3	4478.2	5156.3
Aldehyde dehydrogenase 5 family member A1 isoform B (Fragment)	ALDH5A1	10	2269.1	3610.13 3	3210.7	3125.76 7	3310.63 3	3133.16 7
F-box only protein 30	FBXO30	2	603.166666 7	1045.43 3	1117.03 3	905.2	649.8	705.166 7
Serine/arginine-rich splicing factor 10	SRSF10	5	948.2	1281.93 3	1100.1	1110	943.333 3	982.633 3
Uncharacterized protein C8orf59	C8orf59	3	805.4	1165.63 3	1330.66 7	1009.4	883.133 3	1077.63 3
39S ribosomal protein L17, mitochondrial	MRPL17	5	1350.43333 3	1487.2	1472.2	1288.03 3	1175.9	1215.93 3

cDNA, FLJ96718, highly similar to Homo sapiens splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) (SFRS10), mRNA		9	1670.86666 7	3008.267	2566.63 3	2605.4	2271.33 3	2164.53 3	
Zinc finger protein 384	ZNF384	2	259.933333 3	302.433 3	240.766 7	261.933 3	243.4	280.5	
Deoxynucleotidyltransferase terminal-interacting protein 2	DNTTIP2	24	6226.03333 3	8090.93 3	7970.93 3	7009.2	6319.73 3	6193.43 3	
Isoform 2 of DNA repair protein RAD50	RAD50	50	8197.33333 3	15287.5	13870.0 7	13244.1	11044.9 3	12591.3	
Rho-related GTP-binding protein RhoG	RHOG	5	1242.8	2548.03 3	2692.93 3	2207.6	1682.63 3	1923.53 3	
Liprin-alpha-1	PPFIA1	15	1997.1	2868.16 7	2509.2	2485.23 3	2290.2	2242.66 7	
CREB-regulated transcription coactivator 2	CRTC2	2	430.533333 3	602.566 7	531.066 7	522.166 7	421.5	494.833 3	
Isoform 3 of Unconventional myosin-Va	MYO5A	4	696.6	1123.53 3	959.4	973.633 3	997.433 3	965.133 3	
CCT7 protein	CCT7	1	15491.2333 3	25898.9 3	24305.7 7	22445.5 3	17121.1 7	19645.4 7	
BetaCstF-64 variant 2	CSTF2	5	3581.66666 7	4967.53 3	4413.86 7	4306.23 3	4189.36 7	3961.3	
Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	AIMP1	18	6376.6	10377.9	9142.16 7	8997.76 7	7561.33 3	8481.36 7	
Remodeling and spacing factor 1	RSF1	27	4186.5	8135.1	7242.43 3	7053.3	6592.26 7	6735.6	

cDNA FLJ60154, highly similar to Centrosomal protein of 110 kDa		3	408.866666 7	443.7	399.5	384.7	363.3	375.7	
Alpha- and gamma-adaptin-binding protein p34	AAGAB	4	311.466666 7	532	521.733 3	461.4	364.4	428.533 3	
DNA topoisomerase 1	TOP1	45	14171.5666 7	29073.7	25732.7	25216.6	21601.4 3	22009.1 7	
60S ribosomal export protein NMD3	NMD3	11	1218.66666 7	2181.86 7	2078.63 3	1892.53 3	1330.83 3	1681.66 7	
CDGSH iron-sulfur domain-containing protein 2	CISD2	8	1045.1	2076.7	1501.16 7	1801.43 3	1711.2	1788	
Isoform 3 of Caldesmon	CALD1	2	7464.03333 3	14014.9	10600.4 3	12158.6 7	12599.4	12378.4 7	
Reticulocalbin-1	RCN1	17	4331.1	10896.3	9460.1	9454.43 3	9199.56 7	9215.66 7	
40S ribosomal protein S30	FAU	3	2271.6	3176.23 3	2983.83 3	2756.03 3	2285.26 7	2508.43 3	
Isoform 2 of Protein SCAI	SCAI	2	81.3333333 3	102.3	84.7333 3	88.7666 7	81.4	76.1333 3	
Annexin A1	ANXA1	16	33661.5	52349.3	45478.4 3	45430.1 7	34263.6 3	43684.8	
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	4	566.4	997.433 3	1081.53 3	865.633 3	819.666 7	804.3	
Interferon-stimulated 20 kDa exonuclease-like 2	ISG20L2	4	566.866666 7	702.9	678.5	610.033 3	423.8	519.533 3	
Monocarboxylate transporter 4	SLC16A3	5	625.366666 7	1665.56 7	1377.4	1445.56 7	1190.96 7	1231.2	

Formin-like protein 3	FMNL3	1	459.733333 3	1040.13 3	836.1	902.766 7	799.7	867.666 7
Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	5	558.966666 7	826.166 7	874.133 3	717.1	548.1	801.566 7
cDNA FLJ52798		8	1559.83333 3	2374.46 7	2668.86 7	2061.13 3	1463	1505.43 3
Sulfiredoxin-1	SRXN1	5	803.166666 7	1072.03 3	1143.13 3	930.633 3	688.966 7	840.3
Solute carrier family 35 member E1	SLC35E1	2	178.633333 3	223.366 7	152.766 7	193.933 3	284.8	159.133 3
26S proteasome non-ATPase regulatory subunit 14	PSMD14	8	1724.73333 3	4768.16 7	4275.5	4140.4	3195.1	3392.8
cDNA, FLJ96428, highly similar to Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7), mRNA		12	3538.53333 3	5365.633	5041.76 7	4659.33 3	3688.46 7	4139.23 3
T-complex protein 1 subunit alpha	TCP1	27	12818.2	20357	18786.3	17678.2 3	13794.4 7	16160.1 3
Serine incorporator 1	SERINC1	2	223.666666 7	404.4	393.666 7	351.233 3	284.666 7	316.333 3
Isoform 2 of [Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	5	509.8	889.966 7	580.266 7	773.1	923.1	834.333 3
Arginine and glutamate-rich protein 1	ARGLU1	8	1912.43333 3	4034.6	3495.23 3	3504.83 3	3261.3	3546.96 7

Golgi resident protein GCP60	ACBD3	8	1783.7	3044.7	2646.6	2644.93 3	2173.26 7	2451.03 3
Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	JMJD6	8	928.9	1915.63 3	1715.7	1664.16 7	1325.8	1343.16 7
Isoform 2 of B-cell receptor-associated protein 29	BCAP29	4	568.266666 7	2163.2	2063.7	1879.3	1790.93 3	1525.73 3
PDZ and LIM domain protein 7	PDLIM7	14	4071.83333 3	6724.83 3	5960.56 7	5842.96 7	4819.66 7	4947.83 3
Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	2	3181.73333 3	6196.1	4722.43 3	5383.9	4845.2	5661.43 3
cDNA FLJ55173, highly similar to Nuclear distribution protein nudE-like 1		2	1216.66666 7	1746.667	1358.8	1517.8	1474.13 3	1492.16 7
Serine/threonine-protein kinase TBK1	TBK1	7	1054.66666 7	1837.63 3	1556.2	1596.9	1362.2	1728.46 7
Ribosome biogenesis protein BMS1 homolog	BMS1	13	1850.63333 3	3196.2	2811.6	2779	2424.2	2664.1
Isoform 4 of DNA repair protein RAD51 homolog 1	RAD51	2	289.533333 3	378.966 7	429.733 3	329.533 3	252.433 3	249.366 7
Uncharacterized protein C12orf29	C12orf29	4	441.433333 3	1147.06 7	1290.73 3	997.466 7	661.266 7	1024.73 3
Uncharacterized protein C19orf47	C19orf47	4	796.466666 7	1038.53 3	978.866 7	903.133 3	813.2	815.533 3
Retinoid-inducible serine carboxypeptidase	SCPEP1	3	635.633333 3	1558.63 3	1494.06 7	1355.76 7	1225.73 3	1331.53 3

Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	6	1004.4	1473.33 3	1409.6	1281.63 3	1058.06 7	1178.1
Exosome complex component CSL4	EXOSC1	5	2043	2771.96 7	2624.86 7	2411.66 7	2006.1	2084.16 7
cDNA FLJ10654 fis, clone NT2RP2005901, highly similar to FAST kinase domains-containing protein 2	6	856	1022.767	1191.13 3	889.9	993.2	857.466 7	
Protein tyrosine phosphatase type IVA 2	PTP4A2	3	397.3	547.833 3	454.7	476.666 7	447.133 3	435.166 7
Porphobilinogen deaminase	HMBS	12	2087.53333 3	3623.96 7	3303.86 7	3153.56 7	2580.96 7	3046.03 3
Pleckstrin homology-like domain family A member 1	PHLDA1	2	196.8	340.033 3	301.2	295.9	270.166 7	243.966 7
Peptidyl-prolyl cis-trans isomerase		7	1780.96666 7	3817.73 3	3867.93 3	3322.26 7	2733.73 3	2863.63 3
Large subunit GTPase 1 homolog	LSG1	13	1359.03333 3	2448.86 7	2458	2131.06 7	1624.23 3	1733.36 7
Myopalladin	MYPN	8	754.066666 7	646.1	551	562.3	584.6	537.166 7
Conserved oligomeric Golgi complex subunit 2	COG2	3	521.333333 3	682.133 3	557.8	593.666 7	599.433 3	643.366 7
Guanine nucleotide-binding protein subunit alpha-13	GNA13	6	1037.36666 7	2065.56 7	1801.96 7	1797.7	1700.9	1740.76 7
26S proteasome non-ATPase regulatory subunit 3	PSMD3	27	6343.9	12823.5 7	11812.3 7	11160.9 3	8411.2	10014.8

Phosphoribosyltransferase domain-containing protein 1	PRTFDC1	2	904.733333 3	1290.16 7	1185.76 7	1122.9	883.966 7	1038.2
cDNA FLJ56262, highly similar to M-phase inducer phosphatase 3 (EC 3.1.3.48)		6	460.966666 7	1029.667	1081.26 7	896.366 7	748.666 7	791.366 7
Copper chaperone for superoxide dismutase	CCS	4	566.4	702.633 3	555.9	611.733 3	558.6	636.433 3
Zinc finger protein 830	ZNF830	4	661.333333 3	948.7	942.133 3	826	670.9	713.133 3
60S ribosomal protein L6		22	15988.2	23538.2	23237.0 3	20496.8 7	15622.7 3	17215.8 3
Muscleblind-like protein 2	MBNL2	2	1055.73333 3	2124.73 3	1607.53 3	1850.2	1743	2033.26 7
Ubiquitin carboxyl-terminal hydrolase CYLD	CYLD	3	263.666666 7	773.266 7	665.666 7	673.433 3	561.766 7	686.866 7
Polyglutamine binding protein 1 isoform 2 (Fragment)	PQBP1	8	2379.26666 7	3777.86 7	4075.2	3290.53 3	2933.8	2810.7
Isoform 5 of Kinesin-like protein KIFC3	KIFC3	1	197.466666 7	487.966 7	487.9	425.033 3	343.833 3	363.3
Vasodilator-stimulated phosphoprotein isoform 3 (Fragment)	VASP	3	4515.6	8932.03 3	7433.63 3	7781.03 3	6662.26 7	7026.96 7
Mediator of RNA polymerase II transcription subunit 16	MED16	4	264.566666 7	270.6	222.866 7	235.733 3	206.533 3	211.966 7
Ashwin	C2orf49	6	746.7	1002.26 7	921.233 3	873.233 3	784.466 7	776.433 3
PCK2 protein	PCK2	1	3500.1	6532.2	4962	5692.1	5174.4	5976.33 3

Cystathionine gamma-lyase	CTH	13	1668.73333 3	3542.5	2576.3	3087.03 3	2535.23 3	3029.53 3
Argininosuccinate synthase	ASS1	3	534.833333 3	843.466 7	677.566 7	735.033 3	1123.13 3	999.966 7
Sialic acid synthase	NANS	11	2603.83333 3	5513.13 3	4480.03 3	4804.63 3	4214.4	4921.6
PERQ amino acid-rich with GYF domain-containing protein 2	GIGYF2	23	5342.86666 7	7510.96 7	7327.46 7	6546.2	5004.93 3	5435.73 3
Replication factor C subunit 4	RFC4	17	4370.33333 3	5279.93 3	5575.3	4602.63 3	3971.36 7	3796.3
ATP-dependent RNA helicase DDX19A	DDX19A	6	6359.66666 7	11597.2	10803.3	10109.7 3	7905.66 7	8892.03 3
Isoform 3 of Protein SEC13 homolog	SEC13	7	2189.46666 7	4227.96 7	3691.46 7	3685.8	2850.8	3782.96 7
Isoform 3 of Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	BUB1B	12	1447.13333 3	2060.06 7	2385.43 3	1795.9	1509.4	1394.06 7
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	DHX16	20	3179.56666 7	5939.9	6004.63 3	5178.5	4121.73 3	4422.16 7
ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	6	1631.66666 7	2703.23 3	2548	2356.8	1691	1833.73 3
Protein unc-119 homolog A	UNC119	2	333.966666 7	539.033 3	418.266 7	469.966 7	459.066 7	418.2
Factor VIII intron 22 protein	F8A1	3	276.1	597.733 3	472.833 3	521.266 7	503.4	557.733 3

Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2	PPIP5K2	6	2039.8	2732.46 7	2314.33 3	2383.16 7	2167.9	2327.53 3
Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	HACD3	4	606.8	785.5	753.033 3	685.133 3	590.533 3	674.933 3
Chloride intracellular channel protein 1	CLIC1	17	10483.1333 3	12960	11235.9	11304.6	9106	10580.3 7
PAK2		1	5137.03333 3	5974.5	5044.76 7	5213.16 7	4847.7	5099.13 3
cDNA, FLJ95314, highly similar to Homo sapiens transducin (beta)-like 2 (TBL2), transcript variant 1, mRNA		17	3708.8	7052.5	5808.6	6155.26 7	5682.2	6470.9
Steroid receptor RNA activator 1, isoform CRA_a	SRA1	9	1453.46666 7	2797.33 3	2555.93 3	2441.53 3	1834.23 3	2078
Transcription factor Sp1	SP1	5	644.1	544.933 3	489.333 3	475.7	409.233 3	395.033 3
NmrA-like family domain-containing protein 1	NMRAL1	5	653.066666 7	1060.8	923.9	926.033 3	785.4	917.633 3
Small ubiquitin-related modifier 2	SUMO2	2	3850.93333 3	7297.23 3	6623.2	6372	5437.53 3	5585.06 7
Isoform 3 of Regulator of G-protein signaling 10	RGS10	6	238.666666 7	545.3	515.333 3	476.166 7	461.666 7	524.6
Heat shock protein HSP 90-beta	HSP90AB1	47	64665.4333 3	117555. 6	111819. 7	102652. 2	75082.4 3	88145.2 3
cDNA FLJ75092, highly similar to Homo sapiens golgi associated, gamma adaptin ear		6	924.566666 7	1836.767	1686.83 3	1603.96 7	1367.6	1415.96 7

containing, ARF binding protein 3 (GGA3), transcript variant long, mRNA								
T-complex protein 1 subunit beta	CCT2	43	14840.3333 3	24068.2 7	21812.9 3	21018.9 7	16369.9 7	19180
Catechol O-methyltransferase	COMT	12	1916.1	3830.46 7	3404.3	3345.23 3	2943.13 3	3069.1
High density lipoprotein binding protein (Vigilin), isoform CRA_a	HDLBP	69	17920.4333 3	32461.5 7	27614.6 3	28351.2 3	22236.3 3	27217.6 3
Protein sprouty homolog 1	SPRY1	4	774.966666 7	981.6	860.7	857.433 3	839.466 7	767.766 7
Protein disulfide-isomerase TMX3	TMX3	10	1117.86666 7	1688.76 7	1540.66 7	1475.2	1357.03 3	1530.96 7
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1	7	1328.73333 3	3269.03 3	3043.23 3	2855.7	2466.2	2772.5
TSC22 domain family protein 4	TSC22D4	7	919.633333 3	1541	1338.86 7	1346.3	1232.4	1431.06 7
Heat shock cognate 71 kDa protein (Fragment)	HSPA8	1	23145.1	39741.7 7	35687.5 7	34723.6 7	27413.0 7	34806.5
60S ribosomal protein L13	RPL13	21	12708.4333 3	21450.6 3	21036.5 3	18742.2 7	14496.0 3	16206.6 7
Zinc finger CCHC domain-containing protein 10	ZCCHC10	1	179.1	241.766 7	237.666 7	211.266 7	173.733 3	172.833 3
Melanoma-associated antigen D2	MAGED2	18	2078.96666 7	3987.36 7	3360.8	3484.73 3	2832.8	3169.43 3

Sorcin	SRI	10	2696.9	5695.16 7	4903.43 3	4977.4	4058.86 7	4699.6
ADP-ribosylation factor GTPase-activating protein 1	ARFGAP1	12	1929.56666 7	3417.83 3	3120.63 3	2987.8	2262.16 7	2818.86 7
Isoform 2 of Zinc finger protein 791	ZNF791	1	566.833333 3	1009.66 7	993.866 7	882.633 3	834.666 7	752.2
MICAL-like protein 1	MICALL1	7	1127.3	1683.7	1452.53 3	1471.9	1258.36 7	1363.93 3
Coiled-coil domain-containing protein 117	CCDC117	3	191.066666 7	435.033 3	388.5	380.333 3	321.833 3	380.7
Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	8	1914.66666 7	3093.86 7	3208.5	2704.86 7	2520.2	2302.23 3
Casein kinase I isoform delta	CSNK1D	2	565.466666 7	798	831.566 7	697.666 7	524.566 7	533.666 7
Protein transport protein Sec23A	SEC23A	12	1893.36666 7	4081.63 3	3189.33 3	3569	3144.16 7	3480.63 3
Methyltransferase-like protein 13	METTL13	11	839.566666 7	1268.66 7	1100.53 3	1109.53 3	939.033 3	1107.6
UPF0688 protein C1orf174	C1orf174	4	1358.56666 7	1749.7	1750.23 3	1530.23 3	1390.73 3	1482.73 3
Enhancer of mRNA-decapping protein 3	EDC3	10	1567.3	2485.96 7	2158.76 7	2174.2	2005.13 3	1908.93 3
Calcium-binding and coiled-coil domain-containing protein 1	CALCOCO1	4	444.766666 7	619.3	457.5	541.666 7	472.3	491.6
Thyroid receptor-interacting protein 11	TRIP11	28	3859	6140.13 3	5403.36 7	5371.03 3	4541.03 3	5553.46 7
cDNA FLJ77229, highly similar to Homo sapiens GRIP1	16	1827.2	3720.767	3291.6	3255.13 3	2643.86 7	3191.53 3	

associated protein 1 (GRIPAP1), transcript variant 1, mRNA								
Exosome complex component RRP41	EXOSC4	7	1110.23333 3	1709.63 3	1677.43 3	1495.76 7	1154.3	1223.13 3
PRA1 family protein		2	359.633333 3	459.966 7	385.866 7	402.466 7	472.966 7	418.2
SOSS complex subunit C	INIP	1	157.633333 3	347.633 3	324.633 3	304.2	289.666 7	282.3
Ubiquitin-associated protein 2	UBAP2	10	3025.23333 3	4098.53 3	4181.63 3	3586.56 7	2532.23 3	2593.23 3
Isoform 2 of Chromatin target of PRMT1 protein	CHTOP	4	2431.8	3498.4	2857.53 3	3061.66 7	2887.1	2962.86 7
cDNA, FLJ95547, highly similar to Homo sapiens nuclear receptor coactivator 6 interacting protein (NCOA6IP), mRNA		7	594.966666 7	1444.5	1336.33 3	1264.2	943.966 7	1049.56 7
Integrin-linked protein kinase	ILK	11	1420.1	2816.43 3	2729.36 7	2465.03 3	1981.63 3	2247.96 7
Peptidyl-prolyl cis-trans isomerase D		21	5153.66666 7	9781.5	9213.93 3	8561.86 7	6357.46 7	7531.43 3
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	CHCHD2	3	763.1	2145.96 7	1509.23 3	1878.46 7	1483.8	1364.26 7
WASH complex subunit FAM21A	FAM21A	11	3118.2	4367.73 3	3726.06 7	3824.03 3	3559.8	3793.3
Eukaryotic translation initiation factor 2A	EIF2A	18	4946	9915.66 7	9624.33 3	8681.46 7	6543.8	7677.13 3

Casein kinase II subunit alpha'	CSNK2A2	14	1981.63333 3	4173.1	4260.63 3	3654	2707	3031.96 7
cDNA FLJ77676, highly similar to Homo sapiens TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae) (TRMT1), mRNA		12	1593.23333 3	1928.433	1805.43 3	1688.83 3	1417.33 3	1415.83 3
Cell division cycle associated 1, isoform CRA_a	CDCA1	10	1614.46666 7	2399.03 3	2954.06 7	2101	1544.43 3	1570.73 3
Vasodilator-stimulated phosphoprotein	VASP	5	6355.8	11039.8	9142.1	9668.6	8091.33 3	8726.13 3
CHD9 protein	CHD9	2	218.5	376.9	411.866 7	330.1	241.466 7	259.666 7
Isoform 5 of Splicing factor 1	SF1	15	6347.53333 3	8116.33 3	7685.66 7	7109.1	6576.96 7	6463.06 7
U8 snoRNA-decapping enzyme	NUDT16	5	914.433333 3	1191.6	1128.76 7	1043.73 3	941.5	1064.73 3
Glycylpeptide N-tetradecanoyltransferase	NMT2	9	1754	3572.8	3420.16 7	3129.5	2750.2	2848.6
Protein pelota homolog	hCG_2002731	10	1441.83333 3	3377.8	2652.96 7	2959.23 3	2665.36 7	2887.63 3
Isoform 4 of Calcium-binding and coiled-coil domain-containing protein 2	CALCOCO2	7	343.933333 3	1441.03 3	1766.93 3	1262.46 7	869.5	938.6
Mismatch repair endonuclease PMS2	PMS2	3	201.666666 7	343.433 3	358.933 3	300.933 3	244.4	263.266 7
Isoform 3 of Alpha-adducin	ADD1	4	665.766666 7	709.333 3	658.533 3	621.6	579.4	598.1

Kinesin-associated protein 3	KIFAP3	2	344.2	585.033 3	482.633 3	512.7	459.1	539.766 7
Cip1-interacting zinc finger protein	CIZ1	7	762.366666 7	758.066 7	884.266 7	664.366 7	590.4	535.433 3
Histone-lysine N-methyltransferase SETDB1	SETDB1	4	233	367.033 3	330.466 7	321.666 7	324.3	307.3
EBNA1 binding protein 2, isoform CRA_d	EBNA1BP2	19	4598.53333 3	9129.63 3	8838.76 7	8001.23 3	5714.1	6267.16 7
cDNA, FLJ95843, highly similar to Homo sapiens small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), mRNA		2	189.766666 7	539.7667	489.366 7	473.066 7	455.366 7	436.4
Putative deoxyribonuclease TATDN1 (Fragment)	TATDN1	6	794.233333 3	1683.43 3	1583.2	1475.96 7	1283.66 7	1465.5
40S ribosomal protein S11	RPS11	20	11332.7	13514.5 3	13035.8 7	11849.3 3	9109.8	9987.33 3
Ribosomal protein L4 variant (Fragment)		46	23532.7666 7	42112.4	39017.9 3	36927.0 7	28198.3 7	30380.1 7
Nucleolin	NCL	42	53698.5666 7	74326.0 7	60614.5 7	65181.6	61319.9 3	61005.6
Histone acetyltransferase p300	EP300	8	889.766666 7	1159.7	1171.33 3	1017.03 3	1058	1132.23 3
Zinc transporter SLC39A7	SLC39A7	2	214	1099.86 7	883.033 3	964.7	889.4	974.166 7
Signal transducer and activator of transcription 1-alpha/beta	STAT1	1	4531.56666 7	8736.93 3	8182.3	7663.36 7	5972.43 3	7676.1

Rab GTPase-binding effector protein 1	RABEP1	21	2740.13333 3	4982.7	4551.93 3	4371	3842.16 7	4246.93 3
Small ubiquitin-related modifier 4	SUMO4	2	3286.66666 7	5223.23 3	4848.93 3	4583.9	4223.56 7	3980.76 7
cDNA, FLJ95623, highly similar to Homo sapiens differentially expressed in FDCP 6 homolog (mouse) (DEF6), mRNA	7	811.3	1550.8	1557.86 7	1361.03 3	1022.86 7	1188.23 3	
Tumor susceptibility gene 101 protein	TSG101	13	1401.2	3398.13 3	3007.66 7	2983.6	2159.9	2518.76 7
Activating signal cointegrator 1	TRIP4	10	1241.1	1937.96 7	1686.16 7	1701.6	1443.6	1618.66 7
Zinc finger CCHC domain-containing protein 9	ZCCHC9	6	888.633333 3	1616.56 7	1464.03 3	1419.4	1234.33 3	1295.16 7
Probable ATP-dependent RNA helicase DDX56	DDX56	12	1697.63333 3	2702.7	3271.03 3	2373.2	1821.5	1837.53 3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	UQCRCF1	7	1028.63333 3	1753.8	1803.4	1540.03 3	1533.56 7	1516.1
Lamina-associated polypeptide 2, isoform alpha	TMPO	26	11729.6666 7	16651.6 7	16564.4	14624.3	12380.1	12810.4 7
Chromosome 12 open reading frame 10	C12orf10	7	1246.43333 3	2418	2168.66 7	2123.86 7	1719.66 7	2094.06 7
PIN2/TERF1-interacting telomerase inhibitor 1	PINX1	7	755.3	1153.3	1207.8	1013.03 3	937.966 7	861.5
Cytochrome b-c1 complex subunit 7	UQCRB	8	1068.76666 7	2585.5	2827.06 7	2271.06 7	2270.13 3	2053.33 3
Dihydroorotate dehydrogenase (quinone), mitochondrial	DHODH	8	1390.73333 3	2829.56 7	2946.96 7	2485.6	2201.4	2118.06 7

Mediator of RNA polymerase II transcription subunit 24	MED24	9	722.933333 3	655.1	606.2	575.466 7	561.633 3	491.033 3
Guanine nucleotide binding protein-like 3 (Nucleolar), isoform CRA_b	GNL3	24	4688.6	9129.5	8376.96 7	8019.96 7	6410.13 3	6828.23 3
cDNA, FLJ94230, highly similar to Homo sapiens thioredoxin-like 1 (TXNL1), mRNA	12	5138	8165.867	7645.5	7173.9	5140.26 7	6287.56 7	
Metastasis-associated protein MTA2	MTA2	22	5295.63333 3	9291.53 3	9557.83 3	8163.06 7	6597.6	6578.46 7
CCDC43 protein	CCDC43	2	716.233333 3	1155.8	1009	1015.43 3	923.7	976.366 7
MRN complex-interacting protein	MRNIP	2	146.033333 3	186.4	161	163.766 7	137.7	157.633 3
cDNA FLJ77865		1	105.233333 3	160.2	140.966 7	140.766 7	114.533 3	126.533 3
ER membrane protein complex subunit 8	EMC8	5	854.966666 7	1014.93 3	1021.76 7	891.866 7	732.2	808.066 7
Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1	3	978.9	895.6	730.466 7	787.1	781.833 3	810.766 7
Uncharacterized protein C15orf52	C15orf52	2	423.3	986.733 3	829.933 3	867.2	839.3	812.466 7
60S ribosomal protein L36a	RPL36A	5	5970.33333 3	10979.5 7	10538.5 3	9649.73 3	7502.36 7	7809.56 7
Isoform 2 of Secretory carrier-associated membrane protein 3	SCAMP3	1	2664.96666 7	3827.86 7	3578.26 7	3364.26 7	2953.8	3125.06 7

Serine/threonine-protein kinase RIO3	RIOK3	8	1684.3	3819.06 7	2641.33 3	3357.36 7	2993.46 7	2812.06 7
Eukaryotic translation initiation factor 5	EIF5	28	7550.8	11494.6	10063.9	10105.5 7	8185.46 7	9752.56 7
Disks large-associated protein 4	DLGAP4	2	200.966666 7	335.8	296.633 3	295.233 3	266.733 3	278.333 3
Valine--tRNA ligase, mitochondrial	VARS2	2	245.2	291.7	245.1	256.5	236.366 7	244.966 7
60S ribosomal protein L10a	RPL10A	10	7106.1	11193.2 7	10268.6	9842.63 3	7568.16 7	8456.7
Beta-parvin	PARVB	3	307.1	678	739.266 7	596.266 7	326.066 7	480.4
RNA binding motif protein, X-linked-like-1	RBMXL1	4	4728.6	7874	7033.73 3	6925.16 7	6287.6	5995.6
RNMT-activating mini protein	FAM103A1	4	675.9	946.8	818.633 3	832.733 3	740.3	774.4
Methyltransferase-like protein 2B	METTL2B	4	536.9	683.833 3	652.666 7	601.466 7	515.966 7	560.4
Signal transducing adapter molecule 2	STAM2	6	1166	2326.83 3	2206.96 7	2046.6	1636.53 3	1922.86 7
Pre-mRNA cleavage complex 2 protein Pcf11	PCF11	12	1436.66666 7	3024.56 7	2803.33 3	2660.73 3	2232	2268.16 7
Isoform Mitochondrial of Lysine--tRNA ligase	KARS	27	8097.1	16447.8	15106.0 3	14469.3	9982.73 3	11848.7
RNA-binding protein 34	RBM34	14	1988.93333 3	3815.16 7	3820.56 7	3356.26 7	2800.26 7	2698.5
TIA1 protein variant (Fragment)		4	1134.7	1688.23 3	1437.53 3	1485.66 7	1269.2	1392.8

40S ribosomal protein S15a	RPS15A	13	3439.43333 3	5777.16 7	5295.7	5084.76 7	4089.13 3	4514.93 3
Guanine nucleotide-binding protein subunit beta-like protein 1	GNB1L	5	351.4	620.833 3	585.4	546.433 3	437.6	479.466 7
Mitogen-activated protein kinase kinase kinase 7	MAP3K7	6	1213.4	1910.73 3	1851.3	1681.86 7	1491	1703.56 7
Coatomer subunit gamma-1	COPG1	26	5682.16666 7	11739.4 3	9954.96 7	10335.2 3	7118.03 3	9671.26 7
Signal transducer and activator of transcription	STAT1	1	4414.53333 3	8637.03 3	8101.46 7	7605.5	5917.4	7615.13 3
Peptidyl-prolyl cis-trans isomerase CWC27 homolog	CWC27	7	1101.9	1644.03 3	1637.03 3	1447.76 7	1109	1250.3
Isoform 3 of Inositol monophosphatase 1	IMPA1	9	2112.73333 3	3820.96 7	3379.93 3	3365.43 3	2815.1	3184.73 3
Mitochondrial import receptor subunit TOM20 homolog	TOMM20	4	1069.83333 3	1494.06 7	1368.2	1316.06 7	1291.9	1320.43 3
cDNA FLJ56443, highly similar to Putative ATP-dependent RNA helicase DHX33 (EC 3.6.1.-)		7	1414	1730.133	1737.56 7	1524.03 3	1294.26 7	1347.63 3
Intersex-like (Drosophila)	MED29	4	760.533333 3	817.733 3	792.633 3	720.5	645.733 3	657.233 3
Centrosomal protein of 85 kDa	CEP85	3	369.6	454.833 3	555.733 3	400.8	302.1	328.433 3
G-protein coupled receptor-associated sorting protein 2	GPRASP2	1	253	404.766 7	387.9	356.7	371.4	387.7

EEF1A protein (Fragment)	EEF1A	4	10183.7	11092.8	10647.3	9778.16 7	7691.43 3	9103.7
Glucose-induced degradation protein 8 homolog	GID8	5	1335.03333 3	1836.8	1747.13 3	1619.2	1378.86 7	1381.26 7
Isoform 2 of HCLS1-associated protein X-1	HAX1	6	600.7	745.366 7	720.566 7	657.2	571.266 7	586.033 3
Bystin (Fragment)	BYSL	1	268.2	806.4	856.5	711.066 7	359.2	353.133 3
cDNA, FLJ95853, highly similar to Homo sapiens exosome component Rrp46 (RRP46), mRNA		4	677.366666 7	1129.367	1037.83 3	995.866 7	940.633 3	970.766 7
Protein kinase C and casein kinase substrate in neurons protein 2	PACSIN2	16	3029.13333 3	5626.46 7	4927.06 7	4961.5	4162.33 3	4535.3
Vacuolar protein sorting-associated protein 13C	VPS13C	1	40.4666666 7	70.0333 3	67.7	61.7666 7	53.9333 3	55.8666 7
Protein FAM111B	FAM111B	2	335.6	353.166 7	595.066 7	311.5	233.133 3	210.166 7
Pre-mRNA-splicing factor SPF27	BCAS2	11	1357.93333 3	2714.7	2470.2	2394.9	2174.86 7	2366.36 7
Isoform 3 of Protein DDI1 homolog 2	DDI2	8	1112.96666 7	1770.96 7	1648.53 3	1562.56 7	1349.73 3	1475.83 3
Ganglioside-induced differentiation-associated protein 2	GDAP2	1	113.066666 7	101.466 7	88.5	89.5333 3	78.0333 3	78.1666 7

Leucine-rich repeat and calponin homology domain-containing protein 4	LRCH4	4	144.066666 7	256.333 3	220.666 7	226.2	200.7	224.666 7
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	8	1379.93333 3	2206.8	1990.16 7	1947.43 3	1719.26 7	1868.86 7
cDNA FLJ54710, highly similar to Target of Myb protein 1		7	871.733333 3	1482.1	1206.43 3	1307.96 7	1206.2	1256.83 3
Protein Churchill	CHURC1	3	709.833333 3	1043.7	1058.7	921.233 3	690.333 3	697.233 3
cDNA FLJ60315		3	259.533333 3	238.566 7	216.766 7	210.6	196.966 7	189.5
60S ribosomal protein L5	RPL5	25	13552.1333 3	19180.0 7	16903.3 7	16931.6 3	13206.8 3	15687.8 7
Ras-related protein R-Ras	RRAS	4	870.5	1797.46 7	1541.73 3	1586.76 7	1629.43 3	1585.9
RNA-binding motif, single-stranded-interacting protein 2	RBMS2	3	1092.76666 7	1472.36 7	1456.7	1299.86 7	1128.7	1205
CUG triplet repeat, RNA binding protein 1, isoform CRA_c	CELF1	11	1876.46666 7	4580.53 3	4255.03 3	4044.13 3	3153.53 3	3552.76 7
cDNA FLJ76053, highly similar to Homo sapiens Ras-GTPase activating protein SH3 domain-binding protein 2 (G3BP2), transcript variant 3, mRNA		10	3070.5	6425.467	6841.2	5673.06 7	3887.8	4410.5
Isoform A of Protein CutA	CUTA	3	690.266666 7	733.933 3	597.133 3	648	652.766 7	750.266 7

Probable ATP-dependent RNA helicase DDX10	DDX10	20	3035.66666 7	5697.26 7	5916.4	5030.5	3856.93 3	4068.9
tRNA (guanine-N(7)-)-methyltransferase	METT11	2	669.8	1101.16 7	1007.6	972.366 7	913.133 3	987
Zinc finger protein 428 (Fragment)	ZNF428	3	949.8	1087.26 7	1048.56 7	960.266 7	735.933 3	780.133 3
Tight junction protein 1 (Zona occludens 1), isoform CRA_e	TJP1	22	3588.66666 7	5307.36 7	5460.7	4688.13 3	3442.53 3	3822.33 3
Cysteine and histidine-rich protein 1	CYHR1	9	1166.2	2307.63 3	1958.43 3	2038.5	1864.33 3	1972.2
cDNA FLJ55935, highly similar to Protein FAM21C (Fragment)		2	2543.13333 3	3604.167	3069.23 3	3183.93 3	2949.76 7	3186.1
Probable E3 ubiquitin-protein ligase makorin-2	MKRN2	3	176.1	372.6	365.133 3	329.2	244.066 7	273.733 3
Serine/threonine-protein kinase PAK 4	PAK4	11	1921.73333 3	3582.06 7	3306.33 3	3165.36 7	2184.96 7	2480.36 7
Protein FAM207A	FAM207A	6	445.466666 7	597.566 7	714.066 7	528.133 3	404.566 7	439.333 3
Protein phosphatase 1, regulatory (Inhibitor) subunit 14B, isoform CRA_a	PPP1R14B	2	339.966666 7	407.266 7	344.266 7	360	317.433 3	335.733 3
Armado repeat-containing protein 6	ARMC6	10	1857.66666 7	3162.4	3244.16 7	2795.5	2021.06 7	2350.1
Isoform 4 of NEDD8-activating enzyme E1 regulatory subunit	NAE1	15	2634.46666 7	4646.73 3	4420.13 3	4107.7	3625.6	3735.93 3
Histone H1x	H1FX	13	4030.63333 3	7441.13 3	6054.63 3	6578.46 7	6122.8	6283.3

Probable RNA-binding protein EIF1AD	EIF1AD	6	612.2	1306.16 7	1322.63 3	1154.83 3	813.033 3	954.6
Zinc transporter 1	SLC30A1	7	1234.73333 3	2246.4	2113.46 7	1986.3	1771.56 7	1687.7
60S ribosomal protein L28	RPL28	14	8005.9	12545.4	12017.3 3	11095.0 7	8791.1	9900.73 3
Lysophosphatidylcholine acyltransferase 1	LPCAT1	6	494.466666 7	1746.8	1893.2	1545.03 3	1375.6	1243.5
Isoform 2 of Tyrosyl-DNA phosphodiesterase 2	TDP2	5	404.3	581.933 3	536.966 7	514.733 3	454.266 7	477.133 3
Coiled-coil domain containing 12, isoform CRA_a	CCDC12	7	1404.96666 7	2068.86 7	2061.83 3	1830	1293.2	1405.06 7
Alternative protein SMCR7L	SMCR7L	3	517.966666 7	617.7	562.433 3	546.533 3	495.4	498.766 7
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	3	429.4	992.566 7	960.9	878.233 3	672.433 3	724.3
Vacuolar fusion protein CCZ1 homolog	CCZ1	4	590.666666 7	827.266 7	958.2	732	558.333 3	602.766 7
UBX domain-containing protein 4	UBXN4	7	1923.1	3148.13 3	2645.2	2785.86 7	2675.9	2646.03 3
Zinc finger CCCH domain- containing protein 4	ZC3H4	19	2880.8	3573.46 7	3367.13 3	3162.56 7	3090.53 3	3044.86 7
Annexin A6	ANXA6	50	9617	23370.8	17179.4 7	20686.6 7	16547.7	21735.7 3
Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	5	844.033333 3	724.7	514.966 7	641.566 7	565.066 7	639.466 7

cDNA, FLJ92490, highly similar to Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA		3	374.333333 3	974.7667	1118.3	863.066 7	600.966 7	752.4	
Isoform 2 of Clusterin	CLU	4	423.633333 3	606.9	470.266 7	537.433 3	482.866 7	659.533 3	
Mitochondrial calcium uniporter regulator 1	MCUR1	4	710.933333 3	1163.03 3	1145.63 3	1029.93 3	893.9	1050.8	
Plasminogen receptor (KT)	PLGRKT	2	320.133333 3	600.133 3	555.233 3	531.466 7	485.366 7	500.033 3	
ATP-dependent RNA helicase DDX19B	DDX19B	4	4949.86666 7	9601.93 3	8900.3	8503.46 7	6580.43 3	7809.3	
GTPase NRas	NRAS	2	1249.23333 3	2198.33 3	1795.03 3	1947	1802.7	1709.63 3	
Ras-related protein Rap-1A	RAP1A	2	1487.36666 7	3222.3	3188.86 7	2853.96 7	2564.13 3	2594.6	
28S ribosomal protein S29, mitochondrial	DAP3	9	978.933333 3	1135.76 7	1319.26 7	1006	788.033 3	935.533 3	
Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 36	USP36	6	834.433333 3	1627.8	1572.46 7	1441.93 3	1250.56 7	1280.43 3	
Integrator complex subunit 2	INTS2	2	297.433333 3	580.266 7	497.7	514.033 3	466	501.433 3	
Isoform 6 of ADP-ribosylation factor-binding protein GGA1	GGA1	7	1429.63333 3	2459.33 3	2251.93 3	2178.63 3	1825.56 7	1917.2	
Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	3	334.066666 7	516.2	440.4	457.3	429.066 7	485.366 7	
Phosphomannomutase 1	PMM1	5	463.133333 3	593.633 3	526.1	525.933 3	438.033 3	472.8	

Spatacsin	SPG11	1	178.333333 3	224.633 3	186.033 3	199.033 3	175.5	206.666 7
Isoform 2 of ATP-dependent (S)-NAD(P)H-hydrate dehydratase	NAXD	4	557.633333 3	874.733 3	749.633 3	775.2	764.333 3	813.1
Ubiquitin carboxyl-terminal hydrolase 16	USP16	4	334.366666 7	722.033 3	696.133 3	639.933 3	457.366 7	533.6
Synaptotagmin-1	SYT1	3	630.333333 3	1543.23 3	1572.13 3	1367.8	998.8	1167.93 3
cDNA FLJ59571, highly similar to Eukaryotic translation initiation factor 4gamma 2	25	5536.23333 3	10674.07	10451.1 7	9462.13 3	6751.1	7646.03 3	
Kinesin-like protein KIF14	KIF14	9	956.1	1668.8	1820.16 7	1479.43 3	1066.73 3	1230.96 7
Testis tissue sperm-binding protein Li 46a	24	6792.36666 7	12910.47	11074.0 7	11445.8	10853.8 7	10864.5	
FAM133B protein	FAM133B	3	696.366666 7	1105.53 3	1063.1	980.4	733.066 7	873.733 3
Ubiquitin-like protein ATG12	ATG12	3	567.266666 7	966.266 7	860.4	856.9	727.366 7	816.3
Myocyte enhancer factor 2D/deleted in azoospermia associated protein 1 fusion protein	MEF2D/DAZAP1fusion	3	960.166666 7	284.8	210.066 7	252.6	262.5	235.133 3
cDNA FLJ56285, highly similar to ADP-ribosylation factor-like protein 8B	2	568.4	1641.733	1615.03 3	1456.16 7	1173.76 7	1230.56 7	

STAM-binding protein	STAMPB	8	1042.43333 3	2035.76 7	1879.86 7	1805.73 3	1466.26 7	1712.86 7
Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	11	2644.1	4243.83 3	3772.46 7	3765.03 3	3842.23 3	3406.2
Protein PAXX	C9orf142	7	856.5	1404.43 3	1136.66 7	1246.03 3	994.133 3	1166.46 7
60S ribosomal protein L7a	RPL7A	29	21305.6	30128.6 7	30429.2	26731.9 7	19229.9 7	22605.5 3
ADP-dependent glucokinase	ADPGK	4	459.766666 7	638.233 3	662.8	566.466 7	570.833 3	626.3
Serum response factor-binding protein 1	SRFBP1	5	563.6	868.333 3	912.233 3	770.866 7	599.466 7	575.3
Optineurin	OPTN	6	860.666666 7	1215.13 3	1103.96 7	1078.93 3	1176.66 7	1272.7
Charged multivesicular body protein 1a	CHMP1A	6	1005.5	2406	2260.43 3	2136.46 7	1633.8	1876.53 3
Ribose-5-phosphate isomerase	RPIA	5	990.933333 3	1809.3	1807.8	1607.4	1151.13 3	1431.03 3
DnaJ homolog subfamily A member 2	DNAJA2	15	4259.7	6326.23 3	6235.3	5620.73 3	4186.36 7	4990.53 3
Isoamyl acetate-hydrolyzing esterase 1 homolog	IAH1	2	414.466666 7	778.4	685.666 7	691.633 3	532.866 7	686.333 3
Fructose-2,6-bisphosphatase TIGAR	TIGAR	9	1856.36666 7	3153.16 7	3087.7	2801.7	2171.33 3	2481.46 7
Deoxyhypusine hydroxylase	DOHH	8	1215.06666 7	1672.33 3	1641.06 7	1485.96 7	1110.8	1423.36 7
40S ribosomal protein S24	RPS24	8	4646.23333 3	6835.13 3	6152.36 7	6073.86 7	4529.6	5081.76 7

NudC domain-containing protein 1	NUDCD1	8	1333.1	2298.46 7	2265.1	2042.63 3	1535.03 3	1867.9
Choline kinase alpha	CHKA	3	67.6	99.4333 3	115.233 3	88.3666 7	81.6333 3	96.1666 7
Serpin B8	SERPINB8	17	2454.63333 3	5276.16 7	3828.8	4689.1	3953.13 3	4176.96 7
Ribosome biogenesis regulatory protein homolog	RRS1	18	4281.8	6195.36 7	5978.73 3	5507.6	4667.76 7	4984.4
Ras-related protein Rab-5A	RAB5A	6	1598.13333 3	2516.3	2127.13 3	2237.16 7	1860.4	2210.66 7
Glyceraldehyde-3-phosphate dehydrogenase (Fragment)	1	132.3	234.9333	201	208.9	127.2	352.2	
U6 snRNA-associated Sm-like protein LSM4 (Fragment)	LSM4	4	1106.46666 7	1725.86 7	1470.33 3	1534.76 7	1398.96 7	1500.63 3
Squamous cell carcinoma antigen recognized by T-cells 3	SART3	26	5643.8	9957.36 7	9042.7	8855.66 7	7392.43 3	8077.86 7
Tetratricopeptide repeat protein 17	TTC17	4	873.666666 7	1649.86 7	1890.76 7	1467.33 3	1065.7	1305.13 3
Protein SDE2 homolog	SDE2	4	688.6	1315.63 3	1289.7	1170.26 7	902.533 3	1006.93 3
Zinc finger CCHC domain-containing protein 8	ZCCHC8	15	2372.06666 7	3846.63 3	3381.33 3	3421.73 3	3334.7	3217.76 7
Insulin-induced gene protein	INSIG2	1	87.9	321.433 3	135.266 7	285.933 3	243.9	255.1
DNA fragmentation factor subunit alpha	DFFA	9	4663.66666 7	7694.1	6742.5	6844.36 7	6068.33 3	6457.63 3

NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	5	907.733333 3	1611.93 3	1822.46 7	1434.1	1268.26 7	1166
High mobility group protein HMG-I/HMG-Y	HMGA1	3	4697.36666 7	6872	5621.36 7	6114.43 3	5873.46 7	6354.53 3
Proto-oncogene c-Rel	REL	3	495.866666 7	702.433 3	611.866 7	625.1	584.4	705.466 7
Pyridoxal phosphate phosphatase	PDXP	5	1084	1304.9	1096.03 3	1161.36 7	1058.26 7	1138.1
KIAA1609 protein, isoform CRA_a	KIAA1609	1	495.366666 7	978.466 7	907.7	870.933 3	784.233 3	802.466 7
Isoform AML-1G of Runt-related transcription factor 1	RUNX1	7	847.266666 7	1507.13 3	1577.63 3	1341.63 3	1219.2	1269.53 3
Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2 (Fragment)	PPIP5K2	1	604.5	676.7	575.133 3	602.4	515	611.7
RRP1 protein (Fragment)	RRP1	15	3339.53333 3	5545.2	5302.4	4938.56 7	3960.8	4427.66 7
LDLR chaperone MESD	MESDC2	4	311.6	1050.23 3	890.933 3	935.366 7	1055.93 3	955.233 3
Prefoldin subunit 5	PFDN5	8	2237.03333 3	4130.4	3842.26 7	3678.7	2993.06 7	3491.13 3
Pleiotropic regulator 1	PLRG1	7	1310.26666 7	1552.53 3	1403.53 3	1382.76 7	1303.93 3	1198.63 3
Peptidyl-prolyl cis-trans isomerase E		8	1765.8	2659.9	2250.63 3	2370.06 7	2105.03 3	2146.33 3

Coiled-coil domain-containing protein 102A	CCDC102A	4	413.166666 7	622.766 7	609.833 3	554.933 3	522.033 3	551
Far upstream element-binding protein 3	FUBP3	24	8603.2	10094.7	9018.76 7	8995.5	7729.4	8483.2
Brain-specific angiogenesis inhibitor 1-associated protein 2	BAIAP2	14	2457.93333 3	3695.96 7	4309.46 7	3294.83 3	2645.16 7	2715
cDNA, FLJ94802		3	281.833333 3	584.266 7	622.7	520.866 7	401.633 3	541.133 3
Splicing factor, proline- and glutamine-rich	SFPQ	33	14007.8333 3	24124.5	21930.4 7	21507.3 7	18214.5 7	18855.4 7
60S ribosomal protein L6 (Fragment)	RPL6	1	979	2139.2	2105.26 7	1907.2	1497.73 3	1562.9
Protein CDV3 homolog	CDV3	12	3608.16666 7	6501.13 3	6018.16 7	5797.2	4200.13 3	5078.66 7
WDR13 protein (Fragment)	WDR13	3	577	858.466 7	700.4	765.6	649.2	912.1
Ubiquitin-associated domain-containing protein 1	UBAC1	4	1258.63333 3	1398	1227.23 3	1247.06 7	1281.23 3	1177.5
cDNA FLJ78451		1	127	46.3666 7	40.8	41.3666 7	38.7	37.1
Toll interacting protein variant (Fragment)		3	624.3	934.4	843.633 3	833.666 7	674.333 3	718.033 3
WWC family member 3	WWC3	1	319.266666 7	525.166 7	521.8	468.6	364.666 7	387.633 3
Isoform 4 of Protein FAM65A	FAM65A	7	308.166666 7	758.433 3	976.7	676.8	407.366 7	441.233 3
E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	22	4086.4	7538.93 3	6049	6728.76 7	5996.46 7	7193.03 3

Intraflagellar transport protein 27 homolog	IFT27	7	1035.56666 7	1722.13 3	1513.36 7	1537.2	1307.63 3	1593.36 7
Bromodomain-containing protein 2	BRD2	3	185.266666 7	326.466 7	343.333 3	291.466 7	226	258.133 3
Ataxin-2 (Fragment)	ATXN2	1	201.366666 7	427	442.133 3	381.266 7	139.166 7	152.433 3
Alpha-actinin-4	ACTN4	52	29180.3	51278.9	44984.3 3	45796.8 7	35415.2 7	40801.2 3
Synaptosomal-associated protein 29	SNAP29	9	2825.73333 3	3591.7	3486.4	3207.93 3	2757.9	2895.7
E3 ubiquitin-protein ligase MYCBP2	MYCBP2	5	312.133333 3	448.233 3	389.366 7	400.366 7	334.133 3	396.1
tRNA-dihydrouridine(47) synthase [NAD(P)(+)]		11	1227.86666 7	2080.8	2132.13 3	1858.76 7	1434.53 3	1525.83 3
Transmembrane emp24 domain-containing protein 9	TMED9	4	1468.33333 3	3015.33 3	2663.2	2693.7	2179.63 3	2437.16 7
60S ribosomal protein L18 (Fragment)	RPL18	12	7588.3	9353.93 3	9244.66 7	8358.06 7	7059.63 3	7634.7
cDNA, FLJ79447, highly similar to Nucleosome assembly protein 1-like 4		14	3529.33333 3	5933	5589.7	5305.36 7	3762.33 3	4518.26 7
DnaJ homolog subfamily A member 1	DNAJA1	19	5685.36666 7	7777.36 7	9481.33 3	6954.66 7	4957.23 3	5447.5
Farnesyl pyrophosphate synthase	FDPS	2	2246.66666 7	3063.3	2445.4	2739.4	2669.3	2738.06 7
Isoform 2 of Transcription factor BTF3	BTF3	1	5967.1	7489.5	8047.33 3	6697.76 7	4883.8	5322.2

cDNA FLJ75055		1	463.9	950.233 3	884.033 3	849.8	766.4	773.166 7
Zinc finger protein 800	ZNF800	9	1411.03333 3	3033.4	2511	2712.8	2747.06 7	2702.26 7
Programmed cell death protein 2-like	PDCD2L	6	1048.3	1756.06 7	1697.26 7	1570.66 7	1134.13 3	1368.06 7
Isoform 3 of CAP-Gly domain-containing linker protein 1	CLIP1	58	10138.9	18713.5	17068.6 7	16739.4 3	13683.2 3	14602.1
cDNA FLJ20465 fis, clone KAT06236		9	28278.1333 3	24217.5 7	20642.9	21664.3 7	20258.4	21039
Round spermatid basic protein 1-like protein	RSBN1L	12	2068.06666 7	2942.13 3	2968.83 3	2632.03 3	2301.03 3	2285.03 3
Afadin	AFDN	19	2623.3	4408.4	4060.13 3	3943.9	3585.9	3567.6
Small ubiquitin-related modifier 3	SUMO3	2	2508.33333 3	4156.36 7	4144	3718.66 7	3225.66 7	2943.4
Centromere protein V	CENPV	7	745	1201.4	1178.33 3	1074.96 7	871.166 7	980.633 3
Chromosome 11 open reading frame 48, isoform CRA_c	C11orf98	5	1507.96666 7	1420	1389.86 7	1270.63 3	1010.33 3	1158.26 7
Endothelial differentiation-related factor 1	EDF1	11	3370.5	5884.2	5550.93 3	5265.3	3899.43 3	4608.86 7
Cytochrome c oxidase subunit 7C, mitochondrial	COX7C	2	567.066666 7	865.6	867.866 7	774.566 7	653.5	693.833 3
NHP2-like protein 1	SNU13	7	3056.6	4051.83 3	3423.03 3	3626.16 7	2929.5	3040.1
Uncharacterized protein C14orf119	C14orf119	2	399	625.966 7	680.066 7	560.233 3	406.533 3	457.066 7

Cytochrome c oxidase subunit 6B1	COX6B1	5	1252.93333 3	1935.2	2397.53 3	1732.46 7	1306.36 7	1261.26 7
ETS translocation variant 3	ETV3	2	91.1	43.6	38.4333 3	39.0333 3	33.6666 7	41.1333 3
Isoform 2 of Coiled-coil-helix-coiled-coil-helix domain-containing protein 5	CHCHD5	2	210.9	364.166 7	343.6	326.033 3	282.533 3	255.4
cDNA, FLJ95288, highly similar to Homo sapiens feline leukemia virus subgroup C cellular receptor (FLVCR), mRNA		4	375.066666 7	771.0667	741	690.4	580.766 7	605.233 3
GRIP and coiled-coil domain-containing protein 2	GCC2	14	1623.63333 3	2969.5	2545.16 7	2658.9	2152.16 7	2445.53 3
Ubinuclein-1	UBN1	4	802.166666 7	872	787.533 3	780.9	683.766 7	661.6
Isoform 2 of Elongation factor 1-gamma	EEF1G	23	9851.56666 7	16940.3 3	18532.7 3	15173.8 3	10625.7	13279.1 3
PHD finger protein 3	PHF3	24	2416.23333 3	4535.53 3	4032.86 7	4062.83 3	3891.43 3	4081.53 3
Elongation factor 1-alpha 2	EEF1A2	13	19003.3333 3	30484	28546.8 7	27310.6 7	20616.1 3	24244.2
Isoform 3 of Hyaluronan mediated motility receptor	HMMR	21	3893.2	4615	6472.66 7	4135.16 7	2846.46 7	3042.3
Isoform 2 of Vacuolar protein sorting-associated protein 72 homolog	VPS72	1	193.966666 7	246.366 7	229.5	220.8	209.1	232.133 3

tRNA selenocysteine 1-associated protein 1	TRNAU1AP	2	632.833333 3	1149.36 7	1058.8	1030.13 3	760	922.666 7
Signal peptidase complex subunit 2	SPCS2	7	582.066666 7	2326.23 3	2097.2	2085.63 3	1562.66 7	1932.66 7
ATP-binding cassette sub-family F member 1	ABCF1	22	4422.86666 7	8214	7639.8	7364.6	5716.36 7	6644.2
Golgi-associated PDZ and coiled-coil motif-containing protein	GOPC	6	882.866666 7	1556.2	1373.43 3	1395.36 7	1032.53 3	1350.63 3
NEDD8 ultimate buster 1	NUB1	8	660.033333 3	1267.5	1258.66 7	1136.56 7	903.866 7	1041.5
Isoform 2 of Mannose-1-phosphate guanylttransferase beta	GMPPB	6	1201.46666 7	2490.9	2046.1	2233.96 7	1979.56 7	2318.83 3
Zinc finger protein with KRAB and SCAN domains 1	ZKSCAN1	4	499.366666 7	675.9	506	606.466 7	528.833 3	568.7
Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	7	2155.86666 7	3775.5	3198.56 7	3387.73 3	2782.86 7	2954.93 3
Ribonuclease P protein subunit p25-like protein	RPP25L	4	193.9	328.2	327.9	294.566 7	252.4	248.566 7
Tripartite motif-containing protein 47	TRIM47	1	344.7	485.366 7	444.266 7	435.633 3	400.566 7	431.1
Insulin receptor substrate 2 insertion mutant (Fragment)	IRS2	2	239.033333 3	296.733 3	251	266.333 3	260.1	297.666 7
Coatomer subunit beta'	COPB2	26	4859.96666 7	10049.5 3	8599.66 7	9020.33 3	6634.3	8344.8
Peptidyl-prolyl cis-trans isomerase G	PPIG	11	1815.36666 7	2774.2	2315.9	2490.73 3	2404.73 3	2526.33 3

Peroxisomal membrane protein PEX13	PEX13	2	447.266666 7	605.066 7	572.3	543.266 7	495.5	502.666 7
Isoform 2 of Proto-oncogene tyrosine-protein kinase Src	SRC	7	1160.26666 7	2925.76 7	2895.6	2627.1	2001.96 7	2024.13 3
Signal recognition particle receptor subunit alpha	SRPRA	15	2345.16666 7	3988.76 7	3699.03 3	3582.53 3	2773.6	3435.06 7
Hepatocellular carcinoma related protein 2		7	805.066666 7	1211.633	1302.03 3	1088.43 3	903.833 3	927.7
Tubulin-folding cofactor B	TBCB	15	4848.5	6582.93 3	5621.63 3	5914	5087.9	5495.06 7
Cellular tumor antigen p53	TP53	1	3859.7	7344.1	6351.96 7	6599.53 3	4517.26 7	5744.03 3
26S protease regulatory subunit 10B	PSMC6	29	9387.16666 7	13820.4 7	12461.1 7	12420.7 7	10336.9 7	12310.1 3
Pericentrin	PCNT	14	1012.66666 7	1867.03 3	1867.43 3	1678.23 3	1448.5	1618.53 3
Pre-mRNA-processing factor 17	CDC40	12	1542.6	2881.93 3	2594.86 7	2590.6	2088.93 3	2238.03 3
cDNA, FLJ96419, highly similar to Homo sapiens fructosamine-3-kinase-related protein (FN3KRP), mRNA		3	674.566666 7	949.0333	881.633 3	853.266 7	972.266 7	1028.26 7
Mediator of RNA polymerase II transcription subunit 13	MED13	3	352.333333 3	652.8	576.666 7	586.966 7	555.5	572.5
Translocon-associated protein subunit delta	SSR4	5	1098.13333 3	1750.93 3	1516.23 3	1574.43 3	1345.53 3	1513.9
Isoform 2 of Protein LSM12 homolog	LSM12	2	915.933333 3	1283.13 3	1199.36 7	1153.86 7	880.833 3	1006.66 7

Isoform 2 of Cactin	CACTIN	8	918.466666 7	1137.43 3	1038.03 3	1022.96 7	862.8	945.866 7
Cellular tumor antigen p53	TP53	1	3870.56666 7	7376.3	6381.33 3	6634.56 7	4540.06 7	5776.9
Coiled-coil domain-containing protein 91	CCDC91	10	1598.1	3118.03 3	2691.16 7	2804.86 7	2416.36 7	2719.76 7
cDNA, FLJ93375, highly similar to Homo sapiens ZW10, kinetochore associated, homolog (Drosophila) (ZW10), mRNA		7	526.4	625.9667 7	638.266 7	563.1	462.933 3	484.2
Alpha-galactosidase A	GLA	4	961.766666 7	1281.4	1508.16 7	1152.9	1098.46 7	849.6
Ethanolamine kinase 1	ETNK1	3	163.333333 3	377.133 3	545.433 3	339.366 7	198.1	229.566 7
Biorientation of chromosomes in cell division protein 1-like 1	BOD1L1	16	2236.53333 3	3801.93 3	3443.63 3	3421.4	3313.8	3119.1
Telomeric repeat-binding factor 2-interacting protein 1	TERF2IP	9	1678.33333 3	2201.26 7	2336.73 3	1981.06 7	1635.23 3	1767.23 3
cDNA, FLJ95064, highly similar to Homo sapiens nin one binding protein (NOB1P), mRNA		8	1284.93333 3	2037.033	2555.63 3	1833.53 3	1325.1	1347.56 7
Isoform 3 of E3 ubiquitin-protein ligase TRIP12	TRIP12	2	11079.1666 7	18192.0 3	18412.4 3	16376.9 7	11817.0 3	13102.8 3
Mitogen-activated protein kinase kinase kinase 4	MAP4K4	1	332.1	467.3	457.466 7	420.7	435.066 7	365.8

E3 ubiquitin-protein ligase CBL	CBL	9	901.3	1531.76 7	1361.46 7	1379.43 3	1185.86 7	1212.13 3
Arginine/serine-rich coiled-coil protein 2	RSRC2	8	961.766666 7	1388.46 7	1243.8	1250.4	1106.4	1206.9
mRNA-capping enzyme		6	1019.2	1716.8	1589.96 7	1546.3	1315.1	1448.23 3
N-alpha-acetyltransferase 20	NAA20	2	361.266666 7	736.333 3	679.733 3	663.266 7	486.366 7	595.133 3
Isoform 3 of Protein NEDD1	NEDD1	4	344.633333 3	360.666 7	341.433 3	325	280.466 7	305.433 3
Late secretory pathway protein AVL9 homolog	AVL9	2	239	398.433 3	353.366 7	359.166 7	256.8	326.9
E3 ubiquitin-protein ligase RNF5	RNF5	2	223.766666 7	653.7	516.933 3	589.333 3	434.566 7	423.1
26S proteasome non-ATPase regulatory subunit 9	PSMD9	7	833.1	1317.56 7	1245.16 7	1188.06 7	959.433 3	1071.8
Thioredoxin-like 4B variant (Fragment)		2	80.766666 7	92.3666 7	92.0666 7	83.3	52.8333 3	59.7333 3
Actin-related protein 8	ACTR8	1	175.8	371.366 7	487.8	334.933 3	215.966 7	228.8
DNA-directed RNA polymerases I, II, and III subunit RPABC5	POLR2L	2	183.9	249.2	278.933 3	224.766 7	149.933 3	193.033 3
Fragile X mental retardation autosomal homolog variant p2K	FXR1	24	5928.8	10149.7	9757.93 3	9154.76 7	7306.06 7	7907.76 7
U3 small nucleolar ribonucleoprotein protein MPP10	MPHOSPH10	14	4033.66666 7	6491.73 3	6004.2	5857	4816.23 3	5163.03 3

Isoform 2 of E3 ubiquitin-protein ligase TRIP12	TRIP12	1	10699.7	17604.8	17780.3	15884.2 3	11410.9 7	12654.4 7
AP2-associated protein kinase 1	AAK1	6	790.4	1633.7	1380.3	1474.26 7	1184.53 3	1377.93 3
Guanine nucleotide-binding protein subunit alpha-12	GNA12	2	410.2	900.033 3	797.8	812.2	758.966 7	754.5
Ubiquitin-like modifier-activating enzyme 5	UBA5	9	1878.16666 7	2824.6	2291.26 7	2549.93 3	1979.1	2259.13 3
Centrin-2	CETN2	4	1877.03333 3	2918.36 7	2575.53 3	2634.9	2142.06 7	2186.2
Cyclin-Y-like protein 1	CCNYL1	1	82.0333333 3	91.6333 3	80.3	82.7333 3	83.8333 3	91.0666 7
Ras GTPase-activating protein-binding protein 1	G3BP1	18	7464.76666 7	11285.7 3	11852.6 7	10192.3	7309.83 3	7563.7
E3 ubiquitin-protein ligase Itchy homolog	ITCH	5	591.733333 3	898.1	1016.63 3	811.266 7	533.133 3	760.666 7
N-alpha acetyl transferase 40	NAA40	1	325.166666 7	402.133 3	516.166 7	363.333 3	280.766 7	267.166 7
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	33	10168.2333 3	20283.4	17788.4	18327.1 7	14255.9 3	15724.4 7
RNA-binding motif protein, X chromosome	RBMX	9	6325	10139.5 3	9177.53 3	9161.66 7	8160.7	8004.4
Caprin-1	CAPRIN1	16	5067.96666 7	8562.43 3	10712.3 7	7737.26 7	4895.83 3	5279.73 3
Heat shock-related 70 kDa protein 2	HSPA2	4	19906.7666 7	35516.3	33708.2 7	32095.7 3	24571.3 3	32189.2
Cytosol aminopeptidase	LAP3	18	4298.23333 3	7710.33 3	6284.93 3	6968.13 3	3702.66 7	6758.76 7

Isoform 2 of Tropomyosin alpha-4 chain	TPM4	5	14816.6666 7	27378.8	23115.9 7	24749.2 3	19490.4 7	22926.8
cDNA FLJ57133, highly similar to Bifunctional purine biosynthesis protein PURH		3	12207.3333 3	20780.1	20027.6 7	18789.4 7	14255.9	16659.8
Transcription factor BTF3	BTF3	1	4548.26666 7	5374.03 3	5689.4	4859.26 7	3603.06 7	3943.2
Isoform 2 of Tight junction-associated protein 1	TJAP1	7	1015.4	1523.16 7	1356.73 3	1377.36 7	1227.46 7	1430.36 7
E3 UFM1-protein ligase 1	UFL1	21	2878.26666 7	6545.96 7	5935.53 3	5919.53 3	5335.36 7	5962.4
Something about silencing protein 10	UTP3	3	803.5	1248.06 7	1176.56 7	1128.73 3	1068.56 7	1198.1
Putative G-binding protein (Fragment)		1	2705.13333 3	5551.36 7	6425.66 7	5020.86 7	3414.46 7	3759.26 7
Zinc finger protein 93	ZNF93	1	632.1	1003.86 7	1035.8	907.966 7	809.133 3	761.966 7
Collagen alpha-1(XIII) chain	COL13A1	2	155.5	187.3	174.433 3	169.466 7	153.8	179.433 3
Elongation factor 1-beta	EEF1B2	13	10990.2	14129.5 3	13938.3 7	12785.2 7	9498.36 7	11078.6 3
Tropomyosin 1 (Alpha), isoform CRA_m	TPM1	3	6598.13333 3	10933.1 3	9896.36 7	9893	8109.5	9478.6
Coiled-coil domain-containing protein 86	CCDC86	8	2061.43333 3	3287.73 3	3391.93 3	2975.2	2321.8	2539.4
U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein	SNRNP27	3	364.266666 7	658.266 7	585.233 3	595.733 3	528.366 7	488.033 3

Methionine aminopeptidase 2	METAP2	1	3799.63333 3	4329.23 3	4259.2	3918.3	3048.3	3484.86 7
Triosephosphate isomerase	TPI1	30	17247.8	24710.1 3	20342.0 7	22366.1 3	19420.3	22678.0 7
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	UAP1L1	5	499.066666 7	910.433 3	815.7	824.133 3	574.866 7	743.4
Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	22	2977.96666 7	5218	4567.6	4723.56 7	4072.9	4601.2
Septin 10, isoform CRA_c	Sep 10	10	1494.5	3008.1	2735.53 3	2723.06 7	2364.7	2490.33 3
Serine/threonine-protein kinase 26	STK26	5	3344.33333 3	5743.6	5628.6	5199.76 7	3878.23 3	4274.36 7
Isoform 2 of Cystathionine beta-synthase	CBS	20	2650.56666 7	4675.63 3	4331.33 3	4233.3	2875.96 7	3380.3
Isoform 2 of Golgin subfamily B member 1	GOLGB1	47	6750	11452.8 3	10037.4 3	10369.8 7	8929	10277.6 3
Coatomer subunit delta	ARCN1	25	6722.36666 7	14420.1 3	12628.3 7	13057.7	10007.1 3	12498.9
Neurobeachin-like protein 1	NBEAL1	2	90.6	111.633 3	91.5	101.1	100.233 3	113.433 3
Ribosome-releasing factor 2, mitochondrial	GFM2	3	720.133333 3	1443.06 7	1320.26 7	1307.26 7	1090.3	1298.2
Annexin (Fragment)	ANXA1	1	21135.7333 3	30381.7	26791.8	27524.0 3	20558.7	26590.7 3
Inositol polyphosphate 5- phosphatase OCRL-1	OCRL	14	1724.66666 7	3536.46 7	3383.7	3203.83 3	2666.5	3105.76 7

39S ribosomal protein L14, mitochondrial	MRPL14	5	1165.3	1011.9	1006.73 3	916.8	858.3	868.633 3
DnaJ homolog subfamily C member 15	DNAJC15	3	691.966666 7	1275.86 7	1606.23 3	1156.53 3	919.4	869.933 3
Proteasomal ubiquitin receptor ADRM1	ADRM1	9	1909.66666 7	4822.23 3	5046.96 7	4371.73 3	2924.16 7	3475.63 3
Far upstream element-binding protein 1	FUBP1	2	9349.2	13805	12751.2 3	12515.5 7	9888.66 7	10972.2
Isoform 15 of Fibronectin	FN1	2	315	342.8	317.7	310.8	553.733 3	312.766 7
60S ribosomal protein L34	RPL34	8	6654	9782.7	9160.73 3	8869.9	6337.26 7	7009
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	PLCG2	2	197.3	407.2	391.233 3	369.233 3	289.266 7	353.9
Sjogren syndrome/scleroderma autoantigen 1	SSSCA1	4	499.066666 7	546.033 3	509.5	495.133 3	344.733 3	387.066 7
Isoform 2 of ATP-dependent RNA helicase DDX54	DDX54	18	3145.56666 7	5516.53 3	5662.56 7	5002.36 7	3747.76 7	4104.66 7
cDNA FLJ60373, highly similar to Zinc finger CCCH domain-containing protein11A	1	1795.96666 7	2890.467	2644.9	2621.5	2474.9	2499.33 3	
Serine/threonine-protein phosphatase 1 regulatory subunit 10	PPP1R10	11	836.3	1694.13 3	1680.73 3	1536.63 3	1160.4	1158.86 7
60S ribosomal protein L26 (Fragment)	RPL26	1	4775.26666 7	7881.03 3	7581.33 3	7148.56 7	5294.16 7	5837.9

G protein-binding protein CRFG variant (Fragment)	11	4526.73333 3	8508.467	9415.4	7717.73 3	5505.1	6096.03 3	
cDNA FLJ10695 fis, clone NT2RP3000403, highly similar to WW domain-binding protein 4	3	405	763.5333	734.633 3	692.6	599.2	590.233 3	
Glutathione peroxidase		6	947.533333 3	2177.83 3	2049.1	1975.53 3	1420.2	1570.73 3
E3 ubiquitin-protein ligase KCMF1	KCMF1	4	222.666666 7	466.933 3	394.233 3	423.6	314.866 7	372.933 3
Saccharopine dehydrogenase-like oxidoreductase	SCCPDH	6	1323.76666 7	3046.43 3	2790.56 7	2764.13 3	2607.86 7	2959.66 7
MAP7 domain-containing protein 3	MAP7D3	5	820.933333 3	1292.2	1436.26 7	1172.46 7	926.9	916.2
Putative histone H2B type 2-C	HIST2H2BC	1	3095.4	5688.46 7	4638.73 3	5161.93 3	6723.86 7	3426.33 3
Small ubiquitin-related modifier 1	SUMO1	3	1792.1	2268.23 3	1953.9	2058.56 7	1549.56 7	1702.8
Isoform 2 of Protein BUD31 homolog	BUD31	10	2525.16666 7	3630	3440.5	3294.53 3	2329.3	2857.9
Elongation factor 1-alpha (Fragment)		1	34565.4666 7	50926.2 3	54516.5 7	46225.5 7	33510.2	40493.3 3
MICOS complex subunit	APOOL	6	1142.8	2420.16 7	2230.1	2197.1	1943.33 3	1898.73 3
cDNA, FLJ93255, highly similar to Homo sapiens solute carrier family 7 (cationic amino		4	477.866666 7	997.8667	883.366 7	906	724.166 7	833.3

acidtransporter, γ+ system), member 1 (SLC7A1), mRNA								
Zinc finger protein 644	ZNF644	4	522.466666 7	644.866 7	693.833 3	585.5	517.833 3	543.933 3
Septin-8	Sep 08	2	857.566666 7	1934.53 3	1827.1	1756.5	1496.13 3	1676.4
Tropomyosin alpha-3 chain	TPM3	4	15589.5333 3	28530.2 3	25356.9 7	25906.8	19793.6 7	22986.6 3
Methionine aminopeptidase 2	METAP2	1	3605.86666 7	4138.73 3	4076.13 3	3758.56 7	2865.06 7	3350
Mannosyl (Alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase variant (Fragment)	3	236.3	367.8	419.366 7	334.066 7	250.5	267.1	
Nuclear receptor subfamily 2 group F member 6	NR2F6	1	252.9	698.133 3	745.1	634.133 3	471.466 7	525.533 3
Melanophilin	MLPH	7	954.133333 3	977.6	1185.93 3	888.166 7	791.1	907.666 7
60S ribosomal protein L26-like 1	RPL26L1	2	5267.93333 3	8592.53 3	8192.83 3	7806.73 3	5753.33 3	6464.06 7
Isoform 2 of A-kinase anchor protein 13	AKAP13	11	620.866666 7	930.566 7	830.733 3	845.6	766.833 3	885.533 3
SUZ domain-containing protein 1	SZRD1	7	1783.8	2484	2128.26 7	2257.63 3	2089.96 7	2177.43 3
Selenoprotein H	SELH	2	312.166666 7	560.9	644.733 3	510.133 3	454.2	463
Kanadaptin	SLC4A1AP	12	1387.83333 3	1853.9	1855.23 3	1686.13 3	1327.4	1436.03 3

PHD finger-like domain-containing protein 5A	PHF5A	10	1796.46666 7	3017.2	2792.53 3	2744.16 7	2722.46 7	2539.13 3
Cleavage stimulation factor subunit 2 tau variant	CSTF2T	3	2111.5	2624.36 7	2300.66 7	2386.9	2356.4	2154.8
SPRY2 protein		5	772.566666 7	1513.4	1426.46 7	1376.7	1175.93 3	1225.2
Protein TFG	TFG	8	1884.53333 3	4063.96 7	3665.46 7	3697.26 7	2773.7	3555.46 7
MAGUK p55 subfamily member 6	MPP6	19	2854.83333 3	6473.43 3	6914.5	5890.36 7	4230.93 3	4793.66 7
A-kinase anchor protein 17A	AKAP17A	9	966.366666 7	2212.63 3	2032.16 7	2013.36 7	1636.86 7	1698.36 7
Isoform 3 of NSFL1 cofactor p47	NSFL1C	17	3462.93333 3	5512.83 3	5208.06 7	5016.56 7	4957.03 3	4612.73 3
Isoform 2 of Exosome complex component RRP45	EXOSC9	6	866.366666 7	1010.76 7	908.566 7	919.966 7	829.066 7	974.466 7
Isoform 3 of Golgi reassembly-stacking protein 2	GORASP2	9	1952.76666 7	4173.73 3	3583.86 7	3799.86 7	3115.33 3	3628.36 7
Mitogen-activated protein kinase 12	MAPK12	1	313.533333 3	450.233 3	438.666 7	409.933 3	311.3	387.733 3
Suppressor of hairy wing homolog 4 (Drosophila), isoform CRA_a	SUHW4	3	199.933333 3	262.8	290.633 3	239.333 3	193.833 3	233.8
Ras-related protein Rap-1b	RAP1B	2	1667.06666 7	3630.23 3	3679.93 3	3306.1	2879.63 3	2986.63 3
Putative uncharacterized protein DKFZp586H1823 (Fragment)	DKFZp586H1823	1	500.633333 3	954.733 3	917.366 7	869.666 7	779.1	872.766 7

Isoform 2 of Conserved oligomeric Golgi complex subunit 5	COG5	5	450.833333 3	716.033 3	633.666 7	652.266 7	415.866 7	469.133 3
UAP56-interacting factor	FYTTD1	5	624.966666 7	635.033 3	722.6	578.5	616.833 3	524.6
Mediator of DNA damage checkpoint protein 1	MDC1	19	1980.7	2366.3	2348	2155.96 7	1651.23 3	1921.03 3
Nucleolar protein 6	NOL6	15	1674.13333 3	3051.93 3	2811.3	2781.43 3	2562.23 3	2772.2
Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR	10	1163.43333 3	2109.33 3	1866.23 3	1922.63 3	1856.26 7	1927.46 7
Dual specificity protein phosphatase		2	106.6	94.2	90.9666 7	85.8666 7	58.8	74.2
Isoform 2 of Uncharacterized protein C11orf57	C11orf57	1	231.5	324.166 7	327.133 3	295.666 7	235.933 3	242
cDNA FLJ78127, highly similar to Homo sapiens SFRS protein kinase 1 (SRPK1), mRNA		10	1825.86666 7	2474.233	2613.66 7	2257.16 7	1841.36 7	1878.86 7
Excision repair cross-complementing rodent repair deficiency, complementation group 6	ERCC6	3	254.3	435.466 7	418.1	397.266 7	351.666 7	361.633 3
Peptidyl-prolyl cis-trans isomerase (Fragment)	PPIL3	7	827.2	1632.56 7	1335.06 7	1490.1	1232.33 3	1498.73 3
Xylulose kinase	XYLB	2	107.633333 3	138.766 7	113.633 3	126.733 3	113.766 7	135.2

U6 snRNA-associated Sm-like protein LSM2	LSM2	8	2207.06666 7	2868.53 3	2729.83 3	2620.23 3	2283.73 3	2391
cDNA FLJ38059 fis, clone CTONG2014946, highly similar to Gigaxonin		4	823.666666 7	1181.667	1059.1	1079.56 7	969.266 7	1035.66 7
60S ribosomal protein L8	RPL8	23	11965.2333 3	14478.8 7	13826.6 7	13229.6	9907.73 3	11475.8
Isoform 5 of Tropomyosin alpha-3 chain	TPM3	7	17650.8	30212.1	26987.6 3	27615.6 3	21402.5 7	24848.5 3
cDNA, FLJ94517, highly similar to Homo sapiens baculoviral IAP repeat-containing 4 (BIRC4), mRNA		5	566.366666 7	920.8	856.366 7	841.766 7	660.233 3	823.233 3
COX assembly mitochondrial protein 2 homolog	CMC2	4	884.833333 3	1565.63 3	1565.03 3	1431.33 3	1233.3	1266.6
cDNA FLJ90354 fis, clone NT2RP2003390, highly similar to Translocation protein SEC63 homolog		11	1759.63333 3	3657.933	2925.5	3344.8	2878.1	3333.83 3
Switch-associated protein 70	SWAP70	16	2559.3	4274.36 7	3836.4	3908.6	3312.53 3	3997.26 7
Isoform 3 of Glutaminase kidney isoform, mitochondrial	GLS	20	3248.06666 7	7181.66 7	7538.26 7	6567.83 3	4466.23 3	4949.13 3
cDNA FLJ54637, highly similar to Homo sapiens BAT2 domain containing 1 (BAT2D1), mRNA (Fragment)		1	2121.13333 3	3098.5	3493.66 7	2833.9	2068.03 3	2161.23 3

Bifunctional purine biosynthesis protein PURH	ATIC	8	14724.2	23947.2	23038.4	21909.3 7	16718.2	19698.6 7
Isoform 5 of Activating molecule in BECN1-regulated autophagy protein 1	AMBRA1	1	71.3	86.9666 7	100.8	79.5666 7	70.0666 7	69.1
Prostaglandin reductase 1	PTGR1	10	2273.86666 7	4028.13 3	3556.86 7	3685.46 7	2721.56 7	3548.46 7
Angio-associated migratory cell protein	AAMP	6	1132.53333 3	1719.63 3	2173.5	1573.6	1150.1	1386.33 3
Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	13	2426.03333 3	3732.76 7	3379.3	3416.03 3	2793.23 3	3066.46 7
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	8	1014.86666 7	2175.8	2445.56 7	1991.26 7	1623.43 3	1616.86 7
Zinc finger CCCH domain-containing protein 11A	ZC3H11A	16	4054.86666 7	5951.23 3	5464.6	5451.53 3	4951.76 7	5306.2
Non-histone chromosomal protein HMG-14	HMGN1	2	3805.73333 3	5315.16 7	4969.36 7	4869.83 3	4641.53 3	4178.56 7
Proteasomal ATPase-associated factor 1	PAAF1	4	454.433333 3	912.933 3	842	836.7	663.666 7	630.3
Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase	FTSJ1	6	808.733333 3	1014	1012.1	929.433 3	596.2	717.6
Regulatory-associated protein of mTOR	RPTOR	6	855.666666 7	1241.4	1226.8	1138.36 7	977.6	1193.63 3

Isoform 4 of Nuclear respiratory factor 1	NRF1	3	515.833333 3	894.466 7	776.033 3	820.266 7	838.433 3	866.766 7
Alpha-1,3/1,6-mannosyltransferase ALG2	ALG2	8	1038.63333 3	1998.03 3	1642.7	1832.46 7	1565.33 3	1809.83 3
C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	46	10342.4333 3	19371.7 7	16985.8	17768.0 3	14052.7 3	16041.7 7
Probable RNA polymerase II nuclear localization protein SLC7A6OS	SLC7A6OS	4	426.7	702.033 3	680.433 3	644	469.833 3	519.466 7
Putative phospholipase B-like 2	PLBD2	3	329.9	376.5	436.533 3	345.4	346.466 7	290.566 7
A-kinase anchor protein 10, mitochondrial	AKAP10	4	438.333333 3	935.766 7	859.366 7	858.5	643.833 3	732.333 3
Isoform 4 of La-related protein 4	LARP4	9	1591.46666 7	2308.3	2883.9	2118.13 3	1483.46 7	1556.9
cDNA FLJ76888, highly similar to Homo sapiens RNA binding motif protein 6 (RBM6), mRNA		4	536.433333 3	481.8667	479.4	442.233 3	381.1	392.633 3
Cysteine and histidine-rich domain (CHORD)-containing 1, isoform CRA_c	CHORDC1	18	5413.56666 7	11126.1 7	12098.6	10212.8	6171.16 7	8303.13 3
Protein FAM192A	FAM192A	14	3112.9	4604.36 7	5262.7	4226.7	2954.4	3165.53 3
Fas-activated serine/threonine kinase	FASTK	1	21.1666666 7	16.6666 7	18	15.3	11.8333 3	12.3
Putative uncharacterized protein (Fragment)		8	1915.16666 7	2242.5	1888.76 7	2059.7	1793.8	2101.1

Peroxisomal leader peptide-processing protease	TYSND1	4	442.766666 7	384.133 3	335.633 3	352.866 7	341.266 7	362.1
Wiskott-Aldrich syndrome protein family member 1	WASF1	6	298	531.533 3	509.333 3	488.433 3	420.6	482.566 7
Protein NEDD8-MDP1	NEDD8-MDP1	6	3083.6	5471.03 3	4586	5029.23 3	4595.26 7	4974.1
RNA binding motif single stranded interacting protein 1 isoform 2 (Fragment)	RBMS1	2	1560.13333 3	2045.13 3	2120.9	1880.13 3	1534.4	1676.06 7
WD repeat-containing protein 59	WDR59	4	351.533333 3	563.333 3	493.4	518.1	388.066 7	492.833 3
Isoform 2 of H(+)/Cl(-) exchange transporter 5	CLCN5	3	163.733333 3	405.3	441.8	372.8	252.433 3	312.366 7
ESF1 homolog	ESF1	15	2453.53333 3	4235.1	4261.33 3	3896.06 7	2787.36 7	2911.53 3
Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	6	1143.86666 7	2239.63 3	2210.4	2060.56 7	1658.5	1928.96 7
Isoform 3 of Protein TALPID3	KIAA0586	1	258.433333 3	275.933 3	310.966 7	253.9	189.333 3	207.766 7
Isoform 6 of A-kinase anchor protein 9	AKAP9	19	3422.46666 7	4857.16 7	4278.7	4470.4	4149.66 7	5023.7
cDNA FLJ76981, highly similar to Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA	16	1647.33333 3	3049.7	2359.46 7	2807.6	2561.66 7	3416.93 3	
Proline and serine-rich protein 2	PROSER2	1	148.2	194.066 7	162.266 7	178.666 7	108.366 7	139.6

WD repeat-containing protein 81	WDR81	7	193.5	274.3	241.1	252.533 3	228.5	282.433 3
Prolactin regulatory element-binding protein	PREB	11	1477.63333 3	1965.1	1717	1809.16 7	1673.2	1900.8
cDNA FLJ75187, highly similar to Homo sapiens nap1 P120	7	1081.33333 3	1905.7	1763.4	1754.63 3	1464.2	1571.76 7	
Transcription elongation factor SPT4	SUPT4H1	2	349.333333 3	889.366 7	807.2	818.9	656.166 7	636.633 3
Nuclear fragile X mental retardation-interacting protein 2	NUFIP2	18	3778.13333 3	6148.46 7	7083.76 7	5663.13 3	4044.16 7	4187.76 7
40S ribosomal protein S25	RPS25	13	7662.2	8318.33 3	7911.3	7663.46 7	6160.13 3	6604.43 3
Malic enzyme		9	1707.6	3067.46 7	2838.2	2826.3	2178.83 3	2422.53 3
PDZ and LIM domain protein 7 (Fragment)	PDLIM7	1	1121.43333 3	1684.06 7	1609.46 7	1551.66 7	1246.7	1248.13 3
Kinase D-interacting substrate of 220 kDa	KIDINS220	10	924.966666 7	1511.93 3	1590.66 7	1393.06 7	1197.56 7	1248.13 3
Desumoylating isopeptidase 1	DESI1	1	327.266666 7	727.666 7	751.133 3	670.466 7	471.7	546.266 7
PC4 and SFRS1-interacting protein (Fragment)	PSIP1	1	110.066666 7	104.033 3	98.8	95.8666 7	86.5666 7	87.5666 7
60S ribosomal protein L38	RPL38	5	2203.2	3460.5	3372.56 7	3189.66 7	2486.1	2756.76 7
cDNA, FLJ93464, highly similar to Homo sapiens RAB7,	1	206.566666 7	321.4	300.966 7	296.266 7	240.866 7	339.766 7	

member RAS oncogene family-like 1 (RAB7L1), mRNA								
SF3A2 protein (Fragment)	SF3A2	6	924.133333 3	1027.93 3	826.7	947.833 3	941.866 7	934.033 3
Coronin-1A	CORO1A	6	614.666666 7	1111.03 3	1009.53 3	1025.16 7	872.266 7	955.4
Zinc finger CCCH domain-containing protein 7A	ZC3H7A	8	1030.46666 7	1377.96 7	1390.26 7	1271.9	1023.8	1200.46 7
Galectin (Fragment)		5	947.266666 7	1023.8	803.8	945	1030.7	984.8
Src substrate cortactin	CTTN	32	6763.53333 3	11679.3 3	10282.6 7	10780.7 3	9224.2	9867.06 7
COP9 signalosome complex subunit 7a	COPS7A	6	1539.3	2189.36 7	1855.2	2020.96 7	1932.56 7	2073.56 7
Probable ATP-dependent RNA helicase DHX40	DHX40	5	252.266666 7	353.3	312.866 7	326.166 7	254.533 3	259.666 7
Uncharacterized protein KIAA0513	KIAA0513	1	62.2666666 7	75.1333 3	123.733 3	69.3666 7	77.1333 3	72.7
Ribosomal protein L7-like 1, isoform CRA_b	RPL7L1	7	2773.63333 3	4022.36 7	4395.06 7	3714.26 7	2721.4	2863.86 7
Phosphatidylinositol-binding clathrin assembly protein (Fragment)	PICALM	1	865.233333 3	1657.4	1337.53 3	1530.8	1432.16 7	1563.16 7
Ubiquitin-like protein 4A	UBL4A	5	1009.13333 3	1751.73 3	1523.33 3	1618.06 7	1226.06 7	2212.76 7
Caveolin (Fragment)		3	638.866666 7	2139.4	2209.66 7	1976.16 7	1600.5	1507.56 7

Ataxin-2	ATXN2	16	2559.56666 7	4452.46 7	4342.1	4113.4	2997.36 7	3357.66 7
40S ribosomal protein S12	RPS12	12	7512.06666 7	8337.2	7787.46 7	7702.73 3	6174.83 3	7027.4
Utrophin	UTRN	13	1078.16666 7	2117.43 3	2100.63 3	1956.56 7	1865.96 7	1832.7
Isoform 2 of Transforming acidic coiled-coil-containing protein 1	TACC1	10	1653.73333 3	2850.4	2829.43 3	2633.96 7	2193.83 3	2494.06 7
Serine/threonine-protein kinase VRK2	VRK2	6	1090.4	1214.36 7	1309.56 7	1122.33 3	928.333 3	989.233 3
Dynactin subunit 6	DCTN6	3	442.3	537.6	474.033 3	496.966 7	554.366 7	534.833 3
Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	GATB	4	977.266666 7	1375.23 3	1232.4	1271.3	1139.53 3	1149.13 3
Tropomyosin alpha-4 chain	TPM4	7	16469.8	28906.5 3	25023.6 3	26722.8	20990.5 7	25029.0 3
Pyridoxine 5'-phosphate oxidase variant (Fragment)		3	446.266666 7	748.2	666.933 3	691.733 3	606.3	667.033 3
cDNA FLJ55847		1	103.8	137.533 3	139.666 7	127.166 7	99.9333 3	105.733 3
Calponin	CNN2	11	4174.36666 7	6289.76 7	5917.6	5816.1	4745.53 3	5201.43 3
cDNA FLJ78650, highly similar to Homo sapiens mucosa associated lymphoid tissue lymphoma translocation gene 1		5	524.6	767.1333	738.633 3	709.366 7	594.666 7	653.9

(MALT1), transcript variant 1, mRNA								
Nucleolar RNA helicase 2	DDX21	48	14788.8	29070.3 ₇	32913.7 ₃	26883.2 ₇	17116.9	17833.5 ₇
Gamma-adducin	ADD3	1	112.8	157.966 ₇	160.566 ₇	146.1	132.7	157.766 ₇
MLL/SEPTIN6 fusion protein (Fragment)		4	1683.56666 ₇	3960.7	4080.4	3663.4	3108.56 ₇	3382.6
WD repeat-containing protein 74	WDR74	6	923.033333 ₃	1136.43 ₃	1208.2	1051.16 ₇	782.666 ₇	844.166 ₇
cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA		38	7524.06666 ₇	12669.63 ₃	11095.9 ₃	11720.3	9050.26 ₇	10720.2 ₇
Endophilin-B1	SH3GLB1	10	1942.76666 ₇	2837.66 ₇	2633.36 ₇	2626.2	2206.9	2485.73 ₃
Zinc finger, HIT domain containing 2 variant (Fragment)		9	556.6	738.6	704.633 ₃	683.633 ₃	551.866 ₇	635.1
NAD-dependent protein deacetylase sirtuin-1	SIRT1	7	713.633333 ₃	1273.93 ₃	1500.16 ₇	1179.16 ₇	890.333 ₃	971.666 ₇
cDNA FLJ31974 fis, clone NT2RP7008167, weakly similar to 85.1 kDa PROTEIN IN GREB-FEOA INTERGENIC REGION		8	785.7	1527.733	1528.06 ₇	1414.16 ₇	1166.76 ₇	1276.93 ₃
Opioid growth factor receptor	OGFR	11	674.166666 ₇	995.3	795.4	921.533 ₃	802.3	854.133 ₃
E3 ubiquitin-protein ligase TTC3	TTC3	2	45.2666666 ₇	135.066 ₇	88	125.066 ₇	91.2333 ₃	114.6

Transcription and mRNA export factor ENY2	ENY2	5	1032.6	1448.1	1360.66 7	1341.06 7	1077.4	1216.46 7
Transforming growth factor beta-1-induced transcript 1 protein	TGFB111	4	286.666666 7	476.3	445.966 7	441.333 3	365.6	371.7
Urokinase plasminogen activator surface receptor	PLAUR	3	479.5	564.333 3	542.366 7	522.966 7	390.333 3	429.333 3
Charged multivesicular body protein 6	CHMP6	2	423.866666 7	766.3	669.266 7	710.133 3	653.666 7	713.233 3
Mitochondrial import inner membrane translocase subunit TIM14	DNAJC19	5	1218.7	1946.56 7	1506.56 7	1804.1	1672.76 7	1944.5
Kelch-like ECH-associated protein 1	KEAP1	4	888.3	1114.33 3	1299.56 7	1032.9	842.566 7	876.466 7
cDNA FLJ59877, highly similar to LAG1 longevity assurance homolog 5	1	243.1	387.9333	360.333 3	359.6	272.066 7	291.566 7	
cDNA FLJ76749, highly similar to Homo sapiens Wiskott-Aldrich syndrome-like (WASL), mRNA	5	433.8	853.9333	897.233 3	791.566 7	694.266 7	747.766 7	
Golgi reassembly-stacking protein 1	GORASP1	1	431.9	1243.6	1118.66 7	1152.93 3	949.566 7	1135.33 3
Isoform 5 of Golgin subfamily A member 4	GOLGA4	28	2424.33333 3	4687.13 3	4343.93 3	4345.86 7	3747.26 7	4318.36 7
Cellular nucleic acid-binding protein	CNBP	1	3535.6	4069.5	3714.16 7	3774.03 3	2963.5	3008.56 7

Chromosome 6 open reading frame 11	WDR46	18	4225.96666 7	6578.5	6483.96 7	6102.6	4855.16 7	5381.3
Gamma-aminobutyric acid receptor-associated protein-like 2	GABARAPL2	6	1018.03333 3	2789.53 3	3222.9	2588.43 3	1657.2	2399.1
Spliceosome-associated protein CWC15 homolog	CWC15	4	977.933333 3	1908.4	1800.76 7	1770.83 3	1677.36 7	1577.63 3
Isoform 2 of Translocon-associated protein subunit gamma	SSR3	2	984.733333 3	741.233 3	556.2	687.933 3	598.033 3	751.766 7
Nucleolar protein 16	NOP16	7	1575.43333 3	2670.66 7	2605	2478.93 3	2138.8	1823.7
Granulins	GRN	11	849.733333 3	1211.46 7	1027.5	1124.5	1023.16 7	1414.4
Isoform 2 of Disks large homolog 1	DLG1	10	1573.36666 7	2226.46 7	2247.3	2066.9	1876.76 7	1876.4
Isoform 8 of Erbin	ERBIN	13	1275.9	2892.1	3053.66 7	2685.83 3	2239.26 7	2217.8
Ribosome biogenesis protein BRX1 homolog	BRX1	11	1246.53333 3	1524.66 7	1429.26 7	1416.73 3	1215.86 7	1331.6
Isoform 2 of Phosphatase and actin regulator 4	PHACTR4	4	520.6	539.2	468.2	501.033 3	466.766 7	501
Uracil phosphoribosyltransferase homolog	UPRT	2	407.133333 3	658.766 7	525.966 7	612.266 7	552.766 7	619.666 7
Ubiquitin carboxyl-terminal hydrolase 11	USP11	19	2159.66666 7	3988.33 3	3797.66 7	3707.43 3	2686.1	3028.9

Costars family protein ABRACL	ABRACL	2	88.4666666 7	177.6	220.033 3	165.133 3	117.866 7	165.966 7
Microtubule-associated protein RP/EB family member 2	MAPRE2	2	194.333333 3	474.2	512.433 3	440.933 3	340.333 3	374.366 7
Isoform 2 of Mannose-1-phosphate guanyltrtransferase alpha	GMPPA	3	203.866666 7	323.533 3	252.5	300.933 3	243	357.466 7
cDNA FLJ77685		3	398.533333 3	590.7	569.3	549.466 7	490.833 3	570
Isoform HMG-Y of High mobility group protein HMG-I/HMG-Y	HMGA1	1	3244.53333 3	4672.26 7	3827.53 3	4346.63 3	4323.4	4723.76 7
60S ribosomal protein L35a	RPL35A	9	5989.76666 7	7638.16 7	8111.43 3	7106.3	5364.1	6336.96 7
Golgi integral membrane protein 4	GOLIM4	8	421.066666 7	868	941.433 3	807.633 3	658.033 3	778.433 3
Eukaryotic translation initiation factor 1	EIF1	11	3525.2	5135.4	5264.13 3	4779.03 3	3149.5	3907.43 3
CDKN2AIP N-terminal-like protein	CDKN2AIPNL	3	1022.33333 3	1452.4	1265.16 7	1351.73 3	1219.46 7	1188.03 3
Sequestosome-1	SQSTM1	9	1633.5	2440.43 3	2775.83 3	2272.86 7	2189.33 3	3276.7
UPF0729 protein C18orf32	C18orf32	1	171.766666 7	604.466 7	452.866 7	563	514.1	512.166 7
Prefoldin subunit 4	PFDN4	7	4074.63333 3	4231.3	3810.5	3942.16 7	3230.26 7	3845.46 7
Centrosomal protein of 41 kDa	CEP41	4	279.1	390.633 3	398.166 7	363.966 7	269.9	307.466 7

Glutathione reductase, mitochondrial	GSR	9	1917.23333 3	4572.16 7	4429.43 3	4261.26 7	3043.23 3	4024.96 7
Farnesyl pyrophosphate synthetase like-4 protein (Fragment)		1	2011.66666 7	2553.333	2161.6	2380.06 7	2169.43 3	2374.63 3
Vacuolar protein sorting-associated protein 28 homolog	VPS28	6	1426.13333 3	1730.4	1590.1	1613.16 7	1323.33 3	1566.86 7
Probable arginine--tRNA ligase, mitochondrial	RARS2	6	453.5	929	926.3	866.766 7	679.766 7	774.633 3
Sodium-coupled neutral amino acid transporter 2	SLC38A2	3	1023.2	1469.33 3	1671.73 3	1370.93 3	944.733 3	970.566 7
RNA-binding protein 28	RBM28	34	7076.4	12864.2	13007.4 7	12003.2	8431.36 7	9803.5
Phosphatidylinositol 4-kinase beta	PI4KB	6	1079.2	1392.9	1266.8	1300.16 7	1136.5	1297.6
G patch domain and KOW motifs-containing protein	GPKOW	19	2865.2	4436.26 7	4679.23 3	4141.16 7	2866.1	3045.03 3
PNMA1 protein	PNMA1	2	168.433333 3	365.433 3	506.7	341.2	247.4	259.766 7
Isoform 4 of Cellular nucleic acid-binding protein	CNBP	1	3485.6	3867.7	3520.4	3611.7	2841.66 7	2896.8
Zyxin	ZYX	13	4408.43333 3	7663.36 7	6989.73 3	7159.36 7	5582.66 7	6504.63 3
Protein kinase C alpha type	PRKCA	5	309.833333 3	676	638	631.566 7	533.6	693.3
Core-binding factor subunit beta	CBFB	2	2304.53333 3	3312.63 3	3207.16 7	3096.13 3	2482	2922.5

Isoform DFF35 of DNA fragmentation factor subunit alpha	DFFA	2	2912.866667	4726.1	4294.5	4418.4	3937.467	4116.967
HCG1984214, isoform CRA_a	hCG_1984214	2	63.33333333	45.8	49.06667	42.83333	34.03333	36.56667
Tumor suppressing subtransferable candidate 4, isoform CRA_a	TSSC4	3	459.4	656.4667	629.7333	613.9667	389.6333	677.5333
ZEB (Fragment)		4	284.1	448.0333	484.4667	419.1333	355.5333	329.4667
Probable ATP-dependent RNA helicase DHX37	DHX37	6	417.7	622.7	746.4	582.8	448.6	474.2667
Syndecan binding protein (Syntenin), isoform CRA_a	SDCBP	4	925.4666667	2132.6	1935.167	1996.133	1668.633	2439.067
cDNA FLJ78640, highly similar to Homo sapiens TSPY-like 2 (TSPYL2), mRNA		1	64.73333333	23.56667	24.96667	22.06667	16	27.03333
Guanine nucleotide-binding protein subunit gamma (Fragment)		2	275.6333333	534.4333	551.9333	500.5	289.9667	308.4333
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	NDUFB1	2	425.6	645.8667	827.9667	604.9	542.1333	440.0667
HAUS augmin-like complex subunit 4	HAUS4	5	765.5	1576.4	1533.633	1476.733	1227.5	1225.167
Probable ATP-dependent RNA helicase DDX52	DDX52	11	1945.633333	3302.767	3028.967	3094.333	2651.7	2855.533

Solute carrier organic anion transporter family member 4A1	SLCO4A1	4	751.933333 3	2032.13 3	2073.5	1905	1448.13 3	1306.66 7
Chromosome 6 open reading frame 57	C6orf57	2	756.666666 7	722.666 7	730.2	677.633 3	753.033 3	585.6
Ribosome production factor 1	RPF1	6	314.866666 7	717.8	811.3	673.1	525.366 7	580.5
Transitional endoplasmic reticulum ATPase	VCP	55	19366.1	32798.7 3	28316.8 3	30768.4 3	21914.7 3	28334.4
DNA-directed RNA polymerase III subunit RPC1	POLR3A	7	395.3	615.7	656.5	577.6	403.233 3	409
Supervillin	SVIL	9	1483.36666 7	2439.36 7	2308.93 3	2288.66 7	2147.4	2147.93 3
MRG/MORF4L-binding protein	MRGBP	3	401.2	409.266 7	392.1	384	344.7	353
40S ribosomal protein S23	RPS23	10	3913.13333 3	4836.83 3	4533.96 7	4538.4	3914	3927.46 7
RING finger protein 214	RNF214	6	913.466666 7	1077.3	947.766 7	1010.83 3	862.4	1006.63 3
Heat shock 70 kDa protein 1B	HSPA1B	6	15991.6333 3	29503.4	28390.7 3	27683.5	19917.7 7	28142.3
Zinc finger protein RFP	TRIM27	6	356.566666 7	639.266 7	628.933 3	600.066 7	484.5	565.833 3
cDNA FLJ59240, highly similar to Far upstream element-binding protein 1		3	8318.03333 3	10730.67	10207.5 7	10077.7 3	8050.53 3	9222.73 3
Uncharacterized protein C12orf45	C12orf45	3	1005.33333 3	1362.36 7	1757.96 7	1279.86 7	982.733 3	1065.96 7

Cytochrome c oxidase subunit 7A-related protein, mitochondrial	COX7A2L	2	577.733333 3	1081.36 7	1337.66 7	1016.33 3	928.4	886
60S ribosomal protein L26	RPL26	2	5598.16666 7	9826.03 3	9665.2	9235.96 7	6621.5	7611.86 7
Myotrophin	MTPN	9	5050.36666 7	7628.83 3	6376.43 3	7171.36 7	6504.03 3	7592.7
Protein cereblon	CRBN	1	207.166666 7	271.633 3	232.933 3	255.666 7	269.033 3	326.366 7
TATA box-binding protein-associated factor RNA polymerase I subunit C	TAF1C	3	287.566666 7	372.533 3	376.033 3	350.7	281.166 7	306.633 3
Isoform 3 of Proline-rich AKT1 substrate 1	AKT1S1	3	875.6	1238.63 3	1323.73 3	1166.1	763.4	902.733 3
Isoform 7 of Protein PRRC2C	PRRC2C	38	8984.03333 3	13352.1	14983.4 7	12573.6 3	9007.33 3	9779.26 7
RING finger protein 113A	RNF113A	4	365.633333 3	824.566 7	608.1	776.6	683.433 3	737.833 3
Cell division cycle protein 123 homolog	CDC123	5	717.866666 7	1116.66 7	1276.96 7	1051.73 3	714.866 7	920.533 3
Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	8	1563.26666 7	4123.43 3	4338.03 3	3886.66 7	3462.5	3354.3
Nuclear prelamin A recognition factor	NARF	3	100.1	127.3	101.066 7	120.033 3	119.366 7	122.433 3
Cdc42 effector protein 3	CDC42EP3	6	1045.83333 3	1942.93 3	1966.03 3	1832.13 3	1295.3	1333.2

Dephospho-CoA kinase domain-containing protein	DCAKD	2	357.733333 3	665.766 7	689.3	627.8	473.3	578.966 7
cDNA FLJ30322 fis, clone BRACE2006703, highly similar to Surfeit locus protein 6		17	4039.83333 3	5746.733	5363.1	5419.76 7	4718.8	4986.76 7
Bromodomain adjacent to zinc finger domain protein 2A	BAZ2A	10	1718.06666 7	2372.83 3	2432.26 7	2239.63 3	1843.46 7	2046
Isoform 3 of Phosphoacetylglucosamine mutase	PGM3	12	1949.33333 3	3911.53 3	3060.76 7	3692.8	2788.36 7	4002.13 3
EH domain-containing protein 1	EHD1	17	3845.93333 3	7072.96 7	7080.13 3	6677.63 3	4973.4	6057.26 7
60S ribosomal protein L24	RPL24	16	10542.9333 3	13776.4 7	13267.7 3	13014.6 7	9387.7	10848.8 3
Lactation elevated protein 1	LACE1	1	77.1333333 3	129.1	143.3	121.966 7	92.4333 3	97.0333 3
FLJ00169 protein (Fragment)	FLJ00169	4	367.366666 7	778.5	609.5	735.533 3	702.666 7	745.566 7
5'-nucleotidase domain-containing protein 1	NT5DC1	13	2814	5007.3	5456.26 7	4733.56 7	3557.93 3	4226.4
Isoform 2 of UBX domain-containing protein 1	UBXN1	7	646.166666 7	762.3	742.166 7	720.666 7	542.966 7	628.566 7
Thyroid receptor-interacting protein 6	TRIP6	10	1981.6	2362.7	2437.46 7	2233.9	1661.36 7	2018.96 7
Thyroid transcription factor 1-associated protein 26	CCDC59	4	657.2	1180.13 3	1198.9	1116.36 7	844.433 3	945.166 7
Isoform 5 of PDZ and LIM domain protein 2	PDLIM2	7	1138.23333 3	1557.3	1185.06 7	1473.26 7	1310.13 3	1386.26 7

Protein transport protein Sec31A	SEC31A	21	2985.36666 7	6196.63 3	5090.9	5865.53 3	4555.66 7	6254.83 3
RB1-inducible coiled-coil protein 1	RB1CC1	6	431.966666 7	789.966 7	728.766 7	748.466 7	654	823.6
AP2-associated protein kinase 1 (Fragment)	AAK1	6	1261.4	2352.56 7	2046.93 3	2229.63 3	1739.46 7	2162.33 3
cDNA FLJ55728, highly similar to ADP-ribosylation factor GTPase-activating protein 3		9	1282.73333 3	2544.533	2134.1	2412.2	1945.46 7	2426.6
cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1		1	15225.5	28888.23	27677.7	27390.0 7	19772.2 3	27867.2 3
Isoform 2 of Septin-2	Oct 89	19	4033.76666 7	7520.7	7487.7	7130.73 3	5418.9	6698.46 7
Aspartate aminotransferase, cytoplasmic	GOT1	23	3832.46666 7	7995.06 7	7018.53 3	7583.16 7	5534.4	7361.06 7
Pseudouridylate synthase 7 homolog-like protein	PUS7L	1	126.5	184.066 7	165.7	174.6	135.7	152.533 3
Isoform 4 of Protein CASC4	CASC4	3	231	495.5	430.833 3	470.1	379.266 7	525.133 3
Magnesium transporter protein 1	MAGT1	4	358.466666 7	851.8	829.633 3	808.733 3	657.366 7	816.866 7
U3 small nucleolar RNA-associated protein 14 homolog A	UTP14A	31	5352.23333 3	7602.66 7	7347.46 7	7218.3	6213.06 7	6829.03 3
Ran guanine nucleotide release factor	RANGRF	1	65.5	137.9	102.566 7	130.933 3	94.3	100.4
Isoform 2 of Cilia- and flagella-associated protein 36	CFAP36	6	1105.73333 3	1957.4	1546.26 7	1860	1560.73 3	1762.46 7

Isoform 4 of Magnesium transporter MRS2 homolog, mitochondrial	MRS2	6	804.566666 7	1289.53 3	1334.7	1225.9	1057.9	1149.86 7
Isoform 2 of Protein kinase C delta type	PRKCD	5	282.733333 3	313.166 7	268.166 7	297.766 7	240.2	295.333 3
BSD domain-containing protein 1	BSDC1	3	733.866666 7	1414.46 7	1270.26 7	1345.16 7	1048.1	1299.03 3
Vesicle transport through interaction with t-SNAREs homolog 1A	VTI1A	3	221.133333 3	368.133 3	368.866 7	350.166 7	278.833 3	336.733 3
General vesicular transport factor p115	USO1	32	6330.66666 7	11198	8948.63 3	10654.8 3	8179.36 7	11736.7 7
Transmembrane protein 263	TMEM263	2	468.3	846.6	590.666 7	805.633 3	421.2	676.666 7
NDUFA7 protein (Fragment)	NDUFA7	5	542.9	762.433 3	824.766 7	725.8	633.766 7	562.166 7
Tripartite motif-containing protein 5 alpha	TRIM5	4	612.533333 3	1029.76 7	911.466 7	980.466 7	646.8	731.566 7
Chromobox protein homolog 5	CBX5	8	2583.66666 7	4889.9	5160.9	4656.56 7	3910.03 3	3950.16 7
Microtubule-associated proteins 1A/1B light chain 3 beta 2	MAP1LC3B2	3	411.1	671.9	564	640.033 3	576.166 7	847
Group XV phospholipase A2	PLA2G15	4	480.166666 7	887.2	1063.23 3	845.133 3	610.6	640.4
Peptidyl-prolyl cis-trans isomerase FKBP14	FKBP14	4	362.533333 3	612.066 7	662.033 3	583.1	478.533 3	624.933 3

Alanine aminotransferase 2	GPT2	13	1896	3117.1	2582.13 3	2971.2	2447.13 3	2635.96 7
Isoform 4 of CDK5 regulatory subunit-associated protein 3	CDK5RAP3	16	1754.93333 3	3230.83 3	2908.6	3080.83 3	2760.16 7	3336.06 7
Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	32	5767.06666 7	10832.1	10745.0 3	10333.7 3	8713.73 3	9894.56 7
Transcription factor 25	TCF25	2	109.9	84.1	92.5333 3	80.2666 7	71.0333 3	76.6
cDNA FLJ53206		12	1652.5	3281.53 3	3632.06 7	3133.73 3	2357.1	2395.7
Fibronectin type III and SPRY domain-containing protein 1	FSD1	3	150.9	240.966 7	268.6	230.133 3	143.3	393.7
Ribosomal protein L29	RPL29	8	5786.76666 7	6551.56 7	6143	6257.43 3	5240.43 3	5429.7
RalA-binding protein 1	RALBP1	3	235.233333 3	256.2	248.433 3	244.7	198	221.033 3
Activator of basal transcription 1	ABT1	6	639.033333 3	1406.93 3	1351.2	1344.03 3	894.933 3	857.6
Chromosome transmission fidelity protein 8 homolog (Fragment)	CHTF8	2	91.5666666 7	106.266 7	113.333 3	101.566 7	88.1666 7	93.7666 7
Pre-mRNA-splicing factor CWC25 homolog	CWC25	3	752.8	816.333 3	1005.86 7	780.366 7	543.466 7	574.666 7
Fibronectin type-III domain-containing protein 3A	FNDC3A	7	1408.06666 7	3014.43 3	2607.4	2882.26 7	2340.13 3	2719.96 7
Isoform 2 of Stress-induced-phosphoprotein 1	STIP1	59	19933.5	31964.2	30099.5	30565.6 7	22502.1 7	28455.9 7

5'-nucleotidase domain-containing protein 3	NT5DC3	6	138.766666 7	507.6	427.766 7	485.5	434.466 7	460
Gamma-soluble NSF attachment protein	NAPG	14	1960.4	3932.03 3	4027.23 3	3762.53 3	2687.7	3347.36 7
Oxysterol-binding protein 1	OSBP	17	2562.66666 7	5783.9	5016.36 7	5534.83 3	3915.83 3	5483.23 3
Signal-induced proliferation-associated 1-like protein 3	SIPA1L3	5	431.033333 3	654.6	660.633 3	626.533 3	533.466 7	644.466 7
CWF19-like protein 2	CWF19L2	4	491.033333 3	679.2	656.9	650.3	548.433 3	588.8
Epididymis secretory protein Li 109	HEL-S-109	19	2439.36666 7	6101.5	5128.56 7	5843	4955.63 3	5854.53 3
Pyridoxal kinase	PDXK	5	1110.13333 3	1404.33 3	1134.33 3	1345.13 3	1187.86 7	1450.2
EH domain-containing protein 3	EHD3	1	1236.73333 3	2523.06 7	2582.1	2417.26 7	1808.3	2306.1
Ribonuclease inhibitor	RNH1	28	8820.43333 3	14569.4 7	12973.2 7	13964.3 3	9693.13 3	12901.9 7
Protein misato homolog 1	MSTO1	5	440.133333 3	1170.5	993.633 3	1122.4	751.366 7	1039
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	7	2394.66666 7	3352.53 3	2930.06 7	3214.86 7	2889.16 7	3113.13 3
Septin-7	Sep 07	26	5397.03333 3	10095.6	9400.73 3	9682	8624.13 3	9275.63 3
Signal recognition particle receptor subunit beta	SRPRB	10	3705.43333 3	6248.36 7	6861.83 3	5993.93 3	4118.63 3	5006.73 3

NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12	3	107.133333 3	181.233 3	196.933 3	173.866 7	143.066 7	99.7
Protein ABHD17B	ABHD17B	5	377.133333 3	451.166 7	442.5	432.833 3	403.633 3	480.8
Lysine-rich nucleolar protein 1	KNOP1	3	271.666666 7	425.733 3	398.266 7	408.466 7	355.833 3	347.666 7
Elongation factor 1-delta	EEF1D	20	10979.5	14773.5 3	14325.2 7	14176.8 3	10608.9	12408.2
Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1	PYROXD1	4	331.8	868.6	759.266 7	833.566 7	636.866 7	755.2
Probable ATP-dependent RNA helicase DDX27	DDX27	26	7811.16666 7	10367.5	10296.1 3	9953.46 7	7731.76 7	8449.23 3
Mimitin, mitochondrial	NDUFAF2	13	2668.76666 7	4348.76 7	3889.7	4175.5	3652.73 3	4155.2
EBNA-2 co-activator variant (Fragment)		54	17728.4	28711.1 7	26343.0 3	27568.7	20797.9	26332.9 7
Zinc finger protein 318	ZNF318	16	2405.83333 3	4113.03 3	3707.6	3949.9	3251.66 7	3262.36 7
cDNA FLJ50130, highly similar to Heterogeneous nuclear ribonucleoprotein Q		3	4145.83333 3	5367.833	4442.96 7	5156.03 3	4178.26 7	4848.76 7
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase , mitochondrial	MTHFD2	15	2896.6	4658.03 3	5005.13 3	4478.9	2933.7	3582.96 7

Nucleolar GTP-binding protein 2	GNL2	15	2135.266667	3512.5	3991.867	3377.467	2184.5	2619.4
Tripartite motif-containing protein 26	TRIM26	5	547.0666667	559.4667	626.6667	537.9667	445.4	489.0667
KAT8 regulatory NSL complex subunit 2	KANSL2	3	192.1333333	342.5	348.1667	329.4	304.6333	289.2333
Periodic tryptophan protein 1 homolog	PWP1	11	1705.566667	3295.167	3520.267	3170.867	2336.5	2668.1
cDNA FLJ58045, highly similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 13 (EC 1.6.5.3)		2	381.8666667	724.3333	798	697.3667	570.9667	652.6
Protein kinase C zeta type	PRKCZ	2	282.5333333	569.2667	342.6333	548.1	379.2667	559.7667
Protein SLX4IP	SLX4IP	1	33.7	29.63333	25.63333	28.53333	28.43333	35.96667
Lon protease homolog 2, peroxisomal	LONP2	1	109.2333333	107	108.5667	103.0667	98.2	78.16667
Serine/threonine-protein kinase RIO1	RIOK1	3	434.6666667	596.0333	624.7333	574.2667	369.4333	432.0333
Palmitoyltransferase ZDHHC5	ZDHHC5	4	609.7	1273.4	1202.867	1226.9	1062.267	1047.267
cDNA FLJ37476 fis, clone BRAWH2012827, highly similar to Homo sapiens BH3 interacting domain death		6	1604.2	2079.167	2021.833	2004.4	1581.233	1570.2

agonist (BID), transcript variant 1, mRNA								
Asparagine--tRNA ligase, cytoplasmic	NARS	29	7797.53333 3	15294.9 7	14235.9 3	14745.4 7	10347.4	13413
Ral GTPase-activating protein subunit alpha-2	RALGAPA2	1	186.3	427.066 7	399.033 3	411.766 7	364.666 7	327.033 3
PH and SEC7 domain-containing protein 3 (Fragment)	PSD3	2	531.933333 3	366.6	312.633 3	353.566 7	371	433.466 7
Calreticulin	CALR	31	12801.9	27126.4 7	19209.3 3	26169.6 3	23805.2	34410.2 7
Inhibitor of Bruton tyrosine kinase	IBTK	3	114.466666 7	523.633 3	471.466 7	505.3	294.233 3	411.033 3
UDP-glucose 6-dehydrogenase	UGDH	15	1621.4	2951.76 7	2274.33 3	2848.46 7	2149.56 7	3031.9
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	39	9071.1	18197.7 3	15527.3 7	17561.4 7	15860.6 7	18317.7 3
Isoform 2 of Catenin alpha-1	CTNNA1	22	2724.03333 3	4592.86 7	3871.36 7	4432.9	3240.23 3	3682.2
Rho guanine nucleotide exchange factor 2	ARHGEF2	21	2782.66666 7	5299	5092.66 7	5114.66 7	3781.73 3	4506.63 3
Ferritin (Fragment)	FTH1	2	712.066666 7	1340.9	1213.93 3	1295.36 7	1213.96 7	1599.4
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	3	5669.8	13589.5 3	12628.6 7	13135.9 7	8221.9	11425.6 7

Riboflavin kinase, isoform CRA_a	RFK	3	258.566666 7	301.633 3	395.866 7	291.633 3	186.433 3	220.966 7
Isoform 5 of Radixin	RDX	25	15598.5	29760.5 3	27421.7 7	28778.5 7	22581.9 3	27428.6
BRISC and BRCA1-A complex member 1	BABAM1	6	1364.06666 7	2694.13 3	2415.3	2606.5	1884.26 7	2138.8
Alanine--tRNA ligase, mitochondrial	AARS2	10	1247.96666 7	1983.2	1900.53 3	1920.06 7	1637.4	1886
cDNA FLJ51387, highly similar to Asparagine synthetase (glutamine-hydrolyzing) (EC 6.3.5.4)		1	5763.96666 7	13746.27	12812.8	13313	8232.26 7	11438.9
FGFR1 oncogene partner	FGFR1OP	4	530.566666 7	842.233 3	795.433 3	816.1	553.333 3	684.5
Ribulose-phosphate 3-epimerase	RPE	3	754.6	671.266 7	662.9	651.033 3	536.433 3	626.4
Endoribonuclease LACTB2	LACTB2	7	832.2	1527.43 3	1530.8	1481.56 7	1141.46 7	1460.2
Probable U3 small nucleolar RNA-associated protein 11	UTP11	11	1441.83333 3	3190.53 3	3105.73 3	3095.16 7	2668.96 7	2501.66 7
Nuclear transcription factor Y subunit alpha	NFYA	3	733.233333 3	475.633 3	412.966 7	461.5	436.033 3	461.8
E3 ubiquitin-protein ligase TRIM37	TRIM37	1	153.266666 7	83.7333 3	95.0666 7	81.2666 7	52.7	55.3333 3
Nuclear receptor coactivator 7, isoform CRA_c	NCOA7	8	557.566666 7	918.333 3	891.266 7	891.4	716.666 7	822.7
Protein GPR107	GPR107	2	451.8	830.1	790.166 7	806.333 3	604.666 7	738.4

Beta-2-syntrophin	SNTB2	8	2316.93333 3	2492.56 7	2463.26 7	2421.43 3	2561.56 7	2347.46 7
cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L								
Leucine zipper transcription factor-like protein 1	LZTFL1	11	1267.03333 3	2674.23 3	2196.5	2600.56 7	2029.03 3	3237.4
GTPBP3 protein (Fragment)	GTPBP3	4	419.633333 3	415.7	425.033 3	404.4	348.433 3	385.466 7
Fatty acid-binding protein, epidermal	FABP5	9	1992.86666 7	3975.03 3	4219.36 7	3867.2	2786.63 3	3542.76 7
Small acidic protein	SMAP	4	766.7	1059.83 3	1017.53 3	1031.26 7	730	929.866 7
Probable C-mannosyltransferase DPY19L1	DPY19L1	2	327.766666 7	393.733 3	405.8	383.166 7	369.9	357.466 7
RILP-like protein 2	RILPL2	1	174.566666 7	203.666 7	203.6	198.233 3	156.466 7	166.2
Adenylate kinase isoenzyme 6	AK6	4	1059.06666 7	1246.93 3	1470.06 7	1214.33 3	788.5	1109.76 7
DNA-directed RNA polymerase III 39 kDa polypeptide F variant (Fragment)		1	249.1	296.0333 3	370.633 3	288.833 3	214.933 3	221.266 7
D-tyrosyl-tRNA(Tyr) deacylase	DTD1	4	923.366666 7	1101.7	1012.23 3	1075.16 7	831.766 7	1171.5
Synaptic vesicle membrane protein VAT-1 homolog	VAT1	6	1598.6	2317.06 7	2117.03 3	2261.6	2066.8	2448.46 7
Ligand-dependent nuclear receptor-interacting factor 1	LRIF1	5	415.9	590.433 3	512.566 7	576.866 7	455.033 3	455.1

Ras-related protein Ral-A	RALA	5	951.466666 7	1877.4	2063.93 3	1835.33 3	1551.53 3	1576.3
Isoform 4 of Nuclear factor NF-kappa-B p100 subunit	NFKB2	9	1262.13333 3	2590.63 3	2437.9	2532.6	1844.56 7	2544.26 7
Segment polarity protein dishevelled homolog DVL-2	DVL2	2	393.566666 7	491.666 7	450.5	480.7	449.166 7	481.3
Isoform 3 of Signal peptidase complex catalytic subunit SEC11A	SEC11A	6	656.933333 3	1182.2	1126.1	1157.23 3	1036.2	1280.86 7
Coatomer protein complex, subunit epsilon, isoform CRA_g	COPE	13	1899.66666 7	3020.33 3	2798.8	2957.06 7	2328.23 3	2957.96 7
RalBP1-associated Eps domain-containing protein 1	REPS1	6	276.066666 7	547.733 3	561.433 3	536.3	442.633 3	488.233 3
Peptide deformylase, mitochondrial	PDF	4	558.733333 3	616.266 7	691.5	603.533 3	396.266 7	436.933 3
Protein XRP2		7	1081.1	2631.56 7	2836.4	2577.3	2077.43 3	2342.4
Triple functional domain protein	TRIO	9	494.833333 3	980.033 3	950.966 7	960.2	780.933 3	887.266 7
MAP kinase-interacting serine/threonine-protein kinase 1	MKNK1	1	157.1	125.533 3	154.2	123	115.566 7	117.6
RRP15-like protein	RRP15	8	2158.16666 7	2466.63 3	2733.93 3	2418.7	1914.96 7	1968.33 3
Zinc finger protein 593	ZNF593	4	1014.2	1119.83 3	1366.1	1098.36 7	937.833 3	1071.8
Phosphoserine phosphatase, isoform CRA_b	PSPH	10	2004	3608.76 7	3359.03 3	3539.9	2532.1	3394.63 3

Ubiquitin-40S ribosomal protein S27a	RPS27A	7	10511.2666 7	18249.1 3	16897.9 3	17901.1 3	13653.2	15823.3 7
Alternative protein ASNSD1	ASNSD1	5	544.433333 3	995.466 7	1026.96 7	976.5	756.833 3	847.1
Keratin, type I cytoskeletal 9	KRT9	7	1203.2	2225.36 7	1219.56 7	2188	1595.9	1287.33 3
Coatomer subunit zeta-1	COPZ1	5	1384.76666 7	2497.46 7	2184.66 7	2457.36 7	1916.56 7	2608.46 7
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	16	3336.96666 7	6144.76 7	5925.93 3	6046.5	4735.53 3	5107.2
Protein disulfide-isomerase A3	PDIA3	37	17299.1333 3	31914.7 7	22805.4 3	31413.0 7	30093.2 7	40618
60S ribosomal protein L35	RPL35	12	10395.0333 3	14065.8 3	13988.7 3	13846.8 3	9976.5	11000.7 7
Mediator of RNA polymerase II transcription subunit 17	MED17	5	1355.83333 3	1270.76 7	1221.3	1251.13 3	1026.2	1025
Isoform 3 of Dynactin subunit 4	DCTN4	6	501.433333 3	608.266 7	525.9	599.066 7	499.266 7	543.533 3
UPF0547 protein C16orf87 (Fragment)	C16orf87	1	18.4666666 7	31.9333 3	33.1666 7	31.4666 7	19.5666 7	18.5333 3
Protein disulfide-isomerase A3 (Fragment)	PDIA3	1	4818.33333 3	5442.83 3	4081.23 3	5363.63 3	5575.93 3	7354.03 3
Myotubularin-related protein 14	MTMR14	5	671.266666 7	844.566 7	768.933 3	832.733 3	737.566 7	806.633 3
60S ribosomal protein L19	RPL19	17	7546.76666 7	9194.16 7	9199.1	9073.93 3	6614.1	7800.3
Nibrin	NBN	4	343.033333 3	695.6	677.566 7	686.733 3	594.1	671.966 7

Putative ataxin-7-like protein 3B	ATXN7L3B	2	165.466666 7	395.633 3	389.733 3	390.7	302.833 3	349.233 3
Protein quaking	QKI	11	3124.96666 7	4669.93 3	4625.86 7	4617.2	3793.9	3927
Isoform 2 of Kinesin-like protein KIF16B	KIF16B	2	82.9333333 3	151.566 7	165.2	149.9	112.266 7	136.133 3
Cytochrome c oxidase subunit 6C	COX6C	5	1107.56666 7	1613.03 3	2149.1	1597.03 3	1413.2	1546.56 7
40S ribosomal protein S29	RPS29	3	1944.46666 7	2472.8	2575.33 3	2448.63 3	1066.03 3	2054.66 7
Lysyl oxidase homolog 2	LOXL2	6	768.566666 7	1347.56 7	1026.43 3	1334.5	804.3	1384.46 7
cDNA, FLJ93417, highly similar to Homo sapiens plasminogen activator, urokinase (PLAU), mRNA		3	207.166666 7	258.2333	226.733 3	255.766 7	202.2	270.966 7
HD domain-containing protein 2	HDHC2	5	719.633333 3	1032.93 3	1173.3	1023.6	688.266 7	892.6
cDNA FLJ78114, highly similar to Homo sapiens thymidylate synthetase, mRNA		9	1797.63333 3	1730.533	2559.06 7	1718.56 7	978.7	1017.36 7
cDNA FLJ75950		3	807.2	952.633 3	908.566 7	946.8	721.133 3	870.033 3
CD59 glycoprotein	CD59	5	1067.86666 7	1525.73 3	1943.7	1516.6	1286.13 3	1128.3
Very low-density lipoprotein receptor	VLDLR	3	317.966666 7	926.066 7	585.766 7	921.933 3	777.266 7	934.833 3

Tuberin	TSC2	3	256.533333 3	690.366 7	692.533 3	687.766 7	543.366 7	686.666 7
cDNA FLJ76413, highly similar to Homo sapiens core-binding factor, beta subunit (CBFB), transcript variant 1, mRNA	2	2426.3	3004.4	2884.26 7	2993.66 7	2391.1	2847.26 7	
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8	4	375	677.066 7	848.966 7	675	622.2	549.766 7
cDNA FLJ76697		4	305.666666 7	572.9	584.2	571.466 7	549.633 3	478.2
Syntaxin-7	STX7	6	727.8	1179.56 7	1116.53 3	1177.06 7	894.8	1077.96 7
Probable ATP-dependent RNA helicase DDX31	DDX31	8	739.666666 7	1167.43 3	1153	1165.7	937.7	1312.1
Isoform 2 of Metalloreductase STEAP3	STEAP3	4	494.566666 7	474.1	503.933 3	473.466 7	337.333 3	353.766 7
Syntaxin-5	STX5	5	1213.23333 3	1933.8	1871.9	1932.9	1420.36 7	2007.83 3
Isoform 2 of Protein disulfide-isomerase A6	PDIA6	20	7526.26666 7	11621.7 3	8789	11620.2 3	11033.4	14506.1 7
Zinc finger, NFX1-type containing 1, isoform CRA_b	ZNFX1	6	693.966666 7	656	624.3	656	622.233 3	698.1
Isoform 3 of Cysteine--tRNA ligase, cytoplasmic	CARS	38	7396	12996.9 3	12382.1	13006.6	9144.83 3	12562.1 7
Protein dpy-30 homolog	DPY30	3	1492.53333 3	969.833 3	892.566 7	970.633 3	1037.6	1001.53 3

Zinc finger protein 622	ZNF622	6	544.8	916.166 7	934.3	917.6	624.333 3	966.6
Tyrosine-protein phosphatase non-receptor type	1	135	190.6	189.266 7	191.033 3	135.233 3	166.666 7	
28S ribosomal protein S12, mitochondrial	MRPS12	3	835.766666 7	896.333 3	906.133 3	898.5	795.633 3	807.466 7
Katanin p80 WD40 repeat-containing subunit B1	KATNB1	4	649.166666 7	1222.96 7	1221.63 3	1226.43 3	849.6	1145.33 3
Nuclear receptor-binding factor 2	NRBF2	2	233.833333 3	339.333 3	287.933 3	340.433 3	272.566 7	353.866 7
RNA/RNP complex-1-interacting phosphatase	DUSP11	3	205.933333 3	226.666 7	238.233 3	227.8	167.1	192.733 3
Zinc finger protein 512	ZNF512	6	938.9	1015.86 7	940	1021.46 7	931.4	932.033 3
TANK protein	TANK	5	448.633333 3	678.066 7	673.333 3	682.866 7	480.533 3	670.833 3
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	NDUFS4	2	283.9	288.666 7	329.533 3	290.8	288.266 7	291.066 7
Annexin A5	ANXA5	20	3981.9	7687.3	7156.06 7	7745.66 7	6104.76 7	7863.16 7
DnaJ homolog subfamily B member 6	DNAJB6	12	2258.96666 7	3984.93 3	4133.33 3	4015.7	2733.96 7	3929.86 7
Isoform 4 of Probable helicase senataxin	SETX	12	1251.53333 3	2854.03 3	2880.63 3	2876.36 7	2149.4	2659.06 7
Nestin, isoform CRA_c	NES	7	309.8	466.2	523.333 3	470.266 7	470.433 3	409.166 7

tRNA (guanine-N(7)-)-methyltransferase (Fragment)	METTL1	1	371.233333 3	449.3	421.133 3	453.566 7	442.8	502.233 3
Integrator complex subunit 10	INTS10	2	37	147.433 3	152.7	148.966 7	116.133 3	110.766 7
Zinc finger protein ZPR1	ZPR1	15	2578.5	3233.76 7	3520.06 7	3270.53 3	2321.63 3	2882.36 7
Endoplasmic reticulum resident protein 44	ERP44	13	1999.63333 3	4264.76 7	4086.43 3	4317.06 7	3518.2	4305.93 3
Patatin-like phospholipase domain-containing protein 2	PNPLA2	2	185.666666 7	192.166 7	229.333 3	194.566 7	149.933 3	182.7
Sperm-specific antigen 2	SSFA2	8	743.7	1252.5	1363.23 3	1269.46 7	1044.43 3	1165.13 3
TATA element modulatory factor	TMF1	16	2403.9	5133.13 3	4747.63 3	5207.76 7	4034.83 3	4986.53 3
Histone chaperone ASF1A	ASF1A	3	335.2	1084.76 7	1363.86 7	1100.96 7	638.966 7	759.633 3
Coiled-coil domain-containing protein 50	CCDC50	7	1208.96666 7	1302.43 3	1404.4	1322.4	1024.73 3	1219.96 7
Isoform 3 of Calumenin	CALU	20	4366.06666 7	10701.5	10296.2	10867.5 3	7595.46 7	10544.5 3
Testis-specific Y-encoded-like protein 1	TSPYL1	4	698.433333 3	838.8	996.966 7	851.866 7	698.366 7	762.433 3
cDNA FLJ61695, highly similar to Glioma tumor suppressor candidate region gene 2 protein	5	1226.1	1794.367	2126.13 3	1822.9	1370.46 7	1453.7	
Serine/threonine-protein kinase RIO2	RIOK2	4	345.2	556.333 3	713.266 7	565.466 7	333.833 3	366.466 7

Cytospin-B	SPECC1	5	615.666666 7	559.133 3	675.6	569.633 3	556.633 3	504.466 7
Thiopurine S-methyltransferase	TPMT	4	524.8	1372.7	1023.66 7	1399.7	919.7	1629.16 7
Erythrocyte band 7 integral membrane protein	STOM	2	43.4666666 7	157.9	172.3	161.033 3	128.933 3	142.466 7
Filamin-A	FLNA	1	24120.2666 7	43966.6 3	43645.4 7	44849.5 3	35102.8 3	41296.3 7
Protein disulfide-isomerase	P4HB	47	16164.5	32231.0 3	22711.5	32886.3 7	30885.7 3	41097.8
cDNA, FLJ92476, highly similar to Homo sapiens LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM3), mRNA		3	1310.36666 7	1104.8	1083.53 3	1127.7	985.633 3	1039.4
cDNA, FLJ95758, highly similar to Homo sapiens GCIP-interacting protein p29 (P29), mRNA		1	231.5	166.9	199.4	170.4	143.066 7	152.033 3
m7GpppN-mRNA hydrolase	DCP2	5	436.066666 7	563.9	549.3	575.733 3	431.2	529.3
Type II inositol 3,4-bisphosphate 4-phosphatase	INPP4B	6	448.1	638.833 3	683.033 3	652.333 3	527.5	615.833 3
Protein SPT2 homolog	SPTY2D1	4	1018.03333 3	1266.93 3	1474.66 7	1293.93 3	1030.86 7	1309.56 7
Pumilio homolog 3	PUM3	16	2373.9	2320.96 7	2365.13 3	2372.26 7	1896.03 3	2158.5

DNA oxidative demethylase ALKBH2	ALKBH2	2	171.066666 7	212.2	211.5	216.9	135.533 3	184.9
Moesin	MSN	40	21254.8	39797.2 7	37103.8 7	40688.5	29769.1 3	39585.2 3
Filamin A	FLNA	2	24026.2666 7	43874.8 7	43648.1 3	44863.1 7	35025.2	41331.5 3
Golgin subfamily A member 3	GOLGA3	31	4472.3	7138.06 7	6669.3	7300.9	5952.2	8040.06 7
Werner syndrome ATP- dependent helicase	WRN	3	443.433333 3	640.666 7	744.733 3	655.533 3	470.8	594.866 7
PJA2/FER fusion protein	Pe7Fe14	3	276.033333 3	467.266 7	404	478.166 7	374.366 7	507.866 7
Isoform 1 of Scavenger receptor class B member 1	SCARB1	4	1006.1	2328.63 3	3223	2386.2	1586.8	1763.5
Diphosphoinositol polyphosphate phosphohydrolase 2	NUDT4	3	832.766666 7	1215.8	1290.53 3	1246.96 7	881.333 3	1159.9
Tyrosine-protein kinase	YES1	7	1308.8	3675.16 7	3737.96 7	3770.73 3	2771	3006.3
Ubiquitin-60S ribosomal protein L40	UBA52	3	9527.43333 3	13447.3 3	12383.3 7	13800.3	9871.3	13106.9 3
Nucleolar protein 7	NOL7	12	2469	2967.93 3	3054.3	3049.4	2220.76 7	2413.66 7
Isoform 2 of Tubby-related protein 3	TULP3	3	216.533333 3	268.566 7	263.833 3	276.166 7	242.466 7	213.866 7
Cysteine-rich motor neuron 1 protein	CRIM1	9	997.333333 3	2467.26 7	2211.06 7	2537.26 7	1943.23 3	2694.53 3

Aurora kinase A-interacting protein	AURKAIP1	2	564.1	710.266 7	785	730.633 3	729.666 7	575.833 3
Proepiregulin	EREG	2	652.6	585.4	623.066 7	602.3	467.166 7	497.1
LIM and SH3 domain protein 1	LASP1	16	7271.4	14433.4 3	15363.3	14851.2 3	11659	13870.0 7
UPF0428 protein CXorf56	CXorf56	5	1111.33333 3	2165.96 7	2108.03 3	2228.76 7	1396.7	2178.63 3
Isoform 3 of Neurochondrin	NCDN	5	832.8	1011.36 7	958	1040.73 3	632.966 7	770.066 7
Transcription elongation factor A protein 1	TCEA1	15	3988.5	7100.33 3	7131.8	7307.06 7	5112.86 7	6822
Isoform 7 of Tumor protein D54	TPD52L2	17	5157.5	7773.03 3	7110.76 7	8002.6	6370.83 3	8062.1
Charged multivesicular body protein 5	CHMP5	9	1145.7	1634.7	1570.1	1684.1	1331.36 7	1671.33 3
Thioredoxin-interacting protein	TXNIP	4	512.466666 7	1831.7	720.233 3	1890.6	1363.2	1766.36 7
Prefoldin subunit 6	PFDN6	10	2677.93333 3	3036.56 7	2685.33 3	3137.33 3	2504.26 7	3008.5
Putative sodium-coupled neutral amino acid transporter 10	SLC38A10	4	225.966666 7	326.566 7	314.433 3	337.666 7	294.066 7	358.8
Isoform 2 of Transmembrane protein 245	TMEM245	3	598.033333 3	785.5	714.3	812.5	901.166 7	779.9
Isoform 2 of COMM domain-containing protein 6	COMMD6	4	525.766666 7	524.633 3	505.366 7	542.666 7	360.066 7	486.933 3

Probable ATP-dependent RNA helicase DDX59	DDX59	5	447.533333 3	401.133 3	312.933 3	415.5	460.2	554.266 7
YrdC domain-containing protein, mitochondrial	YRDC	6	1179.16666 7	1550.5	1859.56 7	1607.73 3	1162.9	1376.9
Isoform 2 of Membrane magnesium transporter 1	MMGT1	1	657.6	753.2	734.4	781.7	575.866 7	682.5
Alanine--tRNA ligase, cytoplasmic	AARS	52	17587.0666 7	31566.3	27150.4 7	32777.5 3	23341.2	36369.3
Phosphoserine aminotransferase		23	7078.53333 3	14205.2 7	14269.7 7	14755.1 7	9571.43 3	14256
Cytovillin 2 (Fragment)	VIL2	1	6264.9	11551.0 3	10861.1 7	12026.0 3	9069.7	11560.3
Translocon-associated protein subunit alpha	SSR1	2	332.733333 3	1093.73 3	973.866 7	1138.86 7	817.366 7	1088.46 7
Protein ELFN1	ELFN1	1	80.2	38.4333 3	47.2666 7	40.0333 3	37.8	39.2333 3
Neural cell expressed, developmentally down-regulated 4, isoform CRA_b	NEDD4	5	466.033333 3	769.666 7	859.366 7	801.833 3	515.4	747.433 3
Isoform 3 of Protein YIPF5	YIPF5	2	202.033333 3	438.1	371.2	456.466 7	365.233 3	469.6
Isoform 2 of Protein PRRC1	PRRC1	6	1224.63333 3	1804.6	1514.96 7	1881.56 7	1478.7	2133.86 7
Nicastrin	NCSTN	2	182.466666 7	326.666 7	357.833 3	341.166 7	211.2	362.933 3
Cyclin-dependent kinase 6	CDK6	8	965.833333 3	2091.33 3	2437.96 7	2184.26 7	1471.7	1779.3

cDNA FLJ53470, highly similar to Calcium/calmodulin-dependent protein kinase type II delta chain (EC 2.7.11.17)		2	1028.466667	1333.3	1430.367	1393.133	1218.467	1467.367	
Zinc finger protein 512B	ZNF512B	1	64	37.533333	45.93	39.233333	59.933333	44.33	
Serine--tRNA ligase, cytoplasmic	SARS	27	6169.433333	12846.73	13144.87	13432.53	8225.97	12332.57	
Junctional adhesion molecule C	JAM3	3	329.1	605.4	740.8	633.1667	471.6333	673.2667	
Ribosome biogenesis protein NSA2 homolog	NSA2	11	2093.233333	3409.667	4025.867	3567.167	2212.167	2204.233	
Tyrosine-protein kinase receptor UFO	AXL	4	467.5	895.7667	1085.067	937.3333	677.5667	726.17	
rRNA-processing protein UTP23 homolog	UTP23	5	1075.933333	1201.367	1133.767	1257.233	1122.767	1212.867	
Tax1-binding protein 1	TAX1BP1	7	640.9	957.5	1182.433	1003.067	814.2667	9717	
Solute carrier family 12 member 2	SLC12A2	7	1381.233333	2233.033	2550.867	2341.267	1859.47	2137.933	
Phosphotriesterase-related protein	PTER	10	1271.466666	2857.97	2864.333	2996.967	2113.567	2804.67	
Fascin	FSCN1	11	1564.133333	3832.533	3571.233	4020.067	3066.133	3936.73	
TBC1 domain family member 23	TBC1D23	7	863.3	1834.533	1826.73	1924.4	1288	1848.367	
Profilin (Fragment)	PFN2	3	1914.066666	3556.667	3623.867	3736.433	2543.367	3536.233	

Motile sperm domain-containing protein 2	MOSPD2	2	50.6	329.733 3	303	346.4	267.266 7	317.6
Isoform 3 of UDP-N-acetylhexosamine pyrophosphorylase	UAP1	36	11524.3666 7	23804.3 3	22065.3	25036.5 3	15320.2	21677.2 3
Box C/D snoRNA protein 1	ZNHIT6	7	961.133333 3	1394.6	2158.93 3	1466.9	948.533 3	982.933 3
URCC5	URCC5	2	192.3	229.433 3	215	241.333 3	199.566 7	213.533 3
60S ribosomal protein L11	RPL11	12	4299.36666 7	7051.06 7	7100.26 7	7419.63 3	5039.5	5692.3
DDB1- and CUL4-associated factor 5	DCAF5	1	48.5	82.9666 7	76.9666 7	87.3666 7	56.3666 7	58.4333 3
Cytoskeleton-associated protein 4	CKAP4	30	7767.43333 3	13383.8 7	12914.8 7	14111.5	11693.1	15042.3
Serine/threonine-protein kinase 10	STK10	10	396.3	855.633 3	960.5	902.733 3	632.8	781.7
Myeloid-associated differentiation marker	MYADM	2	438.5	400.833 3	420.066 7	423	329.2	396.2
E3 SUMO-protein ligase CBX4	CBX4	7	851.233333 3	1005.5	946.1	1064.46 7	911.033 3	1086.33 3
Oligoribonuclease, mitochondrial	REXO2	7	2907.06666 7	5045.86 7	4836.46 7	5353.6	3622.5	5434.93 3
RPL14 protein	RPL14	2	9401.13333 3	9083.7	8998.53 3	9665.86 7	7000.03 3	8450.8
Probable tRNA(His) guanylyltransferase	THG1L	3	323.766666 7	482.866 7	427.166 7	514	396.666 7	530.266 7

Isoform 3 of Oxidoreductase HTATIP2	HTATIP2	4	596.766666 7	1359	1592.33 3	1458.76 7	948.733 3	1409.6
Single-stranded DNA-binding protein, mitochondrial	SSBP1	6	887.3	1311.96 7	1197.96 7	1410.46 7	1119.13 3	1497.03 3
Golgi SNAP receptor complex member 2	GOSR2	3	119.6	305.366 7	310.766 7	328.333 3	249.866 7	347.733 3
Golgin subfamily A member 2	GOLGA2	15	2001.3	3092.63 3	3142.66 7	3326.5	2394.7	3125.83 3
Rab11 family-interacting protein 1	RAB11FIP1	7	352.066666 7	451.8	375.866 7	486.466 7	503.133 3	715.433 3
cDNA FLJ31151 fis, clone IMR322001541, highly similar to Probable ribosome biogenesis protein RLP24		3	688.3	1114.2	1316.86 7	1200.1	839.633 3	872.033 3
Aldehyde dehydrogenase family 3 member B1	ALDH3B1	2	173	275.933 3	300.266 7	297.833 3	276.2	319.4
Adenosine deaminase	ADA	2	165.933333 3	341.233 3	371.266 7	368.4	304.666 7	346.466 7
Sterol O-acyltransferase 1	SOAT1	5	487.333333 3	1024.3	1489.5	1107.63 3	633.166 7	757.133 3
cDNA, FLJ92155, highly similar to Homo sapiens ubiquitin-like 5 (UBL5), mRNA		2	1099.63333 3	1120.533	1454.43 3	1212.4	925	915
Ribosome maturation protein SBDS	SBDS	18	3365.5	6642.63 3	7684.56 7	7195.2	4591.5	6613.16 7
Ezrin	EZR	35	25580.2666 7	37199.3 3	34595.4 3	40300.2 3	30630.2	39810.7 3

High mobility group nucleosome-binding domain-containing protein 3	HMGN3	1	1607.36666 7	2519.83 3	2439.96 7	2736.06 7	2897.53 3	2480.3
Myelin protein zero-like protein 1	MPZL1	4	417.466666 7	740.566 7	953.733 3	804.866 7	537.9	643.4
Cyclic GMP-AMP synthase	MB21D1	6	480.2	976.766 7	1311.8	1063.96 7	688.1	903.566 7
Isoform 2 of High mobility group nucleosome-binding domain-containing protein 3	HMGN3	1	1641.56666 7	2586.8	2516.23 3	2826.9	2985.86 7	2564.43 3
PDZ and LIM domain protein 4	PDLIM4	3	292.233333 3	539.766 7	579.633 3	590.166 7	390.433 3	510.7
Profilin-2	PFN2	2	1523.1	2593.53 3	2794.66 7	2836.33 3	1965.56 7	2654
cDNA FLJ54371, highly similar to Serum albumin		3	577.933333 3	1218.433	1126.33 3	1332.66 7	1497.96 7	1291.36 7
cDNA FLJ75556, highly similar to Homo sapiens ribosomal protein L14, mRNA		4	11671.1333 3	10197.17	9932.53 3	11159.2 7	8383.23 3	10332.2 7
Neuroblastoma breakpoint family member 9	NBPF9	2	179.8	75.1333 3	60.0666 7	82.2666 7	87.9333 3	98.5333 3
Protein transport protein Sec61 subunit beta	SEC61B	3	297.866666 7	1049.96 7	792.966 7	1152.1	820.6	1216.5
Protein CMSS1	CMSS1	5	698.2	1683.2	1849	1849.13 3	1215.2	1546.16 7
cDNA FLJ50039, highly similar to Homo sapiens solute carrier		11	2436.43333 3	5266.2	6001.86 7	5801.76 7	4794.7	6055.8

family 25, member 24, transcript variant 1, mRNA								
Zinc transporter ZIP14	SLC39A14	3	866.7	1348.13 3	1859.4	1486.3	888.733 3	1099.43 3
cDNA, FLJ94320		3	384.2	473.966 7	531.966 7	522.8	427.133 3	522.8
Cyclin-dependent kinase inhibitor 1B	CDKN1B	2	43.4666666 7	85.7333 3	45.5666 7	94.5666 7	68.0666 7	133
Band 4.1-like protein 2	EPB41L2	25	3064.33333 3	6140.5	7117.86 7	6775.33 3	4891.6	6027.46 7
Peptidyl-tRNA hydrolase ICT1, mitochondrial	MRPL58	4	434.3	518.5	487.6	572.2	517.266 7	522.566 7
Pirin	PIR	4	283.9	599.033 3	769.866 7	665.166 7	435.866 7	594.9
cDNA FLJ78217		2	567.633333 3	1384.16 7	1174.5	1538.9	942.366 7	1217
Diphosphoinositol polyphosphate phosphohydrolase 3-beta	NUDT11	1	211.033333 3	694.6	805.433 3	772.766 7	498.466 7	706.133 3
Perilipin-2	PLIN2	16	2945.26666 7	6641.03 3	4917.56 7	7393.9	8078.06 7	7230.9
DnaJ homolog subfamily C member 17	DNAJC17	3	628.7	493.066 7	450.133 3	549.2	428.466 7	576.533 3
Small glutamine-rich tetratricopeptide repeat- containing protein beta	SGTB	2	509.766666 7	483.766 7	453.066 7	538.9	373.133 3	525.266 7
Protein LTV1 homolog	LTV1	4	543.433333 3	443.4	755.6	495.966 7	319.2	338

p180/ribosome receptor	RRBP1	100	21760	35025.7 7	28503.2 3	39229.5 3	33608.5 7	43399.3 7
High mobility group nucleosome-binding domain-containing protein 4	HMGN4	7	3613.13333 3	3198.4	2913.93 3	3589.03 3	3622.5	3588.7
Isoform 2 of Leupaxin	LPXN	6	788.433333 3	1724.53 3	1952.66 7	1938.7	1138.96 7	1529.83 3
Isoform 4 of Angiomotin-like protein 2	AMOTL2	5	868.1	1533.1	2225.73 3	1725.06 7	1065.4	1197.96 7
Armadillo repeat-containing X-linked protein 3	ARMCX3	9	1631.16666 7	2791.26 7	2655.76 7	3141.83 3	2380.66 7	3086.3
Isoform 2 of Astrocytic phosphoprotein PEA-15	PEA15	7	1956.7	3996.83 3	4162.26 7	4500.46 7	3150.53 3	4305.26 7
Collagen alpha-1(XIV) chain	COL14A1	1	454.5	228.9	239.2	258.666 7	264.233 3	351.7
Tropomyosin alpha-4 chain (Fragment)	TPM4	1	2837.1	2684.3	2450.56 7	3042.06 7	2409.16 7	3059.43 3
OTU domain-containing protein 3	OTUD3	1	21.7333333 3	59.4666 7	92.4333 3	67.4	27.8333 3	41.4
Solute carrier family 2 (Facilitated glucose transporter), member 1 variant (Fragment)		6	503.966666 7	1404.8	1029.96 7	1594.53 3	1027.83 3	1391.3
Neutral amino acid transporter B(0)	SLC1A5	3	1516.3	2442	3234.5	2784.43 3	1510.36 7	2105.86 7
cDNA FLJ77391, highly similar to Homo sapiens EH-domain containing 4 (EHD4), mRNA		9	1827.66666 7	3452.067	3850.6	3945.3	2696.5	3772.6

Glycine--tRNA ligase	GARS	39	10558.4333 3	20758.3 7	18538.6	23761.5 3	14929.8	25475.3 3
Putative uncharacterized protein Nbla00360	Nbla00360	4	473.066666 7	609.633 3	561.233 3	700.533 3	478	886.866 7
Putative uncharacterized protein (Fragment)	2	172.933333 3	164.9	158.233 3	189.833 3	115.4	162.533 3	
cDNA FLJ55697, highly similar to Protein transport protein Sec23B	9	1866.56666 7	3385.667	3183.36 7	3901.73 3	2305.2	3476.16 7	
Isoform 2 of Septin-11	Oct 89	12	3488.43333 3	7093	8229.83 3	8194.23 3	5734.73 3	7779.16 7
cDNA FLJ58765, highly similar to Neutral amino acid transporter B(0)	1	1340.8	2172.433	2906.6	2510.63 3	1338.03 3	1882.4	
Interferon-related developmental regulator 1	IFRD1	4	465.866666 7	1228.63 3	1535.26 7	1423.33 3	935.9	1390.9
Epidermal growth factor receptor kinase substrate 8	EPS8	7	922.166666 7	1160.26 7	1665.06 7	1346.16 7	980.066 7	1116.56 7
C-type mannose receptor 2	MRC2	3	315.2	254.833 3	306.9	296.5	285.2	292.633 3
CCAAT/enhancer-binding protein beta	CEBPB	2	245.533333 3	367.733 3	438.733 3	428.066 7	324.866 7	418.766 7
Isoform 3 of GRAM domain-containing protein 3	GRAMD3	4	303.2	407.6	454.2	475	323.566 7	340.433 3
Prostaglandin E synthase 3 (Cytosolic), isoform CRA_c	PTGES3	10	2819.13333 3	5097.46 7	6000.43 3	5976.56 7	3188.5	4772.76 7
COX assembly mitochondrial protein homolog (Fragment)	CMC1	2	655.033333 3	610.733 3	826.933 3	716.133 3	523.6	527.966 7

cDNA, FLJ96730, highly similar to Homo sapiens sorting nexin 15 (SNX15), transcript variant A, mRNA		2	187.166666 7	136.8333	132.1	160.466 7	151.333 3	170.133 3	
RNA-binding protein 3	RBM3		4	881.133333 3	1368.93 3	1826.86 7	1609.83 3	1052.43 3	1210.03 3
Ras GTPase-activating protein 1	RASA1		7	857.3	1244.1	1303.56 7	1464.3	1084.5	1460.63 3
cDNA FLJ61541, highly similar to Homo sapiens PDZ and LIM domain 5 (PDLIM5), transcript variant 2, mRNA		2	2032.4	3766.067	4817	4440.9	2465.5	3424.66 7	
STE20/SPS1-related proline-alanine-rich protein kinase	STK39		3	257.133333 3	366.5	518.033 3	432.3	233.466 7	340.7
Cytochrome c oxidase subunit 2	COX2		3	148.333333 3	151.2	176.733 3	178.833 3	157.4	174.233 3
Thioredoxin-related transmembrane protein 2	TMX2		2	356.266666 7	464.233 3	635.4	550.433 3	347.433 3	404.633 3
Ubiquitin-like-conjugating enzyme ATG3	ATG3		7	1143.43333 3	1779.5	2294.9	2112.23 3	1099.6	1900.96 7
Fibronectin type III domain-containing protein 3B	FNDC3B		10	1062.86666 7	2041.5	2184.4	2431.06 7	1656.3	2077.33 3
Protein disulfide-isomerase A3	PDIA3		1	180.833333 3	511.1	287.2	609.133 3	355.366 7	451.566 7
Isoform 4 of Ras-related protein R-Ras2	RRAS2		6	1141.43333 3	2165	2679.83 3	2588.5	1736.56 7	2274.43 3
cDNA, FLJ94436, highly similar to Homo sapiens platelet		1	258.833333 3	288.5333	298.433 3	345.6	245.066 7	472.666 7	

derived growth factor C (PDGFC), mRNA								
Protein spire homolog 1	SPIRE1	4	401.666666 7	760.466 7	866.9	912.2	613.433 3	875.8
Pituitary tumor-transforming gene 1 protein-interacting protein	PTTG1IP	3	920.366666 7	1420.3	1330.56 7	1716.66 7	1530.26 7	1695.13 3
Trans-3-hydroxy-L-proline dehydratase	L3HYPDH	3	292.966666 7	480.7	587.766 7	584.133 3	394.866 7	549.9
cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein		2	473.066666 7	430.2	441.9	524.5	589.666 7	460.233 3
Major prion protein	PRNP	1	119.6	148.8	147.333 3	181.466 7	162.866 7	168.3
Isoform 2 of Secernin-1	SCRN1	6	1278	2190.33 3	2767.66 7	2679.1	1734.16 7	2798.63 3
Protein FAM3C	FAM3C	5	1254.6	2394.53 3	3820.23 3	2948.9	1615.66 7	2351.36 7
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	20	3379.13333 3	6188.33 3	6056.46 7	7648.9	4626.03 3	8258.2
Heat shock 70 kDa protein 13	HSPA13	9	1541.73333 3	2684.56 7	2922.66 7	3344.63 3	2051.8	2901.2
PDZ and LIM domain 5, isoform CRA_c	PDLIM5	8	3112.16666 7	5734.3	7639.36 7	7156.03 3	3736.76 7	5312.93 3
Similar to t-complex 1; T-complex locus TCP-1; t-complex 1 (A murine tcp homolog)	LOC401329	1	561.666666 7	639.266 7	598.933 3	798.233 3	688.5	899.333 3

Y+L amino acid transporter 2	SLC7A6	1	41.4	107.6	163.9	135.233 3	60.5	98.4666 7
Metalloproteinase inhibitor 2	TIMP2	4	493	1134.23 3	997.3	1432.33 3	816.9	2024.33 3
Pleckstrin homology-like domain family B member 3	PHLDB3	1	104.933333 3	122.266 7	139.766 7	154.733 3	115.1	133.333 3
cDNA, FLJ93605, highly similar to Homo sapiens heme oxygenase (decycling) 1 (HMOX1), mRNA		4	448.733333 3	551.9667	528.966 7	698.833 3	505.766 7	670.4
Isoform 4 of Microtubule-associated protein 2	MAP2	3	2332.43333 3	3915.63 3	4819.96 7	5007.26 7	3304.16 7	4999.5
Angiopoietin-related protein 4	ANGPTL4	8	988.633333 3	1451.9	904.8	1867.23 3	1033.73 3	2706.83 3
Ras-related GTP-binding protein B	RRAGB	2	318.166666 7	406.833 3	343.666 7	523.5	501.266 7	849.833 3
cDNA FLJ55486, highly similar to Semaphorin-3C		4	544.333333 3	774.8667	848.1	1002	752.366 7	1210.66 7
E3 ubiquitin-protein ligase NEDD4-like	NEDD4L	15	1808.5	2419.36 7	3125.7	3137.76 7	1858.86 7	2823.23 3
Transgelin	TAGLN	5	240.3	775.766 7	1000.16 7	1011.2	666.166 7	892.666 7
Mesencephalic astrocyte-derived neurotrophic factor	MANF	14	2402.63333 3	4873.03 3	3985.66 7	6456.83 3	3869.83 3	6453.9
Protein disulfide-isomerase A4	PDIA4	55	21161.9	37132.0 7	28338.9	50171.8 3	32526.5	72292.7 7
Isoform 2 of Ras GTPase-activating protein nGAP	RASAL2	4	328.4	505.233 3	928.5	683.766 7	424.766 7	586.966 7

Isoform 4 of 4F2 cell-surface antigen heavy chain	SLC3A2	22	5252.33333 3	8678.76 7	11782.2 7	11835.4	6226.93 3	10419.0 3
Isoform 2 of Melanoma-associated antigen D1	MAGED1	7	1021.13333 3	1609.93 3	1576.16 7	2209.83 3	1134.9	1790.76 7
Hypoxia up-regulated protein 1 (Fragment)	HYOU1	1	2994.03333 3	4842.86 7	4198.26 7	6768.43 3	3959.7	8547.93 3
Serine/threonine-protein kinase LATS2	LATS2	1	67.0666666 7	53.7	70.5666 7	75.9333 3	54.4	65.3333 3
Isoform 2 of Hypoxia up-regulated protein 1	HYOU1	1	6267.86666 7	11095.4	9463.23 3	15763.3	8273.56 7	19817.2 3
ER membrane protein complex subunit 10	EMC10	2	149.266666 7	353.966 7	445.766 7	506.2	268.333 3	560.833 3
Microtubule-associated protein 2	MAP2	19	4263.96666 7	6233.66 7	8268.8	8965.63 3	5664.1	8992.93 3
Endoplasmic	HSP90B1	53	23506.1666 7	45842.4 7	37778.5 7	66069.7 7	39230.8	92735.2 7
D-3-phosphoglycerate dehydrogenase	PHGDH	22	7426.4	10004.5 3	12727.4 3	14461.1 3	8537.16 7	15601.9 3
Isoform 2 of EF-hand calcium-binding domain-containing protein 4B	CRACR2A	1	195.566666 7	301.7	477.6	440.433 3	207.066 7	397.5
cDNA FLJ75428, highly similar to Homo sapiens activating transcription factor 6 (ATF6), mRNA	2	229.4	471.2333	538.833 3	688.766 7	360.933 3	671.566 7	
Hypoxia up-regulated protein 1	HYOU1	20	10446.8333 3	21116.7 7	17954.1	30969.0 3	15267.4 3	37741.8

Endoplasmin (Fragment)	HSP90B1	2	3333.66666 7	8751.5	6971.73 3	13189.6	7542.4	17538.2 7
Derlin-2	DERL2	2	346.033333 3	311.966 7	299.866 7	470.566 7	343.233 3	503.9
Isoform 2 of Protein transport protein Sec24D	SEC24D	8	765.066666 7	1428.23 3	1271.7	2166.53 3	1142.2	2400.96 7
Cytoplasmic polyadenylation element binding protein 4, isoform CRA_b	CPEB4	1	23.6666666 7	28	30.4333 3	44	19.8	34.8666 7
cDNA FLJ76303, highly similar to Homo sapiens armadillo repeat containing, X-linked 2 (ARMCX2), mRNA		2	105.366666 7	172.6667	250.533 3	271.7	183.8	240.166 7
PRKC apoptosis WT1 regulator protein	PAWR	7	554.066666 7	532.766 7	806.866 7	841.866 7	411	665.8
Tumor necrosis factor receptor superfamily member 1A	TNFRSF1A	2	254.366666 7	355.966 7	355.933 3	570.966 7	269.033 3	484.533 3
Protein-glutamine gamma-glutamyltransferase 2	TGM2	30	8637.3	13077.5	23349.2	21069.6 7	9954.76 7	18987.7
Translocating chain-associated membrane protein		1	164.6	200.3333	185.333 3	322.933 3	158.733 3	326.5
Isoform 4 of [F-actin]-methionine sulfoxide oxidase MICAL1	MICAL1	2	230.6	406.766 7	661.2	679.033 3	361.2	693.166 7
Cystine/glutamate transporter	SLC7A11	2	329.3	916.8	1457.36 7	1545.06 7	560	981.866 7
Protein CYR61	CYR61	6	442.066666 7	1031.46 7	910.8	1762.03 3	799.766 7	2382.53 3

DnaJ homolog subfamily C member 3	DNAJC3	11	1700.23333 3	2559.9	2438.86 7	4473.8	2102.9	5408.96 7
Hyaluronan and proteoglycan link protein 1	HAPLN1	4	295.466666 7	261.633 3	535.133 3	457.733 3	185.466 7	428.066 7
cDNA, FLJ94125, highly similar to Homo sapiens tissue factor pathway inhibitor(lipoprotein-associated coagulation inhibitor) (TFPI), mRNA	1	201	281.3333	399	501.333 3	226.6	716.133 3	
Large neutral amino acids transporter small subunit 1	SLC7A5	5	1393.46666 7	1641.53 3	2734.83 3	2988.7	1331.46 7	2583.5
Signal peptidase complex catalytic subunit SEC11C	SEC11C	2	144.7	223.4	277.8	406.766 7	205.866 7	399.466 7
Tumor protein D53	TPD52L1	4	713.033333 3	784.766 7	1583.23 3	1433.5	652.866 7	1247.66 7
cDNA FLJ78675, highly similar to Homo sapiens stroma HMG-box containing protein (HBP2) mRNA	1	108.7	239.2	314.966 7	437.066 7	256.233 3	484.433 3	
Semaphorin-3A	SEMA3A	14	1266.33333 3	1744.83 3	1664.4	3205.43 3	1348.5	4259.36 7
78 kDa glucose-regulated protein	HSPA5	62	43277.4333 3	70337.2	61261.0 3	129387	58481.9	176122. 4
High mobility group protein HMGI-C	HMGA2	2	239.9	214.566 7	286.466 7	418.866 7	223.333 3	484.466 7
Protein Shroom3	SHROOM3	2	64.4	16.8333 3	38.7	35.9666 7	18	24.0666 7

Protein Niban	FAM129A	8	625.133333 3	776.9	1178.56 7	1818.76 7	593.566 7	1905.43 3
cDNA FLJ76864, highly similar to Homo sapiens homocysteine-inducible, endoplasmic reticulumstress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA	2	235.633333 3	169.5333	177.2	442.833 3	174.7	434.2	
cDNA FLJ56136, highly similar to Solute carrier family 2, facilitated glucosetransporter member 14	3	193.633333 3	316.2	316.033 3	883.8	252.433 3	1127.03 3	
Myristoylated alanine-rich C-kinase substrate	MARCKS	8	845.4	1053.43 3	3561.43 3	4128.2	830.266 7	2928.16 7

Chapter 7 (Pull down Proteomics)

Normoxia (Nx) Pull down

Accession	Gene	Name	Nx_Control_e mPAI	Nx_Sample_e mPAI	Nx_Control_ Total Peptide	Nx_Sample_ Total Peptide	Interacts with	Pathway
P35579	MYH9	Myosin-9	2.97	4.28	196	237		

P60709	ACTB	Actin, cytoplasmic 1	11.13	21.22	192	200	Q9Y281; P04626; Q8TCJ0-2; P11142; O14950; P84022; P37802	
P35580	MYH10	Myosin00	1.92	2.6	132	171		
P09211	GSTP1	Glutathione S-transferase P	53.02	69.48	101	145	Q12933	
Q96HE7	ERO1A	ERO1-like protein alpha	0.68	9.16	19	98		
P68032	ACTC1	Actin, alpha cardiac muscle 1	2.09	3.86	75	87		
Q9UHB6	LIMA1	LIM domain and actin-binding protein 1	1.29	1.86	42	58		
P08670	VIM	Vimentin	4.29	3.43	54	61	Itself; P31749; P31751; Q9H6U6; Q14194; O95251; O95361	
Q13813	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	0.39	0.3	57	43	P40692; Q01082	
Q562R1	ACTBL2	Beta-actin-like protein 2	0.83	0.97	56	45		
P35749	MYH11	Myosin01	0.19	0.22	19	24	O14950	
P07237	P4HB	Protein disulfide-isomerase	0	1.44	0	38	Q03518	
Q16643	DBN1	Drebrin	0.56	0.64	18	23		

Q5JP53	TUBB	Tubulin beta chain	0	1.21	0	19		
F5H5D3	TUBA1C	Tubulin alpha0C chain	0.82	0.73	21	24		
P38646	HSPA9	Stress-70 protein, mitochondrial	0.42	0.54	10	18	Q8WX92; P04637; O15350	
P68371	TUBB4B	Tubulin beta-4B chain	0.66	1.28	20	19		
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	1.02	1.2	19	16	P00533; P15927	Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 1/5.
P06733	ENO1	Alpha-enolase	0.5	0.6	10	15	P22303; Q8WZ42	Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 4/5.
G3V1V0	MYL6	Myosin light polypeptide 6	6.6	3.58	24	16		

P62805	HIST1H4A	Histone H4	7.38	9.93	15	21	Q12830; Q12830-4; P49450; O14929; Q9Y468; P49736; P25205; P33992; O14744; Q16576; Q9NQR1	
A0A087W WU8	TPM3	Tropomyosin alpha-3 chain	1.28	2.25	10	15		
P52907	CAPZA1	F-actin-capping protein subunit alpha0	0.95	0.95	12	14		
P06899	HIST1H2B J	Histone H2B type 1-J	0	2.74	0	12		
B2R4S9	HIST1H2B C	Histone H2B	0.93	1.41	9	11		
A0A0U1RR 32	hCG_2039 566	HCG2039566, isoform CRA_b	1.74	1.74	11	12		
Q9NYL9	TMOD3	Tropomodulin-3	0.62	0.49	10	12		
Q7Z406	MYH14	Myosin04	0.12	0.1	15	17		
Q6FI13	HIST2H2A A3	Histone H2A type 2-A	3.55	3.55	13	11		
A0A0A0M TN3	GSTM3	Glutathione S- transferase Mu 3	1.11	1.39	14	14		
P25705	ATP5A1	ATP synthase subunit alpha, mitochondrial	0.24	0.45	8	13	P78537; Q9NTG7	
H0Y449	YBX1	Nuclease-sensitive element-binding protein 1 (Fragment)	0.25	0.16	3	5		

P21589	NT5E	5~-nucleotidase	0.35	0.16	10	7		
P13929	ENO3	Beta-enolase	0	0.14	0	5		Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 4/5.
P04350	TUBB4A	Tubulin beta-4A chain	0.38	0.78	15	13	P22736	
P10809	HSPD1	60 kDa heat shock protein, mitochondrial	0.11	0.37	4	9	P38398; P49789	
B1AK87	CAPZB	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a	0.53	0.38	11	8		
E9PKE3	HSPA8	Heat shock cognate 71 kDa protein	0	0.52	0	19		
A0A087WVQ9	EEF1A1	Elongation factor 1-alpha 1	0.39	0.59	8	12		
Q5TCU3	TPM2	Tropomyosin beta chain	0	0.78	0	12		
H0YKX5	TPM1	Tropomyosin alpha0 chain (Fragment)	0	1.12	0	8		

Q71DI3	HIST2H3A	Histone H3.2	0.82	0.49	3	2		
P68431	HIST1H3A	Histone H3.1	0.48	0.22	2	2		
P04792	HSPB1	Heat shock protein beta0	0.15	0.51	3	6	Q9UER7; Q9UJY1; P49137; Q16644; Q8IW41; P08473	
Q9BUF5	TUBB6	Tubulin beta-6 chain	0.29	0.46	7	8		
A0A0C4DH25	IGKV3D-20	Protein IGKV3D-20 (Fragment)	0.61	0.61	3	4		
P67936	TPM4	Tropomyosin alpha-4 chain	0	0.93	0	11		
P11021	HSPA5	78 kDa glucose-regulated protein	0.14	0.19	8	6	Q96IZ0; Q62627; P04049	
P08238	HSP90AB1	Heat shock protein HSP 90-beta	0.12	0.21	4	9	P36896; P31751; Q9UM73; Q16671; P10398; Q96GD4; P15056; Q06187; Q13555; Q16543; Q15131; O94921; Q96Q40; P11802; Q00534; O14757; P49674; Q13618; Q16832; P00533; P29317; P04626; Q15303; P22607; P09769; P35916; P06241; Q8TF76; P49840; Q9UPZ9; Q2WGI6; P06239;	

							P53671; P41279; P80192; P31152; P42679; O15146; Q8TD19; O75469; Q9P215; Q02156; Q05513; Q15139; P51817; P11801; P04049; P49758; Q01974; Q15831; Q15208; Q96S53; Q9BXA6; P29597	
F5H6E2	MYO1C	Unconventional myosin-Ic	0.08	0.18	4	10		
B4E3S0	CORO1C	Coronin	0	0.16	0	4		
HOYK49	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial	0.29	0.29	4	4		
J3KN67	TPM3	Tropomyosin alpha-3 chain	0.61	0.94	8	10		
HOY2P0	CD44	CD44 antigen (Fragment)	0.22	0.11	3	4		
M0QZN2	RPS5	40S ribosomal protein S5	0.23	0.23	2	2		
HOYN42	ANXA2	Annexin (Fragment)	0	0.55	0	6		
A0A075B6 J7	IGLV3-21	Protein IGLV3-21 (Fragment)	0.27	0.27	2	2		
J3KPX7	PHB2	Prohibitin-2	0	0.33	0	5		

Q96C19	EFHD2	EF-hand domain-containing protein D2	0.26	0.42	2	6		
P0C0S5	H2AFZ	Histone H2A.Z	0.96	0.57	7	5		
M0R1V7	UBA52	Ubiquitin-60S ribosomal protein L40 (Fragment)	0	0.5	0	2		
H3BTN5	PKM	Pyruvate kinase (Fragment)	0.2	0.35	5	8		Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 5/5.
P27348	YWHAQ	14-3-3 protein theta	0	0.25	0	4	Q9P0K1-3; P49407; P32121; O94921; P00533; P23945; Q14678; Q14678-2; Q5S007	
P21796	VDAC1	Voltage-dependent anion-selective channel protein 1	0.36	0.23	4	4	P19367	
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	0.04	0.16	4	6	Itself; O95433; Q96G23; Q9UHD1; P05412; P53041;	

							Q15185; P61247; Q9UNE7	
J3KSP2	RPL38	60S ribosomal protein L38 (Fragment)	1.53	1.53	1	2		
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	0.33	0.21	6	5		
A0A075B6 P5	IGKV2D-28	Protein IGKV2-28 (Fragment)	0.26	0.59	1	3		
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	0.11	0.23	2	4		
P00338	LDHA	L-lactate dehydrogenase A chain	0	0.29	0	3		Fermentation ; pyruvate fermentation to lactate; (S)-lactate from pyruvate: step 1/1.
Q9H853	TUBA4B	Putative tubulin-like protein alpha-4B	0.25	0.25	4	3		
P53597	SUCLG1	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	0.09	0.19	3	6		Carbohydrate metabolism; tricarboxylic acid cycle.

G3V1A4	CFL1	Cofilin 1 (Non-muscle), isoform CRA_a	0.44	0.72	4	6		
A0A0B4J213	RPL30	60S ribosomal protein L30	0.64	1.69	1	3		
A0A0B4J2B5	IGHV3OR16-9	Protein IGHV3OR16-9 (Fragment)	0	0.74	0	3		
Q5TEC6	HIST2H3PS2	Histone H3	0.82	0.82	3	5		
P39019	RPS19	40S ribosomal protein S19	0	0.47	0	4	P62633; O15479; Q96BK5	
B7Z4C8	RPL31	60S ribosomal protein L31	0.22	0.22	2	2		
E7EX29	YWHAZ	14-3-3 protein zeta/delta (Fragment)	0	0.25	0	4		
A0A087WZ27	ZNF90	Zinc finger protein 90	0.23	0.23	2	2		
P05109	S100A8	Protein S100-A8	0.32	0.74	1	3		
A0A087WYY5	PPP1CC	Serine/threonine-protein phosphatase	0	0.2	0	2		
E5RIP1	RPS20	40S ribosomal protein S20	0	0.67	0	1		
Q3BDU5	LMNA	Prelamin-A/C	0	0.12	0	3		
J3KQE5	RAN	GTP-binding nuclear protein Ran (Fragment)	0.12	0.12	2	4		
HOYH81	ATP5B	ATP synthase subunit beta (Fragment)	0.18	0.18	4	5		

A0A024R4M0	RPS9	40S ribosomal protein S9	0.15	0.51	1	4		
P49411	TUFM	Elongation factor Tu, mitochondrial	0	0.14	0	3		
J3KMX5	RPS13	40S ribosomal protein S13	0.2	0.2	1	3		
P61626	LYZ	Lysozyme C	0	0.2	0	3		
F8WE65	PPIA		0.26	0.58	3	3		
HOYE27	RPS2	40S ribosomal protein S2 (Fragment)	0	0.5	0	1		
E7ERL0	NME1	Nucleoside diphosphate kinase A	0	0.49	0	3		
A0A075B7E8	IGHV3OR1603	Protein IGHV3OR1603 (Fragment)	0	0.26	0	3		
P62701	RPS4X	40S ribosomal protein S4, X isoform	0.24	0.11	3	3		
A0A087WY6	IGKV3D05	Protein IGKV3D05 (Fragment)	0.27	0.61	5	7		
K7ELC7	RPL27	60S ribosomal protein L27 (Fragment)	0.21	0.21	2	3		
Q6DN03	HIST2H2B C	Putative histone H2B type 2-C	0	0.33	0	3		
A8MUD9	RPL7	60S ribosomal protein L7	0	0.29	0	2		
E9PJD9	RPL27A	60S ribosomal protein L27a	0.79	0.34	2	1		

A0A087WUT2	MBD3L3	Putative methyl-CpG-binding domain protein 3-like 3	0.15	0.15	11	7		
A0A0D9SFE5	LMNB1	Lamin B1, isoform CRA_a	0	0.18	0	2		
A0A0B4J1T9	IGKV305	Protein IGKV305 (Fragment)	0	0.61	0	6		
Q06830	PRDX1	Peroxioredoxin0	0.15	0.52	4	8	P10275	
P26641	EEF1G	Elongation factor 1-gamma	0	0.14	0	2	P24534; P29692	
H0YB39	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H (Fragment)	0	0.11	0	2		
J3JS69	RPS18	40S ribosomal protein S18	0.36	0.36	2	2		
Q5VVC8	RPL11	60S ribosomal protein L11 (Fragment)	0.17	0.17	2	2		
P10412	HIST1H1E	Histone H1.4	0	0.15	0	3	Q9Y468; P16333	
P16403	HIST1H1C	Histone H1.2	0	0.16	0	3		
P62318	SNRPD3	Small nuclear ribonucleoprotein Sm D3	0	0.24	0	2	P54105	
H7BY16	NCL	Nucleolin (Fragment)	0	0.1	0	3		

A0A087WUS2	IGKV3D01	Protein IGKV3D01	0.29	0.66	1	3		
F5H136	TCP1	T-complex protein 1 subunit alpha (Fragment)	0	0.23	0	2		
P62263	RPS14	40S ribosomal protein S14	0.21	0.21	2	1	O15479; O43353; Q15654	
HOY6E7	RBMX	RNA-binding motif protein, X chromosome (Fragment)	0	0.1	0	1		
D6RBK0	PHB	Prohibitin (Fragment)	0	0.25	0	1		
J3KT29	RPL23	60S ribosomal protein L23	0	0.26	0	1		
G5EA24	MCOLN2	Mucolipin 2, isoform CRA_a	0	0.11	0	2		
E7EPB3	RPL14	60S ribosomal protein L14	0	0.23	0	1		
G3V1N2	HBA2	HCG1745306, isoform CRA_a	1.13	0.29	7	2		
E7ESF5	CALCB	Calcitonin gene-related peptide 2	0	0.23	0	2		
J3QLE5	SNRPN	Small nuclear ribonucleoprotein-associated protein N (Fragment)	0	0.19	0	1		
P09382	LGALS1	Galectin0	0.23	0.23	2	1		

P26373	RPL13	60S ribosomal protein L13	0.67	0.29	4	3	P16333; P27986	
Q8NGR8	OR1L8	Olfactory receptor 1L8	0	0.1	0	2		
Q04917	YWHAH	14-3-3 protein eta	0	0.12	0	4	O94921; O60565; Q14678-2; Q5S007; Q7KZI7; P27448; Q96L34; Q8TEW0; Q9NPB6; Q9BYG5; Q9BYG4; P41743; P04049	
P23284	PPIB	Peptidyl-prolyl cis-trans isomerase B	0	0.14	0	2		
H3BRB3	KIF22	Kinesin-like protein	0.05	0.1	1	3		
A0A0G2JN Q3	HNRNPCL 2	Heterogeneous nuclear ribonucleoprotein C-like 2	0	0.1	0	2		
Q9Y5S9	RBM8A	RNA-binding protein 8A	0.17	0.17	1	1	P38919; P61326; Q9H1J1; Q9BZI7	
MOROP7	RPL18A	60S ribosomal protein L18a	0	0.21	0	2		
I3L3K4	KCTD13	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 1 (Fragment)	0	0.37	0	2		

HOYDP8	TRIM21	E3 ubiquitin-protein ligase TRIM21 (Fragment)	0	0.34	0	1		
Q96HU8	DIRAS2	GTP-binding protein Di-Ras2	0	0.15	0	2		
P30050	RPL12	60S ribosomal protein L12	0	0.19	0	1		
HOYEU2	RPS3	40S ribosomal protein S3 (Fragment)	0.18	0.18	3	4		
P62851	RPS25	40S ribosomal protein S25	0	0.25	0	2	Q9HA U5	
H3BQB0	PPCDC	Phosphopantothenoyl cysteine decarboxylase	0	0.19	0	1		
M0QY31	PSG4	Pregnancy-specific beta0-glycoprotein 4 (Fragment)	0	0.12	0	1		
P62081	RPS7	40S ribosomal protein S7	0	0.15	0	4	Q009 87	
H7BXH9	METTL21 A	Protein N-lysine methyltransferase METTL21A	0	0.12	0	2		
A0A087W VU3	NKX2-3	Homeobox protein Nkx-2.3	0	0.1	0	2		
P14174	MIF	Macrophage migration inhibitory factor	0	0.27	0	1	O4352 1-2	

F8VX48	ZDHHC17	Palmitoyltransferase ZDHHC17 (Fragment)	0	0.19	0	1		
E5RH18	LSM1	LSM1-like protein U6 small nuclear RNA associated isoform 3	0	0.75	0	1		
H0YDB0	GSDMD	Gasdermin-D (Fragment)	0.14	0.14	1	1		
H0YAA1	ATP8A1	Phospholipid-transporting ATPase 1A (Fragment)	0	0.43	0	2		
F2Z3G2	PLA2G6	85/88 kDa calcium-independent phospholipase A2	0	0.31	0	1		
H0Y8U1	CNTN4	Contactin-4 (Fragment)	0	0.21	0	2		
B1ANM0	LGALS8	Galectin (Fragment)	0	0.18	0	1		

Hypoxia (Hx) Pull down

Accession	Gene	Name	Hx_Control_e mPAI	HX_Sample_e mPAI	Hx_Control_ Total Peptide	HX_Sample_ Total Peptide	Interacts with	Pathway
Q96HE7	ERO1A	ERO1-like protein alpha	0.89	20.59	21	226		
P09211	GSTP1	Glutathione S-transferase P	6.35	26.78	47	51	Q12933	

P60709	ACTB	Actin, cytoplasmic 1	8.67	4.28	282	44	Q9Y281; P04626; Q8TCJ0-2; P11142; O14950; P84022; P37802	
P07237	P4HB	Protein disulfide- isomerase	0	2.22	0	48	Q0351 8	
P08670	VIM	Vimentin	1.44	1.92	52	31	Itself; P31749; P31751; Q9H6U6; Q14194; O95251; O95361	
F5H5D3	TUBA1C	Tubulin alpha0C chain	0.73	0.63	22	17		
P68032	ACTC1	Actin, alpha cardiac muscle 1	1.47	1.47	120	23		
Q5JP53	TUBB	Tubulin beta chain	1.21	1.07	21	20		
Q6FI13	HIST2H2A A3	Histone H2A type 2-A	1.95	3.55	12	11		
P68371	TUBB4B	Tubulin beta-4B chain	0.89	0.89	20	17		
P06733	ENO1	Alpha-enolase	0.6	0.96	14	14	P2230 3; Q8WZ 42	Carbohydrate degradation; glycolysis; pyruvate from D- glyceralde- hyde 3- phosphate: step 4/5.

AOA0B4J269	AOA0B4J269	Uncharacterized protein	0.24	0.33	13	13		
P14618	PKM	Pyruvate kinase PKM	0.18	0.83	8	12	P49407; P32121; Q9H6Z9; Q16665; P04049	Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 5/5.
AOA0U1RRF4	IGKV1-8	Protein IGKV1-8	0	1.52	0	15		
AOA0U1RR32	hCG_2039566	HCG2039566, isoform CRA_b	0	1.74	0	9		
P62805	HIST1H4A	Histone H4	1.89	7.38	17	17	Q12830; Q12830-4; P49450; O14929; Q9Y468; P49736; P25205; P33992; O14744; Q16576; Q9NQR1	
B2R4S9	HIST1H2BC	Histone H2B	2	2	9	10		
Q8N257	HIST3H2BB	Histone H2B type 3-B	2.74	1.41	11	10		

P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	1.02	1.02	24	11	P00533; P15927	Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 1/5.
A0A087WZH9	IGKV1D-33	Protein IGKV1-33	0.29	1.13	3	3		
P35579	MYH9	Myosin-9	2.16	0.14	173	11		
P0C0S5	H2AFZ	Histone H2A.Z	0.57	0.96	5	7		
P13929	ENO3	Beta-enolase	0.07	0.14	4	3		Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 4/5.
P38646	HSPA9	Stress-70 protein, mitochondrial	0.3	0.19	10	8	Q8WX92; P04637; O15350	

P11021	HSPA5	78 kDa glucose-regulated protein	0.14	0.14	6	5	Q96IZ0; Q62627; P04049	
Q562R1	ACTBL2	Beta-actin-like protein 2	0.97	0.57	115	11		
E9PKE3	HSPA8	Heat shock cognate 71 kDa protein	0	0.32	0	10		
A0A0B4J1Z6	IGKV3-20	Protein IGKV3-20 (Fragment)	0	0.61	0	2		
A0A087WVQ9	EEF1A1	Elongation factor 1-alpha 1	0.39	0.39	9	10		
F5H0C8	ENO2	Enolase	0	0.2	0	3		Carbohydrate degradation; glycolysis; pyruvate from D-glyceraldehyde 3-phosphate: step 4/5.
A0A0A0MTN3	GSTM3	Glutathione S-transferase Mu 3	0.65	0.86	11	9		
P25705	ATP5A1	ATP synthase subunit alpha, mitochondrial	0.24	0.38	8	9	P78537; Q9NTG7	
A0A0C4DH25	IGKV3D-20	Protein IGKV3D-20 (Fragment)	0	0.27	0	2		
E7ESE2	PHB	Prohibitin (Fragment)	0	0.32	0	2		

A0A0B4J2 B5	IGHV3OR1 6-9	Protein IGHV3OR16-9 (Fragment)	0	0.74	0	4		
P68431	HIST1H3A	Histone H3.1	0.48	0.22	4	1		
A0A0B4J1 T9	IGKV305	Protein IGKV305 (Fragment)	0.61	0.61	13	4		
J3QS39	UBB	Polyubiquitin-B (Fragment)	0.77	0.77	3	2		
E9PJD9	RPL27A	60S ribosomal protein L27a	0	0.79	0	2		
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	0.11	0.23	2	4		
J3KPX7	PHB2	Prohibitin-2	0.1	0.1	1	2		
A0A0B4J1 Z4	IGKV107	Protein IGKV107 (Fragment)	0	0.26	0	1		
A0A075B6 J7	IGLV3-21	Protein IGLV3-21 (Fragment)	0	0.27	0	1		
P21796	VDAC1	Voltage-dependent anion-selective channel protein 1	0.51	0.23	6	4	P1936 7	
P26641	EEF1G	Elongation factor 1- gamma	0	0.14	0	2	P24534; P29692	
E7EX29	YWHAZ	14-3-3 protein zeta/delta (Fragment)	0	0.25	0	3		
H0Y2P0	CD44	CD44 antigen (Fragment)	0.22	0.11	4	1		
P07355	ANXA2	Annexin A2	0	0.18	0	4	P4069 2	

F8VQE1	LIMA1	LIM domain and actin-binding protein 1	0.77	0.1	23	4		
M0QZN2	RPS5	40S ribosomal protein S5	0.23	0.23	2	1		
P06576	ATP5B	ATP synthase subunit beta, mitochondrial	0.19	0.19	7	5		
P10809	HSPD1	60 kDa heat shock protein, mitochondrial	0	0.17	0	4	P38398; P49789	
A0A075B6 P5	IGKV2D-28	Protein IGKV2-28 (Fragment)	0	0.26	0	2		
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	0.16	0.12	5	5	Itself; O95433; Q96G23; Q9UHD1; P05412; P53041; Q15185; P61247; Q9UNE7	
A0A087W SY6	IGKV3D05	Protein IGKV3D05 (Fragment)	0.61	0.61	7	3		
Q8NBS9	TXNDC5	Thioredoxin domain-containing protein 5	0	0.14	0	4		
E7EPB3	RPL14	60S ribosomal protein L14	0	0.23	0	1		
P62263	RPS14	40S ribosomal protein S14	0.21	0.21	2	1	O15479; O43353; Q15654	
Q96IX5	USMG5	Up-regulated during skeletal muscle growth protein 5	0	0.55	0	1		

J3KQE5	RAN	GTP-binding nuclear protein Ran (Fragment)	0.26	0.12	4	3		
P05141	SLC25A5	ADP/ATP translocase 2	0	0.33	0	3	Q9Y6E7	
A0A075B7B8	IGHV3OR1602	Protein IGHV3OR1602 (Fragment)	0	0.6	0	3		
P60842	EIF4A1	Eukaryotic initiation factor 4A-I	0	0.15	0	3	Q04637; P78344; Q15056	
H3BUX2	CYB5B	Cytochrome b5 type B	0	0.21	0	1		
A0A075B6I8	IGLV1-47	Protein IGLV1-47 (Fragment)	0	0.28	0	2		
A0A075B6H7	IGKV3-7	Protein IGKV3-7 (Fragment)	0	0.27	0	4		
E5RIP1	RPS20	40S ribosomal protein S20	0	0.67	0	1		
G3V1A4	CFL1	Cofilin 1 (Non-muscle), isoform CRA_a	0.44	0.44	3	3		
H0YB39	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H (Fragment)	0.11	0.11	2	1		
A0A075B6R2	IGHV4-4	Protein IGHV4-4 (Fragment)	0	0.26	0	1		

HOYK49	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial	0.14	0.29	2	2		
F5H423	F5H423	Uncharacterized protein	0	0.14	0	2		
P62851	RPS25	40S ribosomal protein S25	0	0.25	0	1	Q9HAU5	
Q04917	YWHAH	14-3-3 protein eta	0	0.25	0	3	O94921; O60565; Q14678-2; Q5S007; Q7KZ17; P27448; Q96L34; Q8TEW0; Q9NPB6; Q9BYG5; Q9BYG4; P41743; P04049	
A0A087WUI2	HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	0	0.11	0	1		
A0A087WZ27	ZNF90	Zinc finger protein 90	0.23	0.23	2	2		
HOY6E7	RBMX	RNA-binding motif protein, X chromosome (Fragment)	0	0.1	0	1		
E9PK82	RPS3	40S ribosomal protein S3 (Fragment)	0	0.23	0	2		
J3JS69	RPS18	40S ribosomal protein S18	0.36	0.36	1	1		

A0A0B4J1X5	IGHV3-74	Protein IGHV3-74 (Fragment)	0	0.6	0	5		
A8MUD9	RPL7	60S ribosomal protein L7	0	0.14	0	2		
P62701	RPS4X	40S ribosomal protein S4, X isoform	0.11	0.24	2	2		
F8WE65	PPIA		0.26	0.26	5	1		
A0A0B4J213	RPL30	60S ribosomal protein L30	0.64	0.64	1	1		
G3V1V0	MYL6	Myosin light polypeptide 6	3.58	0.18	20	2		
E7ERL0	NME1	Nucleoside diphosphate kinase A	0	0.22	0	2		
P55769	SNU13	NHP2-like protein 1	0	0.24	0	1	P04591	
Q9NZY4	UQCR10	Cytochrome b-c1 complex subunit 9	0	0.23	0	1		
Q8NGR8	OR1L8	Olfactory receptor 1L8	0	0.1	0	1		
C9JNW5	RPL24	60S ribosomal protein L24	0	0.19	0	1		
H7C3T4	PRDX4	Peroxisredoxin-4 (Fragment)	0	0.18	0	3		
P30041	PRDX6	Peroxisredoxin-6	0.13	0.13	1	1		
I3L3K4	KCTD13	BTB/POZ domain-containing adapter for CUL3-mediated RhoA	0.37	0.37	1	2		

		degradation protein 1 (Fragment)						
P49755	TMED10	Transmembrane emp24 domain-containing protein 10	0	0.13	0	1	Q92542; P49768; Q9NZ42; P177060; Q15363	
F8WE04	HSPB1	Heat shock protein beta0	0.16	0.16	3	1		
E7ESF5	CALCB	Calcitonin gene-related peptide 2	0	0.23	0	1		
H7C0F8	MST1	Hepatocyte growth factor-like protein (Fragment)	0	0.16	0	1		
E9PB61	ALYREF	THO complex subunit 4	0	0.12	0	1		
Q96HU8	DIRAS2	GTP-binding protein Di-Ras2	0	0.15	0	2		
A0A087WUS2	IGKV3D01	Protein IGKV3D01	0	0.29	0	2		
H0Y632	SAMD12	Sterile alpha motif domain-containing protein 12 (Fragment)	0	0.2	0	1		
Q99943	AGPAT1	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	0	0.1	0	2		Phospholipid metabolism; CDP-diacylglycerol biosynthesis

								s; CDP- diacylglyce rol from sn-glycerol 3- phosphate: step 2/3.
D6RA52	RHOH	Rho-related GTP- binding protein RhoH (Fragment)	0	0.28	0	2		
A6NJ46	NKX6-3	Homeobox protein Nkx-6.3	0	0.11	0	1		
G3XAL0	MDH2	Malate dehydrogenase	0	0.13	0	1		
F5H274	NLRC5	Protein NLRC5 (Fragment)	0	0.4	0	1		
J3KRY3	SNRPN	Small nuclear ribonucleoprotein- associated protein N (Fragment)	0	0.5	0	1		
H3BTP7	RPL4	60S ribosomal protein L4 (Fragment)	0	0.18	0	1		
Q5TEC6	HIST2H3P S2	Histone H3	0	0.22	0	1		
J3KSS0	RPL26	60S ribosomal protein L26	0	0.47	0	2		
B1ANM0	LGALS8	Galectin (Fragment)	0	0.18	0	1		

MOR1H5	RPS11	40S ribosomal protein S11	0	0.36	0	1		
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