PROTEOMIC CHARACTERISATION OF PATEAMINE A TREATMENT OF GLIOBLASTOMA

by

VERONICA ADELINE WALKER POT

A thesis
submitted to the Victoria University of Wellington
in fulfilment of the
requirements for the degree of
Master of Drug Discovery and Development
in Chemical Biology.

Te Herenga Waka — Victoria University of Wellington
2022

Abstract

Pateamine A is a potent inhibitor of eukaryotic translation initiation factor eIF4A, with potential application in cancer treatment. Glioblastoma is a highly aggressive and clinically challenging type of brain cancer. Existing evidence shows glioblastoma exhibit an abnormal energy metabolism, and there is also evidence that pateamine A causes alterations in the energy metabolism of other cancer cell lines. This research investigates the effects of eIF4A inhibition on biological pathways in glioblastoma cells, via proteomic analysis and gene ontology analysis. Characterising changes in the proteome as a result of pateamine inhibition of eIF4A contributes to the understanding of pre-initiation influences on mRNA processing, and elucidates alterations in glioblastoma metabolism following pateamine A treatment.

An elongation inhibitor, cycloheximide, was used as a control, as was a human leukaemia cell line. The two glioblastoma cell lines, LN18 and U87, exhibited direct effects on translation ontologies as a result of cycloheximide treatment. When compared to translational inhibition, pateamine A treatment caused alterations in RNA transcription splicing in glioblastoma. Other effects were also seen in ribosomal biogenesis and mitochondrial translation. This research characterised proteomic effects of pateamine A and cycloheximide treatment on two glioblastoma cell lines, and evidenced alterations in a range of cell processes.

Acknowledgments

No study is completed without abundant support, help, and guidance, be it from the academic sphere to the domestic. My own journey completing a Masters degree has produced its own challenges, but I am immensely proud of the achievement.

First, to Paul Teesdale-Spittle - thank you for your ever-patient and unwavering guidance. Our weekly meetings were a pleasure, and your staunch support in preparing, continuing, and finalising everything from experiments to writing up has been invaluable.

To my family, for their encouragement and tolerance as I have completed my studies. To Mum, for reading drafts, to Dad, for his computer wizardry, and to Catherine, for helping with issues that arose during typesetting. I am eternally grateful.

Finally, to my lab colleagues, for advice, suggestions, and practical help in the lab. I certainly avoided a few pitfalls thanks to them.

Contents

List of Tables **xi**

List of Figures **xiii**

1 Introduction **1**

1.1 Regulation of Translation and Role of eIF4A 2

1.2 Pateamine A and Other eIF4A Inhibitors 6

1.3 Glioblastoma 11

1.3.1 Typing and Mutations 11

1.3.2 Cell Models of Glioblastoma 12

1.4 Hypothesis 14

2 Aims and Objectives **17**

3 Materials and Methods **19**

3.1 Reagents and Solutions 19

3.1.1 Materials 19

3.1.2 Cell Culture Reagents 20

3.1.3 Drug Stocks 20

3.1.4 MTT Reagents 20

3.1.5 Proteomics Reagents 21
3.2 Drug Stocks 21
3.3 Cell Culture 22
3.3.1 Adherent Cell Lines 22
3.3.2 Suspension Cell Line 22
3.4 MTT Cell Viability Assays 23
3.4.1 Chemical Principles of the Assay 23
3.4.2 Seeding and Drugging 23
3.4.2.1 Drug Dilutions 24
3.4.2.2 Adherent Cell Lines 25
3.4.2.3 Suspension Cell Lines 25
3.4.3 MTT and Lysis 25
3.5 Pharmacological Challenge 26
3.6 Sample Preparation for LC-MS/MS 26
3.6.1 Cell Lysis 26
3.6.2 Acetone Precipitation 27
3.6.3 Protein Quantification 27
3.6.4 Protein Pre-Treatment and Tryptic Digestion 28
3.6.5 Concentration, Purification, and Desalting Peptides . 28
3.6.6 Peptide Quantification 29
3.6.7 Preparation for LC-MS/MS Analysis 29
3.7 Analysis Pipeline 30
3.7.1 Procedure for Determining IC_{50} 30
3.7.2 Procedure for Collecting Mass Spectroscopic Data . . 30
3.7.3 Procedure for Analysis of Mass Spectroscopic Data . 31
3.7.3.1 Gene Ontology Enrichment 32

3.7.3.2 Subsequent Processing 32

4 Results **35**

4.1 IC_{50} from MTT Assay 35

4.2 Gene Ontological Enrichment Using g:Profiler 38

4.2.1 GO Differences in Cell Lines 38

4.2.1.1 HL60 vs LN18 39

4.2.1.2 HL60 vs U87 41

4.2.1.3 LN18 vs U87 43

4.2.2 GO Differences Following Cycloheximide Treatment 44

4.2.2.1 HL60 Cell Line 44

4.2.2.2 LN18 Cell Line 46

4.2.2.3 U87 Cell Line 50

4.2.3 GO Differences where Pateamine A Treated 52

4.2.3.1 HL60 Cell Line 52

4.2.3.2 LN18 Cell Line 55

4.2.3.3 U87 Cell Line 57

5 Discussion **61**

5.1 Selection of Cell Lines and Culturing 61

5.2 Drugs, Treatments, and Times 62

5.2.1 Positive Control: Cycloheximide 63

5.2.2 Drug Concentrations 63

5.2.3 Duration of Experiments 64

5.2.4 Wells vs Flasks 64

5.3 Whole Proteome Preparation 65

5.4 Statistical Decisions and Limitations 66

5.4.1 Proteome Discoverer 66
5.4.2 Adjusted p-values and Significance 66
5.4.3 Justification for the Top Ten Tables 68
5.4.4 Using UpSet Plots 69
5.5 Notable Features 70
5.5.1 A Comment on Cell Line Comparisons 70
5.5.2 A Note on Treating the U87 Cell Line with Fresh Cycloheximide 71
5.6 Differences in eIF4A vs Translation Inhibition 72
5.6.1 HL60 72
5.6.2 LN18 77
5.6.3 U87 82
5.7 Effect of Pateamine A Treatment on Glioblastoma 86
5.7.1 RNA Processing Alterations 87
5.7.2 Effects on Splicing 91
5.7.3 Energy and Glucose Metabolism 94
5.7.4 Protein Transport 97
5.7.5 Cell Proliferation 98
5.7.6 Comparing Back to HL60s 100
5.8 Investigating Glioblastoma-specific Protein Lists 101
5.9 The Wider Picture 106
5.9.1 Further Work 109
5.10 Final Conclusions 110

6 Appendices **113**
A HL60 vs LN18: Upregulated BP and MF 114

B HL60 vs LN18: Downregulated BP and MF 115
C HL60 vs U87 Upregulated BP and MF 116
D HL60 vs U87 Downregulated BP and MF 118
E LN18 vs U87 Upregulated BP and MF 119
F LN18 vs U87 Downregulated BP and MF 121
G HL60 Cycloheximide Upregulated BP and MF 121
H HL60 Cycloheximide Downregulated BP and MF 122
I LN18 Cycloheximide Upregulated BP and MF 123
J LN18 Cycloheximide Downregulated BP and MF 127
K U87 Cycloheximide Upregulated BP and MF 128
L U87 Cycloheximide Downregulated BP and MF 130
M HL60 Pateamine A Upregulated BP and MF 130
N HL60 Pateamine A Downregulated BP and MF 131
O LN18 Pateamine A Upregulated BP and MF 132
P LN18 Pateamine A Downregulated BP and MF 134
Q U87 Pateamine A Upregulated BP and MF 134
R U87 Pateamine A Downregulated BP and MF 136
S HL60 Cycloheximide Genes 136
T LN18 Cycloheximide Genes 157
U U87 Cycloheximide Genes 204
V HL60 Pateamine A Genes 239
W LN18 Pateamine A Genes 274
X U87 Pateamine A Genes 315
Y Accession Intersection Lists by Drug Treatment 346

Bibliography **353**

Index **366**

List of Tables

3.1 MTT assay drug concentration and dilution 24

4.1 IC_{50} cycloheximide and pateamine A in HL60, LN18 and U87 35
4.2 GO HL60 vs LN18 upregulated 39
4.3 GO HL60 vs LN18 downregulated 40
4.4 GO HL60 vs U87 upregulated 41
4.5 GO HL60 vs U87 downregulated 42
4.6 GO LN18 vs U87 upregulated 43
4.7 GO LN18 vs U87 downregulated 44
4.8 GO HL60 cycloheximide upregulated 45
4.9 GO HL60 cycloheximide downregulated 46
4.10 GO LN18 cycloheximide upregulated 48
4.11 GO LN18 cycloheximide downregulated 49
4.12 GO U87 cycloheximide upregulated 50
4.13 GO U87 cycloheximide downregulated 51
4.14 GO HL60 pateamine A upregulated 53
4.15 GO HL60 pateamine A downregulated 54
4.16 GO LN18 pateamine A upregulated 56
4.17 GO LN18 pateamine A downregulated 57

4.18 GO U87 pateamine A upregulated 58
4.19 GO U87 pateamine A downregulated 59

List of Figures

1.1 Schematic of translation initiation 3
1.2 Ribbon representation of eIF4A 4
1.3 Structure of pateamine 6
1.4 eIF4A:mRNA:patemine A complex 7
1.5 Structure of DMDA pateamine 8
1.6 Structure of rocaglamide A 9
1.7 Structure of hippuristanol 9
1.8 Structure of cycloheximide 10

3.1 Reduction of MTT to formazan 24

4.1 MTT assay: HL60 cycloheximide 36
4.2 MTT assay: LN18 cycloheximide 36
4.3 MTT assay: U87 cycloheximide 36
4.4 MTT assay: HL60 pateamine A 37
4.5 MTT assay: LN18 pateamine A 37
4.6 MTT assay: U87 pateamine A 37

5.1 GO UpSet: HL60 cycloheximide up 73
5.2 GO UpSet: HL60 cycloheximide down 74

5.3 GO UpSet: HL60 pateamine A up 75
5.4 GO UpSet: HL60 pateamine A down 76
5.5 GO UpSet: LN18 cycloheximide up 78
5.6 GO UpSet: LN18 cycloheximide down 79
5.7 GO UpSet: LN18 pateamine A up 80
5.8 GO UpSet: LN18 pateamine A down 81
5.9 GO UpSet: U87 cycloheximide up 82
5.10 GO UpSet: U87 cycloheximide down 83
5.11 GO UpSet: U87 pateamine A up 84
5.12 GO UpSet: U87 pateamine A down 86
5.13 GO UpSet: Cycloheximide 102
5.14 GO UpSet: Pateamine A 103

Chapter 1

Introduction

Glioblastomas are a malignant class of brain tumours with no effective clinical treatments currently available. There is evidence that the eIF4A inhibitor, pateamine A, is effective against glioblastoma in cell culture. Earlier work gave preliminary indications that eIF4A inhibition via pateamine treatment affects the energy metabolism in human cells, but this is yet to be fully characterised on a proteomic basis.

This research focuses on two immortalised glioblastoma cell lines, LN18 and U87. They are compared to an acute myeloid leukaemia cell, HL60, a cell line previously well-studied in relation to pateamine A treatment. Inhibitory growth concentrations of pateamine A and the positive control, the elongation inhibitor cycloheximide, were calculated. The IC_{50} dose was used to treat the cells prior to proteomic analysis, which provided sufficient inhibition levels to limit proliferation and evidenced effects on cellular metabolism. Effects of eIF4A inhibition were studied using gene ontological enrichment analysis to determine changes in cellular pathways. Gene ontological enrichment is a powerful tool that links alterations in

gene expression, from comparing control and treatment samples, in order to determine pathways and processes affected by drug treatment.

1.1 Regulation of Translation and Role of eIF4A

After transcription, mRNA transcripts are exported from the nucleus and processed by various enzymes and cofactors. This regulates protein synthesis and initiation of translation. Translation initiation factors bind to the transcript before recruiting the ribosome to the start codon. mRNA transcripts, and especially those with more complex secondary structures, require helicases to unwind the RNA backbone in preparation for binding factors and translation.

The eukaryotic translation initiation factors 4E (eIF4E) and 4A are complexed to the scaffolding protein 4G (eIF4G) [1]. eIF4E binds to the 7-methylguanosine cap of the 5′ untranslated region (5′ UTR) of the mRNA transcript, enabling eIF4A to bind along the mRNA strand, forming the eIF4F complex [2, 3, 4]. eIF4F then recruits the 43S subunit of the pre-initiation complex, which leads to translation upon recruitment of other initiation factors which assemble the ribosome at the start codon [2, 5]. This thesis focusses on the interdependent ATPase/RNA helicase subunit, eIF4A.

Helicases are separated into two superfamilies, 1 and 2, where the DEA(D/H)-box proteins are in the second superfamily [6, 7]. The DEA(D/H)-box proteins, the protein family to which eIF4A belongs, are so named for containing the D-E-A-D (Asp-Glu-Ala-Asp) motif [7]. In humans, there are three isoforms of eIF4A, with types I and II being 90-95% similar, and III

65% similar to types I and II [5]. The type I isoform is most prevalent, and is part of the eIF4F complex [5]. Pateamine A binds to all three isoforms [5].

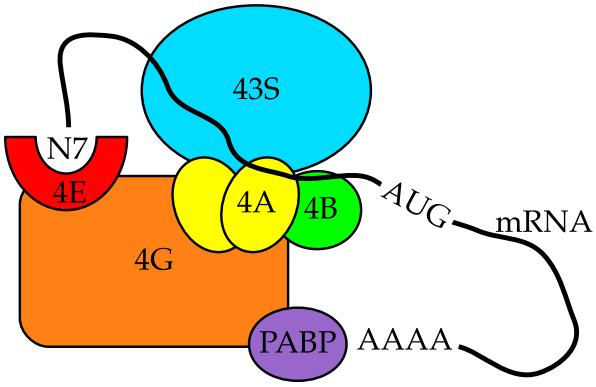

Figure 1.1: A schematic of the pre-translation initiation complex. eIF4E (4E) binds to the N7-methylguanylsine cap (N7) of the mRNA, anchoring the complex. eIF4G (4G) acts as a scaffold and is critical in factor recruitment and activity. eIF4A (4A), the activity of which is improved by eIF4B (4B), binds to the mRNA and unwinds it, allowing the recruitment of the 43S pre-initiation complex to scan for the start codon (AUG). Poly(A)-binding protein (PABP) binds to the poly A tail, circularising the mRNA strand.

A schematic of the eukaryotic translation initiation complex is shown in Figure 1.1. eIF4A consists of C- and N-terminal domains, each forming one half of a dumbbell-like structure joined by a flexible linkage (Figure 1.2) [3]. The mRNA transcript interacts with residues on both lobes, approximately antipodal to the ATP binding site and linkage [3, 8]. ATP binding and hydrolysis occurs on the amino-terminal globular domain near the N-terminus and the linkage to the C-terminal lobe [8]. The RNA helicase and ATPase activity of eIF4A are interdependent, which enables procession along the mRNA strand, but if the RNA binding site is blocked or

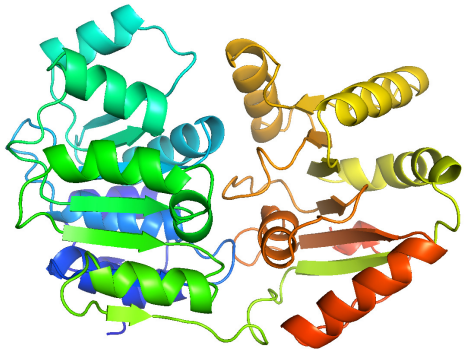

Figure 1.2: Ribbon representation of eIF4A, N-terminus in blue and C-terminus in red. mRNA unwinding occurs across both lobes at the top of the protein and ATP binding on the lowest green α helix.

otherwise disrupted, hydrolysis of ATP can continue [8, 9]. ATPase and RNA helicase activity induce a close-open-close action of the two globular domains, causing the dumbbell ends to scissor towards each other [10, 11]. In order for RNA helicase activity to occur, eIF4A begins in a half-closed formation as a result of eIF4G scaffolding, which becomes fully closed once ATP and mRNA bind [12]. The mRNA binding site on the N-terminal lobe of eIF4A forces secondary mRNA structures to unwind due to an induced kink in the transcript, which forms the linear structure necessary for more complex transcripts to be transcribed [8, 12, 13]. It should also be noted that the interaction of poly(A)-binding protein (PABP) with the poly A tail causes the mRNA strand to form a loop [14]. The RNA strand is unwound, and upon phosphate and ADP release, the unwound RNA is also relaxed as eIF4A resumes the half-closed state [11]. eIF4A helicase activity is markedly improved when it is complexed to the RNA binding protein, eIF4B [2, 9]. Thus, eIF4A is critical for translation control, initiation, and

ultimately, overall peptide synthesis.

The effect of eIF4E inhibition on other cellular pathways has been explored in previous research in the research group. Using gene ontology and STRING analysis, it was found that 4E1RCat inhibition of eIF4E in HL60 and HT29 cells was associated with upregulation of ribosome biogenesis, RNA processing, and protein ER targeting, and downregulation of three mitochondrial proteins and eukaryotic replisome [15]. This indicates that pre-initiation complex inhibition, such as that caused by eIF4E inhibtion, can affect cellular metabolism. However, the use of high DMSO concentrations to deliver drug treatments may have had unforeseen impacts on these results, and it is unclear whether the specific use of pateamine A to inhibit eIF4A has similar effects [15]. This did, however, engender a healthy caution in planning drug concentrations and treatment methodology for the present thesis.

Veronica Venturi, and later Richard Little, researched subinhibitory drug effects on eIF4A activity, and investigated equivalent yeast gene deletion models. The gene encoding for eIF4A in yeast is duplicated, termed *TIF1* and *TIF2* respectively, and disruption, such as in gene deletion sets, affects energy metabolism [16]. Using differential mass spectrometry, it was found that the deletion of either *TIF1* or *TIF2* decreased eIF4A expression [17]. In *tif1*Δ strains, upregulation in protein translation, ATP biosynthesis and oxidative phosphorylation, and downregulation in amino acid production and translation initiation proteins was observed [17]. In *tif2*Δ strains, the same pathways were upregulated, and energy production pathways were downregulated[17]. Thus, in yeast, deletion mutation of either gene resulted in different pathways being affected. When the eIF4A inhibitor

pateamine A is used to generate a 20% reduction in cell proliferation on human leukaemia cells, gene ontology analysis indicated that carbohydrate and monosaccharide catabolism were affected [17].

As eIF4A is a critical factor in translation initiation, it can be surmised that inhibition of eIF4A could be an attractive candidate for medical disorders characterised by rapid cell division. Based on yeast and cancer cell line studies, the outstanding question is: what are the effects of downregulated, or inhibited, eIF4A on cellular pathways? By extension, are there specific effects on energy metabolism and RNA processing? One eIF4A inhibitor, pateamine A, is the topic of this thesis.

1.2 Pateamine A and Other eIF4A Inhibitors

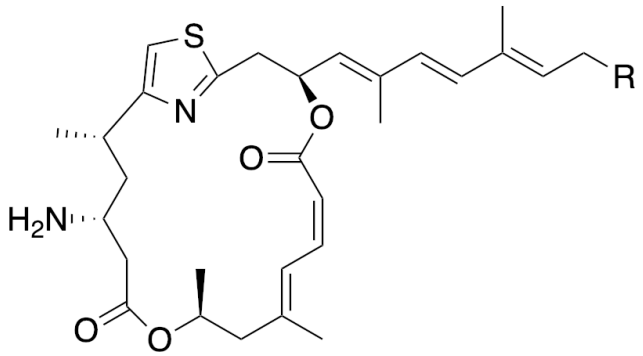

Figure 1.3: Structure of pateamine. Pateamine A R=NMe_2; B R=NHMe; C R=N(O)Me_2.

Pateamine is a heteroaromatic macrolide containing two lactone functionalities, a thiazole, and a trienylamine tail [18, 19]. It was first identified as an antifungal and cytotoxin, with potential for tumour inhibition also

reported in cytotoxicity assays [19]. Three forms are found in the native source, being from sea sponges in the *Mycale* family, of A, B and C, shown in Figure 1.3 [18, 19]. Being the most abundant of the three forms in the biological source, and highly efficacious, pateamine A has been carried through to further cytotoxicity studies.

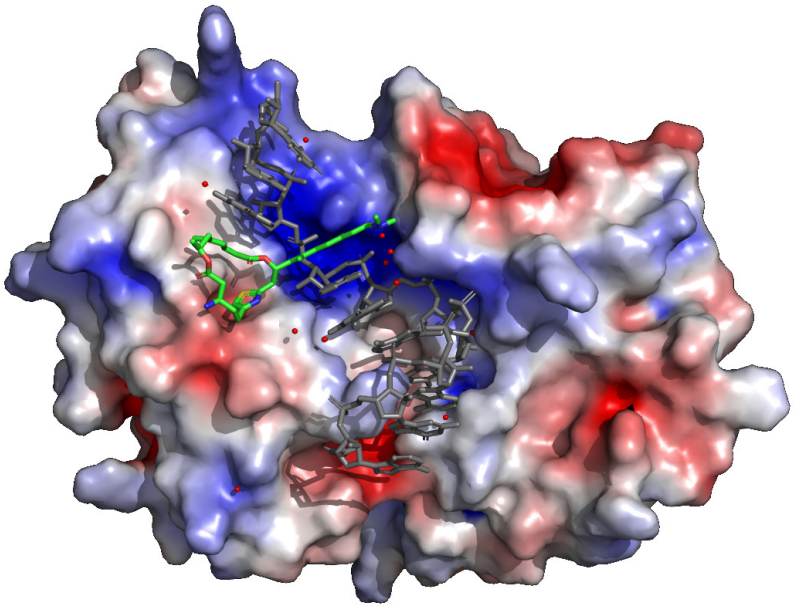

Figure 1.4: Binding site of pateamine A to eIF4A:mRNA complex. eIF4A represented with a space-filling model with electrostatic potentials in red and blue as per convention. mRNA backbone is represented in dark grey. Pateamine A is represented in green. Red dots are water molecules.

Pateamine A binds selectively to eIF4A and mRNA when processing, increasing the stability of helicase:RNA interactions, as shown in Figure 1.4 [20]. This activation mechanism prevents the helicase from disassociating, which disrupts ribosome binding and thus inhibiting translation [20]. Naineni et al's x-ray crystal structure also shows that this pateamine A

binding locks the eIF4A in a closed conformation, which pre-forms the ATP binding site, explaining an increase in perceived affinity for ATP when pateamine A is bound, despite no helicase progression occurring [20, 21].

A key limitation of pateamine A's applicability in the clinical setting is its limited availability. Extractions from *Mycale* sp. are minimal at best, and while synthesis of A, B and C forms are possible, these are all limited by low yield, lengthy experimental procedures, and high costs. Romo et al, and later Pattenden et al, reported an asymmetric full synthesis of pateamine via retrosynthetic methods, but both were long and had low overall yields [18, 22]. More recently, Zhuo and Fürstner reported a full synthesis with a much-improved yield of 5.3% [23]. However, a synthetic equivalent, desmethyl-desamino pateamine (DMDA pateamine), shown in Figure 1.5, is significantly less cumbersome to produce, with yields of over 18% [24]. DMDA pateamine has almost identical biological activity to pateamine A, and appears functionally equivalent in kinetic studies [25]. It is also effective against a variety of human cancers, in culture and when tumours are xenografted to nude mice [26].

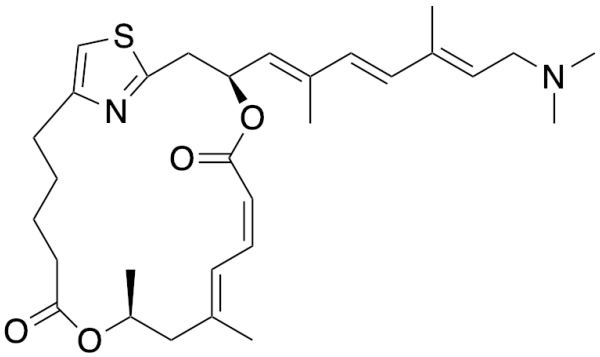

Figure 1.5: Structure of DMDA pateamine.

Rocaglamide A (Figure 1.6) interacts across the binding pocket of the eIF4A:RNA complex [8, 27]. Rocaglamide A was the first cyclopenta[*b*]benzofuran to be isolated from the *Aglaia* genus [27]. It was found that rocaglamide A bound at consecutive purine residues on the mRNA, where the binding to eIF4A caused the mRNA strand to bend sharply, preventing further helicase activity [8]. It must be noted that while rocaglamide A binds in an analogous fashion to the same RNA conformational motif and amino acids of eIF4A as pateamine A, the two inhibitors have markedly different structures [20].

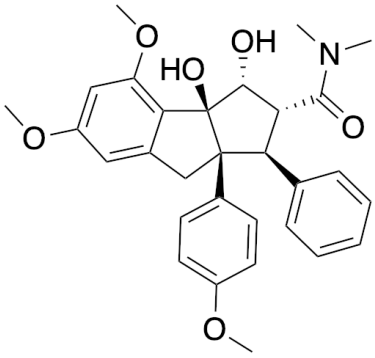

Figure 1.6: Structure of rocaglamide A.

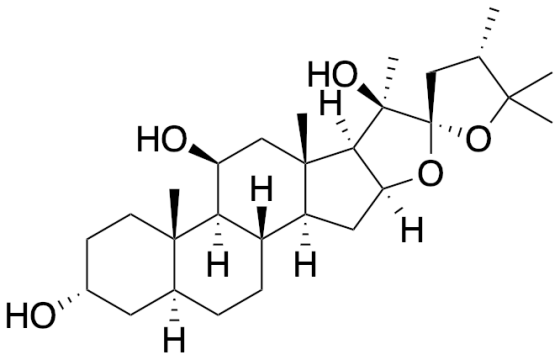

Figure 1.7: Structure of hippuristanol.

Hippuristanol (Figure 1.7) is another small-molecule inhibitor of eIF4A, identified from a screen of cytotoxic polyoxylated steroids of the coral *Isis hippuris* [28]. It binds at the carboxy-terminal domain of eIF4A [28]. In binding to this site, near the domain linkage, hippuristanol locks eIF4A in the closed shape, which prevents mRNA processing and therefore strand progression [10, 28]. ATP dephosphorylation is not impeded, which renders this inhibitor useful for ATP kinetic studies [10]. While not directly studied in this thesis, rocaglamide A and hippuristanol have been utilised in characterisation of eIF4A mechanics and its function in translation initiation.

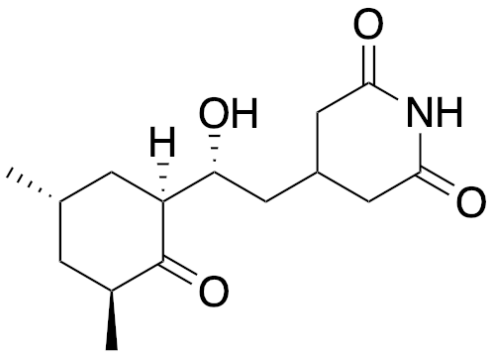

Figure 1.8: Structure of cycloheximide.

For the purposes of this research, pateamine A-specific effects of eIF4A inhibition are compared against overall translation inhibition caused by the drug cycloheximide. The structure of cycloheximide is shown in Figure 1.8. Cycloheximide is a glutarimide which binds in the conserved E-site of the 60S subunit of the eukaryotic ribosome [29]. The deacetylation of tRNA within the E-site in conjunction with cycloheximide causes the ribosome to stall, inhibiting translation irrespective of pre-translational effects [30].

1.3 Glioblastoma

Brain and central nervous system cancers present at an average rate of 23.79 per hundred thousand in United States of America [31]. These are classified as malignant or non-malignant (7.08 and 16.71 respectively), and further classified by pathology [31]. Gliomas account for 14.5% of all tumours, and these are divided into four grades of increasing severity [31]. The highest severity, grade IV, are also termed glioblastoma, and are further subtyped based on location and tumour morphology [32]. Survival prognosis for patients with glioblastoma tumours varies, from five months to one year depending on treatment regime, or median survival of less than two years [32, 33]. Patients commonly develop seizures, altered behaviour, and diminished cognitive ability over the course of disease progression [33].

1.3.1 Typing and Mutations

Oncogenesis requires critical pathways in cell regulation to be disrupted, modified, subverted, or to have otherwise deviated from standard processes. Classifying the type of glioma and glioblastoma can be carried out based on phenotype and genetic mutations, which influence selection of treatment and indicators of patient outcomes [34]. This subtyping refers to the afflicted pathways — classical, mesenchymal, proneural, and neural — of which, proneural, associated with younger age of onset, are commonly TP53 and IDH mutated [34]. Tumour protein P53 (TP53) and isocitrate dehydrogenase (IDH) mutations are both associated with energy metabolism. TP53 is a protein which suppresses tumour formation by triggering apoptosis, and is commonly mutated or silenced in a variety of cancers [35, 36]. IDH,

one of the enzymes of the citric acid cycle involved in glucose metabolism, is mutated in some glioma, and instead of reducing isocitrate, it instead reduces α-ketoglutarate (normally the product of isocitrate dehydrogenation) to 2-hydroxyglutarate [37, 38]. IDH mutations are reported in up to 70% of secondary glioblastoma patients, where the glioblastoma developed from smaller gliomas. One study showed the IDH1 (*R132ΔH*) mutation having occurred prior to TP53 mutations from all 51 patient biopsy samples studied [35]. Verhaak et al also characterise glioma-specific mutations, such as EGFR, NF1, and PGFRA/IDH1, which correlate to different phenotypes of glioma [34].

A recent meta-analysis showed that, based on fourteen studies, glioblastoma exhibit protein upregulation of mRNA splicing and immune system-related proteins, and downregulation of synaptic signalling and glucose/glutamine metabolism [39]. Thus, it is of interest to investigate glioblastoma response to translation inhibition, as the effect of disruption to mRNA splicing pathways and translation inhibition has not been characterised. Moreover, previous yeast studies in the group have indicated overall energy metabolism effects as a result of pateamine treatment, which may synergise with the already-altered pathways of the glioblastoma lines studied [17].

1.3.2 Cell Models of Glioblastoma

Whole exome and RNA sequencing has been completed on six commonly-used glioblastoma cell lines, characterising their genetic subtype [36]. This concurred with Verhaak et al on specific mutations found in this cancer

phenotype, and also expanded this list [34, 36]. As this work is carried out using two of the cell lines discussed, LN18 and U87, a brief discussion of affected genes is provided here.

The LN18 cell line is derived from a 61-year-old Caucasian male [17]. LN18s contain single nucleotide variations (SNVs) in BRCA2 (double stranded break repair regulation), ERCC2 (nuclear localisation of nucleotide excision repair), and TP53 in the DNA binding domain (cell apoptosis and transcriptional regulation) [36]. These regulatory SNVs have flow-on effects in cellular processes, and are considered causal in the oncogenic phenotype.

The U87 cell line, named and distributed as such or alternatively by the term U87MG, however, is not related to the original cells [40]. Genetic profiling and transcriptome analysis has previously been used to compare the distributed U87MG to the original U87MG line kept in Uppsala, Sweden, and found both DNA and mtDNA mismatch; however, the distributed U87MG is indeed a human glioblastoma, of unknown origin [40]. SNVs found in distributed U87 via the whole exome and RNA sequencing include mutations in NF1 (RAS pathway regulator, GTPase activity inhibited), the hTERT promotor (telomerase activation increased) and a frameshift in RAD50 (non-homologous end joining) [36]. No immortalised glioblastoma cell line, such as LN18 or U87, is IDH-mutant, so while this change is particularly evident in the clinic, cultured cell models are unable to reflect this genetic variant [36]. In this research, the distributed U87 cell line was used, and is referred to as such throughout this thesis.

The control cell line used in these experiments is HL60, an acute myeloid leukaemia isolated from a 35-year-old Caucasian female [17]. This cell line is characterised by a large homozygous deletion in TP53 (disrupting tumour

suppression), and is commonly used for cell differentiation studies [41]. The HL60 cell line used as a control cell line against which the glioblastoma cell lines, LN18 and U87, were compared. The HL60 cell line has been used previously in the research group, and more generally, for characterising cell response, specifically the cellular response to eIF4A inhibition by pateamine A treatment.

In summary, glioblastomas are clinically challenging, against which pateamine A treatment is evidenced but not fully characterised, and may have an interesting proteomic response. Two glioblastoma cell lines, with different proteomic characteristics exhibited in preliminary experiments, have been selected for this research: LN18 and U87.

1.4 Hypothesis

The current model of eIF4A inhibition by pateamine A recognises that there are unexplored effects on other cellular pathways. This has been evidenced in energy metabolism differences in yeast, but this has not been characterised in human cancer cell lines. Moreover, the altered expression of energy metabolism in glioblastoma is relevant to further research as their clinical presentation is associated with already-abnormal energy metabolism. Pateamine A is a powerful inhibitor of eIF4A, and thus an attractive cancer treatment, not only for its cytotoxicity profile, but also for its efficacy and low treatment doses.

A proposed general theory has been suggested to explain eIF4A inhibition effects. Higher levels of loaded tRNAs cause the cell to perceive an abundance of amino acids, causing the cellular metabolism to balance in

favour of energy metabolism, amino acid biosynthesis, or possibly lipid accumulation. A link between eIF4A-related translation initiation and energy metabolism, while evidenced in yeast, has yet to be confirmed in human glioma and glioblastoma cell lines.

The hypothesis of this research is as follows: inhibitors of eIF4A, including pateamine A, cause alterations in cellular metabolism, particularly pathways involved in energy metabolism. Specifically, this work will focus on the proteomic characterisation of the effects of pateamine A treatment on two glioblastoma cell lines.

Chapter 2

Aims and Objectives

This research aims to characterise changes to cellular profiles of glioblastoma cell lines in response to eIF4A inhibition via pateamine A treatment. High performance liquid chromatography tandem mass spectrometry (LC-MS/MS) will be used to characterise differences in response to pateamine A of two glioblastoma cell lines to a leukaemia cell line. Three cell lines have been selected for this: HL60 as the leukaemia control, and two glioblastoma cell lines, LN18 and U87. The LC-MS/MS results will be used to carry out gene ontology analysis to show what cell pathways are affected by overall translational inhibition and pateamine A-specific effects.

The objectives of this thesis are as follows:

1. Determine IC_{50} concentration of pateamine A and cycloheximide (positive control) in three cell lines: two glioblastoma (LN18 and U87) and one control (HL60, leukaemia), and;

2. Use these drug treatment concentrations to prepare samples for proteomic LC-MS/MS analysis, as well as negative controls, and;

3. Elucidate the impact of eIF4A inhibition on other metabolic pathways, using gene ontology analysis.

Chapter 3

Materials and Methods

3.1 Reagents and Solutions

3.1.1 Materials

C18 OMIX™ Tips	Agilent Technologies, USA
Cell Culture Treated Flasks, T25 and T75	Grenier Bio-One, Germany
Falcon Tubes (15 and 50 mL)	Corning Incorporated, USA
Flat-bottomed 96-well Plates (Tissue Culture Treated)	Corning Incorporated, USA
Glass Pasteur Pipettes	Poulten & Grat Ltd, UK
Low Protein Binding Microcentrifuge Tubes, 2.0 mL	Thermo Scientific, USA
Microcentrifuge Tubes, 1.7 mL	MultiMax, USA
Parafilm M®	Bemis, USA
Stripettes (5, 10, 25 mL)	Corning Incorporated, USA

3.1.2 Cell Culture Reagents

GlutaMAX™, 100X	Life Technologies, NZ
Dubecco's Phosphate-Buffered Saline, 1X (DPBS)	Life Technologies, NZ
Foetal Bovine Serum (FBS)	Sigma-Aldrich, NZ
Roswell Park Memorial Institute 1640 Media (RPMI), Hyclone™, + L-Glutamine	Life Technologies, NZ
Trypan Blue™, 0.4%	Life Technologies, NZ
Trypsin-EDTA, 0.05%	Life Technologies, NZ

3.1.3 Drug Stocks

Cycloheximide, 95%	Fisher Scientific, USA
Dimethyl sulfoxide (DMSO)	Fisher Scientific, USA
Pateamine A, 400 μM, in DMSO	Previously isolated in-house

3.1.4 MTT Reagents

Phosphate Buffered Saline (PBS)	Sigma-Aldrich, USA
3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT)	ThermoFisher Scientific, USA
Sodium Dodecyl Sulfate (SDS)	BioRad, USA
Distilled water (dH_2O)	High-Q Inc, USA

3.1.5 Proteomics Reagents

Pierce™ MS Grade Trypsin Protease	Thermo Scientific, USA
Pierce™ LC-MS Grade Water (HPLC H_2O)	Thermo Scientific, USA
Urea, anhydrous	Sigma-Aldrich, USA
Dithiothreitol (DTT)	BioRad, USA
Iodoacetamide	Sigma-Aldrich, USA
Pierce™ Rapid Gold BCA Protein Assay Kit	Thermo Scientific, USA
Pierce™ Quantitative Fluorometric Peptide Assay	Thermo Scientific, USA
Formic acid, 98%	Merck, NZ
Acetonitrile, >99.99%	Carl Roth, NZ
Acetone, >99%	Romil Ltd, UK

3.2 Drug Stocks

Cycloheximide was made fresh from powdered 95% cycloheximide, to 10 μM for each assay and flask treatment.

Pateamine A was sourced from existing stock, stored frozen at -20 °C. All pateamine A was sourced from the same parent 400 μM solution, and diluted to an intermediary 100 μM stock. This 100 μM stock was used within one week of dilution. A 10 μM stock was also made for the purpose of flask treatments, and used within one week of dilution.

3.3 Cell Culture

Immediately post-thaw, cell lines were cultured in 5 mL of supplemented media in treated T25 flasks, before passaging and upscaling in T75 flasks. To upscale, cell lines were cultured in 14 to 15 mL of supplemented media in treated T75 flasks at 37 °C and 5% CO_2. Flasks were replaced weekly to prevent development of films. All cultures of each cell line originated from the same frozen source.

3.3.1 Adherent Cell Lines

For LN18 and U87 cell lines, cells were maintained in logarithmic phase in RPMI 1640 media supplemented with 5% FBS in T75 cell culture flasks. Cells were passaged at 80% confluency by washing with DPBS then 0.05% trypsin-EDTA, and incubated for one minute at 37 °C and 5% CO_2 to open the extracellular matrix. A 1:10 dilution of cells was carried out in media, and the total flask volume was made up toopen 14 to 15 mL.

3.3.2 Suspension Cell Line

For the HL60 cell line, cells were maintained in logarithmic phase in RPMI 1640 media supplemented with 10% FBS and 2 mM GlutaMAX™. Cells were passaged every two days by removing two-thirds of the culture volume and replacing this volume with fresh media. At weekly flask replacements, cells were centrifuged at 300 *x g* for four minutes and resuspended in fresh media to 15 mL before passaging.

3.4 MTT Cell Viability Assays

MTT assays are used to determine cell viability, and therefore implicit cell proliferation, in response to drug treatment [42]. This was carried out in 96-well plates, with the outermost wells filled with media to prevent evaporation, leaving six replicates of nine serially-diluted drug-treated wells and of DMSO control wells.

3.4.1 Chemical Principles of the Assay

The MTT assay is based on the intracellular reduction of yellow MTT to purple formazan (Figure 3.1), which is used to measure cellular proliferation [42]. MTT passes through the cell membrane, and is reduced by mitochondrial or cell plasma enzymes using a variety of electron donors (NADH, NADPH, succinate, or pyruvate) to form insoluble formazan [42]. Cell lysis is carried out and the needle-like formazan crystals dissolved before spectroscopic analysis [42]. In practice, this is carried out with a no-treatment control, and a drug dilution series treatment is used to determine the IC_{50} value for flask treatments.

3.4.2 Seeding and Drugging

In preliminary experiments, seeding of adherent cell lines was complicated by surface-area:volume ratio effects on seeding density, which led to misleading IC_{50} results when this IC_{50} drug concentration was used in a full-sized flask of the same seed density. Adherent cells were seeded at lower concentrations in the MTT assay than in the flasks themselves, which

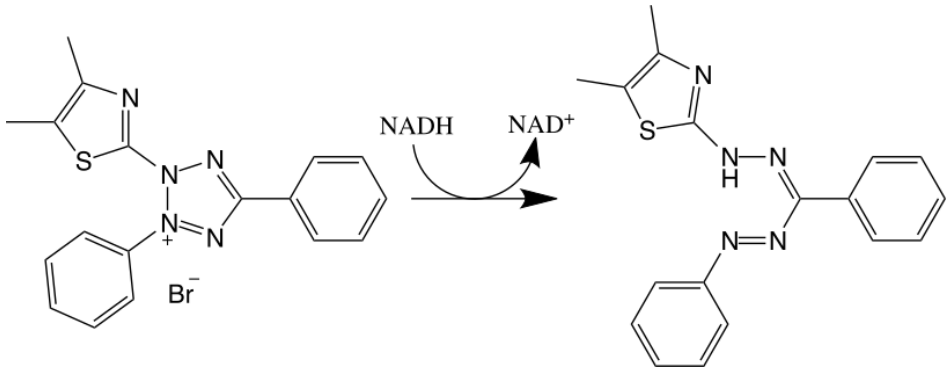

Figure 3.1: Reduction of MTT to formazan.

nonetheless resulted in comparable observed inhibition of cell growth. Suspension cell lines did not exhibit this disparity.

3.4.2.1 Drug Dilutions

Cycloheximide and pateamine A stocks were diluted to twice the top final concentration and serially diluted at 2.5-fold for each cell line (Table 3.1), for a final DMSO/drug volume of 0.8 μL. 400 μL of media was added to each tube, before aliquots of 50 μL were added to six replicates of a 96-well plate.

	HL60	LN18	U87
Cycloheximide	10 μM	5 μM	10 μM
Pateamine A	100 nM	100 nM	100 nM

Table 3.1: Top final concentration of cycloheximide and pateamine in MTT assays, diluted 2.5-fold.

3.4.2.2 Adherent Cell Lines

For LN18 and U87 cell lines, cells were seeded in 100 μL aliquots of 1 x 10^4 cells/mL and incubated at 37 °C and 5% CO_2 for 12-16 hours to adhere. 50 μL aliquots of media was removed, and 50 μL aliquots of the drug dilutions described above were added. Plates were incubated at 37 °C and 5% CO_2 for 48 hours before lysis.

3.4.2.3 Suspension Cell Lines

For HL60 cell lines, cells were seeded in 50 μL aliquots of 2 x 10^{5} cells/mL. 50 μL aliquots of the drug dilutions described above were added. Plates were incubated at 37 °C and 5% CO_2 for 48 hours before lysis.

3.4.3 MTT and Lysis

To determine cellular activity, aliquots of 20 μL of 5 mg/mL MTT in PBS were added to each well prior to a 1-2 hour incubation at 37 °C and 5% CO_2 to allow cells to metabolise MTT to formazan. Cells were checked under the microscope at 1 hour, 1.5 hours, and 2 hour time points and lysed with 100 μL aliquots of 10% SDS when needle-like formazan crystals began to puncture the cells. Plates were incubated at 37 °C and 5% CO_2 for 24 hours at room temperature in the dark for colour to develop before being read.

Plates were read at 570 nm on an EnSpire TM 2300 Multilabel plate reader (Perkin Elmer), with absorbance values normalised to the DMSO-only control.

The IC_{50} concentration of each drug on each cell line was determined using Prism 7 (GraphPad Software, USA) as described in Section 3.7.1.

3.5 Pharmacological Challenge

Four biological replicates were used, and passaged at least once within the T75 flask before seeding. Adherent cell lines were washed with 5 mL DPBS, then 5 mL 0.05% trypsin-EDTA, and seeded at 2 x 10^5 cells/mL and incubated at 37 °C and 5% CO_2 for 12-16 hours to adhere. Media was aspirated off and fresh media, supplemented with the relevant drug dissolved in DMSO to yield a final DMSO concentration of 0.1% and drug at the IC_{50}, was added. For suspension cells, flasks were seeded with 7.5 mL of 2 x 10^5 cell/mL and 7.5 mL of drugged media to yield a final DMSO concentration of 0.1% and the drug at the IC_{50}.

Treated flasks were incubated for 48 hours at 37 °C and 5% CO_2 before lysis. Adherent cell lines were washed with 5 mL DPBS, then 5 mL trypsin-EDTA, and resuspended in 10 mL media. Cells were placed in a 15 mL Falcon tubes for sample preparation, with suspension cells having been transferred directly to the tube.

3.6 Sample Preparation for LC-MS/MS

3.6.1 Cell Lysis

Harvested cells were centrifuged at 300 *x g* for four minutes, and media aspirated off. On ice, the pellet was resuspended in 5 mL PBS, centrifuged at 300 *x g* for four minutes in 4 °C refrigerated centrifuge, and PBS aspirated off. This was repeated in 1 mL of PBS, with the sample being transferred to a low protein-binding tube prior to centrifugation.

The pellet was resuspended in 200 μL of 8 M urea and vortexed well be-

fore freezing at -80 °C for one hour, or until the sample could be processed.

3.6.2 Acetone Precipitation

After thawing and vortexing, 800 μL of ice-cold acetone was added to the sample and incubated for one hour at -20 °C. This was centrifuged at 13,000 *x g* for ten minutes and supernatent removed before air-drying for 10-15 minutes. The sample was resuspended in 50 μL of 8 M urea for quantification.

3.6.3 Protein Quantification

Protein quantification was carried out using Pierce™ Rapid Gold BCA Protein Assay Kit in duplicate using sixteen wells of a 96-well plate. Briefly, a BSA protein standard of 2000 μg/mL was diluted with 2 M urea to generate a standard curve of 2000 μg/mL, 1000 μg/mL, 500 μg/mL, 100 μg/mL, and 10 μg/mL in duplicate. A 2 M urea blank was used, and a 5 μL aliquot of the sample diluted 1:4 with distilled H_2O, and divided equally between two wells. 10 μL of sample/blank/standard was used, and 200 μL of working reagent added to each well. Working reagent was made immediately prior to assay from 2,940 μL of Reagent A and 60 μL of Reagent B (49:1) from the kit.

A 30-second shake was included in the protocol, followed by a five minute incubation at room temperature to allow the colour to develop before reading at 480 nm using an EnSpire TM 2300 Multilabel plate reader (Perkin Elmer). A standard curve was formed in Excel (Microsoft, USA) and linear regression used to calculate mass of protein in the sample.

3.6.4 Protein Pre-Treatment and Tryptic Digestion

5 μL of fresh 100 mM DTT stock was added to the sample, followed by a two hour incubation at 56 °C. 22 μL of fresh 100 mM iodoacetamide stock was added to the sample, and incubated in the dark at room temperature for 45 minutes before adding 231 μL of distilled H_2O to dilute the sample to 2 M urea. Iodoacetamide prevents cysteine residues from forming disulfide bonds. 10 μg/mL mass spectrometry-grade trypsin protease was added in a weight ratio to protein of 1:50 or 1:100 and incubated overnight at 37 °C to digest proteins. These are hereafter referred to as peptides. 3.1 μL of 10% formic acid was used to quench the trypsin digest.

3.6.5 Concentration, Purification, and Desalting Peptides

Peptides were purified using C18 OMIX™ micropipette tips set at 100 μL volumes for all stages and reagents. All solutions used were made fresh from stocks. Tips were wetted with 50% acetonitrile and 0.1% formic acid twice each, and kept wet throughout extraction steps. The peptide solution was passed 20 times through the tip, washed thrice with 0.1% formic acid, and eluted with 50% acetonitrile by passing through the tip 20 times. This was repeated, but eluting with 70% acetonitrile. The tip was then eluted with two further solutions of 50% and 70% acetonitrile, totalling four tubes, to maximise peptide return. 50% and 70% tube pairs were combined to form two tubes with an acetonitrile concentration of 60%.

The two tubes of purified peptide samples were dried at 37 °C in a CentriVap vacuum concentrator (Labconco), resuspended in 50 μL HPLC H_2O and recombined into a single tube. Two 10 μL aliquots were removed

for peptide quantification, and the remaining 80 μL of purified peptides in H_2O was dried at 37 °C in a CentriVap vacuum concentrator.

3.6.6 Peptide Quantification

Peptide quantification was carried out using Pierce™ Quantitative Fluorometric Peptide Assay Kit in duplicate using sixteen wells of a 96-well plate. Briefly an albumin standard of 1000 μg/mL was diluted with HPLC H_2O to generate a standard curve of 500 μg/mL, 250 μg/mL, 125 μg/mL, 62.5 μg/mL and 31.25 μg/mL. 10 μL of sample/HPLC H_2O blank/standard was used, and 70 μL of the provided assay buffer and 20 μL of the provided assay reagent was added to each well.

A 30-second shake was included in the plate reader protocol, followed by a five minute incubation at room temperature to complete the reaction before reading at 390 nm using an EnSpire TM 2300 Multilabel plate reader (Perkin Elmer). A standard curve was formed in Excel and linear regression used to calculate mass of peptide remaining in the sample.

3.6.7 Preparation for LC-MS/MS Analysis

The dried peptide sample was resuspended in 0.1% formic acid to a concentration of 100 ng/mL to store at -20 °C. Samples were dried before sending to the Mass Spectrometry and Proteomics Facility at the Bio21 Molecular Science and Biotechnology Institute for spectroscopic analysis.

3.7 Analysis Pipeline

3.7.1 Procedure for Determining IC_{50}

The calculation of the IC_{50} concentration of each drug on each cell line was carried out using Prism 7 (GraphPad Software, USA). After normalisation to DMSO control, outliers were removed subject to Grubb's test, graphs generated, and IC_{50} determined using the default model for dose inhibition with variable slope.

3.7.2 Procedure for Collecting Mass Spectroscopic Data

All mass spectrometry analysis was carried out by the Mass Spectrometry and Proteomics Facility at the Bio21 Molecular Science and Biotechnology Institute of the University of Melbourne. Samples were resuspended in 2% acetonitrile and 0.05% triflic acid in HPLC H_2O. LC-MS/MS was carried out on a QExactive plus Orbitrap mass spectrometer (Thermo Scientific) with a nanoESI interface in conjunction with an Ultimate 3000 RSLC nanoHPLC (Dionex Ultimate 3000). The LC system was equipped with an Acclaim Pepmap nano-trap column (Dinoex-C18, 100 Å, 75 μm x 2 cm) and an Acclaim Pepmap RSLC analytical column (Dinoex-C18, 100 Å, 75 μm x 50 cm). The tryptic peptides were injected to the enrichment column at an isocratic flow of 5 μL/min of 2% v/v CH_3CN containing 0.1% v/v formic acid for 5 minutes before the enrichment column was switched in-line with the analytical column. The eluents were 5% DMSO in 0.1% v/v formic acid (solvent A) and 5% DMSO in 100% v/v CH_3CN and 0.1% v/v formic acid (solvent B). The flow gradient was (i) 0-6min at 3% B, (ii) 6-95 minutes,

3-22% B (iii) 95-105 minutes 22-40% B (iv) 105-110 minutes, 40-80% B (v) 110-115 minutes, 80-80% B (vi) 115-117 minutes, 80-3% and equilibrated at 3% B for 10 minutes before the next sample injection. The QExactive plus mass spectrometer was operated in the data-dependent mode, whereby full MS1 spectra were acquired in positive mode, 70,000 resolution, AGC target of 3 x 10^6 and maximum IT time of 50 ms. Fifteen of the most intense peptide ions with charge states ≥ 2 and intensity threshold of 1.7 x 10^4 were isolated for MS/MS. The isolation window was set at 1.2 m/z and precursors fragmented using normalised collision energy of 30, 17,500 resolution, AGC target of 1 x 10^5 and maximum IT time of 100 ms. Dynamic exclusion was set to be 30 seconds.

3.7.3 Procedure for Analysis of Mass Spectroscopic Data

Mass spectra files were analysed using Proteome Discoverer (ThermoFisher, version 2.4). The spectra were searched using the Swiss-Prot human proteome database including all proteins with evidence (downloaded on 25-10-2017). Input peptide length was set 6-144 amino acids with a precursor mass tolerance of 10 ppm and fragment mass tolerance of 0.6 Da. The digesting enzyme was set to trypsin, with a maximum of 2 missed cleavages allowed. Cysteine carbamidomethylation was set as a static modification (+57.021 Da) and no dynamic modifications were used. This was completed for both determination of the number of peptides from each sample, and quantitative comparison between replicates and samples. The comparison file was then processed in Excel to filter out changes with an adjusted p-value greater than 0.05 and medium to low confidence hits. The fold

change was then filtered to generate two lists: genes that were upregulated by two-fold or more, and genes that were downregulated by two-fold or more.

3.7.3.1 Gene Ontology Enrichment

Each up- and downregulated list, with isoforms removed, was loaded into the g:Profiler online tool [43], with the organism set to *Homo sapiens*, gene names manually converted into Ensembl IDs where necessary, and duplicates removed. Ontologies were limited to terms with a sum total of 1000 associated genes to remove top-level ontology terms (GO terms). Databases searched included Biological Process, Molecular Function, Cell Component, WikiPathways, KEGG, Reactome, and Transcription Factors to maximise breadth of the search, and all were searched using the default background settings and included a multiple testing correction native to g:Profiler. These GO terms were limited to those with adjusted p-values less than 0.05. As many of the recognised terms were replicated in multiple databases, and this thesis is focussed on pathway effects, only the ten lowest adjusted p-value Biological Process and Molecular Function terms are reported in Results (Chapter 4), with GO terms from other databases being useful in informing the Discussion (Chapter 5).

3.7.3.2 Subsequent Processing

UpSet plots are a method of visualising exclusive intersections of sets, such as those arising from gene ontology analysis [44]. Regrettably, the available interface presents merely a count of those overlaps, and does not present

exactly which genes belong to which term intersections. I would like to thank Michael Pot for developing programs to both print a list the genes contributing to exclusive intersects of terms, and the modified UpSet plots presented in the Discussion (Section 5) to include insets of graphs showing adjusted p-value, and the number of genes within each term annotated with the total size of the term.

Chapter 4

Results

4.1 IC_{50} from MTT Assay

The results from the MTT assays are presented in two forms: first, a summary in Table 4.1 shows the calculated IC_{50} concentrations which were used to treat each flask for LC-MS/MS sample preparations. Second, each MTT curve generated from Prism are shown in Figures 4.1 to 4.6. The x-axis of Figures 4.1 to 4.6 represents to % growth of the control wells, so higher x-value correlates to lesser growth inhibition.

	Cycloheximide (nM)	Pateamine A (nM)
HL60	73.15 (69.26 to 77.27) [0.9933]	0.5377 (0.4828 to 0.5991) [0.9685]
LN18	181.8 (160.2 to 206.3) [0.9675]	2.499 (2.293 to 2.726) [0.9822]
U87	134.9 (100.9 to 181.3) [0.8644]	2.018 (1.862 to 2.188) [0.9831]

Table 4.1: IC_{50} values, with 95% confidence intervals reported in parentheses and R^2 value in square brackets to indicate quality of fit.

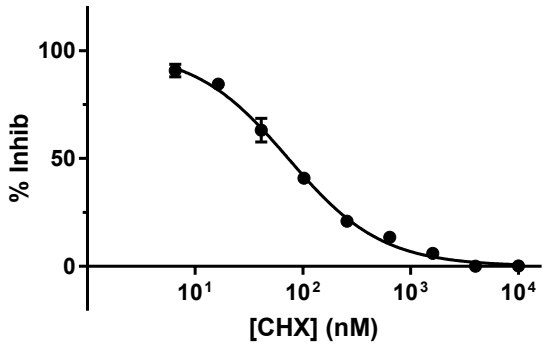

Figure 4.1: MTT assay of cycloheximide treatment effects on HL60 cell line.

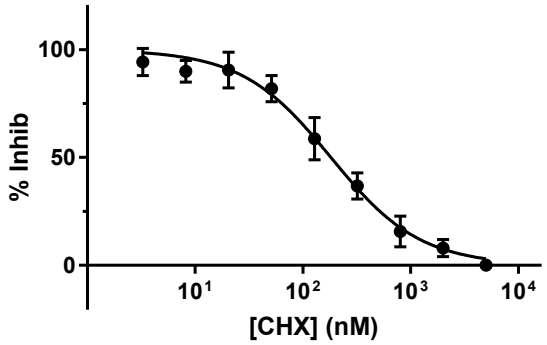

Figure 4.2: MTT assay of cycloheximide treatment effects on LN18 cell line.

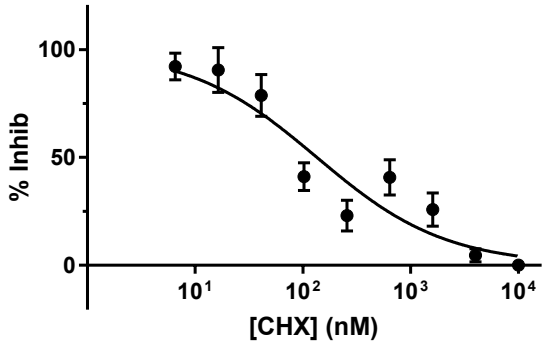

Figure 4.3: MTT assay of cycloheximide treatment effects on U87 cell line.

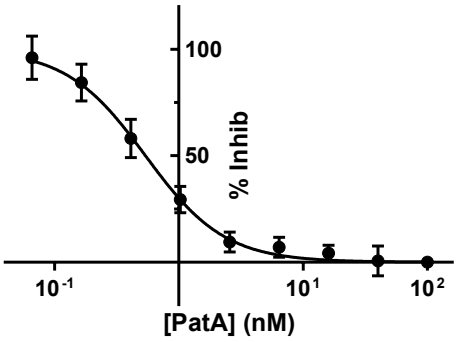

Figure 4.4: MTT assay of pateamine A treatment effects on HL60 cell line.

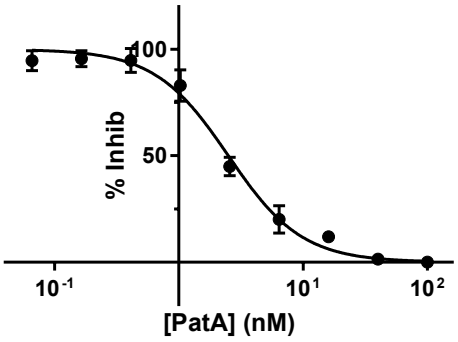

Figure 4.5: MTT assay of pateamine A treatment effects on LN18 cell line.

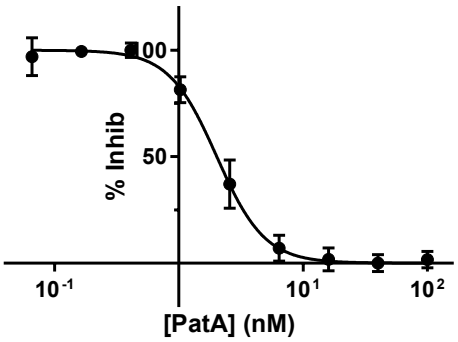

Figure 4.6: MTT assay of pateamine A treatment effects on U87 cell line.

4.2 Gene Ontological Enrichment Using g:Profiler

The results of gene ontology (GO) analysis are presented here. The first group compares differences between the no-treatment control samples (Tables 4.2 to 4.7). Full terms lists are shown in Appendices A to F. Next are the intracellular comparisons (Tables 4.8 to 4.19). They are sorted by drug type, then cell line, and up- and downregulated lists are presented in two separate tables.

The lists contain the ten Biological Processes and Molecular Function terms identified by the g:Profiler algorithm with the lowest adjusted p-value. If fewer than ten GO terms were identified, they are shown below in shorter tables. Full lists of terms for each cell line and drug treatment, sorted as up- or downregulated terms, are shown in Appendices G to Q. Full gene lists, showing accession number, description, fold change, and adjusted p-value for each gene identified as having changed in response to drug treatment, are presented in Appendices U to X.

4.2.1 GO Differences in Cell Lines

The purpose of this data is to elucidate underlying GO differences between the cell lines studied. HL60 has been used as the denominator in comparisons with LN18 and U87, under the principle that it is acting as the control against which future comparisons will be made. For completeness, a comparison has been made between LN18 and U87.

4.2.1.1 HL60 vs LN18

source	term name	adjusted p-value	term size	intersection size
GO:MF	cell adhesion molecule binding	6.53E-09	544	39
GO:MF	actin binding	5.87E-07	449	32
GO:MF	cadherin binding	1.51E-05	333	25
GO:BP	actin filament-based process	2.69E-04	810	41
GO:BP	actin cytoskeleton organization	6.14E-04	712	37
GO:MF	phosphatase binding	2.09E-03	199	16
GO:MF	protein domain specific binding	2.18E-03	706	34
GO:MF	enzyme regulator activity	2.85E-03	911	40
GO:BP	actin filament bundle assembly	3.04E-03	161	15
GO:BP	actin filament bundle organization	3.83E-03	164	15

Table 4.2: Biological processes (BP) and molecular functions (MF) upregulated in LN18 cells compared to HL60 cells. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix A.

source	term name	adjusted p-value	term size	intersection size
GO:MF	catalytic activity, acting on RNA	8.65E-07	394	36
GO:BP	ncRNA metabolic process	4.69E-06	535	43
GO:BP	regulated exocytosis	1.31E-05	790	54
GO:BP	myeloid leukocyte mediated immunity	1.65E-05	558	43
GO:BP	leukocyte degranulation	1.71E-05	538	42
GO:BP	ncRNA processing	1.85E-05	439	37
GO:BP	neutrophil mediated immunity	1.99E-05	500	40
GO:BP	neutrophil degranulation	2.38E-05	483	39
GO:BP	neutrophil activation involved in immune response	3.16E-05	488	39
GO:BP	myeloid cell activation involved in immune response	3.58E-05	552	42

Table 4.3: Biological processes (BP) and molecular functions (MF) downregulated in LN18 cells compared to HL60 cells. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown.See Appendix B.

4.2.1.2 HL60 vs U87

source	term name	adjusted p-value	term size	intersection size
GO:MF	adhesion	6.00E-11	333	31
GO:MF	cell adhesion molecule binding	1.80E-10	544	39
GO:BP	actin cytoskeleton organization	3.94E-07	712	41
GO:BP	actin filament-based process	5.16E-07	810	44
GO:MF	actin binding	5.78E-07	449	30
GO:MF	structural molecule activity	4.27E-05	701	35
GO:BP	supramolecular fiber organization	1.01E-04	863	41
GO:BP	actin filament organization	2.08E-04	445	27
GO:BP	cell morphogenesis involved in differentiation	2.16E-04	754	37
GO:MF	extracellular matrix binding	3.53E-04	56	9

Table 4.4: Biological processes (BP) and molecular functions (MF) upregulated in U87 cells compared to HL60 cells. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix C.

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitochondrial translational elongation	7.16E-06	87	17
GO:BP	mitochondrial translational termination	8.60E-06	88	17
GO:BP	translational termination	1.88E-05	104	18
GO:BP	negative regulation of cell cycle process	1.30E-04	400	36
GO:BP	mitochondrial translation	2.34E-04	135	19
GO:BP	myeloid leukocyte mediated immunity	5.66E-04	558	43
GO:BP	neutrophil mediated immunity	5.71E-04	500	40
GO:BP	neutrophil degranulation	6.39E-04	483	39
GO:BP	leukocyte activation involved in immune response	6.69E-04	723	51
GO:BP	negative regulation of cell cycle	7.89E-04	487	39

Table 4.5: Biological processes (BP) and molecular functions (MF) downregulated in U87 cells compared to HL60 cells. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix D.

4.2.1.3 LN18 vs U87

source	term name	adjusted p-value	term size	intersection size
GO:BP	ribonucleoprotein complex biogenesis	2.39E-06	473	37
GO:BP	rRNA metabolic process	4.05E-06	275	27
GO:BP	ribosome biogenesis	4.43E-06	335	30
GO:BP	rRNA processing	3.74E-05	265	25
GO:BP	ncRNA processing	5.37E-05	439	33
GO:BP	ncRNA metabolic process	6.53E-05	535	37
GO:BP	protein localization to organelle	8.30E-05	974	54
GO:MF	peptidyl-lysine 5-dioxygenase activity	1.84E-04	4	4
GO:BP	mRNA metabolic process	2.07E-03	880	47
GO:BP	intracellular protein transport	2.31E-03	995	51

Table 4.6: Biological processes (BP) and molecular functions (MF) upregulated in U87 cells compared to LN18 cells. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix E.

source	term name	adjusted p-value	term size	intersection size
GO:BP	DNA replication	1.70E-02	338	24
GO:BP	cell division	3.51E-02	630	35
GO:BP	chromosome segregation	3.53E-02	353	24
GO:BP	regulation of DNA-dependent DNA replication initiation	3.90E-02	7	4

Table 4.7: Biological processes (BP) and molecular functions (MF) downregulated in U87 cells compared to LN18 cells. The table shows the four most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix F.

4.2.2 GO Differences Following Cycloheximide Treatment

These tables show the no-treatment control of each cell line compared to the positive control (*i.e.* cycloheximide-treated) of the same cell line.

4.2.2.1 HL60 Cell Line

In HL60 cells, treatment with cycloheximide upregulates processes involved in transcription, such as the mediator complex (shown as vitamin D receptor binding), and regulators of protein stability. Downregulated gene ontologies include translational output (ribosome biogenesis and translation) and mitochondrial ATP synthesis.

source	term name	adjusted p-value	term size	intersection size
GO:BP	cell cycle phase transition	2.74E-06	681	43
GO:BP	mitotic cell cycle process	2.98E-06	956	53
GO:BP	mitotic cell cycle phase transition	4.36E-06	588	39
GO:BP	regulation of cell cycle phase transition	2.05E-04	543	34
GO:BP	regulation of mitotic cell cycle phase transition	3.68E-04	453	30
GO:BP	regulation of cell cycle process	5.00E-04	815	43
GO:MF	transcription factor binding	3.50E-03	556	30
GO:BP	regulation of protein stability	3.69E-03	302	22
GO:BP	protein catabolic process	5.32E-03	983	46
GO:MF	vitamin D receptor binding	6.22E-03	15	5

Table 4.8: Biological processes (BP) and molecular functions (MF) upregulated in HL60 cells in response to cycloheximide treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix G.

source	term name	adjusted p-value	term size	intersection size
GO:BP	ribosome biogenesis	3.96E-06	335	23
GO:BP	rRNA processing	2.85E-04	265	18
GO:BP	rRNA metabolic process	4.96E-04	275	18
GO:BP	ribonucleoprotein complex biogenesis	5.73E-04	473	24
GO:MF	structural constituent of ribosome	9.05E-04	171	13
GO:BP	peptide metabolic process	9.86E-04	998	37
GO:BP	oxidative phosphorylation	1.15E-03	151	13
GO:BP	aerobic electron transport chain	2.88E-03	92	10
GO:BP	translation	4.11E-03	804	31
GO:BP	mitochondrial ATP synthesis coupled electron transport	5.68E-03	99	10

Table 4.9: Biological processes (BP) and molecular functions (MF) downregulated in HL60 cells in response to cycloheximide treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix H.

4.2.2.2 LN18 Cell Line

In LN18 cells, cycloheximide treatment upregulated protein localisation

and transport, and associated biosynthesis. (m)RNA splicing and processing and some protein binding terms are downregulated, indicating increased retention of (m)RNA transcripts as a result of translation inhibition.

source	term name	adjusted p-value	term size	intersection size
GO:BP	intracellular protein transport	7.15E-18	995	119
GO:BP	ribonucleoprotein complex biogenesis	6.04E-16	473	73
GO:BP	ribosome biogenesis	6.60E-14	335	57
GO:BP	translation	8.38E-14	804	96
GO:BP	protein localization to organelle	1.59E-13	974	108
GO:BP	peptide biosynthetic process	9.29E-13	834	96
GO:BP	establishment of protein localization to membrane	2.65E-12	385	59
GO:BP	establishment of protein localization to organelle	7.10E-12	523	70
GO:BP	amide biosynthetic process	8.84E-12	975	104
GO:BP	mRNA metabolic process	2.83E-11	880	96

Table 4.10: Biological processes (BP) and molecular functions (MF) upregulated in LN18 cells in response to cycloheximide treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix I.

source	term name	adjusted p-value	term size	intersection size
GO:BP	mRNA processing	3.92E-14	532	64
GO:BP	mRNA metabolic process	1.32E-11	880	81
GO:BP	RNA splicing, via transesterification reactions	1.32E-11	363	48
GO:BP	mRNA splicing, via spliceosome	4.18E-11	360	47
GO:BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	4.18E-11	360	47
GO:BP	RNA splicing	1.44E-10	459	53
GO:MF	cadherin binding	8.33E-10	333	42
GO:MF	cell adhesion molecule binding	5.79E-06	544	48
GO:MF	phosphatase binding	7.50E-06	199	26
GO:MF	actin binding	9.44E-06	449	42

Table 4.11: Biological processes (BP) and molecular functions (MF) downregulated in LN18 cells in response to cycloheximide treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix J.

4.2.2.3 U87 Cell Line

In cycloheximide-treated U87 cells, the top six upregulated terms relate to

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitochondrial translation	7.79E-08	135	28
GO:BP	mitochondrial gene expression	1.20E-07	166	31
GO:BP	translational elongation	3.55E-05	143	25
GO:BP	translational termination	3.66E-05	104	21
GO:BP	mitochondrial translational elongation	4.59E-05	87	19
GO:BP	mitochondrial translational termination	5.60E-05	88	19
GO:BP	ncRNA transcription	1.03E-04	110	21
GO:BP	DNA metabolic process	2.01E-04	976	84
GO:BP	nucleobase-containing small molecule metabolic process	4.99E-04	628	60
GO:BP	DNA repair	1.27E-03	586	56

Table 4.12: Biological processes (BP) and molecular functions (MF) upregulated in U87 cells in response to cycloheximide treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix K.

translation, with the 19 genes in mitochondrial translational elongation/ termination also being found in the top four terms. DNA repair mechanisms were upregulated, and RNA transcript-related catabolism downregulated.

source	term name	adjusted p-value	term size	intersection size
GO:BP	mRNA metabolic process	1.00E-07	880	43
GO:BP	viral transcription	1.11E-05	181	17
GO:BP	cellular nitrogen compound catabolic process	5.36E-04	623	29
GO:BP	viral gene expression	5.93E-04	237	17
GO:BP	RNA catabolic process	9.91E-04	431	23
GO:BP	nucleobase-containing compound catabolic process	1.13E-03	573	27
GO:BP	heterocycle catabolic process	1.46E-03	617	28
GO:BP	mRNA catabolic process	2.56E-03	388	21
GO:BP	aromatic compound catabolic process	2.66E-03	636	28
GO:BP	translation	3.91E-03	804	32

Table 4.13: Biological processes (BP) and molecular functions (MF) downregulated in U87 cells in response to cycloheximide treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix L.

4.2.3 GO Differences where Pateamine A Treated

These tables show the no-treatment control of each cell line compared to samples treated with the drug of interest (*i.e.* pateamine A-treated) of the same cell line.

4.2.3.1 HL60 Cell Line

In HL60 cells treated with pateamine A, no molecular functions met the p-value threshold for upregulated gene ontologies. The four biological processes that did meet the threshold involved endosomal and protein transport, and mitochondrion organisation. In pateamine A-treated HL60 cells, downregulated gene ontologies included overall and mitotic cell cycle processes, and organisation of chromatin and spindles.

source	term name	adjusted p-value	term size	intersection size
GO:BP	endosomal transport	1.58E-04	244	31
GO:BP	intracellular protein transport	3.84E-04	995	78
GO:BP	mitochondrion organization	2.51E-03	565	50
GO:BP	organelle localization	3.85E-02	657	52

Table 4.14: Biological processes (BP) and molecular functions (MF) upregulated in HL60 cells in response to pateamiine A treatment. The table shows the four most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix M.

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitotic cell cycle process	2.35E-10	956	55
GO:BP	regulation of cell cycle process	4.59E-09	815	48
GO:BP	chromatin organization	1.68E-05	839	42
GO:BP	DNA metabolic process	1.97E-05	976	46
GO:BP	spindle organization	3.95E-05	256	21
GO:BP	cell cycle phase transition	5.48E-05	681	36
GO:BP	regulation of cell cycle phase transition	9.75E-05	543	31
GO:BP	mitotic nuclear division	9.76E-05	346	24
GO:BP	mitotic cell cycle phase transition	1.77E-04	588	32
GO:BP	mitotic sister chromatid segregation	1.78E-04	185	17

Table 4.15: Biological processes (BP) and molecular functions (MF) downregulated in HL60 cells in response to pateamine A treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix N.

4.2.3.2 LN18 Cell Line

In LN18 cells, upregulated pathways upon pateamine A treatment included non-coding and small nuclear RNA transcription, and capping processes

of RNA and mRNA. Downregulated pathways in response to pateamine A treatment of LN18 cells include cell division and related chromatid segregation pathways.

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitochondrion organization	2.26E-09	565	72
GO:BP	ncRNA transcription	6.39E-07	110	25
GO:BP	endosomal transport	6.73E-07	244	39
GO:BP	snRNA transcription by RNA polymerase II	1.16E-06	73	20
GO:BP	snRNA transcription	1.51E-06	74	20
GO:BP	intracellular protein transport	3.86E-06	995	96
GO:BP	7-methylguanosine mRNA capping	9.35E-06	33	13
GO:BP	RNA capping	1.44E-05	34	13
GO:BP	7-methylguanosine RNA capping	1.44E-05	34	13
GO:BP	ncRNA processing	1.19E-04	439	51

Table 4.16: Biological processes (BP) and molecular functions (MF) upregulated in LN18 cells in response to pateamine A treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix O.

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitotic nuclear division	2.19E-03	346	24
GO:BP	mRNA metabolic process	2.41E-03	880	43
GO:BP	cell division	1.13E-02	630	33
GO:BP	sister chromatid segregation	1.51E-02	214	17
GO:BP	mitotic sister chromatid segregation	4.18E-02	185	15

Table 4.17: Biological processes (BP) and molecular functions (MF) downregulated in LN18 cells in response to pateamine A treatment. The table shows the five most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix P.

4.2.3.3 U87 Cell Line

In pateamine A-treated U87 cells, mRNA and non-coding RNA metabolic processes and mitochondrial translation were upregulated. Overall translation was also upregulated. (m)RNA splicing and RNA processing were downregulated.

source	term name	adjusted p-value	term size	intersection size
GO:BP	ncRNA metabolic process	6.29E-06	535	52
GO:BP	mitochondrial gene expression	2.37E-05	166	25
GO:BP	mitochondrial translation	4.19E-05	135	22
GO:BP	ncRNA processing	4.39E-05	439	44
GO:BP	ribonucleoprotein complex biogenesis	5.25E-05	473	46
GO:BP	mitochondrion organization	1.03E-04	565	51
GO:BP	mRNA processing	2.64E-04	532	48
GO:BP	mRNA metabolic process	2.74E-04	880	68
GO:BP	peptide metabolic process	7.89E-04	998	73
GO:BP	translation	1.10E-03	804	62

Table 4.18: Biological processes (BP) and molecular functions (MF) upregulated in U87 cells in response to pateamine A treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix Q.

source	term name	adjusted p-value	term size	intersection size
GO:BP	mRNA processing	5.51E-04	532	26
GO:MF	nucleosomal DNA binding	8.81E-04	39	7
GO:BP	RNA splicing	1.83E-03	459	23
GO:BP	mRNA metabolic process	1.90E-03	880	34
GO:BP	organelle localization	2.93E-03	657	28
GO:BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	8.08E-03	360	19
GO:BP	mRNA splicing, via spliceosome	8.08E-03	360	19
GO:BP	RNA splicing, via transesterification reactions	9.11E-03	363	19
GO:MF	chromatin DNA binding	1.41E-02	103	9
GO:BP	ncRNA processing	3.95E-02	439	20

Table 4.19: Biological processes (BP) and molecular functions (MF) downregulated in U87 cells in response to pateamine A treatment. The table shows the ten most enriched BP and MF terms from gene ontology enrichment analysis, ranked by adjusted p-value. The total number of genes annotated to the term (term size) and the number of identified proteins associated with the ontological term (intersection size) are also shown. See Appendix R.

Chapter 5

Discussion

5.1 Selection of Cell Lines and Culturing

The selection of suitable cell lines was based on those available in cryostorage, and previous experiments in the lab group. All cell lines were grown with the same media (RPMI 1640), with variations on FBS concentration as required for optimal growth conditions.

HL60 was used as the control cell line. It is a cell line with an excellent growth profile, highly sensitive to both cycloheximide and pateamine A, and simple media conditions allowing for rapid passages. Its passage times matched with the glioblastoma cell lines, allowing for comparable experimental time frames to be used. HL60 cells required slight modifications to the glioblastoma media, namely a higher FBS concentration to maintain optimum growth, and the addition of GlutaMax (see Section 3.3.2).

The two glioblastoma cell lines, LN18 and U87, had identical media conditions and comparable growth profiles (see Section 3.3.1). As adherent cell lines, these required extra steps in the protocol to allow for adhesion,

and it was found that a 12-16 hour incubation yielded good seed density pre-treatment with minimal growth exhibited. While the U87 cell line took longer to recover post-thaw — about 1.5 weeks compared to 1 week for LN18 — the growth profile thereafter was suitable for meeting the seeding requirements for treatment flasks and allowed for comparable passage numbers post-thaw between the glioblastoma cell lines.

Excepting one incident with contaminated FBS and new media, no cross-contamination was observed. This caused a two-week delay to allow the thawing and recovery of new cells, from the same original freeze batches. "New" cells exhibited identical growth profiles and drug susceptibility to previous flasks.

5.2 Drugs, Treatments, and Times

One limitation in these experiments is that it was assumed that the small amount of DMSO in media, used to solubilise cycloheximide and pateamine A, had minimal effects on the changes in the proteome. The control flasks were not treated with the same volume of DMSO; however, previous research within the group indicated that limiting overall DMSO concentration to 0.1% prevented any significant effects on cell proliferation and morphology [15].

5.2.1 Positive Control: Cycloheximide

Cycloheximide was the first translational inhibitor of the glutarimide class to be discovered, and has been regularly used for translation inhibition

studies [29]. The selection of a suitable positive control for pateamine A was driven by a few key considerations. First, the control drug should primarily and strongly inhibit translation, to minimise other effects on the proteome, and via a different mechanism than the test drug pateamine A. It should have good cellular uptake and potent effects, which should have been previously studied. It should also be soluble in DMSO, as for pateamine A, to ensure solvent effects (discussed below) are comparable. Conveniently, cycloheximide both meets these requirements, and is commercially available in powdered form.

5.2.2 Drug Concentrations

Cycloheximide and pateamine A were dissolved to the requisite IC_{50} concentration in sufficient DMSO to yield a final DMSO concentration of 0.1% v/v. Neither cycloheximide nor pateamine A failed to dissolve at the requisite concentrations, indicating sufficient solubility.

The selection of drug ranges for the MTT assay was based on previous assays within the group [15, 17]. Repeating the MTT assays for each cell line prior to experimentation was necessary, as cells with different origins, thaw history, and growth conditions can exhibit altered growth and response to drug treatment. Some difficulty was experienced early in the experimental work in balancing seeding requirements and selecting appropriate drug dilution series. No significant variation in the coefficient of determination of the MTT curves was observed.

5.2.3 Duration of Experiments

Of key concern in developing the protocols for these experiments was duration of treatment — overgrowth occurred in no-treatment flasks three days after passages in preliminary experiments across all cell lines. The duration of treatment should match, in no-, cycloheximide-, and pateamine A-treated flasks, but should not be less than a doubling time for the cell line. In shortening MTT duration to two days at the desired seeding concentration with cycloheximide, a decrease in cell growth could be visually observed under the microscope, and compared to pre-treatment wells.

It should also be noted that passage counts were kept comparable across cell lines and between biological replicates in order to minimise variation in cell quality and accumulation of mutations.

5.2.4 Wells vs Flasks

It was observed that adherent cell lines (LN18 and U87) produced different seeding densities in 96-well plates compared to T75 flasks, even when cell concentration was the same. In principle, concentration-per-volume compared to available surface area differed, and as a result, wells seeded at 2×10^5 cells/mL formed a lawn within a 24-hour period. This could lead to variations in drug and MTT uptake, and overabundance of cells produced intense spectrophotometric signals, which were impenetrable for data analysis. It was thus of interest to consider seed density as a product of surface area:volume ratio and concentration-per-volume in respect to T75 flasks and 96-well plates. It was found that seeding concentration in a well of 1×10^4 cells/mL in a 96-well plate yielded comparable post-adhesion

seed density to a T75 flask seeded at 2 x 10^5 cells/mL. In both cases, half the media was removed prior to pharmacological treatment with drugged media.

This was not a consideration in the case of the HL60 control cell line, as seeding of a suspension cell line is not affected by available surface area.

5.3 Whole Proteome Preparation

The use of trypsin to digest protein samples prior to purifications, while convenient, may not necessarily have been consistent across samples. First: early experiments had exceedingly poor protein and peptide yields post-purification, and the weight ratio of trypsin to protein was doubled accordingly. The protein assay used was highly sensitive to timely spectrophotometric reading and, at times, the control wells could markedly differ due to lack of adequate mixing. The results of this assay directly informed the trypsin weight concentration applied to the sample. Third, trypsin stocks for protein digestion was, at times, severely restricted due to shipping delays as a result of the COVID-19 pandemic. When this occurred, the original weight ratio of trypsin (1:50) to protein was used, as by this time, familiarity with the protocol and its execution had significantly improved protein and peptide yields.

5.4 Statistical Decisions and Limitations

5.4.1 Proteome Discoverer

Proteome Discoverer includes a range of options for raw data processing, which has significant impact on the stringency and breadth of the results. Should the conditions be too restrictive, very few hits would be obtained, and too broad would increase false hits. A survey of hits and their quality was carried out on control and cycloheximide raw data of all cell lines when analysed with the protocol outlined in Section 3.7.3, and with the addition of dynamic modifications (max 2 each) of amide deamidation and methionine oxidation. The extra modifications decreased both the amount of identified proteins and the confidence profile in all samples, and so they were not carried through to the quantitative comparison step. The purpose of this step was to ensure that all biological replicates had reasonable hits to be included in the quantitative comparison between treatments. One biological replicate of the LN18 control cell line was of exceedingly poor quality, so was excluded from further analysis. However, Proteome Discoverer required an equal number of samples between treatment groups, so the sample with the least protein hits was excluded from the treatment it was compared against, yielding triplicate data (rather than quadruplicate in the intracellular comparisons of the HL60 and U87 cell lines).

5.4.2 Adjusted p-values and Significance

The use of p-values for indicating statistical significance is widespread — if erroneously so — in many fields of research. A p-value of less than 0.05 is

commonly accepted as sufficient to indicate the finding to be 'statistically significant' [45, 46]. In the case of repeat testing, a correction is applied, such as a Bonferroni correction, to account for multiple statistical tests on the same data [47]. Over time, a 5% threshold has become standard for determining the significance of a statistical change [46]. Other propositions have been made for 'better' statistical measures of significance, but little effort has been made to move away from the entrenched and convenient norm [45].

In the case of Proteome Discoverer, the adjusted p-value reported in quantitative analysis is found using ANOVA. The identification of each protein is assigned a p-value, and in the case of quantitative comparisons between control and drugged replicates, an adjusted p-value is reported. This adjusted p-value is a product of both confidence in the protein's identification (from peptide fragment identification), and the presence (or absence) of that same protein across all the samples.

The lists of up- and downregulated proteins identified in Proteome Discoverer for each control vs drug comparison are then loaded into g:Profiler. g:Profiler reports an adjusted p-value, which indicates the confidence of the gene ontology assignations — also referred to as terms. These terms were sorted by adjusted p-value to reflect the likelihood of the genes associated with the term being up- or downregulated. Often, only a small proportion of all genes that comprise a term were identified as having been altered. This could be for two reasons. First, the gene was not expressed, lost in extraction, or undetectable in the mass spectrometer. Second, the gene may not have met the statistical constraints — adjusted p-value in identification and fold-change quantification, or two-fold change in expression threshold,

or met thresholds for gene ontology enrichment processes. It should also be noted that many genes within the same term could be oppositely affected, as terms of increasing size and breadth necessarily encompass a broader range of genes. It thus becomes necessary to investigate the specific genes identified in each up- or downregulated list to investigate which particular pathways and genes within the term are affected.

5.4.3 Justification for the Top Ten Tables

The use of top ten tables of Biological Process and Molecular Function gene ontology terms presented in the Results chapter (Tables 4.2 to 4.19) was based on the assumption that the smaller the adjusted p-value, the more confident in the observed term's effects on the cell line. The term size and observed size were shown to indicate the relative coverage of the genes identified, and the overall breadth of the term. Translation, for example, occurs in multiple tables, but includes 804 genes (Tables 4.9, 4.10, 4.13, and 4.18). It should also be noted that up- and downregulated genes within a term differ, and therefore result in the same term appearing in both up- and downregulated tables, as different processes within the term may be affected in opposite ways.

In limiting the terms to Biological Process and Molecular Function, it was possible to examine alterations in the proteomic response as a result of drug treatment. This naturally limits the field of view to alterations in cellular processes and functional pathways affected. This is preferable to the inclusion of, for example, Cell Component gene ontologies, which would show which locales and cell contents are altered, not whether their activity

has changed. It should also be noted that a strict adherence to inclusion based wholly on adjusted p-value did, in some tables, eliminate one or the other ontology category, where the ten lowest adjusted p-values of, for example, Biological Process, excluded the presentation of the other (Molecular Function) in the top ten table, such as in Table 4.16. Full tables of Biological Process and Molecular Function terms can be found in Appendices A to R.

5.4.4 Using UpSet Plots

Gene ontology analysis generates a list of terms ranked by increasing adjusted p-value, and shows the genes contributing to the identification of the term. If we consider a simple example of three terms, with genes contributing to one, two, or all three terms, the number of gene intersects can be identified. This can then be plotted on a bar chart with an abacus-like matrix beneath to represent the contributing terms. The trends revealed in this plot, termed an UpSet plot, identify how many genes contribute to multiple terms [44]. It was also possible to identify the exact genes in each exclusive intersection set (see Section 3.7.3.2).

For the remainder of the discussion, UpSet plots are used to depict the intersectionality of up- and down-regulated top ten term lists from Tables 4.8 to 4.19. Black dots indicate which terms are applicable in each overlapping set. The upper inset depicts confidence by -$\log_{10}$ adjusted p-value. The lower inset depicts the number of genes found that contribute to each term, and is annotated by the total number of genes in each term. Both insets retain the same term name order as in the bottom left of the plot. Limiting by adjusted p-value is a convenient way of limiting the potential

number of intersections (maximum 2^n-1) to avoid noisy plots. It should be noted that genes being present in more than one term does not mean they are twice as influential; rather, it can show a group of genes that contribute to multiple ontological terms. An UpSet plot of each drug treatment by up- and downregulated gene lists in each cell line is also presented to enable a discussion of particular gene responses — not terms — across cell lines and their effects.

5.5 Notable Features

This section deals with some notable features found in individual cell lines and treatments, which are not able to be commented on as pateamine A-specific effects.

5.5.1 A Comment on Cell Line Comparisons

During early data processing, it was decided to directly compare the control cell line samples, with the intent of better understanding the differences between cell lines. As such, HL60 was compared to each glioblastoma cell line, and LN18 to U87, the results of which are presented in Tables 4.2 to 4.7, and Appendices A to F.

With HL60 as the control, upregulated processes in glioblastoma include those related to adherence, actin structure, and cadherin binding. The majority of terms identified as up- or downregulated in each cell line comparison were also found in the other cell line, or were included in subsets of other terms, thus concluding both glioblastoma cell lines selected

had similar differences in Molecular Function and Biological Process terms when compared to HL60. This was expected due to underlying differences between glioblastoma (brain cancer, adherent) and leukaemia (blood cancer, suspension) cell lines.

When comparing LN18 to U87 (Tables 4.6 and 4.7), upregulated terms involved those relating to RNA processing and protein transport, and downregulated terms were fairly broad and with high p-values. While this highlights the presence of underlying gene ontology differences between the two glioblastoma cell lines, an in-depth proteomic characterisation and comparison of untreated samples is not the goal of this thesis. For an overview of mRNA profiling of commonly used cell lines, see [36, 38] ; for a meta-analysis of recent proteomic research on glioblastoma see [39].

5.5.2 A Note on Treating the U87 Cell Line with Fresh Cycloheximide

In repeated MTT assays on the U87 cell line, an increased survival was found at approximately 0.64 μM cycloheximide concentrations. When the experiment was repeated by another member of the lab group, Emma Woods, using a four-day-old cycloheximide stock, this feature disappeared. The increased survival at 0.64 μM cycloheximide concentration was not observed in any other cell line.

While this particular assay presented in Figure 4.3 has a diminished R^2 value when compared to the other assays, the IC_{50} value was not significantly altered when this point was removed from the analysis. It remains to be seen what U87-specific, time-specific, and cycloheximide-specific ef-

fects are at play to result in the increased survival rate at the elevated drug concentration. This is not considered in the present work in the interests of time and scope.

5.6 Differences in eIF4A vs Translation Inhibition

This section presents intracellular comparisons between cycloheximide and pateamine A treatment. A brief overview of the gene ontology terms is provided, followed by a discussion on the distribution of terms associated with them.

5.6.1 HL60

The gene ontology terms found to be upregulated in the cycloheximide-treated HL60 cell line were primarily those related to cell cycle processes and protein catabolism (Figure 5.1); downregulated processes included terms related to energy metabolism and ribosome formation and processing (Figure 5.2). Where HL60 cells were treated with pateamine A, few localisation terms were upregulated (Figure 5.3), but cell cycle processes, especially those related to spindle regulation, and mitotic processes were downregulated (Figure 5.4).

Translational inhibition caused increased expression of genes associated with ontologies in the top ten list. When represented in an UpSet plot (Figure 5.1), it can be seen that the many genes are represented in two or more of upregulated terms relating to regulation and (mitotic) cell cycle,

which is consistent with the role of cycloheximide as a translation inhibitor and its interactions with checkpoint activations [48]. In the case of eIF4A-inhibited cells (pateamine A-treated), the majority of genes listed within each set are not found in any other set (Figure 5.3). This is a product of fewer significant sets being identified by the gene ontology investigation.

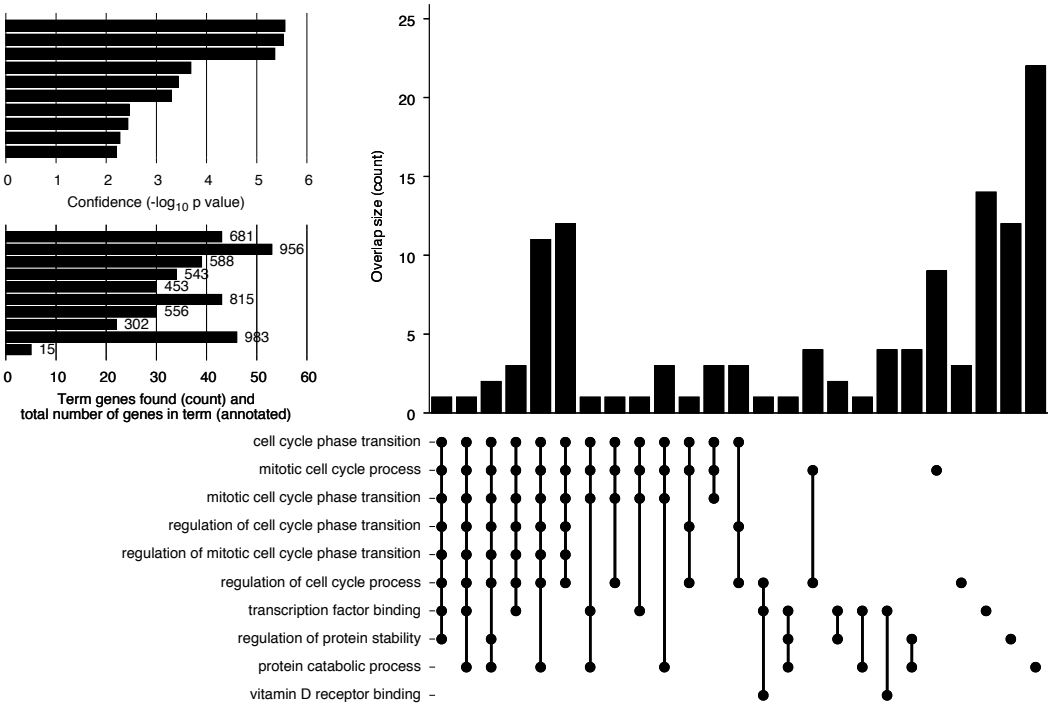

Figure 5.1: Upset plot shows the number of genes upregulated in the HL60 cell line in response to cycloheximide treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

Downregulated terms in response to cycloheximide treatment include gene overlaps in ribosomal and rRNA-related terms (Figure 5.2). In com-

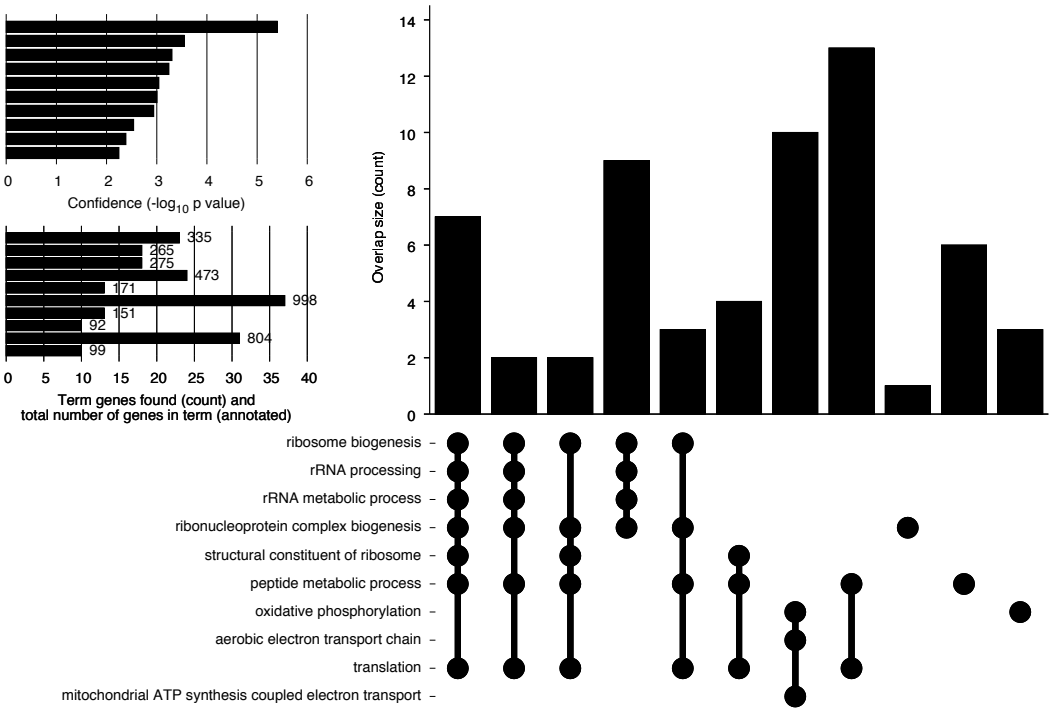

Figure 5.2: Upset plot shows the number of genes downregulated in the HL60 cell line in response to cycloheximide treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

parison, those downregulated terms from pateamine A treatment consist of significantly more numerous, but smaller, overlaps in genes within terms, and two terms, chromatin organization and DNA metabolic process, which had almost half the included genes within the set being independent to them (Figure 5.4).

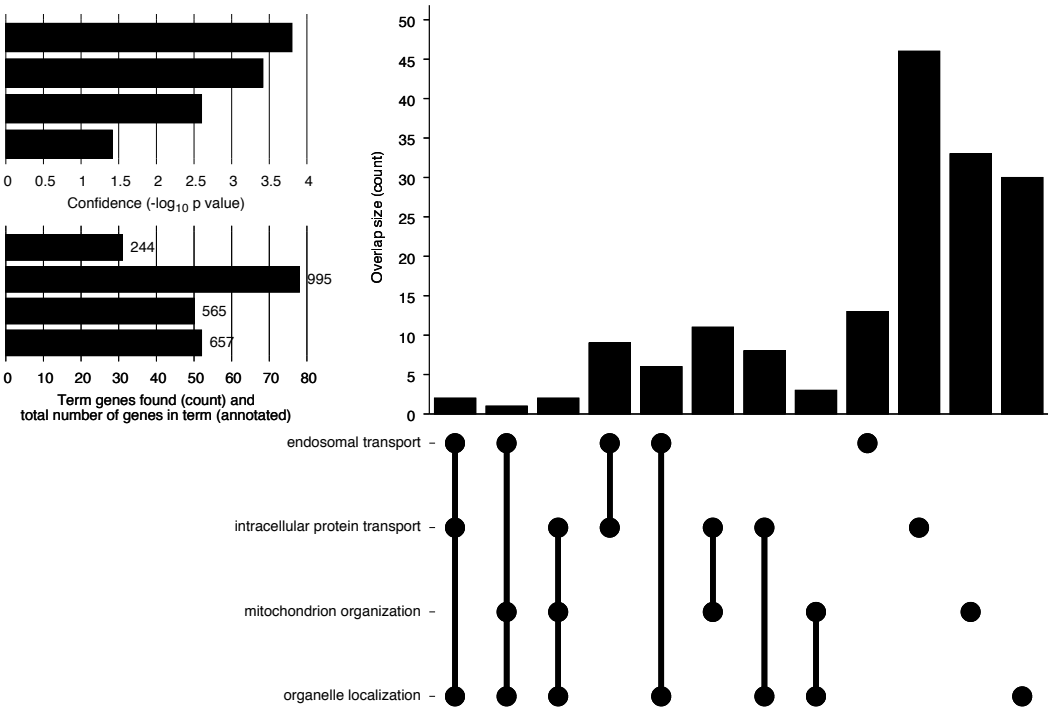

Figure 5.3: Upset plot shows the number of genes upregulated in the HL60 cell line in response to pateamine A treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

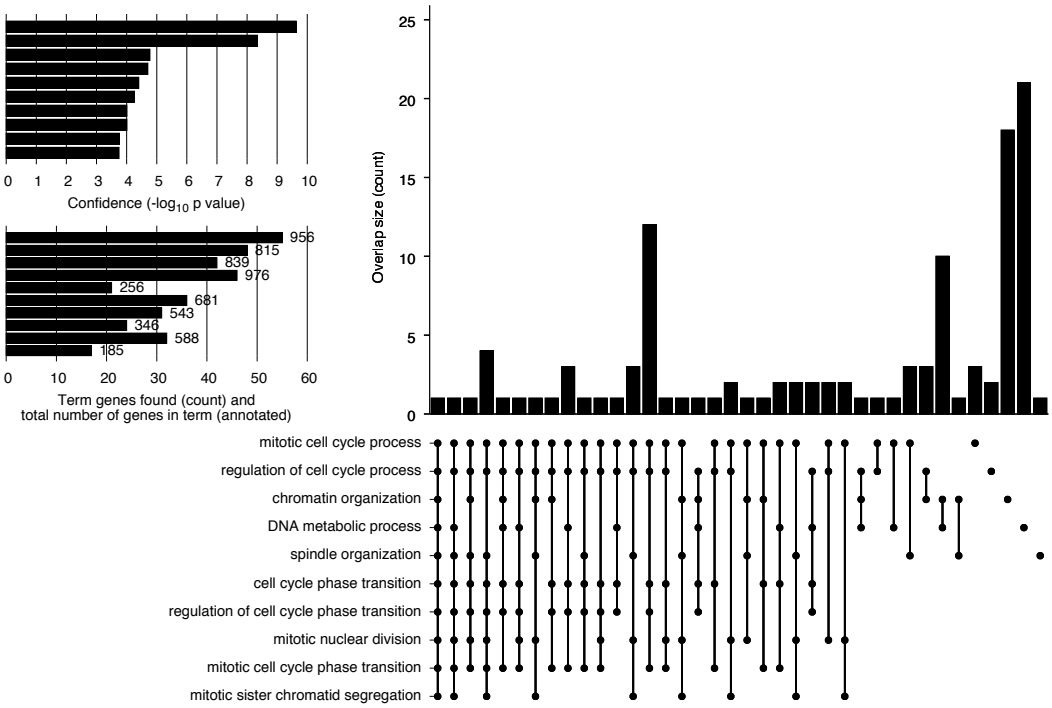

Figure 5.4: Upset plot shows the number of genes downregulated in the HL60 cell line in response to pateamine treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

5.6.2 LN18

Cycloheximide-treated LN18 cells exhibited upregulated translation and associated terms (Figure 5.5), while downregulated terms included RNA splicing and binding terms (cadherin, phosphatase, actin) (Figure 5.6). It should be noted that the upregulated gene ontology terms list had significantly more terms that met the adjusted p-value threshold than the downregulated list. Protein localization specifically was upregulated, with the genes associated with all the three localization terms in the top ten list for cycloheximide-treated LN18 cells being involved in ribosomal assembly and nucleopore protein expression (Figure 5.5).

The pateamine A-treated LN18 cells exhibited upregulated RNA modification and translation terms (Figure 5.7). Three highly similar terms relating to RNA capping were present in the top ten list for upregulated terms from pateamine A treated LN18 cells. (7-methylguanosine (m))RNA capping-related terms likely reached extremely low adjusted p-values as a product of each containing only 33 or 34 genes associated with them, of which 13 genes were identified in the sample. These included genes responsible for seven ribosomal subunits (POLR2C, POLR2E, POLR2F, POLR2G, POLR2H, POLR2I, POLR2J), which are subunits of RNA polymerase II that are involved in core transcription and capping processes [49]. Downregulated terms included division and chromatid segregation (Figure 5.8).

Few of the genes contributing to upregulated terms cycloheximide-treated samples were the same as those found in the pateamine A treated samples. However, those that did were involved in translational processes. When subunits, especially of larger proteins, are considered, the change

in expression in different subunits may not have met p-value thresholds in enough replicates to be present in both drug-treatment lists after gene ontology analysis. When gene overlaps in the top ten terms are considered in UpSet plots, cycloheximide treatment of the LN18 cell line found the most intersections between translation-related terms and protein transport terms, while the pateamine A treatment list was too short to determine useful gene overlaps.

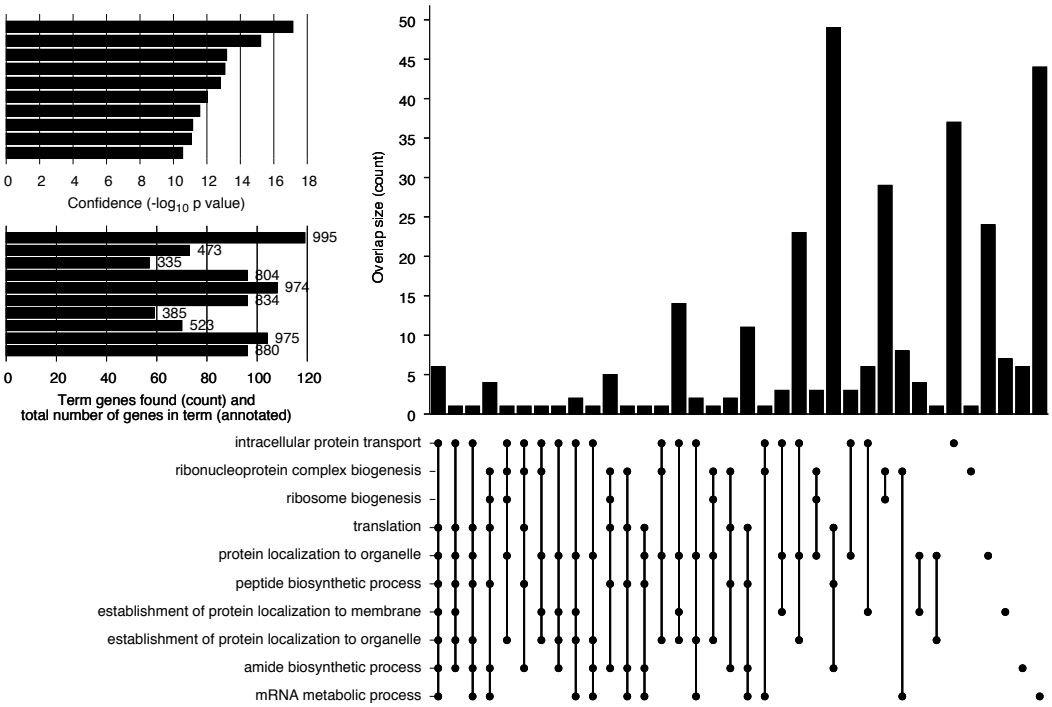

Figure 5.5: Upset plot shows the number of genes upregulated in the LN18 cell line in response to cycloheximide treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

Downregulated genes present in cycloheximide- and pateamine A-treated LN18 cells included some splicing factors, discussed in Section 5.7.2. It should be noted that the downregulated pateamine A gene list was less than half the length of that from the cycloheximide treatment, so this likely contributed to fewer gene ontology terms being identified.

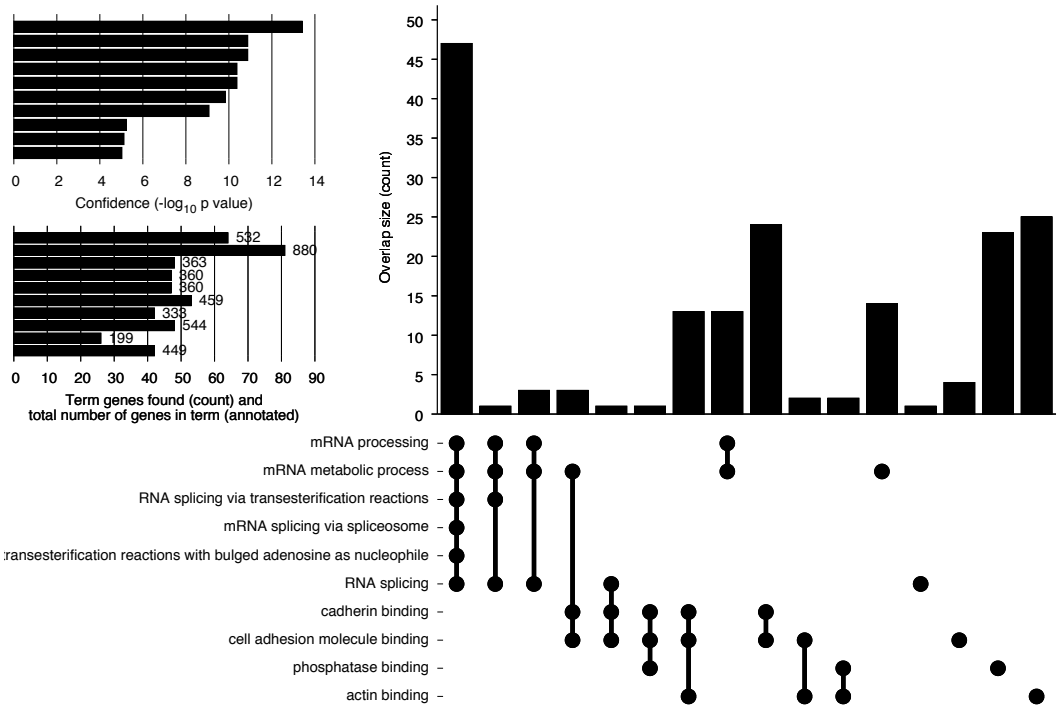

Figure 5.6: Upset plot shows the number of genes downregulated in the LN18 cell line in response to cycloheximide treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

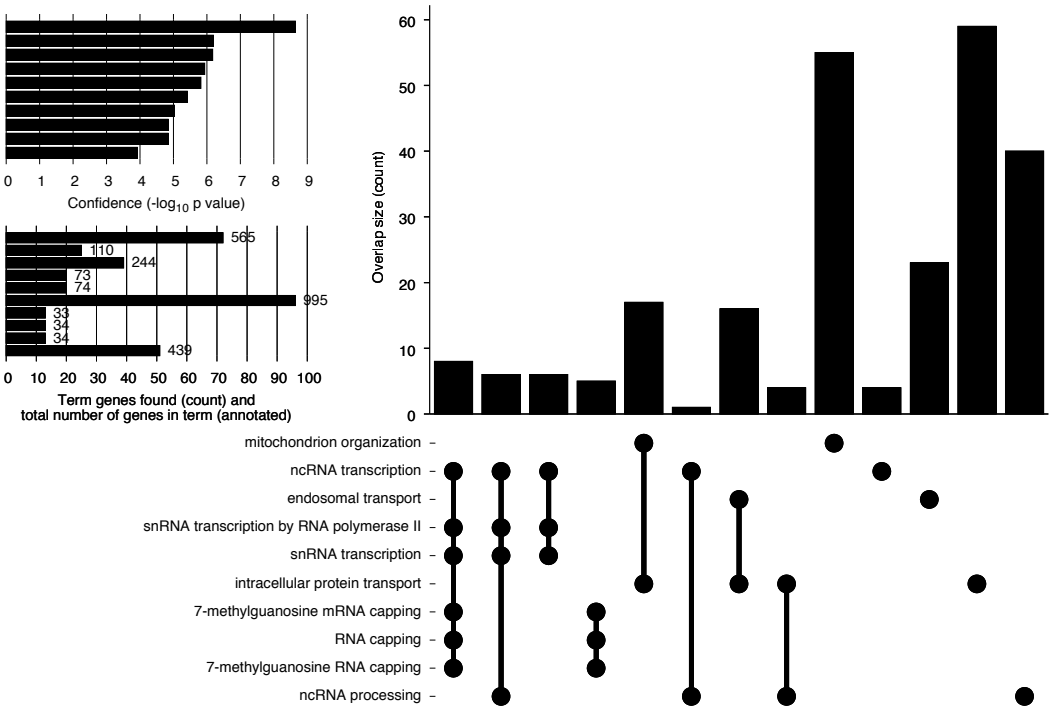

Figure 5.7: Upset plot shows the number of genes upregulated in the LN18 cell line in response to pateamine A treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

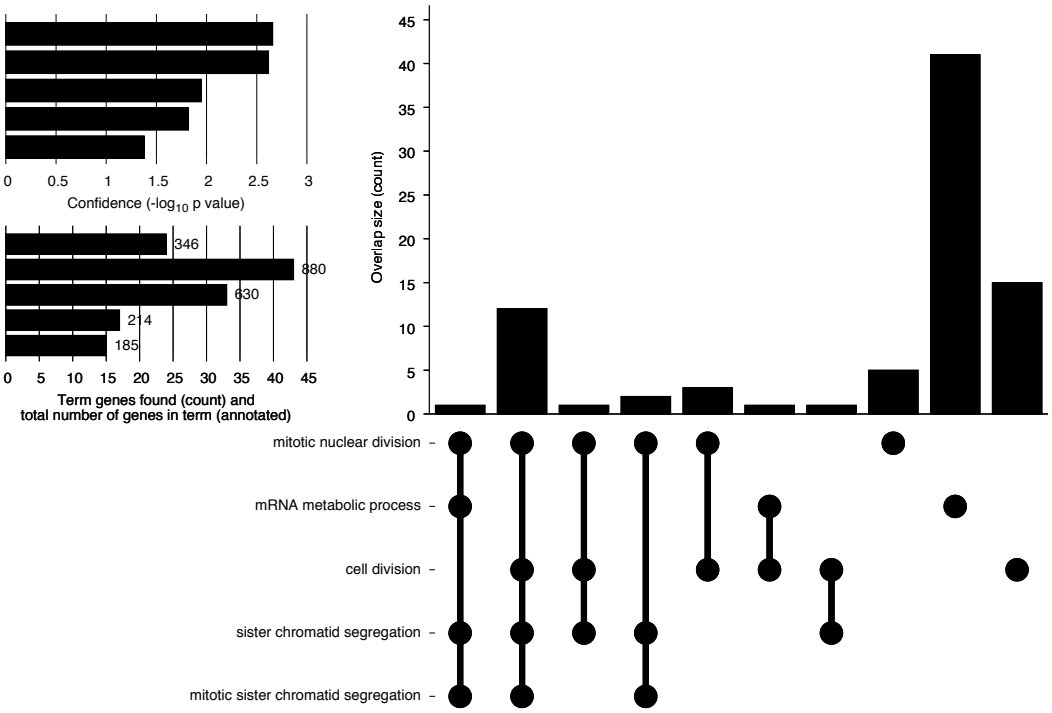

Figure 5.8: Upset plot shows the number of genes downregulated in the LN18 cell line in response to pateamine A treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

5.6.3 U87

For cycloheximide-treated U87 cells, translation and gene expression was upregulated (Figure 5.9), and an assortment of catabolic processes were downregulated (Figure 5.10). This cell line, when treated with pateamine A, exhibited significant overlap in terms identified as both up- and down-regulated (Figure 5.11 and 5.12).

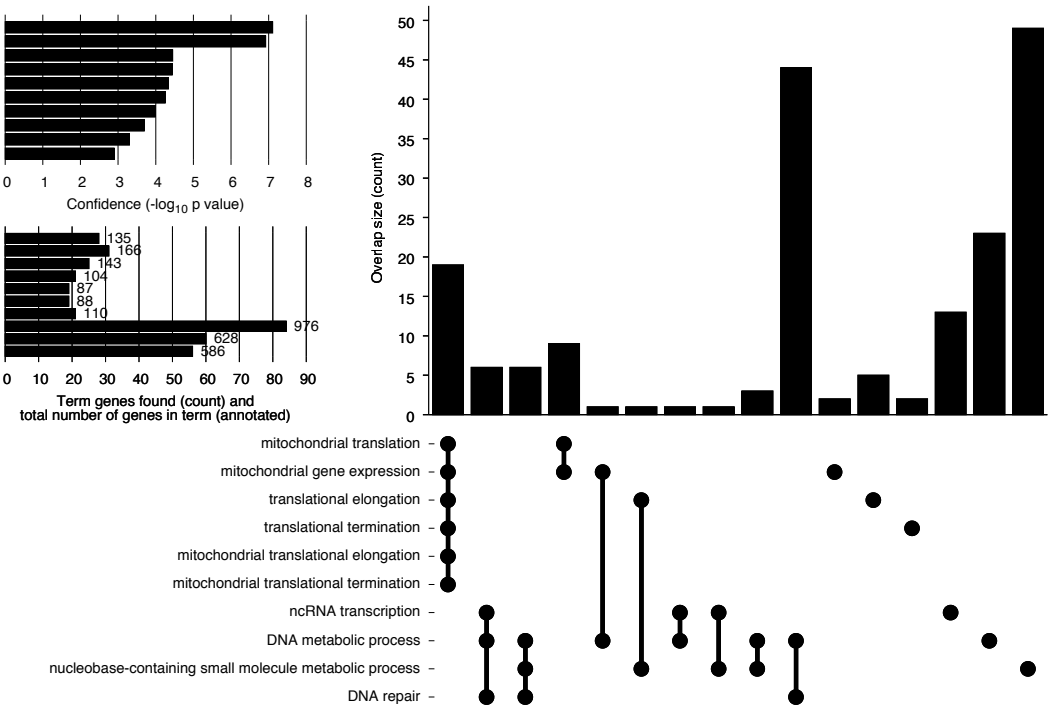

Figure 5.9: Upset plot shows the number of genes upregulated in the U87 cell line in response to cycloheximide treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

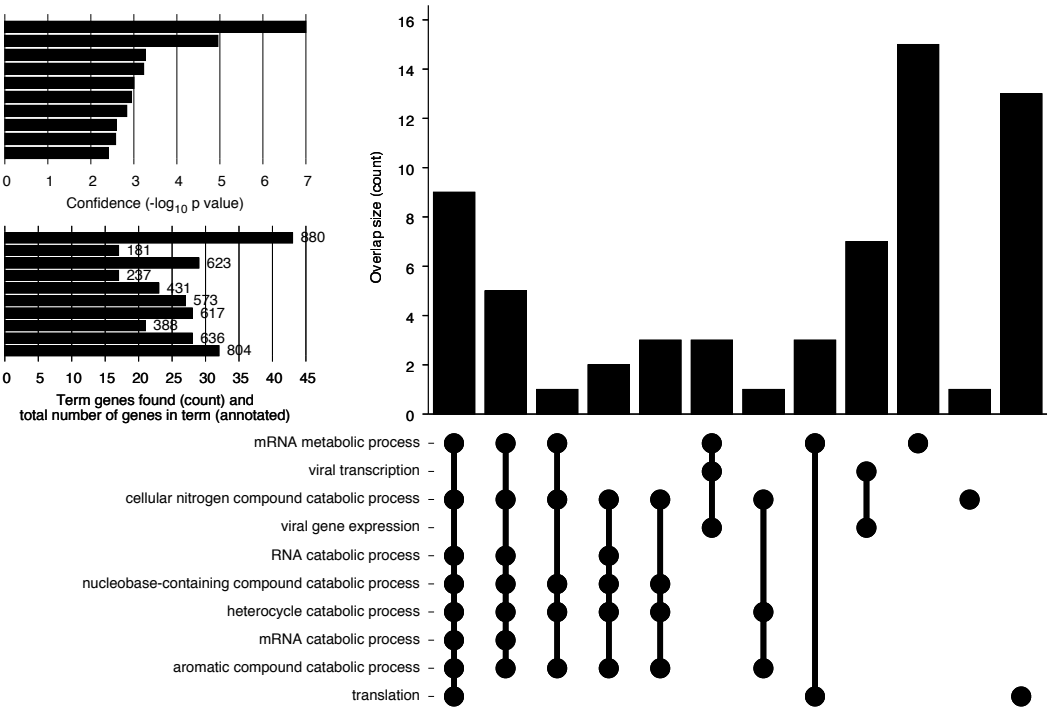

Figure 5.10: Upset plot shows the number of genes downregulated in the U87 cell line in response to cycloheximide treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

For genes that were upregulated in response to cycloheximide treatment, U87 cells exhibited high degrees of overlap of genes within translation terms and in DNA repair terms, which significantly outnumbers all exclusive genes in each term with the exception of nucleobase-containing small molecule processes (Figure 5.9). This indicates two effects of cycloheximide treatment — inhibition of translation, as expected, and inhibition of DNA repair, causing increased need for DNA repair. Cycloheximide has also been implicated in inhibiting DNA crosslinks [50]. When investigating

downregulated cycloheximide-treated U87 gene lists, many of the same genes contribute to different terms (compare Figure 5.9 with Figure 5.10). Both metabolic and catabolic processes related to RNA and its related compounds exhibited significant overlaps, but it should be noted that the sum of genes in each term was significantly less than in other plots.

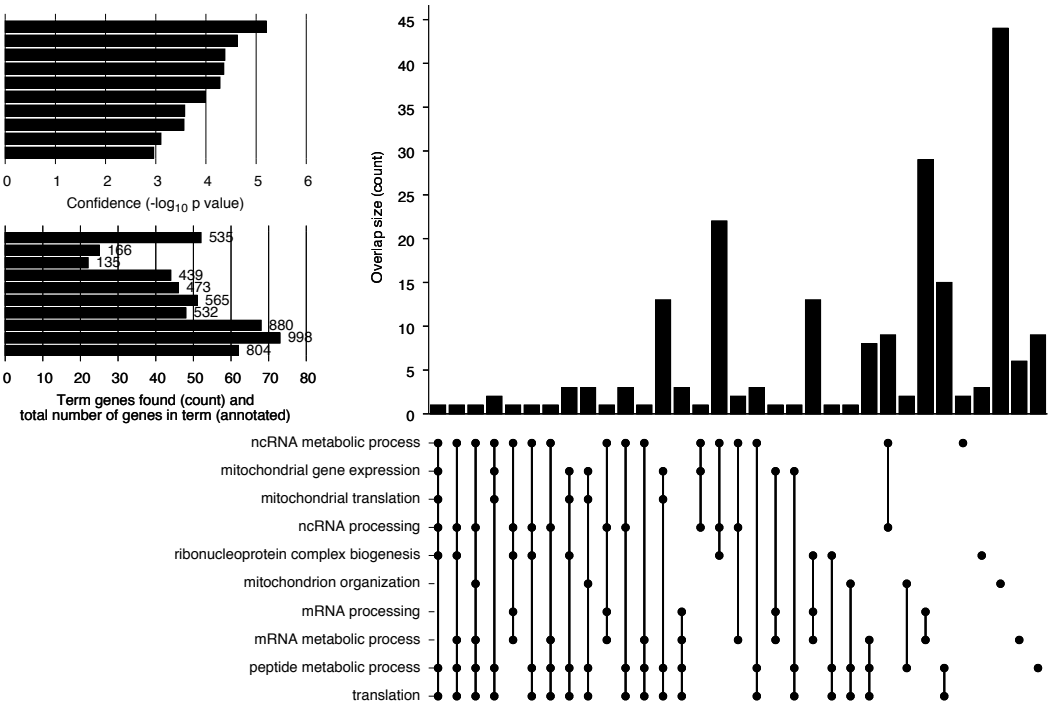

Figure 5.11: Upset plot shows the number of genes upregulated in the U87 cell line in response to pateamine A treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

When treated with pateamine A, U87 cells exhibited significant overlap in terms identified as both up- and downregulated. This can be evidenced in an example term: the biological process term 'mRNA processing' (532

terms) is the seventh upregulated term by adjusted p-value (2.64E-04), including 48 genes. The same term is the most downregulated term by adjusted p-value (5.51E-04), including 26 genes. No gene is found in both sets, indicating the importance of investigating genes in terms identified as up- and downregulated in the same treatment and cell line. This topic is continued in Section 5.7.1.

In pateamine A-treated U87 cells, the top ten terms relate to mitochondrial gene expression and RNA processing. These split into many small overlap sets when considering the genes present in the different terms, with particularly large intersects of non-coding RNA-related terms and mRNA terms. Comparable mRNA terms were also found in the downregulated tables.

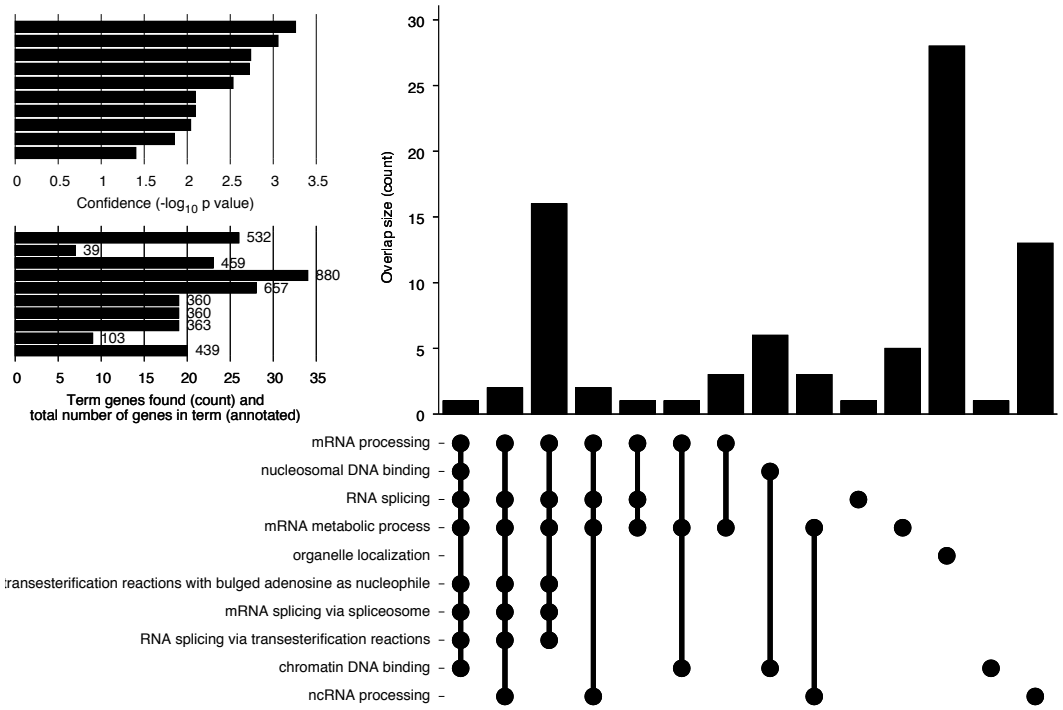

Figure 5.12: Upset plot shows the number of genes downregulated in the U87 cell line in response to pateamine A treatment by exclusive intersection lists identified from the top ten GO:BP/MF terms, given in bottom left. The top inset shows -$\log_{10}$ adjusted p-value, and the lower inset the number of genes found in each term and is annotated by with the sum number of genes.

5.7 Effect of Pateamine A Treatment on Glioblastoma

This section discusses the effects of pateamine A treatment both glioblastoma cell lines (LN18 and U87), but not in the HL60 control cells, with a brief comparison to effects found in cycloheximide treatment and those of the HL60 controls for context.

5.7.1 RNA Processing Alterations

A brief overview of the RNA processing gene ontology (Biological Process), and its situation compared to other RNA metabolic pathways, provides context for the following discussion. The majority of GO terms, in full lists and their top ten equivalents, were related to Biological Process. Nucleic acid metabolic process is divided into three terms — nucleic acid phosphodiester bond hydrolysis, DNA metabolic process and RNA metabolic process. Of primary focus in this section are the terms related to the latter, as these include RNA processing, mRNA metabolic process, and ncRNA metabolic process. These terms, and those that contribute to them, encompass many of the terms mentioned in this sections. Note that some terms are present under more than one parent term — ncRNA processing appears under both RNA processing and ncRNA metabolic process.

In the glioblastoma pateamine A tables (Tables 4.16 to 4.19), RNA processing and multiple related daughter terms were common in both up- and downregulated lists. RNA processing includes processes related to mitochondrial and non-coding RNA, mRNA, 5′- and 3′-end processing, capping, and splicing. Splicing is discussed in the following section; presently we will consider the other RNA processing terms.

In pateamine A-treated LN18 cells, seven terms relating to non-coding RNA and capping processes were in the top ten upregulated list (Table 4.16). Small non-coding RNA transcription (by RNA polymerase II) terms were identified from the same twenty genes, and the two non-coding RNA terms — ncRNA transcription and ncRNA processing — exhibited more overlap with terms by their respective processes (transcription and processing)

than each other. The particulars of the capping terms are discussed above in Section 5.6.2. When transcription processes are considered, the main genes associated with the upregulation across terms are integrator subunits (INTS1, INTS3, INTS5, INTS7, INTS11, INTS13, INTS14). The integrator complex is associated with the POLR2 C-terminal domain, and is critical in regulating snRNA U1 and U2 processing and their 3′-box-dependent processing. The remaining terms — mitochondrion organization, endosomal transport, and intracellular protein transport — exhibit few overlaps within the triad and the majority of each term remains independent of all other terms in the top ten list. As mentioned in Section 5.6.2, the downregulated LN18 list was exceedingly short, and the mRNA metabolic process term is not dependent on RNA processing.

In pateamine A-treated U87 cells, the top ten upregulated terms relating to RNA processes can be divided in by nucleic source — non-coding RNA and mRNA — with both metabolic process and processing being present for each. Other terms include (mitochondrial) translation and three mitochondrial terms — gene expression, translation and organization — as well as translation, ribonucleoprotein complex biogenesis. and peptide metabolic process. This generates a rather noisy UpSet plot (Figure 5.11), as a result of having highly similar terms deriving from having many genes that contribute to a smaller range of terms. The ncRNA processing genes, which are all found as part of the larger term ncRNA metabolic process, include INTS3 and INTS5, and three subunits of RNA polymerase elongator complex (ELP 1, 2, and 3). The same 100% overlap of identified genes found as part of mRNA processing are a full subset mRNA metabolic process. Of those genes, a number of genes related to overall RNA polymerase activity

— POLR2F, PPIE, PPIL1, PPIL3 — and specific mRNA processing genes, such as three core subunits of the snRNP spliceosome (SNRPD1, SNRPD2, SNRPF, SNRPG). The peptidyl propyl isomerase family, and its related -like cyclophilins, are involved in protein folding and splicing [51]. PPIL1 regulates pre-mRNA splicing, PPIL3 is implicating in RNA processing but not fully characterised, and PPIE is also involved in chromatin remodelling [51]. Of the downregulated top ten list, the largest gene overlap list is from mRNA splicing terms, mRNA processing, mRNA metabolic process, and RNA splicing, which includes the downregulation of two RNA polymerase subunits, POLR2C and POLR2D.

As has been alluded to in the above intracellular comparison between cycloheximide and pateamine A inhibition on all three cell lines (Section 5.6), translational inhibition, irrespective of its source, has implications for RNA processing. Cellular stress also leads translation of mRNA transcripts being relegated to stress granules, and these are exported from the cell should translation stall [52].

Inhibition of the elongation step of translation can be caused by a variety of natural products, with cycloheximide being the earliest identified compound and easily synthesised [30]. Like many eukaryotic protein synthesis inhibitors, cycloheximide has failed to deliver as an anticancer drug due to dose-limiting toxicity in mammals, but it remains a useful drug for cell culture studies [30, 29]. As such, the effects on RNA processing as a result of pateamine A treatment, from inhibiting overall translation, are expected.

Pateamine A's potent and exclusive inhibition of eIF4A activity, in both the eIF4F complex and as an unbound enzyme, has significant effect on RNA processing pathways. Previous research supports the identification of

(m/nc)RNA processes being altered in response to extremely low concentrations of pateamine A treatment [17]. As a product of inhibiting translation initiation, overall translation and associated processes must be perturbed by the cell in response to diminished eIF4A activity. It is implicit that these are most likely to impact subunits and factors involved in direct transcript processing. Moreover, many RNA-related processes — and the genes classified as within such terms — are also involved in other cellular pathways and their regulation. It appears that pateamine A inhibition of glioblastoma has particular effect on RNA polymerase subunits and other regulatory factors involved in different RNA-type-specific regulation. This may be especially pertinent as there is evidence that glioblastoma have increased RNA polymerase II-mediated transcription, across multiple sample types (patient-derived, differentiated, and neural stem cells) [53].

It should be noted that the 'baselines' for this section — two different glioblastoma cell lines — are already abnormal and exhibiting altered RNA processing pathways. Firstly, this was evidenced in the preliminary control HL60 to glioblastoma cell line comparison (Section 5.5.1). Second, the abnormality of cancer cells, and specifically glioblastoma, yields cells with alterations in critical pathways, with considerable changes to pathways involved in gene expression and translation — which is closely linked to RNA processing. In particular, glioblastoma-associated proteins have been correlated with altered signalling transduction modulators which have regulatory effects on RNA processes [54]. RNA binding proteins are differentially expressed in glioblastoma and other brain cancer samples, tending to more upregulation than downregulation [55, 56].

5.7.2 Effects on Splicing

RNA splicing is the process of excising introns from an mRNA strand to yield a mature transcript, and is commonly dysfunctional in cancer cells [57]. In clinical presentations of glioblastoma, mutations in splicing-related genes yield dysfunctional or aberrant splicing activity, contributing to malignancy [55]. One early iTRAQ and gene ontology analysis of U87 and U251 cell lines (both derived from glioblastoma) identified that the former exhibited perturbed RNA splicing and the latter did not [58]. Alterations in RNA splicing and related terms have been identified in a meta-analysis of fourteen proteomic studies [39].

Splicing terms (RNA splicing (via transesterification reactions (with bulged adenosine as the nucleophile) or via spliceosome)) are downregulated in pateamine A-treated U87 cells. Of the 23 genes contributing to these four terms, 19 are found in all four terms, one in the RNA splicing term only, and the remaining three also found in others of the top ten terms (Table 4.18 and 4.19, Appendices Q and R).

In pateamine A-treated LN18 cells, only five terms met the adjusted p-value level in the downregulated list, none of which directly included splicing as a term. However, three genes in this list matched those associated with splicing terms in the equivalent list relating to pateamine treatment of U87 cells — P98179 (RNA binding protein 3), Q14011 (cold-inducible RNA-binding protein), and Q9NZ63 (telomere length and silencing protein 1 homolog); the first two of which are implicated in cold and stress response.

While no splicing-related terms were upregulated in LN18 cells, U87 cells evidenced identical terms as those related to splicing in the both up-

and downregulated lists. Specifically, upregulated splicing genes in both LN18 and U87 samples related to ribonucleoprotein polypeptides (SNRPG, SNRPD3, SNRPD1), homologs associated with degradation (LSM1, LSM3, LSM8), and peptidylpropyl(-like) isomerases (PPIE, PPIL1, PPIL3).

This does not present a unified picture of the effects of pateamine A on RNA splicing on these two cell lines. On one hand, U87 cells downregulated splicing-related terms (based on lowest p-values across the two gene lists), but related proteins that bind and interact with splicing machinery were upregulated in LN18. Despite presenting a more convincing p-value, the downregulated genes were in fact associated with shock response and splicing inhibition. There was not an immediately obvious reason why there appeared to be both up- and downregulated lists being involved in splicing, as there appeared to be limited upregulation of proteins associated with promoting splicing. However, it is not inconceivable that splicing could be differentially affected by pateamine A treatment in LN18 and U87 cells, as glioblastoma present differently and have marked genomic alterations.

The question must be asked — is the U87 splicing response to pateamine A treatment glioblastoma or cell line specific? 18 of the 62 RNA-splicing-associated genes present in the relevant U87 gene lists were found the LN18 dataset, including LSM1 and 8, PPIE and PPIL1, and POLR2C. PPIE and PPIL1 were discussed above in Section 5.7.1. LSM proteins are involved in processing most RNA transcripts, and particularly in mediating U6 snRNP localisation [59]. Further research would be necessary to investigate any splicing-specific effects of pateamine A inhibition that may be witnessed across different glioblastoma cell lines, as a result of this heterogeneity.

mRNA splicing terms were upregulated in glioblastoma cell lines compared to normal brain cells across the studies contributing to a meta-analysis, with mRNA splicing via spliceosome the most common subset of this [39]. The implication is that glioblastoma have increased, and perturbed, splicing functionality. This engenders oncogenesis, and isoform variants have been implicated in disease prognosis [60, 61]. A study of U87 and U251 cell lines used comparable techniques to the present work, and corroborates mRNA splicing as upregulated in U87 cells [58]. There is also evidence that further perturbations in alternative splicing pathways are enriched in recurrent glioblastoma samples, and as such, therapies targeting alternative splicing are being explored as treatment options [62].

It is pertinent to note that eIF4A exists in the eIF4F complex, as described in the Introduction (Section 1.1), as a free and unbound helicase, and as eIF4AIII, with 65% homology to eIF4AI, which is involved in nonsense mediated decay [28, 63, 64]. Both cycloheximide and pateamine A inhibit nonsense mediated decay: the former by upregulating Upf1 phosphorylation, and the latter by stabilising the interaction of the exon junction complex with RNA. RNAi-based knockdown of eIF4AIII evidenced the protein's role in nuclear splicing and nonsense mediated decay, providing a link between inhibition of the helicase and its effect on splicing [65]. Pateamine A binds to eIF4A irrespective of isoform; the focus of this thesis on pateamine A's effect on protein synthesis as part of the eIF4F complex is based on prevalence [15, 17]. It is theorised that pateamine A:eIF4AIII interactions inhibit splicing, which contributes to the the presence of specific genes within the RNA splicing gene ontology term.

5.7.3 Energy and Glucose Metabolism

Glioblastoma exhibit abnormal energy metabolic processes, with diverse clinical presentations and range of mutations found in patient samples [34, 36]. This particularly affects glucose metabolism, which provides ATP [66]. IDH, TP53, EGFR, NF1 and PGFRA are used to subtype glioma and glioblastoma samples, with the first two being common across cancer types as they regulate critical oncogenic pathways [34]. The LN18 cell line has SNVs in BRCA2, ERCC2 and RB53 (DNA binding domain), while the U87 cell line has SNVs in NF1, hTERT promotor, and a frameshift in RAD50 [36]. There is evidence that yeast mutants which exhibit comparable eIF4A inhibition through gene deletions have different energy-related responses — in the *tif1*Δ strain, oxidative phosphorylation and ATP biosynthesis are upregulated, and in *tif*2Δ, energy production pathways are also downregulated [17].

When comparing each glioblastoma cell line to HL60, there are no gene ontology terms in the term lists of either cell line that directly link to energy metabolism. Based on ontology analysis, there are no significant perturbations in the energy metabolism of the cell, yet there is an absence of pateamine A interactions with proteins involved in energy-related pathways in all cell lines.

Considering mitochondrial-related terms in pateamine A-treated glioblastoma samples, the top ten lists are all related to mitochondrial genetic processes. In the longer tables, however, NADH-dehydrogenase and mitochondrial pathway-related terms appear, having been displaced due to higher adjusted p-values. In LN18 cells, mitochondrial respiratory chain

(1) complex assembly (adjusted p-value 6.40E-04 (5.25E-04)), mitochondrial electron transport of NADH to ubiquinone (1.02E-02), NADH dehydrogenase complex assembly (5.25E-04), NADH dehydrogenase activity (1.72E-03) and related terms (NADH ubiquinone (1.04E-03) and quinone (1.34E-03); NAD(P)H quinone (2.75E-03)) are upregulated (Appendix O). The upregulated genes in the NADH-related terms exhibit strong overlaps between terms and consist of the relevant oxidoreductase subunits involved in the particular process described by the term. In the list of upregulated terms in the U87 cell line, only the mitochondrial respiratory chain complex assembly (3.21E-02) term is found, with no NADH-related terms meeting the adjusted p-value threshold (Appendix Q). Half of the genes within the assembly term are NADH:ubiquinone oxidoreductase subunits, were also included in the LN18 NADH dehydrogenase complex assembly list.

For the downregulated terms, we again see no terms containing 'NADH' or 'mitochondrial' (except those related to translation and gene expression) in the LN18 and U87 downregulated top ten lists. The LN18 list (Table 4.17) numbers only five terms, none of which relate to energy metabolism. There are also no energy-related terms in the extended U87 list (Appendix R).

There were numerous NADH:ubiquinone dehydrogenase subunits that were upregulated in pateamine A-treated LN18 cells, and some were also evidenced in the U87 cell line. Ubiquinone is a reactive oxidant species that is present in membranes of the cell and mitochondria, primarily being involved in serially reduced forms in the electron transport chain [67].

Significant proportions of clinical and patient-derived glioblastoma contain mutations in genes related to pathways involved in energy metabolism, to which the malignancy of glioblastoma is attributed. In cancer cells, the

perturbation of energy pathways combined with dysfunction in regulatory pathways enables rapid cell growth [66]. The malignancy and aggressiveness of glioblastoma tumours is associated with aberrant energy dynamics, and so the decision was made to investigate this further than merely the top ten lists.

Pateamine A is a potent and exclusive eIF4A inhibitor, across the three isoforms, which appears to bind more strongly with mRNA transcripts with high G:C content and increased tertiary structure [68, 69]. There is no evidence that genes associated with energy metabolism should be particularly susceptible to pateamine A inhibition, based on the structure of their 5′ UTRs [17]. A link to energy metabolism via heightened tRNA loading has not been evidenced.

Whilst it was known that the selected cell lines were not IDH-mutant, there was nonetheless no significant alterations in energy pathways as a result of pateamine A treatment. It should also be noted that no energy or glucose metabolism-related terms were found either up- or downregulated in response to pateamine A treatment in the HL60 cell line. It appears that some subunits of NADH-related proteins may be affected in LN18 and U87 cell lines, but not of sufficiently low adjusted p-value to be of major interest.

5.7.4 Protein Transport

Alterations in protein transport is expected as a result of pateamine A treatment. In pateamine A-treated LN18 cells, upregulated transport processes include endosomal, intracellular protein, Golgi vesicle, and cytosolic transport terms (Table 4.16). When analysed via UpSet, these terms exhibit

significant overlap with the exception of intracellular protein transport, as a consequence of significantly more genes being identified from within this larger term. Notable groups of genes within these terms that were affected include NADH:ubiquinone dehydrogenase subunits (A9, A13, AB1, B4, B5, B7, B8, B9, B10, C2, S2, S4, S6 and S8) and RAS oncogenes (RAB10, RAB23, RAB35, RAB5A, RAB8B, and RAB9A). While the LN18 cell line evidenced particular upregulation of the transport pathways, no 'transport'-containing terms were upregulated in response to pateamine A treatment in the U87 cell line (Appendix O). However, 31 of the 160 'transport' genes from the LN18 terms were found in the U87 whole upregulated gene list, including three NADH:ubiquinone dehydrogenase subunits and three RAS oncogenes. This supports the possibility that pateamine A treatment of LN18 and U87 cells — and other glioblastoma cell lines — may exert effects on protein and intracellular transport. Neither cell line had any 'transport'-containing terms in the downregulated lists.

The HL60 cell line also exhibited upregulated 'endosomal transport' and 'intracellular protein transport' (Table 4.14), with downregulated 'protein localization to organelle' (Table 4.15). With higher adjusted p-values and larger term sizes than the LN18 and U87 cell line, there remains grounds to consider glioblastoma-specific effects on protein transport. KEGG mapping of miRNA and mRNA expression analysis indicated that patient-derived glioblastoma samples concur with the cell type's perturbed protein transport lists, with particular note that these alterations can be attributed to changes in moderators of upper-level signalling pathways [70]. Verhaak's definitive subtyping article recognised that many identified mutations affected higher-level cell growth pathways, and by extension, the regulation

of protein synthesis and transport [34]. In particular, it has been argued that particular changes in protein transport are focussed on mitochondrial transport, which was evidenced in both pateamine A-treated glioblastoma samples [36].

Whilst gene ontology analysis produced few terms relating to protein transport, this could be ascribed to the overall term size limitations that were set. The particular effect on ubiquinone dehydrogenase activity was a novel identification, and indicates the need for continued characterisation of pateamine A's effects. The precise interactions between the mRNA:eIF4A complex and pateamine A, and the consequences for transcripts, expression, and ensuing pathway effects are yet to be characterised. Evidence of upregulated protein transport processes was stronger for the LN18 cell line than the U87 cell line, but this is not unexpected given glioblastoma's heterogeneity.

5.7.5 Cell Proliferation

While RNA processing was altered in both cell lines, the increased cellular stress as a result of eIF4A inhibition yielded both ontological and visual changes in cell proliferation. Flasks treated with either pateamine A or cycloheximide, in all cell lines, had slower cell growth and lower overall protein yields than untreated controls. In the case of pateamine A treatments of the glioblastoma cell lines, specific alterations in chromatid segregation were found. In LN18 cells, mitotic nuclear division, cell division, and (mitotic) sister chromatid segregation terms were downregulated. Most of the genes identified in these terms code for regulators and and cofactors. In

U87 cells, DNA repair was upregulated, and nucleosomal DNA binding, chromatin/single-stranded DNA binding, and nucleosome binding were downregulated.

Cell proliferation is the physical consequence of a range of cellular processes working in concert to yield increased mitosis and growth. In the case of glioblastoma cells, this is easily witnessed through microscopy, where clumps of cells become larger more quickly under good growth conditions, and slower under poor conditions. In the case of pateamine A treatment, the gene ontology analysis suggests that downregulation of chromatid segregation, possibly as a result of alterations in chromatin binding, were key cellular processes that were affected as a consequence.

Inhibition of translation initiation using pateamine A inhibits cell proliferation, with diminished protein synthesis perturbing the balance and amount of proteins available for the cell, especially for division. The evidenced alterations in DNA management, particularly from DNA binding-related processes, indicates the consequences of translation initiation on nuclear processes. Inhibition of eIF4A using silvestrol sensitises T-47D breast cancer cells to radiotherapy, implying a relationship with DNA damage repair and related processes that engender resistance of radiotherapy [71]. As a rocaglate, silvestrol does not exclusively bind to eIF4A, and so the effects observed may be related to its role as an inhibitor of caspase-mediated apoptosis and anaerobic respiration [71].

It should be noted that shutdown of DNA synthesis has been evidenced in response to DMDA pateamine treatment in U937 lymphoma cells; however, these authors noted the inconsistency of the effect across cell lines [26]. Other disruptions in cell cycle processes due to DMDA pateamine were

also evidenced across a range of cancer cell lines, including melanomas, lymphomas, carcinomas, pancreatic, colon and breast cancers [26].

5.7.6 Comparing Back to HL60s

The use of HL60 as a control was primarily driven by convenience — previous work in the group had been based on this reliable, quick-growing cell line [15, 17]. This made experiments early in this research convenient and generally successful, as approximate values for cycloheximide and pateamine A IC_{50} from the MTT assay were already known. It would be valuable to compare the glioblastoma cell lines to non-cancerous glial cells, which would allow comparisons to be made against similar tissue types. As a leukaemia cell line, the use of HL60 for comparisons against the glioblastoma cell line can reveal glioblastoma-specific influences of both cycloheximide and pateamine A. This section focusses on the HL60 cell line response to pateamine A, and how this compares to the effects seen in glioblastoma discussed above.

The upregulated terms relate to transport — endosomal transport and intracellular protein transport — and organelle terms — mitochondrion organization and organelle localization. The alterations in the transport terms support a non-glioblastoma specific response to eIF4A inhibition where perturbations in the proteome of the cell result in adjusted post-folding processes.

The pateamine A-treated HL60 cell line had a far longer and more complex list of downregulated terms than up. When considering the top ten terms, the majority of terms related to cell cycle and its regulation. Down-

regulating mitotic division causes decreased cell proliferation, which, while empirically evidenced across all cell lines, was more supported in the gene ontologies of HL60 and U87 than in LN18. Other downregulated terms that meet the adjusted p-value threshold also include RNA processing terms, but none of these relate directly to splicing. The HL60 cell line's oncogenicity is not attributed to altered splicing activity as seen in glioblastoma cells.

The themes discussed in Section 5.7 were selected for one of two reasons: either preliminary work indicated certain pathways would be of interest to characterise further, or the data provided reason to investigate the theme further. When compared against HL60 cell line, it appears glioblastoma have similar alterations in RNA processing and protein transport. However, RNA splicing terms are not affected in the HL60 cell line, nor are terms related to energy metabolism.

5.8 Investigating Glioblastoma-specific Protein Lists

UpSet plots by cycloheximide and pateamine A treatment depict the full lists of up- and downregulated genes (not terms, unlike the previous UpSet plots) by each cell line (Figures 5.13 and 5.14). This produces, for each drug, lists of genes that were up- or downregulated across all cell lines (HL60, LN18 and U87) or only in both glioblastoma cell lines (LN18 and U87)(Appendix Y).

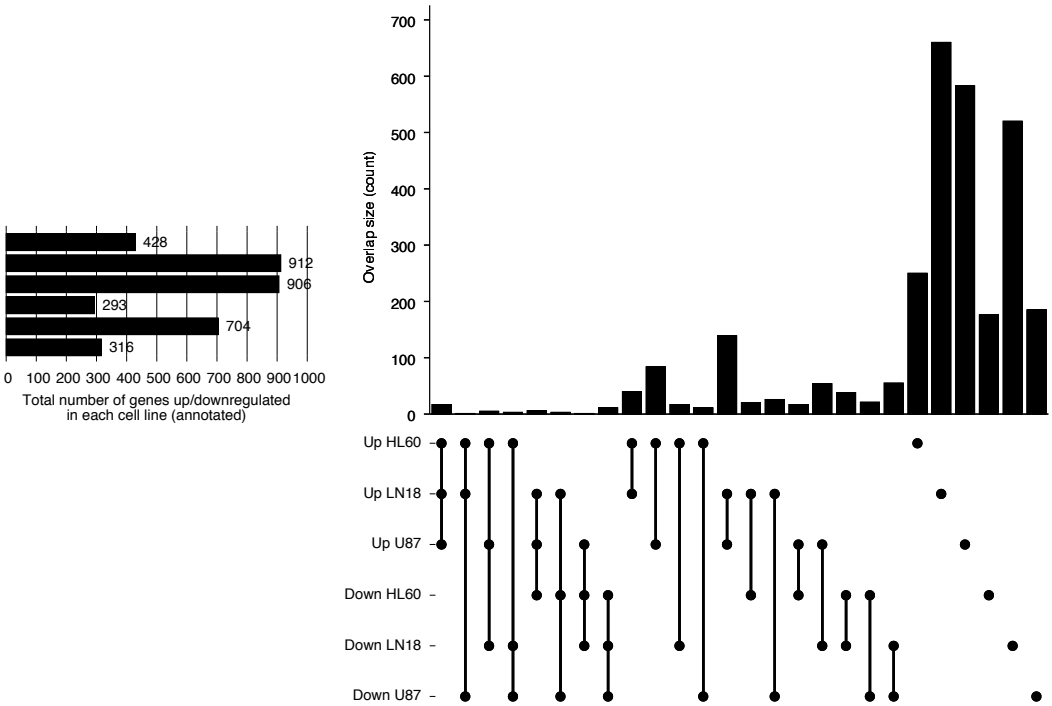

Figure 5.13: UpSet plot shows the number of genes identified in all cell lines in response to cycloheximide treatment by exclusive intersection lists identified from up- and downregulatory effect and cell line, given in bottom left. The inset shows the number of genes found in each list.

The following discussion on genes up- or downregulated in response to cycloheximide or pateamine A treatment in all cell lines or only glioblastoma cell lines is shaped by using gene ontology enrichment, as outlined in Section 3.7.3.1. Adjusted p-values are not reported for the enrichment analysis as it is being used to indicate trends in response to drug treatment, rather than quantitative purposes.

The UpSet plots presented here show how many gene hits were found in each sample, and how many were found in more than one sample. However, the number of isolated hits far exceeded the intersections. If a protein

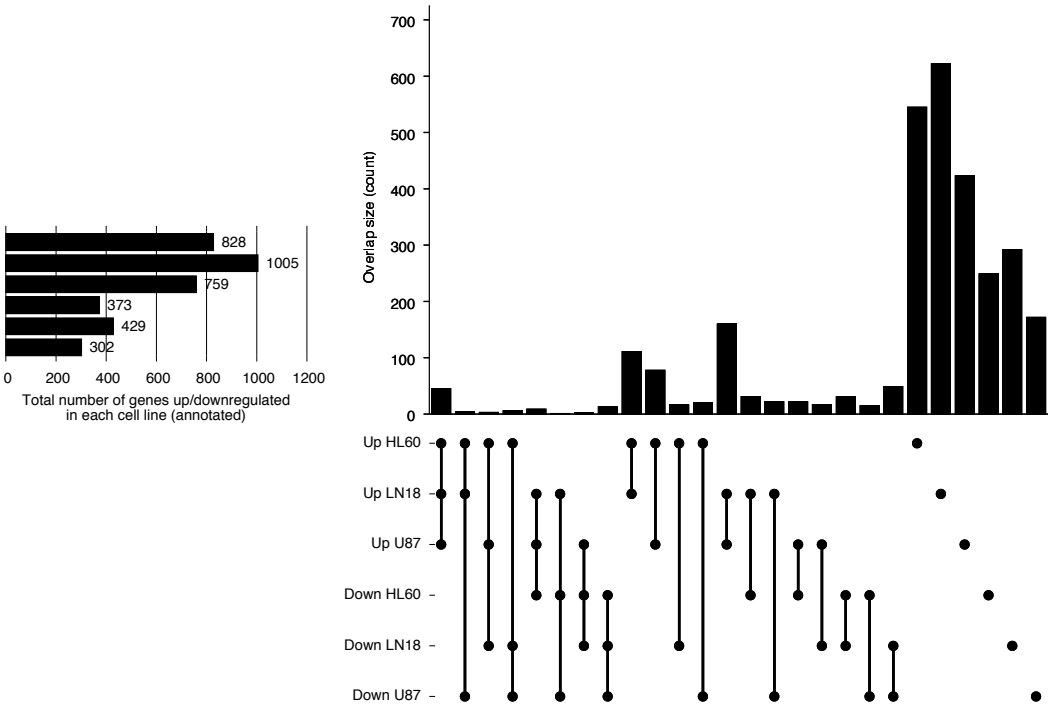

Figure 5.14: UpSet plot shows the number of genes identified in all cell lines in response to pateamine A treatment by exclusive intersection lists identified from up- and downregulatory effect and cell line, given in bottom left. The inset shows the number of genes found in each list.

was found and a gene linked to it in Proteome Discoverer processing, it was included in the analysis list, even if it was just in one of eight replicates (control vs treated, four biological replicates each). What follows is a discussion of four of the intersections in each of the two figures above.

Considering altered gene expression in all cycloheximide samples (Figure 5.13; Appendix Y), five of the upregulated genes were associated with lipid transport and localization process terms, specifically negative regulation regarding transmembrane proteins and their modulation (P31749, Q98ZF1-1, Q9P260-1, Q9Y3D6, and Q9Y6B6). Two of the downregulated

genes (P05114 and P05204) were associated with nucleosomal DNA binding terms, but it should be noted that the downregulated list was very short, and this 'association' is likely as a result of the small sample size.

In contrast, glioblastoma-only altered lists were much longer. Upregulated genes were associated with endoplasmic reticulum transport (exit; (retrograde) to cytosol) (Q13438, Q96CS3, and Q9GZP9); however, this list did include groups of genes being upregulated en masse (VPS25/26B, UBE2L6/2Z, RAB35/3B/5B, NDUFAF7/B9/B11, MRPL10/L21/L24/S33). It should also be noted that a number of these related to NADH:ubiquinone oxidoreductase and dehydrogenase activity, as well as RNA transferases. Glioblastoma-only downregulated genes were associated with protein-specific domain binding (P20248, P52926, Q8N8S7, Q969E4, Q96EI5, Q96I70, Q9NUP9, and Q9P1Y6) and WW domain binding (Q8N8S7, Q969E4, and Q96EI5), indicating diminished protein-protein interactions. The protein-specific domain binding proteins included actin and cyclin regulatory elements (CCNA2, ENAH) that support the observed cell cycle effects of pateamine A.The protein subunit lists of the second ontology term included Golgi membrane proteins 1 and 2, haemoglobin subunits α 1 and 2, and transcription elongation factor-likes 3 and 4.

Pateamine A samples of up- and downregulated genes and their terms had some similarities to the cycloheximide treatments (Figure 5.14; Appendix Y). The list of genes that were upregulated in all cell lines did not yield any associated ontology terms, but genes affected included mitochondrial ribosomal proteins L20 and S24 (the latter also upregulated in cycloheximide-treated glioblastoma), RAB10 and RAB9A, and transmembrane proteins 11, 106B, 126A, and 167A (all transport-related).

The list of genes downregulated in all cell lines were associated with nc/rRNA (metabolic) processing and ribosome biogenesis, and cellular macromolecule metabolic processes. MRPS17 and MRPS22, NDUFAB1, NDUFAF7 and NDUFB5, and UBE2C and UBE2R2 subunits were also affected. Notably, a number of solute carriers that contribute to co-transport mechanisms were downregulated (SLC4A10, 9A6, 12A4, 30A7, 35B2, and 38A14).

For terms upregulated in both glioblastoma samples in response to pateamine A, only ribonucleoprotein complex binding met the size and p-value thresholds (P15531, P98179, Q14978, Q8NC51), but notably included haemoglobin subunit α 1/2 (oppositely affected by cycloheximide treatment in glioblastoma), and MRPL49. These mitochondrial ribosomal subunit proteins (MRPL/S, large and small subunits respectively), seen in earlier combined lists, support the alterations in mitochondrial translation as a result of overall translational inhibition, and particular effects by pateamine A inhibition. The only term identified from the glioblastoma-only downregulated gene list was oxygen binding (P02100, P02768, and Q9NMT6). Five genes (HBE1, HMGN1, MCFD2, PJA2, and PPP1R2) were identical to those found in the cycloheximide treated glioblastoma downregulated list. It should also be noted that while RNA splicing-related terms themselves were not particularly evident, all lists did include RNA polymerase subunits, associated binding proteins, and other proteins that supported pateamine A treatment having effects on RNA splicing activity.

By investigating protein lists that were up- or downregulated in all samples and only in the glioblastoma samples, it is possible to investigate overall translational effects and eIF4A-specific effects. Cycloheximide

negatively regulated lipid transport and localisation across cell lines, and in glioblastoma particular effects included upregulating particular endoplasmic reticulum transport proteins and downregulating protein binding. NADH:ubiquinone and RNA transferase activity was affected by cycloheximide treatment across all cell lines, and particular effects were also seen in glioblastoma cell lines, and when treated with pateamine A.

5.9 The Wider Picture

A range of compounds inhibit eIF4A, to varying degrees of exclusivity, and this section focusses on the effect of this inhibition on a range of cancer models. First, pateamine A and its homologue, DMDA pateamine, are reviewed, before moving to a glioblastoma-focussed discussion of other eIF4A inhibitors. Research on pateamine A inhibition of eIF4A has been restricted by its limited supply, and as the phamacological effects of DMDA pateamine appear identical to that of pateamine A, it is considered as identical in the following discussion of eIF4A inhibition in cancer models.

Early studies on pateamine A's pharmaceutical potential quickly focussed on cancer treatment, as early tests against P388 murine and BSC cell lines indicated its potential as a tumour selective drug [19]. A larger study using DMDA pateamine A found significant regression in xenografted mice models of melanoma, increasing rates of tumour-free survivors; tumour growth inhibition was also evidenced in colon cancer models, and prolonged survival in leukaemia models [26]. Later research, in the context of chronic lymphocytic leukaemia, has also found that DMDA pateamine can bind to human plasma proteins, indicating a need for further analogues

to be developed [72].

Other inhibitors of eIF4A exhibit tumour regression and suppression in a variety of cell lines and test types. A brief selection of examples are described below, based on the chosen inhibitors, with preference given to omics studies (genomics, proteomics) and *in vivo* work.

Rocaglamide A, in spite of its markedly different structure, binds in an analogous fashion as pateamine A to eIF4A [20]. However, it is not an exclusive binding; the compound also binds to DDX3, another DEAD-box helicase, and clamps the enzyme to polypurine mRNA strands [73]. Rocaglamide A inhibits growth and invasion of pancreatic cancer cells in culture and xenografted to mice, and induced apoptosis in leukaemia [74, 75]. The compound also disrupts the regulation of other oncogenic pathways, including activating the ATM/ATR-Chk1/Chk2 checkpoint pathway, preventing cell cycle progression, and inactivating heat shock protein 1 ultimately reducing glucose uptake [27]. Silvestrol, another flavagline, is also a potential anticancer compound, with additional activity as an antiviral [76]. In pancreatic ductal adenocarcinoma tumours, which is characterised by protein synthesis and its regulation being strongly perturbed, eIF4A inhibition of translation proved to overcome uncontrolled DNA replication due to loss of 4E-BP1 [77].

Hippuristanol provides key evidence for eIF4A's dependency on the RNA 5′ UTR length, secondary structure, and cytosine, supporting eIF4A inhibition as a potential treatment route in cancer therapeutics [78]. It resensitises lymphomas to DNA damaging agents, and triggeres cell death of both leukaemia and lymphoma cells when paired with a Bcl-2 family inhibitor [79].

From considering these inhibitors, and background information presented in the Introduction, a few key themes emerge. First, pateamine A and other inhibitors of eIF4A inhibit the growth of various cancer cells, with further effects on both proliferation and cell cycle. Second, the cytotoxicity profile remains favourable in murine models of cancer, indicating a degree of confidence in the application of pateamine A in other cancer types. This was shown through the present work, where proteomic response of glioblastoma cells to pateamine A is presented. When considering the specific nature of eIF4A inhibition and its effects on the cell, we find that alterations in cell cycle, RNA processing, and protein transport GO terms appear across the cell lines.

Above is an eIF4A inhibition-driven approach to considering cancer treatment options. What follows is a discussion of studies on inhibition of overall translation processes in glioblastoma, before finishing on whether pateamime A specific effects have been found in the current work.

An integrated approach to patient glioblastoma profiling recently highlighted both the genetic and proteomic diversity of glioblastoma, and encouraged further research to optimise patient treatment based on targeting specific pathways altered in various subtypes [80]. Particular oncogenic switches identified by the work included phosphorylation of PTPN11 and PLCG1, which are involved in signal transduction at the nucleus, and production of diacylglycerol and inositol respectively [80].

Research involving glioblastoma and cycloheximide treatment tends to investigate combination therapy or viral transcription. For example, apoptosis caused by enterovirus 71 infection in glioblastoma cells is inhibited by treatment with protein synthesis inhibitors, including cycloheximide,

providing insight on mechanisms involved in viral-driven apoptosis [81].

This present work studies the proteomic effects of both cycloheximide and pateamine A on two glioblastoma cell lines, finding that both forms of translational inhibition causes alterations in translation, RNA processing, and mitochondrial processes. Pateamine A caused perturbations in splicing processes and particular effect on chromatid and chromatin management that were not seen in overall translational inhibition.

5.9.1 Further Work

This thesis raises a number of questions as to the particulars of pateamine A inhibition of glioblastoma. Derivatives and synthetic equivalents of pateamine A are likely necessary for future experiments, in the interests of scale and expense. First, a range of glioblastoma and glioma cell lines, as well as patient-derived samples, could help elucidate and quantify glioblastoma subtype-specific effects. Other omics techniques — metabolomics, as was originally considered for this thesis, or genomics and its related techniques — could also be used, in conjunction with other sequencing data to support this (see [80] for a large and integrated approach to this). Ultimately, if development to mammalian models is desired, xenografted murine and rat models would provide *in vivo* evidence for testing the suitability of pateamine A for clinical treatment.

The effects of pateamine A on RNA splicing deserve further research, which could be investigated using RNA-seq coupled with transcriptomics. Studying the effects of pateamine A on protein transport in cell culture would elucidate differences between the impact of translational inhibition

and eIF4A-specific effects, particularly if coupled with a range of translation inhibitors.

5.10 Final Conclusions

The purpose of this thesis was to develop understanding of the effects of pateamine A treatment on glioblastoma using proteomics and gene ontology enrichment. This utilised LN18 and U87 cell lines, which were compared against the HL60 cell line, and used cycloheximide as the control translational inhibitor.

The three aims of the research have been met. The IC_{50} values for pateamine A and cycloheximide were higher in LN18 and U87 cell lines than in the HL60 cell line. The resultant drug concentration used for proteomic sample preparation was not prohibitive to continuing the experiments; however, a more appropriate control would have been media treated with 0.1% DMSO with no drug, rather than untreated media as was used.

Translational inhibition from cycloheximide treatment caused perturbations in cell cycle processes and catabolic processes. Pateamine A treatment caused alterations in mRNA capping processes and RNA splicing processes in glioblastoma cell lines, but in the HL60 cell line, particular effect was seen on chromatid organisation. Both drugs resulted in altered protein transport processes and overall RNA processing across cell lines. Pateamine A was an effective treatment against glioblastoma, despite the cancer's perturbed energy metabolism and translational processes. The use of proteomics with gene ontology enrichment analysis yielded a novel insights to the effects of pateamine A, an eIF4A inhibitor, on glioblastoma cell lines.

Chapter 6

Appendices

The appendices show tables of terms up- and downregulated in comparing cell lines, and in response to drug treatment in each cell line, followed by full lists of genes that altered in each cell line in response to drug treatment.

These first group of tables (Appendices A to F) show the biological processes (BP) and molecular functions (MF) up- and downregulated when comparing the two cell lines, ranked by adjusted p-value, and showing the total number of genes annotated to the term (term size)and the number of identified proteins associated with the ontological term (intersection size).

The second group of tables (Appendices G to R) show the biological processes (BP) and molecular functions (MF) up- and downregulated when each cell line is treated with either cycloheximide or pateamine A, ranked by adjusted p-value, and showing the total number of genes annotated to the term (term size)and the number of identified proteins associated with the ontological term (intersection size).

Finally, the third group of tables (Appendices U to X) presents the genes that changed in response to cycloheximide or pateamine A treatment in

each cell line, ranked by fold change, and showing the accession number, description, and adjusted p-value.

A HL60 vs LN18: Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:MF	cell adhesion molecule binding	6.53E-09	544	39
GO:MF	actin binding	5.87E-07	449	32
GO:MF	cadherin binding	1.51E-05	333	25
GO:BP	actin filament-based process	2.69E-04	810	41
GO:BP	actin cytoskeleton organization	6.14E-04	712	37
GO:MF	phosphatase binding	2.09E-03	199	16
GO:MF	protein domain specific binding	2.18E-03	706	34
GO:MF	enzyme regulator activity	2.85E-03	911	40
GO:BP	actin filament bundle assembly	3.04E-03	161	15
GO:BP	actin filament bundle organization	3.83E-03	164	15
GO:MF	small GTPase binding	5.04E-03	263	18
GO:BP	plasma membrane tubulation	5.36E-03	20	6
GO:MF	GTPase binding	6.77E-03	295	19
GO:MF	actin monomer binding	1.59E-02	30	6
GO:BP	protein localization to cell periphery	1.97E-02	339	21
GO:MF	nucleoside-triphosphatase regulator activity	2.01E-02	526	26
GO:MF	GTPase regulator activity	3.82E-02	484	24
GO:BP	actin filament organization	4.61E-02	445	24
GO:BP	positive regulation of organelle organization	4.78E-02	630	30
End of Table				

B HL60 vs LN18: Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:MF	catalytic activity, acting on RNA	8.65E-07	394	36
GO:BP	ncRNA metabolic process	4.69E-06	535	43
GO:BP	regulated exocytosis	1.31E-05	790	54
GO:BP	myeloid leukocyte mediated immunity	1.65E-05	558	43
GO:BP	leukocyte degranulation	1.71E-05	538	42
GO:BP	ncRNA processing	1.85E-05	439	37
GO:BP	neutrophil mediated immunity	1.99E-05	500	40
GO:BP	neutrophil degranulation	2.38E-05	483	39
GO:BP	neutrophil activation involved in immune response	3.16E-05	488	39
GO:BP	myeloid cell activation involved in immune response	3.58E-05	552	42
GO:BP	exocytosis	3.68E-05	906	58
GO:BP	neutrophil activation	6.80E-05	502	39
GO:BP	granulocyte activation	9.85E-05	509	39
GO:BP	cell activation involved in immune response	1.07E-04	727	49
GO:BP	ribosome biogenesis	1.29E-04	335	30
GO:BP	myeloid leukocyte activation	1.72E-04	671	46
GO:BP	DNA-dependent DNA replication	2.11E-04	216	23
GO:BP	leukocyte activation involved in immune response	2.34E-04	723	48
GO:BP	ncRNA transcription	2.75E-04	110	16
GO:BP	peptidyl-lysine modification	3.17E-04	408	33
GO:BP	ribonucleoprotein complex biogenesis	1.12E-03	473	35
GO:MF	histone deacetylase activity (H3-K14 specific)	4.31E-03	11	5
GO:MF	NAD-dependent histone deacetylase activity (H3-K14 specific)	4.31E-03	11	5
GO:BP	rRNA metabolic process	4.33E-03	275	24
GO:MF	nucleotidyltransferase activity	4.66E-03	134	15
GO:BP	DNA metabolic process	5.18E-03	976	55
GO:MF	structural constituent of nuclear pore	6.29E-03	28	7
GO:BP	rRNA processing	7.75E-03	265	23
GO:BP	regulation of glycolytic process	8.47E-03	81	12
GO:BP	nucleic acid phosphodiester bond hydrolysis	8.72E-03	306	25
GO:BP	mRNA metabolic process	1.22E-02	880	50
GO:MF	catalytic activity, acting on DNA	1.34E-02	299	23
GO:BP	leukocyte mediated immunity	1.57E-02	888	50

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	regulation of DNA-dependent DNA replication	1.61E-02	47	9
GO:BP	regulation of carbohydrate catabolic process	3.25E-02	92	12
GO:BP	signal transduction by p53 class mediator	3.41E-02	290	23
GO:MF	NAD-dependent histone deacetylase activity	3.60E-02	16	5
GO:MF	helicase activity	4.70E-02	163	15
GO:MF	methyltransferase activity	4.81E-02	221	18
GO:MF	NAD-dependent protein deacetylase activity	4.98E-02	17	5
GO:MF	3′-5′ RNA helicase activity	4.99E-02	4	3
End of Table				

C HL60 vs U87 Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:MF	cadherin binding	6.00E-11	333	31
GO:MF	cell adhesion molecule binding	1.80E-10	544	39
GO:BP	actin cytoskeleton organization	3.94E-07	712	41
GO:BP	actin filament-based process	5.16E-07	810	44
GO:MF	actin binding	5.78E-07	449	30
GO:MF	structural molecule activity	4.27E-05	701	35
GO:BP	supramolecular fiber organization	1.01E-04	863	41
GO:BP	actin filament organization	2.08E-04	445	27
GO:BP	cell morphogenesis involved in differentiation	2.16E-04	754	37
GO:MF	extracellular matrix binding	3.53E-04	56	9
GO:BP	response to wounding	4.77E-04	680	34
GO:BP	cell junction organization	2.20E-03	727	34
GO:BP	blood vessel development	2.35E-03	797	36
GO:MF	collagen binding	2.41E-03	70	9
GO:BP	integrin-mediated signaling pathway	2.77E-03	112	12
GO:BP	macroautophagy	3.73E-03	337	21
GO:BP	cell-substrate adhesion	4.19E-03	368	22
GO:BP	blood vessel morphogenesis	4.25E-03	715	33
GO:MF	GTPase binding	4.49E-03	295	18
GO:MF	cell adhesion mediator activity	4.77E-03	58	8
Continued on next page				

source	term name	adjusted p-value	term size	intersection size
GO:BP	cell-matrix adhesion	5.31E-03	236	17
GO:BP	cell-substrate junction assembly	6.52E-03	101	11
GO:BP	vasculature development	6.65E-03	834	36
GO:BP	epithelial cell differentiation	8.28E-03	807	35
GO:MF	structural constituent of cytoskeleton	1.01E-02	104	10
GO:BP	cell-substrate junction organization	1.15E-02	107	11
GO:BP	epithelial cell development	1.24E-02	225	16
GO:BP	receptor-mediated endocytosis	1.25E-02	335	20
GO:BP	plasma membrane bounded cell projection morphogenesis	1.27E-02	684	31
GO:MF	kinase binding	1.33E-02	757	31
GO:BP	small GTPase mediated signal transduction	1.34E-02	520	26
GO:BP	cell projection morphogenesis	1.43E-02	688	31
GO:MF	small GTPase binding	1.45E-02	263	16
GO:BP	wound healing	1.46E-02	555	27
GO:BP	transmembrane receptor protein tyrosine kinase signaling pathway	1.51E-02	759	33
GO:BP	organelle localization	1.56E-02	657	30
GO:BP	positive regulation of cell migration	2.22E-02	568	27
GO:BP	neuron projection morphogenesis	2.28E-02	670	30
GO:BP	cell part morphogenesis	2.32E-02	705	31
GO:BP	endomembrane system organization	2.51E-02	572	27
GO:BP	Ras protein signal transduction	2.60E-02	352	20
GO:MF	protein kinase binding	2.76E-02	677	28
GO:MF	protein kinase C binding	2.92E-02	55	7
GO:BP	regulation of vesicle-mediated transport	2.95E-02	544	26
GO:BP	cellular response to chemical stress	3.06E-02	356	20
GO:MF	nucleosomal DNA binding	3.32E-02	39	6
GO:BP	response to inorganic substance	3.53E-02	583	27
GO:BP	vascular endothelial growth factor receptor signaling pathway	3.59E-02	99	10
GO:MF	exogenous protein binding	3.86E-02	77	8
GO:BP	response to oxidative stress	4.16E-02	457	23
GO:BP	regulation of actin cytoskeleton organization	4.39E-02	365	20
GO:BP	positive regulation of cell motility	4.62E-02	592	27
GO:MF	calmodulin binding	4.75E-02	203	13

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	protein localization to membrane	4.96E-02	698	30
End of Table				

D HL60 vs U87 Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitochondrial translational elongation	7.16E-06	87	17
GO:BP	mitochondrial translational termination	8.60E-06	88	17
GO:BP	translational termination	1.88E-05	104	18
GO:BP	negative regulation of cell cycle process	1.30E-04	400	36
GO:BP	mitochondrial translation	2.34E-04	135	19
GO:BP	myeloid leukocyte mediated immunity	5.66E-04	558	43
GO:BP	neutrophil mediated immunity	5.71E-04	500	40
GO:BP	neutrophil degranulation	6.39E-04	483	39
GO:BP	leukocyte activation involved in immune response	6.69E-04	723	51
GO:BP	negative regulation of cell cycle	7.89E-04	487	39
GO:BP	cell activation involved in immune response	7.91E-04	727	51
GO:BP	neutrophil activation involved in immune response	8.32E-04	488	39
GO:BP	DNA metabolic process	1.33E-03	976	62
GO:BP	mitochondrial gene expression	1.43E-03	166	20
GO:BP	leukocyte degranulation	1.45E-03	538	41
GO:BP	neutrophil activation	1.70E-03	502	39
GO:BP	regulation of cell cycle phase transition	1.84E-03	543	41
GO:MF	ribonuclease activity	2.15E-03	111	15
GO:BP	granulocyte activation	2.40E-03	509	39
GO:BP	translational elongation	2.74E-03	143	18
GO:BP	myeloid cell activation involved in immune response	2.81E-03	552	41
GO:MF	nuclease activity	3.13E-03	207	21
GO:BP	antigen processing and presentation of endogenous peptide antigen	3.49E-03	19	7
GO:BP	cellular response to DNA damage stimulus	3.51E-03	894	57
GO:BP	ncRNA processing	3.53E-03	439	35
GO:BP	negative regulation of cell cycle phase transition	3.93E-03	329	29

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	regulation of cell cycle process	4.68E-03	815	53
GO:MF	catalytic activity, acting on RNA	4.70E-03	394	31
GO:BP	cellular protein complex disassembly	4.94E-03	228	23
GO:BP	covalent chromatin modification	5.30E-03	486	37
GO:BP	ncRNA metabolic process	8.07E-03	535	39
GO:MF	oligosaccharyl transferase activity	9.44E-03	6	4
GO:BP	myeloid leukocyte activation	1.30E-02	671	45
GO:BP	histone modification	1.78E-02	472	35
GO:BP	regulation of mitotic cell cycle phase transition	1.86E-02	453	34
GO:BP	cell cycle checkpoint signaling	1.91E-02	196	20
GO:MF	hydrolase activity, acting on ester bonds	2.04E-02	765	47
GO:BP	chromatin organization	2.29E-02	839	52
GO:BP	DNA-dependent DNA replication	2.42E-02	216	21
GO:MF	peptide antigen binding	2.47E-02	30	7
GO:BP	nucleic acid phosphodiester bond hydrolysis	2.61E-02	306	26
GO:MF	endoribonuclease activity	2.86E-02	65	10
GO:BP	DNA repair	2.90E-02	586	40
GO:BP	antigen processing and presentation of endogenous antigen	3.73E-02	26	7
GO:BP	RNA phosphodiester bond hydrolysis	4.17E-02	157	17
GO:BP	cell cycle phase transition	4.18E-02	681	44
GO:BP	negative regulation of mitotic cell cycle phase transition	4.38E-02	260	23
GO:BP	ribonucleoprotein complex biogenesis	4.59E-02	473	34
GO:BP	ribosome biogenesis	4.60E-02	335	27

End of Table

E LN18 vs U87 Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	ribonucleoprotein complex biogenesis	2.39E-06	473	37
GO:BP	rRNA metabolic process	4.05E-06	275	27
GO:BP	ribosome biogenesis	4.43E-06	335	30
GO:BP	rRNA processing	3.74E-05	265	25

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	ncRNA processing	5.37E-05	439	33
GO:BP	ncRNA metabolic process	6.53E-05	535	37
GO:BP	protein localization to organelle	8.30E-05	974	54
GO:MF	peptidyl-lysine 5-dioxygenase activity	1.84E-04	4	4
GO:BP	mRNA metabolic process	2.07E-03	880	47
GO:BP	intracellular protein transport	2.31E-03	995	51
GO:BP	localization within membrane	2.34E-03	775	43
GO:BP	peptidyl-lysine hydroxylation	3.19E-03	9	5
GO:MF	procollagen-lysine 5-dioxygenase activity	7.52E-03	3	3
GO:BP	mitotic cell cycle process	8.84E-03	956	48
GO:BP	organelle disassembly	9.27E-03	109	13
GO:BP	endoplasmic reticulum tubular network organization	9.73E-03	18	6
GO:BP	endosomal transport	9.81E-03	244	20
GO:BP	regulation of endoplasmic reticulum tubular network organization	1.60E-02	6	4
GO:MF	exonuclease activity	1.82E-02	83	10
GO:BP	vacuolar transport	2.11E-02	154	15
GO:BP	DNA-dependent DNA replication	2.41E-02	216	18
GO:BP	diol biosynthetic process	2.67E-02	21	6
GO:MF	nuclease activity	2.84E-02	207	16
GO:BP	amide biosynthetic process	3.29E-02	975	47
GO:MF	3′-5′ exonuclease activity	3.67E-02	57	8
GO:BP	protein localization to membrane	3.95E-02	698	37
GO:MF	structural constituent of ribosome	4.44E-02	171	14
GO:MF	small GTPase binding	4.85E-02	263	18

End of Table

F LN18 vs U87 Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	DNA replication	1.70E-02	338	24
GO:BP	cell division	3.51E-02	630	35
GO:BP	chromosome segregation	3.53E-02	353	24
GO:BP	regulation of DNA-dependent DNA replication initiation	3.90E-02	7	4
End of Table				

G HL60 Cycloheximide Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	cell cycle phase transition	2.74E-06	681	43
GO:BP	mitotic cell cycle process	2.98E-06	956	53
GO:BP	mitotic cell cycle phase transition	4.36E-06	588	39
GO:BP	regulation of cell cycle phase transition	2.05E-04	543	34
GO:BP	regulation of mitotic cell cycle phase transition	3.68E-04	453	30
GO:BP	regulation of cell cycle process	5.00E-04	815	43
GO:MF	transcription factor binding	3.50E-03	556	30
GO:BP	regulation of protein stability	3.69E-03	302	22
GO:BP	protein catabolic process	5.32E-03	983	46
GO:MF	vitamin D receptor binding	6.22E-03	15	5
GO:BP	protein autophosphorylation	1.58E-02	234	18
GO:BP	proteasome-mediated ubiquitin-dependent protein catabolic process	2.20E-02	442	26
GO:BP	regulation of mitotic cell cycle	2.35E-02	612	32
GO:BP	cellular protein catabolic process	2.43E-02	822	39
GO:BP	proteasomal protein catabolic process	2.58E-02	501	28
GO:MF	DNA-binding transcription factor binding	3.39E-02	234	16
GO:MF	serine-type carboxypeptidase activity	4.98E-02	5	3
End of Table				

H HL60 Cycloheximide Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	ribosome biogenesis	3.96E-06	335	23
GO:BP	rRNA processing	2.85E-04	265	18
GO:BP	rRNA metabolic process	4.96E-04	275	18
GO:BP	ribonucleoprotein complex biogenesis	5.73E-04	473	24
GO:MF	structural constituent of ribosome	9.05E-04	171	13
GO:BP	peptide metabolic process	9.86E-04	998	37
GO:BP	oxidative phosphorylation	1.15E-03	151	13
GO:BP	aerobic electron transport chain	2.88E-03	92	10
GO:BP	translation	4.11E-03	804	31
GO:BP	mitochondrial ATP synthesis coupled electron transport	5.68E-03	99	10
GO:BP	translational initiation	6.08E-03	203	14
GO:BP	ATP synthesis coupled electron transport	6.22E-03	100	10
GO:BP	cotranslational protein targeting to membrane	7.46E-03	102	10
GO:BP	peptide biosynthetic process	8.71E-03	834	31
GO:BP	protein targeting to ER	1.60E-02	111	10
GO:BP	establishment of protein localization to endoplasmic reticulum	2.20E-02	115	10
GO:BP	respiratory electron transport chain	2.56E-02	117	10
GO:BP	aerobic respiration	2.62E-02	200	13
GO:BP	ncRNA processing	2.91E-02	439	20
GO:BP	amide biosynthetic process	2.97E-02	975	33
GO:BP	SRP-dependent cotranslational protein targeting to membrane	3.33E-02	96	9
GO:MF	ribosomal small subunit binding	4.55E-02	17	4

End of Table

I LN18 Cycloheximide Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	intracellular protein transport	7.15E-18	995	119
GO:BP	ribonucleoprotein complex biogenesis	6.04E-16	473	73
GO:MF	structural constituent of ribosome	1.22E-15	171	41
GO:BP	ribosome biogenesis	6.60E-14	335	57
GO:BP	translation	8.38E-14	804	96
GO:BP	protein localization to organelle	1.59E-13	974	108
GO:BP	peptide biosynthetic process	9.29E-13	834	96
GO:BP	establishment of protein localization to membrane	2.65E-12	385	59
GO:BP	establishment of protein localization to organelle	7.10E-12	523	70
GO:BP	amide biosynthetic process	8.84E-12	975	104
GO:BP	mRNA metabolic process	2.83E-11	880	96
GO:BP	cytoplasmic translation	2.84E-11	149	34
GO:BP	rRNA metabolic process	3.62E-11	275	47
GO:BP	rRNA processing	3.83E-11	265	46
GO:BP	ncRNA metabolic process	7.29E-11	535	69
GO:BP	ncRNA processing	8.51E-11	439	61
GO:BP	peptide metabolic process	1.04E-10	998	103
GO:BP	localization within membrane	1.09E-10	775	87
GO:BP	translational initiation	1.33E-10	203	39
GO:MF	rRNA binding	1.21E-09	68	21
GO:BP	protein localization to endoplasmic reticulum	2.22E-09	144	31
GO:BP	protein localization to membrane	8.37E-09	698	77
GO:BP	cotranslational protein targeting to membrane	1.70E-08	102	25
GO:BP	protein targeting	2.74E-08	400	53
GO:BP	establishment of protein localization to endoplasmic reticulum	4.69E-08	115	26
GO:BP	protein targeting to ER	1.25E-07	111	25
GO:MF	cadherin binding	2.86E-07	333	44
GO:BP	vesicle budding from membrane	3.31E-07	107	24
GO:BP	mitochondrial translation	3.87E-07	135	27
GO:MF	structural molecule activity	4.12E-07	701	71
GO:BP	mitochondrial gene expression	5.23E-07	166	30
GO:BP	mRNA catabolic process	9.00E-07	388	49
GO:BP	ribonucleoprotein complex subunit organization	1.19E-06	203	33

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	SRP-dependent cotranslational protein targeting to membrane	1.24E-06	96	22
GO:BP	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	1.28E-06	123	25
GO:BP	RNA catabolic process	1.36E-06	431	52
GO:BP	protein targeting to membrane	2.28E-06	219	34
GO:BP	viral transcription	4.54E-06	181	30
GO:BP	antigen processing and presentation	4.54E-06	236	35
GO:BP	viral gene expression	5.09E-06	237	35
GO:MF	cell adhesion molecule binding	6.21E-06	544	57
GO:BP	organelle localization	6.28E-06	657	67
GO:BP	ribonucleoprotein complex assembly	7.89E-06	196	31
GO:BP	neutrophil degranulation	9.94E-06	483	54
GO:BP	leukocyte degranulation	1.02E-05	538	58
GO:BP	neutrophil activation involved in immune response	1.43E-05	488	54
GO:BP	nuclear-transcribed mRNA catabolic process	1.82E-05	214	32
GO:BP	macroautophagy	2.42E-05	337	42
GO:BP	neutrophil mediated immunity	3.32E-05	500	54
GO:BP	neutrophil activation	3.80E-05	502	54
GO:BP	nucleobase-containing compound catabolic process	4.07E-05	573	59
GO:BP	mitochondrial translational elongation	4.34E-05	87	19
GO:MF	catalytic activity, acting on RNA	4.87E-05	394	44
GO:BP	mitochondrial translational termination	5.29E-05	88	19
GO:BP	aromatic compound catabolic process	5.74E-05	636	63
GO:BP	protein hydroxylation	5.99E-05	28	11
GO:BP	granulocyte activation	6.10E-05	509	54
GO:BP	myeloid cell activation involved in immune response	6.47E-05	552	57
GO:BP	myeloid leukocyte mediated immunity	9.43E-05	558	57
GO:BP	endosomal transport	1.31E-04	244	33
GO:BP	mitochondrion organization	1.45E-04	565	57
GO:BP	cellular nitrogen compound catabolic process	1.46E-04	623	61
GO:BP	translational termination	1.79E-04	104	20
GO:BP	Golgi vesicle transport	1.83E-04	415	46
GO:BP	establishment of organelle localization	1.93E-04	443	48
GO:BP	heterocycle catabolic process	2.40E-04	617	60

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	antigen processing and presentation of exogenous antigen	3.52E-04	183	27
GO:BP	translational elongation	6.02E-04	143	23
GO:BP	organic cyclic compound catabolic process	6.19E-04	664	62
GO:BP	ribosomal small subunit biogenesis	6.62E-04	74	16
GO:BP	cellular component disassembly	6.86E-04	577	56
GO:BP	process utilizing autophagic mechanism	7.53E-04	564	55
GO:BP	autophagy	7.53E-04	564	55
GO:BP	vesicle organization	8.62E-04	342	39
GO:MF	ribonucleoprotein complex binding	1.05E-03	150	22
GO:BP	generation of precursor metabolites and energy	1.35E-03	545	53
GO:MF	L-ascorbic acid binding	1.40E-03	21	8
GO:MF	translation regulator activity	1.63E-03	154	22
GO:BP	organelle disassembly	1.85E-03	109	19
GO:BP	antigen processing and presentation of exogenous peptide antigen	1.87E-03	175	25
GO:BP	ribosome assembly	2.08E-03	62	14
GO:MF	translation regulator activity, nucleic acid binding	2.37E-03	123	19
GO:MF	peptidyl-proline 3-dioxygenase activity	2.51E-03	4	4
GO:BP	ribosomal large subunit biogenesis	2.57E-03	72	15
GO:BP	regulation of translational initiation	2.88E-03	82	16
GO:BP	cell activation involved in immune response	3.10E-03	727	64
GO:BP	regulation of endoplasmic reticulum tubular network organization	3.12E-03	6	5
GO:BP	antigen processing and presentation of peptide antigen	3.54E-03	193	26
GO:BP	exocytosis	3.95E-03	906	75
GO:BP	leukocyte activation involved in immune response	5.28E-03	723	63
GO:MF	procollagen-proline dioxygenase activity	5.84E-03	8	5
GO:BP	nuclear transport	6.16E-03	356	38
GO:BP	regulated exocytosis	6.38E-03	790	67
GO:BP	protein-containing complex localization	6.53E-03	289	33
GO:MF	peptidyl-proline dioxygenase activity	7.08E-03	13	6
GO:MF	translation factor activity, RNA binding	7.38E-03	99	16
GO:BP	myeloid leukocyte activation	8.40E-03	671	59
GO:BP	peptidyl-proline hydroxylation	9.43E-03	16	7
GO:BP	synaptic vesicle recycling via endosome	1.05E-02	7	5

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	protein-containing complex disassembly	1.10E-02	337	36
GO:MF	monosaccharide binding	1.19E-02	71	13
GO:MF	isocitrate dehydrogenase activity	1.21E-02	5	4
GO:BP	endomembrane system organization	1.25E-02	572	52
GO:BP	nucleocytoplasmic transport	1.27E-02	353	37
GO:MF	GTP binding	1.28E-02	381	37
GO:BP	viral life cycle	1.71E-02	386	39
GO:BP	cellular amino acid metabolic process	1.75E-02	344	36
GO:MF	GTPase activity	1.78E-02	300	31
GO:MF	intramolecular oxidoreductase activity	1.79E-02	54	11
GO:MF	guanyl ribonucleotide binding	1.81E-02	402	38
GO:MF	guanyl nucleotide binding	1.81E-02	402	38
GO:BP	organelle assembly	2.52E-02	921	73
GO:BP	nuclear export	2.57E-02	202	25
GO:BP	ribonucleoprotein complex export from nucleus	2.73E-02	130	19
GO:BP	vacuolar transport	2.90E-02	154	21
GO:BP	NADH dehydrogenase complex assembly	3.01E-02	67	13
GO:BP	mitochondrial respiratory chain complex I assembly	3.01E-02	67	13
GO:BP	ribonucleoprotein complex localization	3.06E-02	131	19
GO:MF	ribosome binding	3.56E-02	68	12
GO:MF	translation initiation factor activity	3.59E-02	58	11
GO:BP	obsolete oxidation-reduction process	4.15E-02	475	44
GO:BP	protein stabilization	4.20E-02	195	24
GO:MF	helicase activity	4.24E-02	163	20
GO:BP	endoplasmic reticulum to Golgi vesicle-mediated transport	4.27E-02	208	25

End of Table

J LN18 Cycloheximide Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mRNA processing	3.92E-14	532	64
GO:BP	mRNA metabolic process	1.32E-11	880	81
GO:BP	RNA splicing, via transesterification reactions	1.32E-11	363	48
GO:BP	mRNA splicing, via spliceosome	4.18E-11	360	47
GO:BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	4.18E-11	360	47
GO:BP	RNA splicing	1.44E-10	459	53
GO:MF	cadherin binding	8.33E-10	333	42
GO:MF	cell adhesion molecule binding	5.79E-06	544	48
GO:MF	phosphatase binding	7.50E-06	199	26
GO:MF	actin binding	9.44E-06	449	42
GO:MF	protein domain specific binding	1.47E-05	706	56
GO:BP	actin filament organization	2.51E-04	445	40
GO:BP	regulation of mRNA metabolic process	3.90E-04	384	36
GO:BP	cell division	8.33E-04	630	49
GO:BP	actin cytoskeleton organization	1.09E-03	712	53
GO:BP	protein-containing complex disassembly	1.42E-03	337	32
GO:BP	chromatin organization	1.61E-03	839	59
GO:BP	positive regulation of mRNA metabolic process	2.33E-03	144	19
GO:BP	mitotic nuclear division	2.53E-03	346	32
GO:BP	regulation of mRNA processing	2.59E-03	145	19
GO:BP	histone modification	3.06E-03	472	39
GO:MF	telomerase RNA binding	4.41E-03	22	7
GO:BP	actin filament-based process	5.25E-03	810	56
GO:BP	positive regulation of DNA-templated transcription, elongation	5.26E-03	26	8
GO:BP	covalent chromatin modification	6.24E-03	486	39
GO:BP	supramolecular fiber organization	8.31E-03	863	58
GO:MF	SH3 domain binding	8.89E-03	129	16
GO:MF	protein phosphorylated amino acid binding	1.49E-02	56	10
GO:BP	actin polymerization or depolymerization	3.79E-02	221	22
GO:MF	phosphoprotein binding	3.95E-02	88	12

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:MF	actin monomer binding	4.10E-02	30	7
GO:BP	mitotic spindle assembly	4.76E-02	66	11
GO:BP	mRNA 3′-end processing	4.76E-02	104	14
End of Table				

K U87 Cycloheximide Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitochondrial translation	7.79E-08	135	28
GO:BP	mitochondrial gene expression	1.20E-07	166	31
GO:BP	translational elongation	3.55E-05	143	25
GO:BP	translational termination	3.66E-05	104	21
GO:BP	mitochondrial translational elongation	4.59E-05	87	19
GO:BP	mitochondrial translational termination	5.60E-05	88	19
GO:BP	ncRNA transcription	1.03E-04	110	21
GO:BP	DNA metabolic process	2.01E-04	976	84
GO:BP	nucleobase-containing small molecule metabolic process	4.99E-04	628	60
GO:BP	DNA repair	1.27E-03	586	56
GO:BP	cellular response to DNA damage stimulus	1.39E-03	894	76
GO:BP	protein localization to organelle	1.42E-03	974	81
GO:BP	mRNA metabolic process	1.50E-03	880	75
GO:BP	antigen processing and presentation of endogenous peptide antigen via MHC class I	1.64E-03	13	7
GO:MF	rRNA binding	1.65E-03	68	14
GO:BP	ncRNA processing	2.56E-03	439	45
GO:MF	catalytic activity, acting on RNA	2.89E-03	394	40
GO:BP	intracellular protein transport	3.32E-03	995	81
GO:BP	modification-dependent macromolecule catabolic process	3.51E-03	681	61
GO:BP	ncRNA metabolic process	4.38E-03	535	51
GO:BP	proteolysis involved in cellular protein catabolic process	7.65E-03	760	65
GO:BP	modification-dependent protein catabolic process	8.93E-03	670	59
GO:BP	ribosome biogenesis	1.04E-02	335	36

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:BP	peptide metabolic process	1.29E-02	998	79
GO:BP	translation	1.29E-02	804	67
GO:BP	ubiquitin-dependent protein catabolic process	1.32E-02	663	58
GO:BP	transcription-coupled nucleotide-excision repair	1.43E-02	72	14
GO:BP	snRNA transcription by RNA polymerase II	1.69E-02	73	14
GO:BP	DNA-templated transcription, elongation	1.80E-02	104	17
GO:BP	Golgi vesicle transport	1.89E-02	415	41
GO:BP	snRNA transcription	2.00E-02	74	14
GO:BP	nucleic acid phosphodiester bond hydrolysis	2.39E-02	306	33
GO:BP	cellular protein catabolic process	2.68E-02	822	67
GO:MF	nucleoside-triphosphate diphosphatase activity	2.71E-02	10	5
GO:BP	cellular protein complex disassembly	2.81E-02	228	27
GO:BP	nucleotide metabolic process	2.82E-02	541	49
GO:BP	amide biosynthetic process	3.35E-02	975	76
GO:BP	transcription elongation from RNA polymerase II promoter	3.62E-02	88	15
GO:BP	antigen processing and presentation of endogenous peptide antigen	3.75E-02	19	7
GO:BP	regulation of viral transcription	3.77E-02	41	10
GO:BP	mRNA processing	3.82E-02	532	48
GO:BP	ribonucleoprotein complex biogenesis	4.07E-02	473	44
GO:MF	protein N-terminus binding	4.24E-02	112	16
GO:BP	peptide biosynthetic process	4.26E-02	834	67
End of Table				

L U87 Cycloheximide Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mRNA metabolic process	1.00E-07	880	43
GO:BP	viral transcription	1.11E-05	181	17
GO:BP	cellular nitrogen compound catabolic process	5.36E-04	623	29
GO:BP	viral gene expression	5.93E-04	237	17
GO:BP	RNA catabolic process	9.91E-04	431	23
Continued on next page				

source	term name	adjusted p-value	term size	intersection size
GO:BP	nucleobase-containing compound catabolic process	1.13E-03	573	27
GO:BP	heterocycle catabolic process	1.46E-03	617	28
GO:BP	mRNA catabolic process	2.56E-03	388	21
GO:BP	aromatic compound catabolic process	2.66E-03	636	28
GO:BP	translation	3.91E-03	804	32
GO:MF	structural molecule activity	5.12E-03	701	28
GO:BP	organic cyclic compound catabolic process	6.12E-03	664	28
GO:BP	peptide biosynthetic process	8.46E-03	834	32
GO:BP	nucleus organization	1.01E-02	148	12
GO:MF	structural constituent of ribosome	1.09E-02	171	12
GO:MF	nucleosomal DNA binding	1.69E-02	39	6
GO:BP	nuclear-transcribed mRNA catabolic process	2.01E-02	214	14
GO:MF	chromatin DNA binding	2.12E-02	103	9
GO:BP	mRNA processing	3.36E-02	532	23
End of Table				

M HL60 Pateamine A Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	endosomal transport	1.58E-04	244	31
GO:BP	intracellular protein transport	3.84E-04	995	78
GO:BP	mitochondrion organization	2.51E-03	565	50
GO:BP	organelle localization	3.85E-02	657	52
End of Table				

N HL60 Pateamine A Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitotic cell cycle process	2.35E-10	956	55
GO:BP	regulation of cell cycle process	4.59E-09	815	48
GO:BP	chromatin organization	1.68E-05	839	42
GO:BP	DNA metabolic process	1.97E-05	976	46
GO:BP	spindle organization	3.95E-05	256	21
GO:BP	cell cycle phase transition	5.48E-05	681	36
GO:BP	regulation of cell cycle phase transition	9.75E-05	543	31
GO:BP	mitotic nuclear division	9.76E-05	346	24
GO:BP	mitotic cell cycle phase transition	1.77E-04	588	32
GO:BP	mitotic sister chromatid segregation	1.78E-04	185	17
GO:BP	cell division	2.68E-04	630	33
GO:BP	sister chromatid segregation	2.85E-04	214	18
GO:BP	negative regulation of cell cycle process	3.81E-04	400	25
GO:BP	regulation of mitotic cell cycle	4.37E-04	612	32
GO:BP	regulation of mitotic cell cycle phase transition	1.12E-03	453	26
GO:BP	microtubule cytoskeleton organization involved in mitosis	1.43E-03	214	17
GO:BP	DNA repair	1.66E-03	586	30
GO:BP	cellular response to DNA damage stimulus	2.08E-03	894	39
GO:BP	mRNA metabolic process	3.69E-03	880	38
GO:BP	negative regulation of cell cycle	4.31E-03	487	26
GO:MF	modification-dependent protein binding	6.15E-03	160	13
GO:BP	peptide biosynthetic process	7.11E-03	834	36
GO:BP	translation	8.14E-03	804	35
GO:BP	mitotic spindle organization	9.08E-03	194	15
GO:BP	mitochondrial translational elongation	1.15E-02	87	10
GO:MF	structural constituent of ribosome	1.25E-02	171	13
GO:BP	mitochondrial translational termination	1.28E-02	88	10
GO:BP	ribosome biogenesis	1.31E-02	335	20
GO:BP	cellular response to ionizing radiation	1.51E-02	71	9
GO:BP	protein localization to organelle	1.61E-02	974	39
GO:BP	spindle assembly	2.37E-02	115	11
GO:BP	DNA replication checkpoint signaling	2.49E-02	17	5
GO:BP	nuclear chromosome segregation	2.59E-02	293	18

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:MF	histone binding	3.02E-02	240	15
GO:BP	negative regulation of cell cycle phase transition	3.56E-02	329	19
End of Table				

O LN18 Pateamine A Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitochondrion organization	2.26E-09	565	72
GO:BP	ncRNA transcription	6.39E-07	110	25
GO:BP	endosomal transport	6.73E-07	244	39
GO:BP	snRNA transcription by RNA polymerase II	1.16E-06	73	20
GO:BP	snRNA transcription	1.51E-06	74	20
GO:BP	intracellular protein transport	3.86E-06	995	96
GO:BP	7-methylguanosine mRNA capping	9.35E-06	33	13
GO:BP	RNA capping	1.44E-05	34	13
GO:BP	7-methylguanosine RNA capping	1.44E-05	34	13
GO:BP	ncRNA processing	1.19E-04	439	51
GO:BP	translational termination	1.59E-04	104	21
GO:BP	mitochondrial translational elongation	1.80E-04	87	19
GO:BP	transcription elongation from RNA polymerase II promoter	2.19E-04	88	19
GO:BP	mitochondrial translational termination	2.19E-04	88	19
GO:BP	ribosome biogenesis	2.26E-04	335	42
GO:BP	protein-containing complex disassembly	2.68E-04	337	42
GO:BP	Golgi vesicle transport	3.39E-04	415	48
GO:BP	ncRNA metabolic process	3.93E-04	535	57
GO:BP	mitochondrial respiratory chain complex I assembly	5.25E-04	67	16
GO:BP	NADH dehydrogenase complex assembly	5.25E-04	67	16
GO:BP	mitochondrial respiratory chain complex assembly	6.40E-04	103	20
GO:BP	rRNA metabolic process	6.51E-04	275	36
GO:BP	translational elongation	7.38E-04	143	24
GO:BP	DNA-templated transcription, elongation	7.55E-04	104	20
GO:BP	mitochondrial translation	9.87E-04	135	23

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:MF	NADH dehydrogenase (ubiquinone) activity	1.04E-03	45	12
GO:MF	NADH dehydrogenase (quinone) activity	1.34E-03	46	12
GO:BP	cytosolic transport	1.39E-03	169	26
GO:BP	regulation of viral transcription	1.66E-03	41	12
GO:MF	NADH dehydrogenase activity	1.72E-03	47	12
GO:BP	process utilizing autophagic mechanism	2.23E-03	564	57
GO:BP	autophagy	2.23E-03	564	57
GO:BP	rRNA processing	2.24E-03	265	34
GO:MF	NAD(P)H dehydrogenase (quinone) activity	2.75E-03	49	12
GO:BP	amide biosynthetic process	2.95E-03	975	85
GO:BP	mitochondrial gene expression	3.43E-03	166	25
GO:BP	positive regulation of viral transcription	4.14E-03	24	9
GO:BP	cellular protein complex disassembly	5.79E-03	228	30
GO:MF	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	5.85E-03	61	13
GO:BP	transcription-coupled nucleotide-excision repair	8.05E-03	72	15
GO:BP	vesicle-mediated transport to the plasma membrane	8.08E-03	141	22
GO:MF	nucleotidyltransferase activity	9.49E-03	134	20
GO:BP	cellular component disassembly	9.76E-03	577	56
GO:BP	mitochondrial electron transport, NADH to ubiquinone	1.02E-02	56	13
GO:BP	retrograde transport, endosome to Golgi	1.03E-02	92	17
GO:BP	protein targeting	1.06E-02	400	43
GO:MF	structural constituent of ribosome	1.31E-02	171	23
GO:BP	peptide metabolic process	1.37E-02	998	84
GO:BP	ribonucleoprotein complex biogenesis	1.47E-02	473	48
GO:BP	localization within membrane	1.55E-02	775	69
GO:BP	inner mitochondrial membrane organization	1.55E-02	58	13
GO:BP	oxidative phosphorylation	2.52E-02	151	22
GO:MF	DNA-directed 5′-3′ RNA polymerase activity	2.70E-02	43	10
GO:BP	peptide biosynthetic process	2.82E-02	834	72
GO:BP	translation	2.83E-02	804	70
GO:MF	molecular carrier activity	3.20E-02	71	13
GO:MF	oxidoreductase activity, acting on NAD(P)H	3.66E-02	92	15
GO:BP	DNA-templated transcription, initiation	4.04E-02	289	33
GO:MF	5′-3′ RNA polymerase activity	4.09E-02	45	10
GO:MF	RNA polymerase activity	4.09E-02	45	10

Continued on next page

source	term name	adjusted p-value	term size	intersection size
GO:MF	catalytic activity, acting on RNA	4.28E-02	394	39
GO:BP	transcription initiation from RNA polymerase II promoter	4.29E-02	227	28
GO:BP	glycoside catabolic process	4.60E-02	8	5
End of Table				

P LN18 Pateamine A Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mitotic nuclear division	2.19E-03	346	24
GO:BP	mRNA metabolic process	2.41E-03	880	43
GO:BP	cell division	1.13E-02	630	33
GO:BP	sister chromatid segregation	1.51E-02	214	17
GO:BP	mitotic sister chromatid segregation	4.18E-02	185	15
End of Table				

Q U87 Pateamine A Upregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	ncRNA metabolic process	6.29E-06	535	52
GO:BP	mitochondrial gene expression	2.37E-05	166	25
GO:BP	mitochondrial translation	4.19E-05	135	22
GO:BP	ncRNA processing	4.39E-05	439	44
GO:BP	ribonucleoprotein complex biogenesis	5.25E-05	473	46
GO:BP	mitochondrion organization	1.03E-04	565	51
GO:BP	mRNA processing	2.64E-04	532	48
GO:BP	mRNA metabolic process	2.74E-04	880	68
GO:BP	peptide metabolic process	7.89E-04	998	73
GO:BP	translation	1.10E-03	804	62
GO:BP	amide biosynthetic process	1.37E-03	975	71
Continued on next page				

source	term name	adjusted p-value	term size	intersection size
GO:BP	DNA metabolic process	1.42E-03	976	71
GO:BP	DNA-templated transcription, elongation	1.67E-03	104	17
GO:BP	translational termination	1.67E-03	104	17
GO:MF	catalytic activity, acting on RNA	1.96E-03	394	36
GO:BP	cellular response to DNA damage stimulus	2.18E-03	894	66
GO:BP	mitochondrial translational elongation	3.73E-03	87	15
GO:BP	peptide biosynthetic process	3.77E-03	834	62
GO:BP	transcription elongation from RNA polymerase II promoter	4.34E-03	88	15
GO:BP	mitochondrial translational termination	4.34E-03	88	15
GO:BP	DNA repair	4.39E-03	586	48
GO:BP	ribonucleoprotein complex subunit organization	4.55E-03	203	24
GO:MF	isomerase activity	9.67E-03	171	20
GO:BP	ribosome biogenesis	1.09E-02	335	32
GO:BP	secondary alcohol biosynthetic process	1.68E-02	64	12
GO:BP	cholesterol biosynthetic process	1.68E-02	64	12
GO:BP	RNA splicing	1.75E-02	459	39
GO:BP	RNA splicing, via transesterification reactions	2.21E-02	363	33
GO:BP	RNA-dependent DNA biosynthetic process	2.34E-02	77	13
GO:BP	ribonucleoprotein complex assembly	2.80E-02	196	22
GO:BP	mitochondrial respiratory chain complex assembly	3.21E-02	103	15
GO:BP	sterol biosynthetic process	4.36E-02	70	12
GO:BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	4.73E-02	360	32
GO:BP	mRNA splicing, via spliceosome	4.73E-02	360	32

End of Table

R U87 Pateamine A Downregulated BP and MF

source	term name	adjusted p-value	term size	intersection size
GO:BP	mRNA processing	5.51E-04	532	26
GO:MF	nucleosomal DNA binding	8.81E-04	39	7
GO:BP	RNA splicing	1.83E-03	459	23
GO:BP	mRNA metabolic process	1.90E-03	880	34
GO:BP	organelle localization	2.93E-03	657	28
GO:BP	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	8.08E-03	360	19
GO:BP	mRNA splicing, via spliceosome	8.08E-03	360	19
GO:BP	RNA splicing, via transesterification reactions	9.11E-03	363	19
GO:MF	chromatin DNA binding	1.41E-02	103	9
GO:BP	ncRNA processing	3.95E-02	439	20
GO:MF	nucleosome binding	4.55E-02	70	7
GO:MF	single-stranded DNA binding	4.98E-02	121	9

End of Table

S HL60 Cycloheximide Genes

accession	description	fold p change	adjusted p-value
Q9BVA1	Tubulin beta-2B chain	100.0	9.64E-17
Q96E39	RNA binding motif protein, X-linked-like-1	100.0	9.64E-17
Q15366-4	Isoform 4 of Poly(rC)-binding protein 2	100.0	9.64E-17
Q9Y2Z0-2	Isoform 2 of Protein SGT1 homolog	100.0	9.64E-17
P62714	serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	100.0	9.64E-17
P35749	Myosin-11	100.0	9.64E-17
P29590-5	Isoform PML-4 of Protein PML	100.0	9.64E-17
Q9BZK3	Putative nascent polypeptide-associated complex subunit alpha-like protein	100.0	9.64E-17
Q5JSL3	dedicator of cytokinesis protein 11	100.0	9.64E-17
Q03426	mevalonate kinase	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P63098	Calcineurin subunit B type 1	100.0	9.64E-17
Q6ZNJ1-1	Neurobeachin-like protein 2	100.0	9.64E-17
P60510	Serine/threonine-protein phosphatase 4 catalytic subunit	100.0	9.64E-17
Q8TD16	Protein bicaudal D homolog 2	100.0	9.64E-17
P42345	Serine/threonine-protein kinase mTOR	100.0	9.64E-17
P51617	interleukin-1 receptor-associated kinase 1	100.0	9.64E-17
Q9Y3I1	F-box only protein 7	100.0	9.64E-17
Q03169	Tumor necrosis factor alpha-induced protein 2	100.0	9.64E-17
O60244	Mediator of RNA polymerase II transcription subunit 14	100.0	9.64E-17
P30260	cell division cycle protein 27 homolog	100.0	9.64E-17
Q9Y4R8	telomere length regulation protein TEL2 homolog	100.0	9.64E-17
Q99622	Protein C10	100.0	9.64E-17
Q69YN4	protein virilizer homolog	100.0	9.64E-17
Q8NCG7	Sn1-specific diacylglycerol lipase beta	100.0	9.64E-17
Q2TAL8	Glutamine-rich protein 1	100.0	9.64E-17
O75116	Rho-associated protein kinase 2	100.0	9.64E-17
Q12962	transcription initiation factor TFIID subunit 10	100.0	9.64E-17
Q15386-1	Ubiquitin-protein ligase E3C	100.0	9.64E-17
O60603	toll-like receptor 2	100.0	9.64E-17
Q96SB3	Neurabin-2	100.0	9.64E-17
P50749	Ras association domain-containing protein 2	100.0	9.64E-17
Q96JB2-1	Conserved oligomeric Golgi complex subunit 3	100.0	9.64E-17
Q9UJY5-1	ADP-ribosylation factor-binding protein GGA1	100.0	9.64E-17
Q15257-1	Serine/threonine-protein phosphatase 2A activator	100.0	9.64E-17
Q14149	MORC family CW-type zinc finger protein 3	100.0	9.64E-17
Q96II8-1	Leucine-rich repeat and calponin homology domain-containing protein 3	100.0	9.64E-17
O00762	Ubiquitin-conjugating enzyme E2 C	100.0	9.64E-17
Q5JS54-1	Proteasome assembly chaperone 4	100.0	9.64E-17
Q9UJX4	Anaphase-promoting complex subunit 5	100.0	9.64E-17
Q9Y6B6	GTP-binding protein SAR1b	100.0	9.64E-17
Q13496	Myotubularin	100.0	9.64E-17
O43542	DNA repair protein XRCC3	100.0	9.64E-17
Q86Y82	Syntaxin-12	100.0	9.64E-17
Q6JQN1	Acyl-CoA dehydrogenase family member 10	100.0	9.64E-17
Q9BXW6-1	Oxysterol-binding protein-related protein 1	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O95292	Vesicle-associated membrane protein-associated protein B/C	100.0	9.64E-17
P17612	cAMP-dependent protein kinase catalytic subunit alpha	100.0	9.64E-17
Q96IJ6	Mannose-1-phosphate guanyltransferase alpha	100.0	9.64E-17
O75925	E3 SUMO-protein ligase PIAS1	100.0	9.64E-17
Q96C36	Pyrroline-5-carboxylate reductase 2	100.0	9.64E-17
Q7Z7H5	Transmembrane emp24 domain-containing protein 4	100.0	9.64E-17
Q8WY22	BRI3-binding protein	100.0	9.64E-17
P27986	Phosphatidylinositol 3-kinase regulatory subunit alpha	100.0	9.64E-17
O00411	DNA-directed RNA polymerase, mitochondrial	100.0	9.64E-17
Q8NC56-1	LEM domain-containing protein 2	100.0	9.64E-17
Q53H96	Pyrroline-5-carboxylate reductase 3	100.0	9.64E-17
Q9NZV5-1	Selenoprotein N	100.0	9.64E-17
Q9H2H9	Sodium-coupled neutral amino acid transporter 1	100.0	9.64E-17
O75995	SAM and SH3 domain-containing protein 3	100.0	9.64E-17
Q7Z7A4-1	PX domain-containing protein kinase-like protein	100.0	9.64E-17
P46199	Translation initiation factor IF-2, mitochondrial	100.0	9.64E-17
Q13488	V-type proton ATPase 116 kDa subunit a isoform 3	100.0	9.64E-17
P63172	Dynein light chain Tctex-type 1	100.0	9.64E-17
P43307	Translocon-associated protein subunit alpha	100.0	9.64E-17
Q96RS6	NudC domain-containing protein 1	100.0	9.64E-17
Q9NPJ6-1	mediator of RNA polymerase II transcription subunit 4	100.0	9.64E-17
Q86Y91	Kinesin-like protein KIF18B	100.0	9.64E-17
Q9BW72	HIG1 domain family member 2A, mitochondrial	100.0	9.64E-17
Q9NQW6	Anillin	100.0	9.64E-17
Q9Y6A9	Signal peptidase complex subunit 1	100.0	9.64E-17
P48059	LIM and senescent cell antigen-like-containing domain protein 1	100.0	9.64E-17
Q8N999-1	Uncharacterized protein C12orf29	100.0	9.64E-17
Q1ED39	Lysine-rich nucleolar protein 1	100.0	9.64E-17
Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	100.0	9.64E-17
Q5HYK3-1	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	100.0	9.64E-17
Q9H813	Transmembrane protein 206	100.0	9.64E-17
Q9P2N6	KAT8 regulatory NSL complex subunit 3	100.0	9.64E-17
Q8NB90-1	Spermatogenesis-associated protein 5	100.0	9.64E-17
Q9H0A8-1	COMM domain-containing protein 4	100.0	9.64E-17
P12318	Low affinity immunoglobulin gamma Fc region receptor II-a	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P49761-1	Isoform 1 of Dual specificity protein kinase CLK3	100.0	9.64E-17
Q15018	BRISC complex subunit Abraxas 2	100.0	9.64E-17
Q96I59	probable asparagine–tRNA ligase, mitochondrial	100.0	9.64E-17
Q6ZSR9	Uncharacterized protein FLJ45252	100.0	9.64E-17
Q9NZ53-1	Podocalyxin-like protein 2	100.0	9.64E-17
Q8TEQ8-1	GPI ethanolamine phosphate transferase 3	100.0	9.64E-17
Q15648	Mediator of RNA polymerase II transcription subunit 1	100.0	9.64E-17
Q9C0B0	RING finger protein unkempt homolog	100.0	9.64E-17
Q8N490	Probable hydrolase PNKD	100.0	9.64E-17
Q86VI3	Ras GTPase-activating-like protein IQGAP3	100.0	9.64E-17
Q9UL33-1	Trafficking protein particle complex subunit 2-like protein	100.0	9.64E-17
Q9HBU6-1	ethanolamine kinase 1	100.0	9.64E-17
Q9H840	Gem-associated protein 7	100.0	9.64E-17
Q96SI1-1	BTB/POZ domain-containing protein KCTD15	100.0	9.64E-17
Q9H9Q4-1	non-homologous end-joining factor 1	100.0	9.64E-17
P52758	2-iminobutanoate/2-iminopropanoate deaminase	100.0	9.64E-17
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog	100.0	9.64E-17
Q8NHZ8	Anaphase-promoting complex subunit CDC26	100.0	9.64E-17
Q9BRR9	Rho GTPase-activating protein 9	100.0	9.64E-17
P04004	Vitronectin	100.0	9.64E-17
Q9BVW5	TIMELESS-interacting protein	100.0	9.64E-17
P36888	Receptor-type tyrosine-protein kinase FLT3	100.0	9.64E-17
Q643R3	lysophospholipid acyltransferase LPCAT4	100.0	9.64E-17
Q9Y2X0-1	Mediator of RNA polymerase II transcription subunit 16	100.0	9.64E-17
Q9NRW7	Vacuolar protein sorting-associated protein 45	100.0	9.64E-17
Q9NSU2-1	Three-prime repair exonuclease 1	100.0	9.64E-17
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial	100.0	9.64E-17
Q9NR19-1	Acetyl-coenzyme A synthetase, cytoplasmic	100.0	9.64E-17
Q9H008-1	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	100.0	9.64E-17
Q6NW29	RWD domain-containing protein 4	100.0	9.64E-17
Q86WX3	Active regulator of SIRT1	100.0	9.64E-17
O43865	S-adenosylhomocysteine hydrolase-like protein 1	100.0	9.64E-17
P28749-1	Retinoblastoma-like protein 1	100.0	9.64E-17
Q8WUA7	TBC1 domain family member 22A	100.0	9.64E-17
Q92833	Protein Jumonji	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8N0V3-1	Putative ribosome-binding factor A, mitochondrial	100.0	9.64E-17
Q9Y221-1	60S ribosome subunit biogenesis protein NIP7 homolog	100.0	9.64E-17
O75818-1	Ribonuclease P protein subunit p40	100.0	9.64E-17
Q7L8W6	Diphthine–ammonia ligase	100.0	9.64E-17
Q13627-1	dual specificity tyrosine-phosphorylation-regulated kinase 1A	100.0	9.64E-17
Q96TC7	Regulator of microtubule dynamics protein 3	100.0	9.64E-17
P61803	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase subunit DAD1	100.0	9.64E-17
Q03111	Protein ENL	100.0	9.64E-17
P78362-1	SRSF protein kinase 2	100.0	9.64E-17
Q9H9C1-1	Spermatogenesis-defective protein 39 homolog	100.0	9.64E-17
Q14764	major vault protein	100.0	9.64E-17
Q5TEU4	Arginine-hydroxylase NDUFAF5, mitochondrial	100.0	9.64E-17
Q5J8M3-1	ER membrane protein complex subunit 4	100.0	9.64E-17
Q9Y657	Spindlin-1	100.0	9.64E-17
Q9BQ15-1	SOSS complex subunit B1	100.0	9.64E-17
Q8ND04	Protein SMG8	100.0	9.64E-17
Q9NWZ5-1	Uridine-cytidine kinase-like 1	100.0	9.64E-17
Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	100.0	9.64E-17
P62256	ubiquitin-conjugating enzyme E2 H	100.0	9.64E-17
O60701	UDP-glucose 6-dehydrogenase	100.0	9.64E-17
Q96PV6-2	Isoform 2 of Leukocyte receptor cluster member 8	100.0	9.64E-17
P16383-1	GC-rich sequence DNA-binding factor 2	100.0	9.64E-17
Q9UHB6	LIM domain and actin-binding protein 1	100.0	9.64E-17
Q7KZI7-1	Serine/threonine-protein kinase MARK2	100.0	9.64E-17
Q9P260-1	LisH domain and HEAT repeat-containing protein KIAA1468	100.0	9.64E-17
Q9UPT5	Exocyst complex component 7	100.0	9.64E-17
O75884-1	Putative hydrolase RBBP9	100.0	9.64E-17
Q96CW6	Probable RNA polymerase II nuclear localization protein SLC7A6OS	100.0	9.64E-17
P16234-1	Platelet-derived growth factor receptor alpha	100.0	9.64E-17
P48651	phosphatidylserine synthase 1	100.0	9.64E-17
O75164-1	Lysine-specific demethylase 4A	100.0	9.64E-17
Q13884	Beta-1-syntrophin	100.0	9.64E-17
Q99081-1	Transcription factor 12	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96ME1	F-box/LRR-repeat protein 18	100.0	9.64E-17
Q9ULP9	TBC1 domain family member 24	100.0	9.64E-17
Q8TDW4-1	Suppressor of tumorigenicity 7 protein-like	100.0	9.64E-17
P20585	DNA mismatch repair protein MSH3	100.0	9.64E-17
Q9BXX0	EMILIN-2	100.0	9.64E-17
Q9BW61	DET1- and DDB1-associated protein 1	100.0	9.64E-17
O15554	intermediate conductance calcium-activated potassium channel protein 4	100.0	9.64E-17
Q8TE02-1	elongator complex protein 5	100.0	9.64E-17
Q8NC42	E3 ubiquitin-protein ligase RNF149	100.0	9.64E-17
Q9BRQ0	Pygopus homolog 2	100.0	9.64E-17
O14957	cytochrome b-c1 complex subunit 10	100.0	9.64E-17
Q8WXE1	ATR-interacting protein	100.0	9.64E-17
Q5TA45-1	Integrator complex subunit 11	100.0	9.64E-17
Q93050-1	Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1	100.0	9.64E-17
O14556	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	100.0	9.64E-17
Q2TAA5	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase	100.0	9.64E-17
Q52LR7	enhancer of polycomb homolog 2	100.0	9.64E-17
O75319-1	RNA/RNP complex-1-interacting phosphatase	100.0	9.64E-17
Q5JPH6	Probable glutamate–tRNA ligase, mitochondrial	100.0	9.64E-17
Q68CQ7-1	Glycosyltransferase 8 domain-containing protein 1	100.0	9.64E-17
O00311-1	Cell division cycle 7-related protein kinase	100.0	9.64E-17
A2RUS2	DENN domain-containing protein 3	100.0	9.64E-17
Q9P0U3-1	Sentrin-specific protease 1	100.0	9.64E-17
P50583	Bis(5′-nucleosyl)-tetraphosphatase [asymmetrical]	100.0	9.64E-17
Q9H9T3	elongator complex protein 3	100.0	9.64E-17
Q8WXG6-1	MAP kinase-activating death domain protein	100.0	9.64E-17
Q8N4J0	carnosine N-methyltransferase	100.0	9.64E-17
Q99996	A-kinase anchor protein 9	100.0	9.64E-17
Q6P179	Endoplasmic reticulum aminopeptidase 2	100.0	9.64E-17
P04920-1	Anion exchange protein 2	100.0	9.64E-17
P61225	ras-related protein Rap-2b	100.0	9.64E-17
O60294	tRNA wybutosine-synthesizing protein 4	100.0	9.64E-17
Q5JTD0-1	Tight junction-associated protein 1	100.0	9.64E-17
O60504-1	Vinexin	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q14CZ7	FAST kinase domain-containing protein 3, mitochondrial	100.0	9.64E-17
Q8IUF8	ribosomal oxygenase 2	100.0	9.64E-17
Q92820	Gamma-glutamyl hydrolase	100.0	9.64E-17
Q86VR2	Reticulophagy regulator 3	100.0	9.64E-17
Q15800	Methylsterol monooxygenase 1	100.0	9.64E-17
Q9UKK3	Poly [ADP-ribose] polymerase 4	100.0	9.64E-17
Q9Y3E7	Charged multivesicular body protein 3	100.0	9.64E-17
Q9H967	WD repeat-containing protein 76	100.0	9.64E-17
Q6UXH1	Cysteine-rich with EGF-like domain protein 2	100.0	9.64E-17
Q86UV5	Ubiquitin carboxyl-terminal hydrolase 48	100.0	9.64E-17
Q8IWI9-1	MAX gene-associated protein	100.0	9.64E-17
Q9Y312	Protein AAR2 homolog	100.0	9.64E-17
Q8N884	cyclic GMP-AMP synthase	100.0	9.64E-17
Q9Y4E5	E3 SUMO-protein ligase ZNF451	100.0	9.64E-17
P78346-1	ribonuclease P protein subunit p30	100.0	9.64E-17
Q13617-1	Cullin-2	100.0	9.64E-17
Q86Y07	serine/threonine-protein kinase VRK2	100.0	9.64E-17
Q96NT0	Coiled-coil domain-containing protein 115	100.0	9.64E-17
Q9Y6X3-1	MAU2 chromatid cohesion factor homolog	100.0	9.64E-17
Q9NYV6	RNA polymerase I-specific transcription initiation factor RRN3	100.0	9.64E-17
P31749	RAC-alpha serine/threonine-protein kinase	100.0	9.64E-17
Q15311	RalA-binding protein 1	100.0	9.64E-17
Q3KQV9	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	100.0	9.64E-17
Q15058	Kinesin-like protein KIF14	100.0	9.64E-17
Q6PK04	Coiled-coil domain-containing protein 137	100.0	9.64E-17
Q6P1R4	tRNA-dihydrouridine(16/17) synthase [NAD(P)(+)]-like	100.0	9.64E-17
Q9UDT6-1	CAP-Gly domain-containing linker protein 2	100.0	9.64E-17
Q96ER9	Coiled-coil domain-containing protein 51	100.0	9.64E-17
Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1	100.0	9.64E-17
Q9Y4U1	Methylmalonic aciduria and homocystinuria type C protein	100.0	9.64E-17
Q9BW83-1	Intraflagellar transport protein 27 homolog	100.0	9.64E-17
Q93074-1	Mediator of RNA polymerase II transcription subunit 12	100.0	9.64E-17
Q9UDW1	cytochrome b-c1 complex subunit 9	100.0	9.64E-17
Q8IYL2	probable tRNA (uracil-O(2)-)-methyltransferase	100.0	9.64E-17
Q7Z4G4	tRNA (guanine(10)-N2)-methyltransferase homolog	100.0	9.64E-17
Q92562	Polyphosphoinositide phosphatase	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8TAD8	Smad nuclear-interacting protein 1	100.0	9.64E-17
Q7RTS9-1	dymeclin	100.0	9.64E-17
O75352	Mannose-P-dolichol utilization defect 1 protein	100.0	9.64E-17
Q9UID3-1	Vacuolar protein sorting-associated protein 51 homolog	100.0	9.64E-17
O15091	Mitochondrial ribonuclease P protein 3	100.0	9.64E-17
Q9HAW4	Claspin	100.0	9.64E-17
O94913	Pre-mRNA cleavage complex 2 protein Pcf11	100.0	9.64E-17
Q06330-1	Recombining binding protein suppressor of hairless	100.0	9.64E-17
Q01831	DNA repair protein complementing XP-C cells	100.0	9.64E-17
Q8WV99	AN1-type zinc finger protein 2B	100.0	9.64E-17
P10619	lysosomal protective protein	100.0	9.64E-17
Q9UP83-1	conserved oligomeric Golgi complex subunit 5	100.0	9.64E-17
Q9Y3D6	mitochondrial fission 1 protein	100.0	9.64E-17
P00846	ATP synthase subunit A	100.0	9.64E-17
Q5THK1-1	Protein PRR14L	100.0	9.64E-17
Q13439-1	Golgin subfamily A member 4	100.0	9.64E-17
Q53H82	Endoribonuclease LACTB2	100.0	9.64E-17
Q6P589	Tumor necrosis factor alpha-induced protein 8-like protein 2	100.0	9.64E-17
Q9NVR2	Integrator complex subunit 10	100.0	9.64E-17
Q7Z392	trafficking protein particle complex subunit 11	100.0	9.64E-17
Q8WVX9	Fatty acyl-CoA reductase 1	100.0	9.64E-17
Q92890-1	Isoform Long of Ubiquitin recognition factor in ER-associated degradation protein 1	100.0	9.64E-17
Q9Y239	Nucleotide-binding oligomerization domain-containing protein 1	100.0	9.64E-17
Q6P1M0	Long-chain fatty acid transport protein 4	100.0	9.64E-17
Q96HQ2-1	CDKN2AIP N-terminal-like protein	100.0	9.64E-17
Q8WUK0	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	100.0	9.64E-17
Q2M3X9-1	zinc finger protein 674	100.0	9.64E-17
Q9H6D8	Fibronectin type III domain-containing protein 4	100.0	9.64E-17
Q9H469	F-box/LRR-repeat protein 15	100.0	9.64E-17
O15498	Synaptobrevin homolog YKT6	100.0	9.64E-17
Q9NZA1-1	Chloride intracellular channel protein 5	100.0	9.64E-17
Q9NYR9-1	NF-kappa-B inhibitor-interacting Ras-like protein 2	100.0	9.64E-17
O95613	Pericentrin	100.0	9.64E-17
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1	100.0	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O94915-1	protein furry homolog-like	100.0	9.64E-17
O15228	Dihydroxyacetone phosphate acyltransferase	100.0	9.64E-17
P78332	RNA-binding protein 6	100.0	9.64E-17
Q7L1S5	carbohydrate sulfotransferase 9	100.0	9.64E-17
O75330-1	Hyaluronan mediated motility receptor	100.0	9.64E-17
Q9BSW2-1	EF-hand calcium-binding domain-containing protein 4B	100.0	9.64E-17
Q13291-4	Isoform 4 of Signaling lymphocytic activation molecule	100.0	9.64E-17
O75915	PRA1 family protein 3	100.0	9.64E-17
Q7Z4S6-1	Kinesin-like protein KIF21A	100.0	9.64E-17
P46063	ATP-dependent DNA helicase Q1	100.0	9.64E-17
Q9Y336	Sialic acid-binding Ig-like lectin 9	100.0	9.64E-17
Q96BT1	Putative uncharacterized protein C3orf49	100.0	9.64E-17
Q502W6-1	von Willebrand factor A domain-containing protein 3B	100.0	9.64E-17
O75695	Protein XRP2	100.0	9.64E-17
Q9P283	Semaphorin-5B	49.39	9.64E-17
Q8TB24-1	Ras and Rab interactor 3	39.00	8.55E-15
O43427	Acidic fibroblast growth factor intracellular-binding protein	33.72	1.27E-03
Q9BRK5-1	45 kDa calcium-binding protein	32.21	1.11E-10
Q969F1	General transcription factor 3C polypeptide 6	31.97	8.08E-06
Q01518-2	Isoform 2 of Adenylyl cyclase-associated protein 1	30.28	2.68E-13
P10153	Non-secretory ribonuclease	29.07	6.30E-10
P55789	FAD-linked sulfhydryl oxidase ALR	28.00	9.10E-03
Q9P2W9	Syntaxin-18	27.22	9.27E-03
Q06265-1	Exosome complex component RRP45	24.96	4.18E-05
Q9NWW5	ceroid-lipofuscinosis neuronal protein 6	24.36	2.77E-04
Q8NBM8	Prenylcysteine oxidase-like	24.01	1.97E-02
Q9Y6A4	Cilia- and flagella-associated protein 20	23.57	1.07E-02
O95630	STAM-binding protein	23.26	3.23E-03
Q9BZD4	kinetochore protein nuf2	23.18	8.32E-06
Q92759	General transcription factor IIH subunit 4	22.55	1.65E-03
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	22.04	5.29E-03
Q9BUN8	Derlin-1	21.84	1.30E-02
Q96JB5	CDK5 regulatory subunit-associated protein 3	21.52	2.64E-02
Q15637-6	Isoform 6 of Splicing factor 1	21.43	4.68E-05
Q02241-1	Kinesin-like protein KIF23	21.18	4.52E-02
O43566	Regulator of G-protein signaling 14	20.59	2.52E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q8TBQ9	Protein kish-A	20.46	3.26E-02
Q9NVI1-1	Isoform 1 of Fanconi anemia group I protein	19.74	6.36E-09
Q27J81	Inverted formin-2	19.65	4.00E-04
Q8TED0	U3 small nucleolar RNA-associated protein 15 homolog	18.99	1.65E-02
Q66K14-1	TBC1 domain family member 9B	18.95	1.42E-03
Q13395	Probable methyltransferase TARBP1	18.56	3.15E-02
P49354	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	18.24	5.59E-03
Q8WU79-1	Stromal membrane-associated protein 2	18.23	1.02E-03
Q6STE5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3	17.80	3.96E-02
Q96RR1-1	Twinkle protein, mitochondrial	17.74	4.28E-02
P33981	Dual specificity protein kinase TTK	17.63	4.75E-02
Q96EX2-5	Isoform 5 of RING finger and transmembrane domain-containing protein 2	17.51	1.73E-05
Q9BQC6	Ribosomal protein 63, mitochondrial	17.30	1.45E-04
Q9NS18	Glutaredoxin-2, mitochondrial	17.11	4.59E-02
Q14186	Transcription factor Dp-1	17.08	1.84E-02
Q8NF37	Lysophosphatidylcholine acyltransferase 1	17.00	5.34E-04
Q9GZT9-1	Egl nine homolog 1	16.95	1.48E-02
P42356	phosphatidylinositol 4-kinase alpha	16.93	1.20E-03
Q13444	Disintegrin and metalloproteinase domain-containing protein 15	16.85	3.95E-02
Q9BTA9-1	WW domain-containing adapter protein with coiled-coil	16.76	7.34E-03
Q92576-1	PHD finger protein 3	16.61	5.71E-03
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	16.59	6.97E-03
P48730-1	Casein kinase I isoform delta	16.56	2.62E-03
Q12872	Splicing factor, suppressor of white-apricot homolog	16.46	3.03E-02
Q9NQ48	Leucine zipper transcription factor-like protein 1	16.41	1.36E-03
Q9BV44	THUMP domain-containing protein 3	16.18	6.45E-03
Q9BSR8	protein YIPF4	16.13	6.88E-03
Q6ZQQ2	spermatogenesis-associated protein 31D1	16.10	3.98E-03
Q3KQU3	MAP7 domain-containing protein 1	15.93	1.61E-04
P19474	E3 ubiquitin-protein ligase TRIM21	15.53	4.06E-02
Q96KA5-1	cleft lip and palate transmembrane protein 1-like protein	15.34	2.80E-04
Q6UUV9-1	CREB-regulated transcription coactivator 1	15.24	4.70E-04
Q99496	E3 ubiquitin-protein ligase RING2	15.18	9.33E-05

Continued on next page

accession	description	fold p change	adjusted p-value
P49760-1	Dual specificity protein kinase CLK2	15.18	4.58E-03
Q7Z434	Mitochondrial antiviral-signaling protein	15.12	6.52E-03
Q9UER7-1	Death domain-associated protein 6	15.09	2.19E-04
P53007	Tricarboxylate transport protein, mitochondrial	15.06	3.87E-04
Q02083	N-acylethanolamine-hydrolyzing acid amidase	14.91	3.33E-12
P60604	Ubiquitin-conjugating enzyme E2 G2	14.87	2.66E-02
Q96EV8-1	dysbindin	14.72	5.18E-03
P49593	Protein phosphatase 1F	14.55	8.36E-08
O60344-4	Isoform D of Endothelin-converting enzyme 2	14.32	3.48E-04
P54619-1	5′-AMP-activated protein kinase subunit gamma-1	14.29	4.03E-02
Q9H3S1-1	Semaphorin-4A	14.17	3.94E-02
Q8N1F8	Serine/threonine-protein kinase 11-interacting protein	14.14	3.56E-02
Q9H074	Polyadenylate-binding protein-interacting protein 1	13.88	8.70E-03
P51649-1	Succinate-semialdehyde dehydrogenase, mitochondrial	13.87	1.30E-03
Q8WWI5	choline transporter-like protein 1	13.82	1.03E-02
Q14155-1	Isoform 1 of Rho guanine nucleotide exchange factor 7	13.80	4.92E-02
Q9BYC9	39S ribosomal protein L20, mitochondrial	13.77	3.21E-03
Q49AR2-1	UPF0489 protein C5orf22	13.72	4.12E-03
Q9NV31	U3 small nucleolar ribonucleoprotein protein IMP3	13.71	1.12E-07
O14727	apoptotic protease-activating factor 1	13.51	3.24E-03
P49795	Regulator of G-protein signaling 19	13.47	9.06E-03
P23497	Nuclear autoantigen Sp-100	13.29	2.41E-03
Q93034	Cullin-5	13.20	9.31E-03
P82663	28S ribosomal protein S25, mitochondrial	13.13	6.24E-03
Q9Y4P3	Transducin beta-like protein 2	13.11	1.79E-04
Q9GZT8-1	NIF3-like protein 1	12.99	3.11E-04
Q96NW4	Ankyrin repeat domain-containing protein 27	12.97	4.44E-02
Q9UJX5	Anaphase-promoting complex subunit 4	12.82	4.76E-02
Q9Y244	Proteasome maturation protein	12.79	1.46E-03
P01040	Cystatin-A	12.74	8.81E-04
P79522	Proline-rich protein 3	12.57	4.72E-03
Q9NRY2-1	SOSS complex subunit C	12.53	5.46E-03
Q9NWS8	Required for meiotic nuclear division protein 1 homolog	12.37	3.14E-02
Q86UY6	N-alpha-acetyltransferase 40	12.37	3.16E-03
Q96HR8	H/ACA ribonucleoprotein complex non-core subunit NAF1	12.24	1.07E-03
P17706-1	Tyrosine-protein phosphatase non-receptor type 2	12.16	4.49E-06

Continued on next page

accession	description	fold p change	adjusted p-value
P39880-3	Isoform 3 of Homeobox protein cut-like 1	12.16	2.49E-02
Q9NVM4	Protein arginine N-methyltransferase 7	12.09	8.19E-03
Q14790-1	Caspase-8	12.03	1.43E-02
O00459	Phosphatidylinositol 3-kinase regulatory subunit beta	11.97	4.30E-02
Q9NV56	MRG/MORF4L-binding protein	11.84	2.09E-02
P53602	Diphosphomevalonate decarboxylase	11.81	1.97E-02
P83436	Conserved oligomeric Golgi complex subunit 7	11.81	1.23E-02
Q96GC5-1	39S ribosomal protein L48, mitochondrial	11.64	1.49E-03
Q6ZN55-1	zinc finger protein 574	11.55	1.41E-02
P32780	General transcription factor IIH subunit 1	11.40	3.96E-02
Q15043	Zinc transporter ZIP14	11.25	1.29E-04
P40855-1	Peroxisomal biogenesis factor 19	11.12	2.71E-03
Q14004-1	Cyclin-dependent kinase 13	11.08	6.40E-03
Q96Q83-1	alpha-ketoglutarate-dependent dioxygenase alkB homolog 3	11.04	1.32E-02
O75586	Mediator of RNA polymerase II transcription subunit 6	10.83	1.84E-02
P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial	10.80	6.91E-03
Q8NB37	Glutamine amidotransferase-like class 1 domain-containing protein 1	10.76	2.86E-03
Q9H2H8-1	peptidyl-prolyl cis-trans isomerase-like 3	10.60	3.99E-06
Q9BWS9-1	Chitinase domain-containing protein 1	10.59	7.75E-03
Q8NHQ9	ATP-dependent RNA helicase DDX55	10.24	1.04E-02
Q9H6W3	ribosomal oxygenase 1	10.23	9.06E-03
Q8IUI8	Cytokine receptor-like factor 3	10.20	2.20E-02
Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein	9.841	9.17E-05
Q99684	Zinc finger protein Gfi-1	9.609	4.69E-02
Q9NRP0-1	oligosaccharyltransferase complex subunit OSTC	9.574	6.97E-06
P52294	Importin subunit alpha-5	9.276	7.21E-03
O75976	Carboxypeptidase D	8.872	1.58E-02
Q92793-1	CREB-binding protein	8.369	2.13E-02
O14746	Telomerase reverse transcriptase	8.018	1.06E-02
O95372	acyl-protein thioesterase 2	7.485	4.65E-02
O15164	Transcription intermediary factor 1-alpha	7.287	1.23E-02
Q9Y2Q5	Ragulator complex protein LAMTOR2	6.930	4.64E-02
Q9BWJ5	Splicing factor 3B subunit 5	6.722	5.39E-05
Q9BZF1-1	Oxysterol-binding protein-related protein 8	6.536	2.47E-03
O95644-1	Nuclear factor of activated T-cells, cytoplasmic 1	6.429	1.12E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q969K3-1	E3 ubiquitin-protein ligase RNF34	5.958	7.39E-03
P16104	Histone H2AX	5.785	1.28E-05
O43237	Cytoplasmic dynein 1 light intermediate chain 2	5.309	1.52E-02
Q01804-1	OTU domain-containing protein 4	5.290	3.72E-03
Q96RP8	Potassium voltage-gated channel subfamily A member 7	5.190	1.32E-04
O94992	Protein HEXIM1	5.189	2.48E-04
P0DKV0	Spermatogenesis-associated protein 31C1	4.904	8.30E-03
P07108	acyl-CoA-binding protein	4.854	1.21E-04
O75787	Renin receptor	4.757	7.08E-04
Q9NS87	Kinesin-like protein KIF15	4.747	2.57E-02
O95777	U6 snRNA-associated Sm-like protein LSm8	4.668	1.03E-02
P13727	Bone marrow proteoglycan	4.612	9.94E-04
P42785-1	lysosomal Pro-X carboxypeptidase	4.572	6.80E-03
Q9UHD2	Serine/threonine-protein kinase TBK1	4.505	3.07E-03
Q9Y2S0-2	Isoform 2 of DNA-directed RNA polymerases I and III subunit RPAC2	4.473	1.50E-02
Q15032-1	R3H domain-containing protein 1	4.390	1.27E-02
P17026	zinc finger protein 22	4.173	6.28E-03
O43805	Sjoegren syndrome nuclear autoantigen 1	4.088	3.31E-02
P14406	Cytochrome c oxidase subunit 7A2, mitochondrial	3.994	2.27E-02
Q8N5M4	Tetratricopeptide repeat protein 9C	3.918	2.20E-03
Q96EP0-1	E3 ubiquitin-protein ligase RNF31	3.897	6.39E-03
Q86U42-1	polyadenylate-binding protein 2	3.867	3.26E-03
P09012	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A	3.817	5.18E-03
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	3.716	4.88E-03
P62891	60S ribosomal protein L39	3.716	5.15E-03
Q9UIA9	exportin-7	3.668	3.37E-03
P63173	60s ribosomal protein l38	3.471	6.03E-03
Q16540	39S ribosomal protein L23, mitochondrial	3.465	3.01E-02
P62158	Calmodulin	3.303	1.00E-02
Q9P275	Ubiquitin carboxyl-terminal hydrolase 36	3.296	4.28E-02
Q9UL25	Ras-related protein Rab-21	3.295	3.15E-02
Q14315	Filamin-C	3.266	3.49E-02
Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	3.143	3.58E-02
P51665	26S proteasome non-ATPase regulatory subunit 7	3.126	2.17E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P05387	60S acidic ribosomal protein P2	2.867	3.40E-02
Q9BZZ5-4	Apoptosis inhibitor 5	2.751	4.57E-02
Q9NZR2	Low-density lipoprotein receptor-related protein 1B	0.492	4.75E-02
O00483	Cytochrome c oxidase subunit NDUFA4	0.491	3.29E-02
Q9NVS2	39S ribosomal protein S18a, mitochondrial	0.488	2.72E-02
Q15004-1	PCNA-associated factor	0.483	4.70E-02
P37108	Signal recognition particle 14 kDa protein	0.481	3.65E-02
P62280	40S ribosomal protein S11	0.481	3.95E-02
P07195	L-lactate dehydrogenase B chain	0.475	3.59E-02
Q9UK76	Jupiter microtubule associated homolog 1	0.467	3.87E-02
Q99614	tetratricopeptide repeat protein 1	0.459	4.13E-02
P62937	peptidyl-prolyl cis-trans isomerase A	0.458	2.65E-02
Q9Y334	von Willebrand factor A domain-containing protein 7	0.456	1.58E-02
Q9NX40	OCIA domain-containing protein 1	0.456	1.72E-02
O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	0.455	2.75E-02
P62841	40S ribosomal protein S15	0.453	4.95E-02
Q9BUL8	programmed cell death protein 10	0.444	4.46E-02
O00182-1	Galectin-9	0.439	1.23E-02
O60232	Sjoegren syndrome/scleroderma autoantigen 1	0.439	3.91E-02
P31350-1	ribonucleoside-diphosphate reductase subunit M2	0.438	4.35E-02
Q9NPJ8-3	Isoform 3 of NTF2-related export protein 2	0.437	2.40E-02
Q96K17-1	transcription factor BTF3 homolog 4	0.437	4.79E-02
P61626	lysozyme c	0.435	1.54E-02
Q13951-2	Isoform 2 of Core-binding factor subunit beta	0.433	8.66E-03
P52272	Heterogeneous nuclear ribonucleoprotein M	0.431	1.52E-02
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.426	6.85E-03
P78316	Nucleolar protein 14	0.416	1.78E-02
Q8IUE6	Histone H2A type 2-B	0.412	1.15E-02
P16220-1	Cyclic AMP-responsive element-binding protein 1	0.410	1.15E-02
O75347	Tubulin-specific chaperone A	0.407	9.10E-03
Q9H2W6	39S ribosomal protein L46, mitochondrial	0.405	9.73E-03
Q562R1	Beta-actin-like protein 2	0.398	7.29E-03
P20674	Cytochrome c oxidase subunit 5A, mitochondrial	0.395	6.71E-03
P22061	protein-L-isoaspartate(D-aspartate) O-methyltransferase	0.393	6.04E-03
O60814	Histone H2B type 1-K	0.393	6.44E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q9GZZ1-1	N-alpha-acetyltransferase 50	0.388	5.03E-03
P62910	60S ribosomal protein L32	0.387	6.72E-03
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	0.387	4.38E-02
O15305	Phosphomannomutase 2	0.384	3.76E-02
Q9H7E9-1	UPF0488 protein C8orf33	0.382	3.33E-02
P04908	histone H2A type 1-B/E	0.371	3.59E-03
Q15233	Non-POU domain-containing octamer-binding protein	0.366	3.15E-03
P07919	Cytochrome b-c1 complex subunit 6, mitochondrial	0.364	1.63E-03
O00214-1	Galectin-8	0.364	1.43E-02
P14174	Macrophage Migration inhibitory factor	0.355	2.26E-03
Q8WYP5	protein elys	0.349	1.97E-02
P06748	Nucleophosmin	0.344	1.59E-03
Q32MZ4-3	Isoform 3 of Leucine-rich repeat flightless-interacting protein 1	0.332	1.46E-03
P46778	60S ribosomal protein L21	0.331	9.43E-04
P63220	40S ribosomal protein S21	0.330	9.83E-04
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	0.326	5.51E-04
O75607	Nucleoplasmin-3	0.320	1.26E-02
Q147X3	N-alpha-acetyltransferase 30	0.318	1.07E-02
Q96C01	Protein FAM136A	0.318	3.41E-02
Q9Y3B9	RRP15-like protein	0.317	2.77E-03
P02768-1	Serum albumin	0.317	1.06E-02
P30049	ATP synthase subunit delta, mitochondrial	0.313	7.47E-04
P68133	Actin, alpha skeletal muscle	0.309	1.95E-04
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	0.306	8.97E-03
O75438	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	0.300	5.38E-04
Q495C1-1	Probable E3 SUMO-protein ligase RNF212	0.300	5.48E-03
P42677	40S ribosomal protein S27	0.299	1.65E-04
P05204	Non-histone chromosomal protein HMG-17	0.298	3.02E-04
O75348	V-type proton ATPase subunit G 1	0.283	1.67E-02
Q01650	large neutral amino acids transporter small subunit 1	0.280	5.40E-03
Q8IUR0	Trafficking protein particle complex subunit 5	0.262	6.54E-03
P43308	Translocon-associated protein subunit beta	0.262	1.40E-02
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	0.251	1.28E-05
Q9H4A6	Golgi phosphoprotein 3	0.248	3.96E-02
Q9BYP7	Serine/threonine-protein kinase WNK3	0.247	1.37E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q9P265	Disco-interacting protein 2 homolog B	0.247	3.95E-02
P56385	ATP synthase subunit e, mitochondrial	0.245	3.85E-06
Q8IWL3	iron-sulfur cluster co-chaperone protein HscB, mitochondrial	0.245	1.84E-03
Q01130	serine/arginine-rich splicing factor 2	0.233	7.43E-06
Q71U36	tubulin alpha-1A chain	0.227	2.01E-05
P09669	Cytochrome c oxidase subunit 6C	0.225	5.50E-05
P61956	small ubiquitin-related modifier 2	0.213	2.80E-06
Q99704	docking protein 1	0.209	3.87E-02
P08708	40S ribosomal protein S17	0.205	1.24E-06
P11166	Solute carrier family 2, facilitated glucose transporter member 1	0.205	1.97E-02
P61024	cyclin-dependent kinases regulatory subunit 1	0.202	1.56E-03
P07910-1	Heterogeneous nuclear ribonucleoproteins C1/C2	0.194	2.57E-02
P15531	Nucleoside diphosphate kinase A	0.193	1.46E-07
Q13685	angio-associated migratory cell protein	0.190	1.48E-02
Q8IU81	Interferon regulatory factor 2-binding protein 1	0.190	2.07E-02
P05114	Non-histone chromosomal protein HMG-14	0.186	2.24E-02
Q9BWT6	Meiotic nuclear division protein 1 homolog	0.185	2.98E-03
Q9H0S4	Probable ATP-dependent RNA helicase DDX47	0.173	6.77E-03
Q12912-1	Lymphoid-restricted membrane protein	0.173	1.85E-02
Q9Y399	28S ribosomal protein S2, mitochondrial	0.170	4.57E-02
P02100	Hemoglobin subunit epsilon	0.162	9.50E-04
Q14139	ubiquitin conjugation factor e4 a	0.157	2.08E-02
P56381	ATP synthase subunit epsilon, mitochondrial	0.153	7.14E-03
Q8IXQ4	GPALPP motifs-containing protein 1	0.147	7.31E-03
P61513	60S ribosomal protein L37a	0.142	5.14E-09
P68431	Histone H3.1	0.130	2.65E-10
Q9Y294	Histone chaperone ASF1A	0.128	1.00E-08
Q9BZC7	ATP-binding cassette sub-family A member 2	0.126	3.36E-03
Q14028	Cyclic nucleotide-gated cation channel beta-1	0.124	1.54E-06
Q86Y39-1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	0.122	1.12E-02
Q8NC51-3	Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein	0.121	5.82E-07
Q96EV2	RNA-binding protein 33	0.121	2.48E-03
Q99880	Histone H2B type 1-L	0.119	1.36E-02
Q9H4B7	tubulin beta-1 chain	0.111	3.60E-03
Q8TBK6	zinc finger CCHC domain-containing protein 10	0.111	2.58E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P04070	Vitamin K-dependent protein C	0.108	6.49E-13
O43164	E3 ubiquitin-protein ligase Praja-2	0.107	3.17E-02
Q9BUF5	Tubulin beta-6 chain	0.102	4.54E-02
Q86U90	YrdC domain-containing protein, mitochondrial	0.101	7.61E-03
Q8NI22	Multiple coagulation factor deficiency protein 2	0.098	1.59E-04
Q96L92	Sorting nexin-27	0.097	2.41E-03
O43278	Kunitz-type protease inhibitor 1	0.097	1.81E-02
O60739	eukaryotic translation initiation factor 1b	0.097	4.03E-02
Q9NWB6	Arginine and glutamate-rich protein 1	0.094	8.24E-09
Q9UIA0	Cytohesin-4	0.089	1.23E-04
Q8WUX1-1	Sodium-coupled neutral amino acid transporter 5	0.085	8.27E-03
Q9UIV1-1	CCR4-NOT transcription complex subunit 7	0.083	5.49E-04
O95180	voltage-dependent T-type calcium channel subunit alpha-1H	0.083	1.04E-03
P41236	Protein phosphatase inhibitor 2	0.083	6.21E-03
Q12929	Epidermal growth factor receptor kinase substrate 8	0.083	1.34E-02
Q9UDY4	DnaJ homolog subfamily B member 4	0.082	4.87E-05
O94864-1	STAGA complex 65 subunit gamma	0.078	1.33E-08
Q8N9N8	probable RNA-binding protein EIF1AD	0.078	2.78E-03
Q9H334-1	Forkhead box protein P1	0.075	2.82E-04
Q9ULH0-1	Kinase D-interacting substrate of 220 kDa	0.075	4.39E-02
Q96S52	GPI transamidase component PIG-S	0.074	9.49E-03
Q8NFH5	Nucleoporin NUP53	0.073	1.47E-04
Q04941-1	proteolipid protein 2	0.073	7.46E-04
P46531	Neurogenic locus notch homolog protein 1	0.073	2.08E-02
Q9NR56-5	Isoform 5 of Muscleblind-like protein 1	0.072	3.47E-03
Q9HBL0	Tensin-1	0.071	4.90E-02
Q8N511	Transmembrane protein 199	0.070	1.11E-04
Q8N5K1	CDGSH iron-sulfur domain-containing protein 2	0.068	1.44E-07
Q92990	Glomulin	0.067	1.43E-06
Q7Z5L9-2	Isoform 2 of Interferon regulatory factor 2-binding protein 2	0.066	1.07E-14
Q2M2I8-1	AP2-associated protein kinase 1	0.065	5.78E-05
Q8TBJ4	Phospholipid phosphatase-related protein type 1	0.064	1.52E-05
Q9HD42-1	Charged multivesicular body protein 1a	0.064	2.91E-04
Q5H8C1-1	FRAS1-related extracellular matrix protein 1	0.061	3.46E-02
Q96PZ7-1	CUB and sushi domain-containing protein 1	0.060	1.19E-05
Q8N490-2	Isoform 2 of Probable hydrolase PNKD	0.060	2.88E-05

Continued on next page

accession	description	fold p change	adjusted p-value
Q13158	FAS-associated death domain protein	0.060	7.36E-03
Q9BSY4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5	0.060	1.41E-02
Q9P0U1	Mitochondrial import receptor subunit TOM7 homolog	0.060	1.46E-02
Q9NPE3	H/ACA ribonucleoprotein complex subunit 3	0.059	1.92E-09
Q9UFG5	UPF0449 protein C19orf25	0.059	6.84E-07
Q6IPU0	Centromere protein P	0.059	1.72E-02
Q9H1D9	DNA-directed RNA polymerase III subunit RPC6	0.059	2.83E-02
Q9Y4Y9	U6 snRNA-associated Sm-like protein LSm5	0.057	4.65E-12
Q96MX6	WD repeat-containing protein 92	0.057	7.34E-03
P27540	Aryl hydrocarbon receptor nuclear translocator	0.057	1.91E-02
Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta	0.057	3.21E-02
Q9Y2H0-1	Isoform 2 of Disks large-associated protein 4	0.056	1.15E-04
Q14533	Keratin, type II cuticular Hb1	0.056	3.03E-03
Q9NX55-2	Huntingtin-interacting protein K	0.050	6.83E-04
Q5BJD5-1	Transmembrane protein 41B	0.049	4.92E-02
Q13416	Origin recognition complex subunit 2	0.047	8.20E-03
P42025	Beta-centractin	0.043	1.02E-03
Q99595	Mitochondrial import inner membrane translocase subunit Tim17-A	0.043	5.61E-03
P0DMU8	Cancer/testis antigen family 45 member A5	0.041	1.43E-06
P46734-1	dual specificity mitogen-activated protein kinase kinase 3	0.040	8.15E-03
Q7L590-1	Protein MCM10 homolog	0.038	1.88E-03
O95298-1	NADH dehydrogenase [ubiquinone] 1 subunit C2	0.036	1.68E-04
L0R8F8	MIEF1 upstream open reading frame protein	0.035	1.69E-03
Q9H4L4	Sentrin-specific protease 3	0.034	1.56E-03
O95747	Serine/threonine-protein kinase OSR1	0.034	2.50E-03
Q9NZM1	Myoferlin	0.033	6.20E-03
Q969U7	Proteasome assembly chaperone 2	0.032	2.10E-07
Q9H3Z4	DnaJ homolog subfamily C member 5	0.027	4.35E-05
Q14159	DNA repair-scaffolding protein	0.025	4.14E-08
Q96P66	Probable G-protein coupled receptor 101	0.024	7.35E-07
Q9P2K5-1	Myelin expression factor 2	0.019	4.80E-10
O75970	multiple PDZ domain protein	0.017	4.04E-14
P16403	Histone H1.2	0.010	9.64E-17
Q3ZCM7	tubulin beta-8 chain	0.010	9.64E-17
Q15366-1	Poly(rC)-binding protein 2	0.010	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	0.010	9.64E-17
Q6DN03	Putative histone H2B type 2-C	0.010	9.64E-17
Q9NRR5-1	Ubiquilin-4	0.010	9.64E-17
P62491-1	Ras-related protein Rab-11A	0.010	9.64E-17
Q92901	60S ribosomal protein L3-like	0.010	9.64E-17
P13747	HLA class I histocompatibility antigen, alpha chain E	0.010	9.64E-17
Q58FG1	Putative heat shock protein HSP 90-alpha A4	0.010	9.64E-17
Q13422-2	Isoform Ik2 of DNA-binding protein Ikaros	0.010	9.64E-17
P11234	Ras-related protein Ral-B	0.010	9.64E-17
Q9BRL6-1	serine/arginine-rich splicing factor 8	0.010	9.64E-17
Q9H4A5	Golgi phosphoprotein 3-like	0.010	9.64E-17
Q9NUW8	tyrosyl-DNA phosphodiesterase 1	0.010	9.64E-17
Q00005-1	serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform	0.010	9.64E-17
O60256-1	Phosphoribosyl pyrophosphate synthase-associated protein 2	0.010	9.64E-17
P10124	Serglycin	0.010	9.64E-17
P24557	Thromboxane-A synthase	0.010	9.64E-17
Q9P1U0	DNA-directed RNA polymerase I subunit RPA12	0.010	9.64E-17
P35813	Protein phosphatase 1A	0.010	9.64E-17
P25440-1	Bromodomain-containing protein 2	0.010	9.64E-17
Q05932-1	Folylpolyglutamate synthase, mitochondrial	0.010	9.64E-17
Q9BQE9-1	B-cell CLL/lymphoma 7 protein family member B	0.010	9.64E-17
Q99470	Stromal cell-derived factor 2	0.010	9.64E-17
P41208	centrin-2	0.010	9.64E-17
Q9H467	CUE domain-containing protein 2	0.010	9.64E-17
O15126-1	Secretory carrier-associated membrane protein 1	0.010	9.64E-17
P15260	Interferon gamma receptor 1	0.010	9.64E-17
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.010	9.64E-17
P02686-1	myelin basic protein	0.010	9.64E-17
O60783	28S ribosomal protein S14, mitochondrial	0.010	9.64E-17
P61009	Signal peptidase complex subunit 3	0.010	9.64E-17
P56377	AP-1 complex subunit sigma-2	0.010	9.64E-17
P04921-1	Glycophorin-C	0.010	9.64E-17
Q96RG2-1	PAS domain-containing serine/threonine-protein kinase	0.010	9.64E-17
Q9BUR5-1	MICOS complex subunit MIC26	0.010	9.64E-17
Q9BWE0	Replication initiator 1	0.010	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P49006	MARCKS-related protein	0.010	9.64E-17
Q16643	drebrin	0.010	9.64E-17
Q8NDF8-5	Isoform 5 of Non-canonical poly(A) RNA polymerase PAPD5	0.010	9.64E-17
Q15836	Vesicle-associated membrane protein 3	0.010	9.64E-17
P63218	guanine nucleotide-binding protein g(i)/g(s)/g(o) subunit gamma-5	0.010	9.64E-17
Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase	0.010	9.64E-17
Q99700-1	Ataxin-2	0.010	9.64E-17
Q8NDX1	PH and SEC7 domain-containing protein 4	0.010	9.64E-17
Q96PE3-1	Type I inositol 3,4-bisphosphate 4-phosphatase	0.010	9.64E-17
Q9NXE4-1	Sphingomyelin phosphodiesterase 4	0.010	9.64E-17
Q9NPI1-1	Bromodomain-containing protein 7	0.010	9.64E-17
Q9H582-1	zinc finger protein 644	0.010	9.64E-17
Q16864-1	V-type proton ATPase subunit F	0.010	9.64E-17
Q96SK2	Transmembrane protein 209	0.010	9.64E-17
Q9Y2Z2	Protein MTO1 homolog, mitochondrial	0.010	9.64E-17
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	0.010	9.64E-17
Q8IVS2	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	0.010	9.64E-17
Q4J6C6	prolyl endopeptidase-like	0.010	9.64E-17
P60002	Transcription elongation factor 1 homolog	0.010	9.64E-17
P04156-1	Major prion protein	0.010	9.64E-17
P78345	Ribonuclease P protein subunit p38	0.010	9.64E-17
Q8IUD2-1	ELKS/Rab6-interacting/CAST family member 1	0.010	9.64E-17
Q9Y2Q9	28S ribosomal protein S28, mitochondrial	0.010	9.64E-17
P34896-1	Serine hydroxymethyltransferase, cytosolic	0.010	9.64E-17
O75616-1	GTPase Era, mitochondrial	0.010	9.64E-17
Q8N5F7	NF-kappa-B-activating protein	0.010	9.64E-17
Q9Y289	Sodium-dependent multivitamin transporter	0.010	9.64E-17
Q99640	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	0.010	9.64E-17
Q96JP5-1	E3 ubiquitin-protein ligase ZFP91	0.010	9.64E-17
Q9UBW7	Zinc finger MYM-type protein 2	0.010	9.64E-17
Q15118	[Pyruvate dehydrogenase (Acetyl-transferring)] kinase isozyme 1, mitochondrial	0.010	9.64E-17
Q96F44-1	E3 ubiquitin-protein ligase TRIM11	0.010	9.64E-17
O96005-1	Cleft lip and palate transmembrane protein 1	0.010	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BY66	Lysine-specific demethylase 5D	0.010	9.64E-17
Q86SF2	N-acetylgalactosaminyltransferase 7	0.010	9.64E-17
O75907	Diacylglycerol O-acyltransferase 1	0.010	9.64E-17
P10620	Microsomal glutathione S-transferase 1	0.010	9.64E-17
Q6FIF0	AN1-type zinc finger protein 6	0.010	9.64E-17
O15239	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	0.010	9.64E-17
O43482	Protein Mis18-beta	0.010	9.64E-17
Q96BR1-1	Serine/threonine-protein kinase Sgk3	0.010	9.64E-17
Q9UBM7	7-dehydrocholesterol reductase	0.010	9.64E-17
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	0.010	9.64E-17
Q9NZ32	Actin-related protein 10	0.010	9.64E-17
Q9UNZ5	Leydig cell tumor 10 kDa protein homolog	0.010	9.64E-17
P53680	AP-2 complex subunit sigma	0.010	9.64E-17
O95391	Pre-mRNA-splicing factor SLU7	0.010	9.64E-17
P00352	Retinal dehydrogenase 1	0.010	9.64E-17
Q8WW22-1	DnaJ homolog subfamily A member 4	0.010	9.64E-17
Q8N954-1	G patch domain-containing protein 11	0.010	9.64E-17
Q86TI0	TBC1 domain family member 1	0.010	9.64E-17
P23511	Nuclear transcription factor Y subunit alpha	0.010	9.64E-17
O60308	Centrosomal protein of 104 kDa	0.010	9.64E-17
Q8N4H5	mitochondrial import receptor subunit TOM5 homolog	0.010	9.64E-17
Q9H5V9-1	UPF0428 protein CXorf56	0.010	9.64E-17
O60830-1	Mitochondrial import inner membrane translocase subunit Tim17-B	0.010	9.64E-17
Q9BS18	Anaphase-promoting complex subunit 13	0.010	9.64E-17
Q8N3Z6	Zinc finger CCHC domain-containing protein 7	0.010	9.64E-17
Q15811	Intersectin-1	0.010	9.64E-17
P25208	nuclear transcription factor Y subunit beta	0.010	9.64E-17
Q9BQA9-1	Uncharacterized protein C17orf62	0.010	9.64E-17
Q9Y4D8-1	Probable E3 ubiquitin-protein ligase HECTD4	0.010	9.64E-17
Q6NUS6	tectonic-3	0.010	9.64E-17
Q92994	Transcription factor IIIB 90 kDa subunit	0.010	9.64E-17
O60921	checkpoint protein HUS1	0.010	9.64E-17
A6NLC8	Putative TAF11-like protein ENSP00000332601	0.010	9.64E-17
Q9Y287	Integral membrane protein 2B	0.010	9.64E-17
P35527	Keratin, type I cytoskeletal 9	0.010	9.64E-17
Q8N4U5	T-complex protein 11-like protein 2	0.010	9.64E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q969S8-1	Histone deacetylase 10	0.010	9.64E-17
O15120	1-acyl-sn-glycerol-3-phosphate acyltransferase beta	0.010	9.64E-17
Q9BYF1	angiotensin-converting enzyme 2	0.010	9.64E-17
Q9NRN9	Methyltransferase-like protein 5	0.010	9.64E-17
O15066	Kinesin-like protein KIF3B	0.010	9.64E-17
Q8TCT9-1	Minor histocompatibility antigen H13	0.010	9.64E-17
Q86UB9	transmembrane protein 135	0.010	9.64E-17
Q8IZC7	Zinc finger protein 101	0.010	9.64E-17
Q6TDU7-1	protein CASC1	0.010	9.64E-17
P01906	HLA class II histocompatibility antigen, DQ alpha 2 chain	0.010	9.64E-17
Q9Y5S1	Transient receptor potential cation channel subfamily V member 2	0.010	9.64E-17
Q9HBD1-1	Roquin-2	0.010	9.64E-17
Q9P1Z2-1	Calcium-binding and coiled-coil domain-containing protein 1	0.010	9.64E-17
Q96JB8-1	MAGUK p55 subfamily member 4	0.010	9.64E-17
Q6UWL6-5	Isoform 5 of Kin of IRRE-like protein 2	0.010	9.64E-17
End of Table			

T LN18 Cycloheximide Genes

accession	description	fold p change	adjusted p-value
Q9BQE3	Tubulin alpha-1C chain	100.0	4.62E-17
Q6S8J3	POTE ankyrin domain family member E	100.0	4.62E-17
P29692-3	Isoform 3 of Elongation factor 1-delta	100.0	4.62E-17
O43399-2	Isoform 2 of Tumor protein D54	100.0	4.62E-17
P22090	40S ribosomal protein S4, Y isoform 1	100.0	4.62E-17
P35609	Alpha-actinin-2	100.0	4.62E-17
P13929-1	Beta-enolase	100.0	4.62E-17
P30498	HLA class I histocompatibility antigen, B-78 alpha chain	100.0	4.62E-17
O15523	atp-dependent rna helicase ddx3y	100.0	4.62E-17
Q14240-1	eukaryotic initiation factor 4A-II	100.0	4.62E-17
P07942	Laminin subunit beta-1	100.0	4.62E-17
Q9Y4G6	Talin-2	100.0	4.62E-17
P35908	Keratin, type II cytoskeletal 2 epidermal	100.0	4.62E-17
Continued on next page			

accession	description	fold p change	adjusted p-value
P38606	V-type proton ATPase catalytic subunit A	100.0	4.62E-17
Q6PD62	RNA polymerase-associated protein CTR9 homolog	100.0	4.62E-17
Q96CW1	AP-2 complex subunit mu	100.0	4.62E-17
Q6NUQ4	Transmembrane protein 214	100.0	4.62E-17
P62136-1	serine/threonine-protein phosphatase PP1-alpha catalytic subunit	100.0	4.62E-17
P11908	ribose-phosphate pyrophosphokinase 2	100.0	4.62E-17
Q96FW1	Ubiquitin thioesterase otub1	100.0	4.62E-17
O00429	Dynamin-1-like protein	100.0	4.62E-17
Q9NR56-5	Isoform 5 of Muscleblind-like protein 1	100.0	4.62E-17
Q9H3P7	Golgi resident protein GCP60	100.0	4.62E-17
P08729	Keratin, type II cytoskeletal 7	100.0	4.62E-17
P62834	ras-related protein Rap-1A	100.0	4.62E-17
Q8IVL6-1	Prolyl 3-hydroxylase 3	100.0	4.62E-17
Q6NYC1	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	100.0	4.62E-17
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	100.0	4.62E-17
Q9Y2X3	Nucleolar protein 58	100.0	4.62E-17
Q96FJ2	Dynein light chain 2, cytoplasmic	100.0	4.62E-17
Q96AC1	Fermitin family homolog 2	100.0	4.62E-17
Q9Y2T2	ap-3 complex subunit mu-1	100.0	4.62E-17
Q13547	histone deacetylase 1	100.0	4.62E-17
Q92747	Actin-related protein 2/3 complex subunit 1A	100.0	4.62E-17
Q9H061-1	Transmembrane protein 126A	100.0	4.62E-17
P28370-1	Probable global transcription activator SNF2L1	100.0	4.62E-17
Q6DD88	Atlastin-3	100.0	4.62E-17
O60443	Non-syndromic hearing impairment protein 5	100.0	4.62E-17
Q6DKJ4	nucleoredoxin	100.0	4.62E-17
O95352	Ubiquitin-like modifier-activating enzyme ATG7	100.0	4.62E-17
O43169	Cytochrome b5 type B	100.0	4.62E-17
Q96RP9	Elongation factor G, mitochondrial	100.0	4.62E-17
P52943	Cysteine-rich protein 2	100.0	4.62E-17
P52895	Aldo-keto reductase family 1 member C2	100.0	4.62E-17
Q14651	Plastin-1	100.0	4.62E-17
O60645	exocyst complex component 3	100.0	4.62E-17
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	100.0	4.62E-17
P16278	Beta-galactosidase	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y5A9-1	YTH domain-containing family protein 2	100.0	4.62E-17
Q9BY43	Charged multivesicular body protein 4a	100.0	4.62E-17
Q9Y2Q3-1	Glutathione S-transferase kappa 1	100.0	4.62E-17
O15042	U2 snRNP-associated SURP motif-containing protein	100.0	4.62E-17
Q96QR8	Transcriptional activator protein Pur-beta	100.0	4.62E-17
Q08AM6	Protein VAC14 homolog	100.0	4.62E-17
Q9Y2R4	Probable ATP-dependent RNA helicase DDX52	100.0	4.62E-17
Q9H7E9-1	UPF0488 protein C8orf33	100.0	4.62E-17
Q03154-1	Aminoacylase-1	100.0	4.62E-17
Q8IVL5	Prolyl 3-hydroxylase 2	100.0	4.62E-17
Q8N806	Putative E3 ubiquitin-protein ligase UBR7	100.0	4.62E-17
P42025	Beta-centractin	100.0	4.62E-17
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4	100.0	4.62E-17
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23	100.0	4.62E-17
Q9GZP9	Derlin-2	100.0	4.62E-17
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	100.0	4.62E-17
Q9UHY7	Enolase-phosphatase E1	100.0	4.62E-17
Q9NQ55-1	suppressor of SWI4 1 homolog	100.0	4.62E-17
P30626-1	Sorcin	100.0	4.62E-17
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	100.0	4.62E-17
O96008	Mitochondrial import receptor subunit TOM40 homolog	100.0	4.62E-17
Q9HD33-1	39S ribosomal protein L47, mitochondrial	100.0	4.62E-17
O76071	Probable cytosolic iron-sulfur protein assembly protein Ciao1	100.0	4.62E-17
Q9HCU5	Prolactin regulatory element-binding protein	100.0	4.62E-17
P43307	Translocon-associated protein subunit alpha	100.0	4.62E-17
O15533-1	Tapasin	100.0	4.62E-17
Q93100-1	phosphorylase b kinase regulatory subunit beta	100.0	4.62E-17
O95487-1	Protein transport protein Sec24B	100.0	4.62E-17
O75431	Metaxin-2	100.0	4.62E-17
Q9H444	Charged multivesicular body protein 4b	100.0	4.62E-17
Q99575	Ribonucleases P/MRP protein subunit pop1	100.0	4.62E-17
Q9H267	Vacuolar protein sorting-associated protein 33B	100.0	4.62E-17
O95758-1	Isoform 1 of Polypyrimidine tract-binding protein 3	100.0	4.62E-17
P61326	Protein mago nashi homolog	100.0	4.62E-17
P29992	guanine nucleotide-binding protein subunit alpha-11	100.0	4.62E-17
Q0VDF9	Heat shock 70 kDa protein 14	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P49815	Tuberin	100.0	4.62E-17
Q96ER3	protein saal1	100.0	4.62E-17
P61964	WD repeat-containing protein 5	100.0	4.62E-17
Q9NWS0-1	PIH1 domain-containing protein 1	100.0	4.62E-17
Q92925-1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	100.0	4.62E-17
P51648	Fatty aldehyde dehydrogenase	100.0	4.62E-17
Q9NVG8	TBC1 domain family member 13	100.0	4.62E-17
Q9UNL2	Translocon-associated protein subunit gamma	100.0	4.62E-17
Q9UHD2	Serine/threonine-protein kinase TBK1	100.0	4.62E-17
Q9NW13-1	RNA-binding protein 28	100.0	4.62E-17
O00291	Huntingtin-interacting protein 1	100.0	4.62E-17
Q96FZ7	charged multivesicular body protein 6	100.0	4.62E-17
O95983-1	methyl-CpG-binding domain protein 3	100.0	4.62E-17
Q96KG9	N-terminal kinase-like protein	100.0	4.62E-17
Q9HCD5	Nuclear receptor coactivator 5	100.0	4.62E-17
Q70J99-1	Protein unc-13 homolog D	100.0	4.62E-17
Q8IY95	transmembrane protein 192	100.0	4.62E-17
P49753-2	Isoform 2 of Acyl-coenzyme A thioesterase 2, mitochondrial	100.0	4.62E-17
O76074	cGMP-specific 3′,5′-cyclic phosphodiesterase	100.0	4.62E-17
Q96MU7-1	YTH domain-containing protein 1	100.0	4.62E-17
P57088	Transmembrane protein 33	100.0	4.62E-17
P35237	serpin B6	100.0	4.62E-17
Q9HD26-1	Golgi-associated PDZ and coiled-coil motif-containing protein	100.0	4.62E-17
Q9UET6	Putative tRNA (cytidine(32)/guanosine(34)-2′-O)-methyltransferase	100.0	4.62E-17
Q8NEM2	SHC SH2 domain-binding protein 1	100.0	4.62E-17
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	100.0	4.62E-17
Q9NVH1-1	DnaJ homolog subfamily C member 11	100.0	4.62E-17
P29034	protein S100-A2	100.0	4.62E-17
Q9Y5V3	Melanoma-associated antigen D1	100.0	4.62E-17
Q13190	Syntaxin-5	100.0	4.62E-17
P41214	Eukaryotic translation initiation factor 2d	100.0	4.62E-17
Q14344	Guanine nucleotide-binding protein subunit alpha-13	100.0	4.62E-17
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y6M7-7	Isoform 7 of Sodium bicarbonate cotransporter 3	100.0	4.62E-17
A6NDU8	UPF0600 protein C5orf51	100.0	4.62E-17
P49590	probable histidine–tRNA ligase, mitochondrial	100.0	4.62E-17
Q9Y2X7-1	ARF GTPase-activating protein GIT1	100.0	4.62E-17
Q13868	Exosome complex component Rrp4	100.0	4.62E-17
Q96C36	Pyrroline-5-carboxylate reductase 2	100.0	4.62E-17
Q969Z0-1	Protein TBRG4	100.0	4.62E-17
Q9H977	WD repeat-containing protein 54	100.0	4.62E-17
Q15386-1	Ubiquitin-protein ligase E3C	100.0	4.62E-17
Q15833-1	Syntaxin-binding protein 2	100.0	4.62E-17
Q96Q11-1	CCA tRNA nucleotidyltransferase 1, mitochondrial	100.0	4.62E-17
O43598-1	2′-deoxynucleoside 5′-phosphate N-hydrolase 1	100.0	4.62E-17
Q9UNS1	Protein timeless homolog	100.0	4.62E-17
Q9Y3D6	mitochondrial fission 1 protein	100.0	4.62E-17
A2A3N6	Putative PIP5K1A and PSMD4-like protein	100.0	4.62E-17
P61421	V-type proton ATPase subunit d 1	100.0	4.62E-17
Q13107-1	Ubiquitin carboxyl-terminal hydrolase 4	100.0	4.62E-17
Q8TF05	Serine/threonine-protein phosphatase 4 regulatory subunit 1	100.0	4.62E-17
Q9NX08	COMM domain-containing protein 8	100.0	4.62E-17
Q9H814	Phosphorylated adapter RNA export protein	100.0	4.62E-17
Q9NQZ2	Something about silencing protein 10	100.0	4.62E-17
Q8IUW5	RELT-like protein 1	100.0	4.62E-17
Q9UKG1	DCC-interacting protein 13-alpha	100.0	4.62E-17
Q96SK2	Transmembrane protein 209	100.0	4.62E-17
Q8NFZ8	Cell adhesion molecule 4	100.0	4.62E-17
Q6PJG6-1	BRCA1-associated ATM activator 1	100.0	4.62E-17
Q9BWM7	Sideroflexin-3	100.0	4.62E-17
Q96LR5	Ubiquitin-conjugating enzyme E2 E2	100.0	4.62E-17
Q9BUR4	Telomerase Cajal body protein 1	100.0	4.62E-17
O75592-1	E3 ubiquitin-protein ligase MYCBP2	100.0	4.62E-17
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	100.0	4.62E-17
Q9UKA9-1	Polypyrimidine tract-binding protein 2	100.0	4.62E-17
P11441	Ubiquitin-like protein 4A	100.0	4.62E-17
P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	100.0	4.62E-17
Q15041	ADP-ribosylation factor-like protein 6-interacting protein 1	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q4J6C6	prolyl endopeptidase-like	100.0	4.62E-17
Q8TCD5	5′(3′)-deoxyribonucleotidase, cytosolic type	100.0	4.62E-17
Q13098	COP9 signalosome complex subunit 1	100.0	4.62E-17
Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinase	100.0	4.62E-17
A0FGR8-1	Extended synaptotagmin-2	100.0	4.62E-17
Q9NZ45	CDGSH iron-sulfur domain-containing protein 1	100.0	4.62E-17
Q9BW83-1	Intraflagellar transport protein 27 homolog	100.0	4.62E-17
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	100.0	4.62E-17
Q8WWQ0	PH-interacting protein	100.0	4.62E-17
Q7Z4W1	L-xylulose reductase	100.0	4.62E-17
Q96M27-1	protein PRRC1	100.0	4.62E-17
Q9Y5B8	Nucleoside diphosphate kinase 7	100.0	4.62E-17
O95785	Protein Wiz	100.0	4.62E-17
Q92552	28S ribosomal protein S27, mitochondrial	100.0	4.62E-17
O43747-1	AP-1 complex subunit gamma-1	100.0	4.62E-17
P61020	Ras-related protein Rab-5B	100.0	4.62E-17
Q8N488	RING1 and YY1-binding protein	100.0	4.62E-17
Q8NCN5	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	100.0	4.62E-17
Q15631-1	Translin	100.0	4.62E-17
Q32P28-1	Prolyl 3-hydroxylase 1	100.0	4.62E-17
Q96BP3	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	100.0	4.62E-17
Q6NZ67	Mitotic-spindle organizing protein 2B	100.0	4.62E-17
Q12873-1	Chromodomain-helicase-DNA-binding protein 3	100.0	4.62E-17
Q13217	DnaJ homolog subfamily C member 3	100.0	4.62E-17
Q00653-1	Nuclear factor NF-kappa-B p100 subunit	100.0	4.62E-17
Q9NX14-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	100.0	4.62E-17
Q5VW32	BRO1 domain-containing protein BROX	100.0	4.62E-17
Q96AB3	isochorismatase domain-containing protein 2	100.0	4.62E-17
Q8NEW0	Zinc transporter 7	100.0	4.62E-17
O96019-1	Actin-like protein 6A	100.0	4.62E-17
Q9NQH7-1	Probable Xaa-Pro aminopeptidase 3	100.0	4.62E-17
O95674-1	phosphatidate cytidylyltransferase 2	100.0	4.62E-17
P19474	E3 ubiquitin-protein ligase TRIM21	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P63172	Dynein light chain Tctex-type 1	100.0	4.62E-17
Q7Z478	ATP-dependent RNA helicase Dhx29	100.0	4.62E-17
Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit	100.0	4.62E-17
O75396	Vesicle-trafficking protein SEC22b	100.0	4.62E-17
Q14155-1	Isoform 1 of Rho guanine nucleotide exchange factor 7	100.0	4.62E-17
Q9UJX3-1	Anaphase-promoting complex subunit 7	100.0	4.62E-17
Q6RW13	Type-1 angiotensin II receptor-associated protein	100.0	4.62E-17
Q9Y3I1	F-box only protein 7	100.0	4.62E-17
Q06190	Serine/threonine-protein phosphatase 2A regulatory subunit B″ subunit alpha	100.0	4.62E-17
Q6UWP7-1	Lysocardiolipin acyltransferase 1	100.0	4.62E-17
O14817	Tetraspanin-4	100.0	4.62E-17
Q93050-1	Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1	100.0	4.62E-17
Q9GZS3	WD repeat-containing protein 61	100.0	4.62E-17
Q03518	Antigen peptide transporter 1	100.0	4.62E-17
Q9Y5X3	sorting nexin-5	100.0	4.62E-17
O00566	U3 small nucleolar ribonucleoprotein protein Mpp10	100.0	4.62E-17
P35527	Keratin, type I cytoskeletal 9	100.0	4.62E-17
Q9BRT3	migration and invasion enhancer 1	100.0	4.62E-17
Q7Z2W9	39S ribosomal protein L21, mitochondrial	100.0	4.62E-17
Q9H1Y0-1	Autophagy protein 5	100.0	4.62E-17
P56182	Ribosomal RNA processing protein 1 homolog A	100.0	4.62E-17
Q8TED0	U3 small nucleolar RNA-associated protein 15 homolog	100.0	4.62E-17
Q96GC9	Vacuole membrane protein 1	100.0	4.62E-17
P04062	glucosylceramidase	100.0	4.62E-17
Q92995	Ubiquitin carboxyl-terminal hydrolase 13	100.0	4.62E-17
Q9P2K8-1	eIF-2-alpha kinase GCN2	100.0	4.62E-17
P20337	Ras-related protein Rab-3B	100.0	4.62E-17
Q92466	DNA damage-binding protein 2	100.0	4.62E-17
P54289	Voltage-dependent calcium channel subunit alpha-2/delta-1	100.0	4.62E-17
P10155-1	60 kDa SS-A/Ro ribonucleoprotein	100.0	4.62E-17
Q15286	Ras-related protein Rab-35	100.0	4.62E-17
Q9UBC2-1	Epidermal growth factor receptor substrate 15-like 1	100.0	4.62E-17
Q7Z7N9	Transmembrane protein 179B	100.0	4.62E-17
Q00535	Cyclin-dependent-like kinase 5	100.0	4.62E-17
Q8TDQ7	Glucosamine-6-phosphate isomerase 2	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9UBF8	Phosphatidylinositol 4-kinase beta	100.0	4.62E-17
P79522	Proline-rich protein 3	100.0	4.62E-17
Q6R327-1	Rapamycin-insensitive companion of mTOR	100.0	4.62E-17
Q9BZL6	Serine/threonine-protein kinase D2	100.0	4.62E-17
O95861-1	3′(2′),5′-bisphosphate nucleotidase 1	100.0	4.62E-17
Q8NI27-1	THO complex subunit 2	100.0	4.62E-17
Q96IV0	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	100.0	4.62E-17
Q96TC7	Regulator of microtubule dynamics protein 3	100.0	4.62E-17
Q15031	Probable Leucine–tRNA ligase, mitochondrial	100.0	4.62E-17
Q9UBU8-1	Mortality factor 4-like protein 1	100.0	4.62E-17
P09234	U1 small nuclear ribonucleoprotein C	100.0	4.62E-17
Q96A35	39S ribosomal protein L24, mitochondrial	100.0	4.62E-17
A8MXV4	nucleoside diphosphate-linked moiety X motif 19	100.0	4.62E-17
Q96BW9-1	Phosphatidate cytidylyltransferase, mitochondrial	100.0	4.62E-17
Q7Z7H5	Transmembrane emp24 domain-containing protein 4	100.0	4.62E-17
Q9UGP8	Translocation protein SEC63 homolog	100.0	4.62E-17
Q9NP73-2	Isoform 2 of Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13	100.0	4.62E-17
P37198	nuclear pore glycoprotein p62	100.0	4.62E-17
Q9NXH9-1	tRNA (guanine(26)-N(2))-dimethyltransferase	100.0	4.62E-17
O60934	Nibrin	100.0	4.62E-17
Q6P9B9	Integrator complex subunit 5	100.0	4.62E-17
Q5VSL9-1	striatin-interacting protein 1	100.0	4.62E-17
P17405-1	Sphingomyelin phosphodiesterase	100.0	4.62E-17
O43837-1	isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	100.0	4.62E-17
Q9UQ13	Leucine-rich repeat protein SHOC-2	100.0	4.62E-17
Q8WUX9	Charged multivesicular body protein 7	100.0	4.62E-17
Q9NQ48	Leucine zipper transcription factor-like protein 1	100.0	4.62E-17
Q9UBV2	Protein sel-1 homolog 1	100.0	4.62E-17
O75116	Rho-associated protein kinase 2	100.0	4.62E-17
P49459-1	Ubiquitin-conjugating enzyme E2 A	100.0	4.62E-17
Q99489-1	D-aspartate oxidase	100.0	4.62E-17
Q96G21	U3 small nucleolar ribonucleoprotein protein IMP4	100.0	4.62E-17
P09417	dihydropteridine reductase	100.0	4.62E-17
Q9HC36	rRNA methyltransferase 3, mitochondrial	100.0	4.62E-17
Q9UDR5	Alpha-aminoadipic semialdehyde synthase, mitochondrial	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q86TN4	tRNA 2′-phosphotransferase 1	100.0	4.62E-17
O15344-1	E3 ubiquitin-protein ligase Midline-1	100.0	4.62E-17
O60762	Dolichol-phosphate mannosyltransferase subunit 1	100.0	4.62E-17
Q9NRL3	Striatin-4	100.0	4.62E-17
O96028-1	Histone-lysine N-methyltransferase NSD2	100.0	4.62E-17
Q9H7Z7	Prostaglandin E synthase 2	100.0	4.62E-17
Q9UBB6	Neurochondrin	100.0	4.62E-17
Q9GZM5	protein YIPF3	100.0	4.62E-17
Q15813	Tubulin-specific chaperone E	100.0	4.62E-17
Q96FN4	Copine-2	100.0	4.62E-17
Q96MW5	Conserved oligomeric Golgi complex subunit 8	100.0	4.62E-17
Q6IAN0	Dehydrogenase/reductase SDR family member 7B	100.0	4.62E-17
Q69YQ0-1	Cytospin-A	100.0	4.62E-17
Q9NP92	39S ribosomal protein S30, mitochondrial	100.0	4.62E-17
Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	100.0	4.62E-17
Q2KHR3-1	Glutamine and serine-rich protein 1	100.0	4.62E-17
Q96F63	Coiled-coil domain-containing protein 97	100.0	4.62E-17
Q7LGA3-1	Heparan sulfate 2-O-sulfotransferase 1	100.0	4.62E-17
Q86U86-1	Protein polybromo-1	100.0	4.62E-17
Q9HC07	Transmembrane protein 165	100.0	4.62E-17
Q9GZT8-1	NIF3-like protein 1	100.0	4.62E-17
Q9HBH1	Peptide deformylase, mitochondrial	100.0	4.62E-17
O14933	Ubiquitin/ISG15-conjugating enzyme E2 L6	100.0	4.62E-17
Q9NRW7	Vacuolar protein sorting-associated protein 45	100.0	4.62E-17
P56134	ATP synthase subunit f, mitochondrial	100.0	4.62E-17
Q66LE6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform	100.0	4.62E-17
Q92619	Rho GTPase-activating protein 45	100.0	4.62E-17
P34059	N-acetylgalactosamine-6-sulfatase	100.0	4.62E-17
Q86VR2	Reticulophagy regulator 3	100.0	4.62E-17
Q9HBF4-1	Zinc finger FYVE domain-containing protein 1	100.0	4.62E-17
Q96EF6	F-box only protein 17	100.0	4.62E-17
Q96LD4	Tripartite motif-containing protein 47	100.0	4.62E-17
Q9NVS2	39S ribosomal protein S18a, mitochondrial	100.0	4.62E-17
Q9NYH9	U3 small nucleolar RNA-associated protein 6 homolog	100.0	4.62E-17
Q92692-1	Nectin-2	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q7L7X3	Serine/threonine-protein kinase TAO1	100.0	4.62E-17
Q68CQ7-1	Glycosyltransferase 8 domain-containing protein 1	100.0	4.62E-17
Q13505-1	Metaxin-1	100.0	4.62E-17
Q9Y697	Cysteine desulfurase, mitochondrial	100.0	4.62E-17
Q96AE7	Tetratricopeptide repeat protein 17	100.0	4.62E-17
Q9NPJ6-1	mediator of RNA polymerase II transcription subunit 4	100.0	4.62E-17
P16333-1	Cytoplasmic protein NCK1	100.0	4.62E-17
Q15007	Pre-mRNA-splicing regulator WTAP	100.0	4.62E-17
Q5T447	E3 ubiquitin-protein ligase HECTD3	100.0	4.62E-17
Q15477	Helicase SKI2W	100.0	4.62E-17
Q7L775	EPM2A-interacting protein 1	100.0	4.62E-17
P42785-1	lysosomal Pro-X carboxypeptidase	100.0	4.62E-17
Q5SY16	Polynucleotide 5′-hydroxyl-kinase NOL9	100.0	4.62E-17
O43148-1	mRNA cap guanine-N7 methyltransferase	100.0	4.62E-17
P98170	E3 ubiquitin-protein ligase XIAP	100.0	4.62E-17
P23434	Glycine cleavage system H protein, mitochondrial	100.0	4.62E-17
Q8TB37-1	Iron-sulfur protein NUBPL	100.0	4.62E-17
Q8TCE6-1	Protein FAM45A	100.0	4.62E-17
P07099	epoxide hydrolase 1	100.0	4.62E-17
P49356	protein farnesyltransferase subunit beta	100.0	4.62E-17
Q03426	mevalonate kinase	100.0	4.62E-17
P42356	phosphatidylinositol 4-kinase alpha	100.0	4.62E-17
Q8TCJ2	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase subunit STT3B	100.0	4.62E-17
Q7Z3T8	Zinc finger FYVE domain-containing protein 16	100.0	4.62E-17
Q4V328	GRIP1-associated protein 1	100.0	4.62E-17
P10586-1	Receptor-type tyrosine-protein phosphatase F	100.0	4.62E-17
Q99943	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	100.0	4.62E-17
Q53EP0	Fibronectin type III domain-containing protein 3B	100.0	4.62E-17
P67870	Casein kinase II subunit beta	100.0	4.62E-17
O14730	serine/threonine-protein kinase RIO3	100.0	4.62E-17
P53365	Arfaptin-2	100.0	4.62E-17
O15118	Niemann-Pick C1 protein	100.0	4.62E-17
Q9H9A6	Leucine-rich repeat-containing protein 40	100.0	4.62E-17
Q13325	Interferon-induced protein with tetratricopeptide repeats 5	100.0	4.62E-17
A7E2Y1	Myosin-7B	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q6VMQ6	activating transcription factor 7-interacting protein 1	100.0	4.62E-17
O95084	Serine protease 23	100.0	4.62E-17
P00403	Cytochrome c oxidase subunit 2	100.0	4.62E-17
Q70CQ2	Ubiquitin carboxyl-terminal hydrolase 34	100.0	4.62E-17
O75414	Nucleoside diphosphate kinase 6	100.0	4.62E-17
Q03113	Guanine nucleotide-binding protein subunit alpha-12	100.0	4.62E-17
Q9P260-1	LisH domain and HEAT repeat-containing protein KIAA1468	100.0	4.62E-17
O60711-1	Leupaxin	100.0	4.62E-17
Q9BYX2	TBC1 domain family member 2A	100.0	4.62E-17
O60613-1	selenoprotein F	100.0	4.62E-17
Q6UWU4-1	Bombesin receptor-activated protein C6orf89	100.0	4.62E-17
Q8NDT2	Putative RNA-binding protein 15B	100.0	4.62E-17
Q96BN8	Ubiquitin thioesterase otulin	100.0	4.62E-17
Q9BZH6	WD repeat-containing protein 11	100.0	4.62E-17
Q9BRG1	Vacuolar protein-sorting-associated protein 25	100.0	4.62E-17
Q8IX01-1	SURP and G-patch domain-containing protein 2	100.0	4.62E-17
Q9UK61	Protein TASOR	100.0	4.62E-17
Q14746	Conserved oligomeric Golgi complex subunit 2	100.0	4.62E-17
P98194-1	Calcium-transporting ATPase type 2C member 1	100.0	4.62E-17
O60678	protein arginine N-methyltransferase 3	100.0	4.62E-17
P15927-1	Replication protein A 32 kDa subunit	100.0	4.62E-17
Q14254	Flotillin-2	100.0	4.62E-17
Q53H96	Pyrroline-5-carboxylate reductase 3	100.0	4.62E-17
P62310	U6 snRNA-associated Sm-like protein LSm3	100.0	4.62E-17
Q9Y3B4	Splicing factor 3B subunit 6	100.0	4.62E-17
E9PRG8	Uncharacterized protein C11orf98	100.0	4.62E-17
Q7L592	Protein arginine methyltransferase NDUFAF7, mitochondrial	100.0	4.62E-17
Q9NZD8	Maspardin	100.0	4.62E-17
Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10	100.0	4.62E-17
Q9UKF6	Cleavage and polyadenylation specificity factor subunit 3	100.0	4.62E-17
Q9HA77	probable cysteine–tRNA ligase, mitochondrial	100.0	4.62E-17
Q9NUM4	Transmembrane protein 106B	100.0	4.62E-17
P46926	glucosamine-6-phosphate isomerase 1	100.0	4.62E-17
Q86TC9-1	Myopalladin	100.0	4.62E-17
Q99538	Legumain	100.0	4.62E-17
O95219	sorting nexin-4	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O94919	endonuclease domain-containing 1 protein	100.0	4.62E-17
Q8N954-1	G patch domain-containing protein 11	100.0	4.62E-17
P46977	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase subunit STT3A	100.0	4.62E-17
Q13625-1	Apoptosis-stimulating of p53 protein 2	100.0	4.62E-17
Q9NXG2	THUMP domain-containing protein 1	100.0	4.62E-17
Q7Z392	trafficking protein particle complex subunit 11	100.0	4.62E-17
Q9BV44	THUMP domain-containing protein 3	100.0	4.62E-17
Q4VC31	coiled-coil domain-containing protein 58	100.0	4.62E-17
O75586	Mediator of RNA polymerase II transcription subunit 6	100.0	4.62E-17
Q15910	Histone-lysine N-methyltransferase EZH2	100.0	4.62E-17
Q15070-1	Mitochondrial inner membrane protein OXA1L	100.0	4.62E-17
Q9UJX2-1	cell division cycle protein 23 homolog	100.0	4.62E-17
Q16537	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	100.0	4.62E-17
Q96CW6	Probable RNA polymerase II nuclear localization protein SLC7A6OS	100.0	4.62E-17
Q08AF3-1	schlafen family member 5	100.0	4.62E-17
Q8IWV8	E3 ubiquitin-protein ligase UBR2	100.0	4.62E-17
Q9NXC5-1	GATOR complex protein MIOS	100.0	4.62E-17
P35573-1	glycogen debranching enzyme	100.0	4.62E-17
P23470	Receptor-type tyrosine-protein phosphatase gamma	100.0	4.62E-17
Q8TCF1-1	AN1-type zinc finger protein 1	100.0	4.62E-17
Q9ULJ3	Zinc finger and BTB domain-containing protein 21	100.0	4.62E-17
Q8N612-1	FTS and Hook-interacting protein	100.0	4.62E-17
Q9BTX7	Alpha-tocopherol transfer protein-like	100.0	4.62E-17
Q92947-1	Glutaryl-CoA dehydrogenase, mitochondrial	100.0	4.62E-17
P55039	Developmentally-regulated GTP-binding protein 2	100.0	4.62E-17
O75448	Mediator of RNA polymerase II transcription subunit 24	100.0	4.62E-17
O15382	Branched-chain-amino-acid aminotransferase, mitochondrial	100.0	4.62E-17
O75044	SLIT-ROBO Rho GTPase-activating protein 2	100.0	4.62E-17
Q5TAQ9-1	DDB1- and CUL4-associated factor 8	100.0	4.62E-17
Q9Y5Q8-1	general transcription factor 3C polypeptide 5	100.0	4.62E-17
Q9NZM5	ribosome biogenesis protein NOP53	100.0	4.62E-17
Q6GMV2	SET and MYND domain-containing protein 5	100.0	4.62E-17
O14647	Chromodomain-helicase-DNA-binding protein 2	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P83111-1	Serine beta-lactamase-like protein LACTB, mitochondrial	100.0	4.62E-17
P06732	Creatine kinase M-type	100.0	4.62E-17
Q9H5H4	Zinc finger protein 768	100.0	4.62E-17
Q9Y2L9-1	Leucine-rich repeat and calponin homology domain-containing protein 1	100.0	4.62E-17
Q96K21	Abscission/NoCut checkpoint regulator	100.0	4.62E-17
Q92544	Transmembrane 9 superfamily member 4	100.0	4.62E-17
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24	100.0	4.62E-17
O43813	LanC-like protein 1	100.0	4.62E-17
Q8IX18	probable ATP-dependent RNA helicase DHX40	100.0	4.62E-17
Q9BVG9	phosphatidylserine synthase 2	100.0	4.62E-17
Q5F1R6	DnaJ homolog subfamily C member 21	100.0	4.62E-17
Q06546	GA-binding protein alpha chain	100.0	4.62E-17
O15235	28S ribosomal protein S12, mitochondrial	100.0	4.62E-17
Q16762	thiosulfate sulfurtransferase	100.0	4.62E-17
O75794	Cell division cycle protein 123 homolog	100.0	4.62E-17
Q9Y3C4	EKC/KEOPS complex subunit TPRKB	100.0	4.62E-17
Q14703	Membrane-bound transcription factor site-1 protease	100.0	4.62E-17
Q9Y584	Mitochondrial import inner membrane translocase subunit TIM22	100.0	4.62E-17
Q15262	Receptor-type tyrosine-protein phosphatase kappa	100.0	4.62E-17
Q9Y5K8	V-type proton ATPase subunit D	100.0	4.62E-17
Q5C9Z4	nucleolar MIF4G domain-containing protein 1	100.0	4.62E-17
O95602	DNA-directed RNA polymerase I subunit RPA1	100.0	4.62E-17
Q9Y6J9	TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L	100.0	4.62E-17
P09001	39S ribosomal protein L3, mitochondrial	100.0	4.62E-17
Q14562	ATP-dependent RNA helicase dhx8	100.0	4.62E-17
O94886	CSC1-like protein 1	100.0	4.62E-17
Q15392	Delta(24)-sterol reductase	100.0	4.62E-17
Q6P1X6	UPF0598 protein C8orf82	100.0	4.62E-17
P23458	Tyrosine-protein kinase JAK1	100.0	4.62E-17
Q9Y2Z4	Tyrosine–tRNA ligase, mitochondrial	100.0	4.62E-17
O75530	Polycomb protein EED	100.0	4.62E-17
Q96EK6	glucosamine 6-phosphate N-acetyltransferase	100.0	4.62E-17
Q16850-1	lanosterol 14-alpha demethylase	100.0	4.62E-17
P30837	Aldehyde dehydrogenase X, mitochondrial	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q4G0F5	Vacuolar protein sorting-associated protein 26B	100.0	4.62E-17
Q9Y291	28S ribosomal protein S33, mitochondrial	100.0	4.62E-17
Q9NYY8	FAST kinase domain-containing protein 2, mitochondrial	100.0	4.62E-17
P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial	100.0	4.62E-17
Q06265-1	Exosome complex component RRP45	100.0	4.62E-17
Q9NV06	DDB1- and CUL4-associated factor 13	100.0	4.62E-17
P13473-1	Lysosome-associated membrane glycoprotein 2	100.0	4.62E-17
Q92805	Golgin subfamily A member 1	100.0	4.62E-17
Q15628	Tumor necrosis factor receptor type 1-associated DEATH domain protein	100.0	4.62E-17
Q9C0E8-1	Protein lunapark	100.0	4.62E-17
P42696	RNA-binding protein 34	100.0	4.62E-17
Q9NQS3-1	Nectin-3	100.0	4.62E-17
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	100.0	4.62E-17
O95528	Solute carrier family 2, facilitated glucose transporter member 10	100.0	4.62E-17
O43292-1	Glycosylphosphatidylinositol anchor attachment 1 protein	100.0	4.62E-17
Q8TD08-1	mitogen-activated protein kinase 15	100.0	4.62E-17
Q9NWQ9	Uncharacterized protein C14orf119	100.0	4.62E-17
Q9NRX1	RNA-binding protein pno1	100.0	4.62E-17
Q9Y2P8	RNA 3′-terminal phosphate cyclase-like protein	100.0	4.62E-17
Q08AE8-1	Protein spire homolog 1	100.0	4.62E-17
Q8IV08	Phospholipase D3	100.0	4.62E-17
A6ZKI3	Retrotransposon Gag-like protein 8B	100.0	4.62E-17
Q9HBI6	Phylloquinone omega-hydroxylase CYP4F11	100.0	4.62E-17
Q15126	phosphomevalonate kinase	100.0	4.62E-17
Q969E2-1	Secretory carrier-associated membrane protein 4	100.0	4.62E-17
Q9BSJ2-1	Gamma-tubulin complex component 2	100.0	4.62E-17
P27216-1	Annexin A13	100.0	4.62E-17
Q13228	Selenium-binding protein 1	100.0	4.62E-17
Q8WTX7	Cytosolic arginine sensor for mTORC1 subunit 1	100.0	4.62E-17
P06280	alpha-galactosidase A	100.0	4.62E-17
O15550	Lysine-specific demethylase 6A	100.0	4.62E-17
Q0VDD8	Dynein heavy chain 14, axonemal	100.0	4.62E-17
Q9BVL2	Nucleoporin p58/p45	100.0	4.62E-17
P04637	Cellular tumor antigen p53	100.0	4.62E-17
A6NKD9	Coiled-coil domain-containing protein 85C	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BSH4	Translational activator of cytochrome c oxidase 1	100.0	4.62E-17
Q8NHY2-1	E3 ubiquitin-protein ligase RFWD2	100.0	4.62E-17
Q13451-1	Peptidyl-prolyl cis-trans isomerase FKBP5	100.0	4.62E-17
O95456	Proteasome assembly chaperone 1	100.0	4.62E-17
Q4U2R6	39S ribosomal protein L51, mitochondrial	100.0	4.62E-17
Q9BZI7-1	Regulator of nonsense transcripts 3B	100.0	4.62E-17
Q9Y483	Metal-response element-binding transcription factor 2	100.0	4.62E-17
Q5VU43	Myomegalin	100.0	4.62E-17
Q5VWP2	Putative nucleotidyltransferase FAM46C	100.0	4.62E-17
P28676	Grancalcin	100.0	4.62E-17
Q02040-1	A-kinase anchor protein 17A	100.0	4.62E-17
Q9BYC9	39S ribosomal protein L20, mitochondrial	100.0	4.62E-17
Q9H6Q4	Cytosolic fe-s cluster assembly factor narfl	100.0	4.62E-17
A0AV02	Solute carrier family 12 member 8	100.0	4.62E-17
Q53FA7-1	Quinone oxidoreductase PIG3	100.0	4.62E-17
Q8TDW4-1	Suppressor of tumorigenicity 7 protein-like	100.0	4.62E-17
Q03701	CCAAT/enhancer-binding protein zeta	100.0	4.62E-17
Q9H6K4	Optic atrophy 3 protein	100.0	4.62E-17
Q9UBU7	Protein DBF4 homolog A	100.0	4.62E-17
Q13873	Bone morphogenetic protein receptor type-2	100.0	4.62E-17
Q9H5X1-1	MIP18 family protein FAM96A	100.0	4.62E-17
Q13907	Isopentenyl-diphosphate Delta-isomerase 1	100.0	4.62E-17
Q96GM8	Target of EGR1 protein 1	100.0	4.62E-17
Q6P3R8	serine/threonine-protein kinase Nek5	100.0	4.62E-17
O14686-1	Histone-lysine N-methyltransferase 2D	100.0	4.62E-17
P08912	muscarinic acetylcholine receptor M5	100.0	4.62E-17
Q9BRT9	DNA replication complex GINS protein SLD5	100.0	4.62E-17
O75844	caax prenyl protease 1 homolog	100.0	4.62E-17
Q96GK7	fumarylacetoacetate hydrolase domain-containing protein 2A	100.0	4.62E-17
Q68CZ1	protein fantom	100.0	4.62E-17
Q13438-1	Protein os-9	100.0	4.62E-17
O60942-1	mRNA-capping enzyme	100.0	4.62E-17
Q5VZ46-1	Uncharacterized protein KIAA1614	100.0	4.62E-17
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	100.0	4.62E-17
Q9H7L9	Sin3 histone deacetylase corepressor complex component SDS3	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96N66-1	Lysophospholipid acyltransferase 7	100.0	4.62E-17
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	100.0	4.62E-17
Q9Y2I7-3	Isoform 3 of 1-phosphatidylinositol 3-phosphate 5-kinase	100.0	4.62E-17
P38435-1	vitamin K-dependent gamma-carboxylase	100.0	4.62E-17
O94875-1	Sorbin and SH3 domain-containing protein 2	100.0	4.62E-17
Q9HD20	manganese-transporting ATPase 13A1	100.0	4.62E-17
Q5FBB7-1	shugoshin 1	100.0	4.62E-17
Q96D96-1	voltage-gated hydrogen channel 1	100.0	4.62E-17
Q9UJF2	ras GTPase-activating protein nGAP	100.0	4.62E-17
A8K2U0	Alpha-2-macroglobulin-like protein 1	100.0	4.62E-17
Q2PPJ7-1	Ral GTPase-activating protein subunit alpha-2	100.0	4.62E-17
Q9NZQ3-1	NCK-interacting protein with SH3 domain	100.0	4.62E-17
Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase	100.0	4.62E-17
Q6Q788	Apolipoprotein A-V	100.0	4.62E-17
Q8IYF1	Elongin-A2	100.0	4.62E-17
P49703	ADP-ribosylation factor-like protein 4D	100.0	4.62E-17
Q9NRR4-1	Ribonuclease 3	100.0	4.62E-17
P09525	annexin A4	100.0	4.62E-17
Q9NPL8	Complex I assembly factor TIMMDC1, mitochondrial	100.0	4.62E-17
Q9UBM7	7-dehydrocholesterol reductase	100.0	4.62E-17
P19447	TFIIH basal transcription factor complex helicase XPB subunit	100.0	4.62E-17
Q7Z442	Polycystic kidney disease protein 1-like 2	100.0	4.62E-17
Q8NE35-1	Cytoplasmic polyadenylation element-binding protein 3	100.0	4.62E-17
Q8N5C6	S1 RNA-binding domain-containing protein 1	100.0	4.62E-17
Q9BZF1-1	Oxysterol-binding protein-related protein 8	100.0	4.62E-17
O43716	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	100.0	4.62E-17
Q15784	neurogenic differentiation factor 2	100.0	4.62E-17
P08F94-1	Fibrocystin	100.0	4.62E-17
Q9Y530	O-acetyl-ADP-ribose deacetylase 1	100.0	4.62E-17
Q6P0Q8	microtubule-associated serine/threonine-protein kinase 2	100.0	4.62E-17
Q9NR48	Histone-lysine N-methyltransferase ASH1L	100.0	4.62E-17
O14981	TATA-binding protein-associated factor 172	100.0	4.62E-17
Q9UGI0	Ubiquitin thioesterase Zranb1	100.0	4.62E-17
Q5FWE3-1	Proline-rich transmembrane protein 3	100.0	4.62E-17
Q5JVF3	PCI domain-containing protein 2	100.0	4.62E-17
Q5EBL4-1	RILP-like protein 1	100.0	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9P2R6	Arginine-glutamic acid dipeptide repeats protein	100.0	4.62E-17
Q9HC96	Calpain-10	100.0	4.62E-17
O75362	zinc finger protein 217	100.0	4.62E-17
Q53H12	Acylglycerol kinase, mitochondrial	100.0	4.62E-17
Q6SJ93-1	Protein FAM111B	100.0	4.62E-17
A8K8P3	protein SFI1 homolog	100.0	4.62E-17
Q86VI3	Ras GTPase-activating-like protein IQGAP3	100.0	4.62E-17
Q7Z7M0	Multiple epidermal growth factor-like domains protein 8	100.0	4.62E-17
Q9C0F1-1	centrosomal protein of 44 kDa	100.0	4.62E-17
O75911	Short-chain dehydrogenase/reductase 3	100.0	4.62E-17
Q6ZSB9	Zinc finger and BTB domain-containing protein 49	100.0	4.62E-17
Q8NBA8	DTW domain-containing protein 2	100.0	4.62E-17
Q8ND61-1	Uncharacterized protein C3orf20	100.0	4.62E-17
Q9Y5R2	Matrix metalloproteinase-24	100.0	4.62E-17
P0DKV0	Spermatogenesis-associated protein 31C1	100.0	4.62E-17
Q8NGM9	Olfactory receptor 8D4	100.0	4.62E-17
Q8NFA0	Ubiquitin carboxyl-terminal hydrolase 32	100.0	4.62E-17
Q8IYR2	SET and MYND domain-containing protein 4	100.0	4.62E-17
P61970	nuclear transport factor 2	40.89	1.16E-03
P14653-2	Isoform 2 of Homeobox protein Hox-B1	37.02	9.69E-04
P62820	Ras-related protein Rab-1A	33.49	8.86E-04
Q15061	WD repeat-containing protein 43	25.83	2.55E-02
P36954	DNA-directed RNA polymerase II subunit RPB9	25.20	7.48E-02
Q9H089	Large subunit GTPase 1 homolog	25.14	5.34E-03
Q16777	Histone H2A type 2-C	24.64	1.73E-02
P16104	Histone H2AX	23.25	2.07E-02
Q9UHY1	Nuclear receptor-binding protein	21.42	3.64E-04
Q9H4A6	Golgi phosphoprotein 3	21.34	7.42E-02
P62861	40S ribosomal protein S30	21.23	2.74E-02
P17900	Ganglioside GM2 activator	20.16	4.59E-02
O75306-1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	19.70	2.39E-02
Q92526-1	T-complex protein 1 subunit zeta-2	19.50	2.54E-02
P46776	60S ribosomal protein L27a	18.63	4.01E-02
Q6P5R6	60S ribosomal protein L22-like 1	18.52	1.20E-01
Q9P2B7	Cilia- and flagella-associated protein 97	18.41	3.93E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q14914	Prostaglandin reductase 1	17.40	2.48E-02
O95819	Mitogen-activated protein kinase kinase kinase kinase 4	17.38	4.93E-02
Q16774-1	guanylate kinase	17.08	5.75E-03
Q9BY89-1	Uncharacterized protein KIAA1671	17.00	3.11E-02
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	16.89	6.55E-03
Q86YV9	Hermansky-Pudlak syndrome 6 protein	16.75	1.56E-01
P56537-1	eukaryotic translation initiation factor 6	16.71	5.40E-02
O95260	Arginyl-tRNA–protein transferase 1	16.67	1.50E-01
Q8IYT3	Coiled-coil domain-containing protein 170	16.55	1.21E-01
Q9Y3C8	ubiquitin-fold modifier-conjugating enzyme 1	16.45	2.37E-02
P18124	60S ribosomal protein L7	16.27	5.81E-02
Q14653	interferon regulatory factor 3	16.19	5.56E-02
Q13574	Diacylglycerol kinase zeta	14.96	1.71E-01
Q9H446	rwd domain-containing protein 1	14.87	9.50E-02
Q8NDI1	EH domain-binding protein 1	14.80	1.86E-01
Q66K74	Microtubule-associated protein 1S	14.61	7.05E-02
Q96PZ0	pseudouridylate synthase 7 homolog	14.34	1.77E-01
Q9H2W6	39S ribosomal protein L46, mitochondrial	14.16	7.53E-03
P46777	60S ribosomal protein L5	13.93	8.70E-02
P62241	40S ribosomal protein S8	13.90	8.74E-02
O94874-1	E3 UFM1-protein ligase 1	13.89	6.92E-02
P62633-8	Isoform 8 of Cellular nucleic acid-binding protein	13.73	1.91E-01
Q5GLZ8-1	Probable E3 ubiquitin-protein ligase HERC4	13.48	8.75E-02
Q96C23	aldose 1-epimerase	13.21	1.01E-01
Q96G25	mediator of RNA polymerase II transcription subunit 8	13.21	1.33E-01
P40429	60S ribosomal protein L13a	13.19	9.92E-02
Q2VIQ3	Chromosome-associated kinesin KIF4B	13.07	1.17E-01
P82673-1	28S ribosomal protein S35, mitochondrial	12.88	1.65E-01
Q8TC07-3	Isoform 3 of TBC1 domain family member 15	12.80	1.17E-01
Q01628	Interferon-induced transmembrane protein 3	12.80	1.46E-02
P08648	Integrin alpha-5	12.67	1.90E-01
P49257	Protein ERGIC-53	12.42	4.46E-02
Q05655	protein kinase C delta type	12.40	1.46E-01
Q9BZD4	kinetochore protein nuf2	12.29	1.95E-01
Q08209-1	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	12.25	2.21E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q16778	Histone H2B type 2-E	12.17	1.19E-01
Q96A26	Protein FAM162A	12.05	9.53E-02
Q9Y2G5-1	Isoform A of GDP-fucose protein O-fucosyltransferase 2	11.82	2.70E-02
Q49AR2-1	UPF0489 protein C5orf22	11.55	1.43E-01
Q9H936	Mitochondrial glutamate carrier 1	11.53	2.01E-02
O96013-1	serine/threonine-protein kinase PAK 4	11.45	1.86E-02
Q8N392-1	Rho GTPase-activating protein 18	11.38	5.08E-02
Q9H0U4	ras-related protein Rab-1B	11.33	9.82E-02
Q9H8U3	AN1-type zinc finger protein 3	11.30	1.96E-01
O00442	RNA 3'-terminal phosphate cyclase	11.21	9.64E-02
Q15691	Microtubule-associated protein RP/EB family member 1	11.19	8.57E-02
P62701	40S ribosomal protein S4, X isoform	11.05	1.48E-01
O60763-1	General vesicular transport factor p115	10.86	1.48E-01
P62745	Rho-related GTP-binding protein RhoB	10.60	2.30E-01
O75340	programmed cell death protein 6	10.52	2.73E-02
P36776	Lon protease homolog, mitochondrial	10.46	5.81E-02
Q96K37-1	Solute carrier family 35 member E1	10.33	1.19E-02
Q9H1H9	Kinesin-like protein KIF13A	10.23	1.75E-01
P53007	Tricarboxylate transport protein, mitochondrial	10.20	7.95E-02
Q9BUL8	programmed cell death protein 10	10.19	1.38E-01
P00491	purine nucleoside phosphorylase	10.18	1.50E-02
Q9Y5P4-1	Collagen type IV alpha-3-binding protein	10.10	2.65E-01
Q16563	Synaptophysin-like protein 1	10.02	1.12E-02
Q969N2	GPI transamidase component PIG-T	9.991	2.78E-01
Q96CW5	Gamma-tubulin complex component 3	9.977	2.18E-01
P36578	60S ribosomal protein L4	9.964	1.85E-01
P49914	5-formyltetrahydrofolate cyclo-ligase	9.920	1.06E-02
Q86W92-1	Liprin-beta-1	9.830	1.89E-01
P07602-1	Prosaposin	9.819	1.72E-01
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial	9.808	1.17E-01
Q16864-1	V-type proton ATPase subunit F	9.801	2.64E-01
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	9.782	1.15E-01
Q92667	A-kinase anchor protein 1, mitochondrial	9.737	2.81E-01
O60313	Dynamin-like 120 kDa protein, mitochondrial	9.707	1.19E-01
Q9NR45	sialic acid synthase	9.652	3.42E-02
P46781	40S ribosomal protein S9	9.574	1.99E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BVC6	Transmembrane protein 109	9.469	9.64E-02
Q6NSJ2-1	Pleckstrin homology-like domain family B member 3	9.356	3.08E-01
Q96EA4	protein Spindly	9.341	2.61E-01
O95372	acyl-protein thioesterase 2	9.302	2.40E-01
Q9H944	Mediator of RNA polymerase II transcription subunit 20	9.264	1.65E-01
Q6SZW1	Sterile alpha and TIR motif-containing protein 1	9.230	2.78E-01
P34931	Heat shock 70 kDa protein 1-like	9.207	1.83E-01
Q9BRJ2	39S ribosomal protein L45, mitochondrial	9.128	3.84E-02
P00338-1	L-lactate dehydrogenase A chain	9.128	2.19E-01
Q3ZCM7	tubulin beta-8 chain	9.127	9.29E-02
Q96SU4	Oxysterol-binding protein-related protein 9	9.098	1.23E-01
P06737-1	Glycogen phosphorylase, liver form	9.089	2.20E-01
Q8WTW3	conserved oligomeric Golgi complex subunit 1	9.071	2.44E-01
P30566	adenylosuccinate lyase	9.069	1.26E-01
Q9BU23-1	Lipase maturation factor 2	9.029	2.05E-01
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like	9.025	2.31E-01
P62269	40S ribosomal protein S18	8.901	2.30E-01
P51572	B-cell receptor-associated protein 31	8.877	9.30E-02
Q9Y605	MORF4 family-associated protein 1	8.875	2.16E-01
Q15435	Protein phosphatase 1 regulatory subunit 7	8.868	2.65E-02
Q8N0V4	Leucine-rich repeat LGI family member 2	8.833	5.69E-02
P48426	phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	8.799	3.02E-01
Q9BPZ3	Polyadenylate-binding protein-interacting protein 2	8.689	6.32E-02
Q15811	Intersectin-1	8.626	2.44E-01
Q16540	39S ribosomal protein L23, mitochondrial	8.624	2.55E-02
Q07020	60S ribosomal protein L18	8.615	2.43E-01
P61758	Prefoldin subunit 3	8.591	1.22E-01
P07900	Heat shock protein HSP 90-alpha	8.534	2.46E-01
Q86TU7	Histone-lysine N-methyltransferase setd3	8.517	2.49E-01
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2	8.514	2.77E-02
O94903	Pyridoxal phosphate homeostasis protein	8.454	2.78E-02
Q9H8S9-1	MOB kinase activator 1A	8.434	8.90E-02
P62081	40S ribosomal protein S7	8.409	2.53E-01
Q13643	four and a half LIM domains protein 3	8.340	2.76E-01
Q99442	translocation protein sec62	8.312	6.80E-02
P08865	40S ribosomal protein SA	8.297	2.59E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q15084-1	Protein disulfide-isomerase A6	8.278	2.59E-01
Q8IY37	Probable ATP-dependent RNA helicase DHX37	8.205	2.32E-01
P08238	Heat shock protein HSP 90-beta	8.193	2.63E-01
Q8WX92	Negative elongation factor B	8.110	1.83E-01
Q9NP77	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	8.062	2.31E-01
Q9BS26	Endoplasmic reticulum resident protein 44	8.048	1.30E-01
Q16222-1	UDP-N-acetylhexosamine pyrophosphorylase	8.037	2.54E-01
P51617	interleukin-1 receptor-associated kinase 1	8.027	2.61E-01
Q9Y303	N-acetylglucosamine-6-phosphate deacetylase	8.010	3.35E-01
Q9H832	Ubiquitin-conjugating enzyme E2 Z	8.004	1.29E-01
Q969V3	Nicalin	7.910	3.60E-02
P08574	Cytochrome c1, heme protein, mitochondrial	7.832	1.94E-01
P26196	Probable ATP-dependent RNA helicase DDX6	7.786	8.74E-02
Q68E01	Integrator complex subunit 3	7.779	3.58E-01
Q9Y2Z2	Protein MTO1 homolog, mitochondrial	7.745	2.00E-01
Q02127	Dihydroorotate dehydrogenase (Quinone), mitochondrial	7.579	2.32E-01
Q9BW62	katanin p60 ATPase-containing subunit A-like 1	7.523	3.80E-01
P43355	Melanoma-associated antigen 1	7.511	9.73E-02
Q92973-1	transportin-1	7.488	3.05E-01
Q8NCW5	NAD(P)H-hydrate epimerase	7.432	7.48E-02
Q76FK4	nucleolar protein 8	7.384	3.81E-01
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	7.380	1.08E-01
Q07960	rho GTPase-activating protein 1	7.374	1.98E-01
P56270-1	Myc-associated zinc finger protein	7.316	2.59E-01
O75663	TIP41-like protein	7.298	9.96E-02
P12004	proliferating cell nuclear antigen	7.280	3.16E-01
O00567	Nucleolar protein 56	7.187	3.25E-01
Q9ULT0-1	tetratricopeptide repeat protein 7A	7.164	2.32E-01
Q9Y570	Protein phosphatase methylesterase 1	7.145	3.25E-01
O95159	Zinc finger protein-like 1	7.111	4.04E-01
P62277	40S ribosomal protein S13	7.076	3.31E-01
P60228	Eukaryotic translation initiation factor 3 subunit E	7.028	2.54E-01
Q99436	Proteasome subunit beta type-7	6.997	6.33E-02
P39656	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase 48 kDa subunit	6.951	3.40E-01

Continued on next page

accession	description	fold p change	adjusted p-value
P63167	Dynein light chain 1, cytoplasmic	6.887	2.63E-01
P22694-1	cAMP-dependent protein kinase catalytic subunit beta	6.866	1.52E-01
Q96GA3	protein LTV1 homolog	6.866	1.78E-01
Q969S9	Ribosome-releasing factor 2, mitochondrial	6.862	3.01E-01
P07947	tyrosine-protein kinase Yes	6.833	3.08E-01
P60033	CD81 antigen	6.826	1.21E-01
P16871-1	Interleukin-7 receptor subunit alpha	6.821	2.80E-01
P17096-1	High mobility group protein HMG-I/HMG-Y	6.767	3.56E-01
O00483	Cytochrome c oxidase subunit NDUFA4	6.734	1.27E-01
O15460-1	Prolyl 4-hydroxylase subunit alpha-2	6.726	1.18E-01
Q5J8M3-1	ER membrane protein complex subunit 4	6.708	2.40E-01
Q05048	Cleavage stimulation factor subunit 1	6.689	5.97E-02
Q13888-1	General transcription factor IIH subunit 2	6.655	1.93E-01
Q9Y6C9	Mitochondrial carrier homolog 2	6.641	2.79E-01
Q9Y6E0	Serine/threonine-protein kinase 24	6.567	1.70E-01
P50748	Kinetochore-associated protein 1	6.567	4.29E-01
Q14789	Golgin subfamily B member 1	6.553	3.14E-01
P04908	histone H2A type 1-B/E	6.532	3.73E-01
P78345	Ribonuclease P protein subunit p38	6.518	4.32E-01
Q8NFQ8	Torsin-1A-interacting protein 2	6.516	2.92E-01
P31749	RAC-alpha serine/threonine-protein kinase	6.505	3.42E-01
P51948-1	CDK-activating kinase assembly factor MAT1	6.451	3.25E-01
Q92733	proline-rich protein PRCC	6.446	3.91E-01
Q9HAV4	exportin-5	6.420	1.23E-01
Q9ULH1-1	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1	6.415	2.57E-01
Q08945	FACT complex subunit SSRP1	6.411	2.96E-01
P43360	Melanoma-associated antigen 6	6.401	4.16E-01
Q6P2Q9	Pre-mRNA-processing-splicing factor 8	6.395	3.86E-01
P20936-1	ras GTPase-activating protein 1	6.392	9.83E-02
Q9H7B2	Ribosome production factor 2 homolog	6.355	7.75E-02
Q99567	Nuclear pore complex protein Nup88	6.335	3.10E-01
P61160-1	Actin-related protein 2	6.311	2.92E-01
P62917	60S ribosomal protein L8	6.289	3.93E-01
O95478	Ribosome biogenesis protein NSA2 homolog	6.271	2.16E-01
Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	6.247	2.42E-01

Continued on next page

accession	description	fold p change	adjusted p-value
P60660	Myosin light polypeptide 6	6.240	3.97E-01
P26447	Protein S100-A4	6.183	2.85E-01
Q15185	Prostaglandin E synthase 3	6.169	4.04E-01
Q71U36	tubulin alpha-1A chain	6.143	4.06E-01
O43707	Alpha-actinin-4	6.140	4.06E-01
Q9NSD9	Phenylalanine–tRNA ligase beta subunit	6.140	4.06E-01
P11413-1	Glucose-6-phosphate 1-dehydrogenase	6.102	4.08E-01
Q8WXA9-2	Isoform 2 of Splicing regulatory glutamine/lysine-rich protein 1	6.075	1.22E-01
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	6.048	2.97E-01
P62424	60S ribosomal protein L7a	6.039	4.14E-01
O15554	intermediate conductance calcium-activated potassium channel protein 4	6.020	4.35E-01
Q9BSY4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5	6.012	3.13E-01
Q9BTV4	Transmembrane protein 43	5.968	2.68E-01
Q9BUJ2-1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	5.947	3.18E-01
P62750	60S ribosomal protein L23a	5.930	4.26E-01
Q9NTJ5	Phosphatidylinositide phosphatase SAC1	5.909	1.63E-01
P40306	Proteasome subunit beta type-10	5.895	3.35E-01
Q9Y6B6	GTP-binding protein SAR1b	5.883	2.16E-01
P82933	28S ribosomal protein S9, mitochondrial	5.871	4.08E-01
Q9UQ16	Dynamin-3	5.826	1.75E-01
P18085	ADP-ribosylation factor 4	5.787	3.47E-01
P14618-2	Isoform M1 of Pyruvate kinase PKM	5.775	1.93E-01
Q14165	Malectin	5.746	3.48E-01
Q8NBS9-1	Thioredoxin domain-containing protein 5	5.740	4.45E-01
P50395-1	Rab GDP dissociation inhibitor beta	5.735	4.45E-01
P51553-1	isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	5.590	1.47E-01
Q93034	Cullin-5	5.548	4.86E-01
Q12905	Interleukin enhancer-binding factor 2	5.538	3.16E-01
P59998	Actin-related protein 2/3 complex subunit 4	5.530	3.24E-01
O95684	FGFR1 oncogene partner	5.515	3.66E-01
P50570-1	Dynamin-2	5.492	3.79E-01
Q8IYS2-1	Uncharacterized protein KIAA2013	5.484	2.30E-01
P48047	ATP synthase subunit O, mitochondrial	5.481	3.28E-01
P51149	ras-related protein Rab-7a	5.479	4.74E-01
Q99873	protein arginine N-methyltransferase 1	5.465	2.17E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q99653	Calcineurin B homologous protein 1	5.460	2.00E-01
Q8N543	prolyl 3-hydroxylase OGFOD1	5.437	3.27E-01
Q10567	AP-1 complex subunit beta-1	5.407	3.37E-01
P55263-1	Adenosine kinase	5.391	3.23E-01
Q9BXI6	TBC1 domain family member 10A	5.358	2.15E-01
O15145	Actin-related protein 2/3 complex subunit 3	5.355	3.79E-01
P61201-1	COP9 signalosome complex subunit 2	5.345	3.05E-01
Q8NFH4	Nucleoporin Nup37	5.329	3.32E-01
Q9NVD7	alpha-parvin	5.264	4.21E-01
Q9UHX3	Adhesion G protein-coupled receptor E2	5.183	2.32E-01
O75569-1	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	5.182	1.37E-01
Q969Q0	60S ribosomal protein L36a-like	5.160	3.50E-01
Q8WVB6	Chromosome transmission fidelity protein 18 homolog	5.157	5.00E-01
P62244	40S ribosomal protein S15a	5.127	4.73E-01
Q15417	Calponin-3	5.111	4.25E-01
Q71UM5	40S ribosomal protein S27-like	5.073	3.46E-01
O95391	Pre-mRNA-splicing factor SLU7	5.064	3.99E-01
Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	5.060	4.06E-01
P19623	spermidine synthase	5.056	4.08E-01
Q9Y4C8	Probable RNA-binding protein 19	5.053	4.22E-01
Q9UHI6	Probable ATP-dependent RNA helicase DDX20	5.041	4.05E-01
Q9NTK5-1	obg-like ATPase 1	5.041	4.30E-01
O15212	Prefoldin subunit 6	5.025	3.58E-01
O60826	Coiled-coil domain-containing protein 22	5.025	4.19E-01
P55786	puromycin-sensitive aminopeptidase	5.010	4.12E-01
Q14318	peptidyl-prolyl cis-trans isomerase FKBP8	4.993	4.36E-01
Q99627-1	COP9 signalosome complex subunit 8	4.975	3.58E-01
O14579-1	coatomer subunit epsilon	4.971	2.27E-01
Q13043-1	serine/threonine-protein kinase 4	4.968	2.86E-01
Q9Y3Q0	N-acetylated-alpha-linked acidic dipeptidase 2	4.915	4.34E-01
P52788-1	Spermine synthase	4.911	2.33E-01
P12955	xaa-Pro dipeptidase	4.910	2.66E-01
O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	4.899	3.97E-01
Q96RF0	Sorting nexin-18	4.896	1.71E-01
Q9BT73	Proteasome assembly chaperone 3	4.890	2.71E-01

Continued on next page

accession	description	fold p change	adjusted p-value
P21964-1	Catechol O-methyltransferase	4.882	2.73E-01
Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3	4.880	2.13E-01
O75940	Survival of motor neuron-related-splicing factor 30	4.838	1.79E-01
Q92888-1	Rho guanine nucleotide exchange factor 1	4.832	3.75E-01
P30740	Leukocyte elastase inhibitor	4.826	2.54E-01
P04844-1	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase subunit 2	4.824	4.48E-01
P49721	proteasome subunit beta type-2	4.824	4.66E-01
O75718	Cartilage-associated protein	4.798	3.88E-01
Q9UBQ0	Vacuolar protein sorting-associated protein 29	4.766	4.03E-01
Q9NWV4	UPF0587 protein C1orf123	4.760	2.67E-01
Q9NWZ8	Gem-associated protein 8	4.750	4.96E-01
Q15008-4	Isoform 4 of 26S proteasome non-ATPase regulatory subunit 6	4.720	4.31E-01
Q5K4L6-1	Long-chain fatty acid transport protein 3	4.702	5.00E-01
P08579	U2 small nuclear ribonucleoprotein B″	4.694	4.19E-01
O75694	nuclear pore complex protein nup155	4.660	2.37E-01
Q92930	Ras-related protein Rab-8B	4.641	4.82E-01
P48735	Isocitrate dehydrogenase [NADP], mitochondrial	4.636	3.21E-01
Q14258	E3 ubiquitin/ISG15 ligase TRIM25	4.632	4.70E-01
Q01081	Splicing factor U2AF 35 kDa subunit	4.631	3.73E-01
Q10713	Mitochondrial-processing peptidase subunit alpha	4.628	3.01E-01
P46199	Translation initiation factor IF-2, mitochondrial	4.622	4.63E-01
Q9NSE4	Isoleucine–tRNA ligase, mitochondrial	4.619	3.14E-01
P43363	Melanoma-associated antigen 10	4.613	1.83E-01
P42677	40S ribosomal protein S27	4.612	4.91E-01
P41743	Protein kinase c iota type	4.602	3.19E-01
P49770	Translation initiation factor eIF-2B subunit beta	4.580	2.84E-01
P04424	argininosuccinate lyase	4.569	4.91E-01
Q9BV20-1	methylthioribose-1-phosphate isomerase	4.539	3.19E-01
P13674-1	prolyl 4-hydroxylase subunit alpha-1	4.538	4.32E-01
O94804	Serine/threonine-protein kinase 10	4.509	4.86E-01
Q7KZI7-1	Serine/threonine-protein kinase MARK2	4.455	3.08E-01
Q8IU81	Interferon regulatory factor 2-binding protein 1	4.410	4.97E-01
Q08722	Leukocyte surface antigen CD47	4.389	3.45E-01
P15153	Ras-related C3 botulinum toxin substrate 2	4.358	4.55E-01
Q7Z3J2-1	UPF0505 protein C16orf62	4.353	4.99E-01

Continued on next page

accession	description	fold p change	adjusted p-value
O60573	eukaryotic translation initiation factor 4E type 2	4.346	2.18E-01
Q96EY5-1	Multivesicular body subunit 12A	4.325	4.32E-01
P61599	N-alpha-acetyltransferase 20	4.321	3.82E-01
Q96KA5-1	cleft lip and palate transmembrane protein 1-like protein	4.300	5.00E-01
P57764	Gasdermin-D	4.267	4.55E-01
O95298-1	NADH dehydrogenase [ubiquinone] 1 subunit C2	4.261	2.61E-01
P56211	cAMP-regulated phosphoprotein 19	4.261	4.90E-01
Q9NVJ2	ADP-ribosylation factor-like protein 8B	4.255	4.55E-01
P35658-1	Nuclear pore complex protein Nup214	4.233	2.41E-01
O75436-1	Vacuolar protein sorting-associated protein 26A	4.226	2.52E-01
Q9UBS4	DnaJ homolog subfamily B member 11	4.221	2.26E-01
Q9BYT8	Neurolysin, mitochondrial	4.210	2.46E-01
Q9BV73-1	Centrosome-associated protein CEP250	4.201	2.99E-01
Q9NVC6	mediator of RNA polymerase II transcription subunit 17	4.191	4.96E-01
Q7Z7H8	39S ribosomal protein L10, mitochondrial	4.183	3.94E-01
Q12959	Disks large homolog 1	4.141	2.81E-01
Q8TDN6	Ribosome biogenesis protein BRX1 homolog	4.093	4.93E-01
P25788-1	Proteasome subunit alpha type-3	4.039	4.56E-01
Q53HL2	Borealin	4.015	4.74E-01
O00139	Kinesin-like protein KIF2A	4.007	2.60E-01
Q5T9A4	ATPase family AAA domain-containing protein 3B	3.990	3.82E-01
Q86TX2	acyl-coenzyme A thioesterase 1	3.984	3.62E-01
Q9Y4B6	DDB1- and CUL4-associated factor 1	3.980	4.83E-01
Q8WXC6-2	COP9 signalosome complex subunit 9	3.976	4.37E-01
Q9H074	Polyadenylate-binding protein-interacting protein 1	3.962	3.22E-01
Q16718	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	3.941	4.21E-01
O60749	Sorting nexin-2	3.937	5.00E-01
O15160	DNA-directed RNA polymerases I and III subunit RPAC1	3.908	2.78E-01
Q92979	Ribosomal RNA small subunit methyltransferase Nep1	3.863	2.98E-01
P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	3.804	4.23E-01
P36551	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	3.788	4.98E-01
P42126	Enoyl-CoA delta isomerase 1, mitochondrial	3.773	4.10E-01
O95453	poly(A)-specific ribonuclease PARN	3.766	4.32E-01
Q9UL25	Ras-related protein Rab-21	3.744	4.04E-01
O75970	multiple PDZ domain protein	3.725	4.08E-01
Q9C0J8	pre-mRNA 3′ end processing protein WDR33	3.694	4.61E-01

Continued on next page

accession	description	fold p change	adjusted p-value
P40123	Adenylyl cyclase-associated protein 2	3.666	4.33E-01
Q9H1Z4	WD repeat-containing protein 13	3.631	4.22E-01
Q15545	Transcription initiation factor TFIID subunit 7	3.535	4.21E-01
Q92878	DNA repair protein Rad50	3.496	4.88E-01
Q12800-1	Alpha-globin transcription factor CP2	3.438	4.91E-01
P28074-1	proteasome subunit beta type-5	3.413	4.36E-01
O43432	Eukaryotic translation initiation factor 4 gamma 3	3.388	4.99E-01
P49366-1	deoxyhypusine synthase	3.348	4.84E-01
O00203-1	AP-3 complex subunit beta-1	3.336	3.98E-01
Q96FS4	signal-induced proliferation-associated protein 1	3.332	4.70E-01
Q9GZL7	ribosome biogenesis protein WDR12	3.309	4.87E-01
Q9UIG0	Tyrosine-protein kinase BAZ1B	3.299	4.91E-01
Q13404	Ubiquitin-conjugating enzyme E2 variant 1	3.294	4.74E-01
Q8N2U0	Transmembrane protein 256	3.271	3.92E-01
Q8TBC4-1	NEDD8-activating enzyme E1 catalytic subunit	3.271	3.94E-01
Q8N4V1	Membrane magnesium transporter 1	3.240	4.54E-01
P52294	Importin subunit alpha-5	3.234	4.91E-01
Q96HY6-1	DDRGK domain-containing protein 1	3.233	4.10E-01
Q8WUW1	Protein BRICK1	3.171	4.12E-01
P78316	Nucleolar protein 14	3.136	4.22E-01
Q9Y2R5	28S ribosomal protein S17, mitochondrial	3.129	3.92E-01
Q15369-1	elongin-C	3.117	4.38E-01
Q96CS3	FAS-associated factor 2	3.114	4.29E-01
P49959	Double-strand break repair protein MRE11	3.058	4.33E-01
O14617-1	AP-3 complex subunit delta-1	3.011	4.85E-01
Q8N5G0	Small integral membrane protein 20	2.906	4.95E-01
P63313	thymosin beta-10	0.499	4.63E-01
Q9NQR4	Omega-amidase NIT2	0.495	4.76E-01
O14593	DNA-binding protein RFXANK	0.493	4.75E-01
O60684	Importin subunit alpha-7	0.490	4.55E-01
P30044-1	Peroxiredoxin-5, mitochondrial	0.481	4.94E-01
P14678-1	Small nuclear ribonucleoprotein-associated proteins B and B′	0.479	4.83E-01
Q02880	DNA topoisomerase 2-beta	0.479	4.90E-01
Q9UHB6	LIM domain and actin-binding protein 1	0.479	4.92E-01
P49773	Histidine triad nucleotide-binding protein 1	0.473	4.86E-01
Q96S59-1	Ran-binding protein 9	0.473	4.99E-01

Continued on next page

accession	description	fold p change	adjusted p-value
P50579	methionine aminopeptidase 2	0.469	4.25E-01
Q7Z2W4	zinc finger CCCH-type antiviral protein 1	0.464	4.75E-01
O00244	Copper transport protein ATOX1	0.460	4.92E-01
Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	0.460	4.94E-01
Q07955-1	Serine/arginine-rich splicing factor 1	0.458	4.67E-01
Q15056-2	Isoform Short of Eukaryotic translation initiation factor 4H	0.458	4.67E-01
Q13951-2	Isoform 2 of Core-binding factor subunit beta	0.457	4.64E-01
P41236	Protein phosphatase inhibitor 2	0.456	4.47E-01
P49321	Nuclear autoantigenic sperm protein	0.454	4.97E-01
Q9UHV9	Prefoldin subunit 2	0.447	4.94E-01
O15143	Actin-related protein 2/3 complex subunit 1B	0.441	4.83E-01
Q9NYB0	Telomeric repeat-binding factor 2-interacting protein 1	0.439	4.67E-01
P55010	Eukaryotic translation initiation factor 5	0.439	4.82E-01
Q86SJ2	Amphoterin-induced protein 2	0.437	4.60E-01
Q9ULW0	Targeting protein for Xklp2	0.436	4.02E-01
Q71DI3	histone H3.2	0.434	4.31E-01
O43583	density-regulated protein	0.434	4.95E-01
O75477	erlin-1	0.432	4.92E-01
Q8WWM7-1	ataxin-2-like protein	0.427	4.24E-01
Q9NYF8-3	Isoform 3 of Bcl-2-associated transcription factor 1	0.425	3.97E-01
Q12802-1	A-kinase anchor protein 13	0.424	4.63E-01
Q96C86	M7GpppX diphosphatase	0.421	4.83E-01
Q8TDP1	Ribonuclease H2 subunit C	0.419	4.28E-01
P38117	electron transfer flavoprotein subunit beta	0.418	4.53E-01
P52701	DNA mismatch repair protein MSH6	0.418	4.75E-01
Q14696	LRP chaperone MESD	0.418	4.76E-01
P46109	Crk-like protein	0.418	4.81E-01
P38159-1	RNA-binding motif protein, X chromosome	0.417	4.10E-01
Q05519	serine/arginine-rich splicing factor 11	0.416	4.46E-01
O00151	PDZ and LIM domain protein 1	0.414	4.07E-01
Q9BPW8	Protein NipSnap homolog 1	0.413	4.46E-01
P21291	Cysteine and glycine-rich protein 1	0.411	4.03E-01
Q9H910-1	Jupiter microtubule associated homolog 2	0.409	4.99E-01
P06753-2	Isoform 2 of Tropomyosin alpha-3 chain	0.405	3.94E-01
Q9NQ29	putative RNA-binding protein Luc7-like 1	0.404	4.33E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q9HCS7	Pre-mRNA-splicing factor SYF1	0.403	3.98E-01
P15531	Nucleoside diphosphate kinase A	0.401	3.99E-01
Q14197	Peptidyl-tRNA hydrolase ICT1, mitochondrial	0.401	4.04E-01
Q9H307	Pinin	0.399	4.91E-01
Q6IAA8	ragulator complex protein LAMTOR1	0.397	3.85E-01
Q9P2N5	RNA-binding protein 27	0.396	3.84E-01
Q5JTV8-3	Isoform 3 of Torsin-1A-interacting protein 1	0.396	4.31E-01
Q8N9N8	probable RNA-binding protein EIF1AD	0.395	3.86E-01
Q9Y3B7-1	39S ribosomal protein L11, mitochondrial	0.395	4.36E-01
Q04837	Single-stranded DNA-binding protein, mitochondrial	0.392	3.78E-01
Q9NZT2-1	opioid growth factor receptor	0.391	3.78E-01
Q8TAE8	Growth arrest and DNA damage-inducible proteins-interacting protein 1	0.390	3.49E-01
Q9Y333	U6 snRNA-associated Sm-like protein LSm2	0.390	3.81E-01
P80217	interferon-induced 35 kDa protein	0.389	3.84E-01
P55145	Mesencephalic astrocyte-derived neurotrophic factor	0.388	3.71E-01
O95373	Importin-7	0.387	3.45E-01
Q9NP61-1	ADP-ribosylation factor GTPase-activating protein 3	0.387	4.77E-01
O14974	Protein phosphatase 1 regulatory subunit 12A	0.384	3.40E-01
P51991-1	Heterogeneous nuclear ribonucleoprotein A3	0.384	3.65E-01
P09497-2	Isoform Non-brain of Clathrin light chain B	0.384	3.92E-01
Q99661-1	Kinesin-like protein KIF2C	0.383	4.62E-01
Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein 2	0.382	3.62E-01
P67936	Tropomyosin alpha-4 chain	0.382	3.63E-01
P60174-1	Isoform 2 of Triosephosphate isomerase	0.381	3.62E-01
Q8WX93-1	palladin	0.381	3.62E-01
Q16204	coiled-coil domain-containing protein 6	0.381	3.84E-01
Q9NRG0	Chromatin accessibility complex protein 1	0.380	3.58E-01
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma	0.377	4.00E-01
P52948-1	nuclear pore complex protein Nup98-Nup96	0.376	3.97E-01
Q8IUE6	Histone H2A type 2-B	0.376	4.29E-01
Q96K17-1	transcription factor BTF3 homolog 4	0.374	3.90E-01
Q9UJU6-1	Drebrin-like protein	0.372	3.52E-01
O00154	cytosolic acyl coenzyme A thioester hydrolase	0.371	3.81E-01
Q01130	serine/arginine-rich splicing factor 2	0.368	3.43E-01
P46108-2	Isoform Crk-I of Adapter molecule crk	0.368	3.45E-01

Continued on next page

accession	description	fold p change	adjusted p-value
P61981	14-3-3 protein gamma	0.368	3.77E-01
Q8NFC6	Biorientation of chromosomes in cell division protein 1-like 1	0.365	2.63E-01
P23246-1	splicing factor, proline- and glutamine-rich	0.362	3.35E-01
Q9NQ50	39S ribosomal protein L40, mitochondrial	0.362	3.52E-01
Q9Y3B2	Exosome complex component csl4	0.361	3.18E-01
P46379-1	Large proline-rich protein BAG6	0.361	3.34E-01
O95817	BAG family molecular chaperone regulator 3	0.360	3.65E-01
P22307-1	Non-specific lipid-transfer protein	0.359	3.86E-01
O00330-1	Pyruvate dehydrogenase protein X component, mitochondrial	0.356	3.14E-01
Q08752	peptidyl-prolyl cis-trans isomerase D	0.356	3.58E-01
Q9HAV7	GrpE protein homolog 1, mitochondrial	0.354	3.49E-01
Q9NRR5-1	Ubiquilin-4	0.353	3.89E-01
Q9ULT8	E3 ubiquitin-protein ligase hectd1	0.352	3.90E-01
Q9UBX3	Mitochondrial dicarboxylate carrier	0.351	2.59E-01
Q15459	splicing factor 3A subunit 1	0.350	3.18E-01
Q9H1B7	interferon regulatory factor 2-binding protein-like	0.350	3.20E-01
P45973	chromobox protein homolog 5	0.348	3.07E-01
Q86SX6	Glutaredoxin-related protein 5, mitochondrial	0.346	3.08E-01
Q06587	E3 ubiquitin-protein ligase RING1	0.346	4.26E-01
P53999	Activated RNA polymerase II transcriptional coactivator p15	0.342	3.08E-01
P78318	Immunoglobulin-binding protein 1	0.342	4.63E-01
Q8IYB3	Serine/arginine repetitive matrix protein 1	0.342	4.86E-01
Q96EP5	DAZ-associated protein 1	0.341	3.08E-01
Q9BY32-1	Inosine triphosphate pyrophosphatase	0.341	3.82E-01
Q9NX40	OCIA domain-containing protein 1	0.340	3.06E-01
Q9P1Y6-1	PHD and RING finger domain-containing protein 1	0.340	3.18E-01
Q8NC51-3	Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein	0.339	2.41E-01
P09110-1	3-ketoacyl-CoA thiolase, peroxisomal	0.338	3.02E-01
P35611-1	Alpha-adducin	0.338	3.05E-01
Q14257-2	Isoform 2 of Reticulocalbin-2	0.337	3.23E-01
Q3KQU3	MAP7 domain-containing protein 1	0.337	3.27E-01
P98175-2	Isoform 2 of RNA-binding protein 10	0.336	3.49E-01
Q9BW71-1	HIRA-interacting protein 3	0.336	4.66E-01
P62857	40S ribosomal protein S28	0.335	3.00E-01
Q14839	Chromodomain-helicase-DNA-binding protein 4	0.335	3.21E-01
O75410-1	Transforming acidic coiled-coil-containing protein 1	0.333	2.41E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q99615-1	DnaJ homolog subfamily C member 7	0.333	3.45E-01
Q9BYD2	39S ribosomal protein L9, mitochondrial	0.332	4.05E-01
Q96IZ0	PRKC apoptosis WT1 regulator protein	0.330	3.13E-01
Q96PU8	protein quaking	0.327	3.35E-01
Q12792-2	Twinfilin-1	0.324	3.08E-01
Q9Y520	Protein Prrc2c	0.323	2.81E-01
Q15843	NEDD8	0.323	2.98E-01
P20674	Cytochrome c oxidase subunit 5A, mitochondrial	0.320	2.78E-01
P69905	Hemoglobin subunit alpha	0.320	3.01E-01
Q86U90	YrdC domain-containing protein, mitochondrial	0.319	2.55E-01
Q8NI22	Multiple coagulation factor deficiency protein 2	0.318	3.01E-01
Q8WUH6	Transmembrane protein 263	0.318	3.17E-01
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	0.316	3.13E-01
Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog	0.314	3.01E-01
Q5UIP0	Telomere-associated protein RIF1	0.313	4.07E-01
P00441	Superoxide dismutase [Cu-Zn]	0.312	2.66E-01
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	0.311	2.65E-01
Q92945	Far upstream element-binding protein 2	0.308	2.60E-01
Q92734-1	Protein TFG	0.307	2.94E-01
Q9BRP8	Partner of Y14 and mago	0.306	2.53E-01
P15291	Beta-1,4-galactosyltransferase 1	0.306	2.78E-01
Q9Y3D9	28S ribosomal protein S23, mitochondrial	0.304	3.01E-01
P43121	Cell surface glycoprotein MUC18	0.304	3.27E-01
Q92934	Bcl2-associated agonist of cell death	0.300	4.76E-01
P02788	Lactotransferrin	0.298	3.66E-01
Q9UPT8	Zinc finger CCCH domain-containing protein 4	0.297	2.32E-01
Q12888-1	TP53-binding protein 1	0.295	2.97E-01
P18583-1	Protein SON	0.294	3.13E-01
P62993	Growth factor receptor-bound protein 2	0.293	2.59E-01
P13726-1	tissue factor	0.293	2.63E-01
P20290-2	Isoform 2 of Transcription factor BTF3	0.291	2.37E-01
Q04323-1	UBX domain-containing protein 1	0.290	2.36E-01
Q9H0B6	Kinesin light chain 2	0.290	4.59E-01
Q9NX63	MICOS complex subunit MIC19	0.288	2.46E-01
Q99614	tetratricopeptide repeat protein 1	0.288	2.72E-01
Q96PD2-1	Discoidin, CUB and LCCL domain-containing protein 2	0.287	2.61E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q9C0C2	182 kDa tankyrase-1-binding protein	0.285	1.76E-01
Q9NP97	Dynein light chain roadblock-type 1	0.285	2.32E-01
P50479-1	PDZ and LIM domain protein 4	0.284	2.53E-01
Q14676	Mediator of DNA damage checkpoint protein 1	0.284	3.62E-01
Q9NX55-2	Huntingtin-interacting protein K	0.283	1.88E-01
P07858	Cathepsin B	0.282	2.76E-01
Q9H0W8	protein SMG9	0.281	3.45E-01
P22061	protein-L-isoaspartate(D-aspartate) O-methyltransferase	0.279	1.95E-01
Q9NSI2-1	protein FAM207A	0.278	2.32E-01
O00221	NF-kappa-B inhibitor epsilon	0.277	4.73E-01
P20020	Plasma membrane calcium-transporting ATPase 1	0.275	2.00E-01
Q96EI5	Transcription elongation factor A protein-like 4	0.271	1.88E-01
Q96PK6-5	Isoform 5 of RNA-binding protein 14	0.271	2.50E-01
Q15018	BRISC complex subunit Abraxas 2	0.271	4.91E-01
Q5UCC4-1	ER membrane protein complex subunit 10	0.268	3.20E-01
Q658P3-1	Metalloreductase STEAP3	0.268	4.36E-01
Q8N6N3	UPF0690 protein C1orf52	0.266	2.49E-01
Q8IVM0	Coiled-coil domain-containing protein 50	0.266	2.78E-01
Q9NW82	WD repeat-containing protein 70	0.265	1.77E-01
O95232-1	Luc7-like protein 3	0.264	4.89E-01
Q13242	serine/arginine-rich splicing factor 9	0.263	1.95E-01
Q9Y624	Junctional adhesion molecule A	0.261	3.20E-01
Q15599-2	Isoform 2 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2	0.260	1.51E-01
Q8N4Q1	Mitochondrial intermembrane space import and assembly protein 40	0.260	1.71E-01
P07203	Glutathione peroxidase 1	0.260	2.01E-01
Q6P1N0	Coiled-coil and C2 domain-containing protein 1A	0.259	4.99E-01
Q96CT7	Coiled-coil domain-containing protein 124	0.257	2.33E-01
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	0.256	1.28E-01
P55789	FAD-linked sulfhydryl oxidase ALR	0.256	1.65E-01
Q15427	Splicing factor 3b subunit 4	0.255	1.48E-01
Q9UPQ0-1	LIM and calponin homology domains-containing protein 1	0.255	3.62E-01
P23193	Transcription elongation factor A protein 1	0.254	1.96E-01
P52732	Kinesin-like protein KIF11	0.252	2.90E-01
Q8ND56	protein LSM14 homolog A	0.250	1.60E-01
Q9NRV9	Heme-binding protein 1	0.250	1.75E-01

Continued on next page

accession	description	fold p change	adjusted p-value
P09972	Fructose-bisphosphate aldolase C	0.249	1.75E-01
P17152	Transmembrane protein 11, mitochondrial	0.249	4.56E-01
P05114	Non-histone chromosomal protein HMG-14	0.248	1.39E-01
O95881	Thioredoxin domain-containing protein 12	0.248	2.09E-01
Q71RC2	La-related protein 4	0.247	2.44E-01
O75828	Carbonyl reductase [NADPH] 3	0.247	4.71E-01
Q7Z422	SUZ domain-containing protein 1	0.246	4.60E-01
Q5JTJ3-1	Cytochrome c oxidase assembly factor 6 homolog	0.245	3.58E-01
Q09666-1	Neuroblast differentiation-associated protein AHNAK	0.244	1.69E-01
P29558-1	RNA-binding motif, single-stranded-interacting protein 1	0.244	3.58E-01
P46821	microtubule-associated protein 1B	0.243	1.67E-01
Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2	0.243	1.70E-01
P19883	follistatin	0.241	2.28E-01
Q6P4F2	Ferredoxin-2, mitochondrial	0.240	4.16E-01
P07910-1	Heterogeneous nuclear ribonucleoproteins C1/C2	0.239	4.57E-01
O75475-1	PC4 and SFRS1-interacting protein	0.238	1.63E-01
P0DMU8	Cancer/testis antigen family 45 member A5	0.236	1.11E-01
Q7Z3B3	KAT8 regulatory NSL complex subunit 1	0.236	4.56E-01
Q96B97-1	SH3 domain-containing kinase-binding protein 1	0.235	9.97E-02
A0MZ66	Shootin-1	0.234	1.09E-01
Q15599-3	Isoform 3 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2	0.234	1.54E-01
Q9H2U1	ATP-dependent RNA helicase DHX36	0.234	4.14E-01
P09493-5	Isoform 5 of Tropomyosin alpha-1 chain	0.232	1.14E-01
O75962-1	Triple functional domain protein	0.232	1.59E-01
Q96ME7	Zinc finger protein 512	0.230	5.00E-01
Q9Y3B9	RRP15-like protein	0.229	1.15E-01
Q9H6F5	Coiled-coil domain-containing protein 86	0.229	2.12E-01
Q6P4E1	Protein CASC4	0.229	4.29E-01
Q04941-1	proteolipid protein 2	0.228	9.56E-02
P05783	Keratin, type I cytoskeletal 18	0.228	1.46E-01
Q6P087	Mitochondrial mRNA pseudouridine synthase RPUSD3	0.228	4.30E-01
Q8WVC0-1	RNA polymerase-associated protein LEO1	0.227	2.71E-01
P53985	Monocarboxylate transporter 1	0.224	1.24E-01
Q9Y4B5	Microtubule cross-linking factor 1	0.224	2.35E-01
P04049	RAF proto-oncogene serine/threonine-protein kinase	0.222	4.22E-01
Q58FG1	Putative heat shock protein HSP 90-alpha A4	0.222	4.88E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q86V48-1	Leucine zipper protein 1	0.221	1.82E-01
Q17RB8	LON peptidase N-terminal domain and RING finger protein 1	0.221	4.83E-01
Q8IWS0-1	PHD finger protein 6	0.220	8.89E-02
Q9UMN6	Histone-lysine N-methyltransferase 2B	0.219	1.67E-01
Q15434	RNA-binding motif, single-stranded-interacting protein 2	0.219	3.17E-01
Q8N3D4	EH domain-binding protein 1-like protein 1	0.218	8.72E-02
Q9NYJ1-1	Cytochrome c oxidase assembly factor 4 homolog, mitochondrial	0.217	2.13E-01
Q01804-1	OTU domain-containing protein 4	0.216	4.04E-01
P82909	28S ribosomal protein S36, mitochondrial	0.215	1.20E-01
Q96G23	Ceramide synthase 2	0.215	1.54E-01
Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1	0.215	2.35E-01
Q8WW33	Gametocyte-specific factor 1	0.212	1.54E-01
Q92917	G patch domain and KOW motifs-containing protein	0.211	5.74E-02
P11279	Lysosome-associated membrane glycoprotein 1	0.211	3.01E-01
Q6ZSR9	Uncharacterized protein FLJ45252	0.208	2.86E-01
P30260	cell division cycle protein 27 homolog	0.208	3.86E-01
Q8WWW8	GRB2-associated-binding protein 3	0.208	4.31E-01
Q9H4A3	Serine/threonine-protein kinase WNK1	0.207	3.01E-01
Q9H078-1	Caseinolytic peptidase B protein homolog	0.207	3.59E-01
Q6PJG2	ELM2 and SANT domain-containing protein 1	0.207	4.92E-01
Q9BY42	protein RTF2 homolog	0.205	3.20E-01
Q96AT1	Uncharacterized protein KIAA1143	0.204	6.95E-02
Q96S55-1	ATPase WRNIP1	0.204	7.39E-02
P33240	cleavage stimulation factor subunit 2	0.204	1.15E-01
Q5JTD0-1	Tight junction-associated protein 1	0.202	6.63E-02
Q96C01	Protein FAM136A	0.201	3.80E-01
Q6NYC8	Phostensin	0.200	1.09E-01
Q9UNF1	Melanoma-associated antigen D2	0.200	1.17E-01
Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein 2	0.200	2.84E-01
O76024	Wolframin	0.199	6.31E-02
Q6EMB2	tubulin polyglutamylase TTLL5	0.199	6.37E-02
Q05682-3	Isoform 3 of Caldesmon	0.197	1.05E-01
Q8IXQ3	Uncharacterized protein C9orf40	0.197	3.35E-01
O60664-1	Perilipin-3	0.196	1.04E-01
Q01167	Forkhead box protein K2	0.196	1.13E-01
Q86YP4	Transcriptional repressor p66-alpha	0.196	1.72E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q96FV9-1	THO complex subunit 1	0.196	4.42E-01
O43633	charged multivesicular body protein 2a	0.195	2.50E-01
Q9NRP2	COX assembly mitochondrial protein 2 homolog	0.194	7.40E-02
Q9UQ35	serine/arginine repetitive matrix protein 2	0.193	9.99E-02
P53350	Serine/threonine-protein kinase PLK1	0.189	2.13E-01
P02100	Hemoglobin subunit epsilon	0.188	1.60E-01
P60507	Endogenous retrovirus group FC1 Env polyprotein	0.186	1.17E-01
Q6PK04	Coiled-coil domain-containing protein 137	0.185	4.01E-01
Q86XD8	AN1-type zinc finger protein 4	0.185	4.08E-01
Q9Y2Q9	28S ribosomal protein S28, mitochondrial	0.184	5.16E-02
Q15637	Splicing factor 1	0.184	5.90E-02
Q96DF8	Protein DGCR14	0.183	5.68E-02
Q00587-1	Cdc42 effector protein 1	0.181	5.56E-02
Q9Y6K9	NF-kappa-B essential modulator	0.180	1.47E-01
Q9H7C9-1	Mth938 domain-containing protein	0.180	3.22E-01
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	0.179	5.17E-02
O15056	Synaptojanin-2	0.178	1.38E-01
P55210-1	Caspase-7	0.178	2.81E-01
O00193	Small acidic protein	0.177	7.91E-02
P16989-1	Y-box-binding protein 3	0.176	7.70E-02
Q9HD15	Steroid receptor RNA activator 1	0.175	7.66E-02
Q9UKL0	REST corepressor 1	0.175	2.78E-01
Q9GZR7	ATP-dependent RNA helicase DDX24	0.174	7.92E-02
Q7Z739	YTH domain-containing family protein 3	0.174	2.44E-01
Q8IYS1	Peptidase M20 domain-containing protein 2	0.174	4.97E-01
Q8IZ69	tRNA (uracil-5-)-methyltransferase homolog A	0.173	1.22E-01
Q05D32	CTD small phosphatase-like protein 2	0.172	2.62E-01
Q7LBC6-1	Lysine-specific demethylase 3B	0.172	2.75E-01
Q8N6S5	ADP-ribosylation factor-like protein 6-interacting protein 6	0.171	3.57E-01
Q13151	Heterogeneous nuclear ribonucleoprotein A0	0.169	7.19E-02
Q13442	28 kDa heat- and acid-stable phosphoprotein	0.168	7.01E-02
Q7Z6J0-1	E3 ubiquitin-protein ligase SH3RF1	0.168	3.99E-01
Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	0.166	2.44E-01
Q96DE5	Anaphase-promoting complex subunit 16	0.166	2.52E-01
Q8TEY7-1	Ubiquitin carboxyl-terminal hydrolase 33	0.166	3.82E-01

Continued on next page

accession	description	fold p change	adjusted p-value
Q96ST2	protein IWS1 homolog	0.166	4.10E-01
Q5U5X0	Complex III assembly factor LYRM7	0.163	3.19E-02
Q8N8S7	Protein enabled homolog	0.163	3.86E-02
P52926-1	high mobility group protein HMGI-C	0.163	3.82E-01
P35613	Basigin	0.162	2.87E-02
P07737	profilin-1	0.162	6.36E-02
Q8WX94-1	NACHT, LRR and PYD domains-containing protein 7	0.162	1.93E-01
O75368	SH3 domain-binding glutamic acid-rich-like protein	0.161	6.23E-02
O43768	alpha-endosulfine	0.160	5.96E-02
P20933	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	0.160	1.43E-01
Q63HR2	tensin-2	0.158	3.32E-01
Q92597	Protein NDRG1	0.158	4.45E-01
P61604	10 kDa heat shock protein, mitochondrial	0.155	5.74E-02
Q9BW85	Coiled-coil domain-containing protein 94	0.155	3.45E-01
Q9Y251	Heparanase	0.155	3.62E-01
Q9NWA0	Mediator of RNA polymerase II transcription subunit 9	0.155	4.34E-01
P33316-3	Deoxyuridine 5′-triphosphate nucleotidohydrolase, mitochondrial	0.152	5.37E-02
Q9NSV4-3	Protein diaphanous homolog 3	0.152	3.52E-01
O15541	RING finger protein 113A	0.150	3.00E-02
Q9NRF9	DNA polymerase epsilon subunit 3	0.150	3.95E-02
Q9NUP9	Protein lin-7 homolog C	0.149	5.97E-02
Q8TB72-1	pumilio homolog 2	0.149	2.49E-01
O14618	copper chaperone for superoxide dismutase	0.148	1.86E-02
O43815	striatin	0.148	1.02E-01
P41208	centrin-2	0.148	1.43E-01
P07205	Phosphoglycerate kinase 2	0.147	1.48E-01
Q9HCH5-1	Synaptotagmin-like protein 2	0.147	3.07E-01
Q9BQ61	Uncharacterized protein C19orf43	0.147	4.10E-01
Q9NPE3	H/ACA ribonucleoprotein complex subunit 3	0.146	1.99E-02
Q96JY6-1	PDZ and LIM domain protein 2	0.146	2.05E-01
O75531	Barrier-to-autointegration factor	0.145	4.79E-02
Q9NS25	Sperm protein associated with the nucleus on the X chromosome B1	0.145	1.40E-01
Q05209-1	Tyrosine-protein phosphatase non-receptor type 12	0.145	1.48E-01
O95747	Serine/threonine-protein kinase OSR1	0.145	3.02E-01
Q8IZN3-1	Probable palmitoyltransferase ZDHHC14	0.145	3.32E-01
Q9GZU8	Protein FAM192A	0.143	1.57E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P62330	ADP-ribosylation factor 6	0.142	1.99E-01
P80723	Brain acid soluble protein 1	0.140	4.32E-02
P49918	cyclin-dependent kinase inhibitor 1C	0.140	2.54E-01
Q9UII2-1	ATPase inhibitor, mitochondrial	0.139	3.66E-01
Q8WWH5	probable tRNA pseudouridine synthase 1	0.138	2.22E-01
Q5XKP0	MICOS complex subunit MIC13	0.137	4.41E-02
P02795	metallothionein-2	0.136	3.94E-01
Q8WWI1-3	Isoform 3 of LIM domain only protein 7	0.133	2.78E-01
Q15758-1	Neutral amino acid transporter B(0)	0.132	3.60E-02
Q9P2B4	CTTNBP2 N-terminal-like protein	0.132	3.91E-01
Q96EY8	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	0.127	3.32E-01
Q9Y2U8	inner nuclear membrane protein Man1	0.126	1.06E-02
Q96PU5	E3 ubiquitin-protein ligase NEDD4-like	0.124	1.93E-01
O15126-1	Secretory carrier-associated membrane protein 1	0.123	2.64E-01
O43447	peptidyl-prolyl cis-trans isomerase H	0.121	6.68E-03
P02545-2	Isoform C of Prelamin-A/C	0.121	2.93E-02
Q7RTV0	PHD finger-like domain-containing protein 5A	0.120	9.82E-02
Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4	0.119	3.41E-02
Q96S44	TP53-regulating kinase	0.118	1.91E-02
Q13526	peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	0.118	3.78E-02
P36873-1	serine/threonine-protein phosphatase PP1-gamma catalytic subunit	0.118	2.90E-01
Q96BH1	E3 ubiquitin-protein ligase RNF25	0.117	1.77E-01
O15027-5	Isoform 5 of Protein transport protein Sec16A	0.114	7.58E-03
P57076	UPF0769 protein C21orf59	0.109	2.92E-01
P98082	Disabled homolog 2	0.108	1.10E-01
Q9P275	Ubiquitin carboxyl-terminal hydrolase 36	0.107	2.64E-01
P05204	Non-histone chromosomal protein HMG-17	0.106	8.27E-03
Q96RL7	Vacuolar protein sorting-associated protein 13a	0.106	1.59E-01
Q9UBP6	tRNA (guanine-N(7)-)-methyltransferase	0.104	1.38E-01
O14949	Cytochrome b-c1 complex subunit 8	0.103	1.41E-01
P61024	cyclin-dependent kinases regulatory subunit 1	0.103	2.19E-01
P25208	nuclear transcription factor Y subunit beta	0.103	2.85E-01
P62318	small nuclear ribonucleoprotein sm d3	0.102	4.72E-03
Q13951	Core-binding factor subunit beta	0.102	1.30E-01
A6ND36-1	Protein FAM83G	0.102	2.07E-01
P18615	Negative elongation factor E	0.101	1.66E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q9UHQ1	Nuclear prelamin A recognition factor	0.100	9.52E-02
Q15035	Translocating chain-associated membrane protein 2	0.100	2.83E-01
Q9BTU6	Phosphatidylinositol 4-kinase type 2-alpha	0.099	1.14E-01
Q03164	Histone-lysine N-methyltransferase 2A	0.099	1.30E-01
P53803	DNA-directed RNA polymerases I, II, and III subunit RPABC4	0.097	5.26E-03
Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial	0.096	1.93E-01
Q7Z5J4	Retinoic acid-induced protein 1	0.096	2.44E-01
P52655-1	Transcription initiation factor IIA subunit 1	0.093	4.26E-02
Q9UM22	Mammalian ependymin-related protein 1	0.092	1.03E-01
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	0.091	1.14E-02
Q8NDF8-1	Non-canonical poly(A) RNA polymerase PAPD5	0.089	9.69E-02
Q96D71	RalBP1-associated Eps domain-containing protein 1	0.087	3.51E-02
Q9Y5K5-1	Ubiquitin carboxyl-terminal hydrolase isozyme L5	0.087	1.33E-01
Q9Y5N6	Origin recognition complex subunit 6	0.087	1.83E-01
Q9UKJ3-1	G patch domain-containing protein 8	0.087	2.14E-01
Q96FF9	Sororin	0.087	2.54E-01
O00115	Deoxyribonuclease-2-alpha	0.086	1.73E-03
P20810-6	Isoform 6 of Calpastatin	0.086	9.27E-03
Q99622	Protein C10	0.086	9.44E-02
P15954	Cytochrome c oxidase subunit 7C, mitochondrial	0.085	5.21E-02
O75446	Histone deacetylase complex subunit SAP30	0.085	2.13E-01
O75907	Diacylglycerol O-acyltransferase 1	0.084	2.41E-01
Q9Y3Y2	Chromatin target of PRMT1 protein	0.083	7.15E-02
P20962	Parathymosin	0.081	1.76E-03
P63165-1	Small ubiquitin-related modifier 1	0.081	3.94E-03
Q14699	raftlin	0.080	4.80E-03
P29966	Myristoylated alanine-rich C-kinase substrate	0.080	7.35E-03
Q7L7L0	Histone H2A type 3	0.080	3.87E-02
O43516-1	WAS/WASL-interacting protein family member 1	0.080	1.90E-01
Q3MHD2	Protein LSM12 homolog	0.078	1.53E-03
Q6N021	Methylcytosine dioxygenase TET2	0.078	7.42E-02
Q9P0L2-1	Serine/threonine-protein kinase MARK1	0.078	8.74E-02
P98179	RNA-binding protein 3	0.076	2.10E-03
Q8WUD4	Coiled-coil domain-containing protein 12	0.076	6.79E-03
P07093-1	Glia-derived nexin	0.076	1.15E-01
P16220-1	Cyclic AMP-responsive element-binding protein 1	0.073	1.12E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y2Y1	DNA-directed RNA polymerase III subunit RPC10	0.073	1.12E-01
Q14011	Cold-inducible RNA-binding protein	0.072	2.94E-03
O00401	Neural Wiskott-Aldrich syndrome protein	0.069	1.16E-02
Q8NB16	Mixed lineage kinase domain-like protein	0.069	8.57E-02
Q9NUK0	Muscleblind-like protein 3	0.069	1.21E-01
P49006	MARCKS-related protein	0.068	1.34E-02
O75808-1	Calpain-15	0.068	5.40E-02
Q9HCP6	Protein-cysteine N-palmitoyltransferase HHAT-like protein	0.067	1.74E-01
Q96EX1	small integral membrane protein 12	0.066	1.37E-01
Q08380	Galectin-3-binding protein	0.064	8.16E-02
Q99640	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	0.060	4.13E-02
O43426	Synaptojanin-1	0.058	8.45E-02
Q969H8	Myeloid-derived growth factor	0.057	1.78E-03
O43781-1	dual specificity tyrosine-phosphorylation-regulated kinase 3	0.057	3.99E-02
P55196-5	Isoform 5 of Afadin	0.056	3.03E-02
Q6ZSJ8	Uncharacterized protein C1orf122	0.055	7.85E-02
O43567	E3 ubiquitin-protein ligase RNF13	0.055	1.15E-01
Q99757	Thioredoxin, mitochondrial	0.053	1.12E-01
Q9UK76	Jupiter microtubule associated homolog 1	0.052	1.43E-03
Q14249	endonuclease G, mitochondrial	0.052	3.21E-02
Q9H694-1	Protein bicaudal C homolog 1	0.052	1.11E-01
P05412	transcription factor AP-1	0.051	8.08E-05
Q05682-1	Caldesmon	0.050	4.93E-02
Q6IBS0	Twinfilin-2	0.049	7.07E-04
Q8WUP2	Filamin-binding LIM protein 1	0.049	2.95E-02
P55011	Solute carrier family 12 member 2	0.045	1.88E-02
Q8NHG8	E3 ubiquitin-protein ligase ZNRF2	0.044	4.19E-04
P49458	Signal recognition particle 9 kDa protein	0.043	3.88E-04
Q969E4	transcription elongation factor A protein-like 3	0.041	2.83E-04
Q96CP2	FLYWCH family member 2	0.041	1.63E-02
Q53F19	Nuclear cap-binding protein subunit 3	0.039	1.59E-05
Q6XE24	RNA-binding motif, single-stranded-interacting protein 3	0.039	2.44E-02
Q9BVC5	Ashwin	0.039	7.28E-02
P62328	Thymosin beta-4	0.038	1.28E-05
Q14CZ0	UPF0472 protein C16orf72	0.038	3.41E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NYR9-1	NF-kappa-B inhibitor-interacting Ras-like protein 2	0.037	6.44E-02
Q9Y676	28S ribosomal protein S18b, mitochondrial	0.036	2.54E-05
Q92686	Neurogranin	0.035	5.91E-02
P38405	Guanine nucleotide-binding protein G(olf) subunit alpha	0.034	9.68E-06
O00622	Protein CYR61	0.034	8.23E-03
Q7Z309	Protein FAM122B	0.034	9.77E-03
Q5VUA4	Zinc finger protein 318	0.033	9.54E-03
Q9BXS6	Nucleolar and spindle-associated protein 1	0.032	3.07E-02
Q9H0X4	Protein FAM234A	0.032	4.92E-02
Q12913-1	Receptor-type tyrosine-protein phosphatase eta	0.031	8.52E-03
Q9H4G4	Golgi-associated plant pathogenesis-related protein 1	0.030	6.67E-03
Q96DX5	Ankyrin repeat and SOCS box protein 9	0.030	4.28E-02
Q9Y5Q9	General transcription factor 3C polypeptide 3	0.028	1.93E-03
Q8NBT2	kinetochore protein SPC24	0.028	3.87E-02
Q9P1V8-1	Sterile alpha motif domain-containing protein 15	0.027	3.45E-05
Q9P0P0	E3 ubiquitin-protein ligase RNF181	0.027	3.02E-03
Q5SSJ5-5	Isoform 4 of Heterochromatin protein 1-binding protein 3	0.026	4.33E-03
P17676	CCAAT/enhancer-binding protein beta	0.024	8.73E-04
Q8N5W9	Refilin-B	0.024	1.72E-03
Q86UU0	B-cell CLL/lymphoma 9-like protein	0.024	2.15E-03
O15553	Pyrin	0.024	2.67E-03
Q96IK1	Biorientation of chromosomes in cell division protein 1	0.023	2.62E-02
Q16739	ceramide glucosyltransferase	0.020	4.77E-07
P23141	Liver carboxylesterase 1	0.019	4.43E-06
Q15149-2	Isoform 2 of Plectin	0.010	4.62E-17
Q99880	Histone H2B type 1-L	0.010	4.62E-17
Q5JTV8	Torsin-1A-interacting protein 1	0.010	4.62E-17
P31942-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3	0.010	4.62E-17
Q9H910-2	Isoform 2 of Jupiter microtubule associated homolog 2	0.010	4.62E-17
P13796	Plastin-2	0.010	4.62E-17
Q5JSZ5-1	Protein PRRC2B	0.010	4.62E-17
Q93045	Stathmin-2	0.010	4.62E-17
Q01546	Keratin, type II cytoskeletal 2 oral	0.010	4.62E-17
Q9BRL6-1	serine/arginine-rich splicing factor 8	0.010	4.62E-17
Q14004-1	Cyclin-dependent kinase 13	0.010	4.62E-17
Q9HBR0	Putative sodium-coupled neutral amino acid transporter 10	0.010	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P62491-1	Ras-related protein Rab-11A	0.010	4.62E-17
P20248	Cyclin-A2	0.010	4.62E-17
P61244	Protein max	0.010	4.62E-17
P46976-1	Glycogenin-1	0.010	4.62E-17
O43504	Ragulator complex protein LAMTOR5	0.010	4.62E-17
O95104	Splicing factor, arginine/serine-rich 15	0.010	4.62E-17
P30499	HLA class I histocompatibility antigen, Cw-1 alpha chain	0.010	4.62E-17
Q9Y2X9	Zinc finger protein 281	0.010	4.62E-17
Q53GA4	pleckstrin homology-like domain family A member 2	0.010	4.62E-17
Q2M3G4-1	Protein Shroom1	0.010	4.62E-17
Q92859	neogenin	0.010	4.62E-17
O95251-1	Histone acetyltransferase KAT7	0.010	4.62E-17
Q8WVJ2	NudC domain-containing protein 2	0.010	4.62E-17
Q96EU6	ribosomal RNA processing protein 36 homolog	0.010	4.62E-17
O75157	TSC22 domain family protein 2	0.010	4.62E-17
Q13405	39S ribosomal protein L49, mitochondrial	0.010	4.62E-17
Q9BYN0	sulfiredoxin-1	0.010	4.62E-17
Q12929	Epidermal growth factor receptor kinase substrate 8	0.010	4.62E-17
Q8TAP8	protein phosphatase 1 regulatory subunit 35	0.010	4.62E-17
Q7Z6E9	E3 ubiquitin-protein ligase RBBP6	0.010	4.62E-17
Q9BRF8-1	Serine/threonine-protein phosphatase CPPED1	0.010	4.62E-17
Q9Y2B9	cAMP-dependent protein kinase inhibitor gamma	0.010	4.62E-17
Q9Y4H2	Insulin receptor substrate 2	0.010	4.62E-17
Q12962	transcription initiation factor TFIID subunit 10	0.010	4.62E-17
P17535	Transcription factor jun-D	0.010	4.62E-17
Q8N3F8	MICAL-like protein 1	0.010	4.62E-17
Q9BPX3	Condensin complex subunit 3	0.010	4.62E-17
P08047	Transcription factor Sp1	0.010	4.62E-17
Q6KC79	Nipped-B-like protein	0.010	4.62E-17
O95429	BAG family molecular chaperone regulator 4	0.010	4.62E-17
Q8TEP8-3	Isoform 3 of Centrosomal protein of 192 kDa	0.010	4.62E-17
Q96KQ7	Histone-lysine N-methyltransferase EHMT2	0.010	4.62E-17
Q16676	forkhead box protein D1	0.010	4.62E-17
Q9H4I2	zinc fingers and homeoboxes protein 3	0.010	4.62E-17
Q02241-1	Kinesin-like protein KIF23	0.010	4.62E-17
P61916	Epididymal secretory protein E1	0.010	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O95479	GDH/6PGL endoplasmic bifunctional protein	0.010	4.62E-17
Q9ULV3	Cip1-interacting zinc finger protein	0.010	4.62E-17
Q9H0N5	Pterin-4-alpha-carbinolamine dehydratase 2	0.010	4.62E-17
P78358	Cancer/testis antigen 1	0.010	4.62E-17
Q15398-3	Isoform 3 of Disks large-associated protein 5	0.010	4.62E-17
P39880	Homeobox protein cut-like 1	0.010	4.62E-17
P18846	Cyclic AMP-dependent transcription factor ATF-1	0.010	4.62E-17
Q9BW72	HIG1 domain family member 2A, mitochondrial	0.010	4.62E-17
O75381-1	Peroxisomal membrane protein PEX14	0.010	4.62E-17
Q14135-1	Transcription cofactor vestigial-like protein 4	0.010	4.62E-17
Q8IZP0	abl interactor 1	0.010	4.62E-17
Q6QNY0	biogenesis of lysosome-related organelles complex 1 subunit 3	0.010	4.62E-17
Q9UHW9-2	Isoform 2 of Solute carrier family 12 member 6	0.010	4.62E-17
Q5THK1-1	Protein PRR14L	0.010	4.62E-17
P49757	Protein numb homolog	0.010	4.62E-17
Q6FIF0	AN1-type zinc finger protein 6	0.010	4.62E-17
P02656	Apolipoprotein C-III	0.010	4.62E-17
Q9UPQ9	Trinucleotide repeat-containing gene 6B protein	0.010	4.62E-17
Q9UKN8	General transcription factor 3C polypeptide 4	0.010	4.62E-17
Q8TCG2	Phosphatidylinositol 4-kinase type 2-beta	0.010	4.62E-17
Q9NS87	Kinesin-like protein KIF15	0.010	4.62E-17
Q9NRL2	Bromodomain adjacent to zinc finger domain protein 1A	0.010	4.62E-17
Q9NWT6	Hypoxia-inducible factor 1-alpha inhibitor	0.010	4.62E-17
Q14657	EKC/KEOPS complex subunit LAGE3	0.010	4.62E-17
Q8TBC5	Zinc finger and SCAN domain-containing protein 18	0.010	4.62E-17
Q9P2M7-1	cingulin	0.010	4.62E-17
Q86WP2-1	Vasculin	0.010	4.62E-17
O43164	E3 ubiquitin-protein ligase Praja-2	0.010	4.62E-17
Q9HB20	pleckstrin homology domain-containing family A member 3	0.010	4.62E-17
Q96K76	ubiquitin carboxyl-terminal hydrolase 47	0.010	4.62E-17
Q8NBJ4	Golgi membrane protein 1	0.010	4.62E-17
P02794	Ferritin heavy chain	0.010	4.62E-17
Q7LBR1	Charged multivesicular body protein 1b	0.010	4.62E-17
Q96A19	Coiled-coil domain-containing protein 102A	0.010	4.62E-17
Q9H0E3	Histone deacetylase complex subunit SAP130	0.010	4.62E-17
P49585	choline-phosphate cytidylyltransferase A	0.010	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y6Q9-1	Nuclear receptor coactivator 3	0.010	4.62E-17
Q9ULX9-1	Transcription factor MafF	0.010	4.62E-17
Q15643	Thyroid receptor-interacting protein 11	0.010	4.62E-17
Q02086-1	Transcription factor Sp2	0.010	4.62E-17
O43665	Regulator of G-protein signaling 10	0.010	4.62E-17
P0C7T5	Ataxin-1-like	0.010	4.62E-17
Q15390	Mitochondrial fission regulator 1	0.010	4.62E-17
Q15506	Sperm surface protein Sp17	0.010	4.62E-17
Q9Y4H4	G-protein-signaling modulator 3	0.010	4.62E-17
Q8IYN2	transcription elongation factor A protein-like 8	0.010	4.62E-17
Q6PIW4	Fidgetin-like protein 1	0.010	4.62E-17
Q8IWA4-1	Mitofusin-1	0.010	4.62E-17
Q8TEW0	Partitioning defective 3 homolog	0.010	4.62E-17
Q5SYE7	NHS-like protein 1	0.010	4.62E-17
Q96RD7-1	Pannexin-1	0.010	4.62E-17
P14316-1	Interferon regulatory factor 2	0.010	4.62E-17
Q96RL1	BRCA1-A complex subunit RAP80	0.010	4.62E-17
Q9BTA9-1	WW domain-containing adapter protein with coiled-coil	0.010	4.62E-17
Q68DK7	male-specific lethal 1 homolog	0.010	4.62E-17
Q8N490-2	Isoform 2 of Probable hydrolase PNKD	0.010	4.62E-17
P43007-1	neutral amino acid transporter A	0.010	4.62E-17
Q99618	Cell division cycle-associated protein 3	0.010	4.62E-17
Q16566	calcium/calmodulin-dependent protein kinase type IV	0.010	4.62E-17
Q5TAX3	Terminal uridylyltransferase 4	0.010	4.62E-17
Q8IVH2-1	Forkhead box protein P4	0.010	4.62E-17
Q7Z4H7	HAUS augmin-like complex subunit 6	0.010	4.62E-17
Q9NX70	Mediator of RNA polymerase II transcription subunit 29	0.010	4.62E-17
P49407-1	Beta-arrestin-1	0.010	4.62E-17
Q99583	Max-binding protein MNT	0.010	4.62E-17
Q9H3Q1	Cdc42 effector protein 4	0.010	4.62E-17
Q13111-1	Chromatin assembly factor 1 subunit A	0.010	4.62E-17
Q7Z2K8-1	G protein-regulated inducer of neurite outgrowth 1	0.010	4.62E-17
Q92820	Gamma-glutamyl hydrolase	0.010	4.62E-17
Q00403	Transcription initiation factor IIB	0.010	4.62E-17
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B	0.010	4.62E-17
Q9ULZ3	apoptosis-associated speck-like protein containing a CARD	0.010	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P40337	Von Hippel-Lindau disease tumor suppressor	0.010	4.62E-17
O60563	Cyclin-T1	0.010	4.62E-17
Q53LP3	ankyrin repeat domain-containing protein SOWAHC	0.010	4.62E-17
Q9Y6R0	Numb-like protein	0.010	4.62E-17
Q9H2Y7	Zinc finger protein 106	0.010	4.62E-17
P53567	CCAAT/enhancer-binding protein gamma	0.010	4.62E-17
O95081	Arf-GAP domain and FG repeat-containing protein 2	0.010	4.62E-17
Q01196-1	Runt-related transcription factor 1	0.010	4.62E-17
Q9BTE1	Dynactin subunit 5	0.010	4.62E-17
Q6P3X3	tetratricopeptide repeat protein 27	0.010	4.62E-17
Q14126	Desmoglein-2	0.010	4.62E-17
O75879	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	0.010	4.62E-17
P16144-1	Integrin beta-4	0.010	4.62E-17
Q96MX3	zinc finger protein 48	0.010	4.62E-17
Q96S66	chloride channel CLIC-like protein 1	0.010	4.62E-17
Q96AG3	Solute carrier family 25 member 46	0.010	4.62E-17
Q9BVJ7	Dual specificity protein phosphatase 23	0.010	4.62E-17
Q92871	Phosphomannomutase 1	0.010	4.62E-17
O95382-1	Mitogen-activated protein kinase kinase kinase 6	0.010	4.62E-17
P05164	Myeloperoxidase	0.010	4.62E-17
Q9NVE7	pantothenate kinase 4	0.010	4.62E-17
Q7Z2Z1	Treslin	0.010	4.62E-17
Q8TAP9	M-phase-specific PLK1-interacting protein	0.010	4.62E-17
Q96GD4	Aurora kinase B	0.010	4.62E-17
Q96EK7	Constitutive coactivator of peroxisome proliferator-activated receptor gamma	0.010	4.62E-17
P50443	sulfate transporter	0.010	4.62E-17
Q9P0V9	septin-10	0.010	4.62E-17
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1	0.010	4.62E-17
Q6PI98-1	INO80 complex subunit C	0.010	4.62E-17
Q9UIQ6-1	Leucyl-cystinyl aminopeptidase	0.010	4.62E-17
Q99707	methionine synthase	0.010	4.62E-17
Q6ZUT6-1	Uncharacterized protein C15orf52	0.010	4.62E-17
Q8NFH8-1	RalBP1-associated Eps domain-containing protein 2	0.010	4.62E-17
Q8IVL0	Neuron navigator 3	0.010	4.62E-17
Q71H61	Immunoglobulin-like domain-containing receptor 2	0.010	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q86TB3	Alpha-protein kinase 2	0.010	4.62E-17
Q3KQV9	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	0.010	4.62E-17
Q8IV50	LysM and putative peptidoglycan-binding domain-containing protein 2	0.010	4.62E-17
Q5SXM8	DNL-type zinc finger protein	0.010	4.62E-17
Q9P1U0	DNA-directed RNA polymerase I subunit RPA12	0.010	4.62E-17
Q86US8-1	Telomerase-binding protein EST1A	0.010	4.62E-17
Q8IWI9-1	MAX gene-associated protein	0.010	4.62E-17
P10275	androgen receptor	0.010	4.62E-17
Q96N64	PWWP domain-containing protein 2A	0.010	4.62E-17
O43402	ER membrane protein complex subunit 8	0.010	4.62E-17
Q9NZ63	Telomere length and silencing protein 1 homolog	0.010	4.62E-17
P15822-1	zinc finger protein 40	0.010	4.62E-17
Q99755	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	0.010	4.62E-17
Q9NQS7	Inner centromere protein	0.010	4.62E-17
Q9BXP2-1	Solute carrier family 12 member 9	0.010	4.62E-17
Q9UPN6	Protein SCAF8	0.010	4.62E-17
Q8ND90	paraneoplastic antigen MA1	0.010	4.62E-17
Q6UB99	ankyrin repeat domain-containing protein 11	0.010	4.62E-17
Q9Y4K4	mitogen-activated protein kinase kinase kinase kinase 5	0.010	4.62E-17
P18827	syndecan-1	0.010	4.62E-17
P55199	RNA polymerase II elongation factor ELL	0.010	4.62E-17
Q9Y242	transcription factor 19	0.010	4.62E-17
Q96PE2	Rho guanine nucleotide exchange factor 17	0.010	4.62E-17
P19419-1	ETS domain-containing protein Elk-1	0.010	4.62E-17
Q2NL68-1	Proline and serine-rich protein 3	0.010	4.62E-17
Q5VZL5	Zinc finger MYM-type protein 4	0.010	4.62E-17
Q9HAH7-1	Isoform 1 of Probable fibrosin-1	0.010	4.62E-17
O94916	nuclear factor of activated T-cells 5	0.010	4.62E-17
Q8TCZ2	CD99 antigen-like protein 2	0.010	4.62E-17
O95155	Ubiquitin conjugation factor E4 B	0.010	4.62E-17
A6NFI3	Zinc finger protein 316	0.010	4.62E-17
P0CB38	polyadenylate-binding protein 4-like	0.010	4.62E-17
O60353-1	Frizzled-6	0.010	4.62E-17
Q9P227	Rho GTPase-activating protein 23	0.010	4.62E-17
Q9NYL4	Peptidyl-prolyl cis-trans isomerase FKBP11	0.010	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96AP0	Adrenocortical dysplasia protein homolog	0.010	4.62E-17
Q8IUI8	Cytokine receptor-like factor 3	0.010	4.62E-17
Q8NEH6	Meiosis-specific nuclear structural protein 1	0.010	4.62E-17
Q7L266	isoaspartyl peptidase/L-asparaginase	0.010	4.62E-17
Q8TEU7	Rap guanine nucleotide exchange factor 6	0.010	4.62E-17
Q6MZP7	Protein lin-54 homolog	0.010	4.62E-17
Q2M1P5	Kinesin-like protein KIF7	0.010	4.62E-17
O76080	AN1-type zinc finger protein 5	0.010	4.62E-17
Q9BYC5	Alpha-(1,6)-fucosyltransferase	0.010	4.62E-17
Q9NZM3	Intersectin-2	0.010	4.62E-17
P84157-1	Matrix-remodeling-associated protein 7	0.010	4.62E-17
O60292	Signal-induced proliferation-associated 1-like protein 3	0.010	4.62E-17
Q8IXQ5	kelch-like protein 7	0.010	4.62E-17
Q9BQ89	Protein FAM110A	0.010	4.62E-17
O00762	Ubiquitin-conjugating enzyme E2 C	0.010	4.62E-17
Q96GP6-1	Scavenger receptor class F member 2	0.010	4.62E-17
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	0.010	4.62E-17
P42684	Abelson tyrosine-protein kinase 2	0.010	4.62E-17
Q12841	Follistatin-related protein 1	0.010	4.62E-17
Q8WXD5	gem-associated protein 6	0.010	4.62E-17
O94927	HAUS augmin-like complex subunit 5	0.010	4.62E-17
Q86UE8	Serine/threonine-protein kinase tousled-like 2	0.010	4.62E-17
Q06547-3	Isoform 3 of GA-binding protein subunit beta-1	0.010	4.62E-17
Q96E14	RecQ-mediated genome instability protein 2	0.010	4.62E-17
Q53GG5-1	PDZ and LIM domain protein 3	0.010	4.62E-17
Q9UI43	rRNA methyltransferase 2, mitochondrial	0.010	4.62E-17
P29374-1	AT-rich interactive domain-containing protein 4A	0.010	4.62E-17
O60347	TBC1 domain family member 12	0.010	4.62E-17
P43359	Melanoma-associated antigen 5	0.010	4.62E-17
Q9UQL6-1	histone deacetylase 5	0.010	4.62E-17
P09455-1	Retinol-binding protein 1	0.010	4.62E-17
Q3T8J9-1	GON-4-like protein	0.010	4.62E-17
Q08623	Pseudouridine-5′-phosphatase	0.010	4.62E-17
O14874	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial	0.010	4.62E-17
Q6P2H3-1	Centrosomal protein of 85 kDa	0.010	4.62E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96H55-1	unconventional myosin-XIX	0.010	4.62E-17
Q86V25	Vasohibin-2	0.010	4.62E-17
Q9P253	Vacuolar protein sorting-associated protein 18 homolog	0.010	4.62E-17
Q9P273	Teneurin-3	0.010	4.62E-17
P20929	Nebulin	0.010	4.62E-17
Q6PII5-2	Isoform 2 of Hydroxyacylglutathione hydrolase-like protein	0.010	4.62E-17
Q12815-1	tastin	0.010	4.62E-17
O94864-1	STAGA complex 65 subunit gamma	0.010	4.62E-17
Q96JM4	Leucine-rich repeat and IQ domain-containing protein 1	0.010	4.62E-17
Q9Y4D8-1	Probable E3 ubiquitin-protein ligase HECTD4	0.010	4.62E-17
Q9HA64	Ketosamine-3-kinase	0.010	4.62E-17
Q6N063-1	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2	0.010	4.62E-17
Q96SI1-1	BTB/POZ domain-containing protein KCTD15	0.010	4.62E-17
Q9C0H9-1	SRC kinase signaling inhibitor 1	0.010	4.62E-17
O95206-1	Protocadherin-8	0.010	4.62E-17
Q29983	MHC class I polypeptide-related sequence A	0.010	4.62E-17
Q96B23-1	Uncharacterized protein C18orf25	0.010	4.62E-17
Q9Y485	DmX-like protein 1	0.010	4.62E-17

End of Table

U U87 Cycloheximide Genes

accession	description	fold p change	adjusted p-value
Q12974	Protein tyrosine phosphatase type IVA 2	100.0	4.08E-17
Q8IZ07	ankyrin repeat domain-containing protein 13A	100.0	4.08E-17
Q9Y5B6	PAX3- and PAX7-binding protein 1	100.0	4.08E-17
Q969G6	Riboflavin kinase	100.0	4.08E-17
Q9UL33-1	Trafficking protein particle complex subunit 2-like protein	100.0	4.08E-17
Q9UGR2	Zinc finger CCCH domain-containing protein 7B	100.0	4.08E-17
Q96DE0	U8 snoRNA-decapping enzyme	100.0	4.08E-17
Q96EK6	glucosamine 6-phosphate N-acetyltransferase	100.0	4.08E-17
Q10469	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q5VW32	BRO1 domain-containing protein BROX	100.0	4.08E-17
O95563	Mitochondrial pyruvate carrier 2	100.0	4.08E-17
Q9NZI7	Upstream-binding protein 1	100.0	4.08E-17
Q96EY8	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	100.0	4.08E-17
Q9UFN0	protein NipSnap homolog 3A	100.0	4.08E-17
Q9HC36	rRNA methyltransferase 3, mitochondrial	100.0	4.08E-17
P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	100.0	4.08E-17
O95155	Ubiquitin conjugation factor E4 B	100.0	4.08E-17
Q8IXT5	RNA-binding protein 12B	100.0	4.08E-17
Q9GZP9	Derlin-2	100.0	4.08E-17
Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1	100.0	4.08E-17
Q15833-1	Syntaxin-binding protein 2	100.0	4.08E-17
Q9HCU5	Prolactin regulatory element-binding protein	100.0	4.08E-17
Q9H900-1	Protein zwilch homolog	100.0	4.08E-17
Q7Z5K2-1	Wings apart-like protein homolog	100.0	4.08E-17
A6NDU8	UPF0600 protein C5orf51	100.0	4.08E-17
Q9H7F0-1	probable cation-transporting ATPase 13A3	100.0	4.08E-17
P40818	ubiquitin carboxyl-terminal hydrolase 8	100.0	4.08E-17
Q96FJ0	AMSH-like protease	100.0	4.08E-17
Q8IYB8	ATP-dependent RNA helicase SUPV3L1, mitochondrial	100.0	4.08E-17
Q9BVM2	protein DPCD	100.0	4.08E-17
Q6P4F2	Ferredoxin-2, mitochondrial	100.0	4.08E-17
Q5TEJ8	protein THEMIS2	100.0	4.08E-17
P36639	7,8-dihydro-8-oxoguanine triphosphatase	100.0	4.08E-17
Q9BTW9	Tubulin-specific chaperone D	100.0	4.08E-17
Q92574-1	Hamartin	100.0	4.08E-17
P53384	Cytosolic Fe-S cluster assembly factor nubp1	100.0	4.08E-17
Q9Y3P9	Rab GTPase-activating protein 1	100.0	4.08E-17
Q9H9J2	39S ribosomal protein L44, mitochondrial	100.0	4.08E-17
Q8NEZ5-1	F-box only protein 22	100.0	4.08E-17
Q7LGA3-1	Heparan sulfate 2-O-sulfotransferase 1	100.0	4.08E-17
P42785-1	lysosomal Pro-X carboxypeptidase	100.0	4.08E-17
Q7Z5H3-1	Rho GTPase-activating protein 22	100.0	4.08E-17
P48651	phosphatidylserine synthase 1	100.0	4.08E-17
Q13144	Translation initiation factor eIF-2B subunit epsilon	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8N6R0-5	Methyltransferase-like protein 13	100.0	4.08E-17
Q9NVM6	DnaJ homolog subfamily C member 17	100.0	4.08E-17
Q9Y6A9	Signal peptidase complex subunit 1	100.0	4.08E-17
Q6N063-1	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2	100.0	4.08E-17
P23458	Tyrosine-protein kinase JAK1	100.0	4.08E-17
Q15650	Activating signal cointegrator 1	100.0	4.08E-17
Q8IWT6	volume-regulated anion channel subunit LRRC8A	100.0	4.08E-17
Q14254	Flotillin-2	100.0	4.08E-17
Q9BTZ2	dehydrogenase/reductase sdr family member 4	100.0	4.08E-17
O94901-1	SUN domain-containing protein 1	100.0	4.08E-17
O60231	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	100.0	4.08E-17
Q9Y6Y0	influenza virus NS1A-binding protein	100.0	4.08E-17
Q92562	Polyphosphoinositide phosphatase	100.0	4.08E-17
Q9UBV2	Protein sel-1 homolog 1	100.0	4.08E-17
Q9H1K1	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	100.0	4.08E-17
Q9Y3D5	28S ribosomal protein S18c, mitochondrial	100.0	4.08E-17
Q68CQ7-1	Glycosyltransferase 8 domain-containing protein 1	100.0	4.08E-17
O15382	Branched-chain-amino-acid aminotransferase, mitochondrial	100.0	4.08E-17
Q9UDW1	cytochrome b-c1 complex subunit 9	100.0	4.08E-17
Q13049	E3 ubiquitin-protein ligase TRIM32	100.0	4.08E-17
Q02241-1	Kinesin-like protein KIF23	100.0	4.08E-17
P08253	72 kDa type IV collagenase	100.0	4.08E-17
Q9NSC5-1	homer protein homolog 3	100.0	4.08E-17
Q9NWM3-1	CUE domain-containing protein 1	100.0	4.08E-17
O14925	Mitochondrial import inner membrane translocase subunit tim23	100.0	4.08E-17
P48735	Isocitrate dehydrogenase [NADP], mitochondrial	100.0	4.08E-17
Q75QN2	Integrator complex subunit 8	100.0	4.08E-17
Q9HBM1	Kinetochore protein Spc25	100.0	4.08E-17
Q8IXK2	Polypeptide N-acetylgalactosaminyltransferase 12	100.0	4.08E-17
P51570	galactokinase	100.0	4.08E-17
Q96SY0	Integrator complex subunit 14	100.0	4.08E-17
A8MXV4	nucleoside diphosphate-linked moiety X motif 19	100.0	4.08E-17
Q9P2B2	prostaglandin F2 receptor negative regulator	100.0	4.08E-17
P19388	DNA-directed RNA polymerases I, II, and III subunit RPABC1	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O95671-1	N-acetylserotonin O-methyltransferase-like protein	100.0	4.08E-17
Q643R3	lysophospholipid acyltransferase LPCAT4	100.0	4.08E-17
Q16222-1	UDP-N-acetylhexosamine pyrophosphorylase	100.0	4.08E-17
Q8NB46	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C	100.0	4.08E-17
P12235	ADP/ATP translocase 1	100.0	4.08E-17
Q9NWS8	Required for meiotic nuclear division protein 1 homolog	100.0	4.08E-17
Q9P0I2	ER membrane protein complex subunit 3	100.0	4.08E-17
P48730-1	Casein kinase I isoform delta	100.0	4.08E-17
Q7L592	Protein arginine methyltransferase NDUFAF7, mitochondrial	100.0	4.08E-17
O14880	Microsomal glutathione S-transferase 3	100.0	4.08E-17
Q15628	Tumor necrosis factor receptor type 1-associated DEATH domain protein	100.0	4.08E-17
Q8N5M9	Protein jagunal homolog 1	100.0	4.08E-17
Q9P2E2-1	Kinesin-like protein KIF17	100.0	4.08E-17
Q9ULC3	Ras-related protein Rab-23	100.0	4.08E-17
P42356	phosphatidylinositol 4-kinase alpha	100.0	4.08E-17
Q6ZMZ3	Nesprin-3	100.0	4.08E-17
Q8NCG7	Sn1-specific diacylglycerol lipase beta	100.0	4.08E-17
Q9Y3E7	Charged multivesicular body protein 3	100.0	4.08E-17
Q8TB61	Adenosine 3′-phospho 5′-phosphosulfate transporter 1	100.0	4.08E-17
Q9NUQ2	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	100.0	4.08E-17
P58004	Sestrin-2	100.0	4.08E-17
Q9NUV7	Serine palmitoyltransferase 3	100.0	4.08E-17
Q9UJ72	annexin A10	100.0	4.08E-17
Q96BR5	Cytochrome c oxidase assembly factor 7	100.0	4.08E-17
Q9GZT4	serine racemase	100.0	4.08E-17
Q96SU4	Oxysterol-binding protein-related protein 9	100.0	4.08E-17
O75352	Mannose-P-dolichol utilization defect 1 protein	100.0	4.08E-17
Q8NEW0	Zinc transporter 7	100.0	4.08E-17
Q3MHD2	Protein LSM12 homolog	100.0	4.08E-17
P49917	DNA ligase 4	100.0	4.08E-17
Q92995	Ubiquitin carboxyl-terminal hydrolase 13	100.0	4.08E-17
Q96AB3	isochorismatase domain-containing protein 2	100.0	4.08E-17
Q9NY27	Serine/threonine-protein phosphatase 4 regulatory subunit 2	100.0	4.08E-17
Q01804-1	OTU domain-containing protein 4	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9P000-1	COMM domain-containing protein 9	100.0	4.08E-17
Q8NCW5	NAD(P)H-hydrate epimerase	100.0	4.08E-17
Q4J6C6	prolyl endopeptidase-like	100.0	4.08E-17
Q8NB16	Mixed lineage kinase domain-like protein	100.0	4.08E-17
Q9UBF2	Coatomer subunit gamma-2	100.0	4.08E-17
Q9BU61-1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	100.0	4.08E-17
P54619-1	5′-AMP-activated protein kinase subunit gamma-1	100.0	4.08E-17
Q13619-1	cullin-4A	100.0	4.08E-17
O75122	CLIP-associating protein 2	100.0	4.08E-17
Q5T1M5	FK506-binding protein 15	100.0	4.08E-17
Q86YV9	Hermansky-Pudlak syndrome 6 protein	100.0	4.08E-17
Q9BZH6	WD repeat-containing protein 11	100.0	4.08E-17
Q9NYL2-2	Isoform 2 of Mitogen-activated protein kinase kinase kinase 20	100.0	4.08E-17
Q99598	Translin-associated protein X	100.0	4.08E-17
Q9NZA1-1	Chloride intracellular channel protein 5	100.0	4.08E-17
Q9UBX3	Mitochondrial dicarboxylate carrier	100.0	4.08E-17
Q9NRY4	Rho GTPase-activating protein 35	100.0	4.08E-17
O95487-1	Protein transport protein Sec24B	100.0	4.08E-17
Q9P0K7-1	Ankycorbin	100.0	4.08E-17
Q9UJA5-1	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	100.0	4.08E-17
Q9BXW9-1	Isoform 1 of Fanconi anemia group D2 protein	100.0	4.08E-17
P49427	ubiquitin-conjugating enzyme E2 R1	100.0	4.08E-17
Q14119	Vascular endothelial zinc finger 1	100.0	4.08E-17
Q9HAS0	Protein Njmu-R1	100.0	4.08E-17
P35573-1	glycogen debranching enzyme	100.0	4.08E-17
P63208	s-phase kinase-associated protein 1	100.0	4.08E-17
Q9NYK5-1	39S ribosomal protein L39, mitochondrial	100.0	4.08E-17
Q8IWB7	WD repeat and FYVE domain-containing protein 1	100.0	4.08E-17
Q03426	mevalonate kinase	100.0	4.08E-17
Q9NWM8	Peptidyl-prolyl cis-trans isomerase FKBP14	100.0	4.08E-17
Q9Y3L5	ras-related protein Rap-2c	100.0	4.08E-17
P43003	Excitatory amino acid transporter 1	100.0	4.08E-17
P40938	replication factor C subunit 3	100.0	4.08E-17
Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P56556	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	100.0	4.08E-17
Q9UNQ2	Probable dimethyladenosine transferase	100.0	4.08E-17
Q5PRF9	protein Smaug homolog 2	100.0	4.08E-17
Q9NQY0-1	Bridging integrator 3	100.0	4.08E-17
Q9Y5V3	Melanoma-associated antigen D1	100.0	4.08E-17
Q4KMP7	TBC1 domain family member 10B	100.0	4.08E-17
Q8NBI5	Solute carrier family 43 member 3	100.0	4.08E-17
Q9NSU2-1	Three-prime repair exonuclease 1	100.0	4.08E-17
Q9UFC0	Leucine-rich repeat and WD repeat-containing protein 1	100.0	4.08E-17
Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31	100.0	4.08E-17
O94905-1	Erlin-2	100.0	4.08E-17
P52735	Guanine nucleotide exchange factor VAV2	100.0	4.08E-17
Q96DG6	Carboxymethylenebutenolidase homolog	100.0	4.08E-17
Q9NRP2	COX assembly mitochondrial protein 2 homolog	100.0	4.08E-17
Q9Y282-1	Endoplasmic reticulum-Golgi intermediate compartment protein 3	100.0	4.08E-17
O14732-1	inositol monophosphatase 2	100.0	4.08E-17
Q9NZM3	Intersectin-2	100.0	4.08E-17
P62877	E3 ubiquitin-protein ligase RBX1	100.0	4.08E-17
Q9NRG1	Phosphoribosyltransferase domain-containing protein 1	100.0	4.08E-17
Q6ICB0	Desumoylating isopeptidase 1	100.0	4.08E-17
P15291	Beta-1,4-galactosyltransferase 1	100.0	4.08E-17
Q7L8W6	Diphthine–ammonia ligase	100.0	4.08E-17
Q14997	Proteasome activator complex subunit 4	100.0	4.08E-17
P41134	DNA-binding protein inhibitor ID-1	100.0	4.08E-17
Q9Y376	Calcium-binding protein 39	100.0	4.08E-17
P08397-1	porphobilinogen deaminase	100.0	4.08E-17
O75886	Signal transducing adapter molecule 2	100.0	4.08E-17
P10909-1	Clusterin	100.0	4.08E-17
Q9GZT9-1	Egl nine homolog 1	100.0	4.08E-17
O15533-1	Tapasin	100.0	4.08E-17
Q9Y3C4	EKC/KEOPS complex subunit TPRKB	100.0	4.08E-17
Q8IUF8	ribosomal oxygenase 2	100.0	4.08E-17
O14972	Down syndrome critical region protein 3	100.0	4.08E-17
Q6NXR4	TELO2-interacting protein 2	100.0	4.08E-17
O00767	acyl-CoA desaturase	100.0	4.08E-17
Q5HYI8	Rab-like protein 3	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9P260-1	LisH domain and HEAT repeat-containing protein KIAA1468	100.0	4.08E-17
Q5VZ46-1	Uncharacterized protein KIAA1614	100.0	4.08E-17
P20585	DNA mismatch repair protein MSH3	100.0	4.08E-17
O94766	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3	100.0	4.08E-17
P50750	Cyclin-dependent kinase 9	100.0	4.08E-17
Q14562	ATP-dependent RNA helicase dhx8	100.0	4.08E-17
Q7L311	Armadillo repeat-containing X-linked protein 2	100.0	4.08E-17
Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1	100.0	4.08E-17
Q96JB5	CDK5 regulatory subunit-associated protein 3	100.0	4.08E-17
Q8N999-1	Uncharacterized protein C12orf29	100.0	4.08E-17
Q9Y3B7-1	39S ribosomal protein L11, mitochondrial	100.0	4.08E-17
Q9BW85	Coiled-coil domain-containing protein 94	100.0	4.08E-17
P35226	Polycomb complex protein BMI-1	100.0	4.08E-17
Q9NP73-1	Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13	100.0	4.08E-17
Q9NX47	E3 ubiquitin-protein ligase MARCH5	100.0	4.08E-17
Q8TDQ7	Glucosamine-6-phosphate isomerase 2	100.0	4.08E-17
Q9NVI1-1	Isoform 1 of Fanconi anemia group I protein	100.0	4.08E-17
Q8NEC7-1	Glutathione S-transferase C-terminal domain-containing protein	100.0	4.08E-17
Q9NRP0-1	oligosaccharyltransferase complex subunit OSTC	100.0	4.08E-17
Q9Y2C4	Nuclease EXOG, mitochondrial	100.0	4.08E-17
Q9Y294	Histone chaperone ASF1A	100.0	4.08E-17
O95777	U6 snRNA-associated Sm-like protein LSm8	100.0	4.08E-17
O94763-1	Unconventional prefoldin RPB5 interactor 1	100.0	4.08E-17
Q86TB9	Protein PAT1 homolog 1	100.0	4.08E-17
Q9UNE7-1	E3 ubiquitin-protein ligase CHIP	100.0	4.08E-17
Q13330-1	Metastasis-associated protein MTA1	100.0	4.08E-17
Q9NRX1	RNA-binding protein pno1	100.0	4.08E-17
Q8N392-1	Rho GTPase-activating protein 18	100.0	4.08E-17
Q9H8Y5	Ankyrin repeat and zinc finger domain-containing protein 1	100.0	4.08E-17
O60879	Protein diaphanous homolog 2	100.0	4.08E-17
Q13586	stromal interaction molecule 1	100.0	4.08E-17
Q08380	Galectin-3-binding protein	100.0	4.08E-17
O14933	Ubiquitin/ISG15-conjugating enzyme E2 L6	100.0	4.08E-17
Q96JJ7-1	Protein disulfide-isomerase TMX3	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9H4A5	Golgi phosphoprotein 3-like	100.0	4.08E-17
Q9UQ13	Leucine-rich repeat protein SHOC-2	100.0	4.08E-17
Q9H490	Phosphatidylinositol glycan anchor biosynthesis class U protein	100.0	4.08E-17
O94822	E3 ubiquitin-protein ligase listerin	100.0	4.08E-17
Q96A35	39S ribosomal protein L24, mitochondrial	100.0	4.08E-17
Q9Y223-1	bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	100.0	4.08E-17
Q9Y5Q9	General transcription factor 3C polypeptide 3	100.0	4.08E-17
P31483	nucleolysin TIA-1 isoform p40	100.0	4.08E-17
Q9Y3D6	mitochondrial fission 1 protein	100.0	4.08E-17
P52758	2-iminobutanoate/2-iminopropanoate deaminase	100.0	4.08E-17
Q9UJM3	ERBB receptor feedback inhibitor 1	100.0	4.08E-17
Q5T160	probable arginine–tRNA ligase, mitochondrial	100.0	4.08E-17
Q13485	Mothers against decapentaplegic homolog 4	100.0	4.08E-17
Q9Y2L5-1	trafficking protein particle complex subunit 8	100.0	4.08E-17
Q9Y680-1	Peptidyl-prolyl cis-trans isomerase FKBP7	100.0	4.08E-17
Q14680	Maternal embryonic leucine zipper kinase	100.0	4.08E-17
Q9BZF1-1	Oxysterol-binding protein-related protein 8	100.0	4.08E-17
Q9UBD5-1	Origin recognition complex subunit 3	100.0	4.08E-17
P42226	Signal transducer and activator of transcription 6	100.0	4.08E-17
P09132-1	Signal recognition particle 19 kDa protein	100.0	4.08E-17
P82930	28S ribosomal protein S34, mitochondrial	100.0	4.08E-17
O15116	U6 snRNA-associated Sm-like protein LSm1	100.0	4.08E-17
Q9Y5S2	Serine/threonine-protein kinase MRCK beta	100.0	4.08E-17
Q9UI09	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	100.0	4.08E-17
P32929	Cystathionine gamma-lyase	100.0	4.08E-17
Q15109-1	advanced glycosylation end product-specific receptor	100.0	4.08E-17
Q8TE77	Protein phosphatase Slingshot homolog 3	100.0	4.08E-17
Q92889	DNA repair endonuclease XPF	100.0	4.08E-17
P30481	HLA class I histocompatibility antigen, B-44 alpha chain	100.0	4.08E-17
Q6U841	Sodium-driven chloride bicarbonate exchanger	100.0	4.08E-17
Q9NPJ3-1	Acyl-coenzyme A thioesterase 13	100.0	4.08E-17
Q9UET6	Putative tRNA (cytidine(32)/guanosine(34)-2′-O)-methyltransferase	100.0	4.08E-17
Q9NVH2	Integrator complex subunit 7	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q15646-1	2′-5′-oligoadenylate synthase-like protein	100.0	4.08E-17
P17900	Ganglioside GM2 activator	100.0	4.08E-17
Q9NVS2	39S ribosomal protein S18a, mitochondrial	100.0	4.08E-17
O76054	SEC14-like protein 2	100.0	4.08E-17
Q9H7E9-1	UPF0488 protein C8orf33	100.0	4.08E-17
O95071	E3 ubiquitin-protein ligase UBR5	100.0	4.08E-17
Q8IXK0	Polyhomeotic-like protein 2	100.0	4.08E-17
Q13325	Interferon-induced protein with tetratricopeptide repeats 5	100.0	4.08E-17
Q9BRG1	Vacuolar protein-sorting-associated protein 25	100.0	4.08E-17
P53794	sodium/myo-inositol cotransporter	100.0	4.08E-17
Q9H9Y6-1	DNA-directed RNA polymerase I subunit RPA2	100.0	4.08E-17
Q5VZE5	N-alpha-acetyltransferase 35, NatC auxiliary subunit	100.0	4.08E-17
Q9UBM7	7-dehydrocholesterol reductase	100.0	4.08E-17
Q96JJ3	Engulfment and cell motility protein 2	100.0	4.08E-17
Q86X10-1	Ral GTPase-activating protein subunit beta	100.0	4.08E-17
P05161	Ubiquitin-like protein ISG15	100.0	4.08E-17
P17535	Transcription factor jun-D	100.0	4.08E-17
Q9Y314	nitric oxide synthase-interacting protein	100.0	4.08E-17
Q9GZN8	UPF0687 protein C20orf27	100.0	4.08E-17
O94915-1	protein furry homolog-like	100.0	4.08E-17
Q9Y4X5	E3 ubiquitin-protein ligase ARIH1	100.0	4.08E-17
Q15057	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	100.0	4.08E-17
Q8IZA0	Dyslexia-associated protein KIAA0319-like protein	100.0	4.08E-17
Q2TB10	zinc finger protein 800	100.0	4.08E-17
P61020	Ras-related protein Rab-5B	100.0	4.08E-17
Q9H446	rwd domain-containing protein 1	100.0	4.08E-17
Q01968-1	Inositol polyphosphate 5-phosphatase OCRL-1	100.0	4.08E-17
P21953	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	100.0	4.08E-17
O60921	checkpoint protein HUS1	100.0	4.08E-17
P57076	UPF0769 protein C21orf59	100.0	4.08E-17
Q96HR8	H/ACA ribonucleoprotein complex non-core subunit NAF1	100.0	4.08E-17
Q7Z7H8	39S ribosomal protein L10, mitochondrial	100.0	4.08E-17
O14981	TATA-binding protein-associated factor 172	100.0	4.08E-17
Q9NRW3	DNA dC->dU-editing enzyme APOBEC-3C	100.0	4.08E-17
Q8IYD1	eukaryotic peptide chain release factor GTP-binding subunit ERF3B	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P83111-1	Serine beta-lactamase-like protein LACTB, mitochondrial	100.0	4.08E-17
P30260	cell division cycle protein 27 homolog	100.0	4.08E-17
Q9Y6B6	GTP-binding protein SAR1b	100.0	4.08E-17
Q9BZK7	F-box-like/WD repeat-containing protein TBL1XR1	100.0	4.08E-17
P11166	Solute carrier family 2, facilitated glucose transporter member 1	100.0	4.08E-17
P17706-1	Tyrosine-protein phosphatase non-receptor type 2	100.0	4.08E-17
O60934	Nibrin	100.0	4.08E-17
Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein	100.0	4.08E-17
Q8NDI1	EH domain-binding protein 1	100.0	4.08E-17
P00813	adenosine deaminase	100.0	4.08E-17
P52630-3	signal transducer and activator of transcription 2	100.0	4.08E-17
O60739	eukaryotic translation initiation factor 1b	100.0	4.08E-17
Q92685-1	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase	100.0	4.08E-17
Q86WG3-1	Caytaxin	100.0	4.08E-17
Q9BPW8	Protein NipSnap homolog 1	100.0	4.08E-17
Q9BRU9	rRNA-processing protein UTP23 homolog	100.0	4.08E-17
O15228	Dihydroxyacetone phosphate acyltransferase	100.0	4.08E-17
Q9BYB4-1	Guanine nucleotide-binding protein subunit beta-like protein 1	100.0	4.08E-17
P38571	lysosomal acid lipase/cholesteryl ester hydrolase	100.0	4.08E-17
Q96FZ7	charged multivesicular body protein 6	100.0	4.08E-17
Q0VDG4-1	secernin-3	100.0	4.08E-17
Q9P289	serine/threonine-protein kinase 26	100.0	4.08E-17
Q8WWQ0	PH-interacting protein	100.0	4.08E-17
Q96ER3	protein saal1	100.0	4.08E-17
Q9H967	WD repeat-containing protein 76	100.0	4.08E-17
Q14919-1	Dr1-associated corepressor	100.0	4.08E-17
Q5TZA2	Rootletin	100.0	4.08E-17
Q5JVF3	PCI domain-containing protein 2	100.0	4.08E-17
P51580	Thiopurine S-methyltransferase	100.0	4.08E-17
Q147X3	N-alpha-acetyltransferase 30	100.0	4.08E-17
Q06136	3-ketodihydrosphingosine reductase	100.0	4.08E-17
P37268	squalene synthase	100.0	4.08E-17
O95365	Zinc finger and BTB domain-containing protein 7A	100.0	4.08E-17
Q6P1Q9-1	Methyltransferase-like protein 2B	100.0	4.08E-17
Q9BQB6-1	vitamin K epoxide reductase complex subunit 1	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q6KC79	Nipped-B-like protein	100.0	4.08E-17
Q96RS6	NudC domain-containing protein 1	100.0	4.08E-17
Q7Z3U7-1	Protein MON2 homolog	100.0	4.08E-17
Q9H4L4	Sentrin-specific protease 3	100.0	4.08E-17
Q5TEU4	Arginine-hydroxylase NDUFAF5, mitochondrial	100.0	4.08E-17
P32780	General transcription factor IIH subunit 1	100.0	4.08E-17
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	100.0	4.08E-17
Q9H0F7	ADP-ribosylation factor-like protein 6	100.0	4.08E-17
P10398-1	serine/threonine-protein kinase A-Raf	100.0	4.08E-17
O43665	Regulator of G-protein signaling 10	100.0	4.08E-17
Q16526	Cryptochrome-1	100.0	4.08E-17
O96011-1	Peroxisomal membrane protein 11B	100.0	4.08E-17
Q9BUR5-1	MICOS complex subunit MIC26	100.0	4.08E-17
Q9UHD2	Serine/threonine-protein kinase TBK1	100.0	4.08E-17
O60244	Mediator of RNA polymerase II transcription subunit 14	100.0	4.08E-17
Q6UXN9	WD repeat-containing protein 82	100.0	4.08E-17
Q9Y4R8	telomere length regulation protein TEL2 homolog	100.0	4.08E-17
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1	100.0	4.08E-17
Q5T8P6	RNA-binding protein 26	100.0	4.08E-17
Q96AC1	Fermitin family homolog 2	100.0	4.08E-17
Q12824-1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	100.0	4.08E-17
Q99808	Equilibrative nucleoside transporter 1	100.0	4.08E-17
Q13637	Ras-related protein Rab-32	100.0	4.08E-17
Q9UNX4	WD repeat-containing protein 3	100.0	4.08E-17
Q8NCN5	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	100.0	4.08E-17
Q9ULT8	E3 ubiquitin-protein ligase hectd1	100.0	4.08E-17
Q14728	Major facilitator superfamily domain-containing protein 10	100.0	4.08E-17
Q9UHI6	Probable ATP-dependent RNA helicase DDX20	100.0	4.08E-17
Q14790-1	Caspase-8	100.0	4.08E-17
Q92947-1	Glutaryl-CoA dehydrogenase, mitochondrial	100.0	4.08E-17
P49761-1	Isoform 1 of Dual specificity protein kinase CLK3	100.0	4.08E-17
Q99436	Proteasome subunit beta type-7	100.0	4.08E-17
Q8N201	integrator complex subunit 1	100.0	4.08E-17
Q9Y3R5-1	Protein dopey-2	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9H6E4	Coiled-coil domain-containing protein 134	100.0	4.08E-17
Q14676	Mediator of DNA damage checkpoint protein 1	100.0	4.08E-17
Q8NFF5	FAD synthase	100.0	4.08E-17
Q9Y5Y2	Cytosolic Fe-S cluster assembly factor NUBP2	100.0	4.08E-17
Q8IZK6	Mucolipin-2	100.0	4.08E-17
Q08209-1	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	100.0	4.08E-17
Q9C0I1	Myotubularin-related protein 12	100.0	4.08E-17
Q96PG1	Putative membrane-spanning 4-domains subfamily A member 4E	100.0	4.08E-17
O96007	molybdopterin synthase catalytic subunit	100.0	4.08E-17
Q9H9Q2	COP9 signalosome complex subunit 7b	100.0	4.08E-17
Q86V88	Magnesium-dependent phosphatase 1	100.0	4.08E-17
Q8N2F6-1	Armadillo repeat-containing protein 10	100.0	4.08E-17
Q99836	Myeloid differentiation primary response protein MyD88	100.0	4.08E-17
P51648	Fatty aldehyde dehydrogenase	100.0	4.08E-17
O95379	Tumor necrosis factor alpha-induced protein 8	100.0	4.08E-17
Q9BSC4-1	Nucleolar protein 10	100.0	4.08E-17
Q8WVC0-1	RNA polymerase-associated protein LEO1	100.0	4.08E-17
P36404	ADP-ribosylation factor-like protein 2	100.0	4.08E-17
Q95604	HLA class I histocompatibility antigen, Cw-17 alpha chain	100.0	4.08E-17
Q03154-1	Aminoacylase-1	100.0	4.08E-17
Q86Y39-1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	100.0	4.08E-17
Q13217	DnaJ homolog subfamily C member 3	100.0	4.08E-17
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	100.0	4.08E-17
Q93100-1	phosphorylase b kinase regulatory subunit beta	100.0	4.08E-17
Q86W56	Poly(ADP-ribose) glycohydrolase	100.0	4.08E-17
Q8TBC4-1	NEDD8-activating enzyme E1 catalytic subunit	100.0	4.08E-17
Q92979	Ribosomal RNA small subunit methyltransferase Nep1	100.0	4.08E-17
P50336	protoporphyrinogen oxidase	100.0	4.08E-17
Q9H4L5	Oxysterol-binding protein-related protein 3	100.0	4.08E-17
Q14653	interferon regulatory factor 3	100.0	4.08E-17
Q0VDF9	Heat shock 70 kDa protein 14	100.0	4.08E-17
Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	100.0	4.08E-17
Q7Z434	Mitochondrial antiviral-signaling protein	100.0	4.08E-17
Q9NXG6	Transmembrane prolyl 4-hydroxylase	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q13098	COP9 signalosome complex subunit 1	100.0	4.08E-17
Q15349	Ribosomal protein S6 kinase alpha-2	100.0	4.08E-17
P52756	RNA-binding protein 5	100.0	4.08E-17
Q6P4A7-1	Sideroflexin-4	100.0	4.08E-17
Q9H1A3	Methyltransferase-like protein 9	100.0	4.08E-17
Q9BTE1	Dynactin subunit 5	100.0	4.08E-17
O75208-1	Ubiquinone biosynthesis protein COQ9, mitochondrial	100.0	4.08E-17
Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	100.0	4.08E-17
P20337	Ras-related protein Rab-3B	100.0	4.08E-17
Q16656-1	Nuclear respiratory factor 1	100.0	4.08E-17
P52948-1	nuclear pore complex protein Nup98-Nup96	100.0	4.08E-17
Q86WQ0	nuclear receptor 2C2-associated protein	100.0	4.08E-17
P19474	E3 ubiquitin-protein ligase TRIM21	100.0	4.08E-17
P26022	Pentraxin-related protein PTX3	100.0	4.08E-17
P11169	Solute carrier family 2, facilitated glucose transporter member 3	100.0	4.08E-17
Q9BQ15-1	SOSS complex subunit B1	100.0	4.08E-17
P23434	Glycine cleavage system H protein, mitochondrial	100.0	4.08E-17
Q9Y6N1	Cytochrome c oxidase assembly protein COX11, mitochondrial	100.0	4.08E-17
P62491-1	Ras-related protein Rab-11A	100.0	4.08E-17
Q15554-3	Telomeric repeat-binding factor 2	100.0	4.08E-17
O43251-1	RNA binding protein fox-1 homolog 2	100.0	4.08E-17
Q9BZF3	Oxysterol-binding protein-related protein 6	100.0	4.08E-17
Q96GG9	DCN1-like protein 1	100.0	4.08E-17
Q13769	THO complex subunit 5 homolog	100.0	4.08E-17
Q8NCF5-1	NFATC2-interacting protein	100.0	4.08E-17
Q8WUK0	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	100.0	4.08E-17
P28676	Grancalcin	100.0	4.08E-17
Q9C0D9	Ethanolaminephosphotransferase 1	100.0	4.08E-17
Q9UBV8	Peflin	100.0	4.08E-17
Q12800-1	Alpha-globin transcription factor CP2	100.0	4.08E-17
Q9H2P0	Activity-dependent neuroprotector homeobox protein	100.0	4.08E-17
Q9UKA4	A-kinase anchor protein 11	100.0	4.08E-17
O43598-1	2′-deoxynucleoside 5′-phosphate N-hydrolase 1	100.0	4.08E-17
Q9HBI1-1	Beta-parvin	100.0	4.08E-17
P09972	Fructose-bisphosphate aldolase C	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y4C2-1	TRPM8 channel-associated factor 1	100.0	4.08E-17
P55212	Caspase-6	100.0	4.08E-17
Q9NYT0	pleckstrin-2	100.0	4.08E-17
P82932	28S ribosomal protein S6, mitochondrial	100.0	4.08E-17
P51003	Poly(A) polymerase alpha	100.0	4.08E-17
O00178	GTP-binding protein 1	100.0	4.08E-17
P62380	TATA box-binding protein-like protein 1	100.0	4.08E-17
Q96K76	ubiquitin carboxyl-terminal hydrolase 47	100.0	4.08E-17
P57737	Coronin-7	100.0	4.08E-17
Q12986	Transcriptional repressor NF-X1	100.0	4.08E-17
Q9NZJ4-1	Sacsin	100.0	4.08E-17
Q13888-1	General transcription factor IIH subunit 2	100.0	4.08E-17
Q06481	Amyloid-like protein 2	100.0	4.08E-17
P53701	Cytochrome c-type heme lyase	100.0	4.08E-17
P22612	cAMP-dependent protein kinase catalytic subunit gamma	100.0	4.08E-17
Q9UBU9-1	nuclear RNA export factor 1	100.0	4.08E-17
Q8IZT6-1	Abnormal spindle-like microcephaly-associated protein	100.0	4.08E-17
Q8IZH2-1	5′-3′ exoribonuclease 1	100.0	4.08E-17
P98194-1	Calcium-transporting ATPase type 2C member 1	100.0	4.08E-17
P78357	Contactin-associated protein 1	100.0	4.08E-17
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4	100.0	4.08E-17
P40763	Signal transducer and activator of transcription 3	100.0	4.08E-17
P17152	Transmembrane protein 11, mitochondrial	100.0	4.08E-17
Q12979	active breakpoint cluster region-related protein	100.0	4.08E-17
Q4G0F5	Vacuolar protein sorting-associated protein 26B	100.0	4.08E-17
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	100.0	4.08E-17
Q92805	Golgin subfamily A member 1	100.0	4.08E-17
O75381-1	Peroxisomal membrane protein PEX14	100.0	4.08E-17
Q9BRT3	migration and invasion enhancer 1	100.0	4.08E-17
Q8TED0	U3 small nucleolar RNA-associated protein 15 homolog	100.0	4.08E-17
P83436	Conserved oligomeric Golgi complex subunit 7	100.0	4.08E-17
P62875	DNA-directed RNA polymerases I, II, and III subunit RPABC5	100.0	4.08E-17
O60942-1	mRNA-capping enzyme	100.0	4.08E-17
Q8TF27	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 11	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96FV9-1	THO complex subunit 1	100.0	4.08E-17
Q9P1F3	Costars family protein ABRACL	100.0	4.08E-17
Q9NZV5-1	Selenoprotein N	100.0	4.08E-17
P23497	Nuclear autoantigen Sp-100	100.0	4.08E-17
Q7Z2E3-1	Aprataxin	100.0	4.08E-17
Q8WWV3-1	Reticulon-4-interacting protein 1, mitochondrial	100.0	4.08E-17
O00308	NEDD4-like E3 ubiquitin-protein ligase WWP2	100.0	4.08E-17
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial	100.0	4.08E-17
Q9Y5A7	NEDD8 ultimate buster 1	100.0	4.08E-17
Q03013-1	glutathione S-transferase mu 4	100.0	4.08E-17
Q9Y6I4-1	Ubiquitin carboxyl-terminal hydrolase 3	100.0	4.08E-17
Q9H9Q4-1	non-homologous end-joining factor 1	100.0	4.08E-17
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog	100.0	4.08E-17
Q8IV38	Ankyrin repeat and MYND domain-containing protein 2	100.0	4.08E-17
Q9H0A8-1	COMM domain-containing protein 4	100.0	4.08E-17
Q15648	Mediator of RNA polymerase II transcription subunit 1	100.0	4.08E-17
Q8TDZ2	[F-actin]-monooxygenase MICAL1	100.0	4.08E-17
Q9NYY8	FAST kinase domain-containing protein 2, mitochondrial	100.0	4.08E-17
Q6PL18-1	ATPase family AAA domain-containing protein 2	100.0	4.08E-17
P12236	ADP/ATP translocase 3	100.0	4.08E-17
Q9Y3E1	Hepatoma-derived growth factor-related protein 3	100.0	4.08E-17
Q8IWA4-1	Mitofusin-1	100.0	4.08E-17
Q9BRZ2-1	E3 ubiquitin-protein ligase TRIM56	100.0	4.08E-17
Q9NV31	U3 small nucleolar ribonucleoprotein protein IMP3	100.0	4.08E-17
Q9P2Q2	FERM domain-containing protein 4A	100.0	4.08E-17
Q9BS16	Centromere protein K	100.0	4.08E-17
Q9H832	Ubiquitin-conjugating enzyme E2 Z	100.0	4.08E-17
Q8NBL1	Protein O-glucosyltransferase 1	100.0	4.08E-17
Q13438-1	Protein os-9	100.0	4.08E-17
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1	100.0	4.08E-17
Q969T9	WW domain-binding protein 2	100.0	4.08E-17
Q9BW27	nuclear pore complex protein Nup85	100.0	4.08E-17
Q9NUJ3	T-complex protein 11-like protein 1	100.0	4.08E-17
Q7Z2T5-1	TRMT1-like protein	100.0	4.08E-17
P01116	GTPase KRas	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O43570	Carbonic anhydrase 12	100.0	4.08E-17
Q9NWV4	UPF0587 protein C1orf123	100.0	4.08E-17
Q9NUL3	Double-stranded RNA-binding protein Staufen homolog 2	100.0	4.08E-17
Q96AX1	Vacuolar protein sorting-associated protein 33A	100.0	4.08E-17
Q5HYI7	Metaxin-3	100.0	4.08E-17
Q12981-1	Isoform 3 of Vesicle transport protein SEC20	100.0	4.08E-17
Q5JPH6	Probable glutamate–tRNA ligase, mitochondrial	100.0	4.08E-17
Q92614-1	Unconventional myosin-XVIIIa	100.0	4.08E-17
Q9UJX4	Anaphase-promoting complex subunit 5	100.0	4.08E-17
Q99519	sialidase-1	100.0	4.08E-17
Q03519-1	antigen peptide transporter 2	100.0	4.08E-17
Q9BZD4	kinetochore protein nuf2	100.0	4.08E-17
Q9H2H9	Sodium-coupled neutral amino acid transporter 1	100.0	4.08E-17
Q7L8L6	FAST kinase domain-containing protein 5, mitochondrial	100.0	4.08E-17
Q7Z4H8	KDEL motif-containing protein 2	100.0	4.08E-17
P26572	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	100.0	4.08E-17
Q5VWZ2	Lysophospholipase-like protein 1	100.0	4.08E-17
Q8IZ83	Aldehyde dehydrogenase family 16 member A1	100.0	4.08E-17
Q5W111	SPRY domain-containing protein 7	100.0	4.08E-17
Q13523	Serine/threonine-protein kinase PRP4 homolog	100.0	4.08E-17
Q00653-1	Nuclear factor NF-kappa-B p100 subunit	100.0	4.08E-17
Q96RN5	Mediator of RNA polymerase II transcription subunit 15	100.0	4.08E-17
P29084	transcription initiation factor iie subunit beta	100.0	4.08E-17
P83916	Chromobox protein homolog 1	100.0	4.08E-17
Q9UP95	Solute carrier family 12 member 4	100.0	4.08E-17
Q9NRX5	Serine incorporator 1	100.0	4.08E-17
O43674-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	100.0	4.08E-17
Q99757	Thioredoxin, mitochondrial	100.0	4.08E-17
Q96FQ6	Protein S100-A16	100.0	4.08E-17
Q96P47	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	100.0	4.08E-17
Q9NWU2	Glucose-induced degradation protein 8 homolog	100.0	4.08E-17
Q9BYD6	39S ribosomal protein L1, mitochondrial	100.0	4.08E-17
Q9Y2D4	Exocyst complex component 6B	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8IYS1	Peptidase M20 domain-containing protein 2	100.0	4.08E-17
O95140	Mitofusin-2	100.0	4.08E-17
P62330	ADP-ribosylation factor 6	100.0	4.08E-17
Q86VR2	Reticulophagy regulator 3	100.0	4.08E-17
Q8NB90-1	Spermatogenesis-associated protein 5	100.0	4.08E-17
Q8WX92	Negative elongation factor B	100.0	4.08E-17
Q15345-2	Leucine-rich repeat-containing protein 41	100.0	4.08E-17
Q96DA6	mitochondrial import inner membrane translocase subunit TIM14	100.0	4.08E-17
Q9UP83-1	conserved oligomeric Golgi complex subunit 5	100.0	4.08E-17
Q9UKS6	Protein kinase C and casein kinase substrate in neurons protein 3	100.0	4.08E-17
Q14197	Peptidyl-tRNA hydrolase ICT1, mitochondrial	100.0	4.08E-17
P31942-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3	100.0	4.08E-17
Q8IZD4	mRNA-decapping enzyme 1B	100.0	4.08E-17
Q14146	Unhealthy ribosome biogenesis protein 2 homolog	100.0	4.08E-17
Q96A26	Protein FAM162A	100.0	4.08E-17
Q96S82	ubiquitin-like protein 7	100.0	4.08E-17
Q6VY07	Phosphofurin acidic cluster sorting protein 1	100.0	4.08E-17
Q92643	GPI-anchor transamidase	100.0	4.08E-17
O14965	Aurora kinase A	100.0	4.08E-17
O43837-1	isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	100.0	4.08E-17
P49356	protein farnesyltransferase subunit beta	100.0	4.08E-17
Q9UBW8	COP9 signalosome complex subunit 7a	100.0	4.08E-17
Q9NWY4	Histone PARylation factor 1	100.0	4.08E-17
P25098	Beta-adrenergic receptor kinase 1	100.0	4.08E-17
Q3ZAQ7	Vacuolar ATPase assembly integral membrane protein vma21	100.0	4.08E-17
Q99720	sigma non-opioid intracellular receptor 1	100.0	4.08E-17
Q96F85-1	CB1 cannabinoid receptor-interacting protein 1	100.0	4.08E-17
Q9GZM5	protein YIPF3	100.0	4.08E-17
Q9P0U1	Mitochondrial import receptor subunit TOM7 homolog	100.0	4.08E-17
Q15366-4	Isoform 4 of Poly(rC)-binding protein 2	100.0	4.08E-17
P36873-1	serine/threonine-protein phosphatase PP1-gamma catalytic subunit	100.0	4.08E-17
Q9HAN9	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 1	100.0	4.08E-17
O43264	Centromere/kinetochore protein zw10 homolog	100.0	4.08E-17
O96005-1	Cleft lip and palate transmembrane protein 1	100.0	4.08E-17
Q9HBH1	Peptide deformylase, mitochondrial	100.0	4.08E-17
Q96I51	RCC1-like G exchanging factor-like protein	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8NHZ8	Anaphase-promoting complex subunit CDC26	100.0	4.08E-17
O75446	Histone deacetylase complex subunit SAP30	100.0	4.08E-17
Q9Y6X3-1	MAU2 chromatid cohesion factor homolog	100.0	4.08E-17
Q9Y312	Protein AAR2 homolog	100.0	4.08E-17
Q9HB20	pleckstrin homology domain-containing family A member 3	100.0	4.08E-17
Q16774-1	guanylate kinase	100.0	4.08E-17
Q92599-1	Septin-8	100.0	4.08E-17
Q92963	GTP-binding protein Rit1	100.0	4.08E-17
Q9H201-1	Epsin-3	100.0	4.08E-17
Q8N7H5	RNA polymerase II-associated factor 1 homolog	100.0	4.08E-17
Q9BZG8	2-(3-amino-3-carboxypropyl)histidine synthase subunit 1	100.0	4.08E-17
Q9NR09	Baculoviral IAP repeat-containing protein 6	100.0	4.08E-17
Q9NX14-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	100.0	4.08E-17
Q32P44	Echinoderm microtubule-associated protein-like 3	100.0	4.08E-17
Q9BZV1	UBX domain-containing protein 6	100.0	4.08E-17
P42345	Serine/threonine-protein kinase mTOR	100.0	4.08E-17
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	100.0	4.08E-17
P11441	Ubiquitin-like protein 4A	100.0	4.08E-17
Q9HB40	Retinoid-inducible serine carboxypeptidase	100.0	4.08E-17
O43427	Acidic fibroblast growth factor intracellular-binding protein	100.0	4.08E-17
Q9BY32-1	Inosine triphosphate pyrophosphatase	100.0	4.08E-17
O75427	Leucine-rich repeat and calponin homology domain-containing protein 4	100.0	4.08E-17
Q9BUR4	Telomerase Cajal body protein 1	100.0	4.08E-17
Q8N122	Regulatory-associated protein of mTOR	100.0	4.08E-17
Q8WU76-1	Sec1 family domain-containing protein 2	100.0	4.08E-17
P62341	Thioredoxin reductase-like selenoprotein T	100.0	4.08E-17
Q9UK59	lariat debranching enzyme	100.0	4.08E-17
P46736	Lys-63-specific deubiquitinase BRCC36	100.0	4.08E-17
Q9NZ32	Actin-related protein 10	100.0	4.08E-17
Q9H788	SH2 domain-containing protein 4A	100.0	4.08E-17
Q6ZW31-1	Rho GTPase-activating protein SYDE1	100.0	4.08E-17
Q92759	General transcription factor IIH subunit 4	100.0	4.08E-17
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha	100.0	4.08E-17
Q14657	EKC/KEOPS complex subunit LAGE3	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y3X0	coiled-coil domain-containing protein 9	100.0	4.08E-17
P07311	Acylphosphatase-1	100.0	4.08E-17
Q9Y3E0	vesicle transport protein GOT1B	100.0	4.08E-17
Q9NX20	39S ribosomal protein L16, mitochondrial	100.0	4.08E-17
O60499	Syntaxin-10	100.0	4.08E-17
Q15042-1	Rab3 GTPase-activating protein catalytic subunit	100.0	4.08E-17
P78346-1	ribonuclease P protein subunit p30	100.0	4.08E-17
Q86UY6	N-alpha-acetyltransferase 40	100.0	4.08E-17
Q9BSV6	tRNA-splicing endonuclease subunit sen34	100.0	4.08E-17
P42566-1	epidermal growth factor receptor substrate 15	100.0	4.08E-17
Q9BV20-1	methylthioribose-1-phosphate isomerase	100.0	4.08E-17
Q13057	Bifunctional coenzyme A synthase	100.0	4.08E-17
Q96ND0	Protein FAM210A	100.0	4.08E-17
Q8N8N7-1	Prostaglandin reductase 2	100.0	4.08E-17
P04049	RAF proto-oncogene serine/threonine-protein kinase	100.0	4.08E-17
P29317	Ephrin type-A receptor 2	100.0	4.08E-17
O75127	pentatricopeptide repeat-containing protein 1, mitochondrial	100.0	4.08E-17
Q6PI48	Aspartate–tRNA ligase, mitochondrial	100.0	4.08E-17
Q9Y657	Spindlin-1	100.0	4.08E-17
Q9NW15-1	Anoctamin-10	100.0	4.08E-17
P51608	Methyl-CpG-binding protein 2	100.0	4.08E-17
O60563	Cyclin-T1	100.0	4.08E-17
O43414-1	ERI1 exoribonuclease 3	100.0	4.08E-17
Q86XI2-1	condensin-2 complex subunit G2	100.0	4.08E-17
Q9HAV4	exportin-5	100.0	4.08E-17
Q9BXB4	Oxysterol-binding protein-related protein 11	100.0	4.08E-17
P62308	Small nuclear ribonucleoprotein G	100.0	4.08E-17
Q96JB2-1	Conserved oligomeric Golgi complex subunit 3	100.0	4.08E-17
Q15800	Methylsterol monooxygenase 1	100.0	4.08E-17
Q8IY37	Probable ATP-dependent RNA helicase DHX37	100.0	4.08E-17
Q96B26	Exosome complex component RRP43	100.0	4.08E-17
Q9H501	ESF1 homolog	100.0	4.08E-17
Q9Y3B2	Exosome complex component csl4	100.0	4.08E-17
Q9H2J4	phosducin-like protein 3	100.0	4.08E-17
Q9BYX2	TBC1 domain family member 2A	100.0	4.08E-17
Q15366-1	Poly(rC)-binding protein 2	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O75879	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	100.0	4.08E-17
Q96BN8	Ubiquitin thioesterase otulin	100.0	4.08E-17
Q9UIL1-1	Short coiled-coil protein	100.0	4.08E-17
A2RRP1-1	neuroblastoma-amplified sequence	100.0	4.08E-17
P20339	Ras-related protein Rab-5A	100.0	4.08E-17
Q96M27-1	protein PRRC1	100.0	4.08E-17
O95425	Supervillin	100.0	4.08E-17
O95396	Adenylyltransferase and sulfurtransferase MOCS3	100.0	4.08E-17
Q01518-2	Isoform 2 of Adenylyl cyclase-associated protein 1	100.0	4.08E-17
Q9Y2X7-1	ARF GTPase-activating protein GIT1	100.0	4.08E-17
Q7Z4H7	HAUS augmin-like complex subunit 6	100.0	4.08E-17
Q9Y4B6	DDB1- and CUL4-associated factor 1	100.0	4.08E-17
Q8WTS6	Histone-lysine N-methyltransferase SETD7	100.0	4.08E-17
O75616-1	GTPase Era, mitochondrial	100.0	4.08E-17
Q658Y4	Protein FAM91A1	100.0	4.08E-17
Q9BVC5	Ashwin	100.0	4.08E-17
Q9UHA4	ragulator complex protein LAMTOR3	100.0	4.08E-17
P14735	insulin-degrading enzyme	100.0	4.08E-17
Q96F24-1	Nuclear receptor-binding factor 2	100.0	4.08E-17
O00471	Exocyst complex component 5	100.0	4.08E-17
Q15048	Leucine-rich repeat-containing protein 14	100.0	4.08E-17
Q9BRF8-1	Serine/threonine-protein phosphatase CPPED1	100.0	4.08E-17
Q9UBV7	Beta-1,4-galactosyltransferase 7	100.0	4.08E-17
Q6UXI9	Nephronectin	100.0	4.08E-17
Q6ZMW3	Echinoderm microtubule-associated protein-like 6	100.0	4.08E-17
Q9NTU7	Cerebellin-4	100.0	4.08E-17
Q8IXH7	Negative elongation factor C/D	100.0	4.08E-17
Q9UBK9	protein UXT	100.0	4.08E-17
P02675	Fibrinogen beta chain	100.0	4.08E-17
A6NDN3	Golgin subfamily A member 6B	100.0	4.08E-17
P12109	Collagen alpha-1(VI) chain	100.0	4.08E-17
Q9UL63-1	muskelin	100.0	4.08E-17
Q9NR63-1	Cytochrome P450 26B1	100.0	4.08E-17
P51784	Ubiquitin carboxyl-terminal hydrolase 11	100.0	4.08E-17
Q4G148-1	Glucoside xylosyltransferase 1	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q6STE5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3	100.0	4.08E-17
Q8TCG2	Phosphatidylinositol 4-kinase type 2-beta	100.0	4.08E-17
Q01415-1	N-acetylgalactosamine kinase	100.0	4.08E-17
Q9HB09-1	Bcl-2-like protein 12	100.0	4.08E-17
Q9H5V9-1	UPF0428 protein CXorf56	100.0	4.08E-17
Q96RY7	Intraflagellar transport protein 140 homolog	100.0	4.08E-17
O60637	Tetraspanin-3	100.0	4.08E-17
Q96CN9	GRIP and coiled-coil domain-containing protein 1	100.0	4.08E-17
Q96N46	Tetratricopeptide repeat protein 14	100.0	4.08E-17
Q53HV7-1	single-strand selective monofunctional uracil DNA glycosylase	100.0	4.08E-17
Q9UEU0	vesicle transport through interaction with t-SNAREs homolog 1B	100.0	4.08E-17
P61962	DDB1- and CUL4-associated factor 7	100.0	4.08E-17
Q9H6S1-1	5-azacytidine-induced protein 2	100.0	4.08E-17
P54259	Atrophin-1	100.0	4.08E-17
Q9H0P0-1	Isoform 1 of Cytosolic 5′-nucleotidase 3A	100.0	4.08E-17
Q8N7C3	Probable E3 ubiquitin-protein ligase TRIML2	100.0	4.08E-17
Q6PI78	Transmembrane protein 65	100.0	4.08E-17
O43805	Sjoegren syndrome nuclear autoantigen 1	100.0	4.08E-17
P62487	DNA-directed RNA polymerase II subunit rpb7	100.0	4.08E-17
O14657	Torsin-1B	100.0	4.08E-17
Q8TBQ9	Protein kish-A	100.0	4.08E-17
Q9NXJ5	Pyroglutamyl-peptidase 1	100.0	4.08E-17
Q15772	Striated muscle preferentially expressed protein kinase	100.0	4.08E-17
P82663	28S ribosomal protein S25, mitochondrial	100.0	4.08E-17
Q16875	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	100.0	4.08E-17
Q6ZNF0	Acid phosphatase type 7	100.0	4.08E-17
Q8WZ42	Titin	100.0	4.08E-17
O14646	Chromodomain-helicase-DNA-binding protein 1	100.0	4.08E-17
Q9H981-1	Actin-related protein 8	100.0	4.08E-17
Q8IZX4	transcription initiation factor TFIID subunit 1-like	100.0	4.08E-17
A1A4S6	Rho GTPase-activating protein 10	100.0	4.08E-17
Q07352	mRNA decay activator protein ZFP36L1	100.0	4.08E-17
Q13625-1	Apoptosis-stimulating of p53 protein 2	100.0	4.08E-17
Q5TA45-1	Integrator complex subunit 11	100.0	4.08E-17
Q6IA86-1	elongator complex protein 2	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NYP7-1	elongation of very long chain fatty acids protein 5	100.0	4.08E-17
Q8ND82	zinc finger protein 280c	100.0	4.08E-17
Q9UHP3	ubiquitin carboxyl-terminal hydrolase 25	100.0	4.08E-17
Q8TDB6-1	E3 ubiquitin-protein ligase DTX3L	100.0	4.08E-17
Q9BZL1	ubiquitin-like protein 5	100.0	4.08E-17
P49916-1	DNA ligase 3	100.0	4.08E-17
Q9NQW1-1	Protein transport protein Sec31B	100.0	4.08E-17
Q9UKZ1	CCR4-NOT transcription complex subunit 11	100.0	4.08E-17
Q96IV0	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	100.0	4.08E-17
Q8N954-1	G patch domain-containing protein 11	100.0	4.08E-17
Q5EBL8	PDZ domain-containing protein 11	100.0	4.08E-17
Q9NZJ5	Eukaryotic translation initiation factor 2-alpha kinase 3	100.0	4.08E-17
Q4KWH8-1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1	100.0	4.08E-17
Q8NER1	Transient receptor potential cation channel subfamily V member 1	100.0	4.08E-17
P19021-1	Peptidyl-glycine alpha-amidating monooxygenase	100.0	4.08E-17
Q9Y5H6-1	Protocadherin alpha-8	100.0	4.08E-17
Q6P1Q0	LETM1 domain-containing protein 1	100.0	4.08E-17
Q5W0U4	B box and SPRY domain-containing protein	100.0	4.08E-17
Q9NYQ8	Protocadherin Fat 2	100.0	4.08E-17
P53609	Geranylgeranyl transferase type-1 subunit beta	100.0	4.08E-17
Q6NSX1	Coiled-coil domain-containing protein 70	100.0	4.08E-17
Q9BUT9-1	MAPK regulated corepressor interacting protein 2	100.0	4.08E-17
Q9H410	Kinetochore-associated protein DSN1 homolog	100.0	4.08E-17
P08254	Stromelysin-1	100.0	4.08E-17
Q96DZ1	Endoplasmic reticulum lectin 1	100.0	4.08E-17
Q9C0A1	Zinc finger homeobox protein 2	100.0	4.08E-17
Q7Z6J4-5	Isoform 4 of FYVE, RhoGEF and PH domain-containing protein 2	100.0	4.08E-17
Q9GZN4	Brain-specific serine protease 4	100.0	4.08E-17
Q8IVU3-1	Probable E3 ubiquitin-protein ligase HERC6	100.0	4.08E-17
Q8N8J7	Uncharacterized protein C4orf32	100.0	4.08E-17
Q9Y466	Nuclear receptor subfamily 2 group E member 1	100.0	4.08E-17
P31749	RAC-alpha serine/threonine-protein kinase	100.0	4.08E-17
Q9BYC8	39S ribosomal protein L32, mitochondrial	100.0	4.08E-17
Q9UJV9	Probable ATP-dependent RNA helicase DDX41	100.0	4.08E-17
O95544-2	Isoform 2 of NAD kinase	100.0	4.08E-17
Q96RP8	Potassium voltage-gated channel subfamily A member 7	100.0	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O43708	maleylacetoacetate isomerase	100.0	4.08E-17
Q8WTW3	conserved oligomeric Golgi complex subunit 1	100.0	4.08E-17
Q9UPU9-1	Protein Smaug homolog 1	100.0	4.08E-17
Q8TCB0	Interferon-induced protein 44	100.0	4.08E-17
P16383-1	GC-rich sequence DNA-binding factor 2	100.0	4.08E-17
Q5TCZ1	SH3 and PX domain-containing protein 2A	100.0	4.08E-17
Q8IXQ4	GPALPP motifs-containing protein 1	100.0	4.08E-17
O76024	Wolframin	100.0	4.08E-17
P60323-1	nanos homolog 3	100.0	4.08E-17
P54764	Ephrin type-A receptor 4	100.0	4.08E-17
Q9BXX3	Ankyrin repeat domain-containing protein 30A	100.0	4.08E-17
Q15326	Zinc finger MYND domain-containing protein 11	100.0	4.08E-17
P28749-1	Retinoblastoma-like protein 1	100.0	4.08E-17
Q9BXB1	Leucine-rich repeat-containing G-protein coupled receptor 4	100.0	4.08E-17
Q9Y575	Ankyrin repeat and SOCS box protein 3	100.0	4.08E-17
Q86WZ0	HEAT repeat-containing protein 4	100.0	4.08E-17
Q86SQ0-1	Pleckstrin homology-like domain family B member 2	100.0	4.08E-17
Q9UPV0	centrosomal protein of 164 kDa	100.0	4.08E-17
Q16831	uridine phosphorylase 1	100.0	4.08E-17
O60486	Plexin-C1	100.0	4.08E-17
Q96MM6	Heat shock 70 kDa protein 12B	100.0	4.08E-17
Q9NTX7	E3 ubiquitin-protein ligase rnf146	100.0	4.08E-17
Q9NWT1	p21-activated protein kinase-interacting protein 1	100.0	4.08E-17
Q9Y4F3-1	Meiosis regulator and mRNA stability factor 1	100.0	4.08E-17
P58400	Neurexin-1-beta	51.34	1.74E-04
O00483	Cytochrome c oxidase subunit NDUFA4	51.31	1.74E-04
Q9UQ90	Paraplegin	43.24	4.97E-04
Q01860-2	Isoform B of POU domain, class 5, transcription factor 1	41.05	5.14E-04
P28370-1	Probable global transcription activator SNF2L1	40.73	5.33E-04
Q9H7Z7	Prostaglandin E synthase 2	38.37	1.16E-03
L0R6Q1	SLC35A4 upstream open reading frame protein	37.76	4.02E-03
Q8WXA9-2	Isoform 2 of Splicing regulatory glutamine/lysine-rich protein 1	37.20	1.50E-02
Q06265-1	Exosome complex component RRP45	36.16	9.24E-04
Q9BXW6-1	Oxysterol-binding protein-related protein 1	35.86	1.30E-03
P80192-1	mitogen-activated protein kinase kinase kinase 9	34.24	1.52E-02
O15258	Protein RER1	34.22	1.19E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q96CS3	FAS-associated factor 2	33.89	2.00E-03
O14763	Tumor necrosis factor receptor superfamily member 10B	32.95	1.21E-02
Q9UMS0	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	32.66	1.46E-03
Q86X76	Deaminated glutathione amidase	32.48	8.86E-03
Q8WVQ1	Soluble calcium-activated nucleotidase 1	31.58	1.31E-02
Q9NVH1-1	DnaJ homolog subfamily C member 11	30.84	1.87E-03
P57105	Synaptojanin-2-binding protein	30.31	8.98E-03
P51151	Ras-related protein Rab-9A	29.94	9.75E-03
P49959	Double-strand break repair protein MRE11	29.83	2.54E-03
Q6NXE6-1	Armadillo repeat-containing protein 6	29.78	2.56E-03
Q9Y2P8	RNA 3′-terminal phosphate cyclase-like protein	29.74	2.19E-03
O60565	Gremlin-1	29.62	4.90E-03
Q9BW72	HIG1 domain family member 2A, mitochondrial	29.54	8.85E-03
P61803	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase subunit DAD1	29.43	2.29E-03
A6ZKI3	Retrotransposon Gag-like protein 8B	29.13	7.36E-03
Q93034	Cullin-5	28.85	1.12E-02
Q9Y3A6-1	Transmembrane emp24 domain-containing protein 5	28.85	1.54E-02
Q9H6V9-1	Lipid droplet-associated hydrolase	28.65	1.66E-02
Q96EY7-1	pentatricopeptide repeat domain-containing protein 3, mitochondrial	28.33	6.80E-03
P48449-1	lanosterol synthase	28.23	2.00E-02
O00139-2	Isoform 2 of Kinesin-like protein KIF2A	27.91	3.37E-03
Q7Z7A4-1	PX domain-containing protein kinase-like protein	27.49	2.41E-02
O15016	Tripartite motif-containing protein 66	27.29	1.29E-02
Q15257-1	Serine/threonine-protein phosphatase 2A activator	27.24	3.16E-03
Q9UNW1	Multiple inositol polyphosphate phosphatase 1	27.21	2.19E-02
Q99805	Transmembrane 9 superfamily member 2	27.12	3.22E-03
Q9UBI1	COMM domain-containing protein 3	26.92	3.93E-03
Q96KA5-1	cleft lip and palate transmembrane protein 1-like protein	26.87	1.33E-02
Q86XX4-1	Extracellular matrix protein FRAS1	26.59	1.82E-02
Q9NXF1	Testis-expressed protein 10	26.55	4.25E-03
O43318	mitogen-activated protein kinase kinase kinase 7	26.39	2.10E-02
Q9Y3D3	28S ribosomal protein S16, mitochondrial	26.37	1.09E-02
Q7Z2W9	39S ribosomal protein L21, mitochondrial	26.36	7.71E-03
Q9UNI6	Dual specificity protein phosphatase 12	26.05	1.48E-02

Continued on next page

accession	description	fold p change	adjusted p-value
O96019-1	Actin-like protein 6A	25.73	3.98E-03
P19525	interferon-induced, double-stranded RNA-activated protein kinase	25.66	4.02E-03
Q58FF6	Putative heat shock protein HSP 90-beta 4	25.59	4.06E-03
Q13610	Periodic tryptophan protein 1 homolog	25.51	5.09E-03
Q9BVG4	Protein PBDC1	25.49	4.12E-03
Q9UH17-1	DNA dC->dU-editing enzyme APOBEC-3B	25.45	4.79E-03
Q13616	Cullin-1	25.35	8.15E-03
O60343-1	TBC1 domain family member 4	25.29	4.25E-03
Q92783	signal transducing adapter molecule 1	25.02	4.43E-03
O43148-1	mRNA cap guanine-N7 methyltransferase	24.84	4.56E-03
Q9NY15-1	Stabilin-1	24.74	4.64E-03
Q8N543	prolyl 3-hydroxylase OGFOD1	24.68	4.68E-03
Q9BYN0	sulfiredoxin-1	24.44	3.46E-02
Q9P0J0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	24.35	4.92E-03
O15031	Plexin-B2	24.31	8.54E-03
Q9H8H0	nucleolar protein 11	24.16	4.03E-02
Q00013-1	55 kDa erythrocyte membrane protein	24.14	9.84E-03
A6NMZ7-1	Collagen alpha-6(VI) chain	24.10	7.66E-03
Q96D71	RalBP1-associated Eps domain-containing protein 1	23.95	4.89E-02
P62314	Small nuclear ribonucleoprotein Sm D1	23.94	5.25E-03
Q9H6K4	Optic atrophy 3 protein	23.87	2.38E-02
P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial	23.53	4.06E-02
Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats	23.30	3.56E-02
Q9P0R6	GSK3B-interacting protein	23.22	1.54E-02
P43155	Carnitine O-acetyltransferase	23.22	3.16E-02
P29372	DNA-3-methyladenine glycosylase	23.04	2.19E-02
Q92820	Gamma-glutamyl hydrolase	22.85	6.30E-03
Q86U86-1	Protein polybromo-1	22.50	3.30E-02
Q9P2E5-1	Chondroitin sulfate glucuronyltransferase	22.46	3.96E-02
P19878	Neutrophil cytosol factor 2	22.41	6.78E-03
P61225	ras-related protein Rap-2b	22.37	1.36E-02
Q96I23	Protein preY, mitochondrial	22.27	4.94E-02
P61421	V-type proton ATPase subunit d 1	22.24	6.99E-03
Q69YN2-1	CWF19-like protein 1	21.76	8.54E-03
Q9Y4W2	Ribosomal biogenesis protein LAS1L	21.41	8.98E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BXS5-1	AP-1 complex subunit mu-1	21.32	8.17E-03
Q9NUG6	p53 and DNA damage-regulated protein 1	21.30	8.19E-03
Q96EH3	mitochondrial assembly of ribosomal large subunit protein 1	21.13	4.68E-02
P61619	Protein transport protein Sec61 subunit alpha isoform 1	21.12	8.46E-03
P09884	DNA polymerase alpha catalytic subunit	21.11	1.58E-02
Q9UBQ0-2	Isoform 2 of Vacuolar protein sorting-associated protein 29	21.11	4.61E-02
Q8IVL6-1	Prolyl 3-hydroxylase 3	21.02	2.12E-02
Q9H1E5	Thioredoxin-related transmembrane protein 4	20.91	4.30E-02
Q14241	Elongin-A	20.87	1.77E-02
P35270	Sepiapterin reductase	20.85	8.86E-03
Q63HN8-4	Isoform 2 of E3 ubiquitin-protein ligase RNF213	20.84	4.37E-02
Q8NFH4	Nucleoporin Nup37	20.41	9.56E-03
Q8IUH3	RNA-binding protein 45	20.35	9.65E-03
P98155-1	very low-density lipoprotein receptor	20.30	4.78E-02
P51808	Dynein light chain Tctex-type 3	20.13	1.15E-02
Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	20.11	1.01E-02
Q6P1N9-1	Putative deoxyribonuclease TATDN1	19.87	1.48E-02
P03956	Interstitial collagenase	19.74	1.55E-02
Q9ULP9	TBC1 domain family member 24	19.61	2.65E-02
Q96BW9-1	Phosphatidate cytidylyltransferase, mitochondrial	19.55	2.86E-02
Q14956	Transmembrane glycoprotein NMB	19.54	3.34E-02
P56545	c-terminal-binding protein 2	19.53	1.98E-02
P12110	Collagen alpha-2(VI) chain	19.46	1.13E-02
O95376	E3 ubiquitin-protein ligase ARIH2	19.34	3.91E-02
Q6NUM9-1	all-trans-retinol 13,14-reductase	19.33	1.63E-02
Q96AA3	Protein RFT1 homolog	18.84	1.44E-02
P80303	Nucleobindin-2	18.81	1.28E-02
Q13158	FAS-associated death domain protein	18.49	1.53E-02
Q15436	protein transport protein Sec23A	18.43	1.37E-02
Q9Y291	28S ribosomal protein S33, mitochondrial	18.41	3.01E-02
Q96EM0	Trans-3-Hydroxy-L-proline dehydratase	18.39	1.38E-02
Q68E01	Integrator complex subunit 3	18.32	1.53E-02
Q9P253	Vacuolar protein sorting-associated protein 18 homolog	18.03	3.00E-02
Q9NQ88	Fructose-2,6-bisphosphatase TIGAR	17.93	2.20E-02
Q9NZ08-1	endoplasmic reticulum aminopeptidase 1	17.83	4.21E-02
P49642	DNA primase small subunit	17.33	2.47E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y697	Cysteine desulfurase, mitochondrial	17.17	2.02E-02
Q6ZSB9	Zinc finger and BTB domain-containing protein 49	17.12	3.30E-02
Q14160	protein scribble homolog	17.05	2.01E-02
P98082	Disabled homolog 2	16.97	4.94E-02
Q969Z0-1	Protein TBRG4	16.93	1.85E-02
Q13895	Bystin	16.70	1.93E-02
P28288	ATP-binding cassette sub-family D member 3	16.41	2.03E-02
Q9BSH4	Translational activator of cytochrome c oxidase 1	16.28	2.53E-02
Q9HC07	Transmembrane protein 165	16.27	2.31E-02
Q9NP77	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	16.23	4.08E-02
Q8IWR0	Zinc finger CCCH domain-containing protein 7A	16.10	2.84E-02
Q9P0W8	Spermatogenesis-associated protein 7	15.97	2.52E-02
O94919	endonuclease domain-containing 1 protein	15.75	3.80E-02
Q9UIA9	exportin-7	15.57	2.49E-02
Q9H936	Mitochondrial glutamate carrier 1	15.51	2.44E-02
P61077-1	Ubiquitin-conjugating enzyme E2 D3	15.42	2.48E-02
Q9NXG2	THUMP domain-containing protein 1	15.30	2.53E-02
Q96AJ9-1	Isoform 1 of Vesicle transport through interaction with t-SNAREs homolog 1A	15.29	4.12E-02
Q15286	Ras-related protein Rab-35	14.83	3.69E-02
Q8WVX9	Fatty acyl-CoA reductase 1	14.77	4.60E-02
Q14627	Interleukin-13 receptor subunit alpha-2	14.54	3.78E-02
Q9HD15	Steroid receptor RNA activator 1	14.54	3.59E-02
P06730	Eukaryotic translation initiation factor 4E	14.46	3.03E-02
Q9HD26-1	Golgi-associated PDZ and coiled-coil motif-containing protein	14.40	3.54E-02
Q9BYT8	Neurolysin, mitochondrial	14.37	4.70E-02
P48147	prolyl endopeptidase	14.01	3.35E-02
P61769	Beta-2-microglobulin	13.97	3.38E-02
Q96RE7	Nucleus accumbens-associated protein 1	12.91	4.72E-02
Q9Y3B8-1	Oligoribonuclease, mitochondrial	12.32	4.94E-02
Q15233	Non-POU domain-containing octamer-binding protein	0.204	4.94E-02
P42677	40S ribosomal protein S27	0.203	4.89E-02
P04070	Vitamin K-dependent protein C	0.201	4.73E-02
Q9Y450-1	HBS1-like protein	0.201	4.74E-02
P49773	Histidine triad nucleotide-binding protein 1	0.201	4.74E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q9UK76	Jupiter microtubule associated homolog 1	0.200	4.71E-02
Q92734-1	Protein TFG	0.198	4.53E-02
P61313-1	60S ribosomal protein L15	0.198	4.56E-02
Q9Y4K1	beta/gamma crystallin domain-containing protein 1	0.187	3.81E-02
Q14151	scaffold attachment factor B2	0.185	3.67E-02
Q3KQU3	MAP7 domain-containing protein 1	0.185	3.68E-02
P62899	60S ribosomal protein L31	0.185	3.68E-02
O60784	Target of Myb protein 1	0.179	3.34E-02
P67809	Nuclease-sensitive element-binding protein 1	0.178	3.28E-02
P13987	CD59 glycoprotein	0.174	3.03E-02
P69905	Hemoglobin subunit alpha	0.174	3.04E-02
P02100	Hemoglobin subunit epsilon	0.173	3.01E-02
Q8WVJ2	NudC domain-containing protein 2	0.171	4.21E-02
Q96EP5	DAZ-associated protein 1	0.169	2.77E-02
Q02539	Histone H1.1	0.169	2.80E-02
P26583	High mobility group protein B2	0.167	2.66E-02
Q9BQ75	Protein CMSS1	0.167	2.69E-02
P78316	Nucleolar protein 14	0.167	3.53E-02
P09429	High mobility group protein B1	0.163	2.49E-02
O14593	DNA-binding protein RFXANK	0.162	2.44E-02
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	0.162	2.47E-02
P31350-1	ribonucleoside-diphosphate reductase subunit M2	0.160	2.52E-02
A6NNZ2	Tubulin beta-8 chain-like protein LOC260334	0.153	2.03E-02
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	0.153	2.03E-02
P20929	Nebulin	0.150	1.91E-02
Q52LJ0-2	Isoform 2 of Protein FAM98B	0.150	1.91E-02
P26373-1	60S ribosomal protein L13	0.146	1.76E-02
P82673-1	28S ribosomal protein S35, mitochondrial	0.146	2.93E-02
Q16850-1	lanosterol 14-alpha demethylase	0.145	4.93E-02
Q9Y320	Thioredoxin-related transmembrane protein 2	0.139	4.31E-02
P04264	Keratin, type II cytoskeletal 1	0.136	1.36E-02
P02768-1	Serum albumin	0.130	1.15E-02
P62633-2	Isoform 2 of Cellular nucleic acid-binding protein	0.130	1.17E-02
Q9BXR0	Queuine tRNA-ribosyltransferase catalytic subunit 1	0.129	1.12E-02
Q96S44	TP53-regulating kinase	0.127	3.41E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P16989-1	Y-box-binding protein 3	0.126	1.06E-02
P53350	Serine/threonine-protein kinase PLK1	0.126	1.96E-02
O95470	sphingosine-1-phosphate lyase 1	0.124	1.38E-02
P01023	alpha-2-macroglobulin	0.122	1.31E-02
Q9Y520	Protein Prrc2c	0.121	8.93E-03
Q9GZV5	WW domain-containing transcription regulator protein 1	0.121	4.25E-02
P01584	Interleukin-1 beta	0.120	2.61E-02
Q9NQW6	Anillin	0.119	9.91E-03
P53803	DNA-directed RNA polymerases I, II, and III subunit RPABC4	0.118	1.10E-02
P07919	Cytochrome b-c1 complex subunit 6, mitochondrial	0.117	8.07E-03
Q14011	Cold-inducible RNA-binding protein	0.114	7.14E-03
O15287	Fanconi anemia group G protein	0.112	6.75E-03
Q9UM00-1	Calcium load-activated calcium channel	0.110	6.41E-03
Q9BRP8	Partner of Y14 and mago	0.109	9.45E-03
O43852-4	Isoform 4 of Calumenin	0.109	1.06E-02
Q8TCZ2	CD99 antigen-like protein 2	0.103	3.57E-02
O95267-1	RAS guanyl-releasing protein 1	0.103	4.95E-02
P13645	Keratin, type I cytoskeletal 10	0.102	4.71E-03
Q9Y3B4	Splicing factor 3B subunit 6	0.100	4.45E-03
P02545-2	Isoform C of Prelamin-A/C	0.100	5.08E-03
Q13224	Glutamate receptor ionotropic, NMDA 2B	0.100	3.28E-02
Q96I76	G patch domain-containing protein 3	0.098	4.08E-03
P15407	Fos-related antigen 1	0.097	4.68E-03
Q9H3U5	major facilitator superfamily domain-containing protein 1	0.097	4.63E-02
Q8NBJ4	Golgi membrane protein 1	0.096	2.37E-02
Q7Z7N9	Transmembrane protein 179B	0.092	2.05E-02
P53985	Monocarboxylate transporter 1	0.091	2.00E-02
P06280	alpha-galactosidase A	0.091	4.01E-02
Q9P2X0-1	Dolichol-phosphate mannosyltransferase subunit 3	0.088	1.87E-02
O60783	28S ribosomal protein S14, mitochondrial	0.086	1.22E-02
P47914	60S ribosomal protein L29	0.084	2.10E-03
P80723	Brain acid soluble protein 1	0.084	2.14E-03
P61513	60S ribosomal protein L37a	0.083	2.05E-03
Q96SB4-3	Isoform 1 of SRSF protein kinase 1	0.083	4.05E-03
O00399	Dynactin subunit 6	0.083	1.77E-02
Q99442	translocation protein sec62	0.083	3.47E-02

Continued on next page

accession	description	fold p change	adjusted p-value
O60814	Histone H2B type 1-K	0.081	1.89E-03
Q9H9H4	Vacuolar protein sorting-associated protein 37B	0.081	1.61E-02
Q9BTX1	Nucleoporin Ndc1	0.081	2.05E-02
Q8TCA0-1	Leucine-rich repeat-containing protein 20	0.080	1.22E-02
Q96MU7-1	YTH domain-containing protein 1	0.079	8.61E-03
P48167	Glycine receptor subunit beta	0.078	2.52E-03
Q8NAF0	Zinc finger protein 579	0.077	3.60E-02
Q7Z4V5	Hepatoma-derived growth factor-related protein 2	0.076	4.75E-03
P52926-1	high mobility group protein HMGI-C	0.076	7.59E-03
Q00613	heat shock factor protein 1	0.076	8.79E-03
Q6ZSZ5	Rho guanine nucleotide exchange factor 18	0.076	1.67E-02
O95415	Brain protein I3	0.075	2.05E-02
Q9H0W8	protein SMG9	0.074	7.29E-03
Q7Z3K3-1	Pogo transposable element with ZNF domain	0.071	2.65E-02
Q96L92	Sorting nexin-27	0.069	5.72E-03
P17096-2	Isoform HMG-Y of High mobility group protein HMG-I/HMG-Y	0.067	5.09E-03
P25325	3-mercaptopyruvate sulfurtransferase	0.066	2.94E-02
Q9C0F1-1	centrosomal protein of 44 kDa	0.064	2.35E-03
Q9Y6I9	Testis-expressed protein 264	0.064	3.96E-03
Q86VQ1	Glucocorticoid-induced transcript 1 protein	0.064	8.01E-03
Q96L96	Alpha-protein kinase 3	0.063	2.03E-02
P02788	Lactotransferrin	0.062	1.66E-03
Q9BRP1	Programmed cell death protein 2-like	0.062	1.53E-02
O75410-1	Transforming acidic coiled-coil-containing protein 1	0.059	7.61E-04
Q8WZ82	Esterase OVCA2	0.058	5.06E-04
P14174	Macrophage Migration inhibitory factor	0.056	3.50E-04
P28062-1	Proteasome subunit beta type-8	0.056	1.36E-02
Q9BQ61	Uncharacterized protein C19orf43	0.056	1.38E-02
Q5JVS0	Intracellular hyaluronan-binding protein 4	0.055	2.03E-02
Q96NW7-1	Leucine-rich repeat-containing protein 7	0.055	2.12E-02
O94903	Pyridoxal phosphate homeostasis protein	0.054	8.34E-03
P55199	RNA polymerase II elongation factor ELL	0.054	1.99E-02
Q9NUP9	Protein lin-7 homolog C	0.053	4.64E-04
Q6FIF0	AN1-type zinc finger protein 6	0.052	6.65E-03
Q8WUM9	Sodium-dependent phosphate transporter 1	0.048	2.68E-03
Q9P0P0	E3 ubiquitin-protein ligase RNF181	0.048	6.03E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q96SZ5	2-aminoethanethiol dioxygenase	0.048	1.14E-02
Q9H4A3	Serine/threonine-protein kinase WNK1	0.047	1.09E-02
Q9H6Y5-1	PDZ domain-containing protein MAGIX	0.046	9.99E-03
Q6ZVM7	TOM1-like protein 2	0.045	2.15E-04
A6ND36-1	Protein FAM83G	0.045	5.14E-04
Q9H330	Transmembrane protein 245	0.044	3.42E-03
Q9NQ90-1	Anoctamin-2	0.042	3.92E-03
Q8WUW1	Protein BRICK1	0.041	4.16E-03
Q9Y608-4	Isoform 4 of Leucine-rich repeat flightless-interacting protein 2	0.041	1.08E-02
Q9H3H3	UPF0696 protein C11orf68	0.040	2.75E-03
O75976	Carboxypeptidase D	0.038	2.18E-04
P18827	syndecan-1	0.038	2.90E-04
O43164	E3 ubiquitin-protein ligase Praja-2	0.036	5.49E-03
P28799	Granulins	0.034	1.20E-03
Q8N257	Histone H2B type 3-B	0.034	3.49E-03
Q9BQE9-1	B-cell CLL/lymphoma 7 protein family member B	0.032	3.87E-04
P30414	NK-tumor recognition protein	0.031	1.32E-03
Q92785	Zinc finger protein ubi-d4	0.030	6.15E-04
P16220-1	Cyclic AMP-responsive element-binding protein 1	0.030	2.36E-03
P41236	Protein phosphatase inhibitor 2	0.029	1.42E-03
Q6PRD1	probable G-protein coupled receptor 179	0.028	3.95E-03
Q969E4	transcription elongation factor A protein-like 3	0.021	1.52E-03
Q86WX3	Active regulator of SIRT1	0.020	3.97E-04
Q93045	Stathmin-2	0.019	4.35E-04
Q96EI5	Transcription elongation factor A protein-like 4	0.019	7.05E-04
Q9ULK4	Mediator of RNA polymerase II transcription subunit 23	0.018	1.21E-04
Q15651-1	High mobility group nucleosome-binding domain-containing protein 3	0.017	8.05E-04
Q8WTX7	Cytosolic arginine sensor for mTORC1 subunit 1	0.016	2.77E-06
Q562R1	Beta-actin-like protein 2	0.013	6.26E-08
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	0.011	8.52E-05
Q9BXE9	Vomeronasal type-1 receptor 3	0.011	2.04E-04
P16403	Histone H1.2	0.010	4.08E-17
A8CG34-1	Nuclear envelope pore membrane protein POM 121C	0.010	4.08E-17
Q75N03	E3 ubiquitin-protein ligase Hakai	0.010	4.08E-17
Q8WUA7	TBC1 domain family member 22A	0.010	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O94842	TOX high mobility group box family member 4	0.010	4.08E-17
Q6GMV2	SET and MYND domain-containing protein 5	0.010	4.08E-17
Q8WW01	tRNA-splicing endonuclease subunit Sen15	0.010	4.08E-17
Q8NI22	Multiple coagulation factor deficiency protein 2	0.010	4.08E-17
Q8WUD4	Coiled-coil domain-containing protein 12	0.010	4.08E-17
P56181-2	Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	0.010	4.08E-17
O43924	Retinal rod rhodopsin-sensitive cGMP 3′,5′-cyclic phosphodiesterase subunit delta	0.010	4.08E-17
Q8NFP9-1	Neurobeachin	0.010	4.08E-17
Q70UQ0-4	Isoform 4 of Inhibitor of nuclear factor kappa-B kinase-interacting protein	0.010	4.08E-17
Q8NHV4	Protein NEDD1	0.010	4.08E-17
Q9NXV2	BTB/POZ domain-containing protein KCTD5	0.010	4.08E-17
Q16864-1	V-type proton ATPase subunit F	0.010	4.08E-17
Q9UQN3-1	Charged multivesicular body protein 2b	0.010	4.08E-17
Q9UHQ9	NADH-cytochrome b5 reductase 1	0.010	4.08E-17
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	0.010	4.08E-17
P17676	CCAAT/enhancer-binding protein beta	0.010	4.08E-17
Q99683	Mitogen-activated protein kinase kinase kinase 5	0.010	4.08E-17
Q8IZ21-1	Phosphatase and actin regulator 4	0.010	4.08E-17
O43663-1	Protein regulator of cytokinesis 1	0.010	4.08E-17
Q15004-1	PCNA-associated factor	0.010	4.08E-17
Q16643	drebrin	0.010	4.08E-17
O94992	Protein HEXIM1	0.010	4.08E-17
O95166	Gamma-aminobutyric acid receptor-associated protein	0.010	4.08E-17
O60885-1	Bromodomain-containing protein 4	0.010	4.08E-17
Q9BTE6-1	Alanyl-tRNA editing protein Aarsd1	0.010	4.08E-17
Q8N4L2	Type 2 phosphatidylinositol 4,5-bisphosphate 4-phosphatase	0.010	4.08E-17
Q8N4Q1	Mitochondrial intermembrane space import and assembly protein 40	0.010	4.08E-17
O60333	Kinesin-like protein KIF1B	0.010	4.08E-17
Q9HC52	chromobox protein homolog 8	0.010	4.08E-17
Q8IWE5	pleckstrin homology domain-containing family M member 2	0.010	4.08E-17
Q96L93-1	Kinesin-like protein KIF16B	0.010	4.08E-17
P32519-1	ETS-related transcription factor Elf-1	0.010	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96JY6-1	PDZ and LIM domain protein 2	0.010	4.08E-17
Q8N8S7	Protein enabled homolog	0.010	4.08E-17
P61970	nuclear transport factor 2	0.010	4.08E-17
P50579	methionine aminopeptidase 2	0.010	4.08E-17
O75152	Zinc finger CCCH domain-containing protein 11A	0.010	4.08E-17
Q96JP5-1	E3 ubiquitin-protein ligase ZFP91	0.010	4.08E-17
Q8NFJ5	Retinoic acid-induced protein 3	0.010	4.08E-17
Q9BT09	Protein canopy homolog 3	0.010	4.08E-17
Q96IZ0	PRKC apoptosis WT1 regulator protein	0.010	4.08E-17
O75586	Mediator of RNA polymerase II transcription subunit 6	0.010	4.08E-17
P02795	metallothionein-2	0.010	4.08E-17
Q9P1Y6-1	PHD and RING finger domain-containing protein 1	0.010	4.08E-17
P29323	Ephrin type-B receptor 2	0.010	4.08E-17
P13647	keratin, type II cytoskeletal 5	0.010	4.08E-17
Q6QNY1	biogenesis of lysosome-related organelles complex 1 subunit 2	0.010	4.08E-17
Q9UDY8	Mucosa-associated lymphoid tissue lymphoma translocation protein 1	0.010	4.08E-17
O60936-3	Isoform 3 of Nucleolar protein 3	0.010	4.08E-17
O43768	alpha-endosulfine	0.010	4.08E-17
Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	0.010	4.08E-17
Q9NSI2-1	protein FAM207A	0.010	4.08E-17
Q6PK04	Coiled-coil domain-containing protein 137	0.010	4.08E-17
Q9NVC6	mediator of RNA polymerase II transcription subunit 17	0.010	4.08E-17
Q12802-1	A-kinase anchor protein 13	0.010	4.08E-17
O95163	Elongator complex protein 1	0.010	4.08E-17
P48509	CD151 antigen	0.010	4.08E-17
O00461	Golgi integral membrane protein 4	0.010	4.08E-17
Q14671-1	Pumilio homolog 1	0.010	4.08E-17
Q96GA7	serine dehydratase-like	0.010	4.08E-17
O15027-1	Protein transport protein Sec16A	0.010	4.08E-17
Q01085-2	Isoform 2 of Nucleolysin TIAR	0.010	4.08E-17
Q92536	Y+L amino acid transporter 2	0.010	4.08E-17
Q9Y5A9-1	YTH domain-containing family protein 2	0.010	4.08E-17
Q6NXT1-1	Ankyrin repeat domain-containing protein 54	0.010	4.08E-17
Q9BRX2	Protein pelota homolog	0.010	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P04920-1	Anion exchange protein 2	0.010	4.08E-17
P43308	Translocon-associated protein subunit beta	0.010	4.08E-17
P63272	Transcription elongation factor Spt4	0.010	4.08E-17
Q99747	Gamma-soluble NSF attachment protein	0.010	4.08E-17
Q9ULX6	A-kinase anchor protein 8-like	0.010	4.08E-17
P02533	Keratin, type I cytoskeletal 14	0.010	4.08E-17
Q969E2-1	Secretory carrier-associated membrane protein 4	0.010	4.08E-17
P40189-1	Interleukin-6 receptor subunit beta	0.010	4.08E-17
P46939	Utrophin	0.010	4.08E-17
Q86YZ3	Hornerin	0.010	4.08E-17
Q96BZ8	leukocyte receptor cluster member 1	0.010	4.08E-17
Q8IXQ3	Uncharacterized protein C9orf40	0.010	4.08E-17
Q9Y4Y9	U6 snRNA-associated Sm-like protein LSm5	0.010	4.08E-17
A6NFE2	Single-pass membrane and coiled-coil domain-containing protein 2	0.010	4.08E-17
O14618	copper chaperone for superoxide dismutase	0.010	4.08E-17
P62987	Ubiquitin-60S ribosomal protein L40	0.010	4.08E-17
P60002	Transcription elongation factor 1 homolog	0.010	4.08E-17
Q15334	Lethal(2) giant larvae protein homolog 1	0.010	4.08E-17
P09493-5	Isoform 5 of Tropomyosin alpha-1 chain	0.010	4.08E-17
Q8ND04	Protein SMG8	0.010	4.08E-17
O95456	Proteasome assembly chaperone 1	0.010	4.08E-17
P20248	Cyclin-A2	0.010	4.08E-17
P0DN86	Choriogonadotropin subunit beta 3	0.010	4.08E-17
Q12769	nuclear pore complex protein Nup160	0.010	4.08E-17
P36954	DNA-directed RNA polymerase II subunit RPB9	0.010	4.08E-17
O14562	Ubiquitin domain-containing protein UBFD1	0.010	4.08E-17
Q5JTY5	COBW domain-containing protein 3	0.010	4.08E-17
Q7LG56-1	Ribonucleoside-diphosphate reductase subunit M2 B	0.010	4.08E-17
Q1ED39	Lysine-rich nucleolar protein 1	0.010	4.08E-17
Q96ME7	Zinc finger protein 512	0.010	4.08E-17
Q9P1U0	DNA-directed RNA polymerase I subunit RPA12	0.010	4.08E-17
Q99958	forkhead box protein C2	0.010	4.08E-17
Q9UIS9-1	Methyl-CpG-binding domain protein 1	0.010	4.08E-17
Q71UM5	40S ribosomal protein S27-like	0.010	4.08E-17
Q96G21	U3 small nucleolar ribonucleoprotein protein IMP4	0.010	4.08E-17
Q96E11	Ribosome-recycling factor, mitochondrial	0.010	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P05114	Non-histone chromosomal protein HMG-14	0.010	4.08E-17
Q14573	Inositol 1,4,5-trisphosphate receptor type 3	0.010	4.08E-17
Q8NC51-3	Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein	0.010	4.08E-17
O00592	Podocalyxin	0.010	4.08E-17
P37173-1	TGF-beta receptor type-2	0.010	4.08E-17
Q9Y673	dolichyl-phosphate beta-glucosyltransferase	0.010	4.08E-17
P29692-4	Isoform 4 of Elongation factor 1-delta	0.010	4.08E-17
P04259	keratin, type II cytoskeletal 6B	0.010	4.08E-17
Q6ZSR9	Uncharacterized protein FLJ45252	0.010	4.08E-17
Q13371	Phosducin-like protein	0.010	4.08E-17
Q9Y3D8	Adenylate kinase isoenzyme 6	0.010	4.08E-17
P05204	Non-histone chromosomal protein HMG-17	0.010	4.08E-17
P05423	DNA-directed RNA polymerase III subunit RPC4	0.010	4.08E-17
Q9NVV4-2	Isoform 2 of Poly(A) RNA polymerase, mitochondrial	0.010	4.08E-17
Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	0.010	4.08E-17
Q92733	proline-rich protein PRCC	0.010	4.08E-17
Q96LA6	Fc receptor-like protein 1	0.010	4.08E-17
O95707	Ribonuclease P protein subunit p29	0.010	4.08E-17
Q63HR2-4	Isoform 4 of Tensin-2	0.010	4.08E-17
O95759-1	TBC1 domain family member 8	0.010	4.08E-17
Q6P4E1	Protein CASC4	0.010	4.08E-17
Q6SPF0	Atherin	0.010	4.08E-17
Q9BYN7-1	zinc finger protein 341	0.010	4.08E-17
Q4VX76-1	Synaptotagmin-like protein 3	0.010	4.08E-17
Q6PIJ6-1	F-box only protein 38	0.010	4.08E-17
Q92833	Protein Jumonji	0.010	4.08E-17
Q8N5G2-1	macoilin	0.010	4.08E-17
Q9P013	spliceosome-associated protein CWC15 homolog	0.010	4.08E-17
P24530-3	Isoform C of Endothelin receptor type B	0.010	4.08E-17
Q8TD19	Serine/threonine-protein kinase Nek9	0.010	4.08E-17
Q08AD1	Calmodulin-regulated spectrin-associated protein 2	0.010	4.08E-17
Q04656-3	Isoform 2 of Copper-transporting ATPase 1	0.010	4.08E-17
Q96D96-1	voltage-gated hydrogen channel 1	0.010	4.08E-17
P09455-1	Retinol-binding protein 1	0.010	4.08E-17
Q16740	ATP-dependent Clp protease proteolytic subunit, mitochondrial	0.010	4.08E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O95147	Dual specificity protein phosphatase 14	0.010	4.08E-17
Q14934-1	Nuclear factor of activated T-cells, cytoplasmic 4	0.010	4.08E-17
P51826	AF4/FMR2 family member 3	0.010	4.08E-17
Q9Y2S6	Translation machinery-associated protein 7	0.010	4.08E-17
P82909	28S ribosomal protein S36, mitochondrial	0.010	4.08E-17
Q96AT1	Uncharacterized protein KIAA1143	0.010	4.08E-17
Q96EY5-1	Multivesicular body subunit 12A	0.010	4.08E-17
Q9Y625	Glypican-6	0.010	4.08E-17
Q9H147	Deoxynucleotidyltransferase terminal-interacting protein 1	0.010	4.08E-17
Q8TCC3	39S ribosomal protein L30, mitochondrial	0.010	4.08E-17
Q96G25	mediator of RNA polymerase II transcription subunit 8	0.010	4.08E-17
Q96GN5-1	cell division cycle-associated 7-like protein	0.010	4.08E-17
Q9BPZ3	Polyadenylate-binding protein-interacting protein 2	0.010	4.08E-17
Q12967	Ral guanine nucleotide dissociation stimulator	0.010	4.08E-17
Q9NYI0-1	PH and SEC7 domain-containing protein 3	0.010	4.08E-17
Q6DD87	Zinc finger protein 787	0.010	4.08E-17
Q6MZT1	Regulator of G-protein signaling 7-binding protein	0.010	4.08E-17
P33552	cyclin-dependent kinases regulatory subunit 2	0.010	4.08E-17
Q92844	TRAF family member-associated NF-kappa-B activator	0.010	4.08E-17
Q9NRF2	SH2B adapter protein 1	0.010	4.08E-17
Q9H814	Phosphorylated adapter RNA export protein	0.010	4.08E-17
Q6ZMI0-1	Protein phosphatase 1 regulatory subunit 21	0.010	4.08E-17
Q8NH73	Olfactory receptor 4S2	0.010	4.08E-17
Q86YF9	Zinc finger protein DZIP1	0.010	4.08E-17
Q32M45-1	Anoctamin-4	0.010	4.08E-17
B2RTY4	unconventional myosin-IXa	0.010	4.08E-17
Q07864	DNA polymerase epsilon catalytic subunit A	0.010	4.08E-17
B5MCY1	Tudor domain-containing protein 15	0.010	4.08E-17
Q96Q83-1	alpha-ketoglutarate-dependent dioxygenase alkB homolog 3	0.010	4.08E-17
Q8IY18	structural maintenance of chromosomes protein 5	0.010	4.08E-17
P0C880	Putative uncharacterized protein FLJ40606	0.010	4.08E-17
Q86VL8-1	Multidrug and toxin extrusion protein 2	0.010	4.08E-17
End of Table			

V HL60 Pateamine A Genes

accession	description	fold p change	adjusted p-value
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	100.0	5.37E-17
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	100.0	5.37E-17
Q969G6	Riboflavin kinase	100.0	5.37E-17
P22033	Methylmalonyl-CoA mutase, mitochondrial	100.0	5.37E-17
Q9Y2X0-1	Mediator of RNA polymerase II transcription subunit 16	100.0	5.37E-17
Q9BYJ9-1	YTH domain-containing family protein 1	100.0	5.37E-17
Q9BQP7	mitochondrial genome maintenance exonuclease 1	100.0	5.37E-17
Q9Y6K0	Choline/ethanolaminephosphotransferase 1	100.0	5.37E-17
Q15070-1	Mitochondrial inner membrane protein OXA1L	100.0	5.37E-17
P86790	Vacuolar fusion protein CCZ1 homolog B	100.0	5.37E-17
Q9NZJ9-1	Diphosphoinositol polyphosphate phosphohydrolase 2	100.0	5.37E-17
Q14154	Death ligand signal enhancer	100.0	5.37E-17
Q96CB9	5-methylcytosine rRNA methyltransferase NSUN4	100.0	5.37E-17
Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinase	100.0	5.37E-17
P33527	Multidrug resistance-associated protein 1	100.0	5.37E-17
P62256	ubiquitin-conjugating enzyme E2 H	100.0	5.37E-17
B1ANS9	WD repeat-containing protein 64	100.0	5.37E-17
A8TX70-1	Collagen alpha-5(VI) chain	100.0	5.37E-17
Q9Y2K6	ubiquitin carboxyl-terminal hydrolase 20	100.0	5.37E-17
P48200	iron-responsive element-binding protein 2	100.0	5.37E-17
O75995	SAM and SH3 domain-containing protein 3	100.0	5.37E-17
O60506-3	Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q	100.0	5.37E-17
P54707-1	Potassium-transporting ATPase alpha chain 2	100.0	5.37E-17
P16402	Histone H1.3	100.0	5.37E-17
P19793	retinoic acid receptor RXR-alpha	100.0	5.37E-17
P40818	ubiquitin carboxyl-terminal hydrolase 8	100.0	5.37E-17
O60603	toll-like receptor 2	100.0	5.37E-17
P30273	High affinity immunoglobulin epsilon receptor subunit gamma	100.0	5.37E-17
P42785-1	lysosomal Pro-X carboxypeptidase	100.0	5.37E-17
Q9UKZ1	CCR4-NOT transcription complex subunit 11	100.0	5.37E-17
Q9H8G2-1	Caspase activity and apoptosis inhibitor 1	100.0	5.37E-17
Q8WUR7	UPF0235 protein C15orf40	100.0	5.37E-17
Q99470	Stromal cell-derived factor 2	100.0	5.37E-17
Q96HR3	Mediator of RNA polymerase II transcription subunit 30	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9HAD4-2	Isoform 2 of WD repeat-containing protein 41	100.0	5.37E-17
Q9Y3P9	Rab GTPase-activating protein 1	100.0	5.37E-17
Q8IXU6-1	Solute carrier family 35 member f2	100.0	5.37E-17
O43924	Retinal rod rhodopsin-sensitive cGMP 3′,5′-cyclic phosphodiesterase subunit delta	100.0	5.37E-17
Q96GY3	Protein lin-37 homolog	100.0	5.37E-17
Q9UBF8	Phosphatidylinositol 4-kinase beta	100.0	5.37E-17
Q96PE7	Methylmalonyl-CoA epimerase, mitochondrial	100.0	5.37E-17
Q68CQ7-1	Glycosyltransferase 8 domain-containing protein 1	100.0	5.37E-17
Q9BTZ2	dehydrogenase/reductase sdr family member 4	100.0	5.37E-17
P06756	Integrin alpha-V	100.0	5.37E-17
Q9P0U4	CXXC-type zinc finger protein 1	100.0	5.37E-17
Q7Z6V5-1	tRNA-specific adenosine deaminase 2	100.0	5.37E-17
P07902	Galactose-1-phosphate uridylyltransferase	100.0	5.37E-17
Q5T1A1-1	DC-STAMP domain-containing protein 2	100.0	5.37E-17
Q92625	Ankyrin repeat and SAM domain-containing protein 1A	100.0	5.37E-17
Q6UXV4	MICOS complex subunit MIC27	100.0	5.37E-17
Q8N4C6	ninein	100.0	5.37E-17
O95785	Protein Wiz	100.0	5.37E-17
O15320	Endoplasmic reticulum export factor CTAGE5	100.0	5.37E-17
Q9BSH4	Translational activator of cytochrome c oxidase 1	100.0	5.37E-17
Q9UDW1	cytochrome b-c1 complex subunit 9	100.0	5.37E-17
Q9H061-1	Transmembrane protein 126A	100.0	5.37E-17
Q9NUM4	Transmembrane protein 106B	100.0	5.37E-17
Q9BYV8	centrosomal protein of 41 kDa	100.0	5.37E-17
Q86W28	NACHT, LRR and PYD domains-containing protein 8	100.0	5.37E-17
Q9HBM1	Kinetochore protein Spc25	100.0	5.37E-17
Q9NSC5-1	homer protein homolog 3	100.0	5.37E-17
Q9ULF5	Zinc transporter ZIP10	100.0	5.37E-17
Q9Y2P5	Bile acyl-CoA synthetase	100.0	5.37E-17
Q8N4J0	carnosine N-methyltransferase	100.0	5.37E-17
P17544	Cyclic AMP-dependent transcription factor ATF-7	100.0	5.37E-17
P58335-1	Anthrax toxin receptor 2	100.0	5.37E-17
Q9H6W3	ribosomal oxygenase 1	100.0	5.37E-17
P49137	MAP kinase-activated protein kinase 2	100.0	5.37E-17
P32121	Beta-arrestin-2	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
C9JVW0	putative transmembrane protein INAFM1	100.0	5.37E-17
Q9NPQ8	Synembryn-A	100.0	5.37E-17
Q96RT7	gamma-tubulin complex component 6	100.0	5.37E-17
P42356	phosphatidylinositol 4-kinase alpha	100.0	5.37E-17
Q5J8M3-1	ER membrane protein complex subunit 4	100.0	5.37E-17
Q9BXY5-1	Calcyphosin-2	100.0	5.37E-17
O43663-1	Protein regulator of cytokinesis 1	100.0	5.37E-17
Q13322-1	Growth factor receptor-bound protein 10	100.0	5.37E-17
O75828	Carbonyl reductase [NADPH] 3	100.0	5.37E-17
A0A0U1RRE5	negative regulator of P-body association	100.0	5.37E-17
Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta	100.0	5.37E-17
P06746	DNA polymerase beta	100.0	5.37E-17
Q99996	A-kinase anchor protein 9	100.0	5.37E-17
Q7KYR7	Butyrophilin subfamily 2 member A1	100.0	5.37E-17
Q7L1V2	Vacuolar fusion protein MON1 homolog B	100.0	5.37E-17
P53611	Geranylgeranyl transferase type-2 subunit beta	100.0	5.37E-17
Q9Y547	Intraflagellar transport protein 25 homolog	100.0	5.37E-17
Q03426	mevalonate kinase	100.0	5.37E-17
Q9NSU2-1	Three-prime repair exonuclease 1	100.0	5.37E-17
Q4KMP7	TBC1 domain family member 10B	100.0	5.37E-17
Q9H3K2	Growth hormone-inducible transmembrane protein	100.0	5.37E-17
Q9BVV7	Mitochondrial import inner membrane translocase subunit TIM21	100.0	5.37E-17
Q9NWS8	Required for meiotic nuclear division protein 1 homolog	100.0	5.37E-17
P12235	ADP/ATP translocase 1	100.0	5.37E-17
Q9UQ90	Paraplegin	100.0	5.37E-17
Q12894	Interferon-related developmental regulator 2	100.0	5.37E-17
P31269	Homeobox protein Hox-A9	100.0	5.37E-17
Q96GS4	BLOC-1-related complex subunit 6	100.0	5.37E-17
Q5VZM2	Ras-related GTP-binding protein B	100.0	5.37E-17
Q5T447	E3 ubiquitin-protein ligase HECTD3	100.0	5.37E-17
O14880	Microsomal glutathione S-transferase 3	100.0	5.37E-17
P02686-1	myelin basic protein	100.0	5.37E-17
O14521	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial	100.0	5.37E-17
Q13094	lymphocyte cytosolic protein 2	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O75398	Deformed epidermal autoregulatory factor 1 homolog	100.0	5.37E-17
Q9HCU9	Breast cancer metastasis-suppressor 1	100.0	5.37E-17
Q6N069	N-alpha-acetyltransferase 16, NatA auxiliary subunit	100.0	5.37E-17
Q7Z401-1	C-myc promoter-binding protein	100.0	5.37E-17
Q9H477	ribokinase	100.0	5.37E-17
Q96PM5-1	RING finger and CHY zinc finger domain-containing protein 1	100.0	5.37E-17
P02730	Band 3 anion transport protein	100.0	5.37E-17
Q9NRY4	Rho GTPase-activating protein 35	100.0	5.37E-17
Q9H079	KATNB1-like protein 1	100.0	5.37E-17
Q9H074	Polyadenylate-binding protein-interacting protein 1	100.0	5.37E-17
O75420	GRB10-interacting GYF protein 1	100.0	5.37E-17
Q86U06-1	probable RNA-binding protein 23	100.0	5.37E-17
Q86YH6-1	Decaprenyl-diphosphate synthase subunit 2	100.0	5.37E-17
Q8N5M1	ATP synthase mitochondrial F1 complex assembly factor 2	100.0	5.37E-17
Q7Z591	AT-hook-containing transcription factor	100.0	5.37E-17
Q96Q89-1	Kinesin-like protein KIF20B	100.0	5.37E-17
O95248-1	Myotubularin-related protein 5	100.0	5.37E-17
Q16650	T-box brain protein 1	100.0	5.37E-17
Q02241-1	Kinesin-like protein KIF23	100.0	5.37E-17
P49795	Regulator of G-protein signaling 19	100.0	5.37E-17
Q9H0X9	Oxysterol-binding protein-related protein 5	100.0	5.37E-17
Q96AA3	Protein RFT1 homolog	100.0	5.37E-17
Q9H0E2	Toll-interacting protein	100.0	5.37E-17
Q8NDH3	Probable aminopeptidase NPEPL1	100.0	5.37E-17
Q12933	TNF receptor-associated factor 2	100.0	5.37E-17
Q9Y282-1	Endoplasmic reticulum-Golgi intermediate compartment protein 3	100.0	5.37E-17
Q96RD7-1	Pannexin-1	100.0	5.37E-17
Q8WZA6	Olfactory receptor 1E3	100.0	5.37E-17
Q15018	BRISC complex subunit Abraxas 2	100.0	5.37E-17
Q9BZH6	WD repeat-containing protein 11	100.0	5.37E-17
Q8IVS2	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	100.0	5.37E-17
Q8IVH4	methylmalonic aciduria type A protein, mitochondrial	100.0	5.37E-17
O15117-1	FYN-binding protein 1	100.0	5.37E-17
P27361-1	mitogen-activated protein kinase 3	100.0	5.37E-17
O75122	CLIP-associating protein 2	100.0	5.37E-17
Q9C0K1-1	Zinc transporter zip8	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q92932	Receptor-type tyrosine-protein phosphatase N2	100.0	5.37E-17
Q9NYL2-2	Isoform 2 of Mitogen-activated protein kinase kinase kinase 20	100.0	5.37E-17
Q7L1T6	Cytochrome b5 reductase 4	100.0	5.37E-17
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1	100.0	5.37E-17
Q9UBW5-1	Bridging integrator 2	100.0	5.37E-17
Q8TB52	F-box only protein 30	100.0	5.37E-17
Q8TD26	Chromodomain-helicase-DNA-binding protein 6	100.0	5.37E-17
Q92597	Protein NDRG1	100.0	5.37E-17
Q8TBP6	Solute carrier family 25 member 40	100.0	5.37E-17
Q8IUF8	ribosomal oxygenase 2	100.0	5.37E-17
O95685	Protein phosphatase 1 regulatory subunit 3D	100.0	5.37E-17
Q9UL16	Cilia- and flagella-associated protein 45	100.0	5.37E-17
P20962	Parathymosin	100.0	5.37E-17
Q9BT23	LIM domain-containing protein 2	100.0	5.37E-17
Q8WUH2	Transforming growth factor-beta receptor-associated protein 1	100.0	5.37E-17
Q15831-1	Serine/threonine-protein kinase STK11	100.0	5.37E-17
Q9H3S4	Thiamin pyrophosphokinase 1	100.0	5.37E-17
Q12982	BCL2/adenovirus E1B 19 kDa protein-interacting protein 2	100.0	5.37E-17
Q9BSL1	ubiquitin-associated domain-containing protein 1	100.0	5.37E-17
A6NC98	Coiled-coil domain-containing protein 88B	100.0	5.37E-17
Q9UNY4-1	transcription termination factor 2	100.0	5.37E-17
Q9BVC3	sister chromatid cohesion protein dcc1	100.0	5.37E-17
Q15208	serine/threonine-protein kinase 38	100.0	5.37E-17
Q9BW83-1	Intraflagellar transport protein 27 homolog	100.0	5.37E-17
Q92610	Zinc finger protein 592	100.0	5.37E-17
Q8NEC7-1	Glutathione S-transferase C-terminal domain-containing protein	100.0	5.37E-17
Q9UEG4	zinc finger protein 629	100.0	5.37E-17
Q9UGN4-1	CMRF35-like molecule 8	100.0	5.37E-17
Q9P260-1	LisH domain and HEAT repeat-containing protein KIAA1468	100.0	5.37E-17
Q8IYB5	Stromal membrane-associated protein 1	100.0	5.37E-17
O15258	Protein RER1	100.0	5.37E-17
P04424	argininosuccinate lyase	100.0	5.37E-17
O75915	PRA1 family protein 3	100.0	5.37E-17
Q86SQ7-4	Isoform 4 of Serologically defined colon cancer antigen 8	100.0	5.37E-17
Q9UN19-1	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O94822	E3 ubiquitin-protein ligase listerin	100.0	5.37E-17
Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats	100.0	5.37E-17
Q9Y2Y0	ADP-ribosylation factor-like protein 2-binding protein	100.0	5.37E-17
Q49B96	Cytochrome c oxidase assembly protein COX19	100.0	5.37E-17
Q6QNY1	biogenesis of lysosome-related organelles complex 1 subunit 2	100.0	5.37E-17
Q5T2S8	Armadillo repeat-containing protein 4	100.0	5.37E-17
Q96DE5	Anaphase-promoting complex subunit 16	100.0	5.37E-17
P52758	2-iminobutanoate/2-iminopropanoate deaminase	100.0	5.37E-17
Q9UBK9	protein UXT	100.0	5.37E-17
Q9NZN8-1	CCR4-NOT transcription complex subunit 2	100.0	5.37E-17
Q13485	Mothers against decapentaplegic homolog 4	100.0	5.37E-17
Q9UNZ5	Leydig cell tumor 10 kDa protein homolog	100.0	5.37E-17
P00846	ATP synthase subunit A	100.0	5.37E-17
P52655-1	Transcription initiation factor IIA subunit 1	100.0	5.37E-17
Q8NDZ4	Deleted in autism protein 1	100.0	5.37E-17
P61165	transmembrane protein 258	100.0	5.37E-17
Q96HW7	integrator complex subunit 4	100.0	5.37E-17
P82970	High mobility group nucleosome-binding domain-containing protein 5	100.0	5.37E-17
A5D8V6	Vacuolar protein sorting-associated protein 37C	100.0	5.37E-17
P20585	DNA mismatch repair protein MSH3	100.0	5.37E-17
P61925	cAMP-dependent protein kinase inhibitor alpha	100.0	5.37E-17
Q8NEM7	transcription factor SPT20 homolog	100.0	5.37E-17
Q9NRM7	Serine/threonine-protein kinase LATS2	100.0	5.37E-17
O96006	zinc finger BED domain-containing protein 1	100.0	5.37E-17
P09132-1	Signal recognition particle 19 kDa protein	100.0	5.37E-17
P78332	RNA-binding protein 6	100.0	5.37E-17
Q9NZE8	39S ribosomal protein L35, mitochondrial	100.0	5.37E-17
P17275	transcription factor jun-B	100.0	5.37E-17
Q9Y2K7	Lysine-specific demethylase 2A	100.0	5.37E-17
Q86TN4	tRNA 2′-phosphotransferase 1	100.0	5.37E-17
P46019	Phosphorylase b kinase regulatory subunit alpha, liver isoform	100.0	5.37E-17
Q92783	signal transducing adapter molecule 1	100.0	5.37E-17
Q15072	Zinc finger protein OZF	100.0	5.37E-17
Q96N46	Tetratricopeptide repeat protein 14	100.0	5.37E-17
P35555	Fibrillin-1	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P56378-1	6.8 kDa mitochondrial proteolipid	100.0	5.37E-17
Q14186	Transcription factor Dp-1	100.0	5.37E-17
Q9UJX5	Anaphase-promoting complex subunit 4	100.0	5.37E-17
P82912-1	28S ribosomal protein S11, mitochondrial	100.0	5.37E-17
Q9BSW2-1	EF-hand calcium-binding domain-containing protein 4B	100.0	5.37E-17
Q8IXK0	Polyhomeotic-like protein 2	100.0	5.37E-17
Q9BPU6	Dihydropyrimidinase-related protein 5	100.0	5.37E-17
O95219	sorting nexin-4	100.0	5.37E-17
Q49AR2-1	UPF0489 protein C5orf22	100.0	5.37E-17
P49450-1	Histone H3-like centromeric protein A	100.0	5.37E-17
Q9NW81	distal membrane-arm assembly complex protein 2	100.0	5.37E-17
P51810	G-protein coupled receptor 143	100.0	5.37E-17
P82251	B(0,+)-type amino acid transporter 1	100.0	5.37E-17
Q9UBM7	7-dehydrocholesterol reductase	100.0	5.37E-17
Q9NRW7	Vacuolar protein sorting-associated protein 45	100.0	5.37E-17
Q9H2I8	leucine-rich melanocyte differentiation-associated protein	100.0	5.37E-17
Q5SNV9	Uncharacterized protein C1orf167	100.0	5.37E-17
Q8IXS0	Protein FAM217A	100.0	5.37E-17
Q9Y4F3-1	Meiosis regulator and mRNA stability factor 1	100.0	5.37E-17
Q6PML9	zinc transporter 9	100.0	5.37E-17
Q9H446	rwd domain-containing protein 1	100.0	5.37E-17
Q06033-1	Inter-alpha-trypsin inhibitor heavy chain H3	100.0	5.37E-17
Q9NZ09-1	Ubiquitin-associated protein 1	100.0	5.37E-17
Q12768	WASH complex subunit 5	100.0	5.37E-17
P10153	Non-secretory ribonuclease	100.0	5.37E-17
Q9H0R1	AP-5 complex subunit mu-1	100.0	5.37E-17
P27448-7	Isoform 6 of MAP/microtubule affinity-regulating kinase 3	100.0	5.37E-17
Q6IN84-1	rRNA methyltransferase 1, mitochondrial	100.0	5.37E-17
Q9H6D7	HAUS augmin-like complex subunit 4	100.0	5.37E-17
Q9UNA4	DNA polymerase iota	100.0	5.37E-17
Q9BRU9	rRNA-processing protein UTP23 homolog	100.0	5.37E-17
P51798-1	H(+)/Cl(-) exchange transporter 7	100.0	5.37E-17
Q96E14	RecQ-mediated genome instability protein 2	100.0	5.37E-17
Q8TD16	Protein bicaudal D homolog 2	100.0	5.37E-17
P42167-2	Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O94788-1	retinal dehydrogenase 2	100.0	5.37E-17
Q5TC12-1	ATP synthase mitochondrial F1 complex assembly factor 1	100.0	5.37E-17
Q9Y2I6-1	Ninein-like protein	100.0	5.37E-17
Q6YHU6	Thyroid adenoma-associated protein	100.0	5.37E-17
P07951-1	Tropomyosin beta chain	100.0	5.37E-17
Q9BYB4-1	Guanine nucleotide-binding protein subunit beta-like protein 1	100.0	5.37E-17
Q15633	RISC-loading complex subunit TARBP2	100.0	5.37E-17
Q15797	mothers against decapentaplegic homolog 1	100.0	5.37E-17
Q9UM22	Mammalian ependymin-related protein 1	100.0	5.37E-17
P50570-4	Isoform 4 of Dynamin-2	100.0	5.37E-17
Q5TZA2	Rootletin	100.0	5.37E-17
Q86UK0	ATP-binding cassette sub-family A member 12	100.0	5.37E-17
Q96EK4	THAP domain-containing protein 11	100.0	5.37E-17
P0C870	JmjC domain-containing protein 7	100.0	5.37E-17
Q71F23	Centromere protein U	100.0	5.37E-17
Q6P1X6	UPF0598 protein C8orf82	100.0	5.37E-17
P21817	Ryanodine receptor 1	100.0	5.37E-17
Q8IUC8-1	Polypeptide N-acetylgalactosaminyltransferase 13	100.0	5.37E-17
Q9BZW8-1	Natural killer cell receptor 2B4	100.0	5.37E-17
Q9P0U3-1	Sentrin-specific protease 1	100.0	5.37E-17
Q15283-1	ras GTPase-activating protein 2	100.0	5.37E-17
Q9H4L4	Sentrin-specific protease 3	100.0	5.37E-17
Q9NUY8	TBC1 domain family member 23	100.0	5.37E-17
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	100.0	5.37E-17
Q99643	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	100.0	5.37E-17
Q9GZN2-1	homeobox protein TGIF2	100.0	5.37E-17
P35611-1	Alpha-adducin	100.0	5.37E-17
Q9P2K3-1	REST corepressor 3	100.0	5.37E-17
Q13395	Probable methyltransferase TARBP1	100.0	5.37E-17
O60518	ran-binding protein 6	100.0	5.37E-17
P82094	TATA element modulatory factor	100.0	5.37E-17
O95059	Ribonuclease P protein subunit p14	100.0	5.37E-17
Q96PE3-1	Type I inositol 3,4-bisphosphate 4-phosphatase	100.0	5.37E-17
Q92520	Protein FAM3C	100.0	5.37E-17
Q9GZQ3	COMM domain-containing protein 5	100.0	5.37E-17
Q8NER1	Transient receptor potential cation channel subfamily V member 1	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8N1B4	Vacuolar protein sorting-associated protein 52 homolog	100.0	5.37E-17
O75044	SLIT-ROBO Rho GTPase-activating protein 2	100.0	5.37E-17
Q7L5D6	Golgi to ER traffic protein 4 homolog	100.0	5.37E-17
O75676	Ribosomal protein S6 kinase alpha-4	100.0	5.37E-17
Q9H6E4	Coiled-coil domain-containing protein 134	100.0	5.37E-17
P03905	NADH-ubiquinone oxidoreductase chain 4	100.0	5.37E-17
Q9UBS0	Ribosomal protein S6 kinase beta-2	100.0	5.37E-17
Q96QU8	Exportin-6	100.0	5.37E-17
Q5RHP9	glutamate-rich protein 3	100.0	5.37E-17
Q86UY8	5′-nucleotidase domain-containing protein 3	100.0	5.37E-17
Q8NE63	homeodomain-interacting protein kinase 4	100.0	5.37E-17
O75592-1	E3 ubiquitin-protein ligase MYCBP2	100.0	5.37E-17
Q86Y07	serine/threonine-protein kinase VRK2	100.0	5.37E-17
Q6P3W7	SCY1-like protein 2	100.0	5.37E-17
Q16773	Kynurenine–oxoglutarate transaminase 1	100.0	5.37E-17
Q9H832	Ubiquitin-conjugating enzyme E2 Z	100.0	5.37E-17
P29083	General transcription factor IIE subunit 1	100.0	5.37E-17
P51610-1	Host cell factor 1	100.0	5.37E-17
Q96GX2	Ataxin-7-like protein 3B	100.0	5.37E-17
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2	100.0	5.37E-17
O14662-1	Syntaxin-16	100.0	5.37E-17
Q9NVH6-1	Trimethyllysine dioxygenase, mitochondrial	100.0	5.37E-17
O43379-4	Isoform 4 of WD repeat-containing protein 62	100.0	5.37E-17
P48723	Heat shock 70 kDa protein 13	100.0	5.37E-17
Q8TE02-1	elongator complex protein 5	100.0	5.37E-17
O15239	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	100.0	5.37E-17
Q7Z434	Mitochondrial antiviral-signaling protein	100.0	5.37E-17
Q7Z7A1	Centriolin	100.0	5.37E-17
Q99496	E3 ubiquitin-protein ligase RING2	100.0	5.37E-17
Q9BRR9	Rho GTPase-activating protein 9	100.0	5.37E-17
Q8NFW8	N-acylneuraminate cytidylyltransferase	100.0	5.37E-17
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	100.0	5.37E-17
Q9NSV4-1	Isoform 1 of Protein diaphanous homolog 3	100.0	5.37E-17
P24468	COUP transcription factor 2	100.0	5.37E-17
P11169	Solute carrier family 2, facilitated glucose transporter member 3	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q06330-1	Recombining binding protein suppressor of hairless	100.0	5.37E-17
Q86Y82	Syntaxin-12	100.0	5.37E-17
Q9H9B1	histone-lysine N-methyltransferase EHMT1	100.0	5.37E-17
Q15723-1	Isoform 1 of ETS-related transcription factor Elf-2	100.0	5.37E-17
Q86W56	Poly(ADP-ribose) glycohydrolase	100.0	5.37E-17
O00562	Membrane-associated phosphatidylinositol transfer protein 1	100.0	5.37E-17
P50613	Cyclin-dependent kinase 7	100.0	5.37E-17
Q5T3J3	Ligand-dependent nuclear receptor-interacting factor 1	100.0	5.37E-17
Q13901	nuclear nucleic acid-binding protein C1D	100.0	5.37E-17
Q9NX01	thioredoxin-like protein 4B	100.0	5.37E-17
Q9HBH5	Retinol dehydrogenase 14	100.0	5.37E-17
Q86UE8	Serine/threonine-protein kinase tousled-like 2	100.0	5.37E-17
A2CJ06	Dystrotelin	100.0	5.37E-17
P15954	Cytochrome c oxidase subunit 7C, mitochondrial	100.0	5.37E-17
Q969E2-1	Secretory carrier-associated membrane protein 4	100.0	5.37E-17
Q9Y2E5	Epididymis-specific alpha-mannosidase	100.0	5.37E-17
Q8IVD9	NudC domain-containing protein 3	100.0	5.37E-17
P62380	TATA box-binding protein-like protein 1	100.0	5.37E-17
Q14012	calcium/calmodulin-dependent protein kinase type 1	100.0	5.37E-17
P51854	Transketolase-like protein 1	100.0	5.37E-17
Q14457	Beclin-1	100.0	5.37E-17
Q96M42	Putative uncharacterized protein encoded by LINC00479	100.0	5.37E-17
Q5VIR6-4	Isoform 4 of Vacuolar protein sorting-associated protein 53 homolog	100.0	5.37E-17
P48059	LIM and senescent cell antigen-like-containing domain protein 1	100.0	5.37E-17
Q92890-1	Isoform Long of Ubiquitin recognition factor in ER-associated degradation protein 1	100.0	5.37E-17
Q969Y2	tRNA modification GTPase GTPBP3, mitochondrial	100.0	5.37E-17
P17405-1	Sphingomyelin phosphodiesterase	100.0	5.37E-17
Q6PCT2-1	F-box/LRR-repeat protein 19	100.0	5.37E-17
P20933	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	100.0	5.37E-17
Q06481	Amyloid-like protein 2	100.0	5.37E-17
P17152	Transmembrane protein 11, mitochondrial	100.0	5.37E-17
Q16539-2	Isoform CSBP1 of Mitogen-activated protein kinase 14	100.0	5.37E-17
Q8WZ82	Esterase OVCA2	100.0	5.37E-17
Q01085	Nucleolysin TIAR	100.0	5.37E-17
Q12986	Transcriptional repressor NF-X1	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9HCE5	N6-adenosine-methyltransferase subunit METTL14	100.0	5.37E-17
Q86WC4	Osteopetrosis-associated transmembrane protein 1	100.0	5.37E-17
Q15048	Leucine-rich repeat-containing protein 14	100.0	5.37E-17
Q13445	Transmembrane emp24 domain-containing protein 1	100.0	5.37E-17
Q8WWV3-1	Reticulon-4-interacting protein 1, mitochondrial	100.0	5.37E-17
F8WBI6	Golgin subfamily A member 8N	100.0	5.37E-17
Q5T280	putative methyltransferase C9orf114	100.0	5.37E-17
Q96AP0	Adrenocortical dysplasia protein homolog	100.0	5.37E-17
O75381-1	Peroxisomal membrane protein PEX14	100.0	5.37E-17
Q6JQN1	Acyl-CoA dehydrogenase family member 10	100.0	5.37E-17
O14686-1	Histone-lysine N-methyltransferase 2D	100.0	5.37E-17
P31751	RAC-beta serine/threonine-protein kinase	100.0	5.37E-17
Q71UI9-1	Histone H2A.V	100.0	5.37E-17
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog	100.0	5.37E-17
Q8N1F8	Serine/threonine-protein kinase 11-interacting protein	100.0	5.37E-17
A0PJW6	Transmembrane protein 223	100.0	5.37E-17
Q9HAK2	Transcription factor COE2	100.0	5.37E-17
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	100.0	5.37E-17
Q6ZMG9	Ceramide synthase 6	100.0	5.37E-17
Q9Y6B2-1	EP300-interacting inhibitor of differentiation 1	100.0	5.37E-17
Q6P589	Tumor necrosis factor alpha-induced protein 8-like protein 2	100.0	5.37E-17
O94967-1	WD repeat-containing protein 47	100.0	5.37E-17
Q14554	Protein disulfide-isomerase A5	100.0	5.37E-17
Q15572-1	TATA box-binding protein-associated factor RNA polymerase I subunit C	100.0	5.37E-17
O14562	Ubiquitin domain-containing protein UBFD1	100.0	5.37E-17
P57081-1	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4	100.0	5.37E-17
Q96F44-1	E3 ubiquitin-protein ligase TRIM11	100.0	5.37E-17
Q5VST6-1	Protein ABHD17B	100.0	5.37E-17
Q9Y4C5-1	Carbohydrate sulfotransferase 2	100.0	5.37E-17
Q7L8L6	FAST kinase domain-containing protein 5, mitochondrial	100.0	5.37E-17
Q9H8W3	Protein FAM204A	100.0	5.37E-17
Q96TC7	Regulator of microtubule dynamics protein 3	100.0	5.37E-17
Q13315	Serine-protein kinase ATM	100.0	5.37E-17
Q9H0A8-1	COMM domain-containing protein 4	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96DP5	Methionyl-tRNA formyltransferase, mitochondrial	100.0	5.37E-17
Q9Y4P8-1	WD repeat domain phosphoinositide-interacting protein 2	100.0	5.37E-17
Q14156-1	protein EFR3 homolog A	100.0	5.37E-17
Q9BPY3	Protein FAM118B	100.0	5.37E-17
Q9H008-1	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	100.0	5.37E-17
Q5T440	Putative transferase CAF17, mitochondrial	100.0	5.37E-17
Q9UPV9	Trafficking kinesin-binding protein 1	100.0	5.37E-17
Q8N465	D-2-hydroxyglutarate dehydrogenase, mitochondrial	100.0	5.37E-17
Q12981-1	Isoform 3 of Vesicle transport protein SEC20	100.0	5.37E-17
Q99519	sialidase-1	100.0	5.37E-17
Q9BXK5-1	Bcl-2-like protein 13	100.0	5.37E-17
Q15067	Peroxisomal acyl-coenzyme A oxidase 1	100.0	5.37E-17
Q96DZ1	Endoplasmic reticulum lectin 1	100.0	5.37E-17
Q8TBQ9	Protein kish-A	100.0	5.37E-17
Q9UJX4	Anaphase-promoting complex subunit 5	100.0	5.37E-17
P80297	metallothionein-1X	100.0	5.37E-17
Q8IZT6-1	Abnormal spindle-like microcephaly-associated protein	100.0	5.37E-17
Q5JPH6	Probable glutamate–tRNA ligase, mitochondrial	100.0	5.37E-17
A6NHL2-1	Tubulin alpha chain-like 3	100.0	5.37E-17
Q6ZSC3	RNA-binding protein 43	100.0	5.37E-17
Q5VWZ2	Lysophospholipase-like protein 1	100.0	5.37E-17
Q96Q83-1	alpha-ketoglutarate-dependent dioxygenase alkB homolog 3	100.0	5.37E-17
Q86T03-1	Type 1 phosphatidylinositol 4,5-bisphosphate 4-phosphatase	100.0	5.37E-17
P04062	glucosylceramidase	100.0	5.37E-17
Q03519-1	antigen peptide transporter 2	100.0	5.37E-17
Q8TAF3-1	WD repeat-containing protein 48	100.0	5.37E-17
Q9UDX5	Mitochondrial fission process protein 1	100.0	5.37E-17
Q96EL2	28S ribosomal protein S24, mitochondrial	100.0	5.37E-17
Q9H9L3	Interferon-stimulated 20 kDa exonuclease-like 2	100.0	5.37E-17
Q3V5L5-1	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B	100.0	5.37E-17
Q96BW5-1	Phosphotriesterase-related protein	100.0	5.37E-17
Q969V6	MKL/myocardin-like protein 1	100.0	5.37E-17
Q96I51	RCC1-like G exchanging factor-like protein	100.0	5.37E-17
Q4LE39-1	AT-rich interactive domain-containing protein 4B	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9HBH1	Peptide deformylase, mitochondrial	100.0	5.37E-17
Q99622	Protein C10	100.0	5.37E-17
Q8NHZ8	Anaphase-promoting complex subunit CDC26	100.0	5.37E-17
Q15366-4	Isoform 4 of Poly(rC)-binding protein 2	100.0	5.37E-17
Q9NXR7-1	Isoform 1 of BRISC and BRCA1-A complex member 2	100.0	5.37E-17
P57678	Gem-associated protein 4	100.0	5.37E-17
Q04637-8	Isoform 8 of Eukaryotic translation initiation factor 4 gamma 1	100.0	5.37E-17
Q8WUZ0-1	B-cell CLL/lymphoma 7 protein family member C	100.0	5.37E-17
Q9BVN2	RUN and SH3 domain-containing protein 1	100.0	5.37E-17
P49006	MARCKS-related protein	100.0	5.37E-17
Q96DM3	Uncharacterized protein C18orf8	100.0	5.37E-17
Q8IZU2-1	WD repeat-containing protein 17	100.0	5.37E-17
A6NI56	Coiled-coil domain-containing protein 154	100.0	5.37E-17
Q9BZV1	UBX domain-containing protein 6	100.0	5.37E-17
Q6NYC1	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	100.0	5.37E-17
O00268	Transcription initiation factor TFIID subunit 4	100.0	5.37E-17
Q9P0U1	Mitochondrial import receptor subunit TOM7 homolog	100.0	5.37E-17
P36873-1	serine/threonine-protein phosphatase PP1-gamma catalytic subunit	100.0	5.37E-17
Q9NNW7-1	thioredoxin reductase 2, mitochondrial	100.0	5.37E-17
P51692	Signal transducer and activator of transcription 5B	100.0	5.37E-17
Q8N129	Protein canopy homolog 4	100.0	5.37E-17
Q8N9V3	WD repeat, SAM and U-box domain-containing protein 1	100.0	5.37E-17
Q9UBW8	COP9 signalosome complex subunit 7a	100.0	5.37E-17
Q99720	sigma non-opioid intracellular receptor 1	100.0	5.37E-17
Q9NXN4-1	Ganglioside-induced differentiation-associated protein 2	100.0	5.37E-17
Q9NW68	BSD domain-containing protein 1	100.0	5.37E-17
Q9Y4E5	E3 SUMO-protein ligase ZNF451	100.0	5.37E-17
O00189	AP-4 complex subunit mu-1	100.0	5.37E-17
P03915	NADH-ubiquinone oxidoreductase chain 5	100.0	5.37E-17
P46734-1	dual specificity mitogen-activated protein kinase kinase 3	100.0	5.37E-17
Q9Y312	Protein AAR2 homolog	100.0	5.37E-17
Q96A65	Exocyst complex component 4	100.0	5.37E-17
Q16513	Serine/threonine-protein kinase N2	100.0	5.37E-17
Q9NQS1	Cell death regulator Aven	100.0	5.37E-17
Q10472	Polypeptide N-acetylgalactosaminyltransferase 1	100.0	5.37E-17
Q6P2H3-1	Centrosomal protein of 85 kDa	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
A6NNY8	Ubiquitin carboxyl-terminal hydrolase 27	100.0	5.37E-17
O43390-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein R	100.0	5.37E-17
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	100.0	5.37E-17
Q16670-1	Zinc finger and SCAN domain-containing protein 26	100.0	5.37E-17
Q86X53	Glutamate-rich protein 1	100.0	5.37E-17
Q96LI5-1	CCR4-NOT transcription complex subunit 6-like	100.0	5.37E-17
P78346-1	ribonuclease P protein subunit p30	100.0	5.37E-17
Q8WY22	BRI3-binding protein	100.0	5.37E-17
Q7Z3C6	autophagy-related protein 9A	100.0	5.37E-17
Q6PD74	Alpha- and gamma-adaptin-binding protein p34	100.0	5.37E-17
P32970	CD70 antigen	100.0	5.37E-17
P32189-1	Isoform 1 of Glycerol kinase	100.0	5.37E-17
P0CG39	POTE ankyrin domain family member J	100.0	5.37E-17
Q9UI43	rRNA methyltransferase 2, mitochondrial	100.0	5.37E-17
Q68DK2	Zinc finger FYVE domain-containing protein 26	100.0	5.37E-17
Q12873-1	Chromodomain-helicase-DNA-binding protein 3	100.0	5.37E-17
Q9BTK6	PAXIP1-associated glutamate-rich protein 1	100.0	5.37E-17
Q13546	Receptor-interacting serine/threonine-protein kinase 1	100.0	5.37E-17
Q9HB65	RNA polymerase II elongation factor ELL3	100.0	5.37E-17
O75352	Mannose-P-dolichol utilization defect 1 protein	100.0	5.37E-17
P51151	Ras-related protein Rab-9A	100.0	5.37E-17
Q6NXT2	Histone H3.3C	100.0	5.37E-17
Q9UL63-1	muskelin	100.0	5.37E-17
Q27J81	Inverted formin-2	100.0	5.37E-17
Q9HCN4	GPN-loop GTPase 1	100.0	5.37E-17
O95996-1	adenomatous polyposis coli protein 2	100.0	5.37E-17
O95140	Mitofusin-2	100.0	5.37E-17
Q8WUH1	Protein Churchill	100.0	5.37E-17
O95271	Tankyrase-1	100.0	5.37E-17
Q9ULI0	ATPase family AAA domain-containing protein 2B	100.0	5.37E-17
Q9NZQ3-1	NCK-interacting protein with SH3 domain	100.0	5.37E-17
O60812	Heterogeneous nuclear ribonucleoprotein C-like 1	100.0	5.37E-17
P09104	Gamma-enolase	100.0	5.37E-17
Q9H5H4	Zinc finger protein 768	100.0	5.37E-17
Q9HAD4	WD repeat-containing protein 41	100.0	5.37E-17
Q13496	Myotubularin	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96B36	Proline-rich AKT1 substrate 1	100.0	5.37E-17
P27216-1	Annexin A13	100.0	5.37E-17
P14316-1	Interferon regulatory factor 2	100.0	5.37E-17
Q8IXH7	Negative elongation factor C/D	100.0	5.37E-17
Q9Y2F5	Little elongation complex subunit 1	100.0	5.37E-17
O95834	echinoderm microtubule-associated protein-like 2	100.0	5.37E-17
Q9NZ32	Actin-related protein 10	100.0	5.37E-17
Q96EY5-1	Multivesicular body subunit 12A	100.0	5.37E-17
Q9UGN5-1	Poly [ADP-ribose] polymerase 2	100.0	5.37E-17
Q9BT43	DNA-directed RNA polymerase III subunit RPC7-like	100.0	5.37E-17
Q9NZJ6	Ubiquinone biosynthesis O-methyltransferase, mitochondrial	100.0	5.37E-17
P30047	GTP cyclohydrolase 1 feedback regulatory protein	100.0	5.37E-17
Q96M27-1	protein PRRC1	100.0	5.37E-17
O60423-1	Isoform 2 of Phospholipid-transporting ATPase IK	100.0	5.37E-17
O60318	Germinal-center associated nuclear protein	100.0	5.37E-17
P0CG41	cTAGE family member 8	100.0	5.37E-17
O60476	mannosyl-oligosaccharide 1,2-alpha-mannosidase IB	100.0	5.37E-17
Q658Y4	Protein FAM91A1	100.0	5.37E-17
Q9NVV4-2	Isoform 2 of Poly(A) RNA polymerase, mitochondrial	100.0	5.37E-17
Q969M3	Protein YIPF5	100.0	5.37E-17
Q92934	Bcl2-associated agonist of cell death	100.0	5.37E-17
Q9Y2I9	TBC1 domain family member 30	100.0	5.37E-17
Q53S33	BolA-like protein 3	100.0	5.37E-17
Q8NEY8-2	Isoform 2 of Periphilin-1	100.0	5.37E-17
Q9NXX6	Non-structural maintenance of chromosomes element 4 homolog A	100.0	5.37E-17
Q86VN1	Vacuolar protein-sorting-associated protein 36	100.0	5.37E-17
Q05DH4	Protein FAM160A1	100.0	5.37E-17
Q9NR19-1	Acetyl-coenzyme A synthetase, cytoplasmic	100.0	5.37E-17
Q9NYP7-1	elongation of very long chain fatty acids protein 5	100.0	5.37E-17
Q9UKT5	F-box only protein 4	100.0	5.37E-17
Q8TDX7-1	Serine/threonine-protein kinase Nek7	100.0	5.37E-17
Q5HYK7	SH3 domain-containing protein 19	100.0	5.37E-17
Q8TE73	Dynein heavy chain 5, axonemal	100.0	5.37E-17
Q9UGY1	Nucleolar protein 12	100.0	5.37E-17
Q9H3H3	UPF0696 protein C11orf68	100.0	5.37E-17
Q9UMZ2-1	Synergin gamma	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q6IAN0	Dehydrogenase/reductase SDR family member 7B	100.0	5.37E-17
Q9BSY4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5	100.0	5.37E-17
Q12962	transcription initiation factor TFIID subunit 10	100.0	5.37E-17
Q93073-1	Selenocysteine insertion sequence-binding protein 2-like	100.0	5.37E-17
Q2TBE0	CWF19-like protein 2	100.0	5.37E-17
Q8IU60	m7GpppN-mRNA hydrolase	100.0	5.37E-17
Q8NCH0	Carbohydrate sulfotransferase 14	100.0	5.37E-17
Q66LE6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform	100.0	5.37E-17
Q9Y5X2	Sorting nexin-8	100.0	5.37E-17
P23743-1	diacylglycerol kinase alpha	100.0	5.37E-17
Q86VR2	Reticulophagy regulator 3	100.0	5.37E-17
Q96RN5	Mediator of RNA polymerase II transcription subunit 15	100.0	5.37E-17
P62699	Protein yippee-like 5	100.0	5.37E-17
P12111	Collagen alpha-3(VI) chain	100.0	5.37E-17
Q9HA64	Ketosamine-3-kinase	100.0	5.37E-17
Q9UQR1	Zinc finger protein 148	100.0	5.37E-17
Q9P270	SLAIN motif-containing protein 2	100.0	5.37E-17
Q9Y6W3	Calpain-7	100.0	5.37E-17
Q9BVC5	Ashwin	100.0	5.37E-17
A4D2P6	delphilin	100.0	5.37E-17
Q9NVA1	Ubiquinol-cytochrome-c reductase complex assembly factor 1	100.0	5.37E-17
Q03111	Protein ENL	100.0	5.37E-17
Q96BN8	Ubiquitin thioesterase otulin	100.0	5.37E-17
Q96JB2-1	Conserved oligomeric Golgi complex subunit 3	100.0	5.37E-17
Q6P3S1	DENN domain-containing protein 1B	100.0	5.37E-17
P55082-1	Microfibril-associated glycoprotein 3	100.0	5.37E-17
O14657	Torsin-1B	100.0	5.37E-17
Q9NR77	Peroxisomal membrane protein 2	100.0	5.37E-17
O75909-1	Isoform 3 of Cyclin-K	100.0	5.37E-17
P43146	Netrin receptor DCC	100.0	5.37E-17
Q53ET0	CREB-regulated transcription coactivator 2	100.0	5.37E-17
Q9UKI2	Cdc42 effector protein 3	100.0	5.37E-17
Q96FK6	WD repeat-containing protein 89	100.0	5.37E-17
O43715	TP53-regulated inhibitor of apoptosis 1	100.0	5.37E-17
Q9H2J4	phosducin-like protein 3	100.0	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O43566	Regulator of G-protein signaling 14	100.0	5.37E-17
Q9NWZ3-1	Interleukin-1 receptor-associated kinase 4	99.70	5.37E-17
P0C7P3-1	Protein Slfn14	81.76	5.37E-17
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial	80.62	3.53E-12
Q8IUR6-1	CREB3 regulatory factor	68.85	5.37E-17
Q9UBD5-1	Origin recognition complex subunit 3	66.34	5.37E-17
Q9UEE9-1	Craniofacial development protein 1	58.41	5.37E-17
P08047	Transcription factor Sp1	55.66	1.51E-03
P06454-1	Prothymosin alpha	49.78	5.37E-17
Q86X76	Deaminated glutathione amidase	42.47	1.19E-15
O60637	Tetraspanin-3	40.93	1.50E-07
O14656	Torsin-1A	40.86	1.37E-05
Q03169	Tumor necrosis factor alpha-induced protein 2	39.39	4.94E-04
Q8NEH6	Meiosis-specific nuclear structural protein 1	34.37	9.90E-04
O95379	Tumor necrosis factor alpha-induced protein 8	32.05	1.45E-13
Q14657	EKC/KEOPS complex subunit LAGE3	31.93	2.15E-10
P17900	Ganglioside GM2 activator	31.75	1.47E-05
Q9NYK1	Toll-like receptor 7	30.68	5.11E-14
Q9H2A2-1	aldehyde dehydrogenase family 8 member A1	30.56	1.47E-03
Q92994	Transcription factor IIIB 90 kDa subunit	30.20	2.84E-13
Q99547	M-phase phosphoprotein 6	29.87	4.34E-05
O75970	multiple PDZ domain protein	29.83	5.11E-05
Q96RE7	Nucleus accumbens-associated protein 1	29.09	9.31E-06
Q9BZL6	Serine/threonine-protein kinase D2	28.36	1.86E-03
O14647	Chromodomain-helicase-DNA-binding protein 2	27.80	5.93E-05
Q32P28-1	Prolyl 3-hydroxylase 1	27.59	1.77E-03
Q9Y3E7	Charged multivesicular body protein 3	26.17	6.59E-03
Q9P2X0-1	Dolichol-phosphate mannosyltransferase subunit 3	25.74	7.01E-04
Q96E39	RNA binding motif protein, X-linked-like-1	25.65	6.80E-04
Q86TJ2-1	Transcriptional adapter 2-beta	25.42	2.42E-03
P55854	Small ubiquitin-related modifier 3	25.15	4.45E-05
P68871	Hemoglobin subunit beta	24.27	2.68E-12
Q8NDD1	Uncharacterized protein C1orf131	24.12	3.40E-03
P40763	Signal transducer and activator of transcription 3	23.97	8.61E-03
Q9H2H9	Sodium-coupled neutral amino acid transporter 1	23.85	1.27E-02
Q9H6V9-1	Lipid droplet-associated hydrolase	23.83	1.10E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q9H9E3-1	Conserved oligomeric Golgi complex subunit 4	23.53	1.89E-05
O95249-1	Golgi SNAP receptor complex member 1	23.47	1.40E-02
P21399	Cytoplasmic aconitate hydratase	22.59	5.44E-11
O14730	serine/threonine-protein kinase RIO3	22.33	1.02E-03
Q96FZ7	charged multivesicular body protein 6	22.17	5.12E-03
P10523	S-arrestin	21.96	5.45E-05
O15230	Laminin subunit alpha-5	21.68	6.39E-03
Q5RI15-1	Cytochrome c oxidase protein 20 homolog	21.63	1.42E-04
P08651	Nuclear factor 1 C-type	21.48	2.97E-04
Q6IE36	Ovostatin homolog 2	21.12	3.15E-05
Q8TEA7	TBC domain-containing protein kinase-like protein	21.03	1.40E-02
Q86UA1	Pre-mRNA-processing factor 39	20.92	5.04E-03
Q9ULU4	protein kinase C-binding protein 1	20.85	1.23E-02
Q8NB49-1	Phospholipid-transporting ATPase IG	20.80	1.45E-02
Q9NQA3	WAS protein family homolog 6	20.67	1.08E-02
Q96EV8-1	dysbindin	20.48	1.62E-03
Q9BSR8	protein YIPF4	20.45	1.69E-02
O43760	Synaptogyrin-2	20.29	4.75E-08
Q8NB90-1	Spermatogenesis-associated protein 5	20.24	4.69E-04
Q8WUK0	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1	20.09	4.81E-05
O15379	Histone deacetylase 3	20.05	7.01E-03
Q9UJ70	N-acetyl-D-glucosamine kinase	19.70	7.63E-03
Q9UBB5-1	Methyl-CpG-binding domain protein 2	19.69	1.06E-04
P07311	Acylphosphatase-1	19.67	6.29E-03
Q9Y2H1	serine/threonine-protein kinase 38-like	19.67	2.67E-02
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial	19.35	8.14E-03
Q8NBU5	ATPase family aaa domain-containing protein 1	19.11	7.54E-03
P0CB38	polyadenylate-binding protein 4-like	19.06	2.16E-05
P10109	Adrenodoxin, mitochondrial	18.70	1.69E-02
Q08AG7	Mitotic-spindle organizing protein 1	18.13	1.86E-04
P15735-1	Phosphorylase b kinase gamma catalytic chain, liver/testis isoform	18.06	9.85E-03
Q9NVC6	mediator of RNA polymerase II transcription subunit 17	17.95	9.45E-03
O75208-1	Ubiquinone biosynthesis protein COQ9, mitochondrial	17.94	3.13E-03
Q9NPP4-1	NLR family CARD domain-containing protein 4	17.91	9.49E-06
P50583	Bis(5′-nucleosyl)-tetraphosphatase [asymmetrical]	17.91	2.42E-02

Continued on next page

accession	description	fold p change	adjusted p-value
O95260	Arginyl-tRNA–protein transferase 1	17.90	2.87E-02
Q9NXK8	F-box/LRR-repeat protein 12	17.81	1.89E-02
Q92643	GPI-anchor transamidase	17.71	3.65E-02
Q4VC05	B-cell CLL/lymphoma 7 protein family member A	17.46	7.67E-06
Q8WTX7	Cytosolic arginine sensor for mTORC1 subunit 1	17.35	3.22E-02
Q6S8J3	POTE ankyrin domain family member E	17.23	2.12E-02
Q6P4I2	WD repeat-containing protein 73	17.20	7.44E-03
P09467	Fructose-1,6-bisphosphatase 1	17.03	5.79E-10
Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10	16.87	2.05E-02
Q9ULP9	TBC1 domain family member 24	16.86	3.27E-07
Q8WUX1-1	Sodium-coupled neutral amino acid transporter 5	16.72	2.97E-04
Q9Y305-1	Acyl-coenzyme A thioesterase 9, mitochondrial	16.57	9.43E-05
P20160	Azurocidin	16.54	5.98E-04
Q9NX04	Uncharacterized protein C1orf109	16.53	2.98E-02
Q9HD40-1	O-phosphoseryl-tRNA(Sec) selenium transferase	16.47	3.84E-02
Q9UHQ9	NADH-cytochrome b5 reductase 1	16.22	4.58E-02
Q92609-1	TBC1 domain family member 5	16.17	3.19E-04
Q9BRD0	BUD13 homolog	16.07	2.22E-04
P35908	Keratin, type II cytoskeletal 2 epidermal	15.85	4.21E-02
P18433	Receptor-type tyrosine-protein phosphatase alpha	15.54	2.05E-02
Q8ND76	cyclin-Y	15.51	1.59E-02
Q7LGA3-1	Heparan sulfate 2-O-sulfotransferase 1	15.41	4.34E-04
Q86U28	iron-sulfur cluster assembly 2 homolog, mitochondrial	15.30	1.43E-02
Q53GS7-1	Nucleoporin GLE1	15.22	2.12E-04
P20813	Cytochrome P450 2B6	15.14	1.58E-02
Q9Y3D6	mitochondrial fission 1 protein	15.10	4.23E-04
Q5JTY5	COBW domain-containing protein 3	14.88	4.62E-04
Q69YN4	protein virilizer homolog	14.81	1.32E-03
Q96JA3	pleckstrin homology domain-containing family A member 8	14.74	3.90E-07
P61020	Ras-related protein Rab-5B	14.62	4.54E-02
Q9BV73-1	Centrosome-associated protein CEP250	14.46	3.74E-02
O95864	fatty acid desaturase 2	14.39	6.39E-04
Q8WWN9	Interactor protein for cytohesin exchange factors 1	14.34	2.02E-02
Q9BQC6	Ribosomal protein 63, mitochondrial	14.29	5.93E-04
P61927	60S ribosomal protein L37	14.27	7.13E-06
P61978-3	Isoform 3 of Heterogeneous nuclear ribonucleoprotein K	14.20	1.21E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y5P6	Mannose-1-phosphate guanyltransferase beta	14.10	1.48E-03
P01040	Cystatin-A	14.04	3.49E-03
Q8NF37	Lysophosphatidylcholine acyltransferase 1	14.02	1.66E-03
Q6P179	Endoplasmic reticulum aminopeptidase 2	13.77	1.23E-03
O43759-1	Synaptogyrin-1	13.68	2.39E-02
Q9UBP0-1	spastin	13.31	7.45E-04
Q86WB0	Nuclear-interacting partner of ALK	13.17	4.88E-02
Q6P1K2	polyamine-modulated factor 1	13.03	8.01E-03
O14972	Down syndrome critical region protein 3	12.89	2.73E-02
P20248	Cyclin-A2	12.83	2.26E-03
Q96CB8	integrator complex subunit 12	12.72	8.36E-03
P54132	Bloom syndrome protein	12.71	2.97E-02
Q12899	Tripartite motif-containing protein 26	12.69	4.74E-02
Q9UI26	Importin-11	12.58	2.77E-02
Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	12.57	1.10E-05
Q13232	Nucleoside diphosphate kinase 3	12.50	1.13E-03
Q15057	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	12.35	2.76E-02
Q5DJT8	Cancer/testis antigen family 45 member A2	11.57	2.45E-03
Q9Y223-1	bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	11.45	3.44E-02
P50748	Kinetochore-associated protein 1	11.42	3.59E-02
Q9Y6B6	GTP-binding protein SAR1b	11.36	1.84E-02
Q9Y2Z9-1	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial	11.29	2.25E-03
Q96P16-1	Regulation of nuclear pre-mRNA domain-containing protein 1A	11.27	1.74E-05
Q9BRG1	Vacuolar protein-sorting-associated protein 25	11.24	9.53E-03
P00387	NADH-cytochrome b5 reductase 3	10.96	8.87E-07
P07910-1	Heterogeneous nuclear ribonucleoproteins C1/C2	10.95	4.49E-05
O94905-1	Erlin-2	10.93	3.86E-02
Q9NUP1	Biogenesis of lysosome-related organelles complex 1 subunit 4	10.54	4.03E-02
Q9Y296	Trafficking protein particle complex subunit 4	10.29	9.35E-05
Q99747	Gamma-soluble NSF attachment protein	10.21	3.96E-03
O75027-1	ATP-binding cassette sub-family B member 7, mitochondrial	10.04	3.86E-02
Q53H82	Endoribonuclease LACTB2	10.04	2.35E-02
P37235	Hippocalcin-like protein 1	10.00	1.35E-05
Q8NBM8	Prenylcysteine oxidase-like	9.871	7.04E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q13033	Striatin-3	9.743	3.95E-03
Q7LBC6-1	Lysine-specific demethylase 3B	9.537	2.10E-02
Q2LD37-1	Uncharacterized protein KIAA1109	9.439	2.20E-03
Q9BTW9	Tubulin-specific chaperone D	9.367	1.82E-08
P49848	Transcription initiation factor TFIID subunit 6	9.346	4.84E-03
Q96S52	GPI transamidase component PIG-S	9.288	4.04E-02
P35240-1	merlin	9.262	7.11E-03
Q10567-3	Isoform C of AP-1 complex subunit beta-1	9.223	2.82E-02
Q9BUR5-1	MICOS complex subunit MIC26	9.183	7.91E-03
Q9BXP2-1	Solute carrier family 12 member 9	9.024	1.16E-02
Q9BYC9	39S ribosomal protein L20, mitochondrial	8.896	6.59E-06
Q5HYK3-1	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	8.809	5.71E-03
Q8WUB8	PHD finger protein 10	8.803	2.68E-02
Q9NVH1-1	DnaJ homolog subfamily C member 11	8.510	4.86E-13
O95292	Vesicle-associated membrane protein-associated protein B/C	8.359	4.65E-03
P50749	Ras association domain-containing protein 2	8.258	1.08E-06
O00487	26S proteasome non-ATPase regulatory subunit 14	8.026	2.13E-04
Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase	7.815	6.51E-03
Q969Q0	60S ribosomal protein L36a-like	7.784	1.29E-05
P61026	ras-related protein rab-10	7.755	3.34E-07
Q9Y2S6	Translation machinery-associated protein 7	7.729	1.84E-02
Q86UP0	Cadherin-24	7.685	7.51E-10
P62072	Mitochondrial import inner membrane translocase subunit Tim10	7.524	1.31E-03
Q5JS54-1	Proteasome assembly chaperone 4	7.459	2.53E-02
Q9NWZ5-1	Uridine-cytidine kinase-like 1	7.411	1.06E-03
Q6ZS11	Ras and Rab interactor-like protein	7.388	7.13E-03
Q8N4H5	mitochondrial import receptor subunit TOM5 homolog	7.321	3.84E-05
Q96GX9-1	Methylthioribulose-1-phosphate dehydratase	7.267	1.49E-02
Q14254	Flotillin-2	7.175	6.43E-09
Q96C01	Protein FAM136A	7.009	1.29E-06
A2RUS2	DENN domain-containing protein 3	6.735	7.87E-03
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	6.677	2.11E-02
Q9NVM9	integrator complex subunit 13	6.511	2.33E-02
Q6IPU0	Centromere protein P	6.498	9.30E-03
Q15303	Receptor tyrosine-protein kinase erbB-4	6.359	8.66E-04
Q9UII2-1	ATPase inhibitor, mitochondrial	6.321	2.24E-05

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BZE9	tether containing UBX domain for GLUT4	6.320	3.65E-02
P20338	Ras-related protein Rab-4A	6.246	1.84E-02
Q8WVM8	Sec1 family domain-containing protein 1	6.224	5.49E-06
Q9Y6G5	COMM domain-containing protein 10	6.126	2.68E-02
O15498	Synaptobrevin homolog YKT6	6.051	2.40E-02
Q96J01	THO complex subunit 3	5.984	1.18E-03
Q96B23-1	Uncharacterized protein C18orf25	5.981	3.62E-02
P30042-1	ES1 protein homolog, mitochondrial	5.873	2.33E-03
P31949	protein S100-A11	5.797	4.61E-05
P30536	translocator protein	5.680	7.08E-04
Q6P587-1	Acylpyruvase FAHD1, mitochondrial	5.593	3.78E-02
Q8TDH9	Biogenesis of lysosome-related organelles complex 1 subunit 5	5.506	6.00E-06
Q9H0S4	Probable ATP-dependent RNA helicase DDX47	5.478	8.34E-04
Q8N5M4	Tetratricopeptide repeat protein 9C	5.435	2.23E-08
Q6ZN16-1	Mitogen-activated protein kinase kinase kinase 15	5.322	4.40E-02
O60499	Syntaxin-10	5.273	3.87E-03
Q99436	Proteasome subunit beta type-7	5.260	1.54E-02
Q76FK4	nucleolar protein 8	5.203	9.25E-05
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like	5.077	9.17E-08
Q9UL25	Ras-related protein Rab-21	5.036	2.97E-04
Q8NFC6	Biorientation of chromosomes in cell division protein 1-like 1	4.937	3.16E-02
Q14139	ubiquitin conjugation factor e4 a	4.713	2.81E-03
P62306	Small nuclear ribonucleoprotein F	4.657	8.98E-03
Q9HCJ3	Ribonucleoprotein PTB-binding 2	4.561	4.01E-02
Q6WKZ4-4	Rab11 family-interacting protein 1	4.538	3.86E-04
Q9Y570	Protein phosphatase methylesterase 1	4.537	7.33E-04
P14406	Cytochrome c oxidase subunit 7A2, mitochondrial	4.510	3.43E-02
P02792	Ferritin light chain	4.483	8.21E-04
Q96BM9	ADP-ribosylation factor-like protein 8A	4.436	2.13E-02
Q99442	translocation protein sec62	4.392	9.62E-03
P49458	Signal recognition particle 9 kDa protein	4.389	7.97E-03
P01903	HLA class II histocompatibility antigen, DR alpha chain	4.372	3.22E-03
Q8NAF0	Zinc finger protein 579	4.319	1.44E-02
P17026	zinc finger protein 22	4.290	5.57E-03
Q9H2K8	Serine/threonine-protein kinase TAO3	4.268	1.37E-03
Q96IX5	Up-regulated during skeletal muscle growth protein 5	4.172	7.11E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NRR5-1	Ubiquilin-4	4.165	1.97E-04
Q14161-1	ARF GTPase-activating protein GIT2	4.037	2.42E-04
Q9NWH9-1	SAFB-like transcription modulator	3.815	9.97E-05
Q9BT78	COP9 signalosome complex subunit 4	3.797	1.94E-03
Q96MW5	Conserved oligomeric Golgi complex subunit 8	3.680	1.22E-02
Q9H2G2-1	STE20-like serine/threonine-protein kinase	3.672	8.22E-04
Q6P4F2	Ferredoxin-2, mitochondrial	3.618	3.16E-02
Q5XKP0	MICOS complex subunit MIC13	3.610	2.41E-02
O00221	NF-kappa-B inhibitor epsilon	3.535	1.58E-02
P09960-1	leukotriene A-4 hydrolase	3.494	1.53E-02
Q5TFE4	5′-nucleotidase domain-containing protein 1	3.488	4.47E-02
O60502	protein O-GlcNAcase	3.396	2.53E-02
Q9P1F3	Costars family protein ABRACL	3.393	1.23E-03
Q8NCN5	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	3.374	3.43E-02
Q15293	Reticulocalbin-1	3.371	1.76E-02
O15116	U6 snRNA-associated Sm-like protein LSm1	3.335	2.86E-02
P63208	s-phase kinase-associated protein 1	3.282	5.71E-03
P62847-1	40S ribosomal protein S24	3.281	2.20E-03
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	3.262	2.57E-02
P68032	Actin, alpha cardiac muscle 1	3.259	2.29E-04
O00193	Small acidic protein	3.256	3.48E-02
Q3SY69-1	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	3.163	3.55E-04
P53602	Diphosphomevalonate decarboxylase	3.148	2.95E-02
Q15819	Ubiquitin-conjugating enzyme E2 variant 2	3.142	1.77E-02
P13693	Translationally-controlled tumor protein	3.028	6.55E-04
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	2.984	2.32E-02
Q13123	Protein Red	2.958	8.99E-04
Q15758-1	Neutral amino acid transporter B(0)	2.904	5.08E-03
O00233-1	26S proteasome non-ATPase regulatory subunit 9	2.871	4.66E-02
P46779	60S ribosomal protein L28	2.821	1.89E-03
Q9UBQ0-2	Isoform 2 of Vacuolar protein sorting-associated protein 29	2.819	9.62E-03
Q9UBR2	Cathepsin Z	2.813	1.74E-03
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	2.788	1.95E-03
P62308	Small nuclear ribonucleoprotein G	2.757	2.86E-02
O60496	Docking protein 2	2.720	1.31E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q15366-6	Isoform 6 of Poly(rC)-binding protein 2	2.683	3.73E-03
P08133-1	annexin A6	2.671	3.34E-03
Q13057	Bifunctional coenzyme A synthase	2.628	4.04E-02
O00273-1	DNA fragmentation factor subunit alpha	2.582	2.50E-02
Q9UL46	proteasome activator complex subunit 2	2.557	2.14E-02
P09012	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A	2.544	6.60E-03
Q8N9N8	probable RNA-binding protein EIF1AD	2.535	2.33E-02
Q01813	ATP-dependent 6-phosphofructokinase, platelet type	2.521	6.69E-03
Q04760-1	lactoylglutathione lyase	2.435	9.78E-03
P62899	60S ribosomal protein L31	2.423	1.18E-02
P49721	proteasome subunit beta type-2	2.422	2.97E-02
Q13158	FAS-associated death domain protein	2.393	2.59E-02
P61970	nuclear transport factor 2	2.380	1.88E-02
O00505	Importin subunit alpha-4	2.358	3.28E-02
P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	2.353	1.57E-02
Q13823	Nucleolar GTP-binding protein 2	2.292	1.84E-02
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	2.254	2.18E-02
Q07955-1	Serine/arginine-rich splicing factor 1	2.198	2.79E-02
P23919	thymidylate kinase	2.097	4.47E-02
P62263	40S ribosomal protein S14	0.506	4.68E-02
P41227-1	N-alpha-acetyltransferase 10	0.470	2.35E-02
P62979	Ubiquitin-40S ribosomal protein S27a	0.467	2.20E-02
Q96T88	E3 ubiquitin-protein ligase UHRF1	0.464	4.89E-02
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.455	4.09E-02
P55209	Nucleosome assembly protein 1-like 1	0.442	1.25E-02
P20290-2	Isoform 2 of Transcription factor BTF3	0.436	1.08E-02
P67809	Nuclease-sensitive element-binding protein 1	0.424	7.97E-03
P16220-1	Cyclic AMP-responsive element-binding protein 1	0.417	4.44E-02
P31689-1	DnaJ homolog subfamily A member 1	0.409	4.53E-02
P98179	RNA-binding protein 3	0.408	1.55E-02
Q9BTY7	Protein HGH1 homolog	0.406	4.85E-02
Q01780	exosome component 10	0.398	1.24E-02
P46778	60S ribosomal protein L21	0.390	2.91E-03
Q99661-1	Kinesin-like protein KIF2C	0.376	2.75E-02
P52292	Importin subunit alpha-1	0.365	3.20E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q13765-1	Nascent polypeptide-associated complex subunit alpha	0.355	8.93E-04
P17096-1	High mobility group protein HMG-I/HMG-Y	0.351	4.25E-02
P15531	Nucleoside diphosphate kinase A	0.351	4.40E-02
P31350-1	ribonucleoside-diphosphate reductase subunit M2	0.316	3.45E-02
P40222	alpha-taxilin	0.305	3.49E-02
P50851-1	Lipopolysaccharide-responsive and beige-like anchor protein	0.303	2.19E-02
P42677	40S ribosomal protein S27	0.276	1.96E-05
P24158	Myeloblastin	0.256	1.19E-03
O60306	Intron-binding protein aquarius	0.231	3.50E-02
Q92901	60S ribosomal protein L3-like	0.226	3.16E-03
Q9NX20	39S ribosomal protein L16, mitochondrial	0.212	1.79E-02
O75419	Cell division control protein 45 homolog	0.205	7.14E-03
Q7L2J0-1	7SK snRNA methylphosphate capping enzyme	0.185	1.18E-02
P51532-1	Transcription activator BRG1	0.171	4.81E-04
P50579	methionine aminopeptidase 2	0.166	4.70E-03
Q13405	39S ribosomal protein L49, mitochondrial	0.146	9.38E-04
Q8IWA4-1	Mitofusin-1	0.146	2.80E-03
Q8WTV0-1	Scavenger receptor class B member 1	0.135	4.88E-02
P31323	cAMP-dependent protein kinase type II-beta regulatory subunit	0.132	4.28E-02
P49454	Centromere protein F	0.131	2.06E-03
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	0.130	4.16E-04
Q9Y291	28S ribosomal protein S33, mitochondrial	0.127	3.44E-02
Q969F1	General transcription factor 3C polypeptide 6	0.126	3.45E-02
P69905	Hemoglobin subunit alpha	0.124	6.53E-03
Q9Y697	Cysteine desulfurase, mitochondrial	0.123	1.11E-07
P16455	Methylated-DNA–protein-cysteine methyltransferase	0.123	1.52E-02
Q9BZL4	Protein phosphatase 1 regulatory subunit 12C	0.117	1.75E-02
O75376-1	Nuclear receptor corepressor 1	0.115	1.71E-02
P04818	thymidylate synthase	0.110	2.26E-05
Q6PIY7-1	Poly(A) RNA polymerase GLD2	0.108	2.79E-02
Q5TA45-1	Integrator complex subunit 11	0.108	2.96E-02
Q7Z7K6-1	Centromere protein V	0.108	4.01E-02
Q06587	E3 ubiquitin-protein ligase RING1	0.106	2.64E-05
Q5XPI4	E3 ubiquitin-protein ligase RNF123	0.097	2.01E-02
Q14376	UDP-glucose 4-epimerase	0.095	4.44E-02
Q6UWP7-1	Lysocardiolipin acyltransferase 1	0.094	1.60E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P17612	cAMP-dependent protein kinase catalytic subunit alpha	0.092	4.13E-02
Q15291-1	Retinoblastoma-binding protein 5	0.092	4.20E-02
P49459-1	Ubiquitin-conjugating enzyme E2 A	0.091	1.67E-03
Q9NQZ2	Something about silencing protein 10	0.091	1.28E-02
Q15006	ER membrane protein complex subunit 2	0.090	1.56E-02
Q9BZK3	Putative nascent polypeptide-associated complex subunit alpha-like protein	0.090	4.06E-02
P00352	Retinal dehydrogenase 1	0.089	1.27E-02
Q8NAV1-1	Pre-mRNA-splicing factor 38A	0.088	5.28E-12
Q9Y580	RNA-binding protein 7	0.086	4.24E-03
Q9H0H5	Rac GTPase-activating protein 1	0.085	3.17E-02
Q96GM5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	0.084	3.24E-02
Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	0.082	1.33E-05
Q13951-2	Isoform 2 of Core-binding factor subunit beta	0.081	4.84E-04
Q96DE0	U8 snoRNA-decapping enzyme	0.081	2.73E-02
Q93100-1	phosphorylase b kinase regulatory subunit beta	0.081	2.97E-02
Q9H3U5	major facilitator superfamily domain-containing protein 1	0.078	1.53E-03
Q9H1C4	Protein unc-93 homolog B1	0.078	5.93E-03
O94913	Pre-mRNA cleavage complex 2 protein Pcf11	0.078	4.50E-02
P08246	Neutrophil elastase	0.076	1.39E-02
Q9NVT9	armadillo repeat-containing protein 1	0.075	4.25E-02
Q03405	Urokinase plasminogen activator surface receptor	0.074	2.50E-02
P08962	CD63 antigen	0.073	1.12E-02
Q86U90	YrdC domain-containing protein, mitochondrial	0.072	7.30E-06
Q96RS6	NudC domain-containing protein 1	0.071	3.15E-03
A2A288-1	Probable ribonuclease ZC3H12D	0.071	9.97E-03
P56524	Histone deacetylase 4	0.071	3.58E-02
Q13503	Mediator of RNA polymerase II transcription subunit 21	0.070	2.16E-02
Q9NWV8	BRISC and BRCA1-A complex member 1	0.067	1.82E-02
Q5BJF2	sigma intracellular receptor 2	0.066	3.76E-03
Q9UBU8-1	Mortality factor 4-like protein 1	0.065	1.60E-02
Q7L1W4	volume-regulated anion channel subunit LRRC8D	0.065	4.55E-02
O75794	Cell division cycle protein 123 homolog	0.064	3.01E-03
Q13287	N-myc-interactor	0.064	3.80E-02
Q9Y4Y9	U6 snRNA-associated Sm-like protein LSm5	0.063	1.29E-06

Continued on next page

accession	description	fold p change	adjusted p-value
Q8IYJ2	uncharacterized protein C10orf67, mitochondrial	0.063	1.44E-03
P28074-1	proteasome subunit beta type-5	0.062	1.47E-02
Q96NB3	zinc finger protein 830	0.061	1.48E-07
Q9H6R0-1	Putative ATP-dependent RNA helicase DHX33	0.060	3.38E-03
Q5SNT2-1	Transmembrane protein 201	0.060	3.49E-02
Q9HD26-1	Golgi-associated PDZ and coiled-coil motif-containing protein	0.059	1.96E-03
Q15651-1	High mobility group nucleosome-binding domain-containing protein 3	0.059	1.04E-02
Q9H223	EH domain-containing protein 4	0.058	1.00E-02
Q16626	Male-enhanced antigen 1	0.058	1.04E-02
Q9BYE7-1	Polycomb group RING finger protein 6	0.057	2.01E-02
Q9BXK1	krueppel-like factor 16	0.057	2.51E-02
P17947	transcription factor PU.1	0.055	7.43E-04
P63172	Dynein light chain Tctex-type 1	0.055	9.33E-03
Q9UQR0	Sex comb on midleg-like protein 2	0.055	1.75E-02
Q9NWZ8	Gem-associated protein 8	0.054	1.51E-03
P57764	Gasdermin-D	0.053	1.46E-04
Q9Y478	5′-AMP-activated protein kinase subunit beta-1	0.053	8.59E-03
Q96R06	Sperm-associated antigen 5	0.052	2.25E-02
Q6NT76-1	Homeobox-containing protein 1	0.052	2.34E-02
P05204	Non-histone chromosomal protein HMG-17	0.051	1.45E-10
Q8WW22-1	DnaJ homolog subfamily A member 4	0.051	1.88E-02
Q86V88	Magnesium-dependent phosphatase 1	0.050	8.97E-04
Q6PI98-1	INO80 complex subunit C	0.049	2.13E-03
Q96B54	Zinc finger protein 428	0.049	5.83E-03
O43237	Cytoplasmic dynein 1 light intermediate chain 2	0.049	7.97E-03
P27540	Aryl hydrocarbon receptor nuclear translocator	0.047	9.55E-03
Q8WWK9-1	Cytoskeleton-associated protein 2	0.045	5.04E-03
P10124	Serglycin	0.045	9.52E-03
Q9GZN7	Protein rogdi homolog	0.044	1.01E-03
P17066	Heat shock 70 kDa protein 6	0.044	1.26E-03
Q9BTT4	Mediator of RNA polymerase II transcription subunit 10	0.044	4.75E-03
Q9BVL4	Selenoprotein O	0.043	3.65E-03
Q99595	Mitochondrial import inner membrane translocase subunit Tim17-A	0.043	1.56E-02
Q6DD87	Zinc finger protein 787	0.042	1.49E-04
Q8NC51-3	Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein	0.041	1.76E-04

Continued on next page

accession	description	fold p change	adjusted p-value
O15120	1-acyl-sn-glycerol-3-phosphate acyltransferase beta	0.039	9.02E-03
Q658P3-1	Metalloreductase STEAP3	0.039	1.21E-02
Q8WXC6-2	COP9 signalosome complex subunit 9	0.038	1.63E-05
O95155	Ubiquitin conjugation factor E4 B	0.038	1.34E-02
O95684	FGFR1 oncogene partner	0.036	5.08E-03
Q86XI2-1	condensin-2 complex subunit G2	0.033	5.48E-04
Q6DN03	Putative histone H2B type 2-C	0.033	3.46E-03
Q14116	Interleukin-18	0.029	1.10E-12
Q58FG1	Putative heat shock protein HSP 90-alpha A4	0.029	2.84E-06
Q13535	serine/threonine-protein kinase ATR	0.029	8.34E-04
Q96P66	Probable G-protein coupled receptor 101	0.029	8.82E-04
P12074	Cytochrome c oxidase subunit 6A1, mitochondrial	0.020	1.68E-06
Q9NPJ6-1	mediator of RNA polymerase II transcription subunit 4	0.019	5.37E-17
O00399	Dynactin subunit 6	0.019	1.00E-12
Q5TC84	Opioid growth factor receptor-like protein 1	0.014	1.25E-11
Q8N2C7-1	protein unc-80 homolog	0.010	5.37E-17
Q8WX94-1	NACHT, LRR and PYD domains-containing protein 7	0.010	5.37E-17
Q9BWE0	Replication initiator 1	0.010	5.37E-17
Q9NZM5	ribosome biogenesis protein NOP53	0.010	5.37E-17
O43156	TELO2-interacting protein 1 homolog	0.010	5.37E-17
P46087-2	Isoform 2 of Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	0.010	5.37E-17
Q6FIF0	AN1-type zinc finger protein 6	0.010	5.37E-17
Q96EU6	ribosomal RNA processing protein 36 homolog	0.010	5.37E-17
Q8IVE0	Putative ciliary rootlet coiled-coil protein-like 2 protein	0.010	5.37E-17
Q9P2D3-1	HEAT repeat-containing protein 5B	0.010	5.37E-17
Q9C0B5	Palmitoyltransferase ZDHHC5	0.010	5.37E-17
Q8WWN8	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3	0.010	5.37E-17
A6NDU8	UPF0600 protein C5orf51	0.010	5.37E-17
P48651	phosphatidylserine synthase 1	0.010	5.37E-17
Q9H4A6	Golgi phosphoprotein 3	0.010	5.37E-17
P13498	Cytochrome b-245 light chain	0.010	5.37E-17
Q9Y3D5	28S ribosomal protein S18c, mitochondrial	0.010	5.37E-17
Q9HBL0	Tensin-1	0.010	5.37E-17
Q7Z4G4	tRNA (guanine(10)-N2)-methyltransferase homolog	0.010	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NQS7	Inner centromere protein	0.010	5.37E-17
P02751	fibronectin	0.010	5.37E-17
P23458	Tyrosine-protein kinase JAK1	0.010	5.37E-17
Q8WV92	MIT domain-containing protein 1	0.010	5.37E-17
Q06547-3	Isoform 3 of GA-binding protein subunit beta-1	0.010	5.37E-17
Q4KWH8-1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1	0.010	5.37E-17
Q5T7W0	zinc finger protein 618	0.010	5.37E-17
Q8WU10	pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1	0.010	5.37E-17
Q6T4P5	Phospholipid phosphatase-related protein type 3	0.010	5.37E-17
Q03188	centromere protein C	0.010	5.37E-17
O00479	High mobility group nucleosome-binding domain-containing protein 4	0.010	5.37E-17
Q9HBD1-1	Roquin-2	0.010	5.37E-17
O95229	ZW10 interactor	0.010	5.37E-17
Q99952	Tyrosine-protein phosphatase non-receptor type 18	0.010	5.37E-17
P04222	HLA class I histocompatibility antigen, Cw-3 alpha chain	0.010	5.37E-17
Q58FF6	Putative heat shock protein HSP 90-beta 4	0.010	5.37E-17
Q9BUK0-1	coiled-coil-helix-coiled-coil-helix domain-containing protein 7	0.010	5.37E-17
P79522	Proline-rich protein 3	0.010	5.37E-17
Q96BR1-1	Serine/threonine-protein kinase Sgk3	0.010	5.37E-17
Q9H4I3-1	traB domain-containing protein	0.010	5.37E-17
Q9NQW6	Anillin	0.010	5.37E-17
Q12968-1	Nuclear factor of activated T-cells, cytoplasmic 3	0.010	5.37E-17
P18846	Cyclic AMP-dependent transcription factor ATF-1	0.010	5.37E-17
Q15643	Thyroid receptor-interacting protein 11	0.010	5.37E-17
Q9Y2I1-1	Nischarin	0.010	5.37E-17
Q14004-1	Cyclin-dependent kinase 13	0.010	5.37E-17
Q52LR7	enhancer of polycomb homolog 2	0.010	5.37E-17
Q8N6S5	ADP-ribosylation factor-like protein 6-interacting protein 6	0.010	5.37E-17
Q01664	Transcription factor AP-4	0.010	5.37E-17
Q9NPI1-1	Bromodomain-containing protein 7	0.010	5.37E-17
Q9NR56-5	Isoform 5 of Muscleblind-like protein 1	0.010	5.37E-17
Q9BY41	Histone deacetylase 8	0.010	5.37E-17
Q8TBC3	SH3KBP1-binding protein 1	0.010	5.37E-17
Q9BYC8	39S ribosomal protein L32, mitochondrial	0.010	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P14209	CD99 antigen	0.010	5.37E-17
P35527	Keratin, type I cytoskeletal 9	0.010	5.37E-17
Q8IWI9-1	MAX gene-associated protein	0.010	5.37E-17
Q14978-3	Isoform 3 of Nucleolar and coiled-body phosphoprotein 1	0.010	5.37E-17
P51946	Cyclin-H	0.010	5.37E-17
Q8N999-1	Uncharacterized protein C12orf29	0.010	5.37E-17
Q14159	DNA repair-scaffolding protein	0.010	5.37E-17
Q5VW36	focadhesin	0.010	5.37E-17
Q9BUT9-1	MAPK regulated corepressor interacting protein 2	0.010	5.37E-17
O60291-1	E3 ubiquitin-protein ligase MGRN1	0.010	5.37E-17
Q9BS18	Anaphase-promoting complex subunit 13	0.010	5.37E-17
Q9H0U9	Testis-specific Y-encoded-like protein 1	0.010	5.37E-17
Q15382	GTP-binding protein rheb	0.010	5.37E-17
P40616	ADP-ribosylation factor-like protein 1	0.010	5.37E-17
Q9BQ95	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	0.010	5.37E-17
Q08357	sodium-dependent phosphate transporter 2	0.010	5.37E-17
P29692-3	Isoform 3 of Elongation factor 1-delta	0.010	5.37E-17
Q00613	heat shock factor protein 1	0.010	5.37E-17
P04156-1	Major prion protein	0.010	5.37E-17
Q9P0J7	E3 ubiquitin-protein ligase KCMF1	0.010	5.37E-17
Q15398	Disks large-associated protein 5	0.010	5.37E-17
Q6PCB5-1	Round spermatid basic protein 1-like protein	0.010	5.37E-17
Q9H3S7	Tyrosine-protein phosphatase non-receptor type 23	0.010	5.37E-17
O15235	28S ribosomal protein S12, mitochondrial	0.010	5.37E-17
Q9NPH3	Interleukin-1 receptor accessory protein	0.010	5.37E-17
Q96RK0	Protein capicua homolog	0.010	5.37E-17
Q14738-1	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	0.010	5.37E-17
Q9UHR6	Zinc finger HIT domain-containing protein 2	0.010	5.37E-17
P13646	Keratin, type I cytoskeletal 13	0.010	5.37E-17
Q6P161	39S ribosomal protein L54, mitochondrial	0.010	5.37E-17
Q9UDY4	DnaJ homolog subfamily B member 4	0.010	5.37E-17
Q96PU4-1	E3 ubiquitin-protein ligase UHRF2	0.010	5.37E-17
Q58FF7	Putative heat shock protein HSP 90-beta-3	0.010	5.37E-17
Q96IZ7-1	Serine/Arginine-related protein 53	0.010	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96HR8	H/ACA ribonucleoprotein complex non-core subunit NAF1	0.010	5.37E-17
O60921	checkpoint protein HUS1	0.010	5.37E-17
Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein	0.010	5.37E-17
Q8NDI1	EH domain-binding protein 1	0.010	5.37E-17
Q9NWU5	39S ribosomal protein L22, mitochondrial	0.010	5.37E-17
O75907	Diacylglycerol O-acyltransferase 1	0.010	5.37E-17
P08887-1	Interleukin-6 receptor subunit alpha	0.010	5.37E-17
Q96G74-1	OTU domain-containing protein 5	0.010	5.37E-17
O60739	eukaryotic translation initiation factor 1b	0.010	5.37E-17
Q92854-1	Semaphorin-4D	0.010	5.37E-17
Q9NZM4	BRD4-interacting chromatin-remodeling complex-associated protein	0.010	5.37E-17
Q9NRV9	Heme-binding protein 1	0.010	5.37E-17
Q9Y2X9	Zinc finger protein 281	0.010	5.37E-17
P42695	condensin-2 complex subunit D3	0.010	5.37E-17
Q9BQB6-1	vitamin K epoxide reductase complex subunit 1	0.010	5.37E-17
Q96CX6	Leucine-rich repeat-containing protein 58	0.010	5.37E-17
Q147X3	N-alpha-acetyltransferase 30	0.010	5.37E-17
O15270	Serine palmitoyltransferase 2	0.010	5.37E-17
Q6UWL6-5	Isoform 5 of Kin of IRRE-like protein 2	0.010	5.37E-17
Q04941-1	proteolipid protein 2	0.010	5.37E-17
O75414	Nucleoside diphosphate kinase 6	0.010	5.37E-17
O43824	Putative GTP-binding protein 6	0.010	5.37E-17
O95873	Uncharacterized protein C6orf47	0.010	5.37E-17
Q969R2	Oxysterol-binding protein 2	0.010	5.37E-17
P15260	Interferon gamma receptor 1	0.010	5.37E-17
Q86VW0	SEC14 domain and spectrin repeat-containing protein 1	0.010	5.37E-17
O95714	E3 ubiquitin-protein ligase HERC2	0.010	5.37E-17
Q9UK61	Protein TASOR	0.010	5.37E-17
Q969R8	KICSTOR complex protein ITFG2	0.010	5.37E-17
O75116	Rho-associated protein kinase 2	0.010	5.37E-17
Q9GZU7-1	carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1	0.010	5.37E-17
O95391	Pre-mRNA-splicing factor SLU7	0.010	5.37E-17
Q9UFG5	UPF0449 protein C19orf25	0.010	5.37E-17
Q9UH65	Switch-associated protein 70	0.010	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96N66-1	Lysophospholipid acyltransferase 7	0.010	5.37E-17
Q96SW2-1	Protein cereblon	0.010	5.37E-17
P05413	Fatty acid-binding protein, heart	0.010	5.37E-17
P31321	cAMP-dependent protein kinase type I-beta regulatory subunit	0.010	5.37E-17
Q6QNK2-4	Isoform 4 of Adhesion G-protein coupled receptor D1	0.010	5.37E-17
P11802	Cyclin-dependent kinase 4	0.010	5.37E-17
P62491-1	Ras-related protein Rab-11A	0.010	5.37E-17
Q05932-1	Folylpolyglutamate synthase, mitochondrial	0.010	5.37E-17
Q03518	Antigen peptide transporter 1	0.010	5.37E-17
P50336	protoporphyrinogen oxidase	0.010	5.37E-17
Q8NDW8	Tetratricopeptide repeat protein 21A	0.010	5.37E-17
Q9Y5J6	Mitochondrial import inner membrane translocase subunit Tim10 B	0.010	5.37E-17
Q12834	cell division cycle protein 20 homolog	0.010	5.37E-17
Q8IXQ3	Uncharacterized protein C9orf40	0.010	5.37E-17
Q9H4B7	tubulin beta-1 chain	0.010	5.37E-17
O43482	Protein Mis18-beta	0.010	5.37E-17
Q9C0K3	Actin-related protein 3C	0.010	5.37E-17
Q9Y2I7-3	Isoform 3 of 1-phosphatidylinositol 3-phosphate 5-kinase	0.010	5.37E-17
Q9Y448	Small kinetochore-associated protein	0.010	5.37E-17
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.010	5.37E-17
Q96ES7	SAGA-associated factor 29	0.010	5.37E-17
Q9BQ04	RNA-binding protein 4B	0.010	5.37E-17
O60930	Ribonuclease H1	0.010	5.37E-17
Q13888-1	General transcription factor IIH subunit 2	0.010	5.37E-17
Q99684	Zinc finger protein Gfi-1	0.010	5.37E-17
Q96AJ9-1	Isoform 1 of Vesicle transport through interaction with t-SNAREs homolog 1A	0.010	5.37E-17
Q7L590-1	Protein MCM10 homolog	0.010	5.37E-17
P34059	N-acetylgalactosamine-6-sulfatase	0.010	5.37E-17
Q9BRT3	migration and invasion enhancer 1	0.010	5.37E-17
Q6IC98-1	GRAM domain-containing protein 4	0.010	5.37E-17
Q9ULM3	YEATS domain-containing protein 2	0.010	5.37E-17
Q504U0	Renal cancer differentiation gene 1 protein	0.010	5.37E-17
Q16342-1	Programmed cell death protein 2	0.010	5.37E-17
Q9H2B2	Synaptotagmin-4	0.010	5.37E-17
Q9UNS1	Protein timeless homolog	0.010	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y624	Junctional adhesion molecule A	0.010	5.37E-17
Q96S94	cyclin-L2	0.010	5.37E-17
Q9NX18	Succinate dehydrogenase assembly factor 2, mitochondrial	0.010	5.37E-17
Q9NQH7-1	Probable Xaa-Pro aminopeptidase 3	0.010	5.37E-17
P61204	ADP-ribosylation factor 3	0.010	5.37E-17
O00273-2	Isoform DFF35 of DNA fragmentation factor subunit alpha	0.010	5.37E-17
Q6UW68	Transmembrane protein 205	0.010	5.37E-17
Q7Z2T5-1	TRMT1-like protein	0.010	5.37E-17
Q1ED39	Lysine-rich nucleolar protein 1	0.010	5.37E-17
Q05823	2-5A-dependent ribonuclease	0.010	5.37E-17
Q9NYR9-1	NF-kappa-B inhibitor-interacting Ras-like protein 2	0.010	5.37E-17
Q9Y605	MORF4 family-associated protein 1	0.010	5.37E-17
Q8TED9	Actin filament-associated protein 1-like 1	0.010	5.37E-17
Q2M2I8-1	AP2-associated protein kinase 1	0.010	5.37E-17
Q15366-3	Isoform 3 of Poly(rC)-binding protein 2	0.010	5.37E-17
Q96QV6	Histone H2A type 1-A	0.010	5.37E-17
Q13422-2	Isoform Ik2 of DNA-binding protein Ikaros	0.010	5.37E-17
O94864-1	STAGA complex 65 subunit gamma	0.010	5.37E-17
P55199	RNA polymerase II elongation factor ELL	0.010	5.37E-17
Q8N0V3-1	Putative ribosome-binding factor A, mitochondrial	0.010	5.37E-17
P04183	Thymidine kinase, cytosolic	0.010	5.37E-17
Q8TEK3	Histone-lysine N-methyltransferase, H3 lysine-79 specific	0.010	5.37E-17
Q9ULG1	DNA helicase ino80	0.010	5.37E-17
O14965	Aurora kinase A	0.010	5.37E-17
Q96LR5	Ubiquitin-conjugating enzyme E2 E2	0.010	5.37E-17
Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	0.010	5.37E-17
Q9Y4D8-1	Probable E3 ubiquitin-protein ligase HECTD4	0.010	5.37E-17
Q5VZL5	Zinc finger MYM-type protein 4	0.010	5.37E-17
Q53HL2	Borealin	0.010	5.37E-17
O60830-1	Mitochondrial import inner membrane translocase subunit Tim17-B	0.010	5.37E-17
Q58A45	PAN2-PAN3 deadenylation complex subunit PAN3	0.010	5.37E-17
Q8WVD3-1	E3 ubiquitin-protein ligase RNF138	0.010	5.37E-17
Q9Y421-1	Protein FAM32A	0.010	5.37E-17
P46976-1	Glycogenin-1	0.010	5.37E-17
Q15811	Intersectin-1	0.010	5.37E-17
Q9Y3S2	zinc finger protein 330	0.010	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96PZ7-1	CUB and sushi domain-containing protein 1	0.010	5.37E-17
Q9BXS6	Nucleolar and spindle-associated protein 1	0.010	5.37E-17
Q9NWK9	Box C/D snoRNA protein 1	0.010	5.37E-17
Q9NW08	DNA-directed RNA polymerase III subunit RPC2	0.010	5.37E-17
Q99638	cell cycle checkpoint control protein rad9a	0.010	5.37E-17
B2RBV5	Putative MORF4 family-associated protein 1-like protein UPP	0.010	5.37E-17
Q92995	Ubiquitin carboxyl-terminal hydrolase 13	0.010	5.37E-17
P56282	DNA polymerase epsilon subunit 2	0.010	5.37E-17
Q9BRL6-1	serine/arginine-rich splicing factor 8	0.010	5.37E-17
Q8NCN4	E3 ubiquitin-protein ligase RNF169	0.010	5.37E-17
Q15366-1	Poly(rC)-binding protein 2	0.010	5.37E-17
P56589	Peroxisomal biogenesis factor 3	0.010	5.37E-17
P47974	mRNA decay activator protein ZFP36L2	0.010	5.37E-17
Q8IWC1	MAP7 domain-containing protein 3	0.010	5.37E-17
Q7Z739	YTH domain-containing family protein 3	0.010	5.37E-17
Q99943	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	0.010	5.37E-17
Q7Z4H7	HAUS augmin-like complex subunit 6	0.010	5.37E-17
O75616-1	GTPase Era, mitochondrial	0.010	5.37E-17
Q9NRN9	Methyltransferase-like protein 5	0.010	5.37E-17
Q9Y240	C-type lectin domain family 11 member A	0.010	5.37E-17
Q9NXR5	Ankyrin repeat domain-containing protein 10	0.010	5.37E-17
P04921-1	Glycophorin-C	0.010	5.37E-17
Q8N3Z6	Zinc finger CCHC domain-containing protein 7	0.010	5.37E-17
Q9BXV9	EKC/KEOPS complex subunit GON7	0.010	5.37E-17
Q96RG2-1	PAS domain-containing serine/threonine-protein kinase	0.010	5.37E-17
Q14691	DNA replication complex GINS protein PSF1	0.010	5.37E-17
Q8N6G6-1	Isoform 1 of ADAMTS-like protein 1	0.010	5.37E-17
Q9GZN1	Actin-related protein 6	0.010	5.37E-17
O75164-1	Lysine-specific demethylase 4A	0.010	5.37E-17
Q9H9F9	actin-related protein 5	0.010	5.37E-17
Q9H0Z9	RNA-binding protein 38	0.010	5.37E-17
Q99640	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	0.010	5.37E-17
Q92966	snRNA-activating protein complex subunit 3	0.010	5.37E-17
P04049	RAF proto-oncogene serine/threonine-protein kinase	0.010	5.37E-17
Q9H334-1	Forkhead box protein P1	0.010	5.37E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q502W6-1	von Willebrand factor A domain-containing protein 3B	0.010	5.37E-17
P31483-2	Isoform Short of Nucleolysin TIA-1 isoform p40	0.010	5.37E-17
P14373	Zinc finger protein RFP	0.010	5.37E-17
P82673-1	28S ribosomal protein S35, mitochondrial	0.010	5.37E-17
Q9Y657	Spindlin-1	0.010	5.37E-17
Q96SK2	Transmembrane protein 209	0.010	5.37E-17
P13747	HLA class I histocompatibility antigen, alpha chain E	0.010	5.37E-17
P15104	Glutamine synthetase	0.010	5.37E-17
Q9H467	CUE domain-containing protein 2	0.010	5.37E-17
Q8NHH9	Atlastin-2	0.010	5.37E-17
Q96P47	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	0.010	5.37E-17

End of Table

W LN18 Pateamine A Genes

accession	description	fold p change	adjusted p-value
P14618-2	Isoform M1 of Pyruvate kinase PKM	100.0	3.35E-17
O60506-3	Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q	100.0	3.35E-17
P29692-3	Isoform 3 of Elongation factor 1-delta	100.0	3.35E-17
P34931	Heat shock 70 kDa protein 1-like	100.0	3.35E-17
Q15366-4	Isoform 4 of Poly(rC)-binding protein 2	100.0	3.35E-17
P22090	40S ribosomal protein S4, Y isoform 1	100.0	3.35E-17
Q15056-2	Isoform Short of Eukaryotic translation initiation factor 4H	100.0	3.35E-17
Q3ZCM7	tubulin beta-8 chain	100.0	3.35E-17
Q15637-6	Isoform 6 of Splicing factor 1	100.0	3.35E-17
Q10567	AP-1 complex subunit beta-1	100.0	3.35E-17
Q14315	Filamin-C	100.0	3.35E-17
Q9UNX3	60S ribosomal protein L26-like 1	100.0	3.35E-17
P47813	Eukaryotic translation initiation factor 1A, X-chromosomal	100.0	3.35E-17
P0CG39	POTE ankyrin domain family member J	100.0	3.35E-17
Q9BZZ5-4	Apoptosis inhibitor 5	100.0	3.35E-17
Q9TNN7	HLA class I histocompatibility antigen, Cw-5 alpha chain	100.0	3.35E-17
Q15437	protein transport protein Sec23B	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9UBQ0	Vacuolar protein sorting-associated protein 29	100.0	3.35E-17
Q9NQC3-5	Isoform 5 of Reticulon-4	100.0	3.35E-17
P35908	Keratin, type II cytoskeletal 2 epidermal	100.0	3.35E-17
O14929	histone acetyltransferase type B catalytic subunit	100.0	3.35E-17
Q9BQ04	RNA-binding protein 4B	100.0	3.35E-17
O60282-1	kinesin heavy chain isoform 5C	100.0	3.35E-17
P11908	ribose-phosphate pyrophosphokinase 2	100.0	3.35E-17
O43169	Cytochrome b5 type B	100.0	3.35E-17
Q99986	Serine/threonine-protein kinase VRK1	100.0	3.35E-17
Q58FF6	Putative heat shock protein HSP 90-beta 4	100.0	3.35E-17
Q58FG1	Putative heat shock protein HSP 90-alpha A4	100.0	3.35E-17
Q9Y6M7-7	Isoform 7 of Sodium bicarbonate cotransporter 3	100.0	3.35E-17
Q12789-2	General transcription factor 3C polypeptide 1	100.0	3.35E-17
Q8WUD1	Ras-related protein Rab-2B	100.0	3.35E-17
P22830-1	Ferrochelatase, mitochondrial	100.0	3.35E-17
P30837	Aldehyde dehydrogenase X, mitochondrial	100.0	3.35E-17
O94901-1	SUN domain-containing protein 1	100.0	3.35E-17
O95678	Keratin, type II cytoskeletal 75	100.0	3.35E-17
Q8N543	prolyl 3-hydroxylase OGFOD1	100.0	3.35E-17
P20339	Ras-related protein Rab-5A	100.0	3.35E-17
P08237	ATP-dependent 6-phosphofructokinase, muscle type	100.0	3.35E-17
O75306-1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	100.0	3.35E-17
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4	100.0	3.35E-17
Q8N201	integrator complex subunit 1	100.0	3.35E-17
Q01546	Keratin, type II cytoskeletal 2 oral	100.0	3.35E-17
P83916	Chromobox protein homolog 1	100.0	3.35E-17
P23434	Glycine cleavage system H protein, mitochondrial	100.0	3.35E-17
P06756	Integrin alpha-V	100.0	3.35E-17
Q14004-1	Cyclin-dependent kinase 13	100.0	3.35E-17
Q9Y5X2	Sorting nexin-8	100.0	3.35E-17
P61326	Protein mago nashi homolog	100.0	3.35E-17
Q6NZY4	Zinc finger CCHC domain-containing protein 8	100.0	3.35E-17
Q14165	Malectin	100.0	3.35E-17
Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8IVL6-1	Prolyl 3-hydroxylase 3	100.0	3.35E-17
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	100.0	3.35E-17
O94804	Serine/threonine-protein kinase 10	100.0	3.35E-17
P07602-1	Prosaposin	100.0	3.35E-17
Q9NY27	Serine/threonine-protein phosphatase 4 regulatory subunit 2	100.0	3.35E-17
Q9Y5S9	RNA-binding protein 8A	100.0	3.35E-17
Q8N1B4	Vacuolar protein sorting-associated protein 52 homolog	100.0	3.35E-17
Q96QD8	sodium-coupled neutral amino acid transporter 2	100.0	3.35E-17
P01116-2	Isoform 2B of GTPase KRas	100.0	3.35E-17
Q12873-1	Chromodomain-helicase-DNA-binding protein 3	100.0	3.35E-17
P61619	Protein transport protein Sec61 subunit alpha isoform 1	100.0	3.35E-17
O60234	glia maturation factor gamma	100.0	3.35E-17
Q96M27-1	protein PRRC1	100.0	3.35E-17
Q13153	Serine/threonine-protein kinase PAK 1	100.0	3.35E-17
Q9H1I8-1	Activating signal cointegrator 1 complex subunit 2	100.0	3.35E-17
P40616	ADP-ribosylation factor-like protein 1	100.0	3.35E-17
P10155-1	60 kDa SS-A/Ro ribonucleoprotein	100.0	3.35E-17
Q49AR2-1	UPF0489 protein C5orf22	100.0	3.35E-17
Q96DV4	39S ribosomal protein L38, mitochondrial	100.0	3.35E-17
Q96FJ2	Dynein light chain 2, cytoplasmic	100.0	3.35E-17
Q9Y394	Dehydrogenase/reductase SDR family member 7	100.0	3.35E-17
O95864	fatty acid desaturase 2	100.0	3.35E-17
Q9UKG1	DCC-interacting protein 13-alpha	100.0	3.35E-17
Q8IXI2-1	Mitochondrial Rho GTPase 1	100.0	3.35E-17
Q9H6T3	RNA polymerase II-associated protein 3	100.0	3.35E-17
Q13546	Receptor-interacting serine/threonine-protein kinase 1	100.0	3.35E-17
Q9UHJ6	Sedoheptulokinase	100.0	3.35E-17
Q8N2K0	Monoacylglycerol lipase ABHD12	100.0	3.35E-17
Q9UBL3-1	Set1/Ash2 histone methyltransferase complex subunit ASH2	100.0	3.35E-17
A8MXV4	nucleoside diphosphate-linked moiety X motif 19	100.0	3.35E-17
Q96GM5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	100.0	3.35E-17
P35573-1	glycogen debranching enzyme	100.0	3.35E-17
Q9Y3L3-1	SH3 domain-binding protein 1	100.0	3.35E-17
Q8IYS2-1	Uncharacterized protein KIAA2013	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NV31	U3 small nucleolar ribonucleoprotein protein IMP3	100.0	3.35E-17
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1	100.0	3.35E-17
Q15738	sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	100.0	3.35E-17
Q9NU22	Midasin	100.0	3.35E-17
P22694-1	cAMP-dependent protein kinase catalytic subunit beta	100.0	3.35E-17
Q96CW5	Gamma-tubulin complex component 3	100.0	3.35E-17
Q96C23	aldose 1-epimerase	100.0	3.35E-17
Q96N66-1	Lysophospholipid acyltransferase 7	100.0	3.35E-17
O15084-1	Isoform 3 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	100.0	3.35E-17
Q8NFW8	N-acylneuraminate cytidylyltransferase	100.0	3.35E-17
P04062	glucosylceramidase	100.0	3.35E-17
Q2TAL8	Glutamine-rich protein 1	100.0	3.35E-17
Q96SI9	spermatid perinuclear RNA-binding protein	100.0	3.35E-17
Q8TDZ2	[F-actin]-monooxygenase MICAL1	100.0	3.35E-17
P09884	DNA polymerase alpha catalytic subunit	100.0	3.35E-17
Q14919-1	Dr1-associated corepressor	100.0	3.35E-17
P78332	RNA-binding protein 6	100.0	3.35E-17
Q9HD26-1	Golgi-associated PDZ and coiled-coil motif-containing protein	100.0	3.35E-17
Q9BQS8	fyve and coiled-coil domain-containing protein 1	100.0	3.35E-17
Q8TCD5	5′(3′)-deoxyribonucleotidase, cytosolic type	100.0	3.35E-17
Q9GZP9	Derlin-2	100.0	3.35E-17
Q9UFC0	Leucine-rich repeat and WD repeat-containing protein 1	100.0	3.35E-17
Q63HN8-4	Isoform 2 of E3 ubiquitin-protein ligase RNF213	100.0	3.35E-17
Q96BJ3-1	Axin interactor, dorsalization-associated protein	100.0	3.35E-17
Q9UBN7-1	histone deacetylase 6	100.0	3.35E-17
Q96KA5-1	cleft lip and palate transmembrane protein 1-like protein	100.0	3.35E-17
O60218	Aldo-keto reductase family 1 member B10	100.0	3.35E-17
P12532	Creatine kinase U-type, mitochondrial	100.0	3.35E-17
Q9BTX1	Nucleoporin Ndc1	100.0	3.35E-17
Q8N6R0-5	Methyltransferase-like protein 13	100.0	3.35E-17
Q9H061-1	Transmembrane protein 126A	100.0	3.35E-17
Q8TED0	U3 small nucleolar RNA-associated protein 15 homolog	100.0	3.35E-17
O75976	Carboxypeptidase D	100.0	3.35E-17
Q15404-1	Ras suppressor protein 1	100.0	3.35E-17
Q9Y5P4-1	Collagen type IV alpha-3-binding protein	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BZX2-1	Uridine-cytidine kinase 2	100.0	3.35E-17
P20248	Cyclin-A2	100.0	3.35E-17
Q9BRG1	Vacuolar protein-sorting-associated protein 25	100.0	3.35E-17
Q9Y3P9	Rab GTPase-activating protein 1	100.0	3.35E-17
Q4KMP7	TBC1 domain family member 10B	100.0	3.35E-17
O95983-1	methyl-CpG-binding domain protein 3	100.0	3.35E-17
Q9BRF8-1	Serine/threonine-protein phosphatase CPPED1	100.0	3.35E-17
Q86XI2-1	condensin-2 complex subunit G2	100.0	3.35E-17
Q9BSC4-1	Nucleolar protein 10	100.0	3.35E-17
O15270	Serine palmitoyltransferase 2	100.0	3.35E-17
Q96RE7	Nucleus accumbens-associated protein 1	100.0	3.35E-17
O15118	Niemann-Pick C1 protein	100.0	3.35E-17
Q96KP1	exocyst complex component 2	100.0	3.35E-17
O00217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	100.0	3.35E-17
Q96ER3	protein saal1	100.0	3.35E-17
Q9Y3E1	Hepatoma-derived growth factor-related protein 3	100.0	3.35E-17
P82650	28S ribosomal protein S22, mitochondrial	100.0	3.35E-17
P40855-1	Peroxisomal biogenesis factor 19	100.0	3.35E-17
P51784	Ubiquitin carboxyl-terminal hydrolase 11	100.0	3.35E-17
P29992	guanine nucleotide-binding protein subunit alpha-11	100.0	3.35E-17
Q12824-1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	100.0	3.35E-17
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like	100.0	3.35E-17
P62745	Rho-related GTP-binding protein RhoB	100.0	3.35E-17
Q9UH62	Armadillo repeat-containing X-linked protein 3	100.0	3.35E-17
O00566	U3 small nucleolar ribonucleoprotein protein Mpp10	100.0	3.35E-17
Q7Z2W9	39S ribosomal protein L21, mitochondrial	100.0	3.35E-17
O95819	Mitogen-activated protein kinase kinase kinase kinase 4	100.0	3.35E-17
O95905	Protein ecdysoneless homolog	100.0	3.35E-17
Q9BTY2	Plasma alpha-L-fucosidase	100.0	3.35E-17
Q9NVD7	alpha-parvin	100.0	3.35E-17
O15116	U6 snRNA-associated Sm-like protein LSm1	100.0	3.35E-17
Q9Y2A7-1	Nck-associated protein 1	100.0	3.35E-17
O95292	Vesicle-associated membrane protein-associated protein B/C	100.0	3.35E-17
P19447	TFIIH basal transcription factor complex helicase XPB subunit	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q86U06-1	probable RNA-binding protein 23	100.0	3.35E-17
Q14194-1	Dihydropyrimidinase-related protein 1	100.0	3.35E-17
Q9HC07	Transmembrane protein 165	100.0	3.35E-17
Q08AM6	Protein VAC14 homolog	100.0	3.35E-17
Q99570	Phosphoinositide 3-kinase regulatory subunit 4	100.0	3.35E-17
Q15286	Ras-related protein Rab-35	100.0	3.35E-17
Q6NUM9-1	all-trans-retinol 13,14-reductase	100.0	3.35E-17
Q9NR19-1	Acetyl-coenzyme A synthetase, cytoplasmic	100.0	3.35E-17
Q6UXN9	WD repeat-containing protein 82	100.0	3.35E-17
Q9HC36	rRNA methyltransferase 3, mitochondrial	100.0	3.35E-17
Q7Z7H5	Transmembrane emp24 domain-containing protein 4	100.0	3.35E-17
Q9UID3-1	Vacuolar protein sorting-associated protein 51 homolog	100.0	3.35E-17
Q9Y315	deoxyribose-phosphate aldolase	100.0	3.35E-17
P35610	sterol O-acyltransferase 1	100.0	3.35E-17
Q96QD9-1	UAP56-interacting factor	100.0	3.35E-17
P09619	Platelet-derived growth factor receptor beta	100.0	3.35E-17
Q9H9C1-1	Spermatogenesis-defective protein 39 homolog	100.0	3.35E-17
Q96L92	Sorting nexin-27	100.0	3.35E-17
P49354	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	100.0	3.35E-17
Q03519-1	antigen peptide transporter 2	100.0	3.35E-17
Q96SY0	Integrator complex subunit 14	100.0	3.35E-17
Q02297-1	Pro-neuregulin-1, membrane-bound isoform	100.0	3.35E-17
O94915-1	protein furry homolog-like	100.0	3.35E-17
Q5SRD1	Putative mitochondrial import inner membrane translocase subunit Tim23B	100.0	3.35E-17
Q9Y3Y2	Chromatin target of PRMT1 protein	100.0	3.35E-17
Q8TD30-1	Alanine aminotransferase 2	100.0	3.35E-17
Q96RF0	Sorting nexin-18	100.0	3.35E-17
Q9C0E2	Exportin-4	100.0	3.35E-17
Q9NXH9-1	tRNA (guanine(26)-N(2))-dimethyltransferase	100.0	3.35E-17
P62070	Ras-related protein R-Ras2	100.0	3.35E-17
Q6DKI1	60S ribosomal protein L7-like 1	100.0	3.35E-17
P06400	Retinoblastoma-associated protein	100.0	3.35E-17
O95870-1	Protein ABHD16A	100.0	3.35E-17
Q86WA8	Lon protease homolog 2, peroxisomal	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NVH1-1	DnaJ homolog subfamily C member 11	100.0	3.35E-17
P50336	protoporphyrinogen oxidase	100.0	3.35E-17
Q15262	Receptor-type tyrosine-protein phosphatase kappa	100.0	3.35E-17
Q15052	Rho guanine nucleotide exchange factor 6	100.0	3.35E-17
Q13505-1	Metaxin-1	100.0	3.35E-17
Q86TN4	tRNA 2′-phosphotransferase 1	100.0	3.35E-17
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial	100.0	3.35E-17
Q9UJX2-1	cell division cycle protein 23 homolog	100.0	3.35E-17
Q6NZ67	Mitotic-spindle organizing protein 2B	100.0	3.35E-17
Q13618	Cullin-3	100.0	3.35E-17
Q9NZ32	Actin-related protein 10	100.0	3.35E-17
O60942-1	mRNA-capping enzyme	100.0	3.35E-17
Q9UBB6	Neurochondrin	100.0	3.35E-17
Q5VV42	threonylcarbamoyladenosine tRNA methylthiotransferase	100.0	3.35E-17
Q8IXH7	Negative elongation factor C/D	100.0	3.35E-17
Q8ND24	Ring finger protein 214	100.0	3.35E-17
P17152	Transmembrane protein 11, mitochondrial	100.0	3.35E-17
Q9NX47	E3 ubiquitin-protein ligase MARCH5	100.0	3.35E-17
O60318	Germinal-center associated nuclear protein	100.0	3.35E-17
Q7LGA3-1	Heparan sulfate 2-O-sulfotransferase 1	100.0	3.35E-17
P30536	translocator protein	100.0	3.35E-17
Q9UNL2	Translocon-associated protein subunit gamma	100.0	3.35E-17
Q12768	WASH complex subunit 5	100.0	3.35E-17
Q68E01	Integrator complex subunit 3	100.0	3.35E-17
Q6IAN0	Dehydrogenase/reductase SDR family member 7B	100.0	3.35E-17
Q9Y3I1	F-box only protein 7	100.0	3.35E-17
Q9UBS4	DnaJ homolog subfamily B member 11	100.0	3.35E-17
Q658Y4	Protein FAM91A1	100.0	3.35E-17
Q9P260-1	LisH domain and HEAT repeat-containing protein KIAA1468	100.0	3.35E-17
Q9Y6A9	Signal peptidase complex subunit 1	100.0	3.35E-17
Q6IQ22	Ras-related protein Rab-12	100.0	3.35E-17
Q03113	Guanine nucleotide-binding protein subunit alpha-12	100.0	3.35E-17
P50583	Bis(5′-nucleosyl)-tetraphosphatase [asymmetrical]	100.0	3.35E-17
Q8IYS1	Peptidase M20 domain-containing protein 2	100.0	3.35E-17
Q9HBH1	Peptide deformylase, mitochondrial	100.0	3.35E-17
P13473-1	Lysosome-associated membrane glycoprotein 2	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q15007	Pre-mRNA-splicing regulator WTAP	100.0	3.35E-17
Q9Y5Q9	General transcription factor 3C polypeptide 3	100.0	3.35E-17
P53384	Cytosolic Fe-S cluster assembly factor nubp1	100.0	3.35E-17
Q9NQ55-1	suppressor of SWI4 1 homolog	100.0	3.35E-17
Q96BW9-1	Phosphatidate cytidylyltransferase, mitochondrial	100.0	3.35E-17
Q13015	protein AF1q	100.0	3.35E-17
P41214	Eukaryotic translation initiation factor 2d	100.0	3.35E-17
P18084	Integrin beta-5	100.0	3.35E-17
P38435-1	vitamin K-dependent gamma-carboxylase	100.0	3.35E-17
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial	100.0	3.35E-17
Q659C4-1	La-related protein 1B	100.0	3.35E-17
Q9UM00-1	Calcium load-activated calcium channel	100.0	3.35E-17
Q9NP77	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	100.0	3.35E-17
Q00013-1	55 kDa erythrocyte membrane protein	100.0	3.35E-17
Q9NZQ3-1	NCK-interacting protein with SH3 domain	100.0	3.35E-17
P20585	DNA mismatch repair protein MSH3	100.0	3.35E-17
P15927-1	Replication protein A 32 kDa subunit	100.0	3.35E-17
Q6P1N9-1	Putative deoxyribonuclease TATDN1	100.0	3.35E-17
Q86TU7	Histone-lysine N-methyltransferase setd3	100.0	3.35E-17
Q9Y496	kinesin-like protein KIF3A	100.0	3.35E-17
P42785-1	lysosomal Pro-X carboxypeptidase	100.0	3.35E-17
Q6PJI9-1	GATOR complex protein WDR59	100.0	3.35E-17
Q4V328-2	Isoform 2 of GRIP1-associated protein 1	100.0	3.35E-17
O15382	Branched-chain-amino-acid aminotransferase, mitochondrial	100.0	3.35E-17
Q8TEA8	D-aminoacyl-tRNA deacylase 1	100.0	3.35E-17
Q6U841	Sodium-driven chloride bicarbonate exchanger	100.0	3.35E-17
Q9BYM8	ranBP-type and C3HC4-type zinc finger-containing protein 1	100.0	3.35E-17
P38432	coilin	100.0	3.35E-17
Q9UP95	Solute carrier family 12 member 4	100.0	3.35E-17
Q32P41	tRNA (guanine(37)-N1)-methyltransferase	100.0	3.35E-17
Q9BRX2	Protein pelota homolog	100.0	3.35E-17
Q8IY95	transmembrane protein 192	100.0	3.35E-17
Q8N2U0	Transmembrane protein 256	100.0	3.35E-17
Q9UBV2	Protein sel-1 homolog 1	100.0	3.35E-17
Q9H2P9-1	Diphthine methyl ester synthase	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q969E8	pre-rRNA-processing protein TSR2 homolog	100.0	3.35E-17
Q9Y3A4	Ribosomal RNA-processing protein 7 homolog A	100.0	3.35E-17
Q9UPT5	Exocyst complex component 7	100.0	3.35E-17
Q30201-1	Hereditary hemochromatosis protein	100.0	3.35E-17
Q96AB3	isochorismatase domain-containing protein 2	100.0	3.35E-17
O75616-1	GTPase Era, mitochondrial	100.0	3.35E-17
Q9NRL3	Striatin-4	100.0	3.35E-17
Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	100.0	3.35E-17
P57678	Gem-associated protein 4	100.0	3.35E-17
Q9BZL6	Serine/threonine-protein kinase D2	100.0	3.35E-17
Q8NDT2	Putative RNA-binding protein 15B	100.0	3.35E-17
Q9UIV1-1	CCR4-NOT transcription complex subunit 7	100.0	3.35E-17
Q9NTX5	Ethylmalonyl-CoA decarboxylase	100.0	3.35E-17
Q6RW13	Type-1 angiotensin II receptor-associated protein	100.0	3.35E-17
Q9NRX1	RNA-binding protein pno1	100.0	3.35E-17
Q8TF74	WAS/WASL-interacting protein family member 2	100.0	3.35E-17
P52655-1	Transcription initiation factor IIA subunit 1	100.0	3.35E-17
Q9Y4G8	rap guanine nucleotide exchange factor 2	100.0	3.35E-17
Q9BUL5-1	PHD finger protein 23	100.0	3.35E-17
P48426	phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	100.0	3.35E-17
Q9Y5J6	Mitochondrial import inner membrane translocase subunit Tim10 B	100.0	3.35E-17
P28290	Sperm-specific antigen 2	100.0	3.35E-17
Q7Z7H8	39S ribosomal protein L10, mitochondrial	100.0	3.35E-17
Q9NTM9	Copper homeostasis protein cutC homolog	100.0	3.35E-17
Q13451-1	Peptidyl-prolyl cis-trans isomerase FKBP5	100.0	3.35E-17
Q9UHD2	Serine/threonine-protein kinase TBK1	100.0	3.35E-17
Q8IUI8	Cytokine receptor-like factor 3	100.0	3.35E-17
P19388	DNA-directed RNA polymerases I, II, and III subunit RPABC1	100.0	3.35E-17
P51948-1	CDK-activating kinase assembly factor MAT1	100.0	3.35E-17
Q9NZJ7	Mitochondrial carrier homolog 1	100.0	3.35E-17
P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial	100.0	3.35E-17
P17096-2	Isoform HMG-Y of High mobility group protein HMG-I/HMG-Y	100.0	3.35E-17
Q9UL63-1	muskelin	100.0	3.35E-17
Q9H6E5	Speckle targeted PIP5K1A-regulated poly(A) polymerase	100.0	3.35E-17
Q15043	Zinc transporter ZIP14	100.0	3.35E-17
Q93050-1	Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O43592	Exportin-T	100.0	3.35E-17
Q8NFZ8	Cell adhesion molecule 4	100.0	3.35E-17
O96011-1	Peroxisomal membrane protein 11B	100.0	3.35E-17
O95302	Peptidyl-prolyl cis-trans isomerase FKBP9	100.0	3.35E-17
P09601	heme oxygenase 1	100.0	3.35E-17
Q53EU6	Glycerol-3-phosphate acyltransferase 3	100.0	3.35E-17
Q9UKG9-1	peroxisomal carnitine O-octanoyltransferase	100.0	3.35E-17
Q99836	Myeloid differentiation primary response protein MyD88	100.0	3.35E-17
P56134	ATP synthase subunit f, mitochondrial	100.0	3.35E-17
Q3LXA3	Triokinase/FMN cyclase	100.0	3.35E-17
Q15397	Pumilio homolog 3	100.0	3.35E-17
Q9BV68-1	E3 ubiquitin-protein ligase RNF126	100.0	3.35E-17
Q15276	Rab GTPase-binding effector protein 1	100.0	3.35E-17
Q9NUL3	Double-stranded RNA-binding protein Staufen homolog 2	100.0	3.35E-17
Q8N0U8	Vitamin K epoxide reductase complex subunit 1-like protein 1	100.0	3.35E-17
Q53GG5-1	PDZ and LIM domain protein 3	100.0	3.35E-17
Q96GM8	Target of EGR1 protein 1	100.0	3.35E-17
Q969M3	Protein YIPF5	100.0	3.35E-17
O00767	acyl-CoA desaturase	100.0	3.35E-17
Q12894	Interferon-related developmental regulator 2	100.0	3.35E-17
Q02040-1	A-kinase anchor protein 17A	100.0	3.35E-17
Q8TB52	F-box only protein 30	100.0	3.35E-17
Q8TB61	Adenosine 3′-phospho 5′-phosphosulfate transporter 1	100.0	3.35E-17
Q12830-1	Nucleosome-remodeling factor subunit BPTF	100.0	3.35E-17
O00459	Phosphatidylinositol 3-kinase regulatory subunit beta	100.0	3.35E-17
P43007-1	neutral amino acid transporter A	100.0	3.35E-17
Q9UK41-1	vacuolar protein sorting-associated protein 28 homolog	100.0	3.35E-17
Q7Z4R8	UPF0669 protein C6orf120	100.0	3.35E-17
Q86Y82	Syntaxin-12	100.0	3.35E-17
Q8WUY8	N-acetyltransferase 14	100.0	3.35E-17
O15498	Synaptobrevin homolog YKT6	100.0	3.35E-17
P62699	Protein yippee-like 5	100.0	3.35E-17
O95834	echinoderm microtubule-associated protein-like 2	100.0	3.35E-17
Q13112	Chromatin assembly factor 1 subunit B	100.0	3.35E-17
Q68D91-1	Metallo-beta-lactamase domain-containing protein 2	100.0	3.35E-17
Q969S3	Zinc finger protein 622	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8IV38	Ankyrin repeat and MYND domain-containing protein 2	100.0	3.35E-17
Q6ZVM7	TOM1-like protein 2	100.0	3.35E-17
Q9Y303	N-acetylglucosamine-6-phosphate deacetylase	100.0	3.35E-17
Q99489-1	D-aspartate oxidase	100.0	3.35E-17
Q5T8D3-3	Isoform 3 of Acyl-CoA-binding domain-containing protein 5	100.0	3.35E-17
Q9Y2P8	RNA 3′-terminal phosphate cyclase-like protein	100.0	3.35E-17
Q6SZW1	Sterile alpha and TIR motif-containing protein 1	100.0	3.35E-17
Q9Y2H0-1	Isoform 2 of Disks large-associated protein 4	100.0	3.35E-17
Q9NVS2	39S ribosomal protein S18a, mitochondrial	100.0	3.35E-17
Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	100.0	3.35E-17
Q5T9L3	Protein wntless homolog	100.0	3.35E-17
Q8TCE6-1	Protein FAM45A	100.0	3.35E-17
P51692	Signal transducer and activator of transcription 5B	100.0	3.35E-17
Q9UBF8	Phosphatidylinositol 4-kinase beta	100.0	3.35E-17
O00186	syntaxin-binding protein 3	100.0	3.35E-17
Q6VN20	Ran-binding protein 10	100.0	3.35E-17
O95260	Arginyl-tRNA–protein transferase 1	100.0	3.35E-17
P53365	Arfaptin-2	100.0	3.35E-17
Q15904	V-type proton ATPase subunit S1	100.0	3.35E-17
Q9NP73-1	Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13	100.0	3.35E-17
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	100.0	3.35E-17
Q9NXR7-2	BRISC and BRCA1-A complex member 2	100.0	3.35E-17
Q8NDI1	EH domain-binding protein 1	100.0	3.35E-17
Q9BQ69	O-acetyl-ADP-ribose deacetylase MACROD1	100.0	3.35E-17
Q9H147	Deoxynucleotidyltransferase terminal-interacting protein 1	100.0	3.35E-17
Q13616	Cullin-1	100.0	3.35E-17
Q53F19	Nuclear cap-binding protein subunit 3	100.0	3.35E-17
Q96G21	U3 small nucleolar ribonucleoprotein protein IMP4	100.0	3.35E-17
Q7KZI7-1	Serine/threonine-protein kinase MARK2	100.0	3.35E-17
Q6UX53	Methyltransferase-like protein 7B	100.0	3.35E-17
O60563	Cyclin-T1	100.0	3.35E-17
Q9UNP9-1	Peptidyl-prolyl cis-trans isomerase E	100.0	3.35E-17
Q15147-1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4	100.0	3.35E-17
Q9NUM4	Transmembrane protein 106B	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P08648	Integrin alpha-5	100.0	3.35E-17
P42226	Signal transducer and activator of transcription 6	100.0	3.35E-17
Q9C0E8-1	Protein lunapark	100.0	3.35E-17
Q09472	Histone acetyltransferase p300	100.0	3.35E-17
Q9Y3L5	ras-related protein Rap-2c	100.0	3.35E-17
Q969U7	Proteasome assembly chaperone 2	100.0	3.35E-17
O75530	Polycomb protein EED	100.0	3.35E-17
P27448-7	Isoform 6 of MAP/microtubule affinity-regulating kinase 3	100.0	3.35E-17
Q01628	Interferon-induced transmembrane protein 3	100.0	3.35E-17
P27105	erythrocyte band 7 integral membrane protein	100.0	3.35E-17
O95989	Diphosphoinositol polyphosphate phosphohydrolase 1	100.0	3.35E-17
P52435	DNA-directed RNA polymerase II subunit RPB11-a	100.0	3.35E-17
O95169	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	100.0	3.35E-17
O14653-1	Golgi SNAP receptor complex member 2	100.0	3.35E-17
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1	100.0	3.35E-17
Q9UHG3	prenylcysteine oxidase 1	100.0	3.35E-17
Q4L180	Filamin A-interacting protein 1-like	100.0	3.35E-17
Q12979	active breakpoint cluster region-related protein	100.0	3.35E-17
Q9ULJ7-1	Ankyrin repeat domain-containing protein 50	100.0	3.35E-17
Q9UBI1	COMM domain-containing protein 3	100.0	3.35E-17
Q9UPT9-1	ubiquitin carboxyl-terminal hydrolase 22	100.0	3.35E-17
Q9NVI1-3	Fanconi anemia group I protein	100.0	3.35E-17
Q8IWJ2	GRIP and coiled-coil domain-containing protein 2	100.0	3.35E-17
P78330	phosphoserine phosphatase	100.0	3.35E-17
Q96LW7-2	Isoform 2 of Caspase recruitment domain-containing protein 19	100.0	3.35E-17
Q9NZI7	Upstream-binding protein 1	100.0	3.35E-17
Q9Y4F1	FERM, RhoGEF and pleckstrin domain-containing protein 1	100.0	3.35E-17
Q8NEW0	Zinc transporter 7	100.0	3.35E-17
Q9BYX2	TBC1 domain family member 2A	100.0	3.35E-17
P53794	sodium/myo-inositol cotransporter	100.0	3.35E-17
P22304	iduronate 2-sulfatase	100.0	3.35E-17
P61225	ras-related protein Rap-2b	100.0	3.35E-17
O95785	Protein Wiz	100.0	3.35E-17
O60343-1	TBC1 domain family member 4	100.0	3.35E-17
Q9NR46	Endophilin-B2	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9P286	Serine/threonine-protein kinase PAK 5	100.0	3.35E-17
O43674-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	100.0	3.35E-17
Q13769	THO complex subunit 5 homolog	100.0	3.35E-17
Q9Y2I1-1	Nischarin	100.0	3.35E-17
O75027-1	ATP-binding cassette sub-family B member 7, mitochondrial	100.0	3.35E-17
Q9BUL8	programmed cell death protein 10	100.0	3.35E-17
P60002	Transcription elongation factor 1 homolog	100.0	3.35E-17
Q8TBQ9	Protein kish-A	100.0	3.35E-17
Q8NHG7	Small VCP/p97-interacting protein	100.0	3.35E-17
P25490	Transcriptional repressor protein YY1	100.0	3.35E-17
Q9UBP9	PTB domain-containing engulfment adapter protein 1	100.0	3.35E-17
Q9BZQ8	Protein Niban	100.0	3.35E-17
Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	100.0	3.35E-17
Q13472-1	DNA topoisomerase 3-alpha	100.0	3.35E-17
Q8WX92	Negative elongation factor B	100.0	3.35E-17
Q9BRT9	DNA replication complex GINS protein SLD5	100.0	3.35E-17
Q93074-1	Mediator of RNA polymerase II transcription subunit 12	100.0	3.35E-17
P28161	Glutathione S-transferase Mu 2	100.0	3.35E-17
Q96SB8	structural maintenance of chromosomes protein 6	100.0	3.35E-17
Q15554-3	Telomeric repeat-binding factor 2	100.0	3.35E-17
O43819	Protein SCO2 homolog, mitochondrial	100.0	3.35E-17
Q7Z7N9	Transmembrane protein 179B	100.0	3.35E-17
Q9UHA4	ragulator complex protein LAMTOR3	100.0	3.35E-17
Q8NCC3	Group XV phospholipase A2	100.0	3.35E-17
O95456	Proteasome assembly chaperone 1	100.0	3.35E-17
Q0ZGT2	Nexilin	100.0	3.35E-17
P04424	argininosuccinate lyase	100.0	3.35E-17
Q96EF6	F-box only protein 17	100.0	3.35E-17
Q9P2K5-1	Myelin expression factor 2	100.0	3.35E-17
Q5J8M3-1	ER membrane protein complex subunit 4	100.0	3.35E-17
Q15477	Helicase SKI2W	100.0	3.35E-17
O00221	NF-kappa-B inhibitor epsilon	100.0	3.35E-17
Q643R3	lysophospholipid acyltransferase LPCAT4	100.0	3.35E-17
O75446	Histone deacetylase complex subunit SAP30	100.0	3.35E-17
Q8IWR0	Zinc finger CCCH domain-containing protein 7A	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q7Z2E3-1	Aprataxin	100.0	3.35E-17
Q4G0F5	Vacuolar protein sorting-associated protein 26B	100.0	3.35E-17
Q8NE86	Calcium uniporter protein, mitochondrial	100.0	3.35E-17
Q9BSY4	Coiled-coil-helix-coiled-coil-helix domain-containing protein 5	100.0	3.35E-17
Q9Y3E0	vesicle transport protein GOT1B	100.0	3.35E-17
Q9BV81	ER membrane protein complex subunit 6	100.0	3.35E-17
P56211	cAMP-regulated phosphoprotein 19	100.0	3.35E-17
Q13043-1	serine/threonine-protein kinase 4	100.0	3.35E-17
P17029	Zinc finger protein with KRAB and SCAN domains 1	100.0	3.35E-17
Q9UI26	Importin-11	100.0	3.35E-17
Q9BZJ0	Crooked neck-like protein 1	100.0	3.35E-17
Q6P9B9	Integrator complex subunit 5	100.0	3.35E-17
Q16656-1	Nuclear respiratory factor 1	100.0	3.35E-17
Q9C0I1	Myotubularin-related protein 12	100.0	3.35E-17
Q9UJF2	ras GTPase-activating protein nGAP	100.0	3.35E-17
Q9UPN9-1	E3 ubiquitin-protein ligase TRIM33	100.0	3.35E-17
O60333-3	Isoform 3 of Kinesin-like protein KIF1B	100.0	3.35E-17
P98194-1	Calcium-transporting ATPase type 2C member 1	100.0	3.35E-17
Q8N4H5	mitochondrial import receptor subunit TOM5 homolog	100.0	3.35E-17
Q8TCY9	Up-regulator of cell proliferation	100.0	3.35E-17
Q9H0R4-1	haloacid dehalogenase-like hydrolase domain-containing protein 2	100.0	3.35E-17
Q9HBH5	Retinol dehydrogenase 14	100.0	3.35E-17
P23443-1	Ribosomal protein S6 kinase beta-1	100.0	3.35E-17
O14578	Citron Rho-interacting kinase	100.0	3.35E-17
P05161	Ubiquitin-like protein ISG15	100.0	3.35E-17
Q5HYI7	Metaxin-3	100.0	3.35E-17
Q14139	ubiquitin conjugation factor e4 a	100.0	3.35E-17
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	100.0	3.35E-17
Q6SPF0	Atherin	100.0	3.35E-17
Q8TBM8	dnaJ homolog subfamily B member 14	100.0	3.35E-17
A6NDU8	UPF0600 protein C5orf51	100.0	3.35E-17
Q96ER9	Coiled-coil domain-containing protein 51	100.0	3.35E-17
O60551	Glycylpeptide N-tetradecanoyltransferase 2	100.0	3.35E-17
Q9UKV8	Protein argonaute-2	100.0	3.35E-17
Q8NBL1	Protein O-glucosyltransferase 1	100.0	3.35E-17
Q5JPH6	Probable glutamate–tRNA ligase, mitochondrial	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q6UWU4-1	Bombesin receptor-activated protein C6orf89	100.0	3.35E-17
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	100.0	3.35E-17
E9PRG8	Uncharacterized protein C11orf98	100.0	3.35E-17
Q9UBV8	Peflin	100.0	3.35E-17
P22670	MHC class II regulatory factor RFX1	100.0	3.35E-17
Q9UN81	LINE-1 retrotransposable element ORF1 protein	100.0	3.35E-17
Q8WUX9	Charged multivesicular body protein 7	100.0	3.35E-17
Q96MW1	Coiled-coil domain-containing protein 43	100.0	3.35E-17
O15182	Centrin-3	100.0	3.35E-17
Q86UE8	Serine/threonine-protein kinase tousled-like 2	100.0	3.35E-17
Q9NRP0-1	oligosaccharyltransferase complex subunit OSTC	100.0	3.35E-17
Q9Y4U1	Methylmalonic aciduria and homocystinuria type C protein	100.0	3.35E-17
Q9BQB6-1	vitamin K epoxide reductase complex subunit 1	100.0	3.35E-17
O00411	DNA-directed RNA polymerase, mitochondrial	100.0	3.35E-17
O94929-1	Actin-binding LIM protein 3	100.0	3.35E-17
O95825-1	Quinone oxidoreductase-like protein 1	100.0	3.35E-17
O75817	Ribonuclease P protein subunit p20	100.0	3.35E-17
Q8N5A5-1	Zinc finger CCCH-type with G patch domain-containing protein	100.0	3.35E-17
Q70E73	Ras-associated and pleckstrin homology domains-containing protein 1	100.0	3.35E-17
Q99653	Calcineurin B homologous protein 1	100.0	3.35E-17
Q96FN4	Copine-2	100.0	3.35E-17
Q8NEJ9	neuroguidin	100.0	3.35E-17
P51884	Lumican	100.0	3.35E-17
Q9BQ48	39S ribosomal protein L34, mitochondrial	100.0	3.35E-17
P04156-1	Major prion protein	100.0	3.35E-17
A0PJW6	Transmembrane protein 223	100.0	3.35E-17
Q8WTS6	Histone-lysine N-methyltransferase SETD7	100.0	3.35E-17
Q9Y282-1	Endoplasmic reticulum-Golgi intermediate compartment protein 3	100.0	3.35E-17
Q9Y478	5′-AMP-activated protein kinase subunit beta-1	100.0	3.35E-17
O15479	Melanoma-associated antigen B2	100.0	3.35E-17
Q53FT3	Protein Hikeshi	100.0	3.35E-17
Q7L592	Protein arginine methyltransferase NDUFAF7, mitochondrial	100.0	3.35E-17
Q8TCF1-1	AN1-type zinc finger protein 1	100.0	3.35E-17
Q9H1Z4	WD repeat-containing protein 13	100.0	3.35E-17
Q8NFA0	Ubiquitin carboxyl-terminal hydrolase 32	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q4KMQ2-1	Anoctamin-6	100.0	3.35E-17
P14406	Cytochrome c oxidase subunit 7A2, mitochondrial	100.0	3.35E-17
Q9BU89	Deoxyhypusine hydroxylase	100.0	3.35E-17
Q3YEC7-1	Rab-like protein 6	100.0	3.35E-17
Q9Y2R0	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	100.0	3.35E-17
O95183	vesicle-associated membrane protein 5	100.0	3.35E-17
Q9P265	Disco-interacting protein 2 homolog B	100.0	3.35E-17
Q9NPJ6-1	mediator of RNA polymerase II transcription subunit 4	100.0	3.35E-17
Q8TCC3	39S ribosomal protein L30, mitochondrial	100.0	3.35E-17
Q96R06	Sperm-associated antigen 5	100.0	3.35E-17
Q9BYC8	39S ribosomal protein L32, mitochondrial	100.0	3.35E-17
P32456	Guanylate-binding protein 2	100.0	3.35E-17
Q6ZSJ8	Uncharacterized protein C1orf122	100.0	3.35E-17
Q5VT79	annexin A8-like protein 1	100.0	3.35E-17
Q9H788	SH2 domain-containing protein 4A	100.0	3.35E-17
O43759-1	Synaptogyrin-1	100.0	3.35E-17
P50613	Cyclin-dependent kinase 7	100.0	3.35E-17
Q9H5N1	rab GTPase-binding effector protein 2	100.0	3.35E-17
Q96EH3	mitochondrial assembly of ribosomal large subunit protein 1	100.0	3.35E-17
Q9UG56-3	Phosphatidylserine decarboxylase proenzyme, mitochondrial	100.0	3.35E-17
Q6UWP7-1	Lysocardiolipin acyltransferase 1	100.0	3.35E-17
P08236	beta-glucuronidase	100.0	3.35E-17
Q9BTV5	fibronectin type III and SPRY domain-containing protein 1	100.0	3.35E-17
Q96EV8-1	dysbindin	100.0	3.35E-17
Q9Y4C2-1	TRPM8 channel-associated factor 1	100.0	3.35E-17
Q9H5V9-1	UPF0428 protein CXorf56	100.0	3.35E-17
Q9UQ13	Leucine-rich repeat protein SHOC-2	100.0	3.35E-17
Q9NVH6-1	Trimethyllysine dioxygenase, mitochondrial	100.0	3.35E-17
Q6PD74	Alpha- and gamma-adaptin-binding protein p34	100.0	3.35E-17
Q9UI14	Prenylated Rab acceptor protein 1	100.0	3.35E-17
Q9NWU5	39S ribosomal protein L22, mitochondrial	100.0	3.35E-17
O00418	Eukaryotic elongation factor 2 kinase	100.0	3.35E-17
Q9UBK8-1	Methionine synthase reductase	100.0	3.35E-17
Q5NDL2	EGF domain-specific O-linked N-acetylglucosamine transferase	100.0	3.35E-17
O95363	phenylalanine–tRNA ligase, mitochondrial	100.0	3.35E-17
Q01459	Di-N-acetylchitobiase	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q4VC31	coiled-coil domain-containing protein 58	100.0	3.35E-17
Q96Q15-1	Serine/threonine-protein kinase SMG1	100.0	3.35E-17
Q99735	microsomal glutathione S-transferase 2	100.0	3.35E-17
Q96LA8-1	protein arginine N-methyltransferase 6	100.0	3.35E-17
Q92889	DNA repair endonuclease XPF	100.0	3.35E-17
P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3	100.0	3.35E-17
Q9NUP1	Biogenesis of lysosome-related organelles complex 1 subunit 4	100.0	3.35E-17
Q8N954-1	G patch domain-containing protein 11	100.0	3.35E-17
Q9BSF4	Mitochondrial import inner membrane translocase subunit Tim29	100.0	3.35E-17
Q86TI0	TBC1 domain family member 1	100.0	3.35E-17
P03928	ATP synthase protein 8	100.0	3.35E-17
Q9BRT6	Protein LLP homolog	100.0	3.35E-17
Q6UXH1	Cysteine-rich with EGF-like domain protein 2	100.0	3.35E-17
Q567U6	Coiled-coil domain-containing protein 93	100.0	3.35E-17
O95298-1	NADH dehydrogenase [ubiquinone] 1 subunit C2	100.0	3.35E-17
O75382-1	Tripartite motif-containing protein 3	100.0	3.35E-17
Q96CN9	GRIP and coiled-coil domain-containing protein 1	100.0	3.35E-17
Q9BU76-1	Multiple myeloma tumor-associated protein 2	100.0	3.35E-17
Q9BQC6	Ribosomal protein 63, mitochondrial	100.0	3.35E-17
Q8WWC4	m-AAA protease-interacting protein 1, mitochondrial	100.0	3.35E-17
Q9NXV2	BTB/POZ domain-containing protein KCTD5	100.0	3.35E-17
Q92643	GPI-anchor transamidase	100.0	3.35E-17
Q8N531-1	F-box/LRR-repeat protein 6	100.0	3.35E-17
Q8IZX4	transcription initiation factor TFIID subunit 1-like	100.0	3.35E-17
Q969H6	Ribonuclease P/MRP protein subunit POP5	100.0	3.35E-17
Q5VSL9-1	striatin-interacting protein 1	100.0	3.35E-17
O14561	Acyl carrier protein, mitochondrial	100.0	3.35E-17
O00762	Ubiquitin-conjugating enzyme E2 C	100.0	3.35E-17
Q8IXK0	Polyhomeotic-like protein 2	100.0	3.35E-17
Q12882-1	Dihydropyrimidine dehydrogenase [NADP(+)]	100.0	3.35E-17
Q96IG2-1	F-box/LRR-repeat protein 20	100.0	3.35E-17
Q14746	Conserved oligomeric Golgi complex subunit 2	100.0	3.35E-17
Q9NXS2	Glutaminyl-peptide cyclotransferase-like protein	100.0	3.35E-17
P17050	alpha-N-acetylgalactosaminidase	100.0	3.35E-17
Q6XZF7	Dynamin-binding protein	100.0	3.35E-17
Q9BW60	Elongation of very long chain fatty acids protein 1	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O43414-1	ERI1 exoribonuclease 3	100.0	3.35E-17
Q9BVT8	transmembrane and ubiquitin-like domain-containing protein 1	100.0	3.35E-17
O43181	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	100.0	3.35E-17
P63218	guanine nucleotide-binding protein g(i)/g(s)/g(o) subunit gamma-5	100.0	3.35E-17
Q8WWN8	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3	100.0	3.35E-17
Q15349	Ribosomal protein S6 kinase alpha-2	100.0	3.35E-17
P61803	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase subunit DAD1	100.0	3.35E-17
P21359-1	Neurofibromin	100.0	3.35E-17
O75352	Mannose-P-dolichol utilization defect 1 protein	100.0	3.35E-17
Q96BX8	MOB kinase activator 3A	100.0	3.35E-17
Q7Z7E8-1	Ubiquitin-conjugating enzyme E2 Q1	100.0	3.35E-17
Q5K651	Sterile alpha motif domain-containing protein 9	100.0	3.35E-17
Q9H944	Mediator of RNA polymerase II transcription subunit 20	100.0	3.35E-17
Q9GZR2-1	RNA exonuclease 4	100.0	3.35E-17
Q15811	Intersectin-1	100.0	3.35E-17
O95249-1	Golgi SNAP receptor complex member 1	100.0	3.35E-17
Q9UJY5-1	ADP-ribosylation factor-binding protein GGA1	100.0	3.35E-17
Q9C0B7	Transport and Golgi organization protein 6 homolog	100.0	3.35E-17
Q9UGJ1	gamma-tubulin complex component 4	100.0	3.35E-17
Q3SXM5	Inactive hydroxysteroid dehydrogenase-like protein 1	100.0	3.35E-17
P61218	DNA-directed RNA polymerases I, II, and III subunit RPABC2	100.0	3.35E-17
Q13049	E3 ubiquitin-protein ligase TRIM32	100.0	3.35E-17
Q9BXJ8-1	Transmembrane protein 120A	100.0	3.35E-17
Q9H0W9	Ester hydrolase C11orf54	100.0	3.35E-17
P55268	laminin subunit beta-2	100.0	3.35E-17
Q9BUE0	Mediator of RNA polymerase II transcription subunit 18	100.0	3.35E-17
P51151	Ras-related protein Rab-9A	100.0	3.35E-17
Q9Y2V7-1	Conserved oligomeric Golgi complex subunit 6	100.0	3.35E-17
Q15649	Zinc finger HIT domain-containing protein 3	100.0	3.35E-17
O95777	U6 snRNA-associated Sm-like protein LSm8	100.0	3.35E-17
P23470	Receptor-type tyrosine-protein phosphatase gamma	100.0	3.35E-17
O75319-1	RNA/RNP complex-1-interacting phosphatase	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y4E5	E3 SUMO-protein ligase ZNF451	100.0	3.35E-17
P43155	Carnitine O-acetyltransferase	100.0	3.35E-17
A4D1P6-1	WD repeat-containing protein 91	100.0	3.35E-17
P23468-1	Receptor-type tyrosine-protein phosphatase delta	100.0	3.35E-17
Q9ULC3	Ras-related protein Rab-23	100.0	3.35E-17
Q6PJ69	Tripartite motif-containing protein 65	100.0	3.35E-17
O15260-1	surfeit locus protein 4	100.0	3.35E-17
P42356	phosphatidylinositol 4-kinase alpha	100.0	3.35E-17
Q9UBS0	Ribosomal protein S6 kinase beta-2	100.0	3.35E-17
Q9UNQ0-1	ATP-binding cassette sub-family G member 2	100.0	3.35E-17
Q8N4J0	carnosine N-methyltransferase	100.0	3.35E-17
Q9Y376	Calcium-binding protein 39	100.0	3.35E-17
P82914	28S ribosomal protein S15, mitochondrial	100.0	3.35E-17
Q14728	Major facilitator superfamily domain-containing protein 10	100.0	3.35E-17
P28289	Tropomodulin-1	100.0	3.35E-17
Q9BYC9	39S ribosomal protein L20, mitochondrial	100.0	3.35E-17
Q96HQ2-1	CDKN2AIP N-terminal-like protein	100.0	3.35E-17
Q8WXE0-1	caskin-2	100.0	3.35E-17
Q8IYL3	UPF0688 protein C1orf174	100.0	3.35E-17
P00846	ATP synthase subunit A	100.0	3.35E-17
P48443	Retinoic acid receptor RXR-gamma	100.0	3.35E-17
Q8N8R5	UPF0565 protein C2orf69	100.0	3.35E-17
Q9Y2R5	28S ribosomal protein S17, mitochondrial	100.0	3.35E-17
O43505	beta-1,4-glucuronyltransferase 1	100.0	3.35E-17
Q8IUR0	Trafficking protein particle complex subunit 5	100.0	3.35E-17
Q05DH4	Protein FAM160A1	100.0	3.35E-17
Q9UFN0	protein NipSnap homolog 3A	100.0	3.35E-17
Q49B96	Cytochrome c oxidase assembly protein COX19	100.0	3.35E-17
Q86UY6	N-alpha-acetyltransferase 40	100.0	3.35E-17
P49760-1	Dual specificity protein kinase CLK2	100.0	3.35E-17
Q17RN3-1	Protein Fam98c	100.0	3.35E-17
P19838	Nuclear factor NF-kappa-B p105 subunit	100.0	3.35E-17
O60613-1	selenoprotein F	100.0	3.35E-17
Q9BYB4-1	Guanine nucleotide-binding protein subunit beta-like protein 1	100.0	3.35E-17
Q96RT7	gamma-tubulin complex component 6	100.0	3.35E-17
P10586-1	Receptor-type tyrosine-protein phosphatase F	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8IWV7-1	E3 ubiquitin-protein ligase UBR1	100.0	3.35E-17
Q53H82	Endoribonuclease LACTB2	100.0	3.35E-17
O15379	Histone deacetylase 3	100.0	3.35E-17
Q9Y3C5	Ring finger protein 11	100.0	3.35E-17
Q9H6V9-1	Lipid droplet-associated hydrolase	100.0	3.35E-17
Q5T0N5-1	Formin-binding protein 1-like	100.0	3.35E-17
Q969T7	7-methylguanosine phosphate-specific 5′-nucleotidase	100.0	3.35E-17
Q9Y3E7	Charged multivesicular body protein 3	100.0	3.35E-17
Q96N46	Tetratricopeptide repeat protein 14	100.0	3.35E-17
Q9Y2U5	Mitogen-activated protein kinase kinase kinase 2	100.0	3.35E-17
Q8IV48	3′-5′ exoribonuclease 1	100.0	3.35E-17
Q9NX62	Inositol monophosphatase 3	100.0	3.35E-17
A2RRP1-1	neuroblastoma-amplified sequence	100.0	3.35E-17
P55285-1	Cadherin-6	100.0	3.35E-17
P49454	Centromere protein F	100.0	3.35E-17
Q9H079	KATNB1-like protein 1	100.0	3.35E-17
Q8N6N7	acyl-CoA-binding domain-containing protein 7	100.0	3.35E-17
Q8IXJ6	NAD-dependent protein deacetylase sirtuin-2	100.0	3.35E-17
Q9NYM9	BET1-like protein	100.0	3.35E-17
Q6NW29	RWD domain-containing protein 4	100.0	3.35E-17
P78536-1	Disintegrin and metalloproteinase domain-containing protein 17	100.0	3.35E-17
O75391	Sperm-associated antigen 7	100.0	3.35E-17
P55211-1	caspase-9	100.0	3.35E-17
Q2VPK5-1	Cytoplasmic tRNA 2-thiolation protein 2	100.0	3.35E-17
Q13445	Transmembrane emp24 domain-containing protein 1	100.0	3.35E-17
Q9Y4X5	E3 ubiquitin-protein ligase ARIH1	100.0	3.35E-17
Q9H5H4	Zinc finger protein 768	100.0	3.35E-17
Q9NQE9	Histidine triad nucleotide-binding protein 3	100.0	3.35E-17
O95696	Bromodomain-containing protein 1	100.0	3.35E-17
O15439-1	multidrug resistance-associated protein 4	100.0	3.35E-17
Q9BPZ3	Polyadenylate-binding protein-interacting protein 2	100.0	3.35E-17
A3KMH1	von Willebrand factor A domain-containing protein 8	100.0	3.35E-17
Q9Y3X0	coiled-coil domain-containing protein 9	100.0	3.35E-17
Q5TA45-1	Integrator complex subunit 11	100.0	3.35E-17
Q86WG5	Myotubularin-related protein 13	100.0	3.35E-17
Q13416	Origin recognition complex subunit 2	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96EL2	28S ribosomal protein S24, mitochondrial	100.0	3.35E-17
Q86WG3-1	Caytaxin	100.0	3.35E-17
P56182	Ribosomal RNA processing protein 1 homolog A	100.0	3.35E-17
O14662-1	Syntaxin-16	100.0	3.35E-17
Q5TC12-1	ATP synthase mitochondrial F1 complex assembly factor 1	100.0	3.35E-17
Q92870-1	Amyloid-beta A4 precursor protein-binding family B member 2	100.0	3.35E-17
O43493-1	Trans-Golgi network integral membrane protein 2	100.0	3.35E-17
Q53HC9	EARP-interacting protein	100.0	3.35E-17
Q9NRZ9	Lymphoid-specific helicase	100.0	3.35E-17
Q5VZE5	N-alpha-acetyltransferase 35, NatC auxiliary subunit	100.0	3.35E-17
Q8IWB7	WD repeat and FYVE domain-containing protein 1	100.0	3.35E-17
Q7Z3E5	LisH domain-containing protein ARMC9	100.0	3.35E-17
Q9UNZ5	Leydig cell tumor 10 kDa protein homolog	100.0	3.35E-17
O60930	Ribonuclease H1	100.0	3.35E-17
Q8IXM6-1	Nurim	100.0	3.35E-17
Q9NPG8	probable palmitoyltransferase ZDHHC4	100.0	3.35E-17
Q13485	Mothers against decapentaplegic homolog 4	100.0	3.35E-17
Q969V5	Mitochondrial ubiquitin ligase activator of NFKB 1	100.0	3.35E-17
Q06190	Serine/threonine-protein phosphatase 2A regulatory subunit B″ subunit alpha	100.0	3.35E-17
Q15543	Transcription initiation factor TFIID subunit 13	100.0	3.35E-17
Q5TCS8	Adenylate kinase 9	100.0	3.35E-17
Q8NEF9	serum response factor-binding protein 1	100.0	3.35E-17
Q6IN84-1	rRNA methyltransferase 1, mitochondrial	100.0	3.35E-17
Q9H8Y5	Ankyrin repeat and zinc finger domain-containing protein 1	100.0	3.35E-17
Q8IZH2-1	5′-3′ exoribonuclease 1	100.0	3.35E-17
Q6F5E8	capping protein, Arp2/3 and myosin-I linker protein 2	100.0	3.35E-17
Q9P2N6	KAT8 regulatory NSL complex subunit 3	100.0	3.35E-17
P14621	Acylphosphatase-2	100.0	3.35E-17
O60725	protein-s-isoprenylcysteine O-methyltransferase	100.0	3.35E-17
Q96A73-1	Putative monooxygenase p33MONOX	100.0	3.35E-17
O00471	Exocyst complex component 5	100.0	3.35E-17
Q99453	Paired mesoderm homeobox protein 2B	100.0	3.35E-17
Q9NR77	Peroxisomal membrane protein 2	100.0	3.35E-17
A6ZKI3	Retrotransposon Gag-like protein 8B	100.0	3.35E-17
Q04656-1	copper-transporting ATPase 1	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96NW4	Ankyrin repeat domain-containing protein 27	100.0	3.35E-17
Q92581-1	Sodium/hydrogen exchanger 6	100.0	3.35E-17
Q12981-1	Isoform 3 of Vesicle transport protein SEC20	100.0	3.35E-17
Q9H270	Vacuolar protein sorting-associated protein 11 homolog	100.0	3.35E-17
Q15910	Histone-lysine N-methyltransferase EZH2	100.0	3.35E-17
Q9Y5W7	Sorting nexin-14	100.0	3.35E-17
Q9H7B4-1	Histone-lysine N-methyltransferase SMYD3	100.0	3.35E-17
Q9UGN5-1	Poly [ADP-ribose] polymerase 2	100.0	3.35E-17
O95563	Mitochondrial pyruvate carrier 2	100.0	3.35E-17
Q14667-1	Protein KIAA0100	100.0	3.35E-17
Q8IVV7	Glucose-induced degradation protein 4 homolog	100.0	3.35E-17
Q9ULH0-1	Kinase D-interacting substrate of 220 kDa	100.0	3.35E-17
Q8NHP6-1	motile sperm domain-containing protein 2	100.0	3.35E-17
Q6QHF9	Peroxisomal N(1)-acetyl-spermine/spermidine oxidase	100.0	3.35E-17
P51688	N-sulphoglucosamine sulphohydrolase	100.0	3.35E-17
Q9NVM9	integrator complex subunit 13	100.0	3.35E-17
Q9NRY6	Phospholipid scramblase 3	100.0	3.35E-17
O95847	Mitochondrial uncoupling protein 4	100.0	3.35E-17
Q9H334-1	Forkhead box protein P1	100.0	3.35E-17
Q9BVC3	sister chromatid cohesion protein dcc1	100.0	3.35E-17
Q7Z4H3-1	HD domain-containing protein 2	100.0	3.35E-17
Q6ZTA4	Tripartite motif-containing protein 67	100.0	3.35E-17
Q9BT43	DNA-directed RNA polymerase III subunit RPC7-like	100.0	3.35E-17
Q9UNQ2	Probable dimethyladenosine transferase	100.0	3.35E-17
P40818	ubiquitin carboxyl-terminal hydrolase 8	100.0	3.35E-17
Q0JRZ9-1	F-BAR domain only protein 2	100.0	3.35E-17
Q9UM47	Neurogenic locus notch homolog protein 3	100.0	3.35E-17
Q8IY18	structural maintenance of chromosomes protein 5	100.0	3.35E-17
Q9NUJ3	T-complex protein 11-like protein 1	100.0	3.35E-17
Q8N9E0	Protein FAM133A	100.0	3.35E-17
Q9H3K2	Growth hormone-inducible transmembrane protein	100.0	3.35E-17
P62487	DNA-directed RNA polymerase II subunit rpb7	100.0	3.35E-17
Q6P1M0	Long-chain fatty acid transport protein 4	100.0	3.35E-17
Q6IA69	glutamine-dependent NAD(+) synthetase	100.0	3.35E-17
Q15070-1	Mitochondrial inner membrane protein OXA1L	100.0	3.35E-17
Q9NZ52	ADP-ribosylation factor-binding protein GGA3	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q13488	V-type proton ATPase 116 kDa subunit a isoform 3	100.0	3.35E-17
O60934	Nibrin	100.0	3.35E-17
Q9BZQ6	ER degradation-enhancing alpha-mannosidase-like protein 3	100.0	3.35E-17
P61165	transmembrane protein 258	100.0	3.35E-17
Q9NWZ3-1	Interleukin-1 receptor-associated kinase 4	100.0	3.35E-17
P52848-1	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	100.0	3.35E-17
Q92759	General transcription factor IIH subunit 4	100.0	3.35E-17
Q16864-1	V-type proton ATPase subunit F	100.0	3.35E-17
Q5T2Q4	Cyclin-Y-like protein 2	100.0	3.35E-17
Q15800	Methylsterol monooxygenase 1	100.0	3.35E-17
Q9H0W7	THAP domain-containing protein 2	100.0	3.35E-17
Q9BU02-1	Thiamine-triphosphatase	100.0	3.35E-17
Q8IYT3	Coiled-coil domain-containing protein 170	100.0	3.35E-17
Q5EBL4-1	RILP-like protein 1	100.0	3.35E-17
Q9H9Y6-1	DNA-directed RNA polymerase I subunit RPA2	100.0	3.35E-17
Q5JSP0-1	FYVE, RhoGEF and PH domain-containing protein 3	100.0	3.35E-17
O43663-1	Protein regulator of cytokinesis 1	100.0	3.35E-17
Q8TBC3	SH3KBP1-binding protein 1	100.0	3.35E-17
Q8NDD1	Uncharacterized protein C1orf131	100.0	3.35E-17
Q9NQ88	Fructose-2,6-bisphosphatase TIGAR	100.0	3.35E-17
O14657	Torsin-1B	100.0	3.35E-17
Q9Y6V7	Probable ATP-dependent RNA helicase ddx49	100.0	3.35E-17
Q8TB03	Uncharacterized protein CXorf38	100.0	3.35E-17
Q8NBF6-1	Late secretory pathway protein AVL9 homolog	100.0	3.35E-17
Q9H1Z9	Tetraspanin-10	100.0	3.35E-17
Q15036-1	Sorting nexin-17	100.0	3.35E-17
Q8NG48-1	protein Lines homolog 1	100.0	3.35E-17
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	100.0	3.35E-17
Q7Z7B0	Filamin-A-interacting protein 1	100.0	3.35E-17
P27352	Gastric intrinsic factor	100.0	3.35E-17
Q96GQ5-1	RUS1 family protein C16orf58	100.0	3.35E-17
Q5JVF3	PCI domain-containing protein 2	100.0	3.35E-17
Q5T9S5-1	Coiled-coil domain-containing protein 18	100.0	3.35E-17
Q86X83	COMM domain-containing protein 2	100.0	3.35E-17
Q9Y5E7	Protocadherin beta-2	100.0	3.35E-17
Q712K3	Ubiquitin-conjugating enzyme E2 R2	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NYP7-1	elongation of very long chain fatty acids protein 5	100.0	3.35E-17
P36954	DNA-directed RNA polymerase II subunit RPB9	100.0	3.35E-17
Q9H6K4	Optic atrophy 3 protein	100.0	3.35E-17
Q6RI45	Bromodomain and WD repeat-containing protein 3	100.0	3.35E-17
Q9UKP5-1	A disintegrin and metalloproteinase with thrombospondin motifs 6	100.0	3.35E-17
O14672	Disintegrin and metalloproteinase domain-containing protein 10	100.0	3.35E-17
O75175	CCR4-NOT transcription complex subunit 3	100.0	3.35E-17
Q9Y399	28S ribosomal protein S2, mitochondrial	100.0	3.35E-17
Q9UFW8	CGG triplet repeat-binding protein 1	100.0	3.35E-17
Q9Y3A2	Probable U3 small nucleolar RNA-associated protein 11	100.0	3.35E-17
Q16706	Alpha-mannosidase 2	100.0	3.35E-17
P08151	Zinc finger protein GLI1	100.0	3.35E-17
O75586	Mediator of RNA polymerase II transcription subunit 6	100.0	3.35E-17
O43286	Beta-1,4-galactosyltransferase 5	100.0	3.35E-17
Q7Z4T9-7	Isoform 7 of Cilia- and flagella-associated protein 91	100.0	3.35E-17
Q9HB90	ras-related GTP-binding protein C	100.0	3.35E-17
P42336	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform	100.0	3.35E-17
Q6PHR2-1	Serine/threonine-protein kinase ULK3	100.0	3.35E-17
Q99797	Mitochondrial intermediate peptidase	100.0	3.35E-17
Q08999	Retinoblastoma-like protein 2	100.0	3.35E-17
Q9P2S2-1	Neurexin-2	100.0	3.35E-17
P29084	transcription initiation factor iie subunit beta	100.0	3.35E-17
Q8N5H7-1	SH2 domain-containing protein 3C	100.0	3.35E-17
Q5XUX0-1	F-box only protein 31	100.0	3.35E-17
Q8NDV7	Trinucleotide repeat-containing gene 6A protein	100.0	3.35E-17
Q14154	Death ligand signal enhancer	100.0	3.35E-17
Q2TB10	zinc finger protein 800	100.0	3.35E-17
Q5JYT7	Uncharacterized protein KIAA1755	100.0	3.35E-17
Q9Y2H2-1	Phosphatidylinositide phosphatase SAC2	100.0	3.35E-17
Q14865	AT-rich interactive domain-containing protein 5B	100.0	3.35E-17
Q63HM1	kynurenine formamidase	100.0	3.35E-17
Q86SS6	Synaptotagmin-9	100.0	3.35E-17
Q8IYJ2	uncharacterized protein C10orf67, mitochondrial	100.0	3.35E-17
P47869	Gamma-aminobutyric acid receptor subunit alpha-2	100.0	3.35E-17
Q92733	proline-rich protein PRCC	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O43236	septin-4	100.0	3.35E-17
O95628-1	CCR4-NOT transcription complex subunit 4	100.0	3.35E-17
Q96MT7-1	Cilia- and flagella-associated protein 44	100.0	3.35E-17
A6NKD9	Coiled-coil domain-containing protein 85C	100.0	3.35E-17
Q9HB65	RNA polymerase II elongation factor ELL3	100.0	3.35E-17
Q9BQS2-3	Isoform 3 of Synaptotagmin-15	100.0	3.35E-17
Q9UHC6-1	Contactin-associated protein-like 2	100.0	3.35E-17
Q9BVM2	protein DPCD	100.0	3.35E-17
A2CJ06	Dystrotelin	100.0	3.35E-17
O96006	zinc finger BED domain-containing protein 1	100.0	3.35E-17
Q96GW9	Methionine–tRNA ligase, mitochondrial	100.0	3.35E-17
Q9UIG8-1	solute carrier organic anion transporter family member 3A1	100.0	3.35E-17
Q16595-1	Frataxin, mitochondrial	100.0	3.35E-17
Q8N6G5-1	chondroitin sulfate N-acetylgalactosaminyltransferase 2	100.0	3.35E-17
Q86YR6	POTE ankyrin domain family member D	100.0	3.35E-17
P49917	DNA ligase 4	100.0	3.35E-17
Q9P206-2	Isoform 2 of Uncharacterized protein KIAA1522	100.0	3.35E-17
Q9BQP7	mitochondrial genome maintenance exonuclease 1	100.0	3.35E-17
Q6PFW1-1	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1	100.0	3.35E-17
Q9NYK1	Toll-like receptor 7	100.0	3.35E-17
Q9Y5T5-1	ubiquitin carboxyl-terminal hydrolase 16	100.0	3.35E-17
Q6W3E5	Glycerophosphodiester phosphodiesterase domain-containing protein 4	100.0	3.35E-17
Q6P2D8	X-ray radiation resistance-associated protein 1	100.0	3.35E-17
P35398-1	Isoform 2 of Nuclear receptor ROR-alpha	100.0	3.35E-17
Q0VF96	Cingulin-like protein 1	100.0	3.35E-17
O94762-1	ATP-dependent DNA helicase Q5	100.0	3.35E-17
Q7Z4F1	Low-density lipoprotein receptor-related protein 10	100.0	3.35E-17
Q68D10-1	Protein SPT2 homolog	100.0	3.35E-17
Q96ET8-1	Golgi apparatus membrane protein TVP23 homolog C	100.0	3.35E-17
O95972	Bone morphogenetic protein 15	100.0	3.35E-17
Q8N5B7	Ceramide synthase 5	100.0	3.35E-17
O75815-1	Breast cancer anti-estrogen resistance protein 3	100.0	3.35E-17
Q12879-1	Glutamate receptor ionotropic, NMDA 2A	100.0	3.35E-17
P20749	B-cell lymphoma 3 protein	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NTG7	NAD-dependent protein deacetylase sirtuin-3, mitochondrial	100.0	3.35E-17
Q5VWP2	Putative nucleotidyltransferase FAM46C	100.0	3.35E-17
Q8WVQ1	Soluble calcium-activated nucleotidase 1	100.0	3.35E-17
Q96DT5	Dynein heavy chain 11, axonemal	100.0	3.35E-17
Q9UPY5	Cystine/glutamate transporter	100.0	3.35E-17
Q14517	Protocadherin Fat 1	100.0	3.35E-17
Q9BPU6	Dihydropyrimidinase-related protein 5	100.0	3.35E-17
Q96C11	FGGY carbohydrate kinase domain-containing protein	100.0	3.35E-17
Q14526-1	Hypermethylated in cancer 1 protein	100.0	3.35E-17
O95996-1	adenomatous polyposis coli protein 2	100.0	3.35E-17
Q5SW96	Low density lipoprotein receptor adapter protein 1	100.0	3.35E-17
Q9NZE8	39S ribosomal protein L35, mitochondrial	100.0	3.35E-17
Q8TEB1	DDB1- and CUL4-associated factor 11	100.0	3.35E-17
Q8N9C0	Immunoglobulin superfamily member 22	100.0	3.35E-17
Q3SY69-1	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	100.0	3.35E-17
P50748	Kinetochore-associated protein 1	100.0	3.35E-17
Q7Z3T8	Zinc finger FYVE domain-containing protein 16	100.0	3.35E-17
Q5TB80	Centrosomal protein of 162 kDa	100.0	3.35E-17
Q15526	Surfeit locus protein 1	100.0	3.35E-17
Q04725-2	Isoform 2 of Transducin-like enhancer protein 2	100.0	3.35E-17
Q9UBN1	Voltage-dependent calcium channel gamma-4 subunit	100.0	3.35E-17
Q8WWF5	E3 ubiquitin-protein ligase ZNRF4	100.0	3.35E-17
Q9Y4X3	C-C motif chemokine 27	100.0	3.35E-17
O43299	AP-5 complex subunit zeta-1	100.0	3.35E-17
Q2M243	Coiled-coil domain-containing protein 27	100.0	3.35E-17
Q9H981-1	Actin-related protein 8	100.0	3.35E-17
Q96KX1	Uncharacterized protein C4orf36	100.0	3.35E-17
Q4G0Z9-1	Minichromosome maintenance domain-containing protein 2	100.0	3.35E-17
Q9Y6A1	Protein O-mannosyl-transferase 1	100.0	3.35E-17
Q8WTX7	Cytosolic arginine sensor for mTORC1 subunit 1	100.0	3.35E-17
O15068-3	Isoform 3 of Guanine nucleotide exchange factor DBS	100.0	3.35E-17
Q8IVF6	Ankyrin repeat domain-containing protein 18A	100.0	3.35E-17
Q5VW36	focadhesin	100.0	3.35E-17
O43715	TP53-regulated inhibitor of apoptosis 1	100.0	3.35E-17
Q5VZ46-1	Uncharacterized protein KIAA1614	100.0	3.35E-17
Q15744	CCAAT/enhancer-binding protein epsilon	100.0	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P05107	Integrin beta-2	100.0	3.35E-17
A6NES4	Maestro heat-like repeat-containing protein family member 2A	100.0	3.35E-17
Q9NPD8	Ubiquitin-conjugating enzyme E2 T	100.0	3.35E-17
O75900	Matrix metalloproteinase-23	100.0	3.35E-17
P31639	sodium/glucose cotransporter 2	100.0	3.35E-17
Q8WZ42	Titin	100.0	3.35E-17
P57081-1	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4	100.0	3.35E-17
Q8TDM6-1	disks large homolog 5	100.0	3.35E-17
O00311-1	Cell division cycle 7-related protein kinase	100.0	3.35E-17
Q6NT04	Tigger transposable element-derived protein 7	100.0	3.35E-17
O75899	Gamma-aminobutyric acid type B receptor subunit 2	100.0	3.35E-17
Q9UPR5	Sodium/calcium exchanger 2	100.0	3.35E-17
O95460	matrilin-4	100.0	3.35E-17
Q9BSJ6	Protein PIMREG	100.0	3.35E-17
Q6IWH7	Anoctamin-7	100.0	3.35E-17
P18075	bone morphogenetic protein 7	100.0	3.35E-17
Q9HAD4-2	Isoform 2 of WD repeat-containing protein 41	100.0	3.35E-17
Q9BQ24	Zinc finger FYVE domain-containing protein 21	100.0	3.35E-17
Q9NWS8	Required for meiotic nuclear division protein 1 homolog	100.0	3.35E-17
Q96JB2-1	Conserved oligomeric Golgi complex subunit 3	100.0	3.35E-17
Q9HCT0	fibroblast growth factor 22	100.0	3.35E-17
Q86W26	NACHT, LRR and PYD domains-containing protein 10	100.0	3.35E-17
Q9P2B7	Cilia- and flagella-associated protein 97	100.0	3.35E-17
Q15118	[Pyruvate dehydrogenase (Acetyl-transferring)] kinase isozyme 1, mitochondrial	100.0	3.35E-17
O43854-1	EGF-like repeat and discoidin I-like domain-containing protein 3	100.0	3.35E-17
Q9H930-1	Isoform 1 of Nuclear body protein SP140-like protein	87.57	2.59E-07
Q9H1Y0-1	Autophagy protein 5	85.11	3.99E-08
Q13885	Tubulin beta-2A chain	76.05	2.14E-05
P42766	60S ribosomal protein L35	75.34	2.45E-05
Q9P0J0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	59.45	1.91E-05
P61204	ADP-ribosylation factor 3	54.12	3.71E-05
P08727	Keratin, type I cytoskeletal 19	44.00	1.28E-05
Q9H1B4-1	Nuclear RNA export factor 5	40.19	6.10E-04

Continued on next page

accession	description	fold p change	adjusted p-value
Q9H8H0	nucleolar protein 11	34.23	1.60E-03
Q9GZT8-1	NIF3-like protein 1	32.51	4.20E-04
Q8N4C8-1	Misshapen-like kinase 1	28.16	3.08E-03
Q9UDR5	Alpha-aminoadipic semialdehyde synthase, mitochondrial	27.58	7.97E-03
Q8NCN5	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	27.45	5.70E-04
Q8IUE6	Histone H2A type 2-B	26.47	1.80E-03
P19387	DNA-directed RNA polymerase II subunit RPB3	24.69	5.37E-03
Q96RK0	Protein capicua homolog	24.20	1.30E-02
Q16778	Histone H2B type 2-E	23.39	6.65E-03
P31483	nucleolysin TIA-1 isoform p40	23.35	6.63E-03
Q03169	Tumor necrosis factor alpha-induced protein 2	23.21	8.56E-03
Q9UQL6-1	histone deacetylase 5	23.16	1.57E-03
O60826	Coiled-coil domain-containing protein 22	23.06	1.71E-02
Q9NXU5	ADP-ribosylation factor-like protein 15	22.39	7.21E-03
Q8TE77	Protein phosphatase Slingshot homolog 3	21.96	1.51E-02
O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	21.92	6.85E-03
P82094	TATA element modulatory factor	20.73	2.55E-02
Q8WVM8	Sec1 family domain-containing protein 1	20.44	3.90E-03
O75676	Ribosomal protein S6 kinase alpha-4	20.26	9.84E-03
Q71U36	tubulin alpha-1A chain	20.22	1.17E-02
Q8NBT2	kinetochore protein SPC24	19.98	2.58E-02
O75915	PRA1 family protein 3	19.87	1.64E-03
Q9Y5J9	mitochondrial import inner membrane translocase subunit Tim8 B	19.84	1.07E-02
P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	19.81	9.85E-03
Q99595	Mitochondrial import inner membrane translocase subunit Tim17-A	19.50	3.13E-02
Q9P0U1	Mitochondrial import receptor subunit TOM7 homolog	19.10	1.20E-02
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1	18.87	4.26E-03
P61812	Transforming growth factor beta-2	18.38	1.43E-02
P06280	alpha-galactosidase A	18.02	2.20E-02
Q86UL3	glycerol-3-phosphate acyltransferase 4	17.66	8.12E-03
O14772	fucose-1-phosphate guanylyltransferase	17.42	3.78E-03
Q96QV6	Histone H2A type 1-A	17.31	5.58E-03
Q7Z739	YTH domain-containing family protein 3	17.19	2.44E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q9H7D7	WD repeat-containing protein 26	16.94	1.23E-02
Q8IXQ4	GPALPP motifs-containing protein 1	16.83	3.90E-02
P62891	60S ribosomal protein L39	16.80	3.08E-03
O75691	Small subunit processome component 20 homolog	16.06	7.38E-03
Q9NYL4	Peptidyl-prolyl cis-trans isomerase FKBP11	16.04	2.05E-02
P11234	Ras-related protein Ral-B	15.82	2.33E-02
Q8NEB9	Phosphatidylinositol 3-kinase catalytic subunit type 3	15.45	4.97E-02
Q01860-2	Isoform B of POU domain, class 5, transcription factor 1	15.05	7.29E-03
Q86V88	Magnesium-dependent phosphatase 1	15.03	2.85E-02
Q14332	Frizzled-2	14.91	3.60E-02
Q9NVH2	Integrator complex subunit 7	14.27	4.39E-02
O14981	TATA-binding protein-associated factor 172	14.20	3.08E-02
O15258	Protein RER1	14.16	4.23E-02
Q13257-1	Mitotic spindle assembly checkpoint protein MAD2A	14.06	3.80E-02
Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	13.83	4.20E-02
O00505	Importin subunit alpha-4	13.83	4.37E-02
P36578	60S ribosomal protein L4	13.71	4.49E-02
Q92930	Ras-related protein Rab-8B	13.61	5.56E-03
P19320-1	Vascular cell adhesion protein 1	13.47	3.78E-02
Q70J99-1	Protein unc-13 homolog D	13.45	2.50E-02
Q9C0F1-1	centrosomal protein of 44 kDa	13.42	4.77E-02
Q99707	methionine synthase	13.28	4.95E-02
Q8TD19	Serine/threonine-protein kinase Nek9	12.62	4.34E-02
O95379	Tumor necrosis factor alpha-induced protein 8	12.56	2.30E-02
O95168-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	12.48	3.42E-02
Q8N4V1	Membrane magnesium transporter 1	12.10	4.73E-02
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1	12.00	4.54E-02
Q86SF2	N-acetylgalactosaminyltransferase 7	11.85	1.27E-02
O95466	formin-like protein 1	11.51	4.93E-02
P06746	DNA polymerase beta	11.50	3.30E-02
P52815	39S ribosomal protein L12, mitochondrial	11.46	2.65E-02
Q9BZI7-1	Regulator of nonsense transcripts 3B	10.56	1.95E-02
P62841	40S ribosomal protein S15	10.45	3.80E-02
P61026	ras-related protein rab-10	10.41	2.22E-02
P43364	Melanoma-associated antigen 11	10.28	3.53E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q9UI30	Multifunctional methyltransferase subunit TRM112-like protein	9.906	3.34E-02
Q8N5K1	CDGSH iron-sulfur domain-containing protein 2	9.899	2.82E-02
Q9BTW9	Tubulin-specific chaperone D	9.766	2.75E-02
P17676	CCAAT/enhancer-binding protein beta	9.531	1.91E-02
P67812	Signal peptidase complex catalytic subunit SEC11A	9.234	3.25E-02
P00403	Cytochrome c oxidase subunit 2	8.903	4.12E-02
Q13418	Integrin-linked protein kinase	8.713	4.51E-02
Q9BVC6	Transmembrane protein 109	8.443	4.53E-02
Q9ULW3	activator of basal transcription 1	8.198	4.49E-02
P00491	purine nucleoside phosphorylase	7.415	4.80E-02
Q9NP97	Dynein light chain roadblock-type 1	0.276	4.43E-02
P00568	Adenylate kinase isoenzyme 1	0.257	4.99E-02
P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	0.255	4.55E-02
Q05682-3	Isoform 3 of Caldesmon	0.248	4.19E-02
P62857	40S ribosomal protein S28	0.245	4.03E-02
P49773	Histidine triad nucleotide-binding protein 1	0.241	3.81E-02
P63220	40S ribosomal protein S21	0.240	3.79E-02
P53999	Activated RNA polymerase II transcriptional coactivator p15	0.238	3.68E-02
Q9UHB6	LIM domain and actin-binding protein 1	0.222	2.91E-02
P61604	10 kDa heat shock protein, mitochondrial	0.215	2.63E-02
Q6NYC8	Phostensin	0.214	2.70E-02
O60664-1	Perilipin-3	0.213	2.55E-02
Q92734-1	Protein TFG	0.213	4.56E-02
Q04323-1	UBX domain-containing protein 1	0.210	1.98E-02
P17252	Protein kinase C alpha type	0.209	4.72E-02
Q5VYK3	Proteasome-associated protein ECM29 homolog	0.208	3.75E-02
Q07157	Tight junction protein ZO-1	0.207	1.49E-02
Q96CT7	Coiled-coil domain-containing protein 124	0.204	4.39E-02
Q9P270	SLAIN motif-containing protein 2	0.202	2.11E-02
P60507	Endogenous retrovirus group FC1 Env polyprotein	0.202	4.66E-02
P43487	Ran-specific GTPase-activating protein	0.196	1.88E-02
P50479-1	PDZ and LIM domain protein 4	0.191	1.87E-02
P46821	microtubule-associated protein 1B	0.187	1.61E-02
Q13951	Core-binding factor subunit beta	0.187	2.72E-02
P07737	profilin-1	0.182	1.46E-02
P52788-1	Spermine synthase	0.182	3.40E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P33316-3	Deoxyuridine 5′-triphosphate nucleotidohydrolase, mitochondrial	0.180	1.38E-02
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	0.179	2.55E-02
O43447	peptidyl-prolyl cis-trans isomerase H	0.177	2.31E-02
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	0.174	3.66E-02
Q92917	G patch domain and KOW motifs-containing protein	0.166	3.11E-02
P98179	RNA-binding protein 3	0.165	1.26E-02
Q9H6F5	Coiled-coil domain-containing protein 86	0.162	2.44E-02
Q15459	splicing factor 3A subunit 1	0.161	9.94E-03
P20962	Parathymosin	0.161	2.00E-02
P06753-2	Isoform 2 of Tropomyosin alpha-3 chain	0.159	8.76E-03
Q969H8	Myeloid-derived growth factor	0.155	1.54E-02
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	0.155	4.90E-02
P09493-3	Isoform 3 of Tropomyosin alpha-1 chain	0.154	1.55E-02
Q99614	tetratricopeptide repeat protein 1	0.148	2.96E-02
Q13442	28 kDa heat- and acid-stable phosphoprotein	0.145	8.50E-03
P62910	60S ribosomal protein L32	0.143	5.74E-03
Q13242	serine/arginine-rich splicing factor 9	0.139	4.81E-03
Q9H910-1	Jupiter microtubule associated homolog 2	0.134	8.37E-03
Q9NSI2-1	protein FAM207A	0.133	4.01E-02
P63165-1	Small ubiquitin-related modifier 1	0.128	7.61E-03
P02768-1	Serum albumin	0.127	4.20E-02
Q9UK76	Jupiter microtubule associated homolog 1	0.122	2.99E-03
Q9UHD9	Ubiquilin-2	0.122	2.87E-02
Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein	0.115	1.13E-02
P41236	Protein phosphatase inhibitor 2	0.115	2.03E-02
Q15398-3	Isoform 3 of Disks large-associated protein 5	0.112	4.69E-02
Q92608-1	Dedicator of cytokinesis protein 2	0.112	4.80E-02
O75348	V-type proton ATPase subunit G 1	0.111	3.82E-02
Q9NUP9	Protein lin-7 homolog C	0.108	3.06E-03
Q14116	Interleukin-18	0.108	4.23E-02
P07951-2	Isoform 2 of Tropomyosin beta chain	0.107	1.70E-03
O00233-1	26S proteasome non-ATPase regulatory subunit 9	0.107	4.86E-03
P07203	Glutathione peroxidase 1	0.107	2.64E-02
P55196-5	Isoform 5 of Afadin	0.101	3.56E-02
Q93063	exostosin-2	0.096	4.82E-02
P22794-1	Protein EVI2A	0.095	4.72E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P43897	Elongation factor Ts, mitochondrial	0.093	2.25E-02
P29558-1	RNA-binding motif, single-stranded-interacting protein 1	0.093	2.64E-02
Q8TAP8	protein phosphatase 1 regulatory subunit 35	0.090	4.08E-02
Q5JTD0-1	Tight junction-associated protein 1	0.087	2.59E-02
Q92620	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	0.086	2.17E-02
Q8N5F7	NF-kappa-B-activating protein	0.083	3.41E-02
Q96DB5	regulator of microtubule dynamics protein 1	0.082	2.64E-02
Q9C0B5	Palmitoyltransferase ZDHHC5	0.082	3.30E-02
Q14011	Cold-inducible RNA-binding protein	0.079	5.31E-04
Q9NRF9	DNA polymerase epsilon subunit 3	0.078	6.56E-03
Q92990	Glomulin	0.077	4.30E-03
Q9HBR0	Putative sodium-coupled neutral amino acid transporter 10	0.077	2.59E-02
Q8TEW0	Partitioning defective 3 homolog	0.074	3.95E-02
P45985	Dual specificity mitogen-activated protein kinase kinase 4	0.073	1.09E-02
Q7Z3K3-1	Pogo transposable element with ZNF domain	0.070	8.80E-03
P48723	Heat shock 70 kDa protein 13	0.069	2.19E-02
Q16625-1	Occludin	0.068	1.62E-02
Q99543-1	dnaJ homolog subfamily C member 2	0.063	4.37E-02
Q7Z3C6	autophagy-related protein 9A	0.062	1.43E-02
O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	0.062	4.27E-02
P20810-6	Isoform 6 of Calpastatin	0.061	2.10E-04
P46976-1	Glycogenin-1	0.061	2.57E-02
P14174	Macrophage Migration inhibitory factor	0.060	9.67E-05
Q92503-1	SEC14-like protein 1	0.060	1.20E-02
O14618	copper chaperone for superoxide dismutase	0.059	1.37E-03
Q9UPN6	Protein SCAF8	0.057	3.34E-02
Q9GZY8-1	Mitochondrial fission factor	0.057	3.73E-02
Q8NDF8-5	Isoform 5 of Non-canonical poly(A) RNA polymerase PAPD5	0.056	3.43E-02
O94818-1	Nucleolar protein 4	0.053	4.62E-03
O43504	Ragulator complex protein LAMTOR5	0.052	8.40E-03
Q9HB19	Pleckstrin homology domain-containing family A member 2	0.051	1.88E-02
Q9UJA5-1	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	0.051	1.95E-02
P13051	uracil-DNA glycosylase	0.050	2.81E-02
Q8TEY7-1	Ubiquitin carboxyl-terminal hydrolase 33	0.049	1.44E-02
P43308	Translocon-associated protein subunit beta	0.043	1.83E-03

Continued on next page

accession	description	fold p change	adjusted p-value
P02545-2	Isoform C of Prelamin-A/C	0.042	1.20E-05
O15056	Synaptojanin-2	0.042	2.76E-03
Q96DF8	Protein DGCR14	0.040	1.39E-03
P80723	Brain acid soluble protein 1	0.039	2.19E-06
P05412	transcription factor AP-1	0.039	1.45E-03
Q13888-1	General transcription factor IIH subunit 2	0.039	2.47E-02
Q14CZ0	UPF0472 protein C16orf72	0.036	1.06E-02
Q86UU0	B-cell CLL/lymphoma 9-like protein	0.035	9.51E-04
P0CB38	polyadenylate-binding protein 4-like	0.033	6.78E-03
Q9H2U1	ATP-dependent RNA helicase DHX36	0.031	1.22E-03
P56377	AP-1 complex subunit sigma-2	0.030	1.91E-04
Q13636	ras-related protein rab-31	0.029	3.63E-05
Q13951-2	Isoform 2 of Core-binding factor subunit beta	0.027	9.95E-05
Q9H6R4-1	Nucleolar protein 6	0.024	1.63E-05
O00399	Dynactin subunit 6	0.021	6.74E-05
Q9C0D5	Protein TANC1	0.019	1.43E-04
Q86TB9	Protein PAT1 homolog 1	0.018	2.93E-07
Q9HD15	Steroid receptor RNA activator 1	0.016	4.45E-06
O43768	alpha-endosulfine	0.015	2.90E-06
Q8NC51-3	Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein	0.010	3.35E-17
P07910-1	Heterogeneous nuclear ribonucleoproteins C1/C2	0.010	3.35E-17
Q99880	Histone H2B type 1-L	0.010	3.35E-17
Q15366-3	Isoform 3 of Poly(rC)-binding protein 2	0.010	3.35E-17
P31942-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3	0.010	3.35E-17
Q02539	Histone H1.1	0.010	3.35E-17
P15531	Nucleoside diphosphate kinase A	0.010	3.35E-17
Q5JTV8	Torsin-1A-interacting protein 1	0.010	3.35E-17
P62633-8	Isoform 8 of Cellular nucleic acid-binding protein	0.010	3.35E-17
P07205	Phosphoglycerate kinase 2	0.010	3.35E-17
Q14978-3	Isoform 3 of Nucleolar and coiled-body phosphoprotein 1	0.010	3.35E-17
Q9H910-2	Isoform 2 of Jupiter microtubule associated homolog 2	0.010	3.35E-17
P62491-1	Ras-related protein Rab-11A	0.010	3.35E-17
P13796	Plastin-2	0.010	3.35E-17
Q9H0L4	cleavage stimulation factor subunit 2 tau variant	0.010	3.35E-17
Q9BW19	Kinesin-like protein KIFC1	0.010	3.35E-17
P05114	Non-histone chromosomal protein HMG-14	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P57764	Gasdermin-D	0.010	3.35E-17
Q5JSZ5-1	Protein PRRC2B	0.010	3.35E-17
Q765P7	MTSS1-like protein	0.010	3.35E-17
Q9H4A6	Golgi phosphoprotein 3	0.010	3.35E-17
P62328	Thymosin beta-4	0.010	3.35E-17
Q96PU5	E3 ubiquitin-protein ligase NEDD4-like	0.010	3.35E-17
Q9BW71-1	HIRA-interacting protein 3	0.010	3.35E-17
Q7Z7K6-1	Centromere protein V	0.010	3.35E-17
Q8WVM7	Cohesin subunit SA-1	0.010	3.35E-17
P19634-1	Sodium/hydrogen exchanger 1	0.010	3.35E-17
P61244	Protein max	0.010	3.35E-17
Q9UKI2	Cdc42 effector protein 3	0.010	3.35E-17
Q5PRF9	protein Smaug homolog 2	0.010	3.35E-17
Q5SSJ5-5	Isoform 4 of Heterochromatin protein 1-binding protein 3	0.010	3.35E-17
O94964	Protein SOGA1	0.010	3.35E-17
O95104	Splicing factor, arginine/serine-rich 15	0.010	3.35E-17
Q13405	39S ribosomal protein L49, mitochondrial	0.010	3.35E-17
P69905	Hemoglobin subunit alpha	0.010	3.35E-17
P53985	Monocarboxylate transporter 1	0.010	3.35E-17
Q8IZ21-1	Phosphatase and actin regulator 4	0.010	3.35E-17
Q9HCH5-1	Synaptotagmin-like protein 2	0.010	3.35E-17
Q9BYD2	39S ribosomal protein L9, mitochondrial	0.010	3.35E-17
P15954	Cytochrome c oxidase subunit 7C, mitochondrial	0.010	3.35E-17
Q147X3	N-alpha-acetyltransferase 30	0.010	3.35E-17
Q9NWV8	BRISC and BRCA1-A complex member 1	0.010	3.35E-17
O95295	SNARE-associated protein Snapin	0.010	3.35E-17
Q15629	Translocating chain-associated membrane protein 1	0.010	3.35E-17
O14907	Tax1-binding protein 3	0.010	3.35E-17
Q9BW85	Coiled-coil domain-containing protein 94	0.010	3.35E-17
Q9BQC3	2-(3-amino-3-carboxypropyl)histidine synthase subunit 2	0.010	3.35E-17
Q12929	Epidermal growth factor receptor kinase substrate 8	0.010	3.35E-17
Q9BRA0-1	N-alpha-acetyltransferase 38, NatC auxiliary subunit	0.010	3.35E-17
O75152	Zinc finger CCCH domain-containing protein 11A	0.010	3.35E-17
Q96DA6	mitochondrial import inner membrane translocase subunit TIM14	0.010	3.35E-17
Q96PD2-1	Discoidin, CUB and LCCL domain-containing protein 2	0.010	3.35E-17
Q7Z3B3	KAT8 regulatory NSL complex subunit 1	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8NI22	Multiple coagulation factor deficiency protein 2	0.010	3.35E-17
Q9BQE9-1	B-cell CLL/lymphoma 7 protein family member B	0.010	3.35E-17
Q9Y2X9	Zinc finger protein 281	0.010	3.35E-17
Q9NUK0	Muscleblind-like protein 3	0.010	3.35E-17
Q92859	neogenin	0.010	3.35E-17
Q8NC60	Nitric oxide-associated protein 1	0.010	3.35E-17
Q99470	Stromal cell-derived factor 2	0.010	3.35E-17
Q9P2B4	CTTNBP2 N-terminal-like protein	0.010	3.35E-17
Q9P0J7	E3 ubiquitin-protein ligase KCMF1	0.010	3.35E-17
P57076	UPF0769 protein C21orf59	0.010	3.35E-17
Q8WUP2	Filamin-binding LIM protein 1	0.010	3.35E-17
Q7Z5K2-1	Wings apart-like protein homolog	0.010	3.35E-17
Q2M3G4-1	Protein Shroom1	0.010	3.35E-17
Q9H0W8	protein SMG9	0.010	3.35E-17
Q9H3Q1	Cdc42 effector protein 4	0.010	3.35E-17
Q8WWH5	probable tRNA pseudouridine synthase 1	0.010	3.35E-17
O95251-1	Histone acetyltransferase KAT7	0.010	3.35E-17
Q9UGU0	Transcription factor 20	0.010	3.35E-17
Q96B54	Zinc finger protein 428	0.010	3.35E-17
Q9H4I2	zinc fingers and homeoboxes protein 3	0.010	3.35E-17
P55011	Solute carrier family 12 member 2	0.010	3.35E-17
O60927	Protein phosphatase 1 regulatory subunit 11	0.010	3.35E-17
P08047	Transcription factor Sp1	0.010	3.35E-17
Q9BTE1	Dynactin subunit 5	0.010	3.35E-17
Q9Y2B9	cAMP-dependent protein kinase inhibitor gamma	0.010	3.35E-17
Q92667	A-kinase anchor protein 1, mitochondrial	0.010	3.35E-17
P54725-1	UV excision repair protein RAD23 homolog A	0.010	3.35E-17
Q8N183	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 2	0.010	3.35E-17
Q9NZ63	Telomere length and silencing protein 1 homolog	0.010	3.35E-17
O00268	Transcription initiation factor TFIID subunit 4	0.010	3.35E-17
Q9UET6	Putative tRNA (cytidine(32)/guanosine(34)-2′-O)-methyltransferase	0.010	3.35E-17
Q9BYN0	sulfiredoxin-1	0.010	3.35E-17
Q9UHA3	Probable ribosome biogenesis protein RLP24	0.010	3.35E-17
Q9UHW9-2	Isoform 2 of Solute carrier family 12 member 6	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q86WB0	Nuclear-interacting partner of ALK	0.010	3.35E-17
Q8N3F8	MICAL-like protein 1	0.010	3.35E-17
Q15004-1	PCNA-associated factor	0.010	3.35E-17
Q96CP2	FLYWCH family member 2	0.010	3.35E-17
P18846	Cyclic AMP-dependent transcription factor ATF-1	0.010	3.35E-17
Q9BW72	HIG1 domain family member 2A, mitochondrial	0.010	3.35E-17
Q9H9F9	actin-related protein 5	0.010	3.35E-17
O75808-1	Calpain-15	0.010	3.35E-17
O15066	Kinesin-like protein KIF3B	0.010	3.35E-17
Q9HBM6	Transcription initiation factor TFIID subunit 9B	0.010	3.35E-17
Q32MZ4-4	Isoform 4 of Leucine-rich repeat flightless-interacting protein 1	0.010	3.35E-17
O43402	ER membrane protein complex subunit 8	0.010	3.35E-17
P31146	Coronin-1A	0.010	3.35E-17
Q9BYV8	centrosomal protein of 41 kDa	0.010	3.35E-17
Q16676	forkhead box protein D1	0.010	3.35E-17
Q63HR2	tensin-2	0.010	3.35E-17
Q15035	Translocating chain-associated membrane protein 2	0.010	3.35E-17
Q9NWT6	Hypoxia-inducible factor 1-alpha inhibitor	0.010	3.35E-17
Q8TCG2	Phosphatidylinositol 4-kinase type 2-beta	0.010	3.35E-17
Q9BUT9-1	MAPK regulated corepressor interacting protein 2	0.010	3.35E-17
Q9H161	Homeobox protein aristaless-like 4	0.010	3.35E-17
Q9UHR5-1	SAP30-binding protein	0.010	3.35E-17
P50548	ETS domain-containing transcription factor ERF	0.010	3.35E-17
P42695	condensin-2 complex subunit D3	0.010	3.35E-17
Q6FIF0	AN1-type zinc finger protein 6	0.010	3.35E-17
Q96FX7	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	0.010	3.35E-17
O95429	BAG family molecular chaperone regulator 4	0.010	3.35E-17
P14859-1	POU domain, class 2, transcription factor 1	0.010	3.35E-17
P78358	Cancer/testis antigen 1	0.010	3.35E-17
Q7Z2T5-1	TRMT1-like protein	0.010	3.35E-17
Q5THK1-1	Protein PRR14L	0.010	3.35E-17
Q9ULV3	Cip1-interacting zinc finger protein	0.010	3.35E-17
P63172	Dynein light chain Tctex-type 1	0.010	3.35E-17
Q16566	calcium/calmodulin-dependent protein kinase type IV	0.010	3.35E-17
P30260	cell division cycle protein 27 homolog	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NVM6	DnaJ homolog subfamily C member 17	0.010	3.35E-17
Q9H7C9-1	Mth938 domain-containing protein	0.010	3.35E-17
Q6PK04	Coiled-coil domain-containing protein 137	0.010	3.35E-17
Q9Y448	Small kinetochore-associated protein	0.010	3.35E-17
Q8N490-2	Isoform 2 of Probable hydrolase PNKD	0.010	3.35E-17
Q00613	heat shock factor protein 1	0.010	3.35E-17
Q02086-1	Transcription factor Sp2	0.010	3.35E-17
Q9UPQ9	Trinucleotide repeat-containing gene 6B protein	0.010	3.35E-17
Q15025	TNFAIP3-interacting protein 1	0.010	3.35E-17
Q99755	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	0.010	3.35E-17
P49643-1	DNA primase large subunit	0.010	3.35E-17
Q9NXA8-1	NAD-dependent protein deacylase sirtuin-5, mitochondrial	0.010	3.35E-17
O75381-1	Peroxisomal membrane protein PEX14	0.010	3.35E-17
P02656	Apolipoprotein C-III	0.010	3.35E-17
Q96SZ5	2-aminoethanethiol dioxygenase	0.010	3.35E-17
Q8TEP8-3	Isoform 3 of Centrosomal protein of 192 kDa	0.010	3.35E-17
Q9Y508-1	E3 ubiquitin-protein ligase RNF114	0.010	3.35E-17
P35568	Insulin receptor substrate 1	0.010	3.35E-17
Q9H6R0-1	Putative ATP-dependent RNA helicase DHX33	0.010	3.35E-17
Q14657	EKC/KEOPS complex subunit LAGE3	0.010	3.35E-17
Q92686	Neurogranin	0.010	3.35E-17
Q96A19	Coiled-coil domain-containing protein 102A	0.010	3.35E-17
Q12913-1	Receptor-type tyrosine-protein phosphatase eta	0.010	3.35E-17
P53801	pituitary tumor-transforming gene 1 protein-interacting protein	0.010	3.35E-17
P0C7T5	Ataxin-1-like	0.010	3.35E-17
Q96B49	Mitochondrial import receptor subunit TOM6 homolog	0.010	3.35E-17
Q96DE5	Anaphase-promoting complex subunit 16	0.010	3.35E-17
Q86WP2-1	Vasculin	0.010	3.35E-17
Q15390	Mitochondrial fission regulator 1	0.010	3.35E-17
Q12834	cell division cycle protein 20 homolog	0.010	3.35E-17
P61024	cyclin-dependent kinases regulatory subunit 1	0.010	3.35E-17
Q6PIW4	Fidgetin-like protein 1	0.010	3.35E-17
Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial	0.010	3.35E-17
Q8TBC5	Zinc finger and SCAN domain-containing protein 18	0.010	3.35E-17
A6ND36-1	Protein FAM83G	0.010	3.35E-17
Q9P2M7-1	cingulin	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9H410	Kinetochore-associated protein DSN1 homolog	0.010	3.35E-17
Q9UJK0	Ribosome biogenesis protein TSR3 homolog	0.010	3.35E-17
Q9Y2H6	Fibronectin type-III domain-containing protein 3a	0.010	3.35E-17
Q9HB20	pleckstrin homology domain-containing family A member 3	0.010	3.35E-17
Q5T3I0	G patch domain-containing protein 4	0.010	3.35E-17
Q9ULX6	A-kinase anchor protein 8-like	0.010	3.35E-17
Q9NQH7-1	Probable Xaa-Pro aminopeptidase 3	0.010	3.35E-17
P53350	Serine/threonine-protein kinase PLK1	0.010	3.35E-17
Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinase	0.010	3.35E-17
Q15506	Sperm surface protein Sp17	0.010	3.35E-17
Q96RL1	BRCA1-A complex subunit RAP80	0.010	3.35E-17
O43426	Synaptojanin-1	0.010	3.35E-17
Q8N1F8	Serine/threonine-protein kinase 11-interacting protein	0.010	3.35E-17
Q7Z4G1-1	COMM domain-containing protein 6	0.010	3.35E-17
Q99618	Cell division cycle-associated protein 3	0.010	3.35E-17
Q7Z309	Protein FAM122B	0.010	3.35E-17
Q9NV56	MRG/MORF4L-binding protein	0.010	3.35E-17
P07093-1	Glia-derived nexin	0.010	3.35E-17
Q8TD55	pleckstrin homology domain-containing family O member 2	0.010	3.35E-17
Q7Z5J4	Retinoic acid-induced protein 1	0.010	3.35E-17
O00622	Protein CYR61	0.010	3.35E-17
Q5SYE7	NHS-like protein 1	0.010	3.35E-17
Q9H0F6-1	Sharpin	0.010	3.35E-17
Q8IXQ5	kelch-like protein 7	0.010	3.35E-17
Q7Z6J0-1	E3 ubiquitin-protein ligase SH3RF1	0.010	3.35E-17
P16144-1	Integrin beta-4	0.010	3.35E-17
Q8IYN2	transcription elongation factor A protein-like 8	0.010	3.35E-17
Q12983	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3	0.010	3.35E-17
Q99583	Max-binding protein MNT	0.010	3.35E-17
O43164	E3 ubiquitin-protein ligase Praja-2	0.010	3.35E-17
Q9HCE5	N6-adenosine-methyltransferase subunit METTL14	0.010	3.35E-17
P40337	Von Hippel-Lindau disease tumor suppressor	0.010	3.35E-17
O60504-1	Vinexin	0.010	3.35E-17
Q8N567	Zinc finger CCHC domain-containing protein 9	0.010	3.35E-17
Q7Z2K8-1	G protein-regulated inducer of neurite outgrowth 1	0.010	3.35E-17
Q9ULX9-1	Transcription factor MafF	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8IVH2-1	Forkhead box protein P4	0.010	3.35E-17
Q9Y6Q9-1	Nuclear receptor coactivator 3	0.010	3.35E-17
Q8IX18	probable ATP-dependent RNA helicase DHX40	0.010	3.35E-17
P49918	cyclin-dependent kinase inhibitor 1C	0.010	3.35E-17
O75879	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	0.010	3.35E-17
Q9H0M0-1	NEDD4-like E3 ubiquitin-protein ligase WWP1	0.010	3.35E-17
Q92844	TRAF family member-associated NF-kappa-B activator	0.010	3.35E-17
Q9H3L0	Methylmalonic aciduria and homocystinuria type D protein, mitochondrial	0.010	3.35E-17
Q8NBJ4	Golgi membrane protein 1	0.010	3.35E-17
Q8IWZ8-1	SURP and G-patch domain-containing protein 1	0.010	3.35E-17
Q96DX5	Ankyrin repeat and SOCS box protein 9	0.010	3.35E-17
Q9Y2R4	Probable ATP-dependent RNA helicase DDX52	0.010	3.35E-17
P53567	CCAAT/enhancer-binding protein gamma	0.010	3.35E-17
O14519	Cyclin-dependent kinase 2-associated protein 1	0.010	3.35E-17
Q8TAP9	M-phase-specific PLK1-interacting protein	0.010	3.35E-17
Q96GD4	Aurora kinase B	0.010	3.35E-17
Q9NSC5-1	homer protein homolog 3	0.010	3.35E-17
Q96MX3	zinc finger protein 48	0.010	3.35E-17
Q14126	Desmoglein-2	0.010	3.35E-17
Q01196-1	Runt-related transcription factor 1	0.010	3.35E-17
Q6PIJ6-1	F-box only protein 38	0.010	3.35E-17
O95382-1	Mitogen-activated protein kinase kinase kinase 6	0.010	3.35E-17
Q9HCD6-1	Protein TANC2	0.010	3.35E-17
Q9ULZ3	apoptosis-associated speck-like protein containing a CARD	0.010	3.35E-17
Q53LP3	ankyrin repeat domain-containing protein SOWAHC	0.010	3.35E-17
Q9GZX9	Twisted gastrulation protein homolog 1	0.010	3.35E-17
O00488	Zinc finger protein 593	0.010	3.35E-17
P01130	Low-density lipoprotein receptor	0.010	3.35E-17
Q96I23	Protein preY, mitochondrial	0.010	3.35E-17
O94927	HAUS augmin-like complex subunit 5	0.010	3.35E-17
Q92871	Phosphomannomutase 1	0.010	3.35E-17
Q8IVL0	Neuron navigator 3	0.010	3.35E-17
Q9GZV5	WW domain-containing transcription regulator protein 1	0.010	3.35E-17
Q9NRP7	Serine/threonine-protein kinase 36	0.010	3.35E-17
P05164	Myeloperoxidase	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NQZ5	StAR-related lipid transfer protein 7, mitochondrial	0.010	3.35E-17
A6NED2	RCC1 domain-containing protein 1	0.010	3.35E-17
P15822-1	zinc finger protein 40	0.010	3.35E-17
O75794	Cell division cycle protein 123 homolog	0.010	3.35E-17
Q06547-3	Isoform 3 of GA-binding protein subunit beta-1	0.010	3.35E-17
Q9Y5W9	Sorting nexin-11	0.010	3.35E-17
Q6ZUT6-1	Uncharacterized protein C15orf52	0.010	3.35E-17
P55327	Tumor protein D52	0.010	3.35E-17
P52566	Rho GDP-dissociation inhibitor 2	0.010	3.35E-17
Q96T21	selenocysteine insertion sequence-binding protein 2	0.010	3.35E-17
Q8NFH8-1	RalBP1-associated Eps domain-containing protein 2	0.010	3.35E-17
Q9Y3D5	28S ribosomal protein S18c, mitochondrial	0.010	3.35E-17
Q7Z2Z1	Treslin	0.010	3.35E-17
Q86SX3-1	Uncharacterized protein C14orf80	0.010	3.35E-17
Q86US8-1	Telomerase-binding protein EST1A	0.010	3.35E-17
Q71H61	Immunoglobulin-like domain-containing receptor 2	0.010	3.35E-17
Q8N3X1	Formin-binding protein 4	0.010	3.35E-17
Q86TB3	Alpha-protein kinase 2	0.010	3.35E-17
Q9BXS6	Nucleolar and spindle-associated protein 1	0.010	3.35E-17
Q9NQS7	Inner centromere protein	0.010	3.35E-17
Q9UPN4	centrosomal protein of 131 kDa	0.010	3.35E-17
A7KAX9	rho GTPase-activating protein 32	0.010	3.35E-17
Q8NEY8-2	Isoform 2 of Periphilin-1	0.010	3.35E-17
Q8N488	RING1 and YY1-binding protein	0.010	3.35E-17
Q5SXM8	DNL-type zinc finger protein	0.010	3.35E-17
P15923	Transcription factor E2-alpha	0.010	3.35E-17
Q9Y4K4	mitogen-activated protein kinase kinase kinase kinase 5	0.010	3.35E-17
P43360	Melanoma-associated antigen 6	0.010	3.35E-17
Q96ES7	SAGA-associated factor 29	0.010	3.35E-17
O15553	Pyrin	0.010	3.35E-17
P02100	Hemoglobin subunit epsilon	0.010	3.35E-17
Q5F1R6	DnaJ homolog subfamily C member 21	0.010	3.35E-17
Q9P0V3-1	SH3 domain-binding protein 4	0.010	3.35E-17
Q5VZL5	Zinc finger MYM-type protein 4	0.010	3.35E-17
P22003	Bone morphogenetic protein 5	0.010	3.35E-17
Q96Q89-1	Kinesin-like protein KIF20B	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9Y242	transcription factor 19	0.010	3.35E-17
Q9BWL3	Uncharacterized protein C1orf43	0.010	3.35E-17
Q8N6I1-1	EP300-interacting inhibitor of differentiation 2	0.010	3.35E-17
O75326-1	Semaphorin-7A	0.010	3.35E-17
O95235	kinesin-like protein KIF20A	0.010	3.35E-17
Q6UB99	ankyrin repeat domain-containing protein 11	0.010	3.35E-17
P31944	Caspase-14	0.010	3.35E-17
Q5H9F3-1	BCL-6 corepressor-like protein 1	0.010	3.35E-17
O76080	AN1-type zinc finger protein 5	0.010	3.35E-17
Q6P3W7	SCY1-like protein 2	0.010	3.35E-17
Q5VT97	Rho GTPase-activating protein SYDE2	0.010	3.35E-17
Q16254	Transcription factor E2F4	0.010	3.35E-17
P10275	androgen receptor	0.010	3.35E-17
Q96EK7	Constitutive coactivator of peroxisome proliferator-activated receptor gamma	0.010	3.35E-17
Q6MZP7	Protein lin-54 homolog	0.010	3.35E-17
Q8WX94-1	NACHT, LRR and PYD domains-containing protein 7	0.010	3.35E-17
P15407	Fos-related antigen 1	0.010	3.35E-17
Q7L266	isoaspartyl peptidase/L-asparaginase	0.010	3.35E-17
Q9P227	Rho GTPase-activating protein 23	0.010	3.35E-17
O60353-1	Frizzled-6	0.010	3.35E-17
Q9HCN4	GPN-loop GTPase 1	0.010	3.35E-17
Q9P275	Ubiquitin carboxyl-terminal hydrolase 36	0.010	3.35E-17
Q9BWE0	Replication initiator 1	0.010	3.35E-17
P19419-1	ETS domain-containing protein Elk-1	0.010	3.35E-17
Q92558	wiskott-Aldrich syndrome protein family member 1	0.010	3.35E-17
Q15726	Metastasis-suppressor KiSS-1	0.010	3.35E-17
O60292	Signal-induced proliferation-associated 1-like protein 3	0.010	3.35E-17
Q7Z6E9	E3 ubiquitin-protein ligase RBBP6	0.010	3.35E-17
Q2NL68-1	Proline and serine-rich protein 3	0.010	3.35E-17
O75907	Diacylglycerol O-acyltransferase 1	0.010	3.35E-17
A6NFI3	Zinc finger protein 316	0.010	3.35E-17
Q8IZN3-1	Probable palmitoyltransferase ZDHHC14	0.010	3.35E-17
P43359	Melanoma-associated antigen 5	0.010	3.35E-17
Q6PJG2	ELM2 and SANT domain-containing protein 1	0.010	3.35E-17
Q8NHG8	E3 ubiquitin-protein ligase ZNRF2	0.010	3.35E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BQ89	Protein FAM110A	0.010	3.35E-17
Q8TEU7	Rap guanine nucleotide exchange factor 6	0.010	3.35E-17
Q9NQG7-4	Isoform 4 of Hermansky-Pudlak syndrome 4 protein	0.010	3.35E-17
Q13905-1	Rap guanine nucleotide exchange factor 1	0.010	3.35E-17
Q9Y2Y1	DNA-directed RNA polymerase III subunit RPC10	0.010	3.35E-17
Q5VUA4	Zinc finger protein 318	0.010	3.35E-17
Q5FWE3-1	Proline-rich transmembrane protein 3	0.010	3.35E-17
Q8IYR2	SET and MYND domain-containing protein 4	0.010	3.35E-17
Q92585	Mastermind-like protein 1	0.010	3.35E-17
Q96GP6-1	Scavenger receptor class F member 2	0.010	3.35E-17
Q99467	CD180 antigen	0.010	3.35E-17
Q8NCM8-1	Cytoplasmic dynein 2 heavy chain 1	0.010	3.35E-17
Q96PZ7-1	CUB and sushi domain-containing protein 1	0.010	3.35E-17
End of Table			

X U87 Pateamine A Genes

accession	description	fold p change	adjusted p-value
P62937-2	Isoform 2 of Peptidyl-prolyl cis-trans isomerase A	100.0	4.13E-17
Q15366-1	Poly(rC)-binding protein 2	100.0	4.13E-17
Q9UNX3	60S ribosomal protein L26-like 1	100.0	4.13E-17
Q9NQC3-5	Isoform 5 of Reticulon-4	100.0	4.13E-17
Q8IYD1	eukaryotic peptide chain release factor GTP-binding subunit ERF3B	100.0	4.13E-17
P34931	Heat shock 70 kDa protein 1-like	100.0	4.13E-17
P07205	Phosphoglycerate kinase 2	100.0	4.13E-17
Q5T2N8	ATPase family AAA domain-containing protein 3C	100.0	4.13E-17
P12235	ADP/ATP translocase 1	100.0	4.13E-17
P36873-1	serine/threonine-protein phosphatase PP1-gamma catalytic subunit	100.0	4.13E-17
P30481	HLA class I histocompatibility antigen, B-44 alpha chain	100.0	4.13E-17
P84085	ADP-ribosylation factor 5	100.0	4.13E-17
Q7Z406-1	myosin-14	100.0	4.13E-17
Q15436	protein transport protein Sec23A	100.0	4.13E-17
Q8WWI1-3	Isoform 3 of LIM domain only protein 7	100.0	4.13E-17
Q13619-1	cullin-4A	100.0	4.13E-17
Continued on next page			

accession	description	fold p change	adjusted p-value
P49902	Cytosolic purine 5′-nucleotidase	100.0	4.13E-17
Q9Y2X7-1	ARF GTPase-activating protein GIT1	100.0	4.13E-17
Q9NQ29	putative RNA-binding protein Luc7-like 1	100.0	4.13E-17
Q8WVM8	Sec1 family domain-containing protein 1	100.0	4.13E-17
O00139-2	Isoform 2 of Kinesin-like protein KIF2A	100.0	4.13E-17
O43251-1	RNA binding protein fox-1 homolog 2	100.0	4.13E-17
Q53EP0	Fibronectin type III domain-containing protein 3B	100.0	4.13E-17
Q95604	HLA class I histocompatibility antigen, Cw-17 alpha chain	100.0	4.13E-17
Q92599-1	Septin-8	100.0	4.13E-17
Q5HYI8	Rab-like protein 3	100.0	4.13E-17
P06737-1	Glycogen phosphorylase, liver form	100.0	4.13E-17
P49959	Double-strand break repair protein MRE11	100.0	4.13E-17
Q8NCW5	NAD(P)H-hydrate epimerase	100.0	4.13E-17
Q13363-1	C-terminal-binding protein 1	100.0	4.13E-17
Q96T60	Bifunctional polynucleotide phosphatase/kinase	100.0	4.13E-17
O60443	Non-syndromic hearing impairment protein 5	100.0	4.13E-17
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	100.0	4.13E-17
Q9H8S9-1	MOB kinase activator 1A	100.0	4.13E-17
Q9H267	Vacuolar protein sorting-associated protein 33B	100.0	4.13E-17
Q96JJ7-1	Protein disulfide-isomerase TMX3	100.0	4.13E-17
P43307	Translocon-associated protein subunit alpha	100.0	4.13E-17
O75431	Metaxin-2	100.0	4.13E-17
Q6P996-1	Pyridoxal-dependent decarboxylase domain-containing protein 1	100.0	4.13E-17
O75116	Rho-associated protein kinase 2	100.0	4.13E-17
Q9H3Q1	Cdc42 effector protein 4	100.0	4.13E-17
Q13547	histone deacetylase 1	100.0	4.13E-17
Q9NYH9	U3 small nucleolar RNA-associated protein 6 homolog	100.0	4.13E-17
O75955	Flotillin-1	100.0	4.13E-17
Q00577	Transcriptional activator protein Pur-alpha	100.0	4.13E-17
Q8IYS2-1	Uncharacterized protein KIAA2013	100.0	4.13E-17
P63208	s-phase kinase-associated protein 1	100.0	4.13E-17
P34059	N-acetylgalactosamine-6-sulfatase	100.0	4.13E-17
Q96P16-1	Regulation of nuclear pre-mRNA domain-containing protein 1A	100.0	4.13E-17
Q9UH62	Armadillo repeat-containing X-linked protein 3	100.0	4.13E-17
Q9NXF1	Testis-expressed protein 10	100.0	4.13E-17
Q9Y5K5-1	Ubiquitin carboxyl-terminal hydrolase isozyme L5	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q14232	Translation initiation factor eIF-2B subunit alpha	100.0	4.13E-17
Q96AC1	Fermitin family homolog 2	100.0	4.13E-17
Q14160	protein scribble homolog	100.0	4.13E-17
Q96CN7	Isochorismatase domain-containing protein 1	100.0	4.13E-17
P61020	Ras-related protein Rab-5B	100.0	4.13E-17
Q8IWB7	WD repeat and FYVE domain-containing protein 1	100.0	4.13E-17
P49590	probable histidine–tRNA ligase, mitochondrial	100.0	4.13E-17
Q16706	Alpha-mannosidase 2	100.0	4.13E-17
P61225	ras-related protein Rap-2b	100.0	4.13E-17
Q15628	Tumor necrosis factor receptor type 1-associated DEATH domain protein	100.0	4.13E-17
Q13907	Isopentenyl-diphosphate Delta-isomerase 1	100.0	4.13E-17
Q9NV31	U3 small nucleolar ribonucleoprotein protein IMP3	100.0	4.13E-17
P37268	squalene synthase	100.0	4.13E-17
P52948-1	nuclear pore complex protein Nup98-Nup96	100.0	4.13E-17
O95163	Elongator complex protein 1	100.0	4.13E-17
O75787	Renin receptor	100.0	4.13E-17
Q14738-1	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	100.0	4.13E-17
Q9Y5Q8-1	general transcription factor 3C polypeptide 5	100.0	4.13E-17
Q9UET6	Putative tRNA (cytidine(32)/guanosine(34)-2′-O)-methyltransferase	100.0	4.13E-17
O00754	Lysosomal alpha-mannosidase	100.0	4.13E-17
Q9ULR0-1	Isoform 2 of Pre-mRNA-splicing factor ISY1 homolog	100.0	4.13E-17
Q96EL3	39S ribosomal protein L53, mitochondrial	100.0	4.13E-17
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like	100.0	4.13E-17
Q9H4A6	Golgi phosphoprotein 3	100.0	4.13E-17
Q9H2H8-1	peptidyl-prolyl cis-trans isomerase-like 3	100.0	4.13E-17
P22059	Oxysterol-binding protein 1	100.0	4.13E-17
Q14376	UDP-glucose 4-epimerase	100.0	4.13E-17
Q5SY16	Polynucleotide 5′-hydroxyl-kinase NOL9	100.0	4.13E-17
O00762	Ubiquitin-conjugating enzyme E2 C	100.0	4.13E-17
Q86U90	YrdC domain-containing protein, mitochondrial	100.0	4.13E-17
Q96SI9	spermatid perinuclear RNA-binding protein	100.0	4.13E-17
Q9BTD8-1	RNA-binding protein 42	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BU61-1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	100.0	4.13E-17
O95716	ras-related protein Rab-3D	100.0	4.13E-17
Q13895	Bystin	100.0	4.13E-17
Q9BPW8	Protein NipSnap homolog 1	100.0	4.13E-17
Q92783	signal transducing adapter molecule 1	100.0	4.13E-17
Q6IQ22	Ras-related protein Rab-12	100.0	4.13E-17
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial	100.0	4.13E-17
P62070	Ras-related protein R-Ras2	100.0	4.13E-17
Q9Y4R8	telomere length regulation protein TEL2 homolog	100.0	4.13E-17
Q13671	ras and Rab interactor 1	100.0	4.13E-17
Q96M27-1	protein PRRC1	100.0	4.13E-17
Q5T8D3-3	Isoform 3 of Acyl-CoA-binding domain-containing protein 5	100.0	4.13E-17
Q9NZ32	Actin-related protein 10	100.0	4.13E-17
Q14573	Inositol 1,4,5-trisphosphate receptor type 3	100.0	4.13E-17
Q9Y3S2	zinc finger protein 330	100.0	4.13E-17
P29558-1	RNA-binding motif, single-stranded-interacting protein 1	100.0	4.13E-17
Q8IZQ5	Selenoprotein H	100.0	4.13E-17
Q16514	Transcription initiation factor TFIID subunit 12	100.0	4.13E-17
Q53H82	Endoribonuclease LACTB2	100.0	4.13E-17
Q15392	Delta(24)-sterol reductase	100.0	4.13E-17
Q9UDY4	DnaJ homolog subfamily B member 4	100.0	4.13E-17
Q9H254	Spectrin beta chain, non-erythrocytic 4	100.0	4.13E-17
P62330	ADP-ribosylation factor 6	100.0	4.13E-17
P52758	2-iminobutanoate/2-iminopropanoate deaminase	100.0	4.13E-17
Q9HBM1	Kinetochore protein Spc25	100.0	4.13E-17
Q92917	G patch domain and KOW motifs-containing protein	100.0	4.13E-17
Q12816-1	Trophinin	100.0	4.13E-17
Q5VW32	BRO1 domain-containing protein BROX	100.0	4.13E-17
Q96ST2	protein IWS1 homolog	100.0	4.13E-17
P16333-1	Cytoplasmic protein NCK1	100.0	4.13E-17
Q9BTZ2	dehydrogenase/reductase sdr family member 4	100.0	4.13E-17
Q9H074	Polyadenylate-binding protein-interacting protein 1	100.0	4.13E-17
Q92466	DNA damage-binding protein 2	100.0	4.13E-17
P09960-1	leukotriene A-4 hydrolase	100.0	4.13E-17
Q8IUF8	ribosomal oxygenase 2	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NU22	Midasin	100.0	4.13E-17
Q6NUM9-1	all-trans-retinol 13,14-reductase	100.0	4.13E-17
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	100.0	4.13E-17
P09884	DNA polymerase alpha catalytic subunit	100.0	4.13E-17
Q9Y2H0-1	Isoform 2 of Disks large-associated protein 4	100.0	4.13E-17
Q9GZS3	WD repeat-containing protein 61	100.0	4.13E-17
Q13257-1	Mitotic spindle assembly checkpoint protein MAD2A	100.0	4.13E-17
P51617	interleukin-1 receptor-associated kinase 1	100.0	4.13E-17
Q96FV9-1	THO complex subunit 1	100.0	4.13E-17
Q13144	Translation initiation factor eIF-2B subunit epsilon	100.0	4.13E-17
Q9H832	Ubiquitin-conjugating enzyme E2 Z	100.0	4.13E-17
P22033	Methylmalonyl-CoA mutase, mitochondrial	100.0	4.13E-17
P50750	Cyclin-dependent kinase 9	100.0	4.13E-17
Q9Y3Q8	TSC22 domain family protein 4	100.0	4.13E-17
Q9H061-1	Transmembrane protein 126A	100.0	4.13E-17
Q13610	Periodic tryptophan protein 1 homolog	100.0	4.13E-17
Q6PL18-1	ATPase family AAA domain-containing protein 2	100.0	4.13E-17
Q96Q11-1	CCA tRNA nucleotidyltransferase 1, mitochondrial	100.0	4.13E-17
Q9UFC0	Leucine-rich repeat and WD repeat-containing protein 1	100.0	4.13E-17
Q9Y5U9	immediate early response 3-interacting protein 1	100.0	4.13E-17
O75616-1	GTPase Era, mitochondrial	100.0	4.13E-17
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit	100.0	4.13E-17
Q969E4	transcription elongation factor A protein-like 3	100.0	4.13E-17
P08253	72 kDa type IV collagenase	100.0	4.13E-17
Q5RI15-1	Cytochrome c oxidase protein 20 homolog	100.0	4.13E-17
Q9GZP9	Derlin-2	100.0	4.13E-17
Q16222-1	UDP-N-acetylhexosamine pyrophosphorylase	100.0	4.13E-17
Q96EY8	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	100.0	4.13E-17
Q16539	Mitogen-activated protein kinase 14	100.0	4.13E-17
Q9BYB4-1	Guanine nucleotide-binding protein subunit beta-like protein 1	100.0	4.13E-17
Q99720	sigma non-opioid intracellular receptor 1	100.0	4.13E-17
P57678	Gem-associated protein 4	100.0	4.13E-17
P36639	7,8-dihydro-8-oxoguanine triphosphatase	100.0	4.13E-17
Q8WXI9	Transcriptional repressor p66-beta	100.0	4.13E-17
P36404	ADP-ribosylation factor-like protein 2	100.0	4.13E-17
P35626	beta-adrenergic receptor kinase 2	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P48449-1	lanosterol synthase	100.0	4.13E-17
Q6P1Q9-1	Methyltransferase-like protein 2B	100.0	4.13E-17
P21953	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	100.0	4.13E-17
Q9BUK6	Protein misato homolog 1	100.0	4.13E-17
Q5UIP0	Telomere-associated protein RIF1	100.0	4.13E-17
P12110	Collagen alpha-2(VI) chain	100.0	4.13E-17
Q96A26	Protein FAM162A	100.0	4.13E-17
Q9BYJ9-1	YTH domain-containing family protein 1	100.0	4.13E-17
P49137	MAP kinase-activated protein kinase 2	100.0	4.13E-17
Q99447-1	ethanolamine-phosphate cytidylyltransferase	100.0	4.13E-17
Q15043	Zinc transporter ZIP14	100.0	4.13E-17
Q86XI2-1	condensin-2 complex subunit G2	100.0	4.13E-17
Q9BRT9	DNA replication complex GINS protein SLD5	100.0	4.13E-17
O15116	U6 snRNA-associated Sm-like protein LSm1	100.0	4.13E-17
Q53EL6-1	Programmed cell death protein 4	100.0	4.13E-17
Q9NRY5	Protein FAM114A2	100.0	4.13E-17
P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial	100.0	4.13E-17
Q9UJX3-1	Anaphase-promoting complex subunit 7	100.0	4.13E-17
P58004	Sestrin-2	100.0	4.13E-17
O00165	HCLS1-associated protein X-1	100.0	4.13E-17
O95837	Guanine nucleotide-binding protein subunit alpha-14	100.0	4.13E-17
P49354	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	100.0	4.13E-17
Q9Y4P1-1	Cysteine protease ATG4B	100.0	4.13E-17
P28062-1	Proteasome subunit beta type-8	100.0	4.13E-17
O76054	SEC14-like protein 2	100.0	4.13E-17
P40855-1	Peroxisomal biogenesis factor 19	100.0	4.13E-17
Q9NRG1	Phosphoribosyltransferase domain-containing protein 1	100.0	4.13E-17
Q13432	protein unc-119 homolog A	100.0	4.13E-17
Q969Z0-1	Protein TBRG4	100.0	4.13E-17
Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1	100.0	4.13E-17
Q13107-1	Ubiquitin carboxyl-terminal hydrolase 4	100.0	4.13E-17
Q9UJV9	Probable ATP-dependent RNA helicase DDX41	100.0	4.13E-17
Q92870-1	Amyloid-beta A4 precursor protein-binding family B member 2	100.0	4.13E-17
Q9BY32-1	Inosine triphosphate pyrophosphatase	100.0	4.13E-17
Q9NQI0	Probable ATP-dependent RNA helicase DDX4	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	100.0	4.13E-17
Q8TCE6-1	Protein FAM45A	100.0	4.13E-17
Q9Y3A3	MOB-like protein phocein	100.0	4.13E-17
Q8TBQ9	Protein kish-A	100.0	4.13E-17
Q8N392-1	Rho GTPase-activating protein 18	100.0	4.13E-17
Q8TEA8	D-aminoacyl-tRNA deacylase 1	100.0	4.13E-17
Q6PJG6-1	BRCA1-associated ATM activator 1	100.0	4.13E-17
P42226	Signal transducer and activator of transcription 6	100.0	4.13E-17
Q8IXI2-1	Mitochondrial Rho GTPase 1	100.0	4.13E-17
Q13112	Chromatin assembly factor 1 subunit B	100.0	4.13E-17
O60306	Intron-binding protein aquarius	100.0	4.13E-17
Q9BV20-1	methylthioribose-1-phosphate isomerase	100.0	4.13E-17
Q9UKV5	E3 ubiquitin-protein ligase AMFR	100.0	4.13E-17
Q8N8A6	ATP-dependent RNA helicase DDX51	100.0	4.13E-17
P23434	Glycine cleavage system H protein, mitochondrial	100.0	4.13E-17
Q99496	E3 ubiquitin-protein ligase RING2	100.0	4.13E-17
O14933	Ubiquitin/ISG15-conjugating enzyme E2 L6	100.0	4.13E-17
O43716	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	100.0	4.13E-17
O60678	protein arginine N-methyltransferase 3	100.0	4.13E-17
Q9BTE6-1	Alanyl-tRNA editing protein Aarsd1	100.0	4.13E-17
Q03426	mevalonate kinase	100.0	4.13E-17
O14936	peripheral plasma membrane protein CASK	100.0	4.13E-17
Q9BQ70	Transcription factor 25	100.0	4.13E-17
O95425	Supervillin	100.0	4.13E-17
Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein	100.0	4.13E-17
O95219	sorting nexin-4	100.0	4.13E-17
Q9NSC5-1	homer protein homolog 3	100.0	4.13E-17
Q9BSH4	Translational activator of cytochrome c oxidase 1	100.0	4.13E-17
Q14197	Peptidyl-tRNA hydrolase ICT1, mitochondrial	100.0	4.13E-17
Q9BTL3	RNMT-activating mini protein	100.0	4.13E-17
P49427	ubiquitin-conjugating enzyme E2 R1	100.0	4.13E-17
Q86TX2	acyl-coenzyme A thioesterase 1	100.0	4.13E-17
O75879	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	100.0	4.13E-17
Q8N490-2	Isoform 2 of Probable hydrolase PNKD	100.0	4.13E-17
O60879	Protein diaphanous homolog 2	100.0	4.13E-17
P62310	U6 snRNA-associated Sm-like protein LSm3	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q5JVF3	PCI domain-containing protein 2	100.0	4.13E-17
Q9UJ41-1	Rab5 GDP/GTP exchange factor	100.0	4.13E-17
Q96GG9	DCN1-like protein 1	100.0	4.13E-17
Q96RS6	NudC domain-containing protein 1	100.0	4.13E-17
O95714	E3 ubiquitin-protein ligase HERC2	100.0	4.13E-17
Q9NUM4	Transmembrane protein 106B	100.0	4.13E-17
P12036	Neurofilament heavy polypeptide	100.0	4.13E-17
P18615	Negative elongation factor E	100.0	4.13E-17
Q8TER5	Rho guanine nucleotide exchange factor 40	100.0	4.13E-17
Q8TD30-1	Alanine aminotransferase 2	100.0	4.13E-17
P47712	Cytosolic phospholipase A2	100.0	4.13E-17
Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	100.0	4.13E-17
Q9Y5V3	Melanoma-associated antigen D1	100.0	4.13E-17
Q6R327-1	Rapamycin-insensitive companion of mTOR	100.0	4.13E-17
P62877	E3 ubiquitin-protein ligase RBX1	100.0	4.13E-17
O75394	39S ribosomal protein L33, mitochondrial	100.0	4.13E-17
Q9P1F3	Costars family protein ABRACL	100.0	4.13E-17
Q9NXC5-1	GATOR complex protein MIOS	100.0	4.13E-17
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	100.0	4.13E-17
Q9NZD8	Maspardin	100.0	4.13E-17
Q9BUV8-1	Uncharacterized protein C20orf24	100.0	4.13E-17
Q9UID3-1	Vacuolar protein sorting-associated protein 51 homolog	100.0	4.13E-17
O15121	Sphingolipid delta(4)-desaturase DES1	100.0	4.13E-17
P17535	Transcription factor jun-D	100.0	4.13E-17
Q13416	Origin recognition complex subunit 2	100.0	4.13E-17
O00418	Eukaryotic elongation factor 2 kinase	100.0	4.13E-17
Q9Y4B6	DDB1- and CUL4-associated factor 1	100.0	4.13E-17
Q96FQ6	Protein S100-A16	100.0	4.13E-17
P08397-1	porphobilinogen deaminase	100.0	4.13E-17
Q15054	DNA polymerase delta subunit 3	100.0	4.13E-17
Q9NQE9	Histidine triad nucleotide-binding protein 3	100.0	4.13E-17
Q8NEW0	Zinc transporter 7	100.0	4.13E-17
Q96EC8-1	Protein YIPF6	100.0	4.13E-17
Q9H0R4-1	haloacid dehalogenase-like hydrolase domain-containing protein 2	100.0	4.13E-17
Q96EH3	mitochondrial assembly of ribosomal large subunit protein 1	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P61964	WD repeat-containing protein 5	100.0	4.13E-17
P49768-1	Presenilin-1	100.0	4.13E-17
P56182	Ribosomal RNA processing protein 1 homolog A	100.0	4.13E-17
Q9H330	Transmembrane protein 245	100.0	4.13E-17
O95140	Mitofusin-2	100.0	4.13E-17
Q9NXE4-1	Sphingomyelin phosphodiesterase 4	100.0	4.13E-17
P78330	phosphoserine phosphatase	100.0	4.13E-17
Q9BV81	ER membrane protein complex subunit 6	100.0	4.13E-17
Q9Y3E0	vesicle transport protein GOT1B	100.0	4.13E-17
P60468	protein transport protein Sec61 subunit beta	100.0	4.13E-17
Q8IYB7	DIS3-like exonuclease 2	100.0	4.13E-17
Q8NF37	Lysophosphatidylcholine acyltransferase 1	100.0	4.13E-17
P32970	CD70 antigen	100.0	4.13E-17
Q93050-1	Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1	100.0	4.13E-17
Q8TC07-1	TBC1 domain family member 15	100.0	4.13E-17
Q9UK59	lariat debranching enzyme	100.0	4.13E-17
P61421	V-type proton ATPase subunit d 1	100.0	4.13E-17
Q9Y4J8-1	Dystrobrevin alpha	100.0	4.13E-17
Q9NZQ3-1	NCK-interacting protein with SH3 domain	100.0	4.13E-17
Q9Y2I1-1	Nischarin	100.0	4.13E-17
Q9Y3X0	coiled-coil domain-containing protein 9	100.0	4.13E-17
O15031	Plexin-B2	100.0	4.13E-17
Q8NHQ9	ATP-dependent RNA helicase DDX55	100.0	4.13E-17
Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein	100.0	4.13E-17
Q96EE3	nucleoporin Seh1	100.0	4.13E-17
Q6P9B9	Integrator complex subunit 5	100.0	4.13E-17
Q8TDZ2	[F-actin]-monooxygenase MICAL1	100.0	4.13E-17
Q9Y2P8	RNA 3′-terminal phosphate cyclase-like protein	100.0	4.13E-17
Q9BUM1	Glucose-6-phosphatase 3	100.0	4.13E-17
Q9UBS0	Ribosomal protein S6 kinase beta-2	100.0	4.13E-17
Q5T5P2-1	Sickle tail protein homolog	100.0	4.13E-17
Q15262	Receptor-type tyrosine-protein phosphatase kappa	100.0	4.13E-17
Q9H9T3	elongator complex protein 3	100.0	4.13E-17
Q9BUR4	Telomerase Cajal body protein 1	100.0	4.13E-17
P04424	argininosuccinate lyase	100.0	4.13E-17
Q9BQB6-1	vitamin K epoxide reductase complex subunit 1	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q15554-3	Telomeric repeat-binding factor 2	100.0	4.13E-17
O95674-1	phosphatidate cytidylyltransferase 2	100.0	4.13E-17
Q13769	THO complex subunit 5 homolog	100.0	4.13E-17
Q92979	Ribosomal RNA small subunit methyltransferase Nep1	100.0	4.13E-17
Q99570	Phosphoinositide 3-kinase regulatory subunit 4	100.0	4.13E-17
Q14676	Mediator of DNA damage checkpoint protein 1	100.0	4.13E-17
P62306	Small nuclear ribonucleoprotein F	100.0	4.13E-17
Q9H6L5	Reticulophagy regulator 1	100.0	4.13E-17
Q7Z7A3	Cytoplasmic tRNA 2-thiolation protein 1	100.0	4.13E-17
Q86TB9	Protein PAT1 homolog 1	100.0	4.13E-17
Q9UHA4	ragulator complex protein LAMTOR3	100.0	4.13E-17
Q9BYC9	39S ribosomal protein L20, mitochondrial	100.0	4.13E-17
Q9UP95	Solute carrier family 12 member 4	100.0	4.13E-17
Q8NE86	Calcium uniporter protein, mitochondrial	100.0	4.13E-17
Q7Z2K6	Endoplasmic reticulum metallopeptidase 1	100.0	4.13E-17
P82930	28S ribosomal protein S34, mitochondrial	100.0	4.13E-17
Q5JTJ3-1	Cytochrome c oxidase assembly factor 6 homolog	100.0	4.13E-17
Q9UJA5-1	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	100.0	4.13E-17
O60231	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	100.0	4.13E-17
Q8WXD5	gem-associated protein 6	100.0	4.13E-17
Q9NUV7	Serine palmitoyltransferase 3	100.0	4.13E-17
Q9UDT6-1	CAP-Gly domain-containing linker protein 2	100.0	4.13E-17
Q9BRT6	Protein LLP homolog	100.0	4.13E-17
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial	100.0	4.13E-17
Q9Y6K5	2′-5′-oligoadenylate synthase 3	100.0	4.13E-17
P82932	28S ribosomal protein S6, mitochondrial	100.0	4.13E-17
Q7L592	Protein arginine methyltransferase NDUFAF7, mitochondrial	100.0	4.13E-17
O96007	molybdopterin synthase catalytic subunit	100.0	4.13E-17
Q9Y3C4	EKC/KEOPS complex subunit TPRKB	100.0	4.13E-17
Q9BVS4	Serine/threonine-protein kinase rio2	100.0	4.13E-17
Q6IA86-1	elongator complex protein 2	100.0	4.13E-17
O75530	Polycomb protein EED	100.0	4.13E-17
Q99811	Paired mesoderm homeobox protein 2	100.0	4.13E-17
Q86X76	Deaminated glutathione amidase	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BWT3	Poly(A) polymerase gamma	100.0	4.13E-17
Q5U5X0	Complex III assembly factor LYRM7	100.0	4.13E-17
O00423-1	Echinoderm microtubule-associated protein-like 1	100.0	4.13E-17
O14981	TATA-binding protein-associated factor 172	100.0	4.13E-17
Q01484	Ankyrin-2	100.0	4.13E-17
Q9UBX3	Mitochondrial dicarboxylate carrier	100.0	4.13E-17
O94901-1	SUN domain-containing protein 1	100.0	4.13E-17
Q96HD1-1	Cysteine-rich with EGF-like domain protein 1	100.0	4.13E-17
Q15208	serine/threonine-protein kinase 38	100.0	4.13E-17
O15021	Microtubule-associated serine/threonine-protein kinase 4	100.0	4.13E-17
Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	100.0	4.13E-17
Q03154-1	Aminoacylase-1	100.0	4.13E-17
Q5VZE5	N-alpha-acetyltransferase 35, NatC auxiliary subunit	100.0	4.13E-17
Q86YV9	Hermansky-Pudlak syndrome 6 protein	100.0	4.13E-17
Q7Z2E3-1	Aprataxin	100.0	4.13E-17
O75525-1	KH domain-containing, RNA-binding, signal transduction-associated protein 3	100.0	4.13E-17
Q13867	bleomycin hydrolase	100.0	4.13E-17
O94929-1	Actin-binding LIM protein 3	100.0	4.13E-17
Q96BX8	MOB kinase activator 3A	100.0	4.13E-17
P22607-1	Fibroblast growth factor receptor 3	100.0	4.13E-17
Q96JJ3	Engulfment and cell motility protein 2	100.0	4.13E-17
A3KMH1	von Willebrand factor A domain-containing protein 8	100.0	4.13E-17
Q15007	Pre-mRNA-splicing regulator WTAP	100.0	4.13E-17
Q9NUQ2	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	100.0	4.13E-17
O94856	Neurofascin	100.0	4.13E-17
O75208-1	Ubiquinone biosynthesis protein COQ9, mitochondrial	100.0	4.13E-17
O14561	Acyl carrier protein, mitochondrial	100.0	4.13E-17
P28288	ATP-binding cassette sub-family D member 3	100.0	4.13E-17
Q9BYD6	39S ribosomal protein L1, mitochondrial	100.0	4.13E-17
Q92925-1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	100.0	4.13E-17
Q92542-1	Nicastrin	100.0	4.13E-17
P23458	Tyrosine-protein kinase JAK1	100.0	4.13E-17
Q9NYP7-1	elongation of very long chain fatty acids protein 5	100.0	4.13E-17
Q8NEZ5-1	F-box only protein 22	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8N4H5	mitochondrial import receptor subunit TOM5 homolog	100.0	4.13E-17
Q9NRP0-1	oligosaccharyltransferase complex subunit OSTC	100.0	4.13E-17
Q86WR0	Coiled-coil domain-containing protein 25	100.0	4.13E-17
O95363	phenylalanine–tRNA ligase, mitochondrial	100.0	4.13E-17
Q9NRP2	COX assembly mitochondrial protein 2 homolog	100.0	4.13E-17
P86790	Vacuolar fusion protein CCZ1 homolog B	100.0	4.13E-17
P51151	Ras-related protein Rab-9A	100.0	4.13E-17
Q86U86-1	Protein polybromo-1	100.0	4.13E-17
Q03111	Protein ENL	100.0	4.13E-17
O75446	Histone deacetylase complex subunit SAP30	100.0	4.13E-17
Q8N543	prolyl 3-hydroxylase OGFOD1	100.0	4.13E-17
Q14746	Conserved oligomeric Golgi complex subunit 2	100.0	4.13E-17
P82650	28S ribosomal protein S22, mitochondrial	100.0	4.13E-17
Q8TB61	Adenosine 3′-phospho 5′-phosphosulfate transporter 1	100.0	4.13E-17
Q99418	Cytohesin-2	100.0	4.13E-17
P51948-1	CDK-activating kinase assembly factor MAT1	100.0	4.13E-17
Q9UFN0	protein NipSnap homolog 3A	100.0	4.13E-17
O43674-1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	100.0	4.13E-17
Q8N9Z2-1	Coiled-coil domain-containing protein 71L	100.0	4.13E-17
Q68E01	Integrator complex subunit 3	100.0	4.13E-17
O95999	B-cell lymphoma/leukemia 10	100.0	4.13E-17
P00846	ATP synthase subunit A	100.0	4.13E-17
Q86VZ5-1	Phosphatidylcholine:ceramide cholinephosphotransferase 1	100.0	4.13E-17
Q9H9Q2	COP9 signalosome complex subunit 7b	100.0	4.13E-17
Q9H2J4	phosducin-like protein 3	100.0	4.13E-17
O95260	Arginyl-tRNA–protein transferase 1	100.0	4.13E-17
O14656	Torsin-1A	100.0	4.13E-17
Q9H490	Phosphatidylinositol glycan anchor biosynthesis class U protein	100.0	4.13E-17
Q9UNQ2	Probable dimethyladenosine transferase	100.0	4.13E-17
Q9H1I8-1	Activating signal cointegrator 1 complex subunit 2	100.0	4.13E-17
Q6U841	Sodium-driven chloride bicarbonate exchanger	100.0	4.13E-17
Q8WWV3-1	Reticulon-4-interacting protein 1, mitochondrial	100.0	4.13E-17
Q9Y2R5	28S ribosomal protein S17, mitochondrial	100.0	4.13E-17
Q709C8	Vacuolar protein sorting-associated protein 13C	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96P47	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	100.0	4.13E-17
O75027-1	ATP-binding cassette sub-family B member 7, mitochondrial	100.0	4.13E-17
Q15649	Zinc finger HIT domain-containing protein 3	100.0	4.13E-17
P23610	Factor VIII intron 22 protein	100.0	4.13E-17
Q99996	A-kinase anchor protein 9	100.0	4.13E-17
P40763	Signal transducer and activator of transcription 3	100.0	4.13E-17
Q9BTA9-1	WW domain-containing adapter protein with coiled-coil	100.0	4.13E-17
Q9UKN8	General transcription factor 3C polypeptide 4	100.0	4.13E-17
Q9UJX2-1	cell division cycle protein 23 homolog	100.0	4.13E-17
Q9UNP9-1	Peptidyl-prolyl cis-trans isomerase E	100.0	4.13E-17
P14406	Cytochrome c oxidase subunit 7A2, mitochondrial	100.0	4.13E-17
Q9Y3M8-1	StAR-related lipid transfer protein 13	100.0	4.13E-17
Q9NXR7-1	Isoform 1 of BRISC and BRCA1-A complex member 2	100.0	4.13E-17
Q9UGN5-1	Poly [ADP-ribose] polymerase 2	100.0	4.13E-17
Q96H79	Zinc finger CCCH-type antiviral protein 1-like	100.0	4.13E-17
P55268	laminin subunit beta-2	100.0	4.13E-17
Q8N5L8	Ribonuclease P protein subunit p25-like protein	100.0	4.13E-17
Q9BRG1	Vacuolar protein-sorting-associated protein 25	100.0	4.13E-17
Q9UHG3	prenylcysteine oxidase 1	100.0	4.13E-17
P22304	iduronate 2-sulfatase	100.0	4.13E-17
Q8TCB0	Interferon-induced protein 44	100.0	4.13E-17
O15305	Phosphomannomutase 2	100.0	4.13E-17
Q15067	Peroxisomal acyl-coenzyme A oxidase 1	100.0	4.13E-17
Q12882-1	Dihydropyrimidine dehydrogenase [NADP(+)]	100.0	4.13E-17
O43929	origin recognition complex subunit 4	100.0	4.13E-17
P48651	phosphatidylserine synthase 1	100.0	4.13E-17
Q93100-1	phosphorylase b kinase regulatory subunit beta	100.0	4.13E-17
P46976-1	Glycogenin-1	100.0	4.13E-17
O43708	maleylacetoacetate isomerase	100.0	4.13E-17
Q16527	Cysteine and glycine-rich protein 2	100.0	4.13E-17
O15541	RING finger protein 113A	100.0	4.13E-17
Q9UM13	Anaphase-promoting complex subunit 10	100.0	4.13E-17
Q9NXV6	CDKN2A-interacting protein	100.0	4.13E-17
Q9Y2L5-1	trafficking protein particle complex subunit 8	100.0	4.13E-17
P15927-1	Replication protein A 32 kDa subunit	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q96N46	Tetratricopeptide repeat protein 14	100.0	4.13E-17
Q9HB40	Retinoid-inducible serine carboxypeptidase	100.0	4.13E-17
Q8IY26	Phospholipid phosphatase 6	100.0	4.13E-17
Q8NHP6-1	motile sperm domain-containing protein 2	100.0	4.13E-17
Q5XKP0	MICOS complex subunit MIC13	100.0	4.13E-17
Q9NUQ3-1	Gamma-taxilin	100.0	4.13E-17
Q9NRZ9	Lymphoid-specific helicase	100.0	4.13E-17
Q9NSU2-1	Three-prime repair exonuclease 1	100.0	4.13E-17
Q9P2T1-1	GMP reductase 2	100.0	4.13E-17
Q9Y2R0	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	100.0	4.13E-17
Q8WW22-1	DnaJ homolog subfamily A member 4	100.0	4.13E-17
Q96MW5	Conserved oligomeric Golgi complex subunit 8	100.0	4.13E-17
Q5TBB1	ribonuclease h2 subunit b	100.0	4.13E-17
Q8TBM8	dnaJ homolog subfamily B member 14	100.0	4.13E-17
Q96FZ2	embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein	100.0	4.13E-17
Q9NZV5-1	Selenoprotein N	100.0	4.13E-17
Q96AA3	Protein RFT1 homolog	100.0	4.13E-17
Q58A45	PAN2-PAN3 deadenylation complex subunit PAN3	100.0	4.13E-17
O00458	Interferon-related developmental regulator 1	100.0	4.13E-17
O14733	dual specificity mitogen-activated protein kinase kinase 7	100.0	4.13E-17
Q8N4J0	carnosine N-methyltransferase	100.0	4.13E-17
P35240-1	merlin	100.0	4.13E-17
P38432	coilin	100.0	4.13E-17
Q9Y3C5	Ring finger protein 11	100.0	4.13E-17
Q01831	DNA repair protein complementing XP-C cells	100.0	4.13E-17
Q9Y5Q9	General transcription factor 3C polypeptide 3	100.0	4.13E-17
Q9Y2Z9-1	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial	100.0	4.13E-17
O75352	Mannose-P-dolichol utilization defect 1 protein	100.0	4.13E-17
Q9H0U6	39S ribosomal protein L18, mitochondrial	100.0	4.13E-17
Q9Y2U5	Mitogen-activated protein kinase kinase kinase 2	100.0	4.13E-17
O75323-1	Protein NipSnap homolog 2	100.0	4.13E-17
Q8N5Z5-1	BTB/POZ domain-containing protein KCTD17	100.0	4.13E-17
P53667-1	LIM domain kinase 1	100.0	4.13E-17
Q8N183	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 2	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9H9Y6-1	DNA-directed RNA polymerase I subunit RPA2	100.0	4.13E-17
Q8IX01-1	SURP and G-patch domain-containing protein 2	100.0	4.13E-17
Q8IXT5	RNA-binding protein 12B	100.0	4.13E-17
Q86Y79	Probable peptidyl-tRNA hydrolase	100.0	4.13E-17
Q9NWS8	Required for meiotic nuclear division protein 1 homolog	100.0	4.13E-17
Q9Y376	Calcium-binding protein 39	100.0	4.13E-17
Q9Y324	rRNA-processing protein FCF1 homolog	100.0	4.13E-17
O95777	U6 snRNA-associated Sm-like protein LSm8	100.0	4.13E-17
Q07817-1	bcl-2-like protein 1	100.0	4.13E-17
Q9BQA9-1	Uncharacterized protein C17orf62	100.0	4.13E-17
Q8NF64	Zinc finger MIZ domain-containing protein 2	100.0	4.13E-17
A6ZKI3	Retrotransposon Gag-like protein 8B	100.0	4.13E-17
Q6NXE6-1	Armadillo repeat-containing protein 6	100.0	4.13E-17
O14958	Calsequestrin-2	100.0	4.13E-17
Q6ZMG9	Ceramide synthase 6	100.0	4.13E-17
O95365	Zinc finger and BTB domain-containing protein 7A	100.0	4.13E-17
Q14145	Kelch-like ECH-associated protein 1	100.0	4.13E-17
Q9BQ95	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	100.0	4.13E-17
Q9NRL2	Bromodomain adjacent to zinc finger domain protein 1A	100.0	4.13E-17
Q92934	Bcl2-associated agonist of cell death	100.0	4.13E-17
Q9ULG6	Cell cycle progression protein 1	100.0	4.13E-17
P10646	Tissue factor pathway inhibitor	100.0	4.13E-17
Q8NBI5	Solute carrier family 43 member 3	100.0	4.13E-17
Q9ULH0-1	Kinase D-interacting substrate of 220 kDa	100.0	4.13E-17
O14657	Torsin-1B	100.0	4.13E-17
Q96RY5	Protein cramped-like	100.0	4.13E-17
P27216-1	Annexin A13	100.0	4.13E-17
Q15464	SH2 domain-containing adapter protein B	100.0	4.13E-17
Q9C004-1	Protein sprouty homolog 4	100.0	4.13E-17
P02686-1	myelin basic protein	100.0	4.13E-17
P18084	Integrin beta-5	100.0	4.13E-17
Q92541	RNA polymerase-associated protein RTF1 homolog	100.0	4.13E-17
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1	100.0	4.13E-17
Q9NPJ6-1	mediator of RNA polymerase II transcription subunit 4	100.0	4.13E-17
O43524	Forkhead box protein O3	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8WVQ1	Soluble calcium-activated nucleotidase 1	100.0	4.13E-17
P50613	Cyclin-dependent kinase 7	100.0	4.13E-17
Q5TCZ1	SH3 and PX domain-containing protein 2A	100.0	4.13E-17
Q5EBL4-1	RILP-like protein 1	100.0	4.13E-17
Q9Y6V7	Probable ATP-dependent RNA helicase ddx49	100.0	4.13E-17
Q03519-1	antigen peptide transporter 2	100.0	4.13E-17
A2RRP1-1	neuroblastoma-amplified sequence	100.0	4.13E-17
Q14693-1	Phosphatidate phosphatase LPIN1	100.0	4.13E-17
P26572	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	100.0	4.13E-17
Q9UBU8-1	Mortality factor 4-like protein 1	100.0	4.13E-17
Q96EL2	28S ribosomal protein S24, mitochondrial	100.0	4.13E-17
Q9NRZ5	1-acyl-sn-glycerol-3-phosphate acyltransferase delta	100.0	4.13E-17
Q92581-1	Sodium/hydrogen exchanger 6	100.0	4.13E-17
P11169	Solute carrier family 2, facilitated glucose transporter member 3	100.0	4.13E-17
Q5HYC2-1	Uncharacterized protein KIAA2026	100.0	4.13E-17
O15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	100.0	4.13E-17
Q6IA69	glutamine-dependent NAD(+) synthetase	100.0	4.13E-17
P15291	Beta-1,4-galactosyltransferase 1	100.0	4.13E-17
Q14919-1	Dr1-associated corepressor	100.0	4.13E-17
P61218	DNA-directed RNA polymerases I, II, and III subunit RPABC2	100.0	4.13E-17
Q5K651	Sterile alpha motif domain-containing protein 9	100.0	4.13E-17
Q9UGJ1	gamma-tubulin complex component 4	100.0	4.13E-17
Q8NER1	Transient receptor potential cation channel subfamily V member 1	100.0	4.13E-17
P16083	Ribosyldihydronicotinamide dehydrogenase [quinone]	100.0	4.13E-17
Q96QU8	Exportin-6	100.0	4.13E-17
O60353-1	Frizzled-6	100.0	4.13E-17
Q99759	Mitogen-activated protein kinase kinase kinase 3	100.0	4.13E-17
Q13936	Voltage-dependent L-type calcium channel subunit alpha-1C	100.0	4.13E-17
Q15652	probable JmjC domain-containing histone demethylation protein 2C	100.0	4.13E-17
Q9GZR2-1	RNA exonuclease 4	100.0	4.13E-17
Q9BX95	Sphingosine-1-phosphate phosphatase 1	100.0	4.13E-17
Q5TAX3	Terminal uridylyltransferase 4	100.0	4.13E-17
Q9ULB1-1	Neurexin-1	100.0	4.13E-17
Q6ZUI0	tumor protein p63-regulated gene 1 protein	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
P38571	lysosomal acid lipase/cholesteryl ester hydrolase	100.0	4.13E-17
Q9UBB9-1	Tuftelin-interacting protein 11	100.0	4.13E-17
P52756	RNA-binding protein 5	100.0	4.13E-17
Q7L5L3-1	Isoform 2 of Lysophospholipase D GDPD3	100.0	4.13E-17
Q14686	Nuclear receptor coactivator 6	100.0	4.13E-17
Q06136	3-ketodihydrosphingosine reductase	100.0	4.13E-17
Q7Z7B0	Filamin-A-interacting protein 1	100.0	4.13E-17
Q14679	Tubulin polyglutamylase TTLL4	100.0	4.13E-17
O75781	Paralemmin-1	100.0	4.13E-17
Q7Z333	Probable helicase senataxin	100.0	4.13E-17
O60469-1	Down syndrome cell adhesion molecule	100.0	4.13E-17
Q8IYJ2	uncharacterized protein C10orf67, mitochondrial	100.0	4.13E-17
Q6UWE0	E3 ubiquitin-protein ligase LRSAM1	100.0	4.13E-17
O94763-1	Unconventional prefoldin RPB5 interactor 1	100.0	4.13E-17
Q9HC36	rRNA methyltransferase 3, mitochondrial	100.0	4.13E-17
Q8TDW4-1	Suppressor of tumorigenicity 7 protein-like	100.0	4.13E-17
Q9H788	SH2 domain-containing protein 4A	100.0	4.13E-17
Q8NB46	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C	100.0	4.13E-17
Q96CW6	Probable RNA polymerase II nuclear localization protein SLC7A6OS	100.0	4.13E-17
Q8NEU8-1	DCC-interacting protein 13-beta	100.0	4.13E-17
Q9H2X3-1	C-type lectin domain family 4 member M	100.0	4.13E-17
Q8WTX7	Cytosolic arginine sensor for mTORC1 subunit 1	100.0	4.13E-17
O15379	Histone deacetylase 3	100.0	4.13E-17
Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	100.0	4.13E-17
Q9UKJ3-1	G patch domain-containing protein 8	100.0	4.13E-17
Q9UPN9-1	E3 ubiquitin-protein ligase TRIM33	100.0	4.13E-17
Q8TB03	Uncharacterized protein CXorf38	100.0	4.13E-17
Q9BUE0	Mediator of RNA polymerase II transcription subunit 18	100.0	4.13E-17
Q96HR8	H/ACA ribonucleoprotein complex non-core subunit NAF1	100.0	4.13E-17
O15228	Dihydroxyacetone phosphate acyltransferase	100.0	4.13E-17
P28356	Homeobox protein Hox-D9	100.0	4.13E-17
Q7Z4S6-1	Kinesin-like protein KIF21A	100.0	4.13E-17
Q8WXG1	Radical S-adenosyl methionine domain-containing protein 2	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9NZC9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1	100.0	4.13E-17
Q14703	Membrane-bound transcription factor site-1 protease	100.0	4.13E-17
O14524-1	Nuclear envelope integral membrane protein 1	100.0	4.13E-17
Q15811	Intersectin-1	100.0	4.13E-17
Q00653-1	Nuclear factor NF-kappa-B p100 subunit	100.0	4.13E-17
Q8TE76	MORC family CW-type zinc finger protein 4	100.0	4.13E-17
Q9Y6G5	COMM domain-containing protein 10	100.0	4.13E-17
Q96F24-1	Nuclear receptor-binding factor 2	100.0	4.13E-17
Q96EF0-1	myotubularin-related protein 8	100.0	4.13E-17
Q9UKX5	Integrin alpha-11	100.0	4.13E-17
O75695	Protein XRP2	100.0	4.13E-17
O00311-1	Cell division cycle 7-related protein kinase	100.0	4.13E-17
O75909-1	Isoform 3 of Cyclin-K	100.0	4.13E-17
Q9NWW7	Uncharacterized protein C2orf42	100.0	4.13E-17
Q9UHB7-1	AF4/FMR2 family member 4	100.0	4.13E-17
Q8WW38-1	Zinc finger protein ZFPM2	100.0	4.13E-17
Q2TB10	zinc finger protein 800	100.0	4.13E-17
Q6IF00	Olfactory receptor 2T2	100.0	4.13E-17
Q9H0X4	Protein FAM234A	100.0	4.13E-17
Q16790	Carbonic anhydrase 9	100.0	4.13E-17
O43665	Regulator of G-protein signaling 10	100.0	4.13E-17
Q14112-1	Nidogen-2	100.0	4.13E-17
O43918-1	autoimmune regulator	100.0	4.13E-17
Q9H553-1	Alpha-1,3/1,6-mannosyltransferase ALG2	100.0	4.13E-17
P47869	Gamma-aminobutyric acid receptor subunit alpha-2	100.0	4.13E-17
Q96M42	Putative uncharacterized protein encoded by LINC00479	100.0	4.13E-17
Q9BPU6	Dihydropyrimidinase-related protein 5	100.0	4.13E-17
O75110	Probable phospholipid-transporting ATPase IIA	100.0	4.13E-17
Q7LBC6-1	Lysine-specific demethylase 3B	100.0	4.13E-17
Q8IV38	Ankyrin repeat and MYND domain-containing protein 2	100.0	4.13E-17
Q8NFA0	Ubiquitin carboxyl-terminal hydrolase 32	100.0	4.13E-17
P17152	Transmembrane protein 11, mitochondrial	100.0	4.13E-17
Q8N138	ORM1-like protein 3	100.0	4.13E-17
P47224	Guanine nucleotide exchange factor MSS4	100.0	4.13E-17
Q5TB80	Centrosomal protein of 162 kDa	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q9BU76-1	Multiple myeloma tumor-associated protein 2	100.0	4.13E-17
Q7L3T8	probable proline–tRNA ligase, mitochondrial	100.0	4.13E-17
Q6PI26	Protein SHQ1 homolog	100.0	4.13E-17
O15533-1	Tapasin	100.0	4.13E-17
Q9Y3A2	Probable U3 small nucleolar RNA-associated protein 11	100.0	4.13E-17
Q96FS4	signal-induced proliferation-associated protein 1	100.0	4.13E-17
P63218	guanine nucleotide-binding protein g(i)/g(s)/g(o) subunit gamma-5	100.0	4.13E-17
O43299	AP-5 complex subunit zeta-1	100.0	4.13E-17
O43156	TELO2-interacting protein 1 homolog	100.0	4.13E-17
Q9HB65	RNA polymerase II elongation factor ELL3	100.0	4.13E-17
Q9ULF5	Zinc transporter ZIP10	100.0	4.13E-17
Q9Y2E6	E3 ubiquitin-protein ligase DTX4	100.0	4.13E-17
Q8TCF1-1	AN1-type zinc finger protein 1	100.0	4.13E-17
P31629	Transcription factor HIVEP2	100.0	4.13E-17
Q9HAN9	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 1	100.0	4.13E-17
Q8IWW6-1	Rho GTPase-activating protein 12	100.0	4.13E-17
Q9UBU7	Protein DBF4 homolog A	100.0	4.13E-17
Q8NBS3-1	Sodium bicarbonate transporter-like protein 11	100.0	4.13E-17
O95786	Probable ATP-dependent RNA helicase DDX58	100.0	4.13E-17
Q96Q89-1	Kinesin-like protein KIF20B	100.0	4.13E-17
Q14168-4	Isoform 4 of MAGUK p55 subfamily member 2	100.0	4.13E-17
P80217	interferon-induced 35 kDa protein	100.0	4.13E-17
Q8NI35	InaD-like protein	100.0	4.13E-17
P18075	bone morphogenetic protein 7	100.0	4.13E-17
Q9H1Z9	Tetraspanin-10	100.0	4.13E-17
Q15633	RISC-loading complex subunit TARBP2	100.0	4.13E-17
Q15363	Transmembrane emp24 domain-containing protein 2	100.0	4.13E-17
Q96Q83-1	alpha-ketoglutarate-dependent dioxygenase alkB homolog 3	100.0	4.13E-17
Q99856	AT-rich interactive domain-containing protein 3A	100.0	4.13E-17
Q9H9Z2	Protein lin-28 homolog A	100.0	4.13E-17
Q93063	exostosin-2	100.0	4.13E-17
Q9Y334	von Willebrand factor A domain-containing protein 7	100.0	4.13E-17
Q3V5L5-1	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B	100.0	4.13E-17
Q5VUR7	Ankyrin repeat domain-containing protein 20A3	100.0	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8IVF4-1	Dynein heavy chain 10, axonemal	100.0	4.13E-17
Q7Z3C6	autophagy-related protein 9A	100.0	4.13E-17
Q9NVH6-1	Trimethyllysine dioxygenase, mitochondrial	100.0	4.13E-17
Q712K3	Ubiquitin-conjugating enzyme E2 R2	100.0	4.13E-17
Q8WWH5	probable tRNA pseudouridine synthase 1	100.0	4.13E-17
P09848	Lactase-phlorizin hydrolase	100.0	4.13E-17
Q9Y4C5-1	Carbohydrate sulfotransferase 2	100.0	4.13E-17
P54792	Putative segment polarity protein dishevelled homolog DVL1P1	100.0	4.13E-17
Q5T7P6	Transmembrane protein 78	100.0	4.13E-17
Q14154	Death ligand signal enhancer	100.0	4.13E-17
Q13474	Dystrophin-related protein 2	100.0	4.13E-17
Q9NZV1	Cysteine-rich motor neuron 1 protein	64.26	2.32E-10
Q13158	FAS-associated death domain protein	58.39	5.48E-09
Q14457	Beclin-1	48.86	1.20E-05
Q8TD08-1	mitogen-activated protein kinase 15	47.14	1.99E-06
Q6NUJ5	PWWP domain-containing protein 2B	46.00	9.01E-06
P27144	Adenylate kinase 4, mitochondrial	44.30	2.66E-06
Q9UBL9-7	Isoform K of P2X purinoceptor 2	42.86	8.46E-05
Q96DE9	Protein CXorf40B	41.24	3.79E-05
L0R6Q1	SLC35A4 upstream open reading frame protein	39.73	6.95E-03
O00257-1	E3 SUMO-protein ligase CBX4	35.45	7.19E-03
Q96JD6-1	1,5-anhydro-D-fructose reductase	35.33	1.45E-03
P42126	Enoyl-CoA delta isomerase 1, mitochondrial	32.70	3.41E-02
P10301	Ras-related protein R-Ras	31.63	3.76E-03
Q6UXX5	Inter-alpha-trypsin inhibitor heavy chain H6	30.56	3.63E-04
P68032	Actin, alpha cardiac muscle 1	30.44	6.88E-07
Q8N0U8	Vitamin K epoxide reductase complex subunit 1-like protein 1	30.12	1.18E-02
O43772	mitochondrial carnitine/acylcarnitine carrier protein	29.91	4.21E-02
P00749	Urokinase-type plasminogen activator	29.85	1.07E-05
Q9Y394	Dehydrogenase/reductase SDR family member 7	29.48	8.51E-03
Q16831	uridine phosphorylase 1	29.44	2.32E-02
Q8WV24	Pleckstrin homology-like domain family A member 1	29.31	1.25E-02
Q8IWA0	WD repeat-containing protein 75	28.85	1.25E-02
Q13217	DnaJ homolog subfamily C member 3	28.14	1.30E-02
P32321	deoxycytidylate deaminase	28.03	8.24E-03
Q96F86	Enhancer of mRNA-decapping protein 3	27.38	4.86E-02

Continued on next page

accession	description	fold p change	adjusted p-value
Q92643	GPI-anchor transamidase	27.17	4.94E-02
P57105	Synaptojanin-2-binding protein	26.74	3.29E-02
Q9Y2I6-1	Ninein-like protein	26.19	5.36E-03
Q9H8Y5	Ankyrin repeat and zinc finger domain-containing protein 1	26.11	1.08E-03
Q96C01	Protein FAM136A	25.39	2.53E-02
Q9Y3D3	28S ribosomal protein S16, mitochondrial	24.54	2.20E-02
O43488	aflatoxin B1 aldehyde reductase member 2	23.96	6.96E-03
P55039	Developmentally-regulated GTP-binding protein 2	23.73	1.85E-02
P20339	Ras-related protein Rab-5A	23.68	2.82E-04
Q9UHY7	Enolase-phosphatase E1	23.23	1.41E-02
Q9UI12-1	V-type proton ATPase subunit H	22.92	3.63E-02
Q9Y5V0	Zinc finger protein 706	22.64	3.78E-04
P53602	Diphosphomevalonate decarboxylase	22.50	2.24E-03
P51159-1	Ras-related protein Rab-27A	21.78	3.05E-05
O43823	A-kinase anchor protein 8	21.64	3.97E-02
O95197-3	Isoform 3 of Reticulon-3	21.39	2.59E-03
P46977	Dolichyl-diphosphooligosaccharide–protein glycosyltransferase subunit STT3A	21.33	3.60E-04
O95486-1	Protein transport protein Sec24A	21.12	2.01E-03
Q01860-2	Isoform B of POU domain, class 5, transcription factor 1	21.10	7.87E-04
Q9Y6M7-1	Sodium bicarbonate cotransporter 3	21.09	4.44E-02
Q5T9L3	Protein wntless homolog	21.04	1.34E-03
Q5T653	39S ribosomal protein L2, mitochondrial	21.02	1.01E-03
O14880	Microsomal glutathione S-transferase 3	20.99	4.46E-02
Q9Y5Y2	Cytosolic Fe-S cluster assembly factor NUBP2	20.83	2.82E-02
O43617-1	Trafficking protein particle complex subunit 3	20.55	9.28E-03
Q8NDX2-1	Vesicular glutamate transporter 3	20.14	2.50E-03
Q8WX92	Negative elongation factor B	19.42	4.72E-02
Q9UL46	proteasome activator complex subunit 2	19.37	2.01E-03
Q99797	Mitochondrial intermediate peptidase	19.33	4.35E-02
Q15386-1	Ubiquitin-protein ligase E3C	19.31	3.87E-02
P61599	N-alpha-acetyltransferase 20	19.13	3.60E-02
Q13885	Tubulin beta-2A chain	19.13	4.19E-05
P62308	Small nuclear ribonucleoprotein G	19.10	6.25E-03
Q13459-1	Unconventional myosin-IXb	19.05	4.12E-02
Q5GLZ8-1	Probable E3 ubiquitin-protein ligase HERC4	18.90	3.42E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	18.82	1.58E-02
P35237	serpin B6	18.70	7.50E-04
O60216	Double-strand-break repair protein rad21 homolog	18.68	2.98E-02
Q5T8P6	RNA-binding protein 26	18.61	3.60E-04
O43169	Cytochrome b5 type B	16.74	1.38E-03
Q15738	sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	16.59	1.50E-03
Q9NTX5	Ethylmalonyl-CoA decarboxylase	16.56	1.94E-02
P09132-1	Signal recognition particle 19 kDa protein	16.32	2.82E-02
Q9NVH1-1	DnaJ homolog subfamily C member 11	16.09	8.03E-03
O43676	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	15.99	2.33E-02
Q8IUE6	Histone H2A type 2-B	15.91	2.69E-03
Q96HS1-1	Serine/threonine-protein phosphatase Pgam5, mitochondrial	15.49	1.68E-03
Q9BXB4	Oxysterol-binding protein-related protein 11	15.45	1.48E-02
Q6P1J9	Parafibromin	15.22	2.93E-03
Q9UJY1	Heat shock protein beta-8	15.01	2.97E-02
Q8NF91	Nesprin-1	14.79	2.57E-03
Q9UBN7-1	histone deacetylase 6	14.60	1.59E-04
Q96TC7	Regulator of microtubule dynamics protein 3	14.60	2.97E-03
Q15758-1	Neutral amino acid transporter B(0)	14.56	2.93E-03
P61026	ras-related protein rab-10	13.99	1.68E-03
Q12768	WASH complex subunit 5	13.83	4.28E-02
Q8WVM7	Cohesin subunit SA-1	13.46	1.35E-02
P35251-1	Replication factor C subunit 1	13.35	1.72E-02
P11166	Solute carrier family 2, facilitated glucose transporter member 1	12.94	1.59E-02
Q05193-1	Dynamin-1	12.86	2.65E-02
O14967	calmegin	12.80	6.50E-03
Q9Y4C2-1	TRPM8 channel-associated factor 1	12.77	4.88E-02
P61769	Beta-2-microglobulin	12.48	3.92E-03
Q9NPF0	CD320 antigen	12.28	4.39E-03
Q96N66-1	Lysophospholipid acyltransferase 7	12.20	8.46E-03
Q8NFV4	Protein Abhd11	12.01	1.84E-02
Q9UPT9-1	ubiquitin carboxyl-terminal hydrolase 22	11.96	1.87E-02
Q4U2R6	39S ribosomal protein L51, mitochondrial	11.86	8.36E-03
P56134	ATP synthase subunit f, mitochondrial	11.45	9.54E-03
P29966	Myristoylated alanine-rich C-kinase substrate	10.61	1.48E-02
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	10.40	1.42E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P62841	40S ribosomal protein S15	10.29	3.59E-03
P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	10.13	1.89E-02
O75844	caax prenyl protease 1 homolog	9.960	2.15E-02
Q6ZS17	RHO family-interacting cell polarization regulator 1	9.863	4.61E-03
Q9UBM7	7-dehydrocholesterol reductase	9.521	1.99E-02
O94915-1	protein furry homolog-like	9.456	3.12E-02
O14618	copper chaperone for superoxide dismutase	9.395	2.17E-02
P62318	small nuclear ribonucleoprotein sm d3	9.150	2.05E-02
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	9.044	7.70E-03
Q9P289	serine/threonine-protein kinase 26	8.882	2.32E-02
Q96FW1	Ubiquitin thioesterase otub1	8.443	1.99E-02
P16930	Fumarylacetoacetase	8.415	1.99E-02
P62314	Small nuclear ribonucleoprotein Sm D1	7.533	2.66E-02
P27816-1	Microtubule-associated protein 4	0.401	4.80E-02
O43852	Calumenin	0.397	4.57E-02
O75347	Tubulin-specific chaperone A	0.395	4.47E-02
P06753-2	Isoform 2 of Tropomyosin alpha-3 chain	0.391	4.28E-02
P17096-1	High mobility group protein HMG-I/HMG-Y	0.389	3.76E-02
P35637-1	RNA-binding protein FUS	0.385	3.97E-02
Q9Y266	nuclear migration protein nudC	0.380	2.90E-02
Q14247-1	Src substrate cortactin	0.379	3.69E-02
Q14847	LIM and SH3 domain protein 1	0.374	4.41E-02
P47914	60S ribosomal protein L29	0.359	2.83E-02
Q02539	Histone H1.1	0.349	2.85E-02
P23588	eukaryotic translation initiation factor 4B	0.335	1.99E-02
Q9UMX0-1	Ubiquilin-1	0.333	2.40E-02
Q13501-1	sequestosome-1	0.332	1.64E-02
P13987	CD59 glycoprotein	0.330	4.26E-02
P62633-2	Isoform 2 of Cellular nucleic acid-binding protein	0.324	2.23E-02
Q9Y2W1	Thyroid hormone receptor-associated protein 3	0.321	3.77E-02
Q13409-1	cytoplasmic dynein 1 intermediate chain 2	0.317	2.60E-02
P07919	Cytochrome b-c1 complex subunit 6, mitochondrial	0.311	4.16E-02
O43399	Tumor protein D54	0.303	1.18E-02
P49321	Nuclear autoantigenic sperm protein	0.284	8.19E-03
P16949-1	Stathmin	0.282	7.96E-03
Q86V81	THO complex subunit 4	0.279	7.35E-03

Continued on next page

accession	description	fold p change	adjusted p-value
Q96C90	Protein phosphatase 1 regulatory subunit 14B	0.276	4.88E-02
P33240	cleavage stimulation factor subunit 2	0.264	4.23E-02
Q13162	Peroxiredoxin-4	0.258	4.70E-03
Q13442	28 kDa heat- and acid-stable phosphoprotein	0.257	6.32E-03
P67809	Nuclease-sensitive element-binding protein 1	0.254	4.30E-03
P26583	High mobility group protein B2	0.253	8.27E-03
P62158	Calmodulin	0.252	6.03E-03
P12955	xaa-Pro dipeptidase	0.252	1.43E-02
Q562R1	Beta-actin-like protein 2	0.249	3.83E-03
P11279	Lysosome-associated membrane glycoprotein 1	0.247	4.05E-02
O75822	Eukaryotic translation initiation factor 3 subunit J	0.238	7.83E-03
P13645	Keratin, type I cytoskeletal 10	0.238	2.32E-02
O75348	V-type proton ATPase subunit G 1	0.238	3.60E-02
Q92922	SWI/SNF complex subunit SMARCC1	0.225	3.47E-02
Q02952-1	A-kinase anchor protein 12	0.216	1.53E-03
Q15042-1	Rab3 GTPase-activating protein catalytic subunit	0.216	7.28E-03
Q13636	ras-related protein rab-31	0.211	2.58E-02
Q9P270	SLAIN motif-containing protein 2	0.209	1.73E-03
P98179	RNA-binding protein 3	0.204	9.34E-04
Q04941-1	proteolipid protein 2	0.199	3.31E-02
Q05682-3	Isoform 3 of Caldesmon	0.192	3.95E-04
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	0.191	3.26E-03
P09486	Sparc	0.186	1.41E-02
P02545-2	Isoform C of Prelamin-A/C	0.183	1.91E-02
P05386	60S acidic ribosomal protein P1	0.176	3.72E-04
Q9NYK5-1	39S ribosomal protein L39, mitochondrial	0.151	3.06E-02
Q9UM22	Mammalian ependymin-related protein 1	0.148	4.57E-03
Q9HC07	Transmembrane protein 165	0.142	1.04E-02
P02768-1	Serum albumin	0.138	7.05E-04
Q7Z417	Nuclear fragile X mental retardation-interacting protein 2	0.136	2.17E-02
Q14011	Cold-inducible RNA-binding protein	0.135	2.15E-02
P04049	RAF proto-oncogene serine/threonine-protein kinase	0.131	5.65E-03
P04264	Keratin, type II cytoskeletal 1	0.120	2.32E-05
P20645	Cation-dependent mannose-6-phosphate receptor	0.108	2.29E-03
O60232	Sjoegren syndrome/scleroderma autoantigen 1	0.103	8.82E-03
Q14978-3	Isoform 3 of Nucleolar and coiled-body phosphoprotein 1	0.101	3.02E-02

Continued on next page

accession	description	fold p change	adjusted p-value
O14593	DNA-binding protein RFXANK	0.097	1.14E-02
Q9NWB6	Arginine and glutamate-rich protein 1	0.094	1.69E-03
Q9GZP4	PITH domain-containing protein 1	0.092	4.46E-02
P46937-1	Transcriptional coactivator YAP1	0.086	2.35E-02
P35241-1	radixin	0.085	2.64E-02
Q9HD15	Steroid receptor RNA activator 1	0.083	1.56E-02
Q8N9N8	probable RNA-binding protein EIF1AD	0.083	4.58E-02
P35908	Keratin, type II cytoskeletal 2 epidermal	0.081	6.74E-04
P49674	Casein kinase I isoform epsilon	0.081	2.68E-02
Q9Y5K8	V-type proton ATPase subunit D	0.080	2.26E-02
Q9UMX5	Neudesin	0.077	1.74E-02
Q2M2I8-1	AP2-associated protein kinase 1	0.071	1.68E-02
Q13427	peptidyl-prolyl cis-trans isomerase g	0.071	1.73E-02
P54727	UV excision repair protein RAD23 homolog B	0.071	3.63E-02
P12074	Cytochrome c oxidase subunit 6A1, mitochondrial	0.068	3.90E-03
Q9NSI2-1	protein FAM207A	0.068	3.77E-02
P53814-1	Smoothelin	0.066	1.97E-02
P53801	pituitary tumor-transforming gene 1 protein-interacting protein	0.063	3.98E-03
Q96MW1	Coiled-coil domain-containing protein 43	0.062	1.32E-02
O14732-1	inositol monophosphatase 2	0.062	1.56E-02
Q15118	[Pyruvate dehydrogenase (Acetyl-transferring)] kinase isozyme 1, mitochondrial	0.061	1.21E-02
Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	0.061	2.76E-02
P62837	ubiquitin-conjugating enzyme E2 D2	0.058	4.91E-02
Q92734-1	Protein TFG	0.055	1.56E-05
P05204	Non-histone chromosomal protein HMG-17	0.052	5.14E-06
O94885	SAM and SH3 domain-containing protein 1	0.050	6.34E-03
O94992	Protein HEXIM1	0.049	1.08E-02
Q8NEM2	SHC SH2 domain-binding protein 1	0.049	3.16E-02
P30042-1	ES1 protein homolog, mitochondrial	0.047	2.68E-02
Q9Y4B5	Microtubule cross-linking factor 1	0.047	3.11E-02
P10109	Adrenodoxin, mitochondrial	0.046	3.57E-03
P80723	Brain acid soluble protein 1	0.042	4.45E-07
Q9NQX3	Gephyrin	0.042	1.16E-02
P08779	Keratin, type I cytoskeletal 16	0.041	2.42E-03
Q8IXU6-1	Solute carrier family 35 member f2	0.039	2.90E-02

Continued on next page

accession	description	fold p change	adjusted p-value
P48509	CD151 antigen	0.038	3.91E-03
Q8N1B4	Vacuolar protein sorting-associated protein 52 homolog	0.038	9.82E-03
Q6ZMZ3	Nesprin-3	0.037	4.20E-02
P08174-1	Complement decay-accelerating factor	0.036	2.82E-04
Q8N139	ATP-binding cassette sub-family A member 6	0.036	1.73E-03
Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinase	0.034	4.19E-02
Q9GZV5	WW domain-containing transcription regulator protein 1	0.033	6.97E-03
Q32P41	tRNA (guanine(37)-N1)-methyltransferase	0.032	3.90E-02
P69905	Hemoglobin subunit alpha	0.029	3.53E-05
Q4LDG9-1	Dynein light chain 1, axonemal	0.022	1.16E-13
Q96DB5	regulator of microtubule dynamics protein 1	0.018	2.33E-02
P16403	Histone H1.2	0.010	4.13E-17
P62987	Ubiquitin-60S ribosomal protein L40	0.010	4.13E-17
Q8NC51-3	Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein	0.010	4.13E-17
P07910-1	Heterogeneous nuclear ribonucleoproteins C1/C2	0.010	4.13E-17
P29692-3	Isoform 3 of Elongation factor 1-delta	0.010	4.13E-17
P62633-8	Isoform 8 of Cellular nucleic acid-binding protein	0.010	4.13E-17
Q15366-3	Isoform 3 of Poly(rC)-binding protein 2	0.010	4.13E-17
Q05682-1	Caldesmon	0.010	4.13E-17
P15531	Nucleoside diphosphate kinase A	0.010	4.13E-17
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	0.010	4.13E-17
P29692-4	Isoform 4 of Elongation factor 1-delta	0.010	4.13E-17
P07951-1	Tropomyosin beta chain	0.010	4.13E-17
P62834	ras-related protein Rap-1A	0.010	4.13E-17
P02533	Keratin, type I cytoskeletal 14	0.010	4.13E-17
O94804	Serine/threonine-protein kinase 10	0.010	4.13E-17
Q6EEV4-2	Isoform 5 of DNA-directed RNA polymerase II subunit GRINL1A, isoforms 4/5	0.010	4.13E-17
O00193	Small acidic protein	0.010	4.13E-17
P62328	Thymosin beta-4	0.010	4.13E-17
P05114	Non-histone chromosomal protein HMG-14	0.010	4.13E-17
Q14651	Plastin-1	0.010	4.13E-17
P04259	keratin, type II cytoskeletal 6B	0.010	4.13E-17
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1	0.010	4.13E-17
P84157-2	Isoform 2 of Matrix-remodeling-associated protein 7	0.010	4.13E-17
Q9GZL7	ribosome biogenesis protein WDR12	0.010	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8WXA9-2	Isoform 2 of Splicing regulatory glutamine/lysine-rich protein 1	0.010	4.13E-17
P19387	DNA-directed RNA polymerase II subunit RPB3	0.010	4.13E-17
Q9H977	WD repeat-containing protein 54	0.010	4.13E-17
P42566-1	epidermal growth factor receptor substrate 15	0.010	4.13E-17
Q8N0X7	Spartin	0.010	4.13E-17
O00592	Podocalyxin	0.010	4.13E-17
Q13084	39S ribosomal protein L28, mitochondrial	0.010	4.13E-17
Q96K76	ubiquitin carboxyl-terminal hydrolase 47	0.010	4.13E-17
Q92665	28S ribosomal protein S31, mitochondrial	0.010	4.13E-17
O95232-1	Luc7-like protein 3	0.010	4.13E-17
Q9UBP6	tRNA (guanine-N(7)-)-methyltransferase	0.010	4.13E-17
O75683	Surfeit locus protein 6	0.010	4.13E-17
Q8NC56-1	LEM domain-containing protein 2	0.010	4.13E-17
Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	0.010	4.13E-17
P13647	keratin, type II cytoskeletal 5	0.010	4.13E-17
P28799	Granulins	0.010	4.13E-17
Q8WVJ2	NudC domain-containing protein 2	0.010	4.13E-17
Q96GA7	serine dehydratase-like	0.010	4.13E-17
Q9BQE9-1	B-cell CLL/lymphoma 7 protein family member B	0.010	4.13E-17
Q13206	probable ATP-dependent RNA helicase DDX10	0.010	4.13E-17
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	0.010	4.13E-17
Q9NX55-2	Huntingtin-interacting protein K	0.010	4.13E-17
Q7Z5L9-1	Interferon regulatory factor 2-binding protein 2	0.010	4.13E-17
Q9P1U0	DNA-directed RNA polymerase I subunit RPA12	0.010	4.13E-17
Q9BYV8	centrosomal protein of 41 kDa	0.010	4.13E-17
Q8IWZ8-1	SURP and G-patch domain-containing protein 1	0.010	4.13E-17
Q9UPT8	Zinc finger CCCH domain-containing protein 4	0.010	4.13E-17
Q8TDQ7	Glucosamine-6-phosphate isomerase 2	0.010	4.13E-17
Q96EI5	Transcription elongation factor A protein-like 4	0.010	4.13E-17
Q6PD62	RNA polymerase-associated protein CTR9 homolog	0.010	4.13E-17
Q9NWV8	BRISC and BRCA1-A complex member 1	0.010	4.13E-17
P54725-1	UV excision repair protein RAD23 homolog A	0.010	4.13E-17
Q9NNW5	WD repeat-containing protein 6	0.010	4.13E-17
Q5T3I0	G patch domain-containing protein 4	0.010	4.13E-17
Q14126	Desmoglein-2	0.010	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8NI22	Multiple coagulation factor deficiency protein 2	0.010	4.13E-17
Q9BSV6	tRNA-splicing endonuclease subunit sen34	0.010	4.13E-17
P98155-1	very low-density lipoprotein receptor	0.010	4.13E-17
O60333	Kinesin-like protein KIF1B	0.010	4.13E-17
Q86VI3	Ras GTPase-activating-like protein IQGAP3	0.010	4.13E-17
Q8IY95	transmembrane protein 192	0.010	4.13E-17
Q86WB0	Nuclear-interacting partner of ALK	0.010	4.13E-17
Q9NP77	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	0.010	4.13E-17
O00461	Golgi integral membrane protein 4	0.010	4.13E-17
O75438	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	0.010	4.13E-17
Q86TG7-1	Retrotransposon-derived protein PEG10	0.010	4.13E-17
Q96G46	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	0.010	4.13E-17
Q9UQN3-1	Charged multivesicular body protein 2b	0.010	4.13E-17
O95295	SNARE-associated protein Snapin	0.010	4.13E-17
Q9NRL3	Striatin-4	0.010	4.13E-17
Q8N4Q1	Mitochondrial intermembrane space import and assembly protein 40	0.010	4.13E-17
Q8WYP5	protein elys	0.010	4.13E-17
Q9H0H5	Rac GTPase-activating protein 1	0.010	4.13E-17
Q92536	Y+L amino acid transporter 2	0.010	4.13E-17
O15514	DNA-directed RNA polymerase II subunit RPB4	0.010	4.13E-17
Q96GM8	Target of EGR1 protein 1	0.010	4.13E-17
Q99622	Protein C10	0.010	4.13E-17
Q1ED39	Lysine-rich nucleolar protein 1	0.010	4.13E-17
Q9H9H4	Vacuolar protein sorting-associated protein 37B	0.010	4.13E-17
Q14653	interferon regulatory factor 3	0.010	4.13E-17
Q6ZSR9	Uncharacterized protein FLJ45252	0.010	4.13E-17
P49418	amphiphysin	0.010	4.13E-17
P20337	Ras-related protein Rab-3B	0.010	4.13E-17
Q86YZ3	Hornerin	0.010	4.13E-17
Q13616	Cullin-1	0.010	4.13E-17
Q96SK2	Transmembrane protein 209	0.010	4.13E-17
Q9Y605	MORF4 family-associated protein 1	0.010	4.13E-17
Q969E8	pre-rRNA-processing protein TSR2 homolog	0.010	4.13E-17
Q9C0F1-1	centrosomal protein of 44 kDa	0.010	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q16637	Survival motor neuron protein	0.010	4.13E-17
Q96ME7	Zinc finger protein 512	0.010	4.13E-17
Q99747	Gamma-soluble NSF attachment protein	0.010	4.13E-17
O43768	alpha-endosulfine	0.010	4.13E-17
Q8WW01	tRNA-splicing endonuclease subunit Sen15	0.010	4.13E-17
Q8IXQ3	Uncharacterized protein C9orf40	0.010	4.13E-17
O43164	E3 ubiquitin-protein ligase Praja-2	0.010	4.13E-17
Q8WXC6-2	COP9 signalosome complex subunit 9	0.010	4.13E-17
Q6NZY4	Zinc finger CCHC domain-containing protein 8	0.010	4.13E-17
P04920-1	Anion exchange protein 2	0.010	4.13E-17
Q96B54	Zinc finger protein 428	0.010	4.13E-17
P61457	Pterin-4-alpha-carbinolamine dehydratase	0.010	4.13E-17
Q6QNY0	biogenesis of lysosome-related organelles complex 1 subunit 3	0.010	4.13E-17
Q9BYN0	sulfiredoxin-1	0.010	4.13E-17
P42695	condensin-2 complex subunit D3	0.010	4.13E-17
Q9NXN4-1	Ganglioside-induced differentiation-associated protein 2	0.010	4.13E-17
Q9NYI0-1	PH and SEC7 domain-containing protein 3	0.010	4.13E-17
P16220-1	Cyclic AMP-responsive element-binding protein 1	0.010	4.13E-17
O60508	pre-mRNA-processing factor 17	0.010	4.13E-17
P17900	Ganglioside GM2 activator	0.010	4.13E-17
Q00613	heat shock factor protein 1	0.010	4.13E-17
Q12824-1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	0.010	4.13E-17
Q8IV08	Phospholipase D3	0.010	4.13E-17
Q8NBZ7-1	UDP-glucuronic acid decarboxylase 1	0.010	4.13E-17
Q9UBD5-1	Origin recognition complex subunit 3	0.010	4.13E-17
Q7Z2T5-1	TRMT1-like protein	0.010	4.13E-17
Q9NZ63	Telomere length and silencing protein 1 homolog	0.010	4.13E-17
Q99547	M-phase phosphoprotein 6	0.010	4.13E-17
Q9C0B5	Palmitoyltransferase ZDHHC5	0.010	4.13E-17
P21802-1	Fibroblast growth factor receptor 2	0.010	4.13E-17
Q6ZSZ5	Rho guanine nucleotide exchange factor 18	0.010	4.13E-17
Q9Y3I1	F-box only protein 7	0.010	4.13E-17
P78362-1	SRSF protein kinase 2	0.010	4.13E-17
Q96DZ1	Endoplasmic reticulum lectin 1	0.010	4.13E-17
Q13405	39S ribosomal protein L49, mitochondrial	0.010	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
Q8WUD4	Coiled-coil domain-containing protein 12	0.010	4.13E-17
Q9Y6I3	epsin-1	0.010	4.13E-17
Q7Z6M1-1	Rab9 effector protein with Kelch motifs	0.010	4.13E-17
P40189-1	Interleukin-6 receptor subunit beta	0.010	4.13E-17
Q6P4F2	Ferredoxin-2, mitochondrial	0.010	4.13E-17
Q96IZ0	PRKC apoptosis WT1 regulator protein	0.010	4.13E-17
Q9UBG0	C-type mannose receptor 2	0.010	4.13E-17
Q5VTL8	Pre-mRNA-splicing factor 38B	0.010	4.13E-17
Q7Z6J0-1	E3 ubiquitin-protein ligase SH3RF1	0.010	4.13E-17
P61244	Protein max	0.010	4.13E-17
P49643-1	DNA primase large subunit	0.010	4.13E-17
Q6UXH1	Cysteine-rich with EGF-like domain protein 2	0.010	4.13E-17
Q8NHV4	Protein NEDD1	0.010	4.13E-17
Q6QNY1	biogenesis of lysosome-related organelles complex 1 subunit 2	0.010	4.13E-17
Q8IZ21-1	Phosphatase and actin regulator 4	0.010	4.13E-17
O14562	Ubiquitin domain-containing protein UBFD1	0.010	4.13E-17
Q9P013	spliceosome-associated protein CWC15 homolog	0.010	4.13E-17
Q8TCZ2	CD99 antigen-like protein 2	0.010	4.13E-17
O43924	Retinal rod rhodopsin-sensitive cGMP 3′,5′-cyclic phosphodiesterase subunit delta	0.010	4.13E-17
Q92667	A-kinase anchor protein 1, mitochondrial	0.010	4.13E-17
Q6NXT1-1	Ankyrin repeat domain-containing protein 54	0.010	4.13E-17
Q75N03	E3 ubiquitin-protein ligase Hakai	0.010	4.13E-17
O95470	sphingosine-1-phosphate lyase 1	0.010	4.13E-17
P02100	Hemoglobin subunit epsilon	0.010	4.13E-17
Q9BRP1	Programmed cell death protein 2-like	0.010	4.13E-17
P53350	Serine/threonine-protein kinase PLK1	0.010	4.13E-17
Q96E11	Ribosome-recycling factor, mitochondrial	0.010	4.13E-17
P50579	methionine aminopeptidase 2	0.010	4.13E-17
P48723	Heat shock 70 kDa protein 13	0.010	4.13E-17
O43663-1	Protein regulator of cytokinesis 1	0.010	4.13E-17
Q96SZ5	2-aminoethanethiol dioxygenase	0.010	4.13E-17
Q9H1Z4	WD repeat-containing protein 13	0.010	4.13E-17
Q8N3X1	Formin-binding protein 4	0.010	4.13E-17
P20248	Cyclin-A2	0.010	4.13E-17
A8CG34-1	Nuclear envelope pore membrane protein POM 121C	0.010	4.13E-17

Continued on next page

accession	description	fold p change	adjusted p-value
O43504	Ragulator complex protein LAMTOR5	0.010	4.13E-17
Q9NVC6	mediator of RNA polymerase II transcription subunit 17	0.010	4.13E-17
Q8TCC3	39S ribosomal protein L30, mitochondrial	0.010	4.13E-17
Q9HC52	chromobox protein homolog 8	0.010	4.13E-17
Q96G25	mediator of RNA polymerase II transcription subunit 8	0.010	4.13E-17
P05423	DNA-directed RNA polymerase III subunit RPC4	0.010	4.13E-17
P56945	Breast cancer anti-estrogen resistance protein 1	0.010	4.13E-17
O75152	Zinc finger CCCH domain-containing protein 11A	0.010	4.13E-17
Q9BYD2	39S ribosomal protein L9, mitochondrial	0.010	4.13E-17
Q9NWT6	Hypoxia-inducible factor 1-alpha inhibitor	0.010	4.13E-17
Q9NZ45	CDGSH iron-sulfur domain-containing protein 1	0.010	4.13E-17
Q9UIS9-1	Methyl-CpG-binding domain protein 1	0.010	4.13E-17
Q4VX76-1	Synaptotagmin-like protein 3	0.010	4.13E-17
Q12802-1	A-kinase anchor protein 13	0.010	4.13E-17
Q96SY0	Integrator complex subunit 14	0.010	4.13E-17
P41236	Protein phosphatase inhibitor 2	0.010	4.13E-17
Q9BXK5-1	Bcl-2-like protein 13	0.010	4.13E-17
Q6ZUT9-1	DENN domain-containing protein 5B	0.010	4.13E-17
Q99683	Mitogen-activated protein kinase kinase kinase 5	0.010	4.13E-17
Q8N5G2-1	macoilin	0.010	4.13E-17
Q96L96	Alpha-protein kinase 3	0.010	4.13E-17
Q6MZT1	Regulator of G-protein signaling 7-binding protein	0.010	4.13E-17
Q96GD4	Aurora kinase B	0.010	4.13E-17
Q9BQC3	2-(3-amino-3-carboxypropyl)histidine synthase subunit 2	0.010	4.13E-17
Q96BZ8	leukocyte receptor cluster member 1	0.010	4.13E-17
Q9H0W8	protein SMG9	0.010	4.13E-17
P01011-1	Alpha-1-antichymotrypsin	0.010	4.13E-17
O75586	Mediator of RNA polymerase II transcription subunit 6	0.010	4.13E-17
Q86YF9	Zinc finger protein DZIP1	0.010	4.13E-17
Q96L93-1	Kinesin-like protein KIF16B	0.010	4.13E-17
Q9UL68	Myelin transcription factor 1-like protein	0.010	4.13E-17
Q14916	Sodium-dependent phosphate transport protein 1	0.010	4.13E-17
Q6PIJ6-1	F-box only protein 38	0.010	4.13E-17
Q6ZU64-1	Cilia- and flagella-associated protein 65	0.010	4.13E-17
End of Table			

Y Accession Intersection Lists by Drug Treatment

This appendix contains the lists of up- and downregulated genes across all cell lines (HL60, LN18, and U87), and lists of up- and down-regulated genes in only both glioblastoma cell lines (LN18 and U87), in both drug treatments.

Cycloheximide				Pateamine A			
Upregulated		Downregulated		Upregulated		Downregulated	
All	GBM	All	GBM	All	GBM	All	GBM
P19474	A6NDU8	O43164	A6ND36-1	O14657	A2RRP1-1	P15531	O43164
P31749	A6ZKI3	P02100	O14593	O15116	A3KMH1	P42695	O43504
P42356	A8MXV4	P05114	O14618	O15379	A6ZKI3	P69905	O43768
P42785-1	O14933	P05204	O43768	O75027-1	O00311-1	P98179	O75152
Q03426	O14981	P16220-1	O75410-1	O75352	O00418	Q00613	O75348
Q06265-1	O15382	P41236	P02545-2	O95260	O00762	Q13405	O95295
Q68CQ7-1	O15533-1	Q6FIF0	P02788	P00846	O14561	Q14978-3	P02100
Q86VR2	O43148-1	Q8NC51-3	P02795	P04424	O14981	Q15366-3	P02545-2
Q8TED0	O43598-1	Q8NI22	P09455-1	P14406	O43169	Q7Z2T5-1	P02768-1
Q93034	O43837-1	Q9P1U0	P09493-5	P17152	O43299	Q8NC51-3	P05114
Q96KA5-1	O60934	Q9UK76	P16989-1	P17568	O43674-1	Q96B54	P06753-2
Q9BZD4	O60942-1		P17676	P35914	O75446	Q9C0B5	P41236
Q9BZF1-1	O94919		P18827	P50613	O75530	Q9NWV8	P49643-1
Q9P260-1	O95487-1		P20248	P51151	O94901-1		P53350
Q9UHD2	O96019-1		P20929	P57678	O94915-1		P53801
Q9Y3D6	P11441		P49773	P61026	O94929-1		P54725-1
Q9Y6B6	P17900		P50579	Q03519-1	O95363		P61244
	P20337		P52926-1	Q12768	O95777		P62328
	P22413		P53350	Q14154	P09884		P62633-8
	P23434		P53803	Q53H82	P15927-1		P80723
	P23458		P53985	Q8N4H5	P18075		Q02539
	P28370-1		P55199	Q8N4J0	P18084		Q05682-3
	P28676		P69905	Q8TBQ9	P20339		Q13442
	P35573-1		P80723	Q8WTX7	P22304		Q13636
	P48735		P82909	Q8WVM8	P23434		Q14011
	P49356		Q12802-1	Q8WVV9	P32322		Q14126
	P49959		Q14011	Q92643	P34931		Q32MZ4

Continued on next page

Cycloheximide				Pateamine A			
Upregulated		Downregulated		Upregulated		Downregulated	
All	GBM	All	GBM	All	GBM	All	GBM
	P51648		Q32MZ4	Q96EL2	P38432		Q5T3I0
	P61020		Q6P4E1	Q96M27-1	P40855-1		Q6PIJ6-1
	P61421		Q8IXQ3	Q96N46	P42226		Q7Z6J0-1
	P83111-1		Q8N4Q1	Q9BPU6	P47869		Q8IWZ8-1
	P98194-1		Q8N8S7	Q9BRG1	P49354		Q8IZ21-1
	Q00653-1		Q8NBJ4	Q9BYB4-1	P51948-1		Q8N3X1
	Q03154-1		Q8TCZ2	Q9BYC9	P55268		Q8NI22
	Q08209-1		Q8WUD4	Q9H061-1	P56134		Q92667
	Q0VDF9		Q8WVJ2	Q9HB65	P56182		Q92734-1
	Q12800-1		Q92734-1	Q9NUM4	P61218		Q96DB5
	Q13098		Q93045	Q9NVH1-1	P61225		Q96GD4
	Q13217		Q969E4	Q9NVH6-1	P62070		Q96SZ5
	Q13325		Q96AT1	Q9NWS8	P62841		Q9BQC3
	Q13438-1		Q96EI5	Q9NYP7-1	P63218		Q9BQE9-1
	Q13625-1		Q96EP5	Q9NZ32	P78330		Q9BYD2
	Q13888-1		Q96IZ0	Q9NZQ3-1	P82650		Q9BYN0
	Q14254		Q96JY6-1	Q9UBS0	Q01860-2		Q9GZV5
	Q14562		Q96ME7	Q9UGN5-1	Q12882-1		Q9H0W8
	Q14653		Q96S44		Q13112		Q9HD15
	Q15286		Q9BQ61		Q13257-1		Q9NSI2-1
	Q15628		Q9BRP8		Q13416		Q9NWT6
	Q15833-1		Q9H0W8		Q13769		Q9NZ63
	Q16222-1		Q9H4A3		Q13885		
	Q16774-1		Q9NSI2-1		Q14746		
	Q4G0F5		Q9NUP9		Q14919-1		
	Q5JVF3		Q9P0P0		Q15007		
	Q5VW32		Q9P1Y6-1		Q15043		
	Q5VZ46-1		Q9Y520		Q15262		
	Q68E01				Q15554-3		
	Q6ZSB9				Q15649		
	Q7L592				Q15738		
	Q7LGA3-1				Q16706		
	Q7Z2W9				Q2TB10		
	Q7Z7H8				Q5EBL4-1		
	Q86U86-1				Q5JVF3		

Continued on next page

Cycloheximide				Pateamine A			
Upregulated		Downregulated		Upregulated		Downregulated	
All	GBM	All	GBM	All	GBM	All	GBM
	Q86YV9				Q5K651		
	Q8IVL6-1				Q5T8D3-3		
	Q8IY37				Q5T9L3		
	Q8N392-1				Q5TB80		
	Q8N543				Q5VZE5		
	Q8NCN5				Q68E01		
	Q8NCW5				Q6GMV3		
	Q8NDI1				Q6IA69		
	Q8NEW0				Q6IQ22		
	Q8NFH4				Q6NUM9-1		
	Q8TBC4-1				Q6P9B9		
	Q8TDQ7				Q6U841		
	Q8WTW3				Q712K3		
	Q8WWQ0				Q7L592		
	Q8WX92				Q7Z2E3-1		
	Q8WXA9-2				Q7Z7B0		
	Q92805				Q8IUE6		
	Q92947-1				Q8IV38		
	Q92979				Q8IWB7		
	Q92995				Q8IXI2-1		
	Q93100-1				Q8IYS2-1		
	Q969Z0-1				Q8N0U8		
	Q96A26				Q8N543		
	Q96A35				Q8NE86		
	Q96AB3				Q8NEW0		
	Q96AC1				Q8NFA0		
	Q96BN8				Q8NHP6-1		
	Q96BW9-1				Q8TB03		
	Q96CS3				Q8TB61		
	Q96EK6				Q8TBM8		
	Q96ER3				Q8TCE6-1		
	Q96FZ7				Q8TCF1-1		
	Q96IV0				Q8TD30-1		
	Q96M27-1				Q8TDZ2		
	Q96SU4				Q8TEA8		

Continued on next page

Cycloheximide				Pateamine A			
Upregulated		Downregulated		Upregulated		Downregulated	
All	GBM	All	GBM	All	GBM	All	GBM
	Q99436				Q8WVQ1		
	Q9BRG1				Q8WX92		
	Q9BRT3				Q92581-1		
	Q9BSH4				Q92870-1		
	Q9BUR4				Q93050-1		
	Q9BV20-1				Q96BX8		
	Q9BYT8				Q96EH3		
	Q9BYX2				Q96SI9		
	Q9BZH6				Q99570		
	Q9GZM5				Q99797		
	Q9GZP9				Q9BRT6		
	Q9H446				Q9BRT9		
	Q9H6K4				Q9BU76-1		
	Q9H7Z7				Q9BUE0		
	Q9H832				Q9BV81		
	Q9H936				Q9GZP9		
	Q9HAV0				Q9GZR2-1		
	Q9HAV4				Q9H0R4-1		
	Q9HBH1				Q9H1I8-1		
	Q9HC07				Q9H1Z9		
	Q9HC36				Q9H4L7		
	Q9HCU5				Q9H788		
	Q9HD26-1				Q9H8Y5		
	Q9NP77				Q9H9Y6-1		
	Q9NRX1				Q9HC36		
	Q9NVH1-1				Q9NQC3-5		
	Q9NWV4				Q9NQE9		
	Q9NX14-1				Q9NRP0-1		
	Q9NXG2				Q9NRZ9		
	Q9NYY8				Q9NTX5		
	Q9UBV2				Q9NU22		
	Q9UET6				Q9NV31		
	Q9UHI6				Q9UBN7-1		
	Q9UQ13				Q9UFC0		
	Q9Y291				Q9UFN0		

Continued on next page

Cycloheximide				Pateamine A			
Upregulated		Downregulated		Upregulated		Downregulated	
All	GBM	All	GBM	All	GBM	All	GBM
	Q9Y2P8				Q9UGJ1		
	Q9Y2X7-1				Q9UH62		
	Q9Y3C4				Q9UHA4		
	Q9Y4B6				Q9UHG3		
	Q9Y5V3				Q9UID3-1		
	Q9Y697				Q9UJX2-1		
	Q9Y6M9				Q9ULH0-1		
					Q9UNP9-1		
					Q9UNQ2		
					Q9UNX3		
					Q9UP95		
					Q9UPN9-1		
					Q9UPT9-1		
					Q9Y2H0-1		
					Q9Y2P8		
					Q9Y2R0		
					Q9Y2R5		
					Q9Y2U5		
					Q9Y376		
					Q9Y394		
					Q9Y3A2		
					Q9Y3C5		
					Q9Y3C6		
					Q9Y3E0		
					Q9Y3X0		
					Q9Y4C2-1		
					Q9Y5Q9		
					Q9Y6V7		
End of Table							

Bibliography

[1] N. L. Korneeva, E. A. First, C. A. Benoit, and R. E. Rhoads, "Interaction between the NH_2-terminal domain of eIF4A and the central domain of eIF4G modulates RNA-stimulated ATPase activity," *Journal of Biological Chemistry*, vol. 280, no. 3, pp. 1872–1881, 2005.

[2] L. D. Kapp and J. R. Lorsch, "The molecular mechanics of eukaryotic translation," *Annual Review of Biochemistry*, vol. 73, no. 1, pp. 657–704, 2004.

[3] J. M. Caruthers, E. R. Johnson, and D. B. McKay, "Crystal structure of yeast initiation factor 4A, a DEAD-box RNA helicase," *Proceedings of the National Academy of Sciences*, vol. 97, no. 24, pp. 13080–13085, 2000.

[4] S. C. Conroy, T. E. Dever, C. L. Owens, and W. C. Merrick, "Characterization of the 46,000-dalton subunit of eIF-4F," *Archives of Biochemistry and Biophysics*, vol. 282, no. 2, pp. 363–371, 1990.

[5] M.-E. Bordeleau, J. Matthews, J. M. Wojnar, L. Lindqvist, O. Novac, E. Jankowsky, N. Sonenberg, P. Northcote, P. Teesdale-Spittle, and J. Pelletier, "Stimulation of mammalian translation initiation factor eIF4A activity by a small molecule inhibitor of eukaryotic translation,"

Proceedings of the National Academy of Sciences, vol. 102, no. 30, pp. 10460–10465, 2005.

[6] A. E. Gorbalenya and E. V. Koonin, "Helicases: amino acid sequence comparisons and structure-function relationships," *Current Opinion in Structural Biology*, vol. 3, no. 3, pp. 419–429, 1993.

[7] P. Linder and E. Jankowsky, "From unwinding to clamping—the DEAD-box RNA helicase family," *Nature Reviews Molecular Cell Biology*, vol. 12, no. 8, pp. 505–516, 2011.

[8] S. Iwasaki, W. Iwasaki, M. Takahashi, A. Sakamoto, C. Watanabe, Y. Shichino, S. N. Floor, K. Fujiwara, M. Mito, K. Dodo, *et al.*, "The translation inhibitor rocaglamide targets a bimolecular cavity between eIF4A and polypurine RNA," *Molecular Cell*, vol. 73, no. 4, pp. 738–748, 2019.

[9] G. W. Rogers, N. J. Richter, W. F. Lima, and W. C. Merrick, "Modulation of the helicase activity of eIF4A by eIF4B, eIF4H, and eIF4F," *Journal of Biological Chemistry*, vol. 276, no. 33, pp. 30914–30922, 2001.

[10] Y. Sun, E. Atas, L. M. Lindqvist, N. Sonenberg, J. Pelletier, and A. Meller, "Single-molecule kinetics of the eukaryotic initiation factor 4AI upon RNA unwinding," *Structure*, vol. 22, no. 7, pp. 941–948, 2014.

[11] A. Z. Andreou and D. Klostermeier, "Conformational changes of DEAD-box helicases monitored by single molecule fluorescence resonance energy transfer," *Methods in Enzymology*, vol. 511, pp. 75–109, 2012.

[12] M. Oberer, A. Marintchev, and G. Wagner, "Structural basis for the enhancement of eIF4A helicase activity by eIF4G," *Genes & Development*, vol. 19, no. 18, pp. 2212–2223, 2005.

[13] Y. V. Svitkin, A. Pause, A. Haghighat, S. Pyronnet, G. Witherell, G. J. Belsham, and N. Sonenberg, "The requirement for eukaryotic initiation factor 4A (eIF4A) in translation is in direct proportion to the degree of mRNA 5′ secondary structure," *RNA*, vol. 7, no. 3, pp. 382–394, 2001.

[14] A. Kahvejian, Y. V. Svitkin, R. Sukarieh, M.-N. M'Boutchou, and N. Sonenberg, "Mammalian poly (A)-binding protein is a eukaryotic translation initiation factor, which acts via multiple mechanisms," *Genes & Development*, vol. 19, no. 1, pp. 104–113, 2005.

[15] R. N. Besaans, "Global proteome response of human cancer cell lines to low dose eIF4E/eIF4G inhibition," Master's thesis, Victoria University of Wellington, Wellington, New Zealand, February 2019.

[16] V. Venturi, *The Genetic Profiles of TIF1 and TIF2 Duplicate Genes*. PhD thesis, Victoria University of Wellington, Wellington, New Zealand, June 2012.

[17] R. Little, *Investigation of the Biological Effect of eIF4A Reduction and Inhibition*. PhD thesis, Victoria University of Wellington, Wellington, New Zealand, July 2020.

[18] D. Romo, R. M. Rzasa, H. A. Shea, K. Park, J. M. Langenhan, L. Sun, A. Akhiezer, and J. O. Liu, "Total synthesis and immunosuppressive activity of (-)-pateamine A and related compounds: implementation

of a β-lactam-based macrocyclization," *Journal of the American Chemical Society*, vol. 120, no. 47, pp. 12237–12254, 1998.

[19] P. T. Northcote, J. W. Blunt, and M. H. Munro, "Pateamine: a potent cytotoxin from the New Zealand marine sponge, *Mycale* sp.," *Tetrahedron Letters*, vol. 32, no. 44, pp. 6411–6414, 1991.

[20] S. K. Naineni, J. Liang, K. Hull, R. Cencic, M. Zhu, P. Northcote, P. Teesdale-Spittle, D. Romo, B. Nagar, and J. Pelletier, "Functional mimicry revealed by the crystal structure of an eIF4A: RNA complex bound to the interfacial inhibitor, desmethyl pateamine A," *Cell Chemical Biology*, vol. 28, no. 6, pp. 825–834, 2021.

[21] J. Grifo, S. Tahara, J. Leis, M. Morgan, A. Shatkin, and W. Merrick, "Characterization of eukaryotic initiation factor 4A, a protein involved in ATP-dependent binding of globin mRNA.," *Journal of Biological Chemistry*, vol. 257, no. 9, pp. 5246–5252, 1982.

[22] G. Pattenden, D. J. Critcher, and M. Remuiñán, "Total synthesis of ()-pateamine A, a novel immunosuppressive agent from *Mycale* sp," *Canadian Journal of Chemistry*, vol. 82, no. 2, pp. 353–365, 2004.

[23] C.-X. Zhuo and A. Fürstner, "Catalysis-based total syntheses of pateamine A and DMDA-Pat A," *Journal of the American Chemical Society*, vol. 140, no. 33, pp. 10514–10523, 2018.

[24] C.-X. Zhuo and A. Fürstner, "Concise synthesis of a pateamine A analogue with *in vivo* anticancer activity based on an iron-catalyzed pyrone ring opening/cross-coupling," *Angewandte Chemie International Edition*, vol. 55, no. 20, pp. 6051–6056, 2016.

[25] D. Romo, N. S. Choi, S. Li, I. Buchler, Z. Shi, and J. O. Liu, "Evidence for separate binding and scaffolding domains in the immunosuppressive and antitumor marine natural product, pateamine A: design, synthesis, and activity studies leading to a potent simplified derivative," *Journal of the American Chemical Society*, vol. 126, no. 34, pp. 10582–10588, 2004.

[26] G. Kuznetsov, Q. Xu, L. Rudolph-Owen, K. TenDyke, J. Liu, M. Towle, N. Zhao, J. Marsh, S. Agoulnik, N. Twine, *et al.*, "Potent *in vitro* and *in vivo* anticancer activities of des-methyl, des-amino pateamine A, a synthetic analogue of marine natural product pateamine A," *Molecular Cancer Therapeutics*, vol. 8, no. 5, pp. 1250–1260, 2009.

[27] M. Li-Weber, "Molecular mechanisms and anti-cancer aspects of the medicinal phytochemicals rocaglamides (= flavaglines)," *International Journal of Cancer*, vol. 137, no. 8, pp. 1791–1799, 2015.

[28] L. Lindqvist, M. Oberer, M. Reibarkh, R. Cencic, M.-E. Bordeleau, E. Vogt, A. Marintchev, J. Tanaka, F. Fagotto, M. Altmann, *et al.*, "Selective pharmacological targeting of a DEAD box RNA helicase," *PLOS One*, vol. 3, no. 2, p. e1583, 2008.

[29] N. G. de Loubresse, I. Prokhorova, W. Holtkamp, M. V. Rodnina, G. Yusupova, and M. Yusupov, "Structural basis for the inhibition of the eukaryotic ribosome," *Nature*, vol. 513, no. 7519, pp. 517–522, 2014.

[30] M. Brönstrup and F. Sasse, "Natural products targeting the elongation phase of eukaryotic protein biosynthesis," *Natural Product Reports*, vol. 37, no. 6, pp. 752–762, 2020.

[31] Q. T. Ostrom, N. Patil, G. Cioffi, K. Waite, C. Kruchko, and J. S. Barnholtz-Sloan, "CBTRUS statistical report: primary brain and other central nervous system tumors diagnosed in the United States in 2013–2017," *Neuro-oncology*, vol. 22, no. Supplement_1, pp. iv1–iv96, 2020.

[32] M. Penas-Prado, T. S. Armstrong, and M. R. Gilbert, "Glioblastoma," *Handbook of Clinical Neurology*, vol. 105, pp. 485–506, 2012.

[33] A. C. Tan, D. M. Ashley, G. Y. López, M. Malinzak, H. S. Friedman, and M. Khasraw, "Management of glioblastoma: State of the art and future directions," *CA: A Cancer Journal for Clinicians*, vol. 70, no. 4, pp. 299–312, 2020.

[34] R. G. Verhaak, K. A. Hoadley, E. Purdom, V. Wang, Y. Qi, M. D. Wilkerson, C. R. Miller, L. Ding, T. Golub, J. P. Mesirov, *et al.*, "Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in PDGFRA, IDH1, EGFR, and NF1," *Cancer Cell*, vol. 17, no. 1, pp. 98–110, 2010.

[35] L. Liu and X. Li, "IDH gene mutation in glioma," *Cancer Translational Medicine*, vol. 4, no. 5, pp. 129–133, 2018.

[36] V. Patil, J. Pal, and K. Somasundaram, "Elucidating the cancer-specific genetic alteration spectrum of glioblastoma derived cell lines from whole exome and RNA sequencing," *Oncotarget*, vol. 6, no. 41, p. 43452, 2015.

[37] Z. J. Reitman and H. Yan, "Malignant glioma: isocitrate dehydrogenases 1 and 2 mutations," in *Tumors of the Central Nervous System, Volume 2*, pp. 53–62, Springer, 2011.

[38] D. W. Parsons, S. Jones, X. Zhang, J. C.-H. Lin, R. J. Leary, P. Angenendt, P. Mankoo, H. Carter, I.-M. Siu, G. L. Gallia, *et al.*, "An integrated genomic analysis of human glioblastoma multiforme," *Science*, vol. 321, no. 5897, pp. 1807–1812, 2008.

[39] A. K. Tribe, M. J. McConnell, and P. H. Teesdale-Spittle, "The big picture of glioblastoma malignancy: A meta-analysis of glioblastoma proteomics to identify altered biological pathways," *ACS Omega*, vol. 6, no. 38, pp. 24535–24544, 2021.

[40] M. Allen, M. Bjerke, H. Edlund, S. Nelander, and B. Westermark, "Origin of the U87MG glioma cell line: Good news and bad news," *Science Translational Medicine*, vol. 8, no. 354, pp. 354re3–354re3, 2016.

[41] G. Birnie, "The HL60 cell line: a model system for studying human myeloid cell differentiation.," *The British Journal of Cancer. Supplement*, vol. 9, p. 41, 1988.

[42] K. Präbst, H. Engelhardt, S. Ringgeler, and H. Hübner, "Basic colorimetric proliferation assays: MTT, WST, and resazurin," in *Cell Viability Assays*, pp. 1–17, Springer, 2017.

[43] U. Raudvere, L. Kolberg, I. Kuzmin, T. Arak, P. Adler, H. Peterson, and J. Vilo, "g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019 update)," *Nucleic Acids Research*, vol. 47, no. W1, pp. W191–W198, 2019.

[44] A. Khan and A. Mathelier, "Intervene: a tool for intersection and visualization of multiple gene or genomic region sets," *BMC Bioinformatics*, vol. 18, no. 1, pp. 1–8, 2017.

[45] C. Andrade, "The p value and statistical significance: misunderstandings, explanations, challenges, and alternatives," *Indian Journal of Psychological Medicine*, vol. 41, no. 3, pp. 210–215, 2019.

[46] J. Concato and J. A. Hartigan, "P values: from suggestion to superstition," *Journal of Investigative Medicine*, vol. 64, no. 7, pp. 1166–1171, 2016.

[47] T. J. VanderWeele and M. B. Mathur, "Some desirable properties of the Bonferroni correction: is the Bonferroni correction really so bad?," *American Journal of Epidemiology*, vol. 188, no. 3, pp. 617–618, 2019.

[48] S. Lockhead, A. Moskaleva, J. Kamenz, Y. Chen, M. Kang, A. R. Reddy, S. D. Santos, and J. E. Ferrell Jr, "The apparent requirement for protein synthesis during G2 phase is due to checkpoint activation," *Cell Reports*, vol. 32, no. 2, p. 107901, 2020.

[49] X. Liu, D. A. Bushnell, and R. D. Kornberg, "RNA polymerase II transcription: structure and mechanism," *Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms*, vol. 1829, no. 1, pp. 2–8, 2013.

[50] R. Gantt, "A cell cycle-associated pathway for repair of DNA-protein crosslinks in mammalian cells," *Mutation Research/DNA Repair Reports*, vol. 183, no. 1, pp. 75–87, 1987.

[51] C. Rajiv and T. L. Davis, "Structural and functional insights into human nuclear cyclophilins," *Biomolecules*, vol. 8, no. 4, p. 161, 2018.

[52] D. Mateju, B. Eichenberger, F. Voigt, J. Eglinger, G. Roth, and J. A. Chao, "Single-molecule imaging reveals translation of mrnas localized to stress granules," *Cell*, vol. 183, no. 7, pp. 1801–1812, 2020.

[53] Z. Qiu, L. Zhao, J. Z. Shen, Z. Liang, Q. Wu, K. Yang, L. Min, R. C. Gimple, Q. Yang, S. Bhargava, *et al.*, "Transcription elongation machinery is a druggable dependency and potentiates immunotherapy in glioblastoma stem cells," *Cancer Discovery*, 2021.

[54] B. Bi, F. Li, J. Guo, C. Li, R. Jing, X. Lv, X. Chen, F. Wang, K. M. Azadzoi, L. Wang, *et al.*, "Label-free quantitative proteomics unravels the importance of RNA processing in glioma malignancy," *Neuroscience*, vol. 351, pp. 84–95, 2017.

[55] F. Marcelino Meliso, C. G. Hubert, P. A. Favoretto Galante, and L. O. Penalva, "RNA processing as an alternative route to attack glioblastoma," *Human Genetics*, vol. 136, no. 9, pp. 1129–1141, 2017.

[56] B. R. Correa, P. R. de Araujo, M. Qiao, S. C. Burns, C. Chen, R. Schlegel, S. Agarwal, P. A. Galante, and L. O. Penalva, "Functional genomics analyses of RNA-binding proteins reveal the splicing regulator SNRPB as an oncogenic candidate in glioblastoma," *Genome Biology*, vol. 17, no. 1, pp. 1–16, 2016.

[57] H. Yamauchi, K. Nishimura, and A. Yoshimi, "Aberrant RNA splicing and therapeutic opportunities in cancers," *Cancer Science*, vol. 113, no. 2, p. 373, 2022.

[58] H. Li, B. Lei, W. Xiang, H. Wang, W. Feng, Y. Liu, and S. Qi, "Differences in protein expression between the U251 and U87 cell lines," *Turkish Neurosurgery*, vol. 27, no. 6, pp. 894–903, 2017.

[59] M. P. Spiller, K.-L. Boon, M. A. Reijns, and J. D. Beggs, "The Lsm2-8 complex determines nuclear localization of the spliceosomal U6 snRNA," *Nucleic Acids Research*, vol. 35, no. 3, pp. 923–929, 2007.

[60] H. Climente-González, E. Porta-Pardo, A. Godzik, and E. Eyras, "The functional impact of alternative splicing in cancer," *Cell Reports*, vol. 20, no. 9, pp. 2215–2226, 2017.

[61] Y. Li, Z. Ren, Y. Peng, K. Li, X. Wang, G. Huang, S. Qi, and Y. Liu, "Classification of glioma based on prognostic alternative splicing," *BMC Medical Genomics*, vol. 12, no. 1, pp. 1–16, 2019.

[62] L. Wang, K. Shamardani, H. Babikir, F. Catalan, T. Nejo, S. Chang, J. J. Phillips, H. Okada, and A. A. Diaz, "The evolution of alternative splicing in glioblastoma under therapy," *Genome Biology*, vol. 22, no. 1, pp. 1–15, 2021.

[63] Y. Dang, W.-K. Low, J. Xu, N. H. Gehring, H. C. Dietz, D. Romo, and J. O. Liu, "Inhibition of nonsense-mediated mRNA decay by the natural product pateamine A through eukaryotic initiation factor 4AIII," *Journal of Biological Chemistry*, vol. 284, no. 35, pp. 23613–23621, 2009.

[64] E. D. Karousis, S. Nasif, and O. Mühlemann, "Nonsense-mediated mRNA decay: novel mechanistic insights and biological impact," *Wiley Interdisciplinary Reviews: RNA*, vol. 7, no. 5, pp. 661–682, 2016.

[65] M. A. Ferraiuolo, C.-S. Lee, L. W. Ler, J. L. Hsu, M. Costa-Mattioli, M.-J. Luo, R. Reed, and N. Sonenberg, "A nuclear translation-like factor eIF4AIII is recruited to the mRNA during splicing and functions in nonsense-mediated decay," *Proceedings of the National Academy of Sciences*, vol. 101, no. 12, pp. 4118–4123, 2004.

[66] J. H. Park, W. Y. Pyun, and H. W. Park, "Cancer metabolism: phenotype, signaling and therapeutic targets," *Cells*, vol. 9, no. 10, p. 2308, 2020.

[67] Y. Wang and S. Hekimi, "Understanding ubiquinone," *Trends in Cell Biology*, vol. 26, no. 5, pp. 367–378, 2016.

[68] K. Leppek, R. Das, and M. Barna, "Functional 5′ UTR mRNA sturctures in eukaryotic translation regulation and how to find them," *Nature Reviews Molecular Cell Biology*, vol. 19, no. 3, pp. 158–174, 2018.

[69] J. R. Babendure, J. L. Babendure, J.-H. Ding, and R. Y. Tsien, "Control of mammalian translation by mRNA structure near caps," *RNA*, vol. 12, no. 5, pp. 851–861, 2006.

[70] S. Wang, H. Zhou, R. Zhang, and Y. Zhang, "Integrated analysis of mutations, miRNA and mRNA expression in glioblastoma," *International Journal of General Medicine*, vol. 14, p. 8281, 2021.

[71] T. E. Webb, M. Davies, J. Maher, and D. Sarker, "The eIF4A inhibitor silvestrol sensitizes T-47D ductal breast carcinoma cells to external-beam radiotherapy," *Clinical and Translational Radiation Oncology*, vol. 24, pp. 123–126, 2020.

[72] R. Chen, M. Zhu, R. R. Chaudhari, O. Robles, Y. Chen, W. Skillern, Q. Qin, W. G. Wierda, S. Zhang, K. G. Hull, *et al.*, "Creating novel translation inhibitors to target pro-survival proteins in chronic lymphocytic leukemia," *Leukemia*, vol. 33, no. 7, pp. 1663–1674, 2019.

[73] M. Chen, M. Asanuma, M. Takahashi, Y. Shichino, M. Mito, K. Fujiwara, H. Saito, S. N. Floor, N. T. Ingolia, M. Sodeoka, *et al.*, "Dual targeting of DDX3 and eIF4A by the translation inhibitor rocaglamide A," *Cell Chemical Biology*, vol. 28, no. 4, pp. 475–486, 2021.

[74] B. Wang, Y. Li, F. Tan, and Z. Xiao, "Chinese herb derived-rocaglamide A is a potent inhibitor of pancreatic cancer cells," *American Journal of Translational Research*, vol. 8, no. 2, p. 1047, 2016.

[75] J. Y. Zhu, I. N. Lavrik, U. Mahlknecht, M. Giaisi, P. Proksch, P. H. Krammer, and M. Li-Weber, "The traditional Chinese herbal compound rocaglamide preferentially induces apoptosis in leukemia cells by modulation of mitogen-activated protein kinase activities," *International Journal of Cancer*, vol. 121, no. 8, pp. 1839–1846, 2007.

[76] L. Pan, J. L. Woodard, D. M. Lucas, J. R. Fuchs, and A. D. Kinghorn, "Rocaglamide, silvestrol and structurally related bioactive compounds from *Aglaia* species," *Natural Product Reports*, vol. 31, no. 7, pp. 924–939, 2014.

[77] D. Müller, S. Shin, T. G. de Rugy, R. Samain, R. Baer, M. Strehaiano, L. Masvidal-Sanz, J. Guillermet-Guibert, C. Jean, Y. Tsukumo, *et al.*, "eIF4A inhibition circumvents uncontrolled DNA replication mediated

by 4E-BP1 loss in pancreatic cancer," *Journal of Clinical Investigation Insight*, vol. 4, no. 21, 2019.

[78] J. Steinberger, L. Shen, S. J. Kiniry, S. K. Naineni, R. Cencic, M. Amiri, S. A. Aboushawareb, J. Chu, R. I. Maïga, B. J. Yachnin, *et al.*, "Identification and characterization of hippuristanol-resistant mutants reveals eIF4A1 dependencies within mRNA 5′ leader regions," *Nucleic Acids Research*, vol. 48, no. 17, pp. 9521–9537, 2020.

[79] R. Cencic, F. Robert, G. Galicia-Vazquez, A. Malina, K. Ravindar, R. Somaiah, P. Pierre, J. Tanaka, P. Deslongchamps, and J. Pelletier, "Modifying chemotherapy response by targeted inhibition of eukaryotic initiation factor 4A," *Blood Cancer Journal*, vol. 3, no. 7, pp. e128–e128, 2013.

[80] L.-B. Wang, A. Karpova, M. A. Gritsenko, J. E. Kyle, S. Cao, Y. Li, D. Rykunov, A. Colaprico, J. H. Rothstein, R. Hong, *et al.*, "Proteogenomic and metabolomic characterization of human glioblastoma," *Cancer Cell*, vol. 39, no. 4, pp. 509–528, 2021.

[81] S.-R. Shih, K.-F. Weng, V. Stollar, and M.-L. Li, "Viral protein synthesis is required for enterovirus 71 to induce apoptosis in human glioblastoma cells," *Journal of Neurovirology*, vol. 14, no. 1, pp. 53–61, 2008.

Index

cell lines, 12–14, 61–62, 70–71
- experimental, 22–25
- HL60, 13–14, 61, 72–74, 100–101
- LN18, 13, 61–62, 77–94
- U87, 13, 61–62, 71–72, 82–85, 93, 94

cycloheximide, 10, 63
- effects of, 44–51, 71–72
- experimental use, 20–21, 24, 64

DMDA pateamine, 8, 100, 106–107

eIF4A, 2–8, 107–108

glioblastoma, 11–14
- mutations, 11–12

hippuristanol, 9–108

MTT assay, 23–25, 63–65, 71
- principles, 23
- results, 35–38

pateamine A, 6–8
- activity, 7, 106
- effects of, 52–107
  - in glioblastoma, 86–100
  - in HL60, 100–101
- experimental use, 21, 24, 64

rocaglamide A, 8, 107

silvestrol, 99–100, 107

whole proteome preparation, 26–29, 65–66