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[V L Newton](#), [V L Newton](#), [I Riba-Garcia](#), [Christopher E.M. Griffiths](#) ...+7 more authors

Institutions: [Manchester Academic Health Science Centre](#),
[Central Manchester University Hospitals NHS Foundation Trust](#), [DSM](#)

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Mass spectrometry-based proteomics reveals the distinct nature of the skin proteomes of photoaged compared to intrinsically aged skin

Running Heading: Photoaged versus intrinsically aged skin proteomes

V.L Newton^{1,2}, I Riba-Garcia³, C.E.M Griffiths^{1,2}, A.V Rawlings⁴, R Voegeli⁵, R.D Unwin³, M.J Sherratt^{6,5}
& R.E.B Watson^{1,2,5}

¹Centre for Dermatology Research, Division of Musculoskeletal & Dermatological Sciences, School of Biological Sciences, Manchester Academic Health Science Centre, University of Manchester, and Salford Royal NHS Foundation Trust UK; ²NIHR Manchester Biomedical Research Centre, Central Manchester University Hospitals NHS Foundation Trust, Manchester Academic Health Science Centre, UK; ³Division of Cardiovascular Sciences, School of Medical Sciences, Faculty of Biology, Medicine and Health, University of Manchester, Manchester Academic Health Science Centre, Core Technology facility (3rd Floor), 46 Grafton Street, Manchester, M13 9NT; ⁴AVR Consulting Ltd, Northwich, UK; ⁵DSM Nutritional Products Ltd, Kaiseraugst, Switzerland; ⁶Division of Cell Matrix Biology and Regenerative Medicine, School of Biological Sciences, Manchester Academic Health Science Centre, The University of Manchester, UK.

§ Joint senior authors.

victoria.newton@manchester.ac.uk; isabel_riba@hotmail.com; Christopher.Griffiths@manchester.ac.uk; tonyrawlings@avrconsultingltd.com; rainer.voegeli@dsm.com; r.unwin@manchester.ac.uk; michael.j.sherratt@manchester.ac.uk; rachel.watson@manchester.ac.uk.

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Corresponding author:

Dr Rachel Watson
Division of Musculoskeletal & Dermatological Sciences
The University of Manchester
2.001 Stopford Building
Oxford Road
Manchester M13 9PT
UK

Tel:

+44 161 275 5505

Fax:

+44 161 275 5171

Email:

rachel.watson@manchester.ac.uk

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Abstract

Objective

With increasing age skin is subject to alterations in its organisation, which impacts on its function as well as having clinical consequences. Proteomics is a useful tool for non-targeted, semi-quantitative simultaneous investigation of high numbers of proteins. In the current study we utilise proteomics to characterise and contrast age-associated differences in photoexposed and photoprotected skin, with a focus on the epidermis, dermal-epidermal junction and papillary dermis.

Methods

Skin biopsies from buttock (photoprotected) and forearm (photoexposed) of healthy volunteers (aged 18-30 or ≥ 65 years) were transversely sectioned from the stratum corneum to a depth of 250 μm . Following SDS-PAGE, each sample lane was segmented prior to analysis by liquid chromatography-mass spectrometry/mass spectrometry. Pathways analysis was carried out using Ingenuity IPA.

Results

Comparison of skin proteomes at buttock and forearm sites revealed differences in relative protein abundance. Ageing in skin on the photoexposed forearm resulted in 80% of the altered proteins being increased with age, in contrast to the photoprotected buttock where 74% of altered proteins with age were reduced. Functionally, age-altered proteins in the photoexposed forearm were associated with conferring structure, energy and metabolism. In the photoprotected buttock proteins associated with gene expression, free-radical scavenging, protein synthesis and protein degradation were most frequently altered.

Conclusion

This study highlights the necessity of not considering photoageing as an accelerated intrinsic ageing, but as a distinct physiological process.

Key words:

Genomics/Proteomics/Elisa/Cell culture; Skin physiology/structure; Skin ageing; Proteomics; Epidermis; Dermis; Dermal-epidermal junction;

Abbreviations:

BU, buttock; DEJ, dermal-epidermal junction; ECM, extracellular matrix; FA, forearm; FDR, false discovery rate; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; IQR, interquartile range; LC, liquid chromatography; MS, Mass spectrometry; OCTM, optimal cutting temperature media.

Introduction

The skin changes with the passage of time, resulting from natural changes in the genome, gene expression and metabolism and is termed intrinsic ageing [1, 2]. However, the skin being of a large surface area and often exposed to the external environment means it is further influenced by factors such as weather, light and pollution [3-5]. It is these external factors exposed to throughout a lifetime, or a person's 'exposome', most particularly to sunlight, that contribute additional mechanisms to how the skin ages and is termed extrinsic ageing [6]. While the changes to the appearance of the skin as we age are often more subtle in those areas not frequently exposed, in those areas of skin which often are, most particularly in those who are paler, then skin can become wrinkled, coarse and mottled [7].

Much of the work carried out on how the skin changes with age has been focused on changes to the extracellular matrix (ECM) within the dermal compartment of the skin [8]. In the dermis ECM molecules are often very long lived and so accumulate damage over time, leading to differences in both their structural and mechanical properties. Other changes such as decreased collagen with respect to elastin, loss of small fibres of the elastin network close to the boarder with the dermis and changes to the glycosaminoglycan composition may also occur [8]. Less work has been carried out looking at the changes in the epidermis as we age, though it is known that epidermal thickness may reduce [9, 10], the rate of keratinocyte turnover slow [11] and that some keratinocytes may enter senescence [12]. The dermal-epidermal junction (DEJ) between the epidermal and dermal compartments also undergoes alterations with age and while we know that it flattens, the reasons for this are still not fully understood [13].

Proteomics, using mass spectrometry (MS) to analyse peptide constituents in a sample allowing *post-hoc* identification of protein species [14], can be used as a non-targeted method to identify differences in relative abundance between samples. This has frequently been used successfully to identify novel biomarkers of disease [15, 16]. Applying such a method to the skin, however, is not

without its challenges, especially where the size of a skin sample through biopsy is limited and high concentrations of structural proteins in skin makes protein solubilisation and hence subsequent detection difficult. The high concentrations of ECM proteins present in the dermis and keratins in the epidermis can also mask changes in other less abundant proteins [17, 18].

Although proteomics on the skin has previously been carried out, to the best of our knowledge, ageing studies have thus far only evaluated whole biopsies taken from photoprotected areas. The aims of this study were therefore to use sectioning and SDS-PAGE separation prior to MS to improve skin protein solubilisation and detection. This strategy also allowed enrichment of samples for the epidermis, DEJ and papillary dermis and to reduce noise from proteins contained within the main volume of the dermis, including those from the vasculature. We then compared for the first time young and aged skin taken from a photoexposed site using non-targeted mass spectrometry. To be able to put into better context both the effect of sunlight on the skin as we age and proteomic differences due to anatomical site we also compared results to young and aged skin from a photoprotected skin site.

Methods

Volunteers and biopsy removal

Two panels of volunteers aged 18-30 years (mean: 24 years \pm 3) and 65 years or over (mean: 71 years \pm 4) were recruited into the study ($n= 6$ females per group; University of Manchester Research Ethics Committee ref 13268). All subjects gave written, informed consent and the study was carried out in accordance with the declaration of Helsinki guidelines (2013). Study subjects were Fitzpatrick skin phototype I-III [19]. An area of skin on the mid dorsal forearm (photoexposed) and an area of the photoprotected upper buttock/hip/lower back (photoprotected) were biopsied (6 mm) under local anaesthesia. Biopsies were rinsed in ice-cold phosphate buffered saline (PBS) twice, followed

by ice-cold 0.25 M sucrose to remove external blood before being bisected and snap-frozen in optimal cutting temperature medium (OCTM) using liquid nitrogen.

Proteomics

One half of the biopsy was orientated *stratum corneum* outermost in an OCTM block and as much excess OCTM surrounding the biopsy as possible removed. The first 5 μm thick transverse/horizontal section of the skin was then collected from when the *stratum corneum* first became visible and collection continued to a depth of 250 μm . Sections were placed into 100 μL of ice-cold lysis buffer (7 M urea, 2 M thiourea, 30 mM Tris-HCl to pH 8, followed by 50 mM DTT, 0.1% SDS), vortexed and frozen at -80°C until required. In an attempt to minimise variation, only skin from female volunteers was used in the proteomics analyses.

Protein concentration was measured (FluoroProfile[®] Protein Quantification Kit; Sigma Aldrich; Gillingham, UK) and 30 μg of each sample loaded onto an SDS-PAGE gel. Following separation gels were stained with Coomassie Blue to confirm equal loading and gel lines excised into 11 bands. In-gel digestion was then performed, beginning with three washes (200 mM ammonium bicarbonate, 40% (v/v) acetonitrile), until samples were translucent. Gel pieces were dried by incubation twice in 100% (v/v) acetonitrile, then protein were reduced and alkylated by sequential incubation in 10mM dithiothreitol (20 mins), dehydration in 1 wash with acetonitrile, then incubation in 50mM iodoacetamide (30 mins). Gel pieces were then dried again by incubation in acetonitrile (2x) then rehydrated using 10-20 μL of 20 $\text{ng}/\mu\text{L}$ porcine sequencing grade modified trypsin (Promega: solution in 5% (v/v) acetonitrile, 100 mM ammonium bicarbonate. A further 50 μL of 5% (v/v) acetonitrile, 100 mM ammonium bicarbonate was added and samples left to incubate overnight at 37°C . Samples were then spun, the supernatant collected and 50 μL of buffer (5% acetonitrile, 100 mM ammonium bicarbonate) added to each sample for 15 minutes to extract additional peptides.

This was removed and pooled with the previous supernatant before drying using a SPEEDVAC. Samples were stored at -80°C prior to reversed-phase liquid chromatography (LC)-MS/MS analysis.

For LC-MS/MS analysis, dried fractions were re-dissolved (20 µL; 97%/3% water/acetonitrile v/v, 0.1% v/v trifluoroacetic acid, 10 fmol Glu-fibrinopeptide B, 10 fmol Leu-enkephalin) and 3 µL subjected to LC-MS analysis using a nanoACQUITY LC system (Waters, Elstree, UK) online to a QSTAR Elite mass spectrometer (AB Sciex, Framingham, USA). Briefly, injected samples were loaded onto a trapping column (Symmetry C18 100A, 5 µm; Waters) for 7.5 minutes using a flow rate of 15 µL/min (98%/2% v/v water/acetonitrile, 0.1% formic acid). The samples were resolved on an analytical column (NanoACQUITY UPLC™ BEH 30 c18, 75 µm x 250mm, 1.7µm; Waters, Elstree, UK) using the gradient shown in Table I at a flow rate of 300 nL/min. Columns were maintained at 40°C.

The nanoACQUITY system was coupled to a QSTAR® Elite MS/MS System (AB Sciex) equipped with an electrospray ionisation (ESI) ion source. Ions were emitted from a Distal Coated Silica Tip Emitter needle 10 ± 1 µm (New Objective, Woburn, USA) and MS/MS collected using a standard IDA method where, following a 1 second MS scan, the four top precursor ions were selected and fragmented for 1 second each.

All MS/MS data files acquired from the same sample lane were processed together using ProteinPilot (AB Sciex) or Mascot DEAMON (Matrix Science Ltd, London, UK) and Scaffold 4 (Proteome Software, Portland, USA) to provide a single list of identifications from each sample.

Data analysis

Two data analysis workflows were used to identify differentially expressed proteins between groups.

ProteinPilot workflow: Raw data files were analysed using the Paragon algorithm within ProteinPilot 4.0 using default search settings against a Human-specific Uniprot database (Release April 2015,

20,204 Entries), which was concatenated with a reversed-sequence decoy version of the same database to enable the false discovery rate (FDR) for identifications to be determined. To identify differentially expressed proteins, protein identification data from all of the samples was aligned using the Protein Alignment Template tool from AB Sciex. Proteins with Unscored score >2 were included. To identify potentially differentially expressed proteins, the 'N', a value related to the relative abundance of each protein within each sample was calculated. Mean values were then calculated for each experimental group.

Mascot workflow: Data were also analysed using Mascot and the results processed using Scaffold 4.5.0 for identification of protein differences. Mascot searches were performed by combining data from all bands for a single sample into a single search using Mascot Daemon. Searches were carried out against a SwissProt 2015 Homo sapiens database using fragment tolerances of 0.8Da for precursor ions and 0.6 Da for product ions, with Met oxidation as a variable modification, carbamidomethylation (CAM) modified Cys as a fixed modification and using trypsin as the digesting enzyme with allowance for one missed cleavage. Resulting data files were imported into Scaffold software, where wide protein grouping with binary peptide protein weights was used. Peptide thresholds for positive protein identification were set to a minimum of 95%, protein thresholds were set to 99% minimum and positive identification required at least 2 peptides per protein. FDR were set at 0.3% for peptides and at 0.4% for protein.

The list of proteins produced was manually reviewed in order to identify those that were missed by the software and to verify the results. Expression levels between samples were then compared in Scaffold by spectral counting, with an associated fold change and p-value calculated for each sample. The data were log transformed for graph plotting.

Pathways analysis was carried out using Ingenuity IPA software (Qiagen, Manchester, UK), where the entire user dataset was used as a background and differentially expressed proteins were defined as those with $0.7 \geq \text{fold change} \geq 1.5$.

Results

We first wanted to gain a sense of the influence of anatomical site on the skin proteome by comparing buttock and forearm skin. As buttock and forearm samples were not analysed on the MS on the same run, peptide numbers detected for each protein in buttock skin could not be directly compared with forearm. However, using ProteinPilot relative abundance could be compared, with the most abundant protein detected in an individual's sample designated 1, the second most abundant 2 and so forth. A mean was then taken for each protein across the young individuals at each skin site. A highly abundant protein which was most different in relative abundance between the two sites was filaggrin, being relatively more abundant in the forearm (FA; the most abundantly detected) than the buttock (BU; the 8th most abundantly detected; Fig 1A (i)). A number of other structural proteins that were relatively more abundant in the forearm compared with the buttock, included osteoglycine/mimecan (167th FA vs. 355th BU), periplakin (114th FA vs. 187th BU), a beta actin variant (18th FA vs. 36th BU) and transgelin (62nd FA vs. 191th BU; Fig 1 (i)). 14-3-3 sigma signalling molecule was also relatively more abundant in forearm than the buttock (39th FA vs. 52nd BU). Conversely, alpha-actinin 4 (54th FA vs. 19th BU) and pyruvate kinase (72nd FA vs. 36th BU), were relatively more abundant in the buttock skin than the forearm skin (See Supplementary Table I for full list).

Next we wanted to investigate the effect of ageing on the proteomes at each of the skin sites. Using Mascot and Scaffold software to analyse the data we detected a total of 377 proteins in samples taken from photoprotected buttock, the full list of which is in Supplementary Table II. Of these 377, 29 showed differential expression between young and aged skin ($p < 0.05$ Table II). Those proteins more highly detected in aged buttock skin than young were structural (keratin 6A, fold change (FC) 648, $p < 0.01$ and filamin A, FC 4, $p < 0.05$), along with two associated with clot formation; coagulation factor XIII (FC 6, $p < 0.01$) and fibrinogen alpha chain (FC 3, $p < 0.05$). Inositol monophosphase 2

(FC<0.001, p<0.05) and proteasome subunit alpha type-7-like protein (FC<0.001, p<0.05) were the proteins most dramatically reduced in aged skin. Those proteins that changed were also organised by general function (as listed in UniProt), into stress response-, signalling-, energy and metabolism-, ubiquitin-proteasome-associated system-, immune-, protein synthesis-, structural-, transportation and/or metal-binding- and histone-related (Table 4).

In skin from photoexposed forearm, using Mascot and Scaffold, we detected more proteins than in the buttock (photoprotected) sample, 547 (see Supplementary Table III for full list). The 48 proteins where fold changes between young and aged skin had a p-value of 0.05 or less in photoexposed forearm are displayed in Table III. The most altered of these proteins being increased vitronectin with age (FC 1000, p<0.001) and a reduction with age of leucyl-tRNA synthetase (FC<0.001, p<0.05) and eukaryotic translation initiation factor 3, subunit B (FC<0.001, p<0.05). Those proteins that changed were also organised by general function (as listed in UniProt), with the largest groupings being those proteins associated with energy and metabolism, immune function, structure, and transportation/binding (Table IV).

The number of proteins that changed with age in the photoprotected buttock and photoexposed forearm were similar when considered as the percentage of detected proteins altered with age, 7% and 8% in buttock and forearm, respectively (where fold change was ≤ 0.7 or ≥ 1.5 ; Fig 2A). However, it was striking that not only were most altered proteins different at the two sites, but that in the buttock most altered proteins were reduced with age (74%), whereas in the forearm most were increased with age (80%). Only haemoglobin (alpha subunit), and coagulation factor XIII were altered with age at both sites with fold changes ≤ 0.7 or ≥ 1.5 . Coagulation factor XIII (coag VIII) was increased with age in both the buttock (coag XIII FC 5.7, p<0.01) and forearm skin (coag XIII FC 2.7,

p<0.01), but haemoglobin alpha subunit was reduced with age in the buttock (FC 0.4, p<0.05) and increased with age in the forearm (FC 14, p<0.05; Fig 2B).

To more systematically compare biological functions and molecular and cellular pathways altered as a result of each type of ageing, we carried out pathways analysis using Ingenuity IPA software on Mascot and Scaffold calculated results. In both buttock and forearm proteins changed with age were associated with cell death and survival. However, the actual proteins listed for each were not the same (except albumin) and as previously, while in buttock most of these proteins reduced with age, in forearm most increased. A number of proteins altered in forearm with age were associated with lipid metabolism, post-translational modification and hair and skin functioning. In buttock skin proteins with these function were either not altered or were not altered to the same degree by ageing. Instead, most proteins altered with ageing in the buttock were associated with gene expression, free-radical scavenging, protein synthesis and protein degradation, none of which were specified by IPA as changing with age in the forearm (Fig 3A, Table V).

Discussion

In this study we wanted to investigate photoageing using LC/MS/MS for the first time and to focus on protein changes in the epidermis, DEJ and the papillary dermis by enriching for this region prior to MS.

The horizontal sectioning of the skin biopsies to a depth of 250 μm allowed collection of not only the epidermis, DEJ and upper dermis, but also aided in the solubilisation of proteins, as sections were only 5 μm thick prior to lysis. Issues associated with the presence of OCTM in the samples were

mitigated by the use of SDS-PAGE prior to MS. While probably not as sensitive as the use of stable isotope tagging (e.g. isobaric tags or dimethyl labelling, for example) for detection of differences in protein abundance between samples, the use of label-free proteomics for relative quantification is now common place [16]). Running proteins digested from each of the gel fragments separately allowed for detection of a greater number of proteins. This is because if each of our samples had been loaded onto the MS without gel separation first and using a single injection, keratins and other more common proteins would have swamped the MS signal. Despite our technique enriching the epidermis and upper dermis in our sample preparation and separating the samples using gels, we did not detect some low abundance proteins, including those contained within the DEJ such as nidogen and laminin 5/332. However, this was also the case in a study where laser capture was employed to specifically extract the DEJ [20], highlighting the difficulty in detecting proteins from a region only approximately 150 nm in thickness [21]. Despite this, the number of proteins detected overall using Mascot and Scaffold in this study was broadly comparable to previous studies that used whole biopsies and that would have had more tissue available for analysis [22, 23]. Proteomics studies on the skin are therefore still far short of the 825 epidermal, 1636 dermal and epidermal, 95 dermal and 32 DEJ/basement membrane proteins now known, as reported by a systematic review on proteins present in the skin [24].

Protein abundance in photoexposed forearm skin compared with photoprotected buttock skin

Comparison of the relative abundance of proteins in the forearm skin with the buttock skin in young individuals revealed differences and highlights that the skin proteome varies between anatomical site, even before exposure differences have had time to cause further impact. Many of the differences associated with anatomical site included proteins with a structural- and/or matrix-related role. This was true of filaggrin, which was the most relatively abundant protein in the forearm, but only the eighth most relatively abundant protein in the buttock. Also,

mimelan/osteoglycin, periplakin, a beta actin variant and transgelin were all more relatively abundant in young forearm compared with the buttock. Both filaggrin and periplakin are vital for cornification and barrier function and in a study in which skin keratinocytes were exposed to cigarette smoke condensate, both periplakin and filaggrin were up-regulated [25]. Filaggrin is also enriched in the *stratum corneum* on the cheek compared to a post-auricular site where skin is protected from sunlight [26]. It is possible that differences between forearm and buttock skin were due to external factors, even in young skin, though these differences may have been a consequence of a thicker *stratum corneum*, which has been observed on the dorsal forearm compared with the buttock [27]. The higher relative levels of a beta actin variant and of transgelin, important in actin dynamics, suggests that the actin cytoskeleton may be different in forearm skin compared with buttock skin. So, too does the finding of alpha-catenins being more relatively abundant in buttock than sun-exposed dorsal forearm skin. These proteins are actin filament-associated proteins and important in maintaining cellular adhesion via β -catenin and E-cadherin through the actin network [28]. A reduction of alpha-catenin 1 is associated with an increase in NF- κ B activation and hyperproliferation [29], again suggesting differences in the actin network and differences in the number and properties of adherence junctions in buttock skin compared with forearm skin. The small leucine-rich proteoglycan mimelan/osteoglycin is thought to control collagen fibre development, with increased fibre thickness observed in mutant mice [30]. In human abdominal skin collagen fibres are thicker in aged skin [31], though whether there are differences in fibre thicknesses in the forearm compared with the buttock is not, to the best of our knowledge, known. It is known however that transcription of mimelan is induced in response to UV [32], so it is possible that even short term-exposure to UV might result in more of this protein and so account for the relatively higher amount in forearm skin than buttock. Non-structural proteins less relatively abundant in forearm compared with buttock included pyruvate kinase and ubiquitin carboxyl terminal hydrolase 5. Pyruvate kinase expression has been linked with controlling the rate of nucleotide synthesis by virtue of nucleotide synthesis being critical for cell proliferation [33]. It is

possible that rates of cell proliferation in forearm skin and buttock skin may differ and be linked with levels of pyruvate kinase. Carboxyl terminal hydrolase 5 is a protease that hydrolyses a peptide bond at the C-terminal glycine of ubiquitin [34]. Reductions in this protein *in vitro* reduce the degradation of ubiquitinated p53 and so result in higher levels of activated p53 [35]. Therefore this may be a mechanism by which the presence of activated p53 is increased and so accelerate cellular apoptosis and/or senescence in forearm skin [36]. As a result, given that the ideal of a longitudinal study is not practical in most instances, ageing studies must bear in mind the additional variation induced by variation in anatomical site in addition to changes caused by a person's exposome, such as the variation already shown in fibroblast gene expression of cells located at different anatomical sites [37, 38].

Protein abundance in young & aged photoexposed forearm skin

Comparison of proteins in young and aged skin in the photoexposed forearm showed that while there were reductions of a trifunctional mitochondrial enzyme, a t-RNA synthetase and a translation initiation factor, most proteins increased in detection with age. The increased levels of vitronectin and, in particular, elastin in the photoexposed forearm have been known for many years [39]. Elastin is deposited as a disorganised amorphous mass [solar elastosis] and ECM proteins such as vitronectin and clusterin bind the edges of these dermal elastic fibres [40]. Indeed, clusterin glycoprotein may be produced in response to stress and is found closely associated with elastin in solar elastosis, thought to be as an attempt to reduce elastin aggregation [41]. Agreement of our proteomic results with previous studies therefore help in validating the findings of this study. Transthyretin and amyloid P are also associated with matrix deposition/amyloidosis, with transthyretin a transporter protein of thyroxine and retinol. Abnormal deposition of this protein is known to occur in some elderly individuals, especially in cardiac tissue [42]. It is also found associated with peripheral nerves and amyloid P in cases of familial amyloidotic polyneuropathy

[43], though the increased levels detected with age in the forearm in our experiment may be the result of increased serum levels rather than increased deposition in the skin. Another structure-associated protein higher in aged skin in our study was spectrin. Spectrin helps maintain the stability, shape and structure of the cell contributing to cell adhesion, spreading and the cell cycle. Spectrin can be degraded by the calcium-dependent protease calpain and the activity of this protease is increased in fibroblasts from aged donors than young [44]. It is therefore possible that more of this protein was detected with age as the skin attempts to compensate for the increased cleavage of this protein. However, it may also be that the cleaved spectrin products were more readily detectable by our methodology than the full length protein. With such clear evidence of elastosis in our aged forearm skin samples we expected that we might find evidence of loss of DEJ-associated proteins as has previously been found in photoaged skin [13]. As previously discussed, we did not detect a number of DEJ-associated proteins due to their scarcity, but we did detect collagen VII and alpha-6 and beta-4 integrins. These were not significantly reduced with age in our data set as might be expected. Our skin samples therefore may have exhibited histology such as that surrounding some wrinkles, where ECM deposition is significant, but the DEJ appears relatively normal [45]. Deposition of ECM and other associated proteins was therefore the major driver of the proteomic differences observed in photoageing in this study.

Protein abundance in young & aged photoprotected buttock skin

By comparison ageing changes in photoprotected buttock were very different, where although there was a structural protein, Keratin 6A, top of the list as increased with age, most of the other changes were reductions in the amount of proteins detected with age. Keratin 6A mRNA expression has been shown to be increased with age in sun protected human skin [46, 47], though we did not find a concurrent increase in its binding partner keratin 16 with age. Filamin A is an actin binding protein and is known to be important in the pericellular organisation of collagen [48] and providing tension

to the ECM [49]. Alterations in this protein with age in the skin have not to our knowledge been reported previously, though it is known that mutations in filamin A can lead to cutaneous alterations including fibromas and pigmentary changes [50]. Filamin A is also known to influence TGF- β signalling through modulation of RhoA and SMAD trafficking, but also influence the negative regulation of both ERK1/2 and MMP signalling via a RAS-GRF1 [51, 52]. Therefore, it is possible that the increase in filamin A with age could be a reflection of changes in ECM dynamics in response to increased levels of MMP 9 with age or an attempt to increase SMAD2/TGF- β signalling in the aged skin. Among the most reduced proteins with age in the buttock were phosphoglycerate mutase 1, proteasome alpha subunits and inositol monophosphatase 2. A recent transcriptome study found inositol monophosphatase 2 to be higher in aged skin [53], however in this study we found the opposite to be true at the protein level. It is possible that the increase in the transcription of this enzyme is in response to lower cellular levels of the protein, if with age the rate of turnover increases or rate of translation reduces. It does however suggest that changes to inositol phosphate metabolism are important as we age and may be linked to keratinocyte differentiation and proliferation, as well as their regulation [54]. Protein degradation is affected by ageing [55] and so it is unsurprising that we found proteins associated with the proteasome pathway to be altered with age. This has been shown to manifest as a reduction in proteasome subunit expression [56] and indeed we observed a reduction in both proteasome subunit alpha type 1 and type-7-like protein. Phosphoglycerate mutase catalyses the interconversion of 3-phosphoglycerate and 2-phosphoglycerate in glycolysis, two steps after GAPDH [57] and so suggests more anaerobic metabolism in the young buttock skin. That being said, the balance of glycolytic enzymes is complex, not all have an effect on the rate of glycolysis and not only the presence or absence of a protein needs to be considered, but its activation and inhibition. Temporal factors are also important, as responses may be dependent on what the cell has previously been exposed to in its environment [58]. In embryonic mouse fibroblasts phosphoglycerate mutase upregulation increases the rate of glycolysis and protects against oxidative stress, its depletion induces cellular senescence and, in

contradiction to the anaerobic theory of ageing, in mouse fibroblasts at least, oxidative stress will lead to an inhibition of glycolysis [58]. Reduced levels of phosphoglycerate mutase in aged buttock skin may therefore be a hallmark of cellular senescence in the intrinsically aged skin.

Functionality groupings of those proteins changed with age and sun-exposure

Division of changed proteins with age into functions revealed that proteins associated with structure, energy and metabolism; more specifically, hair and skin functioning, lipid metabolism and post-translational modification were predominant or unique to the forearm site. Hair and skin-specific processes being pulled out by IPA as changing with photoageing was due to the predominance of *de-novo* synthesis of many structural proteins associated with amyloid-type deposition as discussed above. However, it must also be remembered that structural proteins newly synthesised or fragmented as a result of photoexposure do not possess the same physical properties as ECM in its usual architecture [59]. For example, this material may be more soluble and so could be present in higher concentrations in samples prepared for MS. Indeed, this is perhaps the reason for the detection of more collagen in the aged forearm skin in our study, as although in photoexposed sites overall collagen levels may reduce, fibers are fragmented, thickened, and more soluble [60]. It may also be why more proteins overall were detected in the forearm compared with the buttock despite the same mass of protein being loaded for each. More proteins were also detected in a proteomics study using tape strips taken from the photoexposed cheek [436 protein detected] compared with a photoprotected post-auricular site (253 proteins detected) [26], perhaps suggesting that exposure to sunlight either expands the number of proteins present within the skin or changes the properties of those proteins present allowing them to be more readily detected by MS.

Those proteins identified as being associated with lipid metabolism in photoaged skin in this study including apolipoprotein A and clusterin are known to be increased in plasma with age [61, 62] and so their increased presence may less be indicative of changes in lipid metabolism and more point to their detection in any residual blood in the tissue samples and/or increased vessel leakage in aged skin [63]. Many of these proteins are also common to the process of ECM deposition as previously discussed and so their increased presence be linked to the elastosis process rather than changes in lipid metabolism.

Proteins associated with post-translational modification are becoming of more interest as their link with diseases associated with ageing are studied. Protein phosphorylation, acetylation, methylation, and ubiquitination may not just be markers of ageing and ageing-related diseases, but may also be implicated in disease causation [64], though the proteins identified by IPA analysis in our analysis linked to post-translational modification were limited.

In common with photoaged skin, cell death and survival, cellular assembly and organisation, cellular movement and cell-cell signalling were processes in which proteins were altered with intrinsic ageing. However, contrary to photoaged skin, protein function types additionally altered were associated with gene expression, free-radical scavenging, protein synthesis and protein degradation. The proteins involved in protein synthesis, eukaryotic initiation factor 4A, eukaryotic translation initiation factor 3, subunit B, 40S ribosomal protein S3, elongation factor 1-gamma and leucyl-tRNA synthetase, all tended towards a loss with age and it is known from a number of studies that general protein synthesis rates decline with age [65]. Protein synthesis requires a high rate of energy usage and maintaining low levels of protein synthesis helps to aid in longevity. However, protein synthesis is essential to replace damaged proteins [65]. In photoprotected skin this reduction in protein synthesis may be more acceptable due to lower levels of accumulative damage as a result of protection from light and other environmental factors. By contrast, in photoexposed sites, skin is

regularly challenged by external factors causing damage to proteins and so protein synthesis may need to be maintained at a higher rate in order to replace these damaged proteins. Within the group of free-radical scavenging proteins reduced with age, DJ-1, to the best of our knowledge has not before been associated with skin ageing. Reduced levels of DJ-1 have previously been reported with age in the thymus [66], though DJ-1 is best known for its association with Parkinson's disease, as mutations in this protein can lead to early onset [67]. DJ-1 is also important in response to UV and this has been shown *in vitro* in both a human corneal endothelial cell line [68] and also a HaCaT keratinocyte cell line [69]. More recently an increase in DJ-1 expression *in vivo* in the *stratum corneum* has been shown to result from UVB irradiation [70]. Also, higher levels of DJ-1 protein have been measured in the *stratum corneum* of photoexposed cheek compared with the photoprotected post auricular site [26]. Other anti-oxidant/cell repair proteins found reduced with age in the photoprotected buttock were peroxiredoxin-1, RAC 1 and heat shock protein beta-1, all of which have been shown to be reduced as a result of ageing and/or linked to UV exposure previously [71-73]. Ageing in photoprotected skin therefore tends towards reduced proliferation, reduced protein synthesis and a reduction in capacity to react to cellular stress, fitting with the ageing theory in that accumulation of oxidatively damaged proteins in ageing cells results in the loss of function of gene products critical for maintaining genome integrity [74].

Conclusion

In this study we have shown that there are proteome differences in skin at different anatomical sites, even prior to the added complexity of ageing. We have identified filamin A and DJ-1 as potential markers of skin ageing, though the number of volunteers in this study was small and both would need to be confirmed by alternative experimental means. We have found that ageing induces changes in the proteome in the photoexposed forearm and that these predominate in the direction of protein induction, in stark contrast to the photoprotected buttock, where loss of protein

abundance predominates. It is possible that this may be linked to methylation, as hypermethylation has been measured in intristically aged skin, and hypomethylation in extrinsically aged [75]. This coupled with the differences in the functions of the proteins changing with age at the two sites highlights the distinct nature of photoageing compared with ageing at a photoprotected site, even taking into account the differences that already exist as a result of anatomical location. Therefore, this study highlights the necessity of considering photoageing not as an accelerated intrinsic ageing, but as a distinct physiological process.

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Tables Legends

Table I: Solvent gradients applied to the NanoACQUITY UPLC™ BEH 30 c18 column prior to loading onto the MS.

Table II: List of proteins and their accession numbers that showed a significant change in aged photoprotected buttock skin compared with young. Green shading represents where there is more of a protein in aged skin than young by a factor of 1.5 or more and blue shading represents where there is less of a protein in aged skin compared with young by a factor of 0.7 or less. All protein fold changes exhibited possess p values of 0.05 or less.

Table III: List of proteins and their accession numbers that showed a significant change in aged forearm skin compared with young. Green shading represents where there is more of a protein in aged skin than young by a factor of 1.5 or more and blue shading represents where there is less of a protein in aged skin compared with young by a factor of 0.7 or less. All protein fold changes exhibited possess p values of 0.05 or less.

Table IV: General functional groupings of changed proteins with age in the buttock and forearm skin. Proteins where a difference with age was detected grouped into general functions as listed in UniProt. All proteins displayed exhibit p values of 0.05 or less. Green represents an increase in aged skin and blue a reduction.

Table V: IPA grouping of changed proteins by their molecular and cellular functions. Proteins where a difference with age was detected grouped into molecular and cellular functions by IPA Ingenuity. All proteins displayed exhibit p values of 0.05 or less. Green represents an increase in aged skin and blue a reduction. Fold changes of $0.7 \leq \& \geq 1.5$ were considered in the IPA analysis.

Figure Legends

Figure 1: Differences in relative protein abundance between young buttock and forearm skin sites. Comparison between data sets where each protein is ranked by its abundance relative to the other proteins present in the same sample. For example, the most abundant protein in the sample is designated 1, the second most abundant 2 and so forth. Abundance values were averaged across young samples for each skin site. [i] Relative protein abundance between young buttock and young forearm up to the 400th most relatively abundant protein. [ii] Relative protein abundance between young buttock and forearm up to the 75th most relatively abundant protein. $n = 4 \& 5$.

Figure 2: Numbers of proteins increased and decreased with age in buttock and forearm skin. [A] Pie charts displaying the percentage of proteins increased, decreased and unchanged with age in the photoprotected buttock [i] and photoexposed dorsal forearm [ii]. **[B]** Venn diagram displaying the number of proteins in the buttock and forearm skin where fold change was ≤ 0.7 or ≥ 1.5 and $p \leq 0.05$. $n = 4-6$.

Figure 3: Changes in proteins with age organised by functional group. Fold change with age in proteins as grouped into molecular and cellular functions by IPA Ingenuity. Fold changes are plotted as \log_2 values. All changes exhibit p values of 0.05 or less.

Table I.

Time [min]	Gradient	
	% A	% B
0.0	97.0	3.0
5.0	97.0	3.0
30.0	73.0	27.0
35.0	50.0	50.0
36.0	0.0	100.0
41.0	0.0	100.0
42.0	97.0	3.0
55.0	97.0	3.0

Table II.

Identified Proteins	Accession Number	Fold change	T-Test (P-Value)
Keratin, type II cytoskeletal 6A	K2C6A_HUMAN	648	≤0.01
Coagulation factor XIII A	F13A_HUMAN	5.7	≤0.01
Filamin-A	FLNA_HUMAN	4.0	≤0.05
Fibrinogen alpha chain	FIBA_HUMAN	3.0	≤0.05
Serotransferrin OS	TRFE_HUMAN	2.2	≤0.05
Collagen alpha-3(VI) chain	CO6A3_HUMAN	1.5	≤0.001
Histone H1.2	H12_HUMAN	1.5	≤0.01
Serum albumin	ALBU_HUMAN	1.4	≤0.01
Plakophilin-1	PKP1_HUMAN	0.8	≤0.05
40S ribosomal protein S18	RS18_HUMAN	0.5	≤0.05
Heat shock protein beta-1	HSPB1_HUMAN	0.5	≤0.05
40S ribosomal protein S7	RS7_HUMAN	0.4	≤0.05
Hemoglobin subunit alpha	HBA_HUMAN	0.4	≤0.05
Hemoglobin subunit beta	HBB_HUMAN	0.4	≤0.05
Adenine phosphoribosyltransferase	APT_HUMAN	0.3	≤0.05
Cathepsin D	CATD_HUMAN	0.3	≤0.05
GTP-binding nuclear protein Ran	RAN_HUMAN	0.3	≤0.05
Peroxiredoxin-1	PRDX1_HUMAN	0.3	≤0.01
Profilin-1	PROF1_HUMAN	0.3	≤0.01
Protein DJ-1	PARK7_HUMAN	0.3	≤0.05
Ras-related C3 botulinum toxin substrate 1	RAC1_HUMAN	0.3	≤0.05
40S ribosomal protein S3	RS3_HUMAN	0.2	≤0.05
60S ribosomal protein L7a	RL7A_HUMAN	0.2	≤0.01
ADP/ATP translocase 2	ADT2_HUMAN	0.2	≤0.05
NADH-cytochrome b5 reductase 1	NB5R1_HUMAN	0.2	≤0.01
Phosphoglycerate mutase 1	PGAM1_HUMAN	0.2	≤0.01
Proteasome subunit alpha type-1	PSA1_HUMAN	0.2	≤0.05
Inositol monophosphatase 2	IMPA2_HUMAN	<0.001	≤0.05
Proteasome subunit alpha type-7-like	PSA7L_HUMAN	<0.001	≤0.05

Table III.

Identified Proteins	Accession Number	Fold change	T-Test (P-Value)
Vitronectin	VTNC_HUMAN	1000	≤0.001
EH domain-containing protein 2	EHD2_HUMAN	110	≤0.05
Hemoglobin subunit delta	HBD_HUMAN	87	≤0.05
Elastin	ELN_HUMAN	49	≤0.05
2,4-dienoyl-CoA reductase, mitochondrial	DECR_HUMAN	27	≤0.05
Fibrinogen gamma chain	FIBG_HUMAN	24	≤0.05
Serum amyloid P-component	SAMP_HUMAN	17	≤0.01
Alcohol dehydrogenase 1A	ADH1A_HUMAN	15	≤0.001
Hemoglobin subunit alpha	HBA_HUMAN	14	≤0.05
Transthyretin	TTHY_HUMAN	13	≤0.05
Clusterin	CLUS_HUMAN	12	≤0.01
Synaptic vesicle membrane protein VAT-1 homolog	VAT1_HUMAN	9.7	≤0.01
Histone H1.2	H12_HUMAN	7.1	≤0.05
60S ribosomal protein L34	RL34_HUMAN	7.1	≤0.05
Glycogen phosphorylase, brain form	PYGB_HUMAN	4.6	≤0.05
40S ribosomal protein S20	RS20_HUMAN	4.4	≤0.05
Eukaryotic translation initiation factor 3 subunit A	EIF3A_HUMAN	4.3	≤0.05
Small nuclear ribonucleoprotein Sm D3	SMD3_HUMAN	4.1	≤0.05
Sideroflexin-3	SFXN3_HUMAN	4.1	≤0.05
Protein S100-A4	S10A4_HUMAN	3.9	≤0.01
Histone H4	H4_HUMAN	3.8	≤0.05
Apolipoprotein A-II	APOA2_HUMAN	3.8	≤0.05
Myosin light polypeptide 6	MYL6_HUMAN	3.6	≤0.05
60S ribosomal protein L27	RL27_HUMAN	3.6	≤0.01
60S ribosomal protein L22	RL22_HUMAN	3.0	≤0.05
Collagen alpha-1(I) chain	CO1A1_HUMAN	2.8	≤0.05
Spectrin alpha chain, non-erythrocytic 1	SPTN1_HUMAN	2.8	≤0.05
Coagulation factor XIII A chain	F13A_HUMAN	2.7	≤0.01
Collagen alpha-2(VI) chain	CO6A2_HUMAN	2.6	≤0.05
Collagen alpha-2(I) chain	CO1A2_HUMAN	2.4	≤0.05
Heat shock protein HSP 90-alpha	HS90A_HUMAN	2.4	≤0.01
Clathrin heavy chain 1	CLH1_HUMAN	2.3	≤0.05
Arginase-1	ARG1_HUMAN	2.3	≤0.01
Heat shock protein HSP 90-beta	HS90B_HUMAN	2.2	≤0.01
Transitional endoplasmic reticulum ATPase	TERA_HUMAN	2.1	≤0.05
Collagen alpha-1(VI) chain	CO6A1_HUMAN	1.9	≤0.05
Serum albumin	ALBU_HUMAN	1.4	<0.05
Keratin, type I cytoskeletal 14	K1C14_HUMAN	0.8	≤0.05
Keratin, type I cytoskeletal 15	K1C15_HUMAN	0.8	≤0.05
Tubulin beta chain	TBB5_HUMAN	0.7	≤0.01
Tubulin beta-4B chain	TBB4B_HUMAN	0.7	≤0.05
Tubulin beta-4A chain	TBB4A_HUMAN	0.7	≤0.05
Keratin, type II cytoskeletal 78	K2C78_HUMAN	0.4	≤0.05
D-3-phosphoglycerate dehydrogenase	SERA_HUMAN	0.4	≤0.01
Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_HUMAN	0.4	≤0.05
Trifunctional enzyme subunit beta, mitochondrial	ECHB_HUMAN	0.1	≤0.05
Leucyl-tRNA synthetase, cytoplasmic	SYLC_HUMAN	<0.001	≤0.05
Eukaryotic translation initiation factor 3 subunit B	EIF3B_HUMAN	<0.001	≤0.05

Table IV.

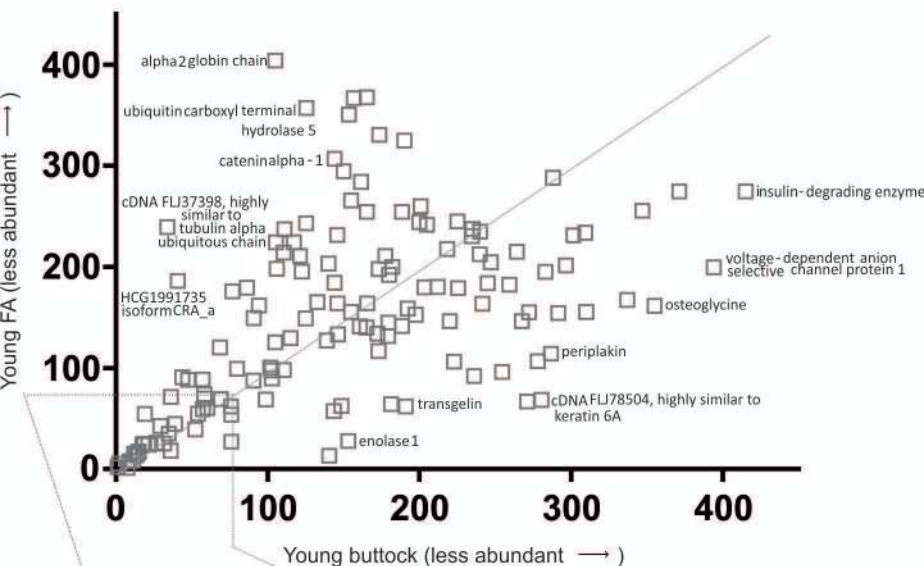
Buttock			Forearm		
	A/Y	p-value		A/Y	p-value
1 Stress response			1 Stress response		
Peroxiredoxin-1	0.3	≤0.01	Serum amyloid P-component	17	≤0.01
Protein DJ-1	0.3	≤0.05	Clusterin	12	≤0.01
			Synaptic vesicle membrane protein VAT-1 homolog	9.7	≤0.01
			Heat shock protein HSP 90-alpha	2.4	≤0.01
			Arginase-1	2.3	≤0.01
			Heat shock protein HSP 90-beta	2.2	≤0.01
			Transitional endoplasmic reticulum ATPase	2.1	≤0.05
			LeucyHRNA synthetase, cytoplasmic	0.001	≤0.05
2 Signalling			2 Signalling		
GTP-binding nuclear protein Ran	0.3	≤0.05	Protein S100-A4	3.9	≤0.01
Peroxiredoxin-1	0.3	≤0.01			
Ras-related C3 botulinum toxin substrate	0.3	≤0.05			
Proteasome subunit alpha type-1	0.2	≤0.05			
3 Energy & Metabolism			3 Energy & Metabolism		
Adenine phosphobosyltransferase	0.3	≤0.05	2,4-dienoyl-CoA reductase, mitochondrial	27	≤0.05
ADP/ATP translocase 2	0.2	≤0.05	Alcohol dehydrogenase 1A	15	≤0.001
NADH-cytochrome b5 reductase 1	0.2	≤0.01	Synaptic vesicle membrane protein VAT-1 homolog	9.7	≤0.01
Phosphoglycerate mutase 1	0.2	≤0.01	Glycogen phosphorylase, brain form	4.6	≤0.05
Inositol monophosphatase 2	0.001	≤0.05	Apolipoprotein A-II	3.8	≤0.05
			Spectrin alpha chain, non-erythrocytic 1	2.8	≤0.05
			Transitional endoplasmic reticulum ATPase	2.1	≤0.05
			D-3-phosphoglycerate dehydrogenase	0.4	≤0.01
			Trifunctional enzyme subunit beta, mitochondrial	0.06	≤0.05
4 Ubiquitin-proteasome & associated systems			4 Ubiquitin-proteasome & associated systems		
Cathepsin D	0.3	≤0.01	EH domain-containing protein 2	110	≤0.05
Proteasome subunit alpha type-1	0.2	≤0.05	Clusterin	12	≤0.01
Proteasome subunit alpha type-7-like	0.001	≤0.05	Heat shock protein HSP 90-alpha	2.4	≤0.01
			Heat shock protein HSP 90-beta	2.2	≤0.01
			Transitional endoplasmic reticulum ATPase	2.1	≤0.05
			Heterogeneous nuclear ribonucleoproteins C1/C2	0.4	≤0.05
5 Immune-related			5 Immune-related		
Coagulation factor XIII	5.7	≤0.01	Vitronectin	1000	≤0.001
Filamin-A	4	≤0.05	EH domain-containing protein 2	110	≤0.05
Fibrinogen alpha chain	3	≤0.05	Fibrinogen gamma chain	24	≤0.05
Cathepsin D	0.3	≤0.01	Serum amyloid P-component	17	≤0.01
Peroxiredoxin-1	0.3	≤0.01	Clusterin	12	≤0.01
Profilin-1	0.3	≤0.01	Apolipoprotein A-II	3.8	≤0.05
Ras-related C3 botulinum toxin substrate	0.3	≤0.05	Collagen alpha-1(I) chain	2.8	≤0.05
Proteasome subunit alpha type-1	0.2	≤0.05	Spectrin alpha chain, non-erythrocytic 1	2.8	≤0.05
			Coagulation factor XIII	2.7	≤0.01
			Heat shock protein HSP 90-alpha	2.4	≤0.01
			Arginase-1	2.3	≤0.01
			Heat shock protein HSP 90-beta	2.2	≤0.01
			Collagen alpha-1(V) chain	1.9	≤0.05
			Tubulin beta-4B chain	0.7	≤0.05
6 Protein Synthesis			6 Protein Synthesis		
40S ribosomal protein S18	0.5	≤0.05	60S ribosomal protein L34	7.1	≤0.05
40S ribosomal protein S7	0.4	≤0.05	40S ribosomal protein S20	4.4	≤0.05
40S ribosomal protein S3	0.2	≤0.05	Eukaryotic translation initiation factor 3 subunit A	4.3	≤0.05
60S ribosomal protein L7a	0.2	≤0.01	Small nuclear ribonucleoprotein Sm D3	4.1	≤0.05
			60S ribosomal protein L27	3.6	≤0.01
			60S ribosomal protein L22	3	≤0.05
			Heterogeneous nuclear ribonucleoproteins C1/C2	0.4	≤0.05
			Eukaryotic translation initiation factor 3 subunit B	0.001	≤0.05
			LeucyHRNA synthetase, cytoplasmic	0.001	≤0.05
7 Structural			7 Structural		
Keratin, type II cytoskeletal 6A	648	≤0.01	Vitronectin	1000	≤0.001
Coagulation factor XIII	5.7	≤0.01	EH domain-containing protein 2	110	≤0.05
Filamin-A	4	≤0.05	Elastin	49	≤0.01
Fibrinogen alpha chain	3	≤0.05	Fibrinogen gamma chain	24	≤0.05
Collagen alpha-3(VI) chain	1.5	≤0.0001	Myosin light polypeptide 6	3.6	≤0.05
Profilin-1	0.3	≤0.01	Collagen alpha-1(I) chain	2.8	≤0.05
Ras-related C3 botulinum toxin substrate	0.3	≤0.05	Spectrin alpha chain, non-erythrocytic 1	2.8	≤0.05
			Coagulation factor XIII	2.7	≤0.01
			Collagen alpha-2(VI) chain	2.6	≤0.05
			Collagen alpha-2(I) chain	2.4	≤0.05
			Collagen alpha-1(V) chain	1.9	≤0.05
			Tubulin beta-4A chain	0.7	≤0.05
			Tubulin beta-4B chain	0.7	≤0.05
			Keratin, type II cytoskeletal 78	0.4	≤0.05
8 Transportation & metal binding			8 Transportation & metal binding		
Coagulation factor XIII	5.7	≤0.01	EH domain-containing protein 2	110	≤0.05
Fibrinogen alpha chain	3	≤0.05	Hemoglobin subunit delta	87	≤0.05
Hemoglobin subunit alpha	0.4	≤0.05	Fibrinogen gamma chain	24	≤0.05
Hemoglobin subunit beta	0.4	≤0.05	Serum amyloid P-component	17	≤0.01
Inositol monophosphatase 2	0.001	≤0.05	Hemoglobin subunit alpha	14	≤0.05
			Transferrin	13	≤0.05
			Synaptic vesicle membrane protein VAT-1 homolog	9.7	≤0.01
			Sideroflexin-3	4.1	≤0.05
			Protein S100-A4	3.9	≤0.01
			Collagen alpha-1(I) chain	2.8	≤0.05
			Spectrin alpha chain, non-erythrocytic 1	2.8	≤0.05
			Coagulation factor XIII	2.7	≤0.01
			Claithrin heavy chain 1	2.3	≤0.05
9 Histone			9 Histone		
Histone H1.2	1.5	≤0.01	Histone H1.2	7.1	≤0.05
			Histone H4	3.8	≤0.05

Table V.

Buttock				Forearm			
		A/Y	p-value			A/Y	p-value
1 Cell death and survival:				1 Cell death and survival:			
FLNA	Filamin-A	4	≤0.05	VTN	Vitronectin	1000	≤0.01
TF	Serotransferrin	2.2	≤0.05	CLU	Clusterin	12	≤0.01
HSPB1	Heat shock protein beta-1	0.5	≤0.05	EIF3A	Eukaryotic translation initiation factor 3 subunit A	4.3	≤0.05
HBB	Hemoglobin subunit beta	0.4	≤0.05	S100A4	Protein S100-A4	3.9	≤0.01
PARK7	Protein DJ-1	0.3	≤0.05	RPL27	60s ribosomal protein L27	3.6	≤0.01
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05	Col1A1	Collagen alpha-1(I) chain	2.8	≤0.05
PSMA1	Proteasome subunit alpha type-1	0.2	≤0.05	HSP90AB1	Heat shock protein HSP 90-beta	2.2	≤0.01
				VCP	Transitional endoplasmic reticulum ATPase	2.1	≤0.05
				TUBB4A	Tubulin beta-4A chain	0.7	≤0.05
2 Lipid metabolism:				2 Lipid metabolism:			
				VTN	Vitronectin	1000	≤0.01
				CLU	Clusterin	12	≤0.01
				APOA2	Apolipoprotein A-II	3.8	≤0.05
3 Cellular assembly and organisation:				3 Cellular assembly and organisation:			
KRT6A	Keratin, type II cytoskeletal 6A	648	≤0.01	VTN	Vitronectin	1000	≤0.01
FLNA	Filamin-A	4	≤0.05	APCS	Serum amyloid P-component	17	≤0.01
Col6A3	Collagen alpha-3(VI) chain	1.5	<0.001	TTR	Transthyretin	13	≤0.05
HSPB1	Heat shock protein beta-1	0.5	≤0.05	S100A4	Protein S100-A4	3.9	≤0.01
PFN1	Profilin-1	0.3	≤0.01	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	2.8	≤0.05
RAN	GTP-binding nuclear protein Ran	0.3	≤0.05				
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05				
RPS3	40S ribosomal protein S3	0.2	≤0.05				
4 Cellular growth and proliferation:				4 Cellular growth and proliferation:			
Rac1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05	TTR	Transthyretin	13	≤0.05
				Clu	Clusterin	12	≤0.01
				HSP90AA1	Heat shock protein HSP 90-alpha	2.4	≤0.01
				HSP90AB1	Heat shock protein HSP 90-beta	2.2	≤0.01
5 Cellular movement:				5 Cellular movement:			
FLNA	Filamin-A	4	≤0.05	VTN	Vitronectin	1000	≤0.01
FGA	Fibrinogen alpha chain	3	≤0.05	S100A4	Protein S100-A4	3.9	≤0.01
HSPB1	Heat shock protein beta-1	0.5	≤0.05	col1A1	Collagen alpha-1(I) chain	2.8	≤0.05
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05				
6 Cell morphology:				6 Cell morphology:			
FLNA	Filamin-A	4	≤0.05	VTN	Vitronectin	1000	≤0.01
PFN1	Profilin-1	0.3	≤0.01	clu	Clusterin	12	≤0.01
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05	hsp90AA1	Heat shock protein HSP 90-alpha	2.4	≤0.01
7 Cell-to-cell signalling:				7 Cell-to-cell signalling:			
FLNA	Filamin-A	4	≤0.05	VTN	Vitronectin	1000	≤0.01
FGA	Fibrinogen alpha chain	3	≤0.05	APCS	Serum amyloid P-component	17	≤0.01
HSPB1	Heat shock protein beta-1	0.5	≤0.05				
HBB	Hemoglobin subunit beta	0.4	≤0.05				
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05				
CTSD	Cathepsin D	0.3	≤0.05				
8 Post-translational modification				8 Post-translational modification:			
				APCS	Serum amyloid P-component	17	≤0.01
				APOA2	Apolipoprotein A-II	3.8	≤0.05
				HSP90AA1	Heat shock protein HSP 90-alpha	2.4	≤0.01
9 Hair and skin development & function:				9 Hair and skin development & function:			
FLNA	Filamin-A	4	≤0.05	TTR	Transthyretin	13	≤0.05
				CLU	Clusterin	12	≤0.01
				COL1A1	Collagen alpha-1(I) chain	2.8	≤0.05
				COL1A2	Collagen alpha-2(I) chain	2.4	≤0.05
				HSP90AA1	Heat shock protein HSP 90-alpha	2.4	≤0.01
				HSP90AB1	Heat shock protein HSP 90-beta	2.2	≤0.01
10 Gene expression:				10 Gene expression:			
FLNA	Filamin-A	4	≤0.05				
TF	Serotransferrin	2.2	≤0.05				
HBB	Hemoglobin subunit beta	0.4	≤0.05				
PRDX1	Peroxisredoxin-1	0.3	≤0.01				
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05				
PARK7	Protein DJ-1	0.3	≤0.05				
RPS3	40S ribosomal protein S3	0.2	≤0.05				
11 Free radical scavenging:				11 Free radical scavenging			
HSPB1	Heat shock protein beta-1	0.5	≤0.05				
HBB	Hemoglobin subunit beta	0.4	≤0.05				
PARK7	Protein DJ-1	0.3	≤0.05				
PRDX1	Peroxisredoxin-1	0.3	≤0.01				
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05				
12 Protein synthesis:				12 Protein synthesis			
FLNA	Filamin-A	4	≤0.05				
FGA	Fibrinogen alpha chain	3	≤0.05				
TF	Serotransferrin	2.2	≤0.05				
HSPB1	Heat shock protein beta-1	0.5	≤0.05				
RPS7	40S ribosomal protein S7	0.4	≤0.05				
CTSD	Cathepsin D	0.3	≤0.05				
PFN1	Profilin-1	0.3	≤0.01				
PARK7	Protein DJ-1	0.3	≤0.05				
RAC1	Ras-related C3 botulinum toxin substrate 1	0.3	≤0.05				
RPS3	40S ribosomal protein S3	0.2	≤0.05				
13 Protein degradation:				13 Protein degradation			
FLNA	Filamin-A	4	≤0.05				
TF	Serotransferrin	2.2	≤0.05				
CTSD	Cathepsin D	0.3	≤0.05				
PFN1	Profilin-1	0.3	≤0.01				
PARK7	Protein DJ-1	0.3	≤0.05				

Figure 1.

A (i) Protein abundance in young forearm skin compared with young buttock skin



(ii)

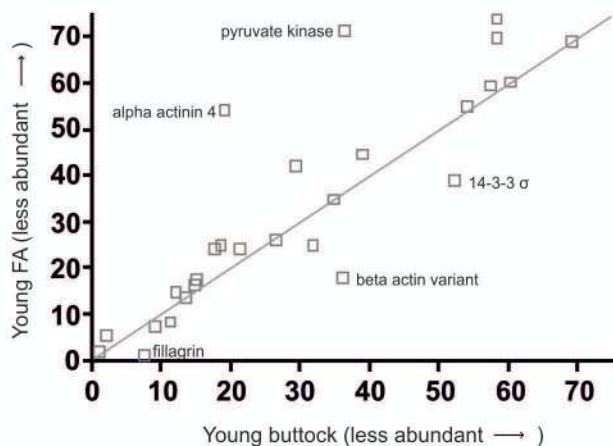
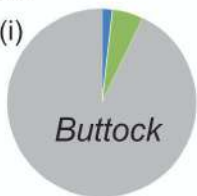


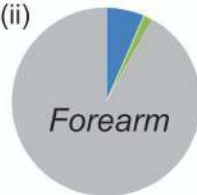
Figure 2.

A

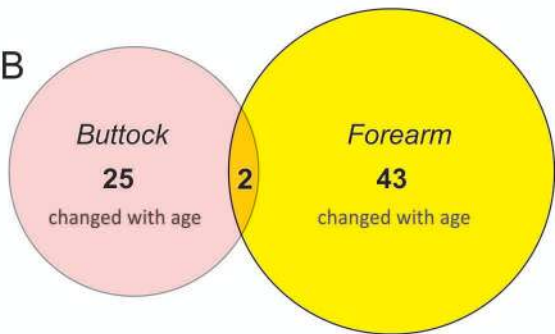
(i)



(ii)



B



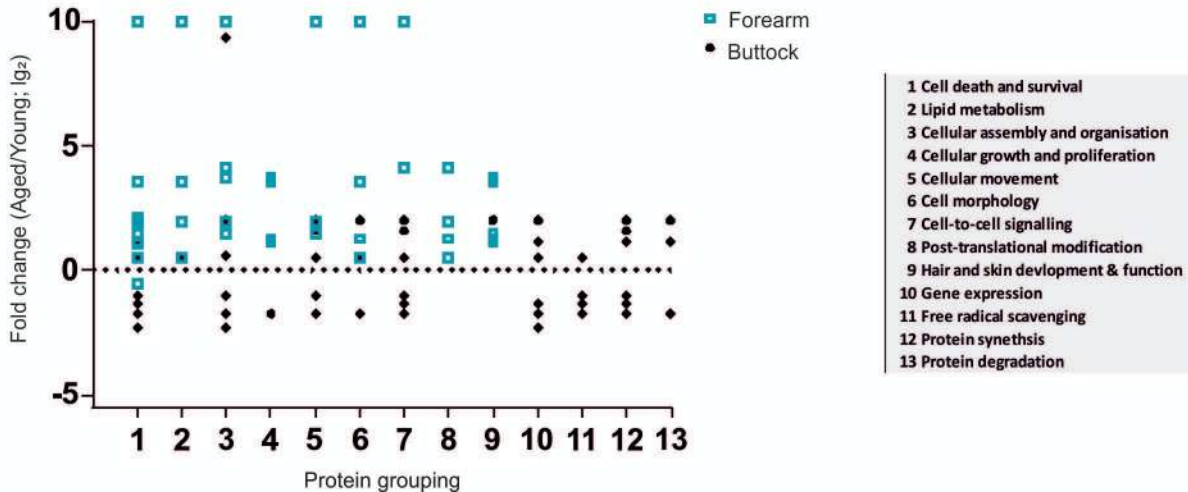
- Increased in aged
- Decreased in aged
- No change

Supp. table 1.

Name	Relative abundance (N; 0 dp)	
	Buttock	Forearm
<i>(alphabetical)</i>		
14-3-3 beta/alpha	259	183
14-3-3 protein sigma	52	39
40S ribosomal protein S11	268	147
60S ribosomal protein L10a	242	164
Actin-related protein 2/3 complex subunit 3	165	140
Adenine phosphoribosyltransferase (Fragment)	166	164
Adenylate kinase 2, mitochondrial	235	231
Alcohol dehydrogenase IB (Class I), beta polypeptide, isoform CRA_a	288	288
Alpha-2 globin chain	105	404
Alpha-actinin-4	19	54
Amyloid P component, serum	255	96
Annexin (Fragment)	141	13
APEX nuclease	189	255
Apolipoprotein A-I, isoform CRA_a	111	98
Arginase-1	192	159
ATP synthase subunit alpha	57	89
ATP-dependent RNA helicase DDX3X	106	198
Beta 5-tubulin	146	164
Beta actin variant (Fragment)	36	18
Biglycan preproprotein variant (Fragment)	117	224
Brain specific protein, isoform CRA_a	111	214
Calmodulin-like skin protein variant (Fragment)	155	266
Calnexin	157	367
Carbonyl reductase [NADPH] 1	57	60
Caspase 14, apoptosis-related cysteine peptidase	103	90
Catenin alpha-1	144	307
Cathepsin D (Lysosomal aspartyl peptidase), isoform CRA_a	198	153
Caveolin	180	145
cDNA FLJ37398 fis, clone BRAMY2027467, highly similar to Tubulin alpha-ubiquitous chain	34	240
cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U	201	260
cDNA FLJ75422, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1, mRNA	182	200
cDNA FLJ78244, highly similar to Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA	235	238
cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA	271	67
cDNA FLJ78674, highly similar to Homo sapiens desmocollin type 4	44	91
cDNA, FLJ94198, highly similar to Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), mRNA	302	231
cDNA, FLJ94268, highly similar to Homo sapiens histone 1, H1e (HIST1H1E), mRNA	48	88
cDNA, FLJ94551	154	351
cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA	115	130
Chaperonin containing TCP1, subunit 2 (Beta), isoform CRA_b	371	275
Chloride intracellular channel protein	337	167
Chromosome 7 open reading frame 24	278	107
Clathrin heavy chain	220	147
Cofilin 1 (Non-muscle), isoform CRA_b	179	132
Collagen alpha-1(I) chain	11	9
Core histone macro-H2A.1	174	331
Cytoplasmic dynein 1 heavy chain 1	94	162
DCN protein	29	42
Desmocollin 1	69	69

Name	Relative abundance (N; 0 dp)	
	Buttock	Forearm
<i>(ordered according to buttock most abundant)</i>		
Desmoplakin	1	2
Keratin 1	2	6
Filaggrin	8	1
Neuroblast differentiation-associated protein AHNAK	9	18
Collagen alpha-1(I) chain	11	9
Serum albumin	12	15
Vimentin	14	14
Epiplakin	15	17
Junction plakoglobin, isoform CRA_a	15	18
Plectin	18	24
Periostin, osteoblast specific factor, isoform CRA_c	19	25
Alpha-actinin-4	19	54
Prelamin-A/C	21	24
Desmoglein-1	27	26
DCN protein	29	42
Plakophilin 1 (Ectodermal dysplasia/skin fragility syndrome), isoform CRA_a	32	25
cDNA FLJ37398 fis, clone BRAMY2027467, highly similar to Tubulin alpha-ubiquitous chain	34	240
Ezrin	35	35
Beta actin variant (Fragment)	36	18
Pyruvate kinase	36	72
Gelsolin	39	45
HCG1991735, isoform CRA_a	41	186
cDNA FLJ78674, highly similar to Homo sapiens desmocollin type 4	44	91
cDNA, FLJ94268, highly similar to Homo sapiens histone 1, H1e (HIST1H1E), mRNA	48	88
14-3-3 protein sigma	52	39
Lumican	54	55
ATP synthase subunit alpha	57	89
Carbonyl reductase [NADPH] 1	57	60
Nucleolin, isoform CRA_b	58	70
PRELP protein (Fragment)	58	74
Transferrin variant (Fragment)	60	60
High-mobility group box 1, isoform CRA_a	69	120
Desmocollin 1	69	69
L-lactate dehydrogenase	76	62
Elongation factor 1-alpha	76	54
Fructose-bisphosphate aldolase	76	53
Glyceraldehyde-3-phosphate dehydrogenase	76	27
Envoplakin	77	176
Peroxiredoxin-1	80	99
Suprabasin	86	180
Serpin peptidase inhibitor, clade B (Ovalbumin), member 5, isoform CRA_b	91	87
Heat shock protein 90kDa alpha (Cytosolic), class B member 1, isoform CRA_a	91	150
Cytoplasmic dynein 1 heavy chain 1	94	162
Hemoglobin, beta	99	69
Profilin-1	102	100
Peroxidoxin 6	103	98
Caspase 14, apoptosis-related cysteine peptidase	103	90
Alpha-2 globin chain	105	404

Figure 3.



Supp. table 1.

Name	Relative abundance (N; 0 dp)	
	Buttock	Forearm
<i>(alphabetical)</i>		
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14-3-3 protein sigma	52	39
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60S ribosomal protein L10a	242	164
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Amyloid P component, serum	255	96
Annexin (Fragment)	141	13
APEX nuclease	189	255
Apolipoprotein A-I, isoform CRA_a	111	98
Arginase-1	192	159
ATP synthase subunit alpha	57	89
ATP-dependent RNA helicase DDX3X	106	198
Beta 5-tubulin	146	164
Beta actin variant (Fragment)	36	18
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<i>(ordered according to buttock most abundant)</i>		
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Keratin 1	2	6
Filaggrin	8	1
Neuroblast differentiation-associated protein AHNAK	9	18
Collagen alpha-1(I) chain	11	9
Serum albumin	12	15
Vimentin	14	14
Epiplakin	15	17
Junction plakoglobin, isoform CRA_a	15	18
Plectin	18	24
Periostin, osteoblast specific factor, isoform CRA_c	19	25
Alpha-actinin-4	19	54
Prelamin-A/C	21	24
Desmoglein-1	27	26
DCN protein	29	42
Plakophilin 1 (Ectodermal dysplasia/skin fragility syndrome), isoform CRA_a	32	25
cDNA FLJ37398 fis, clone BRAMY2027467, highly similar to Tubulin alpha-ubiquitous chain	34	240
Ezrin	35	35
Beta actin variant (Fragment)	36	18
Pyruvate kinase	36	72
Gelsolin	39	45
HCG1991735, isoform CRA_a	41	186
cDNA FLJ78674, highly similar to Homo sapiens desmocollin type 4	44	91
cDNA, FLJ94268, highly similar to Homo sapiens histone 1, H1e (HIST1H1E), mRNA	48	88
14-3-3 protein sigma	52	39
Lumican	54	55
ATP synthase subunit alpha	57	89
Carbonyl reductase [NADPH] 1	57	60
Nucleolin, isoform CRA_b	58	70
PRELP protein (Fragment)	58	74
Transferrin variant (Fragment)	60	60
High-mobility group box 1, isoform CRA_a	69	120
Desmocollin 1	69	69
L-lactate dehydrogenase	76	62
Elongation factor 1-alpha	76	54
Fructose-bisphosphate aldolase	76	53
Glyceraldehyde-3-phosphate dehydrogenase	76	27
Envoplakin	77	176
Peroxiredoxin-1	80	99
Suprabasin	86	180
Serpin peptidase inhibitor, clade B (Ovalbumin), member 5, isoform CRA_b	91	87
Heat shock protein 90kDa alpha (Cytosolic), class B member 1, isoform CRA_a	91	150
Cytoplasmic dynein 1 heavy chain 1	94	162
Hemoglobin, beta	99	69
Profilin-1	102	100
Peroxidoxin 6	103	98
Caspase 14, apoptosis-related cysteine peptidase	103	90
Alpha-2 globin chain	105	404

Supp. table 1 continued1.

Desmoglein-1	27	26
Desmoplakin	1	2
Dopamine receptor interacting protein 4	272	155
Elongation factor 1-alpha	76	54
Enolase 1, (Alpha), isoform CRA_a	153	28
Envoplakin	77	176
Epiplakin	15	17
Extracellular superoxide dismutase [Cu-Zn]	283	195
Ezrin	35	35
Filaggrin	8	1
Filamin A	292	154
Fructose-bisphosphate aldolase	76	53
Galectin	155	155
Gasdermin-A	200	244
Gelsolin	39	45
Glucose-6-phosphate isomerase (Fragment)	247	205
Glutathione S-transferase mu 1 isoform B (Fragment)	150	295
Glyceraldehyde-3-phosphate dehydrogenase	76	27
GTP-binding nuclear protein Ran	133	165
H.sapiens ras-related Hrab6 protein	190	325
HCG1991735, isoform CRA_a	41	186
Heat shock protein 90kDa alpha (Cytosolic), class B member 1, isoform CRA_a	91	150
Hemoglobin, beta	99	69
Heparin-binding protein HBp15	165	255
Heterochromatin protein 1-binding protein 3	205	242
Heterogeneous nuclear ribonucleoprotein A1	146	133
Hexokinase	189	142
High-mobility group box 1, isoform CRA_a	69	120
Histone H1.0	264	215
HNRPK protein	140	203
Insulin-degrading enzyme	415	275
Integrin alpha-6	165	368
Junction plakoglobin, isoform CRA_a	15	18
Keratin 1	2	6
L-lactate dehydrogenase	76	62
Lumican	54	55
Malate dehydrogenase	173	117
Mast cell tryptase beta III	162	284
MHC class I antigen (Fragment)	123	196
Mitochondrial heat shock 60kD protein 1 variant 1	225	245
Myosin light polypeptide 6	125	149
NADH-cytochrome b5 reductase 1	146	232
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	226	179
Neuroblast differentiation-associated protein AHNAK	9	18
Nucleolin, isoform CRA_b	58	70
Nucleoside diphosphate kinase	172	134
Osteoglycin OG	355	162
Peptidyl-prolyl cis-trans isomerase B	181	64
Periostin, osteoblast specific factor, isoform CRA_c	19	25
Periplakin	287	114

Zinc-alpha-2-glycoprotein	105	125
Triosephosphate isomerase	106	58
ATP-dependent RNA helicase DDX3X	106	198
Apolipoprotein A-I, isoform CRA_a	111	98
Brain specific protein, isoform CRA_a	111	214
Phosphoglycerate mutase 1 (Brain)	111	237
cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA	115	130
Biglycan preproprotein variant (Fragment)	117	224
Protein AHNAK2	121	211
MHC class I antigen (Fragment)	123	196
Myosin light polypeptide 6	125	149
Ribosomal protein L11, isoform CRA_b	125	243
Ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing), isoform CRA_a	126	68
GTP-binding nuclear protein Ran	133	165
Prohibitin-2	139	127
HNRPK protein	140	203
Annexin (Fragment)	141	13
Tripartite motif protein TRIM29 isoform alpha variant (Fragment)	144	106
Catenin alpha-1	144	307
Spectrin alpha chain, non-erythrocytic 1	144	184
NADH-cytochrome b5 reductase 1	146	232
Beta 5-tubulin	146	164
Heterogeneous nuclear ribonucleoprotein A1	146	133
Phosphoglycerate kinase	149	63
Glutathione S-transferase mu 1 isoform B (Fragment)	150	295
Enolase 1, (Alpha), isoform CRA_a	153	28
cDNA, FLJ94551	154	351
Calmodulin-like skin protein variant (Fragment)	155	266
Galectin	155	155
Calnexin	157	367
Protein disulfide-isomerase	161	141
Mast cell tryptase beta III	162	284
Actin-related protein 2/3 complex subunit 3	165	140
Heparin-binding protein HBp15	165	255
Integrin alpha-6	165	368
Adenine phosphoribosyltransferase (Fragment)	166	164
Nucleoside diphosphate kinase	172	134
Malate dehydrogenase	173	117
Transforming growth factor, beta-induced, 68kDa variant (Fragment)	173	198
Core histone macro-H2A.1	174	331
Protein IGKV3-11	178	211
Cofilin 1 (Non-muscle), isoform CRA_b	179	132
Caveolin	180	145
Polypyrimidine tract binding protein 1, isoform CRA_b	180	192
Peptidyl-prolyl cis-trans isomerase B	181	64
cDNA FLJ75422, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1, mRNA	182	200
APEX nuclease	189	255
Hexokinase	189	142
H.sapiens ras-related Hrab6 protein	190	325
Transketolase	191	224

Supp. table 1 continued 2.

Peroxi-doxin 6	103	98
Peroxi-redoxin-1	80	99
Phosphoglycerate kinase	149	63
Phosphoglycerate mutase 1 (Brain)	111	237
Plakophilin 1 (Ectodermal dysplasia/skin fragility syndrome), isoform CRA_a	32	25
Plectin	18	24
PMVK protein (Fragment)	240	235
Polypyrimidine tract binding protein 1, isoform CRA_b	180	192
Prelamin-A/C	21	24
PRELP protein (Fragment)	58	74
Profilin-1	102	100
Prohibitin-2	139	127
Proteasome subunit alpha type (Fragment)	203	180
Protein AHNAK2	121	211
Protein disulfide-isomerase	161	141
Protein IGKV3-11	178	211
PSME1 protein (Fragment)	347	256
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	245	184
Pyruvate kinase	36	72
RAB14, member RAS oncogene family, isoform CRA_a	240	213
Ribosomal protein L11, isoform CRA_b	125	243
Serpin peptidase inhibitor, clade B (Ovalbumin), member 5, isoform CRA_b	91	87
Serum albumin	12	15
SFPQ protein (Fragment)	218	218
SLC25A5 protein (Fragment)	236	92
Spectrin alpha chain, non-erythrocytic 1	144	184
Superoxide dismutase [Cu-Zn]	309	234
Suprabasin	86	180
Tenascin	310	155
Transaldolase	212	180
Transferrin variant (Fragment)	60	60
Transforming growth factor, beta-induced, 68kDa variant (Fragment)	173	198
Transketolase	191	224
Triosephosphate isomerase	106	58
Tripartite motif protein TRIM29 isoform alpha variant (Fragment)	144	106
Tubulin alpha-4A chain	223	202
Ubiquitin carboxyl-terminal hydrolase 5	297	357
Ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing), isoform CRA_a	126	68
Vimentin	14	14
Voltage-dependent anion-selective channel protein 1	281	200
Zinc-alpha-2-glycoprotein	105	125

Arginase-1	192	159
Cathepsin D (Lysosomal aspartyl peptidase), isoform CRA_a	198	153
Gasdermin-A	200	244
cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heterogeneous nuclear ribonucleoprotein U	201	260
Proteasome subunit alpha type (Fragment)	203	180
Heterochromatin protein 1-binding protein 3	205	242
Transaldolase	212	180
SFPQ protein (Fragment)	218	218
Clathrin heavy chain	220	147
Tubulin alpha-4A chain	223	202
Mitochondrial heat shock 60kD protein 1 variant 1	225	245
Nascent polypeptide-associated complex subunit alpha, muscle-specific form	226	179
Adenylate kinase 2, mitochondrial	235	231
cDNA FLJ78244, highly similar to Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA	235	238
SLC25A5 protein (Fragment)	236	92
RAB14, member RAS oncogene family, isoform CRA_a	240	213
PMVK protein (Fragment)	240	235
60S ribosomal protein L10a	242	164
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	245	184
Glucose-6-phosphate isomerase (Fragment)	247	205
Amyloid P component, serum	255	96
14-3-3 beta/alpha	259	183
Histone H1.0	264	215
40S ribosomal protein S11	268	147
cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA	271	67
Dopamine receptor interacting protein 4	272	155
Chromosome 7 open reading frame 24	278	107
Voltage-dependent anion-selective channel protein 1	281	200
Extracellular superoxide dismutase [Cu-Zn]	283	195
Periplakin	287	114
Alcohol dehydrogenase IB (Class I), beta polypeptide, isoform CRA_a	288	288
Filamin A	292	154
Ubiquitin carboxyl-terminal hydrolase 5	297	357
cDNA, FLJ94198, highly similar to Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), mRNA	302	231
Superoxide dismutase [Cu-Zn]	309	234
Tenascin	310	155
Chloride intracellular channel protein	337	167
PSME1 protein (Fragment)	347	256
Osteoglycin OG	355	162
Chaperonin containing TCP1, subunit 2 (Beta), isoform CRA_b	371	275
Insulin-degrading enzyme	415	275

Supp. table 2.

Identified Proteins (377)	Accession Number	Fold change	T-Test (p-Value)
10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	CH10_HUMAN	0.5	0.23
14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	1433B_HUMAN	0.7	0.6
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	1433E_HUMAN	0.5	0.26
14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	1433S_HUMAN	0.5	0.082
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	1433Z_HUMAN	0.4	0.057
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	PSMD2_HUMAN	1.4	0.55
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	RS11_HUMAN	0.5	0.26
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	RS12_HUMAN	0.5	0.11
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	RS14_HUMAN	0.7	0.51
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	RS16_HUMAN	0.3	0.074
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	RS18_HUMAN	0.5	0.019
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	RS19_HUMAN	0.7	0.18
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	RS2_HUMAN	0.7	0.41
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	RS20_HUMAN	0.7	0.36
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	RS23_HUMAN	0.4	0.23
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	RS25_HUMAN	0.7	0.27
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	RS28_HUMAN	0.5	0.44
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	RS3_HUMAN	0.2	0.021
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	RS3A_HUMAN	0.5	0.3
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	RS4X_HUMAN	0.2	0.057
40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4	RS5_HUMAN	0.4	0.31
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	RS6_HUMAN	0.5	0.22
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	RS7_HUMAN	0.4	0.037
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	RS8_HUMAN	1.5	0.79
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	RS9_HUMAN	0.5	0.13
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	RSSA_HUMAN	0.4	0.59
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	CH60_HUMAN	0.6	0.42
60S acidic ribosomal protein P0-like OS=Homo sapiens GN=RPLP0P6 PE=5 SV=1	RLA0L_HUMAN	0.9	0.85
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	RL10A_HUMAN	0.5	0.2
60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	RL11_HUMAN	0.6	0.47
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	RL13_HUMAN	0.4	0.16
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	RL17_HUMAN	0.4	0.21
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	RL18_HUMAN	0.7	0.26
60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	RL19_HUMAN	0.3	0.07
60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	RL21_HUMAN	0.4	0.14
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	RL22_HUMAN	0.5	0.16
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	RL23_HUMAN	3.2	0.29
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	RL23A_HUMAN	0.5	0.063
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	RL24_HUMAN	0.6	0.11
60S ribosomal protein L26-like 1 OS=Homo sapiens GN=RPL26L1 PE=1 SV=1	RL26L_HUMAN	0.6	0.11
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	RL27_HUMAN	0.5	0.053
60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	RL27A_HUMAN	0.9	0.86
60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	RL29_HUMAN	0.8	0.67
60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	RL3_HUMAN	<0.001	0.29
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	RL31_HUMAN	0.6	0.3
60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	RL34_HUMAN	1	0.97
60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	RL36_HUMAN	2	0.47
60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	RL5_HUMAN	1.4	0.47
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	RL6_HUMAN	1.1	0.74
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	RL7_HUMAN	0.4	0.38
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	RL7A_HUMAN	0.2	0.0033
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	RL8_HUMAN	0.7	0.53
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	RL9_HUMAN	1.1	0.79
6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2	6PGL_HUMAN	<0.001	0.13
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GRP78_HUMAN	1.1	0.81
Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	ACON_HUMAN	20	0.11
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	ACTB_HUMAN	1.1	0.88
Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	ARP2_HUMAN	1.1	0.94
Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2	ARC1A_HUMAN	0.4	0.59
Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	ARPC3_HUMAN	0.5	0.28
Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3	ARPC4_HUMAN	0.5	0.053
Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	APT_HUMAN	0.3	0.048
Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2	KAD2_HUMAN	0.5	0.52
Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	KAD1_HUMAN	0.4	0.22

Supp. table 2 continued 1.

Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5	CAP1_HUMAN	1.1	0.87
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	ADT2_HUMAN	0.2	0.017
ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	ARF1_HUMAN	<0.001	0.29
ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2	ARF5_HUMAN	1.3	0.76
Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	AK1A1_HUMAN	1.2	0.67
Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3	AL3A1_HUMAN	0.7	0.52
Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2	ALDH2_HUMAN	0.6	0.32
Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1	AK1C1_HUMAN	0.5	0.24
Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	A1AG1_HUMAN	0.4	0.59
Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	A1AT_HUMAN	1.4	0.3
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	A2MG_HUMAN	1.7	0.53
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	ACTN4_HUMAN	0.8	0.61
Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2	CRYAB_HUMAN	<0.001	0.13
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	ENOA_HUMAN	0.8	0.78
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	ANXA1_HUMAN	1.1	0.87
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	ANXA2_HUMAN	0.8	0.47
Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4	ANXA4_HUMAN	0.7	0.38
Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	ANXA5_HUMAN	0.9	0.88
Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	ANXA6_HUMAN	16	0.29
Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	ANT3_HUMAN	16	0.097
Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	APOA1_HUMAN	0.5	0.26
Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	APOA2_HUMAN	<0.001	0.11
Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	APOB_HUMAN	2.6	0.5
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	APOE_HUMAN	1.3	0.7
Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	ARG1_HUMAN	0.7	0.58
Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	AATM_HUMAN	1	0.97
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	ATPA_HUMAN	0.7	0.29
ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	ATPB_HUMAN	0.5	0.16
ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	ATP5H_HUMAN	<0.001	0.12
ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	ATPO_HUMAN	0.5	0.14
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	DDX3X_HUMAN	1.3	0.78
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	PGBM_HUMAN	0.9	0.83
B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3	BAP31_HUMAN	0.4	0.18
Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2	PGS1_HUMAN	1.5	0.26
Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	CALM_HUMAN	0.7	0.6
Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2	CALL3_HUMAN	0.7	0.75
Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	CALL5_HUMAN	0.5	0.077
Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	CALX_HUMAN	1.1	0.87
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	CAN1_HUMAN	2.5	0.26
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	CBR1_HUMAN	1	0.96
Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	CASPE_HUMAN	0.6	0.093
Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	CATA_HUMAN	8	0.41
Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	CTNA1_HUMAN	0.7	0.083
Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1	CTNB1_HUMAN	0.6	0.19
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	CTND1_HUMAN	0.8	0.5
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	CATD_HUMAN	0.3	0.012
Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	CATG_HUMAN	1.6	0.56
Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4	CAV1_HUMAN	0.5	0.54
Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	CERU_HUMAN	1.6	0.42
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	CLIC1_HUMAN	0.6	0.38
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	CLH1_HUMAN	1.1	0.8
Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	F13A_HUMAN	5.7	0.0042
Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	COF1_HUMAN	0.4	0.16
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	CO1A1_HUMAN	1.3	0.081
Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	CO3A1_HUMAN	0.9	0.82
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	CO6A1_HUMAN	1.2	0.43
Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2	CO7A1_HUMAN	1	0.89
Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3	COEA1_HUMAN	0.3	0.2
Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	CO1A2_HUMAN	1.1	0.65
Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	CO6A2_HUMAN	1.2	0.11
Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	CO6A3_HUMAN	1.5	0.0001
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	CO3_HUMAN	11	0.081
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	CO4A_HUMAN	3.8	0.093
Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	H2AY_HUMAN	0.7	0.19
Cystatin-M OS=Homo sapiens GN=CST6 PE=1 SV=1	CYTM_HUMAN	0.4	0.31

Supp. table 2 continued 2.

Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	DYHC1_HUMAN	0.9	0.74
D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	SERA_HUMAN	0.8	0.56
Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	PGS2_HUMAN	1.2	0.42
Desmin OS=Homo sapiens GN=DES PE=1 SV=3	DESM_HUMAN	96	0.11
Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	DSC1_HUMAN	1	0.96
Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3	DSC3_HUMAN	1	0.78
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	DSG1_HUMAN	1.2	0.36
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	DESP_HUMAN	1	0.72
DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2	APEX1_HUMAN	0.8	0.79
ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2	ELAV1_HUMAN	0.4	0.35
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	EF1A1_HUMAN	0.5	0.34
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	EF1D_HUMAN	0.9	0.85
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	EF1G_HUMAN	<0.001	0.29
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	EF2_HUMAN	1.3	0.42
Endoplasmic reticulum protein OS=Homo sapiens GN=ENPL PE=1 SV=1	ENPL_HUMAN	1.1	0.74
Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3	EVPL_HUMAN	0.7	0.11
Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	EPIPL_HUMAN	1.3	0.45
Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	STOM_HUMAN	8	0.41
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	IF4A1_HUMAN	<0.001	0.12
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	EIF3B_HUMAN	1.2	0.8
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	EIF3L_HUMAN	8	0.41
Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2	IF4B_HUMAN	0.4	0.56
Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	IF5A1_HUMAN	0.8	0.64
Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2	SODE_HUMAN	0.8	0.74
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	EZRI_HUMAN	1.1	0.63
F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	CAZA1_HUMAN	0.7	0.53
Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	FUBP2_HUMAN	0.4	0.43
Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	FIBA_HUMAN	3	0.03
Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	FILA_HUMAN	0.9	0.32
Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	FILA2_HUMAN	1	0.99
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	FLNA_HUMAN	4	0.016
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	FLNB_HUMAN	2.1	0.075
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	ALDOA_HUMAN	0.9	0.85
Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	ALDOC_HUMAN	0.4	0.24
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	LEG1_HUMAN	0.8	0.74
Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	LEG3_HUMAN	0.4	0.17
Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	LEG7_HUMAN	0.9	0.86
Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1	GGCT_HUMAN	0.3	0.12
Gasdermin-A OS=Homo sapiens GN=GSDMA PE=2 SV=4	GSDMA_HUMAN	0.7	0.52
GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1	FCL_HUMAN	0.3	0.3
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	GELS_HUMAN	1.4	0.2
Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	G6PI_HUMAN	1	0.96
Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	GSTO1_HUMAN	0.6	0.47
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	G3P_HUMAN	0.5	0.19
Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1	GLOD4_HUMAN	1	0.98
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	RAN_HUMAN	0.3	0.045
Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2	GNAI1_HUMAN	<0.001	0.29
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	GNAI2_HUMAN	4.1	0.21
Guanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2	GNA13_HUMAN	<0.001	0.09
Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	GBLP_HUMAN	0.4	0.22
Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2	HPTR_HUMAN	1.4	0.75
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	HSP71_HUMAN	1	0.91
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	HSP7C_HUMAN	1.5	0.31
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	HSPB1_HUMAN	0.5	0.041
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	HS90A_HUMAN	1.4	0.39
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	HS90B_HUMAN	1.2	0.61
Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	HBA_HUMAN	0.4	0.016
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	HBB_HUMAN	0.4	0.05
Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	HEMO_HUMAN	1.7	0.2
Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	HDGF_HUMAN	12	0.24
Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	HP1B3_HUMAN	0.8	0.36
Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5	ROA1_HUMAN	0.7	0.39
Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	ROA3_HUMAN	0.9	0.92
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	HNRPK_HUMAN	1.3	0.5
Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	HNRPQ_HUMAN	0.2	0.2

Supp. table 2 continued 3.

Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	HNRPU_HUMAN	1.2	0.43
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	ROA2_HUMAN	0.8	0.49
Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4	HNRPC_HUMAN	0.6	0.4
Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3	HXK1_HUMAN	0.8	0.8
High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	HMGB1_HUMAN	0.4	0.056
Histone H1.0 OS=Homo sapiens GN=H1FO PE=1 SV=3	H10_HUMAN	1.1	0.74
Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	H12_HUMAN (+2)	1.5	0.0072
Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	H15_HUMAN	1.2	0.8
Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	H2A1B_HUMAN	0.7	0.67
Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3	H2AV_HUMAN	0.6	0.46
Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	H2B1B_HUMAN	0.8	0.39
Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4	H2B1C_HUMAN	0.9	0.46
Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3	H31T_HUMAN	0.6	0.28
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	H4_HUMAN	0.7	0.33
HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1	1A02_HUMAN	0.6	0.53
HLA class I histocompatibility antigen, B-7 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=3	1B07_HUMAN	0.3	0.47
Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	IGHA1_HUMAN	1.1	0.84
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	IGHG1_HUMAN	0.7	0.3
Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	IGHM_HUMAN	2	0.63
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	IMB1_HUMAN	4.7	0.17
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	IPYR_HUMAN	0.2	0.11
Inositol monophosphatase 2 OS=Homo sapiens GN=IMPA2 PE=1 SV=1	IMPA2_HUMAN	<0.001	0.022
Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	IDE_HUMAN	0.8	0.8
Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5	ITB4_HUMAN	0.9	0.76
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	ILF3_HUMAN	0.8	0.7
Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1	IL18_HUMAN	0.8	0.61
Involucrin OS=Homo sapiens GN=IVL PE=1 SV=2	INVO_HUMAN	12	0.41
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	PLAK_HUMAN	1.2	0.38
Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	K1H1_HUMAN	0.2	0.29
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	K1C10_HUMAN	0.9	0.33
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	K1C14_HUMAN	0.8	0.18
Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	K1C15_HUMAN	0.5	0.11
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	K1C9_HUMAN	1.5	0.57
Keratin, type II cuticular Hb1 OS=Homo sapiens GN=KRT81 PE=1 SV=3	KRT81_HUMAN	<0.001	0.29
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	K2C1_HUMAN	1	0.57
Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3	K2C1B_HUMAN	1.3	0.59
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	K22E_HUMAN	1.1	0.35
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	1	0.55
Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	K2C6A_HUMAN	648	0.01
Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=1 SV=2	K2C78_HUMAN	1.4	0.42
Lactoylglycyl-L-glutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	LGUL_HUMAN	0.8	0.55
LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1	LANC1_HUMAN	0.6	0.31
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	LDHA_HUMAN	0.7	0.3
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	LDHB_HUMAN	12	0.22
Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	LUM_HUMAN	1.3	0.17
Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2	CAPG_HUMAN	1.1	0.9
Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	MDHM_HUMAN	0.9	0.88
Mast cell carboxypeptidase A OS=Homo sapiens GN=CPA3 PE=1 SV=2	CBPA3_HUMAN	2.4	0.11
Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1	PGRC2_HUMAN	<0.001	0.09
Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1	MIME_HUMAN	1	0.98
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	MOES_HUMAN	1.5	0.59
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	MYL6_HUMAN	0.7	0.29
Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	ML12A_HUMAN	0.5	0.3
Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	MYH11_HUMAN	12	0.41
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	MYH9_HUMAN	1.2	0.34
Myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	MYO1C_HUMAN	0.4	0.34
NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1	NB5R1_HUMAN	0.2	0.0096
NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	NB5R3_HUMAN	0.8	0.62
Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1	NACAM_HUMAN	<0.001	0.09
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	AHNAK_HUMAN	1.3	0.4
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	NUCL_HUMAN	1.2	0.36
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	NPM_HUMAN	0.8	0.63
Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	NDKB_HUMAN	0.5	0.14
Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2	PTMS_HUMAN	1	0.94
PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	PDLI1_HUMAN	0.6	0.38

Supp. table 2 continued 4.

Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	PPIA_HUMAN	0.5	0.096
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	PPIB_HUMAN	0.6	0.23
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2	FKBP1A_HUMAN	0.4	0.25
Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	POSTN_HUMAN	1.2	0.35
Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4	PEPL_HUMAN	1.1	0.91
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	PRDX1_HUMAN	0.3	0.0073
Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	PRDX2_HUMAN	0.7	0.25
Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	PRDX5_HUMAN	0.7	0.22
Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	PRDX6_HUMAN	0.5	0.22
Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	PEBP1_HUMAN	0.6	0.53
Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	PGM1_HUMAN	2.3	0.65
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	PGK1_HUMAN	0.5	0.4
Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	PGAM1_HUMAN	0.2	0.0069
Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	PKP1_HUMAN	0.8	0.029
Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	PKP3_HUMAN	0.8	0.23
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	PAIRB_HUMAN	0.7	0.39
Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2	PLSI_HUMAN	0.9	0.88
Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6	PLSL_HUMAN	28	0.27
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	PLEC_HUMAN	1.3	0.22
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	PCBP1_HUMAN	0.6	0.36
Polypprimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	PTBP1_HUMAN	0.7	0.32
Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	UBB_HUMAN	2.2	0.53
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	LMNA_HUMAN	1.4	0.18
Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	PROF1_HUMAN	0.3	0.0023
Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	PDC6I_HUMAN	1.1	0.78
Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	PHB_HUMAN	0.2	0.052
Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2	PHB2_HUMAN	0.7	0.48
Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	PRELP_HUMAN	1.3	0.084
Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	PSA1_HUMAN	0.2	0.024
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	PSA4_HUMAN	0.6	0.41
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	PSA5_HUMAN	0.5	0.49
Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	PSA6_HUMAN	0.6	0.46
Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	PSA7L_HUMAN	<0.001	0.021
Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	PSB5_HUMAN	0.4	0.49
Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	PSB6_HUMAN	0.8	0.54
Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2	AHNK2_HUMAN	1	0.94
Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	PDIA3_HUMAN	1.3	0.39
Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	PDIA1_HUMAN	<0.001	0.29
Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	PARK7_HUMAN	0.3	0.014
Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=2	POF1B_HUMAN	1.4	0.62
Protein S100-A16 OS=Homo sapiens GN=S100A16 PE=1 SV=1	S10AG_HUMAN	0.8	0.76
Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	S10A4_HUMAN	0.5	0.52
Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2	SC61B_HUMAN	0.6	0.086
Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	TGM3_HUMAN	1.6	0.52
Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	PSA_HUMAN	3.4	0.17
Putative 40S ribosomal protein S10-like OS=Homo sapiens GN=RPS10P5 PE=5 SV=1	RS10L_HUMAN	0.8	0.66
Putative 40S ribosomal protein S26-like 1 OS=Homo sapiens GN=RPS26P11 PE=5 SV=1	RS26L_HUMAN	1.1	0.9
Putative 60S ribosomal protein L13a protein RPL13AP3 OS=Homo sapiens GN=RPL13AP3 PE=5 SV=1	R13P3_HUMAN	0.3	0.11
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3	ODPB_HUMAN	0.8	0.74
Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	KPYM_HUMAN	1.4	0.17
Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	QOR_HUMAN	1.6	0.37
Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	GDIA_HUMAN	0.4	0.56
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	IQGA1_HUMAN	0.8	0.11
Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	RAC1_HUMAN	0.3	0.048
Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	RAB10_HUMAN	2.5	0.33
Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3	RB11A_HUMAN	0.8	0.57
Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	RAB14_HUMAN	0.5	0.076
Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	RAB1A_HUMAN	0.7	0.79
Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	RAB1B_HUMAN	0.6	0.51
Ras-related protein Rab-25 OS=Homo sapiens GN=RAB25 PE=1 SV=2	RAB25_HUMAN	0.3	0.16
Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	RAB5C_HUMAN	0.3	0.14
Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	RAB6A_HUMAN	0.3	0.11
Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	RAB7A_HUMAN	1.7	0.28
RelA-associated inhibitor OS=Homo sapiens GN=PPP1R13L PE=1 SV=4	IASPP_HUMAN	4.5	0.42
Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=3	GDIR1_HUMAN	0.3	0.1

Supp. table 2 continued 5.

rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2	FBRL_HUMAN	2	0.39
Sciellin OS=Homo sapiens GN=SCEL PE=1 SV=2	SCEL_HUMAN	<0.001	0.29
Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	SEPT2_HUMAN	<0.001	0.29
Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	SRSF1_HUMAN	1.5	0.79
Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	TRFE_HUMAN	2.2	0.05
Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	SPB12_HUMAN	0.5	0.52
Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2	SPB5_HUMAN	0.4	0.14
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	ALBU_HUMAN	1.4	0.0054
Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	SAMP_HUMAN	2.4	0.27
Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	STAT1_HUMAN	20	0.41
Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1	SMD3_HUMAN	0.7	0.23
Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	SPTN1_HUMAN	1.3	0.26
Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=1	SBSN_HUMAN	0.8	0.61
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	VAT1_HUMAN	<0.001	0.29
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	TLN1_HUMAN	16	0.11
Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3	TENA_HUMAN	6.1	0.2
Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=3	TENX_HUMAN	1.4	0.44
Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2	TYPH_HUMAN	12	0.27
Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	TALDO_HUMAN	1	0.9
Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFB1 PE=1 SV=1	BGH3_HUMAN	1.7	0.078
Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	RHOA_HUMAN	1.2	0.64
Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4	TAGL_HUMAN	8	0.41
Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	TAGL2_HUMAN	0.6	0.2
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	TERA_HUMAN	1.3	0.35
Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	TKT_HUMAN	0.9	0.81
Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1 SV=1	TM109_HUMAN	1	0.95
Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	TMM43_HUMAN	0.8	0.86
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	ECHA_HUMAN	1.5	0.55
Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2	TPIS_HUMAN	0.5	0.23
Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2	TRI29_HUMAN	1.1	0.71
Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	TPM1_HUMAN	32	0.21
Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1	TPM3_HUMAN	<0.001	0.09
Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	TPM4_HUMAN	1.1	0.86
Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	TPM2_HUMAN	6.9	0.48
Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1	TRYB1_HUMAN	2.8	0.14
Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	TBA1A_HUMAN	1.1	0.66
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	TBA4A_HUMAN	0.8	0.68
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	TBB5_HUMAN	0.8	0.44
Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	TBB2B_HUMAN	0.9	0.88
Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	TBB4A_HUMAN	0.8	0.53
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	TBB4B_HUMAN	1	0.83
Tubulin polymerization-promoting protein family member 3 OS=Homo sapiens GN=TPPP3 PE=1 SV=1	TPPP3_HUMAN	0.5	0.092
Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	RS27A_HUMAN	0.4	0.18
Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	UBE2N_HUMAN	0.5	0.24
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	UBA1_HUMAN	1.4	0.37
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	VIME_HUMAN	1.4	0.065
Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	VINC_HUMAN	0.9	0.88
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	VDAC2_HUMAN	0.4	0.17
V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	VATA_HUMAN	0.9	0.89
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	XRCC5_HUMAN	1.7	0.13
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	XRCC6_HUMAN	2.3	0.17
Zinc finger protein 185 OS=Homo sapiens GN=ZNF185 PE=1 SV=3	ZN185_HUMAN	0.1	0.3
Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	ZA2G_HUMAN	0.7	0.53

Supp. table 3

Identified Proteins (547)	Accession Number	Fold change	T-Test (P-Value)
10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	CH10_HUMAN	2.9	0.21
14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	1433B_HUMAN	1.1	0.84
14-3-3 protein epsilon OS=Homo sapiens GN=YWHA E PE=1 SV=1	1433E_HUMAN	1.1	0.83
14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	1433F_HUMAN	1.7	0.52
14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	1433G_HUMAN	1.3	0.56
14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	1433S_HUMAN	1.1	0.81
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	1433T_HUMAN	1.1	0.79
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	1433Z_HUMAN	0.8	0.63
2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1	DECR_HUMAN	27	0.027
26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	PRS6A_HUMAN	0.6	0.053
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	PRS7_HUMAN	1.1	0.91
26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	PRS8_HUMAN	0.9	0.81
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	PSMD2_HUMAN	1.2	0.68
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	PSMD3_HUMAN	1.6	0.48
3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	HCD2_HUMAN	1.5	0.71
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	RS11_HUMAN	1.4	0.64
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	RS12_HUMAN	2.6	0.38
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	RS13_HUMAN	0.6	0.67
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	RS14_HUMAN	3.4	0.085
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	RS15A_HUMAN	1.6	0.57
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	RS16_HUMAN	1.7	0.51
40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1	RS17L_HUMAN	0.6	0.66
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	RS18_HUMAN	2.1	0.38
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	RS19_HUMAN	1	0.99
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	RS2_HUMAN	1	1
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	RS20_HUMAN	4.4	0.016
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	RS23_HUMAN	1.7	0.52
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	RS24_HUMAN	2.8	0.16
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	RS25_HUMAN	2.7	0.054
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	RS28_HUMAN	0.8	0.79
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	RS3_HUMAN	0.7	0.44
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	RS3A_HUMAN	0.5	0.27
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	RS4X_HUMAN	0.7	0.41
40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4	RS5_HUMAN	2	0.21
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	RS6_HUMAN	0.5	0.14
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	RS7_HUMAN	1.6	0.25
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	RS8_HUMAN	0.9	0.9
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	RS9_HUMAN	1.6	0.43
40S ribosomal protein S A OS=Homo sapiens GN=RPSA PE=1 SV=4	RSSA_HUMAN	0.7	0.3
4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	AL9A1_HUMAN	0.7	0.69
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	CH60_HUMAN	0.6	0.18
60S acidic ribosomal protein P0-like OS=Homo sapiens GN=RPLP0P6 PE=5 SV=1	RLA0L_HUMAN	0.9	0.7
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	RLA2_HUMAN	0.3	0.36
60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	RL10_HUMAN	0.2	0.22
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	RL10A_HUMAN	0.9	0.81
60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	RL11_HUMAN	1.5	0.32
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	RL13_HUMAN	0.3	0.48
60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	RL13A_HUMAN	0.5	0.41
60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	RL14_HUMAN	1.2	0.85
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	RL17_HUMAN	1.5	0.51
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	RL18_HUMAN	1.6	0.19
60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	RL18A_HUMAN	1.5	0.46
60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	RL19_HUMAN	1.3	0.74
60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	RL21_HUMAN	1.2	0.73
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	RL22_HUMAN	3	0.034
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	RL23_HUMAN	1.9	0.51
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	RL23A_HUMAN	1.6	0.38
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	RL24_HUMAN	1.5	0.39
60S ribosomal protein L26-like 1 OS=Homo sapiens GN=RPL26L1 PE=1 SV=1	RL26L_HUMAN	1.3	0.68
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	RL27_HUMAN	3.6	0.01
60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	RL28_HUMAN	1.4	0.54
60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	RL29_HUMAN	2.8	0.072
60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	RL3_HUMAN	0.8	0.64
60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	RL34_HUMAN	7.1	0.029

Supp. table 3 continued 1.

60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	RL35_HUMAN	2	0.44
60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	RL36_HUMAN	9.4	0.086
60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	RL4_HUMAN	0.9	0.84
60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	RL5_HUMAN	1.6	0.34
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	RL6_HUMAN	0.8	0.56
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	RL7_HUMAN	1.8	0.27
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	RL7A_HUMAN	0.7	0.65
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	RL8_HUMAN	4.3	0.051
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	RL9_HUMAN	0.8	0.71
6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	6PGD_HUMAN	<0.001	0.084
6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2	6PGL_HUMAN	0.5	0.36
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GRP78_HUMAN	0.9	0.64
Abhydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1	ABHEB_HUMAN	<0.001	0.39
Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=5	ASAH1_HUMAN	2.5	0.17
Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	ACON_HUMAN	1.3	0.45
Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	ACTC_HUMAN	2	0.15
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	ACTB_HUMAN	1	0.82
Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	ARPC3_HUMAN	1.5	0.46
Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3	ARPC4_HUMAN	1.9	0.28
Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	ARP3_HUMAN	0.8	0.78
Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	TCP4_HUMAN	1.2	0.91
Acyl-protein thioesterase 2 OS=Homo sapiens GN=LYPLA2 PE=1 SV=1	LYPA2_HUMAN	<0.001	0.39
Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	APT_HUMAN	1.1	0.84
Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	SAHH_HUMAN	1.2	0.81
Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	KAD1_HUMAN	1.3	0.74
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	ADT2_HUMAN	1.1	0.83
ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	ARF3_HUMAN	1.9	0.57
ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	ARF4_HUMAN	15	0.14
ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2	ARF5_HUMAN	4.3	0.12
ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1	ARL8B_HUMAN	2.2	0.15
Alcohol dehydrogenase [NADP+] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	AK1A1_HUMAN	1.9	0.16
Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2	ADH1A_HUMAN	15	0.00038
Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4	ADHX_HUMAN	6.7	0.08
Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3	AL3A1_HUMAN	0.9	0.87
Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2	ALDH2_HUMAN	0.6	0.52
Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1	AK1C1_HUMAN	1.2	0.68
Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1	AK1C1_HUMAN	0.8	0.86
Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	A1AG1_HUMAN	0.8	0.87
Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	A1AT_HUMAN	1.1	0.84
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	A2MG_HUMAN	14	0.071
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	ACTN4_HUMAN	0.9	0.8
Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2	CRYAB_HUMAN	1.9	0.36
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	ENOA_HUMAN	1	0.89
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	ANXA1_HUMAN	1.2	0.6
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	ANXA2_HUMAN	1.1	0.58
Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4	ANXA4_HUMAN	0.8	0.52
Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	ANXA5_HUMAN	1.6	0.089
Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	ANXA6_HUMAN	9	0.23
Annexin A8 OS=Homo sapiens GN=ANXA8 PE=1 SV=3	ANXA8_HUMAN	5.9	0.3
Annexin A8-like protein 2 OS=Homo sapiens GN=ANXA8L2 PE=2 SV=1	AXA82_HUMAN	0.8	0.8
AP-1 complex subunit sigma-1A OS=Homo sapiens GN=AP1S1 PE=1 SV=1	AP1S1_HUMAN	3	0.1
Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	APOA1_HUMAN	1.6	0.43
Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	APOA2_HUMAN	3.8	0.046
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	APOE_HUMAN	15	0.065
Apoptosis-associated speck-like protein containing a CARD OS=Homo sapiens GN=PYCARD PE=1 SV=2	ASC_HUMAN	0.7	0.62
Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	ARG1_HUMAN	2.3	0.0054
Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	ASSY_HUMAN	3.2	0.36
Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	AATM_HUMAN	1.8	0.56
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	ATPA_HUMAN	1.2	0.51
ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2	AT5F1_HUMAN	1.7	0.73
ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	ATPB_HUMAN	1.4	0.24
ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	ATP5H_HUMAN	0.2	0.32
ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2	ATP5I_HUMAN	0.2	0.47
ATP synthase subunit f, mitochondrial OS=Homo sapiens GN=ATP5J2 PE=1 SV=3	ATPK_HUMAN	3.1	0.23
ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3	ATP5L_HUMAN	5	0.28

Supp. table 3 continued 2.

ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	ATPG_HUMAN	0.05	0.078
ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	ATPO_HUMAN	1.1	0.93
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	DHX9_HUMAN	2.2	0.18
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	DDX3X_HUMAN	1.6	0.061
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	PGBM_HUMAN	3.3	0.11
B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3	BAP31_HUMAN	1.1	0.85
Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2	PGS1_HUMAN	2	0.36
Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	BLMH_HUMAN	1.4	0.25
C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3	C1TC_HUMAN	0.9	0.8
Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2	CALL3_HUMAN	15	0.29
Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	CALL5_HUMAN	3.2	0.27
Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	CALX_HUMAN	1.7	0.2
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	CAN1_HUMAN	0.9	0.86
Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4	ICAL_HUMAN	<0.001	0.39
Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	CAH1_HUMAN	1.4	0.77
Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	CAH2_HUMAN	1	0.95
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	CBR1_HUMAN	0.8	0.6
Carboxypeptidase A4 OS=Homo sapiens GN=CPA4 PE=1 SV=2	CBPA4_HUMAN	1.7	0.61
Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	CASPE_HUMAN	1.4	0.49
Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	CATA_HUMAN	1.2	0.83
Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	CTNA1_HUMAN	0.4	0.45
Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1	CTNB1_HUMAN	0.3	0.13
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	CTND1_HUMAN	0.6	0.46
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	CATD_HUMAN	1.2	0.67
Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	CATG_HUMAN	2	0.5
Cathepsin L2 OS=Homo sapiens GN=CTSL2 PE=1 SV=2	CATL2_HUMAN	14	0.33
Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4	CAV1_HUMAN	2.3	0.3
CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	CD44_HUMAN	5.5	0.13
Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	CDC42_HUMAN	1.8	0.31
Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	CERU_HUMAN	7	0.063
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	CLIC1_HUMAN	0.9	0.66
Chymase OS=Homo sapiens GN=CMA1 PE=1 SV=1	CMA1_HUMAN	6	0.3
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	CLH1_HUMAN	2.3	0.021
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	CLUS_HUMAN	12	0.0018
Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	F13A_HUMAN	2.7	0.0019
Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	COF1_HUMAN	1.5	0.55
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	CO1A1_HUMAN	2.8	0.027
Collagen alpha-1(II) chain OS=Homo sapiens GN=COL2A1 PE=1 SV=3	CO2A1_HUMAN	12	0.3
Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	CO3A1_HUMAN	3	0.24
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	CO6A1_HUMAN	1.9	0.023
Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2	CO7A1_HUMAN	0.6	0.32
Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3	COEA1_HUMAN	1.3	0.61
Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1 PE=1 SV=3	COHA1_HUMAN	1.1	0.87
Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	CO1A2_HUMAN	2.4	0.039
Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	CO6A2_HUMAN	2.6	0.025
Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	CO6A3_HUMAN	1.6	0.085
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	CO3_HUMAN	0.6	0.63
Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	CO9_HUMAN	9	0.14
Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	H2AY_HUMAN	3.6	0.15
Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	KCRB_HUMAN	2.1	0.33
Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1	KCRU_HUMAN	1	1
Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	CAND1_HUMAN	0.02	0.27
Cystatin-M OS=Homo sapiens GN=CST6 PE=1 SV=1	CYTM_HUMAN	1.7	0.46
Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1	CRIP2_HUMAN	0.04	0.41
Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2	CYC_HUMAN	2.6	0.28
Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1	COX2_HUMAN	1	0.96
Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	ACOC_HUMAN	2.9	0.21
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	DYHC1_HUMAN	2.2	0.27
Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3	DC1I2_HUMAN	<0.001	0.36
Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	CYFP1_HUMAN	0.1	0.09
D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	SERA_HUMAN	0.4	0.0061
D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3	DOPD_HUMAN	0.2	0.32
Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	PGS2_HUMAN	1.7	0.088
Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1	HEM2_HUMAN	0.7	0.8
Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	DSC1_HUMAN	0.5	0.21

Supp. table 3 continued 3.

Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3	DSC3_HUMAN	0.8	0.54
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	DSG1_HUMAN	0.9	0.78
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	DESP_HUMAN	1.1	0.62
Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	DEST_HUMAN	3.9	0.076
Dihydropolyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4	ODO2_HUMAN	0.06	0.2
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	DDB1_HUMAN	<0.001	0.15
DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2	APEX1_HUMAN	1.5	0.38
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=1 SV=3	DAD1_HUMAN	2.3	0.58
EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	EHD2_HUMAN	110	0.036
Elastin OS=Homo sapiens GN=ELN PE=1 SV=3	ELN_HUMAN	49	0.012
ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2	ELAV1_HUMAN	0.7	0.55
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	EF1A1_HUMAN	0.9	0.27
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	EF1B_HUMAN	1	1
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	EF1D_HUMAN	1.8	0.073
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	EF1G_HUMAN	1.1	0.76
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	EF2_HUMAN	1.1	0.72
Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	EFTU_HUMAN	1	0.92
Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	EMD_HUMAN	3.5	0.29
Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ENPL_HUMAN	2.3	0.11
Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3	EVPL_HUMAN	0.9	0.87
Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	EPIPL_HUMAN	1.4	0.41
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	IF4A1_HUMAN	0.8	0.76
Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	IF2A_HUMAN	1.5	0.21
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	EIF3A_HUMAN	4.3	0.043
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	EIF3B_HUMAN	<0.001	0.037
Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1	EIF3C_HUMAN	<0.001	0.28
Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2	SODE_HUMAN	1.2	0.86
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	EZRI_HUMAN	0.9	0.84
F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	CAZA1_HUMAN	1	0.92
F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	CAZA2_HUMAN	2.3	0.072
F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	CAPZB_HUMAN	1.2	0.7
Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	FUBP2_HUMAN	1.2	0.81
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	FAS_HUMAN	6	0.3
Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3	FABP7_HUMAN	5.8	0.17
Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	FABP5_HUMAN	0.6	0.63
F-box only protein 50 OS=Homo sapiens GN=NCCRP1 PE=1 SV=1	FBX50_HUMAN	0.7	0.68
Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	FIBG_HUMAN	24	0.033
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	FINC_HUMAN	2.3	0.4
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	FBLN1_HUMAN	100	0.28
Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	FILA_HUMAN	0.8	0.2
Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	FILA2_HUMAN	1.2	0.64
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	FLNA_HUMAN	1.9	0.2
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	FLNB_HUMAN	0.8	0.71
Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3	BLVRB_HUMAN	0.2	0.075
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	ALDOA_HUMAN	1.1	0.66
Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	ALDOC_HUMAN	1.4	0.24
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	LEG1_HUMAN	2.7	0.082
Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	LEG3_HUMAN	1.1	0.85
Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	LEG7_HUMAN	2.7	0.14
Galectin-related protein OS=Homo sapiens GN=GRP PE=1 SV=2	LEGL_HUMAN	1.6	0.46
Gamma-glutamylcystodotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1	GGCT_HUMAN	1.2	0.63
Ganglioside GM2 activator OS=Homo sapiens GN=GM2A PE=1 SV=4	SAP3_HUMAN	3.3	0.083
Gasdermin-A OS=Homo sapiens GN=GSDMA PE=2 SV=4	GSDMA_HUMAN	1.3	0.45
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	GELS_HUMAN	1.4	0.11
Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	G6PI_HUMAN	0.7	0.42
Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2	DHE3_HUMAN	1.2	0.87
Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2	GLRX1_HUMAN	1.7	0.63
Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	GPX3_HUMAN	3.7	0.11
Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3	GSTK1_HUMAN	0.9	0.94
Glutathione S-transferase Mu 2 OS=Homo sapiens GN=GSTM2 PE=1 SV=2	GSTM2_HUMAN	0.6	0.67
Glutathione S-transferase Mu 5 OS=Homo sapiens GN=GSTM5 PE=1 SV=3	GSTM5_HUMAN	6	0.3
Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	GSTP1_HUMAN	1.1	0.79
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	G3P_HUMAN	0.9	0.56
Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	PYGB_HUMAN	4.6	0.026
Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=3	GLTP_HUMAN	1.6	0.62

Supp. table 3 continued 4.

Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=3	SYG_HUMAN	0.4	0.35
Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1	GLOD4_HUMAN	1.4	0.21
GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4	KAD3_HUMAN	1.7	0.46
GTPase HRas OS=Homo sapiens GN=HRAS PE=1 SV=1	RASH_HUMAN	1.8	0.54
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	RAN_HUMAN	2.1	0.47
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	GNAI2_HUMAN	1.1	0.97
Guanine nucleotide-binding protein G(l)/G(s)/G(o) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3	GBG12_HUMAN	7.9	0.069
Guanine nucleotide-binding protein G(l)/G(s)/G(t) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3	GBB1_HUMAN	1.6	0.33
Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	GNAI3_HUMAN	0.6	0.64
Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	GBLP_HUMAN	0.9	0.79
Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	HPT_HUMAN	2.6	0.19
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	HSP71_HUMAN	0.8	0.28
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	HSP74_HUMAN	0.09	0.28
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	HSP7C_HUMAN	0.8	0.32
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	HSPB1_HUMAN	0.8	0.71
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	HS90A_HUMAN	2.4	0.0051
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	HS90B_HUMAN	2.2	0.01
Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1	HEBP1_HUMAN	5	0.3
Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	HBA_HUMAN	14	0.022
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	HBB_HUMAN	7.4	0.069
Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	HBD_HUMAN	87	0.031
Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	HEMO_HUMAN	1.9	0.22
Hepatitis-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	HDGF_HUMAN	0.1	0.45
Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	HP1B3_HUMAN	1.8	0.36
Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2	ROAA_HUMAN	1	0.99
Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5	ROA1_HUMAN	1.1	0.87
Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	ROA3_HUMAN	130	0.14
Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	HNRPD_HUMAN	1.7	0.22
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4	HNRH1_HUMAN	1.1	0.89
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	HNRPK_HUMAN	0.3	0.22
Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	HNRPM_HUMAN	1.7	0.64
Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	HNRPQ_HUMAN	2.2	0.27
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	HNRPU_HUMAN	1.6	0.059
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	ROA2_HUMAN	0.8	0.59
Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4	HNRPC_HUMAN	0.4	0.044
Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3	HXK1_HUMAN	0.3	0.18
Histidine ammonia-lyase OS=Homo sapiens GN=HAL PE=1 SV=1	HUTH_HUMAN	0.8	0.77
Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	HRG_HUMAN	2.8	0.41
Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	H10_HUMAN	10	0.094
Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	H12_HUMAN	7.1	0.019
Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	H12_HUMAN	1.3	0.82
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	H14_HUMAN	<0.001	0.39
Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	H15_HUMAN	1.3	0.74
Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	H2A1B_HUMAN	2	0.18
Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3	H2AV_HUMAN	2.9	0.25
Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	H2B1B_HUMAN	2.3	0.11
Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	H2B1B_HUMAN	1.8	0.37
Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4	H2B1C_HUMAN	31	0.31
Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3	H31T_HUMAN	1.8	0.35
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	H4_HUMAN	3.8	0.025
HLA class I histocompatibility antigen, B-13 alpha chain OS=Homo sapiens GN=HLA-B PE=2 SV=1	1B13_HUMAN	15	0.33
HLA class I histocompatibility antigen, B-15 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=2	1B15_HUMAN	<0.001	0.39
HLA class I histocompatibility antigen, B-51 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1	1B51_HUMAN	15	0.12
HLA class I histocompatibility antigen, B-7 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=3	1B07_HUMAN	0.8	0.91
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	HORN_HUMAN	0.05	0.21
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3	HCDH_HUMAN	0.1	0.13
Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	HPRT_HUMAN	<0.001	0.39
Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	IGHA1_HUMAN	26	0.14
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	IGHG1_HUMAN	1.3	0.39
Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	IGHG2_HUMAN	9	0.29
Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	IGKC_HUMAN	8.1	0.11
Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	KV302_HUMAN	2	0.45
Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	LAC2_HUMAN	1.7	0.27
Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	IGHM_HUMAN	2.2	0.3
Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	IGLL5_HUMAN	2	0.32

Supp. table 3 continued 5.

Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	IMB1_HUMAN	1.5	0.41
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	IPYR_HUMAN	46	0.15
Inositol monophosphatase 2 OS=Homo sapiens GN=IMPA2 PE=1 SV=1	IMPA2_HUMAN	1.8	0.35
Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	IDE_HUMAN	0.9	0.92
Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=4	ITA6_HUMAN	1	0.97
Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5	ITB4_HUMAN	1.3	0.74
Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	ILF2_HUMAN	0.9	0.91
Involucrin OS=Homo sapiens GN=IVL PE=1 SV=2	INVO_HUMAN	22	0.26
Iso citrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	IDHC_HUMAN	1.4	0.29
Iso citrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	IDHP_HUMAN	1	1
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	PLAK_HUMAN	1	0.95
Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	K1H1_HUMAN	240	0.3
Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	K1H1_HUMAN	<0.001	0.34
Keratin, type I cuticular Ha3-I OS=Homo sapiens GN=KRT33A PE=1 SV=2	KT33A_HUMAN	2.4	0.58
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	K1C10_HUMAN	0.9	0.2
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	K1C14_HUMAN	0.8	0.028
Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	K1C15_HUMAN	0.8	0.032
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	K1C16_HUMAN	0.8	0.7
Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	K1C17_HUMAN	0.7	0.57
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	K1C9_HUMAN	2.1	0.4
Keratin, type II cuticular Hb1 OS=Homo sapiens GN=KRT81 PE=1 SV=3	KRT81_HUMAN	4.7	0.35
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	K2C1_HUMAN	0.9	0.47
Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=3	K2C1B_HUMAN	0.5	0.28
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	K22E_HUMAN	1.1	0.63
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	0.9	0.16
Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	K2C6A_HUMAN	0.8	0.77
Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	K2C6C_HUMAN	2.4	0.16
Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=1 SV=2	K2C78_HUMAN	0.4	0.048
Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	K2C80_HUMAN	1.5	0.34
Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4	LGUL_HUMAN	0.9	0.95
LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1	LANCL1_HUMAN	0.8	0.56
Leucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2	SYLC_HUMAN	<0.001	0.048
Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	ILEU_HUMAN	2.2	0.49
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	LDHA_HUMAN	0.9	0.36
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	LDHB_HUMAN	1.7	0.42
Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	LUM_HUMAN	1	0.87
Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	LYSC_HUMAN	44	0.13
Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	MIF_HUMAN	2.9	0.14
Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2	CAPG_HUMAN	0.7	0.17
Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	MDHC_HUMAN	1.1	0.71
Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	MDHM_HUMAN	0.5	0.14
Mast cell carboxypeptidase A OS=Homo sapiens GN=CPA3 PE=1 SV=2	CBPA3_HUMAN	5.4	0.064
Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1	PGRC2_HUMAN	0.08	0.37
Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	MAP4_HUMAN	<0.001	0.38
Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1	MIME_HUMAN	2.1	0.18
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	MOES_HUMAN	0.8	0.57
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	MYL6_HUMAN	3.6	0.041
Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	ML12A_HUMAN	3.4	0.08
Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=1	MYH14_HUMAN	0.2	0.29
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	MYH9_HUMAN	1.2	0.7
Myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	MYO1C_HUMAN	0.007	0.16
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	NDUS3_HUMAN	<0.001	0.39
NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1	NB5R1_HUMAN	1.2	0.85
NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	NB5R3_HUMAN	1.1	0.86
Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1	NACAM_HUMAN	1.1	0.81
Neuroblast differentiation-associated protein AHNK OS=Homo sapiens GN=AHNAK PE=1 SV=2	AHNK_HUMAN	1	0.98
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	GANAB_HUMAN	0.1	0.26
Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=2	NIBL1_HUMAN	0.9	0.76
Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=3	HMGN1_HUMAN	0.7	0.84
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	NUCL_HUMAN	1.7	0.063
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	NPM_HUMAN	1	0.96
Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	NDKA_HUMAN	2.1	0.23
Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	NDKA_HUMAN	<0.001	0.39
Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	OLA1_HUMAN	0.7	0.54
PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	PDL1_HUMAN	0.5	0.54

Supp. table 3 continued 6.

Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	PPIA_HUMAN	2.1	0.19
Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	PPIB_HUMAN	1.6	0.28
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2	FKBP1A_HUMAN	3.1	0.11
Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	POSTN_HUMAN	1.4	0.3
Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4	PEPL_HUMAN	0.8	0.73
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	PRDX1_HUMAN	1	0.91
Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	PRDX2_HUMAN	1.3	0.64
Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	PRDX5_HUMAN	2.3	0.34
Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	PRDX6_HUMAN	1.1	0.79
Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	MPCP_HUMAN	1.6	0.42
Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	PEBP1_HUMAN	1.5	0.39
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	PGK1_HUMAN	1	0.99
Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	PGAM1_HUMAN	1.2	0.84
Phosphomevalonate kinase OS=Homo sapiens GN=PMVK PE=1 SV=3	PMVK_HUMAN	1.5	0.35
Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	PKP1_HUMAN	0.7	0.19
Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	PKP3_HUMAN	1.4	0.46
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	PAIRB_HUMAN	0.9	0.86
Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6	PLSL_HUMAN	6	0.3
Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	PLST_HUMAN	0.7	0.68
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	PLEC_HUMAN	1.3	0.39
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	PCBP1_HUMAN	1.5	0.41
Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	PTBP1_HUMAN	0.6	0.18
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	LMNA_HUMAN	1.2	0.33
Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	PROF1_HUMAN	1.2	0.77
Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	PDC6I_HUMAN	1.7	0.14
Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	PDCD6_HUMAN	1.5	0.63
Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	PHB_HUMAN	0.9	0.92
Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2	PHB2_HUMAN	0.9	0.75
Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1	PRELP_HUMAN	0.5	0.17
Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	PSME2_HUMAN	1.7	0.68
Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	PSA1_HUMAN	0.7	0.56
Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	PSA2_HUMAN	0.6	0.7
Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	PSA3_HUMAN	1.3	0.57
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	PSA4_HUMAN	1.2	0.74
Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	PSA6_HUMAN	0.9	0.88
Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	PSA7L_HUMAN	0.9	0.92
Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	PSB4_HUMAN	1.3	0.71
Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	PSB5_HUMAN	1.5	0.4
Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	PSB6_HUMAN	1.1	0.87
Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2	AHNK2_HUMAN	1.4	0.38
Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	PDIA3_HUMAN	1.1	0.82
Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	PARK7_HUMAN	1.2	0.74
Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=2	POF1B_HUMAN	0.8	0.41
Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2	S10AA_HUMAN	2.1	0.35
Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	S10AB_HUMAN	2.2	0.27
Protein S100-A14 OS=Homo sapiens GN=S100A14 PE=1 SV=1	S10AE_HUMAN	1.6	0.58
Protein S100-A16 OS=Homo sapiens GN=S100A16 PE=1 SV=1	S10AG_HUMAN	2.5	0.17
Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=1 SV=3	S10A2_HUMAN	1.9	0.44
Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	S10A4_HUMAN	3.9	0.0049
Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2	SC61B_HUMAN	2.9	0.38
Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	PSA_HUMAN	0.9	0.92
Putative cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo sapiens GN=UQCRCF1 PE=5 SV=1	UCRIL_HUMAN	0.2	0.21
Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1	HGB1A_HUMAN	1.1	0.74
Putative protein FAM10A4 OS=Homo sapiens GN=ST13P4 PE=5 SV=1	ST134_HUMAN	0.3	0.15
Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4	KPYM_HUMAN	1.3	0.37
Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	QOR_HUMAN	190	0.06
Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	GDI2_HUMAN	1.4	0.36
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	IQGA1_HUMAN	1.2	0.76
Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	RAC1_HUMAN	1.2	0.67
Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	RAB10_HUMAN	1.2	0.65
Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3	RB11A_HUMAN	1.3	0.55
Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	RAB14_HUMAN	0.9	0.84
Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1	RAB18_HUMAN	1.3	0.54
Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	RAB1A_HUMAN	2	0.31
Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	RAB1A_HUMAN	0.7	0.56

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Ras-related protein Rab-25 OS=Homo sapiens GN=RAB25 PE=1 SV=2	RAB25_HUMAN	0.4	0.48
Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1	RAB2A_HUMAN	1.6	0.4
Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1	RAB5B_HUMAN	0.07	0.087
Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	RAB5C_HUMAN	0.7	0.56
Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	RAB6A_HUMAN	1.3	0.62
Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	RAB7A_HUMAN	1.9	0.13
Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	RAB8A_HUMAN	0.9	0.96
Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1	RALA_HUMAN	3.9	0.09
Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1	RAP1A_HUMAN	1.8	0.13
Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1	RAP2B_HUMAN	2	0.32
Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3	REEP5_HUMAN	3.6	0.12
Redox-regulatory protein FAM213A OS=Homo sapiens GN=FAM213A PE=1 SV=3	F213A_HUMAN	1.4	0.59
Retroviral-like aspartic protease 1 OS=Homo sapiens GN=ASPRV1 PE=1 SV=1	APRV1_HUMAN	1.7	0.15
Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=3	GDIR1_HUMAN	1.4	0.41
Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDI2 PE=1 SV=3	GDIR2_HUMAN	1.5	0.68
Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	RINI_HUMAN	0.9	0.77
Sciellin OS=Homo sapiens GN=SCEL PE=1 SV=2	SCEL_HUMAN	0.2	0.28
Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	SEPT2_HUMAN	1.1	0.72
Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2	SEPT7_HUMAN	1.1	0.81
Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	HTRA1_HUMAN	19	0.068
Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4	SRSF2_HUMAN	0.9	0.61
Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1	SRSF3_HUMAN	1.7	0.25
Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	TRFE_HUMAN	1	0.93
Serpin A12 OS=Homo sapiens GN=SERPINA12 PE=2 SV=1	SPA12_HUMAN	7.2	0.13
Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	SPB12_HUMAN	0.8	0.67
Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2	SPB5_HUMAN	1.2	0.52
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	ALBU_HUMAN	1.4	0.012
Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	SAMP_HUMAN	17	0.0014
S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2	ESTD_HUMAN	0.1	0.2
SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGL3 PE=1 SV=1	SH3L3_HUMAN	1.9	0.55
Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=2 SV=2	SFXN3_HUMAN	4.1	0.041
Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	SRP14_HUMAN	1.4	0.73
Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	SMD2_HUMAN	12	0.11
Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1	SMD3_HUMAN	4.1	0.031
Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1	SORCN_HUMAN	1.5	0.6
Spectrin alpha chain, non-erythrocytic 1	SPTN1_HUMAN	2.8	0.047
Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	SPTB2_HUMAN	3.8	0.11
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	SFPQ_HUMAN	0.2	0.18
Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	SND1_HUMAN	0.07	0.37
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	GRP75_HUMAN	0.3	0.4
Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	SODC_HUMAN	2.2	0.25
Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2	SODM_HUMAN	5.6	0.079
Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=1	SBSN_HUMAN	2.1	0.36
Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3	SURF4_HUMAN	0.1	0.45
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	VAT1_HUMAN	9.7	0.0035
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	TLN1_HUMAN	0.7	0.7
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	TCPD_HUMAN	0.8	0.68
Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=3	TENX_HUMAN	0.7	0.5
Thioredoxin domain-containing protein 17 OS=Homo sapiens GN=TXNDC17 PE=1 SV=1	TXD17_HUMAN	0.8	0.84
Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	PRDX3_HUMAN	2.7	0.14
Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	TALDO_HUMAN	1	0.96
Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFB1 PE=1 SV=1	BGH3_HUMAN	0.7	0.42
Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	RHOA_HUMAN	1.4	0.38
Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	TAGL2_HUMAN	1.2	0.65
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	TERA_HUMAN	2.1	0.029
Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	TKT_HUMAN	1.4	0.57
Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1	SSRD_HUMAN	1.1	0.84
Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	TMEDA_HUMAN	2	0.16
Transmembrane glycoprotein NMB OS=Homo sapiens GN=GPNMB PE=1 SV=2	GPNMB_HUMAN	3.8	0.12
Transmembrane protein 33 OS=Homo sapiens GN=TMEM33 PE=1 SV=2	TMM33_HUMAN	1.6	0.72
Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	TMM43_HUMAN	0.3	0.11
Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	TTHY_HUMAN	13	0.019
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	ECHA_HUMAN	0.6	0.4
Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3	ECHB_HUMAN	0.06	0.014
Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2	TPIS_HUMAN	0.8	0.62

Supp. table 3 continued 8.

Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2	TRI29_HUMAN	0.6	0.12
Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1	TPM3_HUMAN	1.8	0.4
Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1	TPM3_HUMAN	1.4	0.66
Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1	TRYB1_HUMAN	1.1	0.91
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	TBA1B_HUMAN	0.9	0.42
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	TBA4A_HUMAN	1.4	0.41
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	TBB5_HUMAN	0.7	0.019
Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	TBB4A_HUMAN	0.7	0.032
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	TBB4B_HUMAN	0.7	0.029
Tubulin polymerization-promoting protein family member 3 OS=Homo sapiens GN=TPPP3 PE=1 SV=1	TPPP3_HUMAN	0.8	0.77
Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	UBP5_HUMAN	0.7	0.8
Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2	RL40_HUMAN	1.6	0.52
Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2	RL40_HUMAN	0.3	0.42
Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	UBE2N_HUMAN	2	0.32
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	UBA1_HUMAN	0.5	0.39
Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	VPS35_HUMAN	3.3	0.27
Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4	SC22B_HUMAN	2.8	0.36
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	VIME_HUMAN	1.2	0.23
Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	VINC_HUMAN	0.1	0.37
Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	VTNC_HUMAN	1000	0.00043
Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	VDAC1_HUMAN	1.3	0.66
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	VDAC2_HUMAN	0.7	0.56
Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	VDAC3_HUMAN	<0.001	0.39
V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	VATA_HUMAN	1.1	0.92
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	XRCC5_HUMAN	2.3	0.12
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	XRCC6_HUMAN	0.5	0.3
Zinc finger protein 185 OS=Homo sapiens GN=ZNF185 PE=1 SV=3	ZN185_HUMAN	0.1	0.44
Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	ZA2G_HUMAN	1.6	0.43