



Proteomics of bronchial biopsies: Galectin-3 as a predictive biomarker of airway remodelling modulation in omalizumab-treated severe asthma patients



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ABSTRACT

Asthma is a chronic inflammatory disease. Reticular basement membrane (RBM) thickening is considered feature of airway remodelling (AR) particularly in severe asthma (SA). Omalizumab, mAb to IgE is effective in SA and can modulate AR. Herein we describe protein profiles of bronchial biopsies to detect biomarkers of anti-IgE effects on AR and to explain potential mechanisms/pathways. We defined the bronchial biopsy protein profiles, before and after treatment. Unsupervised clustering of baseline proteomes resulted in very good agreement with the morphometric analysis of AR. Protein profiles of omalizumab responders (ORs) were significantly different from those of non-omalizumab responders (NORs). The major differences between ORs and NORs lied to smooth muscle and extra cellular matrix proteins. Notably, an IgE-binding protein (galectin-3) was reliable, stable and predictive biomarker of AR modulation. Omalizumab down-regulated bronchial smooth muscle proteins in SA. These findings suggest that omalizumab may exert disease-modifying effects on remodelling components.

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1. Introduction

Asthma is a chronic inflammatory disease of the airways characterised by a variable narrowing of the airways. Asthma is a major health problem worldwide that affects over 300 million patients [1]. Severe asthma affects a minority of the patients with this disease; however, most treatment resources are directed to these patients [2]. Allergies are one of the most common and well-known causes of asthma [3] Omalizumab, an anti-IgE monoclonal antibody, has been approved for the treatment of "severe, uncontrolled allergic asthma", and its effectiveness has been confirmed in several controlled and real-life clinical trials [4–6].

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Personalised medicine [7] and targeted therapies are modern methods of properly treating patients with the most cost-effective approach [8]. There is an absolute need to pursue these approaches and to make them feasible in the identification of biomarkers of clinical response [7].

In recent years, several biomarkers of clinical response have been identified for severe asthma [9]. Among these, periostin is particularly noteworthy, as high blood levels of periostin have been demonstrated to be a reliable biomarker of clinical response to some biotechnology-based treatments, such as lebrikizumab [10] and omalizumab [11]. Reticular basement membrane (RBM) thickening is considered a feature of airway remodelling [12] with increasing prominence in severe asthma [13] with a defined cut-off value.

We recently published a report on the significant effect of omalizumab treatment on bronchial remodelling modulation after 12 months of treatment, which was determined by means of a histological evaluation, according to ATS/ERS guidelines for its use in severe corticosteroid refractory disease. Bronchial biopsies at

baseline and after therapy were analysed [14], and all patients were found to have clinically benefited from the treatment. However, regarding the modulation of airway remodelling, we surprisingly identified two groups: responders (i.e., reduction of RBM thickening) and non-responders (i.e., increasing or stable RBM). No correlation of remodelling reduction with any clinical or functional parameters was detected [14]. Although a relationship between the smooth muscle bronchial component of remodelling and pulmonary function reduction is known [15], evidence of any muscle reduction upon omalizumab or indeed, any other treatment is lacking.

To improve upon the previous study and in the context of the need to understand the molecular pathways in asthma and relationship to specific phenotypes [16], we further investigated the bronchial specimens that were previously analysed, with the aim of identifying candidate biomarkers of response (in terms of bronchial remodelling reduction). For this purpose, we performed a proteomic analysis of the specimens according to a strategy described by Braido [8] and Wheelock [17]. In particular, we used the multi-dimensional protein identification technology (MudPIT) proteomic approach, a high-throughput methodology that allows the simultaneous identification of hundreds/thousands of proteins from a single complex sample [18], an evaluation of differential abundance [19,20], and a characterisation of the involved molecular pathways [21].

The protein profiles obtained from the MudPIT analysis of bronchial biopsies were useful for identifying predictive biomarkers and pathways of anti-IgE effects on remodelling and understanding the potential mechanisms involved.

2. Methods

2.1. Subjects

Eight patients with severe, persistent atopic asthma (7 non-smokers; 3 females; range age 40–62 years; mean age 47.0 ± 9.7 ; mean body mass index (BMI) 23.8 ± 3.1 ; mean total plasma IgE $309.4 \text{ IU/l} \pm 218.2$; mean FEV1 $56.2\% \text{ pred} \pm 14.5\%$; ACT score 11.1 ± 2.9) were enrolled in this study.

All the patients were treated with omalizumab according to the AIFA (Italian Drug Agency) prescription rules. The clinical features of the patients were described in a previous report [14]. The study was approved by the local ethics committee.

Two biopsies were obtained from each patient using a flexible bronchoscope (Pentax FB19-TX, Langley, UK) before and 12 months after omalizumab treatment. Bronchial biopsies were obtained from the right middle lobe.

2.2. Morphometric analysis

The reticular basement membrane (RBM) thickness was measured by performing light microscopy image analysis of all the biopsies before and after treatment according to the ERS/ATS recommendations [22] regarding lung structure, as described in a previous study.

2.3. Immunohistochemistry (IHC) and image analysis

Tissue specimens were fixed in 10% formaldehyde at 4°C for 4 h and were embedded in paraffin. The paraffin sections ($3 \mu\text{m}$) were dewaxed, hydrated, and pretreated with an antigen-unmasking solution for 30 min. The samples were then treated with blocking solution (BLOXALL Blocking Solution, Vector Laboratories) to inactivate endogenous peroxidases, pseudoperoxidases, and alkaline phosphatase. The samples were then incubated for approximately

10 min in a working solution of blocking serum (normal goat serum).

The sections were incubated overnight at 4°C with a primary antibody (anti-human GAL-3 rat monoclonal antibody; Santa Cruz Biotechnology, Santa Cruz, CA, USA) diluted 1:50 in phosphate-buffered saline (PBS). Subsequently, the sections were incubated with a secondary antibody (biotinylated immunoglobulin G diluted 1:200 in PBS) for 10 min. After several washes with PBS, all the slides were incubated with a concentrated labelled enzyme (biotin–streptavidin–peroxidase complex) for 5 min at room temperature. The peroxidase was developed with 0.04% 3,3-diaminobenzidine in 50 mmol/L Tris–HCl buffer containing 0.03% hydrogen peroxide for 10 min. After being rinsed with PBS, the slides were counterstained with haematoxylin, coverslipped with Eukitt, and examined by light microscopy.

The image analysis was performed using the Leica Q500 MC Image Analysis System (Leica, Cambridge, UK). For each biopsy analysed, the optical density of the signals was quantified using a computer. The video images were generated by a charge-coupled device (CCD) camera (Leica) connected by a frame grabber to a computer. Single images were digitised for image analysis at 256 grey levels. The imported data were quantitatively analysed using Q500MC Software-Qwin (Leica). The tissue was selected by the operator using the cursor, and the positive areas were automatically estimated. A constant optical threshold and filter combination was used. The signal quantisation was expressed as the percent positive area in pixels per square micron [23].

2.4. Protein extraction, estimation, and tryptic digestion for proteomic analysis

The dewaxed tissues ($3\text{-}\mu\text{m}$ -thick section from each sample) were dried in a vacuum centrifuge and resuspended in $100 \mu\text{L}$ of $0.1 \text{ M NH}_4\text{HCO}_3$ pH 7.9 buffer with 10% acetonitrile. The tissues were then homogenised and extracted by adding RapigestTM SF reagent (Waters, Milford, MA, USA) at a final concentration of 0.2% (w/v). The resulting suspensions were incubated under stirring, first at 100°C for 20 min and then at 80°C for 2 h. Subsequently, the protein concentration was assayed using the SPNTM Protein Assay Kit (G-Biosciences, Maryland Heights, MO, USA), and $5 \pm 0.5 \mu\text{g}$ of protein from each sample was digested by adding sequencing-grade modified trypsin (Promega, Madison, WI, USA) at an enzyme/substrate ratio of 1:50 (w/w) and incubating it overnight at 37°C . An additional $0.5 \mu\text{g}$ aliquot of trypsin was added the next morning, and the digestion continued for 4 h. The addition of 0.5% trifluoroacetic acid (TFA) stopped the enzymatic reaction, and a subsequent incubation at 37°C for 30 min completed the RapiGest acidic hydrolysis [24]. The water-immiscible degradation products were removed by centrifugation at $14,000 \times g$ for 10 min. The tryptic digest mixture was desalted using PepCleanTM C18 spin columns (Pierce Biotechnology, Rockford, IL, USA) and was resuspended in 0.1% formic acid at a concentration of $0.4 \mu\text{g}/\mu\text{L}$.

2.5. MudPIT analysis

The trypsin-digested samples were analysed using two-dimensional microliquid chromatography coupled online with tandem mass spectrometry (2DC-MS/MS, also referred to as Multi-dimensional Protein Identification Technology, MudPIT) (Thermo Fisher, San José, CA, USA). Briefly, $5 \mu\text{L}$ of each digested peptide mixture was first loaded onto a strong cation exchange column (Biobasic-SCX column, $0.32 \text{ i.d.} \times 100 \text{ mm}$, $5 \mu\text{m}$, Thermo Fisher) using a Micro AS autosampler (Thermo Fisher). The peptide mixture was then eluted stepwise by applying an eleven-step ammonium chloride concentration gradient (0, 10, 20, 30, 40, 80, 120, 200, 400, 600, and 700 mM). Each salt step was directly loaded onto

a reverse-phase C18 column (Biobasic-18, 0.180 i.d. $\times$ 100 mm, 5 μ m, Thermo Fisher) and separated with an acetonitrile gradient (eluent A, 0.1% formic acid in water; eluent B, 0.1% formic acid in acetonitrile). The gradient profile was started and maintained for 5 min with 5% eluent B, followed by 5–45% eluent B for 51 min, 45–80% eluent B for 5 min, and 95% eluent B for 9 min. The flow rate was 100 μ L/min, which was split to achieve a final flux of 2 μ L/min. The peptides that were eluted from the C18 column were directly analysed with a hybrid linear ion trap mass spectrometer (LTQ-Orbitrap XL; Thermo Fischer) equipped with a nanospray ion source. The spray capillary voltage was set at 1.5 kV, and the ion transfer capillary temperature was maintained at 220 °C. For each step of the peptide elution from the C18 column, full mass spectrometry (MS) spectra were recorded in the positive ion mode over a 400–1600 m/z range, with a resolving power of 60,000 (full width at half-maximum) and a scan rate of 2 spectra/s. This step was followed by four low-resolution MS/MS events that were sequentially generated in a data-dependent manner on the first, second, third, and fourth most intense ions selected from the full MS spectrum, using dynamic exclusion for the MS/MS analysis. In particular, the MS/MS scans were acquired by setting a normalised collision energy of 35% on the precursor ion and, when a peptide ion was analysed twice, applying an exclusion duration of 0.5 min.

2.6. Database search

A computer analysis of the MS/MS spectra was performed using Bioworks version 3.3.1, based on the SEQUEST algorithm (University of Washington, licensed to ThermoFinnigan Corp., San Jose, CA, USA). The experimental MS/MS spectra were correlated with the tryptic peptide sequences by comparisons with the theoretical mass spectra, which were obtained by the *in silico* digestion of a human protein database (approximately 226233 entries), downloaded in January 2012 from the National Center for Biotechnology Information (NCBI) website (www.ncbi.nlm.nih.gov). This analysis enabled the identification of peptide sequences and related proteins. Because the confidence of protein identification depends on the stringency of the identification of the peptide sequence and peptide matching, particularly when using data from a single peptide, a high stringency was guaranteed using the following method. The peptide mass search tolerance was set to 1.00 Da; the precursor ion tolerance was set to 50 ppm; and the intensity threshold was set to 100. Moreover, searches were performed with no enzyme, allowing mass measurement tolerance levels of 2.00 mass units for peptides and 1.00 mass units for MS/MS ions. To assign a final score to the proteins, the SEQUEST output data were filtered by setting the peptide probability to 1×10^{-3} , the chosen minimum correlation score values (Xcorr) were 1.5, 2.0, 2.5, and 3.0 for single-, double-, triple-, and quadruple-charged ions, respectively and the consensus score to higher than 10. The false-positive peptide ratio, calculated through a reverse database, was less than 3%.

The output data obtained from the SEQUEST software were compared using an in-house algorithm, namely, the Multidimensional Algorithm Protein Map (MAPProMa) [25].

2.7. Spectral count normalisation and differential analysis

The protein lists were aligned using a specific MAPProMa tool [25] and the average spectral count (SC) for each distinct protein was calculated. Differences in the amount of analysed protein between analyses from the same tissue were balanced by normalising the SC values according to a method proposed by Carvalho et al. [26]. Briefly, the normalised SC (nSC) for each protein was calculated by dividing the SC value of each protein (pSC) by the SC value sum (Σ SC) of all the proteins belonging to the same list ($nS = pSC/\Sigma SC$). In addition, only isoforms identified by the corresponding specific

peptides were considered (or no redundant protein isoforms were considered in the list). The omalizumab responder (OR) and non-omalizumab responder (NOR) protein profiles obtained were compared using the DAVE and DCI algorithms in the MAPProMa software. DAVE is an index of the relative ratio between two compared protein lists, and DCI is an index used to evaluate the confidence of DAVE. Taking into account the spectral count values, the most significant up-represented proteins in the non-responder profile exhibited a DAVE $\geq +0.2$ and a DCI $\geq +50$; the most significant down-represented proteins exhibited a DAVE ≤ -0.2 and a DCI ≤ -50 .

2.8. Linear discriminant analysis

To perform the reduction of data dimensionality, the protein lists obtained using the MudPIT replicate analysis method were processed using linear discriminant analysis (LDA) [27]. This analysis was applied by using a common covariance matrix for all the groups and the Mahalanobis distance [28] from each point to each group's multivariate mean. The identifying features (proteins) that discriminated the analysed samples were considered to be those with the largest *F* ratio (>4) and the smallest *p*-value (<0.05). Specifically, the *F* ratio represented the model mean square divided by the error mean square, whereas the *p*-value indicated the probability of obtaining an *F* value greater than that calculated if, in reality, there was no difference between the population group means.

2.9. Hierarchical clustering

The protein lists were handled and aligned using MAPProMa software [25]. Biological and technical replicates were evaluated using an unsupervised learning method, such as hierarchical clustering (HC) [29] using in-house R-scripts, which was based on the XlsReadWrite, clue, and cValid libraries (<http://cran.r-project.org>). In particular, the Euclidean distance metric was applied, and an agglomerative coefficient was calculated.

2.10. Network analysis

A global *Homo sapiens* protein interactomic network with more than 22,000 nodes and 200,000 interactions was built using the Bionetbuilder Cytoscape plugin [30]. This network combines interactome data sets from major public online repositories, including HPRD, MINT, BioGrid, IntAct, DIP, BIND, KEGG, MPPI, and GO. All types of interactions were retrieved from each repository without applying a *p*-value threshold. Protein-DNA, protein-RNA, protein-metabolite, and protein-drug interactions, if present in the data sets, were removed, as were duplicates and self-interactions. Starting from the list of experimentally identified proteins, the corresponding network was extracted. Proteins that were not mapped or were mapped as isolated components were not considered in the analysis. The network was analysed using Cytoscape software [31]. In particular, the Bingo 2.44 plugin [32] was used to emphasise sub-networks based on functionally organised GO terms, and the MCODE plugin [33] was used to cluster sub-networks based on their topology and, specifically, by considering densely connected regions.

3. Results

Protein profiles of FFPE (formalin fixed paraffin embedded) 16 bronchial biopsies from 8 patients affected by severe asthma were obtained before and 12 months after anti-IgE monoclonal antibody (omalizumab) treatment. Each patient was classified, based on a morphometric analysis [14], as a omalizumab responder or a non-omalizumab responder.

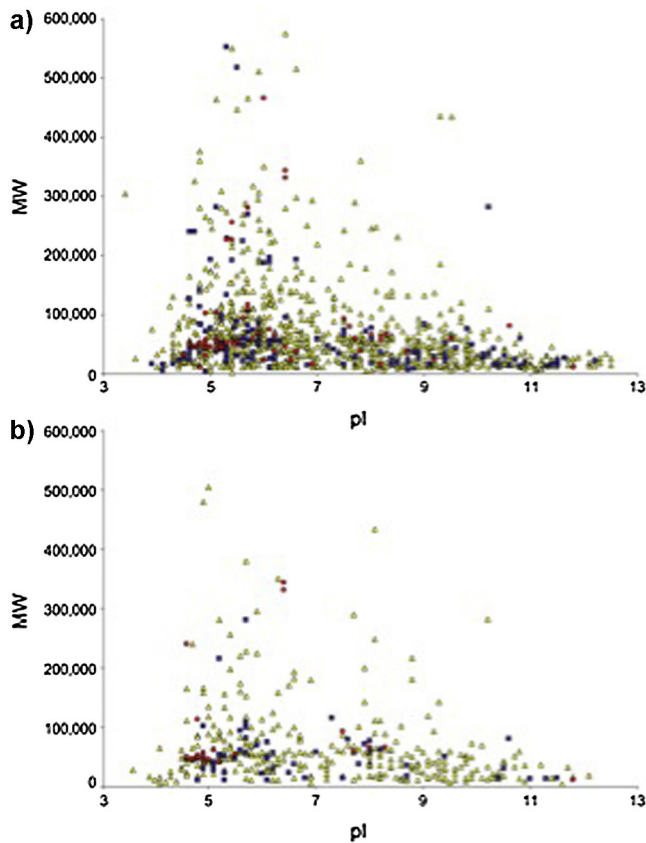


Fig. 1. 2-D virtual map, of FFPE bronchial biopsies proteome obtained plotting MW versus pI of the identified proteins by MaProMa software. The protein lists are reported in Supplementary Information Table 1. A colour/shape code is assigned to each protein according to its SEQUEST score value (yellow/triangle ≤ 15 , blue/square from >15 to <35 , red/circle ≥ 35). (a) Responder (OR), (b) non-responder (NOR).

3.1. Protein profiles

The MudPIT proteomic approach allowed the identification of over one hundred proteins from each sample. Using the MaProMa software, each protein list from the OR and NOR patients was automatically plotted onto a 2-D map according to the theoretical molecular weight (MW) and isoelectric point (pI) of the identified proteins. A representative example is shown in Fig. 1, which shows

the 2-D maps corresponding to all the identified proteins. In particular, it is interesting to note that we were able to characterise a significant number of proteins with extreme theoretical MW values <10 kDa (such as mutant beta-globin, 2 kDa) and >200 kDa (such as neuroblast differentiation-associated protein, AHNK, 628 kDa), along with proteins having a very acidic pI (<4), such as calmodulin (pI = 3.9) or a very basic pI (>10), such as serine/arginine-rich splicing factor 7 isoform 1 (pI = 12.3).

Overall, 1330 distinct proteins were identified, and a complete list of the identified proteins is presented in Supplementary Table 1. To reduce the false-positive peptide identification rate, stringent filtration criteria were applied. Of note, while the weight of the biopsies was stable, the number of identified proteins in the OR samples was always higher than that in the NOR samples; this finding suggested a wider qualitative distribution of proteins in the OR patients.

Considering the 4 biopsy groups (omalizumab responder baseline, ORb; omalizumab responder post-treatment, ORp; non-omalizumab responder baseline, NORb; and non-omalizumab responder post-treatment, NORp), it was observed that a higher number of proteins changed in the OR compared with the NOR due to the anti-IgE treatment. Specifically, 79 and 34 proteins presented a different abundance level after the treatment in ORs and NORs, respectively. In addition, a comparison of OR vs. NOR, both at baseline (ORb vs NORb) and post-treatment (ORp vs NORp), demonstrated a substantial difference with respect to the number of proteins presenting a differential abundance (Fig. 2).

These proteomic findings are in agreement with the morphometric data, confirming the omalizumab effect on ORs. This result indicates that at baseline, ORs possess proteins that are potentially susceptible to the treatment. For this reason we investigated in depth the differences between the ORs and NORs before treatment by performing clustering and label-free differential analyses.

3.2. Clustering and descriptors

Protein lists from bronchial biopsies of each patient were compared and used to perform an unsupervised clustering analysis. The baseline ORs and NORs were segregated into the groups previously defined by the morphometric analysis (Fig. 3). In this context, 81 proteins were identified as descriptors based on a linear discriminant analysis (LDA) performed to discriminate between the two groups (discriminators are listed in Supplementary Table 2).

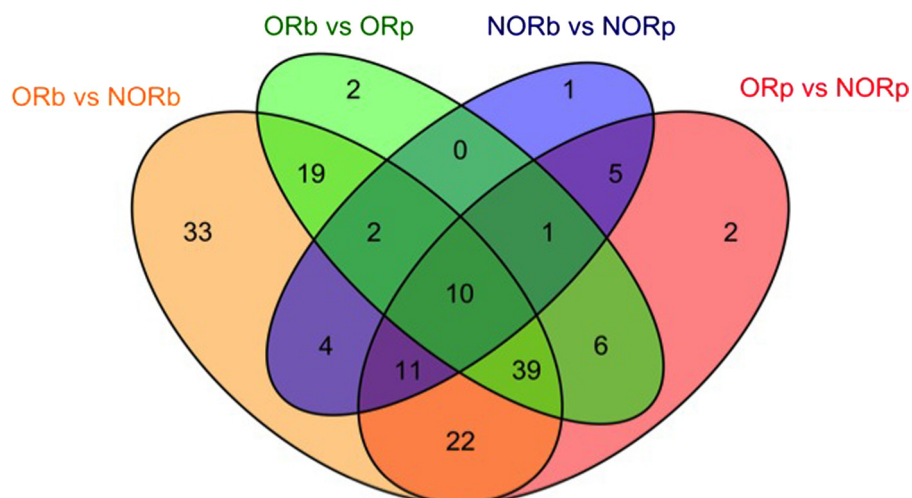


Fig. 2. Venn diagram of differential proteins obtained comparing each other the four groups (ORb, NORb, ORp and NORp), classified according morphometric analysis.

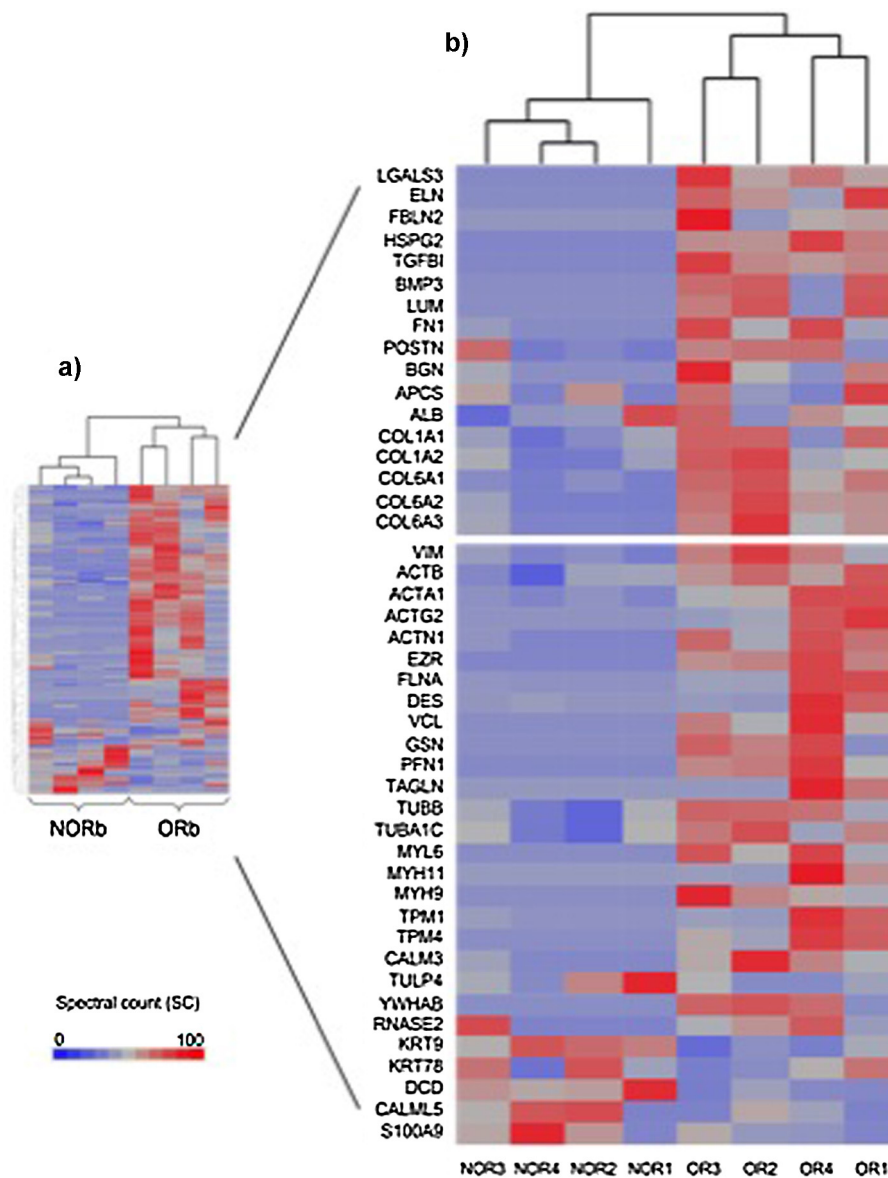


Fig. 3. Unsupervised hierarchical clustering of protein lists obtained by analyzing lung biopsies of responder (ORb) and non-responder (NORb) patients. (a) Total and (b) selected proteins. For each protein the heat map shows the normalised spectral count (SC) values. The obtained cluster resulted well structured (agglomerative coefficient > 0.8).

3.3. Label-free differential analysis

A label-free approach, based on MaProMa algorithms [25], was used for evaluating, independently of the clustering analysis, differential abundance levels of proteins by comparing NORb versus ORb samples. A total of 107 proteins were differentially abundant; in particular, 23 and 84 proteins were up-regulated in the NORb and ORb biopsies, respectively (Supplementary Table 2). Of note, the label-free procedure confirmed 48 descriptor proteins (approximately 60%) selected by LDA. In addition, another 10 descriptors were detected at a low level ($DCI < 50$), but they were present exclusively in ORb; the remaining 23 (out of 81 descriptors) were present in 3 out of 4 omalizumab responders as prevalent compared with NORb.

3.4. Network analysis

The identification of a very large number of proteins and the availability of a *H. sapiens* network dataset constituted the premise

for investigating the functional relationships between groups identified in our proteomic analyses. In this context, the identified proteins, including differentially expressed proteins, were plotted onto the Global Mammalian Protein Interactomic network by means of Cytoscape and its plug-ins (see Section 2). This procedure allowed the mapping of 584 nodes (approximately 72% of the total identified proteins/nodes), involving 4642 interactions, grouped into 7 distinct main networks (Supplementary Fig. 1A–D), including the following: (a) structural proteins (including cytoskeletal and myosin/actin-related proteins, annexins, and keratins), (b) extra-cellular matrix (ECM, including collagens) proteins, (c) metabolism and redox regulation proteins, (d) heat shock proteins, (e) immune system proteins, (f) 14-3-3-interacting proteins, and (g) genetic information-processing proteins (including ribosomal proteins and histones). Figs. 4 and 5 show the most interesting interactions identified in the nodes/proteins plotted on the map. Specifically, Fig. 4 shows the up- (in red) and down-regulated (in blue) proteins in OR vs. NOR at baseline, as well as the identified and unregulated proteins (in white). While Fig. 5 shows the up- (in red) and

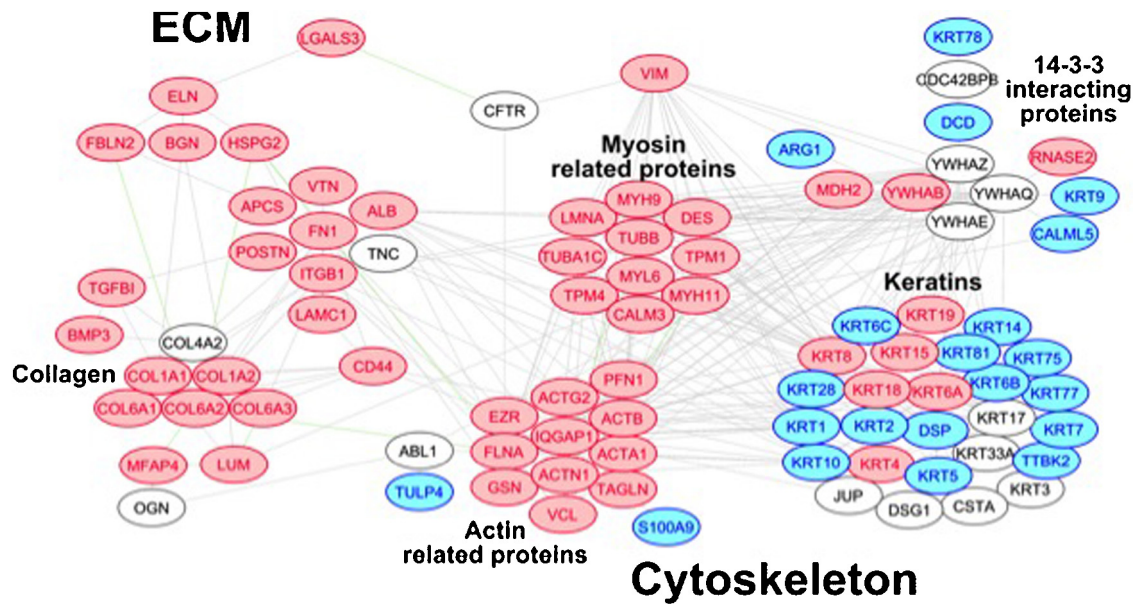


Fig. 4. Network involved the main responder (ORb) versus non-responder (NORb) differences. Red nodes = proteins up-regulated in ORb; blue nodes = proteins up-regulated in NORb; white nodes = unchanged proteins; grey edges = protein–protein interactions; green edges = genetic interactions.

down-regulated (in blue) proteins before and after treatment in the responder patients.

The major differences between the OR and NOR at baseline were detected in the ECM, contractile and structural proteins, including myosin- and actin-related proteins. Specifically, in the OR the up-regulation of vimentin (VIM), COL1A1 and PDGFB fusion transcripts (COL1A1), collagen alpha-2(I) chain (COL1A2), collagen (VI) alpha-1 chain (COL6A1), type VI collagen alpha-2 chain precursor (COL6A2), collagen type VI alpha 3 chain (COL6A3), actin-like protein (ACT), actin, alpha skeletal muscle (ACTA1), actin, cytoplasmic 1 (ACTB), alpha-actinin-1 isoform b (ACTN1), periostin (POSTN), and calmodulin 3 (CALM3) was detected; therefore, these proteins were defined as predominant in the OR. Of note, periostin was detected in all the OR biopsies and in two of the four NOR biopsies.

An IgE-binding protein (LGALS3, galectin-3, Gal-3), perlecan (HSPG2), elastin (ELN), transforming growth factor-beta (TGFB1), vinculin (VCL), ezrin (EZR), myosin 9 (MYH9), myosin light polypeptide 6 (MYL6), myosin-11 (MYH11), actin, gamma-enteric smooth muscle isoform 1 (ACTG2), fibulin-5 (FBLN5), and fibulin-2 (FBLN2) were identified exclusively in the OR. Among these groups (predominant and exclusive proteins), we analysed, by immunochemistry, vimentin (up-regulated) and Gal-3 (exclusive) in bronchial biopsies, confirming the clear difference previously detected by the MudPIT analysis (Fig. 6 and Supplementary Fig. 2).

The proteomic analysis of bronchial tissues after twelve months of omalizumab treatment showed the following: (a) ECM and structural proteins were globally decreased and (b) Gal-3 was the most stable protein marker among the exclusive proteins. Of

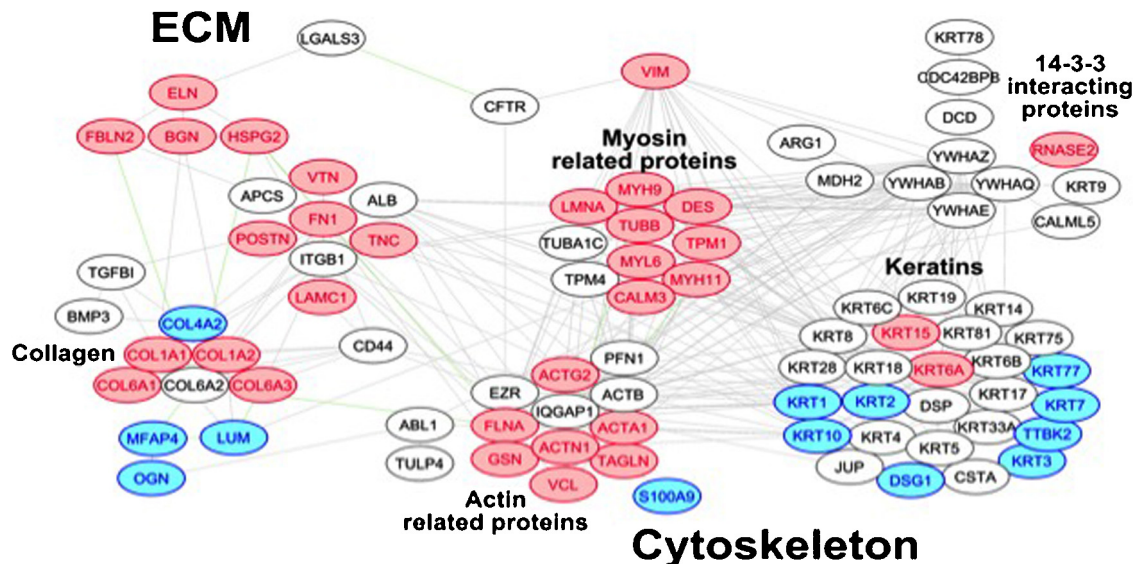


Fig. 5. Network involved the main baseline (ORb) versus post-treatment (ORp) differences in responder patients. Red nodes = proteins down-regulated in ORp; blue nodes = proteins up-regulated in ORp; white nodes = unchanged proteins; grey edges = protein–protein interactions; green edges = genetic interactions.

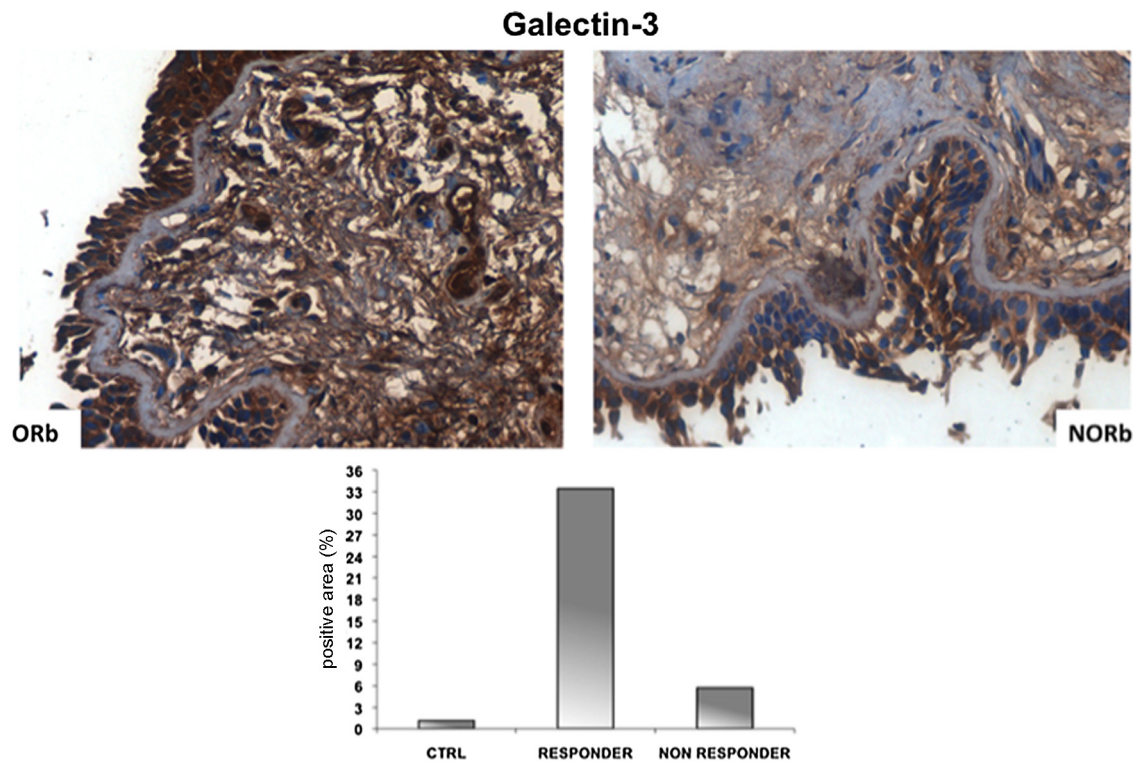


Fig. 6. IHC analysis for galectin-3 in responder (ORb) and non-responder (NORb) patients before anti-IgE treatment.

note, omalizumab treatment induced at 12 months a decrease in muscle-associated components, such as calmodulin 3 (CALM3), myosin light polypeptide 6 (MYL6), prelamins A/C (LMNA), myosin-11 (MYH11), desmin (DES), tropomyosin alpha-1 (TPM1), vinculin (VCN), vimentin (VIM), actin, gamma-enteric smooth muscle isoform 1 (ACTG2), actin alpha skeletal muscle (ACTA1), and transgelin (TAGLN), in the OR bronchial tissues (Fig. 5). In the NORs, the absence of these markers at baseline was confirmed after 12 months of omalizumab treatment. Also, few proteins, mainly keratins, changed their abundance after treatment, according with the stability of RBM.

4. Discussion

In the present work, we investigated the protein profiles of biopsies from asthma patients using a MudPIT approach. Although the relatively few samples and the identification of moderately abundant proteins (cytokines were not detected due to their very low expression levels), it is necessary to underline that the asthma patients were carefully phenotyped by histological evaluation and that the proteomic description produced high-resolution and unbiased results. However, due to the difficulty to obtain biopsies from severe asthmatic patients, this work represents the larger set investigated by proteomics analysis, as far as we know. Specifically, up to now it was not inferred structural and molecular aspects in relation to anti-IgE treatment.

The protein lists from the pre-treatment (baseline) patients were evaluated by hierarchical clustering, and the resulting segregation was in very good agreement between the OR/NOR groups, based on morphometric data from pre- and post-treatment with anti-IgE mAb [14]. The majority of the baseline descriptors were confirmed by an OR vs. NOR differential analysis. Shared descriptors and differentially abundant proteins may represent biomarkers for predicting the remodelling response to anti-IgE therapy.

The major differences between ORs and NORs lied in the cytoskeleton, mainly smooth muscle and ECM proteins. Smooth muscle proteins, mainly myosins and actins, decreased after treatment in the ORs, whereas this was not the case in the NORs, in whom the levels of these proteins at baseline were negligible. This is the first report of a reduction in the muscular component of asthma remodelling due to a therapeutic intervention. The possible relationship between this reduction and lung function parameters should be further investigated in future studies.

ECM predominant proteins, such as vimentin (a marker of airway remodelling), periostin (a marker of clinical response), and other proteins in this group were present in both OR and NOR biopsies; therefore, they are not OR-specific markers. In addition, they were not stable after treatment (see Supplementary Table 2).

Regarding ECM proteins, Gal-3 was the most stable biomarker associated with the prediction of remodelling modulation. Gal-3 gene therapy determines the inhibition of asthmatic reactions [34] and decreases airway remodelling in animals [35]. Also, Sanchez-Cuellar et al. [36] reported that galectins play roles in the resolution phase of inflammatory responses by promoting anti-inflammatory effects. In addition, OVA allergen-induced investigations in Gal-3 KO mice demonstrated that Gal-3 is involved in airway inflammation by influencing the development of profibrotic and angiogenic mediators [37]. In particular, Gal-3 expression is related to alternative macrophage activation (AMA), while classical macrophage activation with LPS reduces Gal-3 expression. In this context, our findings indicate that, before treatment, non-omalizumab responder (NOR) and omalizumab responder (OR) patients belong to distinct sub-groups differentiated by the presence of Gal-3 in bronchial tissue.

Gal-3 is part of a protein complex that includes IgE. Its main receptors, FcεRI (a high-affinity receptor for IgE) and CD23, are where Gal-3 binds both IgE and FcεRI [38]. Of note, Kim et al. [39] reported that IgE–FcεRI complexes dissociate extremely slowly and cannot be disrupted by strictly competitive inhibitors. It may be

speculated that the presence of Gal-3 may have a role in the disruption of IgE–FcεR1 interaction, facilitating the dissociation of this complex, and promoting the effectiveness of anti-IgE therapy for remodelling in Gal-3-positive patients (OR).

In summary, Gal-3 is a regulatory molecule acting at various stages from acute to chronic inflammation and tissue fibrogenesis [40]. In the initial phase of allergic induction, Gal-3 stimulates inflammation through macrophage release and increased IgE production, with the final result being airway remodelling by collagen and fibronectin deposition [41]. These data suggest a possible role of Gal-3 in the omalizumab mechanism of action on remodelling, which further stresses the importance of detecting of Gal-3 as a biomarker of treatment response.

5. Concluding remarks

Our findings indicate the following: (a) the proteomes of anti-IgE mAb OR patients are largely qualitatively and quantitatively different from those of NOR patients; (b) the proteomic state of bronchial tissue before omalizumab treatment represents a selective pattern of anti-IgE response; (c) omalizumab down-regulates bronchial smooth muscle proteins in subtype of severe asthmatics; (d) a possible explanation of the biochemical basis of OR/NOR outcomes of anti-IgE treatment, it may be due to a role of Gal-3 in the disruption of IgE–FcεR1 interaction and (e) Gal-3 can be considered a reliable biomarker with which to predict the modulation of airway remodelling in severe asthma patients treated with omalizumab.

Because Gal-3 is a matrix protein, it is feasible to detect it in serum or urine [42]. This finding could be of great interest for defining the subgroup of candidate patients who are able to modulate bronchial remodelling. Overall, these findings might suggest that blockade of IgE with omalizumab is capable of exerting disease-modifying effects on remodelling components of chronic disease. Also, the reported approach may be considered a proof of principle, and it promises to enhance the ability to type severe asthma and to identify novel potential biomarkers by means of its application on larger independent patient sets, possibly through a multicentre collaboration.

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Appendix A. Supplementary data

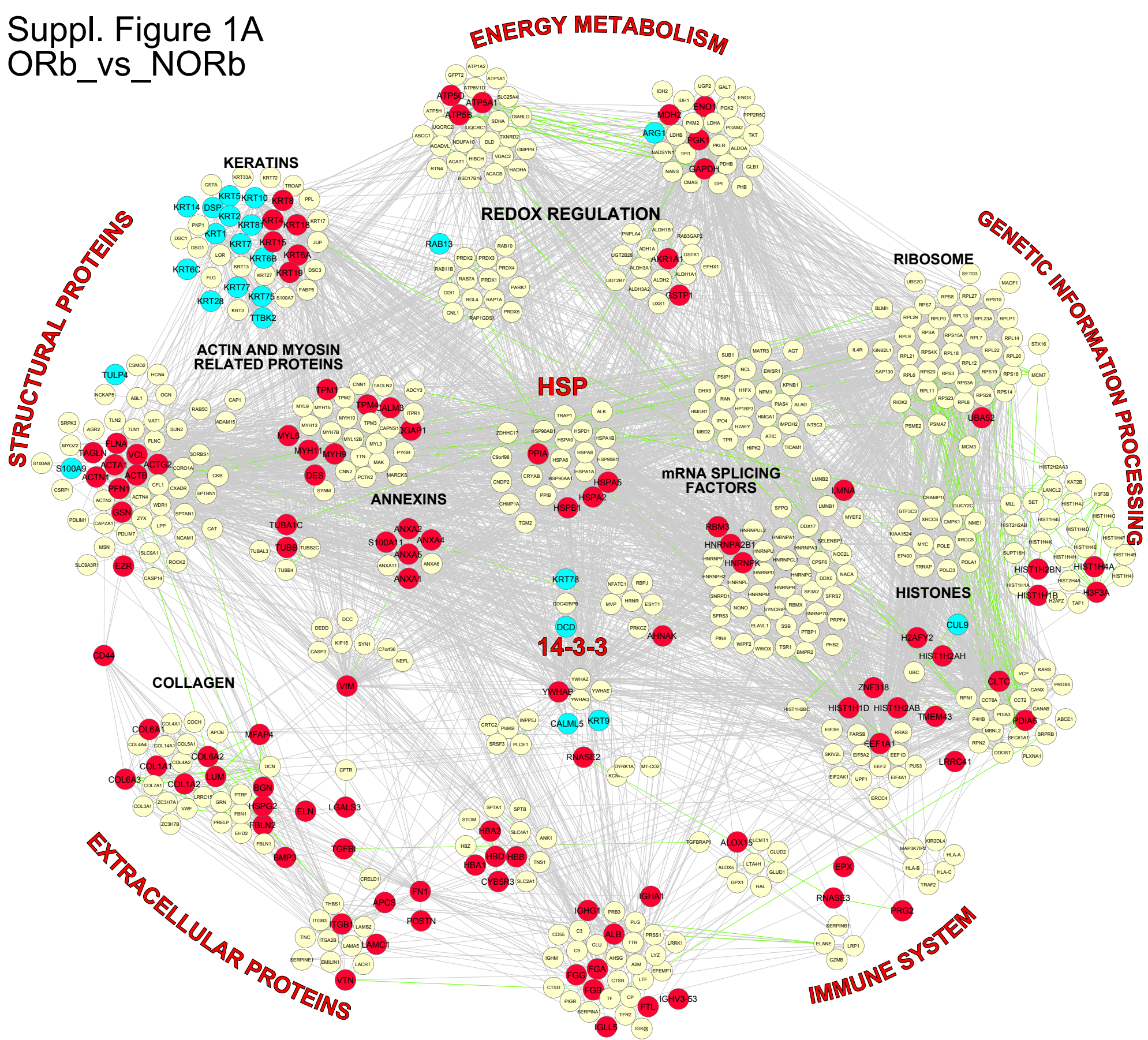
Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.imlet.2014.08.010>.

References

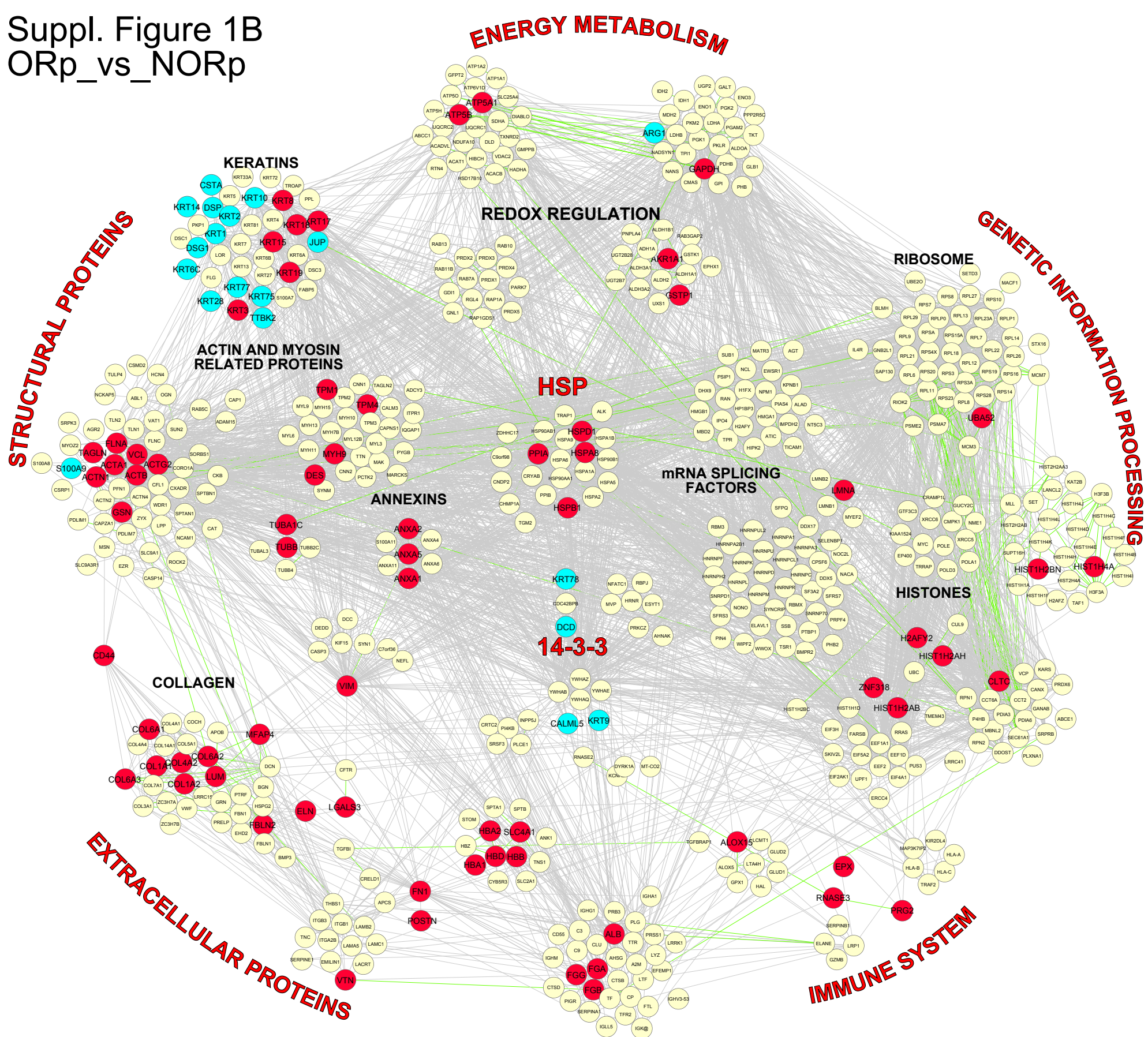
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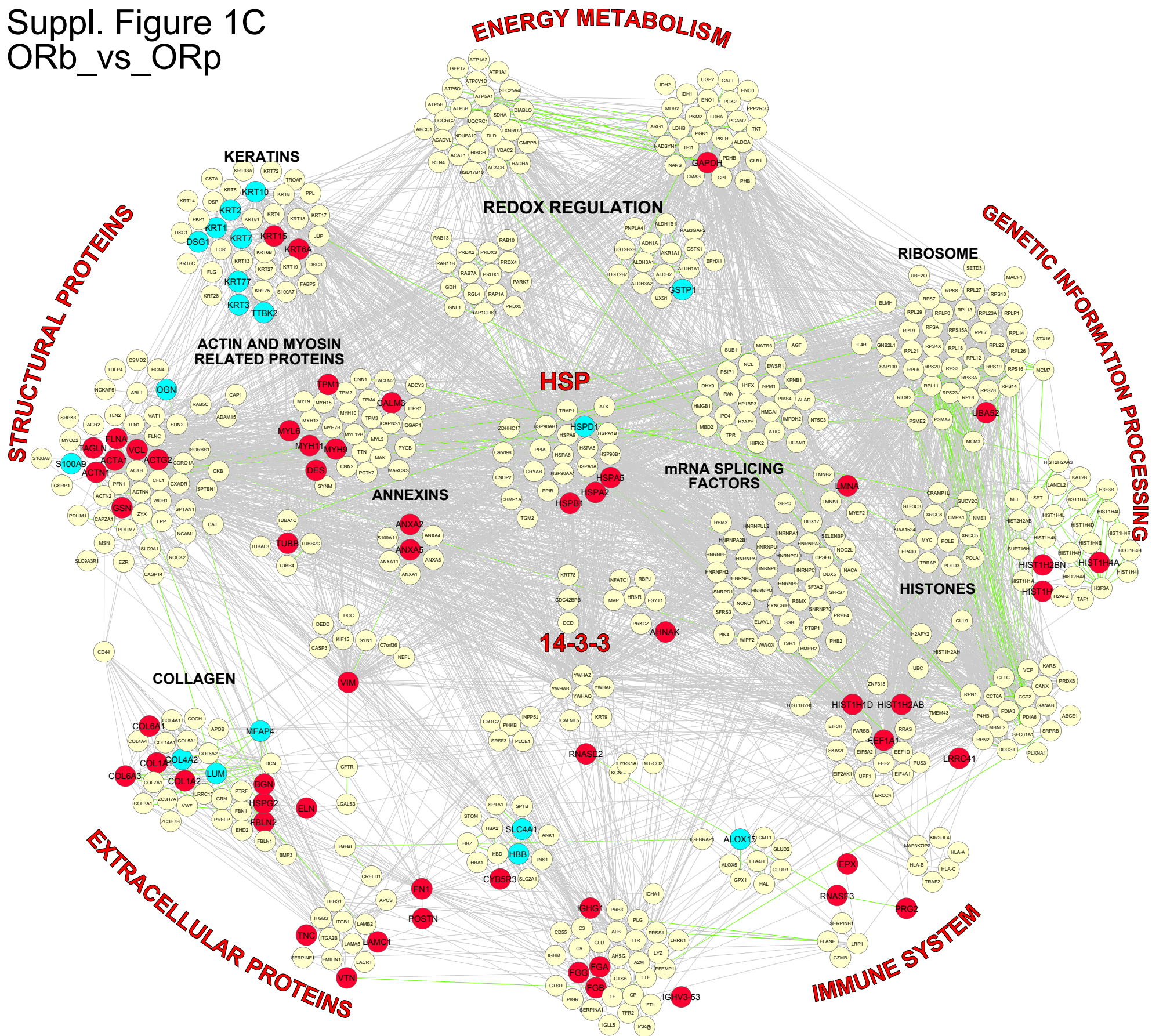
Suppl. Figure 1A
ORb_vs_NORb



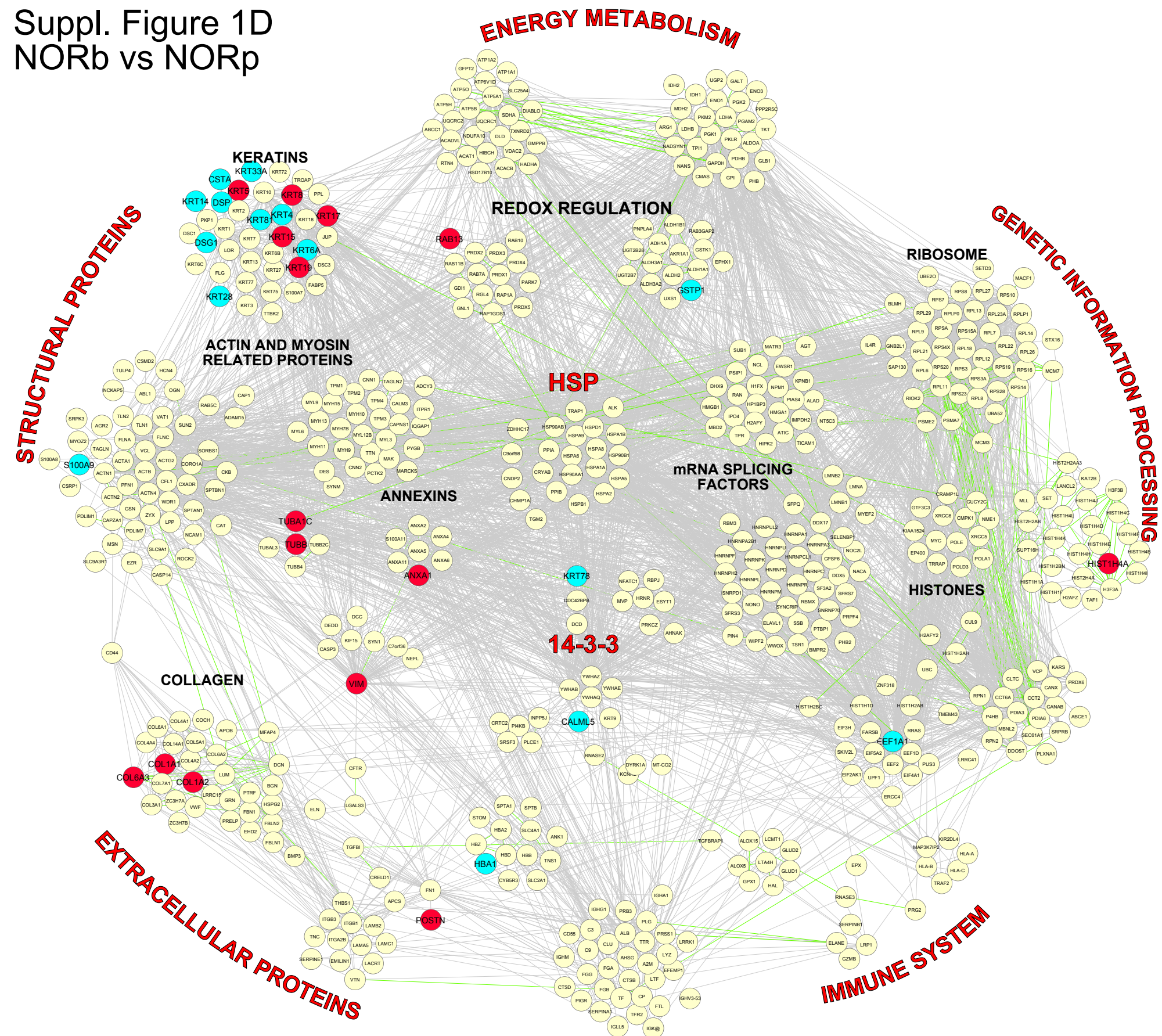
Suppl. Figure 1B
ORp_vs_NORp



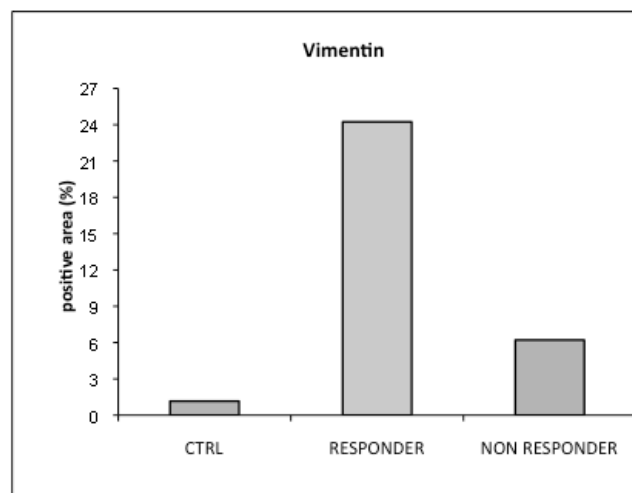
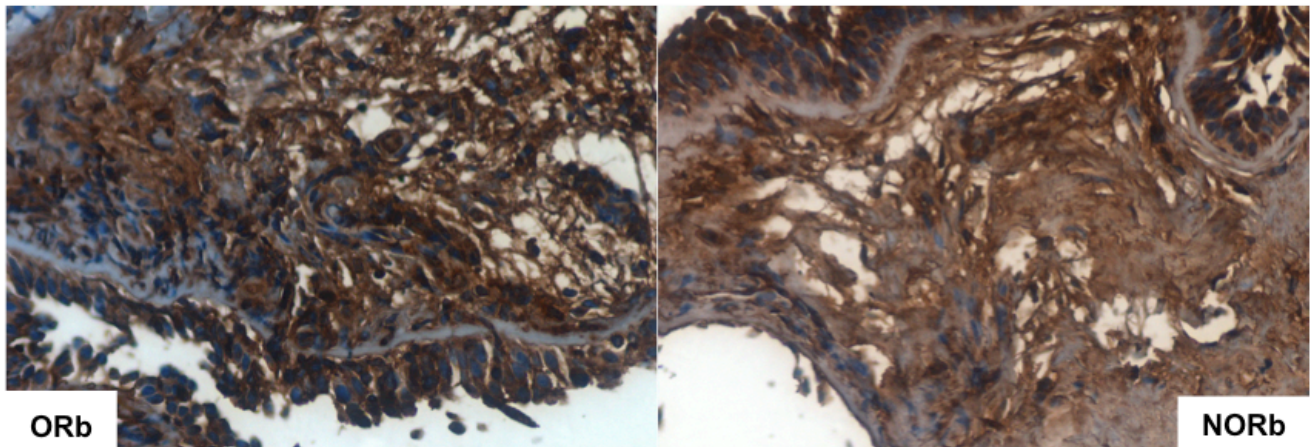
Suppl. Figure 1C
ORb_vs_ORp



Suppl. Figure 1D
NORb vs NORp



Vimentin



Supplementary Table ■■■ List of identified proteins in Responders and Non-Responders before and after omalizumab treatment. ORb=Omalizumab Responder baseline; ORp=Omalizumab Responder post-treatment; NORb= Non Omalizumab Responder baseline; NORp= Non Omalizumab Responder post-treatment. *Average, (n=4) of normalized values.

Annotation				Theoretical		ORb			ORp			NORb			NORp		
Accession NCBI	Entry UNIPROT	Protein name	Gene Name	pI	MW	Frequency (%)	Spectral Count*	Score *	Frequency (%)	Spectral Count*	Score *	Frequency (%)	Spectral Count*	Score *	Frequency (%)	Spectral Count*	Score *
177870		alpha-2-macroglobulin	A2M	6.0	163278	25	1	3	25	1	2	0	0	0	0	0	0
119589967		ATP-binding cassette, sub-family A (ABC1), member 7, isoform CRA_f	ABCA7	8.3	66743	25	1	3	0	0	0	0	0	0	0	0	0
1835659		multidrug resistance-associated protein	ABCC1	6.7	171433	25	1	3	25	1	2	0	0	0	0	0	0
312176403	Q5T3U5	multidrug resistance-associated protein 7 isoform MRP7	ABCC10	6.6	161509	25	1	4	50	2	2	0	0	0	0	0	0
119614196		hCG2010034	ABCE1	5.1	22658	0	0	0	0	0	0	0	0	0	25	1	5
7023681		unnamed protein product	ABCG2	8.1	51156	25	1	3	0	0	0	0	0	0	0	0	0
363543330	Q96IU4	alpha/beta hydrolase domain-containing protein 14B isoform 3	ABHD14B	6.2	18016	0	0	0	25	1	2	0	0	0	0	0	0
4033555		bcr-abl1 e14a2 chimeric protein	ABL1	9.1	37243	50	6	7	75	9	7	50	5	12	25	1	5
17225296	Q8WXZ6	AF324009_1 alpha-3-galactosylaminyltransferase	ABO	6.9	5064	0	0	0	0	0	0	25	2	7	0	0	0
2138330		acetyl-CoA carboxylase	ACACB	6.4	279693	25	1	3	0	0	0	0	0	0	0	0	0
3273228		very-long-chain acyl-CoA dehydrogenase	ACADVL	8.9	70373	25	1	3	25	1	2	0	0	0	0	0	0
27529706	Q15057	KIAA0041	ACAP2	6.5	88299	0	0	0	0	0	0	0	0	0	25	2	10
4557237	P24752	acetyl-CoA acetyltransferase, mitochondrial	ACAT1	9.1	45153	0	0	0	25	1	2	0	0	0	25	1	5
62420912	Q562Z6	actin-like protein	ACT	5.6	11439	25	1	4	0	0	0	0	0	0	0	0	0
62420916	Q562Z4	actin-like protein	ACT	7.7	11556	100	54	15	100	50	10	75	17	24	75	23	19
62421069	Q562R8	actin-like protein	ACT	6.6	11537	0	0	0	25	1	2	0	0	0	0	0	0
62421077	Q562R4	actin-like protein	ACT	6.2	11611	0	0	0	25	1	2	0	0	0	0	0	0
62421162	Q562M3	actin-like protein	ACT	6.2	11537	75	14	11	75	8	12	75	5	20	25	4	5
4501881	P68133	actin, alpha skeletal muscle	ACTA1	5.1	42052	100	128	81	100	98	37	50	10	30	50	10	29
4501885	P60709	actin, cytoplasmic 1	ACTB	5.2	41738	100	54	53	100	52	46	75	19	45	100	20	71
63055057	Q562R1	beta-actin-like protein 2	ACTBL2	5.3	42004	25	2	5	0	0	0	0	0	0	0	0	0
4501889	P63267	actin, gamma-enteric smooth muscle isoform 1	ACTG2	5.2	41832	100	31	27	75	12	9	0	0	0	0	0	0
4501891	P12814	alpha-actinin-1 isoform b	ACTN1	5.1	103058	100	34	52	100	25	23	25	2	5	25	1	5
4501893	P35609	alpha-actinin-2	ACTN2	5.2	103854	25	1	3	0	0	0	0	0	0	0	0	0
2804273	Q43707	alpha actinin 4	ACTN4	5.2	102269	0	0	0	25	1	2	0	0	0	0	0	0
46909592	Q13444	disintegrin and metalloproteinase domain-containing protein 15 isoform 1	ADAM15	5.9	83592	25	1	4	0	0	0	0	0	0	0	0	0
17483854		AF358666_1 a disintegrin-like and metalloprotease with thrombospondin type 1 motif 14	ADAMTS14	6.8	133768	25	1	3	0	0	0	0	0	0	0	0	0
4104226	Q60266	type III adenylyl cyclase	ADCY3	6.1	128970	0	0	0	50	1	5	0	0	0	0	0	0
4501929	P07327	alcohol dehydrogenase 1A	ADH1A	7.8	39860	25	1	3	25	2	4	0	0	0	0	0	0
47077184	Q6ZN18	unnamed protein product	AEBP2	3.6	26169	0	0	0	25	1	2	0	0	0	0	0	0
5453541	Q95994	anterior gradient protein 2 homolog	AGR2	9.4	19949	50	6	17	50	3	9	0	0	0	0	0	0
4557287	P01019	angiotensinogen	AGT	5.9	53155	0	0	0	25	1	2	0	0	0	0	0	0
535177	Q13727	AHNAK-related protein	AHNAK	5.4	57741	50	3	6	50	1	5	0	0	0	0	0	0
897824		AHNAK	AHNAK	8.7	132501	50	3	8	25	2	2	0	0	0	0	0	0
21749456	Q8N274	unnamed protein product	AHNAK	5.6	86053	75	3	9	0	0	0	0	0	0	0	0	0
61743954	Q09666	neuroblast differentiation-associated protein AHNAK isoform 1	AHNAK	5.7	628681	25	1	7	0	0	3	0	0	0	0	0	0
119602294		hCG1817843	AHNAK2	5.4	27568	25	1	3	0	0	0	0	0	0	0	0	0
112910	P02765	FETUA_HUMAN RecName: Full=Alpha-2-HS-glycoprotein	AHSG	5.4	39282	25	1	3	0	0	0	0	0	0	0	0	0
22749187	Q96MA6	adenylate kinase 8	AK8	5.7	54926	75	5	9	25	1	4	50	5	13	0	0	0
5174391	P14550	alcohol dehydrogenase [NADP+]	AKR1A1	6.3	36574	75	5	8	75	5	10	0	0	0	0	0	0
189083849	P13716	delta-aminolevulinic acid dehydratase	ALAD	6.3	36253	0	0	0	25	1	2	0	0	0	0	0	0
28590		unnamed protein product	ALB	5.9	69296	0	0	15	50	1	15	0	0	0	0	0	9
4502027	P02768	serum albumin	ALB	5.9	69367	100	107	94	100	90	66	100	80	99	100	68	96
886258	Q13740	alcam	ALCAM	5.9	65133	0	0	0	25	1	2	0	0	0	0	0	0
21361176	P00352	retinal dehydrogenase 1	ALDH1A1	6.3	54862	25	1	3	25	3	11	0	0	0	0	0	0
1263008		aldehyde dehydrogenase	ALDH1B1	6.4	57218	25	1	4	0	0	0	0	0	0	0	0	0
12804427	P30837	Aldehyde dehydrogenase 1 family, member B1	ALDH1B1	6.4	57184	0	0	0	25	1	2	0	0	0	0	0	0
28606		unnamed protein product	ALDH2	6.1	56105	50	4	9	75	6	19	0	0	0	0	0	0
13325114		Aldehyde dehydrogenase 3 family, member A1	ALDH3A1	6.1	50329	25	2	3	25	2	4	0	0	0	0	0	0
4557303	P51648	fatty aldehyde dehydrogenase isoform 2	ALDH3A2	7.8	54795	0	0	0	25	1	2	0	0	0	0	0	0
28595		aldolase A protein	ALDOA	9.1	11939	25	1	3	25	1	4	0	0	0	0	0	0

4557305	P04075	fructose-bisphosphate aldolase A isoform 1	ALDOA	8.0	39377	25	2	3	50	3	10	0	0	0	25	2	7
1483131		p80 protein	ALK	6.4	75357	50	4	6	50	2	4	0	0	0	0	0	0
40316937	P16050	arachidonate 15-lipoxygenase	ALOX15	6.1	74805	100	37	52	50	46	59	25	3	11	0	0	0
4502057	P09917	arachidonate 5-lipoxygenase isoform 1	ALOX5	5.4	77915	25	1	3	0	0	0	0	0	0	0	0	0
156151441	Q96QP1	alpha-protein kinase 1 isoform 1	ALPK1	5.8	138861	25	1	3	0	0	0	0	0	0	0	0	0
7243041	Q96L96	KIAA1330 protein	ALPK3	5.3	99212	0	0	0	25	1	2	0	0	0	0	0	0
48429165	Q86V81	THOC4_HUMAN RecName: Full=THO complex subunit 4	ALYREF	11.6	26854	0	0	0	50	2	7	0	0	0	0	0	0
169646754	O15123	angiopoietin-2 isoform c	ANGPT2	5.7	50908	25	1	3	0	0	0	0	0	0	0	0	0
28702	P16157	unnamed protein product	ANK1	5.6	206276	0	0	0	25	1	2	0	0	0	0	0	0
38638917	Q6UB99	ankyrin repeat-containing protein	ANKRD11	6.6	298069	0	0	0	25	1	2	0	0	0	0	0	0
120659880	A1L497	ANKRD26 protein	ANKRD26	5.4	198212	0	0	0	0	0	0	0	0	0	25	1	5
89941470	Q69YU3	ankyrin repeat domain-containing protein 34A	ANKRD34A	9.8	52585	0	0	0	0	0	0	0	0	0	25	2	7
256222280	A6QL64	ankyrin repeat domain-containing protein 36A	ANKRD36	8.8	217313	0	0	0	0	0	0	25	2	5	0	0	0
23271804		Ankyrin repeat domain 53	ANKRD53	8.2	38200	25	1	4	25	1	2	0	0	0	0	0	0
90186267	Q3KP44	ankyrin repeat domain-containing protein 55	ANKRD55	6.7	68353	0	0	0	25	1	4	0	0	0	0	0	0
221039678	B7Z1R6	unnamed protein product	ANO4	8.1	111482	0	0	0	0	0	0	0	0	0	25	2	10
4502101	P04083	annexin A1	ANXA1	6.6	38715	100	45	67	100	45	62	100	23	49	75	9	26
4557317	P50995	annexin A11	ANXA11	7.6	54390	25	1	3	0	0	0	0	0	0	0	0	0
4757756	P07355	annexin A2 isoform 2	ANXA2	7.8	38605	100	56	72	75	32	52	50	8	28	75	6	26
4502105	P09525	annexin A4	ANXA4	5.8	36086	100	6	17	50	6	12	0	0	0	0	0	0
194373619	B4DDZ4	unnamed protein product	ANXA4	5.5	33615	0	0	0	25	1	2	0	0	0	0	0	0
4502107	P08758	annexin A5	ANXA5	4.8	35938	100	20	28	100	15	21	50	5	12	50	7	12
71773329	P08133	annexin A6 isoform 1	ANXA6	5.3	75874	50	2	5	25	1	2	0	0	0	0	0	0
4502111	P20073	annexin A7 isoform 1	ANXA7	6.3	50316	0	0	0	25	1	2	0	0	0	0	0	0
6753074	P84091	AP-2 complex subunit mu	Ap2m1	9.9	49655	0	0	0	0	0	6	25	2	5	0	0	0
4502133	P02743	serum amyloid P-component	APCS	6.1	25388	75	13	21	75	8	20	50	7	12	25	3	5
63079709	Q6Q788	apolipoprotein A-V	APOA5	6.0	41213	0	0	0	0	0	0	25	2	5	0	0	0
34331		unnamed protein product	APOB	6.6	515560	25	1	3	0	0	0	0	0	0	0	0	0
8547064	Q0VD83	AF141332_1 apolipoprotein B48 receptor	APOBR	4.2	114835	0	0	0	25	1	2	0	0	0	0	0	0
4502203	P61204	ADP-ribosylation factor 3	ARF3	7.4	20602	0	0	0	25	1	4	0	0	0	0	0	0
10947139	P05089	arginase-1 isoform 2	ARG1	6.8	34736	75	3	9	75	9	6	100	12	39	100	14	35
40788218		KIAA0337	ARHGEF17	5.5	173997	0	0	0	0	0	0	25	2	8	0	0	0
5453704	O75915	PRA1 family protein 3	ARL6IP5	10.1	21616	50	2	6	0	0	0	0	0	0	0	0	0
52545596		hypothetical protein	ARMC2	6.5	79266	0	0	0	0	0	0	25	2	8	0	0	0
119572518		armadillo repeat containing 5, isoform CRA_c	ARMC5	8.4	94549	25	1	3	0	0	0	0	0	0	0	0	0
3808148		ASMTL	ASMTL	5.6	69738	0	0	0	0	0	0	25	2	8	0	0	0
16553768		unnamed protein product	ASPRV1	5.1	28510	0	0	0	0	0	0	25	3	16	50	8	26
1063621	Q13315	mutated in ataxia telangiectasia	ATM	6.3	350643	0	0	0	0	0	0	0	0	0	50	3	12
14424433	O60312	probable phospholipid-transporting ATPase VA	ATP10A	8.2	167564	0	0	0	0	0	0	0	0	0	25	1	7
21361181	P50523	sodium/potassium-transporting ATPase subunit alpha-1 isoform a	ATP1A1	5.2	112806	0	0	0	25	1	2	0	0	0	0	0	0
4502271	P50993	sodium/potassium-transporting ATPase subunit alpha-2	ATP1A2	5.4	112175	0	0	0	25	1	2	0	0	0	0	0	0
4757810	P25705	ATP synthase subunit alpha, mitochondrial isoform a	ATP5A1	9.5	59696	75	18	35	50	18	42	25	2	5	0	0	0
		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle															
15030240		cardiac muscle	ATP5A1	9.4	59754	25	1	3	0	0	0	0	0	0	0	0	0
28940		unnamed protein product	ATP5B	5.8	57956	100	44	62	100	43	56	50	11	18	75	6	19
5453559	O75947	ATP synthase subunit d, mitochondrial isoform a	ATP5H	5.1	18461	25	1	3	25	1	2	0	0	0	0	0	0
4502303	P48047	ATP synthase subunit O, mitochondrial	ATP5O	10.4	23245	75	3	9	50	4	10	0	0	0	0	0	0
5138993	Q9Y5K8	vacuolar H-ATPase subunit D	ATP6V1D	10.0	28417	0	0	0	0	0	0	0	0	0	25	1	5
64174737	P35670	Wilson's disease protein	ATP7B	6.3	145760	0	0	0	25	1	4	0	0	0	0	0	0
119576790		hCG2043250, isoform CRA_a	ATXN7L2	9.1	118868	0	0	0	0	0	0	25	2	7	0	0	0
4502337	P25311	zinc-alpha-2-glycoprotein	AZGP1	5.7	34259	0	0	0	0	0	0	25	3	8	25	4	7
11968003	Q9H6S1	5-azacytidine-induced protein 2 isoform a	AZI2	6.1	44889	75	4	8	75	6	10	75	5	20	50	4	12
6683498		bromodomain adjacent to zinc finger domain 2A	BAZ2A	6.4	208491	0	0	0	0	0	0	25	2	8	0	0	0
4502403	P21810	biglycan	BGN	7.3	41655	75	15	19	50	7	7	25	2	5	25	1	5
4557367	Q13867	bleomycin hydrolase	BLMH	5.8	52563	0	0	0	0	0	0	25	2	8	50	3	14
6807726	Q9NSY1	hypothetical protein	BMP2K	5.9	95534	0	0	0	25	1	2	0	0	0	0	0	0
251736057	D7NTU1	bone morphogenetic protein 3	BMP3	10.1	34957	75	3	9	25	3	2	0	0	0	0	0	0
15451916	Q13873	bone morphogenetic protein receptor type-2	BMPR2	5.8	115111	0	0	0	0	0	0	25	2	8	0	0	0
7706119	Q9NPF5	BPI fold-containing family A member 1	BP1FA1	5.3	26678	0	0	0	0	0	0	0	0	0	25	2	7

40807482	Q8TDL5	BPI fold-containing family B member 1	BPIFB1	6.8	52390	50	2	6	50	4	8	0	0	0	0	0	0
15055535	Q8N4F0	BPI fold-containing family B member 2	BPIFB2	9.0	49124	25	1	3	25	1	4	0	0	0	0	0	0
57012613	Q9BX63	FANCF_HUMAN RecName: Full=Fanconi anemia group J protein	BRIP1	6.5	140771	25	1	3	0	0	0	0	0	0	0	0	0
119630061		high-mobility group nucleosome binding domain 1, isoform CRA_g	C10orf112	12.4	33272	25	1	3	0	0	0	0	0	0	0	0	0
58219030	Q5T4H9	putative uncharacterized protein C10orf114	C10orf114	11.7	14823	50	2	5	25	1	2	0	0	0	0	0	0
119617649		chromosome 12 open reading frame 28	C12orf28	7.3	88929	25	1	3	0	0	0	0	0	0	0	0	0
341913842		PREDICTED: uncharacterized protein C12orf55	C12orf55	8.1	140924	0	0	0	25	1	4	0	0	0	0	0	0
153791218	Q8IXR9	uncharacterized protein C12orf56 isoform 2	C12orf56	9.7	53510	0	0	0	0	0	0	0	0	0	50	4	17
46409512	Q8NAA6	uncharacterized protein C15orf53	C15orf53	10.3	19737	0	0	0	25	1	2	0	0	0	0	0	0
46409514	Q8N8G6	putative uncharacterized protein C15orf54	C15orf54	10.3	21009	0	0	0	0	0	25	2	5	0	0	0	0
24308354	Q96MC5	uncharacterized protein C16orf45 isoform 1	C16orf45	5.9	23698	0	0	0	25	2	0	0	0	0	0	0	0
39795541		C16orf46 protein	C16orf46	8.9	42752	25	1	3	0	0	0	0	0	0	0	0	0
119572590		hypothetical protein LOC90835, isoform CRA_e	C16orf93	9.2	23041	0	0	0	0	0	25	2	8	0	0	0	0
119610683		hCG32827, isoform CRA_c	C17orf49	6.1	28012	0	0	0	0	0	0	0	0	0	25	1	7
12698047		KIAA1751 protein	C1orf222	6.5	81160	25	1	3	0	0	0	0	0	0	0	0	0
119596736		chromosome 20 open reading frame 71, isoform CRA_a	C20orf71	7.3	23709	0	0	0	50	1	4	0	0	0	0	0	0
30425380	Q9H1P6	uncharacterized protein C20orf85	C20orf85	8.6	15720	0	0	0	25	1	2	0	0	0	0	0	0
218749820	Q9H0A9	uncharacterized protein C21orf56 isoform 1	C21orf56	7.2	37571	25	1	3	0	0	0	0	0	0	50	3	12
84570013	Q4AC94	C2CD3 protein	C2CD3	6.6	138848	0	0	0	25	1	4	0	0	0	0	0	0
179665		complement component C3	C3	6.0	187164	75	10	16	50	10	18	0	0	0	0	0	0
16553119	Q96M34	unnamed protein product	C3orf30	5.4	60189	0	0	0	25	2	0	0	0	0	0	0	0
68533033	Q4LE82	C4A variant protein	C4A	6.6	193446	75	10	16	50	7	13	25	2	5	0	0	0
22760732		unnamed protein product	C4orf14	8.7	78431	0	0	0	0	0	0	25	2	8	0	0	0
12751497	Q9H7E9	UPF0488 protein C8orf33	C8orf33	10.4	24993	50	2	6	0	0	0	25	2	5	0	0	0
49169841	Q6P1X6	UPF0598 protein C8orf82	C8orf82	9.3	23890	0	0	0	0	0	0	25	2	5	0	0	0
4502511	P02748	complement component C9	C9	5.3	63174	25	1	3	0	0	0	0	0	0	25	1	5
150036326	A6PVP3	chromosome 9 open reading frame 102	C9orf102	4.7	19476	25	1	3	0	0	0	0	0	0	0	0	0
39930541	Q9BUH6	uncharacterized protein C9orf142	C9orf142	5.2	21640	0	0	0	25	1	2	0	0	0	0	0	0
187019	Q02641	L-type voltage-gated calcium channel B subunit	CACNB1	8.3	57781	0	0	0	25	1	4	0	0	0	0	0	0
114640420		PREDICTED: cell adhesion molecule 1 isoform 7	CADM1	4.6	48599	0	0	0	0	0	0	25	2	8	0	0	0
825635		calmodulin	CALM3	3.9	17164	100	18	20	50	6	11	25	2	5	25	1	5
24657605		Calmodulin-like 5	CALML5	4.1	15891	0	0	0	50	7	6	50	3	13	50	9	26
223278387	Q9NZT1	calmodulin-like protein 5	CALML5	4.1	15893	50	5	11	75	8	10	75	17	20	75	21	35
180631		calnexin	CANX	4.1	40837	25	1	3	50	2	5	0	0	0	0	0	0
10716563	P27824	calnexin	CANX	4.3	67569	25	1	3	0	0	0	0	0	0	0	0	0
5453595	Q01518	adenylyl cyclase-associated protein 1	CAP1	8.0	51623	50	2	6	50	3	9	0	0	0	0	0	0
4502565	P04632	calpain small subunit 1	CAPNS1	4.9	28317	0	0	0	50	2	7	0	0	0	0	0	0
40674605	P04632	CAPNS1 protein	CAPNS1	4.8	28230	0	0	0	25	2	2	0	0	0	0	0	0
5453597	P52907	F-actin-capping protein subunit alpha-1	CAPZA1	5.4	32884	25	1	4	25	1	2	0	0	0	0	0	0
5453599	P47755	F-actin-capping protein subunit alpha-2	CAPZA2	5.5	32911	0	0	0	25	1	2	0	0	0	0	0	0
119609995	I3L414	caspase recruitment domain family, member 14, isoform CRA_d	CARD14	5.8	53910	25	1	4	0	0	0	0	0	0	0	0	0
6912286	P31944	caspase-14	CASP14	5.3	27680	0	0	0	0	0	0	25	4	12	25	2	7
14790115	P42574	caspase-3	CASP3	6.1	31609	0	0	0	0	0	0	25	2	7	0	0	0
6912288	Q9UKL3	CASP8-associated protein 2	CASP8AP2	6.1	222657	0	0	0	25	1	2	0	0	0	0	0	0
4557014	P04040	catalase	CAT	7.0	59757	0	0	0	25	2	6	0	0	0	25	1	7
3549155	O75295	R27328_2	CATSPERG	6.6	46406	0	0	0	25	1	2	0	0	0	0	0	0
4502599	P16152	carbonyl reductase [NADPH] 1	CBR1	8.4	30376	25	1	4	50	2	6	0	0	0	0	0	0
56713254	Q6YP21	kynurenine--oxoglutarate transaminase 3 isoform 1	CCBL2	8.2	51350	0	0	0	0	0	0	0	0	0	25	2	7
119631417	B8ZZB3	hypothetical protein FLJ39502, isoform CRA_b	CCDC141	5.4	74587	0	0	0	25	1	2	0	0	0	0	0	0
144719191	A2VCL2	C6orf184 protein	CCDC162P	7.2	21642	0	0	0	25	2	0	0	0	0	0	0	0
71052023		Coiled-coil domain containing 40	CCDC40	5.2	116979	50	2	7	0	0	0	0	0	0	0	0	0
16552930		unnamed protein product	CCDC42	9.6	38036	25	1	3	0	0	0	0	0	0	0	0	0
119618444		hCG1652305	CCDC42B	8.8	33671	0	0	0	0	0	0	25	2	7	0	0	0
119582086	D3DQH5	coiled-coil domain containing 69, isoform CRA_a	CCDC69	5.4	34601	25	1	3	0	0	0	0	0	0	0	0	0
34534433	Q6ZSE7	unnamed protein product	CCDC78	8.5	30269	0	0	0	25	1	2	0	0	0	0	0	0
5453603	P78371	T-complex protein 1 subunit beta isoform 1	CCT2	6.0	57434	0	0	0	25	1	2	0	0	0	0	0	0
4502643	P40227	T-complex protein 1 subunit zeta isoform a	CCT6A	6.2	57970	0	0	0	25	1	2	0	0	0	0	0	0
180066		CD1c antigen	CD1C	5.7	37595	25	1	3	0	0	0	0	0	0	0	0	0
119609580		hCG1652195, isoform CRA_b	CD300LD	8.9	17747	0	0	0	25	1	2	0	0	0	0	0	0

435700		CD44R5	CD44	4.9	43001	75	3	8	75	5	7	0	0	0	0	0	0
19347597	Q8TD14	decay-accelerating factor 1a	CD55	9.8	33420	25	1	3	0	0	0	0	0	0	0	0	0
4502699	O60729	dual specificity protein phosphatase CDC14B isoform 1	CDC14B	8.7	52700	0	0	0	25	1	4	0	0	0	0	0	0
115527097	Q9Y5S2	serine/threonine-protein kinase MRCK beta	CDC42BPB	5.9	194175	25	1	3	0	0	0	0	0	0	0	0	0
3021388		CDC45 like protein	CDC45	5.2	65555	25	1	3	0	0	0	0	0	0	0	0	0
4826669	P55291	cadherin-15	CDH15	4.7	88916	0	0	0	25	1	2	0	0	0	0	0	0
14625445		KIAA1775 protein	CDHR1	5.2	93464	0	0	0	0	0	0	25	2	5	0	0	0
37595545	Q00537	cyclin-dependent kinase 17 isoform 1	CDK17	9.3	59527	0	0	0	25	1	2	0	0	0	25	1	5
8923040	Q9NXV6	CDKN2A-interacting protein	CDKN2AIIP	9.4	61126	0	0	0	0	0	0	25	2	8	0	0	0
119602269		hCG2040344	CEND1	5.3	16605	0	0	0	25	1	4	0	0	0	0	0	0
21735548	Q9BV73	centrosome-associated protein CEP250	CEP250	4.9	280949	0	0	0	0	0	0	25	2	8	0	0	0
18027302		AF287356_1 centrosome-associated protein 350	CEP350	6.0	350704	25	1	3	0	0	0	0	0	0	0	0	0
14042300	Q96ST8	unnamed protein product	CEP89	6.3	62099	0	0	0	25	1	4	0	0	0	0	0	0
34526693	G0XYE7	unnamed protein product	CERKL	6.6	31260	0	0	0	25	2	0	0	0	0	0	0	0
119592074		hCG2040276	CFL1	4.4	9340	0	0	0	0	0	0	25	2	7	0	0	0
1354931	Q9HD42	PRSM1	CHMP1A	6.5	33250	0	0	0	25	1	4	0	0	0	0	0	0
3513503	O75339	cartilage intermediate layer protein	CILP	8.3	132539	0	0	0	25	1	4	0	0	0	0	0	0
21536286	P12277	creatine kinase B-type	CKB	5.2	42645	0	0	0	25	1	2	0	0	0	0	0	0
4502897	Q96005	cleft lip and palate transmembrane protein 1	CLPTM1	5.9	76030	25	1	3	0	0	0	0	0	0	0	0	0
4758012	Q00610	clathrin heavy chain 1	CLTC	5.4	191614	75	12	21	75	12	29	0	0	0	0	0	0
355594753	P10909	clusterin	CLU	5.9	52495	100	7	21	75	5	14	25	3	5	25	1	5
8923900	Q8NFW8	N-acetylneuraminate cytidyltransferase	CMAS	7.8	48331	25	1	3	0	0	0	0	0	0	0	0	0
12644008	P30085	KCY_HUMAN RecName: Full=UMP-CMP kinase	CMPK1	5.3	22190	0	0	0	25	1	2	0	0	0	0	0	0
21732502		hypothetical protein	CMYA5	4.6	165596	0	0	0	25	1	4	0	0	12	0	0	0
15620780	Q96KP4	glutamate carboxypeptidase	CNDP2	5.7	52853	0	0	0	25	1	2	0	0	0	0	0	0
		CNKR1_HUMAN RecName: Full=Connector enhancer of kinase suppressor of															
50400606	Q969H4	ras 1	CNKSRI	5.1	79638	0	0	0	0	0	0	25	4	12	0	0	0
21361120	P51911	calponin-1	CNN1	9.4	33171	50	5	14	0	0	0	0	0	0	0	0	0
119631098		hCG2002849	CNN2	10.0	19218	0	0	0	0	0	0	0	0	0	25	1	7
4758022	O43405	cochlin	COCH	7.9	59484	0	0	0	25	1	2	0	0	0	0	0	0
23957690	P83436	conserved oligomeric Golgi complex subunit 7	COG7	5.2	86271	0	0	0	0	0	0	0	0	0	25	1	5
2065167	Q05707	collagen type XIV	COL14A1	5.4	78636	0	0	0	25	3	4	0	0	0	0	0	0
55743096	Q05707	collagen alpha-1(XIV) chain	COL14A1	5.0	193376	25	3	6	25	2	2	0	0	0	0	0	0
116008152	P39059	collagen alpha-1(XV) chain	COL15A1	4.8	141614	50	3	8	25	3	6	0	0	0	0	0	0
1082300		A53019 collagen alpha 1(XVIII) chain - human (fragment)	COL18A1	9.4	70369	25	1	5	25	1	2	0	0	0	0	0	0
7717447	P39060	human type XVIII collagen	COL18A1	5.4	154018	0	0	0	25	1	2	0	0	0	0	0	0
30016		unnamed protein product	COL1A1	4.9	44723	75	10	8	25	3	2	0	0	0	0	0	0
180392	P02452	alpha 1 (I) chain propeptide	COL1A1	6.4	98563	0	0	0	25	1	2	0	0	0	0	0	0
1418928		prepro-alpha1(I) collagen	COL1A1	5.6	138912	50	3	7	25	1	2	0	0	0	0	0	0
1888411		COL1A1 and PDGFB fusion transcript	COL1A1	4.4	9563	75	4	9	50	4	2	0	0	0	0	0	0
3288487		COL1A1 and PDGFB fusion transcript	COL1A1	5.1	36987	100	127	34	100	100	25	100	71	75	100	38	54
30023		unnamed protein product	COL1A2	10.1	69344	75	7	11	75	4	14	25	2	5	25	1	7
825646		unnamed protein product	COL1A2	7.9	72260	100	81	35	100	57	20	100	36	75	100	24	53
71296700		COL21A1 protein	COL21A1	9.8	46968	25	1	3	25	1	2	0	0	0	0	0	0
22652113		AF406780_1 alpha 1 type XXII collagen	COL22A1	6.9	161115	25	1	3	0	0	0	0	0	0	0	0	0
32364065		alpha 1 type XXIV collagen	COL24A1	8.3	175504	0	0	0	0	0	0	25	2	8	0	0	0
930045		alpha-1 (III) collagen	COL3A1	9.7	96500	25	1	3	0	0	0	0	0	0	0	0	0
4502951	P02461	collagen alpha-1(III) chain	COL3A1	6.1	138452	25	2	3	0	0	0	0	0	0	0	0	0
		A Chain A, The 1.9-A Crystal Structure Of The Noncollagenous (Nc1) Domain Of															
21466080	P02462	Human Placenta Collagen Iv	COL4A1	7.6	25296	25	1	3	0	0	0	0	0	0	0	0	0
30076	P08572	unnamed protein product	COL4A2	9.3	100676	0	0	0	25	2	0	0	0	0	0	0	0
537329	P08572	alpha-2 type IV collagen	COL4A2	7.8	67175	0	0	0	75	4	7	0	0	0	0	0	0
457161		alpha 4(IV) collagen	COL4A4	6.7	48106	50	2	6	0	0	0	0	0	0	0	0	0
4502955	P29400	collagen alpha-5(IV) chain isoform 1	COL4A5	7.4	160925	0	0	0	25	1	6	0	0	0	0	0	0
30030		alpha-1 collagen VI (AA 574-1009)	COL6A1	5.4	47900	100	26	12	75	16	7	25	2	5	0	0	0
30032		polypeptide (AA -19 to 237)	COL6A1	5.7	28584	100	31	41	75	36	23	0	0	0	25	3	5
1915902		collagen (VI) alpha-1 chain	COL6A1	5.5	47808	100	33	45	75	18	35	50	5	19	0	0	0
105706		C35243 collagen alpha 2(VI) chain , short splice form - human (fragment)	COL6A2	4.5	26563	100	8	24	25	12	6	0	0	0	0	0	0

13603394		type VI collagen alpha 2 chain	COL6A2	5.7	108488	100	25	46	75	22	30	25	3	11	25	3	11
41350923		Collagen, type VI, alpha 2	COL6A2	5.8	108607	75	7	11	50	5	4	0	0	0	0	0	0
49168630	Q6FWH5	COL6A2	COL6A2	6.6	25037	50	5	9	50	7	5	0	0	0	0	0	0
3127926		collagen type VI, alpha 3 chain	COL6A3	6.4	343551	100	328	384	100	188	212	75	37	104	25	8	32
453699		type VII collagen	COL7A1	7.3	115208	75	3	8	75	6	10	25	6	11	25	1	5
4502961	Q59F16	collagen alpha-1(VII) chain	COL7A1	5.9	295023	0	0	0	25	1	2	0	0	0	25	1	5
60219541		hypothetical protein	COLEC11	4.6	23774	0	0	0	0	0	0	25	4	12	0	0	0
109134349	Q9UBF2	coatomer subunit gamma-2	COPG2	5.5	97623	50	3	6	25	1	2	0	0	0	0	0	0
5902134	P31146	coronin-1A	CORO1A	6.2	51027	75	5	11	50	1	4	0	0	0	0	0	0
311893369	O00230	cortistatin	CORT	8.9	11533	0	0	0	0	0	0	25	2	8	0	0	0
288962065	D3YPT7	cytochrome c oxidase subunit II	COX2	4.5	25566	25	1	3	25	1	2	0	0	0	0	0	0
4557485	P00450	ceruloplasmin	CP	5.4	122205	0	0	0	25	1	2	0	0	0	0	0	0
221316749	P15088	mast cell carboxypeptidase A	CPA3	9.3	48621	25	1	3	0	0	0	0	0	0	0	0	0
4503015	O75131	copine-3	CPNE3	5.5	60131	25	1	3	0	0	0	0	0	0	0	0	0
871299	Q16630	Human pre-mRNA cleavage factor I 68 kDa subunit	CPSF6	7.0	59154	0	0	0	25	1	2	0	0	0	0	0	0
239753102		PREDICTED: hypothetical protein LOC100292909	CPSF6	11.8	26240	25	1	3	0	0	0	0	0	0	0	0	0
21739290		hypothetical protein	CRAMP1L	5.4	67847	25	1	3	0	0	0	0	0	0	0	0	0
22095397	Q96HD1	cysteine-rich with EGF-like domain protein 1 isoform 2	CRELD1	4.7	45359	0	0	0	0	0	0	25	4	12	0	0	0
37693043		transducer of regulated CREB protein 2	CRTC2	6.6	73175	25	1	3	0	0	0	0	0	0	0	0	0
4503057	P02511	alpha-crystallin B chain	CRYAB	6.9	20160	25	1	3	0	0	0	0	0	0	0	0	0
27437049	Q8N4W3	granulocyte colony-stimulating factor isoform b	CSF3	5.8	21945	0	0	0	25	1	4	0	0	0	0	0	0
30908443		CUB and sushi multiple domains 2	CSMD2	5.7	380037	0	0	0	0	0	0	25	2	7	0	0	0
148238116	P67963	casein kinase I isoform alpha	csnk1a1	9.9	38902	25	1	3	0	0	0	0	0	0	0	0	0
4758086	P21291	cysteine and glycine-rich protein 1 isoform 1	CSRFP1	8.5	20536	25	2	7	25	2	0	0	0	0	0	0	0
4503109	P01036	cystatin-S	CST4	4.8	16215	0	0	0	25	1	2	0	0	0	0	0	0
4885165	P01040	cystatin-A	CSTA	5.3	11007	75	5	9	75	7	10	50	7	19	100	30	67
4503117	P04080	cystatin-B	CSTB	7.5	11141	50	2	6	50	4	7	0	0	0	0	0	0
4503139	P07858	cathepsin B	CTSB	5.9	37822	0	0	0	25	1	4	0	0	0	0	0	0
4503143	P07339	cathepsin D	CTSD	6.1	44553	0	0	0	25	1	4	0	0	0	0	0	0
24307991	Q8IWT3	cullin-9	CUL9	5.2	281228	0	0	0	75	3	6	75	11	24	50	5	17
219518994	B7ZLS7	CXorf58 protein	CXorf58	10.5	38647	0	0	0	0	0	0	25	2	5	0	0	0
63054828	P49447	cytochrome b561	CYB561	8.7	27560	25	1	3	0	0	0	0	0	0	0	0	0
22760235	Q9UHQ9	unnamed protein product	CYB5R1	9.7	34036	0	0	0	0	0	0	0	0	0	25	2	7
4503327	P00387	NADH-cytochrome b5 reductase 3 isoform 1	CYB5R3	7.4	34195	100	18	26	75	9	17	0	0	0	0	0	0
71052044		Cytochrome P450, family 27, subfamily C, polypeptide 1	CYP27C1	9.5	42588	0	0	0	0	0	0	25	2	8	0	0	0
47077173	Q6ZN67	unnamed protein product	CYP4X1	7.4	57888	0	0	0	50	1	4	0	0	0	0	0	0
399758	Q65ZQ3	FBRNP	D10S102	8.4	29358	0	0	0	25	1	4	0	0	0	0	0	0
20521984		KIAA1743 protein	DAB2IP	6.2	114410	25	1	3	0	0	0	0	0	0	0	0	0
55741849	Q96JK2	DDB1- and CUL4-associated factor 5	DCAF5	5.4	103964	25	1	3	0	0	0	0	0	0	0	0	0
312176366	Q58WW2	DDB1- and CUL4-associated factor 6 isoform c	DCAF6	5.1	106458	0	0	0	25	1	2	0	0	0	0	0	0
453210		tumour suppressor	DCC	6.3	158456	0	0	0	0	0	0	25	4	12	0	0	0
16751921	P81605	dermcidin	DCD	6.1	11285	100	15	24	100	17	17	100	56	93	100	48	50
150456471	A2VCK2	doublecortin domain-containing protein 2B	DCDC2B	8.9	37623	0	0	0	25	1	4	0	0	0	0	0	0
73490260		KIAA1773 protein	DCHS1	4.8	360703	25	1	3	0	0	0	0	0	0	0	0	0
4503271	P07585	decorin isoform a	DCN	8.7	39748	50	3	9	25	4	8	0	0	0	0	0	0
473947		KIAA0115	DDOST	5.9	50712	25	1	3	0	0	0	0	0	0	0	0	0
119615346		dolichyl-diphosphooligosaccharide-protein glycosyltransferase, isoform CRA_d	DDOST	4.7	23606	0	0	0	0	0	0	25	2	8	0	0	0
297261056		PREDICTED: probable ATP-dependent RNA helicase DDX17	DDX17	8.6	72308	0	0	0	25	1	2	0	0	0	0	0	0
19352318		KEO5 protein	DEDD	8.8	40419	25	1	3	0	0	0	0	0	0	0	0	0
56204536	Q5TB30	DEP domain containing 1	DEPDC1	8.1	89359	0	0	0	0	0	0	0	0	0	25	2	7
3411134	Q549R7	mutant desmin	DES	5.1	53535	50	6	5	0	0	0	0	0	0	0	0	0
55749932	P17661	desmin	DES	5.1	53536	75	119	117	50	34	8	25	3	16	0	0	0
71011128	Q45VM6	mutant desmin	DES	5.2	53535	0	0	4	25	2	0	0	0	0	0	0	0
29788751	Q86XP1	diacylglycerol kinase eta isoform 2	DGKH	6.1	134866	0	0	0	25	1	4	0	0	0	0	0	0
149408122	Q96C10	probable ATP-dependent RNA helicase DHX58	DHX58	7.0	76546	0	0	0	25	2	0	0	0	0	0	0	0
1806048		nuclear DNA helicase II	DHX9	6.3	140877	25	1	3	0	0	0	0	0	0	0	0	0
119618717		hCG1782202, isoform CRA_a	DIABLO	9.5	35846	0	0	0	25	1	2	0	0	0	0	0	0
6808091	Q9NT83	hypothetical protein	DKFZp434M1123	6.1	47635	0	0	0	0	0	0	0	0	0	25	1	5

21732332	Q8NDT0	hypothetical protein	DKFZp434P0729	4.7	22225	25	1	3	0	0	0	0	0	0	0	0	0	0
197102950	Q5R6H0	GTP-binding nuclear protein Ran isoform 2	DKFZp468B1019	5.9	14704	50	2	5	0	0	0	0	0	0	0	0	0	0
12224965	Q9H038	hypothetical protein	DKFZp667C165	9.1	11494	0	0	0	50	2	6	0	0	0	0	0	0	0
52545928	Q63HQ4	hypothetical protein	DKFZp686K04147	5.3	133182	75	25	25	75	16	23	25	2	5	25	1	5	5
50949774	Q6AI58	hypothetical protein	DKFZp781A0295	6.1	120312	25	1	3	0	0	0	0	0	0	0	0	0	0
57999503	Q5H9R5	hypothetical protein	DKFZp781F05101	6.5	88281	0	0	0	25	1	4	0	0	0	0	0	0	0
31873734	Q7Z3K9	hypothetical protein	DKFZp781L0540	5.4	90023	0	0	0	25	1	4	0	0	0	0	0	0	0
91199540	P09622	dihydrolipoyl dehydrogenase, mitochondrial isoform 1	DLD	7.7	54125	25	1	3	25	1	2	0	0	0	0	0	0	0
119573998		discs, large homolog 1 (Drosophila), isoform CRA_c	DLG1	11.5	12857	0	0	0	25	1	2	0	0	0	0	0	0	0
1515355	Q92796	neuroendocrine-dlg	DLG3	6.6	90344	0	0	0	0	0	0	0	0	0	25	1	7	7
6624922		DMBT1/8kb.1 protein	DMBT1	5.0	259575	50	2	6	0	0	0	0	0	0	0	0	0	0
61654444		dermokine-gamma 2	DMKN	6.2	38239	0	0	0	0	0	0	25	2	8	25	5	10	10
193785200	B3KX41	unnamed protein product	DMTF1	4.3	54213	25	1	3	0	0	0	0	0	0	0	0	0	0
62945417	Q09019	dystrophia myotonica WD repeat-containing protein	DMWD	6.9	70376	0	0	0	0	0	0	0	0	0	25	1	7	7
119585744		hCG1779312, isoform CRA_b	DNAH12	5.5	447400	25	1	3	0	0	0	0	0	0	0	0	0	0
71891729	Q9P225	KIAA1503 protein	DNAH2	5.9	511494	0	0	0	25	1	4	0	0	0	0	0	0	0
119619962		hypothetical protein FLJ37357, isoform CRA_a	DNAH6	6.4	96097	0	0	0	25	1	4	0	0	0	0	0	0	0
68077166	Q5F1R6	dnaJ homolog subfamily C member 21 isoform 2	DNAJC21	5.2	61971	0	0	0	0	0	0	25	2	8	0	0	0	0
16553740		unnamed protein product	DOK6	5.8	25507	25	1	3	0	0	0	0	0	0	0	0	0	0
4503377	Q16555	dihydropyrimidinase-related protein 2 isoform 2	DPYSL2	5.9	62237	75	3	9	25	1	2	0	0	0	0	0	0	0
4826702	Q08554	desmocollin-1 isoform Dsc1b	DSC1	5.2	93758	25	4	10	25	3	11	25	2	8	50	3	12	12
10801205		AF293359_1 desmocollin 3a	DSC3	5.7	100013	50	2	7	25	2	0	25	2	7	25	3	11	11
30506		desmoglein type 1	DSG1	4.8	113716	75	15	32	100	29	27	75	15	48	100	43	123	123
1147813		desmoplakin l	DSP	6.4	331775	100	27	66	100	28	35	75	38	133	100	63	184	184
18765752	Q13627	dual specificity tyrosine-phosphorylation-regulated kinase 1A isoform 2	DYRK1A	9.0	84485	25	1	3	25	1	2	0	0	0	0	0	0	0
157694516	Q9NTX5	enoyl-CoA hydratase decarboxylase isoform 1	ECHDC1	8.4	32958	0	0	0	0	0	0	50	3	13	25	2	7	7
4503471	P68104	elongation factor 1-alpha 1	EEF1A1	9.4	50142	100	22	38	75	14	27	50	3	13	75	12	31	31
10436857	Q9H7G6	unnamed protein product	EEF1D	6.2	71418	0	0	0	25	1	2	0	0	0	0	0	0	0
4503483	P13639	elongation factor 2	EEF2	6.4	95339	75	5	14	50	6	17	0	0	0	0	0	0	0
38570107	Q5THR3	EF-hand calcium-binding domain-containing protein 6 isoform a	EFCAB6	8.4	172802	25	1	4	0	0	0	0	0	0	0	0	0	0
458228	Q12805	extracellular protein	EFEMP1	5.1	43138	0	0	0	25	1	2	0	0	0	0	0	0	0
21750383	Q8IYU8	unnamed protein product	EFHA1	6.9	40551	0	0	0	25	2	0	0	0	0	0	0	0	0
21361462	Q9NZN4	EH domain-containing protein 2	EHD2	6.0	61162	50	2	6	25	1	2	0	0	0	0	0	0	0
22760314	Q8NCJ3	unnamed protein product	EHD2	6.7	46905	75	6	11	50	3	7	0	0	0	0	0	0	0
11125768	Q9BQI3	eukaryotic translation initiation factor 2-alpha kinase 1 isoform a	EIF2AK1	5.6	71044	0	0	0	25	1	4	0	0	0	0	0	0	0
4503515	O15372	eukaryotic translation initiation factor 3 subunit H	EIF3H	6.1	39887	0	0	0	0	0	0	0	0	0	25	1	7	7
4503529	P60842	eukaryotic initiation factor 4A-l isoform 1	EIF4A1	5.2	46107	50	4	12	25	2	8	0	0	0	0	0	0	0
9966867	Q9GZV4	eukaryotic translation initiation factor 5A-2	EIF5A2	5.3	16764	25	1	3	50	1	5	0	0	0	0	0	0	0
4503549	P08246	neutrophil elastase	ELANE	9.4	28519	25	2	5	50	4	8	25	2	5	0	0	0	0
38201714	Q15717	ELAV-like protein 1	ELAVL1	9.5	36093	0	0	0	25	1	2	0	0	0	0	0	0	0
182021		elastin	ELN	10.8	66136	50	4	6	50	2	6	0	0	0	0	0	0	0
2228743		elastin	ELN	10.7	51808	25	4	3	0	0	0	0	0	0	25	3	5	5
22761674	Q8N2G0	unnamed protein product	ELN	10.5	42266	25	1	3	0	0	0	0	0	0	0	0	0	0
31874660		hypothetical protein	ELN	10.8	59847	100	27	42	75	14	22	0	0	0	25	1	5	5
22761794	Q8N766	unnamed protein product	EMC1	7.6	109519	0	0	0	25	1	2	0	0	0	0	0	0	0
5901944	Q9Y6C2	EMILIN-1	EMILIN1	5.0	106695	25	1	3	0	0	0	0	0	0	0	0	0	0
31179		enolase	ENO1	5.7	49478	75	4	9	25	3	4	0	0	0	0	0	0	0
4503571	P06733	alpha-enolase isoform 1	ENO1	7.2	47170	75	9	19	50	6	20	0	0	0	25	2	7	7
301897469	P13929	beta-enolase isoform 1	ENO3	7.6	46988	25	1	3	25	1	2	0	0	0	0	0	0	0
55597035	H2QI91	PREDICTED: macrophage-capping protein isoform 9	ENSG00000042493	5.8	38476	50	2	6	25	1	2	0	0	0	0	0	0	0
2119276	Q6LC01	I38369 beta-tubulin - human (fragment)	ENSG00000183311	4.6	48881	100	72	84	75	49	51	75	25	71	75	18	61	61
119575481		hCG1978892, isoform CRA_a	ENSG00000203599	8.2	6835	0	0	0	25	1	2	0	0	0	0	0	0	0
114644568	H2Q607	PREDICTED: keratin, type II cytoskeletal 6A	ENSG00000205420	8.0	59963	50	4	6	75	6	6	75	5	20	100	11	29	29
4529894		HSP70-HOM	ENSG00000206383	5.7	70406	75	4	11	75	5	16	25	2	7	25	1	5	5
10435053		unnamed protein product	ENSG00000206488	10.6	36342	0	0	0	0	0	0	25	2	8	0	0	0	0
119613349		hCG2041504	ENSG00000214271	8.7	9884	0	0	0	0	0	0	25	2	7	0	0	0	0
239744846		PREDICTED: putative UPF0607 protein ENSP00000383144	ENSG000000214470	10.9	37593	25	1	3	0	0	0	0	0	0	0	0	0	0
371446015		immunoglobulin G heavy chain variable region	ENSG00000214613	7.2	12778	0	0	0	0	0	0	25	2	7	0	0	0	0
51094986		similar to tropomyosin 3	ENSG00000214869	4.3	24802	50	2	6	25	1	2	0	0	0	0	0	0	0

357529931	G8HXG1	pol/env protein, partial	ENSG00000219665	8.9	81799	0	0	0	25	1	2	0	0	0	0	0	0	0
1841546		tenascin X	ENSG00000233323	5.1	464454	25	1	3	0	0	0	0	0	0	0	0	0	0
47125290		DDR1 protein	ENSG00000234078	6.0	97186	75	4	9	25	1	2	0	0	0	0	0	0	0
6010129		corneodesmosin	ENSG00000237123	8.0	41566	25	2	3	25	2	0	25	2	7	0	0	0	0
14020823	Q96TB7	envelope protein	env	7.7	19985	0	0	0	25	1	2	0	0	0	0	0	0	0
14017853		KIAA1818 protein	EP400	9.5	125525	0	0	0	0	0	0	25	2	8	0	0	0	0
76803654	P29323	EPHB2_HUMAN RecName: Full=Ephrin type-B receptor 2	EPHB2	6.1	117399	0	0	0	25	2	0	0	0	0	0	0	0	0
34538		unnamed protein product	EPHX1	6.6	52905	25	1	3	25	1	2	25	2	5	0	0	0	0
4503595	P11678	eosinophil peroxidase	EPX	10.6	81041	100	52	53	50	36	43	25	6	16	0	0	0	0
71017495	Q4H1F2	ERBB2	ERBB2	8.0	6928	0	0	0	25	1	2	0	0	0	0	0	0	0
1524411	Q92889	DNA repair endonuclease subunit	ERCC4	6.3	103347	0	0	0	0	0	0	0	0	0	25	2	7	0
3600071	Q9BXR3	polymerase	ERVK6	8.9	64717	0	0	0	0	0	0	0	0	0	25	1	5	0
10437984		unnamed protein product	ESYT1	5.3	97131	25	1	3	0	0	0	0	0	0	0	0	0	0
182283		open reading frame	EVI2B	4.5	48683	0	0	0	0	0	0	50	3	13	25	2	7	0
253970502	Q01844	RNA-binding protein EWS isoform 3	EWSR1	9.5	68331	0	0	0	25	1	2	0	0	0	0	0	0	0
117938266	Q17RC7	exocyst complex component 3-like protein 4	EXOC3L4	5.9	79828	0	0	0	0	0	0	0	0	0	25	1	5	0
31283		unnamed protein product	EZR	5.9	69399	100	5	14	25	3	11	0	0	0	0	0	0	0
4557581	Q01469	fatty acid-binding protein, epidermal	FABP5	6.8	15137	50	6	14	50	6	12	75	7	28	25	11	21	0
194306562	Q96GS6	alpha/beta hydrolase domain-containing protein 17A isoform 1	FAM108A1	7.1	39092	25	1	3	0	0	0	0	0	0	0	0	0	0
13375721	Q9BPY3	protein FAM118B	FAM118B	5.6	39500	0	0	0	25	1	4	0	0	0	25	2	10	0
223671925	Q8N0U4	protein FAM185A isoform 1	FAM185A	7.9	42316	0	0	0	25	2	0	0	0	0	0	0	0	0
7023099	Q9NVB8	unnamed protein product	FAM21A	5.7	101182	25	1	3	0	0	0	0	0	0	0	0	0	0
46255030	P58499	protein FAM3B isoform a	FAM3B	8.9	25983	0	0	0	0	0	0	0	0	0	25	1	5	0
22759990	Q8N2R8	unnamed protein product	FAM43A	6.1	45805	0	0	0	25	1	2	0	0	0	0	0	0	0
7020140		unnamed protein product	FAM83E	9.8	51798	0	0	0	0	0	0	0	0	0	25	1	7	0
34191116	Q8TC84	Fibronectin type III and ankyrin repeat domains 1	FANK1	8.9	38327	0	0	0	25	1	2	0	0	0	0	0	0	0
7768938		phenylalanyl tRNA synthetase	FARSB	6.4	66172	25	1	3	0	0	0	0	0	0	0	0	0	0
7407144		AF231022_1 protocadherin Fat 2	FAT2	4.9	479390	0	0	0	0	0	0	25	2	7	0	0	0	0
13661193		AF126110_1 fibulin-1 isoform D	FBLN1	5.0	77205	25	1	3	50	3	2	0	0	0	0	0	0	0
575233		fibulin-2	FBLN2	4.6	126544	75	12	23	75	4	13	0	0	0	0	0	0	0
19743803	Q9UBX5	fibulin-5	FBLN5	4.4	50181	100	6	12	50	4	6	0	0	0	0	0	0	0
1335064		fibrillin	FBN1	4.7	325688	25	1	3	25	1	2	0	0	0	0	0	0	0
148922963	Q9UKT6	F-box/LRR-repeat protein 21	FBXL21	6.0	49152	25	1	3	0	0	0	0	0	0	0	0	0	0
14042214		unnamed protein product	FBXO18	8.3	88295	0	0	0	0	0	0	25	2	5	0	0	0	0
10436278	Q6PIJ6	unnamed protein product	FBXO38	8.9	39954	0	0	0	25	1	2	0	0	0	0	0	0	0
16117781	Q969H0	F-box/WD repeat-containing protein 7 isoform 1	FBXW7	5.4	79595	0	0	0	25	1	2	0	0	0	0	0	0	0
13785945	Q8WWV6	AF354295_1 FKSG87 protein	FCAMR	8.4	56749	0	0	0	25	1	4	0	0	0	0	0	0	0
20810036		FCRL3 protein	FCRL3	6.7	81854	0	0	0	0	0	0	25	2	7	0	0	0	0
		AF343663_1 immunoglobulin superfamily receptor translocation associated protein 2b	FCRL5	7.4	65604	0	0	0	25	1	2	0	0	0	0	0	0	0
13591712	Q96RD9	FER-1-like protein 5	FER1L5	7.5	242326	0	0	0	25	1	4	0	0	0	0	0	0	0
42558478	Q2NNQ7	ffibrinogen alpha chain isoform alpha-E	FGA	5.6	94896	75	65	64	50	39	44	0	0	0	25	6	16	0
4503689	P02671	FGA	FGA	8.7	7044	100	11	17	50	9	11	25	2	8	0	0	0	0
27597169	Q86Z09	FGA	FGB	8.2	55874	75	57	69	50	31	42	0	0	0	25	3	5	0
70906435	P02675	fibrinogen beta chain isoform 1	FGF11	12.1	36430	25	1	3	0	0	0	0	0	0	0	0	0	0
62088360	Q59FR9	fibroblast growth factor 11 variant	FGG	6.5	24091	100	75	50	75	53	38	25	3	16	25	7	16	0
930064		fibrinogen gamma chain (partial) (212 AA)	FGG	5.3	51461	75	10	16	50	7	8	0	0	0	0	0	0	0
70906439	P02679	fibrinogen gamma chain isoform gamma-B	FKBP11	9.8	22148	50	4	6	0	0	0	0	0	0	0	0	0	0
7706131	Q9NYL4	peptidyl-prolyl cis-trans isomerase FKBP11 isoform 1	FKBP15	5.0	135180	0	0	0	0	0	0	0	0	0	25	2	10	0
3327162	Q5T1M5	KIAA0674 protein	FLG	9.5	435167	0	0	0	25	1	2	0	0	0	25	1	7	0
60097902	P20930	filaggrin	FLG2	8.1	248072	25	1	3	0	0	0	25	2	7	75	8	23	0
62122917	Q5D862	filaggrin-2	FLJ00119	5.4	153599	25	1	3	25	1	2	0	0	0	0	0	0	0
18676444	Q8TES4	FLJ00119 protein	FLJ00390	6.2	35037	0	0	0	25	1	2	0	0	0	0	0	0	0
21748626	Q8NF12	FLJ00390 protein	FLJ13231	6.1	238123	25	1	4	0	0	0	0	0	0	0	0	0	0
219841830		C5orf42 protein	FLNA	5.7	280760	100	115	203	100	55	34	25	2	5	25	3	11	0
28243		unnamed protein product	FLNC	9.1	19905	25	2	3	0	0	0	0	0	0	0	0	0	0
5629917		ABP-L, gamma filamin	FN1	5.4	256689	100	29	39	50	15	25	25	2	5	0	0	0	0
31397		fibronectin	FN1	7.1	38430	50	3	8	50	1	4	0	0	0	0	0	0	0
15866734		fibronectin	FN1	6.3	35591	75	8	14	50	1	4	0	0	0	0	0	0	0
15866738		fibronectin																

1911185		forkhead box L1	FOX1	6.3	38092	0	0	0	0	0	0	25	2	5	0	0	0
34365423	Q5H8C1	hypothetical protein	FREM1	9.8	42486	0	0	0	25	1	2	0	0	0	0	0	0
119625474		hCG38879	FREM3	5.9	243495	0	0	0	25	1	2	0	0	0	0	0	0
114656716		PREDICTED: FERM domain-containing protein 5 isoform 1	FRMD5	8.0	63187	50	2	6	0	0	0	0	0	0	0	0	0
14017851		KIAA1817 protein	FRMPD3	9.5	108890	25	1	3	0	0	0	0	0	0	0	0	0
18204301		FRS2 protein	FRS2	5.7	57528	25	1	3	0	0	0	0	0	0	0	0	0
12053063		hypothetical protein	FSCB	3.9	75133	25	1	3	0	0	0	0	0	0	0	0	0
60219464		hypothetical protein	FSIP2	6.5	170866	0	0	0	0	0	0	25	2	7	0	0	0
20149498	P02792	ferritin light chain	FTL	5.4	20021	75	3	8	25	1	4	0	0	0	0	0	0
58257642	Q8N1G2	KIAA0082	FTSJD2	6.6	99843	0	0	0	0	0	0	0	0	0	25	2	10
19913379	Q95866	protein G6b isoform G6b-D	G6B	9.5	20170	25	1	3	0	0	0	0	0	0	0	0	0
194097327	P18505	gamma-aminobutyric acid receptor subunit beta-1	GABRB1	9.0	54182	0	0	0	0	0	0	0	0	0	25	1	7
950395		galactose-1-phosphate uridyl transferase	GALT	7.9	5809	25	1	3	0	0	0	0	0	0	0	0	0
2274968		Glucosidase II	GANAB	5.7	106900	50	5	11	50	4	8	0	0	0	0	0	0
7669492	P04406	glyceraldehyde-3-phosphate dehydrogenase	GAPDH	8.7	36012	100	90	75	100	62	57	100	28	58	100	24	60
119608450		globoside alpha-1,3-N-acetylgalactosaminyltransferase 1, isoform CRA_b	GBGT1	7.1	39681	25	1	3	0	0	0	0	0	0	0	0	0
31873994	Q6ZN66	hypothetical protein	GBP6	5.9	72445	0	0	0	25	1	4	0	0	0	0	0	0
4503971	P31150	rab GDP dissociation inhibitor alpha	GDI1	4.9	50583	75	10	14	50	2	7	0	0	0	0	0	0
4826742	Q94808	glucosamine--fructose-6-phosphate aminotransferase	GFPT2	7.0	76864	25	1	3	0	0	0	0	0	0	0	0	0
179401	P16278	beta-D-galactosidase (EC 3.2.1.23)	GLB1	6.1	76025	0	0	0	0	0	0	0	0	0	25	1	5
3061316	P10070	hGLI2	GLI2	6.7	131579	0	0	0	25	1	4	0	0	0	0	0	0
4885281	P00367	glutamate dehydrogenase 1, mitochondrial	GLUD1	7.7	61341	25	1	3	0	0	0	0	0	0	0	0	0
31815		glutamate dehydrogenase (NAD(P)+)	GLUD2	8.7	61434	50	4	6	50	5	8	0	0	0	0	0	0
7380947		AF132541_1 Gem-interacting protein	GMIP	5.4	106733	25	1	3	0	0	0	0	0	0	0	0	0
11761619	Q9Y5P6	mannose-1-phosphate guanylttransferase beta isoform 1	GMPPB	6.0	42604	25	1	3	0	0	0	0	0	0	0	0	0
5174447	P63244	guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1	7.5	35037	25	1	3	50	3	8	0	0	0	0	0	0
194377678	B4DWZ0	unnamed protein product	GNL1	5.2	45321	0	0	0	0	0	0	0	0	0	25	1	5
405715	Q14789	giantin	GOLGB1	4.8	376076	0	0	0	25	1	2	0	0	0	0	0	0
7020145	Q9NXJ9	unnamed protein product	GON4L	5.3	77609	0	0	0	0	0	0	25	2	5	0	0	0
18201905	P06744	glucose-6-phosphate isomerase isoform 2	GPI	8.4	63089	50	4	6	50	5	8	0	0	0	0	0	0
62088730	Q59F85	glucose phosphate isomerase variant	GPI	9.2	55687	50	3	5	50	2	5	0	0	0	0	0	0
16551407		unnamed protein product	GPR137	8.4	46002	0	0	0	0	0	0	25	4	12	0	0	0
11275368		striatum-specific G protein-coupled receptor	GPR88	9.8	40225	25	1	4	25	1	2	25	2	5	0	0	0
16904208	Q8WXG9	AF435925_1 very large G protein-coupled receptor 1b	GPR98	4.4	692224	0	0	0	25	3	0	0	0	0	0	0	0
4467837	P07203	glutathione peroxidase	GPX1	6.2	21900	0	0	0	25	1	2	0	0	0	0	0	0
32171221	Q7Z6J2	general receptor for phosphoinositides 1-associated scaffold protein isoform 1	GRASP	9.0	42579	0	0	0	25	1	2	0	0	0	0	0	0
51094646	Q13322	growth factor receptor-bound protein 10	GRB10	8.1	66427	0	0	0	0	0	0	0	0	0	25	1	7
20521972		KIAA1719 protein	GRIP2	6.0	113158	0	0	0	0	0	0	25	2	7	0	0	0
221039854	B7Z204	unnamed protein product	GRM3	7.6	52253	0	0	0	25	1	4	0	0	0	0	0	0
183613	P28799	granulin	GRN	6.5	63574	0	0	0	25	1	2	0	0	0	0	0	0
4504165	P06396	gelsolin isoform a	GSN	5.9	85698	75	17	33	75	10	23	0	0	0	0	0	0
10435228	Q8NEC7	unnamed protein product	GSTCD	7.6	51980	0	0	0	25	2	0	0	0	0	0	0	0
7705704	Q9Y2Q3	glutathione S-transferase kappa 1 isoform a	GSTK1	8.7	25462	25	1	3	0	0	0	0	0	0	0	0	0
4504183	P09211	glutathione S-transferase P	GSTP1	5.3	23357	100	20	35	100	25	35	25	3	11	75	15	38
14670350	P78347	general transcription factor II-I isoform 1	GTF2I	6.0	112328	0	0	0	25	1	2	0	0	0	0	0	0
6808030		hypothetical protein	GTF3C3	5.2	82029	0	0	0	0	0	0	25	2	5	0	0	0
338502		heat-stable enterotoxin receptor	GUCY2C	6.8	123369	25	1	3	0	0	0	0	0	0	0	0	0
181186	P10144	granzyme B	GZMB	9.9	27663	0	0	0	25	1	4	0	0	0	0	0	0
5174449	Q92522	histone H1x	H1FX	11.2	22488	0	0	0	25	1	2	0	0	0	0	0	0
10435335		unnamed protein product	H2AFY	10.2	39592	50	2	6	50	3	9	0	0	0	0	0	0
10433885	Q9HA11	unnamed protein product	H2AFY2	10.5	29898	100	16	19	50	14	12	25	3	10	0	0	0
4504255	P0C0S5	histone H2A.Z	H2AFZ	11.0	13554	50	3	8	50	3	7	25	5	11	0	0	0
4504279	P84243	histone H3.3	H3F3A	11.8	15329	75	3	8	50	3	7	0	0	0	0	0	0
		enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of															
862457		trifunctional protein	HADHA	9.4	82889	25	1	3	0	0	0	0	0	0	0	0	0
4504345	P69905	hemoglobin subunit alpha	HBA1;	9.1	15258	100	120	24	100	136	22	50	9	13	75	29	34
183805	P78461	pseudo-a-thal	HBA2	8.8	9079	100	94	22	100	104	23	0	0	0	0	0	0

27902682	Q86YQ1	hemoglobin alpha-2	HBA2	9.8	9672	25	1	3	25	1	2	0	0	0	0	0	0
95115683		hemoglobin alpha 1-2 hybrid	HBA2	9.4	15273	25	2	3	50	3	4	25	2	5	0	0	0
29446		unnamed protein product	HBB	7.5	15969	50	6	9	25	4	11	0	0	0	0	0	0
4504349	D9YZU5	hemoglobin subunit beta	HBB	6.9	15999	75	38	32	100	58	36	75	12	28	75	11	31
13492060		AF319479_1 truncated beta-globin	HBB	9.5	6543	75	14	11	100	12	15	50	7	13	25	3	7
23268683	Q8IUL9	hemoglobin beta chain variant Hb.Sinai-Bel Air	HBB	5.6	11523	25	1	3	50	2	7	0	0	0	0	0	0
66731527	Q4TZM4	hemoglobin beta chain	HBB	6.1	11023	75	21	13	75	32	6	0	0	0	25	6	7
82548237	Q2XP30	mutant beta-globin	HBB	5.4	2398	25	1	3	25	1	2	0	0	0	0	0	0
256028940	C8C504	beta-globin	HBB	8.2	15998	25	7	4	50	8	5	0	0	0	50	3	12
4504351	P02042	hemoglobin subunit delta	HBD	8.2	16056	100	96	59	100	99	54	0	0	0	50	6	25
4885397	P02008	hemoglobin subunit zeta	HBZ	8.6	15638	25	2	3	50	3	7	0	0	0	0	0	0
16554265	Q96LI4	unnamed protein product	hCG_2004368	5.5	26891	0	0	0	0	0	0	0	0	0	25	1	5
73695475	Q9H583	HEAT repeat-containing protein 1	HEATR1	6.1	242370	0	0	0	25	1	2	0	0	0	0	0	0
10440442	Q8NG08	FLJ00057 protein	HELB	4.7	65531	0	0	0	0	0	0	0	0	0	25	2	10
54792138	Q6DFV5	probable helicase with zinc finger domain	Helz	7.0	218843	25	1	3	0	0	0	0	0	0	0	0	0
21040343	Q30201	hereditary hemochromatosis protein isoform 4	HFE	7.5	29157	25	1	3	0	0	0	0	0	0	0	0	0
62988791		unknown	HIBCH	10.1	15966	0	0	0	0	0	0	25	2	8	0	0	0
11907599		AF208291_1 protein kinase HIPK2	HIPK2	8.4	130941	25	1	3	25	1	4	0	0	0	0	0	0
4885373	Q02539	histone H1.1	HIST1H1A	11.5	21843	25	1	3	0	0	0	0	0	0	0	0	0
4885381	P16401	histone H1.5	HIST1H1B	11.4	22581	75	4	8	0	0	0	0	0	0	0	0	0
4885377	P16402	histone H1.3	HIST1H1D	11.5	22351	100	22	25	50	9	15	0	0	0	0	0	0
66365795	Q4VB24	Histone cluster 1, H1e	HIST1H1E	11.5	21894	50	5	14	50	3	4	0	0	0	0	0	0
10645195	P04908	histone H2A type 1-B/E	HIST1H2AB	11.5	14136	75	22	14	50	12	14	25	5	11	25	1	5
18105045	Q96KK5	histone H2A type 1-H	HIST1H2AH	11.3	13907	100	37	32	75	35	25	50	5	18	25	3	11
1568545	Q92646	none	HIST1H2APS4	11.3	12655	0	0	0	25	1	2	0	0	0	0	0	0
78070466		HIST1H2BC protein	HIST1H2BI	10.8	13776	75	5	8	0	0	0	0	0	0	0	0	0
1568557		histone H2B	HIST1H2BN	10.8	13937	100	64	30	100	52	19	50	16	13	75	16	19
31979		histone H2A.2	HIST1H2BO	10.6	13908	50	3	8	0	0	0	0	0	0	0	0	0
4504301	P62805	histone H4	HIST1H4A	11.8	11368	100	209	95	100	163	79	100	55	103	75	31	58
4504251	Q6FI13	histone H2A type 2-A	HIST2H2AA3	11.4	14096	25	12	7	25	47	0	25	38	12	25	8	7
28195394	Q8IUE6	histone H2A type 2-B	HIST2H2AB	11.3	13996	100	53	32	100	57	35	75	50	40	75	48	35
140169749	A4URH5	MHC class I antigen	HLA-A	6.6	31262	25	1	3	0	0	0	0	0	0	0	0	0
238684632	C9WEN0	MHC class I antigen	HLA-A	7.4	21129	25	1	3	25	1	4	0	0	0	0	0	0
32441709	Q7YPH4	MHC class I antigen	HLA-B	5.7	31472	25	1	3	0	0	0	0	0	0	0	0	0
341838808	G1EPS8	MHC class I antigen	HLA-B	6.4	21081	0	0	0	0	0	0	25	2	8	0	0	0
52630342	P10321	HLA class I histocompatibility antigen, Cw-1 alpha chain	HLA-C	5.6	40605	25	1	3	0	0	0	0	0	0	0	0	0
22208967	P17096	high mobility group protein HMG-I/HMG-Y isoform a	HMGAI	10.8	11651	25	1	3	25	1	4	0	0	0	0	0	0
968888		HMG-1	HMGBI	5.6	24994	25	1	4	25	1	2	0	0	0	0	0	0
		high mobility group nucleosome-binding domain-containing protein 3 isoform															
20270186	Q15651	HMGN3a	HMGN3	10.2	10642	25	1	3	0	0	0	0	0	0	0	0	0
194388272	B4E3K8	unnamed protein product	HMHA1	5.4	110539	25	1	3	0	0	0	0	0	0	0	0	0
5803036	Q13151	heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	9.6	30804	0	0	0	0	0	0	25	2	5	0	0	0
1711240		TIS	HNRNPA1	9.2	28898	25	1	3	50	4	13	0	0	0	0	0	0
4504447	P22626	heterogeneous nuclear ribonucleoproteins A2/B1 isoform A2	HNRNPA2B1	8.9	35966	75	10	16	75	9	19	25	2	5	25	1	5
34740329	P51991	heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	9.3	39553	25	2	5	50	3	9	0	0	0	25	1	7
14249959		Heterogeneous nuclear ribonucleoprotein C (C1/C2)	HNRNPC	4.8	32356	50	3	7	50	3	7	0	0	0	0	0	0
61966711	Q60812	heterogeneous nuclear ribonucleoprotein C-like 1	HNRNPCL1	4.8	32105	25	1	3	50	2	7	0	0	0	0	0	0
929663		unnamed protein product	HNRNPD	7.8	24199	0	0	0	25	1	2	0	0	0	0	0	0
4826760	P52597	heterogeneous nuclear ribonucleoprotein F	HNRNPF	5.3	45625	75	4	11	50	6	13	25	2	5	0	0	0
9624998	P55795	heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	5.9	49214	50	2	6	50	4	13	0	0	0	0	0	0
296189587		PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform 8	HNRNPK	5.6	48462	50	10	16	50	8	22	0	0	0	0	0	0
32356	P14866	unnamed protein product	HNRNPL	6.7	60188	0	0	0	25	1	2	0	0	0	0	0	0
14141152	P52272	heterogeneous nuclear ribonucleoprotein M isoform a	HNRNPM	9.0	77446	50	2	7	50	3	10	0	0	0	0	0	0
5031755	O43390	heterogeneous nuclear ribonucleoprotein R isoform 2	HNRNPR	8.2	70881	25	1	3	50	2	6	0	0	0	0	0	0
32358		hnRNP U protein	HNRNPU	5.5	88946	75	4	12	50	4	12	0	0	0	0	0	0
52545896	Q1KMD3	hypothetical protein	HNRNPUL2	5.1	72423	0	0	0	25	1	2	0	0	0	0	0	0
119609188	D3DUR5	hypothetical protein LOC25900, isoform 3, isoform CRA_b	HOM-TES-103	11.9	27530	25	1	3	0	0	0	0	0	0	0	0	0
3237299	O75806	HOXA-9B	HOXA-9	9.5	30614	25	1	3	0	0	0	0	0	0	0	0	0
4504465	P14652	homeobox protein Hox-B2	HOXB2	4.9	37915	25	2	3	0	0	0	0	0	0	0	0	0

11615138	I3L347	hCG2042068, isoform CRA_a	HOXB-AS3	10.2	12834	0	0	0	0	0	0	0	0	0	0	25	1	5
56676330	Q5SSJ5	heterochromatin protein 1-binding protein 3	HP1BP3	10.1	61151	0	0	0	25	1	2	0	0	0	0	0	0	0
1877501	P78365	polyhomeotic 2 homolog	HPH2	9.8	47189	0	0	0	25	1	4	0	0	0	0	0	0	0
28557150		hornerin	HRNR	9.8	48597	0	0	0	0	0	0	50	7	19	50	4	16	
57864582	Q86YZ3	hornerin	HRNR	10.2	282389	25	3	7	25	3	0	0	0	0	25	1	5	
83715985	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 isoform 2	HSD17B10	7.0	25950	0	0	0	50	2	7	0	0	0	0	0	0	0
32486	P07900	unnamed protein product	HSP90AA1	4.4	35761	0	0	0	25	1	4	0	0	0	0	0	0	0
32488		unnamed protein product	HSP90AA1	4.8	84674	0	0	0	25	2	7	0	0	0	25	2	7	
306891	P08238	90kDa heat shock protein	HSP90AB1	4.8	83295	0	0	0	50	2	6	0	0	0	0	0	0	0
4507677	P14625	endoplasmic	HSP90B1	4.6	92469	75	6	11	50	3	9	0	0	0	0	0	0	0
167466173	P08107	heat shock 70 kDa protein 1A/1B	HSPA1A	5.4	70053	0	0	0	25	1	2	0	0	0	0	0	0	0
13676857	P54652	heat shock-related 70 kDa protein 2	HSPA2	5.4	70021	100	13	15	50	7	9	0	0	0	0	0	0	0
16507237	P11021	78 kDa glucose-regulated protein	HSPA5	4.9	72270	100	22	29	75	9	12	0	0	0	0	0	0	0
34419635	P17066	heat shock 70 kDa protein 6	HSPA6	5.8	71029	100	4	15	75	5	12	25	2	5	0	0	0	0
5729877	P11142	heat shock cognate 71 kDa protein isoform 1	HSPA8	5.2	70836	0	0	0	25	1	2	0	0	0	0	0	0	0
24234686	P11142	heat shock cognate 71 kDa protein isoform 2	HSPA8	5.5	53466	0	0	0	50	3	8	0	0	0	0	0	0	0
51095055	A4D111	similar to Chain , Heat-Shock Cognate 70kd Protein	HSPA8	7.8	25564	25	1	3	75	3	8	0	0	0	0	0	0	0
24234688	P38646	stress-70 protein, mitochondrial	HSPA9	5.8	73617	25	1	3	25	2	8	0	0	0	0	0	0	0
4504517	P04792	heat shock protein beta-1	HSPB1	6.0	22783	100	32	52	100	23	36	75	9	29	50	11	25	25
31542947	P10809	60 kDa heat shock protein, mitochondrial	HSPD1	5.6	60998	50	4	6	50	11	13	0	0	0	0	0	0	0
11602963		heparan sulfate proteoglycan perlecan	HSPG2	6.0	466286	100	29	73	75	9	14	0	0	0	0	0	0	0
6807686	Q4G0P3	hypothetical protein	IDIN	7.3	110138	0	0	0	0	0	0	0	0	0	25	1	7	7
119614626		intercellular adhesion molecule 2, isoform CRA_d	ICAM2	8.0	35959	0	0	0	0	0	0	0	0	0	25	2	7	7
28178825	O75874	isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	6.6	46612	50	2	6	50	3	7	0	0	0	0	0	0	0
872121		isocitrate dehydrogenase (NADP+)	IDH2	8.8	50949	25	1	3	25	1	2	0	0	0	0	0	0	0
148727370	Q5T953	immediate early response gene 5-like protein	IER5L	6.5	42065	25	1	3	0	0	0	0	0	0	0	0	0	0
10433963	Q9H9Z0	unnamed protein product	IFT122	6.9	98346	25	1	3	0	0	0	0	0	0	0	0	0	0
56090548	Q8WX77	insulin-like growth factor-binding protein-like 1	IGFBPL1	7.8	28969	0	0	0	0	0	0	25	2	8	0	0	0	0
13375913	Q9H665	IGF-like family receptor 1	IGFLR1	6.7	37852	0	0	0	0	0	0	25	2	7	0	0	0	0
22760231	Q8NCL6	unnamed protein product	IGHA1	6.1	53225	100	8	18	50	4	8	50	3	13	25	2	7	7
11275320		anti HBs antibody heavy-chain Fab fragment	IGHG1	9.8	23133	25	1	3	0	0	0	0	0	0	0	0	0	0
12054072		immunoglobulin heavy chain constant region gamma 1	IGHG1	8.2	36111	100	14	23	75	9	10	0	0	0	25	1	5	5
34527413		unnamed protein product	IGHG1	7.9	52378	25	1	3	0	0	0	0	0	0	0	0	0	0
10334595		immunoglobulin heavy chain	IGHG3	7.7	39662	25	2	3	0	0	0	0	0	0	0	0	0	0
2414492		immunoglobulin heavy chain, constant region	IGHG4	6.0	25716	25	1	3	0	0	0	0	0	0	0	0	0	0
77158017		immunoglobulin epsilon heavy chain variable region	IGHV@	4.8	13263	25	1	3	0	0	0	0	0	0	0	0	0	0
106897590		circulating B cell antibody heavy chain variable region	IGHV@	6.5	14019	25	1	3	0	0	0	0	0	0	0	0	0	0
112698958		immunoglobulin heavy chain variable region	IGHV@	8.9	10777	25	1	3	0	0	0	0	0	0	0	0	0	0
112699833		immunoglobulin heavy chain variable region	IGHV@	8.5	10829	0	0	0	25	1	2	0	0	0	0	0	0	0
112702504		immunoglobulin heavy chain variable region	IGHV@	8.3	10720	25	1	3	0	0	0	0	0	0	0	0	0	0
2344984		IgM heavy chain VH1 region	IGHV1-18	7.8	15460	0	0	0	0	0	0	0	0	0	25	1	7	7
343792811		anti-HIV-1 immunoglobulin heavy chain variable region, partial	IGHV1-2	8.2	14341	0	0	0	0	0	0	0	0	0	25	2	10	10
343793191		anti-HIV-1 immunoglobulin heavy chain variable region, partial	IGHV1-2	9.9	14104	0	0	0	0	0	0	0	0	0	25	1	5	5
9968368		immunoglobulin heavy chain variable region	IGHV1-3	9.2	13031	25	1	3	0	0	0	0	0	0	0	0	0	0
237702092		immunoglobulin heavy chain variable region	IGHV1-46	9.3	13357	0	0	0	25	1	2	25	3	5	0	0	0	0
21668504		immunoglobulin heavy chain VHDJ region	IGHV1-E	6.1	12655	0	0	0	0	0	0	25	2	5	0	0	0	0
190341761		immunoglobulin heavy chain variable region	IGHV1-E	4.8	11843	0	0	0	0	0	0	0	0	0	25	2	7	7
346104		S29543 Ig heavy chain V region (COS 3) - human (fragment)	IGHV3-30	9.4	10815	0	0	0	0	0	0	0	0	0	25	1	5	5
33319336		AF4711396_1 Ig heavy chain variable region, VH3 family	IGHV3-30	6.3	13306	0	0	0	25	1	2	0	0	0	0	0	0	0
47154938		immunoglobulin heavy chain	IGHV3-30	7.0	13591	25	1	4	0	0	0	0	0	0	0	0	0	0
194273220		immunoglobulin heavy chain variable region	IGHV3-30	9.4	10592	25	1	3	0	0	0	0	0	0	0	0	0	0
320042532		immunoglobulin heavy chain variable region	IGHV3-33	9.0	13092	25	1	3	0	0	0	0	0	0	0	0	0	0
281185664		immunoglobulin M heavy chain variable region	IGHV3-53	8.6	10948	75	13	9	50	4	5	50	7	12	25	1	5	5
33451		unnamed protein product	IGHV3-6	5.8	68511	100	11	12	75	7	8	0	0	0	25	1	5	5
1335134		unnamed protein product	IGHV3-6	5.8	11592	50	2	6	25	4	2	0	0	0	25	1	5	5
247422393		immunoglobulin heavy chain variable region	IGHV3-6	9.1	13398	0	0	0	0	0	0	0	0	0	25	1	7	7
323431613		immunoglobulin variable region	IGHV3-64	8.6	14608	0	0	0	0	0	0	0	0	0	25	2	10	10
21670111		immunoglobulin heavy chain VHDJ region	IGHV3-7	6.6	13314	0	0	0	25	1	2	0	0	0	0	0	0	0
157058647		immunoglobulin heavy chain variable region	IGHV3-9	5.6	10817	25	1	3	0	0	0	0	0	0	0	0	0	0

310769592		immunoglobulin mu heavy chain variable region	IGHV3-9	5.7	16898	25	1	3	0	0	0	0	0	0	0	0	0	0
3451168		immunoglobulin heavy chain	IGHV4-34	8.2	12797	25	1	4	0	0	0	0	0	0	0	0	0	0
70797925		immunoglobulin heavy chain variable region	IGHV4-34	7.7	12312	0	0	0	25	1	2	0	0	0	0	0	0	0
197115733		immunoglobulin heavy chain variable region	IGHV4-34	6.1	12418	25	1	4	0	0	0	0	0	0	0	0	0	0
270047229		immunoglobulin heavy chain variable region	IGHV4-34	9.3	11080	25	1	3	0	0	0	0	0	0	0	0	0	0
46253824		immunoglobulin heavy chain	IGHV4-4	7.0	15406	0	0	0	0	0	0	25	2	8	0	0	0	0
106897984		circulating B cell antibody heavy chain variable region	IGHV4-4	8.7	13376	0	0	0	0	0	0	0	0	0	25	2	10	
353254304		anti-tetanus toxoid immunoglobulin heavy chain variable region	IGHV5-51	6.5	13594	25	1	3	0	0	0	0	0	0	0	0	0	0
532598		Ig J-chain	IGJ	4.4	15595	50	2	6	25	1	4	25	2	8	0	0	0	0
13448001		immunoglobulin kappa light chain variable region	IGKV1-39	9.6	11988	0	0	0	25	1	4	0	0	0	0	0	0	0
63103145		anti-rabies virus immunoglobulin light chain variable region	IGKV1-6	6.4	11538	0	0	0	25	1	2	0	0	0	0	0	0	0
90994746		immunoglobulin kappa 1 light chain variable region	IGKV1D-12	9.7	12498	0	0	0	25	1	4	0	0	0	0	0	0	0
37694635		immunoglobulin light chain variable region	IGKV2D-29	9.1	11736	0	0	0	0	0	0	0	0	0	25	1	7	
482003		S40360 Ig kappa chain - human	IGKV3-20	8.2	14198	0	0	0	25	1	2	0	0	0	0	0	0	0
17483730		immunoglobulin kappa light chain variable region	IGKV3-20	10.0	12874	25	1	4	0	0	0	0	0	0	0	0	0	0
70798771		immunoglobulin kappa light chain variable region	IGKV3-20	8.2	11623	0	0	0	0	0	0	25	2	8	0	0	0	0
33569904		immunoglobulin kappa chain variable region	IGKV4-1	9.5	9834	0	0	0	0	0	0	25	2	8	0	0	0	0
237702202		immunoglobulin light chain variable region	IGKV4-1	7.0	12113	0	0	0	25	1	2	0	0	0	0	0	0	0
21669631		immunoglobulin lambda light chain VLJ region	IGLL5	7.0	27839	100	5	12	50	2	5	0	0	0	0	0	0	0
77380088		immunoglobulin lambda chain variable region	IGLL5	4.8	11889	0	0	0	0	0	0	25	2	7	25	2	10	
6643277		immunoglobulin lambda light chain variable region	IGLV2-23	6.9	11295	0	0	0	25	1	4	0	0	0	0	0	0	0
70888265		immunoglobulin lambda light chain variable region	IGLV3-21	5.4	10862	0	0	0	25	1	2	0	0	0	0	0	0	0
54781321		immunoglobulin lambda light chain variable region VL6	IGLV6-57	5.4	15343	25	1	4	0	0	0	0	0	0	0	0	0	0
4504653	Q14116	interleukin-18 isoform 1 protein	IL18	4.4	22327	25	1	3	0	0	0	0	0	0	0	0	0	0
58429948	Q2THG6	interleukin 20 short form	IL20	9.2	17145	25	1	3	0	0	0	0	0	0	0	0	0	0
13385872	Q9CXY6	interleukin enhancer-binding factor 2	ILF2	5.0	43017	0	0	0	25	1	2	0	0	0	0	0	0	0
66933016	P12268	inosine-5'-monophosphate dehydrogenase 2	IMPDH2	6.5	55752	25	1	5	50	4	6	0	0	0	0	0	0	0
194380436	Q9UI26	unnamed protein product	IPO11	5.1	117024	0	0	0	0	0	0	0	0	0	25	1	7	
62087374	Q59H62	IPO4 protein variant	IPO4	4.6	81876	0	0	0	25	1	2	0	0	0	0	0	0	0
5174473	Q9Y573	actin-binding protein IPP isoform 1	IPP	5.4	65262	0	0	0	0	0	0	0	0	0	25	2	7	
4506787	P46940	ras GTPase-activating-like protein IQGAP1	IQGAP1	6.1	189116	75	6	14	50	4	13	0	0	0	0	0	0	0
35520		platelet glycoprotein IIb (648 AA)	ITGA2B	5.0	70547	25	1	3	25	1	4	0	0	0	0	0	0	0
31422	P20701	unnamed protein product	ITGAL	5.3	128850	0	0	0	0	0	0	0	0	0	25	1	7	
31442		unnamed protein product	ITGB1	5.2	88466	25	1	3	0	0	0	0	0	0	0	0	0	0
19743813	P05556	integrin beta-1 isoform 1A	ITGB1	5.1	88339	75	3	9	25	1	2	0	0	0	0	0	0	0
60678566	Q2YFE1	truncated integrin beta 3	ITGB3	5.2	48644	0	0	0	25	1	4	0	0	0	0	0	0	0
38348336	Q6UXX5	inter-alpha-trypsin inhibitor heavy chain H6	ITI16	9.3	143080	0	0	0	0	0	0	25	2	5	0	0	0	0
269954692	Q14643	inositol 1,4,5-trisphosphate receptor type 1 isoform 2	ITPR1	5.9	306560	0	0	0	25	1	2	0	0	0	0	0	0	0
119582225	G5E9Y0	janus kinase and microtubule interacting protein 2, isoform CRA_b	JAKMIP2	5.7	93544	0	0	0	25	1	2	0	0	0	0	0	0	0
1127022	Q7KZ86	plakoglobin	JUP	9.2	18849	25	6	4	25	2	0	0	0	0	25	3	7	
4504811	P14923	junction plakoglobin	JUP	5.7	81745	50	16	25	100	16	22	75	20	48	75	22	49	
505108		KIAA0070	KARS	6.0	68404	25	1	3	0	0	0	0	0	0	0	0	0	0
40805843	Q92831	histone acetyltransferase KAT2B	KAT2B	9.2	93013	0	0	0	0	0	0	0	0	0	25	1	5	
119583307		katanin p60 subunit A-like 2, isoform CRA_c	KATNAL2	9.8	48321	25	1	3	0	0	0	0	0	0	0	0	0	0
28207927	Q86TW6	unnamed protein product	KCNH2	12.3	17523	50	2	6	50	3	2	0	0	0	0	0	0	0
7019439	Q9UNX9	ATP-sensitive inward rectifier potassium channel 14	KCNJ14	5.1	47797	0	0	0	25	2	0	0	0	0	0	0	0	0
		potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3, isoform CRA_a	KCNN3	9.1	81828	25	1	3	25	1	2	0	0	0	0	0	0	0
7243225		KIAA1422 protein	KCNT1	7.3	129779	25	1	3	0	0	0	0	0	0	0	0	0	0
40217617	Q719H9	BTB/POZ domain-containing protein KCTD1 isoform a	KCTD1	6.7	29368	0	0	0	25	1	2	50	4	15	25	5	10	
1661016		SMCY	KDM5D	5.6	174088	25	1	3	0	0	0	0	0	0	25	1	5	
20521009	O15054	KIAA0346	KDM6B	8.8	180751	0	0	0	0	0	0	0	0	0	25	2	10	
20521680	Q9Y6X7	KIAA0864 protein	KIAA0864	4.9	158412	0	0	0	0	0	0	0	0	0	25	2	7	
4240279		KIAA0895 protein	KIAA0895	9.8	61259	25	1	3	0	0	0	0	0	0	0	0	0	0
10435767		unnamed protein product	KIAA0913	7.5	115371	25	1	3	0	0	0	0	0	0	0	0	0	0
20521732		KIAA1024 protein	KIAA1024	7.0	103106	25	1	3	0	0	0	0	0	0	0	0	0	0
10435862		unnamed protein product	KIAA1310	9.8	83173	0	0	0	0	0	0	25	2	8	0	0	0	0
7959315		KIAA1524 protein	KIAA1524	5.8	99842	0	0	0	0	0	0	25	2	5	0	0	0	0
10047313		KIAA1618 protein	KIAA1618	5.6	160273	0	0	0	0	0	0	25	2	5	0	0	0	0

14042774		unnamed protein product	KIF15	5.2	51434	25	1	3	0	0	0	0	0	0	0	0	0	0
15919888	Q96Q89	mitotic kinesin-related protein	KIF20B	5.4	210555	0	0	0	0	0	0	0	0	0	0	25	1	7
6453818	Q14807	kinesin-like protein KIF22 isoform 1	KIF22	9.8	73263	0	0	0	25	1	2	0	0	0	0	0	0	0
56967903	Q5IH82	KIR2DL4	KIR2DL4	7.6	40469	25	1	3	0	0	0	0	0	0	0	0	0	0
14017951		KIAA1867 protein	KIRREL3	6.5	85312	25	1	3	0	0	0	0	0	0	0	0	0	0
51479184	Q9H511	kelch-like protein 31	KLHL31	6.3	70247	0	0	0	0	0	0	0	0	0	0	25	1	7
12697919		KIAA1687 protein	KLHL4	6.4	81334	25	1	4	0	0	0	0	0	0	0	0	0	0
57157125	Q5KU19	G-protein coupled receptor	KPG_009	8.4	101487	0	0	0	0	0	0	0	0	0	0	25	1	7
19923142	Q14974	importin subunit beta-1	KPNB1	4.5	97171	50	2	6	25	1	2	0	0	0	0	0	0	0
68563515	Q5T749	keratinocyte proline-rich protein	KPRP	8.1	64075	0	0	0	0	0	0	25	2	8	25	1	5	
386854	P04264	type II keratin subunit protein	KRT1	5.2	52789	0	0	0	25	1	4	0	0	0	25	1	9	
11935049		AF304164_1 keratin 1	KRT1	8.3	66067	100	874	342	100	1109	356	100	2083	1033	100	2153	1117	
186629		keratin 10	KRT10	4.6	39743	75	12	16	75	18	21	75	29	28	50	10	18	
307086		keratin-10	KRT10	5.0	46387	100	307	124	100	600	144	100	989	539	100	1007	478	
623409		keratin 10	KRT10	4.9	57248	100	236	103	100	422	115	100	515	259	100	513	310	
4557699	Q99456	keratin, type I cytoskeletal 12	KRT12	4.6	53512	25	1	3	0	0	0	0	0	0	0	0	0	
30377		cytokeratin 13	KRT13	4.7	45866	100	115	63	100	129	63	100	130	166	100	120	154	
118835468	A1A4E9	Keratin 13	KRT13	4.8	49587	25	1	3	0	0	0	0	0	0	0	0	0	
12803709		Keratin 14	KRT14	4.9	51652	100	210	168	100	230	153	100	299	341	100	396	383	
34071		unnamed protein product	KRT15	4.6	49168	100	28	53	50	20	45	50	14	40	50	4	17	
186685		keratin type 16	KRT16	4.8	50700	100	218	118	100	207	122	100	225	251	100	240	314	
24430192	P08779	keratin, type I cytoskeletal 16	KRT16	4.8	51268	100	99	58	100	113	58	100	117	104	100	149	125	
194385560	B4E2J5	unnamed protein product	KRT16	4.7	21470	25	2	3	50	3	6	0	0	0	25	1	7	
4557701	Q04695	keratin, type I cytoskeletal 17	KRT17	4.8	48106	100	143	181	100	139	141	100	143	252	100	107	248	
119571624		hCG27965, isoform CRA_a	KRT17	4.6	19566	25	3	3	25	2	4	0	0	0	50	17	12	
4557888	P05783	keratin, type I cytoskeletal 18	KRT18	5.2	48058	75	29	33	75	33	48	25	2	5	0	0	0	
119620881		hCG1988320, isoform CRA_b	KRT18	4.5	36144	0	0	0	50	1	5	0	0	0	0	0	0	
119624166		hCG2040291	KRT18	6.7	29760	25	1	3	25	1	8	0	0	0	0	0	0	
119632243		hCG20535	KRT18	5.7	58193	50	4	6	50	4	7	25	2	5	0	0	0	
34039		unnamed protein product	KRT19	4.9	44107	100	133	128	100	145	127	100	78	172	50	14	55	
386803		40-kDa keratin protein	KRT19	4.9	44093	50	28	11	50	32	9	25	2	5	0	0	0	
7594734		keratin 19	KRT19	4.8	11794	100	36	40	100	34	39	75	40	53	75	24	36	
24234699	P08727	keratin, type I cytoskeletal 19	KRT19	4.9	44107	0	0	0	25	1	2	0	0	0	0	0	0	
181402		epidermal cytokeratin 2	KRT2	8.0	65866	100	172	162	100	423	197	100	614	632	100	596	594	
47132620	P35908	keratin, type II cytoskeletal 2 epidermal	KRT2	8.0	65375	75	11	9	100	14	8	100	59	32	100	48	29	
20306864	Q8TC04	Keratin 23 (histone deacetylase inducible)	KRT23	6.1	48129	50	2	19	25	2	17	50	3	20	50	6	30	
31559829	Q7Z3Z0	keratin, type I cytoskeletal 25	KRT25	4.9	49319	0	0	0	25	1	2	0	0	0	0	0	0	
34526053	Q6ZPD6	unnamed protein product	KRT25	5.0	41380	25	1	3	50	4	2	75	7	27	25	3	7	
31074641		type I inner root sheath specific keratin 25 irs3	KRT27	4.9	49775	25	1	6	0	0	0	25	2	10	25	2	11	
34526448		unnamed protein product	KRT28	5.2	53026	25	2	7	75	9	12	50	13	29	75	25	45	
1335194		unnamed protein product	KRT3	4.1	6102	0	0	0	100	12	17	25	11	12	25	5	11	
3892586		keratin type II	KRT3	9.0	23654	75	9	8	75	5	10	50	7	12	75	10	22	
42760012		keratin 3	KRT3	5.6	61661	25	1	4	0	0	0	25	2	5	0	0	0	
2950168		type I keratin	KRT31	4.7	47233	0	0	0	0	0	0	25	2	7	0	0	0	
386644		type Ia hair keratin a3	KRT33A	4.7	45936	25	4	7	0	0	0	50	5	29	25	31	38	
10337581	Q14525	keratin, type I cuticular Ha3-II	KRT33B	4.7	46214	25	1	4	0	0	0	0	0	0	0	0	0	
1668744		HHa5 hair keratin type I intermediate filament	KRT35	4.6	47522	0	0	0	0	0	0	25	2	7	0	0	0	
12311759	O76015	type I hair keratin 8	KRT38	4.6	50491	0	0	0	25	2	4	0	0	0	0	0	0	
82654947	P19013	K2C4_HUMAN RecName: Full=Keratin, type II cytoskeletal 4	KRT4	6.2	57232	100	26	27	75	30	17	100	21	37	50	26	40	
386850		keratin K5	KRT5	5.5	54512	100	84	99	100	86	93	100	120	216	100	100	221	
9739163		AF274874_1 keratin 5	KRT5	8.2	62462	100	38	40	100	44	45	100	33	64	100	21	57	
18999435		Keratin 5	KRT5	7.8	62379	100	6	12	100	6	10	75	23	24	100	11	29	
908801		keratin type II	KRT6A	8.0	60201	100	28	31	100	20	16	25	9	11	75	10	26	
46812692	P02538	Keratin 6A	KRT6A	7.7	60076	0	0	0	0	0	0	0	0	0	25	2	7	
908790		keratin type II	KRT6B	8.0	59999	0	0	0	50	2	2	50	3	13	0	0	0	
119703753	P04259	keratin, type II cytoskeletal 6B	KRT6B	8.0	60068	75	6	8	50	7	8	75	13	20	50	9	13	
914833		keratin type II	KRT6C	5.2	42469	100	256	180	100	231	148	100	348	352	100	350	369	
84040267		Keratin 6C	KRT6C	7.7	59997	25	2	3	0	0	0	25	3	5	0	0	0	
1200072		keratin	KRT7	5.3	51335	100	45	46	100	59	53	75	66	62	75	60	38	

4688900		sarcolectin	KRT7	5.5	51414	50	4	9	50	3	8	0	0	0	0	0	0
12803727		Keratin 7	KRT7	5.3	51419	25	4	3	50	4	7	0	0	0	0	0	0
193785954	B3KY79	unnamed protein product	KRT7	5.3	49036	0	0	0	25	1	2	0	0	0	0	0	0
197101305	Q5RCY8	keratin, type II cytoskeletal 71	KRT71	6.2	57196	25	1	3	50	5	4	25	2	7	25	7	21
28173564	Q86Y46	keratin, type II cytoskeletal 73	KRT73	7.0	58924	50	5	11	100	9	12	50	6	40	50	14	33
27764565		TPA_exp: keratin 5c	KRT74	7.5	59371	25	1	4	0	0	4	0	0	0	0	0	7
3901030		cytokeratin type II	KRT75	7.7	59505	100	162	97	100	196	101	100	239	212	100	260	258
27764561		TPA_exp: keratin 1b	KRT77	4.9	54248	0	0	0	0	0	0	25	2	8	0	0	0
31074631		keratin 1b	KRT77	5.6	61802	100	20	27	100	35	19	100	53	75	100	57	76
57997474		hypothetical protein	KRT78	5.0	44991	0	0	0	0	0	0	25	2	7	0	0	0
89357932	Q8N1N4	keratin, type II cytoskeletal 78	KRT78	5.7	56866	100	17	22	75	18	8	75	24	42	100	38	80
1419564		cytokeratin	KRT8	4.9	30779	100	56	92	100	58	94	100	13	45	50	8	25
4504919	P05787	keratin, type II cytoskeletal 8 isoform 2	KRT8	5.4	53653	50	16	34	50	15	39	0	0	0	0	0	0
34535144	Q6ZRU0	unnamed protein product	KRT8	4.6	22344	25	1	4	25	1	2	0	0	0	0	0	0
119567961		hCG1643231, isoform CRA_b	KRT8	8.3	35300	0	0	0	25	1	2	0	0	0	0	0	0
119579660		hCG1748768, isoform CRA_a	KRT8	4.6	23921	75	6	16	75	7	19	25	5	5	0	0	0
119607257		hCG1988300, isoform CRA_b	KRT8	4.9	47808	50	2	12	50	3	13	0	0	0	0	0	0
119631362		NCK-associated protein 1, isoform CRA_f	KRT8	4.8	43599	25	2	3	50	1	4	0	0	0	0	0	0
31873640		hypothetical protein	KRT80	5.2	54177	0	0	0	0	0	0	25	2	8	50	4	17
1181996		hair type II basic keratin	KRT81	4.8	47035	0	0	0	0	0	0	50	11	22	25	55	46
22798968		type II hair keratin 2	KRT82	6.4	56684	0	0	0	0	0	0	25	4	7	0	0	0
1903220		type II intermediate filament of hair keratin	KRT86	5.4	53141	0	0	0	0	0	0	0	0	0	25	2	10
435476		cytokeratin 9	KRT9	5.1	62130	100	918	330	100	1089	288	100	2066	924	100	2133	1027
55956899	P35527	keratin, type I cytoskeletal 9	KRT9	5.0	62065	0	0	0	25	2	0	0	0	0	0	0	0
109658980	Q3LI73	Keratin associated protein 19-4	KRTAP19-4	8.5	9047	0	0	0	25	1	4	0	0	0	0	0	0
123702038	P26371	keratin-associated protein 5-9	KRTAP5-9	7.7	16277	25	1	3	25	1	4	0	0	0	0	0	0
119592641		leukocyte-associated Ig-like receptor 1, isoform CRA_c		6.6	38872	0	0	0	0	0	0	25	2	8	0	0	0
1149515	Q16787	alpha3b subunit of laminin 5	LAMA3	6.3	148006	0	0	0	25	1	2	0	0	0	0	0	0
3043590		KIAA0533 protein	LAMA5	7.9	178216	25	1	3	0	0	0	0	0	0	0	0	0
15620873		KIAA1907 protein	LAMA5	5.9	188451	25	1	3	0	0	0	0	0	0	0	0	0
1103585		laminin beta 2 chain	LAMB2	6.1	196080	25	2	5	0	0	0	0	0	0	0	0	0
186964		laminin B2 chain	LAMC1	4.9	177607	75	3	9	0	0	0	0	0	0	0	0	0
112380628	P11279	lysosome-associated membrane glycoprotein 1	LAMP1	8.8	44836	25	1	3	25	1	2	0	0	0	0	0	0
47125269		LanC lantibiotic synthetase componentC-like 2	LANCL2	7.1	50799	25	1	3	0	0	0	0	0	0	0	0	0
6807738		hypothetical protein	LCMT1	5.5	36928	25	1	3	0	0	0	0	0	0	0	0	0
4504963	P31025	lipocalin-1 isoform 1	LCN1	5.3	19251	0	0	0	0	0	0	0	0	0	25	1	7
38455402	P80188	neutrophil gelatinase-associated lipocalin	LCN2	9.2	22556	0	0	0	25	1	4	0	0	0	0	0	0
119613193	C9JI46	transcription factor MLR1, isoform CRA_b	LCORL	8.0	57460	0	0	0	0	0	0	0	0	0	25	2	7
5031857	P00338	L-lactate dehydrogenase A chain isoform 1	LDHA	8.3	36647	50	3	6	0	0	0	0	0	0	0	0	0
4557032	P07195	L-lactate dehydrogenase B chain	LDHB	5.7	36639	25	1	3	0	0	0	0	0	0	0	0	0
93140999	Q8NES3	beta-1,3-N-acetylglucosaminyltransferase lunatic fringe isoform a	LFNG	9.4	41729	0	0	0	0	0	0	0	0	0	25	2	7
179531		IgE-binding protein	LGALS3	8.9	26189	100	7	20	75	5	18	0	0	0	0	0	0
4504985	P47929	galectin-7	LGALS7	7.5	15076	50	3	10	75	5	7	75	7	24	100	19	59
		leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-															
157426829	P0C6S8	interacting protein 3	LINGO3	8.4	64822	0	0	0	25	1	2	0	0	0	0	0	0
119570551		lipase-like, ab-hydrolase domain containing 1, isoform CRA_b	LIPJ	5.6	39366	0	0	0	25	2	0	0	0	0	0	0	0
34228		unnamed protein product	LMNA	7.6	79398	100	52	102	75	34	61	25	6	16	50	3	12
27436946	P02545	prelamin-A/C isoform 1	LMNA	6.6	74140	0	0	0	25	1	2	0	0	0	0	0	0
194379984	B4DI32	unnamed protein product	LMNA	6.8	63992	25	1	3	0	0	0	0	0	0	0	0	0
5031877	P20700	lamin-B1 isoform 1	LMNB1	5.0	66409	0	0	0	25	1	2	0	0	0	0	0	0
345758		A45023 lamin B2 - human (fragment)	LMNB2	5.8	59002	25	1	3	0	0	0	0	0	0	0	0	0
6468766	Q9UIQ6	oxytocinase/insulin-responsive aminopeptidase, varian 1	LNPEP	5.4	117226	0	0	0	0	0	0	0	0	0	25	1	5
296236267	F7H7Y6	PREDICTED: ADP/ATP translocase 2-like	LOC100387000	10.1	32856	0	0	0	25	1	2	0	0	0	0	0	0
51094813	A4D1Q5	similar to 60S ribosomal protein L15	LOC136321	9.8	23771	25	1	3	0	0	0	0	0	0	0	0	0
37610		unnamed protein product	LOC144983	9.8	20038	75	9	11	25	4	4	0	0	0	0	0	0
33872974	Q6PJD4	LOC389906 protein	LOC389906	10.2	21242	0	0	0	0	0	0	25	2	8	0	0	0
51095083	A4D0Y7	similar to 40S ribosomal protein S2	LOC392781	10.3	21070	0	0	0	25	1	2	0	0	0	0	0	0
51095136	A4D0T0	similar to Argininosuccinate synthase	LOC402295	7.6	24146	0	0	0	0	0	0	0	0	0	25	1	7
71051569	Q4G0Q5	LOC442028 protein	LOC442028	10.4	20568	25	1	3	0	0	0	0	0	0	0	0	0

7023623	Q9NUU0	unnamed protein product	LOC645202	5.5	47539	0	0	0	0	0	0	25	4	12	0	0	0
3169770		immunoglobulin kappa light chain	LOC652493	8.1	23052	0	0	0	25	1	2	0	0	0	0	0	0
21669331		immunoglobulin kappa light chain VLJ region	LOC652493	7.6	28831	100	17	12	75	7	8	0	0	0	25	1	7
21669337		immunoglobulin kappa light chain VLJ region	LOC652493	6.2	28690	50	6	13	50	1	6	0	0	0	0	0	0
187185	P23490	loricrin	LOR	8.0	26034	0	0	0	25	1	4	0	0	0	25	1	7
7662022	Q92539	phosphatidate phosphatase LPIN2	LPIN2	5.1	99400	0	0	0	25	1	2	0	0	0	0	0	0
5031887	Q93052	lipoma-preferred partner isoform a	LPP	7.1	65747	25	1	3	0	0	0	0	0	0	0	0	0
34339	Q07954	LDL-receptor related (AA -19 to 4525)	LRP1	5.0	504227	0	0	0	0	0	0	0	0	0	25	2	7
18565270		Lib	LRRC15	6.2	64397	25	10	14	0	0	0	25	3	8	0	0	0
119603533		leucine rich repeat containing 36, isoform CRA_c	LRRC36	8.9	35540	0	0	0	0	0	0	25	3	8	0	0	0
119589283		hCG2045258	LRRC41	8.3	20496	75	11	9	25	1	2	25	2	8	25	1	5
3355597	Q32MZ4	TRIP protein	LRRFIP1	4.4	86438	0	0	0	25	1	4	0	0	0	0	0	0
67107032	Q38SD2	leucine-rich repeat kinase 1	LRRK1	6.2	225150	0	0	0	25	1	2	0	0	0	0	0	0
53729359	Q6UWE0	E3 ubiquitin-protein ligase LRSAM1 isoform 1	LRSAM1	5.6	83523	0	0	0	0	0	0	25	2	5	0	0	0
4505029	P09960	leukotriene A-4 hydrolase	LTA4H	5.8	69286	0	0	0	0	0	0	25	2	8	25	1	7
339548		transforming growth factor-beta 1 binding protein	LTBP1	4.8	152671	25	1	3	0	0	0	0	0	0	0	0	0
34412		unnamed protein product	LTF	8.0	78079	100	10	20	25	2	6	25	12	21	25	2	7
4505047	P51884	lumican	LUM	6.2	38430	75	15	31	50	23	17	0	0	0	25	1	5
		A Chain A, Structural Changes Of The Active Site Cleft And Different Saccharide Binding Modes In Human Lysozyme Co-Crystallized With Hexa-N-Acetyl-						9									
1065033	P61626	Chitohexase At Ph 4.0	LYZ	9.1	14673	75	5		50	4	8	25	4	12	50	3	14
4505061	P20645	cation-dependent mannose-6-phosphate receptor isoform 1	M6PR	5.5	30955	0	0	0	0	0	0	25	3	8	0	0	0
282721057	Q8N8X9	protein mab-21-like 3	MAB21L3	8.5	42358	0	0	0	0	0	0	0	0	0	25	1	7
5821434	Q9UPN3	actin binding protein ABP620	MACF1	5.2	620302	0	0	0	25	1	2	0	0	0	0	0	0
2459681		MAGE-B3	MAGEB3	10.5	39180	0	0	0	0	0	0	25	2	5	0	0	0
29337290	Q8N7X4	melanoma-associated antigen B6	MAGEB6	5.3	43993	0	0	0	25	1	4	0	0	0	0	0	0
5803078	Q9UDY8	mucosa-associated lymphoid tissue lymphoma translocation protein 1 isoform a	MALT1	5.4	92195	0	0	0	0	0	0	0	0	0	25	3	5
10434559	Q5SRI9	unnamed protein product	MANEA	9.5	33629	0	0	0	25	2	0	0	0	0	0	0	0
219894		80K-L protein	MARCKS	4.3	31545	25	1	3	0	0	0	0	0	0	0	0	0
3043646		KIAA0561 protein	MAST3	7.9	143006	0	0	0	0	0	0	25	2	8	25	2	7
2224547		KIAA0303	MAST4	8.5	231795	25	1	4	0	0	0	0	0	0	0	0	0
21626466	P43243	matrin-3 isoform a	MATR3	5.8	94624	0	0	0	25	1	2	0	0	0	0	0	0
4505117	Q9UBB5	methyl-CpG-binding domain protein 2 isoform 1	MBD2	10.5	43210	25	1	3	0	0	0	0	0	0	0	0	0
21464125	Q5VZF2	muscleblind-like protein 2 isoform 1	MBNL2	8.9	39291	0	0	0	0	0	0	0	0	0	25	1	5
34791		melanocyte stimulating hormone receptor	MC4R	8.2	34661	25	2	3	50	1	4	0	0	0	0	0	0
2224665		KIAA0362	MCF2L	6.1	123984	25	1	3	0	0	0	0	0	0	0	0	0
6631095		DNA replication licensing factor MCM3	MCM3	5.4	90906	0	0	0	25	1	2	0	0	0	0	0	0
253735647	C6EMX8	HsMcm7	MCM7	5.9	81280	25	1	3	0	0	0	0	0	0	0	0	0
2906146		malate dehydrogenase	MDH2	8.8	35532	75	4	9	50	6	15	0	0	0	25	1	5
		MDS2_HUMAN RecName: Full=Myelodysplastic syndrome 2 translocation-						3									
74751237	Q8NDY4	associated protein	MDS2	8.4	15356	25	1		0	0	0	0	0	0	0	0	0
23111005	P55083	microfibril-associated glycoprotein 4 isoform 2	MFAP4	5.3	28612	100	50	19	75	65	23	25	6	5	25	8	5
18676484		FLJ00139 protein	MICALL2	10.4	60867	25	1	4	0	0	0	0	0	0	0	0	0
20521812	Q9ULH7	KIAA1243 protein	MKL2	6.0	89453	0	0	0	0	0	0	0	0	0	25	1	5
1490271		ALL-1 protein	MLL	9.3	435830	25	1	3	25	1	4	0	0	0	0	0	0
62088568	Q59FG6	myeloid/lymphoid or mixed-lineage leukemia 2 variant	MLL2	6.9	292985	25	1	4	0	0	0	0	0	0	0	0	0
153070822	Q9Y4U1	methylmalonic aciduria and homocystinuria type C protein	MMACHC	7.7	31690	0	0	0	25	1	2	0	0	0	0	0	0
								3									
7661548	Q9H3L0	methylmalonic aciduria and homocystinuria type D protein, mitochondrial	MMADHC	5.0	32901	25	1		0	0	0	0	0	0	0	0	0
39963607	Q9H8L6	MMRN2 protein	MMRN2	5.3	64623	0	0	0	25	1	2	0	0	0	0	0	0
34719	P05164	unnamed protein product	MPO	9.0	83855	0	0	0	25	1	4	0	0	0	0	0	0
119605074		hypothetical protein MGC12972, isoform CRA_b	MPV17L2	10.7	33503	0	0	0	0	0	0	0	0	0	25	2	7
10047245	Q9HC17	KIAA1585 protein	MSL2	7.5	64198	0	0	0	25	1	2	0	0	0	0	0	0
4505257	P26038	moesin	MSN	6.0	67821	50	2	6	25	1	2	0	0	0	0	0	0
14016		cytochrome C oxidase II subunit	MT-CO2	4.5	20995	25	2	5	50	1	4	0	0	0	0	0	0
28278233	Q9H2K0	Mitochondrial translational initiation factor 3	MTIF3	10.2	31666	0	0	0	25	1	4	0	0	0	0	0	0
221045954	B7ZAG8	unnamed protein product	MTMR7	6.0	75783	0	0	0	25	1	2	0	0	0	0	0	0
119631863		hCG1788572	MT-ND6	4.2	8413	0	0	0	0	0	0	25	2	7	0	0	0

3123852	P98088	mucin	MUC5AC	6.0	119330	0	0	0	25	1	4	0	0	0	0	0	0
547517		gastric mucin	MUC5B	6.7	91763	0	0	0	25	1	4	0	0	0	0	0	0
1834503	Q9HC84	mucin MUC5B	MUC5B	7.8	361018	0	0	0	50	2	6	0	0	0	0	0	0
19913410	Q14764	major vault protein	MVP	5.2	99327	50	2	6	25	2	8	0	0	0	0	0	0
119609832		matrix-remodelling associated 7, isoform CRA_b	MXRA7	4.3	44593	0	0	0	25	2	0	0	0	0	0	0	0
127619	P01106	MYC_HUMAN RecName: Full=Myc proto-oncogene protein	MYC	5.2	48756	25	1	4	0	0	0	0	0	0	0	0	0
10434915	Q9P2K5	unnamed protein product	MYEF2	9.1	61932	0	0	0	25	1	2	0	0	0	0	0	0
641958	P35580	non-muscle myosin B	MYH10	5.3	228938	0	0	0	25	2	4	0	0	0	0	0	0
13124879	P35749	myosin-11 isoform SM1A	MYH11	5.3	227339	75	61	115	75	8	13	0	0	0	0	0	0
4808809		myosin heavy chain	MYH13	5.4	223679	25	2	3	25	1	4	0	0	0	0	0	0
150010558	Q9Y2K3	myosin-15	MYH15	5.6	224618	25	1	6	0	0	0	0	0	0	0	0	0
27529913		KIAA1512 protein	MYH7B	5.7	228519	0	0	0	0	0	0	25	4	12	0	0	0
12667788	P35579	myosin-9	MYH9	5.4	226532	100	23	57	50	13	39	0	0	0	0	0	0
15809016	Q14950	myosin regulatory light chain 12B	MYL12B	4.5	19780	0	0	0	25	1	2	0	0	0	0	0	0
4557777	P08590	myosin light chain 3	MYL3	4.9	21933	0	0	0	25	1	2	0	0	0	0	0	0
33620739	Q60605	myosin light polypeptide 6	MyI6	4.3	16962	100	24	31	50	9	19	0	0	0	25	1	5
188586		myosin light chain 2	MYL9	4.9	19871	25	1	3	0	0	0	0	0	0	0	0	0
7706595	Q9NPC6	myozenin-2	MYO22	8.8	29899	0	0	0	0	0	0	25	2	7	0	0	0
119608650		EGF-like-domain, multiple 7, isoform CRA_a	NACA	7.5	18237	0	0	0	0	0	0	25	4	12	0	0	0
163965364	Q13765	nascent polypeptide-associated complexsubunit alpha isoform b	NACA	4.4	23352	0	0	0	25	1	4	0	0	0	0	0	0
7022784	Q6IA69	unnamed protein product	NADSYN1	6.0	79308	0	0	0	25	2	0	0	0	0	0	0	0
4502169	Q13564	NEDD8-activating enzyme E1 regulatory subunit isoform a	NAE1	5.1	60191	25	1	3	0	0	0	0	0	0	0	0	0
7023053	Q9NR45	unnamed protein product	NANS	6.3	40324	0	0	0	25	1	2	0	0	0	0	0	0
41393547	A2RHP1	neuroblastoma-amplified sequence	NBAS	5.6	268571	0	0	0	25	1	2	0	0	0	0	0	0
115529478	P13591	neural cell adhesion molecule 1 isoform 3	NCAM1	4.6	83700	0	0	0	0	0	0	25	2	8	0	0	0
47825361	Q6ZVX7	F-box only protein 50	NCCRP1	6.2	30810	25	1	3	25	2	0	0	0	0	25	5	13
62956001		peripheral clock protein 2	NCKAP5	7.9	200466	0	0	0	0	0	0	25	2	5	0	0	0
55956788	P19338	nucleolin	NCL	4.4	76615	0	0	0	25	1	2	0	0	0	0	0	0
4505351	P52848	bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	NDST1	7.8	100786	25	1	3	25	1	2	25	2	7	0	0	0
4758768	Q95299	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10	NDUFA10	8.6	40707	50	2	5	50	1	5	0	0	0	0	0	0
105990539	P07196	neurofilament light polypeptide	NEFL	4.5	61517	0	0	0	0	0	0	0	0	0	25	2	10
119621926		hCG1993985	NFATC1	8.7	10583	25	1	3	0	0	0	0	0	0	0	0	0
20521946		KIAA1565 protein	NIN	5.0	151959	25	1	3	0	0	0	0	0	0	0	0	0
4760577	Q6KC79	IDN3-B	NIPBL	8.0	245547	0	0	0	50	2	2	0	0	0	0	0	0
119585635		nischarin, isoform CRA_d	NISCH	5.0	174514	0	0	0	25	1	4	0	0	0	0	0	0
193786538	B3KNF9	unnamed protein product	NISCH	4.9	166686	0	0	0	0	0	0	0	0	0	25	1	5
28912912	Q9C056	homeobox protein Nkx-6.2	NKX6-2	10.1	29236	0	0	0	25	1	2	0	0	0	0	0	0
75709196	Q8WX94	NACHT, LRR and PYD domains-containing protein 7 isoform 2	NLRP7	5.8	111717	0	0	0	25	2	0	0	0	0	0	0	0
4557797	P15531	nucleoside diphosphate kinase A isoform b	NME1	5.8	17120	25	1	3	0	0	0	0	0	0	0	0	0
7018409	Q9Y3T9	hypothetical protein	NOC2L	5.2	84879	0	0	0	25	1	2	0	0	0	0	0	0
194378836	B4DY21	unnamed protein product	NOC2L	6.5	67865	25	1	3	25	1	2	0	0	0	0	0	0
18644728	Q9H6R4	nucleolar protein 6 alpha isoform	NOL6	7.3	127593	0	0	0	25	1	2	0	0	0	0	0	0
348239		unnamed protein product	NONO	9.4	54268	50	3	8	25	1	2	0	0	0	0	0	0
89954541	Q1ZYL4	NADPH oxidase 1 variant NOH-1L	NOX1	8.4	60916	25	1	3	0	0	0	0	0	0	0	0	0
10835063	P06748	nucleophosmin isoform 1	NPM1	4.5	32576	25	1	3	0	0	0	0	0	0	0	0	0
119626600		nephronectin, isoform CRA_b	NPNT	9.8	34970	25	1	3	0	0	0	0	0	0	0	0	0
4505415	P15559	NAD(P)H dehydrogenase [quinone] 1 isoform a	NQO1	9.3	30830	0	0	0	25	1	2	0	0	0	0	0	0
41350305	Q9HDB5	neurexin-3-beta isoform 2	NRXN3	9.4	47271	0	0	0	25	1	2	0	0	0	0	0	0
7020029	Q9H1M0	unnamed protein product	NUP62CL	4.3	20826	0	0	0	0	0	0	0	0	0	25	1	7
7661704	P20774	mimcan	OGN	5.3	33923	50	6	15	25	17	8	0	0	0	0	0	0
52317186	Q8NGV5	olfactory receptor 13D1	OR13D1	7.4	39126	0	0	0	25	2	0	0	0	0	0	0	0
12007434	Q9H210	AF321237_1 hB2 olfactory receptor	OR2D2	9.3	34131	0	0	0	0	0	0	0	0	0	25	1	5
21928842	Q8NGK6	seven transmembrane helix receptor	OR52I1	7.2	34402	0	0	0	0	0	0	0	0	0	25	1	7
119589166		hCG2041519	OR52N2	6.4	22930	25	1	3	0	0	0	25	2	8	0	0	0
53933201	Q96R09	olfactory receptor 5B2	OR5B2	8.2	34569	25	1	3	0	0	0	0	0	0	0	0	0
53828678	Q8NGL1	olfactory receptor 5D18	OR5D18	8.3	35349	0	0	0	25	1	4	0	0	0	0	0	0
21928609		seven transmembrane helix receptor	OR5H6	7.1	34701	0	0	0	0	0	0	50	5	17	0	0	0
50897292	Q9GZM6	olfactory receptor 8D2	OR8D2	8.0	34858	0	0	0	0	0	0	0	0	0	25	2	7
119578392		hCG2044662	OR8S1	8.4	34778	0	0	0	0	0	0	25	4	12	0	0	0

21928989		seven transmembrane helix receptor	OR9K2	8.0	35336	0	0	0	0	0	0	25	2	7	0	0	0
47169546		TPA: ovostatin	OVOS	5.0	118168	0	0	0	0	0	0	0	0	0	25	2	7
23463303	Q96G91	P2Y purinoceptor 11	P2RY11	9.2	40346	0	0	0	0	0	0	0	0	0	50	3	14
20070125	P07237	protein disulfide-isomerase	P4HB	4.6	57063	25	1	3	25	1	2	0	0	0	0	0	0
13376751	Q9BRP4	proteasomal ATPase-associated factor 1	PAAF1	5.9	42145	0	0	0	25	1	2	0	0	0	0	0	0
117938314	Q8WU39	plasma cell-induced resident endoplasmic reticulum	PACAP	5.3	20663	25	2	6	25	1	4	0	0	0	0	0	0
45439836		polyamine oxidase splice variant 6	PAOX	8.5	17012	25	1	3	25	1	4	0	0	0	0	0	0
31543380	Q99497	protein DJ-1	PARK7	6.4	19892	25	3	3	50	5	7	0	0	0	0	0	0
6958293		AF119256_1 PATZ	PATZ1	8.4	57617	0	0	0	0	0	0	25	2	8	0	0	0
10047319	Q9NRJ7	KIAA1621 protein	PCDHB16	4.8	86248	0	0	0	0	0	0	0	0	0	25	2	10
2822161		rab3 effector-like	PCLO	9.6	81797	0	0	0	0	0	0	25	2	8	0	0	0
51476276		hypothetical protein	PDE4DIP	5.6	150175	0	0	0	0	0	0	25	2	8	0	0	0
189754	P11177	pyruvate dehydrogenase beta subunit	PDHB	6.2	39250	0	0	0	25	1	2	0	0	0	0	0	0
1208427		ER-60 protease	PDIA3	5.9	56797	75	5	11	50	4	11	0	0	0	0	0	0
5031973	Q15084	protein disulfide-isomerase A6	PDIA6	4.8	48073	75	8	14	50	4	7	0	0	0	0	0	0
13994151	O00151	PDZ and LIM domain protein 1	PDLIM1	6.6	36072	25	1	3	25	1	4	0	0	0	0	0	0
3138924		alpha-actinin-2 associated LIM protein	PDLIM3	8.1	34267	25	1	3	0	0	0	0	0	0	0	0	0
166235176	Q53GG5	PDZ and LIM domain protein 3 isoform a	PDLIM3	6.4	39189	25	1	4	0	0	0	0	0	0	0	0	0
11496885	Q9NR12	PDZ and LIM domain protein 7 isoform 1	PDLIM7	8.3	49795	25	1	3	25	2	0	0	0	0	0	0	0
4505621	P30086	phosphatidylethanolamine-binding protein 1	PEBP1	7.4	21026	75	3	9	50	3	10	0	0	0	0	0	0
4826898	P07737	profilin-1	PFN1	8.4	15055	100	9	15	75	9	21	0	0	0	0	0	0
51094513	A4D2J6	phosphoglycerate mutase 2	PGAM2	9.8	28220	0	0	0	25	1	2	0	0	0	0	0	0
4505763	P00558	phosphoglycerate kinase 1	PGK1	8.1	44615	75	4	11	50	4	8	0	0	0	0	0	0
35438	P07205	unnamed protein product	PGK2	8.9	44896	0	0	0	50	2	2	0	0	0	0	0	0
4505773	P35232	prohibitin	PHB	5.5	29805	0	0	0	25	1	5	0	0	0	0	0	0
6005854		prohibitin-2 isoform 2	PHB2	10.2	33297	75	5	11	50	7	15	25	2	5	0	0	0
27529704	Q9NQC1	KIAA0239	PHF15	5.4	93690	0	0	0	25	2	0	0	0	0	0	0	0
4505809	Q9UBF8	phosphatidylinositol 4-kinase beta isoform 1	PI4KB	5.9	92648	25	1	3	0	0	0	0	0	0	0	0	0
24850133	Q8N2W9	E3 SUMO-protein ligase PIAS4	PIAS4	5.8	56505	0	0	0	25	1	2	0	0	0	0	0	0
257900451	Q9H5I5	piezo-type mechanosensitive ion channel component 2	PIEZO2	5.8	317840	0	0	0	25	1	2	0	0	0	0	0	0
238236		transmembrane secretory component	PIGR	5.5	83314	25	1	4	0	0	0	0	0	0	0	0	0
193785379	B3KXM0	unnamed protein product	PIN4	10.4	11382	25	1	4	0	0	0	0	0	0	0	0	0
4505821	P12273	prolactin-inducible protein	PIP	8.1	16544	25	1	3	0	0	0	50	5	17	25	1	7
33988793	Q96CM9	PKD1L2 protein	PKD1L2	9.3	24188	0	0	0	0	0	0	25	2	8	0	0	0
28933438		fibrocystin L	PKHD1L1	5.7	465746	25	1	5	25	1	4	0	0	0	0	0	0
10835121	P30613	pyruvate kinase isozymes R/L isoform 1	PKLR	7.6	61773	0	0	0	25	1	2	0	0	0	0	0	0
33286418	P14618	pyruvate kinase isozymes M1/M2 isoform a	PKM	7.7	57882	100	23	33	75	16	40	25	3	5	25	1	5
53729344	Q13835	plakophilin-1 isoform 1a	PKP1	9.1	80497	25	1	4	0	0	0	0	0	0	0	0	0
10433994	Q9P212	unnamed protein product	PLCE1	6.8	91517	0	0	0	25	2	0	0	0	0	0	0	0
1477646		plectin	PLEC	5.5	518486	75	9	25	50	5	18	0	0	0	0	0	0
13548675		epiplakin 1	PLEC	5.3	553091	50	3	9	0	0	0	0	0	0	0	0	0
10440367	Q9H7P9	FLJ00018 protein	PLEKHG2	5.7	152529	0	0	0	25	1	2	0	0	0	25	1	5
4505881	P00747	plasminogen isoform 1	PLG	6.9	90570	0	0	0	25	1	2	0	0	0	0	0	0
15620821		KIAA1881 protein	PLIN4	9.0	133060	25	1	3	0	0	0	0	0	0	0	0	0
6010217	Q9UIW2	NOV/plexin-A1 protein	PLXNA1	6.5	194818	0	0	0	0	0	0	0	0	0	25	1	7
5918167		plexin-B1/SEP receptor	PLXNB1	5.4	214411	25	1	3	0	0	0	0	0	0	0	0	0
29336063	Q9ULL4	plexin-B3 isoform 1	PLXNB3	5.9	206847	0	0	0	25	1	2	0	0	0	0	0	0
42415471	P41247	patatin-like phospholipase domain-containing protei	PNPLA4	9.4	27945	0	0	0	25	1	2	0	0	0	0	0	0
7657465	Q9NZ53	podocalyxin-like protein 2	PODXL2	4.1	65076	0	0	0	0	0	0	0	0	0	25	1	5
106507301	P09884	DNA polymerase alpha catalytic subunit	POLA1	5.5	165789	25	1	3	25	1	4	0	0	0	0	0	0
38492356	Q15054	DNA polymerase delta subunit 3	POLD3	9.8	51401	25	1	3	0	0	0	0	0	0	0	0	0
1206035	Q07864	DNA polymerase epsilon catalytic subunit	POLE	5.9	261207	0	0	0	25	1	2	0	0	0	0	0	0
393317		osteoblast specific factor 2	POSTN	7.5	93332	100	145	132	75	114	72	50	55	84	25	11	21
23345100		extracellular matrix protein periostin-bm	POSTN	7.5	87310	75	11	11	50	10	7	25	5	5	25	3	5
45359384	Q6S5H5	POTE14A	POTEG	6.8	57098	0	0	0	25	1	2	0	0	0	0	0	0
74739412	Q9BYX7	ACTBM_HUMAN RecName: Full=Putative beta-actin-like protein 3	POTEKP	5.9	41971	0	0	0	25	1	2	0	0	0	0	0	0
602106	Q01851	POU domain factor	POU4F1	9.5	43025	0	0	0	25	1	4	0	0	0	0	0	0
458391		Brn-3b	POU4F2	9.5	43160	25	1	3	0	0	0	0	0	0	0	0	0
4505965	Q15319	POU domain, class 4, transcription factor 3	POU4F3	9.3	37011	0	0	0	25	2	0	0	0	0	0	0	0

7020106	Q8NEY8	unnamed protein product	PPHLN1	4.7	13453	0	0	0	25	1	2	0	0	0	0	0	0	0
6679439	P17742	peptidyl-prolyl cis-trans isomerase A	Ppia	8.0	17942	75	27	22	75	23	25	25	3	5	0	0	0	0
10863927	P62937	peptidyl-prolyl cis-trans isomerase A	PPIA	7.8	17983	50	3	6	0	0	0	0	0	0	0	0	0	
181335		cyclophilin B	PPIB	9.8	22743	75	4	13	50	3	7	0	0	0	0	0	0	
119582024		hCG1640224, isoform CRA_a	PPIG	9.7	57229	25	1	3	0	0	0	0	0	0	0	0	0	
7657473	Q13356	peptidyl-prolyl cis-trans isomerase-like 2 isoform a	PPIL2	9.0	58769	0	0	0	0	0	0	25	2	7	0	0	0	
3043660		KIAA0568 protein	PPL	5.1	165871	25	1	3	0	0	0	0	0	0	0	0	0	
40807095	Q5SWA1	Protein phosphatase 1, regulatory (inhibitor) subunit 15B	PPP1R15B	4.4	79058	0	0	0	25	1	2	0	0	0	0	0	0	
452521		KIAA0044	PPP2R5C	6.8	56530	0	0	0	0	0	0	25	2	7	0	0	0	
108936953	Q8TF05	serine/threonine-protein phosphatase 4 regulatory subunit 1 isoform a	PPP4R1	4.5	106918	0	0	0	0	0	0	25	2	8	0	0	0	
4160220		PRAME family member 11	PRAMEF11	8.2	50540	25	1	3	0	0	0	0	0	0	0	0	0	
190486	P04280	salivary proline-rich protein	PRB1	11.7	32597	0	0	0	0	0	0	0	0	0	25	1	5	
117306167	Q04118	basic salivary proline-rich protein 3	PRB3	11.3	30954	25	1	3	0	0	0	0	0	0	0	0	0	
4505591	Q06830	peroxiredoxin-1	PRDX1	8.2	22111	25	1	3	25	2	6	0	0	0	25	2	7	
32189392	P32119	peroxiredoxin-2 isoform a	PRDX2	5.6	21893	75	9	16	75	6	11	0	0	0	0	0	0	
5802974	P30048	thioredoxin-dependent peroxide reductase, mitochondrial isoform a	PRDX3	7.7	27657	25	1	3	50	3	8	0	0	0	0	0	0	
5453549	Q13162	peroxiredoxin-4	PRDX4	5.8	30541	75	11	8	75	10	10	50	5	15	25	1	5	
6912238	P30044	peroxiredoxin-5, mitochondrial isoform a	PRDX5	8.7	21994	50	3	10	50	7	19	0	0	0	0	0	0	
4758638	P30041	peroxiredoxin-6	PRDX6	6.0	25036	0	0	0	25	1	2	0	0	0	0	0	0	
4506041	P51888	prolargin	PRELP	9.6	43811	25	4	7	25	3	4	0	0	0	0	0	0	
31137		unnamed protein product	PRG2	6.2	25232	100	48	17	75	40	11	25	6	5	25	1	5	
157743280	A6NGE7	putative 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	PRHOXNB	5.7	19100	25	1	3	0	0	0	0	0	0	0	0	0	
114635872		PREDICTED: protein kinase C delta-binding protein isoform 2	PRKCDBP	5.8	27607	25	1	3	0	0	0	0	0	0	0	0	0	
52486327	Q05513	protein kinase C zeta type isoform 1	PRKCZ	5.4	67599	25	1	3	0	0	0	0	0	0	0	0	0	
77748060		PROX2 protein	PROX2	9.5	65441	25	1	3	0	0	0	0	0	0	0	0	0	
2653736		U4/U6 snRNP 60 kDa protein	PRPF4	6.7	58552	25	1	3	0	0	0	25	2	7	0	0	0	
1050983		pHL E1F1	PRR4	6.6	15098	50	4	7	0	0	0	0	0	0	25	2	7	
154448886	Q16378	proline-rich protein 4 isoform 2	PRR4	6.6	15070	0	0	0	25	1	4	0	0	0	0	0	0	
4506145	P07477	trypsin-1	PRSS1	6.1	26559	0	0	0	0	0	0	50	9	19	50	6	26	
119572363		hCG22067	PRSS1	7.7	29712	0	0	0	25	1	2	0	0	0	0	0	0	
4731447		pregnancy-specific beta-1-glycoprotein 5	PSG5	8.5	16022	25	1	3	0	0	0	0	0	0	25	1	5	
19923653	O75475	PC4 and SFRS1-interacting protein isoform 2	PSIP1	9.6	60049	0	0	0	25	1	2	0	0	0	0	0	0	
4506189	O14818	proteasome subunit alpha type-7	PSMA7	8.7	27888	0	0	0	25	1	2	0	0	0	0	0	0	
109083120		PREDICTED: proteasome activator complex subunit 2	PSME2	5.3	27326	25	1	3	25	1	2	0	0	0	0	0	0	
4506243	P26599	polypyrimidine tract-binding protein 1 isoform a	PTBP1	9.5	59578	25	1	3	50	3	9	0	0	0	0	0	0	
1381236	Q13635	PATCHED	PTCH1	6.4	160561	0	0	0	25	1	2	0	0	0	0	0	0	
42734430	Q6NZI2	polymerase I and transcript release factor	PTRF	5.4	43432	25	2	4	0	0	0	0	0	0	0	0	0	
16550495	Q9BZE2	unnamed protein product	PUS3	6.9	55582	0	0	0	0	0	0	0	0	0	25	2	10	
7020363	Q7Z7A4	unnamed protein product	PXK	9.9	73061	0	0	0	0	0	0	0	0	0	25	2	7	
21361370	P11216	glycogen phosphorylase, brain form	PYGB	6.4	96696	25	1	3	0	0	0	0	0	0	0	0	0	
40788955	Q15032	KIAA0029	R3HDM1	9.0	108031	0	0	0	0	0	0	0	0	0	25	1	7	
12052826		hypothetical protein	RAB10	8.8	22470	50	2	6	50	1	4	0	0	0	0	0	0	
763130	Q15907	YPT3	RAB11B	5.8	24574	0	0	0	25	1	4	0	0	0	0	0	0	
4506363	P51153	ras-related protein Rab-13	RAB13	9.6	22775	100	10	12	50	2	4	50	19	13	50	7	14	
34485714	Q9ULC3	ras-related protein Rab-23	RAB23	6.2	26660	0	0	0	0	0	0	25	2	5	0	0	0	
19923790	Q9H2M9	rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	5.3	155868	0	0	0	0	0	0	25	2	5	0	0	0	
41393545	P51148	ras-related protein Rab-5C isoform a	RAB5C	8.5	23450	0	0	0	25	1	2	0	0	0	0	0	0	
34147513	P51149	ras-related protein Rab-7a	RAB7A	6.6	23491	0	0	0	25	1	2	0	0	0	0	0	0	
14595132		Raichu404X	RAP1A	6.5	85016	25	1	3	50	5	7	0	0	0	0	0	0	
32080		smg GDS	RAP1GDS1	5.2	61124	25	2	3	50	2	6	0	0	0	0	0	0	
119625255		hCG2036828	RAPGEF6	7.2	21205	0	0	0	0	0	0	0	0	0	25	2	7	
119569941		hCG2036763	RBM20	5.5	137167	25	1	3	0	0	0	0	0	0	0	0	0	
5803137	P98179	putative RNA-binding protein 3	RBM3	9.2	17171	75	3	8	25	3	4	0	0	0	0	0	0	
93277122	Q9BWF3	RNA-binding protein 4 isoform 1	RBM4	6.6	40315	25	1	3	0	0	0	0	0	0	0	0	0	
21450675	Q8TBY0	probable RNA-binding protein 46	RBM46	7.5	60023	0	0	0	25	1	2	0	0	0	0	0	0	
194380344	B4DZ27	unnamed protein product	RBM46	7.5	55284	0	0	0	0	0	0	0	0	0	25	1	7	
56699409	P38159	RNA-binding motif protein, X chromosome isoform 1	RBMX	10.3	42288	50	3	8	25	3	7	0	0	0	0	0	0	
42560225	Q06330	recombining binding protein suppressor of hairless isoform 3	RBPJ	7.9	54093	25	1	3	0	0	0	0	0	0	0	0	0	
23957680	Q8IZJ4	ral-GDS-related protein	RLG4	7.8	52347	25	1	3	0	0	0	0	0	0	0	0	0	

10438686		unnamed protein product	RHBDL2	7.3	69966	0	0	0	0	0	0	25	2	5	0	0	0
7020534	Q9NX52	unnamed protein product	RHBDL2	8.2	32808	0	0	0	25	1	2	0	0	0	0	0	0
2765839	Q9UDZ5	rhesus D category VI type III protein	RHD	9.4	45248	0	0	0	25	1	2	0	0	0	0	0	0
7023651	Q9BVS4	unnamed protein product	RIOK2	5.7	63383	0	0	0	25	1	2	0	0	0	0	0	0
10434636		unnamed protein product	RMI1	4.7	70076	25	1	4	0	0	0	0	0	0	0	0	0
4506549	P10153	non-secretory ribonuclease	RNASE2	8.7	18355	100	12	20	50	3	9	25	6	11	0	0	0
31077		unnamed protein product	RNASE3	10.5	18441	75	15	11	50	10	9	50	8	12	25	3	5
94421471	Q9BXT8	RING finger protein 17 isoform 1	RNF17	5.1	184643	25	1	3	0	0	0	0	0	0	0	0	0
4520225	O75116	Rho kinase	ROCK2	5.7	160885	0	0	0	25	1	2	0	0	0	0	0	0
337465		transmembrane receptor	ROR1	6.7	104313	25	1	3	25	1	2	0	0	0	0	0	0
10435038	Q8IXW5	unnamed protein product	RPAP2	7.6	69449	0	0	0	0	0	0	0	0	0	25	1	5
4506581	Q92834	X-linked retinitis pigmentosa GTPase regulator isoform A	RPGR	4.7	90170	0	0	0	25	2	0	0	0	0	0	0	0
47077429	Q6ZMX3	unnamed protein product	RPGR	4.8	69925	0	0	0	0	0	0	25	2	5	0	0	0
495126	P62913	ribosomal protein L11	RPL11	9.9	20116	0	0	0	25	1	2	0	0	0	0	0	0
4506597	P30050	60S ribosomal protein L12	RPL12	9.9	17819	50	2	6	25	1	2	0	0	0	0	0	0
29383		BBC1	RPL13	12.2	24292	25	1	3	25	1	2	0	0	0	0	0	0
42490910	Q6NZ55	Ribosomal protein L13	RPL13	12.2	24266	25	1	3	0	0	0	0	0	0	0	0	0
3126984		CAG-isl 7	RPL14	11.4	23291	25	1	3	0	0	0	0	0	0	0	0	0
4506607	Q07020	60S ribosomal protein L18	RPL18	12.2	21635	50	2	6	25	3	9	0	0	0	0	0	0
119616019		hCG1979897, isoform CRA_b	RPL18	11.2	16626	0	0	0	25	1	4	0	0	0	0	0	0
18104948	P46778	60S ribosomal protein L21	RPL21	10.9	18566	75	7	13	50	6	11	0	0	0	0	0	0
4506613	P35268	60S ribosomal protein L22 proprotein	RPL22	9.6	14788	25	1	3	0	0	0	0	0	0	0	0	0
17105394	P62750	60S ribosomal protein L23a	RPL23A	10.9	17696	0	0	0	25	1	2	0	0	0	0	0	0
119617809		hCG1646587	RPL23A	10.9	15225	0	0	0	25	1	2	0	0	0	0	0	0
4506621	P61254	60S ribosomal protein L26	RPL26	11.0	17259	0	0	0	25	1	2	0	0	0	0	0	0
4506623	P61353	60S ribosomal protein L27	RPL27	11.0	15799	25	1	3	25	1	2	0	0	0	0	0	0
793843	P47914	ribosomal protein L29	RPL29	12.1	17668	0	0	0	25	1	2	0	0	0	0	0	0
7159730	Q9NY85	ribosomal protein L3	rpl3	10.5	39384	25	1	3	25	1	2	0	0	0	0	0	0
36138		ribosomal protein L6	RPL6	10.8	32862	50	3	9	50	4	8	0	0	0	0	0	0
35903		ribosomal protein L7	RPL7	11.0	29184	50	2	6	50	2	7	0	0	0	0	0	0
4506663	P62917	60S ribosomal protein L8	RPL8	11.5	28025	0	0	0	25	1	2	0	0	0	0	0	0
15431303	P32969	60S ribosomal protein L9	RPL9	10.4	21864	50	3	6	50	4	10	0	0	0	0	0	0
84569966	Q2NKY6	Unknown (protein for MGC:131531)	RPL9	10.5	21761	25	1	3	0	0	0	0	0	0	0	0	0
4506667	P05388	60S acidic ribosomal protein P0	RPLP0	5.6	34274	50	2	6	25	1	4	0	0	0	0	0	0
4506669	P05386	60S acidic ribosomal protein P1 isoform 1	RPLP1	4.0	11489	50	4	5	50	4	7	25	2	5	0	0	0
4506675	P04843	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	5.9	68509	25	1	3	0	0	0	0	0	0	0	0	0
36049		unnamed protein product	RPN2	5.4	69303	50	2	6	50	2	7	0	0	0	25	1	5
3088338		ribosomal protein S10	RPS10	9.8	9436	25	1	3	50	3	6	0	0	0	0	0	0
14277700	P25398	40S ribosomal protein S12	RPS12	7.0	14516	0	0	0	25	1	2	0	0	0	0	0	0
5032051	P62263	40S ribosomal protein S14	RPS14	10.5	16274	25	1	3	0	0	0	0	0	0	0	0	0
36142		ribosomal protein homologous to yeast S24	RPS15A	10.7	14689	50	2	6	50	2	7	0	0	0	0	0	0
4506691	P62249	40S ribosomal protein S16	RPS16	10.6	16446	50	2	6	25	2	7	0	0	0	0	0	0
6755368	P62270	40S ribosomal protein S18	Rps18	11.5	17720	0	0	0	25	1	2	0	0	0	0	0	0
4506695	P39019	40S ribosomal protein S19	RPS19	10.7	16061	25	1	3	25	1	2	0	0	0	0	0	0
3088340		ribosomal protein S20	RPS20	11.1	6858	25	1	3	25	1	2	0	0	0	0	0	0
4506697	P60866	40S ribosomal protein S20 isoform 2	RPS20	10.4	13374	75	3	8	75	5	7	25	2	5	0	0	0
4506701	P62266	40S ribosomal protein S23	RPS23	11.0	15808	0	0	0	25	1	4	0	0	0	0	0	0
46519160	P62849	40S ribosomal protein S24 isoform 3	Rps24	11.4	15198	0	0	0	25	2	6	0	0	0	0	0	0
4506715	P62857	40S ribosomal protein S28	RPS28	11.2	7842	0	0	0	25	1	2	0	0	0	0	0	0
15718687	P23396	40S ribosomal protein S3	RPS3	10.1	26689	0	0	0	25	3	9	0	0	0	0	0	0
4506723	P61247	40S ribosomal protein S3a	RPS3A	10.2	29946	25	2	3	0	0	0	0	0	0	0	0	0
4506725	P62701	40S ribosomal protein S4	RPS4X	10.6	29561	50	2	6	25	1	4	0	0	0	0	0	0
119621546		hCG1643126, isoform CRA_b	RPS4X	8.2	14174	25	1	3	0	0	0	0	0	0	0	0	0
6677809	P62754	40S ribosomal protein S6	Rps6	11.3	28681	25	1	4	25	1	2	0	0	0	0	0	0
15375094	Q96S38	RSK-like protein	RPS6KC1	4.6	118612	0	0	0	25	2	0	0	0	0	0	0	0
4506741	P62081	40S ribosomal protein S7	RPS7	10.6	22128	75	6	8	50	6	10	0	0	0	0	0	0
4506743	P62241	40S ribosomal protein S8	RPS8	10.7	24206	0	0	0	25	2	4	0	0	0	0	0	0
34272	P08865	unnamed protein product	RPSA	4.6	33314	0	0	0	25	2	7	0	0	0	0	0	0

5454028	P10301	ras-related protein R-Ras	RRAS	6.5	23481	25	1	3	0	0	0	0	0	0	0	0	0	0
3288996	Q92766	Raf responsive zinc finger protein	RREB1	5.6	56852	0	0	0	0	0	0	0	0	0	0	25	1	5
6912638	Q15404	ras suppressor protein 1 isoform 1	RSU1	9.1	31541	25	1	3	0	0	0	0	0	0	0	0	0	0
9408096		Nogo-A protein	RTN4	4.3	129942	25	1	3	0	0	0	0	0	0	0	0	0	0
2696015	Q15413	brain ryanodine receptor	RYR3	5.4	551072	0	0	0	25	2	0	0	0	0	0	0	0	0
4522023		similar to calgizzarin; similar to PID:g3115349	S100A11	8.9	11484	100	6	12	50	4	7	0	0	0	50	5	12	
115298657	P31151	protein S100-A7	S100A7	6.3	11472	25	1	3	0	0	0	0	0	0	25	3	7	
29888	P05109	unnamed protein product	S100A8	9.6	10939	0	0	0	0	0	0	0	0	0	25	2	7	
4506773	P06702	protein S100-A9	S100A9	5.7	13243	75	5	8	100	12	10	75	15	20	75	32	37	
38016914	Q9Y3Z3	SAM domain and HD domain-containing protein 1	SAMHD1	6.7	72137	0	0	0	25	1	2	0	0	0	0	0	0	0
19923597	Q9H0E3	histone deacetylase complex subunit SAP130 isoform b	SAP130	10.2	110237	25	1	3	0	0	0	0	0	0	0	0	0	0
10862824	Q9H4B6	WW45 protein	SAV1	9.2	44635	0	0	0	25	1	4	0	0	0	0	0	0	0
260436922	Q6UWP8	suprabasin isoform 1	SBSN	6.5	60541	0	0	0	0	0	0	0	0	0	50	4	16	
62460633	Q9UPN6	protein SCAF8	SCAF8	8.4	140519	25	1	3	0	0	0	0	0	0	0	0	0	0
7657544	Q9UQD0	sodium channel protein type 8 subunit alpha isoform	SCN8A	5.9	225116	0	0	0	0	0	0	0	0	0	25	2	10	
119631065		scratch homolog 2, zinc finger protein (Drosophila), isoform CRA_a	SCRT2	8.6	36039	25	2	3	0	0	0	0	0	0	25	1	5	
31377568	Q8IX30	signal peptide, CUB and EGF-like domain-containing protein 3	SCUBE3	7.3	109192	0	0	0	25	1	2	0	0	0	0	0	0	0
156416003	P31040	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	7.0	72627	25	2	3	50	2	7	0	0	0	0	0	0	0
6755448	O08547	vesicle-trafficking protein SEC22b	SEC22B	8.7	24707	0	0	0	25	1	2	0	0	0	0	0	0	0
1374792	Q13228	selenium-binding protein	SELENBP1	6.1	52314	0	0	0	25	1	2	0	0	0	0	0	0	0
10435945	Q9H8A8	unnamed protein product	SELENBP1	6.2	25954	0	0	0	25	1	2	0	0	0	0	0	0	0
11095320		AF307849_1 sentrin-specific protease SENP6	SENP6	6.3	126049	50	2	6	0	0	0	0	0	0	0	0	0	0
120538355	Q9BQF6	SUMO1/sentrin specific peptidase 7	SENP7	6.1	119658	0	0	0	25	1	2	0	0	0	0	0	0	0
1040689		Human Diff6,H5,CDC10 homologue	SEPT2	7.0	46586	50	2	6	50	1	4	0	0	0	0	0	0	0
47564098	Q6Q137	septin-7	SEPT7	8.9	48759	50	2	6	25	1	2	0	0	0	0	0	0	0
50363217	P01009	alpha-1-antitrypsin	SERPINA1	5.3	46737	0	0	0	50	1	5	0	0	0	0	0	0	0
13489087	P30740	leukocyte elastase inhibitor	SERPINB1	5.9	42743	0	0	0	25	1	2	0	0	0	0	0	0	0
17998551	Q96P63	serpin B12	SERPINB12	5.3	46277	25	1	4	0	0	0	0	0	0	0	0	0	0
239552		squamous cell carcinoma antigen	SERPINB3	6.4	44535	50	6	11	50	17	33	25	3	15	50	6	14	
10835159	P05121	plasminogen activator inhibitor 1 isoform 1	SERPINE1	6.8	45013	0	0	0	25	1	2	0	0	0	0	0	0	0
179619		plasma protease (C1) inhibitor	SERPING1	6.1	55129	0	0	0	0	0	0	25	2	7	0	0	0	0
170763498	Q01105	protein SET isoform 2	SET	4.0	32104	25	1	3	25	1	2	0	0	0	0	0	0	0
10439587		unnamed protein product	SETD3	5.1	57617	0	0	0	0	0	0	25	2	8	0	0	0	0
119595910		transmembrane, prostate androgen induced RNA, isoform CRA_a	SF3A2	12.5	26236	0	0	0	25	1	2	0	0	0	0	0	0	0
4826998	P23246	splicing factor, proline- and glutamine-rich	SFPQ	9.8	76084	50	6	13	50	4	12	0	0	0	0	0	0	0
150010572	Q8TEJ3	SH3 domain-containing RING finger protein 3	SH3RF3	8.9	92700	0	0	0	25	1	2	0	0	0	0	0	0	0
22713420	Q8NDZ2	Chromosome 5 open reading frame 25	SIMC1	6.2	96955	0	0	0	0	0	0	0	0	0	25	2	10	
7363059	Q9NSJ2	human homeobox protein SIX3 (NP_005404)	SIX3	6.3	16656	25	1	3	0	0	0	0	0	0	0	0	0	0
119614828	J3QKN8	family with sequence similarity 33, member A, isoform CRA_c	SKA2	10.9	8657	25	1	3	50	2	2	25	2	7	75	5	22	
4379045	Q15477	helicase	SKIIV2L	5.7	137790	0	0	0	25	1	2	0	0	0	0	0	0	0
24308414	Q96EP9	sodium/bile acid cotransporter 4	SLC10A4	5.0	46505	0	0	0	0	0	0	25	4	12	0	0	0	0
27124713	Q8IV67	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	SLC13A2	8.6	47581	0	0	0	0	0	0	0	0	0	25	1	5	
34916028	Q7RTY1	monocarboxylate transporter 9	SLC16A9	7.9	55794	0	0	0	0	0	0	0	0	0	25	1	5	
21314632	P43007	neutral amino acid transporter A isoform 1	SLC1A4	5.8	55670	0	0	0	0	0	0	0	0	0	25	2	7	
2281942		organic cation transporter	SLC22A2	8.3	62565	0	0	0	0	0	0	25	4	12	0	0	0	0
20070188	Q4U2R8	solute carrier family 22 member 6 isoform a	SLC22A6	8.8	61758	25	1	3	0	0	0	0	0	0	0	0	0	0
55749577	P12235	ADP/ATP translocase 1	SLC25A4	10.1	33065	0	0	0	50	2	7	0	0	0	0	0	0	0
183303		glucose transporter glycoprotein	SLC2A1	8.9	54118	25	1	3	25	1	2	0	0	0	0	0	0	0
4507013	P22732	solute carrier family 2, facilitated glucose transporter member 5 isoform 1	SLC2A5	5.7	54920	0	0	0	0	0	0	25	2	5	0	0	0	0
28193238	Q8IZM9	unnamed protein product	SLC38A6	8.9	57326	0	0	0	25	2	0	0	0	0	0	0	0	0
4507021	P02730	band 3 anion transport protein	SLC4A1	4.9	101793	25	12	18	50	20	31	25	2	8	25	3	11	
2887405	Q92911	sodium iodide symporter	SLC5A5	7.2	68761	0	0	0	25	1	2	0	0	0	0	0	0	0
4759140	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	5.5	38827	0	0	0	25	1	2	0	0	0	0	0	0	0
11990593		AF205075_1 organic anion transporter polypeptide-related protein 4	SLCO5A1	7.5	91800	25	1	3	0	0	0	0	0	0	0	0	0	0
193785674	B3KMU7	unnamed protein product	SLCO5A1	7.8	73816	0	0	0	0	0	0	25	2	8	0	0	0	0
47778925	Q99717	mothers against decapentaplegic homolog 5	SMAD5	7.5	52207	0	0	0	25	1	2	0	0	0	0	0	0	0

987661	P51531	transcriptional activator hSNF2a	SMARCA2	6.9	179334	0	0	0	0	0	0	0	0	0	0	25	2	10
71565160	Q8NDV3	structural maintenance of chromosomes protein 1B	SMC1B	7.2	143729	0	0	0	25	1	2	0	0	0	0	0	0	0
51476898	Q9NRH2	hypothetical protein	SNRK	6.7	86419	0	0	0	0	0	0	0	0	0	0	25	2	7
602021		unnamed protein product	SNRNP70	10.9	35775	0	0	0	0	0	0	25	2	5	0	0	0	0
5902102	P62314	small nuclear ribonucleoprotein Sm D1	SNRPD1	12.1	13255	25	3	3	50	4	7	0	0	0	0	0	0	0
4507135	P63162	small nuclear ribonucleoprotein-associated protein N	SNRPN	11.7	24580	0	0	0	25	1	2	0	0	0	0	0	0	0
3882147	Q9Y5W8	KIAA0713 protein	SNX13	5.6	108277	0	0	0	25	2	0	0	0	0	0	0	0	0
7661700	Q9BX66	sorbin and SH3 domain-containing protein 1 isoform 2	SORBS1	6.0	90129	25	1	3	0	0	0	0	0	0	0	0	0	0
61743973	Q8WY21	VPS10 domain-containing SorCS1 isoform a	SORCS1	7.3	129535	0	0	0	25	1	2	0	0	0	0	0	0	0
15082267		AF345909_1 NYD-SP12	SPATA16	9.5	65232	25	1	3	0	0	0	0	0	0	0	0	0	0
21740171	Q6ZUB1	hypothetical protein	SPATA31E1	9.7	119879	0	0	0	25	1	4	0	0	0	0	0	0	0
75750474	Q5M775	cytospin-B isoform 2	SPECC1	5.6	110243	25	1	3	0	0	0	0	0	0	0	0	0	0
338438		erythroid alpha spectrin	SPTA1	4.8	281056	25	1	3	0	0	0	0	0	0	0	0	0	0
829111	Q13813	alpha-spectrin	SPTAN1	5.1	43819	0	0	0	25	1	2	0	0	0	0	0	0	0
306966132	Q13813	spectrin alpha chain, brain isoform 3	SPTAN1	5.1	282090	25	1	3	25	3	4	0	0	0	0	0	0	0
67782319	P11277	spectrin beta chain, erythrocyte isoform b	SPTB	5.0	246298	0	0	0	25	1	2	0	0	0	0	0	0	0
115430237	Q9H254	spectrin beta chain, brain 3 isoform sigma1	SPTBN4	5.7	288790	0	0	0	25	1	2	0	0	0	0	0	0	0
31874159		hypothetical protein	SPTY2D1	5.9	24474	0	0	0	0	0	0	25	2	7	0	0	0	0
284795266	Q9Y5M8	signal recognition particle subunit beta	SRPRB	9.4	29666	25	1	3	0	0	0	0	0	0	0	0	0	0
119577233		hCG20528, isoform CRA_a	SRRM3	11.8	17084	0	0	0	0	0	0	0	0	0	25	2	7	0
119592206		hCG41366, isoform CRA_b	SRRM3	4.8	17671	0	0	0	0	0	0	0	0	0	25	1	5	0
4506901	P84103	serine/arginine-rich splicing factor 3	SRSF3	12.1	19300	50	3	6	50	3	7	25	2	5	0	0	0	0
72534660	Q16629	serine/arginine-rich splicing factor 7 isoform 1	SRSF7	12.3	27332	25	1	3	25	1	2	0	0	0	0	0	0	0
62822614	Q52MY1	mutant SRY protein	SRY	9.8	19219	0	0	0	0	0	0	0	0	0	25	1	7	0
531106	Q6FGL9	SYT	SS18	6.6	42577	0	0	0	25	1	2	0	0	0	0	0	0	0
10835067	P05455	lupus La protein	SSB	6.8	46838	0	0	0	25	1	2	0	0	0	0	0	0	0
14249150	Q9BWG4	single-stranded DNA-binding protein 4 isoform a	SSBP4	6.3	39344	0	0	0	0	0	0	25	2	7	0	0	0	0
54234057	P61647	alpha-2,8-sialyltransferase 8F	ST8SIA6	9.3	44789	0	0	0	0	0	0	25	2	7	0	0	0	0
56243551	P49675	steroidogenic acute regulatory protein, mitochondrial	STAR	9.4	31875	0	0	0	0	0	0	0	0	0	25	2	7	0
1103842		band 7.2b stomatin	STOM	8.0	32594	25	1	3	0	0	0	0	0	0	0	0	0	0
47778943	Q14662	syntaxin-16 isoform a	STX16	5.7	37032	25	1	4	0	0	0	0	0	0	0	0	0	0
34528063	Q6ZWJ1	unnamed protein product	STXBP4	5.0	61762	0	0	0	25	1	2	0	0	0	0	0	0	0
197098442	Q5R6D0	activated RNA polymerase II transcriptional coactivator p15	SUB1	10.1	14368	75	8	8	50	4	7	0	0	0	0	0	0	0
7656940	Q9UBS9	protein osteopontin homolog isoform 1	SUCO	4.8	139325	0	0	0	25	1	2	0	0	0	0	0	0	0
119582782		hCG1641337, isoform CRA_b	SUGP1	6.3	48273	0	0	0	0	0	0	25	2	7	0	0	0	0
195963398	Q9Y2Z0	suppressor of G2 allele of SKP1 homolog isoform SGT1B	SUGT1	4.9	40980	0	0	0	0	0	0	0	0	0	25	2	10	0
19111164	P61957	small ubiquitin-related modifier 2	Sumo2	5.2	10846	0	0	0	25	1	2	0	0	0	0	0	0	0
3327150		KIAA0668 protein	SUN2	6.3	82968	25	1	3	0	0	0	0	0	0	0	0	0	0
6005757	Q9Y5B9	FACT complex subunit SPT16	SUPT16H	5.4	119914	0	0	0	25	1	2	0	0	0	0	0	0	0
73909146	Q6UWL2	SUSD1 protein	SUSD1	6.3	84510	0	0	0	25	1	2	0	0	0	0	0	0	0
11527207		CGI-85	SUV420H1	9.4	30349	25	1	3	0	0	0	0	0	0	0	0	0	0
19924099	P17600	synapsin-1 isoform Ia	SYN1	10.2	74112	25	1	3	0	0	0	0	0	0	0	0	0	0
26454828	Q60506	SYNCRIP protein	SYNCRIP	9.1	46269	0	0	0	25	1	4	0	0	0	0	0	0	0
20521662	Q8NF91	KIAA0796 protein	SYNE1	5.2	216240	0	0	0	0	0	0	0	0	0	25	2	12	0
18698324		synemin	SYNM	5.0	172479	25	1	3	0	0	0	0	0	0	0	0	0	0
10047269		KIAA1597 protein	SYTL2	8.6	102679	0	0	0	0	0	0	25	2	7	0	0	0	0
14149669	Q9NYJ8	TGF-beta-activated kinase 1 and MAP3K7-binding protein 2	TAB2	8.5	76429	0	0	0	0	0	0	25	2	5	0	0	0	0
166795236	P09758	tumor-associated calcium signal transducer 2	TACSTD2	8.9	35669	0	0	0	25	1	2	0	0	0	0	0	0	0
29733		CCG1 protein	TAF1	6.1	178777	25	1	3	0	0	0	0	0	0	0	0	0	0
48255905	Q01995	transgelin	TAGLN	9.2	22612	50	40	44	50	13	2	0	0	0	0	0	0	0
4507357	P37802	transgelin-2	TAGLN2	8.4	22392	75	7	18	50	6	17	0	0	0	0	0	0	0
1621611	Q92844	TRAF family member-associated NF-kB activator TANK	TANK	5.4	47752	0	0	0	0	0	0	0	0	0	25	1	5	0
221139909	Q9PON9	TBC1 domain family member 7 isoform b	TBC1D7	7.2	30709	0	0	0	0	0	0	25	2	7	0	0	0	0
193784824	B3KW15	unnamed protein product	TBC1D9B	4.3	35146	25	1	3	0	0	0	0	0	0	0	0	0	0
18129690	P57082	T-box transcription factor TBX4	TBX4	7.4	60205	0	0	0	0	0	0	0	0	0	25	2	10	0
2564332		KIAA0292	TCF20	9.3	185896	25	1	3	0	0	0	0	0	0	0	0	0	0
148746195	Q07283	trichohyalin	TCHH	5.6	253924	75	4	9	25	2	4	0	0	0	0	0	0	0
119581916	G3V106	hCG38403, isoform CRA_b	TENM2	6.3	294059	0	0	0	0	0	0	0	0	0	25	1	7	0
1848277	Q99973	telomerase-associated protein TP-1	TEP1	7.7	290414	0	0	0	25	2	0	0	0	0	25	2	10	0

38348356	Q8N6V9	testis-expressed sequence 9 protein	TEX9	6.2	44827	25	3	3	0	0	0	0	0	0	0	0	0	0
4557871	P02787	serotransferrin	TF	6.7	77050	0	0	0	0	0	0	25	4	7	25	3	14	
7020498		unnamed protein product	TFR2	5.9	38534	0	0	0	0	0	0	25	2	5	0	0	0	
4507467	Q15582	transforming growth factor-beta-induced protein ig-h3	TGFB1	7.5	74616	100	5	14	50	5	8	0	0	0	0	0	0	
3150052		TGF beta receptor associated protein-1	TGFBRAP1	6.1	97177	25	1	3	0	0	0	0	0	0	25	1	7	
20151073	P21980	A Chain A, Human Tissue Transglutaminase In Gdp Bound Form	TGM2	5.0	77258	50	4	8	0	0	0	0	0	0	0	0	0	
37138	P07996	unnamed protein product	THBS1	4.6	129413	0	0	0	50	1	4	0	0	0	0	0	0	
41281981	Q8IUC6	TIR domain-containing adapter molecule 1	TICAM1	5.1	76356	0	0	0	25	1	2	0	0	0	0	0	0	
5454120	Q99595	mitochondrial import inner membrane translocase subunit Tim17-A	TIMM17A	8.0	17994	0	0	0	0	0	0	50	9	19	25	3	7	
4507521	P29401	transketolase	TKT	7.5	67878	25	1	3	50	5	12	0	0	0	0	0	0	
223029410	Q9Y490	talin-1	TLN1	5.7	269766	75	9	25	25	4	6	0	0	0	0	0	0	
194382724	B4E0S0	unnamed protein product	TMC8	11.2	36989	0	0	0	0	0	0	25	2	7	0	0	0	
13129092	Q9BVC6	transmembrane protein 109	TMEM109	10.9	26211	25	1	3	0	0	0	0	0	0	0	0	0	
15620871	Q14DG7	KIAA1906 protein	TMEM132B	4.7	66412	0	0	0	25	1	2	0	0	0	0	0	0	
22761276	Q8NBT3	unnamed protein product	TMEM145	8.7	55604	0	0	0	0	0	0	0	0	0	25	1	5	
119592769		hCG1645235, isoform CRA_b	TMEM150B	10.0	26528	0	0	0	25	1	2	0	0	0	0	0	0	
269914178	Q8NBL3	transmembrane protein 178 isoform 1	TMEM178A	8.4	32979	25	1	3	0	0	0	0	0	0	0	0	0	
51095046		similar to RIKEN cDNA A530016O06 gene	TMEM195	6.4	54211	25	1	3	0	0	0	0	0	0	0	0	0	
14042792		unnamed protein product	TMEM43	8.5	25452	75	5	8	25	2	2	0	0	0	0	0	0	
37700256	Q3KNT9	transmembrane protein 95	TMEM95	8.4	20288	0	0	0	25	1	4	0	0	0	0	0	0	
10946578	P20065	thymosin beta-4	Tmsb4x	4.9	5054	25	2	5	25	1	2	0	0	0	0	0	0	
37227		tenascin	TNC	4.7	240718	25	2	5	0	0	0	25	2	5	0	0	0	
556845		human tenascin-C	TNC	4.6	240866	75	13	28	50	4	11	25	12	37	0	0	0	
179331		B94 protein	TNFAIP2	6.0	72663	0	0	0	0	0	0	25	2	8	0	0	0	
26051243	P98066	tumor necrosis factor-inducible gene 6 protein	TNFAIP6	6.3	31165	0	0	0	0	0	0	25	2	8	0	0	0	
11275669		tensin	TNS1	7.6	185677	50	2	8	0	0	0	0	0	0	0	0	0	
4507645	P60174	triosephosphate isomerase isoform 1	TPH1	6.5	26670	50	3	6	50	3	7	0	0	0	0	0	0	
63252898	P09493	tropomyosin alpha-1 chain isoform 1	TPM1	4.5	32671	25	1	3	25	2	0	0	0	0	0	0	0	
63252902	P09493	tropomyosin alpha-1 chain isoform 2	TPM1	4.5	32640	100	41	58	75	12	11	25	2	5	0	0	0	
63252904	P09493	tropomyosin alpha-1 chain isoform 6	TPM1	4.6	28350	0	0	0	25	1	2	0	0	0	0	0	0	
42476296	P07951	tropomyosin beta chain isoform 1	TPM2	4.5	32852	25	2	4	0	0	0	0	0	0	0	0	0	
47519616	P07951	tropomyosin beta chain isoform 2	TPM2	4.5	32991	0	0	0	25	2	0	0	0	0	0	0	0	
38541687	Q5VU62	TPM3 protein	TPM3	4.5	18494	25	1	3	0	0	0	0	0	0	0	0	0	
4507651	P67936	tropomyosin alpha-4 chain isoform 2	TPM4	4.5	28523	100	33	24	100	34	19	0	0	0	0	0	0	
633226		Tpr	TPR	4.9	265600	50	2	6	0	0	0	0	0	0	0	0	0	
217416360	Q86W33	transmembrane protein adipocyte-associated 1 isoform 2	TPRA1	8.9	32078	25	1	3	0	0	0	0	0	0	0	0	0	
119575118		hCG1987691	TPRXL	3.6	28549	0	0	0	0	0	0	0	0	0	25	2	7	
193248252	Q6ZSY7	unnamed protein product	TPRXL	7.8	16605	0	0	0	0	0	0	25	4	12	0	0	0	
1082886		A55877 tumor necrosis factor type 1 receptor associated protein TRAP-1	TRAP1	8.3	75277	0	0	0	25	1	2	0	0	0	0	0	0	
40789021		KIAA1012 protein	TRAPPC8	6.6	162548	25	1	3	0	0	0	0	0	0	0	0	0	
496094		T-cell receptor beta	TRBV2	5.2	12036	0	0	0	0	0	0	25	2	8	0	0	0	
16566786		AF430652_1 T cell receptor beta variable region	TRBV56	5.0	13965	25	1	3	0	0	0	0	0	0	0	0	0	
44680122	Q9C029	tripartite motif-containing protein 7 isoform 1	TRIM7	7.5	56577	0	0	0	25	1	2	0	0	0	0	0	0	
7023747	Q9NUP7	unnamed protein product	TRMT13	8.0	54308	0	0	0	25	2	0	0	0	0	0	0	0	
119593830		tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase, isoform CRA_c	TRMU	10.0	31674	0	0	0	25	1	2	0	0	0	0	0	0	
33304372		tastin	TROAP	6.9	83838	25	1	3	0	0	0	0	0	0	0	0	0	
4507691	Q9Y4A5	transformation/transcription domain-associated protein isoform 2	TRRAP	8.1	434116	0	0	0	0	0	0	25	4	12	0	0	0	
7243183		KIAA1401 protein	TSR1	8.0	97049	0	0	0	25	2	0	25	2	8	0	0	0	
17402865	Q16762	thiosulfate sulfurtransferase	TST	6.9	33430	25	1	3	25	1	4	0	0	0	0	0	0	
27451602	Q8IWI7	tau-tubulin kinase	TTBK2	6.6	182467	0	0	0	50	15	2	50	30	13	50	32	12	
7020708		unnamed protein product	TTC12	5.7	75854	0	0	0	0	0	0	25	2	7	25	1	7	
10435071	Q5W5X9	unnamed protein product	TTC23	7.2	44175	0	0	0	25	1	2	0	0	0	0	0	0	
10436084	Q9Y4R7	unnamed protein product	TTL3	8.3	84685	0	0	0	25	1	2	0	0	0	0	0	0	
4589640		KIAA0998 protein	TTL5	9.2	137392	25	1	3	0	0	0	0	0	0	0	0	0	
17066105	Q8WZ42	Titin	TTN	6.0	3816191	0	0	0	0	0	0	0	0	0	25	1	13	
4507725	E9KL36	transthyretin	TTR	5.4	15888	25	1	3	50	2	5	0	0	0	0	0	0	
14389309	Q9BQE3	tubulin alpha-1C chain	TUBA1C	4.8	49896	100	40	56	100	34	49	100	20	43	50	17	41	
13376181	A6NHL2	tubulin alpha chain-like 3 isoform 1	TUBAL3	5.6	49859	50	2	6	25	1	2	0	0	0	0	0	0	

4507949	P31946	14-3-3 protein beta/alpha	YWHA8	4.6	28083	75	3	8	50	2	6	0	0	0	0	0	0
5803225	P62258	14-3-3 protein epsilon	YWHA8	4.5	29175	25	2	5	50	2	7	0	0	0	25	2	7
5803227	P27348	14-3-3 protein theta	YWHAQ	4.5	27765	0	0	0	25	1	2	0	0	0	0	0	0
4507953	P63104	14-3-3 protein zeta/delta	YWHAZ	4.6	27746	25	1	4	25	1	2	0	0	0	0	0	0
73611156		ligand-gated ion-channel receptor L2	ZACN	8.1	45686	25	1	3	0	0	0	0	0	0	0	0	0
21693132		KIAA1993 protein	ZBTB34	6.0	58623	0	0	0	0	0	0	25	2	7	0	0	0
333609260	Q86UZ6	zinc finger and BTB domain-containing protein 46	ZBTB46	5.5	64025	0	0	0	25	1	2	0	0	0	0	0	0
7020336	Q9NXC8	unnamed protein product	ZC3H7A	8.3	62817	0	0	0	25	2	0	0	0	0	0	0	0
5689399	Q9UGR2	KIAA1031 protein	ZC3H7B	6.7	105441	0	0	0	25	1	2	0	0	0	0	0	0
119580830		zinc finger CCCH-type containing 7B, isoform CRA_b	ZC3H7B	9.4	70230	0	0	0	25	2	0	0	0	0	0	0	0
10439064		unnamed protein product	ZCCHC7	6.0	52267	0	0	0	0	0	0	25	2	7	0	0	0
21361910	Q96GR4	probable palmitoyltransferase ZDHHC12	ZDHHC12	6.8	30760	0	0	0	25	1	2	0	0	0	0	0	0
27693740		ZDHHC17 protein	ZDHHC17	10.0	30469	0	0	0	0	0	0	25	2	8	0	0	0
7959231	Q9P243	KIAA1485 protein	ZFAT	6.9	123578	0	0	0	25	1	2	0	0	0	0	0	0
18916751		KIAA1948 protein	ZFP82	9.2	57087	25	1	3	0	0	0	0	0	0	0	0	0
52546033		hypothetical protein	ZKSCAN2	8.2	110911	0	0	0	25	1	2	0	0	0	25	2	10
10434856	Q9H942	unnamed protein product	ZNF20	8.4	62002	0	0	0	0	0	0	0	0	0	25	2	7
119577668		zinc finger protein 233, isoform CRA_b	ZNF233	6.2	19173	0	0	0	25	1	2	0	0	0	0	0	0
5730196	Q8NDW4	Kruppel-type zinc finger	ZNF248	8.8	39693	0	0	0	25	1	4	0	0	0	0	0	0
21687252	Q8WUU4	zinc finger protein 296	ZNF296	8.8	50811	0	0	0	0	0	0	25	2	5	0	0	0
119624584		zinc finger protein 318	ZNF318	6.8	251084	100	16	12	100	13	10	0	0	0	0	0	0
21327296	Q96SR6	AF513816_1 zinc finger protein 382	ZNF382	9.6	63795	0	0	0	25	1	2	0	0	0	0	0	0
8923887	Q9H8N7	zinc finger protein 395	ZNF395	7.1	54940	0	0	0	0	0	0	25	4	12	0	0	0
194383618	B4E1G8	unnamed protein product	ZNF410	6.1	30582	0	0	0	0	0	0	25	2	8	0	0	0
55661989	Q5VZN3	zinc finger protein 483	ZNF483	4.8	20767	0	0	0	0	0	0	25	2	8	0	0	0
74722910	Q6ZMS7	ZN783_HUMAN RecName: Full=Protein ZNF783	ZNF783	4.8	31423	0	0	0	25	1	2	0	0	0	0	0	0
22760910	Q8NC25	unnamed protein product	ZNF844	9.9	23039	25	1	3	0	0	0	25	2	5	0	0	0
226437632	Q6WRX3	protein zyg-11 homolog A	ZYG11A	7.8	85809	25	1	3	0	0	0	0	0	0	0	0	0
4508047	Q15942	zyxin	ZYX	6.2	61278	25	1	3	0	0	0	0	0	0	0	0	0
7770189	Q9P170	AF119917_38 PRO2325		9.9	22087	0	0	0	25	1	2	0	0	0	0	0	0
27526556	Q8IVM6	hypothetical protein		9.0	14215	25	1	3	0	0	0	0	0	0	0	0	0
119568095		hCG1818486		8.5	22823	0	0	0	0	0	0	25	2	8	0	0	0
119568272		hCG2030186		5.8	15421	25	1	3	0	0	0	0	0	0	0	0	0
119568743		hypothetical protein FLJ37396, isoform CRA_a		6.0	131656	0	0	0	25	1	4	0	0	0	0	0	0
119568790		hCG2030773		9.7	87860	0	0	0	25	1	2	0	0	0	0	0	0
119571977		hCG2038976		9.8	9076	0	0	0	0	0	0	0	0	0	25	2	10
119572106		EF-hand domain family, member D2, isoform CRA_b		9.6	9782	25	1	4	0	0	0	0	0	0	0	0	0
119574455		hCG1991170		7.1	11592	25	1	3	0	0	0	0	0	0	0	0	0
119575068		hCG1992134, isoform CRA_a		12.5	14760	0	0	0	25	1	2	0	0	0	0	0	0
119579409		hCG1651709, isoform CRA_a		6.4	59660	0	0	0	0	0	0	25	2	8	0	0	0
119581503		NudC domain containing 3, isoform CRA_a		10.4	15545	25	1	3	0	0	0	0	0	0	0	0	0
119581544		hCG1808619		4.3	25760	0	0	6	0	0	0	0	0	6	25	2	8
119583448		hCG2045176		8.1	8798	50	2	6	0	0	0	0	0	0	0	0	0
119585987		hCG2041686		10.9	11430	25	1	3	0	0	0	0	0	0	0	0	0
119588003		hCG2032643		11.7	16800	0	0	0	0	0	0	25	2	8	0	0	0
119588250		hCG2032850		10.3	19429	0	0	0	25	1	2	0	0	0	0	0	0
119588928		hCG1992999		9.4	13523	0	0	0	25	1	2	0	0	0	0	0	0
119595577		hCG2021464		9.4	14653	25	1	3	0	0	0	0	0	0	0	0	0
119596354		hCG2038864		11.1	9787	25	1	3	0	0	0	0	0	0	0	0	0
119601725		hCG2042489		8.6	12629	0	0	0	25	1	2	0	0	0	0	0	0
119603253		hCG2045433		11.6	4016	0	0	0	0	0	0	0	0	0	25	1	5
119606313		hCG2040490		5.9	11015	0	0	0	0	0	0	0	0	0	25	1	7
119607314		chromosome 8 open reading frame 46, isoform CRA_a		11.1	8033	0	0	0	25	1	4	0	0	0	0	0	0
119607467		interleukin 7, isoform CRA_b		11.2	10120	0	0	0	25	1	4	0	0	0	0	0	0
119607553		hCG1993372, isoform CRA_b		6.9	17681	0	0	0	25	1	2	0	0	0	25	1	5
119610016		hypothetical protein FLJ35220, isoform CRA_h		7.8	13950	25	1	3	0	0	0	0	0	0	0	0	0
119612236		hCG2009144		9.8	15131	25	1	3	0	0	0	0	0	0	25	1	5
119618896		hCG2015460		6.5	17427	25	1	3	0	0	0	0	0	0	0	0	0
119620456		hCG1658230		10.0	28125	0	0	0	25	1	2	0	0	0	0	0	0

[illegible]

Supplementary Table 2 - List of identified biomarkers in Responders and Non-Responders before and after omalizumab treatment. ORb=Omalizumab Responder baseline; ORp=Omalizumab Responder post-treatment; NORb= Non Omalizumab Responder baseline; NORp= Non Omalizumab Responder post-treatment. In bold type, DAve and DCI values that surpassed the applied thresholds (DAve>|0.2| and DCI>|50|. Red (or positive) DAve and DCI values indicate proteins up-regulated in the first sample used as term of comparison (ES: in the comparison ORb vs NORb in red are shown proteins up-regulated in ORb). Blue (or negative) DAve and DCI values indicate proteins up-regulated in the second sample used as term of comparison (ES: in the comparison ORb vs NORb in blue are shown proteins up-regulated in NORb).

				Spectral count																ORB vs NORb				ORp vs NORp				ORB vs ORp				NORb vs NORp		
Annotations				ORB				ORp				NORb				NORp				MAProMa		Linear Discriminant Analysis		MAProMa		Linear Discriminant Analysis		MAProMa		Linear Discriminant Analysis		MAProMa		
Accession	Entry	Gene Name	Protein name	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	Dave	DCI	F Ratio	Prob>F	Dave	DCI	F Ratio	Prob>F	Dave	DCI	F Ratio	Prob>F	Dave	DCI	
NCBI	UNIPROT																																	
62420916	Q56224	ACT	actin-like protein	54	57	51	54	90	39	50	23	15	29	24	0	31	0	45	18	1.0	1295	31	1.4E-03	0.7	996	-	-	-	-	-	-	-	-0.3	-128
4501881	P68133	ACTA1	actin, alpha skeletal muscle	184	79	62	186	214	99	56	23	0	22	18	0	12	0	28	0	1.7	8101	12	1.3E-02	1.6	4743	-	-	0.3	3357	-	-	-	-	
4501885	P60709	ACTB	actin, cytoplasmic 1	67	61	47	43	34	67	79	27	30	29	18	0	19	19	17	24	0.9	1296	15	8.5E-03	0.9	1156	6.6	4.2E-02	-	-	-	-	-	-	
4501889	P63267	ACTG2	actin, gamma-enteric smooth muscle isoform 1	63	9	4	50	34	11	4	0	0	0	0	0	0	0	0	0	2.0	492	-	-	2.0	76	-	-	-	-	0.9	416	-	-	
4501891	P12814	ACTN1	alpha-actinin-1 isoform b	36	13	39	47	41	32	22	5	0	0	6	0	0	0	6	0	1.8	563	19	4.7E-03	1.8	308	8.6	2.6E-02	0.3	255	-	-	-	-	
21749456	Q8N274	AHNAK	unnamed protein product	4	4	0	4	0	0	0	0	0	0	0	0	0	0	0	0	2.0	5	9	2.6E-02	-	-	-	-	2.0	5	8.7	2.6E-02	-	-	
5174391	P14550	AKR1A1	alcohol dehydrogenase [NADP+]	0	9	8	4	0	7	7	5	0	0	0	0	0	0	0	0	2.0	13	6	4.7E-02	2.0	10	8.0	3.0E-02	-	-	-	-	-	-	
4502027	P02768	ALB	serum albumin	94	52	159	122	90	142	65	64	182	66	12	61	68	29	45	130	0.3	2487	-	-	0.3	1738	-	-	-	-	-	-	-	-	
40316937	P16050	ALOX15	arachidonate 15-lipoxygenase	4	31	74	39	0	99	86	0	0	0	12	0	0	0	0	0	1.7	682	-	-	2.0	1066	-	-	-0.2	-380	-	-	-	-	
4502101	P04083	ANXA1	annexin A1	36	52	62	29	7	67	85	23	45	7	24	14	19	0	11	6	0.7	746	-	-	1.3	993	-	-	-	-	-	-	0.9	216	
4757756	P07355	ANXA2	annexin A2 isoform 2	49	65	82	29	0	42	67	18	0	0	24	7	6	0	6	12	1.5	1553	15	8.6E-03	1.4	495	-	-	0.5	1070	-	-	-	-	
4502105	P09525	ANXA4	annexin A4	4	9	4	7	0	7	15	0	0	0	0	0	0	0	0	0	2.0	18	28	1.8E-03	-	-	-	-	-	-	-	-	-	-	
4502107	P08758	ANXA5	annexin A5	13	31	16	21	7	14	30	9	0	7	12	0	0	0	11	18	1.2	193	10	1.9E-02	0.7	88	-	-	0.3	91	-	-	-	-	
4502133	P02743	APCS	serum amyloid P-component	27	4	19	0	0	4	20	9	0	15	12	0	0	0	11	0	0.6	58	-	-	-	-	-	-	-	-	-	-	-	-	
10947139	P05089	ARG1	arginase-1 isoform 2	4	4	0	4	28	4	0	5	15	22	6	7	19	10	17	12	-1.2	-73	-	-	-0.5	-62	-	-	-	-	-	-	-	-	
4757810	P25705	ATP5A1	ATP synthase subunit alpha, mitochondrial	0	31	39	4	0	14	57	0	0	0	6	0	0	0	0	0	1.7	165	-	-	2.0	157	-	-	-	-	-	-	-	-	
28940		ATP5B	unnamed protein product	18	52	74	32	14	57	85	18	0	0	30	14	12	0	6	6	1.2	912	-	-	1.5	924	-	-	-	-	-	-	-	-	
4502303	P48047	ATP5O	ATP synthase subunit O, mitochondrial	4	4	4	0	0	4	11	0	0	0	0	0	0	0	0	0	2.0	5	9	2.5E-02	-	-	-	-	-	-	-	-	-	-	
4502403	P21810	BGN	biglycan	18	9	35	0	0	21	7	0	0	0	6	0	0	0	6	0	1.6	118	-	-	-	-	-	-	0.8	94	-	-	-	-	
251736057	D7NTU1	BMP3	bone morphogenetic protein 3	4	4	4	0	0	11	0	0	0	0	0	0	0	0	0	0	2.0	5	9	2.5E-02	-	-	-	-	-	-	-	-	-	-	
825635		CALM3	calmodulin	9	35	12	18	0	4	22	0	0	0	6	0	0	0	6	0	1.7	167	8	3.1E-02	-	-	-	-	1.0	148	-	-	-	-	
223278387	Q9NZT1	CALML5	calmodulin-like protein 5	0	13	0	7	0	14	4	14	0	29	12	27	0	38	22	24	-1.1	-135	-	-	-0.9	-191	-	-	-	-	-	-	-0.2	-76	
435700		CD44	CD44R5	0	4	4	4	7	7	4	0	0	0	0	0	0	0	0	0	2.0	4	9	2.5E-02	2.0	11	7.7	3.2E-02	-	-	-	-	-	-	
4758012	Q00610	CLTC	clathrin heavy chain 1	4	26	16	0	0	18	26	5	0	0	0	0	0	0	0	0	2.0	67	-	-	2.0	73	-	-	-	-	-	-	-	-	
3288487		COL1A1	COL1A1 and PDGFB fusion transcript	157	140	148	64	96	170	39	95	91	66	84	41	31	10	51	59	0.6	5602	-	-	0.9	4322	-	-	0.2	3059	-	-	0.6	1779	
825646		COL1A2	unnamed protein product	58	113	101	50	62	88	37	41	45	22	54	20	12	10	45	30	0.8	2629	6	4.4E-02	0.8	1336	-	-	0.3	1632	-	-	0.4	339	
537329	P08572	COL4A2	alpha-2 type IV collagen	0	0	0	0	7	4	4	0	0	0	0	0	0	0	0	0	-	-	-	-	2.0	7	6.7	4.1E-02	-2.0	-7	6.7	4.1E-02	-	-	
1915902		COL6A1	collagen (VI) alpha-1 chain	49	35	27	21	0	35	24	14	0	15	6	0	0	0	0	0	1.5	539	16	6.9E-03	2.0	167	-	-	0.6	385	-	-	-	-	
13603394		COL6A2	type VI collagen alpha 2 chain	18	35	31	18	0	67	13	9	0	0	12	0	0	0	11	0	1.6	320	18	5.7E-03	1.6	245	-	-	-	-	-	-	-	-	
3127926		COL6A3	collagen type VI, alpha 3 chain	269	554	319	172	28	478	159	86	0	7	132	7	0	0	34	0	1.6	53278	11	1.6E-02	1.8	17567	-	-	0.5	36345	-	-	1.3	634	
537329	P08572	CSTA	cystatin-A	13	4	0	4	7	11	0	9	0	22	6	0	31	67	6	18	-	-	-	-	-1.3	-440	-	-	-	-	-	-	-1.3	-437	
24307991	Q8IWT3	CUL9	cullin-9	0	0	0	0	7	0	2	5	30	7	6	0	0	10	0	12	-2.0	-60	-	-	-	-	-	-	-	-	-	-	-	-	
4503327	P00387	CYB5R3	NADH-cytochrome b5 reductase 3 isoform 1	9	17	12	36	0	18	13	5	0	0	0	0	0	0	0	0	2.0	171	9	2.2E-02	-	-	-	-	0.7	131	-	-	-	-	
16751921	P81605	DCD	dermcidin	13	26	8	14	28	14	13	14	91	44	48	41	44	86	39	24	-1.1	-1448	11	1.7E-02	-1.0	-1016	-	-	-	-	-	-	-	-	
55749932	P17661	DES	desmin	188	0	8	279	110	25	0	0	0	0	0	14	0	0	0	0	1.9	7053	-	-	2.0	570	-	-	1.1	6489	-	-	-	-	
4503377	Q16555	DPYSL2	dihydropyrimidinase-related protein 2 isoform 2	4	4	4	0	0	4	0	0	0	0	0	0	0	0	0	0	2.0	5	9	2.5E-02	-	-	-	-	-	-	-	-	-	-	
30506		DSG1	desmoglein type 1	40	13	0	7	48	4	2	64	15	37	0	7	50	19	73	30	-	-	-	-	-0.4	-488	-	-	-0.6	-317	-	-	-1.0	-812	
1147813		DSP	desmoplakin I	76	4	8	18	55	25	4	27	0	59	24	68	118	29	62	41	-0.3	-360	-	-	-0.8	-1568	-	-	-	-	-	-	-0.5	-1244	
4503471	P68104	EEF1A1	elongation factor 1-alpha 1	13	26	27	21	0	28	20	9	0	0	6	7	31	0	11	6	1.5	239	27	2.1E-03	-	-	-	-	0.4	142	-	-	-1.2	-68	
31874660		ELN	hypothetical protein	45	22	35	7	0	25	9	23	0	0	0	0	0	0	6	0	2.0	370	11	1.6E-02	1.6	97	-	-	0.6	272	-	-	-	-	
4503571	P06733	ENO1	alpha-enolase isoform 1	0	9	12	14	0	4	20	0	0	0	0	0	6	0	0</																

21361322	P04350	TUBB4A	tubulin beta-4A chain	0	9	8	4	0	7	33	14	15	0	6	0	6	0	0	0	-	-	-	-	1.6	87	-	-	-0.9	-76	-	-	-	-	
7243175		TULP4	KIAA1397 protein	4	0	8	0	7	0	0	14	30	15	6	0	0	38	0	6	-1.2	-77	-	-	-	-	-	-	-	-	-	-	-	-	
4507761	P62987	UBA52	ubiquitin-60S ribosomal protein L40	9	44	31	18	7	32	26	9	0	15	0	0	12	0	6	18	1.5	316	7	4.2E-02	0.7	131	-	-	0.3	151	-	-	-	-	
4507877	P18206	VCL	vinculin isoform VCL	18	13	31	57	0	25	15	0	0	0	0	0	0	0	0	0	2.0	445	9	2.4E-02	2.0	50	-	-	1.0	395	-	-	-	-	
21757045		VIM	unnamed protein product	139	467	326	311	76	265	286	59	0	59	108	27	0	0	39	6	1.5	47175	14	1.0E-02	1.8	14659	6.9	3.9E-02	0.6	33630	-	-	1.2	1114	
36575		VTN	unnamed protein product	31	22	58	32	0	25	37	14	0	15	18	0	0	0	34	0	1.3	612	9	2.3E-02	0.8	142	-	-	0.6	468	-	-	-	-	
4507949	P31946	YWHAB	14-3-3 protein beta/alpha	0	4	4	4	0	0	5	5	0	0	0	0	0	0	0	0	2.0	4	9	2.5E-02	-	-	-	-	-	-	-	-	-	-	
119624584		ZNFX18	zinc finger protein 318	40	13	4	7	7	28	11	5	0	0	0	0	0	0	0	0	2.0	130	-	-	2.0	81	-	-	-	-	-	-	-	-	-

Supplementary Figure 1:

Sub-network obtained by matching experimental identified proteins against Global Mammalian Interactomic Network. Figure 1A) ORb vs NORb; Figure 1B) ORp vs NORp; Figure 1C) ORb vs ORp; Figure 1D) NORb vs NORp. Red nodes indicate proteins up-regulated in the first sample used as term of comparison (ES: in the comparison ORb vs NORb in red are shown nodes up-regulated in ORb). Blue nodes indicate proteins up-regulated in the second sample used as term of comparison (ES: in the comparison ORb vs NORb in blue are shown nodes up-regulated in NORb).

Supplementary Figure 2:

IHC analysis for Vimentin in Responder (ORb) and Non Responder (NORb) patients before anti-IgE treatment.