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## ORIGINAL ARTICLE

Sperm Biology

# The expression of the new epididymal luminal protein of PDZ domain containing 1 is decreased in asthenozoospermia

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Spermatozoa are not mature until they transit the epididymis where they acquire motility and the ability to fertilize an egg through sequential modifications. The epididymis has three functional regions, caput, corpus, and cauda, and the luminal proteins of the epididymis play important roles in the above modifications. However, the proteins with differential enrichment between the caput and cauda are still largely unknown. To reveal the functions of the caput and cauda during sperm maturation, luminal proteins from caput and cauda of mice were analyzed by isobaric tag for relative and absolute quantitation (iTRAQ). Overall, 128 differentially enriched proteins were found, of which 46 were caput enriched and 82 were cauda enriched. Bioinformatic analysis showed that lipid metabolism was active in the caput; while anion- and cation-binding activity and phosphorus and organophosphate metabolism were active in the cauda. A new epididymal luminal protein, the caput-enriched PDZ domain containing 1 (Pdzk1), also named Na<sup>+</sup>/H<sup>+</sup> exchange regulatory cofactor 3 (NHERF3), which plays a critical role in cholesterol metabolism and carnitine transport, was found in the lipid metabolism. Western blotting and immunofluorescence analyses showed that Pdzk1 was expressed in the epididymis but not in the testis, and localized at the middle piece of the sperm tail. Pdzk1 protein level was also reduced in the spermatozoa in case of asthenozoospermic patients compared with that in normozoospermic men, suggesting that Pdzk1 may participate in sperm maturation regulation and may be associated with male infertility. These results may provide new insights into the mechanisms of sperm maturation and male infertility.

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**Keywords:** asthenozoospermia; epididymis; fertility; PDZ domain containing 1; sperm

## INTRODUCTION

According to the report of World Health Organization (WHO), infertility affects 10%–15% of couples of reproductive age worldwide, and half of the cases are due to male factors.<sup>1</sup> Many factors contribute to male infertility, such as impaired spermatogenesis in the testis<sup>2</sup> and sperm maturational disorders in the epididymis.<sup>3,4</sup> It has been reported that up to 40% of idiopathic male infertility cases are related to sperm maturational disorders. However, the mechanisms underlying the disorders are still unknown.<sup>5</sup>

Spermatozoa in the testis are morphologically complete, but not motile or fertile. They mature in the epididymis to acquire the abilities to move, become capacitated, bind to the zona, and fuse with the oocyte to form an embryo.<sup>6</sup> Mature spermatozoa have a reduced cholesterol level, increased surface-negative charge and disulfide bonds, and modified surface proteins. All of these characteristics are acquired through sequential modifications occurring in the epididymis.<sup>7</sup>

The epididymis is divided into the caput, corpus, and cauda regions, each of which has distinctive functions.<sup>8</sup> The proteins in epididymal

fluid are essential for sperm maturation, since spermatozoa are synthetically inactive.<sup>9</sup> Since the function of the epididymis is region dependent, identifying the differentially enriched proteins in the caput and cauda is critical to the understanding of the mechanism of sperm maturation.

Two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) is a proteomic method that is widely used for the study of luminal proteins. However, it has been reported that no more than twenty proteins account for 80%–90% of the total epididymal luminal proteins, and many proteins are beyond the detection limit of 2D-PAGE.<sup>9</sup> Thus, the proteins that are differentially enriched between the caput and cauda fluid are still largely unknown. Moreover, very little research has been performed on this issue using mouse model.

In this study, iTRAQ was used to profile the different protein compositions of mouse caput and cauda epididymal fluids. We found that the caput-enriched PDZ domain containing 1 (Pdzk1), also called Na<sup>+</sup>/H<sup>+</sup> exchange regulatory cofactor 3 (NHERF3), was associated with male infertility. Our research indicated that identification of the

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differentially enriched proteins in the caput and cauda could provide new clues to how sperm maturation and male infertility develop.

## MATERIALS AND METHODS

### Materials

C57BL/6 mice were purchased from the Department of Laboratory Animal Science, School of Medicine, Shanghai Jiaotong University. The mice were kept at a temperature of 22°C with light cycles of 14 h light and 10 h dark; mice were provided food and water *ad libitum*. Human semen samples were collected at the International Peace Maternity and Child Health Hospital, School of Medicine, Shanghai Jiaotong University, from normozoospermic men (mean age: 29 years) and asthenozoospermic patients (mean age: 30 years) (Table 1). Informed consent was provided by all participants. Semen samples were obtained according to the fifth edition of the WHO Laboratory Manual for the Examination and Processing of Human Semen. This study was approved by the Ethics Committee of the International Peace Maternity and Child Health Hospital.

### Protein extraction

Epididymal luminal proteins were extracted by a modified version of a previously described method.<sup>10</sup> Briefly, five mice were sacrificed and both epididymides of each mouse were collected; thus, ten epididymides in total were harvested. Then, the caput and cauda were dissected from the epididymides, and five capita epididymidum were pooled together as were those from the cauda. The epididymal heads and tails were placed in PBS with protease inhibitor cocktail (Roche, Indianapolis, IN, USA), and several small slits were made in the tubules to promote the release of caput and cauda fluid and spermatozoa into the media. After being incubated at 4°C for 40 min with shaking, the medium was harvested and centrifuged at 800 g for 5 min at 4°C to remove the sperm cells. Then, the supernatant was collected and centrifuged again at 12 000 g for 10 min at 4°C. Finally, proteins of each sample were precipitated using chilled acetone, and the pellets were dried by a vacuum freeze dryer (Thermo Scientific Savant, San Jose, CA, USA). Then, they were dissolved with 50 µl of Dissolution Buffer supplied in the iTRAQ 8-plex Kit (AB SCIEX, Framingham, MA, USA).

### iTRAQ proteome analysis

Proteins were digested by Trypsin Gold (Promega, Madison, WI, USA); the iTRAQ labeling procedure was performed in accordance with the manufacturer's instructions (AB SCIEX). The caput samples were labeled with iTRAQ tag 117 or 119, and the cauda samples were labeled with tags 118 or 121. The labeled peptide mixtures were purified by strong cation exchange chromatography on the Agilent 1200 System (Agilent, Santa Clara, CA, USA). They were analyzed on a TripleTOF 5600 System (AB SCIEX) coupled online to the nanoLC-Ultra 2D System (Eksigent Technologies, Dublin, CA, USA).

**Table 1: Ejaculated sperm characteristics of the 24 men included in the analysis (mean±standard deviation)**

	Normozoospermia (n=12)	Asthenozoospermia (n=12)	P
Age (year)	29±2	30±3	NS
Sperm concentration (10 <sup>6</sup> ml <sup>-1</sup> per ejaculate)	83±23	79±32	<0.01
Total sperm count (10 <sup>6</sup> per ejaculate)	160±77	153±90	<0.05
Progressive motility (%)	59±8	17±7	<0.0001
Nonprogressive motility (%)	9±5	9±2	<0.05

NS: not significant

Data were processed with Protein Pilot Software version 5.0 (AB SCIEX) against the *Mus musculus* database (UniProt release 2015\_12) using the Paragon algorithm.<sup>11</sup> Epididymal luminal proteins that were differentially enriched between the caput and cauda were identified using the following criteria: 1.2-fold cutoff and  $P < 0.05$ . Differentially enriched proteins were analyzed by QuickGO for gene ontology (GO) annotation and enrichment to obtain the information of biological processes and molecular function.<sup>12</sup>

### Western blotting

Western blotting was carried out as described previously.<sup>13</sup> The mouse tissues were lysed in RIPA buffer (50 mmol l<sup>-1</sup> Tris-HCl, pH 7.4, 150 mmol l<sup>-1</sup> NaCl, 1% Triton X-100, 1% SDS, 1% sodium deoxycholate, 1 mmol l<sup>-1</sup> EDTA) with protease inhibitor cocktail (Roche), 1 mmol l<sup>-1</sup> PMSE, and 5 mmol l<sup>-1</sup> sodium orthovanadate. In order to harvest enough luminal fluid, especially the corpus fluid, epididymides from twenty mice were used and processed as mentioned above. The remaining tissues and released spermatozoa were then collected for further analysis. Spermatozoa from the mouse epididymis and human semen were lysed in RIPA buffer with sonication. Proteins were separated by SDS-PAGE and stained by Coomassie Brilliant Blue R-250 (Sigma-Aldrich, St. Louis, MO, USA) or transferred onto nitrocellulose membranes (Amersham Biosciences, Piscataway, NJ, USA). The membranes were blocked by 5% fat-free milk in TBST (10 mmol l<sup>-1</sup> Tris, pH 7.5, 200 mmol l<sup>-1</sup> NaCl, and 0.2% Tween 20) followed by incubation with primary antibodies: Pdzk1 antibody (Abcam, Cambridge, UK), GAPDH antibody (Proteintech, Rosemont, IL, USA),  $\alpha$ -Tubulin (Sigma-Aldrich), and protamine 1 (Briar Patch Biosciences, Livermore, CA, USA). The membranes were probed by goat anti-mouse or rabbit IgG conjugated to HRP (Proteintech), visualized by ECL substrate (Pierce, Rockford, IL, USA) and captured by ImageQuant LAS 4000 mini (GE Healthcare Bioscience, Carlsbad, CA, USA).

### Immunofluorescence

To determine the localization of Pdzk1 in the epididymis and spermatozoa, immunofluorescence was performed. Briefly, 10 µm frozen sections of mouse epididymis, testis, and kidney, or slides spread with spermatozoa from the mouse caput and cauda, and from human semen, were fixed in 4% paraformaldehyde (PFA), permeabilized by 0.1% Triton X-100, and blocked in 5% BSA. The slides were incubated with the Pdzk1 antibodies at 4°C overnight, followed by incubation with Alexa Fluor-488 conjugated donkey anti-rabbit IgG (Molecular Probes, Eugene, OR, USA), and nuclei were stained with Hoechst 33342 (Sigma-Aldrich). Fluorescent signals were captured by confocal microscope LSM 510 (Carl Zeiss, Jena, Germany).

### Statistical analysis

The signal intensity of bands was analyzed by ImageJ software (NIH, Bethesda, MD, USA), and data were analyzed using GraphPad Prism 5.01 (GraphPad Prism, La Jolla, CA, USA). The differences between the normozoospermia and asthenozoospermia group were analyzed by the two-tailed Mann-Whitney U-test, and  $P < 0.05$  was considered statistically significant.

## RESULTS

### The differentially enriched proteins between the caput and cauda

In this study, luminal proteins were extracted from mouse caput and cauda, and the absence of nuclear protein Protamine 1 (Prm1) in all samples showed that they were not contaminated by sperm (Supplementary Figure 1). In the analysis by Protein Pilot 5.0 search engine, a total of 66 794 spectra and 20 799 distinct peptides



were identified. These peptides could be to 2720 proteins with a confidence  $\geq 95\%$ , and a total of 2132 nonredundant proteins with a false discovery rate  $< 1\%$  were detected (Supplementary Table 1). With a criterion of 1.2-fold cutoff and  $P < 0.05$ , 128 differentially enriched proteins were identified, of which 46 were caput fluid enriched and 82 were cauda fluid enriched (Supplementary Table 2). The proteins with no difference in enrichment between the two fluids are listed in Supplementary Table 3.

### The different functions of the caput and cauda epididymidis

The 128 differentially enriched proteins were subjected to bioinformatic analysis by GO annotation and enrichment to analyze the different functions of the caput and cauda regions. Biological process analysis found that processes related to small-molecule metabolism, organic acid metabolism, oxidation-reduction, organonitrogen compound metabolism, and organic substance catabolism existed in both the caput and cauda. However, lipid metabolism was found in the caput, while those associated with phosphorus and organophosphate metabolism were found in the cauda (Figure 1a and 1b). The results of molecular function annotation indicated that binding activity was the main function of these proteins. Identical protein binding, protein domain-specific binding, protein complex binding, and coenzyme binding activities were all identified in the caput and cauda while

anion and cation binding activities were identified only in cauda (Figure 1c and 1d). These results indicate that the caput and cauda play different roles in the process of sperm maturation.

### Pdzk1 is a newly identified epididymal luminal protein

GO analysis showed that Pdzk1 was found in the lipid metabolism group, as an epididymal luminal protein newly identified by iTRAQ (Supplementary Table 2). The expression and localization of Pdzk1 were studied by western blotting and immunofluorescence analyses.

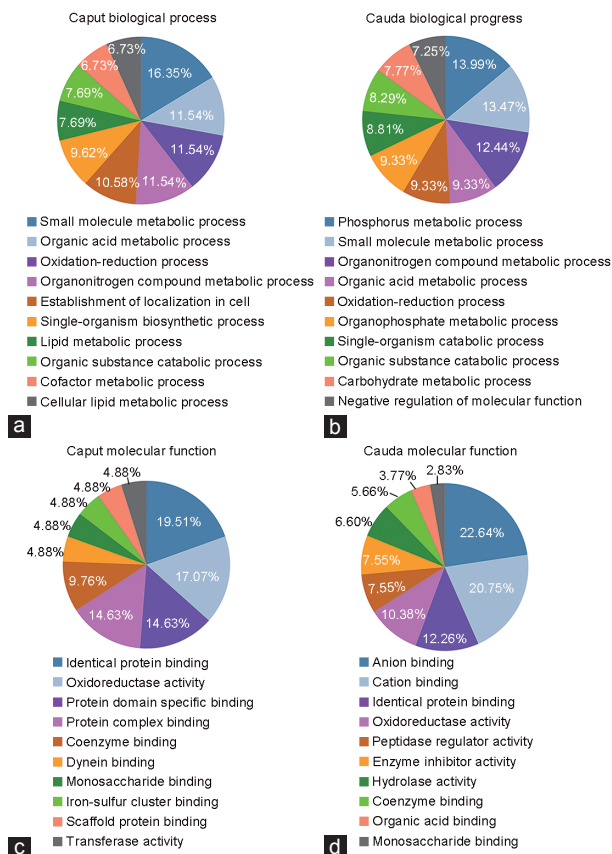
Western blot analysis showed that Pdzk1 was expressed in heart, liver, kidney, epididymis, and efferent ducts, but not in the testis or ovary<sup>14</sup> (Figure 2a and Supplementary Figure 2a). The expression of Pdzk1 in the caput, corpus, and cauda (Figure 2b) was confirmed, and the expression level of Pdzk1 in the spermatozoa and fluid from the caput, corpus, and cauda was also analyzed (Figure 2c and 2d). Immunoblotting result confirmed that Pdzk1 was caput fluid enriched (Figure 2b-2d).

The localization of Pdzk1 was shown by immunofluorescence to have a dynamic expression pattern in the epididymis (Figure 3). In the proximal and distal caput, Pdzk1 was expressed over a wide area and had a stronger signal in the distal caput. Then, an intense signal was observed at the surface of corpus and cauda epithelia. The expression pattern of Pdzk1 in the kidney has been reported and was used here as a positive control.<sup>15</sup>

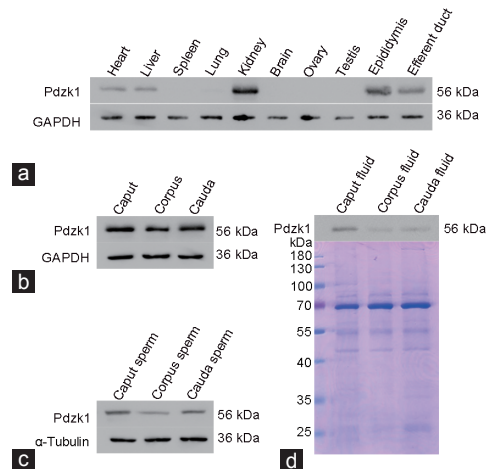
In order to illuminate the sperm localization of Pdzk1, spermatozoa from the mouse caput, corpus, and cauda were analyzed by immunofluorescence (Figure 4). Pdzk1 is localized to the sperm tail, especially in the middle piece, where the mitochondrial sheath lies (Figure 4).

### The expression of Pdzk1 in asthenozoospermia

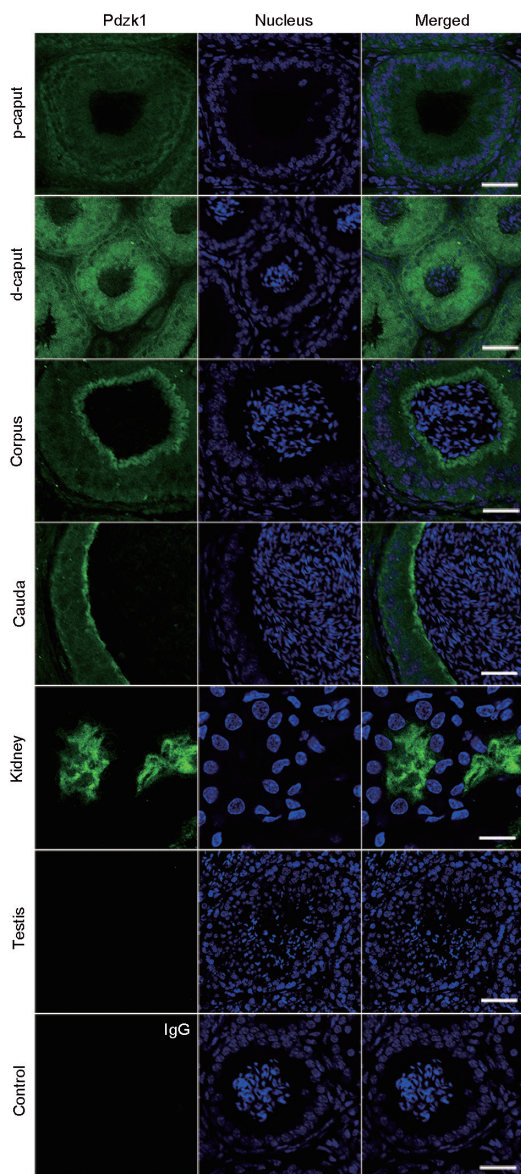
Spermatozoa from normozoospermic men (mean age: 29 years) and asthenozoospermic patients (mean age: 30 years) were collected to investigate the role of Pdzk1 in male fertility (Table 1). The localization of Pdzk1 in human spermatozoa was similar to that in the mouse, and the localization pattern did not differ between normozoospermia and asthenozoospermia (Figure 5). The expression of Pdzk1 was analyzed by western blotting analysis, which showed



**Figure 1:** GO analysis of differentially enriched proteins in the fluids of mouse caput and cauda. A total of 128 differentially enriched proteins were identified by iTRAQ, 46 caput-enriched and 82 cauda-enriched proteins are annotated. The caput (a) and cauda (b) enriched luminal proteins are classified in different categories based on the biological processes, the caput (c) and cauda (d) enriched luminal proteins are also classified based on the molecular functions. The top ten terms of GO enrichment with  $P < 0.05$  were listed. iTRAQ: isobaric tag for relative and absolute quantitation; GO: gene ontology.



**Figure 2:** The expression of Pdzk1 in different organs of the mouse (a) and in the caput, corpus, and cauda (b) is analyzed by western blotting analysis, and also the expression of Pdzk1 in spermatozoa (c) and luminal fluid (d) from the caput, corpus, and cauda is analyzed. The gel is stained by Coomassie Brilliant Blue R-250. Pdzk1: PDZ domain containing 1.



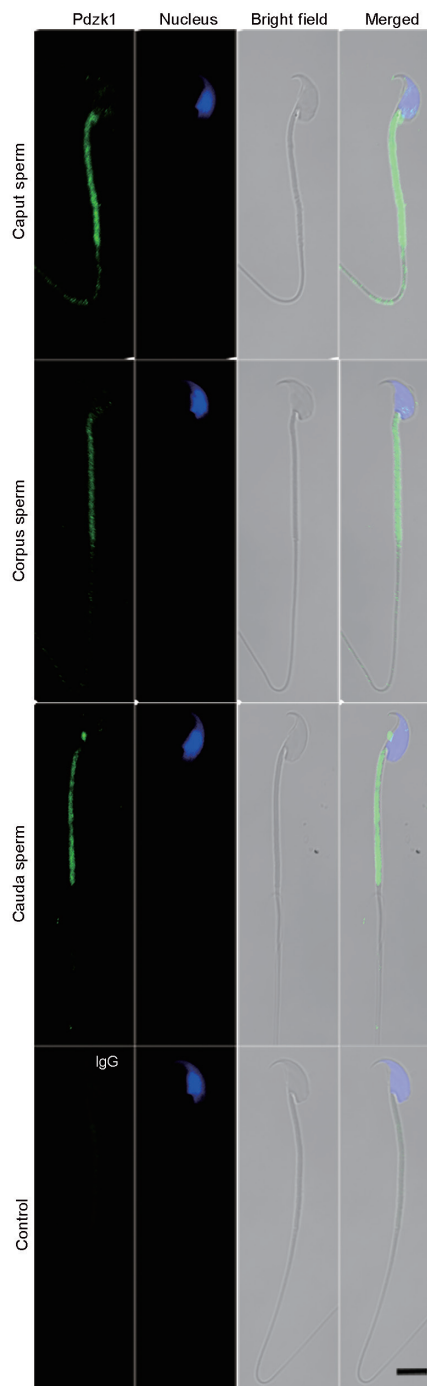
**Figure 3:** Immunofluorescence analysis of the localization of Pdzk1 in the epididymis. p-caput: proximal caput; d-caput: distal caput. IgG was used as control. Antibody dilution: 1:400. Scale bar: 12  $\mu$ m in kidney and 50  $\mu$ m in other panels. Pdzk1: PDZ domain containing 1.

that Pdzk1 was decreased in the spermatozoa in asthenozoospermia (Figure 6 and Supplementary Figure 2b), suggesting that Pdzk1 may function in sperm maturation and may be associated with male infertility.

**DISCUSSION**

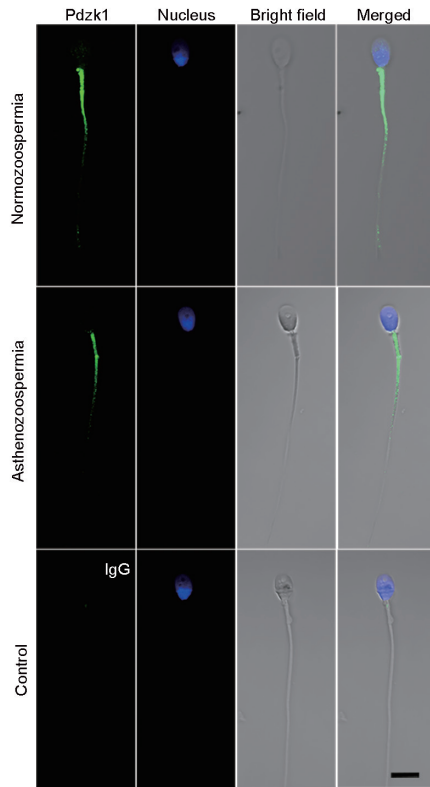
When spermatozoa are transiting through the convoluted epididymal tubule, they successively interact with the epididymal fluid to acquire progressive motility and fertilizing capacity, a process that is called epididymal sperm maturation. To reveal the mechanism of sperm maturation, transcriptomic and proteomic analyses of epididymis,<sup>16-19</sup> proteomic analyses of sperm,<sup>20,21</sup> and proteomic analyses of epididymal fluid<sup>6,9</sup> have been performed by other groups.

Proteomic analyses of luminal proteins were mainly carried out by 2D-PAGE.<sup>6,9</sup> However, this method has drawbacks, in that it is



**Figure 4:** Immunofluorescence analysis of the localization of Pdzk1 in spermatozoa from the mouse. Kidney and testis were used as positive and negative controls, respectively. Antibody dilution: 1:100. IgG was used as control. Scale bar = 5  $\mu$ m. Pdzk1: PDZ domain containing 1.

difficult to use it to analyze low-abundance proteins, hydrophobic proteins, and membrane proteins.<sup>22</sup> The epididymal fluid contains many low-abundance proteins, and studies by 2D-PAGE can only identify hundreds of proteins or fewer in this fluid in various species, such as 525 proteins in human,<sup>23</sup> 146 proteins in boars,<sup>24</sup> 117 proteins in stallions,<sup>25</sup> 172 proteins in bulls,<sup>26</sup> 12 proteins in rams,<sup>27</sup> 198 proteins in monkeys,<sup>28</sup> 27 proteins in platypuses,<sup>29</sup> 19 proteins in rats,<sup>30,31</sup> and 23 proteins in mice.<sup>32</sup> Thus, the epididymal luminal proteins, especially



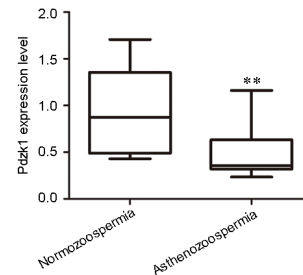
**Figure 5:** Immunofluorescence analysis of the localization of Pdzk1 in spermatozoa from normozoospermic and asthenozoospermic men. Spermatozoa from normozoospermic men were marked as N1 and asthenozoospermia as A1. Antibody dilution: 1:100. IgG was used as control. Scale bar = 10  $\mu$ m. Pdzk1: PDZ domain containing 1.

the proteins differentially enriched between the caput and cauda, are still largely unknown.

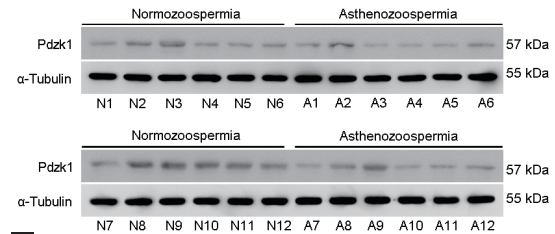
Several methods for epididymal fluid collection have been developed. Mincing and pressing the epididymis was the earliest used method. However, samples processed by this method may be contaminated with serum, lymph, or epididymal cellular proteins. As an alternative, the microperfusion method can provide much purer epididymal fluid, but this method is mainly performed on large animals, and is not suitable for mice, especially for the collection of mouse caput fluid.<sup>25,33</sup> Thus, the method of making small slits in the epididymis tubules with pressing was adopted to collect mouse caput and cauda luminal fluids in the study.

In the present study, the iTRAQ method was applied to reveal the proteins differentially enriched between the caput and cauda. The results of bioinformatic analysis showed that these proteins took part in different biological processes and played different molecular functions. These results indicate that the caput and cauda have distinct functions during sperm maturation.

Pdzk1 is a newly identified epididymal luminal protein by iTRAQ, which was found in lipid metabolism. Pdzk1, also named NHERF3, belongs to the  $\text{Na}^+/\text{H}^+$  exchange regulatory cofactor (NHERF) family. It is a scaffold protein with four PDZ domains and participates in the regulation of cell surface protein expression, cholesterol metabolism, and carnitine transport, which are important for sperm maturation and motility.<sup>15,34–36</sup> Pdzk1 prompts carnitine uptake by upregulating the activity of the carnitine transporter OCTN2.<sup>15,37</sup>



**a**



**b**

**Figure 6:** The sperm expression of Pdzk1 in normozoospermia and asthenozoospermia. **(a)** Box and whiskers plot of Pdzk1 expression in spermatozoa. Boxes indicate the 25<sup>th</sup> and 75<sup>th</sup> percentiles, the middle line indicates arithmetic mean. \*\* $P < 0.01$ , compared with normal control. **(b)** Western blot analysis of the expression of Pdzk1.  $\alpha$ -Tubulin was used as normal control. N: normozoospermia; A: asthenozoospermia; Pdzk1: PDZ domain containing 1.

It has been reported that Pdzk1 is expressed in the epididymis and efferent ducts,<sup>14</sup> which was confirmed by our findings. The cauda has a higher concentration of carnitine and the cauda sperm are more motile than that in the caput.<sup>38</sup> However, we found that Pdzk1 was enriched in the caput fluid but not in the cauda fluid. The function of Pdzk1 in the cauda fluid may be compensated by another NHERF family member, NHERF1, which interacts with another carnitine transporter, OCTN1,<sup>15</sup> since NHERF1 is enriched in the cauda fluid.

Pdzk1 was localized at the sperm tail, but had no expression in the testis. Pdzk1 may be secreted into the luminal fluid from the efferent ducts or epididymis and bound to the sperm surface. Since Pdzk1 has no typical signal sequence (**Supplementary Figure 3**), its secretion may be mediated by epididymosomes, specific exosomes in the epididymis.<sup>5</sup> This manner of secretion was confirmed by the finding that Pdzk1 was present in urinary exosomes.<sup>39,40</sup>

The expression of Pdzk1 in human spermatozoa was analyzed and showed that Pdzk1 was decreased in asthenozoospermia. Mice without Pdzk1 are fertile but have increased serum cholesterol levels, which may affect sperm motility. However, this speculation requires further investigation because the sperm motility and sperm fertilizing ability in the knockout mice are unclear.<sup>41</sup> The results obtained here indicate that Pdzk1 may be associated with sperm maturation and male infertility, but further research is needed to reveal the mechanisms behind this involvement.

## CONCLUSION

Taking the obtained findings together, this work reveals the proteins differentially enriched between the caput and cauda fluid, shedding light on the distinct functions of the caput and cauda in sperm maturation. The epididymal luminal protein Pdzk1 newly identified here by iTRAQ has been associated with asthenozoospermia. This work provides a foundation for future mechanistic research on sperm maturation and male infertility.

## AUTHOR CONTRIBUTIONS

AJL and GSW gathered the epididymal luminal proteins, performed proteomic analysis, and drafted the manuscript. PP and SGH collected human semen and performed western blotting analysis of Pdzk1 in human spermatozoa. YL and YM carried out the immunofluorescence analysis of Pdzk1. ZZD and HSW contributed to the western blotting analysis of Pdzk1 in mouse. FS conceived this study and helped to improve the manuscript. All authors have read and approved the final manuscript.

## COMPETING INTERESTS

The authors declare that they have no competing interests.

## ACKNOWLEDGMENTS

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Supplementary information is linked to the online version of the paper on the *Asian Journal of Andrology* website.

## REFERENCES

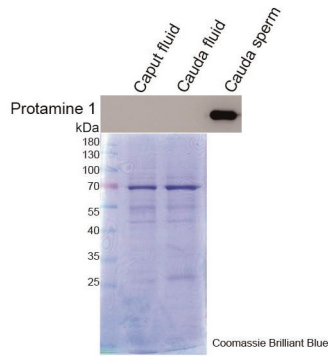
- Lian J, Zhang X, Tian H, Liang N, Wang Y, *et al*. Altered microRNA expression in patients with non-obstructive azoospermia. *Reprod Biol Endocrinol* 2009; 7: 13.
- Navarro-Costa P, Goncalves J, Plancha CE. The AZFc region of the Y chromosome: at the crossroads between genetic diversity and male infertility. *Hum Reprod Update* 2010; 16: 525–42.
- Schoysman R. Epididymal causes of male infertility: pathogenesis and management. *Int J Androl* 1982; 5: 120–34.
- Schoysman R. Management of epididymal dysfunction: Correlation with basic physiology. In: Robaire B, Hinton BT, editors. *The Epididymis: From Molecules to Clinical Practice*. New York: Kluwer Academic/Plenum Publishers; 2002. p. 473–82.
- Cornwall GA. New insights into epididymal biology and function. *Hum Reprod Update* 2009; 15: 213–27.
- Dacheux JL, Dacheux F. New insights into epididymal function in relation to sperm maturation. *Reproduction* 2014; 147: R27–42.
- Dacheux JL, Belleannee C, Guyonnet B, Labas V, Teixeira-Gomes AP, *et al*. The contribution of proteomics to understanding epididymal maturation of mammalian spermatozoa. *Syst Biol Reprod Med* 2012; 58: 197–210.
- Sullivan R, Saez F, Girouard J, Frenette G. Role of exosomes in sperm maturation during the transit along the male reproductive tract. *Blood Cells Mol Dis* 2005; 35: 1–10.
- Baker MA, Nixon B, Naumovski N, Aitken RJ. Proteomic insights into the maturation and capacitation of mammalian spermatozoa. *Syst Biol Reprod Med* 2012; 58: 211–7.
- Roberts KP, Ensrud KM, Hamilton DW. A comparative analysis of expression and processing of the rat epididymal fluid and sperm-bound forms of proteins D and E. *Biol Reprod* 2002; 67: 525–33.
- Shilov IV, Seymour SL, Patel AA, Loboda A, Tang WH, *et al*. The paragon algorithm, a next generation search engine that uses sequence temperature values and feature probabilities to identify peptides from tandem mass spectra. *Mol Cell Proteomics* 2007; 6: 1638–55.
- Binns D, Dimmer E, Huntley R, Barrell D, O'Donovan C, *et al*. QuickGO: a web-based tool for gene ontology searching. *Bioinformatics* 2009; 25: 3045–6.
- Wang G, Zhang H, Wang L, Wang Y, Huang H, *et al*. Ca(2+)/calmodulin-dependent protein kinase IV promotes interplay of proteins in chromatoid body of male germ cells. *Sci Rep* 2015; 5: 12126.
- Trepos-Pouplard M, Lardenois A, Staub C, Guitton N, Dorval-Coiffec I, *et al*. Proteome analysis and genome-wide regulatory motif prediction identify novel potentially sex-hormone regulated proteins in rat efferent ducts. *Int J Androl* 2010; 33: 661–74.
- Kato Y, Sai Y, Yoshida K, Watanabe C, Hirata T, *et al*. PDZK1 directly regulates the function of organic cation/carnitine transporter OCTN2. *Mol Pharmacol* 2005; 67: 734–43.
- Jelinsky SA, Turner TT, Bang HJ, Finger JN, Soltar MK, *et al*. The rat epididymal transcriptome: comparison of segmental gene expression in the rat and mouse epididymides. *Biol Reprod* 2007; 76: 561–70.
- Li JY, Wang HY, Liu J, Liu Q, Zhang JS, *et al*. Transcriptome analysis of a cDNA library from adult human epididymis. *DNA Res* 2008; 15: 115–22.
- Yuan H, Liu A, Zhang L, Zhou H, Wang Y, *et al*. Proteomic profiling of regionalized

- proteins in rat epididymis indicates consistency between specialized distribution and protein functions. *J Proteome Res* 2006; 5: 299–307.
- Liu X, Liu FJ, Jin SH, Shen XF, Wang YW. In-depth proteomic mapping of mouse (*Mus musculus*) epididymal constructive basis for sperm maturation. *Proteome Sci* 2015; 13: 20.
  - Oliva R, de Mateo S, Estanyol JM. Sperm cell proteomics. *Proteomics* 2009; 9: 1004–17.
  - Brewis IA, Gadella BM. Sperm surface proteomics: from protein lists to biological function. *Mol Hum Reprod* 2010; 16: 68–79.
  - Gygi SP, Corthals GL, Zhang Y, Rochon Y, Aebersold R. Evaluation of two-dimensional gel electrophoresis-based proteome analysis technology. *Proc Natl Acad Sci U S A* 2000; 97: 9390–5.
  - Li J, Liu F, Liu X, Liu J, Zhu P, *et al*. Mapping of the human testicular proteome and its relationship with that of the epididymis and spermatozoa. *Mol Cell Proteomics* 2011; 10: M110.004630.
  - Syntin P, Dacheux F, Druart X, Gatti JL, Okamura N, *et al*. Characterization and identification of proteins secreted in the various regions of the adult boar epididymis. *Biol Reprod* 1996; 55: 956–74.
  - Fouchecourt S, Metayer S, Locatelli A, Dacheux F, Dacheux JL. Stallion epididymal fluid proteome: qualitative and quantitative characterization; secretion and dynamic changes of major proteins. *Biol Reprod* 2000; 62: 1790–803.
  - Belleannee C, Labas V, Teixeira-Gomes AP, Gatti JL, Dacheux JL, *et al*. Identification of luminal and secreted proteins in bull epididymis. *J Proteomics* 2011; 74: 59–78.
  - Souza CE, Rego JP, Lobo CH, Oliveira JT, Nogueira FC, *et al*. Proteomic analysis of the reproductive tract fluids from tropically-adapted Santa Ines rams. *J Proteomics* 2012; 75: 4436–56.
  - Liu X, Jin SH, Liu XX, Wang WJ, Liu FJ. Proteome profiling of the sperm maturation milieu in the rhesus monkey (*Macaca mulatta*) epididymis. *Reprod Fertil Dev* 2016; 28: 732–41.
  - Dacheux JL, Dacheux F, Labas V, Ecroyd H, Nixon B, *et al*. New proteins identified in epididymal fluid from the platypus (*Ornithorhynchus anatinus*). *Reprod Fertil Dev* 2009; 21: 1002–7.
  - Turner TT, Miller DW, Avery EA. Protein synthesis and secretion by the rat caput epididymidis *in vivo*: influence of the luminal microenvironment. *Biol Reprod* 1995; 52: 1012–9.
  - Turner TT, Riley TA, Mruk DD, Cheng CY. Obstruction of the vas deferens alters protein secretion by the rat caput epididymidal epithelium *in vivo*. *J Androl* 1999; 20: 289–97.
  - Liu X, Wang W, Liu F. New insight into the castrated mouse epididymis based on comparative proteomics. *Reprod Fertil Dev* 2014; 27: 551–6.
  - Turner TT, Riley TA, Vagnetti M, Flickinger CJ, Caldwell JA, *et al*. Postvasectomy alterations in protein synthesis and secretion in the rat caput epididymidis are not repaired after vasovasostomy. *J Androl* 2000; 21: 276–90.
  - Kocher O, Yesilaltay A, Cirovic C, Pal R, Rigotti A, *et al*. Targeted disruption of the PDZK1 gene in mice causes tissue-specific depletion of the high density lipoprotein receptor scavenger receptor class B type I and altered lipoprotein metabolism. *J Biol Chem* 2003; 278: 52820–5.
  - Wang P, Wang JJ, Xiao Y, Murray JW, Novikoff PM, *et al*. Interaction with PDZK1 is required for expression of organic anion transporting protein 1A1 on the hepatocyte surface. *J Biol Chem* 2005; 280: 30143–9.
  - Mongioli L, Calogero AE, Vicari E, Condorelli RA, Russo GI, *et al*. The role of carnitine in male infertility. *Andrology* 2016; 4: 800–7.
  - Gibb Z, Lambourne SR, Quadrelli J, Smith ND, Aitken RJ. L-carnitine and pyruvate are pro-survival factors during the storage of stallion spermatozoa at room temperature. *Biol Reprod* 2015; 93: 104.
  - Jeulin C, Lewin LM. Role of free L-carnitine and acetyl-L-carnitine in post-gonadal maturation of mammalian spermatozoa. *Hum Reprod Update* 1996; 2: 87–102.
  - Gonzales PA, Pisitkun T, Hoffert JD, Tchapyjnikov D, Star RA, *et al*. Large-scale proteomics and phosphoproteomics of urinary exosomes. *J Am Soc Nephrol* 2009; 20: 363–79.
  - Huebner AR, Cheng L, Somporn P, Knepper MA, Fenton RA, *et al*. Deubiquitylation of protein cargo is not an essential step in exosome formation. *Mol Cell Proteomics* 2016; 15: 1556–71.
  - Kocher O, Pal R, Roberts M, Cirovic C, Gilchrist A. Targeted disruption of the PDZK1 gene by homologous recombination. *Mol Cell Biol* 2003; 23: 1175–80.

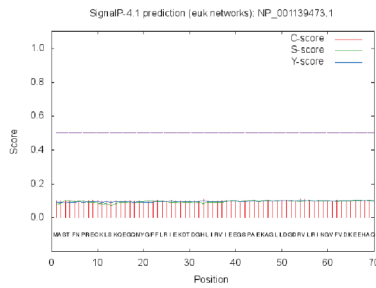
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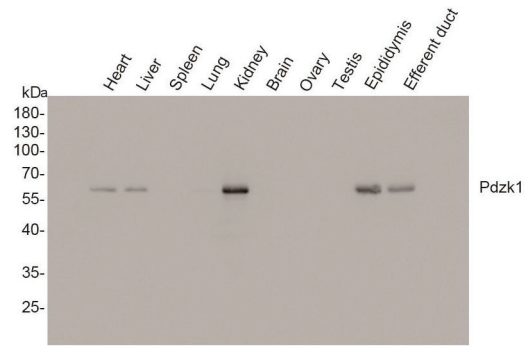
**Supplementary Figure 1:** Western blotting analysis of protamine 1 in the fluid of caput and cauda, and the cauda sperm. Gel is stained by Coomassie Brilliant Blue R-250.



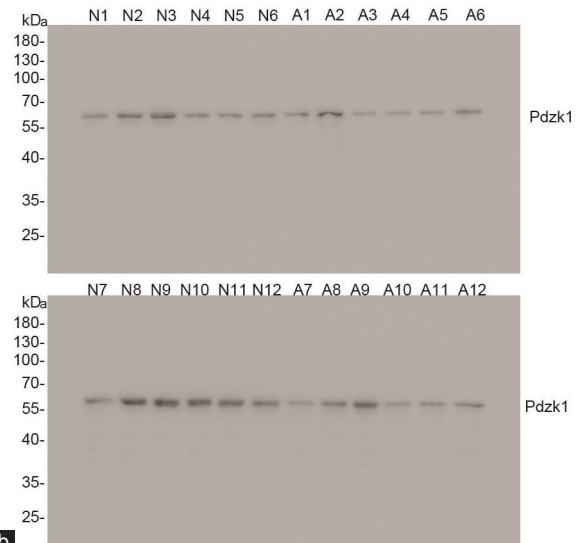
**Supplementary Figure 3:** Pdzk1 has no typical signal sequence. Pdzk1 protein sequence (NP\_001139473) was analyzed by SignalP 4.1 (<http://www.cbs.dtu.dk/services/SignalP>) and no signal peptide was found. Pdzk1: PDZ domain containing 1.

**Supplementary Table 1: The identifications by isobaric tag for relative and absolute quantitation**

Unused cutoff	Proteins detected	Proteins before grouping	Distinct peptides	Spectra identified	Percentage total spectra
>0.05 (10%)	2132	11,097	20,799	66,794	41.2



**a**



**b**

**Supplementary Figure 2:** Complete scans of the different blots presented in **Figure 2** and **Figure 6** indicating the specificity of Pdzk1 antibody. **(a)** Uncropped picture presented in **Figure 2a** showing the expression of Pdzk1 in different organs of mouse. **(b)** Uncropped picture presented in **Figure 6b** showing the expression of Pdzk1 in human spermatozoa. Pdzk1: PDZ domain containing 1.

**Supplementary Table 2: The differentially enriched proteins between the mouse caput and cauda luminal fluids**

<i>Number</i>	<i>Name</i>	<i>Unused ProtScore<sup>a</sup></i>	<i>Total ProtScore<sup>b</sup></i>	<i>Percentage coverage</i>	<i>Peptides (95%)</i>	<i>Cauda/caput</i>
1	Cytochrome c, testis-specific	4.16	6.12	53.3	5	5.024125
2	Acrosin-binding protein	14.54	14.57	28	11	4.27655
3	Prostaglandin-H2 D-isomerase	12.96	13.05	37	11	4.0499
4	CUB and zona pellucida-like domain-containing protein 1	39.8	39.79	49.1	42	3.9259
5	Carboxylesterase 5A	24.15	24.21	32.7	23	3.915625
6	Protein Gm46	26.39	26.49	49.5	18	3.9117
7	Cysteine-rich secretory protein 1	26.88	28	72.5	46	3.6179
8	Wfdc10	3.49	3.83	41.9	13	3.35495
9	Annexin A4	14.93	15.53	36.1	7	3.11155
10	Lactotransferrin	62.63	62.65	70	39	3.0699
11	Acyl-CoA-binding domain-containing protein 7	7.13	7.26	78.4	6	2.925
12	Glutathione peroxidase 3	12.02	15.06	45.1	17	2.80465
13	Myosin regulatory light polypeptide 9	17.45	17.53	79.7	18	2.728075
14	Serine protease inhibitor Kazal-type 2	6	6	50.9	3	2.7052
15	Alpha-1-antitrypsin 1-6	16.25	16.72	39.9	21	2.694375
16	Adenylate kinase 2, mitochondrial	14.26	14.3	57.3	9	2.68195
17	Transgelin	29.56	29.62	83.1	25	2.639525
18	Zona pellucida 3 receptor	20.55	21.03	34.7	11	2.622875
19	Muc5b	98.96	98.95	24.7	64	2.527225
20	NHERF1	12.59	12.67	45.4	7	2.514275
21	L-lactate dehydrogenase C chain	54.59	54.62	89.2	66	2.491375
22	Phosphoglycerate mutase 2	18.73	18.85	71.5	14	2.489025
23	Phosphoglycerate kinase 2	48.58	49.29	80.6	37	2.459625
24	Epididymal secretory protein E1	10.53	13.22	55.7	11	2.431675
25	Inactive ribonuclease-like protein 9	8.51	8.58	32.1	8	2.4102
26	Sorbitol dehydrogenase	31.94	32.02	60.2	21	2.40415
27	Adenylate kinase isoenzyme 1	25.73	25.78	74.2	19	2.391425
28	Tropomyosin beta chain	14.66	32.06	60.2	21	2.38525
29	Ovostatin homolog	2.75	2.84	5.8	2	2.35055
30	Beta-galactosidase-1-like protein	2.65	4.51	14.1	3	2.333125
31	Tropomyosin alpha-1 chain	37.55	37.59	63.5	23	2.330875
32	Annexin	38.68	38.77	43.5	22	2.30755
33	Creatine kinase M-type	15.19	18.19	39.6	9	2.302
34	Lysosomal alpha-mannosidase	29.88	30.04	29	18	2.278325
35	Cystathionine beta-synthase	11.38	11.52	27.3	7	2.27505
36	Cysteine and glycine-rich protein 1	25.99	26.02	67.9	17	2.216425
37	Fructose-bisphosphate aldolase	6.02	26.83	51.4	20	2.1475
38	Sulfhydryl oxidase 1	24.95	25.06	28.9	14	2.119525
39	Galectin-3-binding protein	5.95	6.14	17.5	4	2.091825
40	Angiotensinogen	12.35	12.37	24.1	11	2.084775
41	Myosin light polypeptide 6	18.05	18.06	62.3	15	2.08015
42	Prdx6b	2.98	11.62	46.9	8	2.062575
43	Epididymal-specific lipocalin-5	17.95	18.56	82.3	38	1.97785
44	Fructose-1,6-bisphosphatase 1	19.58	19.66	53.3	13	1.972625
45	Aldo-keto reductase family 1, member C19	11.01	14.02	49.2	8	1.969125
46	PDZ and LIM domain protein 3	5.83	5.98	34.8	5	1.930975
47	Ribonuclease UK114 OS	12.41	12.47	69.6	10	1.929075
48	Myosin light chain kinase, smooth muscle	43.58	43.87	24.2	25	1.878875
49	Malic enzyme	25.36	25.42	51.3	15	1.851325
50	Phospholipase B-like 1	12.16	12.17	19.5	6	1.806875
51	Calponin-1	19.16	20.1	59.3	14	1.799275
52	Phenylethanolamine N-methyltransferase	7.28	7.34	14.9	4	1.79065
53	Epididymis-specific alpha-mannosidase	13.06	13.15	16.1	9	1.76365
54	Spink5	21.08	21.27	24.8	17	1.7589
55	L-amino-acid oxidase	10.05	10.11	23.2	5	1.7543
56	Glucose-6-phosphate isomerase	37.31	37.39	53.6	27	1.7395

Contd...



Supplementary Table 2: Contd...

Number	Name	Unused ProtScore <sup>a</sup>	Total ProtScore <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
57	Annexin A2	27.92	28.4	54.3	16	1.7311
58	Histone deacetylase 6 (fragment)	13.05	13.18	17.8	12	1.717675
59	Dipeptidase 3	19.43	19.45	31.2	12	1.7077
60	Triokinase/FMN cyclase	29.83	29.85	42.7	16	1.6665
61	Protein phosphatase 1 regulatory subunit 7	16.65	17.91	40.7	13	1.6363
62	SH3 domain-binding glutamic acid-rich-like protein	13.92	13.97	70.2	9	1.63015
63	Antithrombin-III	11.09	11.54	22.8	6	1.62045
64	Creatine kinase B-type	34.51	34.55	74	25	1.566225
65	Hexokinase	47.49	47.61	41.1	29	1.564325
66	Lumican	19.36	19.49	39.4	18	1.550125
67	Filamin, alpha	147.06	146.8	51.6	89	1.548575
68	Cytosolic acyl coenzyme A thioester hydrolase	10.58	10.65	25.8	6	1.54185
69	A-kinase anchor protein 12	31.13	31.2	16.3	15	1.490725
70	Methylmalonate-semialdehyde dehydrogenase (acylating), mitochondrial	6.47	6.51	7.9	3	1.48885
71	L-lactate dehydrogenase B chain	24.86	27.69	62	24	1.4714
72	Malate dehydrogenase, mitochondrial	17.35	17.47	48.2	10	1.47115
73	Ahnak	57.94	57.89	32.8	29	1.4579
74	Alcohol dehydrogenase class-3	23.64	23.73	53.7	23	1.42415
75	Alcohol dehydrogenase 1	20.6	22.68	43.7	13	1.4213
76	L-lactate dehydrogenase	30.65	34.89	68.7	29	1.3998
77	Glutathione peroxidase	16.62	16.7	74.1	12	1.37285
78	Tripeptidyl-peptidase 2	23.16	23.38	17.9	13	1.3695
79	T-complex protein 1 subunit delta	24.56	28.28	44.5	17	1.305825
80	Hemopexin	41.8	41.86	55	24	1.291775
81	Serum albumin	116.94	115.2	88.8	143	1.287025
82	Glutathione S-transferase Mu 5	23.62	25.8	69.6	25	1.2795
83	Cytoplasmic aconitate hydratase	61.46	61.47	56.9	39	0.79315
84	Ribonuclease inhibitor	41.98	42.01	76.1	39	0.790325
85	Transaldolase	22.67	22.75	45.1	13	0.785375
86	Dynactin subunit 1	27.37	28.82	20.2	18	0.761225
87	UPF0160 protein MYG1, mitochondrial	16.04	16.09	40.5	9	0.7601
88	Glyoxalase domain-containing protein 4	21.27	21.36	58.7	13	0.757575
89	Microtubule-associated protein 1B	29.15	29.36	16.3	16	0.755475
90	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	25.35	25.35	65.6	20	0.72635
91	Glucose-6-phosphate 1-dehydrogenase X	43.69	43.77	63.1	37	0.721425
92	Acidic leucine-rich nuclear phosphoprotein 32 family member A	11.58	11.63	45.8	10	0.715175
93	HSP 90-beta	71.06	70.93	67.3	55	0.713175
94	Ezrin	54.67	54.73	63.3	33	0.70445
95	Glutathione S-transferase theta-2	11.73	13.97	48	8	0.7018
96	Eukaryotic translation initiation factor 4 gamma 3	6.06	11.16	10	7	0.700925
97	Alcohol dehydrogenase [NADP(+) ]	35.73	35.89	73.2	30	0.699075
98	Lambda-crystallin homolog	15.83	15.97	41.7	11	0.689175
99	Aminopeptidase B	28.85	28.94	46	14	0.68805
100	Glutaredoxin-3	13.92	14.3	41	10	0.67495
101	Glutathione S-transferase Mu 6	22	28.62	75.2	21	0.66255
102	Cytidine monophosphate (UMP-CMP) kinase	8.69	10.06	61.2	6	0.6617
103	Dihydropteridine reductase	18	18	55.6	17	0.6596
104	Epiplakin	28.06	34.5	25.9	18	0.64955
105	ATP-citrate synthase	76.91	76.91	52.2	56	0.64595
106	Huntingtin-interacting protein 1-related protein	33.56	33.7	31.7	17	0.640925
107	Aflatoxin B1 aldehyde reductase member 2	18.63	18.69	44.4	21	0.62655
108	Tryptophan-tRNA ligase, cytoplasmic	59.22	59.22	69.2	45	0.61675
109	Tubulin alpha-4A chain (fragment)	11.46	41.74	61.6	45	0.61045
110	Capping protein (actin filament), gelsolin like	16.08	16.17	44.7	16	0.60995

Contd...

**Supplementary Table 2: Contd...**

Number	Name	Unused ProtScore <sup>a</sup>	Total ProtScore <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
111	Oxysterol-binding protein 1	11.43	11.55	16.4	6	0.608725
112	NHERF3 (Pdzk1)	37.29	37.34	69.2	36	0.6017
113	Guanidinoacetate N-methyltransferase	18.5	18.48	83.9	15	0.60005
114	Aldehyde dehydrogenase, cytosolic 1	21.41	46.98	65.5	41	0.593525
115	Glutathione peroxidase	21.59	21.74	57.4	26	0.59235
116	Plastin-2	62.83	62.8	76.4	52	0.5811
117	Keratin, type I cytoskeletal 18	54.14	54.2	74.2	54	0.5804
118	Inorganic pyrophosphatase	25.8	26.01	65.1	17	0.551425
119	Peroxiredoxin 6	35.43	35.45	88.8	36	0.545925
120	Keratin, type II cytoskeletal 8	53.64	53.7	60	47	0.543625
121	Epididymal-specific lipocalin-8	10.55	10.62	40.6	6	0.535825
122	Glutamine synthetase	33.87	35.29	80.4	50	0.53275
123	14-3-3 protein sigma	12.12	20.32	60.9	16	0.525325
124	Inositol-3-phosphate synthase 1	26.28	28.13	46	42	0.513625
125	Cytosolic nonspecific dipeptidase	44.15	44.15	65.7	36	0.5086
126	Neutrophil gelatinase-associated lipocalin	8.52	8.71	46.5	8	0.466675
127	Cytosol aminopeptidase	55.98	55.97	70.3	51	0.43945
128	Indoleamine 2,3-dioxygenase 1	34.48	34.5	56.5	23	0.43895

<sup>a</sup>Unused ProtScore: reflecting the amount of total, unique peptide evidence related to a given protein; <sup>b</sup>Total ProtScore: reflecting the sum of all peptide evidences related to a given protein. NHERF3: Na<sup>+</sup>/H<sup>+</sup> exchange regulatory cofactor 3; Pdzk1: PDZ domain containing 1; HSP: heat shock protein ; CUB: complement subcomponent /C1s, Uegf, Bmp1; FMN: flavin mononucleotide; NADP: Nicotinamide adenine dinucleotide phosphate; UMP: uridine monophosphate; CMP: cytidine monophosphate

**Supplementary Table 3: The unchanged proteins between the mouse caput and cauda luminal fluids**

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
1	Inorganic pyrophosphatase 2, mitochondrial OS=Mus musculus GN=Ppa2 PE=1 SV=1	10.89	10.95	36.4	5	0.834275
2	Cingulin OS=Mus musculus GN=Cgn PE=1 SV=1	2.56	2.99	8.3	2	0.8346
3	Tropomyosin 3, gamma OS=Mus musculus GN=Tpm3 PE=1 SV=1	1.23	20.63	51.1	14	0.8348
4	GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3	11.96	12.03	42.6	6	0.834875
5	Protein PBDC1 OS=Mus musculus GN=Pbdc1 PE=1 SV=1	6.87	6.92	28.3	5	0.83495
6	Protein prune homolog OS=Mus musculus GN=Prune PE=1 SV=1	5.68	5.75	16.5	3	0.835025
7	V-type proton ATPase subunit D OS=Mus musculus GN=Atp6v1d PE=1 SV=1	3.94	4.14	23.5	2	0.83505
8	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Mus musculus GN=Ciao1 PE=1 SV=1	2	2	11.2	1	0.835475
9	Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1	47.6	47.65	42.8	28	0.8356
10	Carbonyl reductase (NADPH) 3 OS=Mus musculus GN=Cbr3 PE=1 SV=1	14.97	19.18	53.1	11	0.83575
11	Golgin subfamily A member 4 OS=Mus musculus GN=Golga4 PE=1 SV=2	0.74	0.89	5.6	1	0.8363
12	Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=1 SV=2	2.82	2.92	5.9	2	0.836325
13	Tyrosine-tRNA ligase OS=Mus musculus GN=Yars PE=1 SV=1	19.38	19.55	33.2	13	0.836375
14	High mobility group protein B1 OS=Mus musculus GN=Hmgb1 PE=1 SV=2	8.06	8.16	43.7	5	0.836675
15	RAS-related C3 botulinum substrate 1, isoform CRA_a OS=Mus musculus GN=Rac1 PE=1 SV=1	5.88	7.69	30.8	8	0.83685
16	Nuclear migration protein nudC OS=Mus musculus GN=Nudc PE=1 SV=1	17.47	17.58	42.2	8	0.837075
17	Ras-related protein Rab-2A OS=Mus musculus GN=Rab2a PE=1 SV=1	3.29	3.49	47.2	3	0.837125
18	COP9 signalosome complex subunit 5 OS=Mus musculus GN=Cops5 PE=1 SV=3	8.02	8.19	25.8	6	0.83745
19	Fructose-bisphosphate aldolase C OS=Mus musculus GN=Aldoc PE=1 SV=4	16.16	20.78	55.1	18	0.837525
20	Isoprenoid synthase domain-containing protein OS=Mus musculus GN=Ispd PE=2 SV=1	2	2	5.6	1	0.837575
21	40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=1 SV=3	7.8	7.89	27.3	4	0.837875
22	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Mus musculus GN=Dhx15 PE=1 SV=2	13.81	13.86	14.2	7	0.8379
23	Interferon regulatory factor 6 OS=Mus musculus GN=Irf6 PE=1 SV=2	1.08	1.21	5.6	1	0.8381
24	Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV=2	0.86	1.03	18.5	1	0.838375
25	V-type proton ATPase subunit B, brain isoform OS=Mus musculus GN=Atp6v1b2 PE=1 SV=1	18.34	18.41	39.7	13	0.838475

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
26	Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2	8.14	8.15	32.4	4	0.838825
27	Sec1 family domain-containing protein 1 OS=Mus musculus GN=Scfd1 PE=1 SV=1	1.33	1.57	6.3	2	0.83885
28	Bifunctional purine biosynthesis protein PURH OS=Mus musculus GN=Atic PE=1 SV=2	33.39	33.57	44.9	18	0.839575
29	HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	30.79	57.68	53.5	40	0.83965
30	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Mus musculus GN=Ppp3ca PE=1 SV=1	2.86	3.01	10.9	2	0.839675
31	Protein Rap1gds1 OS=Mus musculus GN=Rap1gds1 PE=1 SV=1	18.07	18.29	27.6	9	0.839675
32	Protein Sec24d OS=Mus musculus GN=Sec24d PE=1 SV=1	8.84	9.07	14.8	4	0.839725
33	Neutrophil cytosol factor 2 OS=Mus musculus GN=Ncf2 PE=1 SV=1	5.03	5.13	12.6	3	0.839925
34	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	29.51	29.58	53.6	24	0.840675
35	Hippocalcin-like protein 1 OS=Mus musculus GN=Hpcal1 PE=1 SV=2	2.74	2.82	10.4	2	0.84155
36	N-terminal kinase-like protein OS=Mus musculus GN=Scyl1 PE=1 SV=1	5.31	5.4	7.9	3	0.8417
37	60S ribosomal protein L10 (fragment) OS=Mus musculus GN=Rpl10 PE=1 SV=1	2.56	2.75	18.9	2	0.842375
38	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Mus musculus GN=Pin4 PE=1 SV=1	4	4	17.6	2	0.8425
39	Beta-catenin-interacting protein 1 OS=Mus musculus GN=Ctnnbip1 PE=1 SV=1	3.08	3.16	24.7	2	0.84255
40	Hypoxia upregulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	10.92	11.1	19.3	7	0.84255
41	Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=1 SV=1	34.91	40.22	70.5	27	0.84415
42	Cortactin, isoform CRA_a OS=Mus musculus GN=Cttn PE=1 SV=1	2.04	2.05	6.9	1	0.8448
43	Coatomer subunit beta OS=Mus musculus GN=Copb1 PE=1 SV=1	38.8	38.87	42.9	21	0.8457
44	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Mus musculus GN=Fkbp3 PE=1 SV=2	7.06	7.16	34.4	5	0.84585
45	Poly(ADP-ribose) glycohydrolase ARH3 OS=Mus musculus GN=Adprh12 PE=1 SV=1	5.77	5.89	13	3	0.846825
46	Thymosin beta-4 OS=Mus musculus GN=Tmsb4x PE=1 SV=1	3.27	3.47	40	2	0.846925
47	Twinfilin-2 OS=Mus musculus GN=Twf2 PE=1 SV=1	4.05	4.38	30.4	3	0.84725
48	Protein SET (fragment) OS=Mus musculus GN=Set PE=1 SV=1	7.2	7.29	45.6	4	0.84775
49	Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1	2	2.03	10.2	1	0.8478
50	Protein Gm27029 OS=Mus musculus GN=Gm27029 PE=4 SV=1	7.87	7.96	16	4	0.848275
51	Protein Gm5039 OS=Mus musculus GN=Gm5039 PE=3 SV=1	4.02	4.02	25	2	0.848525
52	Catenin alpha-1 OS=Mus musculus GN=Cttna1 PE=1 SV=1	11.04	11.26	11.8	6	0.84915
53	Proteasome subunit beta type-3 OS=Mus musculus GN=Psmb3 PE=1 SV=1	9.78	9.81	38.5	8	0.84985
54	DnaJ homolog subfamily C member 10 OS=Mus musculus GN=Dnajc10 PE=1 SV=2	2.29	2.89	6.3	1	0.84995
55	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	32.82	32.89	35.4	18	0.850125
56	Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1	13.39	13.43	30.7	10	0.850275
57	Endoplasmic reticulum chaperone protein OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	31.96	36.38	36.2	22	0.85055
58	Thioredoxin domain-containing protein 17 OS=Mus musculus GN=Txndc17 PE=1 SV=1	5.45	5.55	31.7	3	0.850975
59	N-alpha-acetyltransferase 50 OS=Mus musculus GN=Naa50 PE=1 SV=1	0.42	0.47	13.6	1	0.85135
60	SH3 and PX domain-containing protein 2B OS=Mus musculus GN=Sh3pxd2b PE=1 SV=1	1.3	1.48	6.4	2	0.85265
61	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Mus musculus GN=Uap1l1 PE=1 SV=1	20.5	20.52	36.7	11	0.853225
62	Programmed cell death protein 5 OS=Mus musculus GN=Pcdc5 PE=1 SV=3	8.55	8.6	47.6	7	0.8535
63	26S proteasome non-ATPase regulatory subunit 5 OS=Mus musculus GN=Psm5 PE=1 SV=4	16.1	16.48	38.9	9	0.85415
64	Adipocyte enhancer-binding protein 1 OS=Mus musculus GN=Aebp1 PE=1 SV=1	5.78	5.84	5.7	3	0.85495
65	6-pyruvoyl tetrahydrobiopterin synthase OS=Mus musculus GN=Pts PE=1 SV=2	1.79	2	22.2	1	0.8551
66	Transcription elongation factor B polypeptide 2 OS=Mus musculus GN=Tceb2 PE=1 SV=1	12.5	12.57	52.5	8	0.85525
67	Methionine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Mars PE=1 SV=1	12.48	12.59	14.6	7	0.8554
68	Bifunctional glutamate/proline-tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4	36.41	36.5	31.6	18	0.85615
69	DnaJ homolog subfamily C member 7 OS=Mus musculus GN=Dnajc7 PE=1 SV=2	2.02	2.02	7.7	1	0.856275
70	Nuclear protein localization protein 4 homolog OS=Mus musculus GN=Nploc4 PE=1 SV=3	2.41	3.29	9.9	2	0.8569

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
71	Echinoderm microtubule-associated protein-like 2 OS=Mus musculus GN=Eml2 PE=1 SV=1	14.24	14.34	17.5	9	0.857375
72	WD repeat-containing protein 91 OS=Mus musculus GN=Wdr91 PE=1 SV=1	0.45	0.49	3.3	1	0.8575
73	Conserved oligomeric Golgi complex subunit 1 OS=Mus musculus GN=Cog1 PE=1 SV=3	7.14	7.21	9.6	5	0.8575
74	C-type mannose receptor 2 OS=Mus musculus GN=Mrc2 PE=1 SV=3	2	2	1.2	1	0.857775
75	Phospholipid transfer protein OS=Mus musculus GN=Pltp PE=1 SV=1	4.03	4.03	8.4	2	0.857775
76	Fibulin-5 OS=Mus musculus GN=Fbln5 PE=1 SV=1	1.05	1.18	4.5	1	0.8578
77	COMM domain-containing protein 3 OS=Mus musculus GN=Commd3 PE=1 SV=1	4	4.14	21	3	0.858325
78	Aspartate-tRNA ligase, cytoplasmic OS=Mus musculus GN=Dars PE=1 SV=2	28.32	28.38	47.7	17	0.858725
79	Sorting nexin-6 OS=Mus musculus GN=Snx6 PE=1 SV=2	14.43	18.76	29.3	9	0.859
80	KDEL (Lys-Asp-Glu-Leu) containing 2, isoform CRA_b OS=Mus musculus GN=Kdelc2 PE=1 SV=1	1.03	1.19	9.5	1	0.859075
81	1,4-alpha-glucan-branching enzyme OS=Mus musculus GN=Gbe1 PE=1 SV=1	2.77	2.85	6.5	2	0.859725
82	A-kinase anchor protein 9 OS=Mus musculus GN=Akap9 PE=1 SV=1	6.29	6.47	5.7	3	0.86005
83	Serine hydroxymethyltransferase (fragment) OS=Mus musculus GN=Shmt1 PE=1 SV=1	0.69	0.84	13.9	1	0.860175
84	Lysophospholipase-like protein 1 OS=Mus musculus GN=Lyplal1 PE=1 SV=3	1.28	1.71	18.8	1	0.860475
85	Glycerol-3-phosphate dehydrogenase 1-like protein OS=Mus musculus GN=Gpd1l PE=1 SV=2	10.76	13.08	44.4	9	0.861
86	MCG6846, isoform CRA_c OS=Mus musculus GN=Prpsap1 PE=1 SV=1	10	11.07	23.6	7	0.861025
87	AP-1 complex subunit mu-2 OS=Mus musculus GN=Ap1m2 PE=1 SV=3	4.72	4.79	16.3	3	0.8611
88	Replication protein A 14 kDa subunit OS=Mus musculus GN=Rpa3 PE=1 SV=1	2.04	2.05	38.8	1	0.861275
89	26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=1	23.69	23.76	48	11	0.8613
90	Hemoglobin subunit beta-1 OS=Mus musculus GN=Hbb-b1 PE=1 SV=2	1.82	16.22	63.3	25	0.861375
91	Conserved oligomeric Golgi complex subunit 5 OS=Mus musculus GN=Cog5 PE=1 SV=3	8.03	8.21	16.4	4	0.861575
92	Bifunctional coenzyme A synthase OS=Mus musculus GN=Coasy PE=1 SV=2	6.65	6.71	22.2	3	0.8616
93	Heme-binding protein 2 OS=Mus musculus GN=Hebp2 PE=1 SV=1	4.41	4.46	21.5	2	0.861625
94	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	20.35	20.64	40.7	11	0.861825
95	Methylthioribulose-1-phosphate dehydratase OS=Mus musculus GN=Apip PE=1 SV=1	5.19	5.29	26.1	5	0.861975
96	Protein AMBP OS=Mus musculus GN=Ambp PE=1 SV=2	2	2	4.3	1	0.862175
97	Protein misato homolog 1 OS=Mus musculus GN=Msto1 PE=1 SV=1	4.01	4.01	7.6	2	0.862325
98	Phosphoglycolate phosphatase OS=Mus musculus GN=Pgp PE=1 SV=1	15.07	15.11	42.7	9	0.862375
99	BolA-like protein 1 OS=Mus musculus GN=Bola1 PE=1 SV=1	9.05	9.13	56.9	5	0.8624
100	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	75.21	75.21	69.8	44	0.86265
101	WAS/WASL-interacting protein family member 3 OS=Mus musculus GN=Wipf3 PE=1 SV=1	0.52	0.58	5.2	1	0.86295
102	Immunity-related GTPase family Q protein OS=Mus musculus GN=Irgq PE=1 SV=1	2.92	3.02	8.4	2	0.863225
103	Rho GTPase-activating protein 1 OS=Mus musculus GN=Arhgap1 PE=1 SV=1	18.59	18.72	35.3	10	0.863425
104	Calcium-binding protein 39 OS=Mus musculus GN=Cab39 PE=1 SV=2	10.52	10.67	26.7	7	0.86345
105	DNA damage-binding protein 1 OS=Mus musculus GN=Ddb1 PE=1 SV=2	17.23	17.6	24.7	9	0.863675
106	Proteasome subunit beta type-2 OS=Mus musculus GN=Psmb2 PE=1 SV=1	7.75	7.88	42.3	4	0.863775
107	Protein Golgb1 OS=Mus musculus GN=Golgb1 PE=1 SV=1	2.12	2.22	5.2	2	0.86405
108	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1	2.4	2.46	12.1	1	0.86435
109	Glutathione S-transferase Mu 2 OS=Mus musculus GN=Gstm2 PE=1 SV=2	49.13	49.14	91.3	52	0.864775
110	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus GN=Aimp1 PE=1 SV=1	13.07	13.13	39.8	7	0.864825
111	Serpin B5 OS=Mus musculus GN=Serpib5 PE=1 SV=1	5.43	5.62	21.3	4	0.864875
112	26S proteasome non-ATPase regulatory subunit 8 OS=Mus musculus GN=Psm8 PE=1 SV=2	6.35	6.38	28	3	0.8654
113	Cysteine rich with EGF-like domain protein 2 OS=Mus musculus GN=Crel2 PE=1 SV=1	6	6	12	3	0.865425
114	Translin OS=Mus musculus GN=Tsn PE=1 SV=1	4.19	4.6	44.3	5	0.866075
115	Acyl-coenzyme A thioesterase 9, mitochondrial OS=Mus musculus GN=Acot9 PE=1 SV=1	1.48	1.73	7.7	2	0.866125

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
116	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	34.14	34.25	77.7	31	0.866275
117	Caspase-8 OS=Mus musculus GN=Casp8 PE=1 SV=1	3.37	3.92	15.8	3	0.866525
118	Serine/threonine-protein phosphatase CPPED1 (fragment) OS=Mus musculus GN=Cpped1 PE=1 SV=1	2	2	6.3	1	0.866625
119	Proteasome subunit beta type-8 OS=Mus musculus GN=Psm8 PE=1 SV=2	6.11	8.58	29.4	8	0.86725
120	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=1	12.76	12.82	42.7	7	0.867525
121	S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1	17.27	17.43	52.9	18	0.867525
122	Ovarian cancer-associated gene 2 protein homolog OS=Mus musculus GN=Ovca2 PE=1 SV=1	4	4	8.4	2	0.86765
123	Acyl-coenzyme A thioesterase 1 OS=Mus musculus GN=Acot1 PE=1 SV=1	12.32	12.34	28.4	9	0.867675
124	Arginine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Rars PE=1 SV=2	22.26	22.41	25.9	11	0.867675
125	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	76.85	102.84	42.4	60	0.867675
126	Conserved oligomeric Golgi complex subunit 3 OS=Mus musculus GN=Cog3 PE=1 SV=1	2.15	2.17	8.6	1	0.867825
127	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=1 SV=1	2.57	2.63	53	2	0.868025
128	CLIP-associating protein 2 OS=Mus musculus GN=Clasp2 PE=1 SV=1	0.62	0.67	3.6	1	0.868325
129	60S ribosomal protein L9 (fragment) OS=Mus musculus GN=Rpl9 PE=1 SV=1	0.94	1.09	12.6	1	0.86835
130	Basic leucine zipper and W2 domain-containing protein 1 OS=Mus musculus GN=Bzw1 PE=1 SV=1	8.64	8.75	23.3	6	0.8684
131	Nucleobindin-2 OS=Mus musculus GN=Nucb2 PE=1 SV=1	6.18	6.21	12.1	4	0.8684
132	Ras-related GTP-binding protein D OS=Mus musculus GN=Rragd PE=1 SV=1	4.13	4.48	8.4	4	0.86935
133	Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=1	5.82	5.91	24.7	5	0.869475
134	Zinc finger protein 185 OS=Mus musculus GN=Zfp185 PE=1 SV=1	5.09	5.2	25.9	3	0.8701
135	Zinc finger protein ZPR1 (fragment) OS=Mus musculus GN=Zpr1 PE=1 SV=1	2.09	2.12	6.7	1	0.870275
136	EKC/KEOPS complex subunit Tprkb OS=Mus musculus GN=Tprkb PE=1 SV=1	2.03	2.04	13.1	1	0.87175
137	Protein BRICK1 OS=Mus musculus GN=Brk1 PE=1 SV=1	2	2	14.7	1	0.871875
138	Solute carrier family 2, facilitated glucose transporter member 3 OS=Mus musculus GN=Slc2a3 PE=1 SV=1	1.36	1.5	6.3	2	0.87235
139	Proteasome activator complex subunit 3 OS=Mus musculus GN=Psm3 PE=1 SV=1	9.91	10.01	32.3	6	0.872725
140	Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=1	29.02	38.54	55.6	27	0.87275
141	Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=1	7.7	7.74	11.1	7	0.873225
142	Histone H2A OS=Mus musculus GN=H2afz PE=2 SV=1	2	4.02	18.1	3	0.87325
143	Coatomer subunit gamma-1 OS=Mus musculus GN=Copg1 PE=1 SV=1	25.74	25.78	29.5	19	0.8733
144	MCG13402, isoform CRA_c OS=Mus musculus GN=Ptbp1 PE=1 SV=1	10.1	10.2	23.6	7	0.873525
145	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Mus musculus GN=Pip4k2c PE=1 SV=1	8.02	8.2	23.3	7	0.873875
146	Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	9.21	9.34	11	5	0.87395
147	Protein S100 OS=Mus musculus GN=S100a1 PE=1 SV=1	4.82	4.94	69.2	2	0.874275
148	Medium chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadm PE=1 SV=1	1.1	1.28	6.4	1	0.874825
149	Vacuolar protein sorting-associated protein 25 OS=Mus musculus GN=Vps25 PE=1 SV=1	4	4	31.9	2	0.874925
150	WW domain-binding protein 2 OS=Mus musculus GN=Wbp2 PE=1 SV=1	6.3	6.44	24.5	4	0.87525
151	NAD+ ADP-ribosyltransferase 3 PARP-3 OS=Mus musculus GN=Parp3 PE=1 SV=1	4.05	4.06	9.1	2	0.87525
152	G7b alternative form OS=Mus musculus GN=Lsm2 PE=1 SV=1	2	2	5.3	1	0.875875
153	N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate forming) OS=Mus musculus GN=Acy3 PE=1 SV=1	5.01	5.21	20.8	3	0.875875
154	14-3-3 protein theta (fragment) OS=Mus musculus GN=Ywhaq PE=1 SV=1	17.89	26.14	57.5	22	0.876025
155	Glutamine-fructose-6-phosphate aminotransferase (isomerizing) 1 OS=Mus musculus GN=Gfpt1 PE=1 SV=3	15.66	15.81	25.4	8	0.87605
156	Transmembrane 9 superfamily member 2 OS=Mus musculus GN=Tm9sf2 PE=1 SV=1	2.01	2.03	5.6	1	0.87605
157	Rab-like protein 6 OS=Mus musculus GN=Rab16 PE=1 SV=2	8.13	8.26	12.1	6	0.876125
158	TBC1 domain family member 22A OS=Mus musculus GN=Tbc1d22a PE=1 SV=3	2.89	2.99	12	2	0.87625
159	Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=EIF3a PE=1 SV=5	13.61	13.7	17.3	6	0.8769

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
160	E3 ubiquitin-protein ligase MIB2 OS=Mus musculus GN=Mib2 PE=1 SV=2	1.45	1.59	3.3	1	0.877575
161	Prostate- and testis-expressed protein 4 OS=Mus musculus GN=Pate4 PE=1 SV=3	0.82	0.94	13.1	2	0.878275
162	X-ray repair cross-complementing protein 5 OS=Mus musculus GN=Xrcc5 PE=1 SV=4	6.17	6.29	14.9	3	0.8783
163	Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=1	2.35	2.95	39.3	2	0.878625
164	Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1	18.88	19.27	32.2	8	0.879
165	Capping protein (actin filament) muscle Z-line, alpha 1 OS=Mus musculus GN=Capza1 PE=1 SV=1	9.4	13.57	47.2	10	0.879275
166	Glucosamine-6-phosphate isomerase 1 OS=Mus musculus GN=Gnpd1 PE=1 SV=3	8.77	8.81	41.2	5	0.8797
167	Geranylgeranyl transferase type-2 subunit alpha OS=Mus musculus GN=Rabgta PE=1 SV=1	5.13	5.29	27.5	3	0.8805
168	Golgi apparatus protein 1 (fragment) OS=Mus musculus GN=Glg1 PE=1 SV=1	1.43	1.69	4.6	2	0.880825
169	Prefoldin 1 OS=Mus musculus GN=Pfdn1 PE=1 SV=1	2	2	9	1	0.88115
170	Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	8.61	30.89	32.9	18	0.8813
171	AP-3 complex subunit mu-2 OS=Mus musculus GN=Ap3m2 PE=1 SV=1	0.9	1.34	8.6	1	0.88225
172	Lipid phosphate phosphatase-related protein type 3 OS=Mus musculus GN=Lppr3 PE=1 SV=1	1.11	1.24	4.5	1	0.883325
173	Perilipin-3 OS=Mus musculus GN=Plin3 PE=1 SV=1	17.11	17.17	44.6	14	0.8838
174	Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=3	17.82	18.14	34.8	12	0.88405
175	Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	18.19	18.29	74.3	15	0.8849
176	Protein MON2 homolog OS=Mus musculus GN=Mon2 PE=1 SV=2	16.78	17.04	10.1	9	0.885325
177	Conserved oligomeric Golgi complex subunit 8 OS=Mus musculus GN=Cog8 PE=1 SV=3	8.15	8.23	18	5	0.885575
178	UPF0462 protein C4orf33 homolog OS=Mus musculus GN=D3Erd751e PE=2 SV=1	1.15	1.28	13	1	0.8857
179	Platelet-activating factor acetylhydrolase IB subunit beta OS=Mus musculus GN=Pafah1b2 PE=1 SV=2	8.2	8.23	46.7	9	0.88605
180	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	15.58	15.68	55.2	10	0.886675
181	Heterogeneous nuclear ribonucleoprotein A0 OS=Mus musculus GN=Hnrnpa0 PE=1 SV=1	2.02	2.05	19.3	1	0.8873
182	Methylthioribose-1-phosphate isomerase OS=Mus musculus GN=Mri1 PE=1 SV=1	14.44	14.46	48	7	0.887325
183	26S proteasome non-ATPase regulatory subunit 14 OS=Mus musculus GN=Psm14 PE=1 SV=2	12.05	12.17	41.9	12	0.887775
184	Complement component C8 alpha chain OS=Mus musculus GN=C8a PE=1 SV=1	5.9	6.02	8.8	3	0.88785
185	Probable E3 ubiquitin-protein ligase HERC4 OS=Mus musculus GN=Herc4 PE=1 SV=2	1.21	1.37	2.7	1	0.888225
186	Ribosome maturation protein SBDS OS=Mus musculus GN=Sbds PE=1 SV=4	3.35	4.54	24.8	2	0.888625
187	Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4	19.77	21.09	45.4	11	0.889275
188	Cytoplasmic protein NCK1 OS=Mus musculus GN=Nck1 PE=1 SV=1	1.22	2.1	12.8	2	0.889525
189	Transthyretin OS=Mus musculus GN=Ttr PE=1 SV=1	5.41	5.51	44.9	7	0.88985
190	Developmentally regulated GTP-binding protein 2 OS=Mus musculus GN=Drg2 PE=1 SV=1	7.49	9.72	25.6	6	0.890075
191	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	11.45	12.47	40.9	10	0.89035
192	Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=2	6.81	6.86	4	5	0.890375
193	Sedoheptulokinase OS=Mus musculus GN=Shpk PE=1 SV=1	0.84	1.02	9	2	0.89055
194	Thymidylate kinase OS=Mus musculus GN=Dtymk PE=1 SV=2	4.9	4.97	16	3	0.89155
195	Osteoclast-stimulating factor 1 OS=Mus musculus GN=Ostf1 PE=1 SV=2	2.85	2.94	22.8	3	0.891625
196	Dihydrofolate reductase OS=Mus musculus GN=Dhfr PE=1 SV=3	4.87	5.01	35.3	3	0.8917
197	Formin-binding protein 1 OS=Mus musculus GN=Fbnp1 PE=1 SV=1	2.8	3.14	5.4	2	0.8917
198	UPF0600 protein C5 or f51 homolog OS=Mus musculus PE=1 SV=1	3.72	3.83	14.3	2	0.891775
199	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=1 SV=2	4.13	4.15	51.9	3	0.8919
200	40S ribosomal protein S28 (fragment) OS=Mus musculus GN=Rps28 PE=1 SV=1	2.29	2.32	37.5	1	0.89195

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
201	Mitochondrial import inner membrane translocase subunit Tim8 A OS=Mus musculus GN=Timm8a1 PE=1 SV=1	2	2	11.3	1	0.891975
202	TBC1 domain family member 13 OS=Mus musculus GN=Tbc1d13 PE=1 SV=1	2	2	4.5	1	0.892175
203	Ubiquitin-related modifier 1 OS=Mus musculus GN=Urm1 PE=1 SV=1	2	2	14.9	1	0.892725
204	Phosphoacetylglucosamine mutase OS=Mus musculus GN=Pgm3 PE=1 SV=1	16.46	16.53	30.8	11	0.8928
205	Glutathione S-transferase Mu 7 OS=Mus musculus GN=Gstm7 PE=1 SV=1	19.48	42.77	84.9	46	0.89285
206	Hydroxyacyl glutathione hydrolase OS=Mus musculus GN=Hagh PE=1 SV=1	1.53	1.75	17.5	1	0.893225
207	Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	17.38	17.5	71.7	15	0.8937
208	GMP synthase (glutamine hydrolyzing) OS=Mus musculus GN=Gmps PE=1 SV=2	14.82	14.95	31.3	8	0.8938
209	Eukaryotic translation initiation factor 4 gamma 2 OS=Mus musculus GN=Eif4g2 PE=1 SV=1	5.77	6.04	9.9	3	0.8947
210	40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	3.03	3.18	27.3	3	0.89515
211	Glutathione reductase, mitochondrial OS=Mus musculus GN=Gsr PE=1 SV=3	14.22	14.28	30.8	10	0.89575
212	Ribosylidihydroxynicotinamide dehydrogenase (quinone) OS=Mus musculus GN=Nqo2 PE=1 SV=3	2.19	2.21	23.8	1	0.895875
213	Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	5.38	5.48	3.4	3	0.89595
214	Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=1	9.72	10.13	44.5	12	0.896125
215	Protein Skiv2l OS=Mus musculus GN=Skiv2l PE=1 SV=1	2.75	2.82	4.3	2	0.896375
216	Glutathione S-transferase A4 OS=Mus musculus GN=Gsta4 PE=1 SV=3	12.4	12.45	50.5	18	0.89645
217	General transcription factor II-I OS=Mus musculus GN=Gtf2i PE=1 SV=1	2.48	2.66	7.6	2	0.896475
218	Hsp90 co-chaperone Cdc37 OS=Mus musculus GN=Cdc37 PE=1 SV=1	12.09	12.14	25.3	7	0.896725
219	COP9 signalosome complex subunit 6 OS=Mus musculus GN=Cops6 PE=1 SV=1	5.35	5.46	19.5	3	0.8971
220	Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1	23.1	23.18	46	15	0.897275
221	Diazepam-binding inhibitor-like 5 OS=Mus musculus GN=Dbil5 PE=1 SV=1	2.37	2.73	50.6	2	0.897325
222	Neudessin OS=Mus musculus GN=Nenf PE=1 SV=1	4	4	14	2	0.897375
223	Protein phosphatase 1G OS=Mus musculus GN=Ppm1g PE=1 SV=3	3.84	3.97	9.8	3	0.897625
224	AH receptor-interacting protein OS=Mus musculus GN=Aip PE=1 SV=1	4.53	4.68	24.6	2	0.898175
225	Proteasome activator complex subunit 1 (fragment) OS=Mus musculus GN=Psmc1 PE=1 SV=1	18.02	18.11	56.3	12	0.898175
226	Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=1	27.72	27.89	37.1	15	0.8985
227	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	23.7	23.79	79.9	19	0.898575
228	Retinol-binding protein 1 OS=Mus musculus GN=Rbp1 PE=1 SV=2	22.05	22.11	89.6	12	0.898975
229	Serine-threonine kinase receptor-associated protein OS=Mus musculus GN=Strap PE=1 SV=2	4.46	4.66	30	3	0.8992
230	Glycerol kinase OS=Mus musculus GN=Gk PE=1 SV=2	32.01	32.06	42.8	18	0.9006
231	RNA-binding protein 47 OS=Mus musculus GN=Rbm47 PE=1 SV=1	2.02	2.02	6.9	1	0.900775
232	Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2	3.85	4.11	14.2	3	0.900825
233	Diphosphoinositol polyphosphate phosphohydrolase 1 OS=Mus musculus GN=Nudt3 PE=1 SV=1	5.43	5.51	27.4	3	0.901
234	Protein Coq10a OS=Mus musculus GN=Coq10a PE=1 SV=1	0.95	1.08	7.3	1	0.901075
235	Transcriptional activator protein Pur-beta OS=Mus musculus GN=Purb PE=1 SV=3	5.65	5.78	23.8	3	0.901225
236	Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=3	26.5	26.67	30.6	14	0.901775
237	Methionine-R-sulfoxide reductase B3, mitochondrial OS=Mus musculus GN=Msrb3 PE=1 SV=2	2.04	2.05	10.3	1	0.9019
238	Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2	49.98	49.98	34.9	29	0.902
239	ADP-ribosylation factor GTPase-activating protein 3 OS=Mus musculus GN=Arfgap3 PE=1 SV=2	2.33	2.37	10.1	1	0.90255
240	Cell differentiation protein RCD1 homolog OS=Mus musculus GN=Rqcd1 PE=1 SV=1	0.75	0.87	5.7	1	0.902825
241	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	13.67	13.77	49	10	0.902925
242	Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus GN=Uba1 PE=1 SV=1	60.86	60.88	49.5	46	0.903175
243	Seminal vesicle secretory protein 4 OS=Mus musculus GN=Svs4 PE=1 SV=2	0.56	0.63	25.7	1	0.903225
244	Eukaryotic translation initiation factor 3 subunit J-B OS=Mus musculus GN=Eif3j2 PE=1 SV=1	9.27	9.71	26.2	5	0.90335
245	Conserved oligomeric Golgi complex subunit 6 OS=Mus musculus GN=Cog6 PE=1 SV=1	7.29	8.31	19.4	7	0.904225

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
246	Vacuolar protein sorting-associated protein 29 (fragment) OS=Mus musculus GN=Vps29 PE=1 SV=1	2.39	2.43	36.3	1	0.90495
247	Pleckstrin homology domain-containing family A member 3 OS=Mus musculus GN=Plekha3 PE=2 SV=1	2.35	2.38	6.7	2	0.90505
248	Septin-9 OS=Mus musculus GN=Sept9 PE=1 SV=1	7.23	7.41	20.2	4	0.9054
249	Lipopolysaccharide-responsive and beige-like anchor protein OS=Mus musculus GN=Lrba PE=1 SV=1	20.82	21.07	10.4	11	0.905575
250	F-box only protein 6 (fragment) OS=Mus musculus GN=Fbxo6 PE=1 SV=1	0.67	0.77	3.8	1	0.905675
251	Leucine-rich repeat-containing protein 40 OS=Mus musculus GN=Lrrc40 PE=1 SV=2	2.19	2.21	6.1	2	0.90575
252	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5	20.41	20.65	53.7	15	0.905975
253	BRCA1-A complex subunit BRE OS=Mus musculus GN=Bre PE=1 SV=2	4.07	4.09	12.5	2	0.906175
254	40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	0.71	0.82	26.9	1	0.906525
255	Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=1 SV=2	11.56	11.59	30.5	6	0.906725
256	SUMO-activating enzyme subunit 2 OS=Mus musculus GN=Uba2 PE=1 SV=1	14.49	14.59	31.2	10	0.906875
257	mRNA cap guanine-N7 methyltransferase OS=Mus musculus GN=Rnmt PE=1 SV=1	4.04	4.05	9.2	2	0.90735
258	Synapse-associated protein 1 OS=Mus musculus GN=Syap1 PE=1 SV=1	7.12	7.29	32.6	4	0.907425
259	Anaphase-promoting complex subunit CDC26 OS=Mus musculus GN=Cdc26 PE=1 SV=1	2	2	12.9	1	0.907775
260	Galactokinase OS=Mus musculus GN=Galk1 PE=1 SV=2	12.3	12.32	21.7	7	0.907925
261	Putative N-acetylglucosamine-6-phosphate deacetylase OS=Mus musculus GN=Amdhd2 PE=1 SV=1	7.39	7.48	24	4	0.9081
262	Glutathione synthetase OS=Mus musculus GN=Gss PE=1 SV=1	12.83	12.86	25.3	7	0.90835
263	Dynactin 6, isoform CRA_b OS=Mus musculus GN=Dctn6 PE=1 SV=1	2	2	7.6	1	0.9085
264	Putative hydrolase RBBP9 OS=Mus musculus GN=Rbbp9 PE=1 SV=2	5.08	5.36	62.9	4	0.90855
265	Serine/threonine-protein kinase A-Raf OS=Mus musculus GN=Araf PE=1 SV=2	3.06	3.23	13.1	1	0.908675
266	COP9 signalosome complex subunit 7a (fragment) OS=Mus musculus GN=Cops7a PE=1 SV=5	3.57	3.68	11.9	2	0.9092
267	Protein 2310035C23Rik OS=Mus musculus GN=2310035C23Rik PE=1 SV=2	5.46	5.6	7.4	3	0.9093
268	Threonine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Tars PE=1 SV=2	6.29	6.49	21.1	4	0.910475
269	Ribosomal protein S6 kinase alpha-3 OS=Mus musculus GN=Rps6ka3 PE=1 SV=1	10.98	11.23	19.2	5	0.9106
270	Rho-related GTP-binding protein RhoC OS=Mus musculus GN=Rhoc PE=1 SV=2	1.67	10.48	48.2	8	0.910675
271	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	43.25	43.27	70.8	82	0.910775
272	Tumor protein D53 OS=Mus musculus GN=Tpd52l1 PE=1 SV=1	5.11	5.19	20.6	3	0.910925
273	Vacuolar protein sorting-associated protein 52 homolog OS=Mus musculus GN=Vps52 PE=1 SV=1	0.56	0.61	5	1	0.91095
274	Eukaryotic translation initiation factor 3 subunit H OS=Mus musculus GN=Eif3h PE=1 SV=1	10.53	10.61	25.3	6	0.911075
275	Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	16.31	16.37	23.4	12	0.911475
276	26S proteasome non-ATPase regulatory subunit 12 OS=Mus musculus GN=Psm12 PE=1 SV=4	15.5	15.59	29.2	8	0.9117
277	Threonine synthase-like 2 OS=Mus musculus GN=Thns12 PE=1 SV=1	5.92	6	11.4	4	0.9122
278	Small nuclear ribonucleoprotein E OS=Mus musculus GN=Snrpe PE=1 SV=1	2.1	2.12	25	2	0.91235
279	X-prolyl aminopeptidase (Aminopeptidase P) 1, soluble, isoform CRA_b OS=Mus musculus GN=Xpnpep1 PE=1 SV=1	23.75	24.89	25.1	14	0.912525
280	AP-1 complex subunit sigma-2 OS=Mus musculus GN=Ap1s2 PE=1 SV=1	2.3	2.33	15.6	1	0.91395
281	Protein Wbscr27 OS=Mus musculus GN=Wbscr27 PE=1 SV=1	7.74	7.8	24.4	4	0.914325
282	Disintegrin and metalloproteinase domain-containing protein 28 OS=Mus musculus GN=Adam28 PE=1 SV=3	4.76	4.94	7.3	3	0.9149
283	Cullin 5 OS=Mus musculus GN=Cul5 PE=1 SV=1	7.35	7.57	14.3	4	0.915375
284	Lymphocyte antigen 6 complex locus protein G5b OS=Mus musculus GN=Ly6g5b PE=1 SV=1	5.2	5.36	30.9	4	0.9155
285	Olfactory receptor OS=Mus musculus GN=Olfr286 PE=3 SV=1	0.63	0.9	7.8	1	0.9159
286	Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Mus musculus GN=Hmgcs1 PE=1 SV=1	3.44	3.56	11.5	2	0.916325
287	Protein arginine N-methyltransferase 1 OS=Mus musculus GN=Prmt1 PE=1 SV=1	20.15	20.19	45.3	10	0.9164

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
288	Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpysl2 PE=1 SV=2	28.5	28.99	50.9	18	0.9168
289	Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	10.13	10.33	77.1	7	0.9169
290	Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=2	2.22	3.03	3.8	3	0.916925
291	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	34.18	34.26	65.5	28	0.91705
292	Ubiquitin carboxyl-terminal hydrolase OS=Mus musculus GN=Usp5 PE=1 SV=1	33.24	33.36	37.5	18	0.917275
293	Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	13.25	13.28	39	7	0.917425
294	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	11	11.13	45	6	0.9182
295	Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1 PE=1 SV=2	8.97	9.07	29.4	5	0.918525
296	Lysine-tRNA ligase OS=Mus musculus GN=Kars PE=1 SV=1	13.16	13.26	21.5	7	0.91855
297	Probable ATP-dependent RNA helicase DDX6 OS=Mus musculus GN=Ddx6 PE=1 SV=1	10.57	12.81	31.9	6	0.9189
298	Flavin reductase (NADPH) OS=Mus musculus GN=Blvrb PE=1 SV=3	9.92	9.96	42.2	5	0.9191
299	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Mus musculus GN=Pdxdc1 PE=1 SV=2	48.25	48.27	47.1	28	0.919375
300	Thyroid adenoma-associated protein homolog OS=Mus musculus GN=Thada PE=1 SV=1	2.93	3.02	5.6	2	0.91965
301	SET and MYND domain-containing protein 5 OS=Mus musculus GN=Smyd5 PE=1 SV=2	2.33	2.47	6.5	2	0.919825
302	LIM and SH3 domain protein 1 OS=Mus musculus GN=Lasp1 PE=1 SV=1	5.89	5.96	22.1	5	0.920175
303	Protein SEC13 homolog OS=Mus musculus GN=Sec13 PE=1 SV=3	10.14	10.15	35.4	5	0.9207
304	Uncharacterized protein OS=Mus musculus GN=Gm8730 PE=1 SV=1	8.72	8.75	19.6	5	0.9211
305	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	27.35	27.39	69.9	21	0.92115
306	Endoplasmic reticulum-resident protein 44 OS=Mus musculus GN=Erp44 PE=1 SV=1	4.01	4.52	17.5	2	0.921375
307	Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=2	18	18.1	52.7	10	0.921575
308	Valine-tRNA ligase OS=Mus musculus GN=Vars PE=1 SV=1	46.2	46.26	32.9	26	0.92215
309	Protein Noxp20 OS=Mus musculus GN=Fam114a1 PE=1 SV=1	7.25	7.39	13.4	4	0.92235
310	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Mus musculus GN=Prpsap2 PE=1 SV=1	11.1	11.19	32.8	6	0.9224
311	Myotrophin OS=Mus musculus GN=Mtpn PE=1 SV=2	5.2	5.33	55.1	3	0.922925
312	Transportin-1 OS=Mus musculus GN=Tnpo1 PE=1 SV=2	11.75	11.84	12.6	6	0.923275
313	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	23.4	31.74	54.6	33	0.92345
314	Golgi-associated PDZ and coiled-coil motif-containing protein OS=Mus musculus GN=Gopc PE=1 SV=1	8.93	9.03	28.9	5	0.9238
315	Clathrin heavy chain OS=Mus musculus GN=Cltc PE=1 SV=1	54.7	54.73	30.4	28	0.923925
316	Apoptosis inhibitor 5 OS=Mus musculus GN=Api5 PE=1 SV=2	4.9	5.03	12.5	3	0.9241
317	Histidine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Hars PE=1 SV=2	30.35	30.38	38.7	17	0.92425
318	High-mobility group nucleosome-binding domain-containing protein 5 OS=Mus musculus GN=Hmgn5 PE=1 SV=2	2.11	2.13	15	1	0.92435
319	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Mus musculus GN=Camk2d PE=1 SV=1	3.06	3.61	15	4	0.9244
320	Coagulation factor IX OS=Mus musculus GN=F9 PE=2 SV=3	2.01	2.01	5.1	1	0.9245
321	Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3	12.6	12.65	57.6	6	0.9247
322	Eukaryotic translation initiation factor 4H OS=Mus musculus GN=Eif4h PE=1 SV=3	6.15	6.27	29.8	4	0.925
323	Calpain-2 catalytic subunit OS=Mus musculus GN=Capn2 PE=1 SV=4	10.6	10.72	16.7	7	0.92505
324	Casein kinase II subunit alpha OS=Mus musculus GN=Csnk2a1 PE=1 SV=2	2	2.12	5.9	2	0.925625
325	BUB3-interacting and GLEBS motif-containing protein ZNF207 (fragment) OS=Mus musculus GN=Zfp207 PE=1 SV=1	1.05	1.2	5	1	0.925675
326	Glycylpeptide N-tetradecanoyltransferase 1 OS=Mus musculus GN=Nmt1 PE=1 SV=1	2.62	2.67	9.1	2	0.925675
327	TBC1 domain family member 9B OS=Mus musculus GN=Tbc1d9b PE=1 SV=1	2.44	2.5	5.5	1	0.92615
328	UBX domain-containing protein 1 OS=Mus musculus GN=Ubxn1 PE=1 SV=1	6.19	6.33	30.6	4	0.926375
329	ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus GN=Pfkf PE=1 SV=4	25.57	25.66	36.7	13	0.9264
330	Glutaminyl-tRNA synthetase OS=Mus musculus GN=Qars PE=1 SV=1	21.62	21.8	32.7	14	0.926525
331	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	42.01	48.01	47.6	36	0.92665
332	Mitogen-activated protein kinase 3 OS=Mus musculus GN=Mapk3 PE=1 SV=5	3.46	10.1	35.3	7	0.926975

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
333	ATP-dependent RNA helicase DDX42 OS=Mus musculus GN=Ddx42 PE=1 SV=3	0.82	0.93	2.3	1	0.927125
334	S-phase kinase-associated protein 1 OS=Mus musculus GN=Skp1 PE=1 SV=3	4.16	4.19	35.6	2	0.9275
335	Endothelin-converting enzyme 2 OS=Mus musculus GN=Ece2 PE=1 SV=1	2	2	5.3	1	0.927625
336	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Mus musculus GN=Fnta PE=1 SV=1	4.35	4.39	11.1	2	0.927675
337	Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	13.27	13.41	40.4	8	0.9277
338	26S protease regulatory subunit 6A OS=Mus musculus GN=Psmc3 PE=1 SV=1	24.23	24.58	48.3	18	0.9277
339	Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=1	16.41	17.21	56.8	11	0.927775
340	Ran GTPase-activating protein 1 OS=Mus musculus GN=Rangap1 PE=1 SV=2	4.3	4.46	12.9	3	0.928175
341	Apoptosis-associated speck-like protein containing a CARD OS=Mus musculus GN=Pycard PE=1 SV=1	4.97	5.08	35.2	5	0.92905
342	Arylamine N-acetyltransferase 2 OS=Mus musculus GN=Nat2 PE=1 SV=1	4.05	4.05	13.8	2	0.9302
343	Synaptosomal-associated protein 29 OS=Mus musculus GN=Snap29 PE=1 SV=1	1.77	1.92	6.2	1	0.93045
344	Prefoldin subunit 4 OS=Mus musculus GN=Pfdn4 PE=1 SV=1	4.06	4.2	37.3	2	0.9308
345	Protein Ttc37 OS=Mus musculus GN=Ttc37 PE=1 SV=1	1.32	1.51	3.6	1	0.931275
346	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	25.95	33.27	82	29	0.931625
347	Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Elf3c PE=1 SV=1	11.5	11.59	12	6	0.93195
348	Serine/threonine-protein kinase OSR1 OS=Mus musculus GN=Oxsr1 PE=1 SV=1	7.31	7.51	19.9	5	0.93245
349	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnp1 PE=1 SV=1	8.49	8.57	23.1	5	0.932475
350	Basic leucine zipper and W2 domain-containing protein 2 OS=Mus musculus GN=Bzw2 PE=1 SV=1	4.07	5.28	17.9	3	0.932575
351	CAD protein OS=Mus musculus GN=Cad PE=1 SV=1	49.71	49.75	21.6	28	0.933025
352	Tubulin-specific chaperone A OS=Mus musculus GN=Tbca PE=1 SV=3	3.63	3.8	25.9	2	0.933325
353	NAD(P)H dehydrogenase (quinone) 1 OS=Mus musculus GN=Nqo1 PE=1 SV=3	4.69	4.84	29.9	5	0.933375
354	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	24.24	24.31	54.9	12	0.933675
355	Protein Gm20431 OS=Mus musculus GN=Gm20431 PE=4 SV=1	7.18	8.38	23.2	8	0.933775
356	Anaphase-promoting complex subunit 13 OS=Mus musculus GN=Anapc13 PE=3 SV=1	2	2	13.5	1	0.93395
357	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	2.96	3.05	22.9	2	0.934
358	Proteasome subunit beta type-6 OS=Mus musculus GN=Psmb6 PE=1 SV=3	11.22	11.27	43.7	6	0.934125
359	Phosphopantothenate-cysteine ligase OS=Mus musculus GN=Ppcs PE=1 SV=1	7.91	7.95	22.8	4	0.934275
360	Transcription elongation factor A protein 1 OS=Mus musculus GN=Tcea1 PE=1 SV=2	5.02	5.13	21.9	4	0.9352
361	26S proteasome non-ATPase regulatory subunit 6 OS=Mus musculus GN=Psm6 PE=1 SV=1	17.2	18.21	37	8	0.93565
362	Protein FAM49B OS=Mus musculus GN=Fam49b PE=1 SV=1	2.34	2.38	14.5	1	0.935775
363	Heterogeneous nuclear ribonucleoprotein D, isoform CRA_b OS=Mus musculus GN=Hnrnpd PE=1 SV=1	12.87	12.95	45	9	0.9362
364	Twinfilin-1 OS=Mus musculus GN=Twf1 PE=1 SV=2	11.44	11.48	30.9	7	0.936275
365	Kynurenine-oxoglutarate transaminase 1 OS=Mus musculus GN=Ccbl1 PE=1 SV=1	8.11	8.13	30.8	7	0.936375
366	40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	2.4	2.44	16.3	2	0.937
367	Phospholipase D3 OS=Mus musculus GN=Pld3 PE=1 SV=1	2.44	2.48	4.9	1	0.937075
368	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3	27.54	27.61	45.5	15	0.937725
369	Wiskott-Aldrich syndrome protein family member 2 OS=Mus musculus GN=Wasf2 PE=1 SV=1	5.14	5.36	10.9	3	0.9379
370	Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2	9.37	9.46	10.3	5	0.937925
371	HSP beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1	2.08	2.09	22.8	1	0.938
372	Immunoglobulin-binding protein 1 OS=Mus musculus GN=Igbp1 PE=1 SV=1	6.02	7.04	20.3	5	0.93915
373	Epsin-3 OS=Mus musculus GN=Epn3 PE=1 SV=1	1.7	1.82	5.7	1	0.9392
374	Platelet-activating factor acetylhydrolase 1B subunit gamma OS=Mus musculus GN=Pafah1b3 PE=1 SV=1	3.81	3.97	32.2	3	0.939225
375	Alpha-1,4 glucan phosphorylase OS=Mus musculus GN=Pygm PE=1 SV=1	6.23	16.56	25.2	8	0.93955
376	26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	12.57	15.03	47.7	9	0.939625
377	Microtubule-actin cross-linking factor 1 (fragment) OS=Mus musculus GN=Macf1 PE=1 SV=1	2.58	2.8	3.5	3	0.939675

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
378	CCA tRNA nucleotidyltransferase 1, mitochondrial OS=Mus musculus GN=Trnt1 PE=1 SV=1	1.28	1.49	8.8	1	0.939675
379	Adenosine receptor A2b OS=Mus musculus GN=Adora2b PE=2 SV=2	1.46	1.59	3.9	1	0.939675
380	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	7.38	7.5	21.7	4	0.939975
381	Protein Niban OS=Mus musculus GN=Fam129a PE=1 SV=2	4.3	4.35	10.9	2	0.94005
382	COP9 signalosome complex subunit 8 OS=Mus musculus GN=Cops8 PE=1 SV=1	1.92	2.11	20.1	1	0.940125
383	Eukaryotic translation initiation factor 2 subunit 2 OS=Mus musculus GN=Eif2s2 PE=1 SV=1	6.76	6.9	21.2	5	0.94105
384	Casein kinase I isoform alpha OS=Mus musculus GN=Csnk1a1 PE=1 SV=1	1.36	1.5	6	1	0.941125
385	Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=1 SV=1	3.13	3.22	9.4	2	0.941225
386	N-acetylglucosamine-6-sulfatase OS=Mus musculus GN=Gns PE=1 SV=1	5.38	7.62	14.9	5	0.941675
387	Abhydrolase domain-containing protein 4 OS=Mus musculus GN=Abhd4 PE=1 SV=1	2.23	2.36	9.1	2	0.941925
388	Glycogen synthase kinase-3 alpha OS=Mus musculus GN=Gsk3a PE=1 SV=1	3.29	3.4	14.6	2	0.9421
389	Dynein light chain roadblock-type 1 OS=Mus musculus GN=Dynlrb1 PE=1 SV=1	4	4	26.9	4	0.942275
390	Nischarin OS=Mus musculus GN=Nisch PE=1 SV=2	5.81	6.06	8.2	5	0.942975
391	Ectonucleotide pyrophosphatase/phosphodiesterase family member 5 OS=Mus musculus GN=Enpp5 PE=1 SV=3	4.77	4.86	26.6	3	0.943075
392	SEC23-interacting protein OS=Mus musculus GN=Sec23ip PE=1 SV=1	21.79	21.83	20.4	12	0.9435
393	5-oxoprolinase OS=Mus musculus GN=Oplah PE=1 SV=1	2.05	2.07	4.5	1	0.943725
394	Alanine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1	27.62	27.68	36.1	17	0.94495
395	40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3	7.22	7.33	46.9	4	0.945175
396	Inter-alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=1	5.83	6.11	12.2	4	0.945375
397	Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna PE=1 SV=2	2.89	3.5	23.4	3	0.945775
398	MCG64870 OS=Mus musculus GN=Atg4a-ps PE=4 SV=1	9.45	9.55	23.7	6	0.945775
399	Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2	4.21	4.35	16.5	3	0.9462
400	E3 UFM1-protein ligase 1 OS=Mus musculus GN=Ufil1 PE=1 SV=2	2	2.02	3	1	0.946425
401	DNA segment, Chr 16, human D22S680E, expressed, isoform CRA_c OS=Mus musculus GN=Tango2 PE=1 SV=1	0.73	0.88	9.8	1	0.9466
402	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=1 SV=2	6.68	6.81	33.9	4	0.947075
403	Autophagy protein 5 OS=Mus musculus GN=Atg5 PE=1 SV=1	2	2.01	10.9	1	0.94715
404	Conserved oligomeric Golgi complex subunit 7 OS=Mus musculus GN=Cog7 PE=1 SV=1	6.48	7.48	13.5	5	0.947325
405	Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1 PE=1 SV=3	19.43	19.5	43.1	13	0.94735
406	7-methylguanosine phosphate-specific 5'-nucleotidase OS=Mus musculus GN=Nt5c3b PE=1 SV=3	4	4	18.7	2	0.94745
407	Transcription factor p65 OS=Mus musculus GN=Rela PE=1 SV=1	1.74	1.89	3.8	1	0.947675
408	AP-1 complex subunit gamma-1 OS=Mus musculus GN=Ap1g1 PE=1 SV=1	4.72	5.11	11.2	4	0.94785
409	Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=1 SV=3	1.51	1.68	6.9	1	0.94815
410	Protein DEK OS=Mus musculus GN=Dek PE=1 SV=1	4	4	7.4	2	0.948275
411	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Mus musculus GN=Ppp2ca PE=1 SV=1	9.34	10.69	36.9	6	0.948875
412	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3	5.39	5.48	13.4	3	0.949675
413	HemK methyltransferase family member 2, isoform CRA_c OS=Mus musculus GN=N6amt1 PE=1 SV=1	4.95	5.05	28.5	3	0.950025
414	Soluble lamin-associated protein of 75 kDa OS=Mus musculus GN=Fam169a PE=1 SV=3	0.52	0.57	3.6	1	0.950075
415	Annexin A7 OS=Mus musculus GN=Anxa7 PE=1 SV=2	12.33	12.39	20.5	8	0.9501
416	Optineurin OS=Mus musculus GN=Optn PE=1 SV=1	0.58	0.65	7	1	0.951225
417	Beta-actin OS=Mus musculus GN=Actr1b PE=1 SV=1	9.43	9.48	27.7	6	0.951325
418	Leukotriene A-4 hydrolase OS=Mus musculus GN=Lta4h PE=1 SV=4	31.7	31.76	46.2	21	0.95135
419	Testis-expressed sequence 101 protein OS=Mus musculus GN=Tex101 PE=1 SV=1	5.74	5.95	27.6	4	0.95215
420	Protein canopy homolog 2 OS=Mus musculus GN=Cnpy2 PE=1 SV=1	5.7	5.77	26.4	3	0.95255
421	FTS and Hook-interacting protein OS=Mus musculus GN=Fam160a2 PE=1 SV=1	1.33	1.5	6.9	1	0.9528

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
422	60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=1 SV=2	0.72	0.85	24.8	1	0.952825
423	Deoxyhypusine hydroxylase OS=Mus musculus GN=Dohh PE=1 SV=2	10.27	10.28	32.8	5	0.9529
424	Acetoacetyl-CoA synthetase OS=Mus musculus GN=Aacs PE=1 SV=1	11.34	11.4	17.3	6	0.953025
425	Eukaryotic translation initiation factor 3 subunit D OS=Mus musculus GN=Eif3d PE=1 SV=2	5.24	5.34	12.8	3	0.953225
426	CDK-activating kinase assembly factor MAT1 OS=Mus musculus GN=Mnat1 PE=1 SV=1	2	2.01	7.2	1	0.953725
427	Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4 PE=1 SV=3	9.98	10.06	44.1	7	0.954075
428	Proteasome subunit alpha type-4 OS=Mus musculus GN=PsmA4 PE=1 SV=1	12.34	12.4	32.2	7	0.9541
429	Spermidine synthase OS=Mus musculus GN=Srm PE=1 SV=1	12.17	12.3	35.1	8	0.95415
430	N-terminal Xaa-Pro-Lys N-methyltransferase 1 (fragment) OS=Mus musculus GN=Ntmt1 PE=1 SV=1	1.15	1.28	4.8	1	0.9547
431	Adenine phosphoribosyltransferase OS=Mus musculus GN=Aprt PE=1 SV=2	4	4.11	20.6	3	0.9548
432	Protein Sec24c OS=Mus musculus GN=Sec24c PE=1 SV=1	23.5	23.53	20.8	14	0.955125
433	Costars family protein ABRACL OS=Mus musculus GN=Abracl PE=1 SV=1	5.48	5.59	46.9	6	0.95525
434	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform OS=Mus musculus GN=Ppp2r5c PE=1 SV=2	2	2.01	4.6	1	0.95555
435	Prothymosin alpha OS=Mus musculus GN=Ptma PE=1 SV=2	3.83	4.17	33.3	3	0.955925
436	Golgi reassembly-stacking protein 1 OS=Mus musculus GN=Gorasp1 PE=1 SV=3	2.06	2.49	9	1	0.95605
437	Cold shock domain-containing protein E1 OS=Mus musculus GN=Csde1 PE=1 SV=1	5.04	5.2	11.7	4	0.956375
438	Serine/threonine-protein phosphatase 5 OS=Mus musculus GN=Ppp5c PE=1 SV=3	5.08	5.18	12.8	3	0.956425
439	Ribonucleoprotein PTB-binding 1 OS=Mus musculus GN=Raver1 PE=1 SV=2	2.04	2.04	8.2	2	0.95665
440	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus musculus GN=Ugg1 PE=1 SV=4	2.04	2.05	3.7	1	0.9571
441	Echinoderm microtubule-associated protein-like 4 OS=Mus musculus GN=Eml4 PE=1 SV=1	6.24	6.58	12	4	0.95765
442	Golgi reassembly-stacking protein 2 OS=Mus musculus GN=Gorasp2 PE=1 SV=3	12.81	12.84	35.7	7	0.958125
443	Protein DDI1 homolog 2 OS=Mus musculus GN=Ddi2 PE=1 SV=1	0.63	0.74	19.3	1	0.958375
444	Kinectin OS=Mus musculus GN=Ktn1 PE=1 SV=1	4.4	4.54	4.5	2	0.9588
445	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Etf1 PE=1 SV=4	16.85	16.93	25.9	8	0.959125
446	Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnnpk PE=1 SV=1	25.38	25.5	47.1	14	0.959275
447	Inter-alpha trypsin inhibitor, heavy chain 2 OS=Mus musculus GN=Itih2 PE=1 SV=1	1.05	1.21	7.9	1	0.95945
448	Proteasome subunit beta type-5 OS=Mus musculus GN=PsmB5 PE=1 SV=3	21.06	21.08	52.3	13	0.959625
449	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Mus musculus GN=Ddx5 PE=1 SV=1	7.45	9.72	15.5	4	0.9597
450	MCG16669, isoform CRA_a OS=Mus musculus GN=Tardbp PE=1 SV=1	3.68	3.86	14.2	2	0.9598
451	Lysophosphatidic acid phosphatase type 6 OS=Mus musculus GN=Acp6 PE=1 SV=1	1.5	1.63	8.6	1	0.95985
452	Phosphofurin acidic cluster sorting protein 1 OS=Mus musculus GN=Pacs1 PE=1 SV=2	3.69	3.94	7.5	3	0.959975
453	Endophilin-B2 OS=Mus musculus GN=Sh3glb2 PE=1 SV=1	2.39	2.55	13.1	3	0.9604
454	TSC22 domain family protein 3 OS=Mus musculus GN=Tsc22d3 PE=1 SV=1	2	2.03	15	1	0.960625
455	Rho-associated protein kinase 1 OS=Mus musculus GN=Rock1 PE=1 SV=1	2.59	5.05	8.6	2	0.9611
456	Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=Vasp PE=1 SV=4	7.59	7.7	26.9	9	0.962025
457	Protein-tyrosine sulfotransferase 2 OS=Mus musculus GN=Tpst2 PE=1 SV=1	1.89	2.1	10.8	2	0.962275
458	Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2	17.38	17.52	22.2	11	0.962325
459	NADH-cytochrome b5 reductase 2 OS=Mus musculus GN=Cyb5r2 PE=2 SV=2	2.02	2.03	13	1	0.962575
460	Protein transport protein Sec24A OS=Mus musculus GN=Sec24a PE=1 SV=1	2.29	2.34	7.6	1	0.96265
461	Tumor suppressor p53-binding protein 1 OS=Mus musculus GN=Trp53bp1 PE=1 SV=1	1.14	1.27	1.9	1	0.963125
462	Serine/threonine-protein kinase 26 OS=Mus musculus GN=Stk26 PE=1 SV=1	8.33	8.35	23.2	4	0.963275
463	IST1 homolog OS=Mus musculus GN=Ist1 PE=1 SV=1	1.26	1.64	7.2	1	0.963375
464	ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1	2.03	2.16	16.7	1	0.964975

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
465	GDP-L-fucose synthase OS=Mus musculus GN=Tsta3 PE=1 SV=3	13.4	13.5	39.3	10	0.96515
466	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Mus musculus GN=Sart3 PE=1 SV=1	5.43	5.69	12	3	0.966175
467	Adenosylhomocysteinase OS=Mus musculus GN=Ahcyl2 PE=1 SV=1	6.17	8.25	11.1	4	0.966425
468	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=1	6.47	6.59	46.2	4	0.96645
469	Steroid receptor RNA activator 1 (fragment) OS=Mus musculus GN=Sra1 PE=1 SV=1	5.22	6.31	28.7	4	0.966675
470	Kinesin light chain 1 OS=Mus musculus GN=Klc1 PE=1 SV=1	8.07	10.03	17.2	5	0.96685
471	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2	22.58	22.7	31	14	0.966975
472	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2	3.63	3.88	23.7	2	0.967275
473	Dual specificity protein phosphatase 23 OS=Mus musculus GN=Dusp23 PE=1 SV=1	8.52	8.58	42	4	0.967575
474	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1	26.83	26.93	33.4	17	0.96855
475	Charged multivesicular body protein 2b OS=Mus musculus GN=Chmp2b PE=1 SV=1	2.13	2.15	8	1	0.96875
476	Receptor-type tyrosine-protein phosphatase F OS=Mus musculus GN=Ptpfr PE=1 SV=1	1.12	1.25	1.9	1	0.96905
477	Nitrilase homolog 1 OS=Mus musculus GN=Nit1 PE=1 SV=2	12.09	12.19	37.8	8	0.969725
478	Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3	23.01	23.14	33.2	16	0.970025
479	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	8.44	18.56	58.7	18	0.9705
480	Dynammin-1-like protein OS=Mus musculus GN=Dnm1l PE=1 SV=1	27.83	27.88	40.6	15	0.970675
481	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Mus musculus GN=Uchl1 PE=1 SV=1	2.62	2.71	27.4	3	0.970875
482	RILP-like protein 1 OS=Mus musculus GN=Rilpl1 PE=1 SV=1	8.07	8.08	18.5	4	0.9719
483	Glutamate-cysteine ligase regulatory subunit OS=Mus musculus GN=Gclm PE=1 SV=1	4.68	4.86	29.2	5	0.971975
484	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	8.16	8.24	25.4	7	0.97295
485	Protein Ppp2r5d OS=Mus musculus GN=Ppp2r5d PE=1 SV=1	2.91	3.01	8.4	2	0.973525
486	Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1	0.57	36	66.7	63	0.973575
487	1,5-anhydro-D-fructose reductase OS=Mus musculus GN=Akr1e2 PE=1 SV=1	4.85	7.32	19.6	4	0.97385
488	Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=3	18.33	18.48	62	11	0.9741
489	Plectin OS=Mus musculus GN=Plec PE=1 SV=3	49.38	52.07	15	24	0.9741
490	Tyrosine-protein phosphatase nonreceptor type 23 OS=Mus musculus GN=Ptpn23 PE=1 SV=2	4.66	5.12	6.8	2	0.97415
491	Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	13.09	13.14	36.6	6	0.97425
492	Protein Gm10260 OS=Mus musculus GN=Gm10260 PE=3 SV=2	9.32	9.37	47.4	5	0.97445
493	MCG142264, isoform CRA_b OS=Mus musculus GN=Akr1b10 PE=1 SV=1	4.47	4.54	22.8	3	0.97465
494	Oligoribonuclease, mitochondrial OS=Mus musculus GN=Rexo2 PE=1 SV=2	0.44	0.52	14.4	1	0.9749
495	Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3	20.77	21.08	45.3	13	0.974975
496	Protein FAM98B OS=Mus musculus GN=Fam98b PE=1 SV=1	3.62	3.76	11.4	2	0.975275
497	Ral guanine nucleotide dissociation stimulator-like 3 OS=Mus musculus GN=Rgl3 PE=1 SV=2	2.11	2.13	7.2	1	0.9754
498	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=1 SV=1	9.93	10.02	28.5	6	0.97545
499	Gamma-adducin OS=Mus musculus GN=Add3 PE=1 SV=2	2.6	2.75	10.9	2	0.975575
500	PDZ domain-containing protein GIPC1 OS=Mus musculus GN=Gipc1 PE=1 SV=1	6	6	13.5	3	0.9757
501	Interleukin-1 receptor accessory protein OS=Mus musculus GN=Il1rap PE=1 SV=1	3.36	3.44	4.4	2	0.975825
502	Ethylmalonyl-CoA decarboxylase OS=Mus musculus GN=Echdc1 PE=1 SV=2	5	6.37	23.3	5	0.97585
503	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	32.31	32.33	45.8	20	0.975925
504	Fibulin-1 OS=Mus musculus GN=Fbln1 PE=1 SV=2	2.07	2.11	5.5	1	0.976
505	Retinol-binding protein 4 OS=Mus musculus GN=Rbp4 PE=1 SV=1	4.37	4.41	8.2	2	0.976425
506	Beta-lactamase-like protein 2 OS=Mus musculus GN=Lactb2 PE=1 SV=1	3.28	3.43	19.4	2	0.976775
507	Platelet-activating factor acetylhydrolase 1B subunit alpha OS=Mus musculus GN=Pafah1b1 PE=1 SV=2	19.09	19.23	40.2	9	0.97685
508	Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=1	7.29	7.38	8.9	5	0.97715
509	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	17.9	17.97	51.1	24	0.977475
510	Poly (ADP-ribose) polymerase family, member 1 OS=Mus musculus GN=Parp1 PE=1 SV=1	2.06	2.08	6.7	1	0.9775

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
511	Prenylated Rab acceptor protein 1 OS=Mus musculus GN=Rabac1 PE=1 SV=1	3.41	3.55	15.7	2	0.977775
512	Adenylosuccinate synthetase isozyme 2 OS=Mus musculus GN=Adss PE=1 SV=2	11.28	11.38	32.7	6	0.978075
513	Cystatin-B OS=Mus musculus GN=Cstb PE=1 SV=1	6.8	6.87	78.6	3	0.97885
514	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1	43.78	43.8	64.4	48	0.97905
515	Leucine zipper transcription factor-like protein 1 (fragment) OS=Mus musculus GN=Lztf1 PE=1 SV=1	8.95	9	36.7	5	0.9792
516	Mth938 domain-containing protein OS=Mus musculus GN=Aamdc PE=1 SV=1	0.93	1.05	11.5	1	0.980525
517	Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=Hnrnpab PE=1 SV=1	3.96	6.28	18	3	0.980575
518	28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1	4.04	5.03	29.8	3	0.980825
519	60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=1 SV=3	3.19	3.28	13.4	2	0.981125
520	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2	4.01	4.18	22.2	3	0.9828
521	Quinone oxidoreductase OS=Mus musculus GN=Cryz PE=1 SV=1	12.36	13.89	45.9	7	0.98295
522	Prefoldin subunit 2 OS=Mus musculus GN=Pfdn2 PE=1 SV=2	4.08	4.09	31.8	2	0.9832
523	Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=1 SV=2	2.47	2.53	32.6	1	0.983525
524	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2	121.55	121.28	25	61	0.983925
525	Endophilin-A2 OS=Mus musculus GN=Sh3gl1 PE=1 SV=1	6.33	6.38	24.2	4	0.98395
526	UPF0568 protein C14orf166 homolog OS=Mus musculus PE=1 SV=1	11.39	11.43	40.2	7	0.984725
527	Far upstream element-binding protein 1 OS=Mus musculus GN=Fubp1 PE=1 SV=1	3.41	5.72	13.4	3	0.98495
528	Filamin-C OS=Mus musculus GN=Finc PE=1 SV=1	8.02	22.05	9.8	10	0.984975
529	Phosphoglucosyltransferase-2 OS=Mus musculus GN=Pgm2 PE=1 SV=1	4.5	4.67	14.2	3	0.9852
530	Eukaryotic translation initiation factor 3 subunit E OS=Mus musculus GN=Eif3e PE=1 SV=1	3.01	3.34	13	2	0.98545
531	Charged multivesicular body protein 2a OS=Mus musculus GN=Chmp2a PE=1 SV=1	4	4.06	13.1	2	0.985725
532	PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1	15.14	15.2	33.5	7	0.98645
533	Phosphoribosylformylglycinamide synthase OS=Mus musculus GN=Pfas PE=1 SV=1	17.11	17.3	16.9	11	0.9866
534	Transcription intermediary factor 1-beta OS=Mus musculus GN=Trim28 PE=1 SV=3	11.62	11.71	13.9	6	0.9867
535	UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1	4.91	5.03	17.8	3	0.987225
536	Docking protein 1 OS=Mus musculus GN=Dok1 PE=1 SV=2	2.01	2.02	5.2	1	0.987475
537	Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Mus musculus GN=Rprd1b PE=1 SV=2	7.03	7.19	27.6	4	0.9881
538	Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1	16.21	16.33	42	9	0.9885
539	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	17.26	17.31	23.6	9	0.988675
540	Delta-aminolevulinic acid dehydratase OS=Mus musculus GN=Alad PE=1 SV=1	28.62	28.67	63.3	24	0.98875
541	Proteasome subunit beta type-4 OS=Mus musculus GN=Psmb4 PE=1 SV=1	4.64	4.89	39.8	5	0.988775
542	Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1	2.1	2.78	7	1	0.989
543	Uncharacterized protein C1orf50 homolog OS=Mus musculus PE=1 SV=1	2.02	2.82	11.1	2	0.9892
544	UDP-glucose 4-epimerase OS=Mus musculus GN=Gale PE=1 SV=1	1.38	1.59	15	2	0.989275
545	Probable RNA-binding protein EIF1AD OS=Mus musculus GN=Eif1ad PE=1 SV=2	1.09	1.21	8.2	1	0.989325
546	Asparagine synthetase (glutamine-hydrolyzing) OS=Mus musculus GN=Asns PE=1 SV=3	1.49	1.64	10.5	1	0.9897
547	Serine/threonine-protein kinase N2 OS=Mus musculus GN=Pkn2 PE=1 SV=1	1.87	2.39	3.8	1	0.9897
548	Transcription elongation factor A protein-like 5 OS=Mus musculus GN=Tcea5 PE=1 SV=1	4.17	4.2	21	3	0.990075
549	40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=3	4.03	4.04	16.5	2	0.990125
550	Acylophosphatase OS=Mus musculus GN=Acyp1 PE=1 SV=1	9.9	9.98	35.7	5	0.9907
551	Ubiquitin-conjugating enzyme E2 L3 OS=Mus musculus GN=Ube2l3 PE=1 SV=1	5.36	5.56	46.8	4	0.990725
552	Multivesicular body subunit 12A OS=Mus musculus GN=Mvb12a PE=1 SV=1	2.06	2.07	10	1	0.9911
553	Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1	37.88	37.93	76.2	64	0.99155
554	Leiomodin-1 OS=Mus musculus GN=Lmod1 PE=1 SV=1	4	4.08	8.1	2	0.991625

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
555	Serine/threonine-protein phosphatase 2A activator OS=Mus musculus GN=Ppp2r4 PE=1 SV=1	13.7	13.82	42.4	8	0.99215
556	Zinc phosphodiesterase ELAC protein 2 OS=Mus musculus GN=Elac2 PE=1 SV=1	1.3	1.45	2.8	1	0.9923
557	Bifunctional epoxide hydrolase 2 OS=Mus musculus GN=Ephx2 PE=1 SV=2	3.23	3.51	10.1	2	0.992475
558	Cullin-4B OS=Mus musculus GN=Cul4b PE=1 SV=2	2.02	4.54	9.5	3	0.992525
559	Enolase-phosphatase E1 OS=Mus musculus GN=Enoph1 PE=1 SV=1	4.31	4.44	18.7	3	0.992575
560	Receptor-interacting serine/threonine-protein kinase 1 OS=Mus musculus GN=Ripk1 PE=1 SV=1	2.38	2.45	8.7	2	0.993125
561	Protein kinase C and casein kinase substrate in neurons protein 2 OS=Mus musculus GN=Pacsin2 PE=1 SV=1	2.07	2.09	8.8	1	0.99325
562	Semaphorin-4B OS=Mus musculus GN=Sema4b PE=1 SV=2	2.05	2.06	5.7	1	0.99335
563	Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2	39.57	39.61	57	22	0.993675
564	Alpha-aminoacidic semialdehyde dehydrogenase OS=Mus musculus GN=Aldh7a1 PE=1 SV=4	25.24	25.28	46.4	12	0.99375
565	Adapter molecule crk OS=Mus musculus GN=Crk PE=1 SV=1	6.52	6.61	28	4	0.994025
566	Ubiquilin-1 OS=Mus musculus GN=Ubqln1 PE=1 SV=1	4.11	6.67	16	5	0.994225
567	Splicing factor 3B subunit 3 OS=Mus musculus GN=Sf3b3 PE=1 SV=1	4.33	4.38	7.5	2	0.994225
568	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Mus musculus GN=Gsp1 PE=1 SV=2	5.32	5.47	17.5	3	0.994325
569	Pyridoxine-5'-phosphate oxidase OS=Mus musculus GN=Pnpo PE=1 SV=1	4.49	4.53	23.4	2	0.9944
570	ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Carkd PE=1 SV=1	18.37	18.39	41.6	12	0.9945
571	AP-3 complex subunit beta-1 OS=Mus musculus GN=Ap3b1 PE=1 SV=2	10.94	11.21	10.8	7	0.994925
572	Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=Snrpd3 PE=1 SV=1	3.83	3.96	41.3	2	0.994925
573	Ester hydrolase C11orf54 homolog OS=Mus musculus PE=1 SV=1	12.98	13.04	27.3	7	0.995125
574	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	11.57	24.38	64.2	27	0.99535
575	Coatomer subunit beta' OS=Mus musculus GN=Copb2 PE=1 SV=2	27.2	27.25	27.1	17	0.9956
576	60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	8.11	8.19	54.6	4	0.995625
577	AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1	2.53	2.61	11.6	2	0.996
578	Reticulocalbin-1 OS=Mus musculus GN=Rcn1 PE=1 SV=1	7.71	7.88	25.9	4	0.9961
579	40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	15.66	15.74	56.8	9	0.9961
580	Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 SV=3	16.27	16.45	43	8	0.996275
581	Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Eif4a2 PE=1 SV=2	4.09	18.82	44.5	15	0.996775
582	AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 PE=1 SV=1	3.51	8.1	13.5	4	0.99695
583	Beta-glucuronidase OS=Mus musculus GN=Gusb PE=1 SV=2	0.87	1.01	6.6	1	0.9971
584	U6 snRNA-associated Sm-like protein LSm3 OS=Mus musculus GN=Lsm3 PE=1 SV=2	3.43	3.52	19.6	2	0.9976
585	Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 PE=1 SV=3	8.52	8.54	16.5	5	0.9979
586	26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psm3 PE=1 SV=3	17.31	17.52	25.9	12	0.9984
587	Swi5-dependent recombination DNA repair protein 1 homolog OS=Mus musculus GN=Sfr1 PE=1 SV=2	2.03	2.04	17.6	1	0.998975
588	Cleavage and polyadenylation specificity factor subunit 3 OS=Mus musculus GN=Cpsf3 PE=1 SV=2	1.8	1.92	3.4	1	0.999275
589	Cysteine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2	7.27	7.58	16.7	5	0.99945
590	Microtubule-associated protein OS=Mus musculus GN=Map4 PE=1 SV=2	11.94	12.1	13.9	7	1.000325
591	26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	7.27	7.4	32.7	4	1.000525
592	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Mus musculus GN=Gne PE=1 SV=1	2.18	2.21	5.8	1	1.000625
593	Rho GTPase-activating protein 17 OS=Mus musculus GN=Arhgap17 PE=1 SV=1	4.29	4.32	8.9	3	1.0007
594	Interleukin-1 receptor-associated kinase 1 OS=Mus musculus GN=Irak1 PE=1 SV=1	2	2	4	1	1.000725
595	CTP synthase 1 OS=Mus musculus GN=Ctps1 PE=1 SV=2	0.87	3.31	12.2	2	1.00085
596	Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1	12.18	12.28	75	8	1.0012
597	Protein Sf3b2 OS=Mus musculus GN=Sf3b2 PE=1 SV=1	2	2	2.5	1	1.001525
598	Cbx3 protein OS=Mus musculus GN=Cbx3 PE=1 SV=1	6.98	7.16	33.3	4	1.0019

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
599	Alkaline phosphatase, tissue-nonspecific isozyme OS=Mus musculus GN=Alpl PE=1 SV=2	4.05	4.06	9.2	2	1.002425
600	Sperm-associated antigen 7 OS=Mus musculus GN=Spag7 PE=1 SV=1	1.78	2.02	11.5	2	1.0025
601	Elongator complex protein 3 OS=Mus musculus GN=Elp3 PE=1 SV=1	1.43	1.61	5.3	2	1.0028
602	Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=1 SV=2	2.16	2.31	20.8	2	1.003825
603	Vesicle-fusing ATPase OS=Mus musculus GN=Nsf PE=1 SV=2	15.03	15.75	18.8	8	1.00395
604	Type I inositol 3,4-bisphosphate 4-phosphatase OS=Mus musculus GN=Inpp4a PE=1 SV=1	1.88	2.06	4	1	1.0041
605	Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1	17.73	17.87	59.5	11	1.004175
606	Tax1-binding protein 3 OS=Mus musculus GN=Tax1bp3 PE=1 SV=1	2	2	13.7	1	1.0049
607	Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5	7.28	8.96	50.2	7	1.005075
608	KN motif and ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Kank2 PE=1 SV=1	1.64	1.79	6.2	1	1.00525
609	Histidine-rich glycoprotein OS=Mus musculus GN=Hrg PE=1 SV=2	5.87	7.42	12	4	1.005425
610	Proteasome subunit alpha type-1 OS=Mus musculus GN=Pasma1 PE=1 SV=1	23.01	23.13	54.8	14	1.0057
611	NSFL1 cofactor p47 OS=Mus musculus GN=Nsf11c PE=1 SV=1	14.78	14.81	41.1	8	1.005725
612	Clathrin light chain A OS=Mus musculus GN=CltA PE=1 SV=1	5.02	5.14	23.9	5	1.005925
613	Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	5.86	5.99	5.3	3	1.006175
614	Aminoacylase-1 OS=Mus musculus GN=Acy1 PE=1 SV=1	4.53	4.59	16.4	3	1.006175
615	Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5 PE=1 SV=3	4.27	4.31	38.4	3	1.006925
616	Dual-specificity mitogen-activated protein kinase kinase 2 OS=Mus musculus GN=Map2k2 PE=1 SV=1	4.6	4.79	15.3	3	1.007225
617	Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2	7.64	7.79	18.3	5	1.007675
618	Clusterin OS=Mus musculus GN=Clu PE=1 SV=1	32.52	32.67	50.2	31	1.0079
619	Phosphatase and actin regulator 4 OS=Mus musculus GN=Phactr4 PE=1 SV=2	0.78	0.89	2.9	1	1.00795
620	RuvB-like 2 OS=Mus musculus GN=Ruvbl2 PE=1 SV=3	8.23	8.27	25.3	4	1.0086
621	EF-hand domain-containing protein D2 OS=Mus musculus GN=Efhd2 PE=1 SV=1	8.33	8.42	35	5	1.00905
622	NAD(P)H-hydrate epimerase OS=Mus musculus GN=Apoa1bp PE=1 SV=1	6.18	6.43	34.4	4	1.009175
623	Protein VAC14 homolog OS=Mus musculus GN=Vac14 PE=1 SV=1	2	2.01	5	3	1.009575
624	Protein phosphatase methylesterase 1 OS=Mus musculus GN=Ppme1 PE=1 SV=5	8.01	8.02	17.1	4	1.009775
625	Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3	20.08	20.22	60.8	14	1.010675
626	26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1	17.85	18.97	39.9	11	1.0108
627	UV excision repair protein RAD23 homolog B OS=Mus musculus GN=Rad23b PE=1 SV=2	11.42	11.53	30.3	8	1.0111
628	Bis(5'-nucleosyl)-tetrakisphosphatase [asymmetrical] OS=Mus musculus GN=Nudt2 PE=1 SV=3	8.08	8.16	42.2	5	1.011625
629	ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1	6.13	6.25	9.2	3	1.0122
630	Plasminogen OS=Mus musculus GN=Plg PE=1 SV=3	20.71	20.77	22.5	10	1.012625
631	Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculus GN=Eci1 PE=1 SV=2	0.63	0.74	9.7	1	1.01265
632	Signal recognition particle subunit SRP72 OS=Mus musculus GN=Srp72 PE=1 SV=1	6.19	6.21	13.9	3	1.01275
633	Dr1-associated corepressor OS=Mus musculus GN=Drp1 PE=1 SV=1	1.72	1.85	8.1	1	1.013025
634	Transcription activator BRG1 OS=Mus musculus GN=Smarca4 PE=1 SV=1	1.77	1.97	6.1	1	1.01325
635	Tumor susceptibility gene 101 protein OS=Mus musculus GN=Tsg101 PE=1 SV=2	8.02	8.26	14.8	5	1.0134
636	Glia maturation factor beta OS=Mus musculus GN=Gmfb PE=1 SV=3	4.23	4.26	44.4	3	1.01355
637	CapZ-interacting protein OS=Mus musculus GN=Rcsd1 PE=1 SV=1	0.53	0.58	3.9	1	1.0137
638	Cytoplasmic dynein 1 light intermediate chain 1 OS=Mus musculus GN=Dync1li1 PE=1 SV=1	2.1	2.26	15.7	1	1.013725
639	Cellular nucleic acid-binding protein OS=Mus musculus GN=Cnbp PE=1 SV=2	5.7	5.82	32.6	3	1.0145
640	Gamma-glutamylcyclotransferase OS=Mus musculus GN=Ggct PE=1 SV=1	9.24	9.29	35.6	5	1.014575
641	Proteasome subunit alpha type-2 OS=Mus musculus GN=Pasma2 PE=1 SV=3	17.17	17.21	46.6	10	1.0147
642	Arginine-rich, mutated in early-stage tumors, isoform CRA_b OS=Mus musculus GN=Manf PE=1 SV=1	7.71	7.78	31.3	5	1.0148

Contd...



Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
643	26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psmd11 PE=1 SV=3	22.43	22.5	43.1	12	1.01525
644	Extracellular superoxide dismutase (Cu-Zn) OS=Mus musculus GN=Sod3 PE=1 SV=1	4.08	4.09	25.5	2	1.0162
645	Nucleoredoxin OS=Mus musculus GN=Nxn PE=1 SV=1	5.22	5.39	17.2	4	1.016275
646	Epidermal growth factor receptor pathway substrate 15 isoform B OS=Mus musculus GN=Eps15 PE=1 SV=1	1.3	1.52	7.2	1	1.0163
647	Nesprin-2 OS=Mus musculus GN=Syne2 PE=1 SV=1	0.53	0.92	3.4	2	1.0165
648	NEDD8-conjugating enzyme Ubc12 OS=Mus musculus GN=Ube2m PE=1 SV=1	4.6	4.83	37.7	2	1.01695
649	Probable inactive ribonuclease-like protein 13 OS=Mus musculus GN=Rnase13 PE=2 SV=1	1.2	1.35	22.2	1	1.017375
650	Proteasome subunit alpha type-6 OS=Mus musculus GN=Pma6 PE=1 SV=1	16.07	16.12	47.6	12	1.0182
651	COP9 signalosome complex subunit 2 OS=Mus musculus GN=Cops2 PE=1 SV=1	5.18	5.35	24.6	4	1.018525
652	Ubiquitin-fold modifier 1 OS=Mus musculus GN=Ufm1 PE=1 SV=1	6	6	63.5	3	1.018875
653	Transforming growth factor beta-1-induced transcript 1 protein OS=Mus musculus GN=Tgfb1i1 PE=1 SV=1	8	8	18.5	6	1.019
654	Protein CutA OS=Mus musculus GN=Cuta PE=1 SV=1	5.68	5.77	33.8	3	1.019025
655	Serine/threonine-protein kinase Nek9 OS=Mus musculus GN=Nek9 PE=1 SV=2	3.62	3.72	4	2	1.019625
656	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	14.36	14.45	39.3	10	1.019725
657	Thioredoxin reductase 3 OS=Mus musculus GN=Txnr3 PE=1 SV=3	3.25	3.65	14.3	2	1.0202
658	Ectonucleotide pyrophosphatase/phosphodiesterase 1, isoform CRA_d OS=Mus musculus GN=Enpp1 PE=1 SV=1	3.04	3.14	9.9	2	1.020725
659	Desmin OS=Mus musculus GN=Des PE=1 SV=3	14.46	22.51	37.3	13	1.02105
660	AT-rich interactive domain-containing protein 1A OS=Mus musculus GN=Arid1a PE=1 SV=1	1.72	4	2	2	1.02125
661	Ppm1b protein OS=Mus musculus GN=Ppm1b PE=1 SV=1	2.64	5.46	21.2	3	1.0214
662	Tyrosine-protein phosphatase nonreceptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2	9.54	9.61	22.6	5	1.021525
663	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	47.12	47.05	77.3	73	1.02175
664	Exportin-2 OS=Mus musculus GN=Cse1l PE=1 SV=1	10.23	10.29	13	5	1.022525
665	Proteasome subunit alpha type-3 OS=Mus musculus GN=Pma3 PE=1 SV=3	9.17	9.27	26.7	7	1.022775
666	E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3	11.27	11.42	16.7	7	1.022925
667	26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus GN=Psmd13 PE=1 SV=1	15.34	15.49	39.1	8	1.023525
668	Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	2	2.01	5.6	1	1.0236
669	60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	7.26	7.37	26.4	4	1.023725
670	Complement component C8 beta chain OS=Mus musculus GN=C8b PE=1 SV=1	4.01	4.02	11.9	2	1.0238
671	Obg-like ATPase 1 OS=Mus musculus GN=Ola1 PE=1 SV=1	17.79	18.03	50.3	11	1.0242
672	Protein phosphatase 1A OS=Mus musculus GN=Ppm1a PE=1 SV=1	8.2	8.43	32.5	5	1.025775
673	Hermansky-Pudlak syndrome 5 protein homolog OS=Mus musculus GN=Hps5 PE=1 SV=1	2	2.02	4.2	2	1.02595
674	Protein Hook homolog 3 OS=Mus musculus GN=Hook3 PE=1 SV=2	5.03	5.93	11.8	4	1.02605
675	Tubulin-tyrosine ligase-like protein 12 OS=Mus musculus GN=Ttl12 PE=1 SV=1	4.81	5.37	11	4	1.0261
676	Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	2.37	2.49	11.2	2	1.0265
677	Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4	19.09	19.17	74.9	17	1.02685
678	Amidophosphoribosyltransferase OS=Mus musculus GN=Ppat PE=1 SV=1	2.02	2.03	7.4	1	1.027075
679	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=1 SV=2	7.41	8.19	42.6	3	1.02725
680	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	5.93	13.39	30	11	1.027375
681	Capping protein (actin filament) muscle Z-line, beta, isoform CRA_a OS=Mus musculus GN=Capzb PE=1 SV=1	16.02	16.27	67.7	13	1.027925
682	Kinesin light chain 3 OS=Mus musculus GN=Klc3 PE=1 SV=1	4.45	6.17	21.6	5	1.028175
683	Superoxide dismutase (Cu-Zn) OS=Mus musculus GN=Sod1 PE=1 SV=2	15.22	15.38	63	15	1.028325
684	Importin subunit alpha-3 OS=Mus musculus GN=Kpna4 PE=1 SV=1	2.19	2.23	8.7	1	1.028475
685	PITH domain-containing protein 1 OS=Mus musculus GN=Pithd1 PE=1 SV=1	2.34	2.38	9.5	1	1.0285
686	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=1	12	21.77	53.2	13	1.0286
687	Tyrosine-protein phosphatase nonreceptor type 6 OS=Mus musculus GN=Ptpn6 PE=1 SV=2	4.19	4.34	9.6	3	1.0287

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
688	Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=2	12.01	12.01	29.4	6	1.028925
689	Protein dpy-30 homolog OS=Mus musculus GN=Dpy30 PE=1 SV=1	2	2	9.1	1	1.0291
690	Pro-cathepsin H OS=Mus musculus GN=Ctsh PE=1 SV=2	4.01	4.02	24.9	4	1.029625
691	Signal transducer and activator of transcription OS=Mus musculus GN=Stat3 PE=1 SV=1	5.56	5.73	16.9	4	1.030175
692	Conserved oligomeric Golgi complex subunit 2 OS=Mus musculus GN=Cog2 PE=1 SV=2	6.56	6.74	15.7	5	1.03055
693	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=2	5.03	6.63	19	4	1.0308
694	TBC1 domain family member 8 OS=Mus musculus GN=Tbc1d8 PE=1 SV=1	2	2.01	14.7	1	1.030925
695	Protein S100-A11 OS=Mus musculus GN=S100a11 PE=1 SV=1	8.52	8.55	46.9	7	1.031075
696	60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2	2.24	2.28	18.5	1	1.031525
697	Protein Btaf1 OS=Mus musculus GN=Btaf1 PE=1 SV=1	2	2.01	2.7	1	1.031675
698	SEC14-like protein 2 OS=Mus musculus GN=Sec14i2 PE=1 SV=1	6.54	6.62	21.1	3	1.0317
699	Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	24.25	26.33	81.1	60	1.03175
700	Proteasome subunit alpha type-5 OS=Mus musculus GN=Psm5 PE=1 SV=1	17.7	17.73	56.4	14	1.032175
701	RAC-alpha serine/threonine-protein kinase OS=Mus musculus GN=Akt1 PE=1 SV=2	0.96	1.6	5.7	2	1.03225
702	Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	3.31	3.46	15.8	2	1.0325
703	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1	6.13	6.16	11.9	4	1.032825
704	Protein 1300017J02Rik OS=Mus musculus GN=1300017J02Rik PE=1 SV=1	8.38	10.67	17.7	7	1.03295
705	Mothers against decapentaplegic homolog 9 OS=Mus musculus GN=Smad9 PE=1 SV=2	4	4.01	11.4	2	1.033075
706	Protein Gm5786 OS=Mus musculus GN=Gm5786 PE=3 SV=1	3.96	4.29	24.9	3	1.03315
707	MCG5400 OS=Mus musculus GN=Myl12a PE=1 SV=1	6.37	14.01	76.2	11	1.034375
708	Protein AI837181 OS=Mus musculus GN=AI837181 PE=1 SV=1	2.01	2.09	17.5	1	1.034725
709	PDZ and LIM domain protein 1 OS=Mus musculus GN=Pdlim1 PE=1 SV=4	19.45	19.56	48	10	1.03475
710	3'(2'),5'-bisphosphate nucleotidase 1 OS=Mus musculus GN=Bpnt1 PE=1 SV=2	16.6	16.73	54.9	11	1.035125
711	ATPase Asna1 OS=Mus musculus GN=Asna1 PE=1 SV=2	4.08	4.09	12.1	2	1.035875
712	Calponin OS=Mus musculus GN=Cnn3 PE=1 SV=1	6	8.56	18	4	1.0361
713	Protein CREG1 OS=Mus musculus GN=Creg1 PE=1 SV=1	2.01	2.02	20	1	1.0363
714	Parathyrosin OS=Mus musculus GN=Ptms PE=1 SV=3	3.92	4	22.8	2	1.036375
715	Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus GN=Eif4g1 PE=1 SV=1	20.06	21.33	16.1	12	1.0366
716	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=1	15.35	15.38	38	12	1.036975
717	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	6	20.55	52.4	16	1.0376
718	3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3	4.1	5.64	24.2	4	1.037825
719	Peroxisomal carnitine O-octanoyltransferase OS=Mus musculus GN=Crot PE=1 SV=1	3.05	3.15	11.3	2	1.038025
720	Tyrosine-protein phosphatase nonreceptor type OS=Mus musculus GN=Ptpn2 PE=1 SV=1	1.73	1.95	9.4	1	1.038225
721	BolA-like protein 2 OS=Mus musculus GN=Bola2 PE=1 SV=1	2.07	2.09	40.7	1	1.038325
722	m7GpppX diphosphatase OS=Mus musculus GN=Dcps PE=1 SV=1	11.63	11.67	33.1	6	1.038375
723	Signal transducer and activator of transcription OS=Mus musculus GN=Stat2 PE=1 SV=1	2.02	2.02	5.5	2	1.03885
724	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Mus musculus GN=Ppp2r2a PE=1 SV=1	2.26	2.66	12.8	1	1.039075
725	UDP-N-acetylhexosamine pyrophosphorylase OS=Mus musculus GN=Uap1 PE=1 SV=1	3.87	6.03	8.8	3	1.039325
726	Polyubiquitin-B (fragment) OS=Mus musculus GN=Ubb PE=4 SV=2	16.42	16.43	87.7	9	1.03935
727	Coiled-coil and C2 domain-containing protein 1B (fragment) OS=Mus musculus GN=Cc2d1b PE=1 SV=1	1.72	1.99	7.1	2	1.0394
728	Disintegrin and metalloproteinase domain-containing protein 7 OS=Mus musculus GN=Adam7 PE=2 SV=2	2.04	2.04	4.9	1	1.0397
729	Proteasome activator complex subunit 4 OS=Mus musculus GN=Psm4 PE=1 SV=1	5.03	5.39	6.2	4	1.039725
730	Periostin OS=Mus musculus GN=Postn PE=1 SV=2	2	2	2.6	1	1.039775
731	4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1	14.88	15.4	34.2	8	1.0399

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
732	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Mus musculus GN=Adi1 PE=1 SV=1	7.89	8.01	53.6	6	1.039925
733	Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5	55.68	55.68	72.3	65	1.040225
734	Cytoglobin OS=Mus musculus GN=Cygb PE=1 SV=1	0.63	0.75	21.6	1	1.040525
735	Ubiquitin-like-conjugating enzyme ATG3 OS=Mus musculus GN=Atg3 PE=1 SV=1	4.31	4.36	14.7	2	1.040525
736	60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=1 SV=3	3.75	3.89	28.7	2	1.04085
737	Bin1 protein OS=Mus musculus GN=Bin1 PE=1 SV=1	3.89	4.07	12.2	2	1.04125
738	Acidic leucine-rich nuclear phosphoprotein 32 family member E (fragment) OS=Mus musculus GN=Anp32e PE=1 SV=1	1.43	1.66	43	1	1.041325
739	Inositol (Myo)-1(Or 4)-monophosphatase 1 OS=Mus musculus GN=Impa1 PE=1 SV=1	19.22	19.28	53.4	12	1.041325
740	Golgi resident protein GCP60 OS=Mus musculus GN=Acbd3 PE=1 SV=3	2.41	2.45	9.9	2	1.041525
741	Signal transducer and activator of transcription OS=Mus musculus GN=Stat5a PE=1 SV=1	8.54	8.68	10.7	5	1.041675
742	Porphobilinogen deaminase OS=Mus musculus GN=Hmbs PE=1 SV=2	5.32	5.71	22.2	4	1.041875
743	MAP kinase-activated protein kinase 2 (fragment) OS=Mus musculus GN=Mapkapk2 PE=1 SV=1	2	2	13	1	1.04215
744	Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 SV=2	2	10.77	23.5	9	1.04225
745	tRNA (cytosine(34)-C(5))-methyltransferase OS=Mus musculus GN=Nsun2 PE=1 SV=2	3.84	4.02	7.1	4	1.043025
746	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Mus musculus GN=Hgs PE=1 SV=1	2.37	2.81	8	1	1.043575
747	MCG15829, isoform CRA_a OS=Mus musculus GN=Mup3 PE=1 SV=1	2.68	2.75	20.7	2	1.04375
748	CTP synthase 2 OS=Mus musculus GN=Ctps2 PE=1 SV=1	13.5	13.57	17.1	7	1.0441
749	Microtubule-associated protein RP/EB family member 3 OS=Mus musculus GN=Mapre3 PE=1 SV=1	2.02	2.03	9	1	1.044225
750	Protein FAM63A OS=Mus musculus GN=Fam63a PE=1 SV=1	3.81	3.9	10	2	1.04425
751	Trifunctional purine biosynthetic protein adenosine-3 OS=Mus musculus GN=Gart PE=1 SV=3	18.34	18.54	26.8	11	1.0445
752	Parkinson disease 7 domain-containing protein 1 OS=Mus musculus GN=Pddc1 PE=1 SV=1	4	4	12.7	2	1.044625
753	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3	13.98	14.09	29.4	8	1.045475
754	Actin-related protein 2/3 complex subunit 1B OS=Mus musculus GN=Arcp1b PE=1 SV=1	6.72	6.96	33.5	5	1.04575
755	Phosphomannomutase 2 OS=Mus musculus GN=Pmm2 PE=1 SV=1	11.62	11.74	40.9	7	1.046075
756	ATP-dependent RNA helicase DDX1 OS=Mus musculus GN=Ddx1 PE=1 SV=1	14.18	14.28	18.1	7	1.04615
757	Retinal dehydrogenase 2 OS=Mus musculus GN=Aldh1a2 PE=1 SV=2	7.55	9.63	23.4	5	1.046175
758	Clathrin interactor 1 OS=Mus musculus GN=Clint1 PE=1 SV=1	5.36	5.59	7.7	4	1.046175
759	Alpha actinin 1a OS=Mus musculus GN=Actn1 PE=1 SV=1	8.28	28.72	29.8	16	1.046625
760	Vacuolar protein sorting-associated protein 28 homolog OS=Mus musculus GN=Vps28 PE=1 SV=1	6	6	23.1	3	1.046675
761	AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=1 SV=1	19.9	20	22.7	10	1.04685
762	Protein Dr1 OS=Mus musculus GN=Dr1 PE=1 SV=1	2	2	7.4	1	1.04755
763	Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3	25.99	26.02	52.6	15	1.048
764	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4	20.05	20.83	24.3	10	1.0481
765	Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Mus musculus GN=Osgep PE=1 SV=2	3.05	3.17	17.3	2	1.0485
766	Acylamino-acid-releasing enzyme OS=Mus musculus GN=Apeh PE=1 SV=3	12.32	12.96	18.9	6	1.048725
767	Dynamin-2 OS=Mus musculus GN=Dnm2 PE=1 SV=2	19.1	19.73	22.3	11	1.048775
768	Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus GN=Cyfi1 PE=1 SV=1	6.09	6.25	9	4	1.04965
769	Succinyl-CoA ligase (ADP forming) subunit beta, mitochondrial OS=Mus musculus GN=Sucla2 PE=1 SV=2	2.02	2.02	9.1	1	1.049875
770	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4 OS=Mus musculus GN=Pfkfb4 PE=2 SV=4	4.14	4.16	14.5	2	1.0499
771	Lethal(2) giant larvae protein homolog 2 OS=Mus musculus GN=Llg2 PE=1 SV=1	0.92	1.05	1.9	1	1.050125
772	6-phosphogluconolactonase OS=Mus musculus GN=Pgl5 PE=1 SV=1	19.99	20.02	72	15	1.050225

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
773	Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Mus musculus GN=Camk2g PE=1 SV=1	2.05	2.79	11.9	3	1.05025
774	26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1	19.97	21.26	44.3	13	1.050475
775	Caytaxin OS=Mus musculus GN=Atcay PE=4 SV=1	2	2	7.4	1	1.050525
776	Dynein light chain 2, cytoplasmic OS=Mus musculus GN=Dynll2 PE=1 SV=1	4.25	4.38	21.4	3	1.05065
777	Poly(U)-binding-splicing factor PUF60 OS=Mus musculus GN=Puf60 PE=1 SV=2	4.02	4.02	9.9	2	1.0507
778	NAD-dependent protein deacetylase sirtuin-2 OS=Mus musculus GN=Sirt2 PE=1 SV=2	6.43	6.47	17.7	3	1.050875
779	Leucine zipper protein 1 OS=Mus musculus GN=Luzp1 PE=1 SV=2	0.48	0.53	5.2	1	1.051375
780	Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2	1.6	3.82	16.5	2	1.052025
781	Ragulator complex protein LAMTOR1 OS=Mus musculus GN=Lamtor1 PE=1 SV=1	2	2	8.1	1	1.05235
782	Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm PE=1 SV=1	2.03	2.95	8.8	2	1.052625
783	Phospholipase A-2-activating protein OS=Mus musculus GN=Plaa PE=1 SV=4	4.21	4.37	11.5	2	1.05275
784	Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hint1 PE=1 SV=3	7.12	7.42	75.4	10	1.0532
785	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	18.41	18.54	27.3	12	1.053325
786	26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psm2 PE=1 SV=1	29.59	29.64	39.7	20	1.053625
787	Synembryn-A OS=Mus musculus GN=Ric8a PE=1 SV=2	1.42	1.64	8.7	1	1.05385
788	Serine/threonine-protein kinase PAK 2 OS=Mus musculus GN=Pak2 PE=1 SV=1	13.89	13.94	32.1	9	1.0551
789	Sulfurtransferase OS=Mus musculus GN=Mpst PE=1 SV=1	2.01	2.01	8.4	1	1.05675
790	Beta-hexosaminidase subunit alpha OS=Mus musculus GN=Hexa PE=1 SV=2	3.95	4.11	8.5	2	1.057125
791	Protein phosphatase 1 regulatory subunit 12A OS=Mus musculus GN=Ppp1r12a PE=1 SV=2	12.12	12.35	13.4	8	1.05795
792	Endophilin-A1 OS=Mus musculus GN=Sh3gl2 PE=1 SV=1	2.01	2.24	15.6	1	1.05805
793	Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5l PE=1 SV=1	4.02	4.03	31.4	2	1.0583
794	Actin-related protein 2/3 complex subunit 1A OS=Mus musculus GN=Arpc1a PE=1 SV=1	2.77	4.99	15.4	3	1.05895
795	Mitotic spindle-associated MMXD complex subunit MIP18 OS=Mus musculus GN=Fam96b PE=1 SV=1	4.04	4.19	36.8	2	1.059725
796	ATP-dependent RNA helicase DDX39A OS=Mus musculus GN=Ddx39a PE=1 SV=1	1.65	9.38	18.7	6	1.0602
797	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=1 SV=1	6.55	6.59	45.7	3	1.0606
798	Trafficking protein particle complex subunit 3 OS=Mus musculus GN=Trappc3 PE=1 SV=1	4.48	4.53	22.8	4	1.060925
799	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	31.84	31.87	51.9	21	1.061875
800	Proteasome subunit beta type-7 OS=Mus musculus GN=Psb7 PE=1 SV=1	8.21	8.36	23.1	9	1.063575
801	Four and a half LIM domain protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=1	8.15	8.24	24	6	1.0637
802	Probable aminopeptidase NPEPL1 OS=Mus musculus GN=Npepl1 PE=1 SV=1	0.65	1.48	9.4	3	1.06405
803	V-type proton ATPase subunit F OS=Mus musculus GN=Atp6v1f PE=1 SV=2	7.41	7.46	60.5	4	1.065275
804	Methionine adenosyltransferase 2 subunit beta OS=Mus musculus GN=Mat2b PE=1 SV=1	7.49	7.55	13.5	4	1.065425
805	Sorcin OS=Mus musculus GN=Sri PE=1 SV=1	0.89	1.08	20.7	2	1.0665
806	Autophagy-related protein 16-1 OS=Mus musculus GN=Atg16l1 PE=1 SV=1	1.2	1.33	4.6	1	1.067025
807	Isoleucine-tRNA ligase, cytoplasmic OS=Mus musculus GN=lars PE=1 SV=2	15.76	15.93	13.6	10	1.06725
808	Glutamate-cysteine ligase catalytic subunit OS=Mus musculus GN=Gclc PE=1 SV=4	1.58	1.89	16	1	1.06735
809	U6 snRNA-associated Sm-like protein LSm8 OS=Mus musculus GN=Lsm8 PE=1 SV=3	2.01	2.01	27.1	1	1.067475
810	RAC-beta serine/threonine-protein kinase OS=Mus musculus GN=Akt2 PE=1 SV=1	0.92	1.94	8.2	2	1.067925
811	Profilin-2 OS=Mus musculus GN=Pfn2 PE=1 SV=3	8.08	8.13	44.3	5	1.068025
812	Methionine synthase OS=Mus musculus GN=Mtr PE=1 SV=1	2.13	2.16	4.3	1	1.068375
813	Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=1 SV=1	10.89	10.99	32.5	5	1.068425
814	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	9.37	9.4	30.3	5	1.068475

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
815	MCG14616 OS=Mus musculus GN=2810408M09Rik PE=1 SV=1	2.01	2.01	14.8	1	1.068725
816	Heterogeneous nuclear ribonucleoprotein A1 OS=Mus musculus GN=Hnrnpa1 PE=1 SV=1	4.03	7.55	18.2	4	1.068775
817	Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=1 SV=2	11.04	11.2	28.7	11	1.068825
818	Leucine-rich repeat flightless-interacting protein 2 OS=Mus musculus GN=Lrrfip2 PE=1 SV=1	2	2.01	8.3	1	1.069
819	Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Mus musculus GN=Hdh2 PE=1 SV=2	4	4	9.7	2	1.06995
820	26S proteasome non-ATPase regulatory subunit 1 OS=Mus musculus GN=Psm1 PE=1 SV=1	20.24	20.5	29.6	12	1.070525
821	Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	27.53	27.8	37.3	20	1.071025
822	Serine/threonine-protein phosphatase 4 catalytic subunit OS=Mus musculus GN=Ppp4c PE=1 SV=2	2.9	6.22	16.6	4	1.071275
823	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1	8	8	55.3	4	1.0721
824	Rho GDP-dissociation inhibitor 2 OS=Mus musculus GN=Arhgdi2 PE=1 SV=3	4.15	4.18	40	2	1.0727
825	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	113.84	113.79	45.5	64	1.072925
826	Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=1	6.26	6.37	38	4	1.0732
827	60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=1	1.4	1.53	5.7	1	1.0738
828	Beta-globin OS=Mus musculus GN=Hbbt1 PE=1 SV=1	21.46	21.53	77.6	35	1.074625
829	SWI/SNF complex subunit SMARCC2 OS=Mus musculus GN=Smrcc2 PE=1 SV=1	2.68	2.76	5.9	2	1.074975
830	Coronin-7 OS=Mus musculus GN=Coro7 PE=1 SV=2	5.45	5.57	8.9	3	1.075425
831	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Mus musculus GN=Ppp1cb PE=1 SV=3	6.01	20.44	52.9	13	1.07665
832	C-Myc-binding protein OS=Mus musculus GN=Mycbp PE=1 SV=1	2.94	3.03	32.2	2	1.0776
833	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=1 SV=3	4.97	5.05	30.5	4	1.07835
834	NEDD8 OS=Mus musculus GN=Nedd8 PE=1 SV=2	5.72	5.79	58	3	1.07875
835	Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	44.5	50.47	17.9	23	1.079
836	E3 ubiquitin-protein ligase BRE1A OS=Mus musculus GN=Rnf20 PE=1 SV=2	2.01	2.47	4.7	1	1.07955
837	ADP-ribosylation factor-like protein 3 OS=Mus musculus GN=Arl3 PE=1 SV=1	8.56	8.59	43.4	4	1.079725
838	WD repeat-containing protein 61 OS=Mus musculus GN=Wdr61 PE=1 SV=1	2.05	2.15	7.9	1	1.0803
839	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=1	38.96	40.71	73.3	47	1.080725
840	Ankyrin repeat and SAM domain-containing protein 1A OS=Mus musculus GN=Anks1 PE=1 SV=1	2	2.01	2.6	1	1.08125
841	Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3	3.73	4.17	34	3	1.081475
842	Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3	42.35	42.42	35.3	26	1.08225
843	Coatamer subunit epsilon OS=Mus musculus GN=Cope PE=1 SV=3	9.14	9.28	35.1	5	1.0823
844	Histone-lysine N-methyltransferase setd3 OS=Mus musculus GN=Setd3 PE=1 SV=1	2.05	2.32	4.7	1	1.08235
845	Alpha-2-macroglobulin OS=Mus musculus GN=Pzp PE=1 SV=1	42.27	42.39	27.3	24	1.0824
846	Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	14.69	15.53	15.1	8	1.082425
847	Leucine carboxyl methyltransferase 1 OS=Mus musculus GN=Lcmt1 PE=1 SV=1	9.42	9.46	22.9	7	1.08275
848	Tubulin-specific chaperone D OS=Mus musculus GN=Tbcd PE=1 SV=1	13.98	14.04	14.6	8	1.083475
849	Protein Gcn111 OS=Mus musculus GN=Gcn111 PE=1 SV=1	40.43	40.5	19.3	22	1.08365
850	Procollagen C-endopeptidase enhancer 1 OS=Mus musculus GN=Pcolce PE=1 SV=1	1.38	1.53	5.3	2	1.083725
851	Probable ATP-dependent RNA helicase DDX46 OS=Mus musculus GN=Ddx46 PE=1 SV=1	1.33	1.67	8	1	1.0838
852	S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=1 SV=1	10.26	10.33	33.9	6	1.083975
853	Eukaryotic translation initiation factor 1 OS=Mus musculus GN=Eif1 PE=1 SV=2	4.4	4.45	26.6	2	1.084575
854	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3	20.95	21.03	91.4	37	1.084925
855	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	2.09	2.11	12.7	1	1.085225
856	tRNA (guanine(37)-N1)-methyltransferase OS=Mus musculus GN=Trmt5 PE=1 SV=1	3.04	3.14	7.8	2	1.085325

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
857	Small nuclear ribonucleoprotein Sm D1 OS=Mus musculus GN=Snrpd1 PE=1 SV=1	2	2	10.9	1	1.085825
858	Angiotensin-converting enzyme OS=Mus musculus GN=Ace PE=1 SV=3	16.28	16.33	13.3	8	1.086875
859	Glycogenin-1 (fragment) OS=Mus musculus GN=Gyg PE=1 SV=1	0.6	0.72	12.9	1	1.0869
860	Small nuclear ribonucleoprotein-associated protein N OS=Mus musculus GN=Snrpn PE=2 SV=1	2	2.05	3.3	2	1.086975
861	Heterogeneous nuclear ribonucleoprotein U, isoform CRA_b OS=Mus musculus GN=Gm28062 PE=4 SV=1	8.39	8.42	15.6	4	1.087725
862	Dual specificity mitogen-activated protein kinase kinase 4 OS=Mus musculus GN=Map2k4 PE=1 SV=2	3.54	3.73	10.8	2	1.088275
863	Dnaj homolog subfamily A member 1 OS=Mus musculus GN=Dnaja1 PE=1 SV=1	3.51	5.25	24.7	3	1.08845
864	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	28.84	28.92	40.3	17	1.088625
865	Polyadenylate-binding protein-interacting protein 1 OS=Mus musculus GN=Paip1 PE=1 SV=2	0.82	0.95	9.9	1	1.088775
866	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	2.19	2.23	14.3	1	1.0888
867	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	24.61	24.78	49	12	1.08885
868	BTB/POZ domain-containing protein KCTD12 OS=Mus musculus GN=Kctd12 PE=1 SV=1	3.51	3.75	23.6	3	1.089775
869	Importin-7 OS=Mus musculus GN=Ipo7 PE=1 SV=2	7.59	7.7	16.3	6	1.0902
870	Breast cancer anti-estrogen resistance protein 1 OS=Mus musculus GN=Bcar1 PE=1 SV=2	2.05	2.07	7	1	1.0909
871	Protein FAM3C (fragment) OS=Mus musculus GN=Fam3c PE=1 SV=1	7.32	7.42	52	4	1.090925
872	Fructose-bisphosphate aldolase OS=Mus musculus GN=Aldoa PE=1 SV=1	41.29	41.43	78.2	45	1.091225
873	Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap1l1 PE=1 SV=1	8.07	8.13	20.1	4	1.0925
874	3'-phosphoadenosine 5'-phosphosulfate synthase 1, isoform CRA_a OS=Mus musculus GN=Paps1 PE=1 SV=1	7.27	7.56	21.1	5	1.093
875	Geranylgeranyl transferase type-2 subunit beta OS=Mus musculus GN=Rabggtb PE=1 SV=1	2.08	2.09	10	1	1.0934
876	Isoaspartyl peptidase/L-asparaginase OS=Mus musculus GN=Asrgl1 PE=1 SV=1	11.83	12.58	42	6	1.094825
877	Heparin cofactor 2 OS=Mus musculus GN=Serpind1 PE=1 SV=1	3.21	3.35	5.6	2	1.095425
878	E2/E3 hybrid ubiquitin-protein ligase UBE2O OS=Mus musculus GN=Ube2o PE=1 SV=3	2.32	2.37	4.3	2	1.095875
879	Cytoplasmic dynein 1 light intermediate chain 2 OS=Mus musculus GN=Dync1li2 PE=1 SV=2	2.39	4.3	9.6	2	1.09615
880	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Mus musculus GN=Gapvd1 PE=1 SV=2	3.25	3.45	5	3	1.0965
881	von Willebrand factor A domain-containing protein 5A OS=Mus musculus GN=Vwa5a PE=1 SV=2	22.41	22.6	27.4	17	1.097325
882	SAPS domain family, member 3, isoform CRA_c OS=Mus musculus GN=Ppp6r3 PE=1 SV=1	2.14	2.26	10.7	1	1.098075
883	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=1 SV=3	1.55	1.79	21.3	1	1.0986
884	Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	11.14	11.18	30.7	10	1.098625
885	Ubiquitin carboxyl-terminal hydrolase OS=Mus musculus GN=Usp4 PE=1 SV=1	2.51	2.6	8.9	1	1.09875
886	Microtubule-associated protein RP/EB family member 2 OS=Mus musculus GN=Mapre2 PE=1 SV=1	2.02	2.03	7	1	1.099025
887	Ras suppressor protein 1 OS=Mus musculus GN=Rsu1 PE=1 SV=1	12.18	12.25	34.7	6	1.099875
888	Prolyl endopeptidase OS=Mus musculus GN=Prep PE=1 SV=1	31.34	31.37	38.5	18	1.100575
889	Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2	7.96	8.01	12.9	4	1.10105
890	Alpha-1-antitrypsin 1-5 OS=Mus musculus GN=Serpina1e PE=1 SV=1	12.23	34.45	54.2	52	1.101075
891	UTP-glucose-1-phosphate uridylyltransferase OS=Mus musculus GN=Ugp2 PE=1 SV=3	8.7	8.78	21.9	5	1.1015
892	ATP-dependent 6-phosphofructokinase, muscle type OS=Mus musculus GN=Pfkm PE=1 SV=3	4.9	7.41	17.7	4	1.1018
893	Vacuolar protein sorting-associated protein 26A OS=Mus musculus GN=Vps26a PE=1 SV=1	2.92	3.11	24.2	3	1.10275
894	Ran-binding protein 3 OS=Mus musculus GN=Ranbp3 PE=1 SV=2	2.93	3.54	10	2	1.10365
895	Protein FAM114A2 OS=Mus musculus GN=Fam114a2 PE=1 SV=2	2.95	3.05	13.3	2	1.1044
896	Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	10.5	11.23	12.1	8	1.1048
897	Protein Ighg2b (fragment) OS=Mus musculus GN=Ighg2b PE=1 SV=1	6.2	6.22	22.9	3	1.1058

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
898	Granulins OS=Mus musculus GN=Grn PE=1 SV=1	8.01	8.1	15.6	5	1.10645
899	Sorting nexin-30 OS=Mus musculus GN=Snx30 PE=1 SV=1	2.4	2.44	8.2	1	1.1065
900	Protein farnesyltransferase subunit beta OS=Mus musculus GN=Fntb PE=1 SV=1	4.62	4.68	11.4	3	1.1084
901	T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	38.52	38.57	65.1	26	1.108775
902	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	73.24	73.24	54.5	51	1.108825
903	Smoothelin OS=Mus musculus GN=Smtn PE=1 SV=1	1.9	2.07	6.6	1	1.10995
904	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase OS=Mus musculus GN=Lhpp PE=1 SV=1	1.88	2.13	16.7	1	1.11
905	Syntaxin 7 OS=Mus musculus GN=Stx7 PE=1 SV=1	2.42	2.47	19.9	1	1.110175
906	Serine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Sars PE=1 SV=1	20.88	21.04	32.7	12	1.110875
907	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=1 SV=2	2.59	2.64	6.5	2	1.111175
908	Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=1	4.8	4.91	5.9	3	1.11125
909	Probable ATP-dependent RNA helicase DDX58 OS=Mus musculus GN=Ddx58 PE=1 SV=2	2.96	3.07	10.7	2	1.1115
910	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3	2	42.9	53.6	31	1.111775
911	Kininogen-1 OS=Mus musculus GN=Kng1 PE=1 SV=1	21.75	21.92	30.7	12	1.112275
912	Lupus La protein homolog OS=Mus musculus GN=Ssb PE=1 SV=1	11.68	11.8	33.5	6	1.11235
913	Rabankyrin-5 OS=Mus musculus GN=Ankfy1 PE=1 SV=2	1.86	2.04	4.6	1	1.112925
914	Histone H2B OS=Mus musculus GN=Hist1h2bq PE=2 SV=1	1.3	1.76	31.3	2	1.11295
915	EGF-containing fibulin-like extracellular matrix protein 1 OS=Mus musculus GN=Efemp1 PE=1 SV=1	5.92	6.04	13.2	3	1.113325
916	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	41.63	41.73	70.3	48	1.113725
917	Spectrin alpha chain, nonerythrocytic 1 OS=Mus musculus GN=Sptan1 PE=1 SV=1	50.44	50.59	22.3	24	1.114
918	Alpha-N-acetylgalactosaminidase OS=Mus musculus GN=Naga PE=1 SV=2	2.14	2.16	11.6	1	1.114325
919	Sperm surface protein Sp17 OS=Mus musculus GN=Spa17 PE=1 SV=1	2	2	12.8	1	1.1144
920	HIV Tat-specific factor 1 homolog OS=Mus musculus GN=Htatsf1 PE=1 SV=1	5.19	5.28	7.4	3	1.114625
921	Rho GTPase-activating protein 18 OS=Mus musculus GN=Arhgap18 PE=1 SV=1	3.52	3.63	11.2	2	1.11505
922	Fas-activated serine/threonine kinase OS=Mus musculus GN=Fastk PE=2 SV=1	0.84	0.96	9.2	1	1.115375
923	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Mus musculus GN=Arap1 PE=1 SV=2	7.88	7.96	7.7	4	1.1179
924	Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=2	34.22	34.37	25.2	18	1.118175
925	Protein SGT1 homolog OS=Mus musculus GN=Sugt1 PE=1 SV=3	6.16	6.26	18.8	3	1.1185
926	Switch-associated protein 70 OS=Mus musculus GN=Swap70 PE=1 SV=2	4.5	4.56	9.2	2	1.118525
927	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	10.63	16.09	27.9	9	1.1191
928	ATP-binding cassette sub-family F member 3 OS=Mus musculus GN=Abcf3 PE=1 SV=1	6.3	6.61	15.5	3	1.120675
929	Carboxylesterase 1C OS=Mus musculus GN=Ces1c PE=1 SV=4	29.98	30	37.2	20	1.120725
930	Ras-related protein Rab-18 OS=Mus musculus GN=Rab18 PE=1 SV=2	0.55	0.61	12.1	1	1.12075
931	Dynactin subunit 3 OS=Mus musculus GN=Dctn3 PE=1 SV=2	2.85	2.96	23.7	2	1.1213
932	Ketosamine-3-kinase OS=Mus musculus GN=Fn3kpp PE=1 SV=2	2.14	2.19	10.7	1	1.121425
933	Ubiquitin conjugation factor E4 B OS=Mus musculus GN=Ube4b PE=1 SV=3	0.99	1.21	3.3	1	1.122025
934	Ubiquitin carboxyl-terminal hydrolase OS=Mus musculus GN=Usp7 PE=1 SV=1	10.08	10.89	13.8	8	1.1225
935	Syntaxin-binding protein 2 (fragment) OS=Mus musculus GN=Stxbp2 PE=1 SV=1	2.07	2.09	9.6	2	1.12255
936	Hsp70-binding protein 1 OS=Mus musculus GN=Hsbbp1 PE=1 SV=1	6	6	12.3	3	1.122975
937	BAG family molecular chaperone regulator 1 OS=Mus musculus GN=Bag1 PE=1 SV=1	7.06	7.45	26.2	7	1.123475
938	Hematological and neurological expressed 1-like protein OS=Mus musculus GN=Hn1l PE=1 SV=1	2.31	2.34	14.7	1	1.123725
939	Puromycin-sensitive aminopeptidase OS=Mus musculus GN=Npepps PE=1 SV=2	34.05	34.19	34	19	1.124125
940	Carbonyl reductase (NADPH) 1 OS=Mus musculus GN=Cbr1 PE=1 SV=3	25.42	25.53	66.4	21	1.125175
941	Serine/threonine-protein kinase 3 OS=Mus musculus GN=Stk3 PE=1 SV=1	6.25	6.34	12.1	4	1.12575
942	Interferon-induced 35 kDa protein homolog OS=Mus musculus GN=Ifi35 PE=1 SV=3	2.05	2.06	10.8	1	1.125925
943	Pleckstrin homology domain-containing family A member 2 (fragment) OS=Mus musculus GN=Plekha2 PE=1 SV=5	1.35	1.48	6.8	1	1.126425

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Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
944	UBX domain-containing protein 7 OS=Mus musculus GN=Ubxn7 PE=1 SV=2	0.57	0.62	5.8	1	1.127475
945	S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=1 SV=2	11.39	11.5	21.3	6	1.127625
946	N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Mus musculus GN=Naa15 PE=1 SV=1	5.83	6	9.1	4	1.1279
947	Protein transport protein Sec23A OS=Mus musculus GN=Sec23a PE=1 SV=1	13.15	17.56	30.6	13	1.128675
948	Protein Serpinb9 OS=Mus musculus GN=Serpib9 PE=1 SV=1	16.22	16.95	32.9	9	1.1293
949	Sortilin OS=Mus musculus GN=Sort1 PE=1 SV=1	2.01	2.02	4	2	1.12935
950	40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	4.24	4.28	24	2	1.1295
951	MAGUK p55 subfamily member 6 OS=Mus musculus GN=Mpp6 PE=1 SV=1	2.46	2.52	10.7	1	1.1296
952	Golgi to ER traffic protein 4 homolog OS=Mus musculus GN=Get4 PE=1 SV=2	4	4	13.2	2	1.129825
953	Caspase-6 OS=Mus musculus GN=Casp6 PE=1 SV=1	4.49	4.59	26.1	2	1.1301
954	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	22.7	44.7	57.2	35	1.13075
955	ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=2	7.3	15.8	71.1	11	1.130975
956	Retinoid-inducible serine carboxypeptidase OS=Mus musculus GN=Scep1 PE=1 SV=2	2	2	3.3	1	1.1312
957	Alpha-1-antitrypsin 1-2 OS=Mus musculus GN=Serpina1b PE=1 SV=2	6.51	32.44	64.9	49	1.13145
958	Serine/threonine-protein phosphatase OS=Mus musculus GN=Ppp3cb PE=1 SV=1	0.96	1.3	9.5	1	1.1326
959	Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=1	16.29	16.36	45.2	11	1.13315
960	Thimet oligopeptidase OS=Mus musculus GN=Thop1 PE=1 SV=1	24.75	24.84	33.2	12	1.1335
961	BRISC and BRCA1-A complex member 1 OS=Mus musculus GN=Babam1 PE=1 SV=1	2	2	5.7	1	1.13355
962	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Mus musculus GN=Anp32b PE=1 SV=1	4.07	8.35	30.9	7	1.1337
963	Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=1 SV=1	14.51	14.53	54.9	11	1.133825
964	Translationally controlled tumor protein OS=Mus musculus GN=Tpt1 PE=1 SV=1	7.3	7.4	46.5	5	1.13455
965	60S ribosomal protein L30 OS=Mus musculus GN=Rpl30 PE=1 SV=2	4	4	24.4	2	1.1346
966	Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=1 SV=1	4.63	6.55	7.2	3	1.13595
967	Huntingtin OS=Mus musculus GN=Htt PE=1 SV=1	3.75	4.05	4.3	3	1.135975
968	Copper transport protein ATOX1 OS=Mus musculus GN=Atox1 PE=1 SV=1	8.44	8.46	88.2	11	1.1366
969	Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1	12.94	13.05	26.4	7	1.136725
970	T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	44.23	43.97	60.8	24	1.13735
971	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	1.18	1.34	11.4	1	1.138
972	Putative uncharacterized protein Tes OS=Mus musculus GN=Tes PE=1 SV=2	2.71	2.93	22.4	5	1.1382
973	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	7.75	7.83	25.5	5	1.1384
974	Charged multivesicular body protein 3 OS=Mus musculus GN=Chmp3 PE=1 SV=3	2.03	2.03	17	1	1.13845
975	Rho GTPase-activating protein 23 OS=Mus musculus GN=Arhgap23 PE=1 SV=1	1.14	1.28	5.8	1	1.138525
976	Apolipoprotein E OS=Mus musculus GN=Apoe PE=1 SV=2	10.81	10.87	31.5	6	1.13965
977	Insulin-like growth factor-binding protein complex acid labile subunit OS=Mus musculus GN=Igfals PE=1 SV=1	2.01	2.01	7.8	1	1.139725
978	Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4	68.44	67.94	81	51	1.139775
979	ATPase, H+ transporting, lysosomal V1 subunit B1 OS=Mus musculus GN=Atp6v1b1 PE=1 SV=1	2.07	8.19	20.9	6	1.139875
980	Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	5.35	5.51	16.6	4	1.140125
981	Selenide, water dikinase 1 OS=Mus musculus GN=Sephs1 PE=1 SV=1	4.47	4.52	12	4	1.140475
982	T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	18.06	20.25	44.7	13	1.1414
983	Annexin A11 OS=Mus musculus GN=Anxa11 PE=1 SV=2	2	4.16	6.8	2	1.14145
984	Uroporphyrinogen-III synthase OS=Mus musculus GN=Uros PE=1 SV=1	5.92	6	17.4	3	1.141625
985	ADP-ribosylation factor 1 OS=Mus musculus GN=Arf1 PE=1 SV=2	19.55	19.69	85.6	21	1.14195
986	HSP 105 kDa OS=Mus musculus GN=Hsph1 PE=1 SV=1	2.56	5.68	9.3	4	1.141975
987	ATP-binding cassette subfamily E member 1 OS=Mus musculus GN=Abce1 PE=1 SV=1	7.7	7.91	17.5	5	1.142
988	Eukaryotic translation initiation factor 2 subunit 3, X-linked OS=Mus musculus GN=EIF2S3X PE=1 SV=2	10.66	12.19	29.7	9	1.142225

Contd...



Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
989	Cellular nucleic acid-binding protein OS=Mus musculus GN=Cnbp PE=1 SV=1	2	4	25.9	2	1.143
990	Beta-galactosidase OS=Mus musculus GN=Glb1 PE=1 SV=1	15.76	15.92	23	9	1.1441
991	E3 ubiquitin-protein ligase HUWE1 OS=Mus musculus GN=Huwe1 PE=1 SV=1	9.49	9.74	4.8	6	1.144225
992	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	6.99	12.78	32.2	7	1.14435
993	E3 ubiquitin-protein ligase RNF114 OS=Mus musculus GN=Rnf114 PE=1 SV=2	4.08	4.1	26.6	2	1.14445
994	Cytosolic phospholipase A2 OS=Mus musculus GN=Pla2g4a PE=1 SV=1	2.04	2.05	4.3	1	1.14455
995	Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3	64.53	64.53	36.3	37	1.145
996	N-acetylgalactosamine-6-sulfatase OS=Mus musculus GN=Galns PE=1 SV=2	0.51	0.56	6.5	2	1.14565
997	Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2	7.03	7.1	19	5	1.14645
998	Spectrin beta chain, nonerythrocytic 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2	33.79	34.03	16.6	18	1.14675
999	Protein Agl OS=Mus musculus GN=Agl PE=1 SV=1	3.13	3.28	4.8	2	1.14725
1000	Peroxisomal protein 5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2	15.98	16.22	65.7	13	1.14745
1001	Vitamin D-binding protein OS=Mus musculus GN=Gc PE=1 SV=2	19.34	19.4	40.6	11	1.147725
1002	Prothrombin OS=Mus musculus GN=F2 PE=1 SV=1	2.41	2.46	27.4	1	1.14775
1003	Phosphatidylinositol transfer protein alpha isoform OS=Mus musculus GN=Pitpna PE=1 SV=1	5.06	5.26	25.5	3	1.150825
1004	Fibrinogen alpha chain OS=Mus musculus GN=Fga PE=1 SV=1	5.67	5.74	13.2	4	1.152
1005	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=1 SV=2	35.49	35.52	29.7	19	1.15205
1006	Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1	28.93	28.95	53.2	21	1.1525
1007	Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	12.12	12.41	27.8	7	1.152725
1008	Protein Gm20547 OS=Mus musculus GN=Gm20547 PE=3 SV=1	6.82	7.13	9.2	5	1.15315
1009	Flap endonuclease 1 OS=Mus musculus GN=Fen1 PE=1 SV=1	2.02	2.02	8.2	1	1.1546
1010	WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 PE=1 SV=3	19.22	19.35	40.4	10	1.156075
1011	Toll-interacting protein OS=Mus musculus GN=Tollip PE=1 SV=1	2.04	2.05	12	1	1.1561
1012	60S ribosomal protein L5 (fragment) OS=Mus musculus GN=Rpl5 PE=1 SV=1	1.28	1.44	22.1	1	1.15635
1013	PDZ and LIM domain protein 5 OS=Mus musculus GN=Pdlim5 PE=1 SV=4	9.4	9.6	16.1	6	1.156525
1014	CD2-associated protein OS=Mus musculus GN=Cd2ap PE=1 SV=3	8.68	8.8	19.9	6	1.156775
1015	Phospholipid hydroperoxide glutathione peroxidase, nuclear OS=Mus musculus GN=Gpx4 PE=1 SV=3	4.2	4.22	17.4	2	1.15685
1016	Histamine N-methyltransferase OS=Mus musculus GN=Hnmt PE=1 SV=1	2.12	2.14	12.2	1	1.1573
1017	AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=2	9.61	9.77	11.9	7	1.1576
1018	Ribokinase OS=Mus musculus GN=Rbks PE=1 SV=1	2.13	2.15	12.1	1	1.15975
1019	Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2	5.64	5.7	35.7	11	1.160175
1020	Oxysterol-binding protein-related protein 2 OS=Mus musculus GN=Osbp2 PE=1 SV=1	4.65	4.89	18.4	2	1.1602
1021	NEDD8-activating enzyme E1 catalytic subunit OS=Mus musculus GN=Uba3 PE=1 SV=2	5.15	6.26	18.8	4	1.161125
1022	Dihydrolypyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlat PE=1 SV=2	1.19	1.36	5.5	2	1.1619
1023	Phosphoglucosyltransferase-like protein 5 OS=Mus musculus GN=Pgm5 PE=1 SV=2	15.95	17.56	32.1	9	1.163075
1024	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh1 PE=1 SV=2	23.16	24.43	56.3	16	1.1639
1025	Serine protease inhibitor A3K OS=Mus musculus GN=Serpina3k PE=1 SV=2	21.77	21.91	40.2	18	1.164075
1026	Rab GTPase-binding effector protein 2 OS=Mus musculus GN=Rabep2 PE=1 SV=3	8.2	9.59	21.8	6	1.164625
1027	ADP-ribosylation factor GTPase-activating protein 2 OS=Mus musculus GN=Arfgap2 PE=1 SV=1	4.32	4.36	13.3	2	1.16495
1028	CCR4-NOT transcription complex subunit 1 OS=Mus musculus GN=Cnot1 PE=1 SV=2	2.74	2.83	4.2	2	1.1658
1029	Nuclear autoantigenic sperm protein OS=Mus musculus GN=Nasp PE=1 SV=1	3.08	3.33	14.5	3	1.166725
1030	Vacuolar protein sorting-associated protein 4A OS=Mus musculus GN=Vps4a PE=1 SV=1	2.01	4.07	11.9	2	1.16725
1031	182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2	3.32	3.63	4.5	4	1.168275
1032	Dynactin subunit 4 OS=Mus musculus GN=Dctn4 PE=1 SV=1	6.04	6.05	13.9	3	1.16945
1033	Protein Tns1 OS=Mus musculus GN=Tns1 PE=1 SV=1	9.6	9.73	8.3	5	1.17005

Contd...

Supplementary Table 3: Contd...

Number	Name	Unused Prot Score <sup>a</sup>	Total Prot Score <sup>b</sup>	Percentage coverage	Peptides (95%)	Cauda/caput
1034	LIM and senescent cell antigen-like-containing domain protein 1 OS=Mus musculus GN=Lims1 PE=1 SV=1	1.45	1.63	15.8	1	1.170575
1035	Fascin OS=Mus musculus GN=Fscn1 PE=1 SV=4	3.39	3.64	8.3	3	1.171175
1036	Calpastatin OS=Mus musculus GN=Cast PE=1 SV=1	11.17	11.29	15	7	1.17215
1037	Zyxin OS=Mus musculus GN=Zyx PE=1 SV=2	2.13	2.15	5.3	1	1.17235
1038	Beta-1,4-galactosyltransferase 1 OS=Mus musculus GN=B4galt1 PE=1 SV=1	0.68	0.78	8.4	1	1.1736
1039	Chloride intracellular channel protein OS=Mus musculus GN=Clic3 PE=1 SV=1	3	3.12	31.5	2	1.174775
1040	OTU domain-containing protein 4 OS=Mus musculus GN=Otud4 PE=1 SV=1	2	2	2.2	1	1.17495
1041	Coiled-coil domain-containing protein 6 OS=Mus musculus GN=Ccdc6 PE=1 SV=1	7.34	7.43	12.6	4	1.175175
1042	Isopentenyl-diphosphate Delta-isomerase 1 OS=Mus musculus GN=Idi1 PE=1 SV=1	7.89	7.95	22.3	4	1.175225
1043	Septin-11 OS=Mus musculus GN=Sept11 PE=1 SV=4	7.11	7.26	14.9	4	1.175325
1044	Integral membrane protein 2B OS=Mus musculus GN=Itm2b PE=1 SV=1	6.02	6.04	23.7	3	1.1761
1045	Sorting nexin 3 OS=Mus musculus GN=Snx3 PE=1 SV=1	6.27	6.29	35.2	4	1.1762
1046	C-type lectin domain family 3, member b OS=Mus musculus GN=Clec3b PE=1 SV=1	6.31	6.35	37.6	4	1.176275
1047	Alpha-parvin OS=Mus musculus GN=Parva PE=1 SV=1	7.47	7.55	21.1	5	1.176425
1048	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=1 SV=2	1.28	1.41	4.3	1	1.17645
1049	Haptoglobin OS=Mus musculus GN=Hp PE=1 SV=1	15.03	15.12	39.5	9	1.176525
1050	Large proline-rich protein BAG6 OS=Mus musculus GN=Bag6 PE=1 SV=1	13.8	13.9	12.2	10	1.17785
1051	Protein Ighg2c OS=Mus musculus GN=Ighg2c PE=1 SV=1	2	2.43	16.6	2	1.178725
1052	Zinc-alpha-2-glycoprotein OS=Mus musculus GN=Azgp1 PE=1 SV=2	5.27	5.52	32.6	4	1.178975
1053	Peptidyl-prolyl cis-trans isomerase D OS=Mus musculus GN=Ppid PE=1 SV=3	2.17	4.25	14.6	2	1.179075
1054	Peroxisomal biogenesis factor 19 OS=Mus musculus GN=Pex19 PE=1 SV=1	2.02	2.03	8.7	1	1.1795
1055	14 kDa phosphohistidine phosphatase OS=Mus musculus GN=Pht1 PE=1 SV=1	5.52	6.73	54	4	1.18
1056	Complement C4-B OS=Mus musculus GN=C4b PE=1 SV=3	5.66	5.8	6.3	3	1.180225
1057	Ubiquitin-like modifier-activating enzyme 6 OS=Mus musculus GN=Uba6 PE=1 SV=1	11.35	11.71	21.2	6	1.18055
1058	Protein Ahnak2 (fragment) OS=Mus musculus GN=Ahnak2 PE=1 SV=5	2.01	2.05	20.6	1	1.1807
1059	Dicarbonyl L-xylulose reductase, isoform CRA_a OS=Mus musculus GN=Dcxr PE=1 SV=1	6.87	7.02	33.5	8	1.180725
1060	Apolipoprotein A-IV OS=Mus musculus GN=Apoa4 PE=1 SV=3	18.41	18.58	43	12	1.181225
1061	Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2	37.51	37.57	66.7	23	1.181575
1062	Ribonuclease T2 OS=Mus musculus GN=Rnaset2 PE=1 SV=1	3.96	4.21	22	2	1.181825
1063	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	2.63	2.72	9.1	1	1.182125
1064	Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=3	2.92	3.11	3.4	3	1.182475
1065	Phosphoinositide phospholipase C OS=Mus musculus GN=Plcg1 PE=1 SV=1	1.83	1.97	4	1	1.183275
1066	HSP beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	7.56	7.61	32.5	4	1.184175
1067	Coatomer subunit gamma-2 OS=Mus musculus GN=Copg2 PE=1 SV=1	0.7	7.13	7.1	4	1.184225
1068	Dihydropyrimidinase-related protein 3 OS=Mus musculus GN=Dpysl3 PE=1 SV=1	14.02	15.77	27.8	9	1.18485
1069	Diphosphomevalonate decarboxylase OS=Mus musculus GN=Mvd PE=1 SV=2	3.24	3.37	12.2	2	1.186275
1070	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=1 SV=1	0.96	1.12	19.2	1	1.1871
1071	Carboxypeptidase A5 OS=Mus musculus GN=Cpa5 PE=4 SV=1	0.84	1	15.8	1	1.1872
1072	Serotransferrin OS=Mus musculus GN=Tf PE=1 SV=1	67.62	67.64	67.3	62	1.18745
1073	Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1	6.5	6.6	29.6	8	1.187925
1074	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=1 SV=4	6.56	6.72	52.7	5	1.18825
1075	Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2	21.64	25.85	28.8	13	1.1888
1076	COBW domain-containing protein 1 OS=Mus musculus GN=Cbwd1 PE=1 SV=1	4	4	9.9	2	1.189
1077	Sorting nexin-2 OS=Mus musculus GN=Snx2 PE=1 SV=2	8.6	12.92	22.7	7	1.1899
1078	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=1 SV=3	11.07	11.77	55.7	5	1.192225
1079	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=1 SV=1	2.01	4.02	4.3	2	1.192775
1080	Myotubularin-related protein 6 OS=Mus musculus GN=Mtmr6 PE=1 SV=1	0.5	0.55	4.1	1	1.192825
1081	AP-3 complex subunit mu-1 OS=Mus musculus GN=Ap3m1 PE=1 SV=1	2.31	2.35	14.8	1	1.194125
1082	Collagen alpha-1 (XIV) chain OS=Mus musculus GN=Col14a1 PE=1 SV=1	24.93	24.99	13.9	14	1.194525

Contd...

**Supplementary Table 3: Contd...**

<i>Number</i>	<i>Name</i>	<i>Unused Prot Score<sup>a</sup></i>	<i>Total Prot Score<sup>b</sup></i>	<i>Percentage coverage</i>	<i>Peptides (95%)</i>	<i>Cauda/caput</i>
1083	26S proteasome non-ATPase regulatory subunit 9 OS=Mus musculus GN=Psmc9 PE=1 SV=1	6.02	6.08	27.5	5	1.1957
1084	Nicotinamide phosphoribosyltransferase OS=Mus musculus GN=Nampt PE=1 SV=1	14.99	15.09	32	7	1.195875
1085	Exportin-5 OS=Mus musculus GN=Xpo5 PE=1 SV=1	2.14	2.17	3.7	2	1.196525
1086	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Mus musculus GN=Sgta PE=1 SV=2	8.11	8.36	31.4	6	1.196675
1087	Calcineurin subunit B type 1 OS=Mus musculus GN=Ppp3r1 PE=1 SV=3	3.2	3.33	32.9	2	1.197325
1088	Regulator of G-protein signaling 3 OS=Mus musculus GN=Rgs3 PE=1 SV=2	2	2	1.1	1	1.199275

<sup>a</sup>Unused ProtScore: reflecting the amount of total, unique peptide evidence related to a given protein; <sup>b</sup>Total ProtScore: reflecting the sum of all peptide evidences related to a given protein. HSP: heat shock protein. OS: organismName; GN: geneName; PE: proteinExistence; SV: sequence version