Regulation of Cellular Metabolism by Protein Lysine Acetylation

Shimin Zhao, *et al.*

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histone marks, and an interacting splicing regulator (Fig. 5D). Such complexes are a means for epigenetic information to be transmitted to the pre-mRNA processing machinery and probably act by favoring the recruitment of specific splicing regulators to the pre-mRNA, thus defining splicing outcome. We show here that for a subset of PTB-dependent genes, this adaptor system consists of H3-K36me3, its binding protein MRG15, and the splicing regulator PTB. It is tempting to speculate that other combinations of adaptor systems exist that act on other types of alternatively spliced exons. Physical interaction between several chromatin-associated proteins and splicing components has been reported (*9*, *14*). Our results are in line with recent indirect evidence based on genome-wide mapping of histone modifications for a role for chromatin structure and histone modifications in exon definition and alternative splice site selection (*5*, *13*, *15*–*19*).

Although our observations argue for a direct link between histone modifications and the splicing machinery, histone marks may also affect splice site choice indirectly. Extensive evidence demonstrates a role for RNA polymerase II elongation rate or higher-order chromatin structure in splicing outcome, and it is likely that histone modifications act in concert with these mechanisms (*6*–*8*, *10*–*12*). Based on our findings, we propose that the epigenetic memory contained in histone modification patterns is not only used to determine the level of activity of a gene but also transmits information to establish, propagate, and regulate AS patterns during physiological processes such as development and differentiation.

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Supporting Online Material

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Regulation of Cellular Metabolism by Protein Lysine Acetylation

Shimin Zhao,[1,2] Wei Xu,[1,2]* Wenqing Jiang,[1,2]* Wei Yu,[1,2] Yan Lin,[2] Tengfei Zhang,[1,2] Jun Yao,[3] Li Zhou,[4] Yaxue Zeng,[4] Hong Li,[5] Yixue Li,[6] Jiong Shi,[6] Wenlin An,[7] Susan M. Hancock,[7] Fuchu He,[3] Lunxiu Qin,[5] Jason Chin,[7] Pengyuan Yang,[3] Xian Chen,[3,4] Qunying Lei,[1,2,8] Yue Xiong,[1,2,4]† Kun-Liang Guan[1,2,8,9]†

Protein lysine acetylation has emerged as a key posttranslational modification in cellular regulation, in particular through the modification of histones and nuclear transcription regulators. We show that lysine acetylation is a prevalent modification in enzymes that catalyze intermediate metabolism. Virtually every enzyme in glycolysis, gluconeogenesis, the tricarboxylic acid (TCA) cycle, the urea cycle, fatty acid metabolism, and glycogen metabolism was found to be acetylated in human liver tissue. The concentration of metabolic fuels, such as glucose, amino acids, and fatty acids, influenced the acetylation status of metabolic enzymes. Acetylation activated enoyl–coenzyme A hydratase/3-hydroxyacyl–coenzyme A dehydrogenase in fatty acid oxidation and malate dehydrogenase in the TCA cycle, inhibited argininosuccinate lyase in the urea cycle, and destabilized phosphoenolpyruvate carboxykinase in gluconeogenesis. Our study reveals that acetylation plays a major role in metabolic regulation.

Protein acetylation has a key role in the regulation of transcription in the nucleus (*1*), but much less is known about non-nuclear protein acetylation and its role in cellular regulation. To investigate non-nuclear protein acetylation, we separated human liver tissues into nuclear, mitochondrial, and cytosolic fractions. Proteins in cytosolic and mitochondrial fractions were digested with trypsin and acetylated peptides were purified with an antibody to acetyllysine (fig. S1). The purified peptides were analyzed by tandem liquid chromatography–tandem mass spectrometry (LC/LC-MS/MS). From three independent experiments, we identified more than 1300 acetylated peptides, which matched to 1047 distinct human proteins (table S1), including 703 proteins not previously reported to be acetylated. A previous report identified 195 acetylated proteins from mouse liver (*2*), and 135 (70%) of these were also present in our data set (Fig. 1A), indicating that our proteomic analysis reached a high degree of coverage. Choudhary *et al.* very recently reported the identification of 1750 acetylated proteins from a human leukemia cell line (*3*), but only 240 of these were present in our data set (Fig. 1A). Comparison of these three acetylome data sets indicates that the spectrum of acetylated proteins is highly conserved in the liver between mouse and human, but is very different between liver and leukemia cells.

We compared the acetylated proteins with the total liver proteome and discovered that enzymes that participate in intermediate metabolism were preferentially acetylated (Fig. 1B). Indeed, almost

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[1] School of Life Sciences, Fudan University, Shanghai 20032, China. [2] Molecular and Cell Biology Lab, Fudan University, Shanghai 20032, China. [3] Center of Proteomics, Institute of Biomedical Sciences, Fudan University, Shanghai 20032, China. [4] Department of Biochemistry and Biophysics, Lineberger Comprehensive Cancer Center, University of North Carolina, Chapel Hill, NC 27599, USA. [5] Affiliated Zhongshan Hospital, Fudan University, Shanghai 20032, China. [6] Bioinformatics Center, Key Lab of Systems Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 200031, China. [7] Medical Research Council Laboratory of Molecular Biology, Hills Road, Cambridge CB2 OQH, UK. [8] Department of Biological Chemistry, Fudan University, Shanghai 20032, China. [9] Department of Pharmacology and Moores Cancer Center, University of California, San Diego, La Jolla, CA 92093, USA.

*These authors contributed equally to this work.

†To whom correspondence should be addressed. E-mail: yxiong@email.unc.edu (Y.X.); kuguan@ucsd.edu (K.L.G.)

every enzyme in glycolysis, gluconeogenesis, the TCA cycle, the urea cycle, fatty acid metabolism, and glycogen metabolism was acetylated (Fig. 1, C to G). The high occurrence of metabolic enzymes identified in our MS analysis is apparently not due to the abundance of these proteins, because only a few ribosomal proteins (7 of approximately 80 cytosolic ribosomal proteins) were acetylated (table S1). These results indicate a previously unrecognized and potentially extensive role of acetylation in regulation of cellular metabolism. Therefore, we investigated the effect of acetylation on representative enzymes from four metabolic pathways.

Enoyl–coenzyme A hydratase/3-hydroxyacyl–coenzyme A (EHHADH; EC code 1.1.1.35) catalyzes two steps in fatty acid oxidation (Fig. 1E) (*4*, *5*), and its deficiency causes abnormal fatty acid metabolism (*6*). We identified four acetylated lysine residues (Lys^{165}, Lys^{171}, Lys^{346}, and Lys^{584}) in EHHADH (table S2). Immunoprecipitation of ectopically expressed FLAG-tagged EHHADH and Western blotting with antibody to acetyllysine confirmed that EHHADH was indeed acetylated. Its acetylation was enhanced by 80% after treatment of cells with trichostatin A [TSA, an inhibitor of histone deacetylase (HDAC) I and II] and nicotinamide (NAM, an inhibitor of the SIRT family deacetylases) (Fig. 2A and fig. S2A). To quantify the acetylation of EHHADH, we used isobaric tags for relative and absolute quantitation (iTRAQ) MS of immunoprecipitated EHHADH. TSA and NAM treatment increased Lys^{171} acetylation from 43.5% to 62% and Lys^{346} acetylation from 46.8% to 77.8% (Fig. 2B), respectively. Consistently, the corresponding unacetylated peptides were decreased by TSA and NAM treatment. These results show that a substantial portion of EHHADH is acetylated and that EHHADH acetylation can be dynamically regulated in vivo.

To determine the effect of acetylation on enzymatic activity, we treated cultured Chang human liver cells with TSA and NAM and detected a doubling of endogenous EHHADH activity (Fig. 2C). Similar observations were also made with ectopically expressed EHHADH in HEK293T cells (Fig. 2C, right panel). Acetylation of an EHHADH^{4KQ} mutant, which had the four putative acetylation lysine residues replaced by glutamine, was decreased (fig. S2C) and its activity was no longer regulated by TSA and NAM (Fig. 2C). Addition of fatty acids to the culture medium increased acetylation and activity of EHHADH by factors of 1.7 and 1.3, respectively (Fig. 2D and fig. S2D). Thus, acetylation of EHHADH can be regulated by extracellular fuels; this finding supports a physiological role of acetylation in the regulation of EHHADH and fatty acid metabolism.

All seven enzymes in the TCA cycle were acetylated (Fig. 1C and table S1), including malate dehydrogenase (MDH; EC code 1.1.1.37), in which four acetylated lysines were identified (Lys^{185}, Lys^{301}, Lys^{307}, and Lys^{314}; tables S2 and S3). Ectopically expressed MDH was acetylated and its acetylation was increased by a factor of 2.4 in cells treated with TSA and NAM (Fig. 2E and fig. S2E). To quantify MDH acetylation, we performed Fourier transform ion cyclotron resonance (FTICR) MS. This approach identified the unmodified full-length MDH and two additional peaks, each with a mass increment of 42.01 daltons, corresponding to mono- and diacetylation

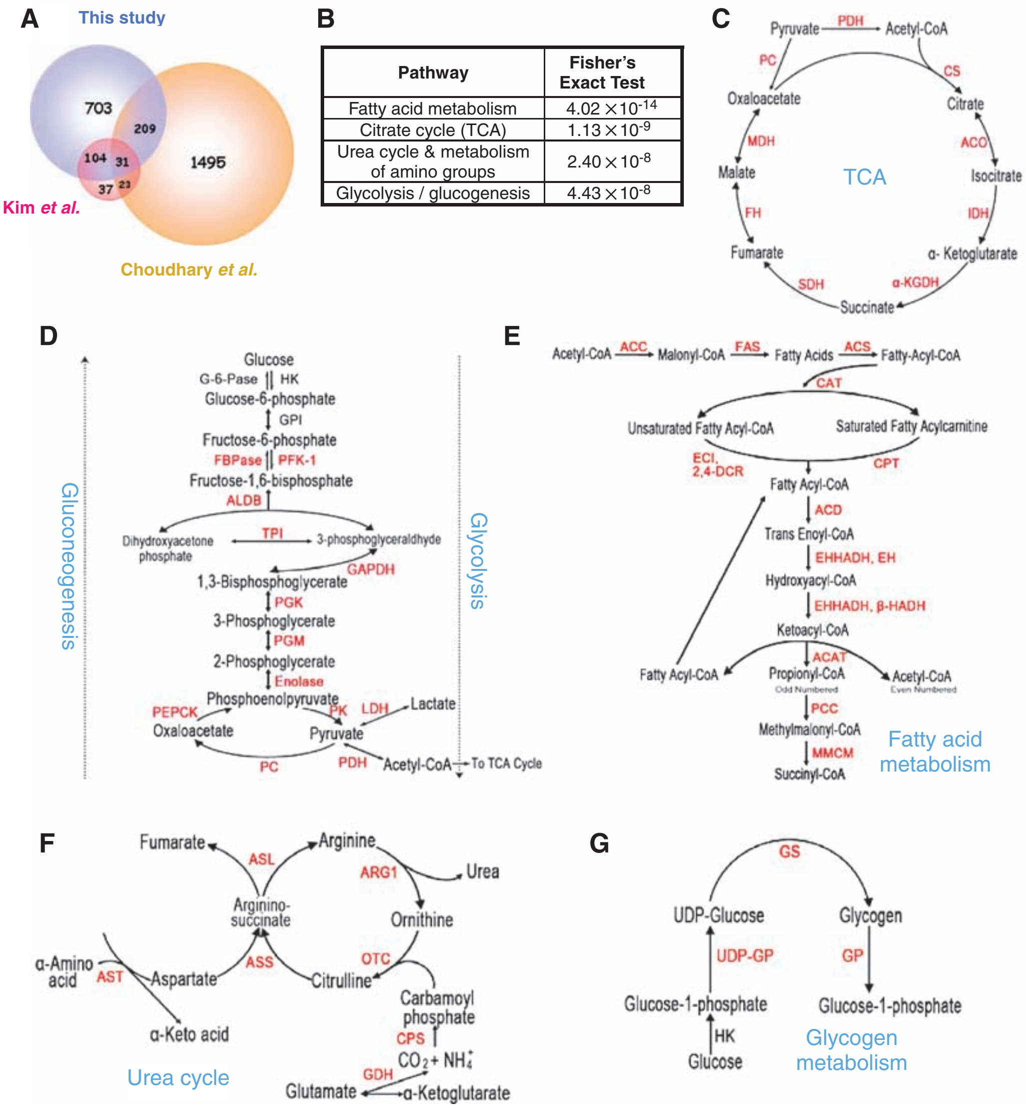
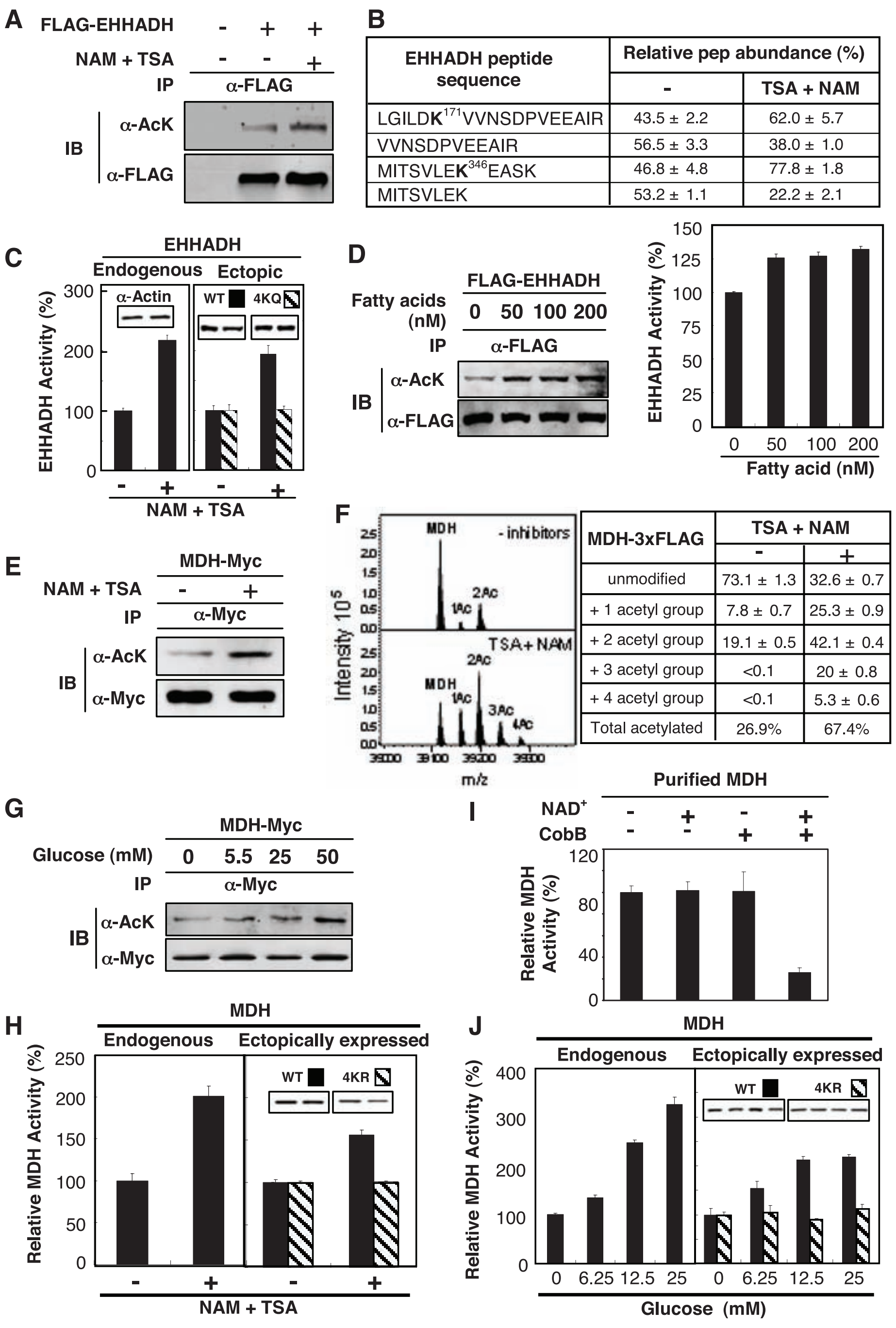


Fig. 1. Acetylation of liver metabolic enzymes. (**A**) Comparison of three acetylation proteomic studies: this study and (*2*, *3*). (**B**) Preferential acetylation of enzymes in intermediary metabolism. Fisher's exact test of comparing acetylated proteins to total liver proteins shows that acetylation is much more prevalent in intermediary metabolic enzymes. (**C** to **G**) Acetylated metabolic enzymes identified by proteomic survey are marked in red. See supporting online material for key to abbreviations.



EHHADH peptide sequence	Relative pep abundance (%)	
	-	TSA + NAM
LGILDK^{171}VVNSDPVEEAIR	43.5 ± 2.2	62.0 ± 5.7
VVNSDPVEEAIR	56.5 ± 3.3	38.0 ± 1.0
MITSVLEK^{346}EASK	46.8 ± 4.8	77.8 ± 1.8
MITSVLEK	53.2 ± 1.1	22.2 ± 2.1

MDH-3xFLAG	TSA + NAM	
	-	+
unmodified	73.1 ± 1.3	32.6 ± 0.7
+ 1 acetyl group	7.8 ± 0.7	25.3 ± 0.9
+ 2 acetyl group	19.1 ± 0.5	42.1 ± 0.4
+ 3 acetyl group	<0.1	20 ± 0.8
+ 4 acetyl group	<0.1	5.3 ± 0.6
Total acetylated	26.9%	67.4%

Fig. 2. Activation of EHHADH and MDH by acetylation. (**A**) Acetylation of EHHADH was increased by deacetylase inhibitors. Ectopically expressed and immunoprecipitated (IP) EHHADH was examined by immunoblotting (IB) with antibody to acetyllysine (α-AcK). (**B**) Quantification of EHHADH acetylation by iTRAQ MS. Quantification of peptides was calculated on the basis of relative intensity of the iTRAQ tags. (**C**) Activation of EHHADH in cells expose to deacetylase inhibitors. Data in this panel and subsequent figures are from triplicate experiments. (**D**) Fatty acid induced EHHADH acetylation and activity. Acetylation and activity of EHHDH ectopically expressed in HEK293T cells were monitored. (**E**) MDH acetylation. MDH-Myc was expressed in HEK293T cells and acetylation was determined by immunoblotting. (**F**) Quantitative MS analysis of MDH. FLAG tagged MDH was overexpressed in HEK293T cells and purified by immunoprecipitation. Eluted intact MDH proteins were analyzed by FTICR MS. (**G**) Glucose enhances MDH acetylation. (**H**) Activation of MDH by acetylation. The activity of endogenous and ectopically expressed MDH from Chang and HEK293T cells, respectively, were assayed and normalized against actin. (**I**) Inactivation of MDH by in vitro deacetylation. Immunoprecipitated MDH was incubated with or without CobB deacetylase and activity was assayed. NAD, an essential cofactor for CobB, was omitted as a negative control. (**J**) Activation of MDH by glucose. Experiments were similar to (H) except cells were treated with glucose.

(Fig. 2F). When cells were treated with TSA and NAM, MDH acetylation was increased from 26.9% to 67.4% with the appearance of tri- and tetraacetylated forms. Subsequent MS/MS analysis confirmed three of four previously identified acetylation sites (fig. S2F and table S1). These data indicate that acetylation is the predominant form of modification and that a substantial fraction of MDH can be acetylated in the cell.

Exposure of cells to high concentrations of glucose enhanced MDH acetylation by 60% (Fig. 2G and fig. S2G). Inhibition of deacetylase doubled endogenous MDH activity in Chang liver cells (Fig. 2H). Consistently, treatment with TSA and NAM activated the wild-type MDH but not the MDH^{4KR} mutant, in which the four acetylation lysine residues were replaced with arginine, in transfected HEK293T cells (Fig. 2H). Furthermore, in vitro deacetylation of immunopurified MDH by CobB deacetylase decreased MDH1 activity (Fig. 2I), indicating that acetylation directly activates MDH. Moreover, high glucose concentrations stimulated enzyme activity of both endogenous and ectopically expressed MDH but had little effect on the MDH^{4KR} mutant (Fig. 2J). These observations indicate that glucose-induced activation of MDH is mediated at least in part through acetylation.

The urea cycle is indispensable for detoxification of ammonium, a product of amino acid catabolism. Mutations in argininosuccinate lyase (ASL; EC code 4.3.2.1) cause argininosuccinic aciduria, the second most common neonatal disorder due to urea cycle malfunction in humans (*7*). We identified two acetylated peptides in ASL—Lys^{69} and Lys^{288} (Fig. 1F and table S2)—and confirmed the acetylation of ectopically expressed ASL (Fig. 3A and fig. S3A). Western blotting with an antibody to acetylated Lys^{288} showed a factor of 2.8 increase of ASL Lys^{288} acetylation in cells treated with TSA and NAM (Fig. 3B and fig. S3B). Addition of extra amino acids decreased both total and Lys^{288} acetylation (Fig. 3C and fig. S3C). An enzymatic assay showed that ASL activity decreased in cells treated with TSA and NAM treatment but increased in cells exposed to amino acids, supporting an inhibitory effect of acetylation on ASL activity (Fig. 3, D and E). The activity of the Lys^{288} → Arg mutant ASL^{K288R} was refractory to inhibition by TSA and NAM (Fig. 3D) or activation by amino acids (Fig. 3E). The ASL^{K288R} mutation did not alter global protein structure, as determined by limited proteolysis and circular dichroism analyses (fig. S3, D and E). Therefore, extra amino acids appear to activate ASL by decreasing acetylation of Lys^{288}.

The urea cycle is coupled with the TCA cycle because fumarate generated from the urea cycle can be fed into the TCA cycle for energy production or gluconeogenesis (*8*). We therefore determined the effect of glucose on ASL activity and acetylation. Glucose increased acetylation of ASL by a factor of 2.7 (Fig. 3F and fig. S3F) and decreased activity of ASL by 50% (Fig. 3G). In vitro incubation of ASL immunopurified from

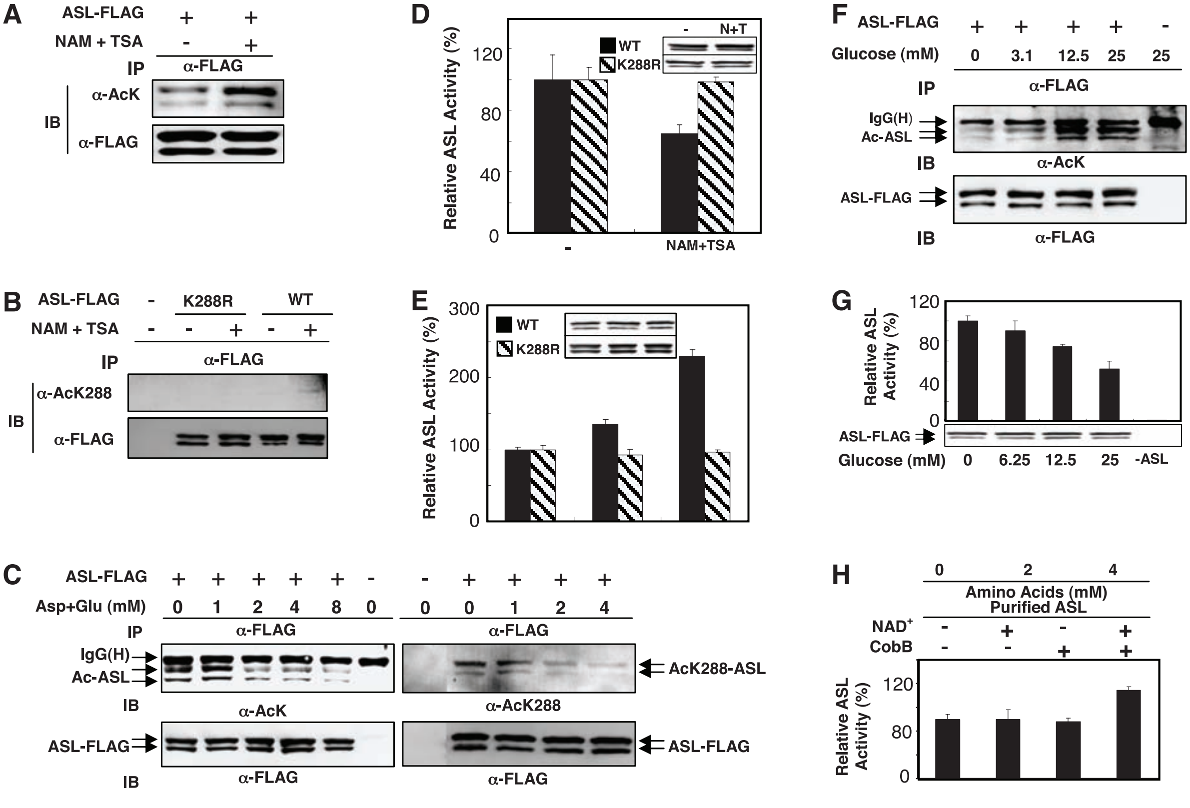


Fig. 3. Inactivation of ASL by acetylation. (**A** and **B**) ASL acetylation. FLAG-tagged ASL or ASL^{K288R} was overexpressed in HEK293T cells, immunoprecipitated, and probed with antibody to acetyllysine (A) or to acetyl-Lys^{288} (B). (**C**) Inhibition of ASL acetylation by extra amino acids. ASL was immunoprecipitated from transfected HEK293T cells, which were treated with various amino acid concentrations. (**D**) Inhibition of ASL in response to NAM and TSA. Wild-type and mutant ASL-K288R (132% of wild-type activity) proteins were expressed in HEK293T cells that were treated with NAM and TSA as indicated. Activity of immunoprecipitated ASL was normalized to total protein. (**E**) Requirement of Lys^{288} acetylation for ASL activation by amino acids. Wild-type and mutant ASL proteins were overexpressed in HEK293T cells incubated in medium containing various amino acid concentrations. (**F** and **G**) Effects of glucose on acetylation and activity of ASL. ASL was overexpressed in HEK293T cells that were treated with various concentrations of glucose. Acetylation and activity of immunoprecipitated ASL were determined. (**H**) Activation of ASL by in vitro deacetylation. In vitro deacetylation was similar to Fig. 2I.

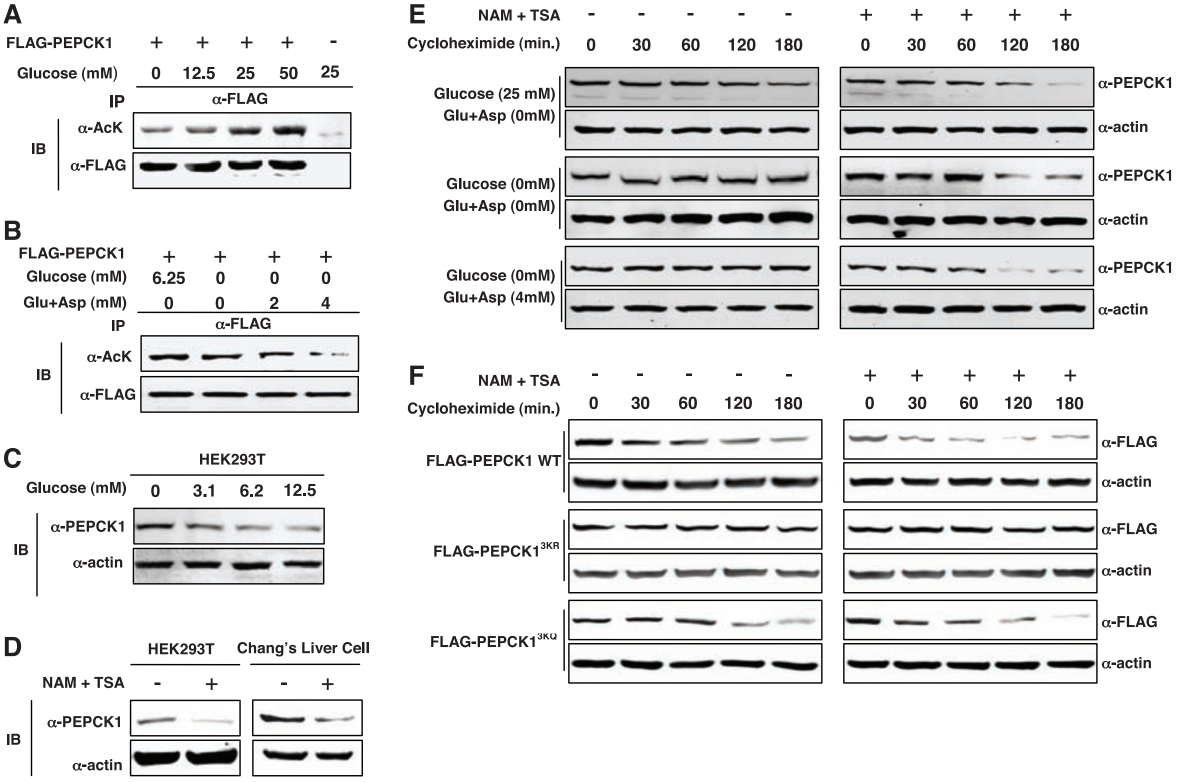


Fig. 4. Destabilization of PEPCK1 by acetylation. (**A**) Glucose induces PEPCK1 acetylation. (**B**) Amino acids decrease PEPCK1 acetylation. (**C**) Glucose induces depletion in of PEPCK1 protein. Endogenous PEPCK levels were detected with a PEPCK1 antibody. (**D**) TSA and NAM reduce PEPCK1 protein abundance. (**E**) Glucose destabilizes PEPCK1. Cycloheximide was added at time zero to block translation in HEK293 cells. PEPCK1 protein abundance was determined by Western blotting. (**F**) Inhibition of deacetylases destabilizes the wild type but not the acetylation-defective mutant PEPCK1.

mammalian cells with CobB deacetylase increased ASL activity (Fig. 3H), supporting a direct role of acetylation in ASL inactivation. The dual regulation of ASL by both amino acids and glucose indicates that acetylation may have an important role in the coordination of metabolic pathways. In the presence of sufficient glucose, amino acid catabolism for energy production and gluconeogenesis would be inhibited. In the presence of abundant amino acids and low glucose, cells would switch to using amino acids for energy production with enhanced urea cycle activity. Cells may use acetylation to coordinate multiple pathways in order to achieve these metabolic adaptations

Phosphoenolpyruvate carboxykinase 1 (PEPCK1; EC code 4.1.1.32) is a key regulatory enzyme in gluconeogenesis (Fig. 1D) (*9*, *10*). Three acetylated lysine residues were identified in PEPCK1 by MS analysis (Lys^{70}, Lys^{71}, and Lys^{594}; table S2). Acetylation of PEPCK1 was enhanced in cells treated with high concentrations of glucose (Fig. 4A) but was decreased by addition of amino acids in glucose-free medium (Fig. 4B). These results suggest a potential mechanism by which cells could regulate gluconeogenesis through regulating acetylation of PEPCK1 in response to the availability of extracellular fuels.

In searching for an effect of acetylation on the regulation of PEPCK1, we noticed that levels of endogenous PEPCK1 protein were decreased by high glucose (Fig. 4C). Furthermore, treatment with TSA and NAM caused a 70% reduction in the amount of PEPCK1 protein in both HEK293T and Chang liver cells (Fig. 4D). PEPCK1 was stable in cells in glucose-free medium but unstable in high-glucose medium (Fig. 4E). When cells were treated with TSA and NAM, PEPCK1 was unstable even in glucose-free medium or in the presence of amino acids. These results indicate that acetylation may regulate the stability of PEPCK1. We replaced the three putative acetylation lysine residues by arginine (PEPCK1^{3KR}) or glutamine (PEPCK1^{3KQ}) to abolish or mimic acetylation, respectively. The PEPCK1^{3KR} mutant was more stable than the wild type, whereas the PEPCK1^{3KQ} mutant remained unstable (Fig. 4F). Moreover, treatment of cells with TSA and NAM failed to destabilize the PEPCK1^{3KR} mutant.

The importance of lysine acetylation in the regulation of chromatin dynamics and gene expression is well appreciated. Our study and others extend the scope of cell regulation by lysine acetylation to an extent comparable to that of other major posttranslational modifications such as phosphorylation and ubiquitination. We show that most intermediate metabolic enzymes are acetylated and that acetylation can directly affect the enzyme activity or stability. We found that acetylation of metabolic enzymes changed in response to the alterations of extracellular nutrient availability, providing evidence for a physiological role of dynamic acetylation in metabolic regulation. The mechanism of acetylation in regulating metabolism may be conserved during evolution. Many metabolic enzymes in *Escherichia coli* are acetylated, although the functional importance of these acetylations has not been investigated (*11*). We propose that lysine acetylation is an evolutionarily conserved mechanism involved in regulation of metabolism in response to nutrient availability and cellular metabolic status. Acetylation may play a key role in the coordination of different metabolic pathways in response to extracellular conditions.

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Acetylation of Metabolic Enzymes Coordinates Carbon Source Utilization and Metabolic Flux

Qijun Wang,[1] Yakun Zhang,[2] Chen Yang,[3] Hui Xiong,[1,2] Yan Lin,[4] Jun Yao,[4] Hong Li,[3] Lu Xie,[3] Wei Zhao,[3] Yufeng Yao,[5] Zhi-Bin Ning,[3] Rong Zeng,[3] Yue Xiong,[4,6] Kun-Liang Guan,[4,7] Shimin Zhao,[1,4]* Guo-Ping Zhao[1,2,3,8]*

Lysine acetylation regulates many eukaryotic cellular processes, but its function in prokaryotes is largely unknown. We demonstrated that central metabolism enzymes in *Salmonella* were acetylated extensively and differentially in response to different carbon sources, concomitantly with changes in cell growth and metabolic flux. The relative activities of key enzymes controlling the direction of glycolysis versus gluconeogenesis and the branching between citrate cycle and glyoxylate bypass were all regulated by acetylation. This modulation is mainly controlled by a pair of lysine acetyltransferase and deacetylase, whose expressions are coordinated with growth status. Reversible acetylation of metabolic enzymes ensure that cells respond environmental changes via promptly sensing cellular energy status and flexibly altering reaction rates or directions. It represents a metabolic regulatory mechanism conserved from bacteria to mammals.

Protein lysine acetylation regulates wide range of cellular functions in eukaryotes, especially transcriptional control in the nucleus (*1*, *2*). It also plays an extensive role in regulation of metabolic enzymes through various mechanisms in human liver (*3*). In prokaryotes such as *Salmonella enterica*, reversible lysine acetylation is known to regulate the activity of acetyl–coenzyme A (CoA) synthetase (*4*). To determine how lysine acetylation globally regulates the metabolism in prokaryotes, we determined the overall acetylation status of *S. enterica* proteins under either fermentable glucose-based glycolysis or under oxidative citrate-based gluconeogenesis. By immunopurification of acetylated peptides with antibody to acetyllysine and peptide identification

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[1] State Key Laboratory of Genetic Engineering, Department of Microbiology, School of Life Sciences and Institute of Biomedical Sciences, Fudan University, Shanghai 200032, China. [2] MOST-Shanghai Laboratory of Disease and Health Genomics, Chinese National Human Genome Center at Shanghai, Shanghai 201203, China. [3] Key Laboratory of Synthetic Biology, Bioinformatics Center and Laboratory of Systems Biology, Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 200032, China. [4] Molecular Cell Biology Laboratory, Institute of Biomedical Sciences, Fudan University, Shanghai 200032, China. [5] Laboratory of Human Bacterial Pathogenesis, Department of Medical Microbiology and Parasitology, Institute of Medical Sciences, Shanghai Jiao Tong University School of Medicine, Shanghai 200025, China. [6] Department of Biochemistry and Biophysics and Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA. [7] Department of Pharmacology and Moores Cancer Center, University of California San Diego, La Jolla, CA 92093, USA. [8] Department of Microbiology and Li Ka Shing Institute of Health Sciences, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, New Territories, Hong Kong SAR, China.

*To whom correspondence should be addressed. E-mail: zhaosm@fudan.edu.cn (S.Z.); gpzhao@sibs.ac.cn (G.-P.Z.)

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Supporting Online Material for

Regulation of Cellular Metabolism by Protein Lysine Acetylation

Shimin Zhao, Wei Xu, Wenqing Jiang, Wei Yu, Yan Lin, Tengfei Zhang, Jun Yao, Li Zhou,
Yaxue Zeng, Hong Li, Yixue Li, Jiong Shi, Wenlin An, Susan M. Hancock, Fuchu He, Lunxiu Qin,
Jason Chin, Pengyuan Yang, Xian Chen, Qunying Lei, Yue Xiong,* Kun-Liang Guan*

*To whom correspondence should be addressed. E-mail: yxiong@email.unc.edu (Y.X.); kuguan@ucsd.edu (K.L.G.)

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Supporting online material (SOM)

Materials and Methods

Proteomic Procedures

Liver tissues were obtained freshly from cancer surgery in Zhongshan Hospital, Fudan University, with consent of patients. Hepatocellular carcinoma tissue was obtained within 2 hours of patient's operation; tumor tissue was isolated by completely removal of surrounding normal liver tissue on ice and the surrounding liver tissue was used as normal tissue. Two grams of normal tissues were subjected to further treatments as described below. The experiments were repeated with samples from three individual patients.

Fractionation and protein extraction from human liver samples

1. Samples were diced to around 1 mm particles and suspended in 10ml ice cold (4°C) PBS buffer (pH 7.5) supplemented with protease inhibitors (SIGMA) as well as deacetylase inhibitors (10μM TSA, 10 mM nicotinamide and 50 mM butyric acid). Cells were broken by Dounce homogenizer with 20 strokes on ice.
2. Homogenized samples were centrifuged at 2000g for 20 minutes at 4°C in horizontal buckets with Eppendorf 5180 centrifuge; pellet and supernatant were separated and subjected to further treatments.

3. Pellet was re-suspended in 10 ml PBS supplemented with deacetylase inhibitors as described above, the suspension were sonicated on ice for 10 minutes with Sonics Ultra Cell ultrasonic apparatus at energy of 50 watts. The resulting suspension was centrifuged at 20,000g in Beckman Avanti J 25 centrifuge for 60 minutes. Supernatant, which should contain the majority of nuclear proteins, was kept and the pellet was discarded.
4. Supernatant from step 2 was centrifuged at 10,000g for 60 minutes in Beckman Avanti J 25 centrifuge, the supernatant and pellet were separated by carefully removal of supernatant with pipette, both fractions were kept for further treatments;
5. Pellet from step 4 was washed by re-suspending in PBS supplemented with deacetylase inhibitors and centrifugation. The pellet was re-suspended in 5ml mitochondria lysis buffer (IMGENX) supplemented with deacetylase inhibitors. After sonicated for 5 minutes on ice, the resulting solution was centrifuged at 20,000g for 60 minutes , the supernatant, which containing mitochondrial proteins, was kept and the pellet was discarded.
6. The supernatant fraction of step 4 is subject to ultracentrifugation at 100,000g for 120 minutes; both supernatant and precipitate were subjected to further treatments.
7. Proteins in supernatant from Step3, 5 and 6 were each precipitated with 80% ice cold acetone. Protein pellet was collected by centrifugation and washed with ice cold 80% acetone one time. Pellet from step 6 contains mainly containing membrane proteins, was washed with 80% ice cold acetone. All acetone precipitated proteins were vacuum dried.

Digestion, peptide enrichment and MS analysis

1. Dried protein pellets were reconstituted in 100 mM ammonium bicarbonate and protein concentrations was determined by BioRad protein assay solution. Proteins were digested with trypsin overnight with gentle shaking at 37°C with a trypsin/protein ratio of 1/50. After overnight digestion, additional trypsin was added to the digestion mixture with a trypsin/protein ratio of 1/500 and incubated at 37°C for another 3-4 hours. The trypsin in the digestion reaction was inactivated by heating at 99 ^{0}C for 5 minutes. The solution was cleared by centrifuge at 10,000 g on desktop centrifuge, solution was vacuum dried two times to remove bicarbonate salts.
2. Anti-acetyllysine antibody was conjugated to protein A beads (Upstate) by mixing 100 μl antiserum (home made) with 50 μl protein A beads in 500 μl pH 7.5 PBS. Conjugated beads were washed by pH 7.5 PBS three times after the conjugation was carried out at 4°C for 3 hours with gentle shaking.
3. Trypsin digested peptide mixture from step 1 was reconstituted in NETN buffer (50 mM Tris [pH 8.0], 100 mM NaCl, 1 mM EDTA, 0.5% NP40). Conjugated antibody was added to the solution and incubated at 4°C for 3-5 hours. Supernatant was removed by carefully washing beads by ETN (50 mM Tris [pH 8.0], 100 mM NaCl, 1 mM EDTA) buffer three times.
4. The bound peptides were eluted by 0.1% trifluoroacetic acid.
5. The resulting peptides were assayed by continuously separated by SCX followed by C18 columns (Dionex) before being subjected to MS/MS analysis in an LTQ-Orbitrap

mass spectrometer (Thermo Electron, Bremen, Germany).

6. The MS data were initially searched against the NCBI database with the aid of the Sequest search engine. Searches for acetylated peptides were done against human proteins database. Two searching approaches were taken: either only single charged fragments were allowed in searching or both single charged and multiple charged fragments were allowed in searching. To collect positive hits, the following selection thresholds were applied: mass accuracy: 5ppm, delta cn: 0.1, primary score: 200, rsp: 5. Those peptides having scores (XC) above 1.5, 2.0 and 2.5 for ion charges at +1, +2 and +3 and higher were automatically selected as positives identification. Peptides with marginal scores were under manual spectra examination to be included in the positive list. The data from three experiments were combined.

Cell culture and transient transfection. HEK293, HEK293T, and Chang's liver cells were cultured in DMEM media supplemented with 10% new born bovine serum (Biochrom Germany). Plasmid transfection was carried out either by calcium phosphate method for HEK293 and HEK293T or Lipofectamine 2000 (Invitrogen) for Chang's liver cell.

Cell treatments. Tricostatin A treatment was carried out by adding 10 μM TSA to the culture medium 16-20 hours before harvest cells, Nicotinamide treatment was carried out by adding 5-10 mM nicotinamide to the culture medium 4-8 hours before harvest cells. Glucose only medium was prepared with DMEM base (SIGMA) and supplemented with glucose to concentrations as indicated; amino acids only medium was prepared with DMEM base and supplemented equal molar of glutamate and aspartate (SIGMA) at total concentrations as indicated; fatty acids only medium was prepared with DMEM base and supplemented with equal molar of linoleic acid and palmitic acid (SIGMA) at total concentrations as indicated.

Antibody generation. To generate pan-Acetyl-Lysine antibody, Chicken Ovalbumin was acetylated by reported method (*1*). Purified acetylated OVA was used to immunize rabbits. Antiserum was collected after four doses of immunization. To generate ASL site specific antibody, synthesized peptide CSTGSSLMPQKK$^{(Ac)}$N (GL Biochem) was coupled to KLH as antigen to immunize rabbit. Antiserum was collected after four doses of immunization.

Immunoprecipitation and Western Blotting. Cells were lysed in NP-40 buffer containing protease inhibitor cocktail (Roche). Immunoprecipitation was carried out either by incubating FLAG/Myc beads at 4°C with lysate for 3-4 hours or by incubate appropriate antibody with cell lysate for 2-3 hours, followed by incubating Protein-A beads (Upstate). Standard Western Blotting procedures were followed for protein and tags analysis. For acetylation Western Blotting, 50 mM Tris (pH 7.5) with 10% (V/V) Tween-20 and 1% peptone (AMRESCO) was used for blocking and 50 mM Tris (pH 7.5) with 0.1% peptone was used to prepare primary and secondary antibodies.

Endogenous enzyme assay was carried out by substrate depletion approaches (*2*). In principle, substrates for a given enzyme in cell lysate were depleted by adding excessive amount of all other substrates except one of them. After the reaction reached equilibrium, the left out substrate is added and endogenous enzyme activity was determined.

Purified enzyme assays

Enoyl-Coenzyme A hydratase/3-hydroxyacyl-Coenzyme A dehydrogenase assay was measured from the direction of consuming NADH (*3*). Reaction mixture consists of 20 mM Tris-chloride buffer (pH 7.0); 0.5 mM acetoacetyl CoA; 10 μM NADH and immuno-precipitation purified enzymes. Total reaction volume was 0.4 ml. Reactions were initiated by addition of enzyme and were assayed at 25°C. The reaction was monitored by the decrease in fluorescence (Ex. 350nm, Em.470nm, HITACH F-4600 fluorescence spectrophotometer) of NADH.

Malate dehydrogenase assay (*4*) reagents included 0.2 mM oxaloacetate, 0.1 mM NADH and immuno-precipitation purified human malate dehydrogenase overexpressed from HEK293T cells. The reaction was carried out in PBS buffer (pH 7.4) with total volume of 400µl. The reaction was started by adding enzyme into the reaction mixture; velocity is determined by measuring the decrease in fluorescence of NADH (Ex. 350nm, Em.470nm) with a HITACH F-4600 fluorescence spectrophotometer.

Argininosuccinate lyase assay. The assay protocol was adapted from previous publication (*5*). Argininosuccinate lyase activity was assayed at 25°C. The consumption of fumarate in the forward direction was assayed by monitoring absorbance changes at 240 nm (absorbance of fumarate) in an Amersham Biosciences Ultrospec p3100 pro spectrophotometer. In a standard assay for the forward reaction, the reaction mixture contained 50 mM Tris/HCl buffer, pH 7.5, 0.2 mM fumarate, 1 mM arginine and immuno-precipitated argininosuccinate lyase in a total volume of 0.3 ml.

Enzyme concentration determination. Protein concentrations were determined by Bradford method using Biorad reagents. Relative enzyme concentrations for immuno-procipitated enzymes were quantified by measuring the band intensity of western blots by using Amersham Bisciences ImageQuant TL 2005v software.

iTRAQ quantification:

Peptide preparation: FLAG-EHHADH protein was expressed from 293T cells treated with or without NAM+ TSA. Protein was purified by FLAG IP and resolved on 10% SDS PAGE and stained by coomassie blue. The amount of protein was estimated by band intensity. Protein bands were sliced and dye was removed by soaking in 50 mM NH_4HCO_3 with 50% acetonitrile. The resulted gel slice was soaked in 100 μl water to remove salts followed by soaking in acetonitrile to remove water. The gel slice was then dried in 37^{0}C incubator and was digested in 100 μl 50 mM

$(NH_4)HCO_3$ with trypsin (trypsin:protein at 1:30) and incubated at 37°C overnight. The resulted peptides were extracted by a solution containing 50% acetonitrile and 0.1% trifluoroacetic acid (TFA) followed by vacuum dry.

Synthesize of internal control peptides: two pairs of peptides, shown in Fig. 2B, corresponding to the acetylated and unacetylated peptide pairs in EHHADH, were synthesized and purified to >99% purity.

Labeling of samples: samples and internal control peptides were labeled by iTRAQ labeling reagents (ABI, Foster City, CA 94404 USA) as indicated in the table:

Sample	Labeling reagent
EHHADH+(TSA+NAM)	Reagents 114
EHHADH	Reagents 116
Internal control peptides	Reagents 117

MS analysis and data process: equal amount (5 nmole, equal molar ratio) of 114,116 and 117 labeled samples were mixed and subjected to LTQ-OrbiTrap (Thermal) analysis under PQD mode. The resulted MS spectra were used to determine the peptide identity and abundance of each peptide in the same spectrum. Relative abundance of a peptide was calculated by comparing the intensity of the corresponding tag. The absolute quantification was calculated by comparing to the internal control peptides. The sum of the acetylated and unacetylated peptide for each pair was set as 100%. Relative abundance of acetylated peptide and unacetylated peptide in HDAC inhibitor treated and untreated EHHADH are shown in

Fig. 2B.

μESI-FTICR-MS Analysis

MDH tagged with 3 copied of FLAG epitope (MDH-3xFLAG) was expressed in HEK293T cells and immunopurified using FLAG antibody (M2, Sigma) and eluted by a low pH glycine buffer. A small portion of eluted samples were examined by both silver staining and western blotting using anti-FLAG antibody. Eluted samples were then analyzed by a top-down approach on a FTICR mass analyzer.

MS spectra were acquired on a hybrid Qe-Fourier Transform Ion Cyclotron Resonance (FTICR) – Mass Spectrometer, equipped with an Apollo II microelectrospray (μESI) source and a 12.0-T actively shielded magnet (Apex Qe-FTICR-MS, 12.0 T AS, Bruker Daltonics, Billerica, MA, USA). The voltages on μESI sprayer, interface plate, heated capillary exit, deflector, ion funnel and skimmer were set at +4.2 kV, +3.6 kV, +320 V, +310 V, +175 V and +25 V, respectively. The temperature of the μESI source was maintained at 180°C. Desolvation was carried out by using a nebulization gas flow (1.5 bar) and a countercurrent drying gas flow (4.0 L second^{-1}). MDH2 samples were prepared by suspending the lyophilized proteins in a mixture of acetonitrile/water/acetic acid (89.0:9.0:2.0 v/v/v) at a concentrations of ~ 0.1 μg μL^{-1}, directly infused with a syringe pump (Harvard Apparatus, Holliston, MA, USA) and a 250-μL syringe (Hamilton, Reno, NV, USA), and electrosprayed at an infusion flow rate of 90 μL hour^{-1}. Before transfer, ion packets were accumulated inside the collision cell in a duration of 1.0 second. 100 MS scans per spectrum were acquired in the ICR cell with a resolution of 580,000 at m/z 400 Da.

Abbreviations for Figure 1.

ACAT, acetyl-CoA acyltransferase; ACC, acetyl-CoA carboxylase; ACD, acyl-CoA dehydrogenase; ACO, aconitase; ACS, acyl-CoA synthetase; ALDB, aldolase B; ARG1, arginase 1; ASL, argininosuccinate lyase; ASS, argino-succinate synthetase; AST, aspartate transaminase; CAT, carnitine acetyltransferase; CPS, carbamoyl phosphate synthase; CPT, carnitine palmitoyltransferase; CS, citrate synthase; ECI,2,4-DCR, enoyl-CoA isomerase,2,4-dienoyl CoA reductase; EHHADH, enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase; FAS, fatty acid synthase; FBPase, fructose-1,6-bisphosphatase; FH, fumarate hydratase; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GDH, glutamate dehydrogenase; G-6-Pase, glucose-6-phosphatase; GPI, phosphohexose isomerase; GP, glycogen phosphorylase; GS, glycogen synthase; HK, hexokinase; IDH, isocitrate dehydrogenase; LDH, lactate dehydrogenase; MDH, malate dehydrogenase; MMCM, methyl-malonyl-CoA mutase; OTC, ornithine carbamoyltransferase; PC, pyruvate carboxylase; PCC, propionyl-CoA carboxylase; PDH, pyruvate dehydrogenase; PEPCK1, phosphoenolpyruvate carboxykinase 1; PFK-1, phosphofructokinase-1; PGK, phosphoglycerate kinase; PGM, phosphoglycerate mutase; PK, pyruvate kinase; SDH, succinate dehydrogenase; TPI, triose phosphate isomerase; UDP-GP, UDP-glucose pyrophosphorylase; α-KGDH, α-ketoglutarate dehydrogenase; β-HADH, β-hydroxyacyl-CoA dehydrogenase.

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Supplementary table S1. Identification of acetylated proteins in human liver. Acetylated peptides identified through only single charged fragments search and through both single charged and multiple charged fragments search are indicated. Green color marks proteins that are reported to be acetylated by proteomic study done with mouse liver samples. Red color marks acetylated proteins that have been previously studied and most are nuclear proteins. Although the cytoplasmic and mitochondrial fractions were analyzed, nuclear proteins were also found in our ms analysis, indicating some contaminations during the subcellular fractionation.

S. Table 1

Accessior	Reference	Representative Peptide	Only Z+1 Allowed	Multiple Charged Fragments Allowec
31662	GATA-3	K.MSSK*SK.K	√	
112983	Aspartate aminotransferase, mitochondrial	R.VESQLK*ILIR.P	√	
119576	similar to Liver carboxylesterase	K.AVEK*PPQTEHIEL.-	√	
126041	L-lactate dehydrogenase B chain	K.SADTLWDIQK*DLK.D	√	
134517	v-ski sarcoma viral oncogene homolog	K.YK*RRVPRVSSEPPASIRPK*TDDTSSQSPAPSE.K	√	
417811	Single-stranded DNA-binding protein, mitochondrial	K.KGSRIYLEGK*IDYGEYMDK.N	√	
545396	neuronal voltage-dependent calcium channel alpha 2d	-.QPK*EPVTLDFLDAELENDIK.V	√	
585079	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	K.LGILDK*VVNSDPVEEAIR.F	√	
1346355	6-phosphofructokinase type C	K.KQTDFEHRIPK*EQWWLK.L	√	
1707896	GTP-binding protein GEM	R.KARRFWGKIVAK*NNK*NMAFK.L	√	
1709683	PMS1 protein homolog 1	R.QLPMYLSK*EDIQDIIYRMK*HQFGNEIK.E	√	
1710488	60S ribosomal protein L14	K.KAPAQKVPAQKATGQK*AAPAPK*AQK*GQK.A	√	
1717972	Glycogen [starch] synthase, liver	K.SPFSLSHVPHGK*K*K*LGHEYK.N	√	
1872205	v-myb myeloblastosis viral oncogene homolog	R.TPTPFK*HALAAQEIK.Y	√	
2370178	P73	R.EQQALNESSAK*NGAASK*R.A	√	
2492935	Arginase-2, mitochondrial	K.GVEHGPAAIREAGLMK*R.L	√	
2498147	apical protein of Xenopus-like	K.K*K*APSSPPPPPPPLR.S	√	
3024341	Histone acetyltransferase p300	K.TSK*NK.S	√	
3041717	Glycogen phosphorylase, muscle form	R.DVAK*VKQENKLKFAAYLER.E	√	
3068761	NF-E2, MafG subunit	R.GYAASCRIK*R.V	√	
3980293	Flap endonuclease-1	K.VTGSLSSAK*R.K	√	
4501859	acyl-Coenzyme A dehydrogenase, short/branched chain	K.VPEANILGQIGHGYK*YAIGSLNEGR.I	√	
4501883	alpha 2 actin	R.HQGVMVGMGQK*DSYVGDEAQSK.R	√	
4501935	class II alcohol dehydrogenase 4 pi subunit	R.DLHK*PIQEVIIELTK.G	√	
4502009	aryl hydrocarbon receptor interacting protein	R.GKPMELIIGK*K.F	√	
4502027	albumin	K.AEFAEVSK*LVTDLTK.V	√	
4502081	amphiphysin isoform 1	-.MADIK*TGIFAKNVQK*R.L	√	
4502099	solute carrier family 25, member 5	K.AFFK*GAWSNVLR.G	√	
4502303	ATP synthase O subunit, mitochondrial	K.LEQVEK*ELLR.V	√	
4502407	betaine-homocysteine methyltransferase	R.IASGRPYNPSMSK*PDGWGVTK.G	√	
4502441	BCL2/adenovirus E1B 19kD interacting protein 1	R.DCSGPLSALTELNTK*VK*EK.F	√	
4502451	breast cancer 2, early onset	R.ISSLPK*SEK.P	√	
4502559	calcium modulating ligand	K.SKQQDSDK*LNSLSVPSVSK*R.V	√	
4502807	chromogranin B	K.LDLK*RQYDR.V	√	
4502917	cyclic nucleotide gated channel alpha 3	R.SAWPLAK*CNTNTSNNTEEEKKTK*K*K.D	√	
4502951	collagen, type III, alpha 1 preproprotein	K.NSIAYMDQASGNVK*KALK.L	√	
4502981	cytochrome c oxidase subunit IV isoform 1	K.FK*ESFAEMNR.G	√	
4503023	carnitine palmitoyltransferase II	R.YLSAQK*PLLNDGQFR.K	√	
4503183	cytochrome b-5 isoform 2	K.VYDLTK*FLEEHPGGEEVLR.E	√	
4503231	cytochrome P450, family 3, subfamily A, polypeptide 5	K.SAISLAEDEEWK*R.I	√	
4503233	cytochrome P450, family 3, subfamily A, polypeptide 7	K.YWTEPEK*FLPER.F	√	
4503247	nucleolar protein NOP52	R.PLTSARAKAANVQEPEK*KK.K	√	
4503301	2,4-dienoyl CoA reductase 1	R.LDPTGTFEK*EMIGR.I	√	
4503327	cytochrome b5 reductase isoform 1	R.STPAITLESPDIK*YPLR.L	√	
4503433	E2F3	R.SPDSPK*TPK*SPSEK.T	√	
4503471	eukaryotic translation elongation factor 1 alpha 1	R.YEEIVK*EVSTYIK.K	√	
4503483	eukaryotic translation elongation factor 2	K.EDLYLK*PIQR.T	√	
4503529	eukaryotic translation initiation factor 4A isoform 1	R.GFK*DQIYDIFQK.L	√	
4503571	enolase 1	K.IDK*LMIEMDGTENK.S	√	
4503579	erythrocyte membrane protein band 4.1-like 2	K.EREEK*VKETQEDK*LEGGAAK*RETK.E	√	
4503583	epoxide hydrolase 1, microsomal (xenobiotic)	K.IEGLDIHFIHVK*PPQLPAGHTPK.P	√	
4503607	electron transfer flavoprotein, alpha polypeptide	K.VLVAQHDVYK*GLLPEELTPLILATQK.Q	√	
4503647	coagulation factor VIII isoform a	K.K*DTILSLNACESNHAIAAINEGQNK.P	√	
4503685	farnesyl diphosphate synthase	K.EVLEYNAIGGK*YNR.G	√	
4503925	GATA-1	R.PLIRPK*K.R	√	
4503933	glycine amidinotransferase	K.MFEK*LGITTIK.V	√	
4504067	aspartate aminotransferase 1	K.NTPVYVSSPTWENHNAVFSAAGFK*DIR.S	√	
4504175	glutathione S-transferase M2	K.PEYLQALPEMLKLYSQFLGK*QPWFLGDK.I	√	
4504183	glutathione transferase	K.YISLIYTNYEAGK*DDYVK.A	√	
4504193	TFIIB	R.K*AVELDLVPGR.S	√	
4504213	guanylate cyclase 1, soluble, alpha 3	R.DFQGK*PNFEYFEILTPK.I	√	
4504239	H2A histone family, member C	R.NDEELNK*LLGK.V	√	
4504259	H2B histone family, member C	K.K*AVTK*AQK.K	√	
4504279	H3 histone family, member C	R.K*STGGK*APR.Y	√	
4504319	H4 histone family, member L	R.GK*AGK*GLGK*GGAK.C	√	
4504327	mitochondrial trifunctional protein, beta subunit	R.TPFLLSGTSYK*DLMPHDLAR.A	√	
4504333	histidine ammonia-lyase	K.SREVIDSIIK*EK.T	√	
4504349	beta globin	K.SAVTALWGK*VNVDEVGGEALGR.L	√	
4504351	delta globin	K.VVAGVANALAHK*YH.	√	
4504503	hydroxysteroid (17-beta) dehydrogenase 2	R.LSVLQMDITK*PVQIK.D	√	
4504505	hydroxysteroid (17-beta) dehydrogenase 4	R.GALVVVNDLGGDFK*GVGK.G	√	
4504523	heat shock 10kDa protein 1 (chaperonin 10)	K.SQGK*VLQATVVAVGSGSK.G	√	
4504707	inositol polyphosphate-4-phosphatase, type II, 105	K.NSLK*MLSEKTELFVHAFK.D	√	
4504733	insulin receptor substrate 4	R.LYFCVDRGATKECKEAK*EVKDAEIPEGAAR.G	√	
4504799	isovaleryl Coenzyme A dehydrogenase	R.SNEFK*NLR.E	√	
4504919	keratin 8	K.DVDEAYMNK*VELESR.L	√	
4505101	microtubule-associated protein 7	K.HLEERK*K.R	√	
4505129	mutated in colorectal cancers	K.EEMAELK*AQLYLLEK*EK.K	√	
4505579	furin preproprotein	R.GERTAFIK*DQSAL.	√	

4505591	peroxiredoxin 1	K.ATAVMPDGQFK*DISLSDYK.G	√
4505611	PARN Poly(A)-specific ribonuclease	K.ERYIVISK*VDEEERK*RREQQK.H	√
4505749	phosphofructokinase, muscle	-.MTHEEHHAAK*TLGIGK.A	√
4505763	phosphoglycerate kinase 1	K.VADK*IQLINNMLDK.V	√
4505789	serine (or cysteine) proteinase inhibitor, clade B	K.FK*VEK*MIDPKACLENLGLK.H	√
4505799	phosphoinositide-3-kinase, class 2, alpha polypeptide	R.ALDIDVEK*LTQAELEKLLLDDSFETK.K	√
4505859	pleiomorphic adenoma gene-like 2 ,PLAGL2	K.KSHSQELLK*IK.T	√
4505917	exosome component 10 isoform 2	K.SDGEMVLPGFPDADSFVK*FALGSVVAVTK.A	√
4505939	DNA directed RNA polymerase II polypeptide A	K.LADIVK*INNQLR.R	√
4505941	DNA directed RNA polymerase II polypeptide B	R.SYK*EQESK*KGFDQEEVFEK.P	√
4506181	proteasome alpha 2 subunit	R.K*LAQQYYLVYQEPIPTAQLVQR.V	√
4506567	RNA (guanine-7-) methyltransferase	K.DKSSTGDGTQNK*RK*IALEDVPEK*QK.N	√
4506713	ubiquitin and ribosomal protein S27a	-.MQIFVK*TLTGK.T	√
4506891	SET translocation (myeloid leukemia-associated)	K.K*ELNSNHDGADETSEK.E	√
4506977	solute carrier family 12, member 3 isoform 1	K.NPEEPVRFGWVK*.G	√
4507149	superoxide dismutase 1, soluble	R.TLVVHEK*ADDLGKGGNEESTK.T	√
4507229	aldehyde dehydrogenase 5A1 , isoform 2	K.WYNLMIQNK*DDLAR.I	√
4507363	TAL1/SCL	K.K*LSK*NEILR.L	√
4507411	treacle; Treacher Collins-Franceschetti syndrome	K.GSLGSQGAK*DEPEEELQK.G	√
4507621	troponin I, skeletal, fast; Troponin I, fast-twit	R.MSADAMLK*ALLGSK.H	√
4507645	triosephosphate isomerase 1	K.ELASQPDVDGFLVGGASLK*PEFVDIINAK.Q	√
4507659	nuclear pore complex-associated protein TPR	K.K*TETMNVVMETNK*MLR.E	√
4507879	voltage-dependent anion channel 1	K.GYGFGLIK*LDLK.T	√
4508005	tripartite motif-containing 26	R.EFQGK*LLRDLEYK.T	√
4557014	catalase	R.LCENIAGHLK*DAQIFIQKK.A	√
4557233	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	R.MAFGAPLTK*LQVIQFK.L	√
4557237	acetyl-Coenzyme A acetyltransferase 1	R.GSTPYGGVK*LEDLIVK.D	√
4557255	adenylate cyclase 7	R.VHITEATLK*HLDK*AYEVEDGHGQQR.D	√
4557349	BRCA1 associated RING domain 1	R.NLLHDNELSDLK*EDK.P	√
4557587	fumarylacetoacetate hydrolase (fumarylacetoacetase)	R.DIQK*WEYVPLGPFLGK.S	√
4557607	gamma-aminobutyric acid A receptor, alpha 6	K.FGSYAYPK*SEIIYTWK.K	√
4557735	monoamine oxidase A	R.TIDNMGK*EIPTDAPWEAQHADK.W	√
4557767	Methyl-malonyl-CoA Mutase	R.LWAHLIEK*MFQPK.N	√
4757862	biphenyl hydrolase-like	K.DAVDLMK*ALK.F	√
4758010	clock	R.DDSSIFDGLVEEDDK*DKAKRVSRNK*SEK.K	√
4758050	carnitine palmitoyltransferase 1B isoform a	K.GRFFK*LWLYEGAR.L	√
4758056	CREB binding protein isoform a	K.TVEVKPGMK*SR.F	√
4758484	glutathione-S-transferase omega 1	K.EFTK*LEEVLTNK.K	√
4758554	homeobox C6 isoform 1	K.K*ESNLTSTLSGGGGGATADSLGGK*EEK.R	√
4758648	kinesin family member 5B	K.ATDQEK*SRK*LHELTVMQDR.R	√
4758696	mitogen-activated protein kinase kinase kinase 13	K.ELIK*REQAVEK.K	√
4758950	peptidylprolyl isomerase B	K.HVVFGK*VLEGMEVVR.K	√
4759080	succinate dehydrogenase complex, subunit A, flavoprotein	K.VPPIKPNAGEESVMNLDK*LR.F	√
4826702	desmocollin 1 isoform Dsc1b preproprotein	R.HGLVATHMLTVRVCDCSTPSECRMK*DK.S	√
4826838	ATP-binding cassette, sub-family C, member 1	K.SK*DNRIK*LMNEILNGIK.V	√
4827008	solute carrier family 15 (oligopeptide transporter), member 1	R.HTLLVWAPNHYQVVK*.D	√
4885079	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isof	R.THSDQFLVAFK*EVGR.K	√
4885281	glutamate dehydrogenase 1	R.ISGASEK*DIVHSGLAYTMER.S	√
4885373	Histone cluster 1, H1a	K.K*PAKAAAASK.K	√
4885399	structural maintenance of chromosomes 3	R.VIGAK*K*DQYFLDK.K	√
4885413	histidine triad nucleotide binding protein 1	R.PGGDTIFGK*IIR.K	√
4885417	huntingtin interacting protein 2; ubiquitin carrier	R.EFK*EVLKSEETSK.N	√
4885615	signal transducer and activator of transcription 2	R.KFNILTSNQK*TLTPEK.G	√
4885649	SUMO-1 activating enzyme subunit 2	R.ASNEDGDIK*RISTK*EWAKSTGYDPVKLFTK.L	√
5031751	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	K.YNNVEAGK*YTVGLGQTR.M	√
5031857	lactate dehydrogenase A	K.DQLIYNLLK*EEQTPQNK.I	√
5031931	nascent-polypeptide-associated complex alpha polypeptide	K.IEDLSQQAQLAAAEK*FK.V	√
5032169	telomeric repeat binding factor 2	K.NK*EFEK*ASK.I	√
17980447	unknown protein	K.K*ENFRPISLMNIDAK*ILNK.I	√
5174387	prominin 1	K.FLQK*AYESKIDYDK.P	√
5174429	acetyl-coenzyme A acyltransferase 2	K.RTPFGAYGGLLK*DFTATDLSEFAAK.A	√
5174457	kinetochore associated 2	K.IKEAEEEDEK*CASELESLEKHK.H	√
5453559	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform a	K.YTAQVDAEEK*EDVK.S	√
5453573	brefeldin A-inhibited guanine nucleotide-exchange protein 1	R.ALEK*ILADK*EVK*R.P	√
5453758	nebulette sarcomeric isoform	K.KASEMASQKQYKK*DLENEIKGK.G	√
5453974	protein kinase N2	R.FNESSQKLDLLK*YSLEQR.L	√
5454014	tripartite motif-containing 38	R.CTEQKLSTAMRITK*WKEK.V	√
5454152	ubiquinol-cytochrome c reductase binding protein	-.AGK*QAVSASGKWLDGIR.K	√
5729858	nuclear receptor coactivator 2	K.TDPASNTK*LIAMK*TEK.E	√
5729877	heat shock 70kDa protein 8 isoform 1	K.IQK*LLQDFFNGK.E	√
5729913	mannosidase, alpha, class 1A, member 2	K.AVQLAEK*LLPAFNTPTGIPWAMVNLK.S	√
5730039	SET domain and mariner transposase fusion	R.LTLETMK*MMLDK*K.Q	√
5730067	Snf2-related CBP activator protein	K.VDVEK*QMPKK.Y	√
5730112	vesicle-associated membrane protein 5 (myobrevin)	R.CQQQANEVTEIMRNNFGK*VLERGVK.L	√
5802970	AFG3 ATPase family gene 3-like 2	K.ESK*PAATTRSSGGGGGGGGKRGGKK.D	√
5802974	peroxiredoxin 3 isoform a	K.GTAVVNGEFK*DLSLDDFK.G	√
5803011	enolase 2	R.LGAEVYHTLK*GVIK*DK.Y	√
5803187	transaldolase 1	K.AAQASDLEK*IHLDEK.S	√
5821726	Era(estrogen receptor alpha)	R.MLK*HK.R	√
5901926	cleavage and polyadenylation specific factor 5	R.GVTQFGNK*YIQQTK.P	√
6005747	ring finger protein 2	R.YIK*TSGNATVDHLSK.Y	√

6005884	signal sequence receptor gamma subunit	R.K*LSEADNRKMSRK*EK.D	√
6166119	Protein diaphanous homolog 2	K.MMEDMNLNEEK*K*APLRNK*DFTTK.R	√
6166208	Hepatocyte nuclear factor 4-alpha , HNF-4	R.QCVVDK*DK.R	√
6453818	kinesin family member 22	R.LLSLDRLLASQGSQGAPLLSTPK*RER.M	√
490044	Serum albumin precursor	K.VFDEFK*PLVEEPQNLIK.Q	√
6685537	Eukaryotic translation initiation factor 3 subunit A	R.ERDRDREREGEK*EKASWRAEKDR.E	√
6715610	Isoform 1 of Tubby-related protein 1	K.EEEEEEEAATVIK*NSNQKGKAKGKGK*K.K	√
6806919	low density lipoprotein-related protein 2	R.PGK*RCAAEGSSPLLLLPDNVR.I	√
6912304	cysteine and histidine-rich domain (CHORD)-containing	R.RK*TSDFNTFLAQEGCTKGKHMWTK*K.D	√
6912352	eukaryotic translation initiation factor 2C, 1	R.GK*QFYNGIEIK.V	√
7019405	host cell factor C2	R.WLQGNNKK*APLN.	√
7242140	ClpX caseinolytic protease X homolog	K.SGSGNSGK*GGNQLRCPK.C	√
7657007	dual adaptor of phosphotyrosine and 3-phosphoinositides	K.TWK*TRWFTLHR.N	√
7657455	pescadillo homolog 1, containing BRCT domain	R.VMAGTLKLEDK*QR.L	√
7657496	RAB guanine nucleotide exchange factor (GEF) 1	K.VPPERVEKIMDQIEK*YIMTR.L	√
7657581	solute carrier family 25, member 13 (citrin)	R.DLGFFGIYK*GAK.A	√
7661786	hormone-regulated proliferation-associated 20 kDa	K.IMQEYQLEQK*DVNSLLK.Y	√
7661858	Rho GTPase activating protein 11A isoform 1	K.QQSPKDK*LNNK.L	√
7661906	hypothetical protein LOC9768 isoform 1	K.ENQIPEEAGSSGLGKAK*R.K	√
7661932	hypothetical protein LOC9816	K.KK*LELK.E	√
7662088	Rho guanine nucleotide exchange factor (GEF) 12	R.FPLKKPIRHGSILNRESPTDK*K.Q	√
7669492	glyceraldehyde-3-phosphate dehydrogenase	R.LEKPAK*YDDIKK.V	√
7705630	mitochondrial ribosomal protein S18C	K.QK*EITK*AIK.R	√
7705664	kruppel-related zinc finger protein hcKrox	R.HLK*GQNCLEVRTR.R	√
7705704	glutathione transferase kappa 1	K.AGMSAEQAQGLLEK*IATPK.V	√
7705793	lactamase, beta 2	K.K*LEKEGKIFSNTDPDKKWK.A	√
7705855	steroid dehydrogenase homolog	R.TIAVDFASEDIYDK*IK.T	√
7705905	hydroxysteroid (17-beta) dehydrogenase 13	K.LVLWDINK*HGLEETAAK.C	√
7706349	mitochondrial ribosomal protein S33	R.GK*EKPKKGEGK.R	√
7706501	WW domain binding protein 11	K.ATATISAK*PQITNPK.A	√
8400738	tumor protein p53	R.KK*GEPHHELPPGSTK.R	√
8475983	Isoform 1 of Regulator of G-protein signaling 9	K.SPIYKDMLAK*AIEPQETTK.K	√
8850217	testes-specific heterogenous nuclear ribonucleopr	K.AAARDMNGK*SLDGK.A	√
8922467	SDA1 domain containing 1	K.TNPFSSSTNK*EKKKQK.N	√
8922477	polymerase (RNA) III (DNA directed) polypeptide E	K.EVATVTKLCAEDVK*DFLEHMAVVR.I	√
8922517	TBCC domain containing 1	R.K*ISTYVQIRATEGAYPR.L	√
8922950	meiosis-specific nuclear structural protein 1	R.QELYQEEQAEIYK*SK*LK.E	√
110815815	hypothetical protein LOC54875	K.FRQK*VNLESNK.S	√
8923588	chromosome 22 open reading frame 8	K.DKTK*VLEWAR.G	√
9257180	adducin 2 isoform c; beta adducin; Adducin-2 (beta)	K.K*LELDGEK*ETAPEEPGSPAK.S	√
9910510	PR domain containing 9	R.GFRNK*SHLLR.H	√
9961252	ATP-binding cassette, subfamily B, member 4	K.NSQMCQK*SLDVETDGLEANVPPVSFLK*VLK.L	√
9966877	Isoform 1 of Golgi-associated PDZ and c	K.AQSVSQINHK*LEAQLVDLK.S	√
9966903	mannosidase, alpha, class 1C, member 1	R.EWGWEVVLALEK*YCR.T	√
4502107	Annexin A5 (Annexin-5) (Annexin V)	R.DLLDDLK*SELTGK.F	√
10140853	diazepam binding inhibitor	K.AYINK*VEELK.K	√
10835063	nucleophosmin 1 isoform 1	K.VEAK*FINYVK.N	√
10835187	manganese superoxide dismutase isoform A precursor	K.HHAAYVNNLNVTEEK*YQEALAK.G	√
10863905	thyroid hormone receptor interactor 11	R.EKEFECHSMK*EK.A	√
10863927	peptidylprolyl isomerase A	R.K*HTGSGILSMANAGPNTNGSQFFICTAK.T	√
10864011	sulfide dehydrogenase like	K.TSPVADAAGWVDVDK*ETLQHR.R	√
10947139	arginase, type I	R.DVDPGEHYILK*TLGIK.Y	√
11055994	SUMO1/sentrin/SMT3 specific protease 2	K.TTQFVPK*QYRLVETR.G	√
11056048	doublesex and mab-3 related transcription factor	R.TPKCARCRNHGVLSWLK*GHK.R	√
11056061	thymosin, beta 4	K.TETQEK*NPLPSK.E	√
11068137	hydroxyacid oxidase 1	K.AIDPSISWEDIK*WLR.R	√
11095441	aldehyde dehydrogenase 6A1	K.FVESK*SDK*WIDIHNPATNEVIGR.V	√
11128019	cytochrome c	K.K*K*EERADLIAYLK*KATNE.	√
11128039	protocadherin gamma subfamily A, 11 isoform 1	K.DLGLEPRELAK*R.G	√
11133608	Dimethylglycine dehydrogenase, mitochondrial	R.EGEEK*PPLSAETQWK.D	√
11230858	HMG-box transcription factor TCF-3	K.PLNAFMLYMK*EMRAK*VVAECTLK.E	√
11321595	integrin, alpha 9; integrin, alpha 4-like	K.ADSK*YSPSVK.S	√
11321601	phosphofructokinase	K.QTDFEHRIPK*EQWWLK.L	√
11386201	UDP-glucose:glycoprotein glucosyltransferase 2	R.K*LLFNALK.H	√
11496237	Glycogen synthase 2 (liver)	R.K*QLWDVAHSVK*EK.F	√
11863154	archain	K.PK*VAPAPARPSGPSK.A	√
11968152	SH3 and multiple ankyrin repeat domains 1	K.QTNLDEK*QLAK.L	√
11968182	ribosomal protein S18	K.DGK*YSQVLANGLDNK.L	√
12383060	cytochrome P450, family 3, subfamily A, polypeptide 43 isoform 1	K.DKQK*HR.V	√
124248539	axin interactor, dorsalization associated	K.LTK*GAAIFFEFK.H	√
13123772	CCR4-NOT transcription complex, subunit 10	K.ALHLLAVLEK*MISQGNNNK.N	√
13236495	crystallin, zeta	R.VFEFGGPEVLK*LR.S	√
13325057	solute carrier family 27 (fatty acid transporter)	R.ESLEEILPK*LQAENIR.C	√
13375727	hypothetical protein LOC79611	K.NQEAFK*HLYFEK.F	√
13375809	hypothetical protein LOC79657	K.EK*PLLIFEILQR.L	√
13376013	hypothetical protein LOC79768	K.SKFEEYVIVGLNWLQAVIK*R.W	√
13376735	Mak3 homolog	K.FYK*DVLEVGELAK.L	√
13376858	Testis-specific protein 10	R.HLAEIQGNVKVLK*SERDK.I	√
13435353	L1 cell adhesion molecule isoform 2	R.STIEK*KGSR.V	√
13435386	cytochrome P450, subfamily IIIA, polypeptide 4	K.SAISIAEDEEWK*R.L	√
13514831	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	K.K*LESILAQDQDLK.E	√

13518015	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	K.REK*LVEILRNIGDER.T	√
13699818	cytochrome P450, family 2, subfamily C, polypeptide 9	K.DQQFLNLMEK*LNENIK.I	√
13699868	methylenetetrahydrofolate dehydrogenase 1	K.VVGDVAYDEAK*ER.A	√
13775174	testis expressed sequence 15	K.AVVHLK*K*AHR.R	√
13775208	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),	R.YFPTQALNFAFK*DK.Y	√
13899231	mitochondrial ribosomal protein L9	K.LEK*IQTK*AGEATVKFLKSCRLEVGMK*NNVK.W	√
13994255	alanine-glyoxylate aminotransferase 2	K.DQYIEQFK*DTLSTSVAK.S	√
14141170	metastasis-associated protein 2	K.LK*QVYIPTYTK*PNPNQIISVGSK.P	√
14149781	hypothetical protein LOC84066	R.PK*KMDGASGVNGAPCALHK.K	√
14150037	ankyrin repeat domain 32	K.KSEGELSCSK*ENCPSVVK.K	√
14285497	Inhibitor of nuclear factor kappa-B kinase subunit beta	K.ELWNLLK*IACSK.V	√
15451916	bone morphogenetic protein receptor type II	K.GDINLVK*QGK*R.C	√
8573114	hemochromatosis protein	K.SGNLSEK*SGDYCDYLKFLYLNFSAQILK.G	√
15617199	histone cluster 3, H2a	-.MSGRGK*QGGKARAK*AK.S	√
15811782	G patch domain and KOW motifs	R.GMGWK*PGEGIGR.T	√
4505205	matrix metalloproteinase 10	R.K*DSNLIVK.K	√
16418343	testis-specific serine kinase 3	R.AK*ALFRQMVEAIR.Y	√
16551574	unnamed protein	R.GVLLK*ASERASGGSK*AVQPGR.K	√
16579888	fructose-1,6-bisphosphatase 1	R.APVILGSPDDVLEFLK*VYEK.H	√
16924319	actin, gamma 1	K.DSYVGDEAQSK*R.G	√
17380137	meiotic recombination 11 homolog A isoform 2	K.YQLEK*TQRFLK.E	√
17384412	similar to methylenetetrahydrofolate dehydrogenase	K.TDLSLSHQPDK*KGVPRDFILPISDVR.V	√
17402865	thiosulfate sulfurtransferase	K.EGHPVTSEPSRPEPAVFK*ATLDR.S	√
17864092	axonemal dynein heavy chain 7	K.KGK*LPHQVDDSYVGPSTSKSK*GK.S	√
18252778	ankyrin repeat and SOCS box-containing protein 2	K.SRETPLYKACERK*NAEAVK.I	√
124297119	BBX protein	R.KNLWWAAKREK*QGKPR.L	√
18390319	adlican	K.EIKDDVATNVDK*HK.S	√
18418630	Smad7	R.AGCCLGK*AVRGAK.G	√
18959200	LATS, large tumor suppressor, homolog 2	K.DK*K*QIQTSPVPVR.K	√
19111150	angiomotin	K.NK*ESQREKEKLEAELATARSTNEDQRR.H	√
19424126	polyamine N-acetyltransferase	R.ELAEFEK*LSDQVK.I	√
19743875	fumarate hydratase	R.AIEMLGGELGSK*IPVHPNDHVNK.S	√
19923191	minichromosome maintenance protein 3 associated	K.ETLQELQCFCK*YLQRWR.E	√
19923315	serine hydroxymethyltransferase 2 (mitochondrial)	K.LQDFK*SFLLK.D	√
19923437	adenylate kinase 3	K.AYEDQTK*PVLEYYQK.K	√
19923653	PC4 and SFRS1 interacting protein 1 isoform 2	K.KQPK*KDEEGQKEEDK.P	√
20070125	prolyl 4-hydroxylase, beta subunit	K.QLAPIWDK*LGETYK.D	√
20070384	Phosphoglycerate mutase family member 5	R.REPLSLINVRK*R.N	√
20127408	mitochondrial trifunctional protein, alpha subuni	K.TILK*DATLTALDR.G	√
20127460	xeroderma pigmentosum, complementation group C	R.REEEEEDAFEDEKPPK*K*SLLSK*VSQGK.R	√
20149500	hydroxymethylbilane synthase	-.MSGNGNAAATAEENSPK*MR.V	√
20149572	optineurin; glaucoma 1, open angle, E	R.LQEK*CQALERK.N	√
20336209	transcriptional regulator ATRX isoform 1	K.VQDGLSDIAEK*FLK.K	√
19584467	hypothetical protein	K.EK*SQLVRPLQPAEYLNSVVVDQDVSLHSRR.L	√
20977052	RGS3 isoform RGS3S	R.RHTMKEAK*DMKNKLGIFR.R	√
21040386	heat shock 70kDa protein 9B	R.HIVK*EFK.R	√
21264485	phosphoglycerate kinase 2	K.K*NQITNNQRIK.A	√
21265070	mitochondrial ribosomal protein L2	R.TKYTITPVK*MR.K	√
21314728	centrosomal protein 76kDa	R.QKTAEK*ER.L	√
21314774	T-cell activation Rho GTPase-activating protein	K.GK*PSREIKKHSMSFTFAPHK.K	√
21359818	Exophilin 5	K.CHSHSPFRNERGK*GKIR.H	√
21361105	retinol dehydrogenase 16	K.VAMIEPGYFK*TAVTSK.E	√
21361202	phosphate cytidylyltransferase 1, choline, beta	R.GYTAK*ELNVSFINEKR.Y	√
21361331	carbamoyl-phosphate synthetase 1 isoform b	K.AIDDNMSLDEIEK*LTYIDK.W	√
21361399	alpha isoform of regulatory subunit A, protein phosphatase 2	K.IGPILDNSTLQSEVK*PILEK.L	√
21361485	TBC1 domain family, member 10B	R.ILK*AYTIYR.P	√
21361539	ring finger protein 138 isoform 1	R.K*CFLTAMRESGAHCPLCR.G	√
21361565	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	K.HVVQSISTQQEK*ETIAK.C	√
21361621	phosphoglucomutase 1	K.ELLSGPNRLK*IR.I	√
21361684	G patch domain containing 1	R.QYK*NQK*ESEK*DLRYVGK.I	√
21389615	hypothetical protein LOC149499	K.PSRAKGIK*IGSR.E	√
21450719	hypothetical protein FLJ31164	R.K*PNFCPQETEVLVSK.V	√
21553321	testis development protein NYD-SP29	R.IENIK*AGDSR.S	√
21614513	aldehyde dehydrogenase 1 family, member L1	K.TDVAAPFGGFK*QSGFGK*DLGEAALNEYLR.V	√
21618334	carnitine acetyltransferase isoform 2	R.LAHYLEK*ALLDMR.A	√
21618342	signal transducer and activator of transcription 5	K.KAEHQVGEDGFLLK*IK.L	√
21626468	zinc finger, matrin-like; CTCL tumor antigen se33	K.ETRMDLQIGTEK*AEK.N	√
21735419	zinc finger, CCHC domain containing 14	K.TQLELEK*EK.S	√
21735621	mitochondrial malate dehydrogenase	K.VSSFEEK*MISDAIPELK.A	√
21928758	Seven transmembrane helix receptor	K.K*AIGK*QTLGK.A	√
21955172	pleckstrin homology-like domain, family B, member 2	K.RTK*LGEK.D	√
22035665	talin 2	R.AAQK*AAFGKADDDDVVVKTK.F	√
22035672	thioredoxin reductase 2	K.GGK*EILLSADHIIIATGGR.P	√
22035679	AT rich interactive domain 4B isoform 2	K.K*YNGLEEKR.K	√
22091454	glutathione S-transferase A1	K.YNLYGK*DIK.E	√
22267436	nipsnap homolog 3A	K.PGGPALWGDAFK*R.A	√
22547182	zinc finger protein of the cerebellum 1	K.PFPCPFPGCGK*VFARSENLK.I	√
22748695	DEP domain containing 4	K.RQK*DAENEFNETLR.P	√
22748943	hypothetical protein LOC145483	K.ENRNNDRK*RAKEYK.K	√
22749327	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog)	K.ISSK*TAAK.L	√
22749351	Tctex1 domain containing 1	R.QMTK*TISEVIK.A	√

22749413	chromosome 10 open reading frame 27	K.EQK*EEPLREQGAK.Y	√
23346420	nuclear factor related to kappaB binding protein	R.LLK*QILASRSDLLEMAR.R	√
23397704	copine I	R.GTITVSAQELK*DNRVVTMEVEARNLDK.K	√
24211029	asp (abnormal spindle)-like, microcephaly associated	K.IQSAFRMAK*AQK*QFR.L	√
24234688	heat shock 70kDa protein 9B	R.YDDPEVQK*DIK.N	√
24307983	hypothetical protein LOC23070	K.LMAK*MGFREGEGLGK.Y	√
24308011	phospholipase C-like 2	-.MPTEK*K*ISSASDCINSMVEGSELK*K.V	√
24308041	Est1p-like protein B	K.MYHQLK*KCETRK*LSPGK.K	√
24308113	KIF1 binding protein	K.IITADPK*K*ELENLATSLEHYK.F	√
24308177	IWS1 homolog	K.K*QDLK*ETFIDSGVMSAIK.E	√
24308239	p90 autoantigen	K.TLQK*EREDK.E	√
24308253	deltex 2	K.VLELLK*VAWK*R.R	√
24308348	polyribonucleotide nucleotidyltransferase 1	K.LFTPSPEIVK*YTHK*LAMER.L	√
24418663	Sec6 protein	R.IIEREEK*IDRRILDRK.K	√
24430183	outer dense fiber of sperm tails 2 isoform 2	K.ENKILK*DEMNK.E	√
24586679	testis-specific histone H2B	K.K*AVVK*TQK.K	√
24797148	selenophosphate synthetase	R.FCAEIK*SPK.Y	√
24797151	dimethylglycine dehydrogenase	K.LYEK*LEEETGQVVGFHQPGSIR.L	√
25092737	histone H2A	K*TESHHHK*AQSK.	√
25121936	RAS protein activator like 2 isoform 2; Ras GTPa	R.SISGTSTSEK*PNSMDTANTSPFK*VPGFFSK.R	√
25188179	voltage-dependent anion channel 3	K.GYGFGMVK*IDLK.T	√
25306287	mitochondrial elongation factor G2 isoform 2	K.TFK*GVVDVVMK.E	√
25777730	aldehyde dehydrogenase 1B1	K.VGNPFELDTQQGPQVDK*EQFER.V	√
25777732	mitochondrial aldehyde dehydrogenase 2	R.VVGNPFDSK*TEQGPQVDETQFK.K	√
25777734	aldehyde dehydrogenase 4A1	K.EEIFGPVLSVYVYPDDK*YK.E	√
25777746	piggyBac transposable element derived 4	R.TDAVGTARLNRK*QIPNDLK.K	√
25901062	hypothetical protein KIAA1434	R.LK*QELPELK.S	√
26190614	pleckstrin homology domain containing, family K	K.K*ISSVLQEEDDEMCLLLSSAVFGVK.Y	√
194217033	phosphatidylinositol-5-phosphate 4-kinase type-2 beta	R.FVIK*TVSSEDVAEMHNILK.K	√
27477095	nuclear receptor binding SET domain protein 1	R.PK*NQPIATEEK*SK.K	√
51316972	actin, aortic smooth muscle (Alpha-actin-2)	R.DLTDYLMK*ILTER.G	√
27545315	clone HQ0477 PRO0477p	K.HMPK*STIETALKMEK.S	√
27597073	epoxide hydrolase 2, cytoplasmic	K.EIFDK*AISAR.K	√
27734925	hypothetical protein LOC285315	K.DNMNNCSLILK*FR.E	√
27734945	zinc finger protein 100	K.RIHTGVKPYK*CTECGK.A	√
27735049	N-terminal Asn amidase	K.ALLYK*KNEDGLWEK.I	√
27764861	myosin heavy chain 6	K.K*NMEQTIKDLQHR.L	√
4507369	tyrosine aminotransferase	K.GNLPSILDVHVNVGGRSSVPGK*MK.G	√
28178832	isocitrate dehydrogenase 2 (NADP+), mitochondrial	R.DQTDDQVTIDSALATQK*YSVAVK.C	√
28466989	ATPase, Class V, type 10D	K.SLEEIK*SLFQRWSVR.R	√
28558977	cofactor required for Sp1 transcriptional activation	K.NEELAK*RAK.K	√
28570172	NADP-dependent leukotriene B4 12-hydroxydehydrogen	K.DLLK*WVLEGK.I	√
28872796	C/EBPb	K.K*TVDK*HSDEYK.I	√
28976154	trafficking protein particle complex 6B isoform	K.FICK*DFWTTVFKK.Q	√
29171694	inorganic pyrophosphatase 2 isoform 2	K.VNSK*EENGIPMK*K.A	√
29244924	chromodomain helicase DNA binding protein 6	K.ASK*EQGPTPVEK.K	√
29336920	BarH-like 1 homeobox protein	R.KARTAFTDHQLAQLERSFERQK*YLSRQDR.M	√
29540545	sulfotransferase family, cytosolic, 2A	R.EEK*NFLLLSYEELK.Q	√
29540551	trophinin isoform 2	K.AAPAAPPVPAANEIATNK*PK.I	√
29734087	similar to ribosomal protein L36	K.RK*QEELSNVLAAMR.K	√
119579853	synaptotagmin-like 5, isoform CRA_b	R.ESQHARHLSSTTPVFLAGVLEYLTANILEK*VGK.E	√
29789000	succinate-CoA ligase, GDP-forming, beta subunit	K.PANFLDLGGGVK*EAQVYQAFK.L	√
29826285	mitochondrial ribosomal protein L47 isoform b	K.VVDSMDALDK*VVQER.E	√
29893552	transient receptor potential cation channel	K.LFLTEEDQK*K.L	√
30181246	doublecortin isoform a	R.TLQALSNEK*K*AK.K	√
168983559	FYVE domain containing 26 zinc finger variant protein	R.QLVEK*EKYSEIQQLLKCVSESGMAAK.S	√
255652953	zinc finger CCCH-type containing 18	K.SSQQPSTPQQAPPGQPQQGTFVAHK*EIK.L	√
31377748	all-trans-13,14-dihydroretinol saturase	K.EK*FPQEEAIIDK.Y	√
31377775	glutamate dehydrogenase 2	R.YSTDVSVDEVK*ALASLMTYK.C	√
31543628	solute carrier family 1 (glial high affinity glutamate transporter), member 3	K.VQNITK*EDVK.S	√
31795563	tryptophan hydroxylase 2	K.NEVGGLVK*ALR.L	√
32171186	B-cell receptor-associated protein 31	K.LEK*AENQVLAMR.K	√
32171205	EF hand domain family, member A2	K.TWK*SLSK*QELNQMLAETPPVWKGSSK.L	√
32189394	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit	K.VLDSGAPIK*IPVGPETLGR.I	√
32455260	peroxiredoxin 5 , isoform b	K.VNLAELFK*GK.K	√
32484975	adenosine kinase isoform b	K.DFLDK*YSLK.P	√
32526576	Acetyl-CoA carboxylase 2	R.IGFPLMIK*ASEGGGGK.G	√
223972685	IQ motif and ubiquitin domain containing	K.CSAPK*IWRTPNGK.T	√
32698718	chromosome 9 open reading frame 36	K.QK*FQAPVCGFPCNHR.H	√
32967514	neurofibromin 2 isoform 7	K.PLDKK*IDVFK.F	√
33112885	Acetyl-CoA carboxylase 1	R.GSVLEPEGTVEIK*FRR.K	√
33239445	eukaryotic translation initiation factor 3, subunit 9 eta	R.LSQSKASK*ELVER.R	√
33286418	pyruvate kinase 3 isoform 1	R.GDLGIEIPAEK*VFLAQK.M	√
33338018	MSTP109	K.QK*LLMNCSLNIDLSMK.L	√
33342280	HECT domain containing 2 isoform a	K.TVKDFQEDVEK*VK.S	√
33519450	NACHT, leucine rich repeat and PYD containing 9	K.LLGFSESEK*K*SYFSYFFGEK.S	√
33624848	spectrin repeat containing, nuclear envelope 2 isoform a	R.EDLDQAK*TQIGMTESLLK.A	√
33695086	nicotinamide nucleotide transhydrogenase	R.MATQASTLYSNNITK*LLK.A	√
33859833	transmembrane 9 superfamily member 3	K.WK*KSDVK.F	√
33859845	zinc finger protein 223	R.K*KPFKCEDCGKK*LVYRSYRK.D	√
215598574	ankyrin 1 isoform 9	R.KK*K*ADAATSFLRAARSGNLDK.A	√

33946293	zinc finger protein 326 isoform 2	K.QQTNNQTEVVK*IIEK.D	√
34147630	Tu translation elongation factor, mitochondrial	R.DLEK*PFLLPVEAVYSVPGR.G	√
34328899	protein tyrosine phosphatase, non-receptor type 14	R.MFMIQTIAQYK*FVYQVLIQFLQNSR.L	√
34335253	disks large-associated protein 4 isoform a	K.ETK*ENNLSEEVLGK.V	√
34452705	bromodomain containing 8 isoform 1	R.GEK*GEVVETVEDVIVR.K	√
34452721	GA binding protein transcription factor, alpha subunit	K.WGQRK*NKPTMNYEK*LSR.A	√
34485727	hematopoietic protein 1	K.DGYNNNIHCLTK*AIIQVSAALFTLYNK.N	√
172046188	GPS, PLAT and transmembrane domain-containing protein FLJ00285	R.K*PLCNRCTYNLVLPGSEKK.Y	√
288557339	sex comb on midleg 1 isoform f	R.GRK*PGK*K.R	√
34577057	fibronectin leucine rich transmembrane protein 1	R.AYNRGSRKKDDYMESGTK*K*DNSILEIR.G	√
34577061	alcohol dehydrogenase 1B (class I), beta polypeptide	K.FSLDALITHVLPFEK*INEGFDLLHSGK.S	√
14149661	RAB6-interacting protein 2 isoform alpha	K.QEALLAAISEKDANIALLELSASK*K.K	√
34577122	NF-kB p50	K.HGTMDTESK*K.D	√
34740331	otoferlin isoform a	K.RSK*PDIK.M	√
35038564	hypothetical protein LOC23240	R.WK*KYKNGDVCKRNVLGTTRFAHLK*K.S	√
35038601	spindle assembly abnormal protein 6	-.MSQVLFHQLVPLQVKCK*DCEER.R	√
38044284	neuron navigator 2 isoform 1	R.DKEMK*LTDIR.L	√
38045952	zinc finger protein 14	K.QCGK*TFIYYQSFQK.H	√
112821690	hypothetical protein LOC285513	K.QLGADSK*LQLK.Q	√
38261962	activating transcription factor 7 interacting protein	K.LEQIQSK*DSLDEK.N	√
38327627	citrate synthase , isoform b	R.GMK*GLVYETSVLDPDEGIR.F	√
196259796	hypothetical protein LOC375484	K.TVEWDWK*LLTYVMEEEGQTLPGR.V	√
38505213	YTH domain containing 2	K.YKK*EKQQEEK*QQTTLTEWYSAQENSFK.P	√
38505218	putative acyl-CoA dehydrogenase	R.IAIEK*IR.L	√
38569411	AP1 gamma subunit binding protein 1 isoform 2	K.GGQNSTAASTK*YDVFR.Q	√
38788333	remodeling and spacing factor 1	K.YLCECQFDDNLK*FK.N	√
38788445	ornithine carbamoyltransferase	R.DLLTLK*NFTGEEIK.Y	√
39540514	pyrin and HIN domain family, member 1 alpha 1	K.MK*EEYDK*IQIADLMEEK.F	√
39753961	IQ motif containing GTPase activating protein 3	K.EQLSDMMVLDK*QKGLK.S	√
40254982	hypothetical protein LOC83641	K.LEQLELEKQK*LQEEQENAPEFVK.V	√
40254986	hydroxysteroid dehydrogenase like 2	R.DEQQISAAVEK*AIK.K	√
40255133	hypothetical protein LOC222256	K.WK*DPLTQMPKWK*ESSHQGAAPR.R	√
40255149	Rho guanine nucleotide exchange factor (GEF) 19	K.QWLFSK*LPEVK*STSER.F	√
40316935	alsin	R.K*LGNLAVPADEK.W	√
40354205	Aldolase B	K.DGVDFGK*WR.A	√
40385867	methionine aminopeptidase 1D	R.KKKK*DGDGDGDGATGK*KKK.K	√
40556361	hypothetical protein LOC56964	K.GQNMYPEGQVK*SQMK.C	√
40789249	aspartyl-tRNA synthetase 2 (mitochondrial)	K.MPTGEIEIK*VK.T	√
40805843	p300/CBP-associated factor	R.IAVK*K*AQLR.S	√
41019126	Eukaryotic translation initiation factor 3 subunit 6	K.LASEILMQNWDAAMEDLTRLK*ETIDNNSVSSPLQSLQQR.T	√
41149376	hypothetical protein XP_373451	K.WSESSVVK*WPYTK.V	√
41281466	endosome-associated FYVE-domain protein	K.VDTTLSDSYNYSGTENLK*DK.K	√
41281499	Rb1-inducible coiled coil protein 1	K.ELLSLKNEYEGKLDGLIK*ETEENENK*IKK.L	√
41281987	nesprin 1 longest	R.AIQERAK*EAVTK.S	√
41322908	plectin 1 isoform 3	K.FK*EMELPAKEADK.N	√
41872631	fatty acid synthase	K.GVDLVLNSLAEEK*LQASVR.C	√
42544130	splicing factor 1 isoform 1	K.K*AVEQIRNILK.Q	√
42544243	dynamin 3	K.GWLTISNIGIMK*GGSK.G	√
42560244	peptidyl-prolyl isomerase G (cyclophilin G)	R.SSVEK*ENQK*SK.G	√
42716289	erythrocyte membrane protein band 4.1	K.LAPNQTK*ELEEK*VMELHK.S	√
44680105	caldesmon 1 isoform 1	K.CFTPK*GSSLK*IEER.A	√
44681484	cell division cycle associated 2	R.LGSGYFSSNGK*LEEVK*TPK.N	√
44890052	stathmin 1	R.SK*ESVPEFPLSPPK.K	√
44917608	mahogunin, ring finger 1	R.VSYLLQEIYGIENK*NNQETK.P	√
45120115	hypothetical protein LOC56905	R.NPLCYGLSTCLGEGAVK*R.P	√
45238851	similar to RPL23AP7 protein	R.YPRK*STPRRNK.L	√
45333906	COMM domain containing 6 isoform b	R.SLK*YPYVAVMLK*VADHSGQVK.T	√
45439357	elongin A2	R.LATK*TEPK.K	√
45505147	protein kinase Njmu-R1	R.LELDK*YIQGLK*NNMNCEAR.G	√
45580730	2-aminoadipic 6-semialdehyde dehydrogenase	R.VPDESLFLNSGGDSLK*SIRLLSEIEK.L	√
45643119	peroxisomal D3,D2-enoyl-CoA isomerase isoform 1	K.WDAWNALGSLPK*EAAR.Q	√
46371197	heart alpha-kinase	R.VGGKDLWSK*R.G	√
46409304	glutamate-rich 1	K.HK*SKK*KFK.N	√
46409324	SPRY domain containing 4	K.WYTMLANEK*APVEGIGQPEK.V	√
46852147	mitochondrial isoleucine tRNA synthetase	R.ELSNFYFSIIK*DR.L	√
74735764	cryptochrome-1	R.ISHTLYDLDKIIELNGGQPPLTYK*R.F	√
47271356	solute carrier family 39 (zinc transporter)	K.VIVGSLSVQDLQASQSACYWLK*GVR.Y	√
47271493	hypothetical protein LOC348654	K.EQALKLIQILK*GQSLLQR.F	√
47575699	KIAA1841 protein	R.FDPTQLTKGCK*VR.D	√
47680169	3-phosphoinositide dependent protein kinase-1	K.LEYDFPEK*FFPK.A	√
47717123	intersectin 1 isoform ITSN-l	K.EQEDIVVLK*AKK.K	√
48255898	SWI/SNF-related actin-dependent regulator of chromatin a2 isoform b	K.GK*GK*K*R.P	√
48255951	plasma membrane calcium ATPase 2 isoform 1	K.SVLQGK*LTK.L	√
48255968	UDP-glucose pyrophosphorylase 2 isoform b	K.AHVDEFK*SVSK.F	√
49258196	syntaxin 19	R.LQELK*QRTK.E	√
49456351	Isocitrate dehydrogenase [NADP] cytoplasm	R.FK*DIFQEIYDK.Q	√
49574537	glycine cleavage system protein H	K.MTLSNPSELDELMSEEAYEK*YIK.S	√
50080162	FYVE, RhoGEF and PH domain containing 5	R.ASESPSSLIFYRDGK*R.K	√
50083285	leucine-rich repeats and IQ motif containing 1	K.DNQQK*K*IQK.V	√
50345984	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit	R.GYLDK*LEPSK.I	√
50345997	E1A binding protein p300	R.EENTSNESTDVTK*GDSK*NAK*K.K	√

50409939	aftiphilin protein isoform a	K.TEEK*LDLLTSK.C	√
50541965	flavin containing monooxygenase 3 isoform 1	K.NLLK*YIQFK.T	√
50659086	prenyl diphosphate synthase, subunit 1	R.DLK*GLYEDIR.K	√
50659095	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	K.TK*KVTK*NEEPSEEEIDAPK.P	√
50659104	Rab coupling protein isoform 3	K.LEEMGLNLRK*DQK*K.T	√
50845386	annexin A2 isoform 2	K.TDLEK*DIISDTSGDFR.K	√
50845388	annexin A2 isoform 1	K.TDLEK*DIISDTSGDFRK.L	√
8051631	RNA-binding protein Raly	K.IK*LK*SSELQAIK.T	√
51467633	nucleoporin 188kDa	R.LSMSLMEQLLK*TLR.Y	√
51472437	similar to Golgin subfamily A member 6	K.SPGIPAGAK*TKK.K	√
91208418	Transcription elongation regulator 1	K.DSRFK*AIEK.M	√
51474256	similar to high-mobility group box 3	R.EEHKK*KNPK*VPINFAEFSK.K	√
51474786	similar to zinc finger protein 528	K.PYNNKECGK*VFSHHAYLAQHRK*IHTGEK.P	√
51475251	hypothetical protein	K.FDDLTAEKEAVSSK*CVDLAK.D	√
51477359	similar to Transcription factor Dp-1	K.QLLPK*TFGQSNVSIAQQVVIGMPQR.P	√
51477505	PREDICTED: similar to Histone H3.3	K*IAK*QTNGYK.S	√
51479141	ATP synthase, H+ transporting, F0 complex, subunit F6 isoform b	K.FEDPK*FEVIEKPQA	√
51479152	ATP synthase, H+ transporting, mitochondrial F0 complex,subunit d	K.NLIPDFLNEIPQMTIEDLNEAFPETKLDK*K.K	√
51592100	ciliary rootlet coiled-coil, rootletin	R.DMLQAEKAEVAEALTK*AEAGR.V	√
51827892	RAB6-interacting protein 2 isoform alpha	K.QEEIDNYKKDLK*DLK*EK.V	√
51972214	lin-28 homolog B	K.K*GPSVQKR.K	√
52138580	xenobiotic/medium-chain fatty acid:CoA ligase	K.FDPLVILK*TLSSYPIK.S	√
52426735	ankyrin 2 isoform 1	R.EAQKTENQTIK*R.G	√
47077105	unnamed protein product	K.DNRHVYEGKDGAIEDIITALK*K.N	√
52486999	THO complex 2	K.EK*ERCTALQDKLLEEEK.K	√
52627166	olfactory receptor, family 52, subfamily H	R.DK*VILLFSK*GTG.-	√
52630322	chromodomain helicase DNA binding protein 3	K.AGSMSK*QELDDILK.F	√
53759107	argininosuccinate synthetase 1	R.NDLMEYAK*QHGIPIPVTPK.N	√
53832003	adenylate kinase 3-like 1 isoform 5	K.DVAK*PVIELYK.S	√
54112380	F-box and leucine-rich repeat protein 10 isoform b	K.MNRDNK*EGQEPAK*RRSECEEAPR.R	√
54112401	calmodulin-binding transcription activator 1	K.HK*LNPEYFQTRQEK.L	√
54291708	zinc finger protein 780B	K.PYK*CKECGK*AFQLHIQLTRHQK.F	√
54606888	hypothetical protein LOC23251	K.DCPQFVPASEPNFLLGVSK*EVKNR.A	√
54607053	GCN1 general control of amino-acid synthesis 1	R.EILSELGK*CVAGK.D	√
54696884	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	K.DFDTALK*HYDK.A	√
54792146	tripartite motif-containing 47	K.FLQLFGTK*GVK.R	√
55418564	RIF1 275 kDa protein	K.KNEPLGK*LTSLFK.L	√
55662117	ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2	K.K*KTIVLRNGMWHTIMWK*EVAVGDIVK.V	√
55741657	CTD-binding SR-like protein rA9	R.EVTK*EEYK*DILR.K	√
55749708	outer dense fiber of sperm tails 2-like isofor	K.QK*TLIEMYK*TQVQK.L	√
55769559	zinc finger protein 21 isoform 2	R.KKGLSLHQRIK*NGEK*PFECTACRK*TFSKK.S	√
55769589	transmembrane protein 63B	K.K*FLAEAAIR.F	√
55956777	sterol carrier protein 2 isoform 1	K.ANLVFK*EIEK.K	√
55956788	nucleolin	K.TLFVK*GLSEDTTEETLK.E	√
55956904	mitogen-activated protein kinase kinase kinase 4	K.DCSK*DSDDVLIDAYLLLTK.H	√
55957186	SH3 multiple domains 1	K.ELDTVPAK*GRQNEGK.S	√
55959987	hypothetical protein LOC126859	K.WQEFFNEK*DILSPNK.G	√
55962098	Zinc finger, MYM-type 1	K.TIWDGTEEICQKITCK*GFKVEK.P	√
56203279	Tubby like protein 1 lng=161	R.KTKKK*GSGEADK.D	√
56204582	hypothetical protein LOC79747	K.EEREQSTRK*ENIQTGPR.T	√
56204992	Superoxide dismutase [Mn], mitochondrial	R.DFGSFDK*FK.E	√
56206277	Ataxin-7-like protein 2	K.GK*DGVEVEAPSRK*R.K	√
56404465	Isoform 1 of Dr1-associated corepressor	R.KPGSGGRK*NGGMGTKSK*DK.K	√
42560225	recombining binding protein suppressor of hairless	R.LIIRK*VDK.Q	√
56549696	E1A binding protein p400	K.LMEEISTSAAPAARPAAAK*LK.A	√
56550055	CGG triplet repeat binding protein 1	R.K*AEFEEQNVR.K	√
56676391	activating signal cointegrator 1 complex subunit 1	R.APSLLYKHIVGKRGDTRK*K.I	√
56806673	high-mobility group (nonhistone chromosomal) protein 1-like 1	R.EMK*TYIPPK*GETK.K	√
5174429	acetyl-coenzyme A acyltransferase 2	R.PQTTLEQLQK*LPPVFK.K	√
57162516	Rho GTPase activating protein 21	K.NK*DGK*EQSETVSLSEDETFSWPGPK*TVTLK.R	√
57164975	Treacher Collins-Franceschetti syndrome 1	R.K*RKLSGDQPAARTPRSK*K.K	√
57208288	transcription elongation factor A (SII)-like 2	R.KTNK*GLAHYLK*EYK.E	√
57232746	nuclear receptor interacting protein 1	K.K*GHK*NNVTNSK.P	√
58197558	Tudor domain-containing protein 6	K.SQVELSTQVIK*SASSK.S	√
58218968	calmodulin 3	R.HVMTNLGEK*LTDEEVDEMIR.E	√
58530842	desmoplakin isoform II	K.EK*EYEIERLR.V	√
58761500	GTP-binding protein PTD004 isoform 1	K.DEEMIGPIIDK*LEK.V	√
60499025	ferrochelatase isoform a	R.WK*SGAAAAAVTTETAQHAQGAKPQVQPQK.R	√
61213484	Isoform 1 of FYVE, RhoGEF and PH domain	K.CDLYGEK*AKNQGGVVLK.A	√
61676193	zinc finger protein 260	K.CGK*AFSQKENFLSHQK.H	√
61676921	axin 2	K.AQSLTLGHFK*EQLSK*KGNYRYYFK*K.A	√
61743954	AHNAK nucleoprotein isoform 1	K.ASLGSLEGEAEAEASSPK*GKFSLFK*SK*K.P	√
61806675	hypothetical protein LOC441242	K.AAATGAK*SRGGAGK.K	√
61966773	zinc finger protein 793	R.ECGK*SFSQK*SCLNKHWR.T	√
62088406	DNA (cytosine-5-)methyltransferase 1 variant	K.GK*GK*GK*GK.P	√
62198232	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	R.DGLQNEK*NIVSTPVK.I	√
62420877	electron-transfer-flavoprotein, beta polypeptide	K.IEVIK*PGDLGVDLTSK.L	√
62530384	dodecenoyl-Coenzyme A delta isomerase	R.DADVQNFVSFISK*DSIQK.S	√
62990154	Isoform 2 of Shugoshin-like	K.K*SNKKTNEHGMKTFRKVK.D	√
63055059	SH3 and PX domains 2B	R.SIVEVKVLDVQK*R.R	√
63252900	tropomyosin 1 alpha chain isoform 4	K.VIESRAQKDEEKMEIQEIQLK*EAK.H	√

189055021	unnamed protein product	K.IVDLVK*ELDR.D	√
65506442	propionyl-Coenzyme A carboxylase, alpha polypeptide	R.MPVIK*PDIANWELSVK.L	√
66346693	FAT tumor suppressor 1	K.FK*LNPDTGELK.T	√
66346721	phosphoenolpyruvate carboxykinase 2 mitochondrial	R.SYLTEQVNQDLPK*EVLAELEALER.R	√
66346737	glucosidase, alpha; neutral C	K.NRFPNPK*RMQELLR.S	√
66347282	hypothetical protein LOC85452	K.PELLHFQDFDIGK*VYKK*K*ITLVNTTYTINYCK.L	√
66347763	FYVE, RhoGEF and PH domain containing 3	R.DK*EKQSCKSCGETFNSITK*R.R	√
66472922	hypothetical protein LOC347273	K.SGK*EHIDNIK.K	√
66912162	histone 2, H2bf	K.K*AVTK*VQK.K	√
66912182	hypothetical protein LOC220416	R.IFGK*QTNK*MESSR.K	√
66912194	RAB3A interacting protein isoform A	R.FVK*ASAVECGGPKK.C	√
66932949	ATPase type 13A4	K.IGSLEDWLSSAK*IHQK.F	√
66933016	inosine monophosphate dehydrogenase 2	K.DK*YPNLQVIGGNVVTAAQAK.N	√
67460390	Isoform 2 of Dipeptidyl peptidase 9	R.TGSKNPK*IALKLAEFQTDSQGK.I	√
67782305	manganese superoxide dismutase isoform A	K.HHAAYVNNLNVTEEK*YQEALAK.G	√
68303542	argininosuccinate lyase isoform 1	K.AEMDQILHGLDK*VAEEWAQGTFK.L	√
68508965	carboxylesterase 1 isoform b	K.ELIPEATEK*YLGGTDDTVK.K	√
71565160	structural maintenance of chromosomes 1B	K.K*IHLLNTK*LEHVNRDLSVK*RESLSHHENIVK.A	√
68989263	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	R.ILADEALK*LGILDK.V	√
71037379	glycogen phosphorylase, liver	K.VFK*DFSELEPDK.F	√
71153325	Artemis protein (DNA cross-link repair 1C protein)	K.REHLQYLYEKLATGESIAVK*KR.K	√
71773106	adaptor-related protein complex 2, beta 1 subunit	K.GEIFELK*AELNNEK*KEK.R	√
71773329	annexin VI isoform 1	R.DLMTDLK*SEISGDLAR.L	√
73622099	Zinc finger CCCH domain-containing protein 11A	K.QGEEPLVRLSLTERLGK*R.K	√
73623035	sperm associated antigen 5	K.AK*EADIEK*LNQALCLRYK.N	√
74136549	AT rich interactive domain 5B (MRF1-like)	K.K*ARAVSPLDPSK.E	√
74315348	transient receptor potential cation channel, subfamily V, member 1	K.TCLLK*AMLNLHDGQNTTIPLLLEIAR.Q	√
74315995	l-myc-1 proto-oncogene isoform 1	K.ALEYLQALVGAEK*RMATEK.R	√
41152074	steroid-sensitive protein 1	K.EKSK*KK*KGGKTEQDGYQK.P	√
21908040	platelet receptor for type III collagen	K.MNNENPLK*SVSR.I	√
74747744	SH2 domain-containing adapter protein E	R.DSLQGLIQAAAGK*GRK.N	√
75677365	dynein heavy chain domain 3	K.ERPELEEQK*DSLVINIAAGKRKLK*.E	√
75750472	spectrin domain with coiled-coils 1 NSP5b3b	R.EYGGSK*RNALLK*WCQKK.T	√
76363520	L-lactate dehydrogenase C chain	K.LK*GEMMDLQHGSLFFSTSK.I	√
11321601	phosphofructokinase, platelet	R.AMEWITAK*LKEARGR.G	√
76800648	Isoform 1 of Large proline-rich protein BAT3	K.EHIAASVSIPSEK*QR.L	√
76825095	Ets variant gene 1, ER81	K.FSYGEK*CLYNVSAYDQK.P	√
77539758	histone cluster 2, H4b	K.GLGK*GGAK*R.H	√
78000165	sorbin and SH3 domain containing 1 isoform 4	R.K*AERGAGER.G	√
82775371	coiled-coil domain containing 93	R.YNEAK*K*TLTELK.T	√
83305198	Olfactory receptor 4C16	R.KLWSK*KLITDDK.R	√
83700225	ATPase, H+/K+ transporting, nongastric, alpha	K.GDGKEKYRGLKNNCLELK*K.K	√
29544726	Docking protein 5	K.KASSK*GPK.R	√
85701377	Oral cancer overexpressed protein 1	K.LHEDLDKIRGKFK*QFCSLLNVQPDFK.I	√
88759339	aster-associated protein	R.LEEK*NKK.K	√
88959048	hypothetical protein LOC57683	K.SGDSK*ITFDSEQLQEAVKKIDQWK.E	√
88959236	similar to male-specific lethal 3-like	R.WQQDMSTSVPKLFLHLEK*K.T	√
88971297	hypothetical protein LOC285264	R.HQQVTSGGLATK*EYLKFNSEQVQK.Q	√
88981318	hypothetical protein	K.GLSK*SMYVFQSLQNVSDSLKYIFSK.C	√
89030110	similar to Protein KIAA0310 isoform	K.K*ETKEPK*K*GESWFFR.W	√
89031341	similar to Protein C6orf182 homolog	K.LYAK*LDKLDVLEK.E	√
89034188	similar to Nucleolar transcription factor 1	K.SQAEELQK*QYK.V	√
89035083	similar to dynein, cytoplasmic, heavy	R.FNRVDEDFRSIMTDIK*K.D	√
89035625	similar to 60S ribosomal protein L26	K.FNPFVTSDRSK*NRK.R	√
89037003	similar to Histone H2a	K.K*TESHLK.V	√
89040240	similar to thyroid hormone receptor	R.FIDNVLK*SSHLNQEK*DIETDALSQK.C	√
89047506	hypothetical protein LOC644041	K.QHDVTQSK*LFSLK.T	√
89059361	similar to 60S ribosomal protein L3	K.IDLK*FIDTTSK.F	√
89061633	similar to zinc finger protein 617	K.K*PYVSKQCGK.S	√
89061842	similar to EC2-V2R pheromone receptor	K.DLYLVMPEWK*YFK.Y	√
89145417	methyltransferase like 7A	K.FLIK*SIAENR.H	√
89242128	dynein, axonemal, intermediate polypeptide 2	R.EKILEARHREMRLKEK*GK.A	√
89274169	cytokine induced apoptosis inhibitor 1	K.PGEK*VLLSDSNLHDA.	√
89276751	collagen, type V, alpha 1	K.K*SEGARITSWPK*ENPGSWFSEFKRGK.L	√
89886480	zinedin isoform 2	R.AKYHKLK*FGTDLNQGEK.K	√
91176325	bromodomain adjacent to zinc finger domain, 2A	R.K*SGYSLNFSEGDGRR.R	√
91199540	dihydrolipoamide dehydrogenase	K.ALTGGIAHLFK*QNK.V	√
91208420	bassoon protein	R.GLPSSASDMSLQTEEQWEASRSGIK*K.R	√
92087060	ankyrin repeat and SOCS box-containing 15	R.TLLEK*GVWPNTKNDK*GETPLLIAVK.K	√
92859630	HSP90AA2 Heat shock protein 90 kDa alpha	K.PEIEDVGSDEEEEKKDGDK*KK*K.K	√
92859701	myosin VI	K.IGLDDEEK*LDLFR.V	√
93138710	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	R.LK*K*YDNCWLALTDPR.D	√
93141018	H2A histone family, member Y isoform 3	R.SAK*AGVIFPVGR.M	√
93204551	Calpain-7-like protein	K.EVK*DVK*EFK*PESSLTTLK.A	√
94536784	coiled-coil domain containing 51	R.EDLEVHQAKLK*EVR.D	√
94557308	L-3-hydroxyacyl-Coenzyme A dehydrogenase	R.GDASK*EDIDTAMK.L	√
94681063	bromodomain adjacent to zinc finger domain, 2B	K.PLSLVNQAK*KETYMK.L	√
94721321	coiled-coil domain containing 11	K.TK*LLK*EKNEKERQDFVAEK.L	√
94721330	Isoform 2 of RUN and FYVE domain-containing	R.SEKSVEITK*QDTK.V	√
94721347	heparanase	R.FGGTK*TDFLIFDPK.K	√
94966757	protein disulfide isomerase-associated 2	K.VIEYK*STRDLETFSK.F	√

94967023	DAB2 interacting protein isoform 1	K.LWVIEAK*DLPAK.K	√
102467235	inner centromere protein antigens 135/155kDa	K.QIEQK*FAQIDEK*TEK.A	√
102470001	PQQ repeat and WD repeat domain containing	R.KLSLK*GHNDWVMDVAISNNK.K	√
103471987	isochorismatase domain containing 1	K.FK*EIQNLIK.A	√
103485496	procollagen (type III) N-endopeptidase o sap	K.AEKDSK*AEQAKVKK.A	√
104526627	triadin	K.GGK*QEK*VKQTAAKVKEVQKTPSK.P	√
106049295	pyruvate carboxylase	R.PGASLPPLDLQALEK*ELVDR.H	√
108773787	Retinoblastoma 1	K.PLKK*LR.F	√
109148533	centrosome-associated protein 350	K.DTIDVLNQISEK*QGR.M	√
109255234	centrosomal protein 290kDa	K.K*NILLEEKVK.K	√
109637791	transcription factor-like nuclear regulator	K.K*TEK*PSTPVQTR.E	√
109659847	filamin A interacting protein 1-like isoform 3	R.VLDMEGK*DEELIK.M	√
109715825	zinc finger protein 690	R.SGLPFPK*SGVVSRLEQGEPWIPDLLGSK.E	√
109809759	leucine rich repeat transmembrane neuronal 3	K.RYPASMK*QLQQR.S	√
109948283	KIAA0020 protein	K.FQPDGRSDESAAK*K*PKWDDFK*KK.K	√
110347443	TATA element modulatory factor 1	R.EAQLLSLSK*EK.A	√
110347568	centrosomal protein 152kDa	R.GQYIK*AVKK*IK*CDMLR.Y	√
110349715	titin isoform N2-B	R.YDSGK*YTLTLENSSGTK*SAFVTVR.V	√
110349786	ALMS1	K.VSIVPGPGDQK*TGIPSAPSSFYSHREK.P	√
110671329	dihydrolipoamide branched chain transacylase	K.GEVYK*AQIMNVSWSADHR.V	√
112293277	DnaJ (Hsp40) homolog, subfamily C, member 8	K.EGK*PTIVEEDDPELFK.Q	√
112380630	leiomodin 1 (smooth muscle)	K.PSEGPAK*VEEEAAPSIFDEPLER.V	√
112421134	hypothetical protein LOC23742	R.K*TPMLPARNPPR.F	√
113411945	similar to forkhead-associated (FHA)	K.ATESLK*AESLALK.L	√
113412878	similar to voltage-dependent anion	K.GFGFGLVK*LDVK.T	√
113413937	Non-histone chromosomal protein HMG-14	R.GAK*GK*QAEVANQETK.E	√
113414558	hypothetical protein	R.GGK*EWAPGGAEKGK.E	√
58530848	destrin isoform b	K.KCIIVEEGKEILVGDVGVTITDPFK*HFVGMLPEK.D	√
113415289	similar to U2-associated SR140 protein	R.DKKDK*EKLESRSK*DK*K.E	√
113416654	similar to Ankyrin repeat domain-containing protein	K.QK*SALDEADDEK*MK.E	√
113416990	similar to CG4502-PA, isoform A	R.QFAASLVK*GQGRICR.K	√
113417201	similar to antiquitin	K.FK*NEEEVFAWNNEVK.Q	√
113417258	hypothetical protein	K.K*VSSICPLQGLGRK.S	√
113419250	similar to Elongation factor 1-gam	R.ILGLLDAYLK*TR.T	√
113419468	Rap guanine nucleotide exchange factor (GEF) 5	K.ARK*SAIEQDEENNDK.H	√
113419615	similar to LYRIC/3D3	-.MVPENQALLTNLRRQK*QK.N	√
113421257	hypothetical protein LOC138311	K.GDLIQPNLAK*VCALLRGYLLPGAPADLR.E	√
113421553	hypothetical protein	R.ENRGK*ATDLAR.W	√
113421796	similar to Glutamate dehydrogenase 1	K.IIAEGANGPTTPEADK*IFLER.N	√
113422189	hypothetical protein	-.MELPK*AIK.S	√
113422807	similar to High mobility group protein	K.GKFGRARGK*FEDMAK*ADKAHYK.R	√
113422811	hypothetical protein	K.SSIQQLNPK*NTR.N	√
113423449	similar to Succinyl-CoA ligase (GDP-forming)	K.SENEPIENEAAK*YDLK.Y	√
113424455	similar to Temporarily Assigned G	K.EIIFNAKCLTMKEK*K.S	√
113424479	similar to family with sequence similarity 70, member B	R.QMTK*RRGK*DIK.P	√
113424851	hypothetical protein	K.FVKMSTIPRHFGLK*YKEESYMFKELEK.V	√
113425040	similar to protein kinase CHK2 isoform b	K.DQITSGK*HNFIPK*VWAEVSEK.A	√
113426970	hypothetical protein	R.GQTTGGEGREGAQTREGK*MGLPDSAR.R	√
113427963	hypothetical protein	R.K*NSGVGRGQIR.L	√
113428240	similar to CG2839-PA	R.K*LAQAYVK*ITQDDREMAQAEGK*FAQK.E	√
113428321	similar to zinc finger protein 16	K.PIK*DQLGSSFYSHLPELHEFQTEGK.I	√
113429587	similar to Collagen alpha-1(X) chain	K.SKLEAK*ENEK.G	√
113722120	G protein-coupled receptor 98	K.RFQIVLFDPK*GGAR.I	√
114155140	tropomyosin 3 isoform 1	R.GMKVIENRALKDEEK*MELQEIQLK.E	√
114326455	chromodomain helicase DNA binding protein 8	K.K*EIEDLLRKGAYAAIMEEDDEGSK.F	√
115298659	spectrin, alpha, erythrocytic 1	R.DVTEAIQWIKEK*EPVLTSEDYGK.D	√
115311627	Probable global transcription activator SNF2L1	R.CNTLISLIEKENMEIEERERAEK*K*K.R	√
115392144	hypothetical protein LOC643155	K.QK*RQENIAKAK*R.L	√
115511030	C6orf150 Isoform 1 of Uncharacterized protein	R.LSFSHIEK*EILNNHGK*SK*TCCENKEEK.C	√
115527082	myosin, heavy chain 1, skeletal muscle, adult	K.TLALLFVGATGAEAEAGGGK*K.G	√
115527120	nebulin	R.VNAYNLSDNVYKQDWEK*SK.A	√
115529475	polymerase (RNA) III (DNA directed) polypeptide	R.QDIERYSK*R.Y	√
116089337	IQ motif containing GTPase activating protein 2	K.LDGK*GEPK*GAK.R	√
116256481	Nef-associated factor 1	K.LLMSNGNK*EGASGR.P	√
116256485	chromosome 6 open reading frame 10	K.IQILK*CGGTAR.S	√
116642889	cyclic nucleotide gated channel beta 3	K.KLVEGDLSSPEASPQTAK*PTAVPPVK.E	√
116805327	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	K.SFNDDAMLIEK*FVDTPR.H	√
117935038	cylicin, basic protein of sperm head cytoskeleto	K.K*ASKNDDK*K*KDAKK.I	√
117956407	Zinc finger protein 568	K.K*QQETLVRK.V	√
18202512	Histone H3.1t (H3t)	R.EIAQDFK*TDLR.F	√
118498356	kinectin 1 isoform a	K.REVIDLLKPDQVEGIQK*SGTK*K*LK.T	√
118572606	hemicentin 1	R.VVVK*YK.P	√
118600975	syntaxin binding protein 3	K.KLLDDIK*MLNK*PK*DK.V	√
119120907	par-3 partitioning defective 3 homolog B isoform a	K.DK*LIAVFEEQEPLHK.I	√
14916543	catenin delta-1 (p120 catenin)	R.K*GGPPPPNWRQPELPEVIAMLGFR.L	√
119583075	kinesin family member 27, isoform CRA_e	K.MK*NLKMVECYHLK*K.N	√
119584314	inositol 1,4,5-triphosphate receptor	K.FLTCDEHRK*KQHVFLR.T	√
166706897	noelin-3 precursor (Olfactomedin-3)	K.EK*MDELLPLIPVLEQYK.T	√
17366994	Glucose transporter type 9	R.NK*AYPPEEK*IDSAVTDGK.I	√
62243484	sarcoma antigen NY-SAR-41	K.K*QELLEMDQALK.E	√
119612317	angiopoietin 1, isoform CRA_c	K.QLLQQTNEILK*IHEK.N	√

119617730	oxysterol binding protein-like 8, isoform CRA_a	K.TQK*NGQWVGTVLLNACEIIERPSK.K	√
119620404	ubiquitin specific peptidase 34	R.NSLQEQEAK*ER.K	√
119621109	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase	R.GQQQVFK*GLNDK.V	√
119625859	hCG2027126	K.QTLGKLNMLHPMSQKKK*K.K	√
119631422	Isoform 2 of Titin	R.PEDLEVK*EVTK.N	√
124106304	Propionyl-CoA carboxylase beta chain, mitochondrial	R.ICCDLDVLASKK*VQR.P	√
126215680	UPF0407 protein C2orf39	K.NVMK*TFREELYNIEK*AFEVERQELLASNKK*K.W	√
113418590	PREDICTED: similar to BAH domain and coiled-coil containing 1	K.IQCAEPSPALLVPSAK*R.R	√
143811385	Isoform 1 of DNA polymerase zeta cataly	R.TRSVTSPRK*PRTPRSTK.Q	√
145699133	KPL2 protein isoform 1	K.EILTTEIAKK*KNKVEK*K*LEEK.E	√
147644956	Isoform 1 of Girdin	K.QKGQLEDLEKMLK*VEQEK*MLLENK.N	√
149363661	Isoform 2 of Septin-8	K.RVHQEEKRKVEEK*R.R	√
150170706	Anaphase-promoting complex subunit 10	R.K*TTVKTLCIYADYK.S	√
154689769	folliculin interacting protein 2	R.QVLFDSK*AVQKIEEVTAQK.T	√
155722990	solute carrier family 4 (anion exchanger), member 1, adaptor protein	K.IVKPAEIPELK*K*.T	√
158563839	Serine protease 33	R.K*SAACGQPRMSSRIVGGRDGR.D	√
160113150	Serine/threonine-protein kinase PLK4	K.KNSDASDNAHSVK*QQNTMK.Y	√
13027380	kinesin binding 2	K.LK*EHVIEKEELK.L	√
169145255	polymerase (DNA-directed), delta interacting protein 3	R.VTEEDIVELFCVCGALK*R.A	√
4885617	Estrogen sulfotransferase	K.EVIK*LIHFLER.K	√
169218082	similar to Phosphodiesterase 4D interacting protein	K.CEECK*DLIESVLEEEVQFQER.E	√
170784817	transcription factor CP2-like 3	R.EGGSVLVK*RMFR.P	√
172044682	Dynein heavy chain 1, Heat shock regulated-1	K.DVEGFLTK*CIQLYETTVVR.H	√
194239711	Zinc finger protein 431	K.IIHTGEKPYKCEECGK*AFNQSSTLSTHK.F	√
194306629	endoplasmic reticulum aminopeptidase 2	K.PGK*ELK*VLSYPAHEQIALLVPEK.L	√
194383430	unnamed protein	K.VTANQMEMEHSLILNNLK*TLLWK.K	√
21039241	Myoferlin (Fer-1-like protein 3)	K.GYSK*LKIYNCELENVAEFEGLTDFSDTFK.L	√
111601563	C14orf102 hypothetical protein LOC55051	R.SHLK*SESSDESDTNKKLK*QTSR.K	√
4758798	Neuro-d4 (rat) homolog	R.K*RQDTASLEDRDKPYVCDK.F	√
116241326	Probable ATP-dependent RNA helicase DDX46	K.INAK*LNYVPLEK*QEEERQDGGQNESFK*R.Y	√
118142875	nexilin	K.EREEKERIK*YEEDK.R	√
118722345	hypothetical protein LOC401024	K.NISAKEK*EEEEREKEKVR.E	√
119569596	fibronectin type III and ankyrin repeat domains 1, isoform CRA_a	K.PHPPVVGK*VTHHSIELYWDLEK*K*AK.R	√
119575211	hCG1788266, isoform CRA_b	R.EKAGFLHHVKK*SDPERGFER.V	√
119579998	Ral-GDS related protein Rgr, isoform CRA_a	K.TWAGVSSK*SMK*ELKELCKKDTAVK.R	√
119602655	zinc finger CCCH-type containing 3	K.IIRRRGSTSLPGDK*KSGTSPAATAK.S	√
120046	Basic fibroblast growth factor receptor 1	K.PNRMPVAPYWTSPEKMEKK*LHAVPAAK*TVK.F	√
123297248	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	K.DRTRNVLERSDK*K*AYEEAQKR.L	√
125765	Ig kappa chain V-I region HK101	R.ARQGISSWLAWYQQK*PEK*APK.S	√
1345662	Calcium signal-modulating cyclophilin ligand	K.SKQQDSDK*LNSLSVPSVSK*R.V	√
13994345	fibroblast growth factor binding protein 2	K.LTEATQLGK*DSMEELGK*AK*PTTRPTAK.P	√
14211935	testes development-related NYD-SP18	K.GLSITTK*DPRILVTHCLVPKNCSSPSGDSKLVQK.K	√
14589856	protein tyrosine phosphatase type IVA, member 3 isoform 1	R.PK*QRLRFKDPHTHK*TRCCVM.-	√
148762940	DVL-binding protein DAPLE	K.ELARCRDAAGKLKELEK*DNRDLTK*QVTVHARTLTTLR.E	√
148806872	lupus brain antigen 1	K.ATSHYK*PLDPNIHK*LQDLR.D	√
150010540	FERM domain containing 4B	K.LQEIENAINEYRIRCGK*K.P	√
150182807	Elongation factor 1-alpha	R.GITIDISLWK*FETSK.Y	√
153945715	myosin VC	K.TIGK*ANDVHSSSGPK*EYLGMLQYK.R	√
166063995	Transcription factor IIIA	K.EEILCEVCRKTFK*RKDYLK*QHMK.T	√
167887702	Isodium channel beta-4 subunit	K.SDPK*VTLKDDDRITLVGSTKEK.M	√
136191	Serotransferrin precursor (Transferrin)	R.NLREGTCPEAPTDECK*PVK.W	√
169208472	similar to cis-Golgi matrix protein GM130	R.QEEK*IREQEEKIREQEKK*MWR.Q	√
1708323	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 2	K.YFELFPQERSPLWQNPCDDK*RHK*DIWSK.E	√
170932473	Zinc finger protein 786	R.PFSCRKCGKGFAK*QCK.L	√
1709337	Nucleosome assembly protein 1-like 1	K.EDPK*GIPEFWLTVFKNVDLLSDMVQ.-	√
172046609	Ankyrin repeat domain-containing protein 6	R.AQSVPRDEVAQSK*GSVSAGDTPSSEQAVARK.E	√
17402886	HEAT-like repeat-containing protein isoform 1	R.GTGNSVDPK*SSGSK*DTQPRKATLKSRK.S	√
18375528	UPF3 regulator of nonsense transcripts homolog B isoform 1	K.K*AESTESIGSSEKTEK*K.E	√
187960084	glutamate receptor, metabotropic 8 isoform c	K.LIQK*GNDRPNGEVKSELCESLETNTSSTK.T	√
194675189	similar to WD repeat-containing protein 87	R.EEEQAQK*KARDMLGLEETQVILK*K.G	√
19923191	minichromosome maintenance complex component 3 associated protein	K.CLQSLK*EMYQDLRNK.G	√
20981706|	CTP synthase 1	K.WK*EMADRYDRLLETCSIALVAK*YTEFSDSYASVIK.A	√
21361116|	versican isoform 1	K.MK*PRYEINSLIRYHCK.D	√
4759154	Synaptosomal-associated protein 29	K.MDQDLK*ISQK.H	√
22538393	Isoform 1 of A-kinase anchor protein 9	K.NQEIK*NMKLELTNSKQK.E	√
23503239	aldehyde dehydrogenase 16 family, member A1	R.QGAELK*AAEAEVELSARR.L	√
2507171	Thioredoxin-dependent peroxide reductase, mitochondrial	K.GTAVVNGEFK*DLSLDDFK.G	√
12025663	ubiquitin-conjugating enzyme E2 variant 1	K.IECGPK*YPEAPPFVR.F	√
28558977	mediator complex subunit 26	K.NEELAK*RAK.K	√
29734087	PREDICTED: similar to ribosomal protein L36 [Homo sapiens]	K.RK*QEELSNVLAAMR.K	√
32949402	BRCA1-associated RING domain protein 1	K.QTVPSENIPLPECSSPPSCKRK*VGGTSGR.K	√
33112673	Kinesin-like protein KIF3A	R.AKNIKNKARINEDPK*DALLRQFQK*EIEELK.K	√
33356179	transcription termination factor, RNA polymerase I	K.K*MSPQELKEVDSK*LQENPESCLSIVR.E	√
118498339	EMI domain containing 2	K.GEEGEK*AATAEGEGVQQLREALK*ILAER.V	√
38708169	sorting nexin 25	K.KVQLPSLSKLPFK*SIDQKFMEKSK.N	√
41281376	ubiquitin specific protease 8	K.KESEQAKKEDK*ETSAKRGK.E	√
41281499	Rb1-inducible coiled coil protein 1	R.EVVEKELLEK*VK.H	√
41281987	nesprin 1 longest	R.AIQERAK*EAVTK.S	√
45387958	1A6/DRIM (down-regulated in metastasis) interacting protein	K.PATPCRPSEAAQNKGGIK*R.S	√
45477317	Angiogenic factor with G patch and FHA domains 1	K.NK*KNWDKARERFTENFPETKPQK.D	√
59853162	thymine-DNA glycosylase	K.EKQEK*ITDTFK.V	√

46852161	MBD6 Methyl-CpG-binding domain protein 6 l	R.RK*YNPTRNSNSSR.Q	√
4757780	Isoform 1 of Beta-arrestin-2	K.TVK*K*IK*VSVRQYADICLFSTAQYK.C	√
50400610	Intraflagellar transport protein 74 homolog	K.MELLESK*MTEEQHSLK.S	√
50428933	C1q domain containing 1 isoform 1	R.NIEK*KK.L	√
55957323	nucleolar protein 8	K.TGGVDFHMK*AVPGTEVPGHK*NWVVSK.F	√
56205148	Protein tyrosine phosphatase, receptor type, C	K.ETEKDCLNLDK*.N	√
56699473	Zinc finger protein 192	K.SGLIEHQRIHTGERPYK*CK*ECGK.A	√
57209105	SNF2 histone linker PHD RING helicase	R.QTTSHKEISYVFTSEK*ANQEEDIPVKGSHSTK.V	√
57232746	nuclear receptor interacting protein 1	K.K*GHK*NNVTNSK.P	√
5803187	transaldolase 1	K.AAQASDLEK*IHLDEK.S	√
5902038	RAB, member of RAS oncogene family-like 2A	K.YDADDNVK*IICLGDSAVGK*S*KLMER.F	√
62511240	Vacuolar protein sorting-associating protein 4A	K.ESIRAK*CVQYLDRAEK*LK*DYLRSK.E	√
62896513	Lysyl oxidase-like 2 variant	R.K*RTPVMEGYVEVK*EGKTWKQICDKHWTAK*NSR.V	√
66529005	ATP-binding cassette, sub-family C, member 5 isoform 1	K.K*ETSGSQKK*SQDKGPKTGSVKK.E	√
6752658	epidermal growth factor repeat containing protein	R.GGNSHGGK*K*GNEEK*MKEGLEDEK.R	√
68303542	argininosuccinate lyase isoform 1	K.AEMDQILHGLDK*VAEEWAQGTFK.L	√
68303809	Zinc finger protein 43	K.HK*KIHTEKKPYKCEECGKAFKWSSLNEHK.R	√
71037379	glycogen phosphorylase, liver	K.VFK*DFSELEPDK.F	√
71565152	class II alcohol dehydrogenase, pi subunit	R.DLHK*PIQEVIIELTK.G	√
73486658	aspartate aminotransferase 2 precursor	R.FFK*FSR.D	√
108796666	hypothetical protein LOC126017	K.CNECGKVFNK*K.A	√
7662062	GRIP and coiled-coil domain-containing 2 isoform b	K.NDPLSSVKELEEK*IENLEK*ECKEK.E	√
83977459	pleckstrin homology-like domain, family A, member 1	K.LKELHFSNMK*TVDCVERK.G	√
84872173	zinc finger protein 131	K.QRTGK*KIHVCQYCEK.Q	√
88959048	zinc finger, DBF-type containing 2	K.LNPQK*EEQVHLENK.E	√
8923289	zinc finger protein 407	R.SSNSMAFLAHIRTHTGSK*PFKCK.I	√
8923421	SARS2 Seryl-tRNA synthetase, mitochondrial	R.SLEEEK*AAVTEAVR.A	√
91718902	myeloid/lymphoid or mixed-lineage leukemia 3	K.LDNQCVSVEPK*KKEQENKTLVLSDK.H	√
106507301	polymerase (DNA-directed), alpha	K.DCIFPYAFK*EVIEK.K	√
11055982	PR domain containing 13	K.TGHLCLYCGK*LYSR.K	√
110624781	myosin, heavy polypeptide 13, skeletal muscle	K.SRDVGSQK*MEE.	√
113430794	similar to Zinc finger protein 93	K.SSHLAAHK*RIHTGEK.P	√
116006967	neuregulin 1 isoform GGF2	R.LKEMK*SQESAAGSK.L	√
13124756	centrosomal protein 68kDa	K.K*DIDEHQSLTESVLQK.G	√
13128970	mitochondrial ribosomal protein 63	R.FIADQLDHLNVTK*K.W	√
13270473	beta-neoendorphin-dynorphin preproprotein	K.SKFLPSISTK*ENTLSK.S	√
13899251	component of golgi transport complex 3	K.LQTQMDQDEGTK*YR.Q	√
15559211	RE1-silencing transcription factor	R.KSVTEVK*EMDVHTGSNSEK*.F	√
16418341	pannexin 2	R.VENSK*AEK*PK.P	√
17149849	FK506-binding protein 6	K.EQPFNHDINNELK*K.L	√
19913381	G6B protein isoform G6b-E precursor	R.TYCK*APGPTHAPLVK.T	√
21071077	dishevelled-associated activator of morphogenesis 1	R.IHTSLIGCIK*ALMNNSQGR.A	√
21237736	mitogen-activated protein kinase 9 isoform JNK2 alpha2	K.VIEQLGTPSAEFMK*K.L	√
21361657	protein disulfide-isomerase A3 precursor	K.TVAYTEQK*MTSGKIK.K	√
21450804	calreticulin 3	K.DNKAQDWEK*HFLDASTSK.Q	√
21541824	transducin-like enhancer protein 1	K.K*DASSSPASTASSASSTSLK.S	√
21902519	pecanex homolog	R.LMAPESIK*PLTTSK.S	√
22749325	zinc finger protein 553	K.SFRLSSDLVK*HQR.T	√
22749515	KM-HN-1 protein	R.PLASDLK*GYFK.V	√
23503331	defensin, beta 123 precursor	K.K*ERVYVYCINNK.M	√
24119274	voltage gated channel like 1	R.INVSVSK*NLNLK.L	√
27478171	PREDICTED: similar to CG10038-PB, isoform B	R.EWVTSPK*PLDK.P	√
29469071	Rho GTPase-activating protein	K.LQRNESEPSEMK*AMALK.G	√
32698714	hypothetical protein LOC284058	R.PVLSCKK*R.R	√
32967601	ankyrin 3 isoform 1	K.LEVIEEEGK*VGPDEDKPPSK.S	√
33342276	hexokinase domain containing 1	K.LEEGVLLSWTK*K*FK.A	√
36031016	CTCL tumor antigen L14-2	K.ELEDLK*RTFK.E	√
38505170	Ras protein-specific guanine nucleotide-releasing factor 2	R.MRPYQSNQEDEDPDIK*K.I	√
40788003	proteasome (prosome, macropain) activator subunit 4	K.HWTFEK*VEK.L	√
41148718	PREDICTED: similar to Myb-related protein A	K.PNPNTSKVVK*LEK.N	√
44955926	hypothetical protein LOC23199	R.GK*PSEQLTPTRAEK.L	√
4501857	acyl-Coenzyme A dehydrogenase, long chain precursor	K.TNAK*KDGSDWILNGSK.V	√
4502351	bile acid Coenzyme A: amino acid N-acyltransferase	K.TINSK*AHAEQAIGQLK.R	√
4502395	beclin 1	K.NRK*IVAENLEK.V	√
4504179	glutathione S-transferase M4 isoform 1	R.FEGLEKISAYMK*SSR.F	√
4504437	heme oxygenase (decyclizing) 1	R.PQPDSMPQDLSEALK*EATK.E	√
4506591	retinal pigment epithelium-specific protein 65kDa	R.YVLPLNIDK*ADTGK.N	√
46049092	nebulin-related anchoring protein isoform C	K.K*AYGLQSDNQYR.A	√
46397394	pogo transposable element with ZNF domain	K.NMYPPPSFPTNK*AATVK.S	√
47578107	delangin isoform B	K.QK*GESRPETPK.Q	√
4758934	phospholipase A2-activating protein isoform 2	R.ESLMSHAIELK*SGSNK.N	√
4885099	carbonic anhydrase III	K.YAAELHLVHWNPK*YNTFK.E	√
4885215	v-erb-a erythroblastic leukemia viral oncogene homolog 4	R.LLEGDEK*EYNADGGK*MPIK.W	√
5031905	MyoD family inhibitor	K.LQTHPSLASQGSKK*SK.S	√
50345870	DENN/MADD domain containing 3	R.VQESGIVK*DASIIHR.L	√
51972256	Fc fragment of IgG, high affinity Ib, receptor (CD64) isoform b	K.K*WNLEISLDSGHEK*K.V	√
54292125	lysosomal trafficking regulator isoform	K.YGK*PVNDYSK*YINK.E	√
5454114	tissue factor pathway inhibitor isoform a precursor	R.ACK*K*GFIQR.I	√
54792129	discoidin, CUB and LCCL domain containing 2	K.IFQGNK*DYHQDVR.N	√
56550039	myeloid/lymphoid or mixed-lineage leukemia	R.FHK*PEEANEPPLNPHGSAR.A	√
5803082	kinesin family member 2C	K.QELAK*K*EIDVISIPSK.C	√

58530857	homocysteine-inducible, ubiquitin-like domain member 1 isoform 2	K.RHVLHLVCNVK*SPSK.M	√	
5901914	Rap guanine nucleotide exchange factor (GEF) 4	K.HK*VLLQQFNTGDER.A	√	
62899035	establishment of cohesion 1 homolog 2	R.STCLK*TNDEDKSFPIVTEK.M	√	
66571327	chromosome 17 open reading frame 27	K.TLHPLLEDGCIEDDPAPHK*K.V	√	
68303635	mutS homolog 3	K.K*VQQKEGGSDLGMSGNSEPK.K	√	
75677363	lectin, mannose-binding, 1 like precursor	K.QLAQAERQWK*K.Q	√	
7657196	zinc finger protein 330	R.K*DSDTESSDLFTNLNLGR.T	√	
7662288	hypothetical protein LOC9851	R.IEKLK*HSYNESYHCK.D	√	
7705682	geminin	K.ENPSSQYWKEVAEK*R.R	√	
7705724	APAF1 interacting protein	K.K*SQCTPLFMNAYTMR.G	√	
78482626	ring finger protein 30 isoform 2	R.QK*SELSDGIAMLVAGNDR.V	√	
83716019	zinc finger protein 284	R.EEK*FWIMETATQREGNSGGK.I	√	
92859678	small nuclear RNA activating complex, polypeptide 4, 190kDa	K.GALDLEK*PPLPQPGPEK.G	√	
98991769	taspase 1 precursor	K.EK*RGGFVLVHAGAGYHSESK.A	√	
9966847	hypothetical protein LOC57102	R.QGIEMEK*VMQELGK.S	√	
20072188	aconitase 2	K.GEFDPGQDTYQHPPK*DSSGQHVDVSPTSQR.L		√
3121765	Actin-related protein 2/3 complex subunit 3	-.MPAYHSSLMDPDTKLIGNMALLPIRSQFKGPAPRETK*DTDIVDEAIYYFK*.A		√
4325111	Isoform 1 of Protein patched homolog 2	K.ICYK*SGVPLIENGMIERMIEK*LFPCVILTPLDCFWEGAK*LQGGSAYLPGR.P		√
4506019	alpha isoform of regulatory subunit B55, protein phosphatase 2	K.IQSHSRGEYNVYSTFQSHEPEFDYLK*SLEIEEKINK*IRWLPQKNAAQFLLSTNDKTIK.L		√
5262689	Hypothetical protein DKFZp434F222	K.KLMAFTLQDLK*EADTPKCEEKERRK*RELHSSATGR.S		√
5902752	A-kinase anchor protein 8	K.KTSLHVAKSVLNNRHIVK*MLEKYLKGEDPFTSETVDPEMEGDDNLGGEDKK.E		√
8922303	ATP5S-like	R.DK*EWIRPDKYGHFSQEFWNFCEVPVEAVDAGDCDINYEGLDNLLRLKELQSLSLQR.C		√
74751538	SH3 and PX domain-containing protein 3A	K.RRAEK*DEMVGASFLLTFQIPTEHQDLQDVEDRVDTFK*AFSK*K.M		√
13124667	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	R.FTDILVRHQSFVLVGETGSGK*TTQIPQWCVEYMRSLPGPK*RGVACTQPR.R		√
13626133	Steroid hormone receptor ERR2	K.LYAMPPPGMPEGDIK*ALTTLCDLADRELVVIIGWAK.H		√
13638390	Myosin-1	K.KLETDISQIQGEMEDIIQEARNAEEK*AKKAITDAAMMAEELK.K		√
13775212	polyamine modulated factor 1 binding protein 1	K.AENTRLCTK*ALGPSRTESTQREKVCGTLGWK*GLPQDMGQR.M		√
13959562	Ras GTPase-activating protein 3	K.TNNPQFDEVFYFEVTRPCSYSKKSHFDFEEEDVDK*LEIRVDLWNASNLKFGDEFLGELR.I		√
14196462	protocadherin gamma subfamily A, 2 isoform 2	R.AFLQTYSHEVSLTADSRKSHLIFPQPNYADTLISQESCEK*K*DFLSAPQSLLEEER.E		√
15150801	Isoform 1 of Zinc finger protein 682	K.KIHTGEKPYTCEDCGRAFNRHSHLTKHK*TIHTGKKPYK.C		√
17225486	Ciliary dynein heavy chain 7	K.SYIEYTKTLPLTPAPEIFGMNANADITK*DQSETQLLFDNILLTQSRSAGAGAK.S		√
22539643	SPHK1 Sphingosine kinase 1	R.GPAAAGNDAGAPTATAPGGEGEPHSRPCDARLGSTDK*ELK.A		√
17380284	Regulator of G-protein signaling 7	R.K*SVYGLQNDIRSHSPTHTPTPETK*PPTEDELQQQIKYWQIQLDR.H		√
19856971	Nebulin	K.ADYNSWMK*GCGWVPFGSLEMEKAKRASDILNEK*KYRQHPDTLK*FTSIEDAPITVQSK.I		√
22324339	platelet glycoprotein Ib alpha	K.AMTSNVASVQCDNSDKFPVYKYPGKGCPTLGDEGDTDLYDYYPEEDTEGDK*VR.A		√
22538495	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-like 3	R.CLVDNSK*SRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTGRCLEVENR.G		√
29171719	glycosylphosphatidylinositol specific phospholipase D1 isoform 2	R.VYVYNGK*ETTLGDMTGKCKSWITPCPEEKAQYVLISPEASSRFGSSLITVR.S		√
30316388	Probable cation-transporting ATPase 13A3	K.MWFCAK*IRVLSLETYPVSSPKSMSNKLSNGHAVCLIENPTEENRHRI		√
32469740	Leucine-rich repeat LGI family member 2	R.DVFSDLDSLIELDLRGNKFECDCK*AK*WLYLWLKMTNSTVSDVLCIGPPEYQEKK.L		√
53832026	IQ motif and Sec7 domain-containing protein 2	K.AQNPAYFEGK*PASLDEGAMAGARSHR.L		√
37537981	Riboflavin kinase	K.QLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVHK*MVVSIGWNPYYK.N		√
46396475	Protein KIAA1199	R.GSAAARVFKLFQTEHGEYFNVSLSSEWVQDVEWTEWFDHDK*VSQTKGGEKISDLWK*AHPGK.I		√
189054904	tropomyosin 3	R.RIQLVEEELDRAQERLATALQKLEEAEK*AADESERGMKVIENRALKDEEK.M		√
55960506	chaperonin containing TCP1, subunit 3	R.PVLVLSQNTKRESGRK*VQSGNINAAK*TIADIIRTCLGPK*SMMK.M		√
55960954	Tropomodulin-4	R.SGDPIANAVADMLRENRSLQSLNIESNFISSTGLMAVLK*AVRENATLIELR.V		√
55976611	RNA-binding protein 28	K.DQQQK*AAQHHTEEQSKVPPEQK*RKAGSTSWTGFQTKAEVEQVELPDGKK.R		√
56748805	Uncharacterized protein C6orf182	K.IHRLELERTQAEDNLNILSREAAQYK*KALENETNERNLAHQELIK*QK.K		√
57471658	acyl-CoA synthetase long-chain family member 4	K.VQEMNYIQK*TLFK*IGYDYK.L		√
68565390	Mediator of DNA damage checkpoint protein 1	R.K*RSLATMDSPPHQKQPQRGEVSQKTVIIKEEEEDTAEKPGK*EEDVVTPK.P		√
119599205	Isoform 1 of Immunoglobulin superfamily, member 10	K.HK*WTMISRDNNTKLEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSK*VRAPYVSEDGR.I		√
74714811	Poly [ADP-ribose] polymerase 8	R.PCPAAVK*SEECLTLK*SHRLLTRSCSGDPRCEHNTNLKPHK*LLSR.S		√
37202123	NMDA receptor-regulated protein 2	R.IGENLNASASSVENEPAVSSATQAK*EK.V		√
74754346	HIV Tat-specific factor 1	K.ESK*K*K*TLKNDCEENGLAKESEDDLNKESEEEVGPTKESEEDDSEKESDEDCSEKQ		√
74762616	Ciliary dynein heavy chain 3	K.KYVDLLDNTAEQNIAAFLK*ENHDIDDFVTKINAIKK.R		√
256985100	TICAM2 protein	R.EAQGRSRAEDLNTRVAYWHSVDTSPGYHESDSK*K*SEDLSLCNVAEHSNTTEGPTGKQ		√
92087039	Proto-oncogene DBL (Proto-oncogene MCF-2)	K.YSKDCEGSALLKKALDAMLDLLKSVNDSMHQIAINGYIGNLNELGK*MIMQGGFSVWIGHKK*GATK.M		√
92090617	Serine/threonine-protein kinase MRCK beta	K.LELSRKLQESTQTVQSLHGSSRALSNSNRDKEIKK*LNEEIER.L		√
113423509	SET domain containing 1B	K.KKLKFCK*SHIHDWGLFAMEPIAADEMVIEYVGQNIRQVIADMR.E		√
60390855	WAS/WASL-interacting protein family member 2	R.SAPILEK*PK*GSSGGYGSGGAALQPK.G		√
118918405	SAC3 domain containing 1	R.VVFLRGRYVEEGLPPASTCK*VLVESK*LRGRTLEEVVMAEEEDEGTDRPGSPA.-		√
121946271	Copine-9	K.K*CGTILLTAEELSNCRDIATMQLCANK*LDK*KDFFGKSDPFLVFYR.S		√
122070147	Src kinase-associated phosphoprotein 1	K.QPK*GTFLIKGYSVRMAPHLRRDSK*K*ESCFELTSQDRR.S		√
124056488	Collagen alpha-2(I) chain	R.GFPGTPGLPGFKGIRGHNGLDGLKGQPGAPGVK*GEPGAPGENGTPGQTGARGLPGERG.R		√
134048493	6-phosphofructokinase, liver type	R.NYGTKLGVKAMLWLSEK*LREVYR.K		√
142976729	Dehydrogenase/reductase SDR family	M.K*FLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAK.L		√
157671919	LOC374864 isoform 1	K.QEMETLLSEAIRLIK*SLETDRADAEEALK*QQR.S		√
157742851	ubiquitin-conjugating enzyme E2Q family member 1	K.ENLAILEK*IK*KNQRQDYLNGAVSGSVQATDR.L		√
167234429	zinc finger and BTB domain containing 17	R.SFSDPTSK*MRHLETHDTDKEHKCPHCDKKFNQVGNLK.A		√
119609006	similar to polyhomeotic 1-like isoform 3	K.PLQTGLPTGLTENQSGGPLGVDSPSAELDK*K*ANLLK.C		√
4503515	EIF3S3 6 kDa protein	R.KEGTGSTATSSSSTAGAAGKGKGKGGSGDSAVKQVQIDGLGNAFK*YVDR.K		√
108935939	Transferrin receptor protein 1	K.ILNIFGVIK*GFVEPDHYVVVGAQRDAWGPGAAK*SGVGTALLLK.L		√
113420417	similar to fatty acid binding protein 9	R.TESSFQDTKISFKLGEEFDETTADNRK*VKSTITLENGSMIHVQKWLGK*.E		√
110347420	structural maintenance of chromosomes 2-like 1	K.ELEK*NMVEDSKTLAAK*EKEVK*KITDGLHALQEASNK.D		√
110611167	ADAM metallopeptidase with thrombospondin type 1 motif, 14	K.EVGSMKADDKCGVCGGDNSHCRTVK*GTLGK*ASKQAGALK.L		√
114205458	NEXN protein	R.KHKLEMEK*QEFEQLRQEMGEEEEENETFGLSREYEELIKLKRSGSIQAK*NLK.-		√
115205	Complement C1s subcomponent	K.MGPTVSPICLPGTSSDYNLMDGDLGLISGWGRTEK*RDRAVRLK.A		√
50845416	WNK3 Isoform 2 of Serine/threonine-protein	K.KLK*GKHK*DNEAIEFSFNLETDTPEEVAYEMVK*SGFFHESDSK.A		√
4557577	fatty acid binding protein 1, liver	K.GK*DIKGVSEIVQNGK*HFKFTITAGSKVIQNEFTVGEECELETMTGEK.V		√
1172837	Ran-specific GTPase-activating protein	K.ICANHYITPMMELK*PNAGSDRAWVWNTHADFADECPK*PELLAIRFLNAENAQKFK*TK.F		√
118572662	Kinesin-like protein KIF13A	K.EGSNINK*SLTTLGLVISSLADQAAGKGKSKFVPYR.D		√
88958985	heterogeneous nuclear ribonucleoprotein A1-like, isoform CRA_b	K.IEVIEIMTDRGSGK*KRGFAFVTFDDHDSVDKIVIQK*YHTVNGHNCEVR.K		√

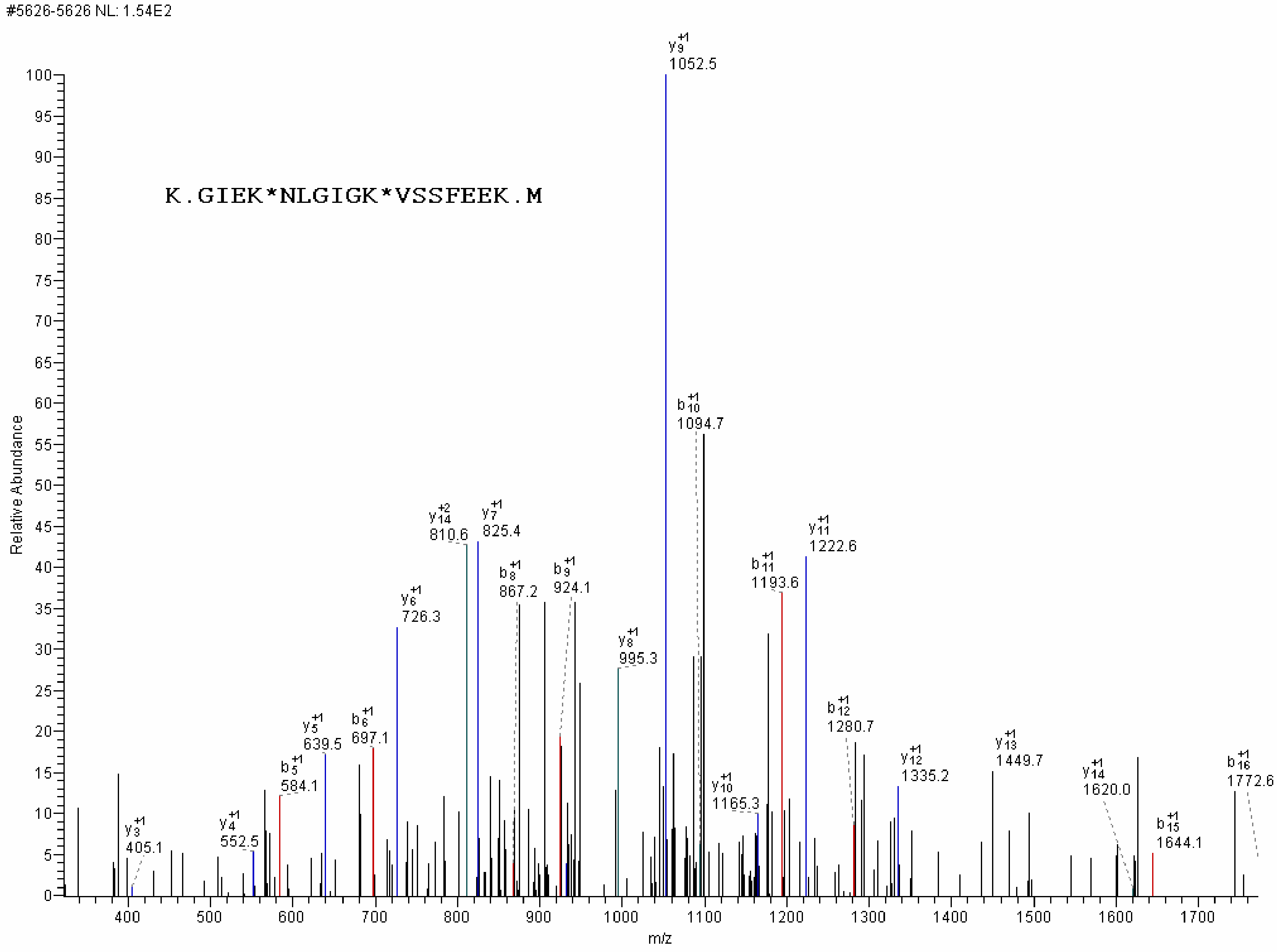
38569482	hypothetical protein LOC57535	R.GNNVLYWRTTAFSVWTK*VPKPVLVRNIAITGVAYTSECFPCK*PGTYADK.Q	√
83523748	hypothetical protein LOC84140	K.KQEEDPEYK*KK*FRANPVPASVFLPLYHDLVKQKEERR.R	√
122890707	mitofusin 2	R.FEECISQSAVK*TKFEQHTVRAKQIAEAVRLIMDSLHMAAREQQVYCEEMREERQDR.L	√
88968962	hypothetical protein isoform 3	K.AIATTALIFRNSSDSDGK*LEK*AIAK*DLLQTQFRNFAELPFTFYHEWK.Q	√
7656991	Coronin-1C	K.KNILDSK*PTANKKCDLISIPKKTTDTASVQNEAK*LDEILK.E	√
28376656	zinc finger, X-linked, duplicated B	K.HQLKMHLLTHSSSQGQRPFKCPLGGCGWTFTTSYK*LK*RHLQSHDKLR.P	√
13375785	steroid 5 alpha-reductase 3	R.NAYITGK*NLLMQARWFHILGMMMFIWSSAHQYKCHVILGNLRK*NK.A	√
14250413	Isoform 1 of Centrosomal protein	R.ENSLTDNLNDLNNELQK*KQKAYNKILREK*EEIDQENDELK.R	√
143811400	G protein-coupled receptor kinase 4	K.WLERQPVTKNTFRHYRVLGK*GGFGEVCACQVRATGKMYACK.K	√
119603744	Reelin precursor	K.NNSADWIQLEK*IRAPSNVSTIIHILYLPEDAK.G	√
53692189	AEBP1	K.SSRGLK*IYAMEISDNPGEHELGEPEFRYTAGIHGNEVLGRELLLLLMQYLCREYR.D	√
150171218	death inducer-obliterator 1	K.DPHGEK*REFQDAPYNEVTGAPAQFEGTEQAPFLGSRGGAPFQFGGQRRPLLSQLK*GPR.G	√
66933018	Indolethylamine N-methyltransferase l	R.EELEK*WLKKEPGAYDWTPAVK*FACELEGNSGRWEEK.E	√
88981318	hypothetical protein	K.GLSK*SMYVFQSLQNVSDSLKYIFSK.C	√
113428240	similar to CG2839-PA	K.VGKIKREMTK*EERDMSEEVEEMATLEEK.V	√
5031805	Insulin receptor substrate 1	R.AASEAGGPARLEYYENEKK*WRHKSSAPK*RSIPLESCFNINK.R	√
38230498	sacsin	K.YLHEALMQNEITK*MSIIDKLKPFSFILVENAYVDSEK*VSFHLNFEAAPYLYQLPNK.Y	√
166989553	Chromosome fragility-associated gene 1 protein	K.HEDFSGGIDFKGSSDDEEESRLCNTVLITGPTGVGKTAAVYACAQELGFK*IFEVNASSQRSGR.Q	√
167003331	N-methyl-D-aspartate receptor subunit 2B	K.KAGNLYDISEDNSLQELDQPAAPVAVTSNASTTK*YPQSPTNSK*AQKKNRNK.L	√
21918844	zinc finger protein 25	K.ECGK*AFSQKSHLTVHQRMHTGEK*PYKCKECGKFFSRNSHLK.T	√
54859722	Nuclear pore complex protein Nup160	R.FIHWK*TSGDTLELMEESLDINLLNNAIRLK.F	√
56118292	sphingosine kinase type 1-interacting protein	K.DSVTECK*QPPVSSLSKTASLTNHSPLDSKKETSSCQDPVPINHK.R	√
187954967	PALM2-AKAP2 protein isoform 1	K.ETEKSFKDFQK*GFSSTDGDAVNYISSQLPDLPILCSRTAEPSPGQDGTSRAAGVGWENVLLK.E	√
187954987	Pleckstrin homology domain containing, family G member 1	R.CESHQDLLPDIADSHQQGTEKLSDLTLQDSQK*VVVVNRNLPLNAQIATQNYFSNFK.E	√
38788288	zinc finger protein 160	R.GIHSGEK*PYKCNECGKVFAQTSQLARHWRVHTGEK*PYK*CNDCGR.A	√
7705897	alpha-aminoadipate aminotransferase	R.NPSPIRTMTDILSRGPK*SMISLAGGLPNPNMFPFK*TAVITVENGKTIQFGEEMMK.R	√
14210488	Dynactin subunit 5	K.SEYIETASGNK*VSRQSVLCGSQNIVLNGK.T	√
21665857	Isoform 1 of Zinc finger protein 33B	R.VHTGEK*HFQCNQCGK*TFWEKSNLTKHQRSHTGEK*PFECNECGK.A	√
22096378	Vacuolar ATP synthase catalytic subunit A	R.EHMGDILYK*LSSMKFKDPLKDGEAK*IKSDYAQLLEDMQNAFR.S	√
23503064	Eukaryotic translation initiation factor 3 subunit 4	K.IVSCRICK*GDHWTTRCPYK*DTLGPMQKELAEQLGLSTGEK*EKLPGELEPVQATQNK.T	√
27804346	BRD4-NUT fusion oncoprotein	K.CCSGILK*EMFAK*K*HAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAR.E	√
27805668	Pantothenate kinase 3	R.ISKLSEVEEQEEEATIDIPEFYSLKVLTGGIDMGFWPFSPK*KADKIK*M.-	√
27805738	Serine/threonine-protein kinase 13	R.K*TMCGTLDYLPPEMIEGRTYDEKVDLWCIGVLCYELLVGYPPFESASHSETYRRILK.V	√
29366828	Synaptotagmin XII	K.NLIWTNDK*TTADPFVKVYLLQDGRKMSK*K*K.T	√
29839561	Isoform 3 of Nesprin-1	R.LEHK*LK*EEEESLPGFVNLHSTETQTAGVIDRWELLQAQALSK*ELRMK.Q	√
30315937	Bullous pemphigoid antigen 1	K.EAKISEIQMTAPLKLTYAEK*LHRLESQYAKLLNTSRNQER.H	√
109637771	Calpastatin (Calpain inhibitor)	K.ESK*EQLPPMSEDFLLDALSEDFSGPQNASSLK*FEDAK.L	√
31077164	Heat shock 70 kDa protein 4L	K.GK*LK*VLATTFDPYLGGRNFDEALVDYFCDEFKTKYKINVK.E	√
117168250	1-phosphatidylinositol-4,5-bisphosphate PPase epsilon-1	R.DLGTPECQSSLPCLK*ASISASILTTQNGEHNALEDLVMR.F	√
31982906	cingulin-like 1	K.DLEYELEAK*SHLKDDRSRLVK*QMEDK*VSQLEMELEEER.N	√
37790762	TRPM6 Isoform TRPM6a of Transient receptor	K.EDLK*K*LHDFEEQCVEKYFHEKMEDVNCSCEERIRVTSERVTEMYFQLKEMNEK.V	√
49640009	tetratricopeptide repeat domain 3	K.EK*EHELHLDQSLEISNTLTNEKMKIEEYIKKGKEDYEESHQRAVAAEVSVLENWK.E	√
39652254	Inter-alpha-trypsin inhibitor heavy chain H3	K.RK*NAHGEEKENLTARALDLSLKYHFVTPLTSMVVTKPEDNEDERAIADK.P	√
44887719	Protein boule-like	K.EVKIVNDRAGVSK*GYGFVTFETQEDAQKILQEAEKLNYK*DK.K	√
4503173	coxsackie virus and adenovirus receptor	K.IYDDYYPDLK*GRVHFTSNDLK*SGDASINVTNLQLSDIGTYQCK*VK.K	√
4504343	nuclear receptor subfamily 5, group A, member 2 isoform 2	K.VSGYHYGLLTCESCKGFFK*RTVQNNKHYTCTESQSCKIDK.T	√
4506529	Rhodopsin kinase	R.IISEPVKYPDK*FSQASK*DFCEALLEKDPEK*RLGFRDETCDK.L	√
4589550	KIAA0953 protein	K.MVAK*LLESEK*PNLQILGTNSFVKFANIEEDTPSYHRSYDFFVSR.F	√
8922301	WD repeat-containing protein 70	R.HAK*AAEDSPYWVSPAYSK*TQPK.T	√
8922712	Septin-11	R.QMFVMRVKEKEAELKEAEK*ELHEKFDLLKRTHQEEK.K	√
4826694	Integral membrane protein DGCR2/IDD	R.HHDLHSWHAESCYEK*SSFLCK*R.S	√
52783149	Serine/threonine-protein kinase LATS2	K.SSVQGLPAGPNSDTSLDAKVLGSK*DATRQQQQMRATPKFGPYQK.A	√
54112397	calcium channel, voltage-dependent, alpha 2/delta 3 subunit	K.KLAKNMEEMFHK*KSEAVRRLVEAAEEAHLK*HEFDADLQYEYFNAVLINERDK.D	√
5453682	hexamethylene bis-acetamide inducible 1	R.DFSETYERYHTESLQNMSK*QELIKEYLELEK*CLSRMEDENNRLR.L	√
5454140	tumor susceptibility gene 101	R.ELMNLTGTIPVPYRGNTYNIPICLWLLDTYPYNPPICFVK*PTSSMTIK.T	√
54633319	PDZ domain-containing guanine nucleotide exchange factor I	R.KSWTSSSSLSDTYEPNYGTVKRRVLESTPAESSEGLDPK*DATDPVYK.T	√
55743102	alpha 3 type VI collagen isoform 3	K.DIQK*EVVQDICSSEACKNSKADIIFLIDGSESISPKDFEKMK.R	√
56757430	Cytochrome P450 4F3	K.AK*SK*TLDFIDVLLLSKDEDGKKLSDEDIRAEADTFMFEGHDTTASGLSWVLYHLAK*.H	√
58331225	Isoform 1 of glycosyltransferase 8 domain containing 1	K.AIYMDDDVIVQGDILALYNTALK*PGHAAAFSEDCDSASTK*VVIRGAGNQYNYIGYLDYK*K.E	√
58331242	formin homology 2 domain containing 3	K.TRGK*MITDSGK*FSGSSPAPPSQPQGLSYAEDAAEHENMKAVLK*TSSPSVEDATPALGVRTR.S	√
18093112	ESF1 homolog (ABT1-associated protein)	K.NIVQHTTDSSLEEK*QRTLDSGTSEIVK.S	√
6306532	cadherin 11, type 2 preproprotein	K.DMGGHMGGLSGSTTVTVTLSDVNDNPPK*FPQSLYQFSVVETAGPGTLVGR.L	√
41281583	Histidine acid phosphatase domain containing 1	R.SSVYSPESNVRKTGSYIYEEFMPTDGTDVK*VYTVGPDYAHAEARKSPALDGK*VERDSEGK.E	√
8923173	Putative Rho guanine nucleotide exchange factor FLJ20184	K.IYCYHHDEAHSILESYEKEEELKEHLSHCIQSLK*.-	√
5902104	SRY (sex determining region Y)-box 10	K.AAQGEAECPGGEAEQGGTAAIQAHYK*SAHLDHR.H	√
5174481	Histone deacetylase 4 (HD4)	K.TQHSSLDQSSPPQSGVSTSYNHPVLGMYDAK*.D	√
74728992	Macoilin (Transmembrane protein 57)	R.KQKEVQK*ENEFYMQLLQQALPPEQQMLQKQEKEAEEAAK.G	√
74743522	Ankyrin repeat domain-containing protein 20A2	K.KLMNECDHLK*ESLFQYEREK*TEVVVVVRQLQQEVADSVK*K.L	√
74751990	POM121-like protein 2	K.SCHRPSSPVPLVSDFESLGGSESSGQQNQKIPQLPSSPENLVSEIPPPQLGYAVSDENLTLGK*.K	√
74759851	Zinc finger protein 664	R.EFFSERADLFMHQKIHTAEKPHKCDKCDK*GFFHISELHIHWR.D	√
74762352	Isoform 1 of Zinc finger protein 549	R.PYECSECGK*GFYLEVKLLQHQRIHTREQLCECNECGKVFSHQKRLLEHQKVHTGEK.P	√
74762600	Protein odd-skipped-related 1	R.GEGPGSPAGGLGALLDVTKLSPEK*K*PTRGRLPSKTK*K.E	√
74762761	ETS homologous factor	K.DENYLYDTNYGSTVDLLDSK*TFCRAQISMTTTSHLPVAESPDMK*KEQDPPAK*CHTKK.H	√
7657526	Ribosomal protein S6 kinase alpha-6	K.REVQPPFK*PASGKPDDTFCFDPEFTAK*TPKDSPGLPASANAHQLFK*GFSFVATSIAEEYK.I	√
88911355	Leucine-rich repeat-containing protein 8B	K.LSK*SKILLSSSGCSADIDSGKQSLPYPQPGLESAGIESPTSSVLDK*K*EGEQAK.A	√
90110077	T-complex protein 10A homolog	R.QEK*FYPNGSKEIVFPDGTVEHLKDGQEETLFPDGTIVRVER.N	√
90577164	RUN and TBC1 domain containing 2 isoform 2	K.K*EMEQVDAVVAARYQQVLAEWK*ACEVVVRQREREAHPATRTKFSSGSSIDSHVQR.L	√

Supplementary table S2. Acetylation sites studied in this study. MS identified acetylation peptides for EHHADH, MDH, ASL and MDH are listed in the table. Acetylated lysine residues are denoted by asterisk.

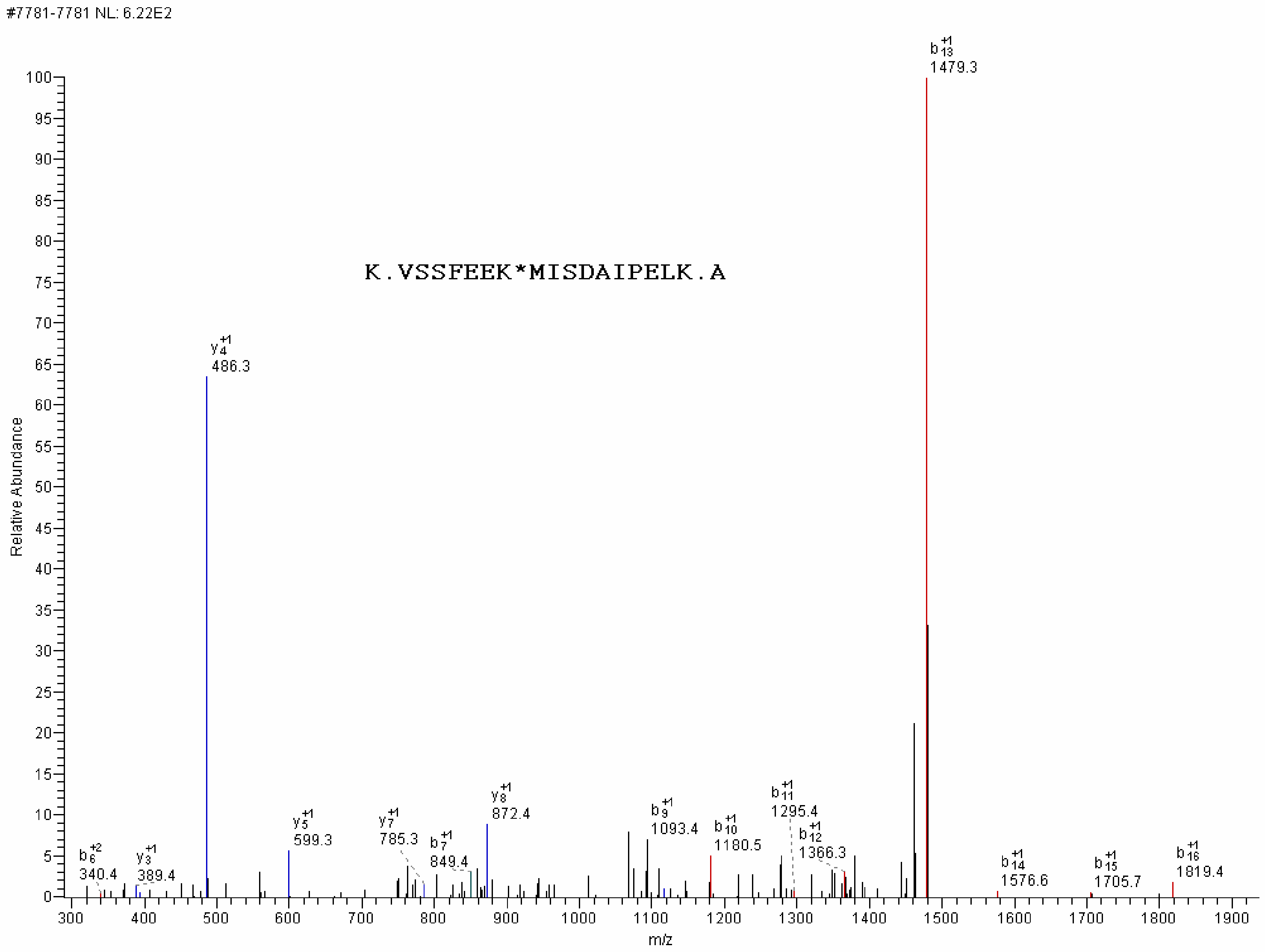
Enzyme Name	**Identified Acetylation Peptides**
EHHADH	K.MITSVLEK*EASK.M
	K.LGILDK*VVNSDPVEEAIR.F
	K.GWYQYDK*PLGR.I
	R.ILADEALK*LGILDK.V
MDH	K.VSSFEEK*MISDAIPELK.A
	K.GIEK*NLGIGK*VSSFEEK.M
	K.NLGIGK*VSSFEEK.M
	R.ANTFVAELK*GLDPAR.V
ASL	K.AEMDQILHGLDK*VAEEWAQGTFK.L
	K.K*NPDSLELIR.S
PEPCK1	R.LK*K*YDNCWLALTDPR.D
	K.EVEDIEK*YLEDQVNADLPCEIER.E

Supplementary table S3. Representative MS spectra of acetylated metabolic enzymes.

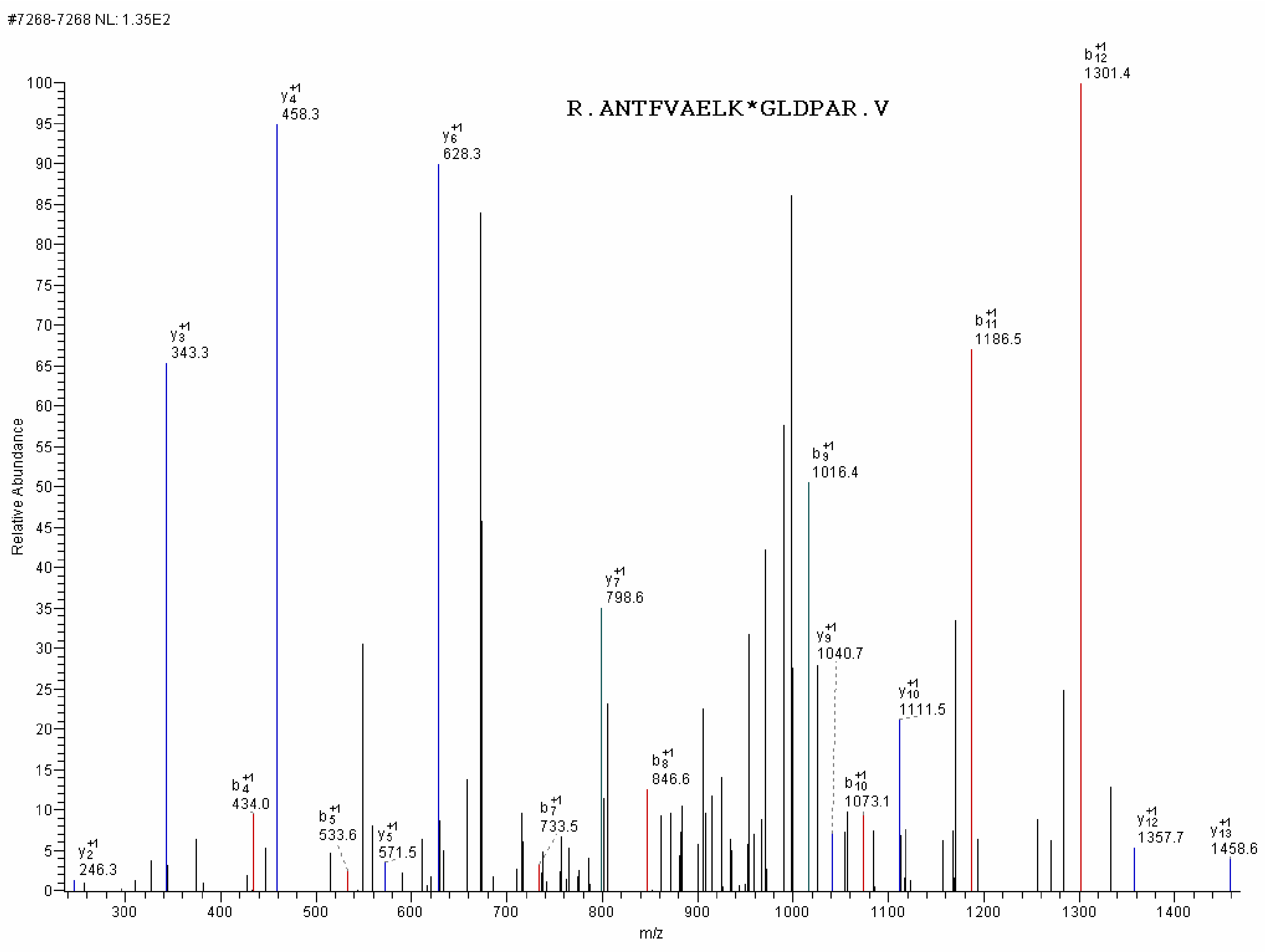
malate dehydrogenase (3-1)



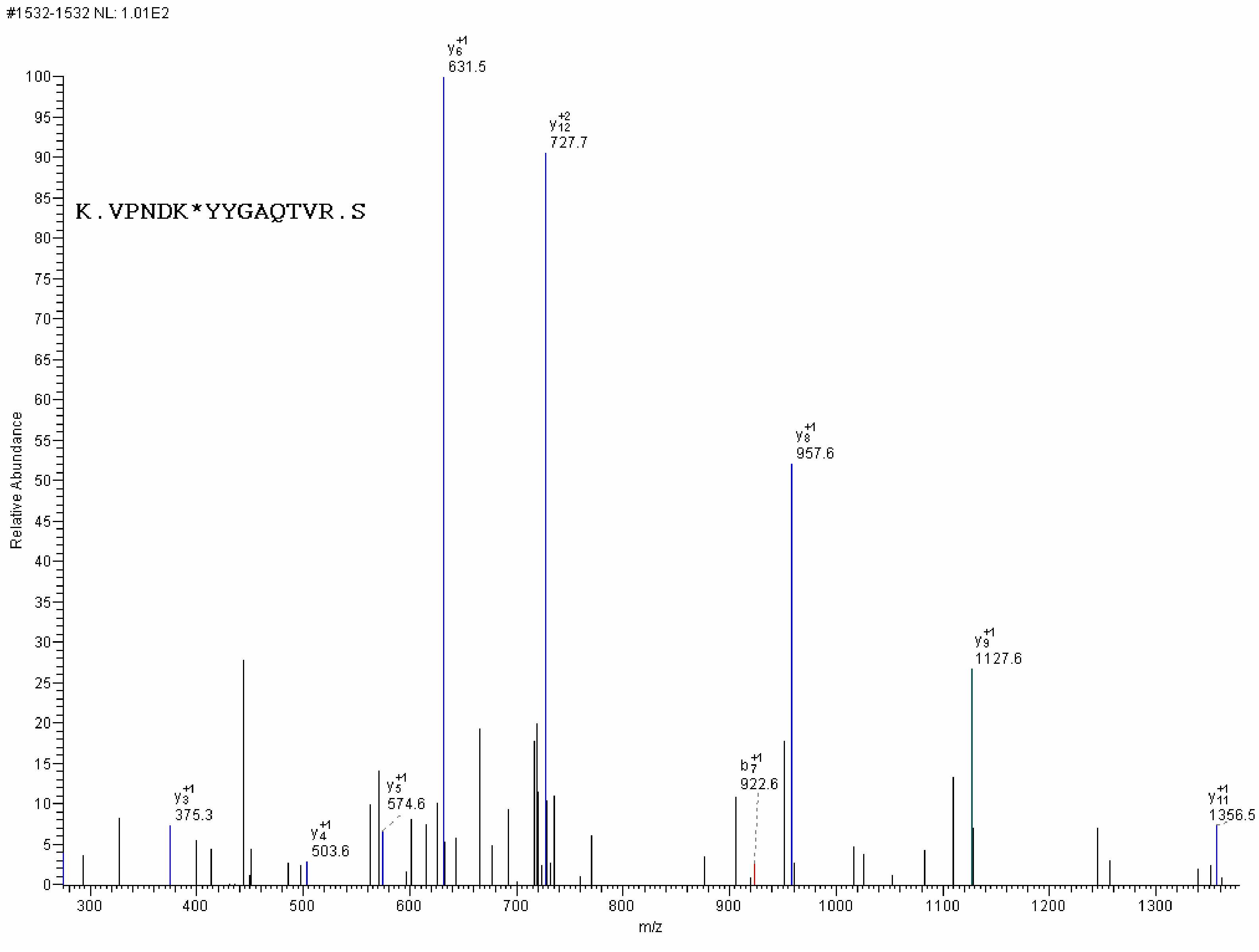
malate dehydrogenase (3-2)



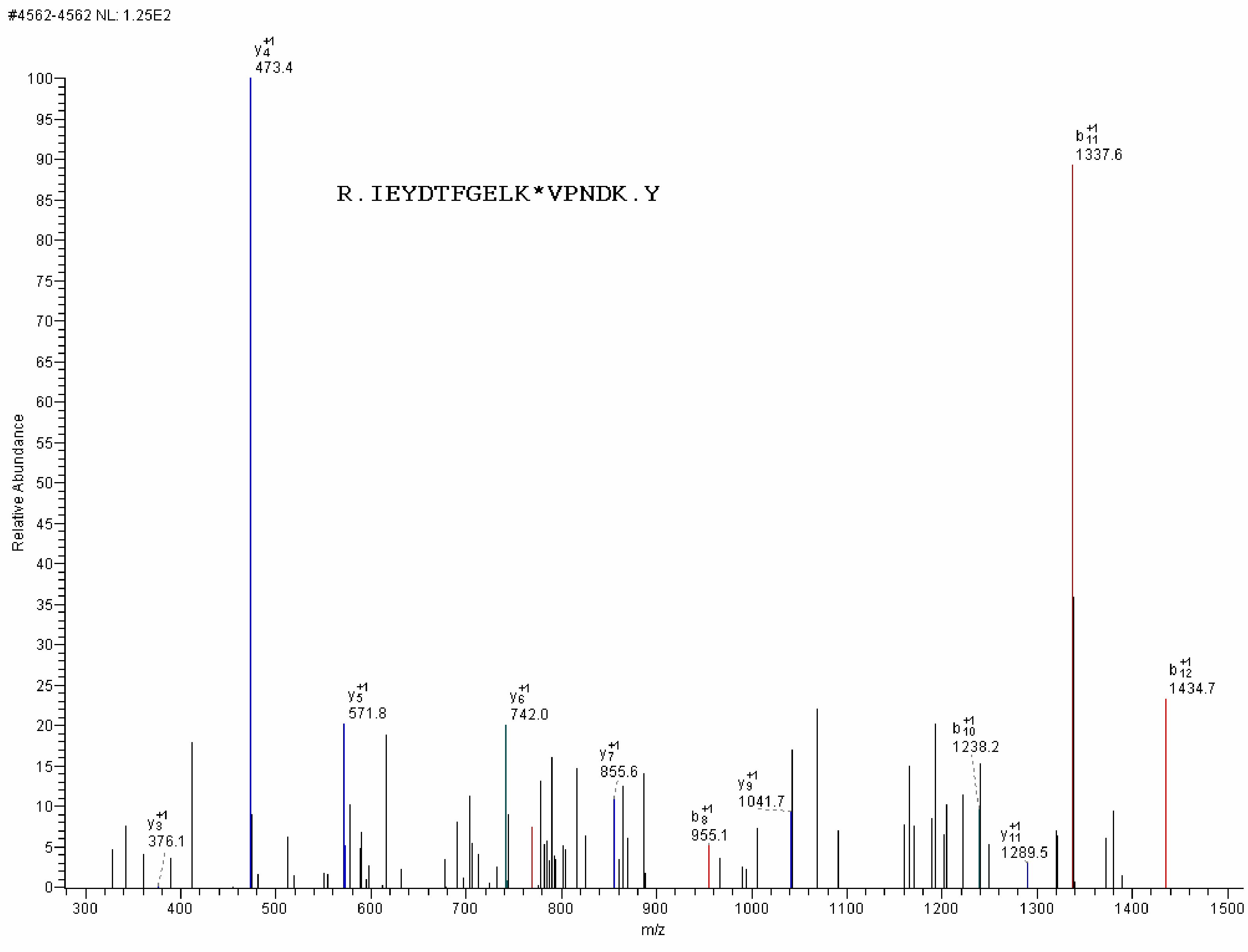
malate dehydrogenase (3-3)



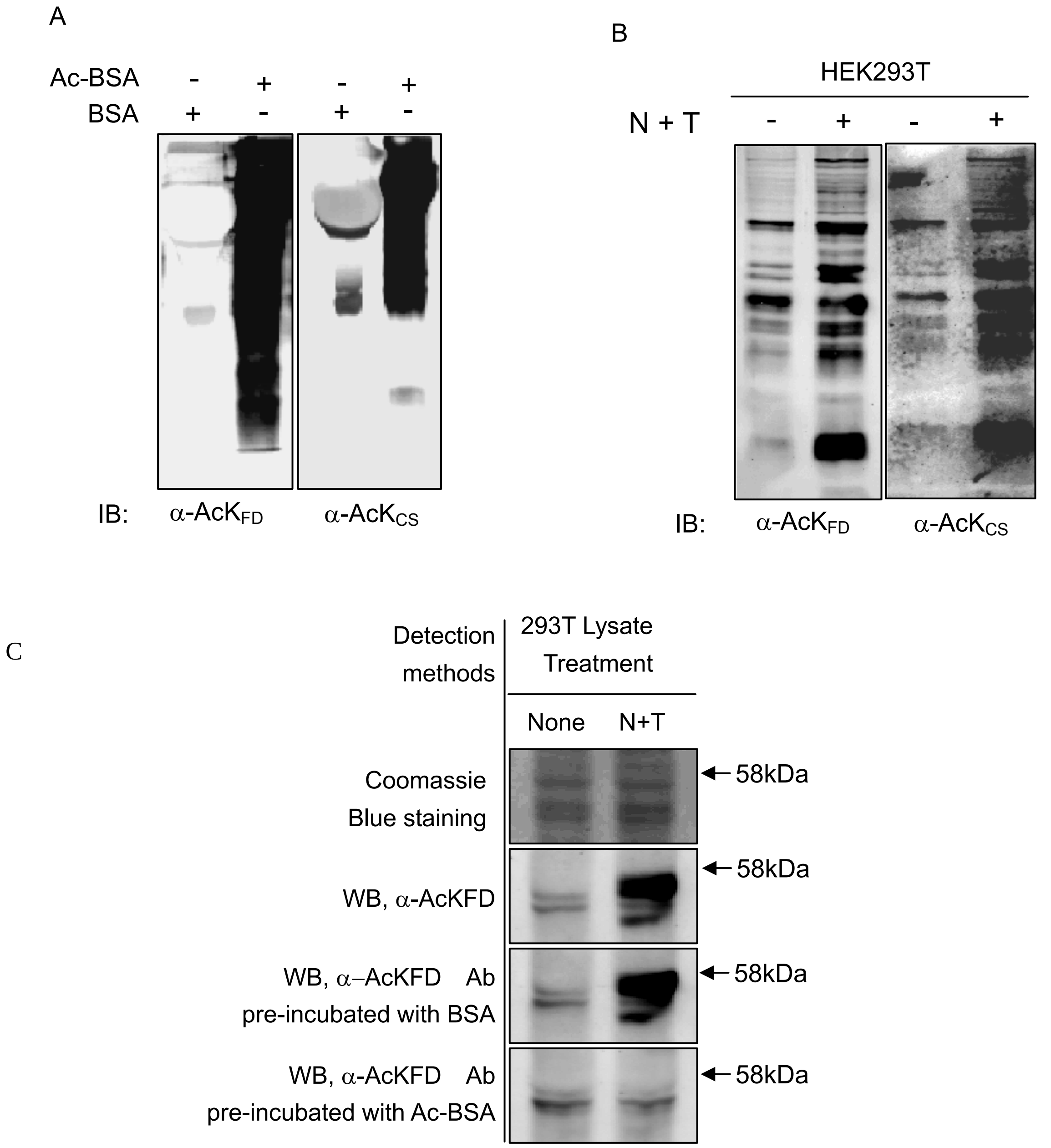
fumarate hydratase (2-1)



fumarate hydratase (2-2)



Zhao et al. Supplement Figure S1



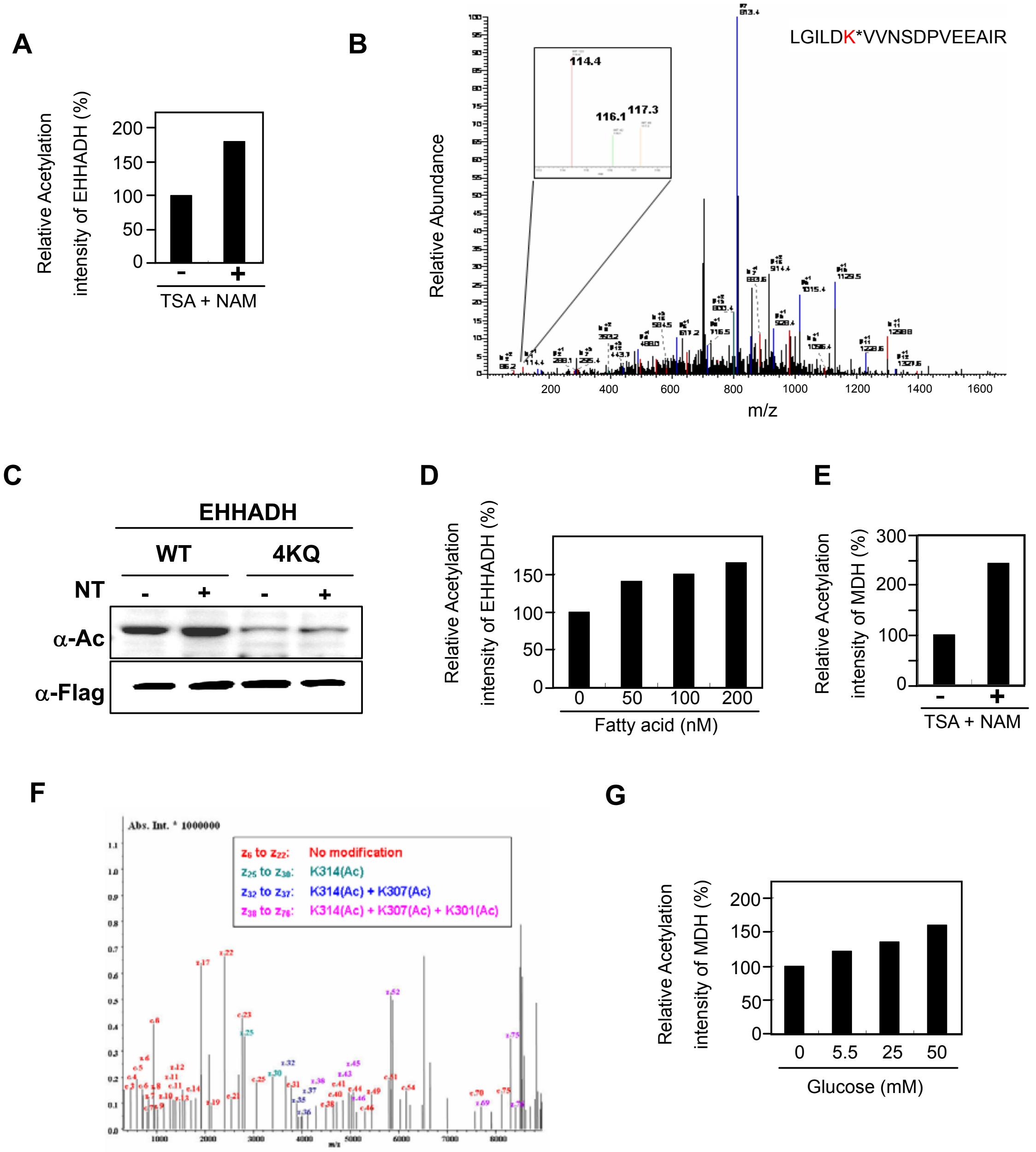
Supplement Fig.S1. Characterization of the anti-acetyllysine antibody

(**A**) The home-made anti-acetyllysine antibody specifically recognizes acetylated proteins. Antibodies were raised in rabbits immunized with chemically acetylated ovalbumin. Western blotting was performed against BSA (5 µg) and acetylated BSA (1 µg) as indicated. α-AcK$_{FD}$ and α-AcK$_{CS}$ denote home-made and Cell Signaling antibodies, respectively.

S1B. HEK293T cells were cultured under either no treatment or nicotinamide plus tricostatin A treatment (N+T) conditions as indicated. Equal amount of cell lysates were loaded onto SDS PAGE and acetylation was detected by either home made or Cell Signaling anti-acetyllysine antibodies.

S1C. Specificity of the α-AcK antibody. The α-AcK antibody was pre-incubated with bovine serum albumin (BSA) or acetylated BSA as indicated before it was used in Western blotting of HEK293T cell lysates. Arrows indicate a prominent 58KD acetylated protein that was detected by the α-AcK antibody. Pre-incubation with acetylated BSA but not the BSA control completely abolished the recognition, demonstrating that our α-AcK antibody specifically recognizes acetyllysine residues in proteins.

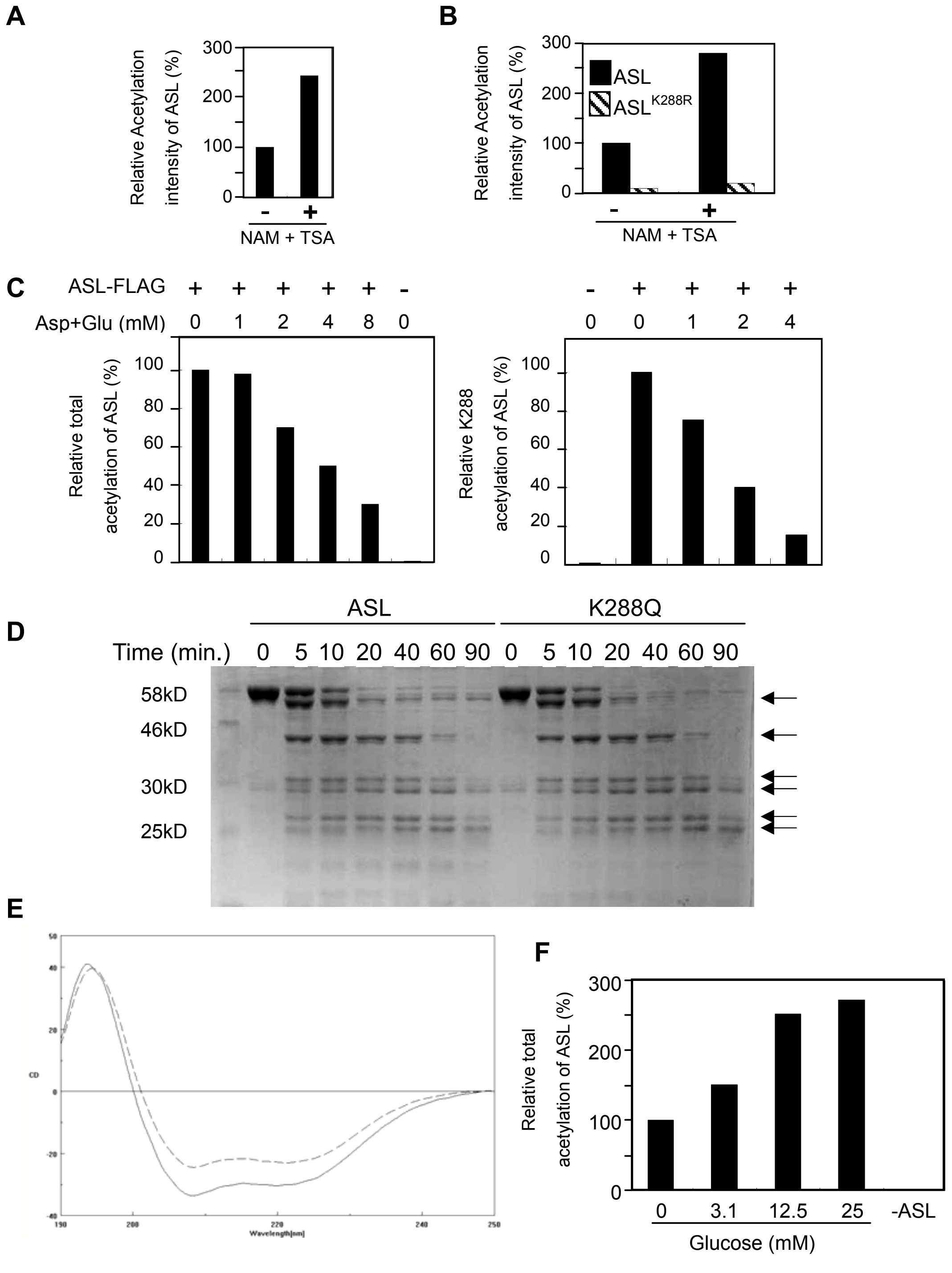
Zhao et al. Supplement Figure S2



Supplement Figure S2. Quantification of EHHADH and MDH acetylation.

(**A, D, E. G**) Individual quantification of protein acetylation shown in this figure corresponds to the immunoblots in Fig. 2A, 2D, 2E, 2G in the main text, respectively. Epitope tagged individual protein was expressed in HEK293T cells. Transfected cells were either left untreated or treated with deacetylase inhibitors TSA + NAM, fatty acid, or glucose as indicated. Proteins were immunoprecipitated, separated by SDS-PAGE and probed by anti-acetyllysine antibody (α-AcK). The intensity of acetylated bands was scanned and quantified on a Typhoon 9410 Imager. Relative acetylation was determined by normalization against total proteins detected by antibody specific to individual epitope tag. (**B**) Quantification of EHHADH acetylation by iTRAQ MS. EHHADH was immunoprecipitated from transfected cells and digested with trypsin. The digested samples from untreated and TSA+NAM treated cells were labeled with the iTRAQ tag of 116 Da and 114 Da, respectively. Synthetic peptides corresponding to the K171 acetylated peptide LGILD**K**(171)VVNSDPVEEAIR and the unacetylated peptide VVNSDPVEEAIR were labeled with iTRAQ tag 117 Da. The three individually labeled samples were mixed and then subjected to MS/MS analysis. The MS peaks of the 114Da, 116Da, and 117Da are shown in the insert. Quantification is based on the peak intensity of the tags. (**C**) EHHADH^{4KQ} mutant lost the majority of acetylation. (**F**) Identification of MDH K301, H307, and K314 acetylation by FTICR-MS. MS/MS spectrum of MDH-FLAG by FTICR analyses.

Zhao et al. Supplement Figure S3



Supplement Figure S3. Quantification of ASL acetylation and characterization of ASL K288Q mutant.

(**A – C, F**) Quantification of protein acetylation corresponding to those shown in Fig. 3A-3C, 3F in the main text, respectively. Epitope tagged individual protein was ectopically expressed in HEK293T cells. Transfected cells were either left untreated or treated with deacetylase inhibitors TSA + NAM, amino acids, or glucose as indicated. Ectopically expressed proteins were immunoprecipitated, separated by SDS-PAGE and probed by anti-acetyllysine antibody (α-AcK). The intensity of acetylated bands was scanned and quantified on a Typhoon 9410 Imager. The relative acetylation was determined after normalization against total proteins detected by antibody recognizing the epitope tag. (**D**, **E**) The K288Q mutation in ASL does not alter global protein structure. Both wild type and K288Q mutant of ASL were expressed and purified from E. coli. The purified ASL was treated with limited trypsin for the indicated times. Both wild type and K288Q mutant ASL showed identical sensitivity and digestion pattern (**D**), indicating that the two proteins have similar folding. Circular dichroism analyses were carried out for both wild-type and K288Q mutant ASL. Again both wild type (solid line) and the K288Q mutant (dashed line) of ASL showed a similar folding (**E**).