SUPPLEMENTARY MATERIAL

Supplementary Methods

Native pre-fractionation of sample pools

For sample preparation before mass spectrometry, our pre-fractionation workflow combined native size exclusion (SEC, first dimension, 1D), followed by native anion exchange (AEC, 2D) chromatography [21]. Briefly, each sample pool was 1D-separated on a HiLoad Superdex™ 200 column controlled by an Äkta purifier™ system (GE Healthcare) at a flow rate of 1 ml/min and at 17 °C. After the void volume, 96 1D-fractions of 600 µl were collected into chilled 96-deepwell microplates (Supplementary Figure S1). After serial 1D-fractionation, all further procedures were performed in microplate format. Thus, beginning with 2D-fractionation, parallelization and automation was achieved for separation, spectrophotometric readout, picking, medium exchange, digest, desalting, and finally storage within the autosampler for LC-MS. 2D-fractionation of all four samples was done simultaneously on four AEC column arrays [21] consisting of 96 micro columns packed with 100 µl Toyopearl DEAE-650M (Tosoh Bioscience). Thus 4128 2D-sub-fractions were generated from each sample pool (Supplementary Figure S2). Within this 2D-matrix the distribution of plasma proteins showed chromatographic spots similar to 2D-PAGE, each with a characteristic native molecular weight and net charge (Supplementary Figure S3). The sub-fractions produced were not entirely mass spectrometric analyzed. The chromatographic distribution of each constituent can be expected within at least nine adjacent sub-fractions. Thus, it is reasonable that we picked only every other sub-fraction (chessboard like) out of the chromatographic spots selected (Supplementary Figure S2). Moreover, due to sensitivity requirements, we selected such sub-fractions with a total protein concentration of >0.03mg/ml (at least in one out of the four corresponding homologous sub-fractions of all four samples). Thereby, each constituent was always identified in at least 3 sub-fractions (e.g. Supplementary Figures S4 to S8). We selected 655 2D-sub-fractions from each sample. These 4 x 655 sub-fractions represent a corresponding set, i.e., they are picked from identical locations after 2D-fractionation of the four sample pools (AM, NM, CF, NF). Corresponding homologous sub-fractions (same location after 2D-separation) out of all four samples were closely placed on the same microplate and thus could be further processed practically simultaneously.

Protease digestion and mass spectrometry

After digest by Trypsin/LysC (enzyme:protein, 1:40, V5072, Promega, Fitchburg, WI, USA), the LC-MS analysis was performed by a Hypersil Gold UHPLC column (1.9 µm, 50×1.0 mm) with an Accela 1250 UHPLC system (both Thermo Fisher Scientific) using binary gradient elution. Tandem mass spectrometry (MS/MS) measurements were carried out (2017 to 2019) on a LTQ Orbitrap Discovery (Thermo Fisher Scientific) by positive heated electrospray ionization (H-ESI). The MS/MS system operated in data-dependent TOP10 mode using 1 microscan. The LC-MS/MS operated via graphical interface of the Xcalibur software 2.1. All sub-fractions were run in duplicate. Human transferrin (holo, SERVA Electrophoresis GmbH, 36756) was simultaneously digested and run with each microplate for quality control.

Data analysis

Raw spectra were analyzed with Proteome Discoverer® 1.3 and Sequest database search algorithm applying a false discovery rate of <0.5% as described previously [19] and the UniProt database of ~47,800 canine entries (date: 10/26/2017). Data of corresponding homologous sub-fractions from affected and unaffected animals were compared with Sieve 2.0®, separately for males (AM versus NM) and females (CF versus NF).

Extraction of BM candidates from mass spectrometric data

Thus, three cases of alteration were considered for selection of BMs from the list of altered proteins: 1) One cluster or multiple exclusively synergistic clusters with increased protein concentration in affected animals with a mean ratio > 2.0 (Sieve®). 2) One or multiple synergistic clusters with increased protein concentration with a mean ratio >5.0, even though other clusters were present. 3) For miscellaneous clusters, an estimated "overall trend" >2.0 based on Formula 1, which identified increased and reduced clusters to estimate a value of global alteration of the protein family (cf. Figure 2). By using "overall trend", the mostly co-existing unaltered forms of a protein family were not included, i.e. proteoforms which showed ratios in the range of ~1.0 (0.51-1.9). However, their presence in a sample might obscure alterations detectable using currently available ELISAs.

$$\text{Overall trend} = (M_i * H_i)/(H_d / M_d) \qquad \text{Formula 1}$$

M_i: mean of all ratios >2 (higher concentration in affected animals in comparison to controls)
H_i: counts of all hits of sub-fractions of ratios >2
M_d: mean of all ratios <0.5 (lower concentration in affected animals in comparison to controls)
H_d: counts of all hits of sub-fractions of ratios <0.5

Analysis of posttranslational modification (PTM)

The search for PTM ran successively using Proteome Discoverer® 1.3 (Thermo) [21] with no more than three dynamic modification types per run. We considered only database matches with high confidence when the sequence coverage was >40% and peptide spectrum match (PSM) was >100. The following dynamic modifications of amino acids were analyzed: deamidation (N, Q, R) and carbamoyl (K, M, R). Multi reports of the related replicates were utilized.

Mean values of the modification rates, #PTM/PSM of albumin and transferrin peptides were determined including the homologous sub-fractions from all animals AM, NM, CF, and NF (cf. Supplementary Figures S10, S11) having database matches with high confidence.

Supplementary results

Proteomic search in blood plasma from AS-dogs

Global protein distribution after pre-fractionation

1D-SEC chromatograms of all sample pools were similar (Supplementary Figure S1). The third, albumin-containing peaks are nearly identical in all samples whereas the first peak, mainly containing lipoproteins, is slightly lower in NM in comparison to all others. After 2D-AEC the global protein distribution is shown exemplarily in Supplementary Figure S2. The high precision of our protein pre-fractionation [21] enabled reliable comparison of the constituents of sub-fractions from different samples.

Proteome comparison

By mass spectrometry altogether 3115 (443) protein chains were identified with the Proteome Discoverer® supported by ≥ 1 (≥ 2) peptide/s, respectively (Supplementary Table S2). Moreover, by Sieve® 918 protein chains were identified by ≥ 2 counts and ≥ 5 hits (Supplementary Table S3) resulting in ~600 and ~300 non-redundant proteins. Aside from counts, their allocation in native sub-fractions is informative. The majority of proteins showed several chromatographic clusters (spots) indicating the existence of diverse proteoforms with different degrees and direction of alteration in AS and only a few were uniformly increased or decreased in affected in comparison to unaffected dogs (Supplementary Figures S3, S4-S7 and Table S4). In the strict sense only heavily altered proteoforms represent BM candidates. Ideally, further application mandatory should use selective measurements of the very increased proteoform (protein variant). However, since the molecular characteristics of these variants are unknown we had to select proteins of high probability to be BM candidates as well as being measurable by currently available ELISA which are mostly not specific for variants. For the assessment of early pathogenesis, both directions of alteration (increase or decrease) of a given protein are similarly valuable. However, for the aimed analytical purposes here, only proteins that were higher in affected animals than in controls were considered.

Posttranslational modifications (PTM)

Albumin concentration is not altered in early AS. Several main clusters identified by Proteome Discoverer® appear not different to heathy controls (Supplementary Figures S1, S3), some minor clusters (#1 and #7 in Supplementary Figure S7) showed lower or higher protein levels. The main and unaltered fractions exhibit uniformly low deamidation rates. Contrarily, the minor clusters, which are higher in AS based on mass spectrometric quantified protein level, exhibit a manifold rate of deamidations (Supplementary Figure S7 D, E). The minor cluster 1 occurred only in male dogs with AS. Notably, in the minor clusters 1 and 7 as well as in the main clusters 2 and 4, the rate of carbamoylation is higher in AS in comparison to healthy controls. Thus, this modification appears increased in early AS in minor parts of albumin in accordance with our preliminary results [21]. Cluster 8 shows remarkably high deamidation rates but no carbamoylation.

Transferrin showed a main cluster (#4 in Supplementary Figure S8) slightly lower in AS compared with unaffected animals, and several minor clusters. The main cluster exhibited a low deamidation rate, close to the values of the main albumin forms (see above). Like albumin, the minor and altered clusters of transferrin showed manifold deamidation rates in dogs with AS. In contrast to albumin and transferrin-cluster 4, the two decreased transferrin clusters 3 and 5 are more Q- and Rdeaminated (mean ~2.2-fold each) in affected dogs in comparison to healthy controls of both genders. Carbamoylation was always lower than 0.01/PSM.

Correlation of BM concentrations measured by ELISA with other clinical parameters

To identify the presence of relationships with individual and clinical parameters that must be considered in clinical practice, and to reveal the surplus of our BM over common parameters, we correlated our BM with these parameters.

Albuminuria (UACR) did not correlate with any of our analyzed BM candidates in blood or urine, except for urinary lumican (Supplementary Table S6). Moreover, urinary lumican at the first visit also correlated with UACR at the second visit (~4 years later). These correlations are mainly due to a few high UACR values in patients with intermediate severity. There was no relation of any of our analyzed BM candidates (in blood and urine) with evidence of late kidney failure, (eGFR, cGFR, SCrea, Supplementary Tables S7, S8), nor inflammation (serum CRP, Supplementary Table S6). Here two high values of CRP, although in the normal range (< 2µg/ml), determine a somewhat moderate correlation.

In our control group, no BM candidate (in blood or urine) correlated with the body mass index (**BMI)** (Supplementary Table S9). The majority of our BM candidates did not correlate with **age** with the exception of *serum* angiotensinogen and C1q (Supplementary Table S9). Thus, there does not appear to be a need for age- and BMI-related cutoffs for any of the promising *urinary* BM.

Supplementary Figures

Figure S1:

Chromatograms of dog serum proteins after native size exclusion chromatography (1D-SEC)

Four sample pools have been separated, non-affected males (NM), affected males (AM), non-affected females (NF), and carrier females (CF). Each sample pool was separated on a HiLoad Superdex™ 200 column controlled by an Äkta purifier™ system (GE Healthcare) at a flow rate of 1 ml/min and at 17 °C. After the void volume, 96 1D-fractions of 600 µl were collected into chilled 96-deepwell microplates. Column calibration [21]. Aliquots of 150 µl were read at 280 nm (SpectraMAX384PLUS, Molecular Devices). Protein concentrations were calculated using BSA as standard. Section of all proteins above 30 kDa.

Figure S2:

Global protein distribution after anion exchange chromatography (2D-AEC)

Example: entire 2D-sub-fractions from one sample pool (NM).

First column: number of 1D-fraction (cf. Figure S1); last column: molecular weight according column calibration.
First line: number of 2D-sub-fraction; second line: designation of the solvent, i.e. sample and the concentration of NaCl in the elution solvent 10mM Tris-HCl.
Frames indicate selected fractions for mass spectrometric analysis.
Total fractional concentrations of proteins were calculated from A280 using BSA as standard. Protein concentrations are given by values (mg/mL) and color code.

Figure S3:

Distribution of two examples of plasma proteins from NM after 2D-AEC

Please enlarge to more than 400%.

Albumin (upper part, P49822) and α2-macroglobulin (lower part, F6UME0).

Results after analysis by the Proteome Discoverer® with the following quantifiers:
A, area; P, PSM; C, coverage. Red intensity code is given for A and P;
Grey: Mass spectrometric analyzed 2D-fractions; empty: without any peptide of the respective protein; frames: these sub-fractions were analyzed for PTM.

Figure S4:

Distribution of serum amyloid after 2D-AEC and mass spectrometry identification of its peptides as example of a uniformly altered protein

The section of 2D-fractions containing serum amyloid peptides is shown. Numbers of 1D- (first column) and 2D-fractions (first line) as in Figure S3. Grey: Mass spectrometric analyzed 2D-fraction.

R: ratio calculated by Sieve® corresponding to the concentration quotient; P: peptide counts; H: hits.
Green figures: Protein signals strongly higher in AM compared to NM. Green highlighting indicate chromatographic clusters. Due to its peptide sequence, the protein is small (~12 kDa). Contrarily, it was found in two high molecular weight clusters. In both clusters, the concentration of this protein are much higher in AM than in NM.

Figure S5:

Distribution of α1B-glycoprotein after 2D-AEC and mass spectrometric identification of its peptides as example of a protein with several proteoforms with different degrees and direction of alteration under AS

The section of 2D-fractions containing α1B-glycoprotein peptides is shown. Numbers of 1D- (first column) and 2D-fractions (first line) as in Figure S3. Grey: Mass spectrometric analyzed 2D-fraction. Frames illustrate chromatographic clusters.

R: ratio calculated by Sieve® corresponding to the concentration quotient; P: peptide counts; H: hits.
Green figures: Protein signals strongly higher in AM compared to NM. Green highlighting: chromatographic cluster with higher concentrations in AM.
Red figures: Protein signals strongly lower in AM compared to NM. Yellow highlighting: chromatographic cluster with lower concentrations in AM.
Black figures: Protein signals are similar in AM and NM, i.e. not altered under disease.

Figure S6:

Distribution of gelsolin after 2D-AEC and mass spectrometric identification of its peptides as example of a second protein with several proteoforms with different degrees and direction of alteration under AS

For explanation, cf. Legend to Figure S5.

Figure S7:

Distribution of BM candidates adiponectin and the complement component C1q after 2D-AEC and mass spectrometric comparison of their peptides in AM to NM

The section of 2D-fractions containing peptides from adiponectin and the tree chains from C1q are shown as indicated.
Numbers of 1D- (first column) and 2D-fractions (first line) as in Figure S3. Grey: Mass spectrometric analyzed 2D-fraction. Frames illustrate chromatographic clusters. For further explanation, cf. Legend to Figure S5.
These protein chains showed at least two proteoforms with different degrees and direction of alteration under AS. The clusters lower under AS of both proteins were found in similar sub-fraction as do the clusters higher under AS.

Figure S8:

Distribution of the BM candidate ColXIII after 2D-AEC and mass spectrometric comparison of its peptides in AM to NM

The section of 2D-fractions containing peptides from ColXIII is shown.
For further explanation, cf. Fig. S5.
This protein showed a singular cluster higher in AM than NM.

Figure S9:

Comparison of the concentrations of BM candidates in serum and urine from patients (set 1 and set 2) and controls

Entire results are given here in box-plots (17 BM candidates each in serum and urine). Second samples were derived about 4 years after the first.

Significance values are given as bars: p < 0.05, bright blue; p < 0.01 (dark blue); all other not significant. To show tendency: 0.05 < p < 0.1 (pale blue).

AS: autosomal or no genetic information; TBMN: thin basement membrane nephropathy; BFH: benign familiar hematuria (set 2).
Less severe, intermediate, and severe show data from patients with AS (set 1) of the three severity groups (cf. main text)
First series: biomarker concentrations in **serum** (S)
Second series: biomarker concentrations in **urine** (U)
Abbreviations of biomarker proteins: cf. main text

Figure S10:

Proteoforms and PTM of albumin

A: Global distribution of plasma protein concentrations after 2D-AEC
Example: NM. Section of sub-fractions containing eight numbered chromatographic clusters of albumin (identified after mass spectrometry). Frames indicate sub-fractions, which form a cluster. Number and color code show the total fractional protein concentration. Black highlighting indicates the sub-fractions analyzed for PTM.

B: Mass spectrometric quantifiers of albumin variants after analysis of sample from males (NM) by the Proteome discoverer®
Estimated percentage of albumin hits in each framed cluster compared to total hits of albumin in all sub-fractions. The analyzed fractions of the main clusters (2 to 6) contained ~48% of all albumin peptides of the sample.
B-F: Grey filling: albumin protein concentration is not altered in AM (ratios around 1.0, >0.5 …<2.0); red filling: protein concentration is increased in AM in comparison to NM due to the ratios calculated by Sieve® (ratios >2, cf. Fig. C).

C: Mass spectrometric comparison of the concentrations of albumin variants from AM and NM determined by Sieve®
The quantifier “ratio” indicates the quotient AM/NM of peptide signals and corresponds to the concentration quotient of albumin of homologous sub-fractions. The mean ratio was built from all sub-fractions of one cluster.
The main clusters of albumin (2 to 6) showed ratios of ~1.0. Thus, the protein concentrations of these proteoforms (clusters) are not altered under AS. Contrarily, the minor clusters 1 and 7 were found about six-fold and the cluster 8 even nearly 50-fold increased under AS.

D-G: Deamidation and carbamoylation rates of albumin proteoforms

The search for PTM ran successively using Proteome Discoverer® 1.3 (Thermo) with no more than three dynamic modifcation types per run. We considered only highly confident database matches when the sequence coverage was >40%. The following dynamic modifications of amino acids were

analyzed: deamidation (N, Q, R) and carbamoylation (K, M, R). Multi reports of the related replicates were utilized.
Mean values of the modification rates, #PTM/PSM of albumin peptides were determined including the homologous sub-fractions from all NM, AM, NF, and CF.
In NM the minor clusters (1, 7, 8), which are elevated under AS, showed higher deamidation and lower carbamoylation rates than the main clusters. However, carbamoylation was significantly increased in minor clusters under AS (Fig. G).

Figure S11:

Proteoforms and PTM of transferrin

A: Global distribution of plasma protein concentrations after 2D-AEC (NM)
Section of sub-fraction containing seven numbered chromatographic clusters of transferrin. Frames indicate sub-fractions, which form a cluster and analyzed by mass spectrometry. Number and color code show the total fractional protein concentration. Black highlighting indicates the sub-fractions analyzed for PTM (see legend to Supplementary Figure S10).

B: Mass spectrometric quantifiers of transferrin variants after analysis of sample from NM by the Proteome discoverer®
Grey: mass spectrometric analyzed sub-fractions. Figures indicate the presence of transferrin peptides. Quantifiers (second line): A: area (red color code); P: number of peptides (green color code); C: sequence coverage. Frames indicate sub-fractions, which form a cluster and analyzed by mass spectrometry.

C: Mass spectrometric comparison of the concentrations of transferrin variants from AM and NM determined by Sieve®
Grey: mass spectrometric analyzed sub-fractions. Figures indicate the presence of transferrin peptides. The quantifier “ratio” (from >>1.0 to <<1.0, color code from red to green) indicate the quotients AM/NM of peptide signals and corresponds to the concentration quotient of transferrin of homologous sub-fractions. P: number of peptides; H: hits. Frames indicate sub-fractions, which form a cluster.

D: Mass spectrometric comparison of the concentrations of transferrin variants from AM and NM determined by the Proteome discoverer®
Estimated percentage of transferrin hits in each framed cluster compared to total hits of transferrin of entire sub-fractions (cf. Fig. C). The analyzed fractions contained ~39% of all transferrin peptides of the sample.

D-G: Grey filling: transferrin protein concentration is lower in AM in comparison to NM (ratios <1.0); red filling: protein concentration is higher in AM in comparison to NM due to the ratios calculated by Sieve® (ratios >2, Fig. E).
The mean ratio was built from all sub-fractions of one cluster.
The main cluster 4 of transferrin (Fig. D) showed a ratio of ~0.6 (Fig. E) like the minor clusters 1, 3, and 6 (<0.5). This is in accordance with the known alteration direction of this APR under inflammation. Surprisingly, there were three minor clusters (2, 5, and 7) 2 to 15-fold increased under AS.

F, G: Deamidation rates of transferrin of proteoforms identified

The search for PTM ran successively using Proteome Discoverer® 1.3 (Thermo) with no more than three dynamic modifcation types per run. We considered only highly confident database matches when the sequence coverage was >40%. The following dynamic modifications of amino acids were analyzed: deamidation (N, Q, R) and carbamoyl (K, M, R). Multi reports of the related replicates were utilized.

Mean values of the modification rates, #PTM/PSM of transferrin peptides were determined including the homologous sub-fractions from all animals AM, NM, CF, and NF (cf. Fig. A-C).

The minor clusters (5, 7), which are elevated under AS, showed much higher deamidation rates than the main cluster and lower clusters under AS. Practically, no carbamoylation was found.

Supplementary Tables

Table S1:

Specification of ELISA-Test kits applied to dog and human samples

Measurement in dog samples: When no dog-specific or reliable kit was available, we applied assays of other species-specificity due to the high sequence similarities. Out of the checked kits those marked by yes (y) produced reliable antigen concentrations. The other kits either were not able to detect the proteoform naturally occurring in our samples or were not sensitive enough.
Measurement in human samples: The kits were performed according the suppliers instructions with the following modifications: all assays from Cloud-Clone and CUSBIO were performed with double incubation times. Samples were pre-incubated with 0.5% Tween 20 before measurement of gelsolin. For the quantification of PICP, TGF-ß1, and CRP in urine either incubation times were prolonged or concentrated specimens were applied. For that samples have been concentrated in Amicon® Ultra - 15 Centrifugal filters (3K, UFC900324) by ~10 to ~60 fold depending on the starting volume available.

Table S2:

List of protein chains identified by the Proteome Discoverer® in four sample pools of blood plasma from dogs

Mass spectrometric data are: Accession number (SwissProt); Description (annotation); ΣCoverage (sequence coverage); Σ# Proteins (number of distinct proteins assigned to the identified sequences); Σ# Unique Peptides (singular peptides assigned to the protein); Σ# Peptides (entire peptide count including repeatedly found peptides); Σ# PSMs.

By mass spectrometry, 3115 (443) proteins in total were identified with the Proteome Discoverer® supported by ≥ 1 (≥ 2) peptide/s, respectively.

Table S3:

List of protein chains identified by the Sieve® in four sample pools of blood plasma from dogs

Mass spectrometric data are: Accession Number (SP: SwissProt); Discription (annotation); Counts (singular peptides assigned to the protein); Sum Hits (entire peptide count including repeatedly found peptides); Hits/Counts.

Using Sieve®, 918 proteins were identified supported by ≥ 2 counts and ≥ 5 hits resulting in ~600 and ~300 non-redundant protein chains in 2D-sub-fractions.

Table S4:

Mass spectrometric identified biomarker candidates

Mean ratios of AM/NM and CF/NF as well as number hits that determine an altered protein as BM candidate. Calculation of mean ratios, cf. Formula 1 in Supplementary Methods. Here all results are given, proteins and protein clusters appearing higher as well as lower in affected animals.

"DIV/0": division by zero, the ratio cannot calculated since there was no hit/peptide in the control sample. The number of hits corresponds to protein concentration in sub-fractions included.
"1000" was set for an extraordinary high ratio, even when much higher, in order to apply value depending color code of Excel ®.
Figure 2 (main document) represent an excerpt from this table.

Table S5:

Concentrations of some BM candidates determined by ELISA in dog samples.

ELISA (last column) have been performed according to the supplier´s instructions each in duplicate and with different dilutions to meet the measuring range of the respective assay.

n: sample count for all of the line, in parenthesis when different from the value given in 8th column. s: serum; p: plasma; u: urine. In urine BM concentrations are normalized by creatinine (c). Sample dilution: [a]1 to 20, [b]1 to 2500. ELISA detects: [c]intact protein, [d]c-terminal fragment.
Bold: trend in blood in accordance with proteomic data of distinct clusters, cf. Figure 2; ***bold and italic***: trend in urine in accordance with the trend in blood. Empty cells: no more samples available.

Table S6:

Correlation of BM concentrations in urine one with each other's

Correlation analyses were performed by SPSS (v.27). Cells contain the correlation coefficients (upper line) and the p-value (lower line). Significant correlations calculated by this software are indicated by stars and p-values below 0.05. We do not follow these proposals rather considered correlation coefficients of > 0.5 (bright color) as moderately and > 0.6 (dark color) as highly correlating.

Lower left halve (blue colors): Correlation analysis according Pearson. Upper right halve: analyses according Spearman (green colors).

Table S7:

Correlation of serum and urinary BM candidates with UACR and serum creatinine in patients with AS and similar diseases

Sample set 1 (first visit) and sample set 2.
Correlation analyses were performed by SPSS (v.27). Cells contain the correlation coefficients (upper line) and the p-value (lower line). Significant correlations calculated by this software are indicated by stars and p-values below 0.05. We do not follow these proposals rather considered correlation coefficients of > 0.5 (bright grey) as moderately and > 0.6 (dark grey) as highly correlating.

Graphical visualization of correlation considered as significant: Urinary lumican (ULUM) of first samples of sample set 1 with UACR of first and additional of the second samples

Table S8:

Correlation of serum and urinary BM candidates with eGFR and cGFR in patients with AS and similar diseases

Correlation analyses see Table S7.

Graphical visualization of correlations considered as significant: Urine CRP with eGFR, and serum PICP and HABP2 with cGFR.

Table S9:

Correlation of serum and urinary BM candidates with serum CRP in patients with AS and similar diseases.

Correlation analyses see Table S7.

Graphical visualization of correlation considered as significant: Serum complement C1q with serum CRP. First samples.

Table S10:

ROC analysis, comparison of patients with AS (set1, first visit) with controls

ROC analysis by SPSS (cf. Methods section). Only BMs with AUC >0.700 are shown.

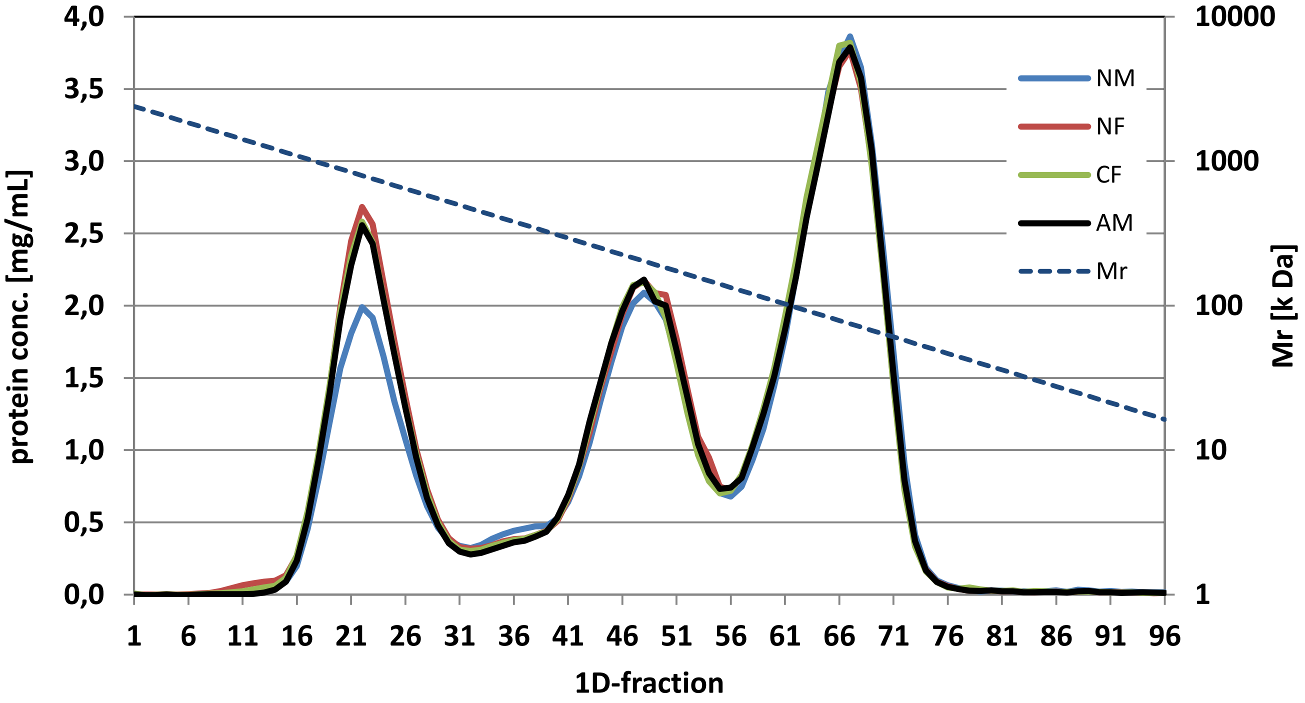
Concentration ranges of BMs: Serum: ColXIII, HABP2, PICP, TGF-ß1 and C1q, ng/mL, GS, µg/mL.

Urine: ColXIII, HABP2, C4BP, CFH, CFI, FGG, GS, LRGP1, a1AGP, and C1q, ng/mg creatinine; CRP, C9 and FMN, pg/mg creatinine.

Supplementary Reference:

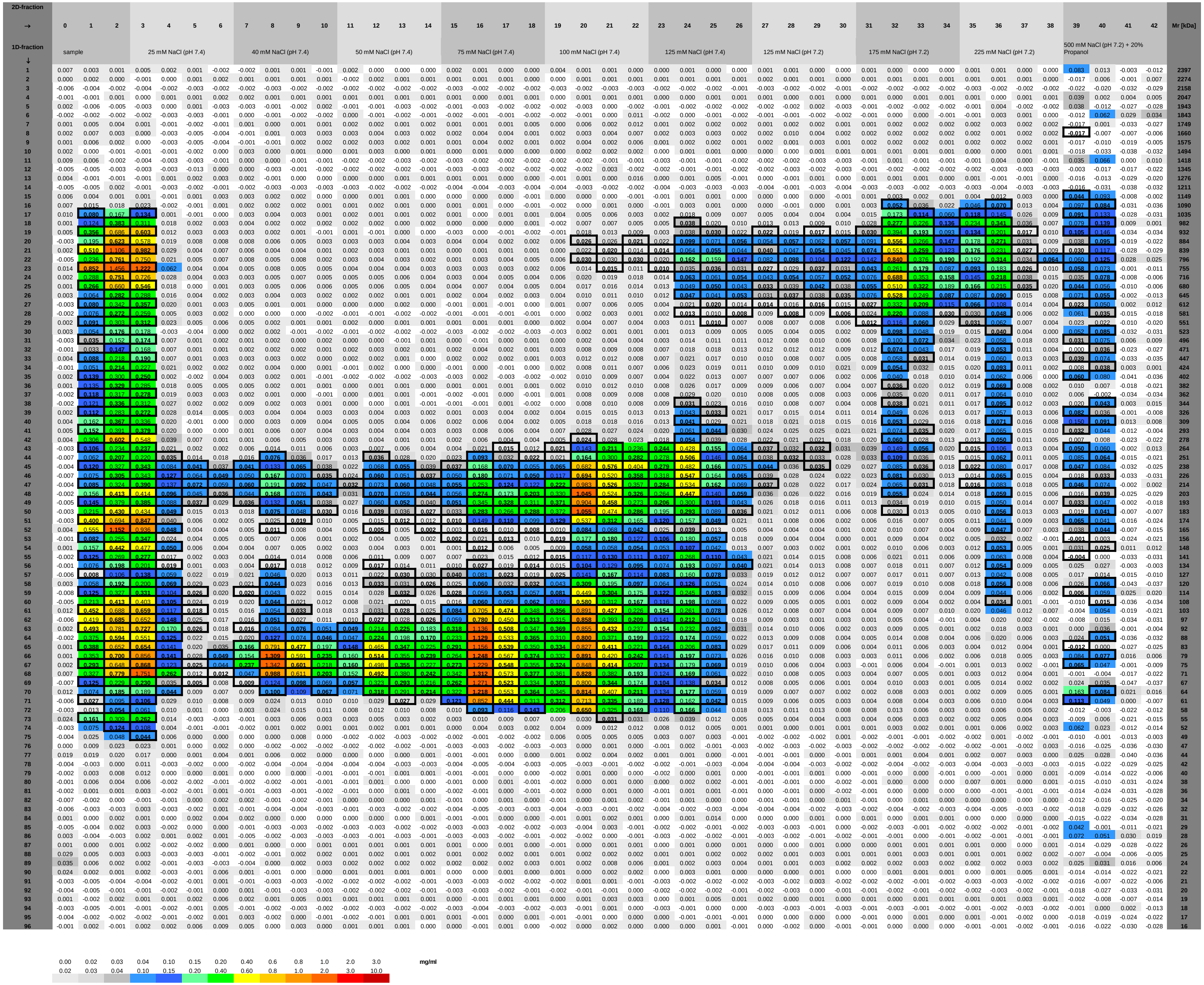
1. Rhode H, Muckova P, Buchler R, et al. A next generation setup for pre-fractionation of non-denatured proteins reveals diverse albumin proteoforms each carrying several post-translational modifications. *Sci Rep*. Aug 13 2019;9(1):11733. doi:10.1038/s41598-019-48278-y
2. Muckova P, Wendler S, Rubel D, et al. Preclinical Alterations in the Serum of COL(IV)A3(-)/(-) Mice as Early Biomarkers of Alport Syndrome. *J Proteome Res*. Dec 4 2015;14(12):5202-14. doi:10.1021/acs.jproteome.5b00814

Figure S1:
Chromatograms of dog serum proteins after native size exclusion chromatography (1D-SEC)



Four sample pools have been separated, non-affected males (NM), affected males (AM), non-affected females (NF), and carrier females (CF). Each sample pool was separated on a HiLoad Superdex™ 200 column controlled by an Äkta purifier™ system (GE Healthcare) at a flow rate of 1 ml/min and at 17 °C. After the void volume, 96 1D-fractions of 600 µl were collected into chilled 96-deepwell microplates. Column calibration [21]. Aliquots of 150 µl were read at 280 nm (SpectraMAX384PLUS, Molecular Devices). Protein concentrations were calculated using BSA as standard. Section of all proteins above 30 kDa.

Figure S2: Global protein distribution after anion exchange chromatography (2D-AEC)



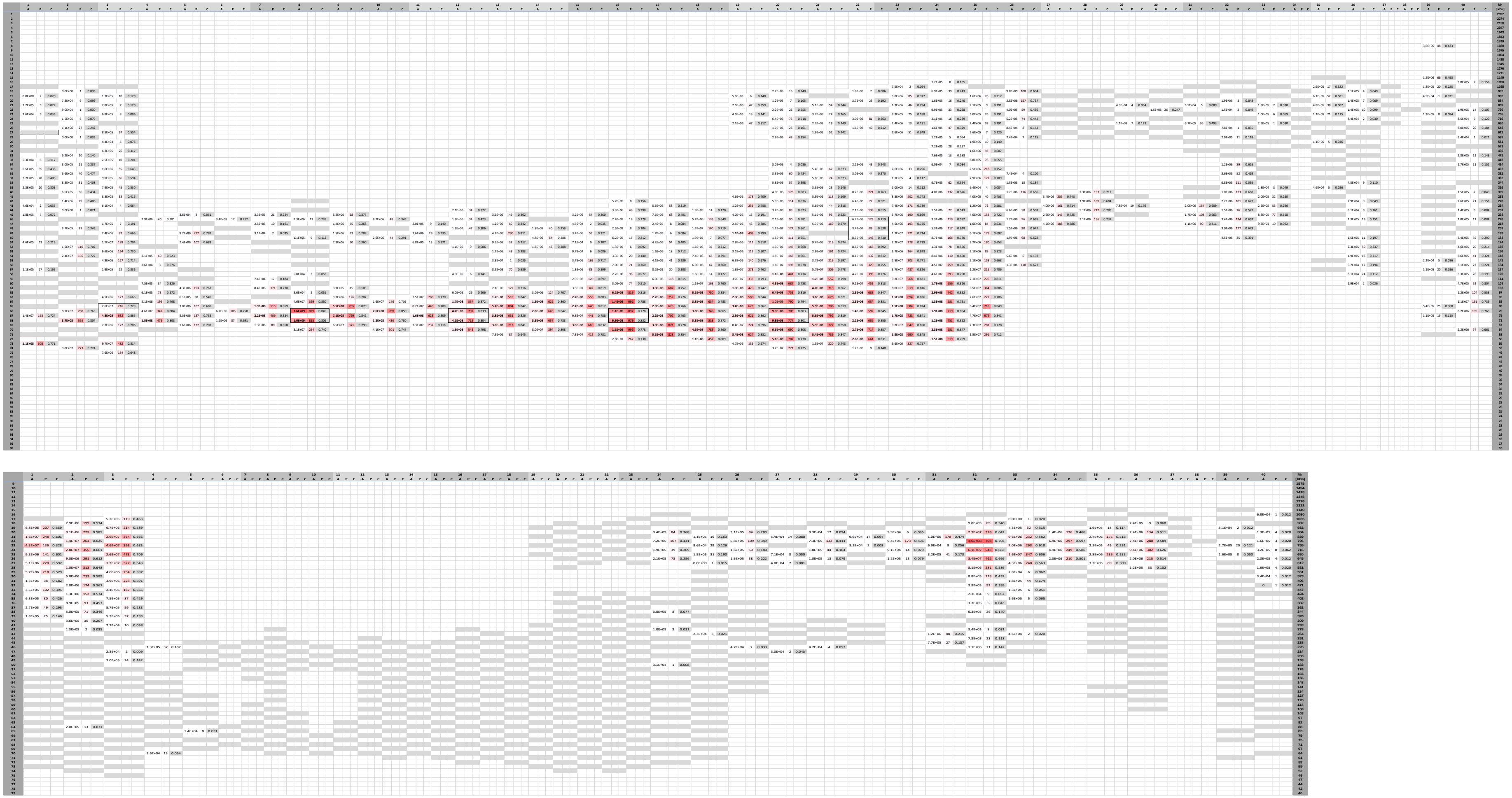
2D-fraction → 1D-fraction ↓	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	Mr [kDa]
	sample			25 mM NaCl (pH 7.4)				40 mM NaCl (pH 7.4)				50 mM NaCl (pH 7.4)				75 mM NaCl (pH 7.4)				100 mM NaCl (pH 7.4)				125 mM NaCl (pH 7.4)				125 mM NaCl (pH 7.2)				175 mM NaCl (pH 7.2)				225 mM NaCl (pH 7.2)				500 mM NaCl (pH 7.2) + 20% Propanol				
1	0.007	0.003	0.001	0.005	0.002	0.001	-0.002	-0.002	0.001	0.001	-0.001	0.002	0.000	0.000	0.000	0.002	0.001	0.000	0.000	0.004	0.001	0.001	0.000	0.000	0.001	0.000	0.000	0.001	0.001	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.001	0.000	0.000	0.083	0.013	-0.003	-0.012	2397
2	0.000	0.002	0.000	-0.001	0.000	0.001	0.002	0.001	0.001	0.001	0.001	-0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.000	0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.002	0.001	0.001	0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	-0.017	0.006	-0.001	0.007	2274
3	-0.006	-0.004	-0.002	-0.004	-0.002	-0.003	-0.002	-0.002	-0.003	-0.002	-0.002	-0.002	-0.002	-0.002	-0.002	-0.003	-0.002	-0.002	-0.002	-0.003	-0.002	-0.003	-0.003	-0.002	-0.002	-0.002	-0.001	-0.003	-0.002	-0.002	-0.001	-0.002	-0.002	-0.002	-0.002	-0.003	-0.002	-0.002	-0.002	-0.022	-0.020	-0.032	-0.029	2158
4	-0.001	-0.001	0.001	0.000	0.001	0.001	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.001	0.000	0.001	0.001	0.001	0.000	0.000	0.001	0.001	0.001	0.000	0.001	0.000	0.001	0.000	0.001	0.001	0.001	0.000	0.001	0.001	0.039	0.002	0.004	0.005	2047
5	0.002	-0.006	-0.005	-0.003	0.000	0.001	-0.003	-0.003	-0.001	-0.002	0.002	-0.001	-0.001	-0.003	-0.002	-0.001	-0.003	-0.002	-0.002	-0.002	-0.003	0.000	-0.002	-0.001	-0.002	-0.002	-0.002	-0.002	-0.002	0.002	-0.003	-0.001	-0.002	-0.002	-0.002	-0.001	0.004	-0.002	-0.002	0.038	-0.012	-0.027	-0.028	1943
6	-0.002	-0.002	-0.002	-0.002	-0.003	-0.003	-0.001	0.000	-0.001	-0.002	-0.002	0.000	-0.001	-0.002	-0.001	-0.002	-0.001	-0.001	-0.002	-0.002	-0.001	0.000	0.011	-0.002	0.000	-0.001	-0.002	-0.001	-0.001	-0.002	-0.002	-0.001	0.000	0.000	-0.001	-0.001	0.003	0.001	0.000	-0.012	0.062	0.029	0.034	1843
7	0.001	0.005	0.004	0.001	-0.001	-0.002	-0.001	0.001	0.000	0.001	0.001	0.002	0.002	0.001	0.002	0.001	0.001	0.001	0.005	0.000	0.006	0.002	0.012	0.001	0.002	0.002	0.002	0.001	0.002	0.002	0.001	0.001	0.002	0.002	0.002	0.002	0.003	0.002	0.002	-0.017	0.001	-0.033	-0.027	1749
8	0.002	0.007	0.003	0.000	-0.003	-0.005	-0.004	-0.001	0.001	0.003	0.003	0.003	0.004	0.003	0.002	0.002	0.004	0.004	0.001	0.002	0.003	0.004	0.007	0.002	0.003	0.003	0.002	0.002	0.010	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.001	0.002	0.002	-0.017	-0.007	-0.007	-0.006	1660
9	0.001	0.006	0.002	0.000	-0.003	-0.005	-0.004	-0.001	-0.001	0.002	0.002	0.002	0.003	0.002	0.001	0.001	0.004	0.002	0.001	0.002	0.004	0.002	0.006	0.001	0.002	0.002	0.001	0.002	0.001	0.003	0.001	0.002	0.002	0.002	0.001	0.002	0.002	0.002	0.001	-0.017	-0.010	-0.019	-0.005	1575
10	0.002	0.000	-0.001	-0.001	-0.001	-0.002	0.000	0.003	0.000	0.001	0.000	0.001	0.003	0.000	0.001	0.000	0.001	0.000	0.000	0.000	0.002	0.002	0.002	0.000	0.001	0.001	0.000	0.000	0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.000	0.001	0.001	-0.018	-0.033	-0.038	-0.032	1494
11	0.009	0.006	-0.002	-0.004	-0.003	-0.003	-0.001	0.000	0.000	-0.001	-0.001	-0.002	-0.002	-0.003	-0.002	-0.003	-0.002	-0.002	-0.002	-0.002	-0.002	-0.001	-0.001	-0.003	-0.001	-0.001	-0.002	-0.002	-0.002	-0.003	-0.003	-0.001	0.001	-0.001	-0.001	-0.001	0.004	0.000	-0.001	0.035	0.066	0.000	0.010	1418
12	-0.005	-0.005	-0.003	-0.003	-0.003	-0.013	0.000	0.000	-0.003	-0.001	-0.002	-0.002	-0.002	-0.002	-0.001	-0.003	-0.003	-0.002	-0.002	-0.002	-0.002	0.003	-0.002	-0.002	-0.001	-0.001	-0.002	-0.002	-0.003	-0.002	-0.003	-0.001	-0.002	-0.002	-0.002	-0.002	-0.003	-0.003	-0.003	-0.003	-0.017	-0.017	-0.022	1345
13	0.004	-0.001	-0.001	-0.001	0.001	0.002	0.003	0.002	-0.001	0.000	0.000	0.000	0.000	0.001	0.001	0.001	0.001	0.000	0.000	-0.001	0.001	0.000	0.016	0.000	0.001	0.005	-0.001	0.000	-0.001	0.001	0.000	0.001	0.001	0.001	0.000	0.001	-0.001	-0.001	0.000	-0.016	-0.013	-0.029	-0.020	1276
14	-0.005	-0.005	0.002	-0.001	-0.003	-0.002	-0.001	-0.002	-0.003	-0.003	-0.003	-0.003	-0.002	-0.002	-0.002	-0.004	-0.004	-0.003	-0.004	-0.004	-0.003	-0.002	-0.002	-0.004	-0.003	-0.003	-0.003	-0.004	-0.001	-0.003	-0.004	-0.003	-0.003	-0.002	-0.003	-0.003	-0.004	-0.003	-0.003	-0.016	-0.031	-0.038	-0.032	1211
15	0.006	0.004	0.001	0.001	-0.001	0.001	0.003	0.003	0.002	0.002	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	0.000	-0.001	-0.001	0.001	0.001	0.000	0.000	0.000	0.000	-0.001	0.001	0.003	0.002	0.001	0.004	0.012	0.003	0.000	0.044	0.093	-0.008	-0.002	1149
16	0.007	0.015	0.018	0.023	-0.002	-0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.002	0.001	0.000	0.001	0.001	0.000	-0.001	-0.002	0.000	0.001	0.000	-0.001	0.003	0.001	0.000	0.000	-0.001	0.000	0.001	0.003	0.052	0.036	0.022	0.046	0.070	0.013	0.004	0.097	0.084	-0.031	-0.036	1090
17	0.010	0.080	0.167	0.134	0.001	-0.001	0.000	0.003	0.004	0.003	0.001	0.002	0.001	0.001	0.002	0.001	0.000	0.001	0.001	0.004	0.005	0.006	0.003	0.002	0.018	0.009	0.007	0.005	0.004	0.004	0.004	0.015	0.173	0.114	0.060	0.118	0.145	0.026	0.009	0.091	0.133	-0.028	-0.031	1035
18	0.001	0.124	0.383	0.311	0.018	0.002	0.003	0.004	0.002	0.002	0.002	0.002	0.002	0.000	0.002	0.000	0.000	0.000	0.001	-0.002	0.007	0.007	0.005	0.005	0.038	0.020	0.010	0.013	0.013	0.009	0.010	0.028	0.277	0.226	0.136	0.234	0.341	0.036	0.007	0.079	0.139	0.009	0.001	982
19	0.005	0.356	0.686	0.603	0.012	0.003	0.003	0.003	0.002	0.001	-0.001	0.001	-0.001	0.000	0.000	-0.003	0.000	-0.001	-0.002	-0.001	0.018	0.013	0.009	0.003	0.038	0.030	0.022	0.022	0.019	0.017	0.015	0.030	0.394	0.193	0.093	0.134	0.201	0.017	0.010	0.105	0.146	-0.034	-0.034	932
20	-0.003	0.195	0.623	0.578	0.019	0.008	0.008	0.008	0.006	0.005	0.003	0.003	0.003	0.004	0.003	0.004	0.004	0.002	0.002	0.006	0.026	0.026	0.021	0.022	0.099	0.071	0.056	0.054	0.057	0.062	0.057	0.091	0.556	0.266	0.147	0.178	0.271	0.031	0.009	0.038	0.095	-0.019	-0.022	884
21	0.002	0.510	1.106	0.982	0.029	0.004	0.007	0.006	0.004	0.004	0.001	0.002	0.003	0.001	0.001	0.000	0.001	0.001	0.001	0.000	0.022	0.020	0.014	0.014	0.064	0.055	0.044	0.040	0.047	0.054	0.045	0.074	0.551	0.259	0.123	0.176	0.231	0.027	0.009	0.030	0.117	-0.028	-0.029	839
22	-0.005	0.236	0.761	0.750	0.021	0.005	0.007	0.008	0.005	0.008	0.002	0.003	0.004	0.003	0.002	0.001	0.003	0.004	0.005	0.006	0.030	0.030	0.030	0.020	0.162	0.159	0.147	0.082	0.098	0.104	0.122	0.142	0.840	0.376	0.190	0.192	0.314	0.034	0.064	0.060	0.125	0.028	0.025	796
23	0.014	0.852	1.456	1.222	0.062	0.004	0.004	0.005	0.008	0.005	0.005	0.004	0.004	0.004	0.003	0.003	0.003	0.003	0.002	0.006	0.014	0.015	0.011	0.010	0.035	0.036	0.031	0.027	0.029	0.037	0.031	0.043	0.261	0.179	0.087	0.093	0.183	0.026	0.010	0.058	0.073	-0.001	-0.011	755
24	0.002	0.288	0.751	0.726	0.028	0.004	0.003	0.003	0.005	0.007	0.005	0.005	0.005	0.006	0.004	0.003	0.004	0.005	0.004	0.006	0.020	0.019	0.018	0.014	0.063	0.061	0.054	0.043	0.054	0.057	0.052	0.076	0.688	0.353	0.158	0.145	0.218	0.038	0.015	0.035	0.078	-0.008	-0.006	716
25	0.001	0.266	0.660	0.546	0.018	0.000	0.001	0.003	0.005	0.006	0.006	0.005	0.006	0.005	0.004	0.004	0.007	0.004	0.005	0.004	0.017	0.016	0.014	0.013	0.049	0.050	0.043	0.033	0.039	0.042	0.038	0.055	0.510	0.322	0.189	0.166	0.215	0.035	0.020	0.044	0.056	-0.010	-0.006	680
26	0.003	0.064	0.282	0.288	0.016	0.004	0.002	0.003	0.004	0.003	0.002	0.002	0.002	0.001	0.001	0.002	0.004	0.002	0.003	0.004	0.010	0.011	0.010	0.012	0.047	0.041	0.053	0.031	0.037	0.038	0.035	0.076	0.528	0.249	0.087	0.087	0.090	0.015	0.008	0.071	0.055	-0.002	-0.013	645
27	-0.003	0.080	0.342	0.357	0.020	0.001	0.003	0.005	0.001	0.001	0.000	0.000	0.000	0.002	0.000	-0.001	0.001	-0.001	0.000	0.001	0.007	0.006	0.005	0.004	0.021	0.020	0.014	0.014	0.016	0.016	0.015	0.027	0.332	0.209	0.115	0.066	0.108	0.014	0.004	0.023	0.050	0.002	0.012	612
28	-0.002	0.076	0.272	0.259	0.005	0.003	0.002	0.000	0.000	0.000	-0.002	-0.001	-0.001	-0.002	-0.002	-0.001	-0.001	-0.001	-0.001	0.000	0.002	0.003	0.001	0.002	0.013	0.010	0.008	0.009	0.008	0.009	0.006	0.024	0.220	0.088	0.030	0.030	0.048	0.006	0.002	0.061	0.035	-0.015	-0.018	581
29	0.002	0.091	0.303	0.312	0.023	0.005	0.006	0.005	0.002	0.001	0.001	0.002	0.000	0.001	0.001	0.001	0.001	0.001	0.000	0.002	0.004	0.007	0.004	0.003	0.011	0.010	0.007	0.008	0.007	0.008	0.006	0.012	0.116	0.060	0.029	0.031	0.062	0.007	0.004	0.023	0.022	-0.010	-0.020	551
30	0.003	0.054	0.176	0.178	-0.003	-0.004	0.000	0.002	0.002	-0.001	-0.002	-0.001	-0.002	-0.002	-0.002	-0.003	-0.002	-0.002	-0.003	-0.003	0.002	0.001	0.001	0.001	0.013	0.009	0.005	0.005	0.004	0.005	0.002	0.009	0.098	0.048	0.019	0.015	0.040	0.004	0.000	0.052	0.085	-0.032	-0.031	523
31	-0.003	0.035	0.152	0.174	0.007	0.001	0.002	0.001	0.002	0.000	0.002	0.000	0.000	-0.001	0.001	0.000	-0.001	0.000	0.001	0.000	0.002	0.004	0.004	0.003	0.014	0.011	0.011	0.012	0.008	0.010	0.006	0.008	0.100	0.072	0.034	0.023	0.058	0.018	0.003	0.031	0.075	0.006	0.009	496
32	-0.001	0.033	0.147	0.168	0.007	0.001	0.001	0.002	0.002	0.002	0.001	0.002	0.003	0.002	0.001	0.002	0.004	0.002	0.001	0.003	0.008	0.009	0.008	0.007	0.018	0.018	0.013	0.012	0.012	0.012	0.009	0.012	0.074	0.043	0.017	0.019	0.053	0.011	0.004	0.000	0.036	-0.023	-0.027	471
33	0.004	0.088	0.218	0.190	0.007	0.001	0.003	0.003	0.003	0.002	0.000	0.002	0.002	0.001	0.000	0.002	0.002	0.002	0.001	0.003	0.012	0.012	0.008	0.007	0.021	0.017	0.010	0.010	0.008	0.007	0.005	0.008	0.058	0.031	0.014	0.019	0.060	0.013	0.003	0.039	0.074	-0.033	-0.035	447
34	-0.001	0.051	0.214	0.227	0.021	0.002	0.002	0.002	0.004	0.000	0.001	-0.001	0.002	0.000	0.000	-0.001	0.000	-0.001	0.000	0.002	0.008	0.011	0.007	0.006	0.023	0.019	0.011	0.010	0.009	0.010	0.021	0.009	0.054	0.032	0.015	0.020	0.093	0.011	0.002	0.008	0.038	0.003	0.001	424
35	0.002	0.139	0.300	0.250	0.002	-0.002	0.004	0.003	0.002	0.001	-0.001	-0.002	-0.002	-0.002	-0.003	-0.003	0.002	-0.003	-0.002	-0.002	0.010	0.009	0.007	0.004	0.022	0.013	0.007	0.007	0.007	0.006	0.002	0.006	0.040	0.018	0.010	0.014	0.062	0.006	0.000	0.060	0.080	-0.041	-0.036	402
36	0.001	0.135	0.329	0.285	0.018	0.005	0.005	0.005	0.002	0.001	0.001	0.000	0.001	0.001	0.000	0.001	0.001	0.001	0.001	0.002	0.010	0.012	0.010	0.008	0.026	0.017	0.009	0.009	0.006	0.007	0.004	0.007	0.036	0.020	0.012	0.019	0.069	0.008	0.002	0.010	0.007	-0.018	-0.021	382
37	-0.002	0.118	0.317	0.278	0.019	0.003	0.003	0.002	0.001	0.000	-0.001	0.000	0.001	0.001	-0.001	-0.002	-0.001	0.000	-0.001	0.001	0.008	0.009	0.008	0.008	0.029	0.020	0.010	0.008	0.005	0.008	0.003	0.006	0.035	0.020	0.011	0.017	0.064	0.010	0.002	0.006	-0.002	-0.034	-0.034	362
38	-0.002	0.121	0.336	0.312	0.027	0.002	0.002	0.009	0.002	0.003	0.001	0.000	0.000	0.001	-0.001	-0.001	-0.001	0.001	-0.002	0.000	0.008	0.010	0.008	0.009	0.031	0.023	0.016	0.010	0.008	0.007	0.004	0.008	0.038	0.021	0.011	0.017	0.095	0.012	0.003	0.020	0.043	0.003	0.015	344
39	0.002	0.112	0.283	0.272	0.028	0.014	0.005	0.003	0.004	0.004	0.003	0.003	0.004	0.003	0.002	0.001	0.003	0.004	0.002	0.004	0.015	0.015	0.013	0.013	0.043	0.033	0.021	0.017	0.015	0.014	0.011	0.014	0.049	0.026	0.013	0.017	0.057	0.013	0.006	0.082	0.036	-0.001	-0.008	326
40	0.004	0.162	0.367	0.336	0.020	-0.001	0.000	0.000	0.003	0.009	0.004	0.005	0.005	0.004	0.006	0.002	0.006	0.004	0.002	0.005	0.018	0.018	0.016	0.013	0.041	0.029	0.021	0.018	0.021	0.018	0.015	0.016	0.053	0.029	0.016	0.018	0.071	0.016	0.008	0.150	0.091	0.013	0.008	309
41	0.005	0.152	0.391	0.379	0.020	0.000	0.000	0.001	0.006	0.007	0.004	0.003	0.004	0.004	0.003	0.003	0.008	0.006	0.004	0.007	0.028	0.027	0.024	0.020	0.061	0.044	0.030	0.024	0.025	0.025	0.021	0.021	0.074	0.035	0.020	0.017	0.065	0.015	0.010	0.032	0.044	-0.012	-0.004	293
42	0.004	0.306	0.602	0.548	0.039	0.007	0.001	0.001	0.006	0.005	0.003	0.003	0.004	0.001	0.001	0.002	0.006	0.004	0.004	0.005	0.024	0.028	0.023	0.018	0.054	0.039	0.028	0.022	0.021	0.021	0.018	0.020	0.060	0.028	0.013	0.013	0.050	0.011	0.005	0.007	0.008	-0.023	-0.022	278
43	-0.003	0.106	0.234	0.237	0.021	0.002	0.002	0.006	0.014	0.011	0.006	0.003	0.007	0.006	0.004	0.004	0.021	0.015	0.012	0.021	0.143	0.211	0.236	0.244	0.428	0.155	0.064	0.037	0.032	0.032	0.031	0.039	0.149	0.056	0.020	0.015	0.106	0.013	0.004	0.050	0.060	-0.002	0.013	264
44	-0.007	0.062	0.207	0.220	0.035	0.014	0.018	0.016	0.076	0.036	0.017	0.013	0.036	0.028	0.020	0.023	0.093	0.032	0.022	0.021	0.164	0.300	0.282	0.278	0.506	0.146	0.064	0.038	0.032	0.033	0.028	0.033	0.109	0.036	0.015	0.015	0.062	0.011	0.005	0.085	0.064	-0.015	-0.021	251
45	-0.004	0.120	0.327	0.343	0.084	0.041	0.037	0.041	0.133	0.065	0.038	0.022	0.068	0.055	0.039	0.037	0.168	0.070	0.055	0.065	0.682	0.576	0.404	0.279	0.482	0.166	0.075	0.044	0.036	0.035	0.029	0.027	0.085	0.036	0.018	0.022	0.080	0.017	0.008	0.047	0.084	-0.032	-0.025	238
46	-0.007	0.075	0.305	0.343	0.127	0.064	0.049	0.050	0.167	0.070	0.035	0.024	0.060	0.051	0.037	0.050	0.180	0.071	0.050	0.117	0.694	0.520	0.358	0.318	0.547	0.164	0.065	0.039	0.028	0.024	0.022	0.023	0.081	0.030	0.013	0.014	0.065	0.015	0.004	0.018	0.033	-0.033	-0.031	226
47	-0.004	0.085	0.324	0.390	0.137	0.072	0.059	0.060	0.191	0.092	0.047	0.032	0.073	0.060	0.048	0.055	0.253	0.124	0.122	0.222	0.983	0.526	0.357	0.284	0.534	0.162	0.069	0.037	0.028	0.022	0.017	0.024	0.065	0.031	0.018	0.016	0.083	0.018	0.005	0.046	0.074	-0.002	0.002	214
48	-0.002	0.156	0.413	0.414	0.096	0.045	0.036	0.044	0.168	0.076	0.043	0.031	0.070	0.059	0.044	0.056	0.274	0.173	0.203	0.330	1.045	0.524	0.326	0.264	0.447	0.140	0.059	0.036	0.026	0.022	0.016	0.019	0.055	0.024	0.014	0.018	0.059	0.015	0.006	0.016	0.039	-0.025	-0.029	203
49	-0.005	0.145	0.379	0.385	0.088	0.037	0.029	0.036	0.132	0.061	0.038	0.027	0.060	0.052	0.040	0.051	0.345	0.328	0.311	0.371	0.904	0.458	0.273	0.206	0.300	0.101	0.043	0.026	0.018	0.016	0.011	0.013	0.034	0.019	0.010	0.015	0.050	0.014	0.007	0.033	0.047	-0.002	-0.018	193
50	-0.003	0.215	0.430	0.434	0.049	0.015	0.013	0.018	0.075	0.048	0.030	0.016	0.039	0.036	0.027	0.033	0.283	0.266	0.288	0.372	1.055	0.474	0.286	0.195	0.293	0.089	0.036	0.021	0.012	0.011	0.006	0.008	0.030	0.013	0.005	0.010	0.056	0.013	0.003	0.019	0.041	-0.007	-0.007	183
51	-0.003	0.400	0.694	0.847	0.040	0.006	0.002	0.005	0.025	0.019	0.010	0.005	0.015	0.012	0.012	0.010	0.149	0.110	0.099	0.129	0.537	0.312	0.165	0.120	0.157	0.049	0.021	0.011	0.008	0.006	0.002	0.006	0.016	0.007	0.005	0.011	0.044	0.009	0.003	0.065	0.041	-0.016	-0.024	174
52	0.004	0.555	1.152	0.936	0.048	0.004	0.004	0.005	0.011	0.008	0.004	0.005	0.005	0.005	0.002	0.003	0.016	0.010	0.008	0.010	0.084	0.068	0.042	0.025	0.039	0.013	0.005	0.004	0.004	0.004	0.001	0.002	0.010	0.007	0.004	0.009	0.047	0.007	0.003	0.038	0.044	-0.007	-0.015	165
53	-0.001	0.082	0.255	0.347	0.024	0.004	0.005	0.005	0.007	0.006	0.001	0.002	0.004	0.005	0.002	0.002	0.021	0.013	0.010	0.019	0.177	0.180	0.127	0.106	0.180	0.057	0.018	0.009	0.004	0.004	0.000	0.001	0.009	0.004	0.002	0.005	0.032	0.002	-0.001	-0.001	0.003	-0.024	-0.021	156
54	0.001	0.157	0.442	0.477	0.050	0.006	0.004	0.004	0.007	0.005	0.002	0.003	0.004	0.003	0.001	0.001	0.012	0.006	0.005	0.009	0.058	0.058	0.054	0.053	0.107	0.042	0.013	0.007	0.003	0.002	0.001	0.002	0.010	0.006	0.003	0.012	0.053	0.005	0.001	0.031	0.025	0.011	0.012	148
55	-0.002	0.125	0.269	0.277	0.017	0.002	0.003	0.004	0.014	0.014	0.008	0.006	0.011	0.009	0.007	0.007	0.023	0.015	0.012	0.015	0.117	0.130	0.111	0.107	0.268	0.110	0.043	0.021	0.014	0.015	0.008	0.006	0.021	0.011	0.006	0.009	0.063	0.008	0.004	-0.004	0.000	-0.033	-0.031	141
56	-0.001	0.076	0.198	0.201	0.019	0.001	0.003	0.004	0.017	0.018	0.012	0.009	0.017	0.014	0.011	0.010	0.027	0.019	0.014	0.015	0.104	0.129	0.095	0.074	0.193	0.097	0.040	0.021	0.014	0.013	0.008	0.007	0.018	0.011	0.007	0.012	0.054	0.009	0.005	0.025	0.027	-0.003	-0.003	134
57	-0.006	0.008	0.106	0.138	0.059	0.022	0.019	0.021	0.046	0.020	0.013	0.011	0.022	0.030	0.030	0.040	0.081	0.023	0.019	0.025	0.141	0.167	0.114	0.083	0.160	0.078	0.033	0.019	0.012	0.012	0.007	0.007	0.017	0.011	0.007	0.013	0.042	0.008	0.005	0.017	0.014	-0.015	-0.010	127
58	0.003	0.058	0.192	0.200	0.069	0.029	0.023	0.021	0.044	0.023	0.016	0.013	0.033	0.031	0.026	0.025	0.060	0.032	0.032	0.043	0.309	0.195	0.097	0.064	0.126	0.051	0.024	0.014	0.010	0.008	0.006	0.007	0.019	0.010	0.008	0.018	0.056	0.008	0.006	0.026	0.066	-0.043	-0.037	120
59	-0.008	0.125	0.327	0.331	0.104	0.026	0.020	0.020	0.043	0.022	0.015	0.014	0.028	0.032	0.026	0.028	0.059	0.053	0.057	0.081	0.449	0.304	0.175	0.122	0.245	0.083	0.032	0.015	0.009	0.006	0.004	0.004	0.015	0.009	0.004	0.009	0.044	0.006	0.002	0.006	0.059	0.025	0.020	114
60	-0.005	0.213	0.413	0.403	0.105	0.024	0.019	0.020	0.044	0.021	0.012	0.008	0.021	0.020	0.015	0.016	0.060	0.059	0.062	0.109	0.580	0.312	0.167	0.116	0.198	0.068	0.022	0.009	0.005	0.005	0.001	0.002	0.009	0.004	0.002	0.004	0.034	0.001	-0.001	-0.010	0.015	-0.036	-0.034	108
61	0.012	0.452	0.688	0.659	0.117	0.018	0.015	0.016	0.054	0.033	0.018	0.013	0.031	0.028	0.025	0.084	0.705	0.474	0.348	0.356	0.891	0.427	0.226	0.154	0.261	0.078	0.026	0.012	0.008	0.007	0.004	0.004	0.009	0.007	0.010	0.020	0.046	0.012	0.007	-0.004	0.054	-0.019	-0.021	103
62	-0.006	0.419	0.685	0.652	0.148	0.025	0.017	0.016	0.051	0.027	0.011	0.010	0.027	0.028	0.026	0.059	0.780	0.450	0.313	0.315	0.858	0.393	0.209	0.141	0.212	0.061	0.018	0.009	0.003	0.001	0.003	0.001	0.005	0.004	-0.001	0.004	0.020	0.002	-0.002	-0.008	0.015	-0.034	-0.031	97
63	0.002	0.493	0.781	0.727	0.170	0.026	0.018	0.016	0.084	0.076	0.051	0.049	0.214	0.225	0.183	0.318	1.136	0.508	0.347	0.369	0.855	0.432	0.237	0.154	0.232	0.082	0.031	0.014	0.010	0.006	0.002	0.003	0.009	0.005	0.001	0.002	0.018	0.003	0.001	0.000	0.036	-0.001	-0.004	92
64	-0.002	0.375	0.594	0.551	0.125	0.022	0.015	0.020	0.127	0.074	0.046	0.047	0.224	0.198	0.170	0.233	1.129	0.533	0.365	0.310	0.800	0.371	0.199	0.122	0.174	0.059	0.022	0.013	0.009	0.008	0.004	0.005	0.014	0.008	0.004	0.006	0.020	0.006	0.003	0.024	0.051	-0.036	-0.032	88
65	0.001	0.388	0.652	0.654	0.141	0.020	0.035	0.166	0.791	0.477	0.197	0.148	0.465	0.347	0.225	0.291	1.156	0.539	0.350	0.334	0.827	0.411	0.221	0.144	0.206	0.083	0.029	0.017	0.011	0.009	0.006	0.004	0.011	0.006	0.003	0.004	0.012	0.004	0.001	-0.012	0.000	-0.027	-0.025	83
66	0.001	0.353	0.700	0.856	0.141	0.028	0.049	0.154	1.309	0.591	0.235	0.160	0.514	0.355	0.239	0.264	1.248	0.567	0.374	0.332	0.891	0.420	0.242	0.141	0.197	0.073	0.026	0.016	0.010	0.008	0.003	0.003	0.011	0.006	0.002	0.006	0.018	0.005	0.003	0.084	0.077	0.016	0.006	79
67	0.002	0.293	0.648	0.868	0.123	0.025	0.044	0.237	1.342	0.601	0.218	0.160	0.498	0.355	0.227	0.273	1.229	0.548	0.355	0.324	0.848	0.414	0.207	0.134	0.179	0.069	0.019	0.010	0.006	0.004	0.003	-0.001	0.006	0.004	-0.001	0.001	0.013	0.002	-0.001	0.065	0.047	-0.001	-0.009	75
68	0.007	0.327	0.779	1.751	0.262	0.012	0.012	0.047	0.988	0.611	0.203	0.152	0.492	0.380	0.242	0.342	1.312	0.573	0.377	0.361	0.828	0.382	0.193	0.124	0.169	0.061	0.022	0.010	0.008	0.005	0.003	0.004	0.007	0.005	0.001	0.003	0.012	0.004	0.001	-0.001	-0.004	-0.017	-0.022	71
69	-0.007	0.125	0.229	0.230	0.035	0.005	0.008	0.009	0.124	0.098	0.069	0.057	0.323	0.293	0.216	0.262	1.271	0.523	0.334	0.303	0.800	0.344	0.174	0.104	0.138	0.034	0.012	0.008	0.005	0.006	0.001	0.004	0.010	0.003	0.001	0.005	0.014	0.002	0.002	0.024	0.035	-0.047	-0.037	67
70	0.012	0.074	0.185	0.189	0.044	0.009	0.007	0.009	0.100	0.109	0.067	0.071	0.318	0.291	0.214	0.322	1.218	0.553	0.364	0.345	0.814	0.407	0.211	0.134	0.177	0.059	0.019	0.009	0.007	0.007	0.002	0.002	0.008	0.003	0.001	0.002	0.009	0.005	0.001	0.163	0.084	0.021	0.016	64
71	-0.006	0.027	0.095	0.106	0.029	0.010	0.008	0.009	0.024	0.013	0.010	0.010	0.029	0.027	0.029	0.121	0.852	0.444	0.313	0.312	0.713	0.335	0.189	0.128	0.162	0.042	0.015	0.009	0.006	0.005	0.003	0.004	0.008	0.004	0.003	0.006	0.010	0.004	0.003	0.113	0.049	0.000	-0.007	61
72	-0.003	0.013	0.054	0.061	0.010	0.001	0.000	0.003	0.024	0.015	0.011	0.008	0.012	0.010	0.008	0.010	0.093	0.116	0.143	0.206	0.650	0.325	0.169	0.110	0.166	0.044	0.018	0.013	0.011	0.013	0.008	0.008	0.013	0.006	0.003	0.003	0.006	0.005	0.002	-0.012	-0.003	-0.022	-0.012	58
73	0.024	0.161	0.309	0.262	0.014	-0.003	-0.003	-0.001	0.003	0.006	0.003	0.003	0.005	0.003	0.002	0.003	0.010	0.009	0.007	0.009	0.030	0.031	0.031	0.026	0.039	0.012	0.005	0.005	0.004	0.004	0.003	0.004	0.006	0.003	0.002	0.002	0.005	0.004	0.003	-0.009	0.006	-0.021	-0.015	55
74	-0.003	0.075	0.124	0.108	0.004	-0.001	-0.001	-0.002	0.001	0.002	0.001	0.001	0.002	0.001	0.001	0.000	0.004	0.003	0.002	0.004	0.009	0.012	0.012	0.008	0.012	0.005	0.001	0.001	0.000	0.001	0.001	0.001	0.003	0.002	0.001	0.001	0.006	0.002	0.003	0.062	0.023	-0.012	-0.014	52
75	-0.004	0.025	0.048	0.044	0.006	0.000	0.000	0.000	0.000	0.008	0.000	-0.002	-0.002	-0.003	-0.002	-0.002	-0.001	-0.002	-0.002	0.006	0.005	0.005	0.005	0.003	0.007	0.003	-0.001	-0.002	-0.002	-0.002	0.001	-0.002	-0.001	-0.001	-0.002	-0.002	0.001	-0.002	-0.001	-0.010	-0.001	-0.013	-0.003	49
76	0.000	0.009	0.023	0.023	0.001	0.000	0.002	0.000	-0.002	-0.002	-0.002	-0.002	-0.002	-0.002	-0.001	-0.003	-0.003	-0.002	-0.003	-0.003	0.000	0.001	0.000	-0.001	0.002	-0.001	-0.003	-0.002	-0.003	-0.002	-0.003	-0.002	-0.002	-0.002	-0.002	-0.002	-0.001	-0.002	0.003	-0.016	-0.025	-0.036	-0.030	47
77	0.019	0.019	0.020	0.017	0.000	0.001	0.004	0.001	0.006	0.002	0.000	0.000	0.000	0.000	0.001	-0.001	-0.001	0.000	0.000	0.001	0.002	0.004	0.002	0.001	0.001	0.000	-0.001	-0.001	-0.001	0.000	-0.001	0.001	0.001	0.004	0.001	0.002	0.007	0.003	0.000	0.025	0.028	-0.040	-0.036	44
78	-0.004	-0.003	0.000	0.011	-0.003	-0.002	0.000	-0.002	-0.004	-0.004	-0.004	-0.004	-0.004	-0.003	-0.003	-0.004	-0.005	-0.004	-0.003	-0.005	-0.003	-0.001	-0.002	-0.002	-0.001	-0.003	-0.004	-0.004	-0.004	-0.003	-0.002	-0.002	-0.004	-0.002	-0.003	-0.004	-0.003	-0.003	-0.003	-0.015	-0.022	-0.029	-0.025	42
79	-0.002	0.003	0.008	0.012	0.000	0.000	0.001	0.000	0.000	0.000	-0.001	-0.001	-0.001	0.001	0.001	-0.001	-0.001	0.000	0.000	-0.002	0.001	0.000	0.000	-0.002	0.000	0.001	0.000	-0.001	-0.001	0.001	0.000	-0.001	0.000	0.000	-0.001	0.000	-0.001	0.000	0.001	-0.009	-0.014	-0.022	-0.006	40
80	-0.001	0.006	0.004	0.006	-0.002	-0.002	-0.001	-0.002	-0.002	-0.001	-0.001	-0.001	0.001	0.000	0.000	-0.001	0.000	0.001	-0.001	-0.002	0.000	0.001	0.000	0.000	0.002	0.002	-0.001	-0.001	-0.001	0.000	-0.002	-0.001	0.000	0.000	0.000	0.007	0.001	0.000	0.001	-0.015	-0.010	-0.031	-0.024	38
81	-0.002	0.001	0.001	0.003	-0.002	-0.001	0.001	-0.001	-0.003	-0.001	-0.002	-0.001	0.000	0.001	0.000	-0.002	-0.001	0.000	-0.001	-0.002	0.000	0.001	0.000	-0.001	0.001	0.001	-0.001	0.000	-0.001	0.000	-0.002	-0.001	0.000	0.000	0.000	0.000	-0.001	-0.001	-0.001	-0.014	-0.024	-0.031	-0.028	36
82	-0.007	-0.002	0.000	-0.001	-0.001	0.000	0.002	0.002	-0.001	-0.002	-0.001	0.000	0.000	0.000	0.001	-0.001	0.000	0.001	0.000	-0.001	0.000	0.001	0.002	-0.001	0.001	0.000	0.000	-0.001	-0.001	0.000	0.001	-0.001	0.000	0.001	0.000	0.000	0.000	0.000	0.000	-0.012	-0.016	-0.025	-0.020	34
83	-0.006	-0.003	-0.003	0.003	-0.003	-0.002	0.001	-0.001	-0.004	-0.004	-0.003	-0.001	-0.003	-0.002	-0.002	-0.004	-0.005	-0.003	-0.003	-0.004	-0.003	-0.001	-0.002	-0.004	-0.002	-0.003	-0.004	-0.004	-0.004	-0.002	-0.003	-0.002	-0.004	-0.002	-0.003	-0.004	-0.005	-0.003	-0.002	-0.018	-0.029	-0.032	-0.026	32
84	0.001	0.000	0.002	0.001	0.000	0.002	0.004	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.001	-0.001	-0.001	0.000	0.000	-0.001	0.001	0.002	0.001	0.000	0.001	0.014	0.000	0.000	0.000	0.001	0.000	0.001	0.000	0.001	0.001	0.000	0.000	0.000	0.000	-0.015	-0.022	-0.034	-0.028	31
85	-0.005	-0.004	0.002	0.003	-0.002	0.000	0.000	-0.001	-0.003	-0.003	-0.002	-0.003	-0.003	-0.002	-0.002	-0.003	-0.003	-0.002	-0.002	-0.003	-0.004	0.003	-0.001	-0.002	-0.002	-0.001	-0.002	-0.003	-0.003	-0.001	0.000	-0.002	-0.003	-0.001	-0.002	-0.002	-0.002	-0.001	-0.002	0.042	-0.001	-0.011	-0.021	29
86	0.003	-0.004	-0.003	0.002	0.001	0.002	0.001	-0.005	-0.002	-0.003	-0.003	-0.003	-0.001	-0.003	-0.001	-0.003	-0.003	-0.002	-0.001	-0.002	-0.002	0.000	-0.001	-0.003	-0.002	-0.002	-0.001	-0.003	-0.002	-0.001	-0.002	-0.001	-0.001	0.000	-0.001	-0.002	-0.001	-0.001	-0.001	0.072	0.051	0.030	0.019	28
87	0.001	0.000	0.001	0.002	-0.002	-0.002	0.000	0.001	0.000	0.000	0.001	0.001	0.001	0.001	0.001	0.001	0.000	0.001	0.000	-0.001	0.000	0.001	0.001	0.000	0.001	0.000	0.001	0.000	0.000	0.001	0.000	0.000	0.001	0.001	0.001	0.001	0.000	0.000	0.001	-0.014	-0.029	-0.028	-0.022	26
88	0.029	0.005	0.003	0.003	-0.003	-0.003	-0.001	-0.002	-0.001	0.002	0.002	0.001	0.002	0.001	0.002	0.001	0.002	0.002	0.001	0.001	0.002	0.002	0.002	0.001	0.001	0.002	0.002	0.002	0.001	0.003	0.001	0.001	0.001	0.003	0.001	0.001	0.001	0.002	0.002	-0.007	-0.004	-0.006	-0.005	25
89	0.035	0.006	0.002	0.002	-0.001	-0.003	-0.003	-0.004	0.000	0.002	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.003	0.001	0.002	0.008	0.006	0.001	0.002	0.003	0.004	0.001	0.001	0.003	0.002	0.002	0.002	0.003	0.002	0.002	0.002	0.003	0.002	0.025	0.031	0.016	0.006	24
90	0.024	0.002	0.001	0.002	-0.003	-0.001	0.006	0.001	-0.001	0.000	0.000	0.001	0.001	0.001	0.001	0.000	0.000	0.001	0.000	0.001	0.000	0.002	0.002	0.000	0.003	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.001	0.001	0.001	0.000	0.001	0.005	0.001	-0.014	-0.014	-0.022	-0.021	22
91	-0.003	-0.005	-0.004	-0.004	-0.002	-0.001	0.001	-0.001	-0.003	-0.003	-0.002	-0.002	-0.002	-0.002	-0.001	-0.003	-0.003	-0.002	-0.002	-0.002	0.001	0.001	-0.001	-0.003	-0.002	-0.002	-0.002	-0.003	-0.002	0.003	-0.002	-0.002	-0.002	-0.001	-0.002	-0.003	-0.003	-0.002	-0.002	-0.016	-0.007	-0.022	-0.006	21
92	-0.004	-0.005	-0.001	-0.001	-0.002	-0.001	0.000	0.001	-0.001	-0.003	-0.003	-0.002	-0.002	-0.002	-0.001	-0.003	-0.003	-0.002	-0.001	-0.002	-0.001	-0.001	0.000	-0.002	-0.002	-0.002	-0.001	-0.002	-0.003	0.000	-0.001	-0.001	-0.002	-0.001	-0.002	-0.002	-0.003	-0.002	-0.001	-0.018	-0.027	-0.033	-0.031	20
93	0.001	-0.002	0.002	0.001	0.001	0.002	0.006	0.002	0.001	0.005	0.001	0.001	0.001	0.001	0.001	0.000	-0.001	0.001	0.001	0.000	0.001	0.003	0.003	0.000	0.001	0.005	0.001	0.002	0.000	0.001	0.000	0.001	0.000	0.001	0.001	0.001	0.001	0.003	0.001	-0.002	-0.008	-0.007	-0.014	19
94	-0.003	-0.005	-0.001	-0.001	-0.002	-0.001	0.005	-0.001	-0.002	-0.003	-0.002	-0.002	-0.003	-0.002	-0.002	-0.003	-0.004	-0.003	-0.002	-0.003	-0.001	0.001	0.000	-0.003	-0.001	0.000	0.000	-0.003	-0.003	-0.001	-0.003	-0.001	-0.003	-0.001	-0.002	-0.001	-0.002	-0.003	-0.002	-0.001	0.000	0.002	-0.013	18
95	-0.004	-0.002	-0.002	-0.002	-0.001	-0.002	0.001	0.003	-0.002	0.000	-0.001	-0.002	-0.001	0.001	0.001	0.001	-0.001	0.000	0.001	-0.001	-0.001	0.000	0.000	0.000	-0.001	-0.001	-0.001	0.000	0.000	0.000	0.000	-0.001	0.000	0.001	0.000	0.001	-0.001	-0.002	0.000	-0.018	-0.019	-0.024	-0.022	17
96	-0.001	0.002	-0.001	0.002	0.002	0.006	0.009	0.005	0.000	0.003	0.000	0.001	0.001	0.001	0.000	0.000	-0.001	0.001	0.000	-0.002	0.000	0.002	0.000	0.000	0.000	0.001	-0.001	0.000	-0.002	0.000	-0.001	-0.001	0.000	0.000	0.000	-0.001	-0.001	-0.002	-0.001	-0.016	-0.022	-0.030	-0.028	16

0.00	0.02	0.03	0.04	0.10	0.15	0.20	0.40	0.6	0.8	1.0	2.0	3.0	mg/ml
0.02	0.03	0.04	0.10	0.15	0.20	0.40	0.60	0.8	1.0	2.0	3.0	10.0	

Example: entire 2D-sub-fractions from one sample pool (NM).

First column: number of 1D-fraction (cf. Figure S1); last column: molecular weight according column
calibration.
First line: number of 2D-sub-fraction; second line: designation of the solvent, i.e. sample and the concentration of NaCl in the elution solvent 10mM Tris-HCl.
Frames indicate selected fractions for mass spectrometric analysis.
Total fractional concentrations of proteins were calculated from A280 using BSA as standard. Protein concentrations are given by values (mg/mL) and color code.

Figure S3: Distribution of two examples of plasma proteins from NM after 2D-AEC



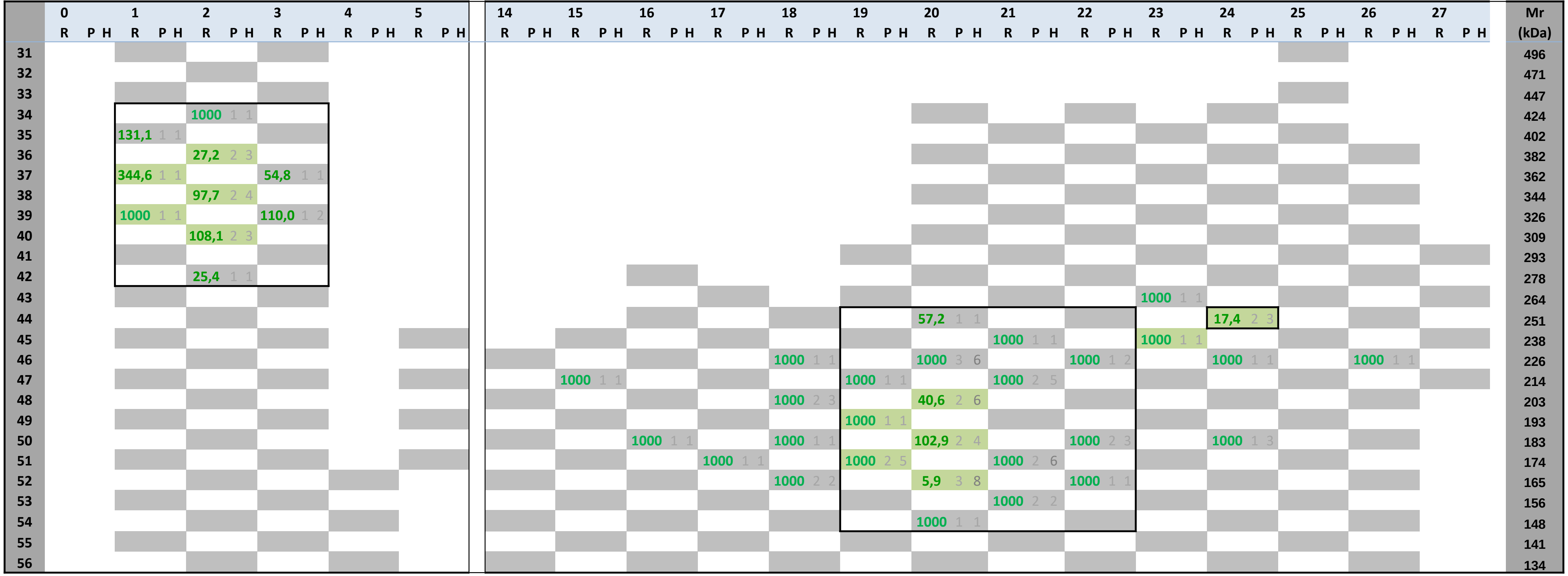
Distribution of two proteins from NM, albumin (upper part, P49822) and α-2-macroglobulin (lower part, F6UME0) after 2D-AEC.
Results after analysis by the Proteome discoverer with the following quantifiers: A, area; P, PSM; C, coverage. Red intensity code is given for A and P; Grey: MS-analyzed 2D-fractions; empty: without any peptide of the respective protein; frames: these sub-fractions from all four samples have been analyzed for PTM.

Please enlarge to more than 400%.

Figuren S4:

Distribution of serum amyloid after 2D-AEC and mass spectrometry identification of its peptides as example of a uniformly altered protein

J9NVE9_Serum amyloid A protein



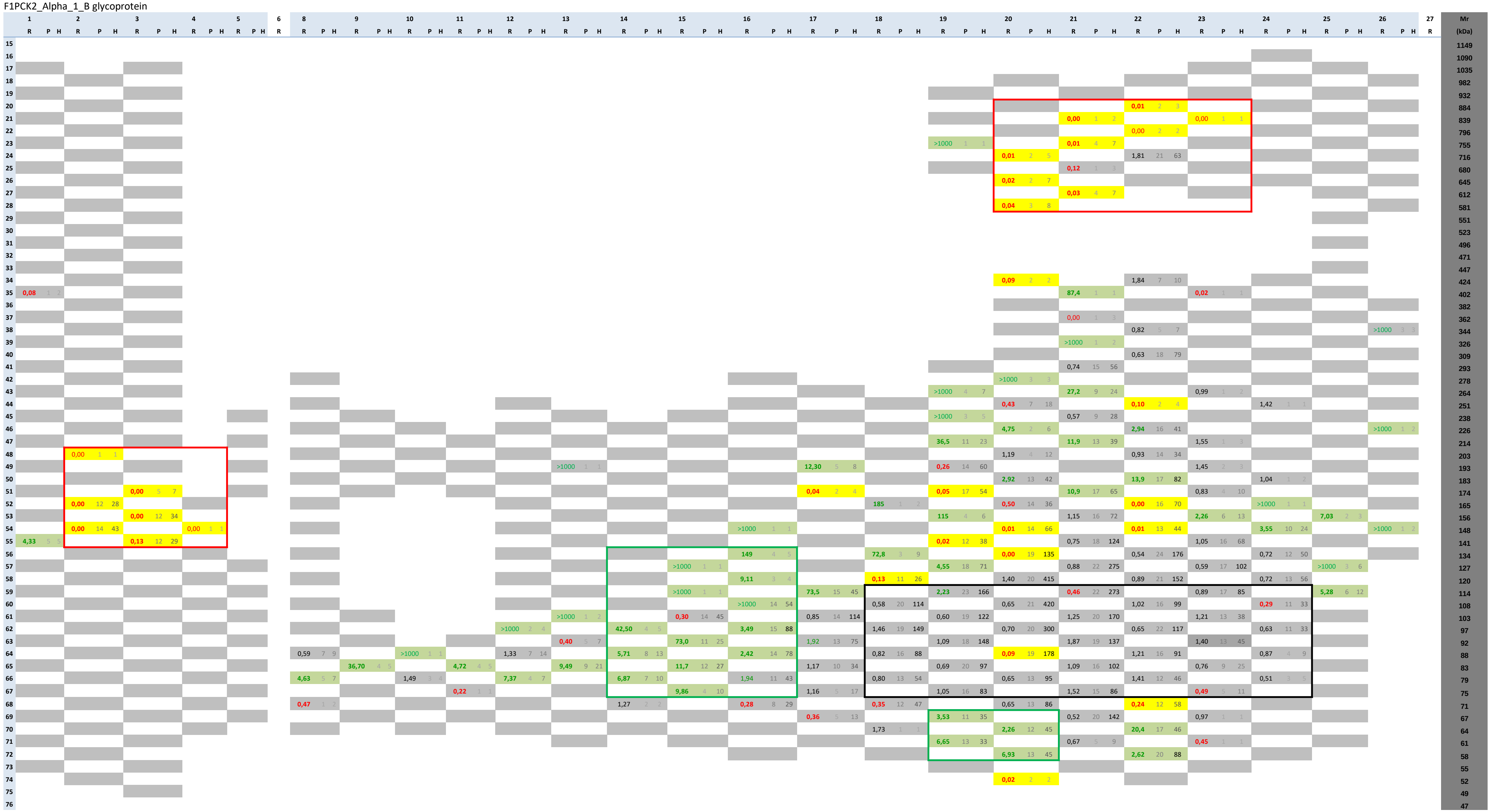
	0			1			2			3			4			5		
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H
31																		
32																		
33																		
34							1000	1	1									
35				131,1	1	1												
36							27,2	2	3									
37				344,6	1	1				54,8	1	1						
38							97,7	2	4									
39				1000	1	1				110,0	1	2						
40							108,1	2	3									
41																		
42							25,4	1	1									
43																		
44																		
45																		
46																		
47																		
48																		
49																		
50																		
51																		
52																		
53																		
54																		
55																		
56																		

	14			15			16			17			18			19			20			21			22			23			24			25			26			27			Mr
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	(kDa)
31																																											496
32																																											471
33																																											447
34																																											424
35																																											402
36																																											382
37																																											362
38																																											344
39																																											326
40																																											309
41																																											293
42																																											278
43																													1000	1	1													264
44																			57,2	1	1										17,4	2	3										251
45																						1000	1	1				1000	1	1													238
46													1000	1	1				1000	3	6				1000	1	2				1000	1	1				1000	1	1				226
47				1000	1	1										1000	1	1				1000	2	5																			214
48													1000	2	3				40,6	2	6																						203
49																1000	1	1																									193
50							1000	1	1				1000	1	1				102,9	2	4				1000	2	3				1000	1	3										183
51										1000	1	1				1000	2	5				1000	2	6																			174
52													1000	2	2				5,9	3	8				1000	1	1																165
53																						1000	2	2																			156
54																			1000	1	1																						148
55																																											141
56																																											134

The section of 2D-fractions containing serum amyloid peptides is shown. Numbers of 1D- (first column) and 2D-fractions (first line) as in Figure S3. Grey: Mass spectrometric analyzed 2D-fraction.

R: ratio calculated by Sieve® corresponding to the concentration quotient; P: peptide counts; H: hits. Green figures: Protein signals strongly higher in AM compared to NM. Green highlighting indicate chromatographic clusters. Due to its peptide sequence, the protein is small (~12 kDa). Contrarily, it was found in two high molecular weight clusters. In both clusters, the concentration of this protein are much higher in AM than in NM.

Figure S5: Distribution of α1B-glycoprotein after 2D-AEC and mass spectrometric identification of its peptides as example of a protein with several proteoforms with different degrees and direction of alteration under AS



F1PCK2_Alpha_1_B glycoprotein

	1	2	3	4	5	6	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	Mr
	R P H	R P H	R P H	R P H	R P H	R	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R P H	R	(kDa)
15																											1149
16																											1090
17																											1035
18																											982
19																											932
20																					0,01 2 3						884
21																				0,00 1 2		0,00 1 1					839
22																					0,00 2 2						796
23																		>1000 1 1		0,01 4 7							755
24																			0,01 2 5		1,81 21 63						716
25																				0,12 1 3							680
26																			0,02 2 7								645
27																				0,03 4 7							612
28																			0,04 3 8								581
29																											551
30																											523
31																											496
32																											471
33																											447
34																			0,09 2 2		1,84 7 10						424
35	0,08 1 2																			87,4 1 1		0,02 1 1					402
36																											382
37																				0,00 1 3							362
38																					0,82 5 7				>1000 3 3		344
39																				>1000 1 2							326
40																					0,63 18 79						309
41																				0,74 15 56							293
42																			>1000 3 3								278
43																		>1000 4 7		27,2 9 24		0,99 1 2					264
44																			0,43 7 18		0,10 2 4		1,42 1 1				251
45																		>1000 3 5		0,57 9 28							238
46																			4,75 2 6		2,94 16 41				>1000 1 2		226
47																		36,5 11 23		11,9 13 39		1,55 1 3					214
48		0,00 1 1																	1,19 4 12		0,93 14 34						203
49												>1000 1 1				12,30 5 8		0,26 14 60				1,45 2 3					193
50																			2,92 13 42		13,9 17 82		1,04 1 2				183
51			0,00 5 7													0,04 2 4		0,05 17 54		10,9 17 65		0,83 4 10					174
52		0,00 12 28															185 1 2		0,50 14 36		0,00 16 70		>1000 1 1				165
53			0,00 12 34															115 4 6		1,15 16 72		2,26 6 13		7,03 2 3			156
54		0,00 14 43		0,00 1 1											>1000 1 1				0,01 14 66		0,01 13 44		3,55 10 24		>1000 1 2		148
55	4,33 5 5		0,13 12 29															0,02 12 38		0,75 18 124		1,05 16 68					141
56															149 4 5		72,8 3 9		0,00 19 135		0,54 24 176		0,72 12 50				134
57														>1000 1 1				4,55 18 71		0,88 22 275		0,59 17 102		>1000 3 6			127
58															9,11 3 4		0,13 11 26		1,40 20 415		0,89 21 152		0,72 13 56				120
59														>1000 1 1		73,5 15 45		2,23 23 166		0,46 22 273		0,89 17 85		5,28 6 12			114
60															>1000 14 54		0,58 20 114		0,65 21 420		1,02 16 99		0,29 11 33				108
61												>1000 1 2		0,30 14 45		0,85 14 114		0,60 19 122		1,25 20 170		1,21 13 38					103
62											>1000 2 4		42,50 4 5		3,49 15 88		1,46 19 149		0,70 20 300		0,65 22 117		0,63 11 33				97
63												0,40 5 7		73,0 11 25		1,92 13 75		1,09 18 148		1,87 19 137		1,40 13 45					92
64							0,59 7 9		>1000 1 1		1,33 7 14		5,71 8 13		2,42 14 78		0,82 16 88		0,09 19 178		1,21 16 91		0,87 4 9				88
65								36,70 4 5		4,72 4 5		9,49 9 21		11,7 12 27		1,17 10 34		0,69 20 97		1,09 16 102		0,76 9 25					83
66							4,63 5 7		1,49 3 4		7,37 4 7		6,87 7 10		1,94 11 43		0,80 13 54		0,65 13 95		1,41 12 46		0,51 3 5				79
67										0,22 1 1				9,86 4 10		1,16 5 17		1,05 16 83		1,52 15 86		0,49 5 11					75
68							0,47 1 2						1,27 2 2		0,28 8 29		0,35 12 47		0,65 13 86		0,24 12 58						71
69																0,36 5 13		3,53 11 35		0,52 20 142		0,97 1 1					67
70																	1,73 1 1		2,26 12 45		20,4 17 46						64
71																		6,65 13 33		0,67 5 9		0,45 1 1					61
72																			6,93 13 45		2,62 20 88						58
73																											55
74																			0,02 2 2								52
75																											49
76																											47

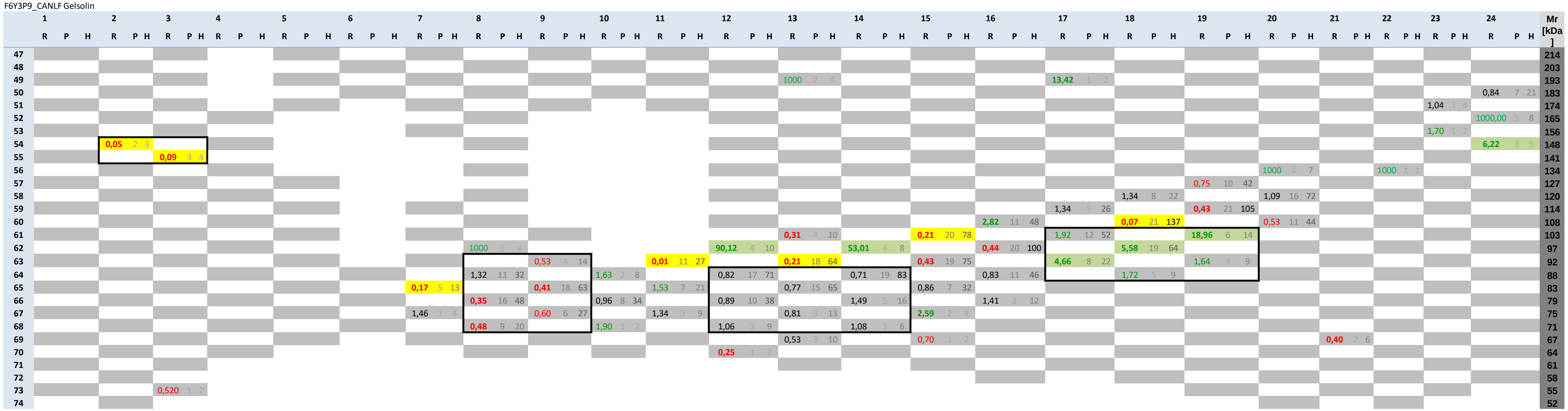
The section of 2D-fractions containing α1B-glycoprotein peptides is shown. Numbers of 1D- (first column) and 2D-fractions (first line) as in Figure S3. Grey: Mass spectrometric analyzed 2D-fraction. Frames illustrate chromatographic clusters.

R: ratio calculated by Sieve® corresponding to the concentration quotient; P: peptide counts; H: hits. Green figures: Protein signals strongly higher in AM compared to NM. Green highlighting: chromatographic cluster with higher concentrations in AM.

Red figures: Protein signals strongly lower in AM compared to NM. Yellow highlighting: chromatographic cluster with lower concentrations in AM.
Black figures: Protein signals are similar in AM and NM, i.e. not altered under disease.

Figure S6:

Distribution of gelsolin after 2D-AEC and mass spectrometric identification of its peptides as example of a second protein with several proteoforms with different degrees and direction of alteration under AS

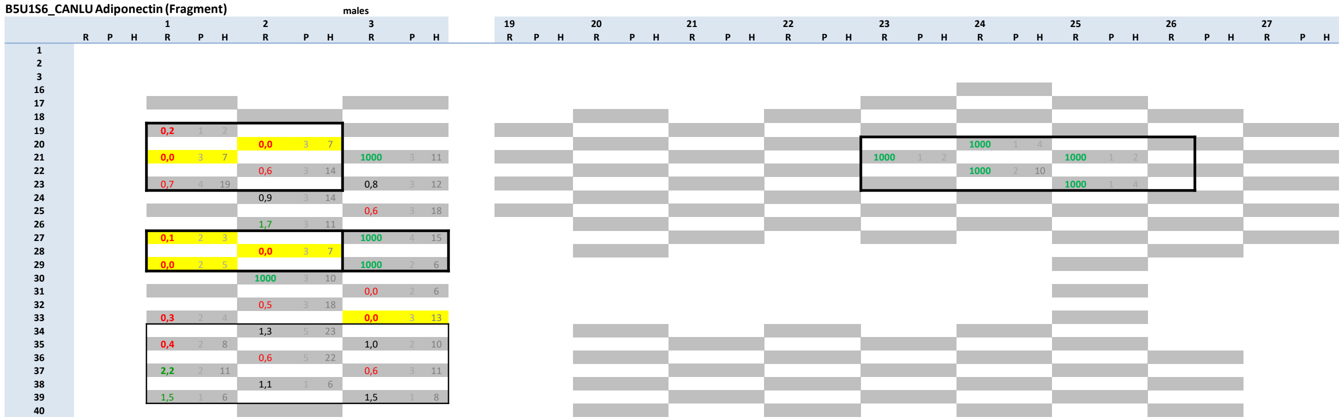


F6Y3P9_CANLF Gelsolin

	1			2			3			4			5			6			7			8			9			10			11			12			13			14			15			16			17			18			19			20			21			22			23			24			Mr [kDa]
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	
47																																																																									214
48																																																																									203
49																																					1000	2	4										13,42	1	2																							193
50																																																																							0,84	7	21	183
51																																																																		1,04	3	4				174
52																																																																						1000,00	5	8	165
53																																																																		1,70	1	2				156
54				0,05	2	3																																																																	6,22	3	5	148
55							0,09	3	4																																																																141
56																																																									1000	4	7				1000	1	1							134
57																																																							0,75	10	42																127
58																																																			1,34	8	22				1,09	16	72													120
59																																																	1,34	5	26				0,43	21	105																	114
60																																														2,82	11	48				0,07	21	137				0,53	11	44													108
61																																					0,31	4	10				0,21	20	78				1,92	12	52				18,96	6	14																103
62																						1000	1	4										90,12	4	10				53,01	4	8				0,44	20	100				5,58	19	64																			97
63																									0,53	4	14				0,01	11	27				0,21	18	64				0,43	19	75				4,66	8	22				1,64	4	9																92
64																						1,32	11	32				1,63	2	8				0,82	17	71				0,71	19	83				0,83	11	46				1,72	5	9																			88
65																			0,17	5	13				0,41	18	63				1,53	7	21				0,77	15	65				0,86	7	32																												83
66																						0,35	16	48				0,96	8	34				0,89	10	38				1,49	5	16				1,41	3	12																									79
67																			1,46	1	4				0,60	6	27				1,34	3	9				0,81	3	13				2,59	2	4																												75
68																						0,48	9	20				1,90	1	2				1,06	3	9				1,08	1	6																															71
69																																					0,53	3	10				0,70	1	2																			0,40	2	6										67
70																																		0,25	1	2																																							64
71																																																																										61
72																																																																										58
73							0,520	1	2																																																																		55
74																																																																										52

For explanation, cf. Legend to Figure S5.

Figure S7:



B5U1S6_CANLU Adiponectin (Fragment)

males

				1			2			3		
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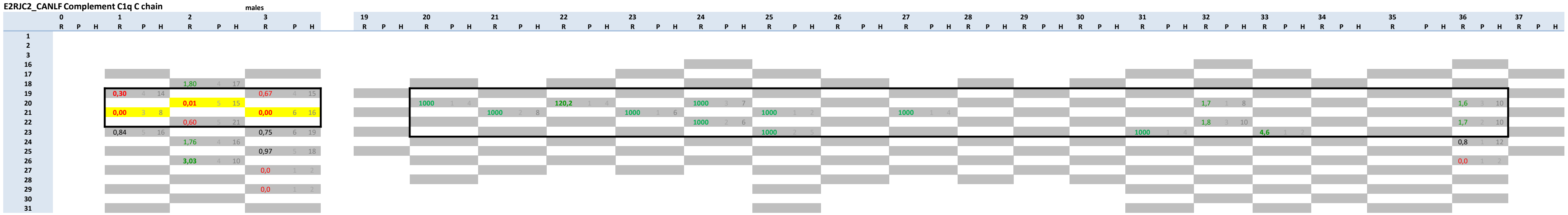
1
2
3
16
17
18
19				0,2	1	2
20							0,0	3	7
21				0,0	3	7				1000	3	11
22							0,6	3	14
23				0,7	4	19				0,8	3	12
24							0,9	3	14
25										0,6	3	18
26							1,7	3	11
27				0,1	2	3				1000	4	15
28							0,0	3	7
29				0,0	2	5				1000	2	6
30							1000	3	10
31										0,0	2	6
32							0,5	3	18
33				0,3	2	4				0,0	3	13
34							1,3	5	23
35				0,4	2	8				1,0	2	10
36							0,6	5	22
37				2,2	2	11				0,6	3	11
38							1,1	1	6
39				1,5	1	6				1,5	1	8
40

	19			20			21			22			23			24			25			26			27		
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H
1
2
3
16
17
18
19
20																1000	1	4
21													1000	1	2				1000	1	2
22																1000	2	10
23																			1000	1	4
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40

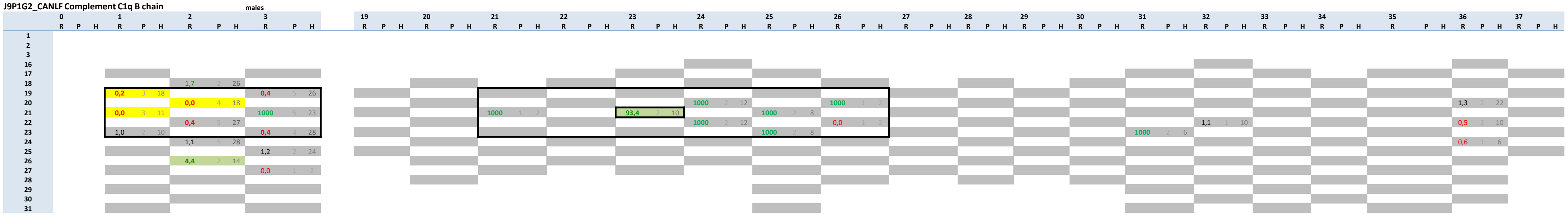


E2RJC2_CANLF Complement C1q C chain

males

	0			1			2			3		
	R	P	H	R	P	H	R	P	H	R	P	H
1
2
3
16
17
18							1,80	4	17
19				0,30	4	14				0,67	4	15
20							0,01	5	15
21				0,00	3	8				0,00	6	16
22							0,60	5	21
23				0,84	5	16				0,75	6	19
24							1,76	4	16
25										0,97	5	18
26							3,03	4	10
27										0,0	1	2
28
29										0,0	1	2
30
31

	19			20			21			22			23			24			25			26			27			28			29			30			31			32			33			34			35			36			37		
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H
1
2
3
16
17
18
19
20				1000	1	4				120,2	1	4				1000	3	7																						1,7	1	8										1,6	3	10
21							1000	2	8				1000	1	6				1000	1	2				1000	1	4
22																1000	2	6																						1,8	3	10										1,7	2	10
23																			1000	2	5																1000	1	4				4,6	1	2
24																																																				0,8	1	12
25
26																																																				0,0	1	2
27
28
29
30
31

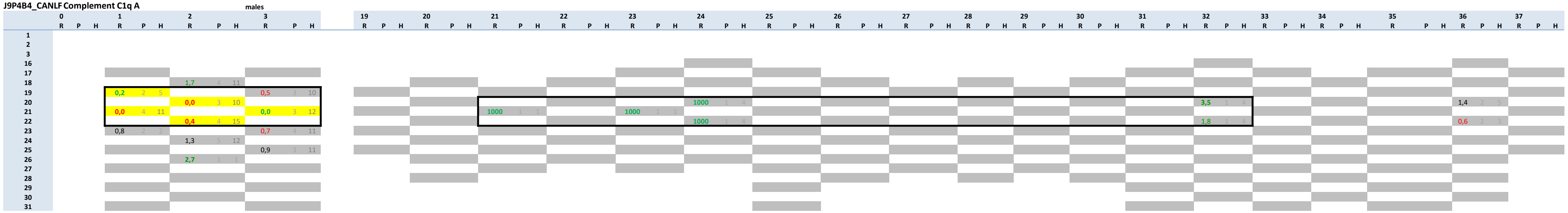


J9P1G2_CANLF Complement C1q B chain

males

	0			1			2			3		
	R	P	H	R	P	H	R	P	H	R	P	H
1
2
3
16
17
18							1,7	2	26
19				0,2	3	18				0,4	5	26
20							0,0	4	18
21				0,0	3	11				1000	5	23
22							0,4	5	27
23				1,0	2	10				0,4	4	28
24							1,1	5	28
25										1,2	2	24
26							4,4	2	14
27										0,0	1	2
28
29
30
31

	19			20			21			22			23			24			25			26			27			28			29			30			31			32			33			34			35			36			37		
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H
1
2
3
16
17
18
19
20																1000	2	12				1000	1	2																												1,3	2	22
21							1000	1	2				93,4	2	10				1000	2	8
22																1000	2	12				0,0	1	2																1,1	1	10										0,5	2	10
23																			1000	2	8																1000	2	6
24																																																				0,6	1	6
25
26
27
28
29
30
31



J9P4B4_CANLF Complement C1q A

males

	0			1			2			3		
	R	P	H	R	P	H	R	P	H	R	P	H
1
2
3
16
17
18							1,7	4	11
19				0,2	2	5				0,5	3	10
20							0,0	3	10
21				0,0	4	11				0,0	3	12
22							0,4	4	15
23				0,8	2	2				0,7	4	11
24							1,3	5	12
25										0,9	3	11
26							2,7	1	1
27
28
29
30
31

	19			20			21			22			23			24			25			26			27			28			29			30			31			32			33			34			35			36			37		
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H
1
2
3
16
17
18
19
20																1000	1	4																						3,5	1	4										1,4	2	5
21							1000	1	1				1000	1	1
22																1000	1	4																						1,8	1	4										0,6	2	3
23
24
25
26
27
28
29
30
31

Figure S7:

Distribution of BM candidates adiponectin and the complement component C1q after 2D-AEC and mass spectrometric comparison of their peptides in AM to NM

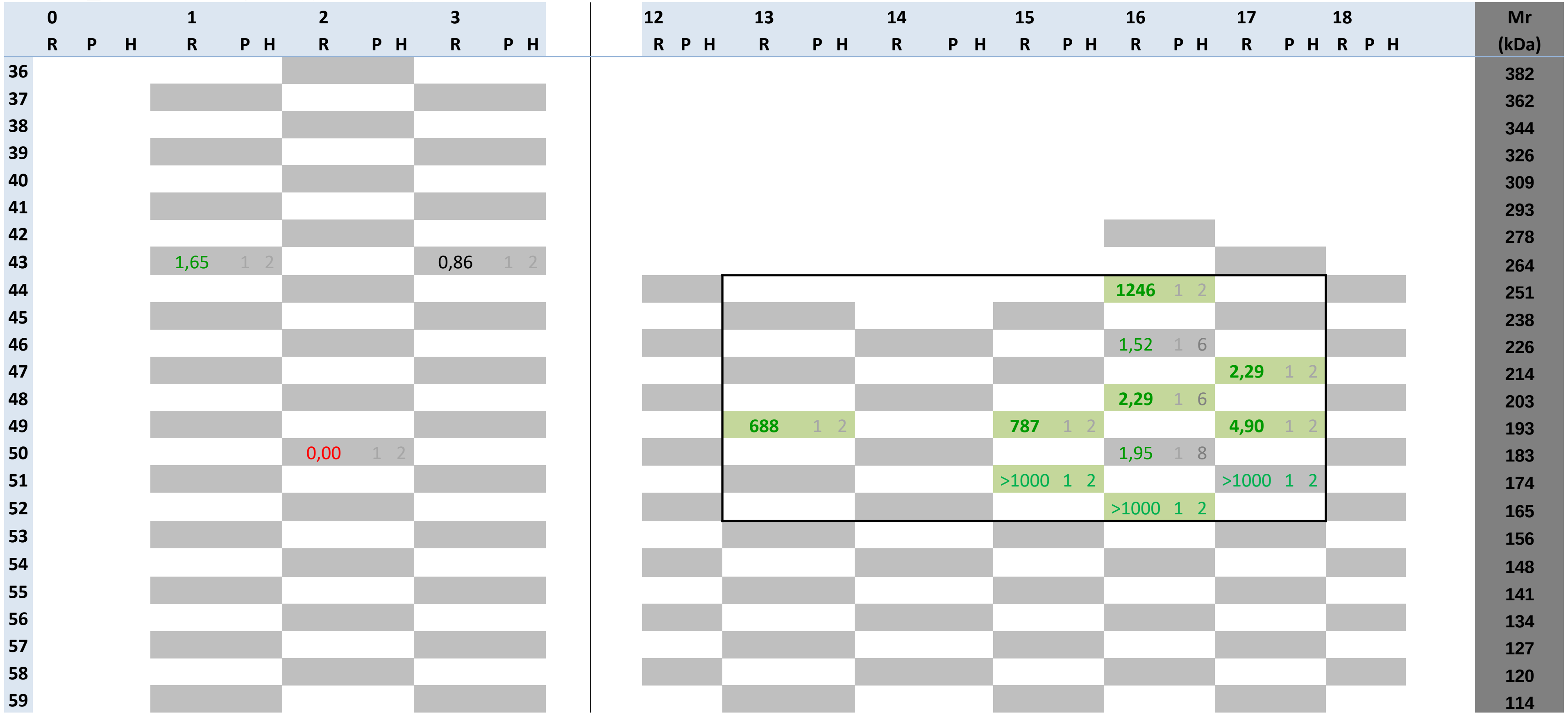
The section of 2D-fractions containing peptides from adiponectin and the tree chains from C1q are shown as indicated.
Numbers of 1D- (first column) and 2D-fractions (first line) as in Figure S3. Grey: Mass spectrometric analyzed 2D-fraction. Frames illustrate chromatographic clusters. For further explanation, cf. Legend to Figure S5.

These protein chains showed at least two proteoforms with different degrees and direction of alteration under AS. The clusters lower under AS of both proteins were found in similar sub-fraction as do the clusters higher under AS.

Figure S8:

Distribution of the BM candidate ColXIII after 2D-AEC and mass spectrometric comparison of its peptides in AM to NM

F1PJH3_CANLF Collagen type XIII alpha 1 chain



	0			1			2			3			12			13			14			15			16			17			18			Mr (kDa)
	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	
36																																		382
37																																		362
38																																		344
39																																		326
40																																		309
41																																		293
42																																		278
43				1,65	1	2				0,86	1	2																						264
44																									1246	1	2							251
45																																		238
46																									1,52	1	6							226
47																												2,29	1	2				214
48																									2,29	1	6							203
49																688	1	2				787	1	2				4,90	1	2				193
50							0,00	1	2																1,95	1	8							183
51																						>1000	1	2				>1000	1	2				174
52																									>1000	1	2							165
53																																		156
54																																		148
55																																		141
56																																		134
57																																		127
58																																		120
59																																		114

The section of 2D-fractions containing peptides from ColXIII is shown. For further explanation, cf. Figure S5.
This protein showed a singular cluster higher in AM than NM.

Figure S9

Entire concentrations biomarker candidates in patients (set 1 and set 2) in comparison to controls

Set 1: less severe, intermediate, and severe show data from patients with X-linked AS of the three severity groups (cf. main text)

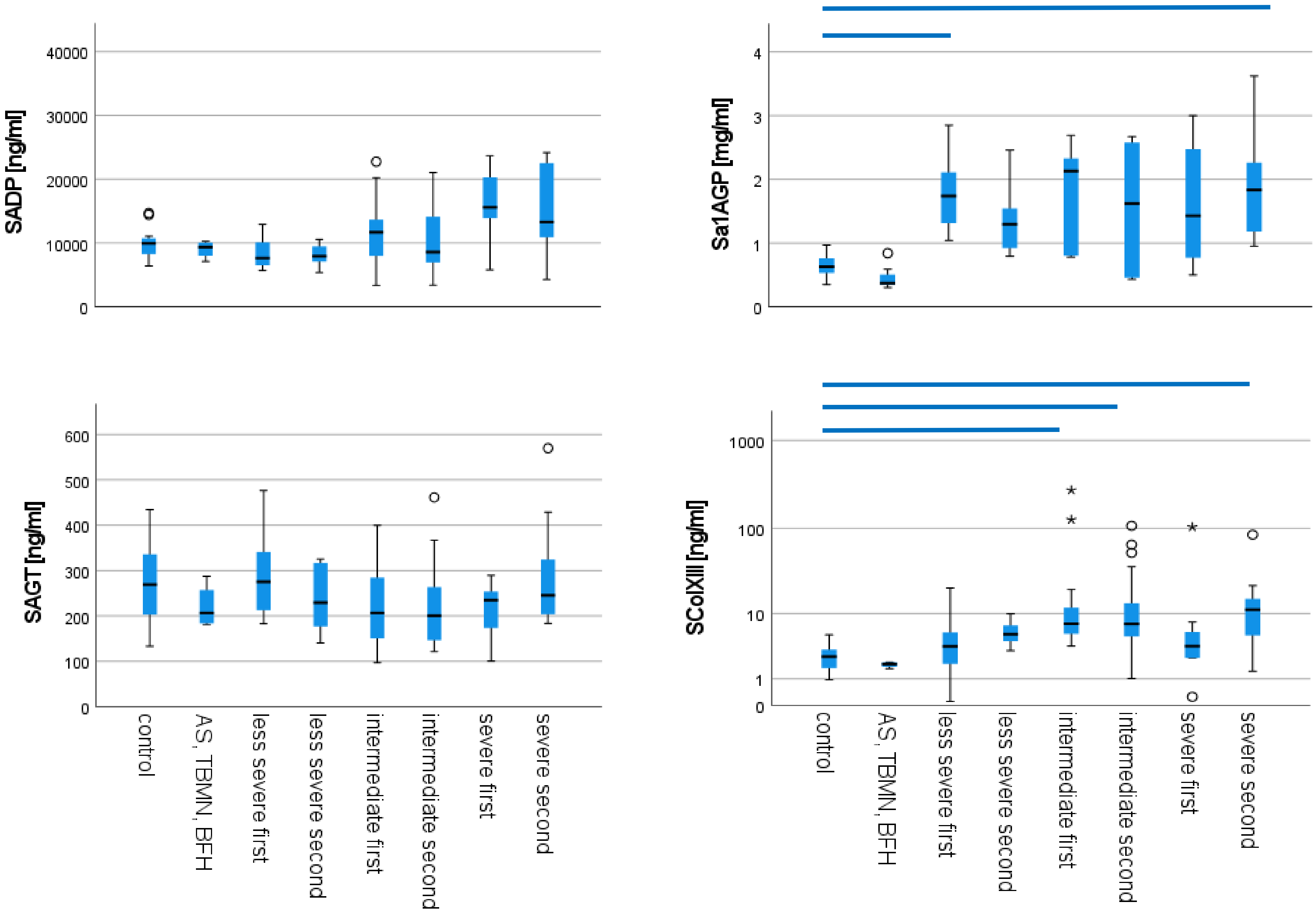
Set 2: AS: autosomal or no genetic information; TBMN: thin basement membrane nephropathy; BFH: benign familiar hematuria.

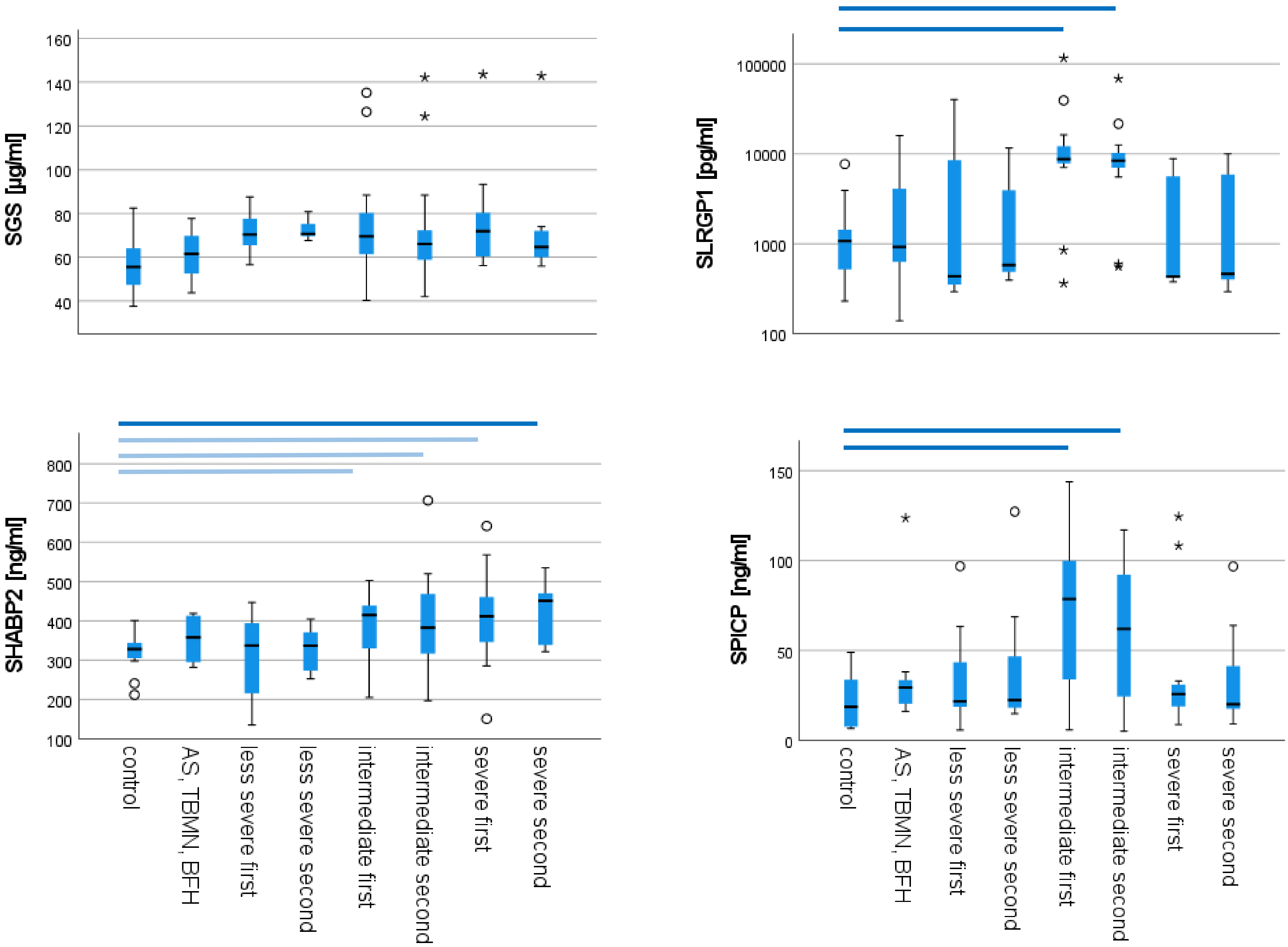
First series: biomarker concentrations in **serum** (S)
Second series: biomarker concentrations in **urine** (U)

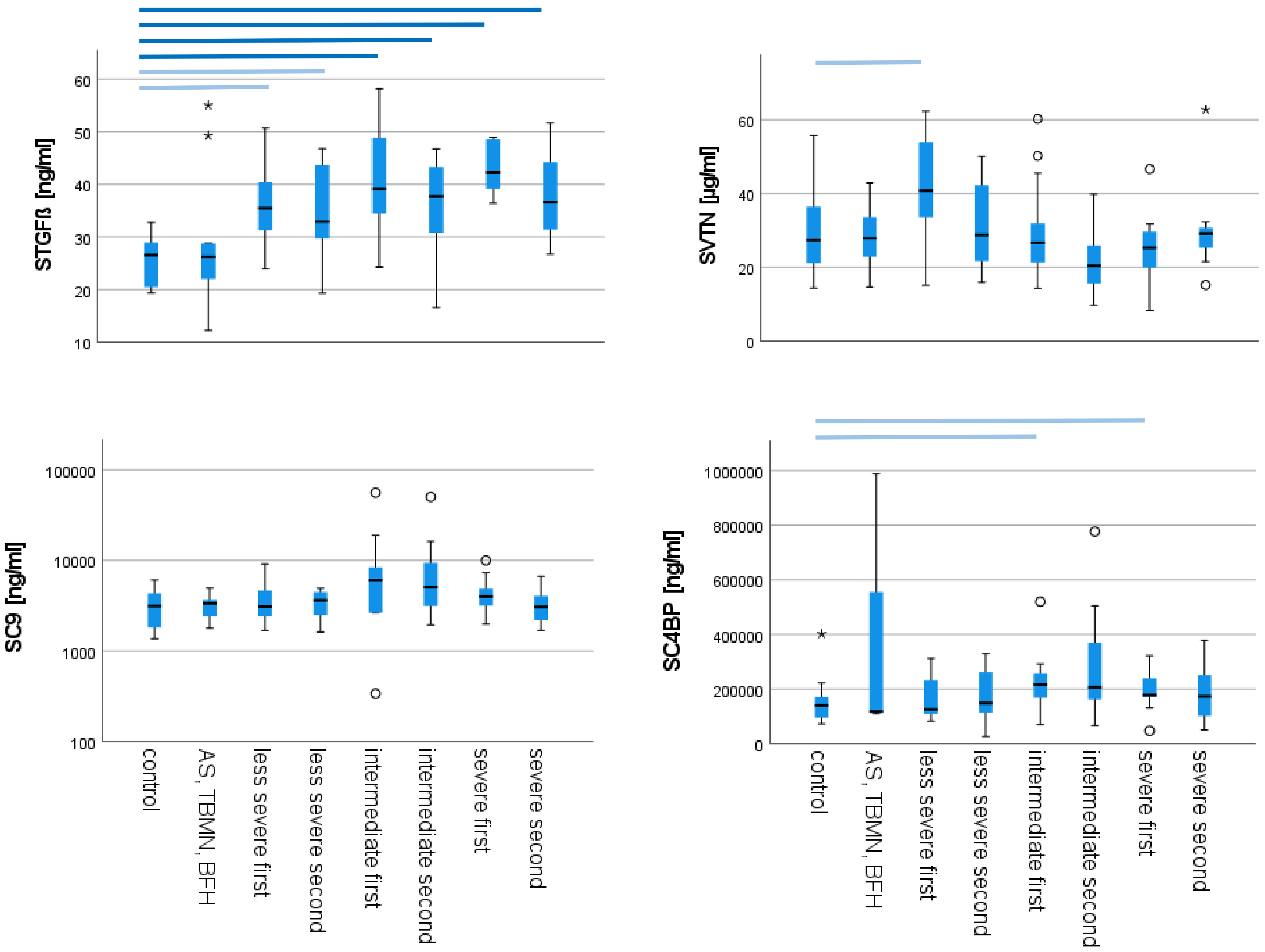
Abbreviations of biomarker proteins: cf. main text

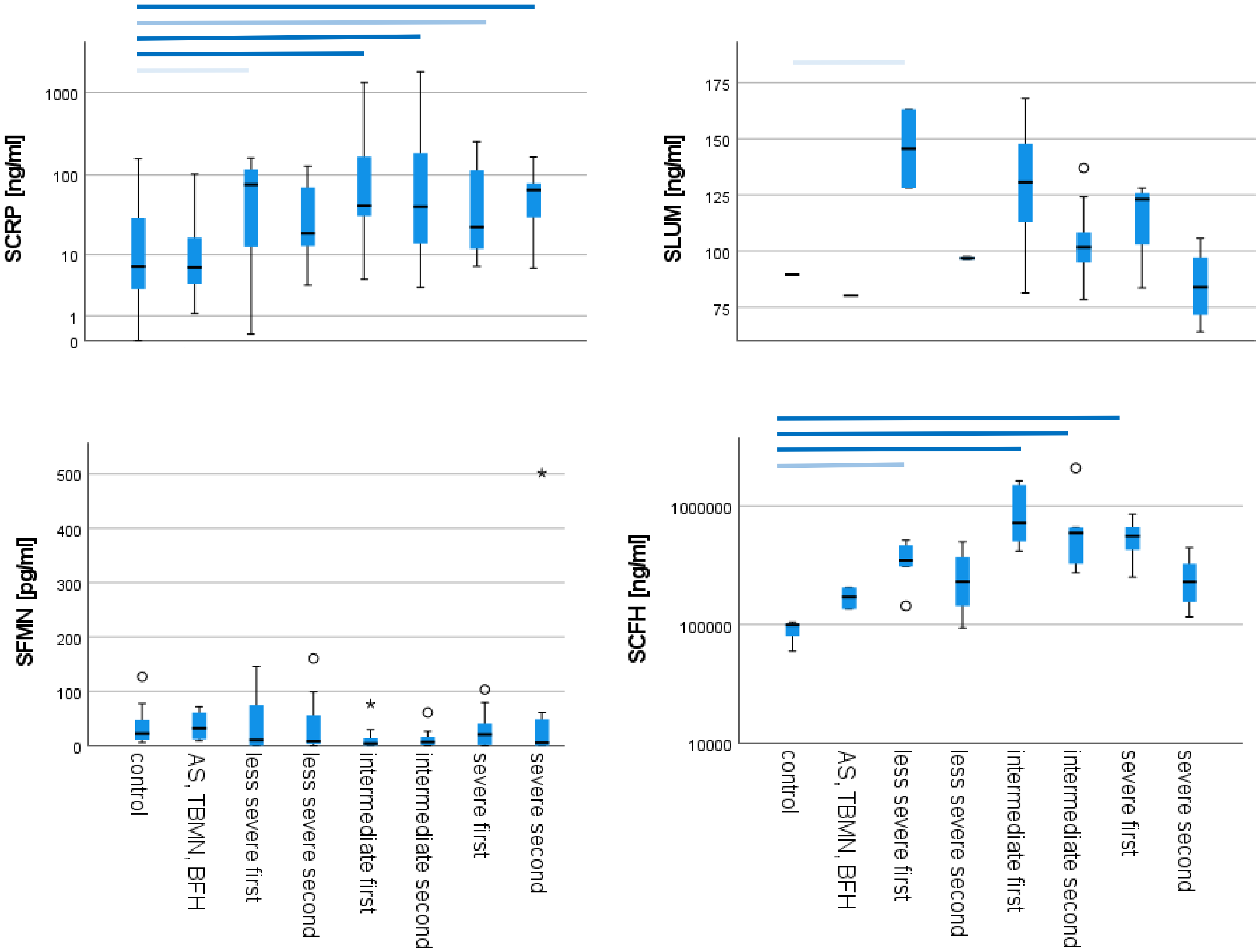
▬ $p < 0.01$
▬ $p < 0.05$
▬ $0.05 < p < 0.10$

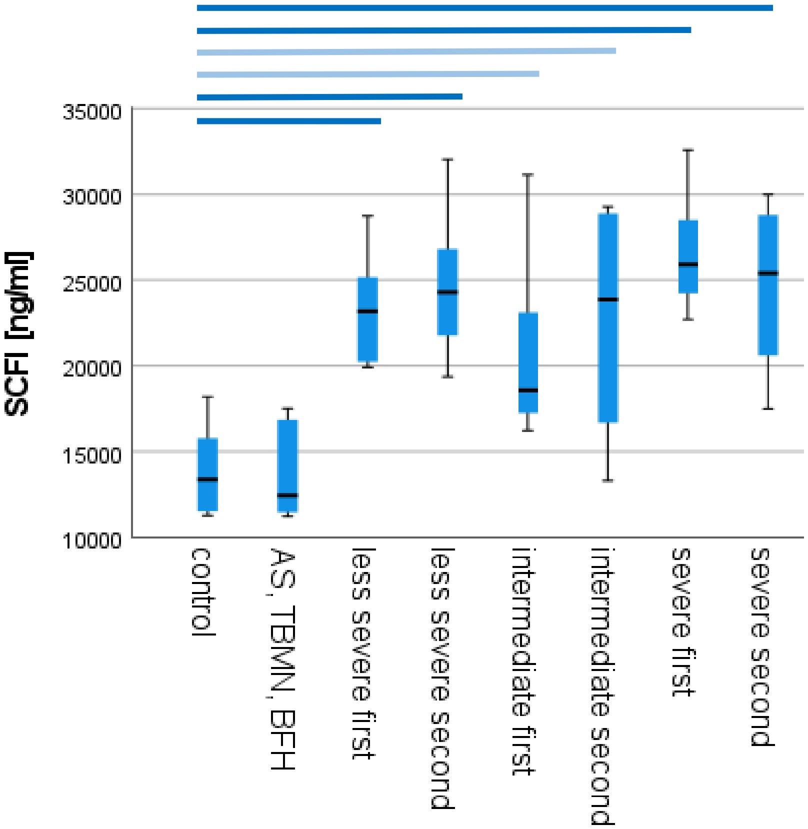
Serum

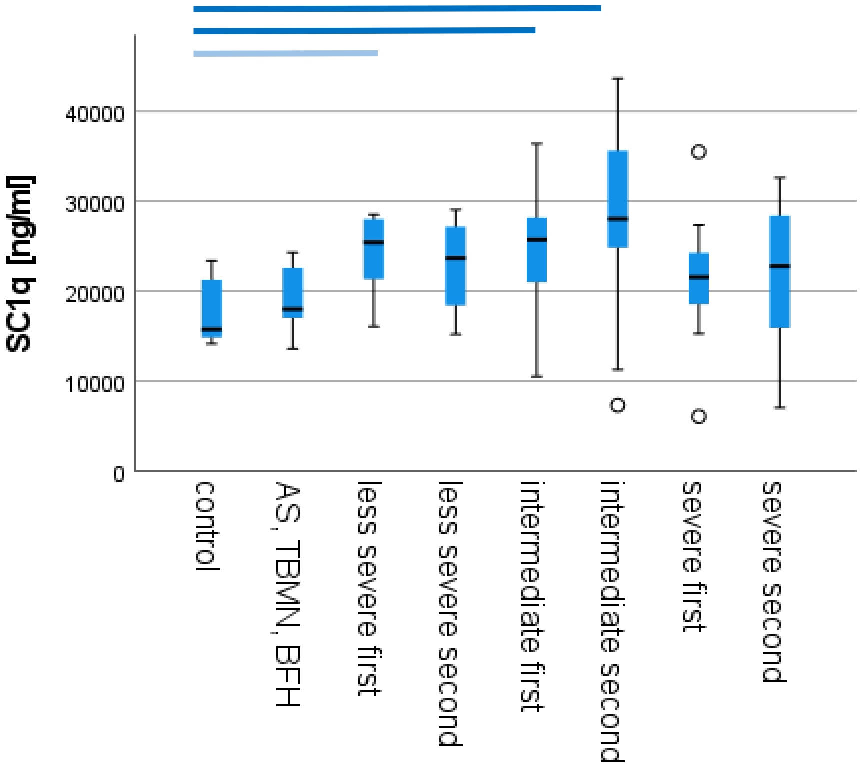

SADP [ng/ml]
40000
30000
20000
10000
0
Sa1AGP [mg/ml]
4
3
2
1
0
SAGT [ng/ml]
600
500
400
300
200
100
0
SColXIII [ng/ml]
1000
100
10
1
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second


SGS [µg/ml]
160
140
120
100
80
60
40
SLRGP1 [pg/ml]
100000
10000
1000
100
SHABP2 [ng/ml]
800
700
600
500
400
300
200
100
SPICP [ng/ml]
150
100
50
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second

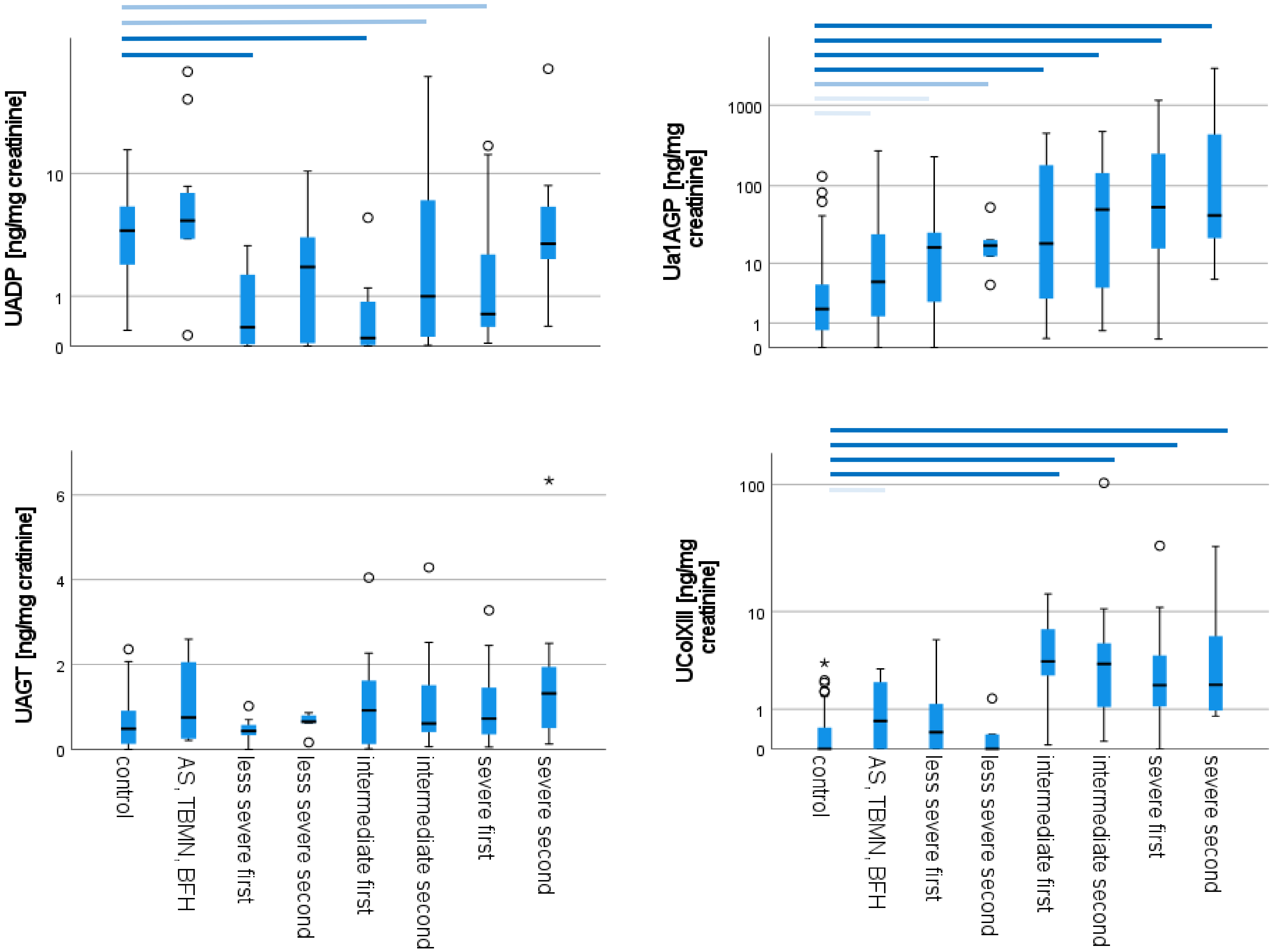

STGFß [ng/ml]
60
50
40
30
20
10
SVTN [µg/ml]
60
40
20
0
SC9 [ng/ml]
100000
10000
1000
100
SC4BP [ng/ml]
1000000
800000
600000
400000
200000
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second

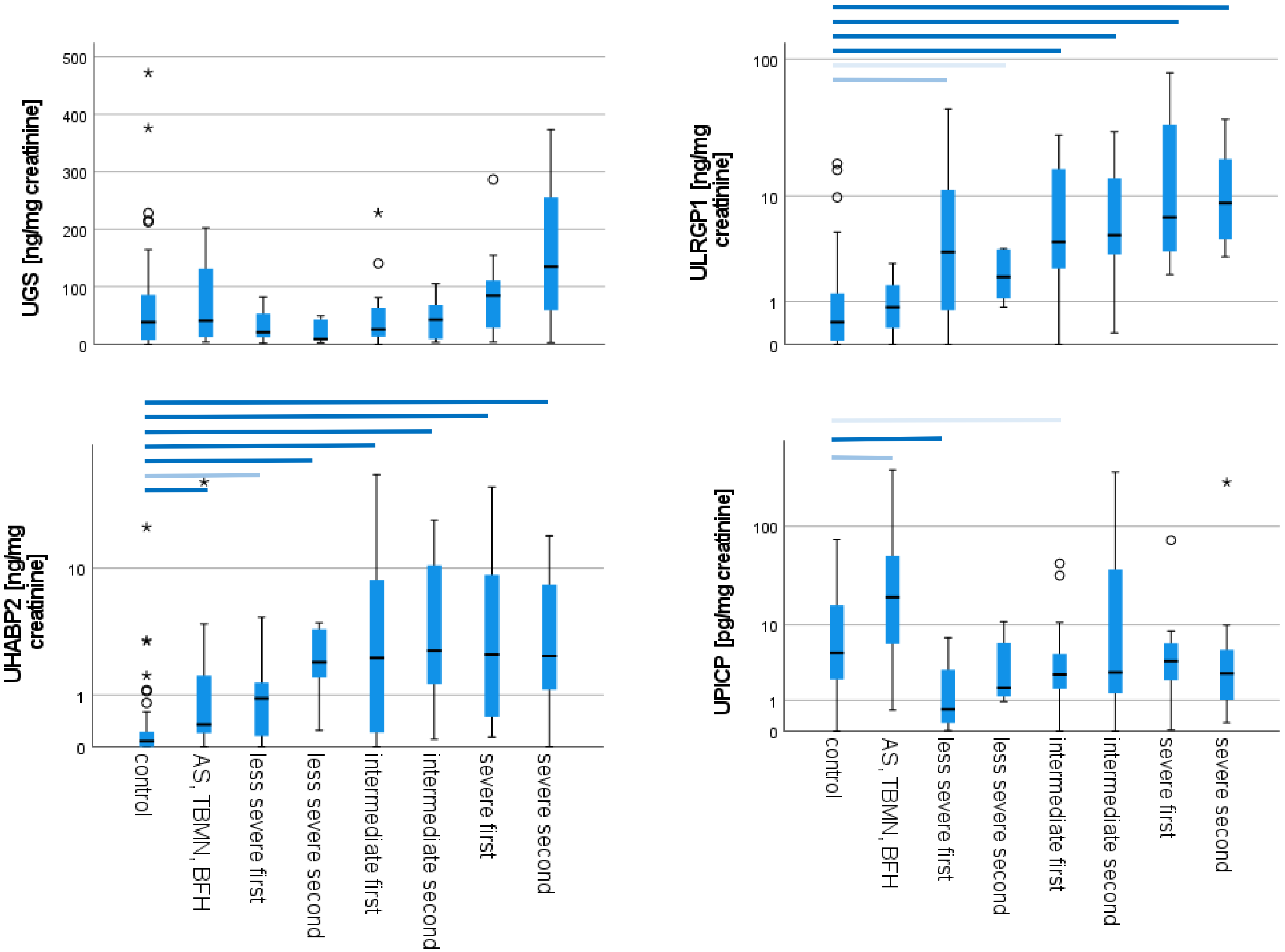

SCRP [ng/ml]
1000
100
10
1
0
SLUM [ng/ml]
175
150
125
100
75
SFMN [pg/ml]
500
400
300
200
100
0
SCFH [ng/ml]
1000000
100000
10000
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second

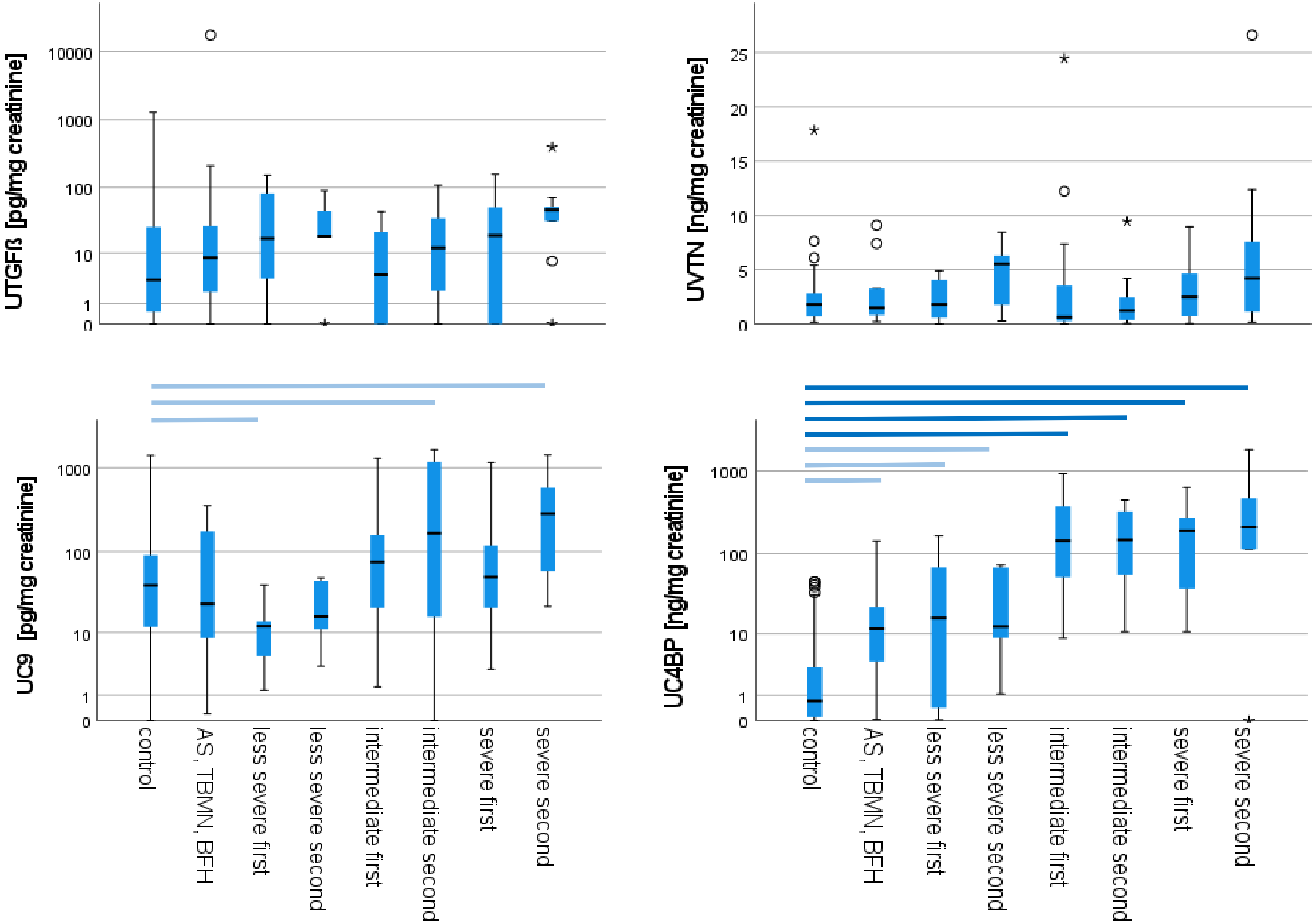

SCFI [ng/ml]
35000
30000
25000
20000
15000
10000
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second

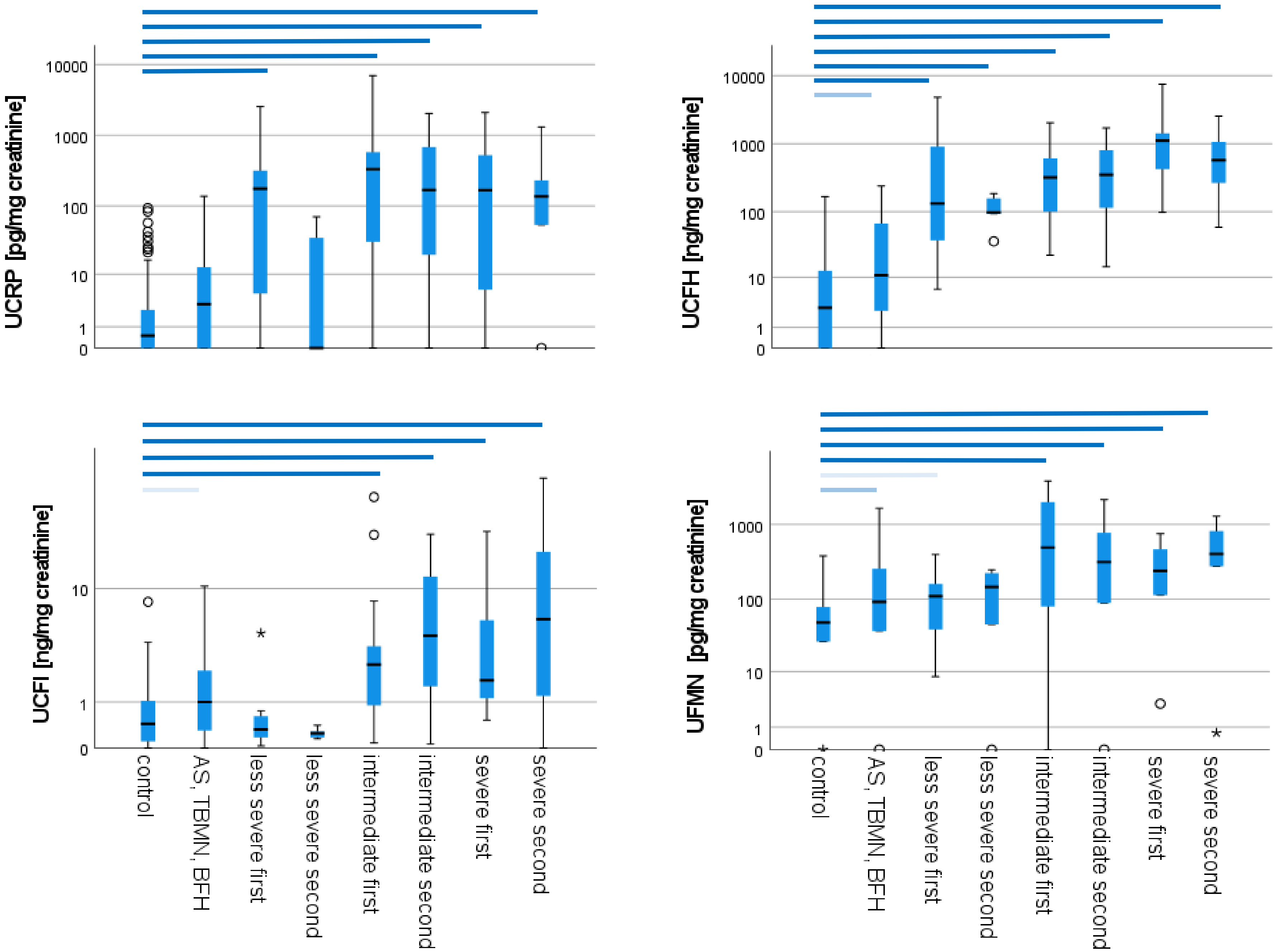

SC1q [ng/ml]
40000
30000
20000
10000
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second

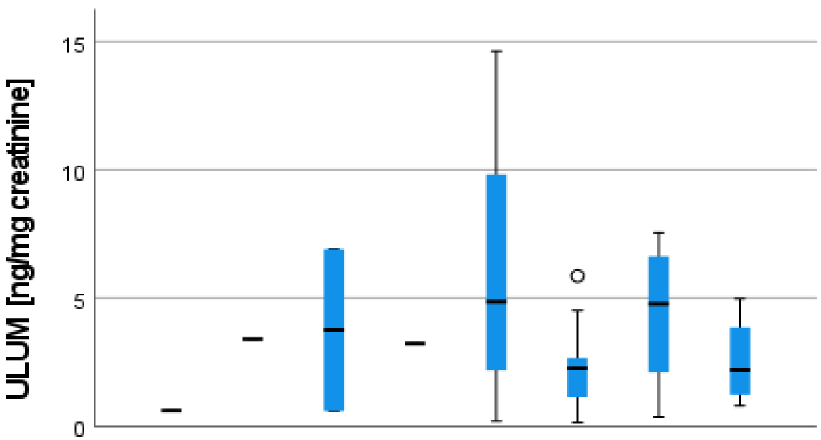
Urine

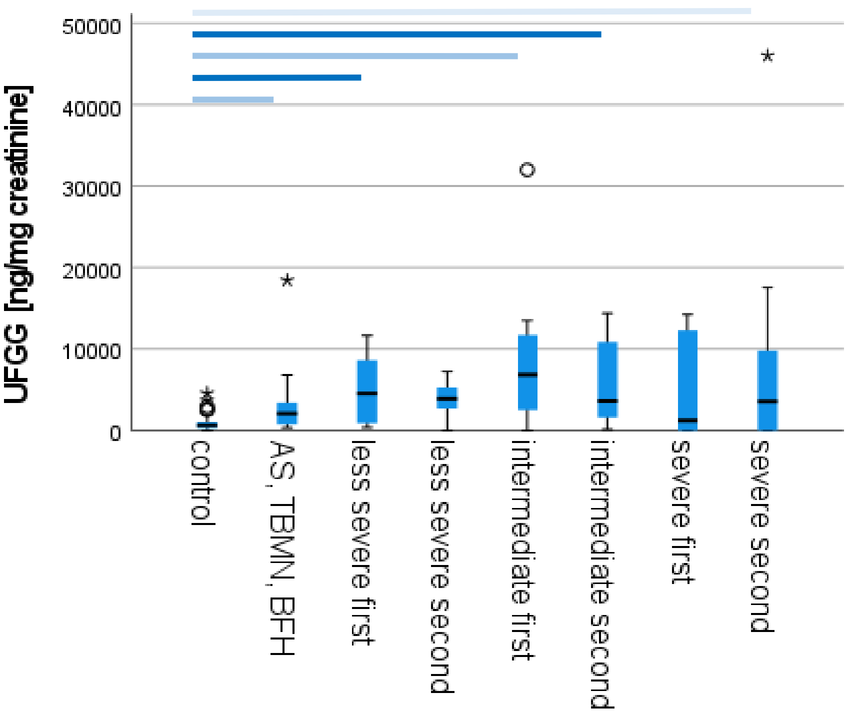

UADP [ng/mg creatinine]
10
1
0
Ua1AGP [ng/mg creatinine]
1000
100
10
1
0
UAGT [ng/mg cratinine]
6
4
2
0
UColXIII [ng/mg creatinine]
100
10
1
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second


UGS [ng/mg creatinine]
500
400
300
200
100
0
ULRGP1 [ng/mg creatinine]
100
10
1
0
UHABP2 [ng/mg creatinine]
10
1
0
UPICP [pg/mg creatinine]
100
10
1
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second


UTGFß [pg/mg creatinine]
10000
1000
100
10
1
0
UVTN [ng/mg creatinine]
25
20
15
10
5
0
UC9 [pg/mg creatinine]
1000
100
10
1
0
UC4BP [ng/mg creatinine]
1000
100
10
1
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second


UCRP [pg/mg creatinine]
10000
1000
100
10
1
0
UCFH [ng/mg creatinine]
10000
1000
100
10
1
0
UCFI [ng/mg creatinine]
10
1
0
UFMN [pg/mg creatinine]
1000
100
10
1
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second


ULUM [ng/mg creatinine]
15
10
5
0


UFGG [ng/mg creatinine]
50000
40000
30000
20000
10000
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second

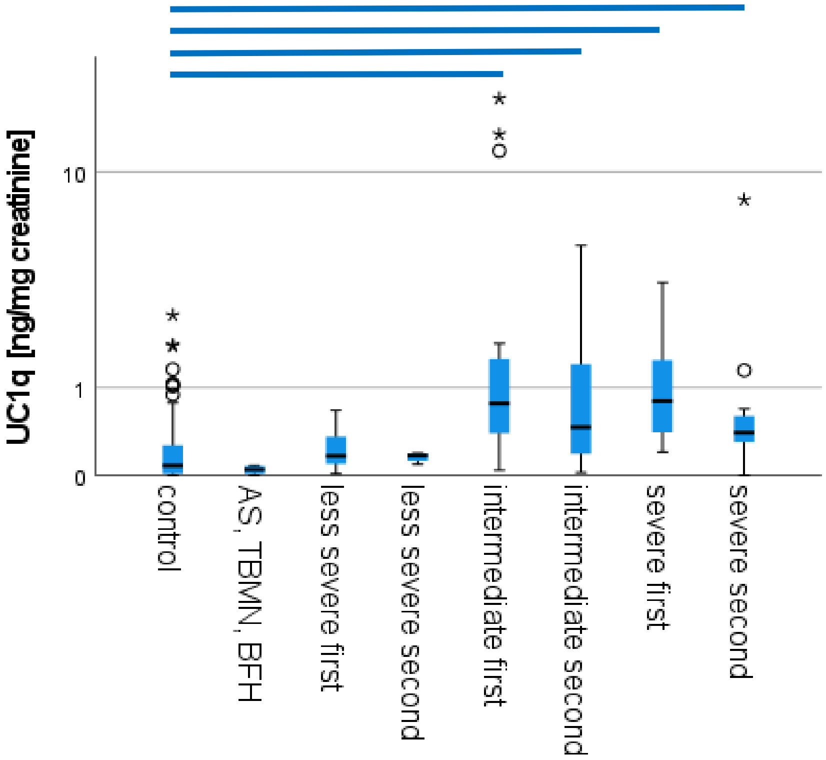

UC1q [ng/mg creatinine]
10
1
0
control
AS, TBMN, BFH
less severe first
less severe second
intermediate first
intermediate second
severe first
severe second

Figure S10: Proteoforms and PTM of albumin

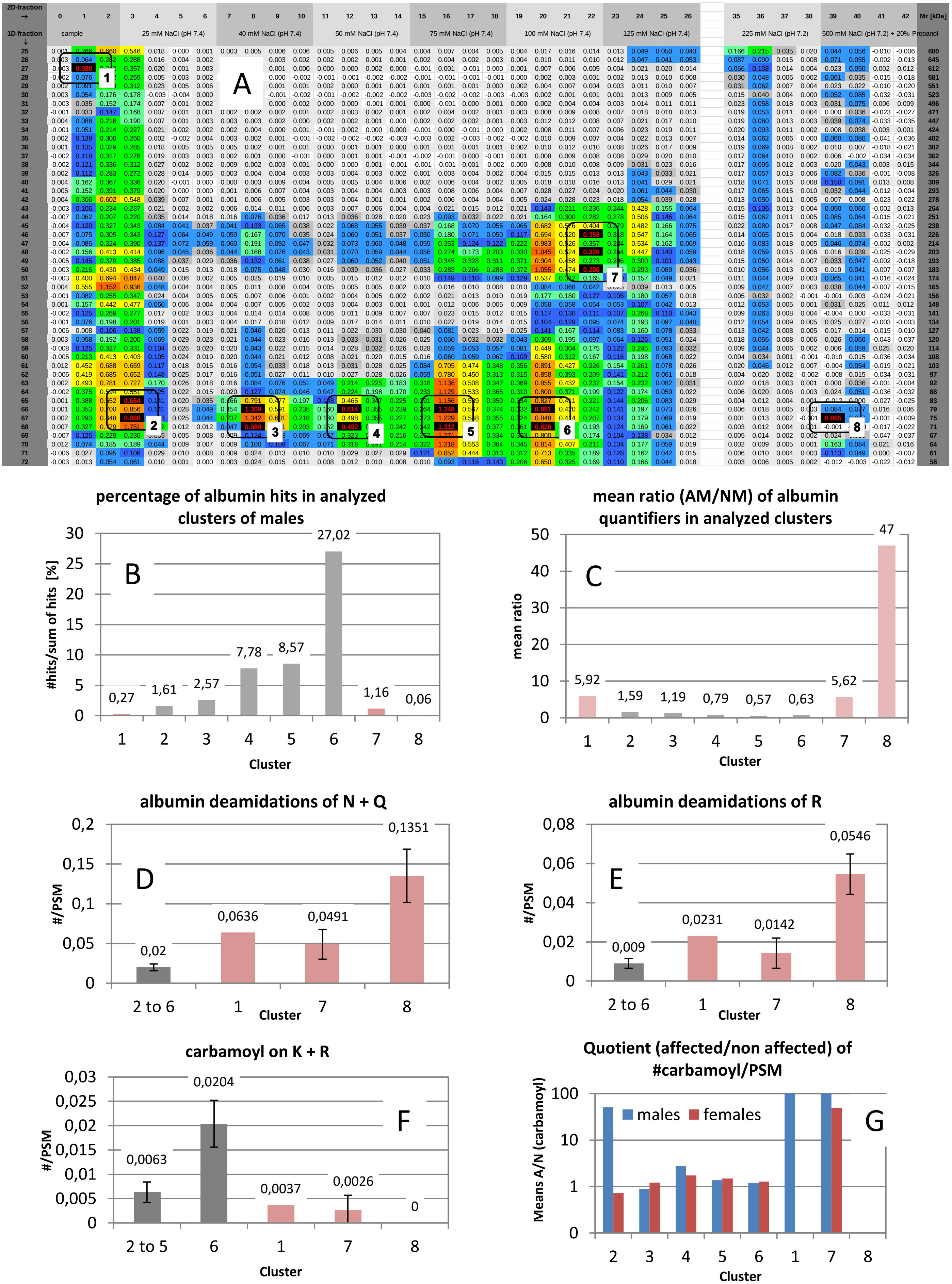
A: Global distribution of plasma protein concentrations after 2D-AEC
Example: NM. Section of sub-fractions containing eight numbered chromatographic clusters of albumin (identified after mass spectrometry). Frames indicate sub-fractions, which form a cluster. Number and color code show the total fractional protein concentration. Black highlighting indicates the sub-fractions analyzed for PTM.

B: Mass spectrometric quantifiers of albumin variants after analysis of sample from males (NM) by the Proteome discoverer®
Estimated percentage of albumin hits in each framed cluster compared to total hits of albumin in all sub-fractions. The analyzed fractions of the main clusters (2 to 6) contained ~48% of all albumin peptides of the sample.
B-F: Grey filling: albumin protein concentration is not altered in AM (ratios around 1.0, >0.5 …<2.0); red filling: protein concentration is increased in AM in comparison to NM due to the ratios calculated by Sieve® (ratios >2, cf. Fig. C).

C: Mass spectrometric comparison of the concentrations of albumin variants from AM and NM determined by Sieve©
The quantifier “ratio” indicates the quotient AM/NM of peptide signals and corresponds to the concentration quotient of albumin of homologous sub-fractions. The mean ratio was built from all sub-fractions of one cluster.
The main clusters of albumin (2 to 6) showed ratios of ~1.0. Thus, the protein concentrations of these proteoforms (clusters) are not altered under AS. Contrarily, the minor clusters 1 and 7 were found about six-fold and the cluster 8 even nearly 50-fold increased under AS.

D-G: Deamidation and carbamoylation rates of albumin proteoforms

The search for PTM ran successively using Proteome Discoverer® 1.3 (Thermo) with no more than three dynamic modifcation types per run. We considered only highly confident database matches when the sequence coverage was >40%. The following dynamic modifications of amino acids were analyzed: deamidation (N, Q, R) and carbamoylation (K, M, R). Multi reports of the related replicates were utilized.
Mean values of the modification rates, #PTM/PSM of albumin peptides were determined including the homologous sub-fractions from all NM, AM, NF, and CF.
In NM the minor clusters (1, 7, 8), which are elevated under AS, showed higher deamidation and lower carbamoylation rates than the main clusters. However, carbamoylation was significantly increased in minor clusters under AS (Fig. G).



2D-fraction →	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	35	36	37	38	39	40	41	42	Mr [kDa]
1D-fraction ↓	sample			25 mM NaCl (pH 7.4)				40 mM NaCl (pH 7.4)				50 mM NaCl (pH 7.4)				75 mM NaCl (pH 7.4)				100 mM NaCl (pH 7.4)				125 mM NaCl (pH 7.4)				225 mM NaCl (pH 7.2)				500 mM NaCl (pH 7.2) + 20% Propanol				
25	0.001	0.266	0.660	0.546	0.018	0.000	0.001	0.003	0.005	0.006	0.006	0.005	0.006	0.005	0.004	0.004	0.007	0.004	0.005	0.004	0.017	0.016	0.014	0.013	0.049	0.050	0.043	0.166	0.215	0.035	0.020	0.044	0.056	-0.010	-0.006	680
26	0.003	0.064	0.282	0.288	0.016	0.004	0.002			0.003	0.002	0.002	0.002	0.001	0.001	0.002	0.004	0.002	0.003	0.004	0.010	0.011	0.010	0.012	0.047	0.041	0.053	0.087	0.090	0.015	0.008	0.071	0.055	-0.002	-0.013	645
27	-0.003	0.080	[illegible]	0.357	0.020	0.001	0.003			0.001	0.000	0.000	0.000	0.002	0.000	-0.001	0.001	-0.001	0.000	0.001	0.007	0.006	0.005	0.004	0.021	0.020	0.014	0.066	0.108	0.014	0.004	0.023	0.050	0.002	0.012	612
28	-0.002	0.076	[illegible]	0.259	0.005	0.003	0.002			0.000	-0.002	-0.001	-0.001	-0.002	-0.002	-0.001	-0.001	-0.001	-0.001	0.000	0.002	0.003	0.001	0.002	0.013	0.010	0.008	0.030	0.048	0.006	0.002	0.061	0.035	-0.015	-0.018	581
29	0.002	0.091	[illegible]	0.312	0.023	0.005	0.006			0.001	0.001	0.002	0.000	0.001	0.001	0.001	0.001	0.001	0.000	0.002	0.004	0.007	0.004	0.003	0.011	0.010	0.007	0.031	0.062	0.007	0.004	0.023	0.022	-0.010	-0.020	551
30	0.003	0.054	0.176	0.178	-0.003	-0.004	0.000			-0.001	-0.002	-0.001	-0.002	-0.002	-0.002	-0.003	-0.002	-0.002	-0.003	-0.003	0.002	0.001	0.001	0.001	0.013	0.009	0.005	0.015	0.040	0.004	0.000	0.052	0.085	-0.032	-0.031	523
31	-0.003	0.035	0.152	0.174	0.007	0.001	0.002			0.000	0.002	0.000	0.000	-0.001	0.001	0.000	-0.001	0.000	0.001	0.000	0.002	0.004	0.004	0.003	0.014	0.011	0.011	0.023	0.058	0.018	0.003	0.031	0.075	0.006	0.009	496
32	-0.001	0.033	0.147	0.168	0.007	0.001	0.001	0.002	0.002	0.002	0.001	0.002	0.003	0.002	0.001	0.002	0.004	0.002	0.001	0.003	0.008	0.009	0.008	0.007	0.018	0.018	0.013	0.019	0.053	0.011	0.004	0.000	0.036	-0.023	-0.027	471
33	0.004	0.088	0.218	0.190	0.007	0.001	0.003	0.003	0.003	0.002	0.000	0.002	0.002	0.001	0.000	0.002	0.002	0.002	0.001	0.003	0.012	0.012	0.008	0.007	0.021	0.017	0.010	0.019	0.060	0.013	0.003	0.039	0.074	-0.033	-0.035	447
34	-0.001	0.051	0.214	0.227	0.021	0.002	0.002	0.002	0.004	0.000	0.001	-0.001	0.002	0.000	0.000	-0.001	0.000	-0.001	0.000	0.002	0.008	0.011	0.007	0.006	0.023	0.019	0.011	0.020	0.093	0.011	0.002	0.008	0.038	0.003	0.001	424
35	0.002	0.139	0.300	0.250	0.002	-0.002	0.004	0.003	0.002	0.001	-0.001	-0.002	-0.002	-0.002	-0.003	-0.003	0.002	-0.003	-0.002	-0.002	0.010	0.009	0.007	0.004	0.022	0.013	0.007	0.014	0.062	0.006	0.000	0.060	0.080	-0.041	-0.036	402
36	0.001	0.135	0.329	0.285	0.018	0.005	0.005	0.005	0.002	0.001	0.001	0.000	0.001	0.001	0.000	0.001	0.001	0.001	0.001	0.002	0.010	0.012	0.010	0.008	0.026	0.017	0.009	0.019	0.069	0.008	0.002	0.010	0.007	-0.018	-0.021	382
37	-0.002	0.118	0.317	0.278	0.019	0.003	0.003	0.002	0.001	0.000	-0.001	0.000	0.001	0.001	-0.001	-0.002	-0.001	0.000	-0.001	0.001	0.008	0.009	0.008	0.008	0.029	0.020	0.010	0.017	0.064	0.010	0.002	0.006	-0.002	-0.034	-0.034	362
38	-0.002	0.121	0.336	0.312	0.027	0.002	0.002	0.009	0.002	0.003	0.001	0.000	0.000	0.001	-0.001	-0.001	-0.001	0.001	-0.002	0.000	0.008	0.010	0.008	0.009	0.031	0.023	0.016	0.017	0.095	0.012	0.003	0.020	0.043	0.003	0.015	344
39	0.002	0.112	0.283	0.272	0.028	0.014	0.005	0.003	0.004	0.004	0.003	0.003	0.004	0.003	0.002	0.001	0.003	0.004	0.002	0.004	0.015	0.015	0.013	0.013	0.043	0.033	0.021	0.017	0.057	0.013	0.006	0.082	0.036	-0.001	-0.008	326
40	0.004	0.162	0.367	0.336	0.020	-0.001	0.000	0.000	0.003	0.009	0.004	0.005	0.005	0.004	0.006	0.002	0.006	0.004	0.002	0.005	0.018	0.018	0.016	0.013	0.041	0.029	0.021	0.018	0.071	0.016	0.008	0.150	0.091	0.013	0.008	309
41	0.005	0.152	0.391	0.379	0.020	0.000	0.000	0.001	0.006	0.007	0.004	0.003	0.004	0.004	0.003	0.003	0.008	0.006	0.004	0.007	0.028	0.027	0.024	0.020	0.061	0.044	0.030	0.017	0.065	0.015	0.010	0.032	0.044	-0.012	-0.004	293
42	0.004	0.306	0.602	0.548	0.039	0.007	0.001	0.001	0.006	0.005	0.003	0.003	0.004	0.001	0.001	0.002	0.006	0.004	0.004	0.005	0.024	0.028	0.023	0.018	0.054	0.039	0.028	0.013	0.050	0.011	0.005	0.007	0.008	-0.023	-0.022	278
43	-0.003	0.106	0.234	0.237	0.021	0.002	0.002	0.006	0.014	0.011	0.006	0.003	0.007	0.006	0.004	0.004	0.021	0.015	0.012	0.021	0.143	0.211	0.236	0.244	0.428	0.155	0.064	0.015	0.106	0.013	0.004	0.050	0.060	-0.002	0.013	264
44	-0.007	0.062	0.207	0.220	0.035	0.014	0.018	0.016	0.076	0.036	0.017	0.013	0.036	0.028	0.020	0.023	0.093	0.032	0.022	0.021	0.164	0.300	0.282	0.278	0.506	0.146	0.064	0.015	0.062	0.011	0.005	0.085	0.064	-0.015	-0.021	251
45	-0.004	0.120	0.327	0.343	0.084	0.041	0.037	0.041	0.133	0.065	0.038	0.022	0.068	0.055	0.039	0.037	0.168	0.070	0.055	0.065	0.682	0.576	0.404	0.279	0.482	0.166	0.075	0.022	0.080	0.017	0.008	0.047	0.084	-0.032	-0.025	238
46	-0.007	0.075	0.305	0.343	0.127	0.064	0.049	0.050	0.167	0.070	0.035	0.024	0.060	0.051	0.037	0.050	0.180	0.071	0.050	0.117	0.694	0.520	0.358	0.318	0.547	0.164	0.065	0.014	0.065	0.015	0.004	0.018	0.033	-0.033	-0.031	226
47	-0.004	0.085	0.324	0.390	0.137	0.072	0.059	0.060	0.191	0.092	0.047	0.032	0.073	0.060	0.048	0.055	0.253	0.124	0.122	0.222	0.983	0.526	0.357	0.284	0.534	0.162	0.069	0.016	0.083	0.018	0.005	0.046	0.074	-0.002	0.002	214
48	-0.002	0.156	0.413	0.414	0.096	0.045	0.036	0.044	0.168	0.076	0.043	0.031	0.070	0.059	0.044	0.056	0.274	0.173	0.203	0.330	1.045	0.524	0.326	0.264	0.447	0.140	0.059	0.018	0.059	0.015	0.006	0.016	0.039	-0.025	-0.029	203
49	-0.005	0.145	0.379	0.385	0.088	0.037	0.029	0.036	0.132	0.061	0.038	0.027	0.060	0.052	0.040	0.051	0.345	0.328	0.311	0.371	0.904	0.458	0.273	0.206	0.300	0.101	0.043	0.015	0.050	0.014	0.007	0.033	0.047	-0.002	-0.018	193
50	-0.003	0.215	0.430	0.434	0.049	0.015	0.013	0.018	0.075	0.048	0.030	0.016	0.039	0.036	0.027	0.033	0.283	0.266	0.288	0.372	1.055	0.474	0.286	[illegible]	0.293	0.089	0.036	0.010	0.056	0.013	0.003	0.019	0.041	-0.007	-0.007	183
51	-0.003	0.400	0.694	0.847	0.040	0.006	0.002	0.005	0.025	0.019	0.010	0.005	0.015	0.012	0.012	0.010	0.149	0.110	0.099	0.129	0.537	0.312	0.165	[illegible]	0.157	0.049	0.021	0.011	0.044	0.009	0.003	0.065	0.041	-0.016	-0.024	174
52	0.004	0.555	1.152	0.936	0.048	0.004	0.004	0.005	0.011	0.008	0.004	0.005	0.005	0.005	0.002	0.003	0.016	0.010	0.008	0.010	0.084	0.068	0.042	[illegible]	0.039	0.013	0.005	0.009	0.047	0.007	0.003	0.038	0.044	-0.007	-0.015	165
53	-0.001	0.082	0.255	0.347	0.024	0.004	0.005	0.005	0.007	0.006	0.001	0.002	0.004	0.005	0.002	0.002	0.021	0.013	0.010	0.019	0.177	0.180	0.127	0.106	0.180	0.057	0.018	0.005	0.032	0.002	-0.001	-0.001	0.003	-0.024	-0.021	156
54	0.001	0.157	0.442	0.477	0.050	0.006	0.004	0.004	0.007	0.005	0.002	0.003	0.004	0.003	0.001	0.001	0.012	0.006	0.005	0.009	0.058	0.058	0.054	0.053	0.107	0.042	0.013	0.012	0.053	0.005	0.001	0.031	0.025	0.011	0.012	148
55	-0.002	0.125	0.269	0.277	0.017	0.002	0.003	0.004	0.014	0.014	0.008	0.006	0.011	0.009	0.007	0.007	0.023	0.015	0.012	0.015	0.117	0.130	0.111	0.107	0.268	0.110	0.043	0.009	0.063	0.008	0.004	-0.004	0.000	-0.033	-0.031	141
56	-0.001	0.076	0.198	0.201	0.019	0.001	0.003	0.004	0.017	0.018	0.012	0.009	0.017	0.014	0.011	0.010	0.027	0.019	0.014	0.015	0.104	0.129	0.095	0.074	0.193	0.097	0.040	0.012	0.054	0.009	0.005	0.025	0.027	-0.003	-0.003	134
57	-0.006	0.008	0.106	0.138	0.059	0.022	0.019	0.021	0.046	0.020	0.013	0.011	0.022	0.030	0.030	0.040	0.081	0.023	0.019	0.025	0.141	0.167	0.114	0.083	0.160	0.078	0.033	0.013	0.042	0.008	0.005	0.017	0.014	-0.015	-0.010	127
58	0.003	0.058	0.192	0.200	0.069	0.029	0.023	0.021	0.044	0.023	0.016	0.013	0.033	0.031	0.026	0.025	0.060	0.032	0.032	0.043	0.309	0.195	0.097	0.064	0.126	0.051	0.024	0.018	0.056	0.008	0.006	0.026	0.066	-0.043	-0.037	120
59	-0.008	0.125	0.327	0.331	0.104	0.026	0.020	0.020	0.043	0.022	0.015	0.014	0.028	0.032	0.026	0.028	0.059	0.053	0.057	0.081	0.449	0.304	0.175	0.122	0.245	0.083	0.032	0.009	0.044	0.006	0.002	0.006	0.059	0.025	0.020	114
60	-0.005	0.213	0.413	0.403	0.105	0.024	0.019	0.020	0.044	0.021	0.012	0.008	0.021	0.020	0.015	0.016	0.060	0.059	0.062	0.109	0.580	0.312	0.167	0.116	0.198	0.068	0.022	0.004	0.034	0.001	-0.001	-0.010	0.015	-0.036	-0.034	108
61	0.012	0.452	0.688	0.659	0.117	0.018	0.015	0.016	0.054	0.033	0.018	0.013	0.031	0.028	0.025	0.084	0.705	0.474	0.348	0.356	0.891	0.427	0.226	0.154	0.261	0.078	0.026	0.020	0.046	0.012	0.007	-0.004	0.054	-0.019	-0.021	103
62	-0.006	0.419	0.685	0.652	0.148	0.025	0.017	0.016	0.051	0.027	0.011	0.010	0.027	0.028	0.026	0.059	0.780	0.450	0.313	0.315	0.858	0.393	0.209	0.141	0.212	0.061	0.018	0.004	0.020	0.002	-0.002	-0.008	0.015	-0.034	-0.031	97
63	0.002	0.493	0.781	0.727	0.170	0.026	0.018	0.016	0.084	0.076	0.051	0.049	0.214	0.225	0.183	0.318	1.136	0.508	0.347	0.369	0.855	0.432	0.237	0.154	0.232	0.082	0.031	0.002	0.018	0.003	0.001	0.000	0.036	-0.001	-0.004	92
64	-0.002	0.375	0.594	0.551	0.125	0.022	0.015	0.020	0.127	0.074	0.046	0.047	0.224	0.198	0.170	0.233	1.129	0.533	0.365	0.310	0.800	0.371	0.199	0.122	0.174	0.059	0.022	0.006	0.020	0.006	0.003	0.024	0.051	-0.036	-0.032	88
65	0.001	0.388	0.652	0.654	0.141	0.020	0.035	0.166	0.791	0.477	0.197	0.148	0.465	0.347	0.225	0.291	1.156	0.539	0.350	0.334	0.827	0.411	0.221	0.144	0.206	0.083	0.029	0.004	0.012	0.004	0.001	-0.012	0.000	-0.027	-0.025	83
66	0.001	0.353	0.700	0.856	0.141	0.028	0.049	0.154	1.309	0.591	0.235	0.160	0.514	0.355	0.239	0.264	1.248	0.567	0.374	0.332	0.891	0.420	0.242	0.141	0.197	0.073	0.026	0.006	0.018	0.005	0.003	0.084	0.077	0.016	0.006	79
67	0.002	0.293	0.648	0.868	[illegible]	0.025	0.044	0.237	1.342	0.601	0.218	0.160	0.498	0.355	0.227	0.273	1.229	0.548	0.355	0.324	0.848	0.414	0.207	0.134	0.179	0.069	0.019	0.001	0.013	0.002	-0.001	0.065	[illegible]	-0.001	-0.009	75
68	0.007	0.327	0.779	1.751	[illegible]	0.012	0.012	0.047	0.988	[illegible]	0.203	0.152	0.492	[illegible]	0.242	0.342	1.312	[illegible]	0.377	0.361	0.828	[illegible]	0.193	0.124	0.169	0.061	0.022	0.003	0.012	0.004	0.001	-0.001	[illegible]	-0.017	-0.022	71
69	-0.007	0.125	0.229	0.230	0.035	0.005	0.008	0.009	0.124	[illegible]	0.069	0.057	0.323	[illegible]	0.216	0.262	1.271	[illegible]	0.334	0.303	0.800	[illegible]	0.174	0.104	0.138	0.034	0.012	0.005	0.014	0.002	0.002	0.024	[illegible]	-0.047	-0.037	67
70	0.012	0.074	0.185	0.189	0.044	0.009	0.007	0.009	0.100	0.109	0.067	0.071	0.318	0.291	0.214	0.322	1.218	0.553	0.364	0.345	0.814	0.407	0.211	0.134	0.177	0.059	0.019	0.002	0.009	0.005	0.001	0.163	0.084	0.021	0.016	64
71	-0.006	0.027	0.095	0.106	0.029	0.010	0.008	0.009	0.024	0.013	0.010	0.010	0.029	0.027	0.029	0.121	0.852	0.444	0.313	0.312	0.713	0.335	0.189	0.128	0.162	0.042	0.015	0.006	0.010	0.004	0.003	0.113	0.049	0.000	-0.007	61
72	-0.003	0.013	0.054	0.061	0.010	0.001	0.000	0.003	0.024	0.015	0.011	0.008	0.012	0.010	0.008	0.010	0.093	0.116	0.143	0.206	0.650	0.325	0.169	0.110	0.166	0.044	0.018	0.003	0.006	0.005	0.002	-0.012	-0.003	-0.022	-0.012	58

percentage of albumin hits in analyzed clusters of males

mean ratio (AM/NM) of albumin quantifiers in analyzed clusters

albumin deamidations of N + Q

albumin deamidations of R

carbamoyl on K + R

Quotient (affected/non affected) of #carbamoyl/PSM

Figure S11: Proteoforms and PTM of transferrin

A: Global distribution of plasma protein concentrations after 2D-AEC (NM)

Section of sub-fraction containing seven numbered chromatographic clusters of transferrin. Frames indicate sub-fractions, which form a cluster and analyzed by mass spectrometry. Number and color code show the total fractional protein concentration. Black highlighting indicates the sub-fractions analyzed for PTM (see legend to Fig. S7).

B: Mass spectrometric quantifiers of transferrin variants after analysis of sample from NM by the Proteome discoverer®

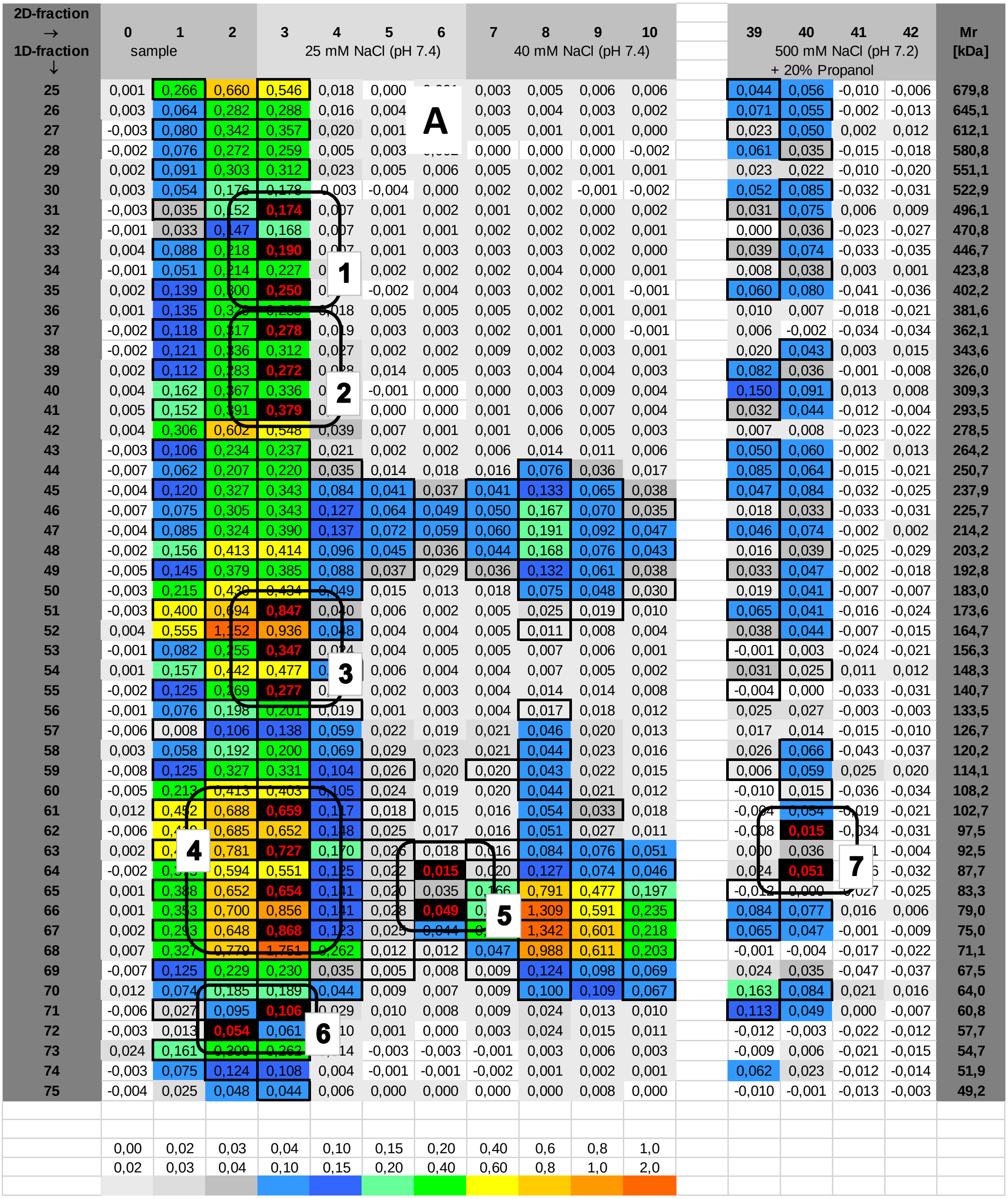
Grey: mass spectrometric analyzed sub-fractions. Figures indicate the presence of transferrin peptides. Quantifiers (second line): A: area (red color code); P: number of peptides (green color code); C: sequence coverage. Frames indicate sub-fractions, which form a cluster and analyzed by mass spectrometry.

C: Mass spectrometric comparison of the concentrations of transferrin variants from AM and NM determined by Sieve®

Grey: mass spectrometric analyzed sub-fractions. Figures indicate the presence of transferrin peptides. The quantifier “ratio” (from >>1.0 to <<1.0, color code from red to green) indicate the quotients AM/NM of peptide signals and corresponds to the concentration quotient of transferrin of homologous sub-fractions. P: number of peptides; H: hits. Frames indicate sub-fractions, which form a cluster.

D: Mass spectrometric comparison of the concentrations of transferrin variants from AM and NM determined by the Proteome discoverer®

Estimated percentage of transferrin hits in each framed cluster compared to total hits of transferrin of entire sub-fractions (cf. Fig. C). The analyzed fractions contained ~39% of all transferrin peptides of the sample.



2D-fraction → 1D-fraction ↓	0	1	2	3	4	5	6	7	8	9	10	39	40	41	42	Mr [kDa]
	sample			25 mM NaCl (pH 7.4)				40 mM NaCl (pH 7.4)				500 mM NaCl (pH 7.2) + 20% Propanol				
25	0,001	0,266	0,660	0,546	0,018	0,000	[illegible]	0,003	0,005	0,006	0,006	0,044	0,056	-0,010	-0,006	679,8
26	0,003	0,064	0,282	0,288	0,016	0,004	[illegible]	0,003	0,004	0,003	0,002	0,071	0,055	-0,002	-0,013	645,1
27	-0,003	0,080	0,342	0,357	0,020	0,001	[illegible]	0,005	0,001	0,001	0,000	0,023	0,050	0,002	0,012	612,1
28	-0,002	0,076	0,272	0,259	0,005	0,003	[illegible]	0,000	0,000	0,000	-0,002	0,061	0,035	-0,015	-0,018	580,8
29	0,002	0,091	0,303	0,312	0,023	0,005	0,006	0,005	0,002	0,001	0,001	0,023	0,022	-0,010	-0,020	551,1
30	0,003	0,054	0,176	0,178	0,003	-0,004	0,000	0,002	0,002	-0,001	-0,002	0,052	0,085	-0,032	-0,031	522,9
31	-0,003	0,035	0,152	0,174	0,007	0,001	0,002	0,001	0,002	0,000	0,002	0,031	0,075	0,006	0,009	496,1
32	-0,001	0,033	0,147	0,168	0,007	0,001	0,001	0,002	0,002	0,002	0,001	0,000	0,036	-0,023	-0,027	470,8
33	0,004	0,088	0,218	0,190	0,007	0,001	0,003	0,003	0,003	0,002	0,000	0,039	0,074	-0,033	-0,035	446,7
34	-0,001	0,051	0,214	0,227	[illegible]	0,002	0,002	0,002	0,004	0,000	0,001	0,008	0,038	0,003	0,001	423,8
35	0,002	0,139	0,300	0,250	[illegible]	-0,002	0,004	0,003	0,002	0,001	-0,001	0,060	0,080	-0,041	-0,036	402,2
36	0,001	0,135	0,320	0,265	0,018	0,005	0,005	0,005	0,002	0,001	0,001	0,010	0,007	-0,018	-0,021	381,6
37	-0,002	0,118	0,317	0,278	0,019	0,003	0,003	0,002	0,001	0,000	-0,001	0,006	-0,002	-0,034	-0,034	362,1
38	-0,002	0,121	0,336	0,312	0,027	0,002	0,002	0,009	0,002	0,003	0,001	0,020	0,043	0,003	0,015	343,6
39	0,002	0,112	0,283	0,272	0,028	0,014	0,005	0,003	0,004	0,004	0,003	0,082	0,036	-0,001	-0,008	326,0
40	0,004	0,162	0,367	0,336	[illegible]	-0,001	0,000	0,000	0,003	0,009	0,004	0,150	0,091	0,013	0,008	309,3
41	0,005	0,152	0,391	0,379	[illegible]	0,000	0,000	0,001	0,006	0,007	0,004	0,032	0,044	-0,012	-0,004	293,5
42	0,004	0,306	0,602	0,548	0,039	0,007	0,001	0,001	0,006	0,005	0,003	0,007	0,008	-0,023	-0,022	278,5
43	-0,003	0,106	0,234	0,237	0,021	0,002	0,002	0,006	0,014	0,011	0,006	0,050	0,060	-0,002	0,013	264,2
44	-0,007	0,062	0,207	0,220	0,035	0,014	0,018	0,016	0,076	0,036	0,017	0,085	0,064	-0,015	-0,021	250,7
45	-0,004	0,120	0,327	0,343	0,084	0,041	0,037	0,041	0,133	0,065	0,038	0,047	0,084	-0,032	-0,025	237,9
46	-0,007	0,075	0,305	0,343	0,127	0,064	0,049	0,050	0,167	0,070	0,035	0,018	0,033	-0,033	-0,031	225,7
47	-0,004	0,085	0,324	0,390	0,137	0,072	0,059	0,060	0,191	0,092	0,047	0,046	0,074	-0,002	0,002	214,2
48	-0,002	0,156	0,413	0,414	0,096	0,045	0,036	0,044	0,168	0,076	0,043	0,016	0,039	-0,025	-0,029	203,2
49	-0,005	0,145	0,379	0,385	0,088	0,037	0,029	0,036	0,132	0,061	0,038	0,033	0,047	-0,002	-0,018	192,8
50	-0,003	0,215	0,430	0,434	0,049	0,015	0,013	0,018	0,075	0,048	0,030	0,019	0,041	-0,007	-0,007	183,0
51	-0,003	0,400	0,694	0,847	0,040	0,006	0,002	0,005	0,025	0,019	0,010	0,065	0,041	-0,016	-0,024	173,6
52	0,004	0,555	1,152	0,936	0,048	0,004	0,004	0,005	0,011	0,008	0,004	0,038	0,044	-0,007	-0,015	164,7
53	-0,001	0,082	0,255	0,347	0,024	0,004	0,005	0,005	0,007	0,006	0,001	-0,001	0,003	-0,024	-0,021	156,3
54	0,001	0,157	0,442	0,477	[illegible]	0,006	0,004	0,004	0,007	0,005	0,002	0,031	0,025	0,011	0,012	148,3
55	-0,002	0,125	0,269	0,277	[illegible]	0,002	0,003	0,004	0,014	0,014	0,008	-0,004	0,000	-0,033	-0,031	140,7
56	-0,001	0,076	0,198	0,201	0,019	0,001	0,003	0,004	0,017	0,018	0,012	0,025	0,027	-0,003	-0,003	133,5
57	-0,006	0,008	0,106	0,138	0,059	0,022	0,019	0,021	0,046	0,020	0,013	0,017	0,014	-0,015	-0,010	126,7
58	0,003	0,058	0,192	0,200	0,069	0,029	0,023	0,021	0,044	0,023	0,016	0,026	0,066	-0,043	-0,037	120,2
59	-0,008	0,125	0,327	0,331	0,104	0,026	0,020	0,020	0,043	0,022	0,015	0,006	0,059	0,025	0,020	114,1
60	-0,005	0,213	0,413	0,403	0,105	0,024	0,019	0,020	0,044	0,021	0,012	-0,010	0,015	-0,036	-0,034	108,2
61	0,012	0,452	0,688	0,659	0,117	0,018	0,015	0,016	0,054	0,033	0,018	-0,004	0,054	-0,019	-0,021	102,7
62	-0,006	[illegible]	0,685	0,652	0,148	0,025	0,017	0,016	0,051	0,027	0,011	-0,008	0,015	-0,034	-0,031	97,5
63	0,002	[illegible]	0,781	0,727	0,170	0,026	0,018	0,016	0,084	0,076	0,051	0,000	0,036	[illegible]	-0,004	92,5
64	-0,002	[illegible]	0,594	0,551	0,125	0,022	0,015	0,020	0,127	0,074	0,046	0,024	0,051	[illegible]	-0,032	87,7
65	0,001	0,388	0,652	0,654	0,141	0,020	0,035	0,166	0,791	0,477	0,197	-0,012	0,000	-0,027	-0,025	83,3
66	0,001	0,353	0,700	0,856	0,141	0,028	0,049	[illegible]	1,309	0,591	0,235	0,084	0,077	0,016	0,006	79,0
67	0,002	0,293	0,648	0,868	0,123	0,025	0,044	[illegible]	1,342	0,601	0,218	0,065	0,047	-0,001	-0,009	75,0
68	0,007	0,327	0,779	1,751	0,262	0,012	0,012	0,047	0,988	0,611	0,203	-0,001	-0,004	-0,017	-0,022	71,1
69	-0,007	0,125	0,229	0,230	0,035	0,005	0,008	0,009	0,124	0,098	0,069	0,024	0,035	-0,047	-0,037	67,5
70	0,012	0,074	0,185	0,189	0,044	0,009	0,007	0,009	0,100	0,109	0,067	0,163	0,084	0,021	0,016	64,0
71	-0,006	0,027	0,095	0,106	0,029	0,010	0,008	0,009	0,024	0,013	0,010	0,113	0,049	0,000	-0,007	60,8
72	-0,003	0,013	0,054	0,061	[illegible]	0,001	0,000	0,003	0,024	0,015	0,011	-0,012	-0,003	-0,022	-0,012	57,7
73	0,024	0,161	0,309	0,262	[illegible]	-0,003	-0,003	-0,001	0,003	0,006	0,003	-0,009	0,006	-0,021	-0,015	54,7
74	-0,003	0,075	0,124	0,108	0,004	-0,001	-0,001	-0,002	0,001	0,002	0,001	0,062	0,023	-0,012	-0,014	51,9
75	-0,004	0,025	0,048	0,044	0,006	0,000	0,000	0,000	0,000	0,008	0,000	-0,010	-0,001	-0,013	-0,003	49,2

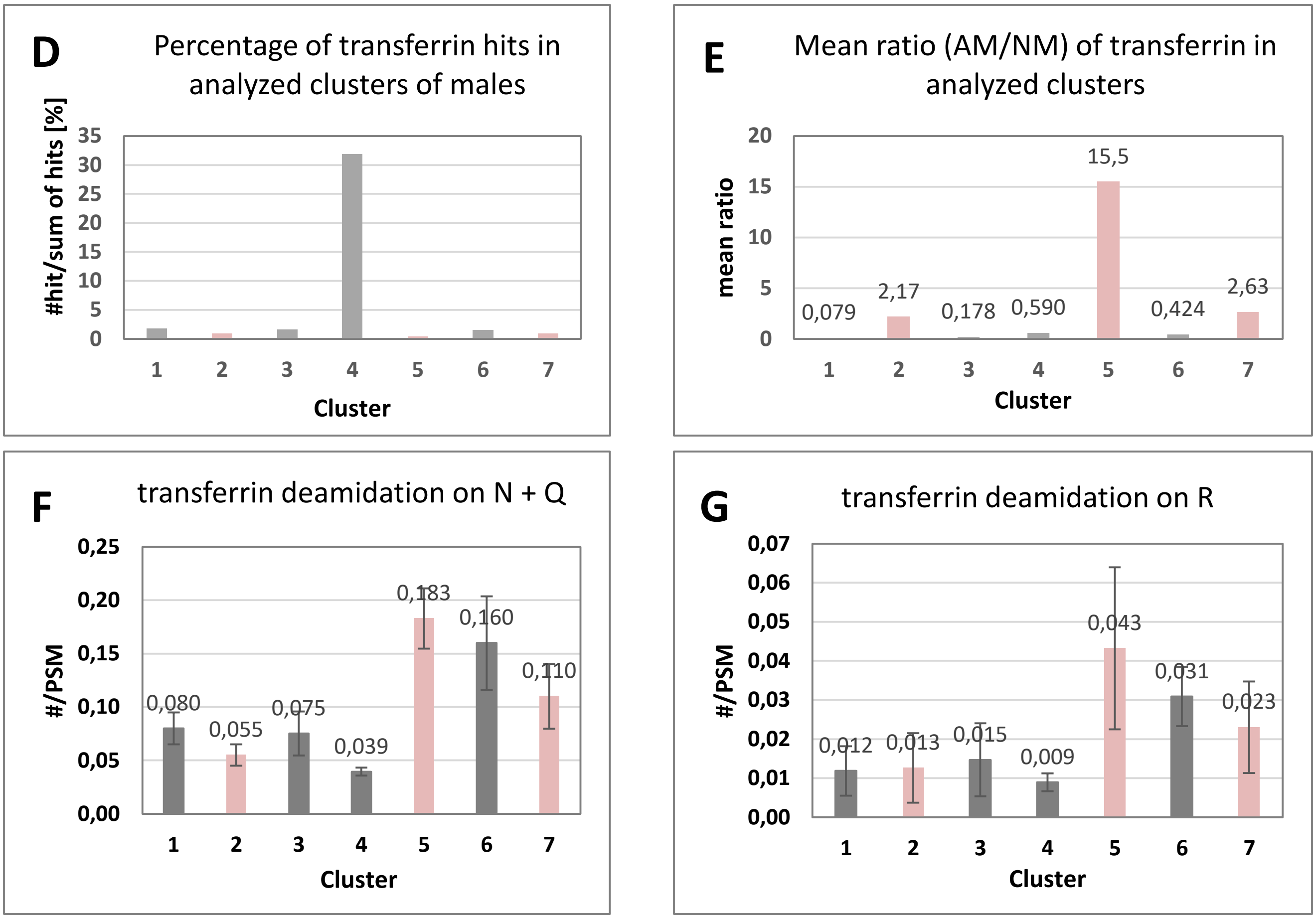
0,00	0,02	0,03	0,04	0,10	0,15	0,20	0,40	0,6	0,8	1,0
0,02	0,03	0,04	0,10	0,15	0,20	0,40	0,60	0,8	1,0	2,0

B

2D-fraction →	1			2			3			4			5			6			7			8			9			10			40			MW [kDa]
1D-fraction ↓	A	P	C	A	P	C	A	P	C	A	P	C	A	P	C	A	P	C	A	P	C	A	P	C	A	P	C	A	P	C	A	P	C	
15																																		1149
16																																		1090
17							1,2E+06	78	0,21																									1035
18																																		982
19							2,5E+05	34	0,19																									932
20																																		884
21							0,0E+00	1	0,02																									839
22				4,5E+05	24	0,19																												796
23							6,5E+05	40	0,17																									755
24				5,5E+05	29	0,19																												716
25		2	0,03				1,8E+05	15	0,14																									680
26																																		645
27	8,5E+04	13	0,09				8,0E+05	89	0,50																									612
28																																		581
29	7,8E+05	33	0,16				2,8E+05	52	0,34																									551
30																																		523
31							1,6E+06	91	0,39																									496
32																																		471
33							1,9E+06	121	0,59																									447
34																																		424
35	9,4E+04	6	0,07				2,5E+06	131	0,65																									402
36				5,0E+04	12	0,13																												382
37	8,9E+04	15	0,12				2,9E+05	32	0,23																									362
38				2,4E+05	37	0,28																												344
39	1,4E+05	31	0,26				3,9E+05	58	0,37																									326
40				3,2E+05	49	0,38																												309
41	8,6E+03	1	0,03				2,4E+05	50	0,35																									293
42				2,4E+05	32	0,20																												278
43	3,5E+04	15	0,17				2,2E+05	37	0,33																									264
44				2,8E+04	15	0,11				4,2E+04	10	0,12																						251
45	7,0E+04	33	0,23				3,1E+05	55	0,40				4,4E+05	102	0,48																			238
46				8,4E+04	21	0,16				2,4E+06	102	0,37				8,1E+04	42	0,29																226
47							2,3E+06	97	0,37																									214
48				2,3E+05	48	0,29				0,0E+00	2	0,02				5,4E+04	2	0,02																203
49							8,8E+06	209	0,70				1,2E+07	289	0,67																			193
50				2,4E+05	43	0,25				7,4E+04	20	0,20				1,0E+04	6	0,07																183
51	6,8E+05	55	0,39				4,4E+06	136	0,66				5,3E+05	95	0,51																			174
52				1,7E+06	63	0,41				7,4E+05	118	0,57										8,2E+04	32	0,21										165
53	6,6E+05	79	0,39				1,1E+06	92	0,53																									156
54				3,0E+06	133	0,61				2,2E+05	62	0,34																						148
55	2,6E+06	153	0,63				3,2E+06	143	0,67																									141
56				2,7E+06	141	0,69				2,3E+04	10	0,11																						134
57	5,7E+04	25	0,17				7,3E+06	217	0,71																									127
58				1,6E+07	342	0,74				8,5E+05	102	0,54																			4,6E+04	4	0,05	120
59	1,9E+07	320	0,71				1,1E+07	241	0,70				2,4E+04	6	0,07				2,6E+05	83	0,40													114
60				3,9E+07	571	0,75				2,0E+06	115	0,50																			2,7E+05	31	0,27	108
61	1,2E+08	704	0,76				5,4E+07	708	0,76				3,8E+06	221	0,64				1,6E+06	153	0,61													103
62				1,4E+08	1119	0,75				2,0E+07	444	0,72										2,9E+04	10	0,08							1,1E+06	80	0,44	97
63	7,5E+07	794	0,76				1,2E+08	1061	0,80				5,9E+05	101	0,45				1,6E+05	46	0,30				1,3E+05	33	0,23							92
64				1,0E+08	1081	0,80				3,6E+07	536	0,72										7,4E+05	111	0,55							8,5E+05	111	0,52	88
65	6,7E+07	879	0,74				1,1E+08	986	0,78				9,0E+06	288	0,64				3,5E+05	110	0,56													83
66				1,9E+08	1013	0,75				3,1E+07	440	0,70				4,5E+04	32	0,20				4,9E+05	5	0,04				1,9E+05	13	0,11	7,4E+05	97	0,53	79
67	4,6E+07	719	0,74				1,6E+08	684	0,80				2,9E+05	64	0,38				1,9E+05	25	0,24				1,9E+05	11	0,08							75
68				1,9E+08	676	0,77				1,9E+07	280	0,64				3,4E+05	101	0,48				3,1E+05	10	0,07				5,0E+04	7	0,07				71
69	1,5E+07	369	0,71				3,9E+07	585	0,77				7,8E+05	99	0,48										1,1E+05	28	0,20							67
70				2,8E+07	528	0,75				2,2E+06	159	0,61										5,1E+05	85	0,52				1,4E+04	4	0,06	1,4E+05	44	0,27	64
71	8,8E+05	101	0,42				9,3E+06	119	0,61																									61
72				9,6E+05	109	0,59																												58
73	1,9E+06	130	0,60				2,7E+06	128	0,63																									55
74				6,4E+05	68	0,47																												52
75							1,6E+06	166	0,54																									49
76																																		47

C

2D-fraction →	1			2			3			4			5			6			7			8			9			10			40			MW [kDa]
1D-fraction ↓	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	R	P	H	
15																																		1149
16																																		1090
17							0,036	8	54																									1035
18																																		982
19							0,771	11	42																									932
20																																		884
21							71,3	5	14																									839
22				0,099	7	20																												796
23							0,113	6	33																									755
24				0,132	7	20																												716
25							2,80	14	43																									680
26				45,9	6	15																												645
27	0,493	19	72				0,002	24	92																									612
28				10	1	2																												581
29	0,155	16	68				0,012	12	50																									551
30				2,260	7	19																												523
31							0,030	18	120																									496
32																																		471
33							0,010	37	188																									447
34																																		424
35	0,184	2	6				0,198	34	201																									402
36				0,592	3	7																												382
37	1,241	4	13				3,39	25	101																									362
38				0,471	11	40																												344
39	1,287	10	31				0,873	18	79																									326
40				0,681	13	45																												309
41							2,25	18	79																									293
42				0,514	9	34																												278
43	0,533	1	2				0,015	13	43																									264
44										0,887	3	11										10	2	3										251
45	0,300	4	21				0,962	22	81				0,439	17	61																			238
46				0,366	4	12				0,002	29	151				0,981	5	13																226
47							0,005	26	142				21,6	10	25																			214
48				0,274	10	23				83,1	16	50				0,480	2	3																203
49							1,55	44	354				1,140	54	410																			193
50				0,420	9	43				0,778	3	6				6,72	13	33																183
51	0,007	15	55				0,003	30	151				0,617	21	105																			174
52				0,047	20	76				0,017	21	74										0,008	6	17										165
53	0,186	16	72				0,151	24	116																									156
54				0,364	32	181				0,131	15	48																						148
55	0,755	32	191				0,381	32	186																									141
56				0,996	35	195				2,47	5	13										21,1	2	4										134
57	16,2	21	69				0,800	47	307																									127
58				1,168	62	507				0,053	23	105																			3,42	5	11	120
59	1,043	51	446				1,011	49	327				6,92	11	33				0,046	24	80													114
60				0,563	73	798				0,107	32	122																			1,029	8	28	108
61	0,689	65	977				0,728	72	933				0,002	40	154				0,005	43	222													103
62				0,370	84	1547				0,794	56	486										0,218	15	48							2,29	22	126	97
63	1,018	68	1172				0,969	84	1520				1,256	20	83				0,015	27	99				0,702	5	19							92
64				0,115	84	1321				0,353	57	583				24,3	26	77				0,917	25	103							2,97	30	143	88
65	1,173	69	1197				0,597	78	1316				0,003	40	250				1,57	29	150				1,55	1	4							83
66				0,719	81	1426				0,597	55	514				6,71	7	22				0,564	4	13				0,330	2	4	1,000	21	103	79
67	0,896	66	1006				0,635	76	1134				0,080	22	103				1,63	13	42				0,625	5	14							75
68				0,760	79	1304				0,593	47	361				0,003	17	69				1,305	4	16				1,419	2	4				71
69	0,817	47	447				0,746	69	870				0,006	25	121				44,7	7	16				1,359	8	26							67
70				0,601	58	661				2,90	37	161										0,594	22	104							1,119	4	7	64
71	0,067	17	79				0,005	41	209																									61
72				0,094	30	149																												58
73	1,328	32	199				0,843	34	208																									55
74				0,004	20	98																												52
75							0,002	27	191																									49
76																																		47



D-G: Grey filling: transferrin protein concentration is lower in AM in comparison to NM (ratios <1.0); red filling: protein concentration is higher in AM in comparison to NM due to the ratios calculated by Sieve (ratios >2, Fig. E).
The mean ratio was built from all sub-fractions of one cluster.
The main cluster 4 of transferrin (Fig. D) showed a ratio of ~0.6 (Fig. E) like the minor clusters 1, 3, and 6 (<0.5). This is in accordance with the known alteration direction of this APR under inflammation. Surprisingly, there were three minor clusters (2, 5, and 7) 2 to 15-fold increased under AS.

F, G: Deamidation rates of transferrin of proteoforms identified

The search for PTM ran successively using Proteome Discoverer® 1.3 (Thermo) with no more than three dynamic modifcation types per run. We considered only highly confident database matches when the sequence coverage was >40%. The following dynamic modifications of amino acids were analyzed: deamidation (N, Q, R) and carbamoyl (K, M, R). Multi reports of the related replicates were utilized.
Mean values of the modification rates, #PTM/PSM of transferrin peptides were determined including the homologous sub-fractions from all animals AM, NM, CF, and NF (cf. Fig. A-C).
The minor clusters (5, 7), which are elevated under AS, showed much higher deamidation rates than the main cluster and lower clusters under AS. Practically, no carbamoylation was found.

Supplementary Table S1:

Specification of ELISA-Test kits applied to dog and human samples

Measurements in dog samples				
Antigen	**Supplier**	**Code**	**Species**	**Function**
kallikrein	Abbkine	KTE20170	dog	**n**
vitronectin		KTE20161	dog	**n**
dynein		KTE20163	dog	**n**
hyaluronan binding protein 2		KTE20164	dog	**n**
fukutin		KTE20171	dog	**n**
myosin IXA		KTE20175	dog	**n**
collagen 1 alpha 1		KTE20165	dog	**n**
collagen 1 alpha 2		KTE20166	dog	**n**
collagen 13 alpha 1		KTE20169	dog	**n**
formin 1		KTE20173	dog	**n**
talin-1	CUSABIO	CSB-EL023597HU	man	**n**
Serum amyloid A	Genorise	GR115278	dog	**n**
leucin rich alpha-2-glycoprotein 1	MyBioSource	MBS075175	dog	**y**
gelsolin		MBS2603447	dog	**y**
adiponectin		MBS778758	dog	**n**
adiponectin		MBS080454	cat	**y**
lumican		MBS2607240	dog	**y**
procollagen I C-terminal propeptide		MBS2608196	dog	**y**
talin-1		MBS2604628	dog	**y**
serum amyloid		MBS740421	dog	**y**
serum amyloid		MBS1602508	dog	**y**
lumican	Cloud-Clone	USC-SEB496HU	man	**y**
collagen type 13		SEC138HU	man	**y**
vitronectin	RayBiotech:	ELH-VTN	man	**y**
adiponectin		RD19102310	man	**y**
TGFß1	Biovendor	BVD-RAF122R	man	**y**
adiponectin		BVD-RD191023100	man	**y**

Measurement in dog samples: When no dog-specific or reliable kit was available, we applied assays of other species-specificity due to the high sequence similarities. Out of the checked kits those marked by yes (y) produced reliable antigen concentrations. The other kits either were not able to detect the proteoform naturally occurring in our samples or were not sensitive enough.

Measurements in human samples				
Antigen	**Supplier**	**Code**	**Species**	**Function**
angiotensinogen	Abbexa	abx573778	man	**y**
formin 1		abx387383	man	y
alpha-1-acid glycoprotein	Cloud-Clone	HEA816Hu	man	y
coagulation factor XIIIB		CEB613Hu	man	y
complement C1q		SEA747Hu	man	y
complement factor H		SEA635Hu	man	y
complement factor I		SEB978Hu	man	y
collagen type XIII		SEC138Hu	man	y
c-reactive protein		SEA821Hu	man	y
fibronectin		USC-HEA037HU	man	y
ficolin		SEA786Hu	man	y
hemopexin		SEB986HU	man	y
gelsolin		SEA372Hu	man	y
C4 binding protein alpha		SEB620Hu	man	y
retinol binding protein 4		SEA929Hu	man	y
talin		SEA278Hu	man	y
leucine rich alpha-2-glycoprotein 1		HEB934Hu high sensitive	man	y
lumican	RayBiotech	ELH-LUM-1	man	y
serum amyloid A		ELH-SAA-1	man	y
vitronectin		(ELH-VTN	man	y
carboxyterminal propeptide of	CUSABIO	CSB-E08079h	man	y
fibrinogen gamma chain		CSB-E13319h	man	y
alpha-trypsin inhibitor heavy chain		CSB-E17022h	man	y
hyaluronan-binding protein 2		CSB-EL010113HU	man	y
complement component C9		CSB-E14011h	man	y
serum amyloid A	Boster	BOS-EK1544, SAA/SAA1	man	y
TGFß1	Biovendor	BVD-RAF122R*	man	y
adiponectin		BVD-RD191023100*	man	y

Measurement in human samples: The kits were performed according the suppliers instructions with the following modifications: all assays from Cloud-Clone and CUSBIO were performed with double incubation times. Samples were pre-incubated with 0.5% Tween 20 before measurement of gelsolin. For the quantification of PICP, TGFß1, and CRP in urine either incubation times were prolonged or concentrated specimens were applied. For that samples have been concentrated in Amicon® Ultra - 15 Centrifugal filters (3K, UFC900324) by ~10 to ~60 fold depending on the starting volume available.

Table S2: **List of protein chains identified by the Proteome Discoverer® in four sample pools of blood plasma from dogs**

Mass spectrometric data are: Accession number (SwissProt); Description (annotation);
ΣCoverage (sequence coverage); Σ# Proteins (number of distinct proteins assigned to the identified sequences);
Σ# Unique Peptides (singular peptides assigned to the protein); Σ# Peptides (entire peptide count including repeatedly found peptides); Σ# PSMs.
By mass spectrometry, 3115 (443) proteins in total were identified with the Proteome Discoverer® supported by ≥ 1 (≥ 2) peptide/s, respectively.

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Pe	Σ# Peptides	Σ# PSMs
F1P8Z5	Apolipoprotein B OS=Canis lupus familiaris GN=APOB PE=4 SV=1 - [F1P8Z5_CANLF]	66,12	1	239	245	3734
F1PIX8	Complement C3 OS=Canis lupus familiaris GN=C3 PE=4 SV=2 - [F1PIX8_CANLF]	72,98	1	23	98	1730
J9PBN6	Uncharacterized protein OS=Canis lupus familiaris GN=LOC611458 PE=4 SV=1 - [J9PBN6_CANLF]	70,91	1	14	81	2455
J9P430	Transferrin OS=Canis lupus familiaris GN=TF PE=3 SV=1 - [J9P430_CANLF]	80,29	1	32	76	7792
J9P8M2	Fibronectin OS=Canis lupus familiaris GN=FN1 PE=4 SV=1 - [J9P8M2_CANLF]	51,55	1	2	73	766
F6UME0	Alpha-2-macroglobulin OS=Canis lupus familiaris GN=A2M PE=4 SV=1 - [F6UME0_CANLF]	65,9	1	71	71	2430
F1P6H7	Fibronectin OS=Canis lupus familiaris GN=FN1 PE=4 SV=2 - [F1P6H7_CANLF]	46,21	1	0	71	763
J9NTL7	Uncharacterized protein OS=Canis lupus familiaris GN=CFH PE=4 SV=1 - [J9NTL7_CANLF]	65,77	1	53	64	1387
E2RS80	Uncharacterized protein OS=Canis lupus familiaris GN=CFB PE=3 SV=2 - [E2RS80_CANLF]	55,99	1	30	61	1354
F6UMP8	Uncharacterized protein OS=Canis lupus familiaris GN=LOC611458 PE=4 SV=1 - [F6UMP8_CANLF]	53,07	1	2	59	322
F1PGM1	Complement C3 OS=Canis lupus familiaris GN=C3 PE=4 SV=2 - [F1PGM1_CANLF]	46,23	1	0	53	370
F1PWR2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PWR2_CANLF]	45,07	1	27	50	283
F1Q421	Plasminogen OS=Canis lupus familiaris GN=PLG PE=3 SV=2 - [F1Q421_CANLF]	71,18	1	15	49	1588
P49822	Serum albumin OS=Canis lupus familiaris GN=ALB PE=1 SV=3 - [ALBU_CANLF]	75,99	1	2	47	402
F2Z4Q6	Serum albumin OS=Canis lupus familiaris GN=ALB PE=3 SV=1 - [F2Z4Q6_CANLF]	75,99	1	2	47	641
F1PN98	Coagulation factor V OS=Canis lupus familiaris GN=F5 PE=3 SV=2 - [F1PN98_CANLF]	26,15	1	45	45	439
F1PDJ5	Apolipoprotein A-I OS=Canis lupus familiaris GN=APOA1 PE=3 SV=1 - [F1PDJ5_CANLF]	85,34	1	15	41	1930
Q28295	von Willebrand factor OS=Canis lupus familiaris GN=VWF PE=1 SV=2 - [VWF_CANLF]	22,75	1	0	41	237
F5XVB0	von Willebrand factor OS=Canis lupus familiaris GN=VWF PE=2 SV=1 - [F5XVB0_CANLF]	22,75	1	0	41	237
G1K2B9	von Willebrand factor OS=Canis lupus familiaris GN=VWF PE=4 SV=1 - [G1K2B9_CANLF]	22,75	1	0	41	237
F1PBL4	Fibrinogen alpha chain OS=Canis lupus familiaris GN=FGA PE=4 SV=1 - [F1PBL4_CANLF]	38,12	1	8	40	990
F6V1W9	Transferrin OS=Canis lupus familiaris GN=TF PE=4 SV=1 - [F6V1W9_CANLF]	39,06	1	1	38	537
A0A219Y8W3	von Willebrand factor OS=Canis lupus familiaris PE=2 SV=1 - [A0A219Y8W3_CANLF]	18,59	1	0	35	174
F1PZR4	Hemopexin OS=Canis lupus familiaris GN=HPX PE=3 SV=2 - [F1PZR4_CANLF]	75,33	1	34	34	2201
F1PW65	Fibrinogen beta chain OS=Canis lupus familiaris GN=FGB PE=4 SV=2 - [F1PW65_CANLF]	75,15	1	1	34	1156
F1P8G0	Fibrinogen gamma chain OS=Canis lupus familiaris GN=FGG PE=4 SV=2 - [F1P8G0_CANLF]	81,24	1	29	31	1008
P19006	Haptoglobin OS=Canis lupus familiaris GN=HP PE=1 SV=2 - [HPT_CANLF]	78,72	1	0	28	1300
G1K2D9	Haptoglobin OS=Canis lupus familiaris GN=LOC479668 PE=3 SV=1 - [G1K2D9_CANLF]	74,64	1	0	28	1242
F1Q117	Attractin OS=Canis lupus familiaris GN=ATRN PE=4 SV=2 - [F1Q117_CANLF]	26,53	1	23	28	239
E2RS79	Uncharacterized protein OS=Canis lupus familiaris GN=CFB PE=3 SV=2 - [E2RS79_CANLF]	42,05	1	7	27	291
J9NRV7	Fibrinogen alpha chain OS=Canis lupus familiaris GN=FGA PE=4 SV=1 - [J9NRV7_CANLF]	31,71	1	0	27	298
F1PGS2	Fibrinogen beta chain OS=Canis lupus familiaris GN=FGB PE=4 SV=2 - [F1PGS2_CANLF]	66,6	1	0	26	498
E2QZQ1	Uncharacterized protein OS=Canis lupus familiaris GN=TF PE=3 SV=1 - [E2QZQ1_CANLF]	47,66	1	8	26	374
Q076A4	Myosin-8 OS=Canis lupus familiaris GN=MYH8 PE=3 SV=1 - [MYH8_CANLF]	17,79	1	0	26	55
E2R7A3	Complement factor I OS=Canis lupus familiaris GN=CFI PE=3 SV=2 - [E2R7A3_CANLF]	57,88	1	4	25	703
P02648	Apolipoprotein A-I OS=Canis lupus familiaris GN=APOA1 PE=1 SV=2 - [APOA1_CANLF]	68,42	1	1	23	438
E2RCC8	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=2 - [E2RCC8_CANLF]	55,18	1	4	22	2838
F1PY40	Complement factor I OS=Canis lupus familiaris GN=CFI PE=4 SV=2 - [F1PY40_CANLF]	46,9	1	2	22	672
F1PGM9	Complement component 4 binding protein alpha OS=Canis lupus familiaris GN=C4BPA PE=4 SV=2 - [F1PGM9_C	56,61	1	21	21	314
E2RE76	Apolipoprotein A-IV OS=Canis lupus familiaris GN=APOA4 PE=3 SV=2 - [APOA4_CANLF]	53,97	1	21	21	301
F1P7J4	Complement C5 OS=Canis lupus familiaris GN=C5 PE=4 SV=2 - [F1P7J4_CANLF]	21,14	1	21	21	58
E2R4V3	Serpin family F member 2 OS=Canis lupus familiaris GN=SERPINF2 PE=3 SV=1 - [E2R4V3_CANLF]	54,99	1	20	20	338
F1P903	Complement C1r OS=Canis lupus familiaris GN=C1R PE=3 SV=2 - [F1P903_CANLF]	41,99	1	0	20	137
F1PNG7	Complement C1r OS=Canis lupus familiaris GN=C1R PE=3 SV=2 - [F1PNG7_CANLF]	41,17	1	0	20	137
F1Q418	Inter-alpha-trypsin inhibitor heavy chain 1 OS=Canis lupus familiaris GN=ITIH1 PE=4 SV=2 - [F1Q418_CANLF]	35,16	1	20	20	101
P80009	Plasminogen (Fragment) OS=Canis lupus familiaris GN=PLG PE=1 SV=1 - [PLMN_CANLF]	80,18	1	0	19	126
J9PAD1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAD1_CANLF]	22,01	1	0	18	75
P33703	Beta-2-glycoprotein 1 OS=Canis lupus familiaris GN=APOH PE=2 SV=1 - [APOH_CANLF]	53,33	1	17	17	789
F1PG39	Inter-alpha-trypsin inhibitor heavy chain 2 OS=Canis lupus familiaris GN=ITIH2 PE=4 SV=2 - [F1PG39_CANLF]	33,86	1	17	17	81
H9GWY3	Inter-alpha-trypsin inhibitor heavy chain family member 4 OS=Canis lupus familiaris GN=ITIH4 PE=4 SV=2 - [H9	25,36	1	12	17	50
F1P707	Uncharacterized protein OS=Canis lupus familiaris GN=LOC484960 PE=4 SV=2 - [F1P707_CANLF]	17,94	1	17	17	42
E2QZ19	Afamin OS=Canis lupus familiaris GN=AFM PE=3 SV=1 - [E2QZ19_CANLF]	37,87	1	0	16	38
E2R4E7	Afamin OS=Canis lupus familiaris GN=AFM PE=3 SV=2 - [E2R4E7_CANLF]	37,5	1	0	16	38
F1PQ85	Mannan binding lectin serine peptidase 1 OS=Canis lupus familiaris GN=MASP1 PE=3 SV=2 - [F1PQ85_CANLF]	30,67	1	7	16	137
F1PP08	Dipeptidyl peptidase 4 OS=Canis lupus familiaris GN=DPP4 PE=4 SV=2 - [F1PP08_CANLF]	20,83	1	14	15	65
F1PUM6	Vitronectin OS=Canis lupus familiaris GN=VTN PE=4 SV=1 - [F1PUM6_CANLF]	31,06	1	13	15	278
P60524	Hemoglobin subunit beta OS=Canis lupus familiaris GN=HBB PE=1 SV=1 - [HBB_CANLF]	92,47	1	1	14	193
J9NVC6	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=1 - [J9NVC6_CANLF]	31,61	1	0	14	281
J9JHX7	Uncharacterized protein OS=Canis lupus familiaris GN=TF PE=3 SV=1 - [J9JHX7_CANLF]	28,14	1	0	14	94
F1PKX3	Coagulation factor XIII A chain OS=Canis lupus familiaris GN=F13A1 PE=4 SV=2 - [F1PKX3_CANLF]	28,1	1	14	14	67
F1PNV5	Kallikrein B1 OS=Canis lupus familiaris GN=KLKB1 PE=2 SV=2 - [F1PNV5_CANLF]	26,57	1	13	14	121
E2RK02	Glycosylphosphatidylinositol specific phospholipase D1 OS=Canis lupus familiaris GN=GPLD1 PE=4 SV=2 - [E2RK	24,47	1	14	14	49
O46392	Collagen alpha-2(I) chain OS=Canis lupus familiaris GN=COL1A2 PE=2 SV=2 - [CO1A2_CANLF]	11,71	1	0	13	165
F1PHY1	Collagen alpha-2(I) chain OS=Canis lupus familiaris GN=COL1A2 PE=4 SV=1 - [F1PHY1_CANLF]	11,71	1	0	13	165
F1PAL5	Angiotensinogen OS=Canis lupus familiaris GN=AGT PE=3 SV=2 - [F1PAL5_CANLF]	34,8	1	13	13	93
A0A1K0GGH0	Globin A2 OS=Canis lupus familiaris GN=GLNA2 PE=3 SV=1 - [A0A1K0GGH0_CANLF]	82,31	1	0	12	114
J9NYW7	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=1 - [J9NYW7_CANLF]	38,46	1	1	12	299
J9PAA4	Carboxypeptidase N subunit 2 OS=Canis lupus familiaris GN=CPN2 PE=4 SV=1 - [J9PAA4_CANLF]	37,11	1	12	12	130
E2R3R2	Proteasome subunit beta type OS=Canis lupus familiaris GN=PSMB5 PE=3 SV=1 - [E2R3R2_CANLF]	60,84	1	12	12	159
E2RNG3	Carboxypeptidase N subunit 1 OS=Canis lupus familiaris GN=CPN1 PE=4 SV=1 - [E2RNG3_CANLF]	41,36	1	3	11	55
F1PKB2	Alpha-mannosidase OS=Canis lupus familiaris GN=MAN2B1 PE=3 SV=2 - [F1PKB2_CANLF]	16,48	1	11	11	31
F1PDJ7	Uncharacterized protein OS=Canis lupus familiaris GN=AZGP1 PE=3 SV=2 - [F1PDJ7_CANLF]	47,62	1	11	11	61
E2RMF9	Serpin family A member 5 OS=Canis lupus familiaris GN=SERPINA5 PE=3 SV=1 - [E2RMF9_CANLF]	38,08	1	11	11	125
F1PMS8	Neural cell adhesion molecule 1 OS=Canis lupus familiaris GN=NCAM1 PE=4 SV=2 - [F1PMS8_CANLF]	22,14	1	0	11	197
Q5I2D5	CD56 120 kDa GPI-linked isoform OS=Canis lupus familiaris PE=2 SV=1 - [Q5I2D5_CANLF]	21,66	1	0	11	197
Q5I2D7	CD56 140 kDa isoform OS=Canis lupus familiaris PE=2 SV=1 - [Q5I2D7_CANLF]	18,54	1	0	11	197
Q6QNF3	Platelet-derived growth factor receptor beta OS=Canis lupus familiaris GN=PDGFRB PE=2 SV=1 - [PGFRB_CANL	12,06	1	0	11	81
F1PE35	Platelet-derived growth factor receptor beta OS=Canis lupus familiaris GN=PDGFRB PE=3 SV=2 - [F1PE35_CANL	11,73	1	0	11	81
E2RMN2	Proteasome subunit alpha type OS=Canis lupus familiaris GN=PSMA6 PE=3 SV=1 - [E2RMN2_CANLF]	49,19	1	11	11	320
E2R5U8	Transthyretin OS=Canis lupus familiaris GN=TTR PE=3 SV=1 - [E2R5U8_CANLF]	73,47	1	10	10	133
E2R9B6	Fetuin B OS=Canis lupus familiaris GN=FETUB PE=4 SV=1 - [E2R9B6_CANLF]	33,51	1	10	10	62
E2RE31	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=2 - [E2RE31_CANLF]	27,03	1	0	10	60
E2RES2	Serpin family C member 1 OS=Canis lupus familiaris GN=SERPINC1 PE=3 SV=2 - [E2RES2_CANLF]	26,02	1	10	10	18

E2RG01	Complement C7 OS=Canis lupus familiaris GN=C7 PE=4 SV=2 - [E2RG01_CANLF]	19,93	1	10	10	19
Q9XSJ7	Collagen alpha-1(I) chain OS=Canis lupus familiaris GN=COL1A1 PE=1 SV=1 - [CO1A1_CANLF]	9,73	1	0	10	230
F1Q3I5	Collagen alpha-1(I) chain OS=Canis lupus familiaris GN=COL1A1 PE=4 SV=2 - [F1Q3I5_CANLF]	9,7	1	0	10	230
F2Z4N7	Actin, alpha, cardiac muscle 1 OS=Canis lupus familiaris GN=ACTC1 PE=3 SV=1 - [F2Z4N7_CANLF]	32,1	1	3	10	35
E2R5B2	Enolase 3 OS=Canis lupus familiaris GN=ENO3 PE=3 SV=1 - [E2R5B2_CANLF]	37,79	1	8	10	23
F1PMU2	Neural cell adhesion molecule 1 OS=Canis lupus familiaris GN=NCAM1 PE=4 SV=2 - [F1PMU2_CANLF]	17,6	1	0	10	196
Q5I2D6	CD56 140 kDa VASE isoform OS=Canis lupus familiaris PE=2 SV=1 - [Q5I2D6_CANLF]	17,27	1	0	10	196
E2QW34	Proteasome subunit beta type OS=Canis lupus familiaris GN=PSMB2 PE=3 SV=1 - [E2QW34_CANLF]	54,23	1	10	10	138
E2RLH6	Uncharacterized protein OS=Canis lupus familiaris GN=LOC609402 PE=3 SV=2 - [E2RLH6_CANLF]	67,11	1	0	9	85
E2QUV3	Alpha 2-HS glycoprotein OS=Canis lupus familiaris GN=AHSG PE=3 SV=2 - [E2QUV3_CANLF]	36,16	1	9	9	216
F1PJ74	Apolipoprotein E OS=Canis lupus familiaris GN=APOE PE=3 SV=1 - [F1PJ74_CANLF]	34,98	1	1	9	65
Q28243	Fibrinogen A-alpha-chain (Fragment) OS=Canis lupus familiaris PE=4 SV=1 - [Q28243_CANLF]	20,99	1	0	9	75
Q6EIZ0	Keratin, type I cytoskeletal 10 OS=Canis lupus familiaris GN=KRT10 PE=2 SV=1 - [K1C10_CANLF]	17,78	1	0	9	66
F1PYU9	Keratin, type I cytoskeletal 10 OS=Canis lupus familiaris GN=KRT10 PE=3 SV=2 - [F1PYU9_CANLF]	17,78	1	0	9	66
E2R833	Leucine rich alpha-2-glycoprotein 1 OS=Canis lupus familiaris GN=LRG1 PE=4 SV=2 - [E2R833_CANLF]	27,95	1	0	9	38
J9NSS7	Leucine rich alpha-2-glycoprotein 1 OS=Canis lupus familiaris GN=LRG1 PE=4 SV=1 - [J9NSS7_CANLF]	27,4	1	0	9	38
F1PHS2	Serpin family A member 6 OS=Canis lupus familiaris GN=SERPINA6 PE=3 SV=2 - [F1PHS2_CANLF]	26,73	1	9	9	54
J9JHW4	Proteasome endopeptidase complex OS=Canis lupus familiaris PE=3 SV=1 - [J9JHW4_CANLF]	36,12	1	1	9	47
Q7M321	Plasmin (Fragments) OS=Canis lupus familiaris PE=4 SV=1 - [Q7M321_CANLF]	78,33	1	1	8	376
E2RAK7	Apolipoprotein A-II OS=Canis lupus familiaris GN=APOA2 PE=1 SV=2 - [APOA2_CANLF]	67	1	8	8	234
J9P028	Glutathione peroxidase OS=Canis lupus familiaris GN=GPX3 PE=3 SV=1 - [J9P028_CANLF]	54,9	1	8	8	135
P56595	Apolipoprotein C-I OS=Canis lupus familiaris GN=APOC1 PE=1 SV=1 - [APOC1_CANLF]	40,91	1	8	8	56
P18649	Apolipoprotein E OS=Canis lupus familiaris GN=APOE PE=1 SV=2 - [APOE_CANLF]	35,08	1	1	8	48
F1PCK2	Alpha-1-B glycoprotein OS=Canis lupus familiaris GN=A1BG PE=4 SV=2 - [F1PCK2_CANLF]	26,08	1	8	8	22
P25473	Clusterin OS=Canis lupus familiaris GN=CLU PE=2 SV=1 - [CLUS_CANLF]	21,12	1	0	8	26
E2QYU2	Clusterin OS=Canis lupus familiaris GN=CLU PE=3 SV=1 - [E2QYU2_CANLF]	21,03	1	0	8	26
E2RS75	Uncharacterized protein OS=Canis lupus familiaris GN=CFB PE=3 SV=1 - [E2RS75_CANLF]	14,34	1	0	8	13
E2RK21	Uncharacterized protein OS=Canis lupus familiaris GN=CFH PE=4 SV=2 - [E2RK21_CANLF]	12,36	1	0	8	20
Q6EIY9	Keratin, type II cytoskeletal 1 OS=Canis lupus familiaris GN=KRT1 PE=2 SV=1 - [K2C1_CANLF]	10,99	1	0	8	107
F1PTY1	Keratin, type II cytoskeletal 1 OS=Canis lupus familiaris GN=KRT1 PE=3 SV=1 - [F1PTY1_CANLF]	10,99	1	0	8	107
E2RAH4	Tropomyosin 2 (beta) OS=Canis lupus familiaris GN=TPM2 PE=2 SV=2 - [E2RAH4_CANLF]	23,94	1	2	8	15
F1PVC1	Actin, alpha 1, skeletal muscle OS=Canis lupus familiaris GN=ACTA1 PE=3 SV=2 - [F1PVC1_CANLF]	28,01	1	1	8	28
E2RC23	Procollagen C-endopeptidase enhancer OS=Canis lupus familiaris GN=PCOLCE PE=4 SV=1 - [E2RC23_CANLF]	33,19	1	8	8	39
E2RLN1	Serpin family D member 1 OS=Canis lupus familiaris GN=SERPIND1 PE=3 SV=1 - [E2RLN1_CANLF]	23,19	1	4	8	19
J9P849	Proteasome subunit alpha type OS=Canis lupus familiaris GN=PSMA3 PE=3 SV=1 - [J9P849_CANLF]	34,55	1	0	8	123
E2RKR4	Proteasome subunit alpha type OS=Canis lupus familiaris GN=PSMA3 PE=3 SV=1 - [E2RKR4_CANLF]	33,33	1	0	8	123
J9P9G4	Proteasome subunit alpha type OS=Canis lupus familiaris PE=3 SV=1 - [J9P9G4_CANLF]	32,7	1	1	8	62
F1PQ99	Mannan binding lectin serine peptidase 1 OS=Canis lupus familiaris GN=MASP1 PE=3 SV=1 - [F1PQ99_CANLF]	15,91	1	0	8	62
F1PSX2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PSX2_CANLF]	84,91	1	0	7	2482
L7N0F2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0F2_CANLF]	71,43	1	0	7	2314
J9PAW5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAW5_CANLF]	71,43	1	0	7	2374
H9GWR8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [H9GWR8_CANLF]	69,77	1	0	7	2482
J9NSQ1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NSQ1_CANLF]	58,44	1	0	7	2314
J9P9J6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P9J6_CANLF]	31,07	1	7	7	133
A1ILJ0	Alpha 1 antitrypsin OS=Canis lupus familiaris PE=2 SV=1 - [A1ILJ0_CANLF]	21,2	1	1	7	104
F1PYM4	Insulin like growth factor binding protein acid labile subunit OS=Canis lupus familiaris GN=IGFALS PE=4 SV=2 - [	16,06	1	7	7	17
F1PZC6	Histidine rich glycoprotein OS=Canis lupus familiaris GN=HRG PE=4 SV=2 - [F1PZC6_CANLF]	16,01	1	7	7	17
F1PHR2	Pyruvate kinase OS=Canis lupus familiaris GN=PKM PE=3 SV=2 - [F1PHR2_CANLF]	16,82	1	5	7	10
Q076A3	Myosin-13 OS=Canis lupus familiaris GN=MYH13 PE=3 SV=1 - [MYH13_CANLF]	3,97	1	0	7	7
F1P916	Tropomyosin 1 OS=Canis lupus familiaris GN=TPM1 PE=3 SV=2 - [F1P916_CANLF]	18,71	1	0	7	11
F1PQU7	Myosin-13 OS=Canis lupus familiaris GN=MYH13 PE=3 SV=2 - [F1PQU7_CANLF]	3,97	1	0	7	7
A0A0N9JIB9	Tropomyosin 1 alpha OS=Canis lupus familiaris GN=Tpm1 PE=2 SV=1 - [A0A0N9JIB9_CANLF]	18,31	1	0	7	11
E2RRM2	Coagulation factor II, thrombin OS=Canis lupus familiaris GN=F2 PE=3 SV=2 - [E2RRM2_CANLF]	15,17	1	0	7	15
J9NSF9	Prothrombin OS=Canis lupus familiaris GN=F2 PE=3 SV=1 - [J9NSF9_CANLF]	14,65	1	0	7	15
O18840	Actin, cytoplasmic 1 OS=Canis lupus familiaris GN=ACTB PE=2 SV=3 - [ACTB_CANLF]	29,33	1	0	7	12
Z4YHI2	Uncharacterized protein OS=Canis lupus familiaris GN=ACTG1 PE=3 SV=1 - [Z4YHI2_CANLF]	29,1	1	0	7	12
J9NXE2	Actin, cytoplasmic 1 Actin, cytoplasmic 1, N-terminally processed OS=Canis lupus familiaris GN=ACTBL2 PE=3 S	35,12	1	0	7	39
F1PQL8	Uncharacterized protein OS=Canis lupus familiaris GN=ACTG1 PE=3 SV=2 - [F1PQL8_CANLF]	35,12	1	0	7	39
E2QX17	Proteasome subunit beta type OS=Canis lupus familiaris GN=PSMB3 PE=3 SV=1 - [E2QX17_CANLF]	43,41	1	7	7	114
E2R416	Lumican OS=Canis lupus familiaris GN=LUM PE=4 SV=1 - [E2R416_CANLF]	27,81	1	7	7	57
L7N0K2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0K2_CANLF]	67,77	1	4	6	191
P60529	Hemoglobin subunit alpha OS=Canis lupus familiaris GN=HBA PE=1 SV=1 - [HBA_CANLF]	63,83	1	0	6	87
J9JHF7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100855540 PE=3 SV=1 - [J9JHF7_CANLF]	63,38	1	1	6	56
J9NXL3	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100855558 PE=3 SV=1 - [J9NXL3_CANLF]	63,38	1	0	6	87
E2RQ71	Apolipoprotein M OS=Canis lupus familiaris GN=APOM PE=4 SV=2 - [E2RQ71_CANLF]	47,87	1	6	6	47
J9P4B4	Complement C1q A chain OS=Canis lupus familiaris GN=C1QA PE=4 SV=1 - [J9P4B4_CANLF]	37,5	1	6	6	43
F1PD34	Secreted phosphoprotein 2 OS=Canis lupus familiaris GN=SPP2 PE=4 SV=2 - [F1PD34_CANLF]	34,67	1	0	6	34
J9P1G2	Complement C1q B chain OS=Canis lupus familiaris GN=C1QB PE=4 SV=1 - [J9P1G2_CANLF]	34,4	1	6	6	64
E2RQP5	Secreted phosphoprotein 2 OS=Canis lupus familiaris GN=SPP2 PE=4 SV=1 - [E2RQP5_CANLF]	33,82	1	0	6	34
E2RPW3	Paraoxonase 1 OS=Canis lupus familiaris GN=PON1 PE=4 SV=2 - [E2RPW3_CANLF]	31,18	1	6	6	12
Q8WMR1	Plasminogen (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q8WMR1_CANLF]	30,64	1	0	6	33
F1PCE5	Serpin family A member 1 OS=Canis lupus familiaris GN=SERPINA1 PE=3 SV=2 - [F1PCE5_CANLF]	17,9	1	0	6	103
F1PEN8	Carboxylic ester hydrolase OS=Canis lupus familiaris GN=BCHE PE=3 SV=1 - [F1PEN8_CANLF]	16,28	1	6	6	11
F1PE28	Transketolase OS=Canis lupus familiaris GN=TKT PE=4 SV=2 - [F1PE28_CANLF]	15,97	1	6	6	20
E2RFB7	Amine oxidase OS=Canis lupus familiaris GN=AOC3 PE=3 SV=2 - [E2RFB7_CANLF]	11,01	1	0	6	18
E2RFC0	Amine oxidase OS=Canis lupus familiaris GN=AOC3 PE=3 SV=2 - [E2RFC0_CANLF]	10,95	1	0	6	18
F1P912	Tropomyosin 1 OS=Canis lupus familiaris GN=TPM1 PE=3 SV=1 - [F1P912_CANLF]	11,96	1	0	6	9
J9P7I3	Inter-alpha-trypsin inhibitor heavy chain 3 OS=Canis lupus familiaris GN=ITIH3 PE=4 SV=1 - [J9P7I3_CANLF]	13,83	1	0	6	12
H9GWG4	Inter-alpha-trypsin inhibitor heavy chain 3 OS=Canis lupus familiaris GN=ITIH3 PE=4 SV=2 - [H9GWG4_CANLF]	11,24	1	0	6	12
E7BUP9	Proteasome subunit beta type OS=Canis lupus familiaris GN=PSMB7 PE=2 SV=1 - [E7BUP9_CANLF]	33,57	1	0	6	68
E2RPC6	Proteasome subunit beta type OS=Canis lupus familiaris GN=PSMB7 PE=3 SV=2 - [E2RPC6_CANLF]	32,75	1	0	6	68
F1PGD4	Neural EGFL like 2 OS=Canis lupus familiaris GN=NELL2 PE=4 SV=2 - [F1PGD4_CANLF]	9,8	1	6	6	16
E2R7G9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2R7G9_CANLF]	58,09	1	5	5	89
F1PF90	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PF90_CANLF]	54,68	1	5	5	42
L7N0E8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0E8_CANLF]	44,72	1	5	5	11
A0A1K0FUG1	Globin A1 OS=Canis lupus familiaris GN=GLNA1 PE=3 SV=1 - [A0A1K0FUG1_CANLF]	43,54	1	0	5	20
J9JHZ3	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9JHZ3_CANLF]	42,11	1	0	5	20
F1PNY2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PNY2_CANLF]	40,76	1	2	5	234
P12278	Apolipoprotein C-II OS=Canis lupus familiaris GN=APOC2 PE=1 SV=1 - [APOC2_CANLF]	39,6	1	0	5	143
J9JHH5	Joining chain of multimeric IgA and IgM OS=Canis lupus familiaris GN=JCHAIN PE=4 SV=1 - [J9JHH5_CANLF]	35,85	1	5	5	20
Q95J95	Adiponectin (Fragment) OS=Canis lupus familiaris GN=APM1 PE=2 SV=1 - [Q95J95_CANLF]	31,44	1	0	5	104
E2RNL8	Apolipoprotein D OS=Canis lupus familiaris GN=APOD PE=3 SV=2 - [E2RNL8_CANLF]	28,78	1	0	5	28
E2RNM1	Apolipoprotein D OS=Canis lupus familiaris GN=APOD PE=3 SV=1 - [E2RNM1_CANLF]	27,83	1	0	5	28

F6XTZ1	Carboxypeptidase N subunit 1 OS=Canis lupus familiaris GN=CPN1 PE=4 SV=1 - [F6XTZ1_CANLF]	27,39	1	0	5	13
F1Q4D9	Retinol binding protein 4 OS=Canis lupus familiaris GN=RBP4 PE=3 SV=1 - [F1Q4D9_CANLF]	27,01	1	5	5	15
J9NWG4	Uncharacterized protein OS=Canis lupus familiaris GN=LOC610540 PE=4 SV=1 - [J9NWG4_CANLF]	26,75	1	1	5	91
B5U1S6	Adiponectin (Fragment) OS=Canis lupus PE=2 SV=1 - [B5U1S6_CANLU]	26,64	1	0	5	104
J9NWJ6	Apolipoprotein C-II OS=Canis lupus familiaris GN=APOC2 PE=4 SV=1 - [J9NWJ6_CANLF]	25,64	1	0	5	143
L7N0F1	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100687054 PE=4 SV=1 - [L7N0F1_CANLF]	25,47	1	0	5	277
E2RJC2	Complement C1q C chain OS=Canis lupus familiaris GN=C1QC PE=4 SV=1 - [E2RJC2_CANLF]	25,31	1	5	5	57
J9NYG8	Complement component 4 binding protein beta OS=Canis lupus familiaris GN=C4BPB PE=4 SV=1 - [J9NYG8_CA	25,1	1	0	5	13
A0A0B4J198	Adiponectin, C1Q and collagen domain containing OS=Canis lupus familiaris GN=ADIPOQ PE=4 SV=1 - [A0A0B4	25	1	0	5	104
Q76C76	Adiponectin OS=Canis lupus familiaris GN=apM1 PE=2 SV=1 - [Q76C76_CANLF]	25	1	0	5	104
F1PVL0	Complement component 4 binding protein beta OS=Canis lupus familiaris GN=C4BPB PE=4 SV=2 - [F1PVL0_CA	25	1	0	5	13
F6Y713	Alpha-1-acid glycoprotein OS=Canis lupus familiaris GN=LOC100685620 PE=3 SV=1 - [F6Y713_CANLF]	23,9	1	5	5	18
F1PYX9	Serpin family G member 1 OS=Canis lupus familiaris GN=SERPING1 PE=3 SV=2 - [F1PYX9_CANLF]	19,3	1	5	5	19
J9NUI6	Alpha-1-microglobulin/bikunin precursor OS=Canis lupus familiaris GN=AMBP PE=4 SV=1 - [J9NUI6_CANLF]	17,48	1	0	5	9
E2R796	Alpha-1-microglobulin/bikunin precursor OS=Canis lupus familiaris GN=AMBP PE=4 SV=2 - [E2R796_CANLF]	17,23	1	0	5	9
E2R2F7	Sex hormone binding globulin OS=Canis lupus familiaris GN=SHBG PE=4 SV=1 - [E2R2F7_CANLF]	17,04	1	5	5	19
F1Q041	Coagulation factor XIII B chain OS=Canis lupus familiaris GN=F13B PE=4 SV=2 - [F1Q041_CANLF]	13,41	1	5	5	10
E2RGT6	Complement C6 OS=Canis lupus familiaris GN=C6 PE=4 SV=2 - [E2RGT6_CANLF]	9,08	1	5	5	8
E2RT38	Maltase-glucoamylase OS=Canis lupus familiaris GN=MGAM PE=3 SV=2 - [E2RT38_CANLF]	4,64	1	0	5	6
F1PAQ3	Maltase-glucoamylase OS=Canis lupus familiaris GN=MGAM PE=3 SV=2 - [F1PAQ3_CANLF]	4,59	1	0	5	6
F1PA63	Lecithin-cholesterol acyltransferase OS=Canis lupus familiaris GN=LCAT PE=4 SV=1 - [F1PA63_CANLF]	19,41	1	5	5	43
F1PLT8	Sulfhydryl oxidase OS=Canis lupus familiaris GN=QSOX1 PE=4 SV=2 - [F1PLT8_CANLF]	9,54	1	5	5	10
T2KEN6	Pentaxin OS=Canis lupus familiaris GN=CRP PE=2 SV=1 - [T2KEN6_CANLF]	39,91	1	0	5	21
E2R5J0	Pentaxin OS=Canis lupus familiaris GN=CRP PE=3 SV=2 - [E2R5J0_CANLF]	35,89	1	0	5	21
F1PH86	Serpin family A member 3 OS=Canis lupus familiaris GN=SERPINA3 PE=3 SV=2 - [F1PH86_CANLF]	16,15	1	0	5	15
F1PH87	Serpin family A member 3 OS=Canis lupus familiaris GN=SERPINA3 PE=3 SV=2 - [F1PH87_CANLF]	15,11	1	0	5	15
P05123	Creatine kinase M-type OS=Canis lupus familiaris GN=CKM PE=1 SV=3 - [KCRM_CANLF]	15,75	1	5	5	16
Q28259	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris GN=GAPDH PE=2 SV=3 - [G3P_CANLF]	26,73	1	0	5	12
E2RQ24	Myosin light chain 1 OS=Canis lupus familiaris GN=MYL1 PE=4 SV=2 - [E2RQ24_CANLF]	26,63	1	0	5	9
F1P7C9	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris GN=LOC106559694 PE=3 SV=2 - [F1P7C	26,73	1	0	5	12
F1PBT3	Fructose-bisphosphate aldolase OS=Canis lupus familiaris PE=3 SV=2 - [F1PBT3_CANLF]	8,27	1	0	5	12
F1PTZ9	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris GN=GAPDH PE=3 SV=2 - [F1PTZ9_CANL	26,97	1	0	5	12
F1PV96	Myosin light chain 1 OS=Canis lupus familiaris GN=MYL1 PE=4 SV=2 - [F1PV96_CANLF]	25,98	1	0	5	9
J9P7A6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P7A6_CANLF]	22,57	1	0	5	12
J9P9X0	Interleukin 1 receptor accessory protein OS=Canis lupus familiaris GN=IL1RAP PE=4 SV=1 - [J9P9X0_CANLF]	12,24	1	0	5	13
F1PIL9	Interleukin 1 receptor accessory protein OS=Canis lupus familiaris GN=IL1RAP PE=4 SV=2 - [F1PIL9_CANLF]	11,19	1	0	5	13
J9NU59	Interleukin 1 receptor accessory protein OS=Canis lupus familiaris GN=IL1RAP PE=4 SV=1 - [J9NU59_CANLF]	11,19	1	0	5	13
F1PEM7	Insulin like growth factor binding protein 2 OS=Canis lupus familiaris GN=IGFBP2 PE=4 SV=1 - [F1PEM7_CANLF]	30,77	1	5	5	16
E2RN74	Carboxypeptidase B2 OS=Canis lupus familiaris GN=CPB2 PE=3 SV=1 - [E2RN74_CANLF]	20,57	1	5	5	36
F1PF02	Proteasome subunit beta type OS=Canis lupus familiaris GN=PSMB1 PE=3 SV=2 - [F1PF02_CANLF]	41,27	1	5	5	97
E2R0B6	Proteasome subunit beta type OS=Canis lupus familiaris GN=PSMB6 PE=3 SV=1 - [E2R0B6_CANLF]	36,4	1	5	5	95
E2RF52	Proteasome subunit alpha type OS=Canis lupus familiaris GN=PSMA8 PE=3 SV=2 - [E2RF52_CANLF]	24,8	1	2	5	81
J9P915	Proteasome endopeptidase complex OS=Canis lupus familiaris PE=3 SV=1 - [J9P915_CANLF]	21,29	1	0	5	22
L7N0I0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0I0_CANLF]	63,77	1	2	4	143
F1PH61	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PH61_CANLF]	58,82	1	4	4	29
J9P5C8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P5C8_CANLF]	53,85	1	2	4	241
J9NYY8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NYY8_CANLF]	53,61	1	2	4	347
F1PKI5	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=2 - [F1PKI5_CANLF]	52,07	1	1	4	18
J9P9H8	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100855558 PE=3 SV=1 - [J9P9H8_CANLF]	50,36	1	0	4	8
J9PAX5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAX5_CANLF]	47,37	1	2	4	215
J9P3B7	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=1 - [J9P3B7_CANLF]	44,68	1	0	4	43
F1PL50	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PL50_CANLF]	42,41	1	4	4	55
J9P0D4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P0D4_CANLF]	30,5	1	3	4	47
F1PYR5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PYR5_CANLF]	30,17	1	4	4	160
F1Q184	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1Q184_CANLF]	24,26	1	4	4	112
J9P7F7	Uncharacterized protein OS=Canis lupus familiaris GN=FCN2 PE=4 SV=1 - [J9P7F7_CANLF]	22,98	1	4	4	26
F1Q1W7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC610540 PE=4 SV=2 - [F1Q1W7_CANLF]	19,78	1	0	4	58
F1PCE2	Exostosin like glycosyltransferase 2 OS=Canis lupus familiaris GN=EXTL2 PE=4 SV=2 - [F1PCE2_CANLF]	17,72	1	0	4	6
J9P983	Exostosin like glycosyltransferase 2 OS=Canis lupus familiaris GN=EXTL2 PE=4 SV=1 - [J9P983_CANLF]	16,97	1	0	4	6
B5LX43	Factor XI OS=Canis lupus familiaris PE=2 SV=1 - [B5LX43_CANLF]	9,62	1	0	4	8
F1PPK8	Coagulation factor XI OS=Canis lupus familiaris GN=F11 PE=3 SV=2 - [F1PPK8_CANLF]	9,43	1	0	4	8
F6Y6T8	Uncharacterized protein OS=Canis lupus familiaris GN=PIGR PE=4 SV=1 - [F6Y6T8_CANLF]	8,27	1	1	4	4
F6XKC0	Complement C8 gamma chain OS=Canis lupus familiaris GN=C8G PE=3 SV=1 - [F6XKC0_CANLF]	39,11	1	2	4	16
F2Z4Q7	Serpin family F member 1 OS=Canis lupus familiaris GN=SERPINF1 PE=3 SV=1 - [F2Z4Q7_CANLF]	16,51	1	4	4	7
E2R674	Tropomyosin 2 (beta) OS=Canis lupus familiaris GN=TPM2 PE=4 SV=2 - [E2R674_CANLF]	13,59	1	0	4	5
F1PYE8	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris PE=3 SV=2 - [F1PYE8_CANLF]	22,66	1	0	4	10
F1PNS6	Peptidase D OS=Canis lupus familiaris GN=PEPD PE=3 SV=2 - [F1PNS6_CANLF]	18,65	1	4	4	6
J9P8Q8	Serpin family D member 1 OS=Canis lupus familiaris GN=SERPIND1 PE=3 SV=1 - [J9P8Q8_CANLF]	13,02	1	0	4	5
J9NWY1	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9NWY1_CANLF]	23,35	1	0	4	13
H9GWB5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [H9GWB5_CANLF]	34,78	1	0	4	8
J9P8Z6	Complement C9 OS=Canis lupus familiaris GN=C9 PE=4 SV=1 - [J9P8Z6_CANLF]	25,45	1	0	4	11
F1PSK2	Deleted in malignant brain tumors 1 OS=Canis lupus familiaris GN=DMBT1 PE=4 SV=2 - [F1PSK2_CANLF]	14,39	1	0	4	8
L7N0D6	Deleted in malignant brain tumors 1 OS=Canis lupus familiaris GN=DMBT1 PE=4 SV=1 - [L7N0D6_CANLF]	9,03	1	0	4	8
F1PRV8	Deleted in malignant brain tumors 1 OS=Canis lupus familiaris GN=DMBT1 PE=4 SV=2 - [F1PRV8_CANLF]	8,51	1	0	4	8
F1PSS2	Thrombospondin 4 OS=Canis lupus familiaris GN=THBS4 PE=4 SV=2 - [F1PSS2_CANLF]	8,25	1	3	4	13
Q28278	Vitamin K-dependent protein C OS=Canis lupus familiaris GN=PROC PE=2 SV=2 - [PROC_CANLF]	15,35	1	0	4	27
J9NVK0	Vitamin K-dependent protein C OS=Canis lupus familiaris GN=PROC PE=3 SV=1 - [J9NVK0_CANLF]	13,67	1	0	4	27
J9P482	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=1 - [J9P482_CANLF]	44,83	1	0	3	17
J9P6Z9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P6Z9_CANLF]	44,83	1	2	3	14
J9P182	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=1 - [J9P182_CANLF]	44,07	1	2	3	59
H9GWR0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [H9GWR0_CANLF]	36	1	0	3	159
J9PAD4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAD4_CANLF]	36	1	0	3	82
F1PDJ0	Apolipoprotein C-III OS=Canis lupus familiaris GN=APOC3 PE=4 SV=1 - [F1PDJ0_CANLF]	35	1	1	3	85
J9P8P3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P8P3_CANLF]	34,88	1	0	3	82
F6V8B5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F6V8B5_CANLF]	33,82	1	2	3	16
J9NYC0	Microfibril associated protein 4 OS=Canis lupus familiaris GN=MFAP4 PE=4 SV=1 - [J9NYC0_CANLF]	33,46	1	3	3	21
J9P1F6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P1F6_CANLF]	31,91	1	1	3	94
J9P1M7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P1M7_CANLF]	31,91	1	0	3	113
J9NWX7	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=1 - [J9NWX7_CANLF]	31,43	1	1	3	54
L7N0E7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC612180 PE=4 SV=1 - [L7N0E7_CANLF]	31,03	1	1	3	107
J9P455	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P455_CANLF]	30,95	1	1	3	18
J9P3L5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P3L5_CANLF]	30,61	1	1	3	58
J9P843	Apolipoprotein A-I OS=Canis lupus familiaris GN=APOA1 PE=4 SV=1 - [J9P843_CANLF]	27,54	1	0	3	14

P19708	Serum amyloid A protein OS=Canis lupus familiaris GN=SAA1 PE=1 SV=2 - [SAA_CANLF]	19,38	1	1	3	8
D5G335	Apolipoprotein E4 (Fragment) OS=Canis lupus familiaris PE=3 SV=1 - [D5G335_CANLF]	17,65	1	0	3	13
D5G341	Apolipoprotein E4 (Fragment) OS=Canis lupus familiaris PE=3 SV=1 - [D5G341_CANLF]	17,65	1	0	3	13
D5G334	Apolipoprotein E4 (Fragment) OS=Canis lupus familiaris PE=3 SV=1 - [D5G334_CANLF]	17,65	1	0	3	13
E2RNL3	Peroxiredoxin 4 OS=Canis lupus familiaris GN=PRDX4 PE=4 SV=1 - [E2RNL3_CANLF]	15,44	1	2	3	4
Q8MJZ1	Polymeric immunoglobulin receptor (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q8MJZ1_CANLF]	14,44	1	0	3	3
E2R109	Complement C8 alpha chain OS=Canis lupus familiaris GN=C8A PE=4 SV=1 - [E2R109_CANLF]	9,51	1	3	3	15
E2QYG1	Periostin OS=Canis lupus familiaris GN=POSTN PE=2 SV=2 - [E2QYG1_CANLF]	7,55	1	0	3	5
E2QUG4	Periostin OS=Canis lupus familiaris GN=POSTN PE=4 SV=2 - [E2QUG4_CANLF]	7,06	1	0	3	5
F1PAX2	Ceruloplasmin OS=Canis lupus familiaris GN=CP PE=3 SV=2 - [F1PAX2_CANLF]	3,94	1	3	3	6
F6PNA4	Uncharacterized protein OS=Canis lupus familiaris GN=LOC609402 PE=3 SV=1 - [F6PNA4_CANLF]	25,85	1	0	3	10
E2RN10	Beta-2-microglobulin OS=Canis lupus familiaris GN=B2M PE=1 SV=2 - [E2RN10_CANLF]	21,6	1	3	3	16
F1PR54	Uncharacterized protein OS=Canis lupus familiaris GN=LTF PE=3 SV=1 - [F1PR54_CANLF]	3,53	1	0	3	14
E2RRB2	Calcium-transporting ATPase OS=Canis lupus familiaris GN=ATP2A1 PE=3 SV=1 - [E2RRB2_CANLF]	4,6	1	0	3	8
J9P9P2	Calcium-transporting ATPase OS=Canis lupus familiaris GN=ATP2A1 PE=3 SV=1 - [J9P9P2_CANLF]	4,63	1	0	3	8
F1PGU1	Myosin light chain, phosphorylatable, fast skeletal muscle OS=Canis lupus familiaris GN=MYLPF PE=4 SV=2 - [F1	22,35	1	3	3	3
J9NST4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NST4_CANLF]	19,63	1	3	3	43
E2RFV9	Complement C9 OS=Canis lupus familiaris GN=C9 PE=4 SV=2 - [E2RFV9_CANLF]	8,68	1	3	3	22
Q8WN71	Myosin light chain 2 OS=Canis lupus familiaris GN=MYL2 PE=2 SV=1 - [Q8WN71_CANLF]	19,28	1	3	3	6
F6XIP5	Myosin light chain 6B OS=Canis lupus familiaris GN=MYL6B PE=4 SV=1 - [F6XIP5_CANLF]	14,35	1	2	3	5
J9PB14	Biotinidase OS=Canis lupus familiaris GN=BTD PE=4 SV=1 - [J9PB14_CANLF]	6,39	1	0	3	7
E2QY64	Biotinidase OS=Canis lupus familiaris GN=BTD PE=4 SV=2 - [E2QY64_CANLF]	6,24	1	0	3	7
Q6TEQ7	Annexin A2 OS=Canis lupus familiaris GN=ANXA2 PE=1 SV=1 - [ANXA2_CANLF]	13,57	1	3	3	7
E2R612	EGF containing fibulin like extracellular matrix protein 1 OS=Canis lupus familiaris GN=EFEMP1 PE=4 SV=1 - [E2	9,36	1	3	3	5
Q28284	CD44 antigen (Fragment) OS=Canis lupus familiaris GN=CD44 PE=2 SV=1 - [CD44_CANLF]	8,83	1	0	3	48
J9P423	CD44 antigen OS=Canis lupus familiaris GN=CD44 PE=4 SV=1 - [J9P423_CANLF]	8,54	1	0	3	48
F1PTZ7	CD44 antigen OS=Canis lupus familiaris GN=CD44 PE=4 SV=2 - [F1PTZ7_CANLF]	4,4	1	0	3	48
F1PCD8	Laminin subunit beta 1 OS=Canis lupus familiaris GN=LAMB1 PE=4 SV=2 - [F1PCD8_CANLF]	2,55	1	3	3	6
Q28262	Platelet-activating factor acetylhydrolase OS=Canis lupus familiaris GN=PLA2G7 PE=2 SV=1 - [PAFA_CANLF]	10,36	1	0	3	5
F1P9E5	Platelet-activating factor acetylhydrolase OS=Canis lupus familiaris GN=PLA2G7 PE=4 SV=1 - [F1P9E5_CANLF]	10,36	1	0	3	5
E2RKQ6	Galectin 3 binding protein OS=Canis lupus familiaris GN=LGALS3BP PE=4 SV=1 - [E2RKQ6_CANLF]	6,8	1	3	3	7
P02677	Fibrinogen beta chain (Fragment) OS=Canis lupus familiaris GN=FGB PE=1 SV=2 - [FIBB_CANLF]	61,29	1	1	2	22
P12800	Fibrinogen gamma chain (Fragment) OS=Canis lupus familiaris GN=FGG PE=1 SV=1 - [FIBG_CANLF]	58,33	1	1	2	19
J9NVZ4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NVZ4_CANLF]	38,14	1	0	2	45
L7N098	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N098_CANLF]	37,69	1	0	2	71
J9P4E8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P4E8_CANLF]	32,74	1	0	2	45
F1PSJ5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PSJ5_CANLF]	31,25	1	0	2	253
J9P050	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P050_CANLF]	30,46	1	1	2	39
F1PKN5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PKN5_CANLF]	29,45	1	2	2	33
L7N0E6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0E6_CANLF]	28,67	1	1	2	15
P12279	Apolipoprotein C-III OS=Canis lupus familiaris GN=APOC3 PE=2 SV=1 - [APOC3_CANLF]	28	1	0	2	68
J9P590	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P590_CANLF]	27,94	1	2	2	24
E2QYB2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2QYB2_CANLF]	27,93	1	0	2	16
L7N0K1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0K1_CANLF]	26,44	1	1	2	40
J9NS91	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NS91_CANLF]	25,83	1	0	2	16
J9P6L3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P6L3_CANLF]	25,41	1	0	2	13
J9JHN3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9JHN3_CANLF]	24,81	1	1	2	29
J9P0X4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P0X4_CANLF]	24,6	1	0	2	16
J9P3U4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P3U4_CANLF]	24,6	1	0	2	16
J9P7N3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P7N3_CANLF]	24,6	1	0	2	13
J9PBB2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PBB2_CANLF]	24,6	1	0	2	16
F1Q185	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1Q185_CANLF]	22,67	1	2	2	4
F1PQU0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PQU0_CANLF]	21,43	1	1	2	62
J9P0V6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P0V6_CANLF]	20,57	1	1	2	21
J9P9B9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P9B9_CANLF]	19,05	1	1	2	31
J9NZT2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NZT2_CANLF]	17,6	1	1	2	13
L7N0E5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0E5_CANLF]	17,24	1	1	2	45
J9NY02	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NY02_CANLF]	15,71	1	0	2	67
A0A096P6K5	Serum amyloid A protein OS=Canis lupus familiaris GN=LOC476879 PE=3 SV=1 - [A0A096P6K5_CANLF]	14,73	1	0	2	6
J9NVE9	Serum amyloid A protein OS=Canis lupus familiaris GN=LOC102155886 PE=3 SV=1 - [J9NVE9_CANLF]	14,62	1	0	2	6
E2RBD4	Serum amyloid A protein OS=Canis lupus familiaris PE=3 SV=1 - [E2RBD4_CANLF]	13,01	1	0	2	6
E2R9D2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2R9D2_CANLF]	8,52	1	2	2	9
J9PAK7	Guanine nucleotide-binding protein subunit gamma OS=Canis lupus familiaris GN=GNG2 PE=3 SV=1 - [J9PAK7_	6,73	1	0	2	5
E2R886	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2R886_CANLF]	6,73	1	2	2	4
J9PB28	Fibrinogen like 2 OS=Canis lupus familiaris GN=FGL2 PE=4 SV=1 - [J9PB28_CANLF]	5,9	1	2	2	33
E2RH18	Complement factor properdin OS=Canis lupus familiaris GN=CFP PE=4 SV=1 - [E2RH18_CANLF]	5,6	1	2	2	4
E2R141	Complement C8 beta chain OS=Canis lupus familiaris GN=C8B PE=4 SV=1 - [E2R141_CANLF]	5,25	1	2	2	3
O97624	Keratin 17 (Fragment) OS=Canis lupus familiaris PE=3 SV=1 - [O97624_CANLF]	5	1	0	2	2
Q28275	Fibronectin (Fragment) OS=Canis lupus familiaris GN=FN1 PE=2 SV=2 - [FINC_CANLF]	4,98	1	0	2	3
F1PRB0	Uncharacterized protein OS=Canis lupus familiaris GN=LOC486530 PE=3 SV=2 - [F1PRB0_CANLF]	4,56	1	0	2	4
F1PVL5	Keratin 79 OS=Canis lupus familiaris GN=KRT79 PE=3 SV=2 - [F1PVL5_CANLF]	4,3	1	0	2	66
E2R917	Keratin 75 OS=Canis lupus familiaris GN=KRT75 PE=3 SV=2 - [E2R917_CANLF]	4,17	1	0	2	66
F1PTS8	Uncharacterized protein OS=Canis lupus familiaris GN=LOC486523 PE=3 SV=1 - [F1PTS8_CANLF]	4,03	1	0	2	13
L7N095	Keratin 5 OS=Canis lupus familiaris GN=KRT5 PE=3 SV=1 - [L7N095_CANLF]	4,03	1	0	2	13
E2R8Z5	Keratin 5 OS=Canis lupus familiaris GN=KRT5 PE=3 SV=2 - [E2R8Z5_CANLF]	3,86	1	0	2	67
L7N094	Keratin 3 OS=Canis lupus familiaris GN=KRT3 PE=3 SV=1 - [L7N094_CANLF]	3,65	1	0	2	66
Q6EIZ1	Keratin, type II cytoskeletal 2 epidermal OS=Canis lupus familiaris GN=KRT2 PE=2 SV=1 - [K22E_CANLF]	3,63	1	0	2	17
F1PTX4	Keratin, type II cytoskeletal 2 epidermal OS=Canis lupus familiaris GN=KRT2 PE=3 SV=2 - [F1PTX4_CANLF]	3,62	1	0	2	17
F1Q0N9	Keratin 19 OS=Canis lupus familiaris GN=KRT19 PE=3 SV=1 - [F1Q0N9_CANLF]	3,51	1	0	2	2
F1PSS8	Protein S (alpha) OS=Canis lupus familiaris GN=PROS1 PE=4 SV=2 - [F1PSS8_CANLF]	3,39	1	2	2	2
Q9GLD3	Transferrin receptor protein 1 OS=Canis lupus familiaris GN=TFRC PE=1 SV=1 - [TFR1_CANLF]	3,38	1	0	2	3
F1PEN6	Transferrin receptor protein 1 OS=Canis lupus familiaris GN=TFRC PE=2 SV=1 - [F1PEN6_CANLF]	3,38	1	0	2	3
F1Q0Q9	Keratin 17 OS=Canis lupus familiaris GN=KRT17 PE=3 SV=2 - [F1Q0Q9_CANLF]	3,23	1	0	2	2
E2R7U2	Keratin 13 OS=Canis lupus familiaris GN=KRT13 PE=3 SV=2 - [E2R7U2_CANLF]	3,2	1	0	2	2
E2R7W6	Uncharacterized protein OS=Canis lupus familiaris GN=KRT42 PE=3 SV=1 - [E2R7W6_CANLF]	3,09	1	0	2	2
E2R8Q7	Keratin 15 OS=Canis lupus familiaris GN=KRT15 PE=3 SV=2 - [E2R8Q7_CANLF]	3,06	1	0	2	2
J9P4H9	Keratin 13 OS=Canis lupus familiaris GN=KRT13 PE=3 SV=1 - [J9P4H9_CANLF]	3,05	1	0	2	2
J9P4Q9	Keratin 15 OS=Canis lupus familiaris GN=KRT15 PE=3 SV=1 - [J9P4Q9_CANLF]	2,97	1	0	2	2
F1Q0R0	Keratin 14 OS=Canis lupus familiaris GN=KRT14 PE=3 SV=2 - [F1Q0R0_CANLF]	2,9	1	0	2	2
J9NWS3	Keratin, type I cytoskeletal 9 OS=Canis lupus familiaris GN=KRT9 PE=3 SV=1 - [J9NWS3_CANLF]	2,69	1	0	2	15
H9GWY1	Inter-alpha-trypsin inhibitor heavy chain family member 4 OS=Canis lupus familiaris GN=ITIH4 PE=4 SV=2 - [H9	2,61	1	0	2	3
H2BF45	Attractin (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [H2BF45_CANLF]	2,6	1	0	2	2
E2R150	Keratin 24 OS=Canis lupus familiaris GN=KRT24 PE=3 SV=2 - [E2R150_CANLF]	2,59	1	0	2	2

J9P0I1	Keratin, type I cytoskeletal 9 OS=Canis lupus familiaris GN=KRT9 PE=3 SV=1 - [J9P0I1_CANLF]	2,58	1	0	2	15
F1Q0N7	Keratin, type I cytoskeletal 9 OS=Canis lupus familiaris GN=KRT9 PE=3 SV=1 - [F1Q0N7_CANLF]	2,47	1	0	2	15
E2RR43	Coiled-coil domain containing 18 OS=Canis lupus familiaris GN=CCDC18 PE=4 SV=2 - [E2RR43_CANLF]	2,41	1	0	2	2
J9NUU7	Coiled-coil domain containing 18 OS=Canis lupus familiaris GN=CCDC18 PE=4 SV=1 - [J9NUU7_CANLF]	2,41	1	0	2	2
J9P196	Coiled-coil domain containing 18 OS=Canis lupus familiaris GN=CCDC18 PE=4 SV=1 - [J9P196_CANLF]	2,33	1	0	2	2
O18740	Keratin, type I cytoskeletal 9 OS=Canis lupus familiaris GN=KRT9 PE=3 SV=1 - [K1C9_CANLF]	2,04	1	0	2	15
F1PG69	Collagen type III alpha 1 chain OS=Canis lupus familiaris GN=COL3A1 PE=4 SV=2 - [F1PG69_CANLF]	1,43	1	0	2	7
J9P0L0	Collagen type III alpha 1 chain OS=Canis lupus familiaris GN=COL3A1 PE=4 SV=1 - [J9P0L0_CANLF]	1,43	1	0	2	7
F1PBY8	A-kinase anchoring protein 9 OS=Canis lupus familiaris GN=AKAP9 PE=4 SV=2 - [F1PBY8_CANLF]	0,31	1	0	2	7
J9P4D9	A-kinase anchoring protein 9 OS=Canis lupus familiaris GN=AKAP9 PE=4 SV=1 - [J9P4D9_CANLF]	0,3	1	0	2	7
E2RGB0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2RGB0_CANLF]	20,66	1	2	2	3
E2RRN8	Vasorin OS=Canis lupus familiaris GN=VASN PE=4 SV=1 - [E2RRN8_CANLF]	6,7	1	2	2	6
F1PAB0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PAB0_CANLF]	5,27	1	2	2	2
J9P654	Peptidoglycan recognition protein 2 OS=Canis lupus familiaris GN=PGLYRP2 PE=4 SV=1 - [J9P654_CANLF]	8,82	1	0	2	2
F6XZU1	Peptidoglycan recognition protein 2 OS=Canis lupus familiaris GN=PGLYRP2 PE=4 SV=1 - [F6XZU1_CANLF]	7,83	1	0	2	2
J9P7Q8	Carboxylic ester hydrolase OS=Canis lupus familiaris GN=CEL PE=3 SV=1 - [J9P7Q8_CANLF]	4,35	1	0	2	13
F1PHD0	Carboxyl ester lipase OS=Canis lupus familiaris GN=CEL PE=3 SV=1 - [F1PHD0_CANLF]	3,93	1	0	2	13
F6Y3P9	Gelsolin OS=Canis lupus familiaris GN=GSN PE=4 SV=1 - [F6Y3P9_CANLF]	3,58	1	2	2	2
E2RPP1	Laminin subunit alpha 3 OS=Canis lupus familiaris GN=LAMA3 PE=4 SV=2 - [E2RPP1_CANLF]	1,86	1	2	2	2
F1Q2D1	Centrosomal protein 290 OS=Canis lupus familiaris GN=CEP290 PE=4 SV=2 - [F1Q2D1_CANLF]	0,87	1	0	2	3
E2R0F5	Centrosomal protein 290 OS=Canis lupus familiaris GN=CEP290 PE=4 SV=1 - [E2R0F5_CANLF]	0,85	1	0	2	3
F1PEV3	Deltex E3 ubiquitin ligase 3L OS=Canis lupus familiaris GN=DTX3L PE=4 SV=2 - [F1PEV3_CANLF]	3,26	1	1	2	2
Q9TV65	Angiotensinogen (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q9TV65_CANLF]	20,44	1	0	2	10
F6X7L0	Tropomyosin 4 OS=Canis lupus familiaris GN=TPM4 PE=3 SV=1 - [F6X7L0_CANLF]	8,45	1	0	2	3
F1PCH3	Enolase 1 OS=Canis lupus familiaris GN=ENO1 PE=3 SV=2 - [F1PCH3_CANLF]	7,69	1	0	2	6
A0A0N9JE84	Tropomyosin 4 delta OS=Canis lupus familiaris GN=Tpm4 PE=2 SV=1 - [A0A0N9JE84_CANLF]	8,45	1	0	2	3
O62755	Pyruvate kinase M (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [O62755_CANLF]	41,38	1	0	2	2
F1PJP1	Dynein axonemal heavy chain 11 OS=Canis lupus familiaris GN=DNAH11 PE=4 SV=2 - [F1PJP1_CANLF]	0,97	1	0	2	2
J9P9P6	Dynein axonemal heavy chain 11 OS=Canis lupus familiaris GN=DNAH11 PE=4 SV=1 - [J9P9P6_CANLF]	0,97	1	0	2	2
Q2YF02	Vitronectin (Fragment) OS=Canis lupus familiaris PE=4 SV=1 - [Q2YF02_CANLF]	40,54	1	0	2	7
E2RMA3	Secreted protein acidic and cysteine rich OS=Canis lupus familiaris GN=SPARC PE=4 SV=1 - [E2RMA3_CANLF]	13,53	1	2	2	3
F1PHN8	Serpin family A member 4 OS=Canis lupus familiaris GN=SERPINA4 PE=3 SV=2 - [F1PHN8_CANLF]	6,35	1	2	2	6
P19540	Coagulation factor IX OS=Canis lupus familiaris GN=F9 PE=1 SV=1 - [FA9_CANLF]	6,19	1	0	2	7
G1K2D7	Coagulation factor IX OS=Canis lupus familiaris GN=F9 PE=3 SV=1 - [G1K2D7_CANLF]	6,1	1	0	2	7
E2R8F7	Myosin light chain 3 OS=Canis lupus familiaris GN=MYL3 PE=4 SV=2 - [E2R8F7_CANLF]	10,48	1	2	2	2
E2R1Z0	Four and a half LIM domains 1 OS=Canis lupus familiaris GN=FHL1 PE=4 SV=2 - [E2R1Z0_CANLF]	8,45	1	2	2	3
E2REZ4	Coiled-coil and C2 domain containing 2A OS=Canis lupus familiaris GN=CC2D2A PE=4 SV=2 - [E2REZ4_CANLF]	2,96	1	2	2	3
E2RT39	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [E2RT39_CANLF]	2,14	1	0	2	18
J9NV81	ALG13, UDP-N-acetylglucosaminyltransferase subunit OS=Canis lupus familiaris GN=ALG13 PE=4 SV=1 - [J9NV8	2,86	1	2	2	3
F1P6B7	Annexin OS=Canis lupus familiaris GN=ANXA1 PE=3 SV=1 - [F1P6B7_CANLF]	6,96	1	2	2	5
F2Z4N0	Uncharacterized protein OS=Canis lupus familiaris GN=ACTA2 PE=3 SV=1 - [F2Z4N0_CANLF]	6,1	1	0	2	3
J9PB40	Erbb2 interacting protein OS=Canis lupus familiaris GN=ERBIN PE=4 SV=1 - [J9PB40_CANLF]	0,92	1	0	2	3
E2QWR8	Erbb2 interacting protein OS=Canis lupus familiaris GN=ERBIN PE=4 SV=2 - [E2QWR8_CANLF]	0,85	1	0	2	3
J9P2B7	Histone H2A OS=Canis lupus familiaris GN=LOC611231 PE=3 SV=1 - [J9P2B7_CANLF]	17,97	1	0	2	4
E2QX34	Histone H2A OS=Canis lupus familiaris PE=3 SV=2 - [E2QX34_CANLF]	17,97	1	0	2	4
F1PFZ6	Histone H2A OS=Canis lupus familiaris GN=LOC488254 PE=3 SV=2 - [F1PFZ6_CANLF]	17,97	1	0	2	4
F1PFZ7	Histone H2A OS=Canis lupus familiaris GN=HIST2H2AC PE=3 SV=2 - [F1PFZ7_CANLF]	17,83	1	0	2	4
L7N0D9	Histone H2A OS=Canis lupus familiaris GN=H2AFJ PE=3 SV=1 - [L7N0D9_CANLF]	17,83	1	0	2	4
J9JHP2	Histone H2A OS=Canis lupus familiaris GN=LOC100856200 PE=3 SV=1 - [J9JHP2_CANLF]	17,69	1	0	2	4
J9P664	Histone H2A OS=Canis lupus familiaris GN=LOC100855609 PE=3 SV=1 - [J9P664_CANLF]	17,69	1	0	2	4
J9NRH7	Histone H2A OS=Canis lupus familiaris GN=LOC106558252 PE=3 SV=1 - [J9NRH7_CANLF]	17,69	1	0	2	4
J9P6M9	Histone H2A OS=Canis lupus familiaris GN=LOC488297 PE=3 SV=1 - [J9P6M9_CANLF]	17,69	1	0	2	4
J9P0L5	Histone H2A OS=Canis lupus familiaris GN=HIST2H2AA4 PE=3 SV=1 - [J9P0L5_CANLF]	17,69	1	0	2	4
F1P790	Histone H2A OS=Canis lupus familiaris GN=HIST3H2A PE=3 SV=2 - [F1P790_CANLF]	17,69	1	0	2	4
J9P5B1	Histone H2A OS=Canis lupus familiaris GN=LOC488289 PE=3 SV=1 - [J9P5B1_CANLF]	17,69	1	0	2	4
F1P7D1	Histone H2A OS=Canis lupus familiaris GN=HIST1H2AA PE=3 SV=2 - [F1P7D1_CANLF]	17,56	1	0	2	4
J9NZY9	Histone H2A OS=Canis lupus familiaris PE=3 SV=1 - [J9NZY9_CANLF]	17,16	1	0	2	4
J9P0B2	Histone H2A OS=Canis lupus familiaris GN=LOC488291 PE=3 SV=1 - [J9P0B2_CANLF]	17,04	1	0	2	4
E2RNB0	Histone H2A OS=Canis lupus familiaris GN=H2AFX PE=3 SV=1 - [E2RNB0_CANLF]	16,08	1	0	2	4
F6XXE7	Follicle-stimulating hormone receptor OS=Canis lupus familiaris GN=FSHR PE=3 SV=1 - [F6XXE7_CANLF]	8,56	1	1	2	3
J9P5S6	Uncharacterized protein OS=Canis lupus familiaris GN=LOC490399 PE=4 SV=1 - [J9P5S6_CANLF]	6,83	1	0	2	4
E2R8K8	Uncharacterized protein OS=Canis lupus familiaris GN=LOC490399 PE=4 SV=2 - [E2R8K8_CANLF]	6,81	1	0	2	4
F1PSC8	Tyrosine-protein kinase OS=Canis lupus familiaris GN=SYK PE=3 SV=1 - [F1PSC8_CANLF]	6	1	1	2	2
F1PLV6	Fibulin-1 OS=Canis lupus familiaris GN=FBLN1 PE=3 SV=2 - [F1PLV6_CANLF]	5,08	1	2	2	9
E2R1C3	Proteasome subunit alpha type OS=Canis lupus familiaris PE=3 SV=2 - [E2R1C3_CANLF]	16,53	1	2	2	4
A0A0E3ZQS9	XynC protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08580 PE=4 SV=1 - [A0A0E3ZQS9_I	15,24	1	2	2	2
F1PUB5	Proteasome endopeptidase complex OS=Canis lupus familiaris GN=PSMA7 PE=3 SV=2 - [F1PUB5_CANLF]	13,24	1	1	2	2
Q2VCP3	von Willebrand factor (Fragment) OS=Canis lupus GN=VWF PE=4 SV=1 - [Q2VCP3_CANLU]	10,66	1	0	2	4
C7G0S1	von Willebrand factor (Fragment) OS=Canis lupus GN=vwf PE=4 SV=1 - [C7G0S1_CANLU]	6,57	1	0	2	4
F1PCS8	CD93 molecule OS=Canis lupus familiaris GN=CD93 PE=4 SV=1 - [F1PCS8_CANLF]	4,94	1	2	2	3
F1PF31	Tenascin C OS=Canis lupus familiaris GN=TNC PE=4 SV=1 - [F1PF31_CANLF]	1,43	1	0	2	3
J9NRP5	Tenascin C OS=Canis lupus familiaris GN=TNC PE=4 SV=1 - [J9NRP5_CANLF]	1,34	1	0	2	3
J9NUH6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NUH6_CANLF]	11,19	1	0	2	2
E2R161	Secreted phosphoprotein 1 OS=Canis lupus familiaris GN=SPP1 PE=4 SV=1 - [E2R161_CANLF]	12,04	1	0	2	7
E2R231	Dickkopf WNT signaling pathway inhibitor 3 OS=Canis lupus familiaris GN=DKK3 PE=4 SV=2 - [E2R231_CANLF]	11,53	1	0	2	8
E2RNR9	Osteomodulin OS=Canis lupus familiaris GN=OMD PE=4 SV=2 - [E2RNR9_CANLF]	4,81	1	0	2	4
J9P319	Osteomodulin OS=Canis lupus familiaris GN=OMD PE=4 SV=1 - [J9P319_CANLF]	4,83	1	0	2	4
Q3HTT3	Osteopontin (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q3HTT3_CANLF]	11,28	1	1	2	24
W0RY37	Dickkopf 3 homolog OS=Canis lupus familiaris GN=Dkk-3 PE=2 SV=1 - [W0RY37_CANLF]	11,49	1	0	2	8
E2QYM7	Thrombospondin 3 OS=Canis lupus familiaris GN=THBS3 PE=4 SV=1 - [E2QYM7_CANLF]	4,71	1	1	2	4
F1PE53	Rho associated coiled-coil containing protein kinase 2 OS=Canis lupus familiaris GN=ROCK2 PE=3 SV=2 - [F1PE5	1,15	1	2	2	2
A0A0M5JRD3	Fibrinogen gamma chain (Fragment) OS=Canis lupus baileyi GN=FGG PE=4 SV=1 - [A0A0M5JRD3_CANLU]	91,3	1	0	1	20
A0A0H4NYY6	Plasminogen (Fragment) OS=Canis lupus familiaris GN=plg PE=4 SV=1 - [A0A0H4NYY6_CANLF]	88	1	0	1	67
P68213	Fibrinogen alpha chain (Fragment) OS=Canis lupus familiaris GN=FGA PE=1 SV=1 - [FIBA_CANLF]	42,86	1	0	1	1
P01784	Ig heavy chain V region GOM OS=Canis lupus familiaris PE=1 SV=1 - [HV01_CANLF]	16,67	1	0	1	61
E2QYB1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2QYB1_CANLF]	14,61	1	0	1	5
L7N0L4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0L4_CANLF]	14,18	1	0	1	61
P01785	Ig heavy chain V region MOO OS=Canis lupus familiaris PE=1 SV=1 - [HV02_CANLF]	13,68	1	1	1	1
E2R8C5	Immunoglobulin lambda variable 2-33 (non-functional) OS=Canis lupus familiaris GN=IGLV2-33 PE=4 SV=2 - [E2	12,9	1	1	1	10
L7N0G5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0G5_CANLF]	12,75	1	0	1	5
P01618	Ig kappa chain V region GOM OS=Canis lupus familiaris PE=1 SV=1 - [KV1_CANLF]	12,04	1	0	1	5
L7N0J0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0J0_CANLF]	11,35	1	0	1	3
J9PAL2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAL2_CANLF]	10,66	1	0	1	5

J9PAM5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAM5_CANLF]	10,32	1	0	1	5
L7N0P9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0P9_CANLF]	10,32	1	0	1	5
F1PPK4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PPK4_CANLF]	10,16	1	0	1	5
J9NTU3	FGFR1OP N-terminal like OS=Canis lupus familiaris GN=FOPNL PE=4 SV=1 - [J9NTU3_CANLF]	9,77	1	1	1	2
J9NVY7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NVY7_CANLF]	9,77	1	0	1	5
J9NSV4	Immunoglobulin heavy constant mu OS=Canis lupus familiaris GN=IGHM PE=4 SV=1 - [J9NSV4_CANLF]	9,48	1	0	1	1
L7N0J5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0J5_CANLF]	9,41	1	1	1	1
J9PAP4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAP4_CANLF]	9,38	1	0	1	1
F1PKL6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PKL6_CANLF]	8,22	1	1	1	6
E2R047	Uncharacterized protein OS=Canis lupus familiaris GN=BLOC1S1 PE=4 SV=2 - [E2R047_CANLF]	8	1	1	1	1
F1PVJ7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PVJ7_CANLF]	7,54	1	1	1	1
J9P477	PAXX, non-homologous end joining factor OS=Canis lupus familiaris GN=PAXX PE=4 SV=1 - [J9P477_CANLF]	6,95	1	0	1	1
F6XGN4	PAXX, non-homologous end joining factor OS=Canis lupus familiaris GN=PAXX PE=4 SV=1 - [F6XGN4_CANLF]	6,37	1	0	1	1
E2QUU8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2QUU8_CANLF]	6,21	1	0	1	4
M9PM25	RNA-binding protein Raly short isoform OS=Canis lupus familiaris GN=RALY PE=2 SV=1 - [M9PM25_CANLF]	6,14	1	0	1	2
E2RLM4	Cyclin dependent kinase 6 OS=Canis lupus familiaris GN=CDK6 PE=3 SV=1 - [E2RLM4_CANLF]	6,13	1	1	1	1
A0A059Q851	Cytochrome b (Fragment) OS=Canis lupus familiaris GN=CYTB PE=3 SV=1 - [A0A059Q851_CANLF]	6,02	1	0	1	1
B2XXZ0	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [B2XXZ0_MOKV]	5,94	1	0	1	2
B2XXZ5	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [B2XXZ5_MOKV]	5,94	1	0	1	2
A0A0S1U081	Glial fibrillary acidic protein transcript variant gamma OS=Canis lupus familiaris GN=GFAP PE=2 SV=1 - [A0A0S1	5,85	1	0	1	2
E2R552	RALY heterogeneous nuclear ribonucleoprotein OS=Canis lupus familiaris GN=RALY PE=4 SV=1 - [E2R552_CANL	5,8	1	0	1	2
J9NTG9	Eukaryotic translation initiation factor 3 subunit I OS=Canis lupus familiaris GN=EIF3I PE=4 SV=1 - [J9NTG9_CAN	5,74	1	1	1	3
A0A0M4HNB4	Apolipoprotein B-100 (Fragment) OS=Canis lupus baileyi GN=APOB PE=4 SV=1 - [A0A0M4HNB4_CANLU]	5,61	1	0	1	2
A0A0M5JRC1	Apolipoprotein B-100 (Fragment) OS=Canis lupus GN=APOB PE=4 SV=1 - [A0A0M5JRC1_CANLU]	5,61	1	0	1	2
D6N0H1	Apolipoprotein B (Fragment) OS=Canis lupus GN=APOB PE=4 SV=1 - [D6N0H1_CANLU]	5,43	1	0	1	2
Q3ZEB8	Apolipoprotein B (Fragment) OS=Canis lupus GN=APOB PE=4 SV=1 - [Q3ZEB8_CANLU]	5,43	1	0	1	2
E2RTL7	Uncharacterized protein OS=Canis lupus familiaris GN=RTP4 PE=4 SV=2 - [E2RTL7_CANLF]	5,37	1	1	1	1
C7G0N2	Apolipoprotein B (Fragment) OS=Canis lupus GN=APOB PE=4 SV=1 - [C7G0N2_CANLU]	5,31	1	0	1	2
H8Y2Y6	Cytochrome b OS=Canis lupus familiaris GN=CYTB PE=3 SV=1 - [H8Y2Y6_CANLF]	5,28	1	0	1	1
Q49RE5	Cytochrome b OS=Canis lupus familiaris GN=CYTB PE=3 SV=1 - [Q49RE5_CANLF]	5,28	1	0	1	1
E2RQF8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2RQF8_CANLF]	5,11	1	1	1	2
J9JH97	Transient receptor potential cation channel subfamily M member 1 OS=Canis lupus familiaris GN=TRPM1 PE=4	4,76	1	0	1	2
J9P831	Uncharacterized protein OS=Canis lupus familiaris GN=LOC491421 PE=4 SV=1 - [J9P831_CANLF]	4,75	1	1	1	2
J9P8U3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P8U3_CANLF]	4,53	1	0	1	15
J9P8U8	RWD domain containing 1 OS=Canis lupus familiaris GN=RWDD1 PE=4 SV=1 - [J9P8U8_CANLF]	4,53	1	1	1	1
E2RLY1	Cysteine protease OS=Canis lupus familiaris GN=ATG4A PE=3 SV=2 - [E2RLY1_CANLF]	4,51	1	1	1	2
F1PD33	Peptidyl-prolyl cis-trans isomerase OS=Canis lupus familiaris GN=PPIL6 PE=3 SV=1 - [F1PD33_CANLF]	4,51	1	1	1	1
F1P8E4	Mitochondrial ribosomal protein L39 OS=Canis lupus familiaris GN=MRPL39 PE=4 SV=2 - [F1P8E4_CANLF]	4,48	1	1	1	1
A0A0E3ZPC2	Penicillin-binding protein 2 OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_04260 PE=4 SV=1 - [	4,35	1	1	1	1
F1Q187	Interleukin 3 receptor subunit alpha OS=Canis lupus familiaris GN=IL3RA PE=4 SV=2 - [F1Q187_CANLF]	4,32	1	1	1	1
J9P8B0	Dipeptidyl peptidase 4 OS=Canis lupus familiaris GN=DPP4 PE=4 SV=1 - [J9P8B0_CANLF]	4,32	1	0	1	2
E2R4Z8	High mobility group 20B OS=Canis lupus familiaris GN=HMG20B PE=4 SV=1 - [E2R4Z8_CANLF]	4,11	1	1	1	2
P06871	Cationic trypsin OS=Canis lupus familiaris PE=2 SV=1 - [TRY1_CANLF]	4,07	1	0	1	18
F1PCE8	Uncharacterized protein OS=Canis lupus familiaris GN=LOC475521 PE=3 SV=1 - [F1PCE8_CANLF]	4,07	1	0	1	18
E2RHG2	Uncharacterized protein OS=Canis lupus familiaris GN=PRDX1 PE=4 SV=1 - [E2RHG2_CANLF]	4,02	1	0	1	1
H9GW62	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [H9GW62_CANLF]	3,99	1	0	1	1
E2R3K2	Cytochrome P450 family 2 subfamily R member 1 OS=Canis lupus familiaris GN=CYP2R1 PE=3 SV=1 - [E2R3K2_	3,99	1	1	1	1
F1PWG0	Uncharacterized protein OS=Canis lupus familiaris GN=IFIT5 PE=4 SV=2 - [F1PWG0_CANLF]	3,94	1	1	1	1
E2RKT9	Ubiquitin conjugating enzyme E2 L5, pseudogene OS=Canis lupus familiaris GN=UBE2L5P PE=3 SV=1 - [E2RKT9_	3,9	1	0	1	1
F1PHI1	RIC8 guanine nucleotide exchange factor B OS=Canis lupus familiaris GN=RIC8B PE=4 SV=2 - [F1PHI1_CANLF]	3,85	1	0	1	1
F1PG16	Uncharacterized protein OS=Canis lupus familiaris GN=CD5L PE=4 SV=2 - [F1PG16_CANLF]	3,82	1	0	1	1
W8VYQ1	Apoptosis inhibitor of macrophage OS=Canis lupus familiaris GN=CD5L PE=2 SV=1 - [W8VYQ1_CANLF]	3,82	1	0	1	1
F1PHI2	RIC8 guanine nucleotide exchange factor B OS=Canis lupus familiaris GN=RIC8B PE=4 SV=2 - [F1PHI2_CANLF]	3,78	1	0	1	1
F1PAX5	Uncharacterized protein OS=Canis lupus familiaris GN=CD5L PE=4 SV=2 - [F1PAX5_CANLF]	3,75	1	0	1	1
E2RG47	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Canis lupus familiaris GN=ST	3,63	1	1	1	1
J9PAG6	Growth arrest specific 8 OS=Canis lupus familiaris GN=GAS8 PE=4 SV=1 - [J9PAG6_CANLF]	3,56	1	0	1	1
F1P7H0	Growth arrest specific 8 OS=Canis lupus familiaris GN=GAS8 PE=4 SV=2 - [F1P7H0_CANLF]	3,51	1	0	1	1
J9P488	Uncharacterized protein n=1 Tax=Canis lupus familiaris RepID=J9P488_CANLF	3,24	1	0	1	1
Q95LG6	Skeletal muscle ryanodine receptor (Fragment) OS=Canis lupus familiaris GN=RYR1 PE=2 SV=1 - [Q95LG6_CANL	3,13	1	1	1	1
E2RM11	Nucleobindin 2 OS=Canis lupus familiaris GN=NUCB2 PE=4 SV=2 - [E2RM11_CANLF]	3,1	1	1	1	3
E2R984	Polycomb group ring finger 1 OS=Canis lupus familiaris GN=PCGF1 PE=4 SV=2 - [E2R984_CANLF]	3,09	1	1	1	1
F6X6Y7	Transcription elongation factor A3 OS=Canis lupus familiaris GN=TCEA3 PE=4 SV=1 - [F6X6Y7_CANLF]	2,99	1	0	1	1
E2R1N7	Prenylcysteine oxidase 1 OS=Canis lupus familiaris GN=PCYOX1 PE=3 SV=1 - [E2R1N7_CANLF]	2,97	1	1	1	1
F1PP29	Immunoglobulin heavy constant epsilon OS=Canis lupus familiaris GN=IGHE PE=4 SV=1 - [F1PP29_CANLF]	2,95	1	1	1	1
J9NZM2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NZM2_CANLF]	2,87	1	0	1	1
E2RLF1	Prosaposin OS=Canis lupus familiaris GN=PSAP PE=4 SV=1 - [E2RLF1_CANLF]	2,86	1	1	1	4
J9NZ31	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 OS=Canis lupus familiaris GN=P	2,81	1	0	1	5
E2RI96	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 OS=Canis lupus familiaris GN=P	2,77	1	0	1	5
L7N096	Keratin 4 OS=Canis lupus familiaris GN=LOC608027 PE=3 SV=1 - [L7N096_CANLF]	2,67	1	0	1	2
E2RCT8	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [E2RCT8_CANLF]	2,65	1	0	1	4
F1PXT2	Rho guanine nucleotide exchange factor 38 OS=Canis lupus familiaris GN=ARHGEF38 PE=4 SV=2 - [F1PXT2_CA	2,58	1	0	1	1
E2QUS3	Rho guanine nucleotide exchange factor 38 OS=Canis lupus familiaris GN=ARHGEF38 PE=4 SV=2 - [E2QUS3_CA	2,57	1	0	1	1
A0A0S1U0J7	Glial fibrillary acidic protein transcript variant delta/epsilon OS=Canis lupus familiaris GN=GFAP PE=2 SV=1 - [A	2,55	1	0	1	2
A0A0S1U281	Glial fibrillary acidic protein transcript variant alpha OS=Canis lupus familiaris GN=GFAP PE=2 SV=1 - [A0A0S1U	2,54	1	0	1	2
E2RS09	Glial fibrillary acidic protein OS=Canis lupus familiaris GN=GFAP PE=3 SV=1 - [E2RS09_CANLF]	2,54	1	0	1	2
E2R2C8	Keratin 80 OS=Canis lupus familiaris GN=KRT80 PE=3 SV=1 - [E2R2C8_CANLF]	2,43	1	0	1	2
F1PB85	Serpin family A member 7 OS=Canis lupus familiaris GN=SERPINA7 PE=3 SV=2 - [F1PB85_CANLF]	2,42	1	1	1	16
F1PSB5	Uncharacterized protein OS=Canis lupus familiaris GN=CFH PE=4 SV=2 - [F1PSB5_CANLF]	2,4	1	0	1	2
E2RJG1	Armadillo repeat containing, X-linked 3 OS=Canis lupus familiaris GN=ARMCX3 PE=4 SV=2 - [E2RJG1_CANLF]	2,37	1	1	1	1
E2R5W6	GC, vitamin D binding protein OS=Canis lupus familiaris GN=GC PE=3 SV=2 - [E2R5W6_CANLF]	2,32	1	0	1	2
E2RIY6	Transcription elongation factor A3 OS=Canis lupus familiaris GN=TCEA3 PE=4 SV=2 - [E2RIY6_CANLF]	2,3	1	0	1	1
F1PFZ8	Serine/threonine kinase 40 OS=Canis lupus familiaris GN=STK40 PE=4 SV=2 - [F1PFZ8_CANLF]	2,3	1	1	1	1
A0A0S1U0N3	Glial fibrillary acidic protein transcript variant kappa OS=Canis lupus familiaris GN=GFAP PE=2 SV=1 - [A0A0S1U	2,29	1	0	1	2
F1PNZ8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PNZ8_CANLF]	2,27	1	1	1	5
F1P841	GC, vitamin D binding protein OS=Canis lupus familiaris GN=GC PE=3 SV=2 - [F1P841_CANLF]	2,26	1	0	1	2
F1PW98	Uncharacterized protein OS=Canis lupus familiaris GN=KRT8 PE=3 SV=2 - [F1PW98_CANLF]	2,23	1	0	1	2
J9PBJ0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PBJ0_CANLF]	2,21	1	0	1	1
F1PJM6	MAP7 domain containing 3 OS=Canis lupus familiaris GN=MAP7D3 PE=4 SV=2 - [F1PJM6_CANLF]	2,2	1	0	1	2
Q9TU80	Coxsackie-adenovirus-receptor homolog (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q9TU80_CANLF]	2,19	1	1	1	1
J9P314	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P314_CANLF]	2,15	1	0	1	1
F1PU95	HtrA serine peptidase 1 OS=Canis lupus familiaris GN=HTRA1 PE=4 SV=2 - [F1PU95_CANLF]	2,13	1	0	1	59
E2QST8	Protein phosphatase 1 regulatory subunit 16B OS=Canis lupus familiaris GN=PPP1R16B PE=4 SV=1 - [E2QST8_C	2,11	1	1	1	1
F1P9G4	DEK proto-oncogene OS=Canis lupus familiaris GN=DEK PE=4 SV=2 - [F1P9G4_CANLF]	2,1	1	1	1	3

E2QYQ4	Cytidine monophosphate N-acetylneuraminic acid synthetase OS=Canis lupus familiaris GN=CMAS PE=4 SV=1 -	2,07	1	1	1	1
J9NVE8	MAP7 domain containing 3 OS=Canis lupus familiaris GN=MAP7D3 PE=4 SV=1 - [J9NVE8_CANLF]	2,05	1	0	1	2
E2REU6	Uncharacterized protein OS=Canis lupus familiaris GN=KRT18 PE=3 SV=2 - [E2REU6_CANLF]	2,01	1	0	1	1
F1Q4H9	Uncharacterized protein n=1 Tax=Canis lupus familiaris RepID=F1Q4H9_CANLF	1,95	1	1	1	1
A0A189RMP1	Major outer capsid protein OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A189RMP1_AHSV8]	1,89	1	0	1	1
A0A189RMT5	Major outer capsid protein OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A189RMT5_AHSV8]	1,89	1	0	1	1
A0A0U2DHR4	VP2 OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A0U2DHR4_AHSV8]	1,89	1	0	1	1
A0A0U2DD11	VP2 OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A0U2DD11_AHSV8]	1,89	1	0	1	1
A0A189RMR3	Major outer capsid protein OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A189RMR3_AHSV8]	1,89	1	0	1	1
A0A0U2DGT4	VP2 OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A0U2DGT4_AHSV8]	1,89	1	0	1	1
E2R489	Keratin 84 OS=Canis lupus familiaris GN=KRT84 PE=3 SV=1 - [E2R489_CANLF]	1,88	1	0	1	2
E2R568	Keratin 4 OS=Canis lupus familiaris GN=LOC608027 PE=3 SV=2 - [E2R568_CANLF]	1,86	1	0	1	2
F1PW10	Transforming growth factor beta induced OS=Canis lupus familiaris GN=TGFBI PE=4 SV=2 - [F1PW10_CANLF]	1,85	1	0	1	1
E2R959	Keratin 4 OS=Canis lupus familiaris GN=LOC608027 PE=3 SV=2 - [E2R959_CANLF]	1,85	1	0	1	2
J9P2W2	Transforming growth factor beta induced OS=Canis lupus familiaris GN=TGFBI PE=4 SV=1 - [J9P2W2_CANLF]	1,83	1	0	1	1
E2QT78	Uncharacterized protein n=1 Tax=Canis lupus familiaris RepID=E2QT78_CANLF	1,77	1	1	1	1
J9P2L4	HtrA serine peptidase 1 OS=Canis lupus familiaris GN=HTRA1 PE=4 SV=1 - [J9P2L4_CANLF]	1,77	1	0	1	59
F1PQ21	Astrotactin 1 OS=Canis lupus familiaris GN=ASTN1 PE=4 SV=2 - [F1PQ21_CANLF]	1,77	1	1	1	1
A0A0U2DH70	VP2 OS=African horse sickness virus 7 GN=VP2 PE=4 SV=1 - [A0A0U2DH70_AHSV7]	1,7	1	1	1	1
F1PBD4	PDZ domain containing 7 OS=Canis lupus familiaris GN=PDZD7 PE=4 SV=2 - [F1PBD4_CANLF]	1,7	1	0	1	5
E2RKK3	Coiled-coil domain containing 151 OS=Canis lupus familiaris GN=CCDC151 PE=4 SV=2 - [E2RKK3_CANLF]	1,68	1	1	1	2
A0A0E3ZQT8	Sulfate transporter OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08670 PE=3 SV=1 - [A0A0E3Z	1,63	1	1	1	1
E2RSZ2	Hedgehog acyltransferase OS=Canis lupus familiaris GN=HHAT PE=3 SV=2 - [E2RSZ2_CANLF]	1,62	1	1	1	1
A0MJA4	Niemann-Pick C1-like 1 protein OS=Canis lupus familiaris GN=NPC1L1 PE=2 SV=1 - [A0MJA4_CANLF]	1,58	1	0	1	1
A0A0K2CW84	Capsid protein OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A0K2CW84_AHSV2]	1,52	1	0	1	1
A0A189RMI6	Major outer capsid protein OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A189RMI6_AHSV2]	1,52	1	0	1	1
A0A0N9LU47	Capsid protein OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A0N9LU47_AHSV2]	1,52	1	0	1	1
A0A189RMM8	Major outer capsid protein OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A189RMM8_AHSV2]	1,52	1	0	1	1
A0A0U2DHN5	VP2 OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A0U2DHN5_AHSV2]	1,52	1	0	1	1
A0A189RMK9	Major outer capsid protein OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A189RMK9_AHSV2]	1,52	1	0	1	1
A0A0U1XQZ7	Outer capsid protein OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A0U1XQZ7_AHSV2]	1,52	1	0	1	1
A0A189RMN7	Major outer capsid protein OS=African horse sickness virus 2 GN=VP2 PE=4 SV=1 - [A0A189RMN7_AHSV2]	1,52	1	0	1	1
F1PYT6	Diacylglycerol kinase OS=Canis lupus familiaris GN=DGKK PE=3 SV=2 - [F1PYT6_CANLF]	1,51	1	1	1	1
F1PMS2	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Canis lupus familiaris GN=PPP2R5A PE	1,49	1	0	1	1
J9NTU6	YEATS domain containing 2 OS=Canis lupus familiaris GN=YEATS2 PE=4 SV=1 - [J9NTU6_CANLF]	1,35	1	0	1	1
F6UZ61	YEATS domain containing 2 OS=Canis lupus familiaris GN=YEATS2 PE=4 SV=1 - [F6UZ61_CANLF]	1,34	1	0	1	1
E2RQR3	Leucyl-tRNA synthetase 2, mitochondrial OS=Canis lupus familiaris GN=LARS2 PE=3 SV=1 - [E2RQR3_CANLF]	1,33	1	1	1	1
F1PDT5	Centlein OS=Canis lupus familiaris GN=CNTLN PE=4 SV=2 - [F1PDT5_CANLF]	1,29	1	0	1	1
E2RQU1	Ankyrin repeat domain 26 OS=Canis lupus familiaris GN=ANKRD26 PE=4 SV=2 - [E2RQU1_CANLF]	1,27	1	1	1	1
F6URD2	Serine/threonine kinase 3 OS=Canis lupus familiaris GN=STK3 PE=4 SV=1 - [F6URD2_CANLF]	1,22	1	0	1	1
E2RS10	Eukaryotic translation initiation factor 2 alpha kinase 4 OS=Canis lupus familiaris GN=EIF2AK4 PE=4 SV=1 - [E2R	1,21	1	1	1	1
E2REE8	Amine oxidase OS=Canis lupus familiaris GN=AOC2 PE=3 SV=1 - [E2REE8_CANLF]	1,19	1	0	1	2
Q8MJU5	Alpha-fetoprotein OS=Canis lupus familiaris GN=AFP PE=2 SV=1 - [FETA_CANLF]	1,15	1	0	1	8
F1PXN2	Alpha-fetoprotein OS=Canis lupus familiaris GN=AFP PE=3 SV=1 - [F1PXN2_CANLF]	1,15	1	0	1	8
F1Q4B9	Centlein OS=Canis lupus familiaris GN=CNTLN PE=4 SV=2 - [F1Q4B9_CANLF]	1,14	1	0	1	1
F1P9F6	Uncharacterized protein n=1 Tax=Canis lupus familiaris RepID=F1P9F6_CANLF	1,13	1	1	1	1
F1Q4J4	Lysine demethylase 5A OS=Canis lupus familiaris GN=KDM5A PE=4 SV=2 - [F1Q4J4_CANLF]	1,13	1	1	1	1
E2RQA6	Bardet-Biedl syndrome 7 protein homolog n=1 Tax=Canis lupus familiaris RepID=E2RQA6_CANLF	1,12	1	1	1	1
F1PM26	CD109 molecule OS=Canis lupus familiaris GN=CD109 PE=4 SV=2 - [F1PM26_CANLF]	1,11	1	1	1	1
E2RKW5	Nuclear receptor corepressor 1 OS=Canis lupus familiaris GN=NCOR1 PE=4 SV=2 - [E2RKW5_CANLF]	1,1	1	1	1	1
F1PRL9	Transient receptor potential cation channel subfamily M member 1 OS=Canis lupus familiaris GN=TRPM1 PE=4	1,09	1	0	1	2
E2RI36	Nuclear transcription factor, X-box binding 1 OS=Canis lupus familiaris GN=NFX1 PE=4 SV=2 - [E2RI36_CANLF]	1,07	1	1	1	1
F6V049	Alpha-mannosidase OS=Canis lupus familiaris GN=MAN2A2 PE=3 SV=1 - [F6V049_CANLF]	1,04	1	0	1	18
J9NRR7	GRAM domain containing 1A OS=Canis lupus familiaris GN=GRAMD1A PE=4 SV=1 - [J9NRR7_CANLF]	1,03	1	0	1	1
E2RSC3	Chromosome 16 open reading frame 58 OS=Canis lupus familiaris GN=C16orf58 PE=4 SV=2 - [E2RSC3_CANLF]	1,02	1	0	1	1
F1PD61	Uncharacterized protein n=1 Tax=Canis lupus familiaris RepID=F1PD61_CANLF	1,02	1	0	1	1
J9P435	Uncharacterized protein n=1 Tax=Canis lupus familiaris RepID=J9P435_CANLF	1,02	1	0	1	1
F1PJ75	PCF11 cleavage and polyadenylation factor subunit OS=Canis lupus familiaris GN=PCF11 PE=4 SV=2 - [F1PJ75_	0,99	1	1	1	1
F1Q4I0	Microtubule associated serine/threonine kinase family member 4 OS=Canis lupus familiaris GN=MAST4 PE=4 S	0,94	1	1	1	1
E2RNZ8	Tudor domain containing 9 OS=Canis lupus familiaris GN=TDRD9 PE=4 SV=2 - [E2RNZ8_CANLF]	0,9	1	0	1	3
E2QVB0	ADP ribosylation factor guanine nucleotide exchange factor 2 OS=Canis lupus familiaris GN=ARFGEF2 PE=4 SV=	0,9	1	1	1	1
E2RNZ9	Tudor domain containing 9 OS=Canis lupus familiaris GN=TDRD9 PE=4 SV=2 - [E2RNZ9_CANLF]	0,89	1	0	1	3
J9P8U1	Tudor domain containing 9 OS=Canis lupus familiaris GN=TDRD9 PE=4 SV=1 - [J9P8U1_CANLF]	0,89	1	0	1	3
E2RJ91	BTB domain containing 7 OS=Canis lupus familiaris GN=BTBD7 PE=4 SV=1 - [E2RJ91_CANLF]	0,89	1	1	1	3
E2REY7	GRAM domain containing 1A OS=Canis lupus familiaris GN=GRAMD1A PE=4 SV=2 - [E2REY7_CANLF]	0,87	1	0	1	1
F1PUE8	Centrosomal protein 85 like OS=Canis lupus familiaris GN=CEP85L PE=4 SV=2 - [F1PUE8_CANLF]	0,85	1	0	1	1
F1PAK4	Transmembrane 9 superfamily member OS=Canis lupus familiaris PE=3 SV=2 - [F1PAK4_CANLF]	0,85	1	0	1	4
E2RTG6	Ras protein specific guanine nucleotide releasing factor 2 OS=Canis lupus familiaris GN=RASGRF2 PE=4 SV=2 - [	0,85	1	0	1	1
J9NYT7	Ras protein specific guanine nucleotide releasing factor 2 OS=Canis lupus familiaris GN=RASGRF2 PE=4 SV=1 - [	0,83	1	0	1	1
E2RR68	Family with sequence similarity 129 member B OS=Canis lupus familiaris GN=FAM129B PE=4 SV=1 - [E2RR68_C	0,81	1	0	1	4
J9NUI8	Ras protein specific guanine nucleotide releasing factor 2 OS=Canis lupus familiaris GN=RASGRF2 PE=4 SV=1 - [	0,81	1	0	1	1
J9PAM7	Ras protein specific guanine nucleotide releasing factor 2 OS=Canis lupus familiaris GN=RASGRF2 PE=4 SV=1 - [	0,8	1	0	1	1
A0A0N7CYP2	VP1 OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A0N7CYP2_AHSV4]	0,77	1	0	1	1
A0A189RN00	RNA-dependent RNA polymerase OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A189RN00_AHSV8	0,77	1	0	1	1
F1PKV6	NLR family pyrin domain containing 14 OS=Canis lupus familiaris GN=NLRP14 PE=4 SV=2 - [F1PKV6_CANLF]	0,75	1	0	1	1
F1P818	SART1, U4/U6.U5 tri-snRNP-associated protein 1 OS=Canis lupus familiaris GN=SART1 PE=4 SV=2 - [F1P818_CA	0,75	1	0	1	1
F1PGJ8	Leucine rich repeat and coiled-coil centrosomal protein 1 OS=Canis lupus familiaris GN=LRRCC1 PE=4 SV=2 - [F1	0,68	1	1	1	43
E2R754	PDZ domain containing 7 OS=Canis lupus familiaris GN=PDZD7 PE=4 SV=2 - [E2R754_CANLF]	0,66	1	0	1	5
E2RJ74	NLR family pyrin domain containing 14 OS=Canis lupus familiaris GN=NLRP14 PE=4 SV=1 - [E2RJ74_CANLF]	0,64	1	0	1	1
F1PXC8	WWC family member 3 OS=Canis lupus familiaris GN=WWC3 PE=4 SV=2 - [F1PXC8_CANLF]	0,64	1	0	1	6
J9P0N3	Activating transcription factor 7 interacting protein OS=Canis lupus familiaris GN=ATF7IP PE=4 SV=1 - [J9P0N3_	0,64	1	0	1	1
E2R990	CCR4-NOT transcription complex subunit 1 OS=Canis lupus familiaris GN=CNOT1 PE=4 SV=2 - [E2R990_CANLF]	0,63	1	0	1	1
E2REJ6	Activating transcription factor 7 interacting protein OS=Canis lupus familiaris GN=ATF7IP PE=4 SV=2 - [E2REJ6_	0,63	1	0	1	1
H9GWC8	Tubulin folding cofactor D OS=Canis lupus familiaris GN=TBCD PE=4 SV=1 - [H9GWC8_CANLF]	0,62	1	1	1	2
F1P8M0	F-box protein, helicase, 18 OS=Canis lupus familiaris GN=FBXO18 PE=4 SV=2 - [F1P8M0_CANLF]	0,62	1	0	1	1
F1PLK8	Programmed cell death 11 OS=Canis lupus familiaris GN=PDCD11 PE=4 SV=2 - [F1PLK8_CANLF]	0,59	1	1	1	1
A0A091DVX3	Alpha-mannosidase 2x n=102 Tax=Theria RepID=A0A091DVX3_FUKDA	0,56	1	0	1	2
E2QXZ2	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Canis lupus familiaris GN=SART3 PE=4 SV=2 - [E2C	0,55	1	0	1	1
E2RK31	Centrosomal protein 152 OS=Canis lupus familiaris GN=CEP152 PE=4 SV=2 - [E2RK31_CANLF]	0,54	1	0	1	28
J9JHU7	Centromere protein E OS=Canis lupus familiaris GN=CENPE PE=3 SV=1 - [J9JHU7_CANLF]	0,53	1	0	1	38
J9NTC4	Centrosomal protein 152 OS=Canis lupus familiaris GN=CEP152 PE=4 SV=1 - [J9NTC4_CANLF]	0,52	1	0	1	28
J9P002	Centrosomal protein 152 OS=Canis lupus familiaris GN=CEP152 PE=4 SV=1 - [J9P002_CANLF]	0,51	1	0	1	28
F1PWF3	Zinc finger CCCH-type containing 6 OS=Canis lupus familiaris GN=ZC3H6 PE=4 SV=2 - [F1PWF3_CANLF]	0,51	1	0	1	1

F1PUS9	Dystonin OS=Canis lupus familiaris GN=DST PE=4 SV=2 - [F1PUS9_CANLF]	0,41	1	0	1	1
F6UMS1	Suppressor of glucose, autophagy associated 1 OS=Canis lupus familiaris GN=SOGA1 PE=4 SV=1 - [F6UMS1_CA	0,41	1	0	1	1
F1Q188	Kinesin family member 21B OS=Canis lupus familiaris GN=KIF21B PE=3 SV=2 - [F1Q188_CANLF]	0,37	1	0	1	1
J9P991	Kinesin family member 21B OS=Canis lupus familiaris GN=KIF21B PE=3 SV=1 - [J9P991_CANLF]	0,37	1	0	1	1
E2RPN3	Citron rho-interacting serine/threonine kinase OS=Canis lupus familiaris GN=CIT PE=3 SV=2 - [E2RPN3_CANLF]	0,34	1	0	1	38
J9P1U4	Nuclear mitotic apparatus protein 1 OS=Canis lupus familiaris GN=NUMA1 PE=4 SV=1 - [J9P1U4_CANLF]	0,33	1	0	1	1
E2R099	Upstream transcription factor family member 3 OS=Canis lupus familiaris GN=USF3 PE=4 SV=1 - [E2R099_CANL	0,31	1	1	1	1
E2R5Y7	Nuclear mitotic apparatus protein 1 OS=Canis lupus familiaris GN=NUMA1 PE=4 SV=2 - [E2R5Y7_CANLF]	0,29	1	0	1	1
J9P0W8	Dystonin OS=Canis lupus familiaris GN=DST PE=4 SV=1 - [J9P0W8_CANLF]	0,27	1	0	1	1
F1PV45	Titin OS=Canis lupus familiaris GN=TTN PE=4 SV=2 - [F1PV45_CANLF]	0,03	1	1	1	2
P32750	Cholinesterase (Fragment) OS=Canis lupus familiaris GN=BCHE PE=2 SV=1 - [CHLE_CANLF]	23,4	1	0	1	1
E2RI73	RNA polymerase I subunit D OS=Canis lupus familiaris GN=POLR1D PE=4 SV=1 - [E2RI73_CANLF]	18,05	1	1	1	1
Q9TS44	Cholecystokinins OS=Canis lupus familiaris GN=CCK PE=1 SV=1 - [CCKN_CANLF]	17,24	1	0	1	1
F1PAE2	ATP synthase subunit d, mitochondrial OS=Canis lupus familiaris PE=3 SV=2 - [F1PAE2_CANLF]	16,67	1	1	1	1
J9JHX3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9JHX3_CANLF]	16,35	1	1	1	2
E2QXV4	IZUMO family member 4 OS=Canis lupus familiaris GN=IZUMO4 PE=4 SV=2 - [E2QXV4_CANLF]	16,06	1	1	1	1
F6XCB0	Stathmin OS=Canis lupus familiaris GN=STMN2 PE=3 SV=1 - [F6XCB0_CANLF]	13,97	1	1	1	1
E2RQ33	Transmembrane protein 89 OS=Canis lupus familiaris GN=TMEM89 PE=4 SV=1 - [E2RQ33_CANLF]	11,95	1	0	1	3
A0A0E3ZQE7	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_01685 PE=4 SV=1 - [A0/	11,89	1	1	1	1
F1PGG1	Polycomb group ring finger 3 OS=Canis lupus familiaris GN=PCGF3 PE=4 SV=2 - [F1PGG1_CANLF]	9,09	1	1	1	1
E2RDW8	Single-pass membrane protein with coiled-coil domains 3 OS=Canis lupus familiaris GN=SMCO3 PE=4 SV=2 - [E2	8,89	1	1	1	1
G1K283	Cholecystokinins OS=Canis lupus familiaris GN=CCK PE=3 SV=2 - [G1K283_CANLF]	8,77	1	0	1	1
E2QXZ5	Ankyrin repeat and SOCS box containing 12 OS=Canis lupus familiaris GN=ASB12 PE=4 SV=1 - [E2QXZ5_CANLF]	8,46	1	1	1	1
J9JHH2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9JHH2_CANLF]	8,33	1	0	1	1
F1PYW6	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [F1PYW6_CANLF]	8,15	1	1	1	1
U6C2S1	Prekallikrein OS=Canis lupus familiaris GN=PK PE=2 SV=1 - [U6C2S1_CANLF]	7,94	1	0	1	1
E2RAT7	Sulfotransferase OS=Canis lupus familiaris GN=CHST1 PE=3 SV=1 - [E2RAT7_CANLF]	7,54	1	0	1	1
E9ABV3	Sulfotransferase (Fragment) OS=Canis lupus familiaris GN=sulfo1 PE=2 SV=1 - [E9ABV3_CANLF]	7,54	1	0	1	1
J9P6C1	Uncharacterized protein OS=Canis lupus familiaris GN=LOC477516 PE=4 SV=1 - [J9P6C1_CANLF]	7,36	1	1	1	1
J9NRX7	Docking protein 4 OS=Canis lupus familiaris GN=DOK4 PE=4 SV=1 - [J9NRX7_CANLF]	7,36	1	1	1	1
E2RBF4	THUMP domain containing 1 OS=Canis lupus familiaris GN=THUMPD1 PE=4 SV=2 - [E2RBF4_CANLF]	7,26	1	1	1	1
J9P9J8	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P9J8_CANLF]	6,94	1	0	1	1
J9P7S6	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P7S6_CANLF]	6,71	1	0	1	1
E2QXN3	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [E2QXN3_CANLF]	6,62	1	0	1	1
L7N0H6	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [L7N0H6_CANLF]	6,49	1	0	1	1
J9NZS5	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9NZS5_CANLF]	6,45	1	0	1	1
J9P608	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P608_CANLF]	6,45	1	0	1	1
J9P9Q1	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P9Q1_CANLF]	6,45	1	0	1	1
E2QZG2	Ribosomal protein L23a OS=Canis lupus familiaris GN=RPL23A PE=3 SV=1 - [E2QZG2_CANLF]	6,41	1	0	1	1
J9NZX1	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9NZX1_CANLF]	6,41	1	0	1	1
J9P168	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P168_CANLF]	6,41	1	0	1	1
J9P1I4	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P1I4_CANLF]	6,41	1	0	1	1
J9PAG2	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9PAG2_CANLF]	6,41	1	0	1	1
J9P016	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P016_CANLF]	6,37	1	0	1	1
J9P690	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P690_CANLF]	6,37	1	1	1	1
A0A0E3V3J9	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_01870 PE=4 SV=1 - [A0/	6,23	1	1	1	1
E2QYE5	Cilia and flagella associated protein 36 OS=Canis lupus familiaris GN=CFAP36 PE=4 SV=2 - [E2QYE5_CANLF]	5,8	1	1	1	1
F1PV43	Capping actin protein of muscle Z-line alpha subunit 3 OS=Canis lupus familiaris GN=CAPZA3 PE=3 SV=2 - [F1PV	5,69	1	1	1	1
J9P785	Myb like, SWIRM and MPN domains 1 OS=Canis lupus familiaris GN=MYSM1 PE=4 SV=1 - [J9P785_CANLF]	5,59	1	0	1	1
J9P2L1	Regulatory factor X associated protein OS=Canis lupus familiaris GN=RFXAP PE=4 SV=1 - [J9P2L1_CANLF]	5,58	1	1	1	1
J9NWP1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NWP1_CANLF]	5,42	1	1	1	1
J9P2D6	Methyl-CpG-binding protein 2 OS=Canis lupus familiaris GN=MECP2 PE=4 SV=1 - [J9P2D6_CANLF]	5,35	1	0	1	1
A0A0E3ZQM7	DctP OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08940 PE=4 SV=1 - [A0A0E3ZQM7_PASMD	5,29	1	1	1	1
E2QX15	Methyl-CpG-binding protein 2 OS=Canis lupus familiaris GN=MECP2 PE=4 SV=1 - [E2QX15_CANLF]	5,22	1	0	1	1
J9P653	Uncharacterized protein OS=Canis lupus familiaris GN=CATIP PE=4 SV=1 - [J9P653_CANLF]	5,15	1	1	1	3
E2RFJ8	Translational activator of cytochrome c oxidase I OS=Canis lupus familiaris GN=TACO1 PE=4 SV=1 - [E2RFJ8_CA	5,03	1	1	1	1
E2QZ36	Fasciculation and elongation protein zeta 2 OS=Canis lupus familiaris GN=FEZ2 PE=4 SV=1 - [E2QZ36_CANLF]	4,58	1	0	1	2
E2RE57	Ectonucleoside triphosphate diphosphohydrolase 3 OS=Canis lupus familiaris GN=ENTPD3 PE=3 SV=1 - [E2RE57	4,54	1	1	1	1
F1PDG2	Uncharacterized protein OS=Canis lupus familiaris GN=LOC607286 PE=4 SV=2 - [F1PDG2_CANLF]	4,44	1	0	1	1
Q8HY39	Prenylated Rab acceptor protein 1 OS=Canis lupus familiaris GN=RABAC1 PE=2 SV=1 - [PRAF1_CANLF]	4,32	1	0	1	4
F1P766	PRA1 family protein OS=Canis lupus familiaris GN=RABAC1 PE=3 SV=1 - [F1P766_CANLF]	4,32	1	0	1	4
E2QZ38	Fasciculation and elongation protein zeta 2 OS=Canis lupus familiaris GN=FEZ2 PE=4 SV=1 - [E2QZ38_CANLF]	4,26	1	0	1	2
F1PIF2	Cathepsin Z OS=Canis lupus familiaris GN=CTSZ PE=3 SV=2 - [F1PIF2_CANLF]	4,21	1	1	1	2
J9NU80	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102156332 PE=4 SV=1 - [J9NU80_CANLF]	4,11	1	0	1	1
E2R926	Fukutin OS=Canis lupus familiaris GN=FKTN PE=4 SV=1 - [E2R926_CANLF]	3,9	1	1	1	4
E2R550	Calcyphosine like OS=Canis lupus familiaris GN=CAPSL PE=4 SV=2 - [E2R550_CANLF]	3,85	1	1	1	2
J9P2P7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC607286 PE=4 SV=1 - [J9P2P7_CANLF]	3,73	1	0	1	1
F1Q2W3	Prune homolog 2 OS=Canis lupus familiaris GN=PRUNE2 PE=4 SV=2 - [F1Q2W3_CANLF]	3,58	1	0	1	1
F1P9J2	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102156332 PE=4 SV=2 - [F1P9J2_CANLF]	3,51	1	0	1	1
F1PG90	Leucine rich repeat LGI family member 3 OS=Canis lupus familiaris GN=LGI3 PE=4 SV=2 - [F1PG90_CANLF]	3,43	1	1	1	2
J9P1S6	Cyclin dependent kinase 1 OS=Canis lupus familiaris GN=CDK1 PE=3 SV=1 - [J9P1S6_CANLF]	3,24	1	0	1	1
J9P5Z0	Myosin-1 OS=Canis lupus familiaris GN=MYH1 PE=4 SV=1 - [J9P5Z0_CANLF]	3,23	1	0	1	2
E2RGJ9	Cyclin dependent kinase 1 OS=Canis lupus familiaris GN=CDK1 PE=3 SV=1 - [E2RGJ9_CANLF]	3,03	1	0	1	1
J9P6T3	Phospholipid transfer protein OS=Canis lupus familiaris GN=PLTP PE=4 SV=1 - [J9P6T3_CANLF]	3,03	1	0	1	1
E2R9P0	Protein phosphatase 1 regulatory inhibitor subunit 1B OS=Canis lupus familiaris GN=PPP1R1B PE=4 SV=2 - [E2R	2,93	1	1	1	1
F1P8V0	Phospholipid transfer protein OS=Canis lupus familiaris GN=PLTP PE=4 SV=2 - [F1P8V0_CANLF]	2,92	1	0	1	1
F1PXA5	Uncharacterized protein OS=Canis lupus familiaris GN=cOR10D5P PE=3 SV=2 - [F1PXA5_CANLF]	2,9	1	0	1	1
L7N0C7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC489338 PE=3 SV=1 - [L7N0C7_CANLF]	2,87	1	0	1	1
F1PAC5	Mitogen-activated protein kinase kinase kinase 11 OS=Canis lupus familiaris GN=MAP3K11 PE=4 SV=2 - [F1PAC	2,86	1	1	1	6
J9PBI2	MMS22 like, DNA repair protein OS=Canis lupus familiaris GN=MMS22L PE=4 SV=1 - [J9PBI2_CANLF]	2,86	1	0	1	2
F1Q321	Olfactory receptor OS=Canis lupus familiaris GN=LOC100687027 PE=3 SV=2 - [F1Q321_CANLF]	2,83	1	0	1	1
F1P9B7	Nuclear receptor interacting protein 2 OS=Canis lupus familiaris GN=NRIP2 PE=4 SV=2 - [F1P9B7_CANLF]	2,78	1	1	1	2
I2FJU3	55 kDa erythrocyte membrane protein OS=Canis lupus familiaris GN=MPP1 PE=2 SV=1 - [I2FJU3_CANLF]	2,76	1	1	1	1
E2RCS2	Regulatory factor X5 OS=Canis lupus familiaris GN=RFX5 PE=4 SV=1 - [E2RCS2_CANLF]	2,75	1	1	1	1
J9NUB7	Forkhead box P3 OS=Canis lupus familiaris GN=FOXP3 PE=4 SV=1 - [J9NUB7_CANLF]	2,61	1	0	1	1
J9P514	RB associated KRAB zinc finger OS=Canis lupus familiaris GN=RBAK PE=3 SV=1 - [J9P514_CANLF]	2,61	1	1	1	2
E2QY95	DExD-box helicase 39A OS=Canis lupus familiaris GN=DDX39A PE=4 SV=1 - [E2QY95_CANLF]	2,58	1	1	1	1
E2QY00	Potassium voltage-gated channel subfamily B member 1 OS=Canis lupus familiaris GN=KCNB1 PE=3 SV=1 - [E2C	2,56	1	1	1	1
J9P5K5	Centromere protein H OS=Canis lupus familiaris GN=CENPH PE=4 SV=1 - [J9P5K5_CANLF]	2,55	1	0	1	1
E2R8X4	Centromere protein H OS=Canis lupus familiaris GN=CENPH PE=4 SV=2 - [E2R8X4_CANLF]	2,51	1	0	1	1
Q9TU44	Platelet glycoprotein IIb OS=Canis lupus familiaris GN=GPIIb PE=2 SV=1 - [Q9TU44_CANLF]	2,51	1	0	1	1
Q9TUN8	Glycoprotein GPIIb OS=Canis lupus familiaris GN=GPIIb PE=2 SV=1 - [Q9TUN8_CANLF]	2,51	1	0	1	1
F1PLC7	Myb like, SWIRM and MPN domains 1 OS=Canis lupus familiaris GN=MYSM1 PE=4 SV=2 - [F1PLC7_CANLF]	2,48	1	0	1	1

F1PIE1	Rab geranylgeranyltransferase alpha subunit OS=Canis lupus familiaris GN=RABGGTA PE=4 SV=2 - [F1PIE1_CAN	2,47	1	1	1	1
E2RJP3	GTP binding protein 8 (putative) OS=Canis lupus familiaris GN=GTPBP8 PE=4 SV=1 - [E2RJP3_CANLF]	2,43	1	1	1	2
F1PAB7	Aldehyde dehydrogenase 9 family member A1 OS=Canis lupus familiaris GN=ALDH9A1 PE=3 SV=2 - [F1PAB7_C	2,43	1	1	1	1
F1PRU9	Uncharacterized protein OS=Canis lupus familiaris GN=ITGA2B PE=3 SV=2 - [F1PRU9_CANLF]	2,4	1	0	1	1
E2RNS0	Mitogen-activated protein kinase kinase kinase 13 OS=Canis lupus familiaris GN=MAP3K13 PE=3 SV=2 - [E2RNS	2,38	1	1	1	1
F1PJH3	Collagen type XIII alpha 1 chain OS=Canis lupus familiaris GN=COL13A1 PE=4 SV=2 - [F1PJH3_CANLF]	2,35	1	1	1	1
F1PF21	MMS22 like, DNA repair protein OS=Canis lupus familiaris GN=MMS22L PE=4 SV=2 - [F1PF21_CANLF]	2,34	1	0	1	2
D0VYJ3	Forkhead box P3 OS=Canis lupus familiaris GN=FOXP3 PE=2 SV=1 - [D0VYJ3_CANLF]	2,33	1	0	1	1
E2RM97	Potassium channel tetramerization domain containing 4 OS=Canis lupus familiaris GN=KCTD4 PE=4 SV=1 - [E2R	2,32	1	0	1	2
P0C569	Phosphoprotein OS=Mokola virus GN=P PE=1 SV=1 - [PHOSP_MOKV]	2,31	1	0	1	2
Q91RE1	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [Q91RE1_MOKV]	2,31	1	0	1	2
Q910M0	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [Q910M0_MOKV]	2,31	1	0	1	2
A0A1L2C227	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [A0A1L2C227_MOKV]	2,31	1	0	1	2
R9Q7B8	Phosphoprotein OS=Mokola virus PE=3 SV=1 - [R9Q7B8_MOKV]	2,31	1	0	1	2
A0A1L2C1Z1	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [A0A1L2C1Z1_MOKV]	2,31	1	0	1	2
A0A1L2C1Z5	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [A0A1L2C1Z5_MOKV]	2,31	1	0	1	2
S5DMU3	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [S5DMU3_MOKV]	2,31	1	0	1	2
S5DMW2	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [S5DMW2_MOKV]	2,31	1	0	1	2
S4S267	Phosphoprotein OS=Mokola virus PE=3 SV=1 - [S4S267_MOKV]	2,31	1	0	1	2
Q91RE0	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [Q91RE0_MOKV]	2,31	1	0	1	2
O56775	Phosphoprotein OS=Mokola virus GN=P PE=2 SV=1 - [O56775_MOKV]	2,31	1	0	1	2
R9Q7N9	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [R9Q7N9_MOKV]	2,31	1	0	1	2
U5L226	Phosphoprotein OS=Mokola virus PE=3 SV=1 - [U5L226_MOKV]	2,31	1	0	1	2
S4S2C5	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [S4S2C5_MOKV]	2,31	1	0	1	2
O56777	Phosphoprotein OS=Mokola virus GN=P PE=2 SV=1 - [O56777_MOKV]	2,31	1	0	1	2
S4S2C0	Phosphoprotein OS=Mokola virus GN=P PE=3 SV=1 - [S4S2C0_MOKV]	2,31	1	0	1	2
E2R6C1	Platelet and endothelial cell adhesion molecule 1 OS=Canis lupus familiaris GN=PECAM1 PE=4 SV=1 - [E2R6C1_	2,3	1	1	1	1
F1PLU9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PLU9_CANLF]	2,26	1	1	1	1
F6UVE0	Protein phosphatase 1 regulatory subunit 18 OS=Canis lupus familiaris GN=PPP1R18 PE=4 SV=1 - [F6UVE0_CAN	2,22	1	1	1	1
F1PXQ2	TLR4 interactor with leucine rich repeats OS=Canis lupus familiaris GN=TRIL PE=4 SV=2 - [F1PXQ2_CANLF]	2,18	1	1	1	1
J9P3F0	Zinc finger protein 473 OS=Canis lupus familiaris GN=ZNF473 PE=3 SV=1 - [J9P3F0_CANLF]	2,16	1	1	1	1
E2RBF2	Pumilio RNA binding family member 3 OS=Canis lupus familiaris GN=PUM3 PE=4 SV=2 - [E2RBF2_CANLF]	2,16	1	1	1	1
E2R8E8	Deltex E3 ubiquitin ligase 2 OS=Canis lupus familiaris GN=DTX2 PE=4 SV=1 - [E2R8E8_CANLF]	2,09	1	1	1	1
F1PKA6	Ectonucleoside triphosphate diphosphohydrolase 4 OS=Canis lupus familiaris GN=ENTPD4 PE=3 SV=2 - [F1PKA	1,95	1	1	1	1
E2RCX4	Structural maintenance of chromosomes protein OS=Canis lupus familiaris GN=SMC4 PE=3 SV=2 - [E2RCX4_CA	1,94	1	1	1	1
J9P6J8	Glucosylceramidase beta 2 OS=Canis lupus familiaris GN=GBA2 PE=4 SV=1 - [J9P6J8_CANLF]	1,94	1	1	1	1
Q867B7	Hepatocyte growth factor OS=Canis lupus familiaris GN=HGF PE=2 SV=1 - [HGF_CANLF]	1,92	1	1	1	1
E2RHR8	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100856515 PE=3 SV=1 - [E2RHR8_CANLF]	1,87	1	1	1	1
E2RD34	BCL2 like 14 OS=Canis lupus familiaris GN=BCL2L14 PE=4 SV=1 - [E2RD34_CANLF]	1,82	1	0	1	1
F1PYV6	Adhesion G protein-coupled receptor A2 OS=Canis lupus familiaris GN=ADGRA2 PE=3 SV=2 - [F1PYV6_CANLF]	1,8	1	0	1	1
J9NRV9	Adhesion G protein-coupled receptor A2 OS=Canis lupus familiaris GN=ADGRA2 PE=3 SV=1 - [J9NRV9_CANLF]	1,8	1	0	1	1
F1Q3I3	Condensin complex subunit 2 OS=Canis lupus familiaris GN=NCAPH PE=3 SV=2 - [F1Q3I3_CANLF]	1,79	1	1	1	1
E2R8W7	Calcium binding protein 39 OS=Canis lupus familiaris GN=CAB39 PE=4 SV=1 - [E2R8W7_CANLF]	1,76	1	1	1	1
E2R8P3	Signal induced proliferation associated 1 like 3 OS=Canis lupus familiaris GN=SIPA1L3 PE=4 SV=2 - [E2R8P3_CAN	1,75	1	0	1	1
J9P197	Signal induced proliferation associated 1 like 3 OS=Canis lupus familiaris GN=SIPA1L3 PE=4 SV=1 - [J9P197_CAN	1,75	1	0	1	1
F1PJA7	Maestro heat like repeat family member 9 OS=Canis lupus familiaris GN=MROH9 PE=4 SV=2 - [F1PJA7_CANLF]	1,75	1	1	1	1
J9P4S4	Pre-mRNA processing factor 40 homolog A OS=Canis lupus familiaris GN=PRPF40A PE=4 SV=1 - [J9P4S4_CANLF	1,72	1	0	1	1
F6X487	Wiskott-Aldrich syndrome OS=Canis lupus familiaris GN=WAS PE=4 SV=1 - [F6X487_CANLF]	1,72	1	1	1	1
F1PKD4	Transmembrane protein 67 OS=Canis lupus familiaris GN=TMEM67 PE=4 SV=2 - [F1PKD4_CANLF]	1,72	1	1	1	1
F1P666	Casein kinase 2 alpha 2 OS=Canis lupus familiaris GN=CSNK2A2 PE=3 SV=2 - [F1P666_CANLF]	1,7	1	0	1	1
E2RQ78	RB transcriptional corepressor like 1 OS=Canis lupus familiaris GN=RBL1 PE=4 SV=2 - [E2RQ78_CANLF]	1,69	1	0	1	2
F1PBK3	RB transcriptional corepressor like 1 OS=Canis lupus familiaris GN=RBL1 PE=4 SV=2 - [F1PBK3_CANLF]	1,69	1	0	1	2
E2R5V6	Pre-mRNA processing factor 40 homolog A OS=Canis lupus familiaris GN=PRPF40A PE=4 SV=2 - [E2R5V6_CANL	1,67	1	0	1	1
E2QVP1	Coiled-coil domain containing 13 OS=Canis lupus familiaris GN=CCDC13 PE=4 SV=2 - [E2QVP1_CANLF]	1,64	1	1	1	1
J9PB32	Striatin OS=Canis lupus familiaris GN=STRN PE=4 SV=1 - [J9PB32_CANLF]	1,63	1	0	1	1
F1Q1J3	Single-pass membrane protein with coiled-coil domains 2 OS=Canis lupus familiaris GN=SMCO2 PE=4 SV=2 - [F1	1,63	1	1	1	1
E2RGN3	ERCC excision repair 6 like 2 OS=Canis lupus familiaris GN=ERCC6L2 PE=4 SV=2 - [E2RGN3_CANLF]	1,62	1	1	1	1
F1PCM3	Axin 1 OS=Canis lupus familiaris GN=AXIN1 PE=4 SV=2 - [F1PCM3_CANLF]	1,61	1	1	1	2
F6XFF5	Cilia and flagella associated protein 58 OS=Canis lupus familiaris GN=CFAP58 PE=4 SV=1 - [F6XFF5_CANLF]	1,6	1	1	1	1
E2QZU5	Protein geranylgeranyltransferase type I subunit beta OS=Canis lupus familiaris GN=PGGT1B PE=4 SV=1 - [E2Q	1,59	1	0	1	1
F1PBH4	Fibrous sheath interacting protein 1 OS=Canis lupus familiaris GN=FSIP1 PE=4 SV=2 - [F1PBH4_CANLF]	1,59	1	1	1	1
F1P610	Oligophrenin 1 OS=Canis lupus familiaris GN=OPHN1 PE=4 SV=2 - [F1P610_CANLF]	1,57	1	1	1	1
F1P999	Striatin OS=Canis lupus familiaris GN=STRN PE=4 SV=2 - [F1P999_CANLF]	1,56	1	0	1	1
E2R8X7	Nuclear receptor binding SET domain protein 3 OS=Canis lupus familiaris GN=NSD3 PE=4 SV=1 - [E2R8X7_CANL	1,55	1	0	1	1
E2RLT7	5-azacytidine induced 2 OS=Canis lupus familiaris GN=AZI2 PE=4 SV=2 - [E2RLT7_CANLF]	1,53	1	0	1	1
E2RHZ1	Casein kinase 2 alpha 3 OS=Canis lupus familiaris GN=CSNK2A3 PE=3 SV=1 - [E2RHZ1_CANLF]	1,53	1	0	1	1
J9JHE4	Tripeptidyl peptidase 2 OS=Canis lupus familiaris GN=TPP2 PE=4 SV=1 - [J9JHE4_CANLF]	1,52	1	0	1	1
E2R9J9	Tripeptidyl peptidase 2 OS=Canis lupus familiaris GN=TPP2 PE=4 SV=2 - [E2R9J9_CANLF]	1,51	1	0	1	1
F6X7Y8	Peptidyl arginine deiminase 1 OS=Canis lupus familiaris GN=PADI1 PE=4 SV=1 - [F6X7Y8_CANLF]	1,51	1	1	1	1
J9NSF2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NSF2_CANLF]	1,49	1	0	1	1
D0FHK7	KIF1A OS=Canis lupus familiaris PE=2 SV=1 - [D0FHK7_CANLF]	1,48	1	0	1	1
H9GWG2	Kinesin family member 1A OS=Canis lupus familiaris GN=KIF1A PE=3 SV=2 - [H9GWG2_CANLF]	1,48	1	0	1	1
F1PFD9	Diacylglycerol kinase OS=Canis lupus familiaris GN=DGKH PE=3 SV=2 - [F1PFD9_CANLF]	1,46	1	1	1	1
F1PBD8	Coiled-coil domain containing 33 OS=Canis lupus familiaris GN=CCDC33 PE=4 SV=2 - [F1PBD8_CANLF]	1,45	1	0	1	2
Q076A1	Alpha-cardiac myosin heavy chain (Fragment) OS=Canis lupus familiaris PE=3 SV=1 - [Q076A1_CANLF]	1,44	1	1	1	1
E2RAF1	Uncharacterized protein OS=Canis lupus familiaris GN=HYPK PE=3 SV=1 - [E2RAF1_CANLF]	1,44	1	0	1	1
J9P8V3	KIAA0753 OS=Canis lupus familiaris GN=KIAA0753 PE=4 SV=1 - [J9P8V3_CANLF]	1,44	1	1	1	1
E2RQ77	Creatine kinase, mitochondrial 2 OS=Canis lupus familiaris GN=CKMT2 PE=3 SV=1 - [E2RQ77_CANLF]	1,43	1	0	1	1
J9NYI2	Tripartite motif containing 7 OS=Canis lupus familiaris GN=TRIM7 PE=4 SV=1 - [J9NYI2_CANLF]	1,39	1	0	1	1
E2RN64	Kinesin family member 1A OS=Canis lupus familiaris GN=KIF1A PE=3 SV=2 - [E2RN64_CANLF]	1,38	1	0	1	1
J9P2U6	Protein tyrosine phosphatase, receptor type Q OS=Canis lupus familiaris GN=PTPRQ PE=4 SV=1 - [J9P2U6_CAN	1,35	1	0	1	4
F1PMJ2	Myosin-1 OS=Canis lupus familiaris GN=MYH1 PE=3 SV=2 - [F1PMJ2_CANLF]	1,34	1	0	1	2
J9PB02	Ubiquitin carboxyl-terminal hydrolase 11 OS=Canis lupus familiaris GN=USP11 PE=3 SV=1 - [J9PB02_CANLF]	1,32	1	0	1	1
J9P3M3	Ubiquitin carboxyl-terminal hydrolase 11 OS=Canis lupus familiaris GN=USP11 PE=3 SV=1 - [J9P3M3_CANLF]	1,3	1	0	1	1
Q076A6	Myosin-1 OS=Canis lupus familiaris GN=MYH1 PE=3 SV=2 - [MYH1_CANLF]	1,29	1	0	1	2
Q076A7	Myosin-2 OS=Canis lupus familiaris GN=MYH2 PE=3 SV=1 - [MYH2_CANLF]	1,29	1	0	1	2
A0A140T8E7	Myosin-1 OS=Canis lupus familiaris GN=MYH1 PE=3 SV=1 - [A0A140T8E7_CANLF]	1,28	1	0	1	2
J9NZ48	Uncharacterized protein OS=Canis lupus familiaris GN=HYPK PE=3 SV=1 - [J9NZ48_CANLF]	1,25	1	0	1	1
E2R017	Mitogen-activated protein kinase kinase kinase kinase OS=Canis lupus familiaris GN=MAP4K1 PE=3 SV=2 - [E2R	1,22	1	0	1	2
E2R041	Mitogen-activated protein kinase kinase kinase kinase OS=Canis lupus familiaris GN=MAP4K1 PE=3 SV=2 - [E2R	1,22	1	0	1	2
Q076A0	Masticatory myosin heavy chain 2M OS=Canis lupus familiaris PE=3 SV=1 - [Q076A0_CANLF]	1,22	1	0	1	1
F1PT61	Myosin-16 OS=Canis lupus familiaris GN=MYH16 PE=3 SV=2 - [MYH16_CANLF]	1,19	1	0	1	1
E2RPV3	Stereocilin OS=Canis lupus familiaris GN=STRC PE=4 SV=2 - [E2RPV3_CANLF]	1,18	1	1	1	2

J9P588	Tripartite motif containing 7 OS=Canis lupus familiaris GN=TRIM7 PE=4 SV=1 - [J9P588_CANLF]	1,17	1	0	1	1
H8Y3D0	NADH-ubiquinone oxidoreductase chain 5 OS=Canis lupus familiaris GN=ND5 PE=3 SV=1 - [H8Y3D0_CANLF]	1,16	1	0	1	1
J9NUG8	Coiled-coil domain containing 33 OS=Canis lupus familiaris GN=CCDC33 PE=4 SV=1 - [J9NUG8_CANLF]	1,16	1	0	1	2
F1PDD8	Protein tyrosine phosphatase, receptor type U OS=Canis lupus familiaris GN=PTPRU PE=4 SV=2 - [F1PDD8_CAN	1,11	1	1	1	1
F1PB17	Zinc finger DBF-type containing 2 OS=Canis lupus familiaris GN=ZDBF2 PE=4 SV=2 - [F1PB17_CANLF]	1,11	1	0	1	1
J9NS68	Zinc finger DBF-type containing 2 OS=Canis lupus familiaris GN=ZDBF2 PE=4 SV=1 - [J9NS68_CANLF]	1,11	1	0	1	1
F1PWM6	Ubiquitin carboxyl-terminal hydrolase 11 OS=Canis lupus familiaris GN=USP11 PE=3 SV=2 - [F1PWM6_CANLF]	1,05	1	0	1	1
J9P7B0	Zinc finger DBF-type containing 2 OS=Canis lupus familiaris GN=ZDBF2 PE=4 SV=1 - [J9P7B0_CANLF]	1,03	1	0	1	1
E2QXI8	Tyrosine-protein phosphatase non-receptor type OS=Canis lupus familiaris GN=PTPN3 PE=3 SV=1 - [E2QXI8_CA	0,99	1	1	1	1
F1PR64	UHRF1 binding protein 1 like OS=Canis lupus familiaris GN=UHRF1BP1L PE=4 SV=2 - [F1PR64_CANLF]	0,96	1	1	1	1
E2RDL1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2RDL1_CANLF]	0,96	1	0	1	1
E2QUY9	Uncharacterized protein OS=Canis lupus familiaris GN=ADAMTS13 PE=4 SV=2 - [E2QUY9_CANLF]	0,93	1	0	1	1
F7J124	A disintegrin and metalloproteinase with thrombospondin motifs 13 OS=Canis lupus familiaris GN=ADAMTS13	0,93	1	0	1	1
E2QYE9	MKL1/myocardin like 2 OS=Canis lupus familiaris GN=MKL2 PE=4 SV=1 - [E2QYE9_CANLF]	0,93	1	0	1	1
F1PPD2	Striatin 4 OS=Canis lupus familiaris GN=STRN4 PE=4 SV=2 - [F1PPD2_CANLF]	0,92	1	1	1	1
J9NSB2	MKL1/myocardin like 2 OS=Canis lupus familiaris GN=MKL2 PE=4 SV=1 - [J9NSB2_CANLF]	0,92	1	0	1	1
E2RI01	Solute carrier family 7 member 2 OS=Canis lupus familiaris GN=SLC7A2 PE=4 SV=1 - [E2RI01_CANLF]	0,91	1	0	1	2
F1Q332	Glycyl-tRNA synthetase OS=Canis lupus familiaris GN=GARS PE=4 SV=2 - [F1Q332_CANLF]	0,88	1	1	1	1
F1PT14	Calcium-activated potassium channel subunit alpha-1 OS=Canis lupus familiaris GN=KCNMA1 PE=4 SV=1 - [F1P	0,87	1	0	1	2
J9P0G6	Calcium-activated potassium channel subunit alpha-1 OS=Canis lupus familiaris GN=KCNMA1 PE=3 SV=1 - [J9P(	0,86	1	0	1	2
E2QWE6	Protein tyrosine phosphatase, receptor type Q OS=Canis lupus familiaris GN=PTPRQ PE=4 SV=2 - [E2QWE6_CA	0,86	1	0	1	4
E2REZ1	Coiled-coil domain containing 40 OS=Canis lupus familiaris GN=CCDC40 PE=4 SV=2 - [E2REZ1_CANLF]	0,83	1	1	1	1
F1PT15	Calcium-activated potassium channel subunit alpha-1 OS=Canis lupus familiaris GN=KCNMA1 PE=3 SV=2 - [F1P	0,82	1	0	1	2
E2RPG7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [E2RPG7_CANLF]	0,82	1	0	1	1
F1PL04	ATP/GTP binding protein 1 OS=Canis lupus familiaris GN=AGTPBP1 PE=4 SV=2 - [F1PL04_CANLF]	0,8	1	0	1	1
E2RHS2	Zinc finger and BTB domain containing 49 OS=Canis lupus familiaris GN=ZBTB49 PE=4 SV=2 - [E2RHS2_CANLF]	0,78	1	1	1	1
E2R8N3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2R8N3_CANLF]	0,75	1	1	1	1
F1PAP3	Pericentrin OS=Canis lupus familiaris GN=PCNT PE=4 SV=2 - [F1PAP3_CANLF]	0,74	1	1	1	1
F6UMQ8	Ubiquitin carboxyl-terminal hydrolase 16 OS=Canis lupus familiaris GN=USP16 PE=3 SV=1 - [F6UMQ8_CANLF]	0,73	1	1	1	1
J9NSE2	ATP/GTP binding protein 1 OS=Canis lupus familiaris GN=AGTPBP1 PE=4 SV=1 - [J9NSE2_CANLF]	0,73	1	0	1	1
Q258K2	Myosin-9 OS=Canis lupus familiaris GN=MYH9 PE=2 SV=1 - [MYH9_CANLF]	0,71	1	0	1	2
F1P9J3	Myosin-9 OS=Canis lupus familiaris GN=MYH9 PE=3 SV=2 - [F1P9J3_CANLF]	0,71	1	0	1	2
E2QUJ0	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=NSD3 PE=4 SV=1 - [E2QUJ0_CANLF]	0,7	1	0	1	1
J9NVX7	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=NSD1 PE=4 SV=1 - [J9NVX7_CANLF]	0,7	1	0	1	1
F1Q0K3	Microtubule associated monooxygenase, calponin and LIM domain containing 3 OS=Canis lupus familiaris GN=I	0,64	1	1	1	1
E2R3Q9	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=NSD1 PE=4 SV=2 - [E2R3Q9_CANLF]	0,63	1	0	1	1
J9P0B4	Tudor domain containing 15 OS=Canis lupus familiaris GN=TDRD15 PE=4 SV=1 - [J9P0B4_CANLF]	0,61	1	1	1	1
F6XMT1	Ankyrin repeat domain 35 OS=Canis lupus familiaris GN=ANKRD35 PE=4 SV=1 - [F6XMT1_CANLF]	0,6	1	0	1	1
F1PPE5	Biorientation of chromosomes in cell division 1 like 1 OS=Canis lupus familiaris GN=BOD1L1 PE=4 SV=2 - [F1PPE	0,59	1	0	1	1
E2RFL4	Integrator complex subunit 3 OS=Canis lupus familiaris GN=INTS3 PE=4 SV=2 - [E2RFL4_CANLF]	0,57	1	0	1	6
E2RDY9	Biorientation of chromosomes in cell division 1 like 1 OS=Canis lupus familiaris GN=BOD1L1 PE=4 SV=2 - [E2RDY	0,56	1	0	1	1
E2RB62	Myosin IB OS=Canis lupus familiaris GN=MYO1B PE=3 SV=2 - [E2RB62_CANLF]	0,53	1	0	1	1
J9P0X3	Adenylate kinase 9 OS=Canis lupus familiaris GN=AK9 PE=4 SV=1 - [J9P0X3_CANLF]	0,53	1	0	1	1
E2RT62	Adenylate kinase 9 OS=Canis lupus familiaris GN=AK9 PE=4 SV=2 - [E2RT62_CANLF]	0,52	1	0	1	1
F1Q2M4	DNA topoisomerase 2 OS=Canis lupus familiaris GN=TOP2A PE=3 SV=2 - [F1Q2M4_CANLF]	0,52	1	0	1	1
J9PAY8	DNA topoisomerase 2 OS=Canis lupus familiaris GN=TOP2A PE=3 SV=1 - [J9PAY8_CANLF]	0,52	1	0	1	1
F1PN11	Histone deacetylase OS=Canis lupus familiaris GN=HDAC6 PE=4 SV=2 - [F1PN11_CANLF]	0,52	1	0	1	1
E2RG72	WASH complex subunit 4 OS=Canis lupus familiaris GN=WASHC4 PE=4 SV=2 - [E2RG72_CANLF]	0,51	1	0	1	1
J9P227	WASH complex subunit 4 OS=Canis lupus familiaris GN=WASHC4 PE=4 SV=1 - [J9P227_CANLF]	0,51	1	0	1	1
F1PIZ3	Maestro heat like repeat family member 2B OS=Canis lupus familiaris GN=MROH2B PE=4 SV=2 - [F1PIZ3_CANL	0,5	1	1	1	1
E2RKP7	Pericentriolar material 1 OS=Canis lupus familiaris GN=PCM1 PE=4 SV=2 - [E2RKP7_CANLF]	0,49	1	0	1	3
F1PCE7	Tetratricopeptide repeat and ankyrin repeat containing 1 OS=Canis lupus familiaris GN=TRANK1 PE=4 SV=2 - [F	0,48	1	0	1	1
F1PD19	Tetratricopeptide repeat and ankyrin repeat containing 1 OS=Canis lupus familiaris GN=TRANK1 PE=4 SV=2 - [F	0,48	1	0	1	1
F1PGN5	Protein tyrosine phosphatase, receptor type Z1 OS=Canis lupus familiaris GN=PTPRZ1 PE=4 SV=2 - [F1PGN5_C	0,48	1	1	1	2
J9NSW6	Tetratricopeptide repeat and ankyrin repeat containing 1 OS=Canis lupus familiaris GN=TRANK1 PE=4 SV=1 - [J	0,47	1	0	1	1
J9NWJ8	Pericentriolar material 1 OS=Canis lupus familiaris GN=PCM1 PE=4 SV=1 - [J9NWJ8_CANLF]	0,47	1	0	1	3
J9P8W5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P8W5_CANLF]	0,47	1	0	1	1
E2REB1	Structural maintenance of chromosomes flexible hinge domain containing 1 OS=Canis lupus familiaris GN=SMC	0,45	1	1	1	1
F1PZF8	Ubiquitin specific peptidase 47 OS=Canis lupus familiaris GN=USP47 PE=3 SV=2 - [F1PZF8_CANLF]	0,44	1	1	1	1
E2RSC5	Talin 2 OS=Canis lupus familiaris GN=TLN2 PE=4 SV=2 - [E2RSC5_CANLF]	0,43	1	1	1	1
Q5U820	Cystic fibrosis transmembrane conductance regulator OS=Canis lupus familiaris GN=CFTR PE=2 SV=2 - [CFTR_C	0,4	1	0	1	1
F6V7I1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F6V7I1_CANLF]	0,38	1	1	1	1
J9NU82	Myosin heavy chain 14 OS=Canis lupus familiaris GN=MYH14 PE=3 SV=1 - [J9NU82_CANLF]	0,35	1	0	1	1
J9P1C1	Kinesin family member 20B OS=Canis lupus familiaris GN=KIF20B PE=3 SV=1 - [J9P1C1_CANLF]	0,34	1	0	1	1
F1PYS6	Myosin heavy chain 14 OS=Canis lupus familiaris GN=MYH14 PE=3 SV=2 - [F1PYS6_CANLF]	0,34	1	0	1	1
E2RN40	Prune homolog 2 OS=Canis lupus familiaris GN=PRUNE2 PE=4 SV=2 - [E2RN40_CANLF]	0,33	1	0	1	1
E2QUT0	Kinesin family member 20B OS=Canis lupus familiaris GN=KIF20B PE=3 SV=2 - [E2QUT0_CANLF]	0,33	1	0	1	1
F1PIQ7	Inositol 1,4,5-trisphosphate receptor type 1 OS=Canis lupus familiaris GN=ITPR1 PE=4 SV=2 - [F1PIQ7_CANLF]	0,33	1	0	1	1
F1PW86	Inositol 1,4,5-trisphosphate receptor type 1 OS=Canis lupus familiaris GN=ITPR1 PE=4 SV=2 - [F1PW86_CANLF]	0,33	1	0	1	1
F6XBJ5	Integrator complex subunit 1 OS=Canis lupus familiaris GN=INTS1 PE=4 SV=1 - [F6XBJ5_CANLF]	0,32	1	0	1	1
J9P992	Myosin XVIIIA OS=Canis lupus familiaris GN=MYO18A PE=3 SV=1 - [J9P992_CANLF]	0,31	1	0	1	1
F6Y037	Myosin XVIIIA OS=Canis lupus familiaris GN=MYO18A PE=3 SV=1 - [F6Y037_CANLF]	0,29	1	0	1	1
F6XLF1	Matrix remodeling associated 5 OS=Canis lupus familiaris GN=MXRA5 PE=4 SV=1 - [F6XLF1_CANLF]	0,28	1	1	1	1
F1PYB2	Cilia and flagella associated protein 46 OS=Canis lupus familiaris GN=CFAP46 PE=4 SV=2 - [F1PYB2_CANLF]	0,25	1	0	1	1
E2R021	Cilia and flagella associated protein 46 OS=Canis lupus familiaris GN=CFAP46 PE=4 SV=2 - [E2R021_CANLF]	0,22	1	0	1	1
E2RBM4	Helicase with zinc finger 2 OS=Canis lupus familiaris GN=HELZ2 PE=4 SV=2 - [E2RBM4_CANLF]	0,21	1	0	1	10
F1PRB7	Testis expressed 15, meiosis and synapsis associated OS=Canis lupus familiaris GN=TEX15 PE=4 SV=2 - [F1PRB7	0,19	1	0	1	1
F1PN38	Baculoviral IAP repeat containing 6 OS=Canis lupus familiaris GN=BIRC6 PE=3 SV=2 - [F1PN38_CANLF]	0,15	1	1	1	1
F6XXM1	FAT atypical cadherin 1 OS=Canis lupus familiaris GN=FAT1 PE=3 SV=1 - [F6XXM1_CANLF]	0,14	1	1	1	1
F1PHS5	Plectin OS=Canis lupus familiaris GN=PLEC PE=4 SV=2 - [F1PHS5_CANLF]	0,13	1	0	1	2
E2R4N3	Midasin OS=Canis lupus familiaris GN=MDN1 PE=3 SV=2 - [E2R4N3_CANLF]	0,13	1	0	1	6
J9NZY7	Midasin OS=Canis lupus familiaris GN=MDN1 PE=3 SV=1 - [J9NZY7_CANLF]	0,13	1	0	1	6
J9PAW7	Microtubule-actin crosslinking factor 1 OS=Canis lupus familiaris GN=MACF1 PE=4 SV=1 - [J9PAW7_CANLF]	0,08	1	1	1	1
Q7M310	Angiotensin I (Fragment) OS=Canis lupus familiaris PE=1 SV=1 - [Q7M310_CANLF]	100	1	1	1	1
E2RS77	CDC42 small effector 1 OS=Canis lupus familiaris GN=CDC42SE1 PE=4 SV=1 - [E2RS77_CANLF]	50,63	1	1	1	1
E5G723	Collagen alpha 1 type I (Fragment) OS=Canis lupus familiaris GN=COL1A1 PE=2 SV=1 - [E5G723_CANLF]	25,32	1	0	1	1
A0A0E3V495	30S ribosomal protein S17 OS=Pasteurella multocida subsp. multocida OH4807 GN=rpsQ PE=3 SV=1 - [A0A0E3\	12,94	1	1	1	1
O62801	Prepro-alpha 1 type I collagen (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [O62801_CANLF]	11,3	1	0	1	1
E2RH59	Glucosamine-6-phosphate isomerase OS=Canis lupus familiaris GN=GNPDA2 PE=3 SV=2 - [E2RH59_CANLF]	10,51	1	1	1	1
A0A0E3V418	Inorganic pyrophosphatase OS=Pasteurella multocida subsp. multocida OH4807 GN=ppa PE=3 SV=1 - [A0A0E3\	10,29	1	1	1	1
A0A0E3ZQY8	Bifunctional protein HldE OS=Pasteurella multocida subsp. multocida OH4807 GN=hldE PE=3 SV=1 - [A0A0E3ZC	9,66	1	1	1	1
E2R7F8	Interleukin 19 OS=Canis lupus familiaris GN=IL19 PE=4 SV=1 - [E2R7F8_CANLF]	9,6	1	1	1	1
F6XEW2	RNA binding protein with serine rich domain 1 OS=Canis lupus familiaris GN=RNPS1 PE=4 SV=1 - [F6XEW2_CAN	9,51	1	1	1	1

J9NYH3	LLP homolog, long-term synaptic facilitation OS=Canis lupus familiaris GN=LLPH PE=4 SV=1 - [J9NYH3_CANLF]	9,46	1	1	1	1
Q9GLN4	Type I collagen alpha 1 chain (Fragment) OS=Canis lupus familiaris GN=COL1A1 PE=2 SV=1 - [Q9GLN4_CANLF]	9,26	1	0	1	1
I7ENE2	Ubiquitin carboxyl-terminal hydrolase (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [I7ENE2_CANLF]	8,84	1	0	1	7
E2R9G5	Guanine nucleotide-binding protein subunit gamma OS=Canis lupus familiaris GN=GNG10 PE=3 SV=1 - [E2R9G5	8,82	1	0	1	2
J9NTE7	40S ribosomal protein S24 OS=Canis lupus familiaris PE=3 SV=1 - [J9NTE7_CANLF]	8,33	1	0	1	1
L7N0I3	40S ribosomal protein S24 OS=Canis lupus familiaris PE=3 SV=1 - [L7N0I3_CANLF]	8,33	1	0	1	1
E2RPB8	C-type lectin domain family 3 member B OS=Canis lupus familiaris GN=CLEC3B PE=4 SV=2 - [E2RPB8_CANLF]	8	1	1	1	2
A0A0E3ZRP3	Protein YigB OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_07430 PE=4 SV=1 - [A0A0E3ZRP3_P	7,2	1	1	1	2
F1PUK5	Meis homeobox 3 OS=Canis lupus familiaris GN=MEIS3 PE=4 SV=2 - [F1PUK5_CANLF]	6,98	1	0	1	1
J9P5S4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P5S4_CANLF]	6,67	1	1	1	1
F1PMQ3	Meis homeobox 3 OS=Canis lupus familiaris GN=MEIS3 PE=4 SV=2 - [F1PMQ3_CANLF]	6,47	1	0	1	1
E2R6K2	Adenosine deaminase 2 OS=Canis lupus familiaris GN=ADA2 PE=4 SV=1 - [E2R6K2_CANLF]	6,43	1	1	1	1
F1PDY8	Carbonic anhydrase 2 OS=Canis lupus familiaris GN=CA2 PE=4 SV=2 - [F1PDY8_CANLF]	6,15	1	1	1	3
F6XVD7	Ubiquitin carboxyl-terminal hydrolase OS=Canis lupus familiaris GN=UCHL1 PE=3 SV=1 - [F6XVD7_CANLF]	5,8	1	0	1	7
F1PP63	Acyl-CoA dehydrogenase, short/branched chain OS=Canis lupus familiaris GN=ACADSB PE=3 SV=2 - [F1PP63_C	5,79	1	1	1	1
F1P897	Glycoprotein M6A OS=Canis lupus familiaris GN=GPM6A PE=4 SV=2 - [F1P897_CANLF]	5,76	1	1	1	1
F1PPV4	Uncharacterized protein OS=Canis lupus familiaris GN=NUTM2F PE=4 SV=2 - [F1PPV4_CANLF]	5,76	1	1	1	1
E2RN49	Zinc finger SWIM-type containing 1 OS=Canis lupus familiaris GN=ZSWIM1 PE=4 SV=1 - [E2RN49_CANLF]	5,48	1	1	1	1
J9PAD7	Cerebellar degeneration related protein 2 OS=Canis lupus familiaris GN=CDR2 PE=4 SV=1 - [J9PAD7_CANLF]	5,37	1	0	1	1
E2QWA4	Tripartite motif containing 22 OS=Canis lupus familiaris GN=TRIM22 PE=4 SV=1 - [E2QWA4_CANLF]	5,26	1	0	1	1
F1PYW1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PYW1_CANLF]	5,23	1	1	1	1
E2R278	tRNA-yW synthesizing protein 5 OS=Canis lupus familiaris GN=TYW5 PE=4 SV=2 - [E2R278_CANLF]	5,08	1	1	1	1
F1P7T7	Collagen beta(1-O)galactosyltransferase 2 OS=Canis lupus familiaris GN=COLGALT2 PE=4 SV=2 - [F1P7T7_CANL	4,79	1	1	1	1
J9NYP3	THAP domain containing 7 OS=Canis lupus familiaris GN=THAP7 PE=4 SV=1 - [J9NYP3_CANLF]	4,79	1	1	1	1
J9P814	RNA polymerase III subunit E OS=Canis lupus familiaris GN=POLR3E PE=4 SV=1 - [J9P814_CANLF]	4,71	1	0	1	1
E2R6D2	Complement C8 gamma chain OS=Canis lupus familiaris GN=C8G PE=3 SV=1 - [E2R6D2_CANLF]	4,46	1	0	1	1
F1PH83	Component of oligomeric golgi complex 7 OS=Canis lupus familiaris GN=COG7 PE=4 SV=2 - [F1PH83_CANLF]	4,37	1	0	1	2
F1PG79	Cerebellar degeneration related protein 2 OS=Canis lupus familiaris GN=CDR2 PE=4 SV=1 - [F1PG79_CANLF]	4,24	1	0	1	1
E2RHP6	Uncharacterized protein OS=Canis lupus familiaris GN=ZNF445 PE=4 SV=2 - [E2RHP6_CANLF]	4,2	1	1	1	1
E2QWE0	COP9 signalosome subunit 5 OS=Canis lupus familiaris GN=COPS5 PE=4 SV=1 - [E2QWE0_CANLF]	4,19	1	1	1	3
F1P6Y3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F1P6Y3_CANLF]	4,04	1	1	1	2
E2RMD6	Component of oligomeric golgi complex 7 OS=Canis lupus familiaris GN=COG7 PE=4 SV=1 - [E2RMD6_CANLF]	3,9	1	0	1	2
E2RHN7	RNA polymerase III subunit E OS=Canis lupus familiaris GN=POLR3E PE=4 SV=2 - [E2RHN7_CANLF]	3,85	1	0	1	1
F1Q114	Kelch like family member 5 OS=Canis lupus familiaris GN=KLHL5 PE=4 SV=2 - [F1Q114_CANLF]	3,84	1	1	1	1
J9P6G7	Coiled-coil domain containing 136 OS=Canis lupus familiaris GN=CCDC136 PE=4 SV=1 - [J9P6G7_CANLF]	3,78	1	1	1	1
J9PB03	LDL receptor related protein 12 OS=Canis lupus familiaris GN=LRP12 PE=4 SV=1 - [J9PB03_CANLF]	3,72	1	0	1	1
J9NZC6	Uncharacterized protein OS=Canis lupus familiaris GN=HADHB PE=3 SV=1 - [J9NZC6_CANLF]	3,56	1	1	1	2
F1PR89	Adhesion G protein-coupled receptor D1 OS=Canis lupus familiaris GN=ADGRD1 PE=3 SV=2 - [F1PR89_CANLF]	3,44	1	0	1	2
P32553	Outer capsid protein VP2 OS=African horse sickness virus 4 GN=S2 PE=3 SV=2 - [VP2_AHSV4]	3,3	1	0	1	1
A0A0K2CWP3	Major outer capsid protein OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A0K2CWP3_AHSV4]	3,3	1	0	1	1
A0A0H4NVK8	Major outer capsid protein OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A0H4NVK8_AHSV4]	3,3	1	0	1	1
A0A189RMP4	Major outer capsid protein OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A189RMP4_AHSV4]	3,3	1	0	1	1
A0A189RMP5	Major outer capsid protein OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A189RMP5_AHSV4]	3,3	1	0	1	1
A0A0U1XN16	Outer capsid protein OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A0U1XN16_AHSV4]	3,3	1	0	1	1
A0A0N7CZJ3	VP2 OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A0N7CZJ3_AHSV4]	3,3	1	0	1	1
A0A0S1NIU3	VP2 OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A0S1NIU3_AHSV4]	3,3	1	0	1	1
A0A189RMQ5	Major outer capsid protein OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A189RMQ5_AHSV4]	3,3	1	0	1	1
A0A0U1XN65	Outer capsid protein OS=African horse sickness virus 4 GN=VP2 PE=4 SV=1 - [A0A0U1XN65_AHSV4]	3,3	1	0	1	1
F1PJY9	Nucleolar GTP-binding protein 1 OS=Canis lupus familiaris GN=GTPBP4 PE=3 SV=2 - [F1PJY9_CANLF]	3,24	1	1	1	1
F1PT94	Myotubularin related protein 7 OS=Canis lupus familiaris GN=MTMR7 PE=3 SV=2 - [F1PT94_CANLF]	3,18	1	1	1	1
J9P7L5	Uncharacterized protein OS=Canis lupus familiaris GN=LOC607552 PE=4 SV=1 - [J9P7L5_CANLF]	3,17	1	0	1	2
A0A0E3ZQ87	Leucine--tRNA ligase OS=Pasteurella multocida subsp. multocida OH4807 GN=leuS PE=3 SV=1 - [A0A0E3ZQ87_	3,14	1	1	1	1
F1PPF3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PPF3_CANLF]	3,11	1	1	1	1
E2REK8	Uncharacterized protein OS=Canis lupus familiaris GN=LOC482089 PE=4 SV=2 - [E2REK8_CANLF]	3,02	1	1	1	1
J9PBJ7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PBJ7_CANLF]	2,99	1	1	1	1
F1PMB5	Sorting nexin 2 OS=Canis lupus familiaris GN=SNX2 PE=4 SV=2 - [F1PMB5_CANLF]	2,99	1	1	1	1
F1P9S8	LDL receptor related protein 12 OS=Canis lupus familiaris GN=LRP12 PE=4 SV=2 - [F1P9S8_CANLF]	2,93	1	0	1	1
Q4VSN4	Dual serine/threonine and tyrosine protein kinase OS=Canis lupus familiaris GN=DSTYK PE=2 SV=1 - [DUSTY_C	2,9	1	1	1	1
J9NV31	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NV31_CANLF]	2,76	1	0	1	1
E2RG62	Uncharacterized protein OS=Canis lupus familiaris GN=SMARCAD1 PE=4 SV=1 - [E2RG62_CANLF]	2,73	1	0	1	1
J9PA79	Uncharacterized protein OS=Canis lupus familiaris GN=SMARCAD1 PE=4 SV=1 - [J9PA79_CANLF]	2,73	1	0	1	1
J9P362	DNA cross-link repair 1C OS=Canis lupus familiaris GN=DCLRE1C PE=4 SV=1 - [J9P362_CANLF]	2,65	1	0	1	1
E2RBE9	DNA cross-link repair 1C OS=Canis lupus familiaris GN=DCLRE1C PE=4 SV=1 - [E2RBE9_CANLF]	2,6	1	0	1	1
E2R074	Uncharacterized protein OS=Canis lupus familiaris GN=LOC607552 PE=4 SV=1 - [E2R074_CANLF]	2,56	1	0	1	2
E2RL61	Myomesin 3 OS=Canis lupus familiaris GN=MYOM3 PE=4 SV=2 - [E2RL61_CANLF]	2,55	1	1	1	1
F1P9Q4	Cullin 5 OS=Canis lupus familiaris GN=CUL5 PE=3 SV=2 - [F1P9Q4_CANLF]	2,52	1	0	1	1
E2R3V1	Fc receptor like 4 OS=Canis lupus familiaris GN=FCRL4 PE=4 SV=1 - [E2R3V1_CANLF]	2,52	1	1	1	2
Q6QNF4	Hepatocyte growth factor activator OS=Canis lupus familiaris GN=HGFAC PE=2 SV=1 - [HGFA_CANLF]	2,45	1	0	1	2
F1PAF3	Hepatocyte growth factor activator OS=Canis lupus familiaris GN=HGFAC PE=3 SV=1 - [F1PAF3_CANLF]	2,45	1	0	1	2
E2R0R2	Nephrocystin 3 OS=Canis lupus familiaris GN=NPHP3 PE=4 SV=2 - [E2R0R2_CANLF]	2,45	1	1	1	1
E2RNJ2	EF-hand calcium binding domain 3 OS=Canis lupus familiaris GN=EFCAB3 PE=4 SV=2 - [E2RNJ2_CANLF]	2,38	1	1	1	2
F1PK57	Uncharacterized protein OS=Canis lupus familiaris PE=1 SV=2 - [F1PK57_CANLF]	2,38	1	0	1	1
F1Q4F4	Zinc finger protein 536 OS=Canis lupus familiaris GN=ZNF536 PE=4 SV=2 - [F1Q4F4_CANLF]	2,38	1	1	1	1
J9PAX0	Cullin 5 OS=Canis lupus familiaris GN=CUL5 PE=3 SV=1 - [J9PAX0_CANLF]	2,37	1	0	1	1
E2RSP9	Testis specific serine kinase 4 OS=Canis lupus familiaris GN=TSSK4 PE=4 SV=1 - [E2RSP9_CANLF]	2,37	1	1	1	2
F1PYZ5	A-kinase anchoring protein 4 OS=Canis lupus familiaris GN=AKAP4 PE=4 SV=2 - [F1PYZ5_CANLF]	2,36	1	1	1	1
E2RQJ7	Angiomotin like 2 OS=Canis lupus familiaris GN=AMOTL2 PE=4 SV=2 - [E2RQJ7_CANLF]	2,32	1	0	1	1
E2R1Z3	Keratin 27 OS=Canis lupus familiaris GN=KRT27 PE=3 SV=2 - [E2R1Z3_CANLF]	2,26	1	0	1	3
F1PFV3	Rho GTPase activating protein 6 OS=Canis lupus familiaris GN=ARHGAP6 PE=4 SV=2 - [F1PFV3_CANLF]	2,24	1	1	1	2
E2RJ63	Angiomotin like 2 OS=Canis lupus familiaris GN=AMOTL2 PE=4 SV=2 - [E2RJ63_CANLF]	2,15	1	0	1	1
E2RCS6	Mortality factor 4 like 2 OS=Canis lupus familiaris GN=MORF4L2 PE=4 SV=1 - [E2RCS6_CANLF]	2,08	1	0	1	2
E2QYD6	ERCC excision repair 4, endonuclease catalytic subunit OS=Canis lupus familiaris GN=ERCC4 PE=4 SV=2 - [E2QY	2,07	1	1	1	1
A0A0E3ZQ40	DNA topoisomerase 1 OS=Pasteurella multocida subsp. multocida OH4807 GN=topA PE=3 SV=1 - [A0A0E3ZQ4	2,07	1	1	1	2
E2QS80	Keratin 25 OS=Canis lupus familiaris GN=KRT25 PE=3 SV=1 - [E2QS80_CANLF]	2	1	0	1	3
F1Q170	LDL receptor related protein 8 OS=Canis lupus familiaris GN=LRP8 PE=4 SV=2 - [F1Q170_CANLF]	2	1	0	1	1
E2QUU4	Keratin 4 OS=Canis lupus familiaris GN=LOC608027 PE=3 SV=2 - [E2QUU4_CANLF]	2	1	1	1	1
F1Q179	LDL receptor related protein 8 OS=Canis lupus familiaris GN=LRP8 PE=4 SV=2 - [F1Q179_CANLF]	1,99	1	0	1	1
E2R170	Keratin 27 OS=Canis lupus familiaris GN=KRT27 PE=3 SV=2 - [E2R170_CANLF]	1,97	1	0	1	3
F6USG7	Keratin 25 OS=Canis lupus familiaris GN=KRT25 PE=3 SV=1 - [F6USG7_CANLF]	1,96	1	0	1	3
F1PPU4	FANCD2 and FANCI associated nuclease 1 OS=Canis lupus familiaris GN=FAN1 PE=4 SV=2 - [F1PPU4_CANLF]	1,94	1	1	1	1
E2R164	Keratin 26 OS=Canis lupus familiaris GN=KRT26 PE=3 SV=1 - [E2R164_CANLF]	1,94	1	0	1	3
E2R978	Myelin transcription factor 1 like OS=Canis lupus familiaris GN=MYT1L PE=4 SV=2 - [E2R978_CANLF]	1,94	1	1	1	1
F1PKX9	Plexin A2 OS=Canis lupus familiaris GN=PLXNA2 PE=4 SV=1 - [F1PKX9_CANLF]	1,93	1	0	1	1

J9NU32	Coiled-coil domain containing 150 OS=Canis lupus familiaris GN=CCDC150 PE=4 SV=1 - [J9NU32_CANLF]	1,83	1	0	1	2
E2RSE4	Peptidylprolyl isomerase G OS=Canis lupus familiaris GN=PPIG PE=4 SV=2 - [E2RSE4_CANLF]	1,76	1	0	1	1
J9PAE8	Peptidylprolyl isomerase G OS=Canis lupus familiaris GN=PPIG PE=4 SV=1 - [J9PAE8_CANLF]	1,73	1	0	1	1
E2QUS6	Large tumor suppressor kinase 2 OS=Canis lupus familiaris GN=LATS2 PE=4 SV=1 - [E2QUS6_CANLF]	1,66	1	1	1	1
E2RNY6	DIS3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease OS=Canis lupus familiaris GN=DIS3 PE=3 S	1,57	1	1	1	1
F1PNA7	Transmembrane protein 260 OS=Canis lupus familiaris GN=TMEM260 PE=4 SV=2 - [F1PNA7_CANLF]	1,56	1	1	1	1
J9P966	LUC7 like 3 pre-mRNA splicing factor OS=Canis lupus familiaris GN=LUC7L3 PE=4 SV=1 - [J9P966_CANLF]	1,53	1	0	1	4
F1PVL6	Kinesin-like protein OS=Canis lupus familiaris GN=KIF2A PE=3 SV=2 - [F1PVL6_CANLF]	1,48	1	0	1	1
F1PPN5	Coiled-coil domain containing 150 OS=Canis lupus familiaris GN=CCDC150 PE=4 SV=2 - [F1PPN5_CANLF]	1,45	1	0	1	2
E2R093	Janus kinase and microtubule interacting protein 1 OS=Canis lupus familiaris GN=JAKMIP1 PE=4 SV=2 - [E2R093	1,44	1	1	1	6
Q076A5	Myosin-4 OS=Canis lupus familiaris GN=MYH4 PE=3 SV=1 - [MYH4_CANLF]	1,44	1	0	1	1
F1PHZ1	Plexin A2 OS=Canis lupus familiaris GN=PLXNA2 PE=4 SV=2 - [F1PHZ1_CANLF]	1,42	1	0	1	1
E2RSS5	LUC7 like 3 pre-mRNA splicing factor OS=Canis lupus familiaris GN=LUC7L3 PE=4 SV=2 - [E2RSS5_CANLF]	1,39	1	0	1	4
E2RPQ9	WD repeat domain 63 OS=Canis lupus familiaris GN=WDR63 PE=4 SV=1 - [E2RPQ9_CANLF]	1,34	1	1	1	1
F1PSN6	DENN domain containing 4B OS=Canis lupus familiaris GN=DENND4B PE=4 SV=2 - [F1PSN6_CANLF]	1,34	1	1	1	1
F1Q070	Shroom family member 2 OS=Canis lupus familiaris GN=SHROOM2 PE=4 SV=1 - [F1Q070_CANLF]	1,33	1	0	1	1
J9NXX4	Shroom family member 2 OS=Canis lupus familiaris GN=SHROOM2 PE=4 SV=1 - [J9NXX4_CANLF]	1,28	1	0	1	1
E2RQG7	Beta-carotene oxygenase 1 OS=Canis lupus familiaris GN=BCO1 PE=3 SV=2 - [E2RQG7_CANLF]	1,28	1	0	1	3
J9P4F5	Beta-carotene oxygenase 1 OS=Canis lupus familiaris GN=BCO1 PE=3 SV=1 - [J9P4F5_CANLF]	1,28	1	0	1	3
J9P9X3	Kinesin-like protein OS=Canis lupus familiaris GN=KIF2A PE=3 SV=1 - [J9P9X3_CANLF]	1,24	1	0	1	1
E2R723	Cytochrome P450 family 26 subfamily A member 1 OS=Canis lupus familiaris GN=CYP26A1 PE=3 SV=1 - [E2R723	1,21	1	1	1	1
E2QUS2	Kinesin-like protein OS=Canis lupus familiaris GN=KIF3B PE=3 SV=1 - [E2QUS2_CANLF]	1,2	1	1	1	1
J9P6W0	Nuclear protein, coactivator of histone transcription OS=Canis lupus familiaris GN=NPAT PE=4 SV=1 - [J9P6W0_	1,18	1	0	1	1
F1PCZ7	Nuclear protein, coactivator of histone transcription OS=Canis lupus familiaris GN=NPAT PE=4 SV=2 - [F1PCZ7_	1,17	1	0	1	1
E2R2P0	Nucleoporin 62 OS=Canis lupus familiaris GN=NUP62 PE=4 SV=1 - [E2R2P0_CANLF]	1,14	1	1	1	1
A0A0E3V2J2	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_00575 PE=4 SV=1 - [A0A	1,12	1	0	1	4
E2RN39	Transcriptional regulating factor 1 OS=Canis lupus familiaris GN=TRERF1 PE=4 SV=1 - [E2RN39_CANLF]	1,08	1	1	1	2
F1PUF3	Tyrosine-protein kinase receptor OS=Canis lupus familiaris GN=ROS1 PE=3 SV=2 - [F1PUF3_CANLF]	1,07	1	1	1	1
E2RH24	Suppression of tumorigenicity 5 OS=Canis lupus familiaris GN=ST5 PE=4 SV=1 - [E2RH24_CANLF]	1,06	1	1	1	1
E2R8W2	Cell cycle progression 1 OS=Canis lupus familiaris GN=CCPG1 PE=4 SV=2 - [E2R8W2_CANLF]	1,02	1	0	1	1
E2QTX0	Calcium binding and coiled-coil domain 1 OS=Canis lupus familiaris GN=CALCOCO1 PE=4 SV=1 - [E2QTX0_CANL	1,01	1	1	1	2
F1PX83	Ubiquitin specific peptidase 7 OS=Canis lupus familiaris GN=USP7 PE=3 SV=2 - [F1PX83_CANLF]	1,01	1	1	1	2
F1PNH8	Sperm specific antigen 2 OS=Canis lupus familiaris GN=SSFA2 PE=4 SV=2 - [F1PNH8_CANLF]	1,01	1	1	1	1
F1P834	Component of oligomeric golgi complex 5 OS=Canis lupus familiaris GN=COG5 PE=4 SV=2 - [F1P834_CANLF]	1	1	1	1	1
E2R8W0	Cell cycle progression 1 OS=Canis lupus familiaris GN=CCPG1 PE=4 SV=1 - [E2R8W0_CANLF]	0,99	1	0	1	1
F1PUV3	Unc-45 myosin chaperone B OS=Canis lupus familiaris GN=UNC45B PE=4 SV=2 - [F1PUV3_CANLF]	0,95	1	1	1	1
F1PIP7	Collagen type VII alpha 1 chain OS=Canis lupus familiaris GN=COL7A1 PE=4 SV=1 - [F1PIP7_CANLF]	0,92	1	0	1	1
Q7YRK8	Type VII collagen OS=Canis lupus familiaris PE=2 SV=1 - [Q7YRK8_CANLF]	0,92	1	0	1	1
A0A0E3ZQT3	Ribonuclease R OS=Pasteurella multocida subsp. multocida OH4807 GN=rnr PE=3 SV=1 - [A0A0E3ZQT3_PASMD	0,88	1	1	1	1
F1P8U0	Family with sequence similarity 13 member A OS=Canis lupus familiaris GN=FAM13A PE=4 SV=2 - [F1P8U0_CAN	0,87	1	1	1	1
P82179	Triadin OS=Canis lupus familiaris GN=TRDN PE=1 SV=2 - [TRDN_CANLF]	0,86	1	0	1	2
F1PKD7	Triadin OS=Canis lupus familiaris GN=TRDN PE=4 SV=1 - [F1PKD7_CANLF]	0,86	1	0	1	2
F1PW82	Fermitin family member 1 OS=Canis lupus familiaris GN=FERMT1 PE=4 SV=2 - [F1PW82_CANLF]	0,86	1	0	1	4
G1K275	Triadin OS=Canis lupus familiaris GN=TRDN PE=4 SV=2 - [G1K275_CANLF]	0,85	1	0	1	2
A0A0A0MPA9	Triadin OS=Canis lupus familiaris GN=TRDN PE=4 SV=1 - [A0A0A0MPA9_CANLF]	0,84	1	0	1	2
J9P596	Triadin OS=Canis lupus familiaris GN=TRDN PE=4 SV=1 - [J9P596_CANLF]	0,84	1	0	1	2
F1P8I4	G-patch domain containing 1 OS=Canis lupus familiaris GN=GPATCH1 PE=4 SV=2 - [F1P8I4_CANLF]	0,81	1	1	1	1
E2RIC4	DEAD-box helicase 24 OS=Canis lupus familiaris GN=DDX24 PE=4 SV=2 - [E2RIC4_CANLF]	0,73	1	0	1	2
E2QYP0	NIMA related kinase 9 OS=Canis lupus familiaris GN=NEK9 PE=4 SV=1 - [E2QYP0_CANLF]	0,72	1	1	1	2
F1PBU5	SMG1, nonsense mediated mRNA decay associated PI3K related kinase OS=Canis lupus familiaris GN=SMG1 PE	0,69	1	0	1	1
J9NTC0	SMG1, nonsense mediated mRNA decay associated PI3K related kinase OS=Canis lupus familiaris GN=SMG1 PE	0,69	1	0	1	1
E2R498	Coiled-coil domain containing 88A OS=Canis lupus familiaris GN=CCDC88A PE=4 SV=2 - [E2R498_CANLF]	0,64	1	1	1	1
F1PI98	NCK associated protein 5 OS=Canis lupus familiaris GN=NCKAP5 PE=4 SV=2 - [F1PI98_CANLF]	0,62	1	1	1	1
F1PLE0	RNA binding motif protein 20 OS=Canis lupus familiaris GN=RBM20 PE=4 SV=2 - [F1PLE0_CANLF]	0,59	1	0	1	1
F1PKQ6	RPGR-interacting protein 1 OS=Canis lupus familiaris GN=RPGRIP1 PE=2 SV=2 - [F1PKQ6_CANLF]	0,58	1	0	1	2
Q076A8	Developmental myosin heavy chain embryonic OS=Canis lupus familiaris GN=MYH3 PE=3 SV=1 - [Q076A8_CAN	0,57	1	1	1	2
F1PXN8	RNA binding motif protein 20 OS=Canis lupus familiaris GN=RBM20 PE=4 SV=2 - [F1PXN8_CANLF]	0,57	1	0	1	1
F1PKC1	ATRX, chromatin remodeler OS=Canis lupus familiaris GN=ATRX PE=4 SV=2 - [F1PKC1_CANLF]	0,56	1	1	1	2
F6Y4Y7	TATA element modulatory factor 1 OS=Canis lupus familiaris GN=TMF1 PE=4 SV=1 - [F6Y4Y7_CANLF]	0,55	1	1	1	1
F1PS32	Family with sequence similarity 184 member A OS=Canis lupus familiaris GN=FAM184A PE=4 SV=2 - [F1PS32_C	0,54	1	0	1	1
F1PS31	Family with sequence similarity 184 member A OS=Canis lupus familiaris GN=FAM184A PE=4 SV=2 - [F1PS31_C	0,53	1	0	1	1
E2RRQ0	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100856585 PE=4 SV=1 - [E2RRQ0_CANLF]	0,5	1	0	1	1
E2RRP5	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100856585 PE=4 SV=2 - [E2RRP5_CANLF]	0,49	1	0	1	1
E2REQ8	Phosphorylase kinase regulatory subunit alpha 2 OS=Canis lupus familiaris GN=PHKA2 PE=4 SV=2 - [E2REQ8_CA	0,49	1	0	1	4
F1PDF4	Myosin-7 OS=Canis lupus familiaris GN=MYH7 PE=3 SV=2 - [F1PDF4_CANLF]	0,48	1	0	1	2
E2RJD1	Myosin-7 OS=Canis lupus familiaris GN=MYH7 PE=3 SV=2 - [E2RJD1_CANLF]	0,45	1	0	1	2
P49824	Myosin-7 OS=Canis lupus familiaris GN=MYH7 PE=1 SV=3 - [MYH7_CANLF]	0,41	1	0	1	2
F1PWR1	Insulin like growth factor 2 receptor OS=Canis lupus familiaris GN=IGF2R PE=4 SV=2 - [F1PWR1_CANLF]	0,41	1	0	1	1
B1H0W0	Cation-independent mannose-6-phosphate/insulin-like growth factor 2 receptor protein OS=Canis lupus familia	0,4	1	0	1	1
E2RLJ0	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF OS=Canis lupus familiaris GN=OBSCN PE=4 SV=2	0,4	1	0	1	1
J9NYI6	Leucine rich repeats and IQ motif containing 1 OS=Canis lupus familiaris GN=LRRIQ1 PE=4 SV=1 - [J9NYI6_CANL	0,36	1	0	1	1
F6XPP6	Golgin B1 OS=Canis lupus familiaris GN=GOLGB1 PE=4 SV=1 - [F6XPP6_CANLF]	0,34	1	1	1	1
E2R200	Centromere protein E OS=Canis lupus familiaris GN=CENPE PE=3 SV=2 - [E2R200_CANLF]	0,3	1	1	1	1
F1PVV4	Trio Rho guanine nucleotide exchange factor OS=Canis lupus familiaris GN=TRIO PE=4 SV=2 - [F1PVV4_CANLF]	0,29	1	1	1	1
J9JHM0	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF OS=Canis lupus familiaris GN=OBSCN PE=4 SV=1	0,29	1	0	1	1
J9P6H1	Dynein axonemal heavy chain 5 OS=Canis lupus familiaris GN=DNAH5 PE=4 SV=1 - [J9P6H1_CANLF]	0,27	1	1	1	1
E2R1Q3	Myosin XVIIIB OS=Canis lupus familiaris GN=MYO18B PE=4 SV=2 - [E2R1Q3_CANLF]	0,27	1	1	1	1
F1PIW3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PIW3_CANLF]	0,17	1	1	1	1
J9P9T0	NADH:ubiquinone oxidoreductase complex assembly factor 8 OS=Canis lupus familiaris GN=NDUFAF8 PE=4 SV=	27,03	1	1	1	1
E2R6S4	Stannin OS=Canis lupus familiaris GN=SNN PE=4 SV=1 - [E2R6S4_CANLF]	20,69	1	1	1	1
E2QXJ3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [E2QXJ3_CANLF]	18,1	1	1	1	1
A0A0E3V485	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_07720 PE=4 SV=1 - [A0A	15,19	1	1	1	1
E2RNR3	Decapping enzyme, scavenger OS=Canis lupus familiaris GN=DCPS PE=4 SV=2 - [E2RNR3_CANLF]	9,94	1	1	1	1
E2R8T6	REM2 and RAB like small GTPase 1 OS=Canis lupus familiaris GN=RSG1 PE=4 SV=2 - [E2R8T6_CANLF]	9,54	1	1	1	1
E2RK84	Testis expressed 35 OS=Canis lupus familiaris GN=TEX35 PE=4 SV=2 - [E2RK84_CANLF]	7,89	1	1	1	1
F6UXG8	TBC/LysM-associated domain containing 1 OS=Canis lupus familiaris GN=TLDC1 PE=4 SV=1 - [F6UXG8_CANLF]	7,03	1	1	1	1
A0A0E3V4P5	Bifunctional protein PyrR OS=Pasteurella multocida subsp. multocida OH4807 GN=pyrR PE=3 SV=1 - [A0A0E3V4	6,08	1	1	1	2
F1PBM4	Potassium voltage-gated channel subfamily C member 4 OS=Canis lupus familiaris GN=KCNC4 PE=3 SV=2 - [F1P	6,02	1	0	1	1
J9NTS6	Potassium voltage-gated channel subfamily C member 4 OS=Canis lupus familiaris GN=KCNC4 PE=3 SV=1 - [J9N	5,71	1	0	1	1
E2RLA8	Platelet activating factor acetylhydrolase 1b catalytic subunit 3 OS=Canis lupus familiaris GN=PAFAH1B3 PE=4 S	5,56	1	1	1	1
A0A0E3ZP46	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_03340 PE=4 SV=1 - [A0A	4,49	1	1	1	2
F1PXU8	Uncharacterized protein OS=Canis lupus familiaris GN=C33H3orf30 PE=4 SV=2 - [F1PXU8_CANLF]	4,48	1	1	1	1
J9P8R6	Cornulin OS=Canis lupus familiaris GN=CRNN PE=4 SV=1 - [J9P8R6_CANLF]	4,35	1	0	1	1

E2R9U5	Cornulin OS=Canis lupus familiaris GN=CRNN PE=4 SV=1 - [E2R9U5_CANLF]	4,33	1	0	1	1
F6XBZ5	Tyrosine-protein kinase receptor OS=Canis lupus familiaris GN=NTRK1 PE=3 SV=1 - [F6XBZ5_CANLF]	4,27	1	1	1	1
A0A0E3V3W3	Protein NrfC OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_03380 PE=4 SV=1 - [A0A0E3V3W3_	3,98	1	1	1	1
E2REJ3	BCAS3, microtubule associated cell migration factor OS=Canis lupus familiaris GN=BCAS3 PE=4 SV=2 - [E2REJ3_	3,9	1	0	1	1
E2RHM7	BCAS3, microtubule associated cell migration factor OS=Canis lupus familiaris GN=BCAS3 PE=4 SV=2 - [E2RHM7	3,85	1	0	1	1
E2RFT3	PAF1 homolog, Paf1/RNA polymerase II complex component OS=Canis lupus familiaris GN=PAF1 PE=4 SV=2 - [	3,75	1	1	1	1
E2QXF9	tRNA methyltransferase 11 homolog OS=Canis lupus familiaris GN=TRMT11 PE=4 SV=2 - [E2QXF9_CANLF]	3,56	1	0	1	1
F1PQW2	Kelch like family member 4 OS=Canis lupus familiaris GN=KLHL4 PE=4 SV=2 - [F1PQW2_CANLF]	3,48	1	0	1	2
F1Q115	Kelch like family member 4 OS=Canis lupus familiaris GN=KLHL4 PE=4 SV=2 - [F1Q115_CANLF]	3,46	1	0	1	2
E2R0B0	Caveolae associated protein 4 OS=Canis lupus familiaris GN=CAVIN4 PE=4 SV=2 - [E2R0B0_CANLF]	3,32	1	1	1	1
E2RA71	Uncharacterized protein OS=Canis lupus familiaris GN=VPS4A PE=3 SV=2 - [E2RA71_CANLF]	3,2	1	1	1	1
F1PER3	Calcyphosine 2 OS=Canis lupus familiaris GN=CAPS2 PE=4 SV=2 - [F1PER3_CANLF]	3,18	1	1	1	1
F1PG50	Synaptonemal complex central element protein 1 OS=Canis lupus familiaris GN=SYCE1 PE=4 SV=2 - [F1PG50_C	3,17	1	0	1	1
F1PZ02	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [F1PZ02_CANLF]	3,08	1	1	1	1
E2QRY7	BCL2 interacting protein 1 OS=Canis lupus familiaris GN=BNIP1 PE=4 SV=2 - [E2QRY7_CANLF]	3,07	1	0	1	1
E2QYJ3	Sorting nexin 1 OS=Canis lupus familiaris GN=SNX1 PE=4 SV=1 - [E2QYJ3_CANLF]	3,07	1	1	1	1
E2RRG7	tRNA methyltransferase 11 homolog OS=Canis lupus familiaris GN=TRMT11 PE=4 SV=2 - [E2RRG7_CANLF]	3,02	1	0	1	1
Q8SPL7	Paired-box 3 protein (Fragment) OS=Canis lupus familiaris GN=pax3 PE=4 SV=1 - [Q8SPL7_CANLF]	3,02	1	0	1	1
E2RK45	Exocyst complex component 7 OS=Canis lupus familiaris GN=EXOC7 PE=4 SV=1 - [E2RK45_CANLF]	2,99	1	0	1	1
E2RI52	Synaptonemal complex central element protein 1 OS=Canis lupus familiaris GN=SYCE1 PE=4 SV=2 - [E2RI52_CA	2,98	1	0	1	1
F1PGV3	Exocyst complex component 7 OS=Canis lupus familiaris GN=EXOC7 PE=4 SV=2 - [F1PGV3_CANLF]	2,97	1	0	1	1
F1PZG6	Solute carrier family 16 member 11 OS=Canis lupus familiaris GN=SLC16A11 PE=4 SV=2 - [F1PZG6_CANLF]	2,79	1	1	1	2
E2R961	Transmembrane protein 41B OS=Canis lupus familiaris GN=TMEM41B PE=4 SV=1 - [E2R961_CANLF]	2,75	1	1	1	1
J9NVH2	Ring finger protein 103 OS=Canis lupus familiaris GN=RNF103 PE=4 SV=1 - [J9NVH2_CANLF]	2,63	1	1	1	1
E2RH85	Uncharacterized protein OS=Canis lupus familiaris GN=PIK3R2 PE=4 SV=1 - [E2RH85_CANLF]	2,62	1	1	1	1
F1PUD1	Mab-21 domain containing 2 OS=Canis lupus familiaris GN=MB21D2 PE=4 SV=2 - [F1PUD1_CANLF]	2,6	1	1	1	1
F1Q335	Uncharacterized protein OS=Canis lupus familiaris GN=NLGN4X PE=4 SV=2 - [F1Q335_CANLF]	2,33	1	1	1	2
E2RMJ7	Inositol monophosphatase domain containing 1 OS=Canis lupus familiaris GN=IMPAD1 PE=4 SV=2 - [E2RMJ7_C	2,22	1	1	1	1
F1PD85	EPH receptor B6 OS=Canis lupus familiaris GN=EPHB6 PE=4 SV=2 - [F1PD85_CANLF]	2,08	1	1	1	1
F1PFM6	Collagen type VI alpha 1 chain OS=Canis lupus familiaris GN=COL6A1 PE=4 SV=2 - [F1PFM6_CANLF]	2,05	1	1	1	2
J9P9N2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P9N2_CANLF]	2,04	1	1	1	1
F1PDF7	GRAM domain containing 1B OS=Canis lupus familiaris GN=GRAMD1B PE=4 SV=2 - [F1PDF7_CANLF]	2,02	1	0	1	1
J9P2D0	Spalt like transcription factor 1 OS=Canis lupus familiaris GN=SALL1 PE=4 SV=1 - [J9P2D0_CANLF]	2	1	0	1	1
F1PRN5	SECIS binding protein 2 OS=Canis lupus familiaris GN=SECISBP2 PE=4 SV=2 - [F1PRN5_CANLF]	1,99	1	1	1	1
E2RAC3	Uncharacterized protein OS=Canis lupus familiaris GN=LOC476047 PE=4 SV=2 - [E2RAC3_CANLF]	1,94	1	1	1	1
F1PDF6	GRAM domain containing 1B OS=Canis lupus familiaris GN=GRAMD1B PE=4 SV=2 - [F1PDF6_CANLF]	1,89	1	0	1	1
J9P3E8	Zinc finger protein 770 OS=Canis lupus familiaris GN=ZNF770 PE=4 SV=1 - [J9P3E8_CANLF]	1,88	1	1	1	1
E2RRZ8	Regulation of nuclear pre-mRNA domain containing 1B OS=Canis lupus familiaris GN=RPRD1B PE=4 SV=1 - [E2R	1,84	1	0	1	1
E2RN85	Spalt like transcription factor 1 OS=Canis lupus familiaris GN=SALL1 PE=4 SV=2 - [E2RN85_CANLF]	1,81	1	0	1	1
J9P7U4	Spalt like transcription factor 1 OS=Canis lupus familiaris GN=SALL1 PE=4 SV=1 - [J9P7U4_CANLF]	1,81	1	0	1	1
J9NV61	L3MBTL1, histone methyl-lysine binding protein OS=Canis lupus familiaris GN=L3MBTL1 PE=4 SV=1 - [J9NV61_	1,68	1	1	1	2
J9P3V1	Listerin E3 ubiquitin protein ligase 1 OS=Canis lupus familiaris GN=LTN1 PE=4 SV=1 - [J9P3V1_CANLF]	1,58	1	0	1	1
E2R1P6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2R1P6_CANLF]	1,57	1	1	1	1
J9P6F5	Shroom family member 4 OS=Canis lupus familiaris GN=SHROOM4 PE=4 SV=1 - [J9P6F5_CANLF]	1,55	1	0	1	1
F6XEY1	Vaccinia related kinase 3 OS=Canis lupus familiaris GN=VRK3 PE=4 SV=1 - [F6XEY1_CANLF]	1,54	1	0	1	1
E2RSW0	Cytoskeleton associated protein 5 OS=Canis lupus familiaris GN=CKAP5 PE=4 SV=2 - [E2RSW0_CANLF]	1,52	1	1	1	1
F1PSB3	Dedicator of cytokinesis 10 OS=Canis lupus familiaris GN=DOCK10 PE=3 SV=2 - [F1PSB3_CANLF]	1,51	1	0	1	1
J9P6I4	Dedicator of cytokinesis 10 OS=Canis lupus familiaris GN=DOCK10 PE=3 SV=1 - [J9P6I4_CANLF]	1,5	1	0	1	1
F1PX06	Shroom family member 4 OS=Canis lupus familiaris GN=SHROOM4 PE=4 SV=2 - [F1PX06_CANLF]	1,48	1	0	1	1
E2RN65	Phosphatidylinositol-glycan biosynthesis class W protein OS=Canis lupus familiaris GN=PIGW PE=3 SV=1 - [E2R	1,39	1	1	1	1
E2REW3	ESF1 nucleolar pre-rRNA processing protein homolog OS=Canis lupus familiaris GN=ESF1 PE=4 SV=2 - [E2REW3_	1,3	1	1	1	1
E2RIB3	CYLD lysine 63 deubiquitinase OS=Canis lupus familiaris GN=CYLD PE=3 SV=1 - [E2RIB3_CANLF]	1,26	1	1	1	1
F1P9Y1	ARFGEF family member 3 OS=Canis lupus familiaris GN=ARFGEF3 PE=4 SV=2 - [F1P9Y1_CANLF]	1,24	1	0	1	1
E2QX72	Paired box 3 OS=Canis lupus familiaris GN=PAX3 PE=4 SV=2 - [E2QX72_CANLF]	1,24	1	0	1	1
F1P991	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 OS=Canis lupus familiaris GN=ST8SIA3 PE=4 SV=2	1,23	1	1	1	1
J9PAY0	ARFGEF family member 3 OS=Canis lupus familiaris GN=ARFGEF3 PE=4 SV=1 - [J9PAY0_CANLF]	1,23	1	0	1	1
F1PNX6	Paired box 7 OS=Canis lupus familiaris GN=PAX7 PE=3 SV=2 - [F1PNX6_CANLF]	1,19	1	0	1	1
F1PWM1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PWM1_CANLF]	1,14	1	1	1	1
E2RM22	Cyclin D binding myb like transcription factor 1 OS=Canis lupus familiaris GN=DMTF1 PE=4 SV=1 - [E2RM22_CA	1,05	1	1	1	1
F1PAH2	Voltage-dependent R-type calcium channel subunit alpha OS=Canis lupus familiaris GN=CACNA1E PE=3 SV=2 -	1,01	1	1	1	1
J9NZ73	Sodium/potassium-transporting ATPase subunit alpha OS=Canis lupus familiaris GN=ATP12A PE=3 SV=1 - [J9NZ	0,96	1	0	1	1
F1PE12	Regulator of G protein signaling 22 OS=Canis lupus familiaris GN=RGS22 PE=4 SV=2 - [F1PE12_CANLF]	0,94	1	1	1	1
F1P8N4	Sodium/potassium-transporting ATPase subunit alpha OS=Canis lupus familiaris GN=ATP12A PE=3 SV=2 - [F1P8	0,91	1	0	1	1
F1PNE0	Patched 1 OS=Canis lupus familiaris GN=PTCH1 PE=4 SV=2 - [F1PNE0_CANLF]	0,9	1	1	1	1
F6XG82	Strawberry notch homolog 2 OS=Canis lupus familiaris GN=SBNO2 PE=4 SV=1 - [F6XG82_CANLF]	0,88	1	1	1	1
F1PAF5	Tyrosine-protein phosphatase non-receptor type OS=Canis lupus familiaris GN=PTPN4 PE=3 SV=2 - [F1PAF5_C	0,86	1	1	1	1
E2RP24	RB binding protein 6, ubiquitin ligase OS=Canis lupus familiaris GN=RBBP6 PE=4 SV=2 - [E2RP24_CANLF]	0,82	1	0	1	1
F1PGL8	A-kinase anchoring protein 12 OS=Canis lupus familiaris GN=AKAP12 PE=4 SV=2 - [F1PGL8_CANLF]	0,8	1	1	1	1
F1PGK0	Listerin E3 ubiquitin protein ligase 1 OS=Canis lupus familiaris GN=LTN1 PE=4 SV=2 - [F1PGK0_CANLF]	0,79	1	0	1	1
E2RL41	Plexin A4 OS=Canis lupus familiaris GN=PLXNA4 PE=4 SV=2 - [E2RL41_CANLF]	0,79	1	0	1	2
F1P6G0	Plexin A1 OS=Canis lupus familiaris GN=PLXNA1 PE=4 SV=2 - [F1P6G0_CANLF]	0,79	1	0	1	2
F1PJ65	IQ motif containing GTPase activating protein 1 OS=Canis lupus familiaris GN=IQGAP1 PE=4 SV=2 - [F1PJ65_CA	0,78	1	1	1	1
J9P0A5	RB binding protein 6, ubiquitin ligase OS=Canis lupus familiaris GN=RBBP6 PE=4 SV=1 - [J9P0A5_CANLF]	0,78	1	0	1	1
E2R4X9	Pre-mRNA processing factor 8 OS=Canis lupus familiaris GN=PRPF8 PE=4 SV=2 - [E2R4X9_CANLF]	0,73	1	1	1	1
J9NW31	Ryanodine receptor 1 OS=Canis lupus familiaris GN=RYR1 PE=4 SV=1 - [J9NW31_CANLF]	0,66	1	0	1	1
E2R571	Meiosis regulator and mRNA stability factor 1 OS=Canis lupus familiaris GN=MARF1 PE=4 SV=1 - [E2R571_CAN	0,63	1	1	1	1
F1PCD9	Microtubule associated monooxygenase, calponin and LIM domain containing 1 OS=Canis lupus familiaris GN=	0,62	1	1	1	1
J9P3Y9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P3Y9_CANLF]	0,6	1	0	1	2
F1P780	Exophilin 5 OS=Canis lupus familiaris GN=EXPH5 PE=4 SV=1 - [F1P780_CANLF]	0,57	1	0	1	1
J9NSZ6	Dynein axonemal heavy chain 8 OS=Canis lupus familiaris GN=DNAH8 PE=4 SV=1 - [J9NSZ6_CANLF]	0,57	1	0	1	1
J9P4W7	von Willebrand factor A domain containing 3B OS=Canis lupus familiaris GN=VWA3B PE=4 SV=1 - [J9P4W7_CA	0,56	1	0	1	1
J9NT90	Exophilin 5 OS=Canis lupus familiaris GN=EXPH5 PE=4 SV=1 - [J9NT90_CANLF]	0,55	1	0	1	1
E2QUR1	Chromodomain helicase DNA binding protein 8 OS=Canis lupus familiaris GN=CHD8 PE=4 SV=2 - [E2QUR1_CAN	0,55	1	0	1	1
J9NUZ2	Dynein axonemal heavy chain 8 OS=Canis lupus familiaris GN=DNAH8 PE=4 SV=1 - [J9NUZ2_CANLF]	0,55	1	0	1	1
E2REK9	Dynein axonemal heavy chain 8 OS=Canis lupus familiaris GN=DNAH8 PE=4 SV=2 - [E2REK9_CANLF]	0,54	1	0	1	1
E2RIS0	von Willebrand factor A domain containing 3B OS=Canis lupus familiaris GN=VWA3B PE=4 SV=2 - [E2RIS0_CAN	0,54	1	0	1	1
F1PIS0	Ryanodine receptor 1 OS=Canis lupus familiaris GN=RYR1 PE=4 SV=2 - [F1PIS0_CANLF]	0,53	1	0	1	1
E2RLY8	Cullin 9 OS=Canis lupus familiaris GN=CUL9 PE=3 SV=2 - [E2RLY8_CANLF]	0,52	1	1	1	2
J9NWD8	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1 OS=Canis lupus familiaris GN=HE	0,51	1	0	1	2
E2R280	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2R280_CANLF]	0,49	1	0	1	2
E2QUS7	Chromodomain-helicase-DNA-binding protein 8 OS=Canis lupus familiaris GN=CHD8 PE=3 SV=2 - [E2QUS7_CAN	0,46	1	0	1	1
F1PBL9	Human immunodeficiency virus type I enhancer binding protein 2 OS=Canis lupus familiaris GN=HIVEP2 PE=4 S	0,45	1	1	1	1
J9NRQ0	Teneurin transmembrane protein 3 OS=Canis lupus familiaris GN=TENM3 PE=4 SV=1 - [J9NRQ0_CANLF]	0,45	1	0	1	3

E2QYQ5	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1 OS=Canis lupus familiaris GN=HE	0,43	1	0	1	2
F1P9A6	Teneurin transmembrane protein 3 OS=Canis lupus familiaris GN=TENM3 PE=4 SV=2 - [F1P9A6_CANLF]	0,41	1	0	1	3
F1Q450	HECT domain E3 ubiquitin protein ligase 4 OS=Canis lupus familiaris GN=HECTD4 PE=4 SV=2 - [F1Q450_CANLF]	0,38	1	0	1	1
E2R054	Kinesin family member 14 OS=Canis lupus familiaris GN=KIF14 PE=3 SV=1 - [E2R054_CANLF]	0,36	1	0	1	1
E2R0K6	HECT domain E3 ubiquitin protein ligase 4 OS=Canis lupus familiaris GN=HECTD4 PE=4 SV=2 - [E2R0K6_CANLF]	0,35	1	0	1	1
E2QSC2	Tet methylcytosine dioxygenase 1 OS=Canis lupus familiaris GN=TET1 PE=4 SV=1 - [E2QSC2_CANLF]	0,33	1	0	1	1
F1P9A1	Vacuolar protein sorting 13 homolog D OS=Canis lupus familiaris GN=VPS13D PE=4 SV=2 - [F1P9A1_CANLF]	0,32	1	1	1	1
J9NZV6	Tet methylcytosine dioxygenase 1 OS=Canis lupus familiaris GN=TET1 PE=4 SV=1 - [J9NZV6_CANLF]	0,32	1	0	1	1
F1PGL1	Versican OS=Canis lupus familiaris GN=VCAN PE=4 SV=2 - [F1PGL1_CANLF]	0,32	1	1	1	1
E2RNI0	Myosin IXA OS=Canis lupus familiaris GN=MYO9A PE=4 SV=2 - [E2RNI0_CANLF]	0,23	1	0	1	1
J9P187	Myosin IXA OS=Canis lupus familiaris GN=MYO9A PE=4 SV=1 - [J9P187_CANLF]	0,23	1	0	1	1
J9NW38	Uncharacterized protein OS=Canis lupus familiaris GN=LOC611589 PE=4 SV=1 - [J9NW38_CANLF]	0,14	1	0	1	1
F1PRF6	Uncharacterized protein OS=Canis lupus familiaris GN=LOC611589 PE=4 SV=2 - [F1PRF6_CANLF]	0,13	1	0	1	1
E2RI62	Molybdopterin synthase catalytic subunit OS=Canis lupus familiaris GN=MOCS2 PE=3 SV=2 - [E2RI62_CANLF]	5,95	1	0	1	1
E2R9Q9	SPC24, NDC80 kinetochore complex component OS=Canis lupus familiaris GN=SPC24 PE=4 SV=2 - [E2R9Q9_CA	5,58	1	1	1	1
E2R0Y2	Molybdopterin synthase catalytic subunit OS=Canis lupus familiaris GN=MOCS2 PE=3 SV=1 - [E2R0Y2_CANLF]	5,5	1	0	1	1
E2QUT6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [E2QUT6_CANLF]	4,77	1	1	1	1
A0A0E3ZP33	Isochorismate synthase MenF OS=Pasteurella multocida subsp. multocida OH4807 GN=menF PE=3 SV=1 - [A0A	4,64	1	1	1	1
E2QVS8	Olfactory receptor OS=Canis lupus familiaris GN=OR4N2 PE=3 SV=2 - [E2QVS8_CANLF]	4,3	1	0	1	1
F1PJI2	Solute carrier family 36 member 4 OS=Canis lupus familiaris GN=SLC36A4 PE=4 SV=2 - [F1PJI2_CANLF]	4,28	1	1	1	1
E2RD57	Olfactory receptor OS=Canis lupus familiaris GN=LOC482537 PE=3 SV=2 - [E2RD57_CANLF]	4,22	1	0	1	1
J9PB63	Keratin 5 OS=Canis lupus familiaris GN=KRT5 PE=4 SV=1 - [J9PB63_CANLF]	3,88	1	0	1	1
J9P969	AHNAK nucleoprotein OS=Canis lupus familiaris GN=AHNAK PE=4 SV=1 - [J9P969_CANLF]	3,81	1	1	1	1
E2RAF2	Uncharacterized protein OS=Canis lupus familiaris GN=KLC1 PE=4 SV=2 - [E2RAF2_CANLF]	1,95	1	0	1	1
E2RAF0	Uncharacterized protein OS=Canis lupus familiaris GN=KLC1 PE=4 SV=2 - [E2RAF0_CANLF]	1,74	1	0	1	1
J9P7J3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P7J3_CANLF]	1,67	1	1	1	1
J9P925	Rac/Cdc42 guanine nucleotide exchange factor 6 OS=Canis lupus familiaris GN=ARHGEF6 PE=4 SV=1 - [J9P925_	1,61	1	0	1	1
E2R0Z1	Rac/Cdc42 guanine nucleotide exchange factor 6 OS=Canis lupus familiaris GN=ARHGEF6 PE=4 SV=2 - [E2R0Z1_	1,29	1	0	1	1
E2REP7	Zinc finger with KRAB and SCAN domains 2 OS=Canis lupus familiaris GN=ZKSCAN2 PE=4 SV=2 - [E2REP7_CANL	1,24	1	1	1	1
F1PF23	Fanconi anemia complementation group I OS=Canis lupus familiaris GN=FANCI PE=4 SV=2 - [F1PF23_CANLF]	0,98	1	1	1	1
F1PKR8	Tensin 2 OS=Canis lupus familiaris GN=TNS2 PE=4 SV=2 - [F1PKR8_CANLF]	0,78	1	0	1	1
E2R0D7	Collagen type VI alpha 6 chain OS=Canis lupus familiaris GN=COL6A6 PE=4 SV=2 - [E2R0D7_CANLF]	0,66	1	1	1	1
F1PX71	Myosin VB OS=Canis lupus familiaris GN=MYO5B PE=4 SV=2 - [F1PX71_CANLF]	0,49	1	1	1	1
O97592	Dystrophin OS=Canis lupus familiaris GN=DMD PE=2 SV=1 - [DMD_CANLF]	0,41	1	0	1	1
D1MEQ0	Dystrophin OS=Canis lupus familiaris PE=2 SV=1 - [D1MEQ0_CANLF]	0,41	1	0	1	1
F1P7G4	Dystrophin (Fragment) OS=Canis lupus familiaris GN=DMD PE=4 SV=2 - [F1P7G4_CANLF]	0,41	1	0	1	1
E2RQ26	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=KMT2D PE=4 SV=2 - [E2RQ26_CANLF]	0,23	1	0	1	1
J9P0X8	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=KMT2D PE=4 SV=1 - [J9P0X8_CANLF]	0,23	1	0	1	1
E2R9Z6	Kinesin family member 27 OS=Canis lupus familiaris GN=KIF27 PE=3 SV=1 - [E2R9Z6_CANLF]	0,64	1	1	1	1
E2RJK6	Zinc finger and BTB domain containing 11 OS=Canis lupus familiaris GN=ZBTB11 PE=4 SV=1 - [E2RJK6_CANLF]	2,66	1	0	1	1
J9P4R3	Zinc finger and BTB domain containing 11 OS=Canis lupus familiaris GN=ZBTB11 PE=4 SV=1 - [J9P4R3_CANLF]	3,04	1	0	1	1
A0A0E3ZS10	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08325 PE=4 SV=1 - [A0	3,89	1	1	1	1
E2QV33	Mediator complex subunit 22 OS=Canis lupus familiaris GN=MED22 PE=4 SV=1 - [E2QV33_CANLF]	5,39	1	1	1	1
F1Q0F4	Peptidylprolyl isomerase OS=Canis lupus familiaris GN=FKBP15 PE=4 SV=2 - [F1Q0F4_CANLF]	0,75	1	1	1	1
Q864L3	Sodium channel subunit beta-2 OS=Canis lupus familiaris GN=SCN2B PE=2 SV=2 - [SCN2B_CANLF]	4,65	1	0	1	1
J9P9N8	Sodium channel subunit beta-2 OS=Canis lupus familiaris GN=SCN2B PE=4 SV=1 - [J9P9N8_CANLF]	3,86	1	0	1	1
F1PYB7	Centrosomal protein 162 OS=Canis lupus familiaris GN=CEP162 PE=4 SV=2 - [F1PYB7_CANLF]	0,64	1	1	1	1
J9NWK0	RAD51 associated protein 2 OS=Canis lupus familiaris GN=RAD51AP2 PE=4 SV=1 - [J9NWK0_CANLF]	1,14	1	0	1	1
J9P2K3	RAD51 associated protein 2 OS=Canis lupus familiaris GN=RAD51AP2 PE=4 SV=1 - [J9P2K3_CANLF]	1,15	1	0	1	1
E2R9H8	WNK lysine deficient protein kinase 3 OS=Canis lupus familiaris GN=WNK3 PE=4 SV=1 - [E2R9H8_CANLF]	2,98	1	0	1	1
J9P5T2	WNK lysine deficient protein kinase 3 OS=Canis lupus familiaris GN=WNK3 PE=4 SV=1 - [J9P5T2_CANLF]	1,24	1	0	1	1
F1P8L4	Family with sequence similarity 208 member B OS=Canis lupus familiaris GN=FAM208B PE=4 SV=2 - [F1P8L4_C	0,76	1	1	1	1
E2RFH8	Uncharacterized protein OS=Canis lupus familiaris GN=TRIM16 PE=4 SV=2 - [E2RFH8_CANLF]	1,14	1	1	1	1
F1PF40	G protein-coupled receptor 63 OS=Canis lupus familiaris GN=GPR63 PE=4 SV=2 - [F1PF40_CANLF]	6,55	1	1	1	1
A0A0E3ZNT4	Putative deoxyribonuclease YjjV OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_02590 PE=4 SV=	4,56	1	1	1	1
F1PLG0	Uncharacterized protein OS=Canis lupus familiaris GN=EMR4 PE=3 SV=2 - [F1PLG0_CANLF]	2,51	1	0	1	1
Q2Q419	EMR4 OS=Canis lupus familiaris PE=2 SV=1 - [Q2Q419_CANLF]	2,51	1	0	1	1
F1PCZ6	Actin binding LIM protein family member 2 OS=Canis lupus familiaris GN=ABLIM2 PE=4 SV=2 - [F1PCZ6_CANLF]	3,11	1	1	1	1
E2RFF1	DEAD-box helicase 42 OS=Canis lupus familiaris GN=DDX42 PE=4 SV=1 - [E2RFF1_CANLF]	2,57	1	1	1	1
E2RPF7	Phospholipase A2 group VI OS=Canis lupus familiaris GN=PLA2G6 PE=4 SV=2 - [E2RPF7_CANLF]	4,33	1	0	1	2
E2RPF9	Phospholipase A2 group VI OS=Canis lupus familiaris GN=PLA2G6 PE=4 SV=1 - [E2RPF9_CANLF]	2,61	1	0	1	2
E2RFS7	ERCC excision repair 8, CSA ubiquitin ligase complex subunit OS=Canis lupus familiaris GN=ERCC8 PE=4 SV=1 - [	5,3	1	1	1	2
E2RFJ1	Uncharacterized protein OS=Canis lupus familiaris GN=PCDH11X PE=4 SV=2 - [E2RFJ1_CANLF]	2,32	1	1	1	1
E2R985	Actin-related protein 2/3 complex subunit 3 OS=Canis lupus familiaris PE=3 SV=2 - [E2R985_CANLF]	6,9	1	0	1	1
J9P309	Actin-related protein 2/3 complex subunit 3 OS=Canis lupus familiaris GN=ARPC3 PE=3 SV=1 - [J9P309_CANLF]	7,87	1	0	1	1
P24460	Cytochrome P450 2B11 OS=Canis lupus familiaris GN=CYP2B11 PE=2 SV=1 - [CP2BB_CANLF]	3,85	1	0	1	1
E2R970	Ubiquitin specific peptidase 24 OS=Canis lupus familiaris GN=USP24 PE=3 SV=2 - [E2R970_CANLF]	0,87	1	1	1	1
F1PNK2	Uncharacterized protein OS=Canis lupus familiaris GN=CYP2B6 PE=3 SV=2 - [F1PNK2_CANLF]	3,63	1	0	1	1
X5KJB3	Cytochrome-P450-2B11 OS=Canis lupus familiaris GN=CYP2B11 PE=2 SV=1 - [X5KJB3_CANLF]	3,85	1	0	1	1
F6Y1C9	DNA polymerase OS=Canis lupus familiaris GN=POLA1 PE=3 SV=1 - [F6Y1C9_CANLF]	1,3	1	1	1	1
F6UWX1	THO complex 5 OS=Canis lupus familiaris GN=THOC5 PE=4 SV=1 - [F6UWX1_CANLF]	1,46	1	1	1	1
F1PTP2	Sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) OS=Canis lupus familiaris GN=SPR PE=4 S	4,87	1	1	1	1
A0A0E3ZS08	Signal recognition particle protein OS=Pasteurella multocida subsp. multocida OH4807 GN=ffh PE=3 SV=1 - [A0	4,59	1	0	1	6
E2R289	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=SUV39H1 PE=3 SV=1 - [E2R289_CANLF]	2,43	1	1	1	1
O46674	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Canis lupus familiaris GN=ATP2A2 PE=2 SV=1 - [AT2	1,5	1	0	1	1
E2QUQ0	Actinin alpha 2 OS=Canis lupus familiaris GN=ACTN2 PE=4 SV=2 - [E2QUQ0_CANLF]	1,34	1	1	1	1
E2RLK0	L-lactate dehydrogenase OS=Canis lupus familiaris GN=LDHC PE=3 SV=1 - [E2RLK0_CANLF]	3,6	1	0	1	1
E2RRC9	Phosphoglycerate kinase OS=Canis lupus familiaris GN=PGK1 PE=3 SV=1 - [E2RRC9_CANLF]	3,6	1	1	1	1
F1PS82	Fructose-bisphosphate aldolase OS=Canis lupus familiaris GN=ALDOC PE=3 SV=2 - [F1PS82_CANLF]	5,83	1	0	1	1
H9N9H3	Lactate dehydrogenase C isoform 4 OS=Canis lupus familiaris GN=LDHC PE=2 SV=1 - [H9N9H3_CANLF]	3,28	1	0	1	1
J9P540	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris GN=LOC477441 PE=3 SV=1 - [J9P540_C	4,19	1	0	1	2
F1PL63	Fructose-bisphosphate aldolase OS=Canis lupus familiaris GN=ALDOC PE=3 SV=1 - [F1PL63_CANLF]	7,14	1	0	1	1
E2R1B9	HERV-H LTR-associating 1 OS=Canis lupus familiaris GN=HHLA1 PE=4 SV=2 - [E2R1B9_CANLF]	1,4	1	0	1	1
F1PVW0	L-lactate dehydrogenase OS=Canis lupus familiaris GN=LOC476882 PE=3 SV=2 - [F1PVW0_CANLF]	4,71	1	0	1	4
J9P8V2	HERV-H LTR-associating 1 OS=Canis lupus familiaris GN=HHLA1 PE=4 SV=1 - [J9P8V2_CANLF]	1,34	1	0	1	1
E2RA64	L-lactate dehydrogenase OS=Canis lupus familiaris GN=LOC476882 PE=3 SV=2 - [E2RA64_CANLF]	6,09	1	0	1	4
Q95159	Angiotensinogen (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q95159_CANLF]	38,46	1	0	1	1
Q95LE3	Interleukin-10 (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q95LE3_CANLF]	30,33	1	0	1	1
Q28251	Sex-determining region Y protein (Fragment) OS=Canis lupus familiaris GN=sry PE=3 SV=1 - [Q28251_CANLF]	29,09	1	0	1	1
B0M0J2	Interleukin 10 OS=Canis lupus familiaris PE=2 SV=1 - [B0M0J2_CANLF]	20,67	1	0	1	1
F1PZ65	Interleukin-10 OS=Canis lupus familiaris GN=IL10 PE=4 SV=1 - [F1PZ65_CANLF]	20,67	1	0	1	1
P48411	Interleukin-10 OS=Canis lupus familiaris GN=IL10 PE=2 SV=1 - [IL10_CANLF]	20,44	1	0	1	1
Q643X2	Protein kinase B (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q643X2_CANLF]	20	1	0	1	1

J9NSK3	NANOG neighbor homeobox OS=Canis lupus familiaris GN=NANOGNB PE=4 SV=1 - [J9NSK3_CANLF]	15,97	1	1	1	1
F1PF97	Retinitis pigmentosa 9 (autosomal dominant) OS=Canis lupus familiaris GN=RP9 PE=4 SV=2 - [F1PF97_CANLF]	10,9	1	0	1	2
A0A0E3V455	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_04765 PE=4 SV=1 - [A0	10,66	1	1	1	1
L7N062	Retinitis pigmentosa 9 (autosomal dominant) OS=Canis lupus familiaris GN=RP9 PE=4 SV=1 - [L7N062_CANLF]	10,45	1	0	1	2
E2RSY6	NudC domain containing 2 OS=Canis lupus familiaris GN=NUDCD2 PE=4 SV=2 - [E2RSY6_CANLF]	10,42	1	1	1	1
A0A0E3ZPT6	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_06515 PE=4 SV=1 - [A0	9,47	1	1	1	1
O62729	Neuropeptide Y receptor type 5 OS=Canis lupus familiaris GN=NPY5R PE=2 SV=1 - [NPY5R_CANLF]	9,42	1	1	1	1
F1PQ93	Stratifin OS=Canis lupus familiaris GN=SFN PE=3 SV=2 - [F1PQ93_CANLF]	8,87	1	1	1	2
J9NXM6	Nucleolar protein interacting with the FHA domain of MKI67 OS=Canis lupus familiaris GN=NIFK PE=4 SV=1 - [J	8,42	1	0	1	1
E2RHG8	Nucleolar protein interacting with the FHA domain of MKI67 OS=Canis lupus familiaris GN=NIFK PE=4 SV=2 - [E	8,36	1	0	1	1
J9NV30	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NV30_CANLF]	7,48	1	1	1	1
Q9XT60	Sex-determining region Y protein OS=Canis lupus familiaris GN=SRY PE=3 SV=1 - [SRY_CANLF]	7,27	1	0	1	1
J9NWC1	MOB kinase activator 2 OS=Canis lupus familiaris GN=MOB2 PE=4 SV=1 - [J9NWC1_CANLF]	6,38	1	0	1	1
P68280	Alpha-crystallin A chain OS=Canis lupus familiaris GN=CRYAA PE=1 SV=1 - [CRYAA_CANLF]	6,36	1	1	1	2
E2R0N3	Annexin OS=Canis lupus familiaris GN=ANXA3 PE=3 SV=1 - [E2R0N3_CANLF]	6,19	1	1	1	1
F1PF62	MOB kinase activator 2 OS=Canis lupus familiaris GN=MOB2 PE=4 SV=2 - [F1PF62_CANLF]	5,64	1	0	1	1
F6XJI8	Mitochondrial ribosomal protein S31 OS=Canis lupus familiaris GN=MRPS31 PE=4 SV=1 - [F6XJI8_CANLF]	5,57	1	0	1	1
F1PDH5	Apolipoprotein A5 OS=Canis lupus familiaris GN=APOA5 PE=3 SV=1 - [F1PDH5_CANLF]	5,41	1	1	1	2
E2RB38	Tropomyosin 3 OS=Canis lupus familiaris GN=TPM3 PE=3 SV=2 - [E2RB38_CANLF]	5,24	1	0	1	1
E2R9J7	Mitochondrial ribosomal protein S31 OS=Canis lupus familiaris GN=MRPS31 PE=4 SV=2 - [E2R9J7_CANLF]	5	1	0	1	1
J9P5D6	Mitochondrial ribosomal protein S31 OS=Canis lupus familiaris GN=MRPS31 PE=4 SV=1 - [J9P5D6_CANLF]	4,92	1	0	1	1
E2RBS0	IKAROS family zinc finger 2 OS=Canis lupus familiaris GN=IKZF2 PE=4 SV=1 - [E2RBS0_CANLF]	4,75	1	1	1	1
A0A0E3ZPX3	Coproporphyrinogen III oxidase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_02065 PE=4 SV=	4,64	1	1	1	1
Q4ZHS0	Guanylate cyclase soluble subunit alpha-3 OS=Canis lupus familiaris GN=GUCY1A3 PE=2 SV=1 - [GCYA3_CANLF]	4,64	1	0	1	1
F1P649	Guanylate cyclase soluble subunit alpha-3 OS=Canis lupus familiaris GN=GUCY1A3 PE=3 SV=1 - [F1P649_CANLF	4,64	1	0	1	1
A0A0N9JS23	Tropomyosin 3 gamma OS=Canis lupus familiaris GN=Tpm3 PE=2 SV=1 - [A0A0N9JS23_CANLF]	4,58	1	0	1	1
E2RBW4	Tropomyosin 3 OS=Canis lupus familiaris GN=TPM3 PE=3 SV=2 - [E2RBW4_CANLF]	4,56	1	0	1	1
J9NTU0	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9NTU0_CANLF]	4,36	1	0	1	1
J9P1L8	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9P1L8_CANLF]	4,36	1	0	1	1
F1PBK4	Lamin B1 OS=Canis lupus familiaris GN=LMNB1 PE=3 SV=2 - [F1PBK4_CANLF]	4,19	1	0	1	1
F1PT35	HECT domain E3 ubiquitin protein ligase 2 OS=Canis lupus familiaris GN=HECTD2 PE=4 SV=2 - [F1PT35_CANLF]	4,19	1	1	1	2
J9P3G1	Lamin B1 OS=Canis lupus familiaris GN=LMNB1 PE=3 SV=1 - [J9P3G1_CANLF]	4	1	0	1	1
F1PPW9	Thyroid hormone receptor beta OS=Canis lupus familiaris GN=THRB PE=3 SV=2 - [F1PPW9_CANLF]	3,9	1	1	1	1
F1Q3Y2	Dihydropyrimidinase like 3 OS=Canis lupus familiaris GN=DPYSL3 PE=4 SV=2 - [F1Q3Y2_CANLF]	3,86	1	1	1	1
H9GWH6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [H9GWH6_CANLF]	3,78	1	0	1	1
J9P620	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P620_CANLF]	3,67	1	1	1	1
J9P545	Ring finger protein 219 OS=Canis lupus familiaris GN=RNF219 PE=4 SV=1 - [J9P545_CANLF]	3,63	1	1	1	1
Q5I9W4	Protein kinase B (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q5I9W4_CANLF]	3,33	1	0	1	1
F1PEE4	Exportin 5 OS=Canis lupus familiaris GN=XPO5 PE=4 SV=2 - [F1PEE4_CANLF]	3,32	1	0	1	1
F6XYR9	CXXC finger protein 1 OS=Canis lupus familiaris GN=CXXC1 PE=4 SV=1 - [F6XYR9_CANLF]	3,31	1	1	1	1
Q5I9W5	Protein kinase B OS=Canis lupus familiaris PE=2 SV=1 - [Q5I9W5_CANLF]	3,1	1	0	1	1
J9P8X1	Exportin 5 OS=Canis lupus familiaris GN=XPO5 PE=4 SV=1 - [J9P8X1_CANLF]	2,97	1	0	1	1
F1PSA7	AKT serine/threonine kinase 2 OS=Canis lupus familiaris GN=AKT2 PE=3 SV=2 - [F1PSA7_CANLF]	2,91	1	0	1	1
E2R5C6	Neural precursor cell expressed, developmentally down-regulated 1 OS=Canis lupus familiaris GN=NEDD1 PE=4	2,86	1	1	1	1
F1P8G4	Fucosidase, alpha-L- 2, plasma OS=Canis lupus familiaris GN=FUCA2 PE=4 SV=1 - [F1P8G4_CANLF]	2,77	1	1	1	2
E2RJX4	AKT serine/threonine kinase 1 OS=Canis lupus familiaris GN=AKT1 PE=3 SV=1 - [E2RJX4_CANLF]	2,71	1	0	1	1
F1Q4F8	AKT serine/threonine kinase 3 OS=Canis lupus familiaris GN=AKT3 PE=3 SV=2 - [F1Q4F8_CANLF]	2,71	1	0	1	1
F1PRG4	AKT serine/threonine kinase 2 OS=Canis lupus familiaris GN=AKT2 PE=3 SV=1 - [F1PRG4_CANLF]	2,7	1	0	1	1
J9PB82	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PB82_CANLF]	2,62	1	0	1	1
J9NRX1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NRX1_CANLF]	2,61	1	0	1	1
E2RB36	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2RB36_CANLF]	2,57	1	0	1	1
H9GWJ2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [H9GWJ2_CANLF]	2,56	1	0	1	1
J9P2R2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P2R2_CANLF]	2,56	1	0	1	1
J9P6P3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P6P3_CANLF]	2,56	1	0	1	1
E2R4V0	SET and MYND domain containing 4 OS=Canis lupus familiaris GN=SMYD4 PE=4 SV=1 - [E2R4V0_CANLF]	2,52	1	0	1	1
J9NYI0	SET and MYND domain containing 4 OS=Canis lupus familiaris GN=SMYD4 PE=4 SV=1 - [J9NYI0_CANLF]	2,48	1	0	1	1
F1PYW3	Neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase OS=Canis lupus	2,27	1	1	1	1
F1PMG0	Integrin beta OS=Canis lupus familiaris GN=ITGB7 PE=3 SV=2 - [F1PMG0_CANLF]	2,26	1	1	1	1
F1PKP8	Leucine rich repeat LGI family member 4 OS=Canis lupus familiaris GN=LGI4 PE=4 SV=2 - [F1PKP8_CANLF]	2,25	1	1	1	2
A0A0E3V4L4	Protein TadG OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_09475 PE=4 SV=1 - [A0A0E3V4L4_	2,16	1	1	1	2
E2QX80	Ring finger protein 14 OS=Canis lupus familiaris GN=RNF14 PE=3 SV=1 - [E2QX80_CANLF]	2,11	1	1	1	1
J9P7Y3	Fms related tyrosine kinase 3 OS=Canis lupus familiaris GN=FLT3 PE=3 SV=1 - [J9P7Y3_CANLF]	1,95	1	0	1	1
F1PKV4	Fms related tyrosine kinase 3 OS=Canis lupus familiaris GN=FLT3 PE=3 SV=2 - [F1PKV4_CANLF]	1,91	1	0	1	1
J9P9L5	Fms related tyrosine kinase 3 OS=Canis lupus familiaris GN=FLT3 PE=3 SV=1 - [J9P9L5_CANLF]	1,91	1	0	1	1
Q4ZHV8	Flt3 OS=Canis lupus familiaris GN=Flt3 PE=2 SV=1 - [Q4ZHV8_CANLF]	1,91	1	0	1	1
F1Q2J3	Solute carrier family 12 member 6 OS=Canis lupus familiaris GN=SLC12A6 PE=4 SV=2 - [F1Q2J3_CANLF]	1,82	1	1	1	1
F1PV47	RAS protein activator like 2 OS=Canis lupus familiaris GN=RASAL2 PE=4 SV=2 - [F1PV47_CANLF]	1,8	1	1	1	1
J9P3H7	Regulator of solute carriers 1 OS=Canis lupus familiaris GN=RSC1A1 PE=4 SV=1 - [J9P3H7_CANLF]	1,78	1	1	1	1
X5KCU7	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5KCU7_CANLF]	1,78	1	0	1	1
X5KNV4	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5KNV4_CANLF]	1,78	1	0	1	1
X5KNV9	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5KNV9_CANLF]	1,78	1	0	1	1
F1PHX8	Collagen type V alpha 1 chain OS=Canis lupus familiaris GN=COL5A1 PE=4 SV=2 - [F1PHX8_CANLF]	1,65	1	1	1	1
Q29473	Cytochrome P450 2D15 OS=Canis lupus familiaris GN=CYP2D15 PE=1 SV=3 - [CP2DF_CANLF]	1,6	1	0	1	1
X5KJD2	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5KJD2_CANLF]	1,6	1	0	1	1
X5KJD8	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5KJD8_CANLF]	1,6	1	0	1	1
X5KNW5	Cytochrome-P450-2D15 OS=Canis lupus familiaris GN=CYP2D15 PE=2 SV=1 - [X5KNW5_CANLF]	1,6	1	0	1	1
X5L1N0	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5L1N0_CANLF]	1,6	1	0	1	1
X5L571	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5L571_CANLF]	1,6	1	0	1	1
X5L576	CYP2D15 OS=Canis lupus familiaris GN=Cytochrome-P450-2D15 PE=2 SV=1 - [X5L576_CANLF]	1,6	1	0	1	1
E2R1A3	Phosphatidylinositol transfer protein membrane associated 2 OS=Canis lupus familiaris GN=PITPNM2 PE=4 SV=	1,58	1	1	1	1
E2RJI2	Glutamate metabotropic receptor 5 OS=Canis lupus familiaris GN=GRM5 PE=3 SV=1 - [E2RJI2_CANLF]	1,56	1	0	1	1
J9JH96	Glutamate metabotropic receptor 5 OS=Canis lupus familiaris GN=GRM5 PE=3 SV=1 - [J9JH96_CANLF]	1,53	1	0	1	1
E2QW14	Neurochondrin OS=Canis lupus familiaris GN=NCDN PE=4 SV=2 - [E2QW14_CANLF]	1,51	1	1	1	2
F1PND2	Fanconi anemia group C protein homolog OS=Canis lupus familiaris GN=FANCC PE=4 SV=2 - [F1PND2_CANLF]	1,5	1	0	1	4
F1PZ45	EvC ciliary complex subunit 2 OS=Canis lupus familiaris GN=EVC2 PE=4 SV=2 - [F1PZ45_CANLF]	1,49	1	1	1	1
F1PHQ5	FERM domain containing 3 OS=Canis lupus familiaris GN=FRMD3 PE=4 SV=2 - [F1PHQ5_CANLF]	1,48	1	1	1	1
J9P077	Ankyrin repeat domain 12 OS=Canis lupus familiaris GN=ANKRD12 PE=4 SV=1 - [J9P077_CANLF]	1,47	1	0	1	1
F1PYP5	Tyrosine-protein kinase receptor OS=Canis lupus familiaris GN=NTRK3 PE=3 SV=2 - [F1PYP5_CANLF]	1,47	1	0	1	2
E2QVN0	Ankyrin repeat domain 12 OS=Canis lupus familiaris GN=ANKRD12 PE=4 SV=1 - [E2QVN0_CANLF]	1,46	1	0	1	1
J9PAA8	Baculoviral IAP repeat containing 6 OS=Canis lupus familiaris GN=BIRC6 PE=4 SV=1 - [J9PAA8_CANLF]	1,46	1	0	1	1
F1PQE3	ADP ribosylation factor like GTPase 13B OS=Canis lupus familiaris GN=ARL13B PE=3 SV=2 - [F1PQE3_CANLF]	1,4	1	0	1	1
F1PAN1	Tubby like protein 2 OS=Canis lupus familiaris GN=TULP2 PE=3 SV=2 - [F1PAN1_CANLF]	1,37	1	0	1	1
F1PZY5	Phosphatidylinositol-4-phosphate 5-kinase type 1 gamma OS=Canis lupus familiaris GN=PIP5K1C PE=4 SV=2 - [	1,3	1	1	1	1

F1PTE4	Collagen type XXII alpha 1 chain OS=Canis lupus familiaris GN=COL22A1 PE=4 SV=2 - [F1PTE4_CANLF]	1,29	1	1	1	3
F1PHA7	Fanconi anemia complementation group C OS=Canis lupus familiaris GN=FANCC PE=4 SV=2 - [F1PHA7_CANLF]	1,16	1	0	1	4
F1PND8	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 OS=Canis lupus familiaris GN=TANC1 PE=	1,15	1	1	1	2
E2RSD6	Ski2 like RNA helicase OS=Canis lupus familiaris GN=SKIV2L PE=4 SV=1 - [E2RSD6_CANLF]	1,12	1	1	1	1
E2RKA1	Tyrosine-protein kinase receptor OS=Canis lupus familiaris GN=NTRK2 PE=3 SV=2 - [E2RKA1_CANLF]	1,09	1	0	1	2
F1PIY4	Calcium voltage-gated channel auxiliary subunit alpha2delta 2 OS=Canis lupus familiaris GN=CACNA2D2 PE=4	1,08	1	0	1	1
J9P579	Calcium voltage-gated channel auxiliary subunit alpha2delta 2 OS=Canis lupus familiaris GN=CACNA2D2 PE=4	1,08	1	0	1	1
F1PEA8	Inositol polyphosphate-5-phosphatase D OS=Canis lupus familiaris GN=INPP5D PE=4 SV=2 - [F1PEA8_CANLF]	1,05	1	1	1	1
J9P2Q9	Zinc fingers and homeoboxes 1 OS=Canis lupus familiaris GN=ZHX1 PE=4 SV=1 - [J9P2Q9_CANLF]	1,03	1	1	1	1
F1PAY7	Sorbin and SH3 domain containing 1 OS=Canis lupus familiaris GN=SORBS1 PE=4 SV=2 - [F1PAY7_CANLF]	0,93	1	1	1	1
J9P3Q0	Ubiquitin specific peptidase 25 OS=Canis lupus familiaris GN=USP25 PE=3 SV=1 - [J9P3Q0_CANLF]	0,85	1	0	1	1
E2QW53	Ubiquitin specific peptidase 25 OS=Canis lupus familiaris GN=USP25 PE=3 SV=2 - [E2QW53_CANLF]	0,83	1	0	1	1
F1P8K4	Phospholipase B1 OS=Canis lupus familiaris GN=PLB1 PE=4 SV=1 - [F1P8K4_CANLF]	0,82	1	1	1	1
F1PBI9	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [F1PBI9_CANLF]	0,81	1	1	1	1
J9PA48	Ubiquitin specific peptidase 25 OS=Canis lupus familiaris GN=USP25 PE=3 SV=1 - [J9PA48_CANLF]	0,8	1	0	1	1
F1P9S3	Myosin binding protein C, cardiac OS=Canis lupus familiaris GN=MYBPC3 PE=4 SV=2 - [F1P9S3_CANLF]	0,71	1	0	1	1
Q2Q1P6	Cardiac myosin binding protein C OS=Canis lupus familiaris PE=2 SV=1 - [Q2Q1P6_CANLF]	0,71	1	0	1	1
J9P3T7	Myosin binding protein C, cardiac OS=Canis lupus familiaris GN=MYBPC3 PE=4 SV=1 - [J9P3T7_CANLF]	0,7	1	0	1	1
F1PMI5	Coiled-coil domain containing 88C OS=Canis lupus familiaris GN=CCDC88C PE=4 SV=2 - [F1PMI5_CANLF]	0,65	1	1	1	1
F1PIT6	Forkhead associated phosphopeptide binding domain 1 OS=Canis lupus familiaris GN=FHAD1 PE=4 SV=2 - [F1PI	0,63	1	0	1	3
F1PA81	RAN binding protein 2 OS=Canis lupus familiaris GN=RANBP2 PE=4 SV=2 - [F1PA81_CANLF]	0,62	1	1	1	2
L7N0H2	Forkhead associated phosphopeptide binding domain 1 OS=Canis lupus familiaris GN=FHAD1 PE=4 SV=1 - [L7N	0,61	1	0	1	3
E2RRT5	Mediator complex subunit 12 OS=Canis lupus familiaris GN=MED12 PE=4 SV=2 - [E2RRT5_CANLF]	0,6	1	0	1	1
J9PAD2	Mediator complex subunit 12 OS=Canis lupus familiaris GN=MED12 PE=4 SV=1 - [J9PAD2_CANLF]	0,6	1	0	1	1
F1PGY9	Uncharacterized protein OS=Canis lupus familiaris GN=DYNC1H1 PE=4 SV=2 - [F1PGY9_CANLF]	0,6	1	1	1	1
F1PQK5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PQK5_CANLF]	0,58	1	0	1	1
E2QXC0	Nuclear receptor coactivator 2 OS=Canis lupus familiaris GN=NCOA2 PE=4 SV=2 - [E2QXC0_CANLF]	0,55	1	0	1	1
E2QY25	Nuclear receptor coactivator 2 OS=Canis lupus familiaris GN=NCOA2 PE=4 SV=1 - [E2QY25_CANLF]	0,55	1	0	1	1
F1Q4D5	DNA polymerase epsilon, catalytic subunit OS=Canis lupus familiaris GN=POLE PE=4 SV=2 - [F1Q4D5_CANLF]	0,49	1	1	1	1
F1Q074	A-kinase anchoring protein 13 OS=Canis lupus familiaris GN=AKAP13 PE=4 SV=2 - [F1Q074_CANLF]	0,47	1	1	1	1
A2VEC8	SCO-spondin OS=Canis lupus familiaris GN=sspo PE=2 SV=1 - [A2VEC8_CANLF]	0,27	1	0	1	2
F1PLT3	SCO-spondin OS=Canis lupus familiaris GN=SSPO PE=4 SV=2 - [F1PLT3_CANLF]	0,27	1	0	1	2
J9P3R7	SCO-spondin OS=Canis lupus familiaris GN=SSPO PE=4 SV=1 - [J9P3R7_CANLF]	0,27	1	0	1	2
J9P6N7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P6N7_CANLF]	33,9	1	1	1	1
C6GJL5	VP2 (Fragment) OS=Canine parvovirus type 2 GN=VP2 PE=4 SV=1 - [C6GJL5_PAVC]	18,34	1	1	1	1
J9P1T5	Phospholipase A2 group XIIB OS=Canis lupus familiaris GN=PLA2G12B PE=4 SV=1 - [J9P1T5_CANLF]	12,31	1	1	1	2
Q65AS0	RIM ABC transporter (Fragment) OS=Canis lupus familiaris GN=abca4 PE=4 SV=1 - [Q65AS0_CANLF]	10,16	1	0	1	1
Q4GX49	Zinc alpha-2-glycoprotein 1 (Fragment) OS=Canis lupus familiaris GN=azgp1 PE=2 SV=1 - [Q4GX49_CANLF]	9,25	1	0	1	1
P33712	Insulin-like growth factor I OS=Canis lupus familiaris GN=IGF1 PE=2 SV=2 - [IGF1_CANLF]	9,15	1	0	1	1
E2RKF7	Ring finger protein 224 OS=Canis lupus familiaris GN=RNF224 PE=4 SV=2 - [E2RKF7_CANLF]	7,89	1	1	1	2
E2R442	Insulin-like growth factor I OS=Canis lupus familiaris GN=IGF1 PE=3 SV=1 - [E2R442_CANLF]	7,49	1	0	1	1
F1P774	Cytokine receptor like factor 1 OS=Canis lupus familiaris GN=CRLF1 PE=4 SV=2 - [F1P774_CANLF]	5,19	1	1	1	1
E2RAG4	MACRO domain containing 1 OS=Canis lupus familiaris GN=MACROD1 PE=4 SV=2 - [E2RAG4_CANLF]	4,32	1	0	1	1
E2QU14	Exoribonuclease 1 OS=Canis lupus familiaris GN=ERI1 PE=4 SV=1 - [E2QU14_CANLF]	4,3	1	1	1	2
J9P0Q0	MACRO domain containing 1 OS=Canis lupus familiaris GN=MACROD1 PE=4 SV=1 - [J9P0Q0_CANLF]	4,28	1	0	1	1
F1PM35	Glypican 4 OS=Canis lupus familiaris GN=GPC4 PE=3 SV=2 - [F1PM35_CANLF]	3,96	1	1	1	1
E2R8D5	Protein phosphatase, Mg2+/Mn2+ dependent 1H OS=Canis lupus familiaris GN=PPM1H PE=4 SV=1 - [E2R8D5_	3,7	1	1	1	2
F6ULS6	DALR anticodon binding domain containing 3 OS=Canis lupus familiaris GN=DALRD3 PE=4 SV=1 - [F6ULS6_CAN	3,14	1	1	1	1
E2RBA5	Chloride channel accessory 1 OS=Canis lupus familiaris GN=CLCA1 PE=4 SV=2 - [E2RBA5_CANLF]	2,96	1	1	1	2
E2RSE6	Furin, paired basic amino acid cleaving enzyme OS=Canis lupus familiaris GN=FURIN PE=3 SV=1 - [E2RSE6_CAN	2,9	1	1	1	1
J9PAA1	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9PAA1_CANLF]	2,88	1	0	1	1
E2RJZ5	Secernin 3 OS=Canis lupus familiaris GN=SCRN3 PE=4 SV=2 - [E2RJZ5_CANLF]	2,84	1	1	1	1
J9PBM0	MCF.2 cell line derived transforming sequence OS=Canis lupus familiaris GN=MCF2 PE=4 SV=1 - [J9PBM0_CAN	2,74	1	0	1	1
E2RT67	ADAM metallopeptidase domain 7 OS=Canis lupus familiaris GN=ADAM7 PE=4 SV=1 - [E2RT67_CANLF]	2,52	1	1	1	1
F1Q2N1	Unc-5 netrin receptor D OS=Canis lupus familiaris GN=UNC5D PE=4 SV=2 - [F1Q2N1_CANLF]	2,29	1	1	1	1
F1PNY6	Transient receptor potential cation channel subfamily C member 6 OS=Canis lupus familiaris GN=TRPC6 PE=3	2,13	1	1	1	2
F1Q3K9	AUTS2, activator of transcription and developmental regulator OS=Canis lupus familiaris GN=AUTS2 PE=4 SV=2	1,65	1	1	1	2
J9JHK5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9JHK5_CANLF]	1,58	1	1	1	1
F1Q280	FYVE, RhoGEF and PH domain containing 6 OS=Canis lupus familiaris GN=FGD6 PE=4 SV=1 - [F1Q280_CANLF]	1,55	1	0	1	1
J9NYT0	FYVE, RhoGEF and PH domain containing 6 OS=Canis lupus familiaris GN=FGD6 PE=4 SV=1 - [J9NYT0_CANLF]	1,55	1	0	1	1
E2RN66	Neuronal PAS domain protein 4 OS=Canis lupus familiaris GN=NPAS4 PE=4 SV=2 - [E2RN66_CANLF]	1,38	1	1	1	1
F1PX82	MCF.2 cell line derived transforming sequence OS=Canis lupus familiaris GN=MCF2 PE=4 SV=2 - [F1PX82_CANL	1,35	1	0	1	1
E2RRM8	Fer-1 like family member 6 OS=Canis lupus familiaris GN=FER1L6 PE=4 SV=2 - [E2RRM8_CANLF]	1,29	1	0	1	1
J9P6N0	Fer-1 like family member 6 OS=Canis lupus familiaris GN=FER1L6 PE=4 SV=1 - [J9P6N0_CANLF]	1,28	1	0	1	1
F1PH90	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1 like OS=Canis lupus familiaris GN=MTHFD1L	1,27	1	1	1	1
F1PQV2	Lysine demethylase 3B OS=Canis lupus familiaris GN=KDM3B PE=4 SV=2 - [F1PQV2_CANLF]	1,25	1	1	1	1
F1P8K1	Uncharacterized protein OS=Canis lupus familiaris GN=HNRNPUL2 PE=4 SV=2 - [F1P8K1_CANLF]	1,07	1	0	1	1
J9PAS2	Uncharacterized protein OS=Canis lupus familiaris GN=HNRNPUL2 PE=4 SV=1 - [J9PAS2_CANLF]	1,05	1	0	1	1
F1PD76	TOPBP1 interacting checkpoint and replication regulator OS=Canis lupus familiaris GN=TICRR PE=4 SV=2 - [F1P	1,01	1	1	1	1
F6VA50	Nestin OS=Canis lupus familiaris GN=NES PE=3 SV=1 - [F6VA50_CANLF]	1	1	1	1	1
E2RJB0	Centromere protein I OS=Canis lupus familiaris GN=CENPI PE=4 SV=1 - [E2RJB0_CANLF]	0,94	1	0	1	1
F1PBJ0	Rap guanine nucleotide exchange factor 2 OS=Canis lupus familiaris GN=RAPGEF2 PE=1 SV=2 - [RPGF2_CANLF]	0,73	1	1	1	1
J9P747	Uncharacterized protein OS=Canis lupus familiaris GN=ABCA4 PE=4 SV=1 - [J9P747_CANLF]	0,61	1	0	1	1
F1P7E4	Uncharacterized protein OS=Canis lupus familiaris GN=ABCA4 PE=4 SV=2 - [F1P7E4_CANLF]	0,57	1	0	1	1
F1PWT8	Uncharacterized protein OS=Canis lupus familiaris GN=ABCA4 PE=4 SV=2 - [F1PWT8_CANLF]	0,57	1	0	1	1
Q5ZGW1	Retinal-specific ATP-binding cassette transporter OS=Canis lupus familiaris GN=abcr PE=2 SV=1 - [Q5ZGW1_CA	0,57	1	0	1	1
Q6T940	ABCA4 OS=Canis lupus familiaris PE=2 SV=1 - [Q6T940_CANLF]	0,57	1	0	1	1
Q6T941	ABCA4 OS=Canis lupus familiaris PE=2 SV=1 - [Q6T941_CANLF]	0,57	1	0	1	1
Q6T942	ABCA4 OS=Canis lupus familiaris PE=2 SV=1 - [Q6T942_CANLF]	0,57	1	0	1	1
E2R8M8	Host cell factor C1 regulator 1 OS=Canis lupus familiaris GN=HCFC1R1 PE=4 SV=2 - [E2R8M8_CANLF]	16,67	1	0	1	2
E2R8M7	Host cell factor C1 regulator 1 OS=Canis lupus familiaris GN=HCFC1R1 PE=4 SV=2 - [E2R8M7_CANLF]	16,55	1	0	1	2
J9NSU9	Uncharacterized protein OS=Canis lupus familiaris GN=PSMD9 PE=4 SV=1 - [J9NSU9_CANLF]	14,42	1	0	1	1
E2R0R1	Uncharacterized protein OS=Canis lupus familiaris GN=PSMD9 PE=4 SV=2 - [E2R0R1_CANLF]	13,9	1	0	1	1
E2RCA4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2RCA4_CANLF]	11,81	1	1	1	1
F1PYI3	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Canis lupus familiaris GN=CNP PE=3 SV=2 - [F1PYI3_CANLF]	7,14	1	1	1	1
E2RDY4	NK3 homeobox 2 OS=Canis lupus familiaris GN=NKX3-2 PE=4 SV=1 - [E2RDY4_CANLF]	6,91	1	1	1	1
J9P9J7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P9J7_CANLF]	5,9	1	1	1	2
E2R8U4	Dynein axonemal assembly factor 4 OS=Canis lupus familiaris GN=DNAAF4 PE=4 SV=2 - [E2R8U4_CANLF]	5,71	1	1	1	1
J9P065	Lysine acetyltransferase 2B OS=Canis lupus familiaris GN=KAT2B PE=4 SV=1 - [J9P065_CANLF]	4,63	1	0	1	1
Q2HNR1	Collagen type X alpha 1 (Fragment) OS=Canis lupus familiaris GN=COL10A1 PE=4 SV=1 - [Q2HNR1_CANLF]	4,33	1	0	1	1
J9P1I7	Collagen type X alpha 1 chain OS=Canis lupus familiaris GN=COL10A1 PE=4 SV=1 - [J9P1I7_CANLF]	3,99	1	0	1	1
B6SAL5	NSP3 protein OS=Rotavirus A (isolate RVA/Dog/United States/K9/1981/G3P5A[3]) GN=NSP3 PE=4 SV=1 - [B6SA	3,83	1	0	1	1
B6SAK4	NSP3 protein OS=Rotavirus A (isolate RVA/Dog/United States/Cu-1/1982/G3P5A[3]) GN=NSP3 PE=4 SV=1 - [B6	3,83	1	0	1	1

F1PN31	Lysine acetyltransferase 2B OS=Canis lupus familiaris GN=KAT2B PE=4 SV=1 - [F1PN31_CANLF]	3,65	1	0	1	1
F1Q0I3	Dpy-19 like 2 OS=Canis lupus familiaris GN=DPY19L2 PE=4 SV=2 - [F1Q0I3_CANLF]	3,62	1	1	1	1
F1P637	Ligand dependent nuclear receptor corepressor like OS=Canis lupus familiaris GN=LCORL PE=4 SV=1 - [F1P637_	3,58	1	1	1	1
E2QW54	LIM domain and actin binding 1 OS=Canis lupus familiaris GN=LIMA1 PE=4 SV=2 - [E2QW54_CANLF]	3,54	1	1	1	1
P61010	Signal recognition particle 54 kDa protein OS=Canis lupus familiaris GN=SRP54 PE=1 SV=1 - [SRP54_CANLF]	3,37	1	1	1	1
E2RLW5	Uncharacterized protein OS=Canis lupus familiaris GN=CCDC124 PE=4 SV=1 - [E2RLW5_CANLF]	3,14	1	0	1	1
J9NWZ8	Asparagine synthetase domain containing 1 OS=Canis lupus familiaris GN=ASNSD1 PE=4 SV=1 - [J9NWZ8_CANL	2,92	1	0	1	1
J9PAR9	Pappalysin 2 OS=Canis lupus familiaris GN=PAPPA2 PE=4 SV=1 - [J9PAR9_CANLF]	2,77	1	0	1	1
A0A0E3ZR95	Putative serine protease OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_06150 PE=4 SV=1 - [A0	2,69	1	1	1	1
E2RFA3	RNA helicase OS=Canis lupus familiaris GN=DDX18 PE=3 SV=2 - [E2RFA3_CANLF]	2,69	1	0	1	1
E2REQ1	Asparagine synthetase domain containing 1 OS=Canis lupus familiaris GN=ASNSD1 PE=4 SV=1 - [E2REQ1_CANL	2,66	1	0	1	1
F1Q3U4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1Q3U4_CANLF]	2,64	1	0	1	1
E2RPN4	Solute carrier family 22 member 10 OS=Canis lupus familiaris GN=SLC22A10 PE=4 SV=2 - [E2RPN4_CANLF]	2,5	1	1	1	1
F1Q342	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F1Q342_CANLF]	2,45	1	0	1	1
F1PB46	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PB46_CANLF]	2,38	1	0	1	1
E2QWQ5	Solute carrier family 25 member 23 OS=Canis lupus familiaris GN=SLC25A23 PE=3 SV=2 - [E2QWQ5_CANLF]	2,16	1	1	1	1
F1PNG6	Pappalysin 2 OS=Canis lupus familiaris GN=PAPPA2 PE=4 SV=2 - [F1PNG6_CANLF]	1,96	1	0	1	1
E2RRE3	HPS5, biogenesis of lysosomal organelles complex 2 subunit 2 OS=Canis lupus familiaris GN=HPS5 PE=4 SV=2 - [	1,77	1	1	1	1
Q6E7G6	Receptor protein-tyrosine kinase (Fragment) OS=Canis lupus familiaris GN=PDGFRA PE=2 SV=2 - [Q6E7G6_CAN	1,76	1	1	1	1
J9P815	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P815_CANLF]	1,61	1	0	1	1
E2RHM1	GEM interacting protein OS=Canis lupus familiaris GN=GMIP PE=4 SV=2 - [E2RHM1_CANLF]	1,34	1	0	1	1
J9P1X5	GEM interacting protein OS=Canis lupus familiaris GN=GMIP PE=4 SV=1 - [J9P1X5_CANLF]	1,34	1	0	1	1
F1P9P3	POZ/BTB and AT hook containing zinc finger 1 OS=Canis lupus familiaris GN=PATZ1 PE=4 SV=1 - [F1P9P3_CANL	1,23	1	0	1	1
E2RCK9	Peroxisomal biogenesis factor 1 OS=Canis lupus familiaris GN=PEX1 PE=4 SV=2 - [E2RCK9_CANLF]	1,2	1	1	1	1
F1PZ30	SET binding factor 2 OS=Canis lupus familiaris GN=SBF2 PE=3 SV=2 - [F1PZ30_CANLF]	1,19	1	1	1	1
Q8SPS5	Periplakin (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q8SPS5_CANLF]	1,17	1	0	1	1
E2RJC1	POZ/BTB and AT hook containing zinc finger 1 OS=Canis lupus familiaris GN=PATZ1 PE=4 SV=1 - [E2RJC1_CANL	1,16	1	0	1	1
F1P8S5	Retrotransposon Gag like 1 OS=Canis lupus familiaris GN=RTL1 PE=4 SV=2 - [F1P8S5_CANLF]	1,04	1	1	1	1
F1PXQ7	SLX4 structure-specific endonuclease subunit OS=Canis lupus familiaris GN=SLX4 PE=4 SV=2 - [F1PXQ7_CANLF]	1,04	1	1	1	1
F1PHA4	Senataxin OS=Canis lupus familiaris GN=SETX PE=4 SV=2 - [F1PHA4_CANLF]	0,99	1	1	1	1
E2RMG8	MIS18 binding protein 1 OS=Canis lupus familiaris GN=MIS18BP1 PE=4 SV=2 - [E2RMG8_CANLF]	0,97	1	0	1	1
J9NTS4	MIS18 binding protein 1 OS=Canis lupus familiaris GN=MIS18BP1 PE=4 SV=1 - [J9NTS4_CANLF]	0,96	1	0	1	1
E2R9M1	Minichromosome maintenance 8 homologous recombination repair factor OS=Canis lupus familiaris GN=MCM	0,96	1	1	1	1
E2RMJ1	MIS18 binding protein 1 OS=Canis lupus familiaris GN=MIS18BP1 PE=4 SV=2 - [E2RMJ1_CANLF]	0,95	1	0	1	1
J9P8L3	Uncharacterized protein OS=Canis lupus familiaris GN=LOC489591 PE=4 SV=1 - [J9P8L3_CANLF]	0,94	1	0	1	1
F6UWI0	Ribosomal protein S6 kinase OS=Canis lupus familiaris GN=RPS6KA2 PE=3 SV=1 - [F6UWI0_CANLF]	0,93	1	1	1	1
J9NTS7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC489591 PE=4 SV=1 - [J9NTS7_CANLF]	0,9	1	0	1	1
J9NW55	Uncharacterized protein OS=Canis lupus familiaris GN=LOC489591 PE=4 SV=1 - [J9NW55_CANLF]	0,89	1	0	1	1
E2R4W7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC489591 PE=4 SV=2 - [E2R4W7_CANLF]	0,87	1	0	1	1
F6XKL7	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase OS=Canis lupus familiaris GN=HUWE1 PE	0,59	1	0	1	1
F6XM35	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase OS=Canis lupus familiaris GN=HUWE1 PE	0,59	1	0	1	1
F1P7Q1	Ral GTPase activating protein catalytic alpha subunit 2 OS=Canis lupus familiaris GN=RALGAPA2 PE=4 SV=2 - [F	0,48	1	1	1	1
F1Q1I3	Periplakin OS=Canis lupus familiaris GN=PPL PE=4 SV=2 - [F1Q1I3_CANLF]	0,46	1	0	1	1
J9NU37	Periplakin OS=Canis lupus familiaris GN=PPL PE=4 SV=1 - [J9NU37_CANLF]	0,46	1	0	1	1
F1Q3V9	Spectrin repeat containing nuclear envelope protein 2 OS=Canis lupus familiaris GN=SYNE2 PE=4 SV=2 - [F1Q3	0,1	1	1	1	1
F1Q1B9	Zinc finger MYND-type containing 19 OS=Canis lupus familiaris GN=ZMYND19 PE=4 SV=1 - [F1Q1B9_CANLF]	13,78	1	1	1	1
A0A0E3V3A1	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_00545 PE=4 SV=1 - [A0	11,11	1	1	1	1
E0W6Z3	Insulin-like growth factor 2 splice variant 1 OS=Canis lupus familiaris PE=2 SV=1 - [E0W6Z3_CANLF]	8,79	1	0	1	1
A0A0E3ZS86	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08120 PE=3 SV=1 - [A0	8,7	1	1	1	1
E0W6Z5	Insulin-like growth factor 2 splice variant 2 OS=Canis lupus familiaris PE=2 SV=1 - [E0W6Z5_CANLF]	8,65	1	0	1	1
J9NYS6	Insulin like growth factor 2 OS=Canis lupus familiaris GN=IGF2 PE=3 SV=1 - [J9NYS6_CANLF]	8,56	1	0	1	1
F6X9Z7	Centrin 3 OS=Canis lupus familiaris GN=CETN3 PE=4 SV=1 - [F6X9Z7_CANLF]	8,44	1	1	1	1
F1PBX5	Insulin like growth factor 2 OS=Canis lupus familiaris GN=IGF2 PE=3 SV=2 - [F1PBX5_CANLF]	8,25	1	0	1	1
A0A0E3ZQ53	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_06790 PE=3 SV=1 - [A0	6,63	1	1	1	1
F1PP91	DnaJ heat shock protein family (Hsp40) member A4 OS=Canis lupus familiaris GN=DNAJA4 PE=3 SV=1 - [F1PP91	6,27	1	1	1	1
J9P961	Insulin like growth factor 2 OS=Canis lupus familiaris GN=IGF2 PE=3 SV=1 - [J9P961_CANLF]	6,18	1	0	1	1
E2RNF9	Methyltransferase like 27 OS=Canis lupus familiaris GN=METTL27 PE=4 SV=2 - [E2RNF9_CANLF]	5,84	1	1	1	1
J9NRF8	ATP synthase subunit d, mitochondrial OS=Canis lupus familiaris PE=3 SV=1 - [J9NRF8_CANLF]	5,63	1	1	1	1
F1PPR0	Eukaryotic translation initiation factor 3 subunit I OS=Canis lupus familiaris GN=EIF3I PE=3 SV=1 - [F1PPR0_CAN	5,54	1	1	1	1
Q2VD95	Carbohydrate sulfotransferase (Fragment) OS=Canis lupus GN=CHST12 PE=3 SV=1 - [Q2VD95_CANLU]	5,53	1	0	1	1
F1PCA4	Chromodomain Y like 2 OS=Canis lupus familiaris GN=CDYL2 PE=4 SV=2 - [F1PCA4_CANLF]	5,44	1	1	1	1
F1PEB7	Carbohydrate sulfotransferase OS=Canis lupus familiaris GN=CHST9 PE=3 SV=2 - [F1PEB7_CANLF]	5,23	1	1	1	1
E2RPE5	Ribosomal protein L35 OS=Canis lupus familiaris GN=RPL35 PE=3 SV=2 - [E2RPE5_CANLF]	4,88	1	0	1	3
A0A0E3ZQL3	Membrane-bound metallopeptidase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08805 PE=	4,4	1	1	1	2
J9NXP7	KAT8 regulatory NSL complex subunit 2 OS=Canis lupus familiaris GN=KANSL2 PE=4 SV=1 - [J9NXP7_CANLF]	4,27	1	1	1	1
F1Q1C5	Staufen double-stranded RNA binding protein 1 OS=Canis lupus familiaris GN=STAU1 PE=4 SV=2 - [F1Q1C5_CA	4,23	1	0	1	1
F1PAM9	Epidermal growth factor receptor pathway substrate 15 OS=Canis lupus familiaris GN=EPS15 PE=4 SV=2 - [F1P	3,87	1	1	1	1
J9PA02	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PA02_CANLF]	3,76	1	1	1	1
J9JHS6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9JHS6_CANLF]	3,72	1	1	1	1
J9NZL0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NZL0_CANLF]	3,7	1	0	1	2
J9P393	Staufen double-stranded RNA binding protein 1 OS=Canis lupus familiaris GN=STAU1 PE=4 SV=1 - [J9P393_CAN	3,69	1	0	1	1
E2R4V7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2R4V7_CANLF]	3,53	1	0	1	2
S4S268	Glycoprotein OS=Mokola virus PE=4 SV=1 - [S4S268_MOKV]	3,26	1	0	1	1
R9Q7B7	Glycoprotein OS=Mokola virus PE=4 SV=1 - [R9Q7B7_MOKV]	3,26	1	0	1	1
S5DTC1	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [S5DTC1_MOKV]	3,26	1	0	1	1
J9NUW3	Uncharacterized protein OS=Canis lupus familiaris GN=GGTA1 PE=4 SV=1 - [J9NUW3_CANLF]	3,24	1	1	1	1
A0A0E3V3Y2	Ribosome-recycling factor OS=Pasteurella multocida subsp. multocida OH4807 GN=frr PE=3 SV=1 - [A0A0E3V3	3,24	1	0	1	1
F1PJI0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PJI0_CANLF]	3,17	1	1	1	1
J9NS69	Carbohydrate sulfotransferase OS=Canis lupus familiaris GN=CHST12 PE=3 SV=1 - [J9NS69_CANLF]	3,1	1	0	1	1
F1PH10	Protein disulfide isomerase like, testis expressed OS=Canis lupus familiaris GN=PDILT PE=4 SV=2 - [F1PH10_CA	3,1	1	1	1	1
A0A0A0MPD2	Ribosomal protein L19 OS=Canis lupus familiaris GN=RPL19 PE=3 SV=1 - [A0A0A0MPD2_CANLF]	3,09	1	0	1	3
E2REX9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2REX9_CANLF]	3,09	1	0	1	2
D0VWQ5	60S ribosomal protein L19 OS=Canis lupus familiaris GN=RPL19 PE=1 SV=1 - [RL19_CANLF]	3,06	1	0	1	3
E2RTB1	Uncharacterized protein OS=Canis lupus familiaris GN=NPM1 PE=4 SV=2 - [E2RTB1_CANLF]	3,06	1	0	1	2
J9P3P1	Arginase OS=Canis lupus familiaris GN=ARG2 PE=3 SV=1 - [J9P3P1_CANLF]	2,96	1	0	1	1
J9P062	Nuclear receptor subfamily 1 group I member 2 OS=Canis lupus familiaris GN=NR1I2 PE=3 SV=1 - [J9P062_CAN	2,74	1	0	1	1
Q8SQ02	Pregnane X receptor (Fragment) OS=Canis lupus familiaris GN=PXR PE=2 SV=1 - [Q8SQ02_CANLF]	2,74	1	0	1	1
E2R8N6	Arginase OS=Canis lupus familiaris GN=ARG2 PE=3 SV=2 - [E2R8N6_CANLF]	2,67	1	0	1	1
F6V8I0	Uncharacterized protein OS=Canis lupus familiaris GN=MLPH PE=4 SV=1 - [F6V8I0_CANLF]	2,58	1	0	1	1
Q4KKT7	Melanophilin OS=Canis lupus familiaris GN=mlph PE=4 SV=2 - [Q4KKT7_CANLF]	2,58	1	0	1	1
Q4QZB9	Melanophilin OS=Canis lupus familiaris GN=mlph PE=2 SV=1 - [Q4QZB9_CANLF]	2,58	1	0	1	1
F6XG74	IQ motif and ubiquitin domain containing OS=Canis lupus familiaris GN=IQUB PE=4 SV=1 - [F6XG74_CANLF]	2,52	1	0	1	1
F6V2B9	G protein signaling modulator 2 OS=Canis lupus familiaris GN=GPSM2 PE=4 SV=1 - [F6V2B9_CANLF]	2,5	1	1	1	1

E2R6C5	IQ motif and ubiquitin domain containing OS=Canis lupus familiaris GN=IQUB PE=4 SV=1 - [E2R6C5_CANLF]	2,48	1	0	1	1
J9NV47	Hyaluronan binding protein 2 OS=Canis lupus familiaris GN=HABP2 PE=3 SV=1 - [J9NV47_CANLF]	2,42	1	0	1	1
E2RI51	Anoctamin OS=Canis lupus familiaris GN=ANO4 PE=3 SV=1 - [E2RI51_CANLF]	2,41	1	1	1	1
F6Y4R5	Patatin like phospholipase domain containing 8 OS=Canis lupus familiaris GN=PNPLA8 PE=4 SV=1 - [F6Y4R5_CA	2,38	1	1	1	1
F1Q1K9	Hyaluronan binding protein 2 OS=Canis lupus familiaris GN=HABP2 PE=3 SV=2 - [F1Q1K9_CANLF]	2,15	1	0	1	1
F1Q075	Nuclear receptor subfamily 1 group I member 2 OS=Canis lupus familiaris GN=NR1I2 PE=3 SV=2 - [F1Q075_CAN	2,05	1	0	1	1
F1PHI8	Transmembrane channel-like protein OS=Canis lupus familiaris GN=TMC1 PE=3 SV=2 - [F1PHI8_CANLF]	1,98	1	1	1	1
F1PC09	RAB GTPase activating protein 1 OS=Canis lupus familiaris GN=RABGAP1 PE=4 SV=2 - [F1PC09_CANLF]	1,78	1	1	1	1
J9NYA9	Short chain dehydrogenase/reductase family 42E, member 1 OS=Canis lupus familiaris GN=SDR42E1 PE=3 SV=1	1,78	1	1	1	1
E2RQD5	Leucine rich repeat containing 8 family member A OS=Canis lupus familiaris GN=LRRC8A PE=4 SV=1 - [E2RQD5_	1,73	1	1	1	1
D6C6L9	Matrix extracellular phosphoglycoprotein OS=Canis lupus familiaris GN=MEPE PE=4 SV=1 - [D6C6L9_CANLF]	1,62	1	1	1	3
J9NU33	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100684878 PE=3 SV=1 - [J9NU33_CANLF]	1,62	1	1	1	1
F1PHV9	Tetratricopeptide repeat domain 28 OS=Canis lupus familiaris GN=TTC28 PE=4 SV=2 - [F1PHV9_CANLF]	1,38	1	1	1	1
F5C3N2	Neprilysin-749 OS=Canis lupus familiaris GN=MME PE=2 SV=1 - [F5C3N2_CANLF]	1,34	1	0	1	2
E2RQ25	Uncharacterized protein OS=Canis lupus familiaris GN=MME PE=4 SV=1 - [E2RQ25_CANLF]	1,33	1	0	1	2
E2RP26	Filamin C OS=Canis lupus familiaris GN=FLNC PE=4 SV=1 - [E2RP26_CANLF]	1,32	1	1	1	1
F1PG19	Tetratricopeptide repeat domain 21A OS=Canis lupus familiaris GN=TTC21A PE=4 SV=2 - [F1PG19_CANLF]	1,3	1	1	1	1
J9P0S8	Sortilin related VPS10 domain containing receptor 3 OS=Canis lupus familiaris GN=SORCS3 PE=4 SV=1 - [J9P0S8	1,24	1	0	1	1
F1PS95	Sortilin related VPS10 domain containing receptor 3 OS=Canis lupus familiaris GN=SORCS3 PE=4 SV=2 - [F1PS95	1,23	1	0	1	1
F1PVV7	Myosin heavy chain 10 OS=Canis lupus familiaris GN=MYH10 PE=3 SV=2 - [F1PVV7_CANLF]	1,22	1	1	1	2
J9P0I6	PR/SET domain 16 OS=Canis lupus familiaris GN=PRDM16 PE=4 SV=1 - [J9P0I6_CANLF]	1,21	1	0	1	1
F1P8R4	TBC1 domain family member 8B OS=Canis lupus familiaris GN=TBC1D8B PE=4 SV=2 - [F1P8R4_CANLF]	1,16	1	0	1	1
J9P659	TBC1 domain family member 8B OS=Canis lupus familiaris GN=TBC1D8B PE=4 SV=1 - [J9P659_CANLF]	1,16	1	0	1	1
J9PB56	TBC1 domain family member 8B OS=Canis lupus familiaris GN=TBC1D8B PE=4 SV=1 - [J9PB56_CANLF]	1,16	1	0	1	1
E2RPZ2	Eukaryotic translation initiation factor 4E nuclear import factor 1 OS=Canis lupus familiaris GN=EIF4ENIF1 PE=4	1,12	1	1	1	2
F1Q029	PR/SET domain 16 OS=Canis lupus familiaris GN=PRDM16 PE=4 SV=2 - [F1Q029_CANLF]	1,11	1	0	1	1
J9P9J1	CWC22 spliceosome associated protein homolog OS=Canis lupus familiaris GN=CWC22 PE=4 SV=1 - [J9P9J1_CA	1,1	1	0	1	4
E2RIF6	CWC22 spliceosome associated protein homolog OS=Canis lupus familiaris GN=CWC22 PE=4 SV=2 - [E2RIF6_CA	1,09	1	0	1	4
J9P725	Uncharacterized protein OS=Canis lupus familiaris GN=CCDC141 PE=4 SV=1 - [J9P725_CANLF]	1,08	1	0	1	1
E2RMR3	Heterogeneous nuclear ribonucleoprotein M OS=Canis lupus familiaris GN=HNRNPM PE=4 SV=2 - [E2RMR3_CA	1,08	1	1	1	3
E2RDM3	Uncharacterized protein OS=Canis lupus familiaris GN=LOC479816 PE=4 SV=2 - [E2RDM3_CANLF]	1,01	1	0	1	1
J9P0N5	Uncharacterized protein OS=Canis lupus familiaris GN=LOC479816 PE=4 SV=1 - [J9P0N5_CANLF]	1,01	1	0	1	1
F1PRX7	EPH receptor A6 OS=Canis lupus familiaris GN=EPHA6 PE=3 SV=2 - [F1PRX7_CANLF]	0,99	1	0	1	1
F1PRX3	EPH receptor A6 OS=Canis lupus familiaris GN=EPHA6 PE=3 SV=2 - [F1PRX3_CANLF]	0,92	1	0	1	1
E2RS86	G protein-coupled receptor 158 OS=Canis lupus familiaris GN=GPR158 PE=4 SV=2 - [E2RS86_CANLF]	0,92	1	1	1	1
E2RI02	Microtubule associated protein 6 OS=Canis lupus familiaris GN=MAP6 PE=4 SV=2 - [E2RI02_CANLF]	0,9	1	0	1	1
F1PUC2	Uncharacterized protein OS=Canis lupus familiaris GN=CCDC141 PE=4 SV=2 - [F1PUC2_CANLF]	0,89	1	0	1	1
F6XIY7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F6XIY7_CANLF]	0,82	1	1	1	1
E2QUI5	Chromodomain helicase DNA binding protein 1 OS=Canis lupus familiaris GN=CHD1 PE=4 SV=1 - [E2QUI5_CANL	0,82	1	0	1	1
F1PYH1	Reelin OS=Canis lupus familiaris GN=RELN PE=4 SV=2 - [F1PYH1_CANLF]	0,81	1	0	1	1
J9NZL6	Reelin OS=Canis lupus familiaris GN=RELN PE=4 SV=1 - [J9NZL6_CANLF]	0,81	1	0	1	1
J9P6Y8	Chromodomain helicase DNA binding protein 1 OS=Canis lupus familiaris GN=CHD1 PE=4 SV=1 - [J9P6Y8_CANL	0,79	1	0	1	1
F1PTH1	Megakaryoblastic leukemia (translocation) 1 OS=Canis lupus familiaris GN=MKL1 PE=4 SV=2 - [F1PTH1_CANLF]	0,75	1	0	1	1
J9P8E5	Microtubule associated protein 6 OS=Canis lupus familiaris GN=MAP6 PE=4 SV=1 - [J9P8E5_CANLF]	0,74	1	0	1	1
E2RDZ9	Kinesin-like protein OS=Canis lupus familiaris GN=KIF5C PE=3 SV=2 - [E2RDZ9_CANLF]	0,73	1	0	1	1
E2R4M6	Caspase 8 associated protein 2 OS=Canis lupus familiaris GN=CASP8AP2 PE=4 SV=2 - [E2R4M6_CANLF]	0,71	1	1	1	1
E2QYI5	Unc-13 homolog C OS=Canis lupus familiaris GN=UNC13C PE=4 SV=2 - [E2QYI5_CANLF]	0,63	1	0	1	1
E2QUU0	Thyroid hormone receptor interactor 11 OS=Canis lupus familiaris GN=TRIP11 PE=4 SV=2 - [E2QUU0_CANLF]	0,61	1	1	1	1
A0A0E3ZQQ4	DNA-directed RNA polymerase subunit beta OS=Pasteurella multocida subsp. multocida OH4807 GN=rpoB PE=	0,6	1	1	1	1
F1P872	ATP binding cassette subfamily A member 12 OS=Canis lupus familiaris GN=ABCA12 PE=4 SV=2 - [F1P872_CAN	0,35	1	1	1	1
E2RMC0	Inositol 1,4,5-trisphosphate receptor type 3 OS=Canis lupus familiaris GN=ITPR3 PE=4 SV=2 - [E2RMC0_CANLF]	0,22	1	0	1	3
F1Q0H6	Inositol 1,4,5-trisphosphate receptor type 2 OS=Canis lupus familiaris GN=ITPR2 PE=4 SV=2 - [F1Q0H6_CANLF]	0,22	1	0	1	3
F1Q1P4	Microtubule-actin crosslinking factor 1 OS=Canis lupus familiaris GN=MACF1 PE=4 SV=2 - [F1Q1P4_CANLF]	0,14	1	0	1	1
I0BWQ3	Potassium voltage-gated channel subfamily KQT member 2 (Fragment) OS=Canis lupus familiaris GN=KCNQ2 P	94,12	1	1	1	1
Q6PXD8	Ceruloplasmin (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q6PXD8_CANLF]	19,18	1	0	1	1
J9P260	CDGSH iron sulfur domain 3 OS=Canis lupus familiaris GN=CISD3 PE=4 SV=1 - [J9P260_CANLF]	16,8	1	1	1	2
L7N0G6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0G6_CANLF]	16,18	1	1	1	2
A0A0E3V563	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_09195 PE=4 SV=1 - [A0	14,09	1	1	1	1
A0A0E3V475	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_07595 PE=4 SV=1 - [A0	11,49	1	1	1	1
F1PGD3	Kelch domain containing 10 OS=Canis lupus familiaris GN=KLHDC10 PE=4 SV=2 - [F1PGD3_CANLF]	9,51	1	1	1	1
E2R1B0	Uncharacterized protein OS=Canis lupus familiaris GN=LOC612524 PE=4 SV=2 - [E2R1B0_CANLF]	9,04	1	1	1	1
J9P1P3	Zinc finger protein 322 OS=Canis lupus familiaris GN=ZNF322 PE=4 SV=1 - [J9P1P3_CANLF]	6,97	1	1	1	1
J9NSD1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NSD1_CANLF]	6,46	1	0	1	1
J9P9V6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P9V6_CANLF]	6,19	1	0	1	1
E2R3C5	DFNA5, deafness associated tumor suppressor OS=Canis lupus familiaris GN=DFNA5 PE=4 SV=1 - [E2R3C5_CAN	5,86	1	1	1	1
E2QW61	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2QW61_CANLF]	5,67	1	1	1	7
A0A0E3ZQR5	TnaB OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08420 PE=4 SV=1 - [A0A0E3ZQR5_PASMD]	4,95	1	1	1	1
J9NY89	Sulfurtransferase OS=Canis lupus familiaris GN=TSTD3 PE=4 SV=1 - [J9NY89_CANLF]	4,4	1	0	1	1
E2R0K1	SRY-box 8 OS=Canis lupus familiaris GN=SOX8 PE=4 SV=1 - [E2R0K1_CANLF]	4,33	1	0	1	1
J9NRL8	SRY-box 8 OS=Canis lupus familiaris GN=SOX8 PE=4 SV=1 - [J9NRL8_CANLF]	4,33	1	0	1	1
J9NTC6	Uncharacterized protein OS=Canis lupus familiaris GN=ZNF41 PE=3 SV=1 - [J9NTC6_CANLF]	4,26	1	1	1	1
F6X9Q8	DDB1 and CUL4 associated factor 15 OS=Canis lupus familiaris GN=DCAF15 PE=4 SV=1 - [F6X9Q8_CANLF]	3,71	1	1	1	1
E2RJ29	Developmentally regulated GTP binding protein 2 OS=Canis lupus familiaris GN=DRG2 PE=4 SV=1 - [E2RJ29_CA	3,57	1	1	1	1
J9P576	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P576_CANLF]	3,53	1	0	1	1
F1P6X2	MutS homolog 4 OS=Canis lupus familiaris GN=MSH4 PE=4 SV=2 - [F1P6X2_CANLF]	3,51	1	0	1	1
E2RTJ9	Pyridine nucleotide-disulphide oxidoreductase domain 1 OS=Canis lupus familiaris GN=PYROXD1 PE=4 SV=2 - [	3,47	1	1	1	2
E2RJA9	MutS homolog 4 OS=Canis lupus familiaris GN=MSH4 PE=4 SV=2 - [E2RJA9_CANLF]	3,01	1	0	1	1
J9P1I8	XK-related protein OS=Canis lupus familiaris GN=XK PE=3 SV=1 - [J9P1I8_CANLF]	2,93	1	1	1	1
E2RJI5	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase OS=Canis lupus familiaris GN=MFNG PE=4 SV	2,86	1	1	1	1
F1PZ34	Epidermal growth factor receptor pathway substrate 15 like 1 OS=Canis lupus familiaris GN=EPS15L1 PE=4 SV=	2,53	1	0	1	1
J9P7A9	Epidermal growth factor receptor pathway substrate 15 like 1 OS=Canis lupus familiaris GN=EPS15L1 PE=4 SV=	2,48	1	0	1	1
F1PK60	Transglutaminase 3 OS=Canis lupus familiaris GN=TGM3 PE=4 SV=1 - [F1PK60_CANLF]	2,45	1	1	1	1
F1PSJ2	CD84 molecule OS=Canis lupus familiaris GN=CD84 PE=4 SV=2 - [F1PSJ2_CANLF]	2,35	1	1	1	1
E2QUI7	EPS8 like 1 OS=Canis lupus familiaris GN=EPS8L1 PE=4 SV=2 - [E2QUI7_CANLF]	2,25	1	1	1	1
F1PGL0	ADAM metallopeptidase with thrombospondin type 1 motif 1 OS=Canis lupus familiaris GN=ADAMTS1 PE=4 SV	2,21	1	1	1	1
J9P6J2	Armadillo repeat containing 9 OS=Canis lupus familiaris GN=ARMC9 PE=4 SV=1 - [J9P6J2_CANLF]	1,85	1	0	1	1
E2RHR9	Neuroepithelial cell transforming 1 OS=Canis lupus familiaris GN=NET1 PE=4 SV=1 - [E2RHR9_CANLF]	1,85	1	1	1	1
F1PCZ0	Septin 5 OS=Canis lupus familiaris GN=SEPT5 PE=3 SV=2 - [F1PCZ0_CANLF]	1,85	1	1	1	1
J9P5E1	TAR (HIV-1) RNA binding protein 1 OS=Canis lupus familiaris GN=TARBP1 PE=4 SV=1 - [J9P5E1_CANLF]	1,84	1	0	1	1
E2QYA7	Armadillo repeat containing 9 OS=Canis lupus familiaris GN=ARMC9 PE=4 SV=2 - [E2QYA7_CANLF]	1,84	1	0	1	1
F1PWU0	TAR (HIV-1) RNA binding protein 1 OS=Canis lupus familiaris GN=TARBP1 PE=4 SV=2 - [F1PWU0_CANLF]	1,81	1	0	1	1
E2RDS2	Zinc finger protein 282 OS=Canis lupus familiaris GN=ZNF282 PE=4 SV=2 - [E2RDS2_CANLF]	1,7	1	1	1	1
F1PZ23	Tyrosine-protein phosphatase OS=Canis lupus familiaris GN=PTPN12 PE=4 SV=2 - [F1PZ23_CANLF]	1,6	1	1	1	1

J9P7H5	Catenin delta 1 OS=Canis lupus familiaris GN=CTNND1 PE=4 SV=1 - [J9P7H5_CANLF]	1,5	1	1	1	1
E2RJF8	Kinesin family member 15 OS=Canis lupus familiaris GN=KIF15 PE=3 SV=2 - [E2RJF8_CANLF]	1,44	1	0	1	1
F1PSL9	Kinesin family member 15 OS=Canis lupus familiaris GN=KIF15 PE=3 SV=2 - [F1PSL9_CANLF]	1,37	1	0	1	1
E2QSF3	Spermatogenesis associated serine rich 2 OS=Canis lupus familiaris GN=SPATS2 PE=4 SV=1 - [E2QSF3_CANLF]	1,28	1	0	1	1
F6UV93	Spermatogenesis associated serine rich 2 OS=Canis lupus familiaris GN=SPATS2 PE=4 SV=1 - [F6UV93_CANLF]	1,28	1	0	1	1
J9P5V6	Talin 1 OS=Canis lupus familiaris GN=TLN1 PE=4 SV=1 - [J9P5V6_CANLF]	1,28	1	0	1	1
F1PSC2	Talin 1 OS=Canis lupus familiaris GN=TLN1 PE=4 SV=2 - [F1PSC2_CANLF]	1,22	1	0	1	1
J9P3J2	Bromodomain adjacent to zinc finger domain 1B OS=Canis lupus familiaris GN=BAZ1B PE=4 SV=1 - [J9P3J2_CAN	1,08	1	0	1	2
E2RED7	Bromodomain adjacent to zinc finger domain 1B OS=Canis lupus familiaris GN=BAZ1B PE=4 SV=2 - [E2RED7_CA	1,01	1	0	1	2
J9PAU7	Bromodomain adjacent to zinc finger domain 1B OS=Canis lupus familiaris GN=BAZ1B PE=4 SV=1 - [J9PAU7_CA	1,01	1	0	1	2
F1PKH7	Cation channel sperm associated auxiliary subunit beta OS=Canis lupus familiaris GN=CATSPERB PE=4 SV=2 - [F	0,99	1	1	1	1
A8WA74	L polyprotein OS=Bunyavirus snowshoe hare GN=L PE=4 SV=2 - [A8WA74_BUNSH]	0,88	1	1	1	1
F1PQM0	BAH domain and coiled-coil containing 1 OS=Canis lupus familiaris GN=BAHCC1 PE=4 SV=2 - [F1PQM0_CANLF]	0,63	1	1	1	1
E2R1I7	KIAA1109 OS=Canis lupus familiaris GN=KIAA1109 PE=4 SV=2 - [E2R1I7_CANLF]	0,28	1	0	1	1
F1PIE9	KIAA1109 OS=Canis lupus familiaris GN=KIAA1109 PE=4 SV=2 - [F1PIE9_CANLF]	0,28	1	0	1	1
O97575	Atrial myosin light chain homolog (Fragment) OS=Canis lupus familiaris PE=4 SV=1 - [O97575_CANLF]	19,7	1	0	1	1
Q9GKN4	Mitosin (Fragment) OS=Canis lupus familiaris PE=4 SV=1 - [Q9GKN4_CANLF]	8,95	1	0	1	1
E2QYQ7	SPC25, NDC80 kinetochore complex component OS=Canis lupus familiaris GN=SPC25 PE=4 SV=1 - [E2QYQ7_CA	8,85	1	1	1	1
F1PS70	Uncharacterized protein OS=Canis lupus familiaris GN=RFPL4A PE=4 SV=2 - [F1PS70_CANLF]	8,01	1	1	1	2
F1Q3Z9	Aspartate beta-hydroxylase domain containing 1 OS=Canis lupus familiaris GN=ASPHD1 PE=4 SV=2 - [F1Q3Z9_	7,63	1	1	1	1
E2RJH5	Heterogeneous nuclear ribonucleoprotein H2 OS=Canis lupus familiaris GN=HNRNPH2 PE=4 SV=2 - [E2RJH5_CA	7,35	1	0	1	1
F1PA67	SPT3 homolog, SAGA and STAGA complex component OS=Canis lupus familiaris GN=SUPT3H PE=4 SV=2 - [F1PA	6,41	1	1	1	1
J9NZU9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NZU9_CANLF]	6,38	1	1	1	1
E2R629	Atypical chemokine receptor 1 (Duffy blood group) OS=Canis lupus familiaris GN=ACKR1 PE=4 SV=1 - [E2R629_	6,04	1	1	1	1
Q7YRB7	Amine oxidase [flavin-containing] B OS=Canis lupus familiaris GN=MAOB PE=2 SV=3 - [AOFB_CANLF]	5,77	1	0	1	1
F1PFF8	Amine oxidase OS=Canis lupus familiaris GN=MAOB PE=3 SV=1 - [F1PFF8_CANLF]	5,77	1	0	1	1
E2RGR9	Fumarate hydratase OS=Canis lupus familiaris GN=FH PE=3 SV=1 - [E2RGR9_CANLF]	5,51	1	1	1	1
E2R008	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [E2R008_CANLF]	5,14	1	0	1	1
E2RRU2	Sphingomyelin phosphodiesterase acid like 3A OS=Canis lupus familiaris GN=SMPDL3A PE=4 SV=2 - [E2RRU2_C	4,87	1	0	1	2
E2RCR9	BTG anti-proliferation factor 4 OS=Canis lupus familiaris GN=BTG4 PE=4 SV=2 - [E2RCR9_CANLF]	4,84	1	1	1	1
F1P840	POU domain protein OS=Canis lupus familiaris GN=POU3F1 PE=3 SV=2 - [F1P840_CANLF]	4,39	1	1	1	2
F1Q3E5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1Q3E5_CANLF]	4,35	1	0	1	1
E2QZG0	Prolactin receptor OS=Canis lupus familiaris GN=PRLR PE=4 SV=1 - [E2QZG0_CANLF]	4	1	1	1	2
E2RAS8	Enolase 2 OS=Canis lupus familiaris GN=ENO2 PE=3 SV=2 - [E2RAS8_CANLF]	3,81	1	0	1	1
J9P7F2	Ubiquitin conjugating enzyme E2 R2 OS=Canis lupus familiaris GN=UBE2R2 PE=3 SV=1 - [J9P7F2_CANLF]	3,78	1	1	1	1
E2R2H9	FMR1 autosomal homolog 2 OS=Canis lupus familiaris GN=FXR2 PE=4 SV=1 - [E2R2H9_CANLF]	3,72	1	1	1	1
J9NYQ3	Sphingomyelin phosphodiesterase acid like 3A OS=Canis lupus familiaris GN=SMPDL3A PE=4 SV=1 - [J9NYQ3_C	3,71	1	0	1	2
J9NVM0	L-lactate dehydrogenase OS=Canis lupus familiaris PE=3 SV=1 - [J9NVM0_CANLF]	3,65	1	0	1	2
J9NU05	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9NU05_CANLF]	3,63	1	0	1	2
E2R761	L-lactate dehydrogenase OS=Canis lupus familiaris GN=LDHB PE=3 SV=1 - [E2R761_CANLF]	3,59	1	0	1	2
J9NT18	L-lactate dehydrogenase OS=Canis lupus familiaris PE=3 SV=1 - [J9NT18_CANLF]	3,59	1	0	1	2
J9P3N9	L-lactate dehydrogenase OS=Canis lupus familiaris PE=3 SV=1 - [J9P3N9_CANLF]	3,59	1	0	1	2
J9P290	BTB domain containing 16 OS=Canis lupus familiaris GN=BTBD16 PE=4 SV=1 - [J9P290_CANLF]	3,59	1	0	1	1
F1P746	BTB domain containing 16 OS=Canis lupus familiaris GN=BTBD16 PE=4 SV=2 - [F1P746_CANLF]	3,56	1	0	1	1
F1PUB4	BTB domain containing 16 OS=Canis lupus familiaris GN=BTBD16 PE=4 SV=2 - [F1PUB4_CANLF]	3,56	1	0	1	1
J9P386	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P386_CANLF]	3,46	1	0	1	1
J9P5H9	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102156555 PE=4 SV=1 - [J9P5H9_CANLF]	3,46	1	0	1	1
F1PIB3	L-lactate dehydrogenase OS=Canis lupus familiaris GN=LDHB PE=3 SV=2 - [F1PIB3_CANLF]	3,37	1	0	1	2
E2R785	Uncharacterized protein OS=Canis lupus familiaris GN=LOC608989 PE=4 SV=2 - [E2R785_CANLF]	3,33	1	1	1	1
A0A0E3V567	Deoxyguanosinetriphosphate triphosphohydrolase-like protein OS=Pasteurella multocida subsp. multocida OH	3,33	1	1	1	2
E2RLX8	Transient receptor potential cation channel subfamily V member 2 OS=Canis lupus familiaris GN=TRPV2 PE=3 S	3,27	1	1	1	2
F1PB47	Chromosome 18 open reading frame 8 OS=Canis lupus familiaris GN=C18orf8 PE=4 SV=2 - [F1PB47_CANLF]	3,17	1	1	1	1
E2RAG5	CWF19 like 2, cell cycle control (S. pombe) OS=Canis lupus familiaris GN=CWF19L2 PE=4 SV=2 - [E2RAG5_CANL	2,92	1	1	1	2
E2QX23	Endonuclease III-like protein 1 OS=Canis lupus familiaris GN=NTHL1 PE=3 SV=2 - [E2QX23_CANLF]	2,88	1	1	1	1
J9P6N1	Phosphatidylinositol glycan anchor biosynthesis class K OS=Canis lupus familiaris GN=PIGK PE=4 SV=1 - [J9P6N	2,78	1	1	1	1
E2RDL5	Centrosomal protein 78 OS=Canis lupus familiaris GN=CEP78 PE=4 SV=2 - [E2RDL5_CANLF]	2,64	1	1	1	1
E2RPG3	Adaptor related protein complex 1 gamma 1 subunit OS=Canis lupus familiaris GN=AP1G1 PE=4 SV=2 - [E2RPG	2,55	1	1	1	1
F1PNI3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PNI3_CANLF]	2,47	1	0	1	1
A0A0E3V335	Galactose/methyl galactoside import ATP-binding protein MglA OS=Pasteurella multocida subsp. multocida O	2,37	1	1	1	1
F6V4A2	Nuclear receptor subfamily 0 group B member 2 OS=Canis lupus familiaris GN=NR0B2 PE=3 SV=1 - [F6V4A2_CA	2,15	1	1	1	1
F1PX21	Trafficking protein particle complex 11 OS=Canis lupus familiaris GN=TRAPPC11 PE=4 SV=2 - [F1PX21_CANLF]	1,94	1	1	1	1
A2VBC2	Sialyltransferase 8 (Alpha 2,8-sialyltransferase) E (Fragment) OS=Canis lupus familiaris GN=siat8E PE=2 SV=1 - [	1,93	1	0	1	1
E2RDN7	Phosphoseryl-tRNA kinase OS=Canis lupus familiaris GN=PSTK PE=4 SV=2 - [E2RDN7_CANLF]	1,93	1	1	1	1
J9JHL8	IKAROS family zinc finger 5 OS=Canis lupus familiaris GN=IKZF5 PE=4 SV=1 - [J9JHL8_CANLF]	1,91	1	1	1	1
A0A0E3ZPZ5	Glycerol-3-phosphate acyltransferase OS=Pasteurella multocida subsp. multocida OH4807 GN=plsB PE=3 SV=1	1,85	1	1	1	1
J9P1T8	Dual specificity tyrosine phosphorylation regulated kinase 3 OS=Canis lupus familiaris GN=DYRK3 PE=4 SV=1 - [	1,81	1	0	1	1
F1PSF2	Uncharacterized protein OS=Canis lupus familiaris GN=IL1RL2 PE=4 SV=1 - [F1PSF2_CANLF]	1,81	1	1	1	1
F1PD83	Forkhead box O3 OS=Canis lupus familiaris GN=FOXO3 PE=4 SV=2 - [F1PD83_CANLF]	1,79	1	1	1	1
F1PKV8	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 OS=Canis lupus familiaris GN=ST8SIA5 PE=3 SV=1	1,7	1	0	1	1
E2R8C3	Dual specificity tyrosine phosphorylation regulated kinase 3 OS=Canis lupus familiaris GN=DYRK3 PE=4 SV=2 - [	1,7	1	0	1	1
F1PBL2	T-cell lymphoma invasion and metastasis 2 OS=Canis lupus familiaris GN=TIAM2 PE=4 SV=2 - [F1PBL2_CANLF]	1,7	1	1	1	2
F6UNP7	Neurofilament medium OS=Canis lupus familiaris GN=NEFM PE=3 SV=1 - [F6UNP7_CANLF]	1,62	1	1	1	1
F1PRS3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PRS3_CANLF]	1,55	1	0	1	1
E2R211	Methyl-CpG binding domain protein 1 (Fragment) OS=Canis lupus familiaris GN=MBD1 PE=4 SV=2 - [E2R211_C	1,52	1	0	1	1
E2RMK4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2RMK4_CANLF]	1,51	1	0	1	1
L7N0N8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0N8_CANLF]	1,5	1	0	1	1
E2RK65	Kelch like family member 8 OS=Canis lupus familiaris GN=KLHL8 PE=4 SV=1 - [E2RK65_CANLF]	1,46	1	0	1	1
J9JHW1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9JHW1_CANLF]	1,44	1	0	1	1
J9P6U0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P6U0_CANLF]	1,43	1	0	1	1
E2R214	Methyl-CpG binding domain protein 1 OS=Canis lupus familiaris GN=MBD1 PE=4 SV=2 - [E2R214_CANLF]	1,38	1	0	1	1
B8K1W7	ATP-binding cassette protein C4 OS=Canis lupus familiaris GN=Abcc4 PE=2 SV=1 - [B8K1W7_CANLF]	1,36	1	0	1	1
F1PNA2	ATP binding cassette subfamily C member 4 OS=Canis lupus familiaris GN=ABCC4 PE=4 SV=2 - [F1PNA2_CANLF	1,36	1	0	1	1
F1PB26	Uncharacterized protein OS=Canis lupus familiaris GN=MRPL33 PE=4 SV=2 - [F1PB26_CANLF]	1,35	1	0	1	1
F1P832	Alpha-1,4 glucan phosphorylase OS=Canis lupus familiaris GN=PYGM PE=3 SV=2 - [F1P832_CANLF]	1,31	1	1	1	2
E2RBQ6	Adhesion G protein-coupled receptor B1 OS=Canis lupus familiaris GN=ADGRB1 PE=4 SV=2 - [E2RBQ6_CANLF]	1,28	1	1	1	1
J9NV18	Uncharacterized protein OS=Canis lupus familiaris GN=MRPL33 PE=4 SV=1 - [J9NV18_CANLF]	1,26	1	0	1	1
J9PAI3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAI3_CANLF]	1,23	1	1	1	1
E2R151	Synemin OS=Canis lupus familiaris GN=SYNM PE=3 SV=2 - [E2R151_CANLF]	1,18	1	1	1	1
Q32KH2	Sulfatase 1 OS=Canis lupus familiaris GN=sulf1 PE=2 SV=1 - [Q32KH2_CANLF]	1,15	1	0	1	1
F1Q233	Sulfatase 1 OS=Canis lupus familiaris GN=SULF1 PE=4 SV=2 - [F1Q233_CANLF]	1,12	1	0	1	1
J9P9Y4	Uncharacterized protein OS=Canis lupus familiaris GN=LOC606788 PE=4 SV=1 - [J9P9Y4_CANLF]	1,04	1	0	1	1
E2R8R6	Mitochondrial tRNA translation optimization 1 OS=Canis lupus familiaris GN=MTO1 PE=3 SV=1 - [E2R8R6_CANL	1,04	1	1	1	1
J9P0J6	Coiled-coil domain containing 154 OS=Canis lupus familiaris GN=CCDC154 PE=4 SV=1 - [J9P0J6_CANLF]	1,04	1	1	1	3

F1PXV0	Uncharacterized protein OS=Canis lupus familiaris GN=LOC606788 PE=4 SV=2 - [F1PXV0_CANLF]	1,03	1	0	1	1
F1PMX4	Protein kinase C epsilon type OS=Canis lupus familiaris GN=PRKCE PE=3 SV=2 - [F1PMX4_CANLF]	0,95	1	1	1	1
F1PWQ3	Zinc finger BED-type containing 4 OS=Canis lupus familiaris GN=ZBED4 PE=4 SV=2 - [F1PWQ3_CANLF]	0,86	1	1	1	1
J9NYP9	Ring finger protein 213 OS=Canis lupus familiaris GN=RNF213 PE=4 SV=1 - [J9NYP9_CANLF]	0,55	1	1	1	1
J9P0G8	Intraflagellar transport 122 OS=Canis lupus familiaris GN=IFT122 PE=4 SV=1 - [J9P0G8_CANLF]	0,51	1	0	1	1
E2RID8	ATP-dependent RNA helicase DHX29 OS=Canis lupus familiaris GN=DHX29 PE=3 SV=1 - [E2RID8_CANLF]	0,51	1	0	1	1
J9P6V4	ATP-dependent RNA helicase DHX29 OS=Canis lupus familiaris GN=DHX29 PE=3 SV=1 - [J9P6V4_CANLF]	0,51	1	0	1	1
E2RL93	Intraflagellar transport 122 OS=Canis lupus familiaris GN=IFT122 PE=4 SV=2 - [E2RL93_CANLF]	0,48	1	0	1	1
F1P8S2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1P8S2_CANLF]	16,74	1	1	1	1
J9P1E0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P1E0_CANLF]	12,02	1	0	1	1
A0A0E3ZQV0	SlpA OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_04935 PE=4 SV=1 - [A0A0E3ZQV0_PASMD]	10,77	1	1	1	1
Q8WMS4	Peroxisome proliferator-activated receptor-gamma (Fragment) OS=Canis lupus familiaris GN=PPAR-gamma PE	8,8	1	1	1	1
E2R4R5	Somatomedin B and thrombospondin type 1 domain containing OS=Canis lupus familiaris GN=SBSPON PE=4 SV	8,71	1	1	1	2
F1PNS9	GH3 domain containing OS=Canis lupus familiaris GN=GHDC PE=4 SV=2 - [F1PNS9_CANLF]	6,62	1	1	1	1
O97626	CD40 ligand OS=Canis lupus familiaris GN=CD40LG PE=2 SV=1 - [CD40L_CANLF]	6,54	1	1	1	1
A0A0A0MPC5	Trafficking protein particle complex subunit 2 OS=Canis lupus familiaris GN=TRAPPC2 PE=4 SV=1 - [A0A0A0MP	6,42	1	1	1	1
J9P0D1	Uncharacterized protein OS=Canis lupus familiaris GN=DUSP15 PE=3 SV=1 - [J9P0D1_CANLF]	5,96	1	1	1	1
E2RAG6	BCL2 associated athanogene 5 OS=Canis lupus familiaris GN=BAG5 PE=4 SV=2 - [E2RAG6_CANLF]	5,69	1	1	1	1
J9NTH3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NTH3_CANLF]	5,64	1	0	1	1
E2RI79	Cell division cycle 20B OS=Canis lupus familiaris GN=CDC20B PE=4 SV=1 - [E2RI79_CANLF]	5,56	1	0	1	2
J9P571	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P571_CANLF]	5,54	1	1	1	1
E2RI78	Cell division cycle 20B OS=Canis lupus familiaris GN=CDC20B PE=4 SV=2 - [E2RI78_CANLF]	5,28	1	0	1	2
J9PAZ9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAZ9_CANLF]	5,08	1	0	1	1
F1PJK1	Family with sequence similarity 69 member C OS=Canis lupus familiaris GN=FAM69C PE=4 SV=2 - [F1PJK1_CAN	4,81	1	1	1	1
J9P9Q7	Leucine rich repeat containing 6 OS=Canis lupus familiaris GN=LRRC6 PE=4 SV=1 - [J9P9Q7_CANLF]	4,72	1	0	1	1
E2RC46	Transmembrane protein 252 OS=Canis lupus familiaris GN=TMEM252 PE=4 SV=1 - [E2RC46_CANLF]	4,68	1	1	1	1
J9NXJ5	Olfactory receptor OS=Canis lupus familiaris GN=OR6C6 PE=3 SV=1 - [J9NXJ5_CANLF]	4,52	1	1	1	1
E2QYX5	Solute carrier family 35 member D3 OS=Canis lupus familiaris GN=SLC35D3 PE=4 SV=1 - [E2QYX5_CANLF]	4,26	1	1	1	1
E2RHU6	Tyrosine--tRNA ligase OS=Canis lupus familiaris GN=YARS2 PE=3 SV=1 - [E2RHU6_CANLF]	4,19	1	1	1	1
F1PX34	Polypeptide N-acetylgalactosaminyltransferase OS=Canis lupus familiaris PE=3 SV=2 - [F1PX34_CANLF]	3,95	1	0	1	1
L7N0P4	Keratin 74 OS=Canis lupus familiaris GN=KRT74 PE=3 SV=1 - [L7N0P4_CANLF]	3,92	1	1	1	1
J9P3W3	Leucine rich repeat containing 6 OS=Canis lupus familiaris GN=LRRC6 PE=4 SV=1 - [J9P3W3_CANLF]	3,91	1	0	1	1
F1PZ47	Eukaryotic translation initiation factor 2 subunit beta OS=Canis lupus familiaris GN=EIF2S2 PE=4 SV=2 - [F1PZ47	3,9	1	1	1	1
E2RC31	Leucine rich repeat containing 6 OS=Canis lupus familiaris GN=LRRC6 PE=4 SV=2 - [E2RC31_CANLF]	3,9	1	0	1	1
E2RIJ8	Uncharacterized protein OS=Canis lupus familiaris GN=BBS1 PE=4 SV=1 - [E2RIJ8_CANLF]	3,88	1	1	1	1
J9P6W7	Leucine rich repeat containing 6 OS=Canis lupus familiaris GN=LRRC6 PE=4 SV=1 - [J9P6W7_CANLF]	3,78	1	0	1	1
F1PEM3	Tyrosine-protein kinase OS=Canis lupus familiaris GN=SRMS PE=3 SV=1 - [F1PEM3_CANLF]	3,73	1	1	1	2
F1Q3F3	Polypeptide N-acetylgalactosaminyltransferase OS=Canis lupus familiaris GN=LOC102152620 PE=3 SV=2 - [F1Q	3,65	1	0	1	1
E2RCP9	Proteasome 26S subunit, non-ATPase 2 OS=Canis lupus familiaris GN=PSMD2 PE=4 SV=1 - [E2RCP9_CANLF]	3,63	1	1	1	1
P49926	Corticoliberin OS=Canis lupus familiaris GN=CRH PE=2 SV=2 - [CRF_CANLF]	3,57	1	0	1	1
J9P572	Corticoliberin OS=Canis lupus familiaris GN=CRH PE=4 SV=1 - [J9P572_CANLF]	3,57	1	0	1	1
L7N050	Heat shock protein family A (Hsp70) member 1 like OS=Canis lupus familiaris GN=HSPA1L PE=3 SV=1 - [L7N050_	3,43	1	0	1	1
E2REF5	Cilia and flagella associated protein 70 OS=Canis lupus familiaris GN=CFAP70 PE=4 SV=2 - [E2REF5_CANLF]	3,35	1	0	1	1
J9NXI9	Cilia and flagella associated protein 70 OS=Canis lupus familiaris GN=CFAP70 PE=4 SV=1 - [J9NXI9_CANLF]	3,3	1	0	1	1
J9NYG5	Uncharacterized protein OS=Canis lupus familiaris GN=LOC484365 PE=4 SV=1 - [J9NYG5_CANLF]	3,23	1	1	1	1
F1PWE1	Plasminogen activator OS=Canis lupus familiaris GN=PLAT PE=3 SV=2 - [F1PWE1_CANLF]	3,19	1	0	1	1
E2QWN7	Lymphocyte cytosolic protein 1 OS=Canis lupus familiaris GN=LCP1 PE=4 SV=1 - [E2QWN7_CANLF]	3,03	1	1	1	1
F1PPP8	BR serine/threonine kinase 1 OS=Canis lupus familiaris GN=BRSK1 PE=4 SV=2 - [F1PPP8_CANLF]	2,91	1	1	1	1
F1P6E1	Complement C1s OS=Canis lupus familiaris GN=C1S PE=3 SV=2 - [F1P6E1_CANLF]	2,88	1	1	1	15
F6XSA9	Roundabout guidance receptor 4 OS=Canis lupus familiaris GN=ROBO4 PE=4 SV=1 - [F6XSA9_CANLF]	2,88	1	1	1	1
F1PVE3	SAP domain containing ribonucleoprotein OS=Canis lupus familiaris GN=SARNP PE=4 SV=1 - [F1PVE3_CANLF]	2,86	1	0	1	1
H9GW85	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100856005 PE=4 SV=2 - [H9GW85_CANLF]	2,81	1	0	1	1
E2RT77	Junction mediating and regulatory protein, p53 cofactor OS=Canis lupus familiaris GN=JMY PE=4 SV=2 - [E2RT7	2,76	1	1	1	1
J9PAF7	Anion exchange protein OS=Canis lupus familiaris GN=SLC4A7 PE=3 SV=1 - [J9PAF7_CANLF]	2,67	1	0	1	1
E2R5Y4	Fanconi anemia complementation group L OS=Canis lupus familiaris GN=FANCL PE=4 SV=2 - [E2R5Y4_CANLF]	2,65	1	1	1	1
J9NVV4	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100856005 PE=4 SV=1 - [J9NVV4_CANLF]	2,57	1	0	1	1
J9P6T7	Uncharacterized protein OS=Canis lupus familiaris GN=ARHGEF1 PE=4 SV=1 - [J9P6T7_CANLF]	2,55	1	0	1	1
J9P8E3	Uncharacterized protein OS=Canis lupus familiaris GN=ARHGEF1 PE=4 SV=1 - [J9P8E3_CANLF]	2,46	1	0	1	1
F1PTY0	Anion exchange protein OS=Canis lupus familiaris GN=SLC4A7 PE=3 SV=2 - [F1PTY0_CANLF]	2,43	1	0	1	1
F1Q0Q8	Coiled-coil serine rich protein 2 OS=Canis lupus familiaris GN=CCSER2 PE=4 SV=2 - [F1Q0Q8_CANLF]	2,34	1	1	1	1
E2RDL8	Splicing factor 3a subunit 1 OS=Canis lupus familiaris GN=SF3A1 PE=4 SV=1 - [E2RDL8_CANLF]	2,27	1	1	1	1
F1Q231	Reticulon OS=Canis lupus familiaris GN=RTN1 PE=4 SV=2 - [F1Q231_CANLF]	2,27	1	0	1	1
F1Q311	Uncharacterized protein OS=Canis lupus familiaris GN=LOC611363 PE=4 SV=2 - [F1Q311_CANLF]	2,26	1	0	1	1
F1Q2B3	Reticulon OS=Canis lupus familiaris GN=RTN1 PE=4 SV=2 - [F1Q2B3_CANLF]	2,24	1	0	1	1
A0A0E3V4W2	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_07840 PE=4 SV=1 - [A0	2,05	1	1	1	2
E2QSJ2	Acidic residue methyltransferase 1 OS=Canis lupus familiaris GN=ARMT1 PE=4 SV=1 - [E2QSJ2_CANLF]	2,04	1	1	1	1
J9P559	Diphosphoinositol pentakisphosphate kinase 2 OS=Canis lupus familiaris GN=PPIP5K2 PE=3 SV=1 - [J9P559_CA	2,03	1	0	1	1
E2R1Q4	PNN interacting serine and arginine rich protein OS=Canis lupus familiaris GN=PNISR PE=4 SV=2 - [E2R1Q4_CA	1,97	1	1	1	1
F1PZ17	Diphosphoinositol pentakisphosphate kinase 2 OS=Canis lupus familiaris GN=PPIP5K2 PE=3 SV=2 - [F1PZ17_CA	1,93	1	0	1	1
E2RSY2	Chloride anion exchanger OS=Canis lupus familiaris GN=SLC26A3 PE=3 SV=2 - [E2RSY2_CANLF]	1,92	1	0	1	1
E2RTK4	DExH-box helicase 34 OS=Canis lupus familiaris GN=DHX34 PE=4 SV=2 - [E2RTK4_CANLF]	1,84	1	0	1	1
F1PMS7	Ribosomal modification protein rimK like family member B OS=Canis lupus familiaris GN=RIMKLB PE=4 SV=2 - [	1,79	1	1	1	1
E2RTK2	DExH-box helicase 34 OS=Canis lupus familiaris GN=DHX34 PE=4 SV=2 - [E2RTK2_CANLF]	1,78	1	0	1	1
F1PYQ9	Anthrax toxin receptor 1 OS=Canis lupus familiaris GN=ANTXR1 PE=4 SV=2 - [F1PYQ9_CANLF]	1,65	1	1	1	1
J9NX38	Uncharacterized protein OS=Canis lupus familiaris GN=LOC611363 PE=4 SV=1 - [J9NX38_CANLF]	1,65	1	0	1	1
E2RSY4	Chloride anion exchanger OS=Canis lupus familiaris GN=SLC26A3 PE=3 SV=1 - [E2RSY4_CANLF]	1,58	1	0	1	1
F1PEK4	DS cell adhesion molecule like 1 OS=Canis lupus familiaris GN=DSCAML1 PE=4 SV=2 - [F1PEK4_CANLF]	1,54	1	1	1	1
F1PYB5	REL proto-oncogene, NF-kB subunit OS=Canis lupus familiaris GN=REL PE=4 SV=2 - [F1PYB5_CANLF]	1,52	1	1	1	1
J9P4U4	PR/SET domain 15 OS=Canis lupus familiaris GN=PRDM15 PE=4 SV=1 - [J9P4U4_CANLF]	1,49	1	0	1	1
J9P9V3	Ring finger protein 17 OS=Canis lupus familiaris GN=RNF17 PE=4 SV=1 - [J9P9V3_CANLF]	1,47	1	0	1	2
F6XNH4	Methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1 OS=Canis	1,44	1	0	1	1
F1PYV1	Methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1 OS=Canis	1,42	1	0	1	1
E2RIS2	Ring finger protein 17 OS=Canis lupus familiaris GN=RNF17 PE=4 SV=2 - [E2RIS2_CANLF]	1,39	1	0	1	2
J9NYU9	Ring finger protein 17 OS=Canis lupus familiaris GN=RNF17 PE=4 SV=1 - [J9NYU9_CANLF]	1,37	1	0	1	2
J9PAT4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAT4_CANLF]	1,36	1	1	1	1
F1PFQ1	Zyg-11 family member B, cell cycle regulator OS=Canis lupus familiaris GN=ZYG11B PE=4 SV=2 - [F1PFQ1_CANL	1,36	1	1	1	1
E2RS76	Bloom syndrome RecQ like helicase OS=Canis lupus familiaris GN=BLM PE=4 SV=2 - [E2RS76_CANLF]	1,35	1	0	1	1
J9PB86	Bloom syndrome RecQ like helicase OS=Canis lupus familiaris GN=BLM PE=4 SV=1 - [J9PB86_CANLF]	1,34	1	0	1	1
E2RLE0	Trafficking protein particle complex 9 OS=Canis lupus familiaris GN=TRAPPC9 PE=4 SV=2 - [E2RLE0_CANLF]	1,31	1	1	1	1
F1PNX9	Neuron navigator 3 OS=Canis lupus familiaris GN=NAV3 PE=4 SV=2 - [F1PNX9_CANLF]	1,28	1	0	1	1
F1PNY1	Neuron navigator 3 OS=Canis lupus familiaris GN=NAV3 PE=4 SV=2 - [F1PNY1_CANLF]	1,26	1	0	1	1
F1Q3J3	Bactericidal/permeability-increasing protein OS=Canis lupus familiaris GN=BPI PE=4 SV=2 - [F1Q3J3_CANLF]	1,24	1	0	1	1
F1PZ05	Pleckstrin and Sec7 domain containing 3 OS=Canis lupus familiaris GN=PSD3 PE=4 SV=2 - [F1PZ05_CANLF]	1,23	1	1	1	1

A0A0E3ZQ89	Acetyl-coenzyme A synthetase OS=Pasteurella multocida subsp. multocida OH4807 GN=acsA PE=3 SV=1 - [A0A	1,23	1	1	1	1
F1PF60	Chromosome 12 open reading frame 40 OS=Canis lupus familiaris GN=C12orf40 PE=4 SV=2 - [F1PF60_CANLF]	1,19	1	1	1	1
Q28226	Mucin OS=Canis lupus familiaris PE=2 SV=1 - [Q28226_CANLF]	1,16	1	1	1	1
E2RAJ3	PR/SET domain 15 OS=Canis lupus familiaris GN=PRDM15 PE=4 SV=2 - [E2RAJ3_CANLF]	1,12	1	0	1	1
E2RNS7	Uncharacterized protein OS=Canis lupus familiaris GN=VPS25 PE=4 SV=2 - [E2RNS7_CANLF]	1,05	1	0	1	1
F6UP34	EF-hand calcium binding domain 6 OS=Canis lupus familiaris GN=EFCAB6 PE=4 SV=1 - [F6UP34_CANLF]	1,03	1	1	1	1
E2QWK2	Polyribonucleotide nucleotidyltransferase 1 OS=Canis lupus familiaris GN=PNPT1 PE=4 SV=2 - [E2QWK2_CANL	1,01	1	1	1	1
J9NV24	Testis expressed 14, intercellular bridge forming factor OS=Canis lupus familiaris GN=TEX14 PE=4 SV=1 - [J9NV	0,98	1	0	1	1
E2RP33	Testis expressed 14, intercellular bridge forming factor OS=Canis lupus familiaris GN=TEX14 PE=4 SV=2 - [E2RP	0,97	1	0	1	1
E2RP34	Testis expressed 14, intercellular bridge forming factor OS=Canis lupus familiaris GN=TEX14 PE=4 SV=2 - [E2RP	0,94	1	0	1	1
F6V2Q3	Anion exchange protein OS=Canis lupus familiaris GN=SLC4A5 PE=3 SV=1 - [F6V2Q3_CANLF]	0,9	1	1	1	1
F1PY87	CREB binding protein OS=Canis lupus familiaris GN=CREBBP PE=4 SV=1 - [F1PY87_CANLF]	0,89	1	1	1	1
J9PB95	Phospholipid-transporting ATPase OS=Canis lupus familiaris GN=ATP10A PE=3 SV=1 - [J9PB95_CANLF]	0,89	1	0	1	1
E2RB85	Phospholipid-transporting ATPase OS=Canis lupus familiaris GN=ATP10A PE=3 SV=2 - [E2RB85_CANLF]	0,86	1	0	1	1
E2R9W6	Acyl-coenzyme A oxidase OS=Canis lupus familiaris GN=ACOX3 PE=3 SV=1 - [E2R9W6_CANLF]	0,86	1	0	1	1
E2RDR0	SEC31 homolog B, COPII coat complex component OS=Canis lupus familiaris GN=SEC31B PE=4 SV=2 - [E2RDR0_	0,85	1	1	1	1
E2QWU6	Zinc finger protein 451 OS=Canis lupus familiaris GN=ZNF451 PE=4 SV=1 - [E2QWU6_CANLF]	0,85	1	1	1	1
F1PA39	Calmodulin regulated spectrin associated protein 1 OS=Canis lupus familiaris GN=CAMSAP1 PE=3 SV=2 - [F1PA	0,76	1	1	1	1
E2R698	Nuclear receptor coactivator 6 OS=Canis lupus familiaris GN=NCOA6 PE=4 SV=1 - [E2R698_CANLF]	0,73	1	1	1	1
E2RNW6	Uncharacterized protein OS=Canis lupus familiaris GN=VPS25 PE=4 SV=2 - [E2RNW6_CANLF]	0,7	1	0	1	1
E2RHB2	Ubiquitin protein ligase E3 component n-recognin 2 OS=Canis lupus familiaris GN=UBR2 PE=4 SV=2 - [E2RHB2_	0,68	1	0	1	1
J9P5Z7	Ubiquitin protein ligase E3 component n-recognin 2 OS=Canis lupus familiaris GN=UBR2 PE=4 SV=1 - [J9P5Z7_C	0,68	1	0	1	1
F1PUB9	Elongation factor Tu GTP binding domain containing 2 OS=Canis lupus familiaris GN=EFTUD2 PE=4 SV=2 - [F1PU	0,62	1	0	1	1
J9PAM3	YTH domain containing 2 OS=Canis lupus familiaris GN=YTHDC2 PE=4 SV=1 - [J9PAM3_CANLF]	0,6	1	0	1	1
F1PPS8	AF4/FMR2 family member 3 OS=Canis lupus familiaris GN=AFF3 PE=4 SV=2 - [F1PPS8_CANLF]	0,57	1	0	1	1
E2R4Q1	LDL receptor related protein 1 OS=Canis lupus familiaris GN=LRP1 PE=4 SV=2 - [E2R4Q1_CANLF]	0,55	1	0	1	1
J9P315	LDL receptor related protein 1 OS=Canis lupus familiaris GN=LRP1 PE=4 SV=1 - [J9P315_CANLF]	0,55	1	0	1	1
F1PPS9	AF4/FMR2 family member 3 OS=Canis lupus familiaris GN=AFF3 PE=4 SV=2 - [F1PPS9_CANLF]	0,55	1	0	1	1
F1PB98	Neuron navigator 2 OS=Canis lupus familiaris GN=NAV2 PE=4 SV=2 - [F1PB98_CANLF]	0,54	1	0	1	1
F1P9L3	Neuron navigator 2 OS=Canis lupus familiaris GN=NAV2 PE=4 SV=2 - [F1P9L3_CANLF]	0,53	1	0	1	1
A7YH32	Cingulin OS=Canis lupus familiaris GN=CGN PE=2 SV=1 - [CING_CANLF]	0,5	1	0	1	2
F1PLU8	Cingulin OS=Canis lupus familiaris GN=CGN PE=4 SV=2 - [F1PLU8_CANLF]	0,5	1	0	1	2
F1Q2H7	Kinesin family member 26B OS=Canis lupus familiaris GN=KIF26B PE=3 SV=2 - [F1Q2H7_CANLF]	0,48	1	0	1	1
J9PAB8	Kinesin family member 26B OS=Canis lupus familiaris GN=KIF26B PE=3 SV=1 - [J9PAB8_CANLF]	0,48	1	0	1	1
E2RE65	WNK lysine deficient protein kinase 2 OS=Canis lupus familiaris GN=WNK2 PE=4 SV=2 - [E2RE65_CANLF]	0,48	1	0	1	1
F1Q3Y6	WNK lysine deficient protein kinase 1 OS=Canis lupus familiaris GN=WNK1 PE=4 SV=2 - [F1Q3Y6_CANLF]	0,47	1	0	1	1
J9P404	WNK lysine deficient protein kinase 1 OS=Canis lupus familiaris GN=WNK1 PE=4 SV=1 - [J9P404_CANLF]	0,46	1	0	1	1
E2QZR7	YTH domain containing 2 OS=Canis lupus familiaris GN=YTHDC2 PE=4 SV=2 - [E2QZR7_CANLF]	0,44	1	0	1	1
F1PWZ2	Myosin heavy chain 7B OS=Canis lupus familiaris GN=MYH7B PE=3 SV=2 - [F1PWZ2_CANLF]	0,41	1	1	1	1
F6XJV3	Uncharacterized protein OS=Canis lupus familiaris GN=EIF4EBP3 PE=4 SV=1 - [F6XJV3_CANLF]	0,39	1	0	1	1
F6XSE4	Uncharacterized protein OS=Canis lupus familiaris GN=EIF4EBP3 PE=4 SV=1 - [F6XSE4_CANLF]	0,38	1	0	1	1
F6XQD6	Microtubule associated protein 1B OS=Canis lupus familiaris GN=MAP1B PE=4 SV=1 - [F6XQD6_CANLF]	0,27	1	1	1	1
F1Q3G0	WDFY family member 4 OS=Canis lupus familiaris GN=WDFY4 PE=4 SV=2 - [F1Q3G0_CANLF]	0,19	1	0	1	1
F1Q3G4	WDFY family member 4 OS=Canis lupus familiaris GN=WDFY4 PE=4 SV=2 - [F1Q3G4_CANLF]	0,19	1	0	1	1
F1PIH9	HYDIN, axonemal central pair apparatus protein OS=Canis lupus familiaris GN=HYDIN PE=4 SV=2 - [F1PIH9_CA	0,12	1	0	1	1
J9PAK0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAK0_CANLF]	30,16	1	1	1	1
B2CRU9	p2Y purinoceptor 2 (Fragment) OS=Canis lupus familiaris GN=P2Y2 PE=2 SV=1 - [B2CRU9_CANLF]	20	1	0	1	1
E2R0E8	SplA/ryanodine receptor domain and SOCS box containing 4 OS=Canis lupus familiaris GN=SPSB4 PE=4 SV=1 - [	14,29	1	1	1	1
P52212	Parathyroid hormone OS=Canis lupus familiaris GN=PTH PE=3 SV=1 - [PTHY_CANLF]	11,3	1	1	1	1
F1PM28	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PM28_CANLF]	9,71	1	1	1	1
F2Z4N8	Uncharacterized protein OS=Canis lupus familiaris GN=ACTG2 PE=3 SV=1 - [F2Z4N8_CANLF]	9,57	1	1	1	1
E2RNV3	PITH domain containing 1 OS=Canis lupus familiaris GN=PITHD1 PE=4 SV=2 - [E2RNV3_CANLF]	9	1	1	1	1
E2RQW8	Apoptosis inducing factor, mitochondria associated 2 OS=Canis lupus familiaris GN=AIFM2 PE=4 SV=1 - [E2RQW	5,63	1	1	1	1
A0A0E3V4J3	Glutathione biosynthesis bifunctional protein GshAB OS=Pasteurella multocida subsp. multocida OH4807 GN=	5,54	1	1	1	1
F1PAH5	Uncharacterized protein OS=Canis lupus familiaris GN=CXCR1 PE=3 SV=2 - [F1PAH5_CANLF]	5,03	1	1	1	1
E2RLR0	Cytochrome P450 family 7 subfamily A member 1 OS=Canis lupus familiaris GN=CYP7A1 PE=3 SV=1 - [E2RLR0_	4,99	1	0	1	1
F1P9J8	HIV-1 Tat interactive protein 2 OS=Canis lupus familiaris GN=HTATIP2 PE=4 SV=2 - [F1P9J8_CANLF]	4,71	1	1	1	1
F1PM53	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100855928 PE=4 SV=2 - [F1PM53_CANLF]	4,58	1	1	1	1
F1PXU2	Pyrophosphatase (inorganic) 2 OS=Canis lupus familiaris GN=PPA2 PE=4 SV=2 - [F1PXU2_CANLF]	4,41	1	1	1	1
J9P757	Cytochrome P450 family 7 subfamily A member 1 OS=Canis lupus familiaris GN=CYP7A1 PE=3 SV=1 - [J9P757_	4,31	1	0	1	1
E2R3Z4	Nipsnap homolog 3B OS=Canis lupus familiaris GN=NIPSNAP3B PE=4 SV=2 - [E2R3Z4_CANLF]	4,05	1	1	1	1
E2R1L5	Ring finger protein 40 OS=Canis lupus familiaris GN=RNF40 PE=4 SV=1 - [E2R1L5_CANLF]	4	1	1	1	1
E2RBA0	Tyrosine-protein kinase OS=Canis lupus familiaris GN=TXK PE=3 SV=2 - [E2RBA0_CANLF]	3,99	1	1	1	1
E2RDZ5	Purinergic receptor P2Y2 OS=Canis lupus familiaris GN=P2RY2 PE=3 SV=2 - [E2RDZ5_CANLF]	3,98	1	0	1	1
F1PBF6	Basal body orientation factor 1 OS=Canis lupus familiaris GN=BBOF1 PE=4 SV=2 - [F1PBF6_CANLF]	3,97	1	1	1	1
E2QXN9	Cystathionine beta-synthase OS=Canis lupus familiaris GN=CBS PE=3 SV=2 - [E2QXN9_CANLF]	3,85	1	1	1	2
E2QTV5	Sulfotransferase OS=Canis lupus familiaris GN=HS3ST5 PE=3 SV=1 - [E2QTV5_CANLF]	3,77	1	1	1	1
J9PA32	Myosin-13 OS=Canis lupus familiaris GN=MYH13 PE=4 SV=1 - [J9PA32_CANLF]	3,75	1	0	1	1
J9NYT2	KIAA1755 OS=Canis lupus familiaris GN=KIAA1755 PE=4 SV=1 - [J9NYT2_CANLF]	3,55	1	0	1	1
E2QWF5	Peptidylprolyl isomerase OS=Canis lupus familiaris GN=FKBP4 PE=4 SV=2 - [E2QWF5_CANLF]	3,49	1	1	1	1
F6UYL9	Thyroid hormone receptor interactor 4 OS=Canis lupus familiaris GN=TRIP4 PE=4 SV=1 - [F6UYL9_CANLF]	3,27	1	1	1	1
E2QRU4	Syntaxin 10 OS=Canis lupus familiaris GN=STX10 PE=3 SV=1 - [E2QRU4_CANLF]	3,2	1	1	1	1
F1Q0R1	Protogenin OS=Canis lupus familiaris GN=PRTG PE=4 SV=2 - [F1Q0R1_CANLF]	3,2	1	1	1	1
J9NWW8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NWW8_CANLF]	2,94	1	0	1	1
E2RQ46	Spi-1 proto-oncogene OS=Canis lupus familiaris GN=SPI1 PE=3 SV=2 - [E2RQ46_CANLF]	2,8	1	1	1	1
E2RH91	Staphylococcal nuclease and tudor domain containing 1 OS=Canis lupus familiaris GN=SND1 PE=4 SV=2 - [E2RH	2,53	1	1	1	2
E2RLA5	Golgi membrane protein 1 OS=Canis lupus familiaris GN=GOLM1 PE=4 SV=2 - [E2RLA5_CANLF]	2,46	1	1	1	1
F1PWL8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PWL8_CANLF]	2,19	1	1	1	1
Q32KH1	Sulfatase 2 OS=Canis lupus familiaris GN=sulf2 PE=2 SV=1 - [Q32KH1_CANLF]	2,07	1	1	1	1
E2RM73	Discs large MAGUK scaffold protein 2 OS=Canis lupus familiaris GN=DLG2 PE=4 SV=2 - [E2RM73_CANLF]	2	1	1	1	1
E2R3P0	NOC2 like nucleolar associated transcriptional repressor OS=Canis lupus familiaris GN=NOC2L PE=4 SV=2 - [E2R	1,85	1	1	1	1
F1Q417	KIAA1755 OS=Canis lupus familiaris GN=KIAA1755 PE=4 SV=2 - [F1Q417_CANLF]	1,84	1	0	1	1
F1PBG1	Phosphoinositide phospholipase C OS=Canis lupus familiaris GN=PLCH1 PE=4 SV=2 - [F1PBG1_CANLF]	1,82	1	0	1	1
E2R1U0	Multiple C2 and transmembrane domain containing 1 OS=Canis lupus familiaris GN=MCTP1 PE=4 SV=2 - [E2R1	1,8	1	1	1	1
E2REP2	TRK-fused gene OS=Canis lupus familiaris GN=TFG PE=4 SV=1 - [E2REP2_CANLF]	1,75	1	0	1	1
F1PA82	Cell wall biogenesis 43 C-terminal homolog OS=Canis lupus familiaris GN=CWH43 PE=4 SV=1 - [F1PA82_CANLF]	1,6	1	1	1	1
E2RJV1	Angiomotin OS=Canis lupus familiaris GN=AMOT PE=1 SV=1 - [E2RJV1_CANLF]	1,57	1	1	1	1
J9NWT6	Integrin subunit alpha L OS=Canis lupus familiaris GN=ITGAL PE=3 SV=1 - [J9NWT6_CANLF]	1,55	1	0	1	1
F1PIQ2	Calcineurin binding protein 1 OS=Canis lupus familiaris GN=CABIN1 PE=4 SV=2 - [F1PIQ2_CANLF]	1,43	1	0	1	1
J9NTT6	Calcineurin binding protein 1 OS=Canis lupus familiaris GN=CABIN1 PE=4 SV=1 - [J9NTT6_CANLF]	1,42	1	0	1	1
F1PJD2	Calcineurin binding protein 1 OS=Canis lupus familiaris GN=CABIN1 PE=4 SV=1 - [F1PJD2_CANLF]	1,4	1	0	1	1
J9NSP8	StAR related lipid transfer domain containing 8 OS=Canis lupus familiaris GN=STARD8 PE=4 SV=1 - [J9NSP8_CA	1,36	1	0	1	1
F1PTV7	Disco interacting protein 2 homolog C OS=Canis lupus familiaris GN=DIP2C PE=4 SV=2 - [F1PTV7_CANLF]	1,34	1	1	1	1

E2RHE6	SCY1 like pseudokinase 2 OS=Canis lupus familiaris GN=SCYL2 PE=4 SV=2 - [E2RHE6_CANLF]	1,33	1	1	1	1
F1PBG2	Phosphoinositide phospholipase C OS=Canis lupus familiaris GN=PLCH1 PE=4 SV=2 - [F1PBG2_CANLF]	1,32	1	0	1	1
F1PI22	StAR related lipid transfer domain containing 8 OS=Canis lupus familiaris GN=STARD8 PE=4 SV=2 - [F1PI22_CA	1,27	1	0	1	1
F1PKW2	Receptor-like tyrosine kinase OS=Canis lupus familiaris GN=RYK PE=4 SV=2 - [F1PKW2_CANLF]	1,22	1	1	1	1
F1PBJ3	Uncharacterized protein OS=Canis lupus familiaris GN=LMNA PE=3 SV=1 - [F1PBJ3_CANLF]	1,2	1	0	1	1
J9P775	Bromodomain containing 7 OS=Canis lupus familiaris GN=BRD7 PE=4 SV=1 - [J9P775_CANLF]	1,18	1	0	1	1
F1Q3J6	Tyrosine-protein phosphatase non-receptor type OS=Canis lupus familiaris GN=PTPN11 PE=3 SV=2 - [F1Q3J6_C	1,18	1	1	1	1
F6XTA3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F6XTA3_CANLF]	1,12	1	1	1	1
F1P9T3	Regulating synaptic membrane exocytosis 2 OS=Canis lupus familiaris GN=RIMS2 PE=4 SV=2 - [F1P9T3_CANLF]	1,08	1	0	1	1
J9NSW5	Uncharacterized protein OS=Canis lupus familiaris GN=LMNA PE=3 SV=1 - [J9NSW5_CANLF]	1,05	1	0	1	1
F1P8D8	Integrin subunit alpha L OS=Canis lupus familiaris GN=ITGAL PE=3 SV=2 - [F1P8D8_CANLF]	1,03	1	0	1	1
J9NYS3	Regulating synaptic membrane exocytosis 2 OS=Canis lupus familiaris GN=RIMS2 PE=4 SV=1 - [J9NYS3_CANLF]	0,99	1	0	1	1
E2QW89	Uncharacterized protein OS=Canis lupus familiaris GN=LOC480926 PE=4 SV=1 - [E2QW89_CANLF]	0,94	1	0	1	1
F1P726	Bromodomain containing 7 OS=Canis lupus familiaris GN=BRD7 PE=4 SV=2 - [F1P726_CANLF]	0,92	1	0	1	1
J9NT00	Dynein axonemal heavy chain 3 OS=Canis lupus familiaris GN=DNAH3 PE=4 SV=1 - [J9NT00_CANLF]	0,84	1	0	1	1
F1PBB5	Dynein axonemal heavy chain 3 OS=Canis lupus familiaris GN=DNAH3 PE=4 SV=2 - [F1PBB5_CANLF]	0,83	1	0	1	1
J9NWH9	Dynein axonemal heavy chain 3 OS=Canis lupus familiaris GN=DNAH3 PE=4 SV=1 - [J9NWH9_CANLF]	0,83	1	0	1	1
A0A189RMR6	RNA-dependent RNA polymerase OS=African horse sickness virus 2 GN=VP1 PE=4 SV=1 - [A0A189RMR6_AHSV	0,77	1	1	1	1
J9P1H1	Utrophin OS=Canis lupus familiaris GN=UTRN PE=4 SV=1 - [J9P1H1_CANLF]	0,2	1	0	1	1
Q5JCF5	Utrophin OS=Canis lupus familiaris PE=2 SV=1 - [Q5JCF5_CANLF]	0,2	1	0	1	1
E2RRD8	Chromosome 1 open reading frame 43 OS=Canis lupus familiaris GN=C1orf43 PE=4 SV=2 - [E2RRD8_CANLF]	14,62	1	1	1	1
A0A0E3ZQP1	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_09065 PE=3 SV=1 - [A0	11,2	1	1	1	1
J9P885	Translocase of outer mitochondrial membrane 20 like OS=Canis lupus familiaris GN=TOMM20L PE=3 SV=1 - [J9	9,93	1	1	1	1
B6VCV6	LEF1 (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [B6VCV6_CANLF]	9,73	1	0	1	2
J9NUS8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NUS8_CANLF]	8,91	1	1	1	1
P86218	Oligosaccharyltransferase complex subunit OSTC OS=Canis lupus familiaris GN=OSTC PE=1 SV=1 - [OSTC_CANL	8,72	1	1	1	1
A0A0E3ZND1	Colicin uptake protein TolR OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_02725 PE=3 SV=1 - [	8,57	1	1	1	1
J9P853	40S ribosomal protein S3a OS=Canis lupus familiaris GN=RPS3A PE=3 SV=1 - [J9P853_CANLF]	7,98	1	0	1	1
J9P8N5	40S ribosomal protein S3a OS=Canis lupus familiaris GN=RPS3A PE=3 SV=1 - [J9P8N5_CANLF]	7,95	1	0	1	1
E2RRB7	VAMP associated protein B and C OS=Canis lupus familiaris GN=VAPB PE=4 SV=1 - [E2RRB7_CANLF]	7,82	1	1	1	1
E2RBM2	Phosphate cytidylyltransferase 1, choline, alpha OS=Canis lupus familiaris GN=PCYT1A PE=4 SV=2 - [E2RBM2_C	7,63	1	1	1	1
J9P498	Serum amyloid A protein OS=Canis lupus familiaris GN=LOC476879 PE=3 SV=1 - [J9P498_CANLF]	6,98	1	0	1	1
E2RBD0	Serum amyloid A protein OS=Canis lupus familiaris GN=LOC476879 PE=3 SV=1 - [E2RBD0_CANLF]	6,92	1	0	1	1
Q2VDR4	Apolipoprotein B (Fragment) OS=Canis lupus GN=APOB PE=4 SV=1 - [Q2VDR4_CANLU]	6,84	1	0	1	1
A0A0K0NQY3	Capsid protein VP2 OS=Canine parvovirus type 2 PE=4 SV=1 - [A0A0K0NQY3_PAVC]	5,65	1	1	1	1
J9P5I7	Clusterin associated protein 1 OS=Canis lupus familiaris GN=CLUAP1 PE=4 SV=1 - [J9P5I7_CANLF]	5,25	1	1	1	1
E7BUQ0	Beta-type proteasome 7 subunit OS=Canis lupus familiaris GN=PSMB7 PE=2 SV=1 - [E7BUQ0_CANLF]	4,33	1	1	1	1
F1Q1X7	Transcription factor 7 like 2 OS=Canis lupus familiaris GN=TCF7L2 PE=4 SV=2 - [F1Q1X7_CANLF]	4,23	1	0	1	2
E2RMH6	Poly(ADP-ribose) polymerase family member 6 OS=Canis lupus familiaris GN=PARP6 PE=4 SV=2 - [E2RMH6_CA	4,22	1	0	1	2
E2R9U3	Delta-like protein OS=Canis lupus familiaris GN=DLL4 PE=4 SV=1 - [E2R9U3_CANLF]	4,09	1	1	1	1
F1P6E4	Thromboxane A synthase 1 OS=Canis lupus familiaris GN=TBXAS1 PE=3 SV=2 - [F1P6E4_CANLF]	3,75	1	1	1	1
F1Q0G5	WD repeat domain 91 OS=Canis lupus familiaris GN=WDR91 PE=4 SV=2 - [F1Q0G5_CANLF]	3,31	1	1	1	1
E2RMU1	Histidine decarboxylase OS=Canis lupus familiaris GN=HDC PE=4 SV=1 - [E2RMU1_CANLF]	3,02	1	1	1	1
E2RCD6	tRNA-splicing ligase RtcB homolog OS=Canis lupus familiaris GN=RTCB PE=3 SV=1 - [E2RCD6_CANLF]	2,97	1	1	1	1
E2QZH1	Tetraspanin OS=Canis lupus familiaris GN=TSPAN14 PE=3 SV=1 - [E2QZH1_CANLF]	2,96	1	1	1	1
J9JHB3	Poly [ADP-ribose] polymerase OS=Canis lupus familiaris GN=PARP6 PE=4 SV=1 - [J9JHB3_CANLF]	2,88	1	0	1	2
J9P3M9	Abraxas 1, BRCA1 A complex subunit OS=Canis lupus familiaris GN=ABRAXAS1 PE=4 SV=1 - [J9P3M9_CANLF]	2,78	1	0	1	1
J9P2D2	HKR1, GLI-Kruppel zinc finger family member OS=Canis lupus familiaris GN=HKR1 PE=3 SV=1 - [J9P2D2_CANLF]	2,77	1	1	1	1
F1Q334	Lymphoid enhancer binding factor 1 OS=Canis lupus familiaris GN=LEF1 PE=4 SV=2 - [F1Q334_CANLF]	2,75	1	0	1	2
E2QTH7	Enhancer of polycomb homolog OS=Canis lupus familiaris GN=EPC1 PE=3 SV=1 - [E2QTH7_CANLF]	2,71	1	0	1	1
J9NZA2	Dynamin 1 like OS=Canis lupus familiaris GN=DNM1L PE=3 SV=1 - [J9NZA2_CANLF]	2,71	1	0	1	1
E2RRW8	Transcription factor 7 OS=Canis lupus familiaris GN=TCF7 PE=4 SV=2 - [E2RRW8_CANLF]	2,63	1	0	1	2
E2QTH5	Enhancer of polycomb homolog OS=Canis lupus familiaris GN=EPC1 PE=3 SV=1 - [E2QTH5_CANLF]	2,61	1	0	1	1
J9NRH1	Dynamin 1 like OS=Canis lupus familiaris GN=DNM1L PE=3 SV=1 - [J9NRH1_CANLF]	2,58	1	0	1	1
F1PDK6	Lactase OS=Canis lupus familiaris GN=LCT PE=4 SV=2 - [F1PDK6_CANLF]	2,57	1	1	1	1
E2QXL2	Dynamin 1 like OS=Canis lupus familiaris GN=DNM1L PE=3 SV=2 - [E2QXL2_CANLF]	2,54	1	0	1	1
F1Q1X1	Transcription factor 7 like 2 OS=Canis lupus familiaris GN=TCF7L2 PE=4 SV=2 - [F1Q1X1_CANLF]	2,51	1	0	1	2
F1PR27	Uncharacterized protein OS=Canis lupus familiaris GN=LOC490896 PE=4 SV=1 - [F1PR27_CANLF]	2,45	1	1	1	1
F1PKD8	Abraxas 1, BRCA1 A complex subunit OS=Canis lupus familiaris GN=ABRAXAS1 PE=4 SV=2 - [F1PKD8_CANLF]	2,44	1	0	1	1
F1PYV9	Transcription factor 7 like 1 OS=Canis lupus familiaris GN=TCF7L1 PE=4 SV=2 - [F1PYV9_CANLF]	2,38	1	0	1	2
J9P2V1	Transcription factor 7 like 2 OS=Canis lupus familiaris GN=TCF7L2 PE=4 SV=1 - [J9P2V1_CANLF]	2,26	1	0	1	2
A0A0E3V543	Cell division protein FtsX OS=Pasteurella multocida subsp. multocida OH4807 GN=ftsX PE=3 SV=1 - [A0A0E3V5	2,25	1	1	1	1
E2R9S7	Catenin alpha 1 OS=Canis lupus familiaris GN=CTNNA1 PE=4 SV=1 - [E2R9S7_CANLF]	2,21	1	1	1	1
J9P0N4	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100855888 PE=4 SV=1 - [J9P0N4_CANLF]	2,18	1	1	1	1
E2QXK1	Transcription factor 7 like 2 OS=Canis lupus familiaris GN=TCF7L2 PE=4 SV=2 - [E2QXK1_CANLF]	2,17	1	0	1	2
J9PBB3	EH domain binding protein 1 like 1 OS=Canis lupus familiaris GN=EHBP1L1 PE=4 SV=1 - [J9PBB3_CANLF]	2,02	1	0	1	1
F1PX33	Transcription factor 7 like 1 OS=Canis lupus familiaris GN=TCF7L1 PE=4 SV=2 - [F1PX33_CANLF]	1,88	1	0	1	2
E2RRQ1	Pendrin OS=Canis lupus familiaris GN=SLC26A4 PE=3 SV=1 - [E2RRQ1_CANLF]	1,79	1	1	1	1
J9NXS4	SIN3 transcription regulator family member B OS=Canis lupus familiaris GN=SIN3B PE=4 SV=1 - [J9NXS4_CANLF	1,77	1	0	1	1
B6SAK7	RNA-directed RNA polymerase OS=Rotavirus A (isolate RVA/Dog/United States/K9/1981/G3P5A[3]) GN=VP1 P	1,75	1	0	1	1
B6SAJ6	RNA-directed RNA polymerase OS=Rotavirus A (isolate RVA/Dog/United States/Cu-1/1982/G3P5A[3]) GN=VP1	1,75	1	0	1	1
F1PN34	SIN3 transcription regulator family member B OS=Canis lupus familiaris GN=SIN3B PE=4 SV=2 - [F1PN34_CANL	1,73	1	0	1	1
F1P798	Tenascin R OS=Canis lupus familiaris GN=TNR PE=4 SV=2 - [F1P798_CANLF]	1,69	1	1	1	1
E2RNN5	DNA-directed RNA polymerase subunit beta OS=Canis lupus familiaris GN=POLR2B PE=3 SV=2 - [E2RNN5_CANL	1,62	1	1	1	1
F1PP35	Aldehyde dehydrogenase 5 family member A1 OS=Canis lupus familiaris GN=ALDH5A1 PE=4 SV=2 - [F1PP35_C	1,58	1	1	1	1
F1P907	Dedicator of cytokinesis 2 OS=Canis lupus familiaris GN=DOCK2 PE=3 SV=2 - [F1P907_CANLF]	1,48	1	1	1	1
F1PDU1	Neogenin 1 OS=Canis lupus familiaris GN=NEO1 PE=4 SV=2 - [F1PDU1_CANLF]	1,4	1	0	1	1
J9P8Y2	DENN domain containing 5B OS=Canis lupus familiaris GN=DENND5B PE=4 SV=1 - [J9P8Y2_CANLF]	1,39	1	0	1	1
F1PQG0	DENN domain containing 5B OS=Canis lupus familiaris GN=DENND5B PE=4 SV=2 - [F1PQG0_CANLF]	1,38	1	0	1	1
J9P2T1	Neogenin 1 OS=Canis lupus familiaris GN=NEO1 PE=4 SV=1 - [J9P2T1_CANLF]	1,37	1	0	1	1
F1P7S2	EH domain binding protein 1 like 1 OS=Canis lupus familiaris GN=EHBP1L1 PE=4 SV=2 - [F1P7S2_CANLF]	1,23	1	0	1	1
E2REX6	Myosin binding protein C, slow type OS=Canis lupus familiaris GN=MYBPC1 PE=4 SV=2 - [E2REX6_CANLF]	1,23	1	0	1	1
F1PYX6	IQ motif containing M OS=Canis lupus familiaris GN=IQCM PE=4 SV=2 - [F1PYX6_CANLF]	1,22	1	1	1	1
J9P126	Phosphoinositide phospholipase C OS=Canis lupus familiaris GN=PLCB1 PE=4 SV=1 - [J9P126_CANLF]	1,12	1	0	1	1
E2RH23	Bromodomain and PHD finger containing 1 OS=Canis lupus familiaris GN=BRPF1 PE=4 SV=1 - [E2RH23_CANLF]	1,07	1	1	1	1
F1PL90	Phosphoinositide phospholipase C OS=Canis lupus familiaris GN=PLCB1 PE=4 SV=2 - [F1PL90_CANLF]	1,06	1	0	1	1
F6XHG2	Tubulin tyrosine ligase like 7 OS=Canis lupus familiaris GN=TTLL7 PE=4 SV=1 - [F6XHG2_CANLF]	1,02	1	0	1	1
F1PWA8	Myosin binding protein C, slow type OS=Canis lupus familiaris GN=MYBPC1 PE=4 SV=2 - [F1PWA8_CANLF]	1,02	1	0	1	1
E2RLL0	Tubulin tyrosine ligase like 7 OS=Canis lupus familiaris GN=TTLL7 PE=4 SV=2 - [E2RLL0_CANLF]	1,01	1	0	1	1
J9P1E6	Bromodomain containing 1 OS=Canis lupus familiaris GN=BRD1 PE=4 SV=1 - [J9P1E6_CANLF]	0,99	1	1	1	1
E2RT08	Transcription factor 20 OS=Canis lupus familiaris GN=TCF20 PE=4 SV=1 - [E2RT08_CANLF]	0,97	1	1	1	1
J9P2A4	Ataxin 2 OS=Canis lupus familiaris GN=ATXN2 PE=4 SV=1 - [J9P2A4_CANLF]	0,96	1	0	1	1
F6UUY0	Ataxin 2 OS=Canis lupus familiaris GN=ATXN2 PE=4 SV=1 - [F6UUY0_CANLF]	0,92	1	0	1	1

J9P9T2	Fer-1 like family member 5 OS=Canis lupus familiaris GN=FER1L5 PE=4 SV=1 - [J9P9T2_CANLF]	0,86	1	0	1	1
F6XRY2	Uncharacterized protein OS=Canis lupus familiaris GN=EEF2 PE=4 SV=1 - [F6XRY2_CANLF]	0,82	1	1	1	1
J9P9L3	Fer-1 like family member 5 OS=Canis lupus familiaris GN=FER1L5 PE=4 SV=1 - [J9P9L3_CANLF]	0,78	1	0	1	1
E2RDW0	Fer-1 like family member 5 OS=Canis lupus familiaris GN=FER1L5 PE=4 SV=2 - [E2RDW0_CANLF]	0,77	1	0	1	1
F1PFL8	Nucleoporin 214 OS=Canis lupus familiaris GN=NUP214 PE=4 SV=2 - [F1PFL8_CANLF]	0,77	1	1	1	1
F1P9S5	Plexin B2 OS=Canis lupus familiaris GN=PLXNB2 PE=4 SV=2 - [F1P9S5_CANLF]	0,76	1	1	1	1
A0A0E3ZPK4	RecBCD enzyme subunit RecB OS=Pasteurella multocida subsp. multocida OH4807 GN=recB PE=3 SV=1 - [A0A	0,74	1	1	1	1
F6XWS5	Collagen type XII alpha 1 chain OS=Canis lupus familiaris GN=COL12A1 PE=4 SV=1 - [F6XWS5_CANLF]	0,72	1	0	1	1
J9P6G0	Collagen type XII alpha 1 chain OS=Canis lupus familiaris GN=COL12A1 PE=4 SV=1 - [J9P6G0_CANLF]	0,72	1	0	1	1
F1PJ90	Ankyrin 3 OS=Canis lupus familiaris GN=ANK3 PE=4 SV=2 - [F1PJ90_CANLF]	0,67	1	0	1	1
J9P6X8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P6X8_CANLF]	0,64	1	1	1	1
J9NTT5	Myosin VC OS=Canis lupus familiaris GN=MYO5C PE=4 SV=1 - [J9NTT5_CANLF]	0,49	1	0	1	1
F1P8I8	Myosin VC OS=Canis lupus familiaris GN=MYO5C PE=4 SV=2 - [F1P8I8_CANLF]	0,46	1	0	1	1
E2RN56	Zinc finger CCCH-type containing 13 OS=Canis lupus familiaris GN=ZC3H13 PE=4 SV=2 - [E2RN56_CANLF]	0,42	1	1	1	2
F1PJ98	Ankyrin 3 OS=Canis lupus familiaris GN=ANK3 PE=4 SV=2 - [F1PJ98_CANLF]	0,27	1	0	1	1
J9P348	Proteasome endopeptidase complex OS=Canis lupus familiaris PE=3 SV=1 - [J9P348_CANLF]	13,41	1	1	1	1
E2RKI6	Achaete-scute family bHLH transcription factor 3 OS=Canis lupus familiaris GN=ASCL3 PE=4 SV=1 - [E2RKI6_CA	13,33	1	1	1	1
F1PHB6	Cystatin A OS=Canis lupus familiaris GN=CSTA PE=4 SV=2 - [F1PHB6_CANLF]	12,24	1	1	1	1
F6XMW7	Ras related GTP binding B OS=Canis lupus familiaris GN=RRAGB PE=4 SV=1 - [F6XMW7_CANLF]	9,63	1	1	1	1
A0A0E3ZMY5	NAD(P) transhydrogenase subunit alpha OS=Pasteurella multocida subsp. multocida OH4807 GN=pntA PE=3 S	7,66	1	1	1	1
J9NSK6	Uncharacterized protein OS=Canis lupus familiaris GN=DLG3 PE=4 SV=1 - [J9NSK6_CANLF]	6,95	1	1	1	1
F1PMM9	Cathepsin L1 OS=Canis lupus familiaris GN=CTSL PE=3 SV=1 - [F1PMM9_CANLF]	6,45	1	1	1	1
E2QZS8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [E2QZS8_CANLF]	5,67	1	1	1	1
F1PLM8	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Canis lupus familiaris GN=HIBCH PE=3 SV=2 - [F1PLM8_	5,24	1	0	1	3
E2RL58	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Canis lupus familiaris GN=HIBCH PE=3 SV=2 - [E2RL58_C	5,21	1	0	1	3
J9P3E6	Zinc finger protein 250 OS=Canis lupus familiaris GN=ZNF250 PE=4 SV=1 - [J9P3E6_CANLF]	4,84	1	1	1	1
F1Q067	Septin 7 OS=Canis lupus familiaris GN=SEPT7 PE=3 SV=2 - [F1Q067_CANLF]	4,69	1	1	1	1
F1PVT3	Mastermind like transcriptional coactivator 1 OS=Canis lupus familiaris GN=MAML1 PE=4 SV=2 - [F1PVT3_CAN	4,31	1	0	1	2
E2RLS3	Heat shock protein 90 alpha family class B member 1 OS=Canis lupus familiaris GN=HSP90AB1 PE=3 SV=2 - [E2	4,14	1	1	1	1
A0A0E3ZPE8	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Pasteurella multocida subsp. multocida	4,1	1	1	1	1
E2RM53	Sorting nexin family member 27 OS=Canis lupus familiaris GN=SNX27 PE=4 SV=1 - [E2RM53_CANLF]	3,87	1	1	1	1
Q9MZV5	Bone morphogenetic protein 4 (Fragment) OS=Canis lupus familiaris GN=bmp4 PE=3 SV=1 - [Q9MZV5_CANLF]	3,86	1	0	1	1
F1P6M2	Mastermind like transcriptional coactivator 1 OS=Canis lupus familiaris GN=MAML1 PE=4 SV=2 - [F1P6M2_CA	3,62	1	0	1	2
Q95LA2	Dimethylaniline monooxygenase [N-oxide-forming] 1 OS=Canis lupus familiaris GN=FMO1 PE=2 SV=3 - [FMO1_	3,38	1	1	1	1
F1PVT2	Mastermind like transcriptional coactivator 1 OS=Canis lupus familiaris GN=MAML1 PE=4 SV=2 - [F1PVT2_CAN	3,32	1	0	1	2
F1PDL1	Uncharacterized protein OS=Canis lupus familiaris GN=BMP4 PE=3 SV=1 - [F1PDL1_CANLF]	3,18	1	0	1	1
E2RNU4	DNA helicase OS=Canis lupus familiaris GN=MCM7 PE=3 SV=1 - [E2RNU4_CANLF]	3,06	1	1	1	1
F1PGH5	E2F transcription factor 5 OS=Canis lupus familiaris GN=E2F5 PE=3 SV=1 - [F1PGH5_CANLF]	2,91	1	0	1	1
O77746	cGMP-specific 3',5'-cyclic phosphodiesterase OS=Canis lupus familiaris GN=PDE5A PE=2 SV=1 - [PDE5A_CANLF]	2,89	1	1	1	1
J9P8J1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P8J1_CANLF]	2,87	1	0	1	4
E2R6D5	Carnitine palmitoyltransferase 1C OS=Canis lupus familiaris GN=CPT1C PE=3 SV=1 - [E2R6D5_CANLF]	2,62	1	1	1	1
E2RG74	Amyloid beta precursor protein binding family A member 1 OS=Canis lupus familiaris GN=APBA1 PE=4 SV=2 - [	2,61	1	0	1	1
E2RG71	Amyloid beta precursor protein binding family A member 1 OS=Canis lupus familiaris GN=APBA1 PE=4 SV=2 - [	2,54	1	0	1	1
E2R246	Cell division cycle 25B OS=Canis lupus familiaris GN=CDC25B PE=4 SV=1 - [E2R246_CANLF]	2,44	1	0	1	1
F1PJY4	MER proto-oncogene, tyrosine kinase OS=Canis lupus familiaris GN=MERTK PE=3 SV=1 - [F1PJY4_CANLF]	2,41	1	0	1	1
J9P347	MER proto-oncogene, tyrosine kinase OS=Canis lupus familiaris GN=MERTK PE=3 SV=1 - [J9P347_CANLF]	2,41	1	0	1	1
J9P5G7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P5G7_CANLF]	2,39	1	1	1	1
F1PYX3	Cell division cycle 25B OS=Canis lupus familiaris GN=CDC25B PE=4 SV=2 - [F1PYX3_CANLF]	2,29	1	0	1	1
E2R0S7	LUC7 like OS=Canis lupus familiaris GN=LUC7L PE=4 SV=2 - [E2R0S7_CANLF]	2,16	1	0	1	1
F6UQJ5	Uncharacterized protein OS=Canis lupus familiaris GN=LUC7L2 PE=4 SV=1 - [F6UQJ5_CANLF]	2,05	1	0	1	1
E2QTS3	Uncharacterized protein OS=Canis lupus familiaris GN=LUC7L2 PE=4 SV=1 - [E2QTS3_CANLF]	2,04	1	0	1	1
J9P2R1	PR/SET domain 5 OS=Canis lupus familiaris GN=PRDM5 PE=4 SV=1 - [J9P2R1_CANLF]	2	1	0	1	1
F1PKR9	MYB binding protein 1a OS=Canis lupus familiaris GN=MYBBP1A PE=4 SV=2 - [F1PKR9_CANLF]	1,99	1	0	1	1
F1PML2	Low density lipoprotein receptor OS=Canis lupus familiaris GN=LDLR PE=4 SV=2 - [F1PML2_CANLF]	1,97	1	0	1	1
J9NXB0	Low density lipoprotein receptor OS=Canis lupus familiaris GN=LDLR PE=4 SV=1 - [J9NXB0_CANLF]	1,97	1	0	1	1
S5U8I9	CUL4BY transcript 1 OS=Canis lupus familiaris PE=2 SV=1 - [S5U8I9_CANLF]	1,96	1	0	1	1
J9NRL1	Zinc finger protein 454 OS=Canis lupus familiaris GN=ZNF454 PE=4 SV=1 - [J9NRL1_CANLF]	1,77	1	0	1	1
F6UQI5	Uncharacterized protein OS=Canis lupus familiaris GN=LUC7L2 PE=4 SV=1 - [F6UQI5_CANLF]	1,75	1	0	1	1
E2RDB9	Pleckstrin homology like domain family B member 2 OS=Canis lupus familiaris GN=PHLDB2 PE=4 SV=2 - [E2RDB	1,74	1	1	1	1
J9NU42	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NU42_CANLF]	1,66	1	0	1	1
F6XRW3	Kinesin family member 1C OS=Canis lupus familiaris GN=KIF1C PE=3 SV=1 - [F6XRW3_CANLF]	1,6	1	1	1	1
E2RSL4	PR/SET domain 5 OS=Canis lupus familiaris GN=PRDM5 PE=4 SV=2 - [E2RSL4_CANLF]	1,55	1	0	1	1
S5THS2	CUL4BY transcript 2 OS=Canis lupus familiaris PE=2 SV=1 - [S5THS2_CANLF]	1,54	1	0	1	1
A0A0E3ZPQ1	Bifunctional protein PutA OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_00630 PE=3 SV=1 - [A	1,42	1	1	1	1
E2RB71	Ring finger protein 169 OS=Canis lupus familiaris GN=RNF169 PE=4 SV=1 - [E2RB71_CANLF]	1,4	1	1	1	1
F6XGX8	APC2, WNT signaling pathway regulator OS=Canis lupus familiaris GN=APC2 PE=4 SV=1 - [F6XGX8_CANLF]	1,33	1	1	1	1
F1PFK4	Par-3 family cell polarity regulator OS=Canis lupus familiaris GN=PARD3 PE=1 SV=2 - [F1PFK4_CANLF]	1,31	1	1	1	1
E2RBL8	HECT domain E3 ubiquitin protein ligase 3 OS=Canis lupus familiaris GN=HECTD3 PE=4 SV=2 - [E2RBL8_CANLF]	1,21	1	1	1	1
E2RF27	UBX domain protein 4 OS=Canis lupus familiaris GN=UBXN4 PE=4 SV=2 - [E2RF27_CANLF]	1,18	1	1	1	1
F1PZL7	Transportin 1 OS=Canis lupus familiaris GN=TNPO1 PE=4 SV=2 - [F1PZL7_CANLF]	1,17	1	1	1	1
E2RA65	Tetratricopeptide repeat domain 39C OS=Canis lupus familiaris GN=TTC39C PE=4 SV=1 - [E2RA65_CANLF]	1,15	1	0	1	4
J9NYX5	Ankyrin repeat and zinc finger domain containing 1 OS=Canis lupus familiaris GN=ANKZF1 PE=4 SV=1 - [J9NYX5_	1,11	1	0	1	1
E2RH72	Ankyrin repeat and zinc finger domain containing 1 OS=Canis lupus familiaris GN=ANKZF1 PE=4 SV=2 - [E2RH72	1,07	1	0	1	1
E2QXZ0	Pantothenate kinase 4 OS=Canis lupus familiaris GN=PANK4 PE=3 SV=2 - [E2QXZ0_CANLF]	0,78	1	1	1	1
E2RRF5	RNA binding motif protein 19 OS=Canis lupus familiaris GN=RBM19 PE=4 SV=2 - [E2RRF5_CANLF]	0,72	1	1	1	1
E2RM62	FAT atypical cadherin 2 OS=Canis lupus familiaris GN=FAT2 PE=4 SV=1 - [E2RM62_CANLF]	0,69	1	1	1	1
F1PDR4	Dynein axonemal heavy chain 9 OS=Canis lupus familiaris GN=DNAH9 PE=4 SV=2 - [F1PDR4_CANLF]	0,42	1	1	1	1
Q8WN22	DNA-dependent protein kinase catalytic subunit OS=Canis lupus familiaris GN=PRKDC PE=2 SV=1 - [PRKDC_CA	0,41	1	0	1	1
F1Q3H1	DNA-dependent protein kinase catalytic subunit OS=Canis lupus familiaris GN=PRKDC PE=3 SV=2 - [F1Q3H1_C	0,41	1	0	1	1
F1PXF9	Hemicentin 1 OS=Canis lupus familiaris GN=HMCN1 PE=4 SV=2 - [F1PXF9_CANLF]	0,39	1	1	1	2
Q56JJ8	Apolipoprotein E (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q56JJ8_CANLF]	28,3	1	0	1	1
Q6B829	Histone H4 (Fragment) OS=Canis lupus familiaris PE=3 SV=1 - [Q6B829_CANLF]	18,6	1	0	1	2
B9A1S4	Phosphatidylinositol 3-kinase regulatory subunit alpha (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [B9A1	15,47	1	1	1	2
J9NWG3	Histone H2B OS=Canis lupus familiaris GN=LOC611089 PE=3 SV=1 - [J9NWG3_CANLF]	11,9	1	0	1	4
H9GWB1	Histone H2B OS=Canis lupus familiaris GN=LOC106558265 PE=3 SV=1 - [H9GWB1_CANLF]	11,9	1	0	1	4
J9NRF4	Histone H2B OS=Canis lupus familiaris GN=HIST1H2BJ PE=3 SV=1 - [J9NRF4_CANLF]	11,9	1	0	1	4
J9P6S8	Histone H2B OS=Canis lupus familiaris GN=LOC488303 PE=3 SV=1 - [J9P6S8_CANLF]	11,9	1	0	1	4
L7N0L5	Histone H2B OS=Canis lupus familiaris GN=HIST3H2BB PE=3 SV=1 - [L7N0L5_CANLF]	11,9	1	0	1	4
F1P782	Histone H2B OS=Canis lupus familiaris PE=3 SV=2 - [F1P782_CANLF]	11,9	1	0	1	4
J9P604	Histone H2B OS=Canis lupus familiaris GN=HIST1H2BB PE=3 SV=1 - [J9P604_CANLF]	11,9	1	0	1	4
L7N0C3	Histone H2B OS=Canis lupus familiaris GN=LOC488253 PE=3 SV=1 - [L7N0C3_CANLF]	11,81	1	0	1	4
J9NS47	Histone H2B OS=Canis lupus familiaris GN=LOC106558265 PE=3 SV=1 - [J9NS47_CANLF]	11,36	1	0	1	4
J9PAN7	Histone H2B OS=Canis lupus familiaris GN=LOC100855574 PE=3 SV=1 - [J9PAN7_CANLF]	11,28	1	0	1	4

E2RNW2	Histone H2B OS=Canis lupus familiaris GN=LOC488303 PE=3 SV=1 - [E2RNW2_CANLF]	11,19	1	0	1	4
J9P086	Histone H2B OS=Canis lupus familiaris GN=LOC100855574 PE=3 SV=1 - [J9P086_CANLF]	11,19	1	0	1	4
E2RNW3	Histone H2B OS=Canis lupus familiaris GN=LOC488303 PE=3 SV=1 - [E2RNW3_CANLF]	11,11	1	0	1	4
J9NX76	Histone H2B OS=Canis lupus familiaris GN=LOC106558265 PE=3 SV=1 - [J9NX76_CANLF]	11,11	1	0	1	4
J9NZE4	Histone H2B OS=Canis lupus familiaris GN=LOC100855574 PE=3 SV=1 - [J9NZE4_CANLF]	11,11	1	0	1	4
L7N0M4	Histone H2B OS=Canis lupus familiaris GN=LOC106558265 PE=3 SV=1 - [L7N0M4_CANLF]	11,11	1	0	1	4
L7N0M5	Histone H2B OS=Canis lupus familiaris GN=LOC106558265 PE=3 SV=1 - [L7N0M5_CANLF]	11,11	1	0	1	4
J9P2Y4	Histone H2B OS=Canis lupus familiaris GN=HIST2H2BF PE=3 SV=1 - [J9P2Y4_CANLF]	11,03	1	0	1	4
J9P533	Histone H2B OS=Canis lupus familiaris GN=LOC100855574 PE=3 SV=1 - [J9P533_CANLF]	10,87	1	0	1	4
J9P8B6	Histone H2B OS=Canis lupus familiaris GN=LOC100855574 PE=3 SV=1 - [J9P8B6_CANLF]	10,87	1	0	1	4
L7N0M7	Histone H2B OS=Canis lupus familiaris GN=HIST1H2BA PE=3 SV=1 - [L7N0M7_CANLF]	10,79	1	0	1	4
J9NYU5	Histone H2B OS=Canis lupus familiaris GN=LOC100855574 PE=3 SV=1 - [J9NYU5_CANLF]	9,38	1	0	1	4
P81709	Lysozyme C, spleen isozyme OS=Canis lupus familiaris PE=1 SV=1 - [LYSC2_CANLF]	9,23	1	0	1	2
J9NTD9	Histone H2B OS=Canis lupus familiaris PE=3 SV=1 - [J9NTD9_CANLF]	8,47	1	0	1	4
L7N0L3	Histone H4 OS=Canis lupus familiaris PE=3 SV=1 - [L7N0L3_CANLF]	8,33	1	0	1	2
F1Q2K3	Olfactory receptor OS=Canis lupus familiaris GN=cOR52P3 PE=3 SV=2 - [F1Q2K3_CANLF]	8,21	1	1	1	1
G1K265	Lysozyme OS=Canis lupus familiaris GN=LYZ PE=2 SV=1 - [G1K265_CANLF]	8,11	1	0	1	2
F2Z4N2	Histone H4 OS=Canis lupus familiaris GN=HIST1H4A PE=3 SV=1 - [F2Z4N2_CANLF]	7,77	1	0	1	2
J9NRV0	Histone H4 OS=Canis lupus familiaris PE=3 SV=1 - [J9NRV0_CANLF]	7,77	1	0	1	2
Q9GK59	Na+/H+ exchanger isoform 1 (Fragment) OS=Canis lupus familiaris GN=NHE1 PE=2 SV=1 - [Q9GK59_CANLF]	7,25	1	0	1	1
J9NXA7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NXA7_CANLF]	5,84	1	0	1	1
F1PEH8	Proline-serine-threonine phosphatase interacting protein 1 OS=Canis lupus familiaris GN=PSTPIP1 PE=4 SV=2 -	5,81	1	1	1	1
F1PD15	Mitochondrial calcium uniporter OS=Canis lupus familiaris GN=MCU PE=4 SV=1 - [F1PD15_CANLF]	5,65	1	1	1	1
J9NXE7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NXE7_CANLF]	5,31	1	0	1	1
E2QVP0	Phospholipase D family member 3 OS=Canis lupus familiaris GN=PLD3 PE=4 SV=1 - [E2QVP0_CANLF]	5,31	1	1	1	1
E2RFT8	Thymocyte selection associated high mobility group box OS=Canis lupus familiaris GN=TOX PE=4 SV=1 - [E2RFT	4,94	1	1	1	1
F1PQ43	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Canis lupus familiaris GN=ANP32A PE=4 SV	4,76	1	0	1	1
F1P9Z5	Scavenger receptor class A member 3 OS=Canis lupus familiaris GN=SCARA3 PE=4 SV=2 - [F1P9Z5_CANLF]	4,66	1	1	1	1
E2R525	Rab interacting lysosomal protein OS=Canis lupus familiaris GN=RILP PE=4 SV=2 - [E2R525_CANLF]	4,63	1	1	1	1
Q8HY67	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Canis lupus familiaris GN=ANP32A PE=2 SV	4,42	1	0	1	1
E2QSS0	Interferon regulatory factor 6 OS=Canis lupus familiaris GN=IRF6 PE=3 SV=1 - [E2QSS0_CANLF]	4,33	1	0	1	1
E2R2A6	Retinoic acid receptor beta OS=Canis lupus familiaris GN=RARB PE=3 SV=1 - [E2R2A6_CANLF]	4,24	1	1	1	1
F1PUN9	Acidic nuclear phosphoprotein 32 family member B OS=Canis lupus familiaris GN=ANP32B PE=4 SV=2 - [F1PUN	4,21	1	0	1	1
J9P5D2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P5D2_CANLF]	4,2	1	0	1	1
F1PD68	Interferon regulatory factor 6 OS=Canis lupus familiaris GN=IRF6 PE=3 SV=1 - [F1PD68_CANLF]	4,2	1	0	1	1
E2QT51	Interferon-gamma-inducible GTPase IFGGC1 protein OS=Canis lupus familiaris GN=IFGGC1 PE=4 SV=2 - [E2QT5	4,06	1	1	1	1
F1PPY4	Plasminogen activator, urokinase OS=Canis lupus familiaris GN=PLAU PE=3 SV=2 - [F1PPY4_CANLF]	3,68	1	1	1	1
A0A0E3ZP69	Ribonuclease HII OS=Pasteurella multocida subsp. multocida OH4807 GN=rnhB PE=3 SV=1 - [A0A0E3ZP69_PAS	3,55	1	1	1	1
J9PAT2	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9PAT2_CANLF]	3,25	1	0	1	1
J9PAH9	Uncharacterized protein OS=Canis lupus familiaris GN=SOGA3 PE=4 SV=1 - [J9PAH9_CANLF]	3,23	1	0	1	1
E2RD03	Uncharacterized protein OS=Canis lupus familiaris GN=SOGA3 PE=4 SV=1 - [E2RD03_CANLF]	3,17	1	0	1	1
F1PX30	Heart and neural crest derivatives expressed 2 OS=Canis lupus familiaris GN=HAND2 PE=4 SV=2 - [F1PX30_CAN	3,15	1	0	1	1
O97571	C-X-C chemokine receptor type 2 OS=Canis lupus familiaris GN=CXCR2 PE=2 SV=1 - [CXCR2_CANLF]	2,81	1	0	1	1
F1PAH6	C-X-C chemokine receptor type 2 OS=Canis lupus familiaris GN=CXCR2 PE=3 SV=2 - [F1PAH6_CANLF]	2,79	1	0	1	1
F1PC37	Stabilizer of axonemal microtubules 1 OS=Canis lupus familiaris GN=SAXO1 PE=4 SV=1 - [F1PC37_CANLF]	2,74	1	0	1	1
F1PC38	Stabilizer of axonemal microtubules 1 OS=Canis lupus familiaris GN=SAXO1 PE=4 SV=1 - [F1PC38_CANLF]	2,74	1	0	1	1
E2R2B8	Uncharacterized protein OS=Canis lupus familiaris GN=ZBTB7C PE=4 SV=1 - [E2R2B8_CANLF]	2,58	1	1	1	1
E2RF44	Transcobalamin 1 OS=Canis lupus familiaris GN=TCN1 PE=4 SV=2 - [E2RF44_CANLF]	2,54	1	1	1	3
F1PVV1	ELAV-like protein OS=Canis lupus familiaris GN=ELAVL3 PE=3 SV=2 - [F1PVV1_CANLF]	2,45	1	1	1	3
E2RCC5	3-hydroxybutyrate dehydrogenase 1 OS=Canis lupus familiaris GN=BDH1 PE=3 SV=2 - [E2RCC5_CANLF]	2,33	1	1	1	1
E2RCY8	Aconitate hydratase, mitochondrial OS=Canis lupus familiaris GN=ACO2 PE=3 SV=1 - [E2RCY8_CANLF]	2,3	1	1	1	1
F6Y8N2	TBC1 domain family member 2 OS=Canis lupus familiaris GN=TBC1D2 PE=4 SV=1 - [F6Y8N2_CANLF]	2,27	1	1	1	1
O71025	Core protein VP3 OS=African horse sickness virus 6 GN=S3 PE=2 SV=1 - [VP3_AHSV6]	2,1	1	1	1	1
E2R450	Clathrin heavy chain linker domain-containing protein 1 OS=Canis lupus familiaris GN=CLHC1 PE=4 SV=2 - [E2R4	2,05	1	1	1	1
E2RNT6	DNA ligase OS=Canis lupus familiaris GN=LIG3 PE=3 SV=2 - [E2RNT6_CANLF]	2,03	1	0	1	1
J9P597	DNA ligase OS=Canis lupus familiaris GN=LIG3 PE=3 SV=1 - [J9P597_CANLF]	1,99	1	0	1	1
F1PXD6	Uncharacterized protein OS=Canis lupus familiaris GN=PRG4 PE=4 SV=2 - [F1PXD6_CANLF]	1,99	1	1	1	2
F1PXE8	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PXE8_CANLF]	1,97	1	0	1	1
E2RRQ2	Meiotic double-stranded break formation protein 1 OS=Canis lupus familiaris GN=MEI1 PE=4 SV=2 - [E2RRQ2_	1,96	1	1	1	1
J9P4P7	Fidgetin like 1 OS=Canis lupus familiaris GN=FIGNL1 PE=3 SV=1 - [J9P4P7_CANLF]	1,92	1	1	1	1
J9P9G8	Cartilage intermediate layer protein 2 OS=Canis lupus familiaris GN=CILP2 PE=4 SV=1 - [J9P9G8_CANLF]	1,87	1	0	1	1
E2QUG9	Transmembrane and tetratricopeptide repeat containing 3 OS=Canis lupus familiaris GN=TMTC3 PE=4 SV=2 - [E	1,86	1	1	1	1
E2RFL9	Salvador family WW domain containing protein 1 OS=Canis lupus familiaris GN=SAV1 PE=4 SV=2 - [E2RFL9_CAN	1,82	1	1	1	2
E2RDU7	Palladin, cytoskeletal associated protein OS=Canis lupus familiaris GN=PALLD PE=4 SV=2 - [E2RDU7_CANLF]	1,81	1	0	1	1
E2R0D5	Testis expressed 10 OS=Canis lupus familiaris GN=TEX10 PE=4 SV=1 - [E2R0D5_CANLF]	1,72	1	1	1	1
F1PID1	Sodium/hydrogen exchanger OS=Canis lupus familiaris GN=SLC9A1 PE=3 SV=2 - [F1PID1_CANLF]	1,72	1	0	1	1
E2QZ61	Uncharacterized protein OS=Canis lupus familiaris GN=ATAD3A PE=4 SV=1 - [E2QZ61_CANLF]	1,69	1	1	1	1
F1PK81	Histone deacetylase OS=Canis lupus familiaris GN=HDAC7 PE=3 SV=2 - [F1PK81_CANLF]	1,68	1	1	1	1
E2R0L7	BMP2 inducible kinase OS=Canis lupus familiaris GN=BMP2K PE=4 SV=2 - [E2R0L7_CANLF]	1,67	1	1	1	1
J9NXF7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NXF7_CANLF]	1,66	1	1	1	1
J9P970	Uncharacterized protein OS=Canis lupus familiaris GN=LOC610614 PE=4 SV=1 - [J9P970_CANLF]	1,65	1	0	1	1
F1PZ55	Palladin, cytoskeletal associated protein OS=Canis lupus familiaris GN=PALLD PE=4 SV=2 - [F1PZ55_CANLF]	1,51	1	0	1	1
P68947	Penton protein OS=Canine adenovirus serotype 1 (strain RI261) GN=L2 PE=3 SV=1 - [CAPSP_ADECR]	1,47	1	0	1	1
P87557	Penton base protein OS=Canine adenovirus serotype 2 PE=4 SV=1 - [P87557_ADEC2]	1,47	1	0	1	1
E2RCP2	Cartilage intermediate layer protein 2 OS=Canis lupus familiaris GN=CILP2 PE=4 SV=2 - [E2RCP2_CANLF]	1,47	1	0	1	1
J9P5L6	Phospholipase D family member 4 OS=Canis lupus familiaris GN=PLD4 PE=4 SV=1 - [J9P5L6_CANLF]	1,43	1	0	1	1
E2R269	Valosin containing protein interacting protein 1 OS=Canis lupus familiaris GN=VCPIP1 PE=4 SV=1 - [E2R269_CA	1,39	1	1	1	2
F1PRL4	Phospholipase D family member 4 OS=Canis lupus familiaris GN=PLD4 PE=4 SV=2 - [F1PRL4_CANLF]	1,36	1	0	1	1
F6V533	Structural maintenance of chromosomes 1B OS=Canis lupus familiaris GN=SMC1B PE=4 SV=1 - [F6V533_CANLF	1,3	1	0	1	1
F1PJH4	Uncharacterized protein OS=Canis lupus familiaris GN=LOC610614 PE=4 SV=2 - [F1PJH4_CANLF]	1,26	1	0	1	1
A0A0E3ZRM9	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_06340 PE=4 SV=1 - [A0	1,19	1	0	1	1
E2QRT5	Structural maintenance of chromosomes protein OS=Canis lupus familiaris GN=SMC1B PE=3 SV=1 - [E2QRT5_C	1,13	1	0	1	1
F1PR91	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PR91_CANLF]	1,06	1	1	1	2
E2RMT6	WD repeat domain 3 OS=Canis lupus familiaris GN=WDR3 PE=4 SV=2 - [E2RMT6_CANLF]	1,06	1	0	1	1
J9P8Y5	WD repeat domain 3 OS=Canis lupus familiaris GN=WDR3 PE=4 SV=1 - [J9P8Y5_CANLF]	1,06	1	0	1	1
E2R302	Aminopeptidase OS=Canis lupus familiaris GN=ERAP1 PE=3 SV=1 - [E2R302_CANLF]	0,96	1	1	1	1
S5THR7	OFD1 (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [S5THR7_CANLF]	0,95	1	1	1	5
F1PLN6	Tripartite motif containing 33 OS=Canis lupus familiaris GN=TRIM33 PE=4 SV=2 - [F1PLN6_CANLF]	0,9	1	0	1	1
F1Q1V0	Chromosome segregation 1 like OS=Canis lupus familiaris GN=CSE1L PE=4 SV=2 - [F1Q1V0_CANLF]	0,82	1	1	1	1
A0A0H4NDU4	VP1 OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A0H4NDU4_AHSV4]	0,61	1	0	1	1
A0A0U2DCY1	VP1 OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A0U2DCY1_AHSV8]	0,61	1	0	1	1
A0A0U2DGX2	RNA-dependent RNA polymerase OS=African horse sickness virus 7 GN=VP1 PE=4 SV=1 - [A0A0U2DGX2_AHSV	0,61	1	0	1	1
A0A0N6WIG8	VP1 OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A0N6WIG8_AHSV4]	0,61	1	0	1	1

A0A189RMV2	RNA-dependent RNA polymerase OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A189RMV2_AHSV	0,61	1	0	1	1
A0A0N7CXH2	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0N7CXH2_AHSV1]	0,61	1	0	1	1
A0A0N6WII0	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0N6WII0_AHSV1]	0,61	1	0	1	1
A0A189RN06	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RN06_AHSV6	0,61	1	0	1	1
A0A189RN02	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RN02_AHSV6	0,61	1	0	1	1
A0A0U2DHH7	VP1 OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A0U2DHH7_AHSV6]	0,61	1	0	1	1
A0A189RN23	RNA-dependent RNA polymerase OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A189RN23_AHSV8	0,61	1	0	1	1
E2RRY0	Zinc finger FYVE-type containing 16 OS=Canis lupus familiaris GN=ZFYVE16 PE=4 SV=2 - [E2RRY0_CANLF]	0,52	1	1	1	1
J9NY43	Fanconi anemia complementation group M OS=Canis lupus familiaris GN=FANCM PE=4 SV=1 - [J9NY43_CANLF]	0,4	1	0	1	1
E2RNF7	Fanconi anemia complementation group M OS=Canis lupus familiaris GN=FANCM PE=4 SV=2 - [E2RNF7_CANLF	0,39	1	0	1	1
J9P777	Fanconi anemia complementation group M OS=Canis lupus familiaris GN=FANCM PE=4 SV=1 - [J9P777_CANLF]	0,39	1	0	1	1
E2RLD7	WD repeat and FYVE domain containing 3 OS=Canis lupus familiaris GN=WDFY3 PE=4 SV=2 - [E2RLD7_CANLF]	0,37	1	0	1	1
J9PB38	WD repeat and FYVE domain containing 3 OS=Canis lupus familiaris GN=WDFY3 PE=4 SV=1 - [J9PB38_CANLF]	0,37	1	0	1	1
F1P6C6	Dynein axonemal heavy chain 5 OS=Canis lupus familiaris GN=DNAH5 PE=4 SV=2 - [F1P6C6_CANLF]	0,15	1	0	1	3
F1P6D8	Dynein axonemal heavy chain 5 OS=Canis lupus familiaris GN=DNAH5 PE=4 SV=2 - [F1P6D8_CANLF]	0,15	1	0	1	3
E2RF02	Ubiquitin protein ligase E3 component n-recognin 4 OS=Canis lupus familiaris GN=UBR4 PE=4 SV=1 - [E2RF02_	0,12	1	1	1	1
Q38QA2	Actin (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q38QA2_CANLF]	25,45	1	0	1	1
A0A0E3V486	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_05125 PE=4 SV=1 - [A0	21,69	1	1	1	1
F1Q3U1	Chromosome 8 open reading frame 46 OS=Canis lupus familiaris GN=C8orf46 PE=4 SV=2 - [F1Q3U1_CANLF]	15,27	1	1	1	2
A0A0E3ZRB3	Hypoxanthine phosphoribosyltransferase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_06285	15,08	1	1	1	1
Q95156	Olfactory receptor-like protein OLF3 OS=Canis lupus familiaris PE=3 SV=1 - [OLF3_CANLF]	9,15	1	0	1	1
F1PGN0	Olfactory receptor OS=Canis lupus familiaris GN=LOC100687207 PE=3 SV=2 - [F1PGN0_CANLF]	9,15	1	0	1	1
J9NVI1	T-cell immunoglobulin and mucin domain containing 4 OS=Canis lupus familiaris GN=TIMD4 PE=4 SV=1 - [J9NVI	8,61	1	1	1	1
F1PXI3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PXI3_CANLF]	8,26	1	1	1	31
E2RFG1	Microtubule associated protein RP/EB family member 2 OS=Canis lupus familiaris GN=MAPRE2 PE=4 SV=2 - [E2	7,9	1	1	1	1
F6UXI8	Inosine-5'-monophosphate dehydrogenase OS=Canis lupus familiaris GN=IMPDH2 PE=3 SV=1 - [F6UXI8_CANLF	7,76	1	1	1	1
A0A0E3V4H4	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08925 PE=4 SV=1 - [A0	7,19	1	1	1	1
E2RJN1	Adaptor related protein complex 3 mu 1 subunit OS=Canis lupus familiaris GN=AP3M1 PE=3 SV=1 - [E2RJN1_C	6,9	1	1	1	1
J9P426	PIH1 domain containing 2 OS=Canis lupus familiaris GN=PIH1D2 PE=4 SV=1 - [J9P426_CANLF]	6,07	1	1	1	1
E2RKJ3	Serine/threonine-protein kinase receptor OS=Canis lupus familiaris GN=ACVR1 PE=3 SV=1 - [E2RKJ3_CANLF]	5,97	1	1	1	1
J9P848	Tyrosine-protein phosphatase OS=Canis lupus familiaris GN=PTPRN2 PE=4 SV=1 - [J9P848_CANLF]	4,7	1	1	1	1
E2RFU7	Flavin-containing monooxygenase OS=Canis lupus familiaris GN=LOC478994 PE=3 SV=1 - [E2RFU7_CANLF]	3,89	1	1	1	1
A0A0E3V3F8	Uroporphyrinogen decarboxylase OS=Pasteurella multocida subsp. multocida OH4807 GN=hemE PE=3 SV=1 - [	3,67	1	1	1	1
F1PAY5	Mothers against decapentaplegic homolog OS=Canis lupus familiaris GN=SMAD4 PE=3 SV=2 - [F1PAY5_CANLF]	3,62	1	1	1	1
F1Q1E1	Lamin B2 OS=Canis lupus familiaris GN=LMNB2 PE=3 SV=2 - [F1Q1E1_CANLF]	3,34	1	1	1	2
Q2KNA0	Cytospin-A OS=Canis lupus familiaris GN=SPECC1L PE=2 SV=1 - [CYTSA_CANLF]	2,86	1	1	1	1
E2RRT2	Prospero homeobox 2 OS=Canis lupus familiaris GN=PROX2 PE=4 SV=2 - [E2RRT2_CANLF]	2,85	1	1	1	1
J9NSL9	Sciellin OS=Canis lupus familiaris GN=SCEL PE=4 SV=1 - [J9NSL9_CANLF]	2,76	1	1	1	1
E2QWJ5	PX domain containing serine/threonine kinase like OS=Canis lupus familiaris GN=PXK PE=4 SV=2 - [E2QWJ5_CA	2,75	1	0	1	1
F1PXC4	Ubiquitin specific peptidase 28 OS=Canis lupus familiaris GN=USP28 PE=3 SV=2 - [F1PXC4_CANLF]	2,73	1	0	1	1
P01874	Ig mu chain C region OS=Canis lupus familiaris PE=1 SV=1 - [IGHM_CANLF]	2,67	1	0	1	1
F1PXC1	Ubiquitin specific peptidase 28 OS=Canis lupus familiaris GN=USP28 PE=3 SV=2 - [F1PXC1_CANLF]	2,59	1	0	1	1
F1PFB3	Glutaredoxin 3 OS=Canis lupus familiaris GN=GLRX3 PE=4 SV=2 - [F1PFB3_CANLF]	2,4	1	1	1	1
J9P9L6	PX domain containing serine/threonine kinase like OS=Canis lupus familiaris GN=PXK PE=4 SV=1 - [J9P9L6_CAN	2,35	1	0	1	1
F1PEH6	NEDD4 binding protein 1 OS=Canis lupus familiaris GN=N4BP1 PE=4 SV=2 - [F1PEH6_CANLF]	2,35	1	1	1	2
J9NX93	Sodium channel protein OS=Canis lupus familiaris GN=SCN5A PE=3 SV=1 - [J9NX93_CANLF]	2,29	1	0	1	1
F1PFN4	N(alpha)-acetyltransferase 15, NatA auxiliary subunit OS=Canis lupus familiaris GN=NAA15 PE=4 SV=2 - [F1PFN	2,24	1	1	1	1
J9NTM1	Guanine monophosphate synthase OS=Canis lupus familiaris GN=GMPS PE=4 SV=1 - [J9NTM1_CANLF]	2,23	1	0	1	1
F1PQF9	Anoctamin OS=Canis lupus familiaris GN=ANO1 PE=3 SV=2 - [F1PQF9_CANLF]	2,18	1	1	1	1
F1PGU3	Sodium channel protein OS=Canis lupus familiaris GN=SCN5A PE=3 SV=2 - [F1PGU3_CANLF]	2,14	1	0	1	1
Q865W3	Sodium channel protein OS=Canis lupus familiaris GN=scn5A PE=2 SV=1 - [Q865W3_CANLF]	2,14	1	0	1	1
F1P9U2	Guanine monophosphate synthase OS=Canis lupus familiaris GN=GMPS PE=4 SV=2 - [F1P9U2_CANLF]	2,13	1	0	1	1
A0A0E3V391	Alpha-1,4 glucan phosphorylase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_00420 PE=3 SV=	1,96	1	1	1	1
F1PEB3	Uncharacterized protein OS=Canis lupus familiaris GN=TCAF2 PE=4 SV=2 - [F1PEB3_CANLF]	1,96	1	1	1	1
J9NYW6	Mov10 RISC complex RNA helicase like 1 OS=Canis lupus familiaris GN=MOV10L1 PE=4 SV=1 - [J9NYW6_CANLF	1,86	1	0	1	1
F1PU34	Cysteinyl-tRNA synthetase OS=Canis lupus familiaris GN=CARS PE=3 SV=2 - [F1PU34_CANLF]	1,81	1	1	1	1
F1P7K2	AF4/FMR2 family member 2 OS=Canis lupus familiaris GN=AFF2 PE=4 SV=2 - [F1P7K2_CANLF]	1,8	1	0	1	1
E2R1J7	Mov10 RISC complex RNA helicase like 1 OS=Canis lupus familiaris GN=MOV10L1 PE=4 SV=2 - [E2R1J7_CANLF]	1,73	1	0	1	1
F1P9B2	SWAP switching B-cell complex subunit 70 OS=Canis lupus familiaris GN=SWAP70 PE=4 SV=2 - [F1P9B2_CANLF]	1,71	1	1	1	1
J9NZK5	Lysyl oxidase OS=Canis lupus familiaris GN=LOX PE=4 SV=1 - [J9NZK5_CANLF]	1,71	1	0	1	2
F6XXW3	ClpB homolog, mitochondrial AAA ATPase chaperonin OS=Canis lupus familiaris GN=CLPB PE=4 SV=1 - [F6XXW	1,7	1	1	1	1
F1PJX3	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100688697 PE=3 SV=2 - [F1PJX3_CANLF]	1,61	1	1	1	1
E2RHQ0	Aldehyde dehydrogenase 1 family member B1 OS=Canis lupus familiaris GN=ALDH1B1 PE=3 SV=2 - [E2RHQ0_C	1,56	1	0	1	2
F1Q2T5	AF4/FMR2 family member 2 OS=Canis lupus familiaris GN=AFF2 PE=4 SV=2 - [F1Q2T5_CANLF]	1,55	1	0	1	1
J9P229	Phosphodiesterase OS=Canis lupus familiaris GN=PDE9A PE=3 SV=1 - [J9P229_CANLF]	1,5	1	0	1	1
F1PBB2	Tetratricopeptide repeat domain 3 OS=Canis lupus familiaris GN=TTC3 PE=4 SV=2 - [F1PBB2_CANLF]	1,45	1	1	1	1
F1PK98	Multiple EGF like domains 11 OS=Canis lupus familiaris GN=MEGF11 PE=4 SV=2 - [F1PK98_CANLF]	1,44	1	0	1	1
F1PJ47	Phosphodiesterase OS=Canis lupus familiaris GN=PDE9A PE=3 SV=2 - [F1PJ47_CANLF]	1,39	1	0	1	1
F1PXK3	Nidogen 1 OS=Canis lupus familiaris GN=NID1 PE=4 SV=2 - [F1PXK3_CANLF]	1,37	1	1	1	1
F1PNL7	Oxysterol-binding protein OS=Canis lupus familiaris GN=OSBPL6 PE=3 SV=2 - [F1PNL7_CANLF]	1,36	1	1	1	1
F1PK96	Multiple EGF like domains 11 OS=Canis lupus familiaris GN=MEGF11 PE=4 SV=2 - [F1PK96_CANLF]	1,32	1	0	1	1
E2RDB1	Leucine zipper protein 1 OS=Canis lupus familiaris GN=LUZP1 PE=4 SV=1 - [E2RDB1_CANLF]	1,3	1	1	1	1
F1PNK9	Cytochrome P450 family 4 subfamily B member 1 OS=Canis lupus familiaris GN=CYP4B1 PE=3 SV=2 - [F1PNK9_	1,17	1	1	1	1
F1PML1	Uncharacterized protein OS=Canis lupus familiaris GN=LOC480571 PE=3 SV=2 - [F1PML1_CANLF]	1,09	1	1	1	1
E2RHX5	FERM and PDZ domain containing 1 OS=Canis lupus familiaris GN=FRMPD1 PE=4 SV=2 - [E2RHX5_CANLF]	1,08	1	1	1	1
F1PND4	Uncharacterized protein OS=Canis lupus familiaris GN=TNRC6B PE=4 SV=2 - [F1PND4_CANLF]	1,04	1	0	1	1
F1Q4D2	Elastin microfibril interfacer 3 OS=Canis lupus familiaris GN=EMILIN3 PE=4 SV=2 - [F1Q4D2_CANLF]	1,04	1	0	1	1
F1PUV5	Rho guanine nucleotide exchange factor 37 OS=Canis lupus familiaris GN=ARHGEF37 PE=4 SV=2 - [F1PUV5_CA	1,04	1	1	1	2
E2RKX1	Interleukin 18 receptor accessory protein OS=Canis lupus familiaris GN=IL18RAP PE=4 SV=2 - [E2RKX1_CANLF]	1,03	1	1	1	1
J9NXD6	Uncharacterized protein OS=Canis lupus familiaris GN=TNRC6B PE=4 SV=1 - [J9NXD6_CANLF]	0,98	1	0	1	1
E2RR98	Elastin microfibril interfacer 3 OS=Canis lupus familiaris GN=EMILIN3 PE=4 SV=1 - [E2RR98_CANLF]	0,91	1	0	1	1
F1Q154	Carnitine palmitoyltransferase 2 OS=Canis lupus familiaris GN=CPT2 PE=3 SV=2 - [F1Q154_CANLF]	0,87	1	1	1	1
F1PLW8	CUB and Sushi multiple domains 3 OS=Canis lupus familiaris GN=CSMD3 PE=4 SV=2 - [F1PLW8_CANLF]	0,84	1	1	1	1
J9JHC8	Uncharacterized protein OS=Canis lupus familiaris GN=TNRC6B PE=4 SV=1 - [J9JHC8_CANLF]	0,81	1	0	1	1
E2R0W5	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102157092 PE=4 SV=2 - [E2R0W5_CANLF]	0,8	1	1	1	1
E2RHZ2	DNA-directed RNA polymerase subunit beta OS=Canis lupus familiaris GN=POLR3B PE=3 SV=1 - [E2RHZ2_CANL	0,79	1	1	1	1
J9NWE5	Ubinuclein 2 OS=Canis lupus familiaris GN=UBN2 PE=4 SV=1 - [J9NWE5_CANLF]	0,76	1	0	1	1
F6V8V7	Ubinuclein 2 OS=Canis lupus familiaris GN=UBN2 PE=4 SV=1 - [F6V8V7_CANLF]	0,75	1	0	1	1
F1PF36	Zinc finger homeobox 2 OS=Canis lupus familiaris GN=ZFHX2 PE=4 SV=2 - [F1PF36_CANLF]	0,7	1	1	1	1
F1PJP0	Ectonucleotide pyrophosphatase/phosphodiesterase 1 OS=Canis lupus familiaris GN=ENPP1 PE=4 SV=2 - [F1PJ	0,66	1	1	1	1
J9P3E2	Sodium channel protein OS=Canis lupus familiaris GN=SCN1A PE=3 SV=1 - [J9P3E2_CANLF]	0,64	1	0	1	1
J9P355	Ryanodine receptor 3 OS=Canis lupus familiaris GN=RYR3 PE=4 SV=1 - [J9P355_CANLF]	0,6	1	0	1	1
F1PXD7	Sodium channel protein OS=Canis lupus familiaris GN=SCN1A PE=3 SV=2 - [F1PXD7_CANLF]	0,6	1	0	1	1

F1PJL2	Ryanodine receptor 3 OS=Canis lupus familiaris GN=RYR3 PE=4 SV=2 - [F1PJL2_CANLF]	0,58	1	0	1	1
J9P7M0	Ligand dependent nuclear receptor corepressor OS=Canis lupus familiaris GN=LCOR PE=4 SV=1 - [J9P7M0_CAN	0,56	1	1	1	2
E2R8N9	WD repeat domain 87 OS=Canis lupus familiaris GN=WDR87 PE=4 SV=2 - [E2R8N9_CANLF]	0,55	1	1	1	1
F1PUQ9	Cilia and flagella associated protein 43 OS=Canis lupus familiaris GN=CFAP43 PE=4 SV=2 - [F1PUQ9_CANLF]	0,42	1	0	1	1
F1PUR0	Cilia and flagella associated protein 43 OS=Canis lupus familiaris GN=CFAP43 PE=4 SV=2 - [F1PUR0_CANLF]	0,42	1	0	1	1
J9NVH4	Cilia and flagella associated protein 43 OS=Canis lupus familiaris GN=CFAP43 PE=4 SV=1 - [J9NVH4_CANLF]	0,42	1	0	1	1
E2QWM4	Spectrin beta, non-erythrocytic 4 OS=Canis lupus familiaris GN=SPTBN4 PE=4 SV=1 - [E2QWM4_CANLF]	0,27	1	0	1	2
E2RDK8	Chromodomain helicase DNA binding protein 9 OS=Canis lupus familiaris GN=CHD9 PE=4 SV=1 - [E2RDK8_CAN	0,24	1	0	1	1
F1PWD8	Chromodomain helicase DNA binding protein 7 OS=Canis lupus familiaris GN=CHD7 PE=4 SV=2 - [F1PWD8_CAN	0,23	1	0	1	1
J9PB22	Histone H3 OS=Canis lupus familiaris GN=HIST1H3F PE=3 SV=1 - [J9PB22_CANLF]	23,53	1	1	1	1
F1Q249	Uncharacterized protein OS=Canis lupus familiaris GN=LOC106557533 PE=4 SV=2 - [F1Q249_CANLF]	14,14	1	0	1	2
Q95407	Dqb1 protein (Fragment) OS=Canis lupus familiaris GN=dqb1 PE=2 SV=1 - [Q95407_CANLF]	13,46	1	0	1	1
F1PLY9	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102155424 PE=3 SV=2 - [F1PLY9_CANLF]	12,07	1	0	1	2
F1PQN5	Cofilin 1 OS=Canis lupus familiaris GN=CFL1 PE=3 SV=2 - [F1PQN5_CANLF]	12,05	1	0	1	4
J9P0G4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P0G4_CANLF]	11,58	1	1	1	1
A0A0E3ZQI2	Shikimate 5-dehydrogenase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08475 PE=4 SV=1 -	11,07	1	1	1	1
F1Q1C8	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [F1Q1C8_CANLF]	10,36	1	0	1	4
Q95HI5	MHC Class II antigen (Fragment) OS=Canis lupus GN=Calu-DRB PE=4 SV=1 - [Q95HI5_CANLU]	10,14	1	0	1	1
J9NZQ2	Mesoderm posterior bHLH transcription factor 2 OS=Canis lupus familiaris GN=MESP2 PE=4 SV=1 - [J9NZQ2_C	9,59	1	1	1	1
O19253	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DRB PE=4 SV=1 - [O19253_CANLF]	8,86	1	0	1	1
Q30426	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DRB1 PE=4 SV=1 - [Q30426_CANLF]	8,86	1	0	1	1
O19254	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DRB PE=4 SV=1 - [O19254_CANLF]	8,86	1	0	1	1
O19249	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DQB PE=4 SV=1 - [O19249_CANLF]	8,43	1	0	1	1
E2RAM9	Sulfotransferase OS=Canis lupus familiaris GN=SULT1C4 PE=3 SV=2 - [E2RAM9_CANLF]	8,25	1	1	1	1
A0A0K0KQS3	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [A0A0K0KQS3_CANLF]	8,24	1	0	1	1
A0A0K0KPW8	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [A0A0K0KPW8_CANLF]	8,24	1	0	1	1
B2ZWI5	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [B2ZWI5_CANLF]	7,87	1	0	1	1
C4PLD2	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [C4PLD2_CANLF]	7,87	1	0	1	1
C4PLD3	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [C4PLD3_CANLF]	7,87	1	0	1	1
D8MJ29	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [D8MJ29_CANLF]	7,87	1	0	1	1
G3FMN6	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G3FMN6_CA	7,87	1	0	1	1
G5D4Z8	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D4Z8_CANLF]	7,87	1	0	1	1
G5D4Z9	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D4Z9_CANLF]	7,87	1	0	1	1
G5D500	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D500_CANLF]	7,87	1	0	1	1
G5D513	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D513_CANLF]	7,87	1	0	1	1
G5D515	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D515_CANLF]	7,87	1	0	1	1
G5D516	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D516_CANLF]	7,87	1	0	1	1
G5D517	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D517_CANLF]	7,87	1	0	1	1
G5D520	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D520_CANLF]	7,87	1	0	1	1
Q8MHR6	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q8MHR6_CANLF]	7,87	1	0	1	1
G5D537	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D537_CANLF]	7,87	1	0	1	1
Q9TQP1	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q9TQP1_CANLF]	7,87	1	0	1	1
G5D545	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G5D545_CANLF]	7,87	1	0	1	1
G8XQN5	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQN5_CANLF]	7,87	1	0	1	1
G8XQP1	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQP1_CANLF]	7,87	1	0	1	1
G8XQP2	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQP2_CANLF]	7,87	1	0	1	1
G8XQP9	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQP9_CANLF]	7,87	1	0	1	1
G8XQQ4	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQQ4_CANLF]	7,87	1	0	1	1
G8XQQ5	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQQ5_CANLF]	7,87	1	0	1	1
G8XQR0	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQR0_CANLF]	7,87	1	0	1	1
G8XQR1	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G8XQR1_CANLF]	7,87	1	0	1	1
I0CHI7	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [I0CHI7_CANLF]	7,87	1	0	1	1
I0CHI9	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [I0CHI9_CANLF]	7,87	1	0	1	1
I0CHJ0	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [I0CHJ0_CANLF]	7,87	1	0	1	1
O62926	Major histocompatability complex class II DLA-DRB1 (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1*1503	7,87	1	0	1	1
O62931	Major histocompatability complex class II DLA-DRB1 (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1*2501	7,87	1	0	1	1
O78112	MHC class II DLA-DQ beta chain b1 domain (Fragment) OS=Canis lupus familiaris GN=DLA-DQBC1 PE=4 SV=1 - [	7,87	1	0	1	1
Q19D42	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q19D42_CAN	7,87	1	0	1	1
Q1JRY8	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q1JRY8_CANLF]	7,87	1	0	1	1
Q1JRY9	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q1JRY9_CANLF]	7,87	1	0	1	1
Q2WCC8	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q2WCC8_CANLF]	7,87	1	0	1	1
Q2WCD4	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q2WCD4_CANLF]	7,87	1	0	1	1
Q30411	DLA-DR beta (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q30411_CANLF]	7,87	1	0	1	1
Q860T8	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q860T8_CAN	7,87	1	0	1	1
Q95HP3	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DQB1 PE=4 SV=1 - [Q95HP3_CANLF]	7,87	1	0	1	1
Q95HQ6	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q95HQ6_CANLF]	7,87	1	0	1	1
Q95HQ9	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q95HQ9_CANLF]	7,87	1	0	1	1
Q9BD70	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q9BD70_CAN	7,87	1	0	1	1
Q9BD81	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DQB1 PE=4 SV=1 - [Q9BD81_CA	7,87	1	0	1	1
Q9GIW0	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DQB1 PE=4 SV=1 - [Q9GIW0_CA	7,87	1	0	1	1
Q2WCD6	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q2WCD6_CANLF]	7,87	1	0	1	1
Q1AN76	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DRB1 PE=4 SV=1 - [Q1AN76_CANLF]	7,87	1	0	1	1
J7ICR9	MHC class II antigen (Fragment) OS=Canis lupus GN=DLA-DRB1 PE=4 SV=1 - [J7ICR9_CANLU]	7,87	1	0	1	1
Q8MGV3	MHC class II antigen (Fragment) OS=Canis lupus GN=DLA-DRB1 PE=4 SV=1 - [Q8MGV3_CANLU]	7,87	1	0	1	1
Q9BD66	MHC class II antigen beta chain (Fragment) OS=Canis lupus GN=DLA-DRB1 PE=4 SV=1 - [Q9BD66_CANLU]	7,87	1	0	1	1
A5HXN8	MHC class II antigen (Fragment) OS=Canis lupus GN=DLA-DRB1 PE=4 SV=1 - [A5HXN8_CANLU]	7,87	1	0	1	1
Q8MGV2	MHC class II antigen (Fragment) OS=Canis lupus GN=Calu-DRB1 PE=4 SV=1 - [Q8MGV2_CANLU]	7,87	1	0	1	1
A5HXN7	MHC class II antigen (Fragment) OS=Canis lupus GN=DLA-DRB1 PE=4 SV=1 - [A5HXN7_CANLU]	7,87	1	0	1	1
Q1AN75	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DRB1 PE=4 SV=1 - [Q1AN75_CANLF]	7,87	1	0	1	1
G3FMN7	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G3FMN7_CA	7,69	1	0	1	1
G3FMP2	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G3FMP2_CAN	7,69	1	0	1	1
G3FMP3	MHC class II antigen beta chain (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [G3FMP3_CAN	7,69	1	0	1	1
E2QZ99	BRX1, biogenesis of ribosomes OS=Canis lupus familiaris GN=BRIX1 PE=4 SV=1 - [E2QZ99_CANLF]	7,49	1	1	1	1
Q8MHQ8	MHC class II antigen (Fragment) OS=Canis lupus familiaris GN=DLA-DRB1 PE=4 SV=1 - [Q8MHQ8_CANLF]	7,14	1	0	1	1
A2SXS8	Ret proto-oncogene (Fragment) OS=Canis lupus familiaris GN=RET PE=2 SV=1 - [A2SXS8_CANLF]	6,67	1	0	1	1
F1PIJ5	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100685341 PE=4 SV=2 - [F1PIJ5_CANLF]	6,61	1	1	1	1
J9P587	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102152567 PE=4 SV=1 - [J9P587_CANLF]	6,37	1	1	1	1
F1PKR6	Ribosomal protein S16 OS=Canis lupus familiaris GN=RPS16 PE=3 SV=2 - [F1PKR6_CANLF]	5,63	1	1	1	2
J9NZA4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NZA4_CANLF]	5,62	1	1	1	1
C7G0Q9	Recombination activating gene 1 (Fragment) OS=Canis lupus GN=rag1 PE=4 SV=1 - [C7G0Q9_CANLU]	5,49	1	1	1	1
J9P5L8	Mesoderm posterior bHLH transcription factor 1 OS=Canis lupus familiaris GN=MESP1 PE=4 SV=1 - [J9P5L8_CA	5,28	1	1	1	1
F1PJS1	Tyrosine-protein kinase OS=Canis lupus familiaris GN=ZAP70 PE=3 SV=2 - [F1PJS1_CANLF]	5,25	1	1	1	1
A0A0E3V3D2	Protein DacA OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_04245 PE=3 SV=1 - [A0A0E3V3D2_	4,57	1	1	1	1

E2RCN2	Vaccinia related kinase 1 OS=Canis lupus familiaris GN=VRK1 PE=3 SV=2 - [E2RCN2_CANLF]	4,56	1	1	1	1
J9NZG4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NZG4_CANLF]	4,49	1	1	1	1
F1P8X0	Membrane palmitoylated protein 7 OS=Canis lupus familiaris GN=MPP7 PE=3 SV=2 - [F1P8X0_CANLF]	4,34	1	1	1	3
J9NXA4	FERM, ARH/RhoGEF and pleckstrin domain protein 2 OS=Canis lupus familiaris GN=FARP2 PE=4 SV=1 - [J9NXA4	4,25	1	0	1	1
E2RLI2	Angiogenic factor with G-patch and FHA domains 1 OS=Canis lupus familiaris GN=AGGF1 PE=4 SV=2 - [E2RLI2_	3,8	1	1	1	1
E2R9S2	E3 ubiquitin-protein ligase RNF168 OS=Canis lupus familiaris GN=RNF168 PE=3 SV=1 - [E2R9S2_CANLF]	3,68	1	1	1	1
J9P3Q8	Par-6 family cell polarity regulator alpha OS=Canis lupus familiaris GN=PARD6A PE=4 SV=1 - [J9P3Q8_CANLF]	3,31	1	1	1	1
E2RBH7	Uncharacterized protein OS=Canis lupus familiaris GN=NOL4 PE=4 SV=2 - [E2RBH7_CANLF]	3,13	1	1	1	1
F1PZJ9	Coiled-coil domain containing 152 OS=Canis lupus familiaris GN=CCDC152 PE=4 SV=2 - [F1PZJ9_CANLF]	3,04	1	1	1	1
E2RB31	Hypoxia up-regulated 1 OS=Canis lupus familiaris GN=HYOU1 PE=3 SV=2 - [E2RB31_CANLF]	3,01	1	1	1	1
F1PBF3	Mitogen-activated protein kinase-activated protein kinase 5 OS=Canis lupus familiaris GN=MAPKAPK5 PE=4 SV	2,96	1	1	1	1
E2QWC9	Methylcrotonoyl-CoA carboxylase 2 OS=Canis lupus familiaris GN=MCCC2 PE=4 SV=2 - [E2QWC9_CANLF]	2,84	1	1	1	1
Q30347	Integral membrane glycoprotein (Fragment) OS=Canis lupus familiaris GN=LA-DRB PE=2 SV=1 - [Q30347_CANL	2,72	1	0	1	1
Q30349	Integral membrane glycoprotein (Fragment) OS=Canis lupus familiaris GN=LA-DRB PE=2 SV=1 - [Q30349_CANL	2,72	1	0	1	1
Q30346	Integral membrane glycoprotein (Fragment) OS=Canis lupus familiaris GN=Dw1 PE=2 SV=1 - [Q30346_CANLF]	2,72	1	0	1	1
A0A140KFN7	MHC class II antigen beta chain OS=Canis lupus familiaris GN=DLA-DRB1 PE=2 SV=1 - [A0A140KFN7_CANLF]	2,63	1	0	1	1
Q5W424	MHC class II DR beta 1 OS=Canis lupus familiaris GN=DLA-DRB1 PE=3 SV=1 - [Q5W424_CANLF]	2,63	1	0	1	1
E2R9K6	Arginyl-tRNA synthetase 2, mitochondrial OS=Canis lupus familiaris GN=RARS2 PE=3 SV=2 - [E2R9K6_CANLF]	2,6	1	1	1	1
F1Q298	Glucocorticoid receptor OS=Canis lupus familiaris GN=NR3C1 PE=2 SV=2 - [F1Q298_CANLF]	2,56	1	1	1	1
E2R9U9	FERM, ARH/RhoGEF and pleckstrin domain protein 2 OS=Canis lupus familiaris GN=FARP2 PE=4 SV=2 - [E2R9U9	2,5	1	0	1	1
E2RGA9	ATP/GTP binding protein like 5 OS=Canis lupus familiaris GN=AGBL5 PE=4 SV=2 - [E2RGA9_CANLF]	2,15	1	1	1	1
J9P5Y5	Immunoglobulin superfamily DCC subclass member 4 OS=Canis lupus familiaris GN=IGDCC4 PE=4 SV=1 - [J9P5Y	2,13	1	0	1	1
J9P669	Cadherin 5 OS=Canis lupus familiaris GN=CDH5 PE=4 SV=1 - [J9P669_CANLF]	2,07	1	0	1	1
E2RE03	Cadherin 5 OS=Canis lupus familiaris GN=CDH5 PE=4 SV=2 - [E2RE03_CANLF]	2,02	1	0	1	1
J9P330	Caspase recruitment domain family member 6 OS=Canis lupus familiaris GN=CARD6 PE=4 SV=1 - [J9P330_CAN	1,96	1	0	1	1
A0A0E3ZQT4	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08625 PE=4 SV=1 - [A0	1,69	1	1	1	1
F1PQB8	Immunoglobulin superfamily DCC subclass member 4 OS=Canis lupus familiaris GN=IGDCC4 PE=4 SV=2 - [F1PQ	1,69	1	0	1	1
F1PDX5	Uncharacterized protein OS=Canis lupus familiaris GN=KIF4A PE=3 SV=2 - [F1PDX5_CANLF]	1,62	1	1	1	1
F1PIZ1	Caspase recruitment domain family member 6 OS=Canis lupus familiaris GN=CARD6 PE=4 SV=2 - [F1PIZ1_CANL	1,45	1	0	1	1
F1PBE7	Guanylate cyclase OS=Canis lupus familiaris GN=GUCY2D PE=3 SV=1 - [F1PBE7_CANLF]	1,43	1	0	1	1
F1PHK9	Laminin subunit gamma 1 OS=Canis lupus familiaris GN=LAMC1 PE=4 SV=2 - [F1PHK9_CANLF]	1,41	1	1	1	1
E2QX66	Caspase recruitment domain family member 6 OS=Canis lupus familiaris GN=CARD6 PE=4 SV=2 - [E2QX66_CAN	1,39	1	0	1	1
O19179	Retinal guanylyl cyclase 1 OS=Canis lupus familiaris GN=GUCY2D PE=2 SV=1 - [GUC2D_CANLF]	1,35	1	0	1	1
J9NXS8	Zinc finger MYM-type containing 4 OS=Canis lupus familiaris GN=ZMYM4 PE=4 SV=1 - [J9NXS8_CANLF]	1,32	1	0	1	1
E2RKG5	SR-related CTD associated factor 11 OS=Canis lupus familiaris GN=SCAF11 PE=4 SV=1 - [E2RKG5_CANLF]	1,3	1	1	1	1
E2R4F8	NADH:ubiquinone oxidoreductase core subunit S1 OS=Canis lupus familiaris GN=NDUFS1 PE=3 SV=1 - [E2R4F8_	1,24	1	0	1	1
E2RD75	NADH:ubiquinone oxidoreductase core subunit S1 OS=Canis lupus familiaris GN=NDUFS1 PE=3 SV=1 - [E2RD75_	1,22	1	0	1	1
J9NTW1	Uncharacterized protein OS=Canis lupus familiaris GN=GON4L PE=4 SV=1 - [J9NTW1_CANLF]	1,21	1	0	1	1
E2RQX5	Myosin IIIA OS=Canis lupus familiaris GN=MYO3A PE=4 SV=2 - [E2RQX5_CANLF]	1,18	1	1	1	1
F1PLF6	Proto-oncogene tyrosine-protein kinase receptor Ret OS=Canis lupus familiaris GN=RET PE=3 SV=2 - [F1PLF6_C	1,17	1	0	1	1
F1P7J3	Zinc finger MYM-type containing 4 OS=Canis lupus familiaris GN=ZMYM4 PE=4 SV=2 - [F1P7J3_CANLF]	1,12	1	0	1	1
F1PQC8	Cardiomyopathy associated 5 OS=Canis lupus familiaris GN=CMYA5 PE=4 SV=2 - [F1PQC8_CANLF]	0,56	1	1	1	1
A8C750	Thyroid adenoma-associated protein homolog OS=Canis lupus familiaris GN=THADA PE=2 SV=1 - [THADA_CAN	0,46	1	1	1	1
F1PHP9	Ectopic P-granules autophagy protein 5 homolog OS=Canis lupus familiaris GN=EPG5 PE=4 SV=2 - [F1PHP9_CA	0,39	1	1	1	1
F1PHH5	Mucin 5B, oligomeric mucus/gel-forming OS=Canis lupus familiaris GN=MUC5B PE=4 SV=2 - [F1PHH5_CANLF]	0,36	1	0	1	2
J9JHJ8	Mucin 5B, oligomeric mucus/gel-forming OS=Canis lupus familiaris GN=MUC5B PE=4 SV=1 - [J9JHJ8_CANLF]	0,35	1	0	1	2
E2RT89	Uncharacterized protein OS=Canis lupus familiaris GN=GON4L PE=4 SV=2 - [E2RT89_CANLF]	0,31	1	0	1	1
E2RFS6	Sacsin molecular chaperone OS=Canis lupus familiaris GN=SACS PE=4 SV=2 - [E2RFS6_CANLF]	0,22	1	1	1	1
Q91NH3	Antigenic glycoprotein (Fragment) OS=Mokola virus PE=4 SV=1 - [Q91NH3_MOKV]	13,08	1	0	1	1
E2RLM9	Fibroblast growth factor binding protein 1 OS=Canis lupus familiaris GN=FGFBP1 PE=4 SV=2 - [E2RLM9_CANLF]	7,45	1	1	1	1
E2QS67	Glycine receptor beta OS=Canis lupus familiaris GN=GLRB PE=3 SV=1 - [E2QS67_CANLF]	5,23	1	1	1	1
F1Q0B8	Uncharacterized protein OS=Canis lupus familiaris GN=KLK1 PE=3 SV=2 - [F1Q0B8_CANLF]	5,12	1	1	1	1
E5E503	Glycoprotein (Fragment) OS=Mokola virus GN=G PE=2 SV=1 - [E5E503_MOKV]	3,87	1	0	1	1
F1PD97	Solute carrier family 25 member 44 OS=Canis lupus familiaris GN=SLC25A44 PE=3 SV=2 - [F1PD97_CANLF]	3,51	1	1	1	2
E2QYQ8	Zinc finger C2HC-type containing 1C OS=Canis lupus familiaris GN=ZC2HC1C PE=4 SV=1 - [E2QYQ8_CANLF]	3,4	1	1	1	2
P0C572	Glycoprotein OS=Mokola virus GN=G PE=1 SV=1 - [GLYCO_MOKV]	3,26	1	0	1	1
A0A1L2C213	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [A0A1L2C213_MOKV]	3,26	1	0	1	1
R9Q7B6	Glycoprotein OS=Mokola virus PE=4 SV=1 - [R9Q7B6_MOKV]	3,26	1	0	1	1
R9Q9C4	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [R9Q9C4_MOKV]	3,26	1	0	1	1
S5DTA7	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [S5DTA7_MOKV]	3,26	1	0	1	1
S4S2B6	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [S4S2B6_MOKV]	3,26	1	0	1	1
Q83543	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [Q83543_MOKV]	3,26	1	0	1	1
F2VIE2	Glycoprotein OS=Mokola virus PE=4 SV=1 - [F2VIE2_MOKV]	3,26	1	0	1	1
R9Q7P2	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [R9Q7P2_MOKV]	3,26	1	0	1	1
S5DTB2	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [S5DTB2_MOKV]	3,26	1	0	1	1
S5DTB7	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [S5DTB7_MOKV]	3,26	1	0	1	1
B2XXZ2	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [B2XXZ2_MOKV]	3,26	1	0	1	1
A0A1L2C207	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [A0A1L2C207_MOKV]	3,26	1	0	1	1
B2XXZ7	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [B2XXZ7_MOKV]	3,26	1	0	1	1
S4S290	Glycoprotein OS=Mokola virus GN=G PE=4 SV=1 - [S4S290_MOKV]	3,26	1	0	1	1
J9NRP8	Twinfilin actin binding protein 1 OS=Canis lupus familiaris GN=TWF1 PE=4 SV=1 - [J9NRP8_CANLF]	3,14	1	0	1	1
F1PFK0	Twinfilin actin binding protein 1 OS=Canis lupus familiaris GN=TWF1 PE=4 SV=2 - [F1PFK0_CANLF]	3,08	1	0	1	1
E2RCT9	DNA polymerase epsilon subunit OS=Canis lupus familiaris GN=DNAAF2 PE=3 SV=2 - [E2RCT9_CANLF]	3,04	1	0	1	1
J9PBE8	DNA polymerase epsilon subunit OS=Canis lupus familiaris GN=DNAAF2 PE=3 SV=1 - [J9PBE8_CANLF]	2,93	1	0	1	1
A0A0E3ZRL4	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_05385 PE=4 SV=1 - [A0	2,87	1	1	1	2
F1P9V1	Frizzled-6 OS=Canis lupus familiaris GN=FZD6 PE=3 SV=1 - [F1P9V1_CANLF]	2,39	1	1	1	1
E2RR69	Deoxynucleotidyltransferase terminal interacting protein 2 OS=Canis lupus familiaris GN=DNTTIP2 PE=4 SV=2 -	2,39	1	1	1	1
F1PX27	FCH and double SH3 domains 1 OS=Canis lupus familiaris GN=FCHSD1 PE=4 SV=2 - [F1PX27_CANLF]	1,88	1	1	1	1
F6XTC9	CTD small phosphatase like 2 OS=Canis lupus familiaris GN=CTDSPL2 PE=4 SV=1 - [F6XTC9_CANLF]	1,5	1	1	1	1
E2RGV7	Cation-transporting ATPase OS=Canis lupus familiaris GN=ATP13A3 PE=3 SV=2 - [E2RGV7_CANLF]	1,47	1	0	1	1
F1PMU4	Neural cell adhesion molecule 1 OS=Canis lupus familiaris GN=NCAM1 PE=4 SV=2 - [F1PMU4_CANLF]	1,45	1	1	1	1
J9P4P2	Cation-transporting ATPase OS=Canis lupus familiaris GN=ATP13A3 PE=3 SV=1 - [J9P4P2_CANLF]	1,43	1	0	1	1
F1PER6	Membrane bound transcription factor peptidase, site 1 OS=Canis lupus familiaris GN=MBTPS1 PE=4 SV=2 - [F1	1,33	1	1	1	1
E2RJ59	Serine/threonine-protein phosphatase OS=Canis lupus familiaris GN=PPP3CB PE=3 SV=2 - [E2RJ59_CANLF]	1,15	1	0	1	1
E2RCS3	Uncharacterized protein OS=Canis lupus familiaris GN=LOC489979 PE=4 SV=2 - [E2RCS3_CANLF]	0,36	1	0	1	1
E2R030	Gremlin OS=Canis lupus familiaris GN=GREM1 PE=3 SV=1 - [E2R030_CANLF]	15,76	1	1	1	1
A0A0E3V305	DNA-directed RNA polymerase subunit omega OS=Pasteurella multocida subsp. multocida OH4807 GN=rpoZ P	14,61	1	1	1	1
E2QTV8	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=2 - [E2QTV8_CANLF]	14,56	1	1	1	1
F1Q2K0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1Q2K0_CANLF]	11,4	1	1	1	1
A0A0E3V3T5	ADP-ribose pyrophosphatase NudF OS=Pasteurella multocida subsp. multocida OH4807 GN=nudF PE=4 SV=1 -	10,34	1	1	1	1
J9P611	Olfactory receptor OS=Canis lupus familiaris GN=LOC484983 PE=3 SV=1 - [J9P611_CANLF]	7,72	1	1	1	2
A0A0E3ZRI0	Ribose import ATP-binding protein RbsA OS=Pasteurella multocida subsp. multocida OH4807 GN=rbsA PE=3 SV	5,17	1	1	1	1
E2RMX4	Cryptochrome circadian clock 1 OS=Canis lupus familiaris GN=CRY1 PE=4 SV=2 - [E2RMX4_CANLF]	4,94	1	1	1	1

J9NVZ9	Transcription factor AP-2 alpha OS=Canis lupus familiaris GN=TFAP2A PE=4 SV=1 - [J9NVZ9_CANLF]	4,41	1	0	1	1
A0A0E3V3N2	tRNA(Ile)-lysidine synthase OS=Pasteurella multocida subsp. multocida OH4807 GN=tilS PE=3 SV=1 - [A0A0E3V	4,37	1	1	1	1
F1PFJ9	Transcription factor AP-2 alpha OS=Canis lupus familiaris GN=TFAP2A PE=4 SV=2 - [F1PFJ9_CANLF]	4,33	1	0	1	1
J9P605	Mitogen-activated protein kinase kinase kinase 20 OS=Canis lupus familiaris GN=MAP3K20 PE=4 SV=1 - [J9P60	3,52	1	0	1	1
F1PIB8	RAB44, member RAS oncogene family OS=Canis lupus familiaris GN=RAB44 PE=4 SV=1 - [F1PIB8_CANLF]	3,38	1	1	1	1
F1PMK8	NADH:ubiquinone oxidoreductase complex assembly factor 6 OS=Canis lupus familiaris GN=NDUFAF6 PE=4 SV	3,29	1	1	1	2
E2R7W8	Family with sequence similarity 193 member B OS=Canis lupus familiaris GN=FAM193B PE=4 SV=2 - [E2R7W8_	2,93	1	0	1	1
E2RDJ9	Testin OS=Canis lupus familiaris GN=TES PE=4 SV=1 - [E2RDJ9_CANLF]	2,91	1	0	1	1
A0M8U6	Testin OS=Canis lupus familiaris GN=TES PE=3 SV=1 - [TES_CANLF]	2,85	1	0	1	1
F1PFX9	Testin OS=Canis lupus familiaris GN=TES PE=4 SV=1 - [F1PFX9_CANLF]	2,85	1	0	1	1
E2R9U0	Synaptotagmin like 4 OS=Canis lupus familiaris GN=SYTL4 PE=4 SV=2 - [E2R9U0_CANLF]	2,83	1	1	1	1
J9NZW2	Uncharacterized protein OS=Canis lupus familiaris GN=MICALL2 PE=4 SV=1 - [J9NZW2_CANLF]	2,8	1	0	1	1
F6XRD6	Sosondowah ankyrin repeat domain family member C OS=Canis lupus familiaris GN=SOWAHC PE=4 SV=1 - [F6X	2,79	1	0	1	1
F1PM58	Family with sequence similarity 193 member B OS=Canis lupus familiaris GN=FAM193B PE=4 SV=2 - [F1PM58_	2,56	1	0	1	1
J9P7M6	tRNA (guanine(37)-N1)-methyltransferase OS=Canis lupus familiaris GN=TRMT5 PE=3 SV=1 - [J9P7M6_CANLF]	2,42	1	0	1	1
J9P199	tRNA (guanine(37)-N1)-methyltransferase OS=Canis lupus familiaris GN=TRMT5 PE=3 SV=1 - [J9P199_CANLF]	2,41	1	0	1	1
F1PN08	tRNA (guanine(37)-N1)-methyltransferase OS=Canis lupus familiaris GN=TRMT5 PE=3 SV=2 - [F1PN08_CANLF]	2,39	1	0	1	1
F1PGZ7	Phospholipase A2 OS=Canis lupus familiaris GN=PLA2G4E PE=4 SV=1 - [F1PGZ7_CANLF]	2,36	1	1	1	1
E2RSL5	SUMO1 activating enzyme subunit 1 OS=Canis lupus familiaris GN=SAE1 PE=4 SV=2 - [E2RSL5_CANLF]	2,31	1	1	1	3
F1PHR8	Uncharacterized protein OS=Canis lupus familiaris GN=MICALL2 PE=4 SV=2 - [F1PHR8_CANLF]	2,31	1	0	1	1
E2REE9	Mitogen-activated protein kinase kinase kinase 20 OS=Canis lupus familiaris GN=MAP3K20 PE=4 SV=2 - [E2REE	2	1	0	1	1
E2RR39	Kinesin-like protein OS=Canis lupus familiaris GN=KIF3C PE=3 SV=1 - [E2RR39_CANLF]	1,76	1	0	1	1
E2RJ94	PTGES3L-AARSD1 readthrough OS=Canis lupus familiaris GN=PTGES3L-AARSD1 PE=4 SV=2 - [E2RJ94_CANLF]	1,71	1	0	1	1
E2QY99	Membrane palmitoylated protein 5 OS=Canis lupus familiaris GN=MPP5 PE=3 SV=1 - [E2QY99_CANLF]	1,63	1	1	1	1
F1PLB0	SATB homeobox 1 OS=Canis lupus familiaris GN=SATB1 PE=4 SV=2 - [F1PLB0_CANLF]	1,58	1	0	1	1
E2RME8	BCL6 corepressor OS=Canis lupus familiaris GN=BCOR PE=4 SV=2 - [E2RME8_CANLF]	1,52	1	0	1	1
A0A0E3ZSN6	Site-specific recombinase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08865 PE=4 SV=1 - [A	1,52	1	0	1	1
J9NRQ8	DNA-binding protein SATB OS=Canis lupus familiaris GN=SATB2 PE=3 SV=1 - [J9NRQ8_CANLF]	1,5	1	0	1	1
E2RME7	BCL6 corepressor OS=Canis lupus familiaris GN=BCOR PE=4 SV=2 - [E2RME7_CANLF]	1,48	1	0	1	1
F1Q2V6	DNA-binding protein SATB OS=Canis lupus familiaris GN=SATB2 PE=3 SV=2 - [F1Q2V6_CANLF]	1,44	1	0	1	1
F1PIS1	Stromal interaction molecule 1 OS=Canis lupus familiaris GN=STIM1 PE=4 SV=2 - [F1PIS1_CANLF]	1,31	1	1	1	1
J9NZQ6	Family with sequence similarity 186 member A OS=Canis lupus familiaris GN=FAM186A PE=4 SV=1 - [J9NZQ6_	1,2	1	0	1	1
E2R727	PHD finger protein 3 OS=Canis lupus familiaris GN=PHF3 PE=4 SV=1 - [E2R727_CANLF]	1,17	1	1	1	1
E2QXT4	DExH-box helicase 58 OS=Canis lupus familiaris GN=DHX58 PE=4 SV=2 - [E2QXT4_CANLF]	1,03	1	0	1	1
J9JHC0	Family with sequence similarity 186 member A OS=Canis lupus familiaris GN=FAM186A PE=4 SV=1 - [J9JHC0_C	0,99	1	0	1	1
F1PRA7	DNA topoisomerase 2 OS=Canis lupus familiaris GN=TOP2B PE=3 SV=2 - [F1PRA7_CANLF]	0,87	1	1	1	1
F1PI29	Pecanex homolog 1 OS=Canis lupus familiaris GN=PCNX1 PE=4 SV=2 - [F1PI29_CANLF]	0,87	1	1	1	1
E2QSX9	Laminin subunit beta 4 OS=Canis lupus familiaris GN=LAMB4 PE=4 SV=1 - [E2QSX9_CANLF]	0,69	1	1	1	1
F6XNI2	Phosphodiesterase 4D interacting protein OS=Canis lupus familiaris GN=PDE4DIP PE=4 SV=1 - [F6XNI2_CANLF]	0,58	1	0	1	1
J9NW79	Phosphodiesterase 4D interacting protein OS=Canis lupus familiaris GN=PDE4DIP PE=4 SV=1 - [J9NW79_CANLF	0,53	1	0	1	1
J9P2H2	ATR serine/threonine kinase OS=Canis lupus familiaris GN=ATR PE=3 SV=1 - [J9P2H2_CANLF]	0,27	1	0	1	1
E2QXA4	ATR serine/threonine kinase OS=Canis lupus familiaris GN=ATR PE=3 SV=2 - [E2QXA4_CANLF]	0,26	1	0	1	1
Q28279	cGMP-gated cation channel alpha-1 OS=Canis lupus familiaris GN=CNGA1 PE=2 SV=1 - [CNGA1_CANLF]	4,49	1	0	1	1
Q2PQH8	Glycogen debranching enzyme OS=Canis lupus familiaris GN=AGL PE=2 SV=1 - [GDE_CANLF]	1,63	1	0	1	2
E2R8G0	SNF2 histone linker PHD RING helicase OS=Canis lupus familiaris GN=SHPRH PE=4 SV=2 - [E2R8G0_CANLF]	0,36	1	1	1	1
F1PBL3	Glycogen debranching enzyme OS=Canis lupus familiaris GN=AGL PE=4 SV=2 - [F1PBL3_CANLF]	1,63	1	0	1	2
F1Q3U8	cGMP-gated cation channel alpha-1 OS=Canis lupus familiaris GN=CNGA1 PE=4 SV=2 - [F1Q3U8_CANLF]	4,68	1	0	1	1
E2RB00	STIL, centriolar assembly protein OS=Canis lupus familiaris GN=STIL PE=4 SV=2 - [E2RB00_CANLF]	0,55	1	1	1	1
J9P2P3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P2P3_CANLF]	2,3	1	0	1	1
E2R8G2	ADAM metallopeptidase with thrombospondin type 1 motif 2 OS=Canis lupus familiaris GN=ADAMTS2 PE=4 SV	0,83	1	1	1	1
E2RIH2	Calcium binding protein 39 like OS=Canis lupus familiaris GN=CAB39L PE=4 SV=2 - [E2RIH2_CANLF]	1,78	1	0	1	1
F6X6W7	Uncharacterized protein OS=Canis lupus familiaris GN=LMOD1 PE=4 SV=1 - [F6X6W7_CANLF]	7,87	1	1	1	1
F1P6U3	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102151511 PE=4 SV=2 - [F1P6U3_CANLF]	2,03	1	1	1	1
F1PZT6	Kinesin-like protein OS=Canis lupus familiaris GN=KIFC3 PE=3 SV=2 - [F1PZT6_CANLF]	2,79	1	0	1	1
F6UN94	Kinesin-like protein OS=Canis lupus familiaris GN=KIFC3 PE=3 SV=1 - [F6UN94_CANLF]	3,09	1	0	1	1
E2QXM3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2QXM3_CANLF]	4,12	1	1	1	1
E2RA01	Zinc finger protein 644 OS=Canis lupus familiaris GN=ZNF644 PE=4 SV=2 - [E2RA01_CANLF]	1,28	1	1	1	1
F1PLH1	Interleukin 12 receptor subunit beta 2 OS=Canis lupus familiaris GN=IL12RB2 PE=4 SV=2 - [F1PLH1_CANLF]	0,93	1	0	1	1
F1PNV3	Dedicator of cytokinesis 9 OS=Canis lupus familiaris GN=DOCK9 PE=3 SV=2 - [F1PNV3_CANLF]	0,97	1	1	1	1
H9GWQ7	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102153516 PE=4 SV=2 - [H9GWQ7_CANLF]	4,52	1	0	1	1
L7N0G0	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102153516 PE=4 SV=1 - [L7N0G0_CANLF]	4,21	1	0	1	1
L7N0J3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0J3_CANLF]	2,19	1	0	1	1
L7N0M1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0M1_CANLF]	1,76	1	0	1	1
Q4QYC8	Interleukin 12 receptor beta-2 OS=Canis lupus familiaris PE=2 SV=1 - [Q4QYC8_CANLF]	0,93	1	0	1	1
F1Q2S9	Synaptophysin like 2 OS=Canis lupus familiaris GN=SYPL2 PE=4 SV=1 - [F1Q2S9_CANLF]	9,96	1	1	1	1
J9NZT4	N(alpha)-acetyltransferase 15, NatA auxiliary subunit OS=Canis lupus familiaris GN=NAA15 PE=4 SV=1 - [J9NZT	2,21	1	0	1	1
F1PUH1	WD repeat domain 11 OS=Canis lupus familiaris GN=WDR11 PE=4 SV=2 - [F1PUH1_CANLF]	1,55	1	1	1	1
F1Q156	Uncharacterized protein OS=Canis lupus familiaris GN=CETN2 PE=4 SV=2 - [F1Q156_CANLF]	9,8	1	1	1	1
F1P7D2	Syntaxin binding protein 1 OS=Canis lupus familiaris GN=STXBP1 PE=3 SV=2 - [F1P7D2_CANLF]	3,21	1	0	1	1
J9NUA1	Syntaxin binding protein 1 OS=Canis lupus familiaris GN=STXBP1 PE=3 SV=1 - [J9NUA1_CANLF]	3,47	1	0	1	1
J9NTI1	Syntaxin binding protein 1 OS=Canis lupus familiaris GN=STXBP1 PE=3 SV=1 - [J9NTI1_CANLF]	3,28	1	0	1	1
J9P0P4	MGAT4 family member D OS=Canis lupus familiaris GN=MGAT4D PE=4 SV=1 - [J9P0P4_CANLF]	2,13	1	0	1	1
J9P431	MGAT4 family member D OS=Canis lupus familiaris GN=MGAT4D PE=4 SV=1 - [J9P431_CANLF]	2,03	1	0	1	1
Q98637	Outer capsid protein VP4 OS=Rotavirus A (isolate RVA/Dog/United States/Cu-1/1982/G3P5A[3]) PE=2 SV=1 - [V	1,68	1	0	1	1
Q06894	Outer capsid protein VP4 OS=Rotavirus A (isolate RVA/Dog/United States/K9/1981/G3P5A[3]) PE=2 SV=1 - [VP	1,68	1	0	1	1
B6SAL0	Outer capsid protein VP4 OS=Rotavirus A (isolate RVA/Dog/United States/K9/1981/G3P5A[3]) GN=VP4 PE=3 S	1,68	1	0	1	1
B6SAJ9	Outer capsid protein VP4 OS=Rotavirus A (isolate RVA/Dog/United States/Cu-1/1982/G3P5A[3]) GN=VP4 PE=3	1,68	1	0	1	1
F1Q4F5	Adenylosuccinate synthetase isozyme 2 OS=Canis lupus familiaris GN=ADSS PE=3 SV=2 - [F1Q4F5_CANLF]	3,95	1	1	1	1
E2RDH6	Dynein cytoplasmic 2 heavy chain 1 OS=Canis lupus familiaris GN=DYNC2H1 PE=4 SV=2 - [E2RDH6_CANLF]	0,44	1	1	1	1
J9P9G3	LY6/PLAUR domain containing 8 OS=Canis lupus familiaris GN=LYPD8 PE=4 SV=1 - [J9P9G3_CANLF]	14,53	1	1	1	2
E2RAC1	Zinc finger HIT-type containing 6 OS=Canis lupus familiaris GN=ZNHIT6 PE=4 SV=2 - [E2RAC1_CANLF]	6,41	1	1	1	1
A0A0E3ZPV7	Fumarate/nitrate reduction transcriptional regulator OS=Pasteurella multocida subsp. multocida OH4807 GN=	7,14	1	1	1	1
F1PRK7	ATP synthase mitochondrial F1 complex assembly factor 2 OS=Canis lupus familiaris GN=ATPAF2 PE=4 SV=2 - [	8,07	1	0	1	1
J9P3Y1	ATP synthase mitochondrial F1 complex assembly factor 2 OS=Canis lupus familiaris GN=ATPAF2 PE=4 SV=1 - [J	9,43	1	0	1	1
E2RAV2	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase OS=Canis lupus familiari	0,4	1	0	1	1
J9P266	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase OS=Canis lupus familiari	0,42	1	0	1	1
E2QXK2	TBC1 domain containing kinase OS=Canis lupus familiaris GN=TBCK PE=4 SV=2 - [E2QXK2_CANLF]	0,9	1	1	1	1
E2R1R4	Uncharacterized protein OS=Canis lupus familiaris GN=ATP6V1E1 PE=3 SV=1 - [E2R1R4_CANLF]	11,5	1	0	1	1
J9NUC4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NUC4_CANLF]	15,85	1	0	1	1
Q6JDG6	Spleen tyrosine kinase (Fragment) OS=Canis lupus familiaris GN=SYK PE=4 SV=1 - [Q6JDG6_CANLF]	60	1	0	1	1
A0A097ZQL4	Periostin (Fragment) OS=Canis lupus familiaris GN=POSTN PE=2 SV=1 - [A0A097ZQL4_CANLF]	17,39	1	0	1	2
A0A0E3V4W0	WecD protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_07815 PE=4 SV=1 - [A0A0E3V4W0	17,36	1	1	1	1
A0A0E3ZP41	Na(+)-translocating NADH-quinone reductase subunit E OS=Pasteurella multocida subsp. multocida OH4807 G	16,67	1	1	1	1

E2RA93	Uncharacterized protein OS=Canis lupus familiaris GN=MORN5 PE=4 SV=2 - [E2RA93_CANLF]	15,53	1	0	1	1
J9P563	Uncharacterized protein OS=Canis lupus familiaris GN=LOC102151297 PE=4 SV=1 - [J9P563_CANLF]	14,64	1	1	1	2
E2RG58	Hematopoietic prostaglandin D synthase OS=Canis lupus familiaris GN=HPGDS PE=4 SV=1 - [E2RG58_CANLF]	13,47	1	0	1	1
E5RQH2	Hematopoietic PGD synthase OS=Canis lupus familiaris GN=H-PGDS PE=2 SV=1 - [E5RQH2_CANLF]	13,07	1	0	1	1
E2R9G8	Hexosyltransferase OS=Canis lupus familiaris GN=B3GALT6 PE=3 SV=1 - [E2R9G8_CANLF]	12,7	1	1	1	2
D7PBH4	Allergen Can f 4 OS=Canis lupus familiaris PE=2 SV=1 - [D7PBH4_CANLF]	12,64	1	1	1	1
E2RMY0	Transmembrane protein 33 OS=Canis lupus familiaris GN=TMEM33 PE=4 SV=1 - [E2RMY0_CANLF]	12,55	1	0	1	2
J9NXD3	Transmembrane protein 35A OS=Canis lupus familiaris GN=TMEM35A PE=4 SV=1 - [J9NXD3_CANLF]	12,21	1	1	1	1
F1Q3N3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1Q3N3_CANLF]	11,95	1	1	1	1
A0A0E3V3V2	tRNA-specific adenosine deaminase OS=Pasteurella multocida subsp. multocida OH4807 GN=tadA PE=3 SV=1 -	11,88	1	1	1	1
E2QWK3	Dehydrogenase/reductase 7 OS=Canis lupus familiaris GN=DHRS7 PE=3 SV=1 - [E2QWK3_CANLF]	11,5	1	1	1	1
Q65954	Pre-protein VI OS=Canine adenovirus serotype 1 (strain CLL) GN=L3 PE=3 SV=1 - [CAP6_ADECC]	10,92	1	0	1	1
Q96686	Pre-protein VI OS=Canine adenovirus serotype 1 (strain RI261) GN=L3 PE=3 SV=1 - [CAP6_ADECR]	10,92	1	0	1	1
F1PFG7	Protein phosphatase 1 regulatory subunit 35 OS=Canis lupus familiaris GN=PPP1R35 PE=4 SV=1 - [F1PFG7_CAN	10,82	1	1	1	1
J9NZH5	Olfactory receptor (Fragment) OS=Canis lupus familiaris GN=OR51V1 PE=3 SV=1 - [J9NZH5_CANLF]	10,73	1	1	1	1
P87561	Protein VI OS=Canine adenovirus serotype 2 PE=4 SV=1 - [P87561_ADEC2]	10,44	1	0	1	1
E2QXR2	Tetraspanin 13 OS=Canis lupus familiaris GN=TSPAN13 PE=3 SV=1 - [E2QXR2_CANLF]	10,29	1	0	1	1
J9NY90	Uncharacterized protein OS=Canis lupus familiaris GN=MORN5 PE=4 SV=1 - [J9NY90_CANLF]	9,92	1	0	1	1
E2RM07	RIC3 acetylcholine receptor chaperone OS=Canis lupus familiaris GN=RIC3 PE=4 SV=2 - [E2RM07_CANLF]	9,76	1	1	1	1
E2RNC4	Peroxisomal biogenesis factor 19 OS=Canis lupus familiaris GN=PEX19 PE=4 SV=1 - [E2RNC4_CANLF]	9,36	1	1	1	1
E2QXX6	Aquaporin 9 OS=Canis lupus familiaris GN=AQP9 PE=3 SV=1 - [E2QXX6_CANLF]	9,15	1	1	1	1
F6X6A0	C-type lectin domain containing 11A OS=Canis lupus familiaris GN=CLEC11A PE=4 SV=1 - [F6X6A0_CANLF]	8,36	1	1	1	1
E2RBR6	Proteasome subunit beta OS=Canis lupus familiaris GN=PSMB4 PE=3 SV=1 - [E2RBR6_CANLF]	8,33	1	1	1	1
F1PWV5	Tetraspanin 13 OS=Canis lupus familiaris GN=TSPAN13 PE=3 SV=2 - [F1PWV5_CANLF]	8,27	1	0	1	1
E2R4J2	Uncharacterized protein OS=Canis lupus familiaris GN=TMPO PE=4 SV=1 - [E2R4J2_CANLF]	7,93	1	1	1	1
F1PGW8	Ankyrin repeat domain 9 OS=Canis lupus familiaris GN=ANKRD9 PE=4 SV=2 - [F1PGW8_CANLF]	7,74	1	1	1	2
E2RK90	Transmembrane protein 177 OS=Canis lupus familiaris GN=TMEM177 PE=4 SV=1 - [E2RK90_CANLF]	7,72	1	1	1	1
J9NSK2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NSK2_CANLF]	7,69	1	1	1	1
J9PAQ5	Protein S100 OS=Canis lupus familiaris GN=S100A12 PE=3 SV=1 - [J9PAQ5_CANLF]	7,61	1	0	1	1
F1CL89	Follicle-stimulating hormone receptor (Fragment) OS=Canis lupus familiaris GN=FSHR PE=3 SV=1 - [F1CL89_CA	7,39	1	0	1	2
J9P1D7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P1D7_CANLF]	7,2	1	1	1	1
F1PMK3	Protein S100 OS=Canis lupus familiaris GN=S100A12 PE=3 SV=2 - [F1PMK3_CANLF]	7,14	1	0	1	1
F1P8T1	Angiopoietin like 6 OS=Canis lupus familiaris GN=ANGPTL6 PE=4 SV=2 - [F1P8T1_CANLF]	6,85	1	1	1	1
E2RHD8	TBC1 domain family member 7 OS=Canis lupus familiaris GN=TBC1D7 PE=4 SV=2 - [E2RHD8_CANLF]	6,83	1	1	1	1
E2RBW8	Asporin OS=Canis lupus familiaris GN=ASPN PE=3 SV=1 - [E2RBW8_CANLF]	6,72	1	1	1	1
J9P8N2	Acid sensing ion channel subunit 1 OS=Canis lupus familiaris GN=ASIC1 PE=3 SV=1 - [J9P8N2_CANLF]	6,65	1	0	1	1
E2R4M9	Acid sensing ion channel subunit 1 OS=Canis lupus familiaris GN=ASIC1 PE=3 SV=1 - [E2R4M9_CANLF]	6,26	1	0	1	1
F1Q3A2	Transmembrane protease serine OS=Canis lupus familiaris GN=TMPRSS11E PE=3 SV=2 - [F1Q3A2_CANLF]	6,16	1	1	1	1
F1P6Z9	Cell adhesion molecule 1 OS=Canis lupus familiaris GN=CADM1 PE=4 SV=2 - [F1P6Z9_CANLF]	6	1	0	1	1
E2RR20	5-formyltetrahydrofolate cyclo-ligase OS=Canis lupus familiaris GN=MTHFS PE=3 SV=1 - [E2RR20_CANLF]	5,91	1	1	1	1
F1P702	Cell adhesion molecule 1 OS=Canis lupus familiaris GN=CADM1 PE=4 SV=2 - [F1P702_CANLF]	5,81	1	0	1	1
J9NXC3	Reticulophagy regulator family member 2 OS=Canis lupus familiaris GN=RETREG2 PE=4 SV=1 - [J9NXC3_CANLF]	5,75	1	0	1	1
J9P8L6	Pim-3 proto-oncogene, serine/threonine kinase OS=Canis lupus familiaris GN=PIM3 PE=4 SV=1 - [J9P8L6_CANL	5,65	1	1	1	1
J9JHX9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9JHX9_CANLF]	5,6	1	0	1	1
J9NUF3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NUF3_CANLF]	5,6	1	0	1	1
F1PTB5	Reticulophagy regulator family member 2 OS=Canis lupus familiaris GN=RETREG2 PE=4 SV=1 - [F1PTB5_CANLF]	5,52	1	0	1	1
J9NX69	Cleavage stimulation factor subunit 2 OS=Canis lupus familiaris GN=CSTF2 PE=4 SV=1 - [J9NX69_CANLF]	5,5	1	0	1	1
A0A0E3V377	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_03560 PE=4 SV=1 - [A0	5,42	1	1	1	1
E2QTQ8	Uncharacterized protein OS=Canis lupus familiaris GN=SQRDL PE=4 SV=1 - [E2QTQ8_CANLF]	5,33	1	1	1	1
F1P7M7	Cell adhesion molecule 1 OS=Canis lupus familiaris GN=CADM1 PE=4 SV=2 - [F1P7M7_CANLF]	5,26	1	0	1	1
F1PYN6	Ribonucleoprotein, PTB binding 2 OS=Canis lupus familiaris GN=RAVER2 PE=4 SV=2 - [F1PYN6_CANLF]	5,12	1	1	1	1
E2RJ41	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 OS=Canis lupus familiaris GN=P	5,08	1	1	1	1
E2RP40	Cleavage stimulation factor subunit 2 OS=Canis lupus familiaris GN=CSTF2 PE=4 SV=2 - [E2RP40_CANLF]	4,85	1	0	1	1
J9P0Y5	Transmembrane protein 225 OS=Canis lupus familiaris GN=TMEM225 PE=4 SV=1 - [J9P0Y5_CANLF]	4,82	1	1	1	1
F1PCT5	DNA polymerase nu OS=Canis lupus familiaris GN=POLN PE=4 SV=1 - [F1PCT5_CANLF]	4,76	1	0	1	1
J9NYP5	Ubiquitin conjugating enzyme E2 J2 OS=Canis lupus familiaris GN=UBE2J2 PE=3 SV=1 - [J9NYP5_CANLF]	4,63	1	1	1	1
F1PTD0	F-box and WD repeat domain containing 8 OS=Canis lupus familiaris GN=FBXW8 PE=4 SV=2 - [F1PTD0_CANLF]	4,5	1	0	1	1
E2RJ60	DEAD-box helicase 17 OS=Canis lupus familiaris GN=DDX17 PE=3 SV=2 - [E2RJ60_CANLF]	4,31	1	0	1	1
J9PAP3	Formin binding protein 1 OS=Canis lupus familiaris GN=FNBP1 PE=4 SV=1 - [J9PAP3_CANLF]	4,25	1	0	1	1
F1PM22	GTP:AMP phosphotransferase AK3, mitochondrial OS=Canis lupus familiaris GN=AK3 PE=3 SV=2 - [F1PM22_CA	4,24	1	1	1	1
F1P9I9	Carboxypeptidase OS=Canis lupus familiaris GN=CTSA PE=3 SV=1 - [F1P9I9_CANLF]	4,21	1	1	1	1
E2QX45	A-kinase anchoring protein 8 like OS=Canis lupus familiaris GN=AKAP8L PE=3 SV=2 - [E2QX45_CANLF]	4,07	1	1	1	1
E2RP13	Interferon regulatory factor 5 OS=Canis lupus familiaris GN=IRF5 PE=3 SV=2 - [E2RP13_CANLF]	4,05	1	0	1	1
J9NT77	F-box and WD repeat domain containing 8 OS=Canis lupus familiaris GN=FBXW8 PE=4 SV=1 - [J9NT77_CANLF]	3,99	1	0	1	1
J9P5P1	HDGF like 2 OS=Canis lupus familiaris GN=HDGFL2 PE=4 SV=1 - [J9P5P1_CANLF]	3,9	1	0	1	1
F1PDC8	Sine oculis binding protein homolog OS=Canis lupus familiaris GN=SOBP PE=4 SV=2 - [F1PDC8_CANLF]	3,89	1	1	1	1
F1PID8	DEAD-box helicase 17 OS=Canis lupus familiaris GN=DDX17 PE=3 SV=2 - [F1PID8_CANLF]	3,8	1	0	1	1
J9NT05	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NT05_CANLF]	3,74	1	1	1	1
F1P787	Very low density lipoprotein receptor OS=Canis lupus familiaris GN=VLDLR PE=4 SV=2 - [F1P787_CANLF]	3,67	1	0	1	1
F1PPG7	Armadillo repeat containing 3 OS=Canis lupus familiaris GN=ARMC3 PE=4 SV=2 - [F1PPG7_CANLF]	3,58	1	1	1	1
F1P783	Very low density lipoprotein receptor OS=Canis lupus familiaris GN=VLDLR PE=4 SV=2 - [F1P783_CANLF]	3,55	1	0	1	1
E2QW67	TSPY like 2 OS=Canis lupus familiaris GN=TSPYL2 PE=3 SV=2 - [E2QW67_CANLF]	3,47	1	1	1	1
E2RP14	Interferon regulatory factor 5 OS=Canis lupus familiaris GN=IRF5 PE=3 SV=2 - [E2RP14_CANLF]	3,47	1	0	1	1
E2RGE1	Ras and Rab interactor 1 OS=Canis lupus familiaris GN=RIN1 PE=4 SV=2 - [E2RGE1_CANLF]	3,18	1	1	1	1
A0A0E3V3R3	Fumarate reductase flavoprotein subunit OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_05880	3,16	1	1	1	1
F1PER9	Formin binding protein 1 OS=Canis lupus familiaris GN=FNBP1 PE=4 SV=2 - [F1PER9_CANLF]	3,09	1	0	1	1
J9NXC0	DNA polymerase nu OS=Canis lupus familiaris GN=POLN PE=4 SV=1 - [J9NXC0_CANLF]	3,01	1	0	1	1
F1Q4K4	HDGF like 2 OS=Canis lupus familiaris GN=HDGFL2 PE=4 SV=2 - [F1Q4K4_CANLF]	3	1	0	1	1
J9PBM9	Carnitine O-octanoyltransferase OS=Canis lupus familiaris GN=CROT PE=3 SV=1 - [J9PBM9_CANLF]	2,94	1	0	1	1
E2RLZ3	Carnitine O-octanoyltransferase OS=Canis lupus familiaris GN=CROT PE=3 SV=1 - [E2RLZ3_CANLF]	2,93	1	0	1	1
J9JHF4	DNA polymerase nu OS=Canis lupus familiaris GN=POLN PE=4 SV=1 - [J9JHF4_CANLF]	2,89	1	0	1	1
F1PGI5	BRCA1 associated protein OS=Canis lupus familiaris GN=BRAP PE=4 SV=2 - [F1PGI5_CANLF]	2,87	1	1	1	1
J9NZ53	Nucleoporin like 2 OS=Canis lupus familiaris GN=NUPL2 PE=4 SV=1 - [J9NZ53_CANLF]	2,86	1	1	1	1
A0A0E3V4M4	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_06745 PE=3 SV=1 - [A0	2,73	1	1	1	1
F6XHP7	Centrosomal protein 104 OS=Canis lupus familiaris GN=CEP104 PE=4 SV=1 - [F6XHP7_CANLF]	2,7	1	1	1	1
G3FJC4	Olfactory receptor OS=Canis lupus familiaris PE=3 SV=1 - [G3FJC4_CANLF]	2,61	1	0	1	1
E2RA74	Serine/threonine-protein kinase receptor OS=Canis lupus familiaris GN=BMPR1B PE=3 SV=2 - [E2RA74_CANLF]	2,59	1	1	1	1
G3FJD0	Olfactory receptor OS=Canis lupus familiaris PE=3 SV=1 - [G3FJD0_CANLF]	2,48	1	0	1	1
F1PW78	Olfactory receptor OS=Canis lupus familiaris GN=OR11H6 PE=3 SV=2 - [F1PW78_CANLF]	2,42	1	0	1	1
F1P6G8	Olfactory receptor OS=Canis lupus familiaris GN=LOC610553 PE=3 SV=1 - [F1P6G8_CANLF]	2,41	1	0	1	1
E2RB43	RNA polymerase II associated protein 3 OS=Canis lupus familiaris GN=RPAP3 PE=4 SV=1 - [E2RB43_CANLF]	2,41	1	1	1	1
E2QUA0	Structural maintenance of chromosomes 6 OS=Canis lupus familiaris GN=SMC6 PE=4 SV=1 - [E2QUA0_CANLF]	2,37	1	1	1	1
J9NZ10	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100684414 PE=3 SV=1 - [J9NZ10_CANLF]	2,3	1	1	1	1

A0A0E3ZSC1	TonB-dependent receptor, beta-barrel domain protein OS=Pasteurella multocida subsp. multocida OH4807 GN	2,28	1	1	1	1
A0A0K2CW89	Major outer capsid protein OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A0K2CW89_AHSV8]	2,27	1	0	1	1
A0A189RMU8	Major outer capsid protein OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A189RMU8_AHSV8]	2,27	1	0	1	1
A0A189RMP6	Major outer capsid protein OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A189RMP6_AHSV8]	2,27	1	0	1	1
A0A189RMU0	Major outer capsid protein OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A189RMU0_AHSV8]	2,27	1	0	1	1
A0A0N9M0B3	VP2 OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A0N9M0B3_AHSV8]	2,27	1	0	1	1
A0A0U2DCW1	VP2 OS=African horse sickness virus 8 GN=VP2 PE=4 SV=1 - [A0A0U2DCW1_AHSV8]	2,27	1	0	1	1
F1PKP6	Cytohesin 1 OS=Canis lupus familiaris GN=CYTH1 PE=4 SV=2 - [F1PKP6_CANLF]	2,25	1	1	1	1
Q8HYB7	Thyroid peroxidase OS=Canis lupus familiaris GN=TPO PE=2 SV=2 - [PERT_CANLF]	2,01	1	1	1	1
A0A0E3ZPY5	Molybdenum import ATP-binding protein ModC OS=Pasteurella multocida subsp. multocida OH4807 GN=mod	1,99	1	1	1	1
A0A0K2UX58	Phospholipase A2activating protein [Canis lupus familiaris] OS=Lepeophtheirus salmonis GN=PLAA PE=4 SV=1 -	1,88	1	1	1	1
J9P7J2	Procollagen C-endopeptidase enhancer 2 OS=Canis lupus familiaris GN=PCOLCE2 PE=4 SV=1 - [J9P7J2_CANLF]	1,88	1	0	1	1
B5LBI2	Nephroretinin 4 OS=Canis lupus familiaris GN=NPHP4 PE=2 SV=1 - [B5LBI2_CANLF]	1,82	1	0	1	1
F1PP46	PHD finger protein 2 OS=Canis lupus familiaris GN=PHF2 PE=4 SV=2 - [F1PP46_CANLF]	1,78	1	0	1	1
F1PH12	Serum response factor OS=Canis lupus familiaris GN=SRF PE=4 SV=2 - [F1PH12_CANLF]	1,77	1	1	1	1
F1PY38	Nephrocystin 4 OS=Canis lupus familiaris GN=NPHP4 PE=4 SV=2 - [F1PY38_CANLF]	1,73	1	0	1	1
J9P6K3	PHD finger protein 2 OS=Canis lupus familiaris GN=PHF2 PE=4 SV=1 - [J9P6K3_CANLF]	1,73	1	0	1	1
E2R7L9	Procollagen C-endopeptidase enhancer 2 OS=Canis lupus familiaris GN=PCOLCE2 PE=4 SV=1 - [E2R7L9_CANLF]	1,69	1	0	1	1
F1Q2U2	Chromodomain helicase DNA binding protein 1 like OS=Canis lupus familiaris GN=CHD1L PE=4 SV=2 - [F1Q2U2_	1,67	1	1	1	1
F1PHQ7	Calcium-transporting ATPase OS=Canis lupus familiaris GN=ATP2B4 PE=3 SV=2 - [F1PHQ7_CANLF]	1,58	1	1	1	1
F1P759	Membrane associated guanylate kinase, WW and PDZ domain containing 3 OS=Canis lupus familiaris GN=MAG	1,56	1	0	1	1
J9P535	Membrane associated guanylate kinase, WW and PDZ domain containing 3 OS=Canis lupus familiaris GN=MAG	1,48	1	0	1	1
F1Q129	Collagen type IV alpha 2 chain OS=Canis lupus familiaris GN=COL4A2 PE=3 SV=2 - [F1Q129_CANLF]	1,43	1	1	1	1
A0A0E3ZNI0	Pyruvate formate-lyase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_03145 PE=4 SV=1 - [A0A	1,42	1	1	1	1
E2RL01	Uncharacterized protein OS=Canis lupus familiaris GN=ACACA PE=4 SV=2 - [E2RL01_CANLF]	1,41	1	1	1	1
A0A189RMV9	RNA-dependent RNA polymerase OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A189RMV9_AHSV	1,38	1	0	1	2
A0A189RMT6	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A189RMT6_AHSV	1,38	1	0	1	2
A0A0U2DHF6	VP1 OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A0U2DHF6_AHSV8]	1,38	1	0	1	2
O70695	RNA-directed RNA polymerase OS=African horse sickness virus 9 GN=S1 PE=3 SV=1 - [RDRP_AHSV9]	1,38	1	0	1	2
A0A0H4M9Q0	RNA-dependent RNA polymerase OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A0H4M9Q0_AHSV	1,38	1	0	1	2
A0A189RMZ1	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A189RMZ1_AHSV	1,38	1	0	1	2
A0A0H4M9P0	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A0H4M9P0_AHSV	1,38	1	0	1	2
A0A189RMW1	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A189RMW1_AHS	1,38	1	0	1	2
A0A0N7CXB9	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A0N7CXB9_AHSV4	1,38	1	0	1	2
A0A0S1MMR4	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0S1MMR4_AHSV1]	1,38	1	0	1	2
A0A0N7CWH4	RNA-dependant RNA polymerase OS=African horse sickness virus 2 GN=VP1 PE=4 SV=1 - [A0A0N7CWH4_AHSV	1,38	1	0	1	2
A0A0N7CZP1	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0N7CZP1_AHSV1]	1,38	1	0	1	2
A0A189RN03	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RN03_AHSV6	1,38	1	0	1	2
A0A0N9LTY4	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A0N9LTY4_AHSV6	1,38	1	0	1	2
A0A189RMZ7	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RMZ7_AHSV	1,38	1	0	1	2
A0A189RN01	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RN01_AHSV5	1,38	1	0	1	2
A0A0N6WIG9	RNA-dependent RNA polymerase OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A0N6WIG9_AHSV	1,38	1	0	1	2
A0A191JFA6	RNA-dependent RNA polymerase OS=African horse sickness virus 9 GN=VP1 PE=4 SV=1 - [A0A191JFA6_AHSV9]	1,38	1	0	1	2
A0A0N7CWA7	RNA-dependent RNA polymerase OS=African horse sickness virus 9 GN=VP1 PE=4 SV=1 - [A0A0N7CWA7_AHSV	1,38	1	0	1	2
A0A191JF81	RNA-dependent RNA polymerase OS=African horse sickness virus 9 GN=VP1 PE=4 SV=1 - [A0A191JF81_AHSV9]	1,38	1	0	1	2
A0A0N7CWB3	RNA-dependent RNA polymerase OS=African horse sickness virus 7 GN=VP1 PE=4 SV=2 - [A0A0N7CWB3_AHSV	1,38	1	0	1	2
A0A189RN13	RNA-dependent RNA polymerase OS=African horse sickness virus 7 GN=VP1 PE=4 SV=1 - [A0A189RN13_AHSV7	1,38	1	0	1	2
A0A189RMT8	RNA-dependent RNA polymerase OS=African horse sickness virus 2 GN=VP1 PE=4 SV=1 - [A0A189RMT8_AHSV	1,38	1	0	1	2
A0A0S1NJ35	RNA-dependant RNA polymerase OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0S1NJ35_AHSV1]	1,38	1	0	1	2
A0A0P0R4M5	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0P0R4M5_AHSV1]	1,38	1	0	1	2
A0A0N7CZY0	RNA-dependent RNA polymerase OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0N7CZY0_AHSV1	1,38	1	0	1	2
A0A0S1NIK5	VP1 OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A0S1NIK5_AHSV4]	1,38	1	0	1	2
A0A189RMY3	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A189RMY3_AHSV	1,38	1	0	1	2
A0A189RMX8	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A189RMX8_AHSV	1,38	1	0	1	2
A0A189RMX9	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A189RMX9_AHSV	1,38	1	0	1	2
A0A189RMY2	RNA-dependent RNA polymerase OS=African horse sickness virus 4 GN=VP1 PE=4 SV=1 - [A0A189RMY2_AHSV	1,38	1	0	1	2
A0A0S1MMI4	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0S1MMI4_AHSV1]	1,38	1	0	1	2
A0A0P0IR13	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0P0IR13_AHSV1]	1,38	1	0	1	2
A0A0S1MMG5	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0S1MMG5_AHSV1]	1,38	1	0	1	2
A0A1V0CK12	RNA-dependant RNA polymerase OS=African horse sickness virus 1 PE=4 SV=1 - [A0A1V0CK12_AHSV1]	1,38	1	0	1	2
A0A1S6Q499	VP1 OS=African horse sickness virus 1 PE=4 SV=1 - [A0A1S6Q499_AHSV1]	1,38	1	0	1	2
A0A0S1MMZ5	VP1 OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A0S1MMZ5_AHSV1]	1,38	1	0	1	2
A0A189RMW2	RNA-dependent RNA polymerase OS=African horse sickness virus 1 GN=VP1 PE=4 SV=1 - [A0A189RMW2_AHS	1,38	1	0	1	2
A0A191JF95	RNA-dependent RNA polymerase OS=African horse sickness virus 9 GN=VP1 PE=4 SV=1 - [A0A191JF95_AHSV9]	1,38	1	0	1	2
A0A189RMZ2	RNA-dependent RNA polymerase OS=African horse sickness virus 9 GN=VP1 PE=4 SV=1 - [A0A189RMZ2_AHSV	1,38	1	0	1	2
A0A189RN11	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RN11_AHSV6	1,38	1	0	1	2
A0A189RMZ0	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RMZ0_AHSV	1,38	1	0	1	2
A0A0N7CWA1	VP1 OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A0N7CWA1_AHSV6]	1,38	1	0	1	2
A0A189RMV1	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RMV1_AHSV	1,38	1	0	1	2
A0A189RMY1	RNA-dependent RNA polymerase OS=African horse sickness virus 6 GN=VP1 PE=4 SV=1 - [A0A189RMY1_AHSV	1,38	1	0	1	2
A0A0N7FMJ0	VP1 OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A0N7FMJ0_AHSV8]	1,38	1	0	1	2
A0A189RN07	RNA-dependent RNA polymerase OS=African horse sickness virus 7 GN=VP1 PE=4 SV=1 - [A0A189RN07_AHSV7	1,38	1	0	1	2
A0A189RN20	RNA-dependent RNA polymerase OS=African horse sickness virus 7 GN=VP1 PE=4 SV=1 - [A0A189RN20_AHSV7	1,38	1	0	1	2
A0A189RMZ5	RNA-dependent RNA polymerase OS=African horse sickness virus 7 GN=VP1 PE=4 SV=1 - [A0A189RMZ5_AHSV	1,38	1	0	1	2
A0A0N9LPF7	VP1 OS=African horse sickness virus 7 GN=VP1 PE=4 SV=1 - [A0A0N9LPF7_AHSV7]	1,38	1	0	1	2
A0A189RMW9	RNA-dependent RNA polymerase OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A189RMW9_AHS	1,38	1	0	1	2
A0A189RMV0	RNA-dependent RNA polymerase OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A189RMV0_AHSV	1,38	1	0	1	2
A0A0N7CXM3	VP1 OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A0N7CXM3_AHSV3]	1,38	1	0	1	2
A0A189RMX7	RNA-dependent RNA polymerase OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A189RMX7_AHSV	1,38	1	0	1	2
A0A189RMX2	RNA-dependent RNA polymerase OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A189RMX2_AHSV	1,38	1	0	1	2
A0A0U2DGS4	VP1 OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A0U2DGS4_AHSV5]	1,38	1	0	1	2
A0A189RMU6	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMU6_AHSV	1,38	1	0	1	2
A0A189RMZ3	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMZ3_AHSV	1,38	1	0	1	2
A0A0N7CW95	VP1 OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A0N7CW95_AHSV5]	1,38	1	0	1	2
A0A189RMZ6	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMZ6_AHSV	1,38	1	0	1	2
A0A189RMX1	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMX1_AHSV	1,38	1	0	1	2
A0A189RN25	RNA-dependent RNA polymerase OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A189RN25_AHSV8	1,38	1	0	1	2
A0A189RN04	RNA-dependent RNA polymerase OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A189RN04_AHSV8	1,38	1	0	1	2
A0A189RN24	RNA-dependent RNA polymerase OS=African horse sickness virus 8 GN=VP1 PE=4 SV=1 - [A0A189RN24_AHSV8	1,38	1	0	1	2
A0A189RMW7	RNA-dependent RNA polymerase OS=African horse sickness virus 2 GN=VP1 PE=4 SV=1 - [A0A189RMW7_AHS	1,38	1	0	1	2
A0A0N7CWG8	RNA-dependent RNA polymerase OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A0N7CWG8_AHS	1,38	1	0	1	2
A0A189RN28	RNA-dependent RNA polymerase OS=African horse sickness virus 9 GN=VP1 PE=4 SV=1 - [A0A189RN28_AHSV9	1,38	1	0	1	2
A0A189RMS1	RNA-dependent RNA polymerase OS=African horse sickness virus 3 GN=VP1 PE=4 SV=1 - [A0A189RMS1_AHSV	1,38	1	0	1	2

A0A189RMY8	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMY8_AHSV	1,38	1	0	1	2
A0A189RMY9	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMY9_AHSV	1,38	1	0	1	2
A0A0U2DH27	VP1 OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A0U2DH27_AHSV5]	1,38	1	0	1	2
A0A189RMU1	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMU1_AHSV	1,38	1	0	1	2
A0A189RMX6	RNA-dependent RNA polymerase OS=African horse sickness virus 5 GN=VP1 PE=4 SV=1 - [A0A189RMX6_AHSV	1,38	1	0	1	2
J9P7W0	Coiled-coil domain containing 180 OS=Canis lupus familiaris GN=CCDC180 PE=4 SV=1 - [J9P7W0_CANLF]	1,33	1	0	1	1
A0A0E3ZPT2	Aconitate hydratase B OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_05860 PE=3 SV=1 - [A0A0	1,27	1	1	1	1
F1PHT0	La ribonucleoprotein domain family member 1 OS=Canis lupus familiaris GN=LARP1 PE=4 SV=2 - [F1PHT0_CAN	1,26	1	1	1	4
J9P224	Interleukin 1 receptor like 1 OS=Canis lupus familiaris GN=IL1RL1 PE=4 SV=1 - [J9P224_CANLF]	1,26	1	0	1	1
F1PMN6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PMN6_CANLF]	1,26	1	0	1	1
E2RBJ9	Tudor and KH domain containing OS=Canis lupus familiaris GN=TDRKH PE=4 SV=2 - [E2RBJ9_CANLF]	1,24	1	0	1	1
E2RTL2	Tubulin tyrosine ligase like 6 OS=Canis lupus familiaris GN=TTLL6 PE=4 SV=2 - [E2RTL2_CANLF]	1,24	1	1	1	1
F1PSF7	Interleukin 1 receptor like 1 OS=Canis lupus familiaris GN=IL1RL1 PE=4 SV=1 - [F1PSF7_CANLF]	1,23	1	0	1	1
F1PJ16	Coiled-coil domain containing 180 OS=Canis lupus familiaris GN=CCDC180 PE=4 SV=2 - [F1PJ16_CANLF]	1,19	1	0	1	1
J9NTK0	Transmembrane protein 94 OS=Canis lupus familiaris GN=TMEM94 PE=4 SV=1 - [J9NTK0_CANLF]	1,18	1	0	1	1
F1PD09	Transmembrane protein 94 OS=Canis lupus familiaris GN=TMEM94 PE=4 SV=2 - [F1PD09_CANLF]	1,17	1	0	1	1
J9PAM1	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAM1_CANLF]	1,17	1	0	1	1
J9P0T0	Tudor and KH domain containing OS=Canis lupus familiaris GN=TDRKH PE=4 SV=1 - [J9P0T0_CANLF]	1,16	1	0	1	1
J9NWE2	Mbt domain containing 1 OS=Canis lupus familiaris GN=MBTD1 PE=4 SV=1 - [J9NWE2_CANLF]	1,12	1	0	1	2
F6V7F8	Vacuolar protein sorting 13 homolog C OS=Canis lupus familiaris GN=VPS13C PE=4 SV=1 - [F6V7F8_CANLF]	1,03	1	1	1	1
F1PHJ2	BTB domain containing 11 OS=Canis lupus familiaris GN=BTBD11 PE=4 SV=2 - [F1PHJ2_CANLF]	0,99	1	1	1	1
E2RBZ1	Mbt domain containing 1 OS=Canis lupus familiaris GN=MBTD1 PE=4 SV=2 - [E2RBZ1_CANLF]	0,92	1	0	1	2
F1PGV0	Clathrin heavy chain OS=Canis lupus familiaris GN=CLTCL1 PE=3 SV=2 - [F1PGV0_CANLF]	0,91	1	1	1	1
E2RNJ6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [E2RNJ6_CANLF]	0,91	1	1	1	1
F1PTY4	ZFP28 zinc finger protein OS=Canis lupus familiaris GN=ZFP28 PE=3 SV=2 - [F1PTY4_CANLF]	0,87	1	0	1	1
Q5I2M8	Toll-like receptor 9 OS=Canis lupus familiaris GN=TLR9 PE=2 SV=1 - [TLR9_CANLF]	0,87	1	0	1	1
Q865B9	Toll-like receptor 9 protein OS=Canis lupus familiaris GN=TLR9 PE=2 SV=2 - [Q865B9_CANLF]	0,87	1	0	1	1
E2R8V4	Uncharacterized protein OS=Canis lupus familiaris GN=LOC478038 PE=4 SV=2 - [E2R8V4_CANLF]	0,86	1	1	1	1
E2RR85	FAT atypical cadherin 4 OS=Canis lupus familiaris GN=FAT4 PE=4 SV=2 - [E2RR85_CANLF]	0,84	1	1	1	1
J9P0I0	ZFP28 zinc finger protein OS=Canis lupus familiaris GN=ZFP28 PE=3 SV=1 - [J9P0I0_CANLF]	0,81	1	0	1	1
F1Q4D7	Uncharacterized protein OS=Canis lupus familiaris GN=DNAH12 PE=4 SV=2 - [F1Q4D7_CANLF]	0,78	1	0	1	1
F1P9F8	GRIP and coiled-coil domain containing 2 OS=Canis lupus familiaris GN=GCC2 PE=4 SV=2 - [F1P9F8_CANLF]	0,77	1	1	1	1
F1PF68	Transient receptor potential cation channel subfamily M member 3 OS=Canis lupus familiaris GN=TRPM3 PE=4	0,76	1	1	1	1
Q7YRF5	Cardiac titin (Fragment) OS=Canis lupus familiaris GN=TTN PE=2 SV=1 - [Q7YRF5_CANLF]	0,76	1	0	1	1
J9NWP4	Dedicator of cytokinesis 7 OS=Canis lupus familiaris GN=DOCK7 PE=3 SV=1 - [J9NWP4_CANLF]	0,74	1	0	1	2
F1PTH3	Chromodomain helicase DNA binding protein 6 OS=Canis lupus familiaris GN=CHD6 PE=4 SV=2 - [F1PTH3_CAN	0,74	1	0	1	1
J9P0F6	Chromodomain helicase DNA binding protein 6 OS=Canis lupus familiaris GN=CHD6 PE=4 SV=1 - [J9P0F6_CAN	0,74	1	0	1	1
E2RIX9	Family with sequence similarity 193 member A OS=Canis lupus familiaris GN=FAM193A PE=4 SV=2 - [E2RIX9_C	0,71	1	1	1	1
F1PPR3	Dedicator of cytokinesis 7 OS=Canis lupus familiaris GN=DOCK7 PE=3 SV=2 - [F1PPR3_CANLF]	0,7	1	0	1	2
J9NYC7	Uncharacterized protein OS=Canis lupus familiaris GN=DNAH12 PE=4 SV=1 - [J9NYC7_CANLF]	0,66	1	0	1	1
F1P988	Vacuolar protein sorting 13 homolog D OS=Canis lupus familiaris GN=VPS13D PE=4 SV=2 - [F1P988_CANLF]	0,66	1	0	1	1
E2RIU6	Inositol polyphosphate-4-phosphatase type I A OS=Canis lupus familiaris GN=INPP4A PE=4 SV=2 - [E2RIU6_CA	0,62	1	0	1	3
F1PAP5	Spectrin alpha, non-erythrocytic 1 OS=Canis lupus familiaris GN=SPTAN1 PE=4 SV=2 - [F1PAP5_CANLF]	0,61	1	0	1	1
J9P2H0	Spectrin alpha, non-erythrocytic 1 OS=Canis lupus familiaris GN=SPTAN1 PE=4 SV=1 - [J9P2H0_CANLF]	0,61	1	0	1	1
J9NTH2	Ankyrin 2 OS=Canis lupus familiaris GN=ANK2 PE=4 SV=1 - [J9NTH2_CANLF]	0,58	1	0	1	1
F1PE29	Shroom family member 3 OS=Canis lupus familiaris GN=SHROOM3 PE=4 SV=2 - [F1PE29_CANLF]	0,55	1	1	1	4
F1PB36	MYC binding protein 2, E3 ubiquitin protein ligase OS=Canis lupus familiaris GN=MYCBP2 PE=4 SV=2 - [F1PB36_	0,54	1	0	1	3
J9PB77	MYC binding protein 2, E3 ubiquitin protein ligase OS=Canis lupus familiaris GN=MYCBP2 PE=4 SV=1 - [J9PB77_	0,53	1	0	1	3
E2R4S1	Zinc finger homeobox 4 OS=Canis lupus familiaris GN=ZFHX4 PE=4 SV=1 - [E2R4S1_CANLF]	0,52	1	1	1	1
E2RNN1	Inositol polyphosphate-4-phosphatase type I A OS=Canis lupus familiaris GN=INPP4A PE=4 SV=2 - [E2RNN1_CA	0,5	1	0	1	3
J9NY57	Ankyrin 2 OS=Canis lupus familiaris GN=ANK2 PE=4 SV=1 - [J9NY57_CANLF]	0,4	1	0	1	1
F1P6P1	Ankyrin 2 OS=Canis lupus familiaris GN=ANK2 PE=4 SV=1 - [F1P6P1_CANLF]	0,31	1	0	1	1
F1Q262	Spen family transcriptional repressor OS=Canis lupus familiaris GN=SPEN PE=4 SV=2 - [F1Q262_CANLF]	0,24	1	1	1	1
Q6QT48	Proteasome alpha subunit type 7 (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q6QT48_CANLF]	13,89	1	0	1	1
J9P8C8	Synaptonemal complex protein 1 OS=Canis lupus familiaris GN=SYCP1 PE=4 SV=1 - [J9P8C8_CANLF]	11,07	1	0	1	2
E2RNT5	Inverted formin, FH2 and WH2 domain containing OS=Canis lupus familiaris GN=INF2 PE=4 SV=2 - [E2RNT5_CA	6,8	1	0	1	1
F1PL72	Dystrobrevin beta OS=Canis lupus familiaris GN=DTNB PE=4 SV=2 - [F1PL72_CANLF]	5,88	1	0	1	1
E2RE92	Uncharacterized protein OS=Canis lupus familiaris GN=RNF113A PE=4 SV=2 - [E2RE92_CANLF]	5,46	1	1	1	1
E2R4H4	Proteasome endopeptidase complex OS=Canis lupus familiaris GN=PSMA5 PE=3 SV=2 - [E2R4H4_CANLF]	5,46	1	1	1	2
P06940	Phosphoprotein OS=Canine distemper virus (strain Onderstepoort) GN=P/V PE=3 SV=1 - [PHOSP_CDVO]	5,33	1	0	1	1
Q77K13	Phosphoprotein P OS=Canine distemper virus (strain Onderstepoort) PE=4 SV=1 - [Q77K13_CDVO]	5,33	1	0	1	1
J9NVA0	Phosphoribosyl pyrophosphate synthetase associated protein 1 OS=Canis lupus familiaris GN=PRPSAP1 PE=4 S	5,19	1	1	1	1
J9NVX0	Coenzyme Q8A OS=Canis lupus familiaris GN=COQ8A PE=4 SV=1 - [J9NVX0_CANLF]	4,37	1	0	1	1
F6UP97	DC-STAMP domain containing 2 OS=Canis lupus familiaris GN=DCST2 PE=4 SV=1 - [F6UP97_CANLF]	4,14	1	1	1	1
E2QUB6	Epsin 3 OS=Canis lupus familiaris GN=EPN3 PE=4 SV=1 - [E2QUB6_CANLF]	4,09	1	1	1	1
F1P8R3	Villin like OS=Canis lupus familiaris GN=VILL PE=4 SV=2 - [F1P8R3_CANLF]	4,04	1	1	1	1
E2RGU8	Vasoactive intestinal peptide receptor 1 OS=Canis lupus familiaris GN=VIPR1 PE=3 SV=2 - [E2RGU8_CANLF]	3,68	1	1	1	2
F1PI91	Homer scaffolding protein 2 OS=Canis lupus familiaris GN=HOMER2 PE=4 SV=2 - [F1PI91_CANLF]	3,58	1	1	1	1
F1PXX1	EH domain containing 3 OS=Canis lupus familiaris GN=EHD3 PE=3 SV=2 - [F1PXX1_CANLF]	3,55	1	1	1	1
F1PYN7	Tumor protein p73 OS=Canis lupus familiaris GN=TP73 PE=3 SV=2 - [F1PYN7_CANLF]	3,48	1	1	1	1
E2QXA2	Coenzyme Q8A OS=Canis lupus familiaris GN=COQ8A PE=4 SV=2 - [E2QXA2_CANLF]	3,1	1	0	1	1
J9NYW3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NYW3_CANLF]	3,06	1	1	1	1
E2RDK6	Synaptonemal complex protein 1 OS=Canis lupus familiaris GN=SYCP1 PE=4 SV=2 - [E2RDK6_CANLF]	2,96	1	0	1	2
J9NX31	Synaptonemal complex protein 1 OS=Canis lupus familiaris GN=SYCP1 PE=4 SV=1 - [J9NX31_CANLF]	2,96	1	0	1	2
E2RS84	Dystrobrevin beta OS=Canis lupus familiaris GN=DTNB PE=4 SV=2 - [E2RS84_CANLF]	2,91	1	0	1	1
F1PJJ0	Rabaptin, RAB GTPase binding effector protein 2 OS=Canis lupus familiaris GN=RABEP2 PE=4 SV=2 - [F1PJJ0_CA	2,83	1	0	1	2
E2RFB0	Uncharacterized protein OS=Canis lupus familiaris GN=TRIM50 PE=4 SV=1 - [E2RFB0_CANLF]	2,46	1	1	1	1
E2RFP7	Tyrosine kinase non receptor 2 OS=Canis lupus familiaris GN=TNK2 PE=3 SV=2 - [E2RFP7_CANLF]	2,4	1	1	1	1
D6BR72	Keratin 4 OS=Canis lupus familiaris GN=KRT71 PE=2 SV=1 - [D6BR72_CANLF]	2,29	1	0	1	1
E2QUT7	Keratin 72 OS=Canis lupus familiaris GN=KRT72 PE=3 SV=2 - [E2QUT7_CANLF]	2,29	1	0	1	1
J9NXP4	Sperm specific antigen 2 OS=Canis lupus familiaris GN=SSFA2 PE=4 SV=1 - [J9NXP4_CANLF]	2,27	1	0	1	1
J9NU18	ATP binding cassette subfamily A member 9 OS=Canis lupus familiaris GN=ABCA9 PE=4 SV=1 - [J9NU18_CANLF	2,23	1	0	1	1
J9NVW2	NME/NM23 family member 8 OS=Canis lupus familiaris GN=NME8 PE=4 SV=1 - [J9NVW2_CANLF]	2,12	1	0	1	1
E2R0H3	NME/NM23 family member 8 OS=Canis lupus familiaris GN=NME8 PE=4 SV=2 - [E2R0H3_CANLF]	2,05	1	0	1	1
A0A0E3ZQ68	Bacteriophage Mu transposase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_00980 PE=4 SV=	1,93	1	0	1	1
F1PNY0	Inositol polyphosphate phosphatase like 1 OS=Canis lupus familiaris GN=INPPL1 PE=4 SV=2 - [F1PNY0_CANLF]	1,74	1	1	1	1
F1PU24	Inverted formin, FH2 and WH2 domain containing OS=Canis lupus familiaris GN=INF2 PE=4 SV=2 - [F1PU24_CA	1,6	1	0	1	1
E2RPX4	WD repeat domain 44 OS=Canis lupus familiaris GN=WDR44 PE=4 SV=2 - [E2RPX4_CANLF]	1,54	1	1	1	1
F1PFQ6	Maestro heat like repeat family member 2A OS=Canis lupus familiaris GN=MROH2A PE=4 SV=2 - [F1PFQ6_CAN	1,52	1	1	1	1
F1PHF2	Protein phosphatase 1 regulatory subunit 26 OS=Canis lupus familiaris GN=PPP1R26 PE=4 SV=2 - [F1PHF2_CAN	1,44	1	1	1	1
F1PPN9	Immunoglobulin superfamily member 1 OS=Canis lupus familiaris GN=IGSF1 PE=4 SV=2 - [F1PPN9_CANLF]	1,35	1	1	1	1
E2R490	ATP binding cassette subfamily A member 9 OS=Canis lupus familiaris GN=ABCA9 PE=4 SV=1 - [E2R490_CANLF]	1,29	1	0	1	1
J9PAE4	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PAE4_CANLF]	1,14	1	0	1	1

F1PHU6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [F1PHU6_CANLF]	1,12	1	0	1	1
J9P0F7	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P0F7_CANLF]	1,06	1	0	1	1
E2RQR8	Ubiquitin protein ligase E3 component n-recognin 3 (putative) OS=Canis lupus familiaris GN=UBR3 PE=4 SV=2 -	1,05	1	1	1	1
J9P486	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P486_CANLF]	0,75	1	1	1	1
J9P5E9	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P5E9_CANLF]	14,29	1	1	1	2
J9PBH5	Proteasome endopeptidase complex OS=Canis lupus familiaris GN=PSMA8 PE=3 SV=1 - [J9PBH5_CANLF]	13,86	1	0	1	7
J9NU62	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NU62_CANLF]	10,8	1	1	1	1
J9JHC2	Coiled-coil domain containing 167 OS=Canis lupus familiaris GN=CCDC167 PE=4 SV=1 - [J9JHC2_CANLF]	8,87	1	1	1	1
J9P0X0	LYR motif containing 1 OS=Canis lupus familiaris GN=LYRM1 PE=3 SV=1 - [J9P0X0_CANLF]	8,86	1	1	1	1
A0A0E3ZQZ9	Fatty acid metabolism regulator protein OS=Pasteurella multocida subsp. multocida OH4807 GN=fadR PE=3 SV	7,88	1	1	1	1
F1PFR3	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=SETD7 PE=3 SV=2 - [F1PFR3_CANLF]	7,65	1	1	1	1
H9GX39	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=2 - [H9GX39_CANLF]	5,58	1	1	1	1
E2R6F4	Suppressor APC domain containing 2 OS=Canis lupus familiaris GN=SAPCD2 PE=4 SV=1 - [E2R6F4_CANLF]	5,56	1	1	1	1
E2R7F2	Proteasome 26S subunit, non-ATPase 12 OS=Canis lupus familiaris GN=PSMD12 PE=4 SV=2 - [E2R7F2_CANLF]	5,28	1	0	1	1
J9JHD9	Proteasome 26S subunit, non-ATPase 12 OS=Canis lupus familiaris GN=PSMD12 PE=4 SV=1 - [J9JHD9_CANLF]	5,04	1	0	1	1
F1PN51	Basic leucine zipper nuclear factor 1 OS=Canis lupus familiaris GN=BLZF1 PE=4 SV=2 - [F1PN51_CANLF]	4,75	1	0	1	1
J9NUY0	Basic leucine zipper nuclear factor 1 OS=Canis lupus familiaris GN=BLZF1 PE=4 SV=1 - [J9NUY0_CANLF]	4,74	1	0	1	1
H9GWB6	Uncharacterized protein OS=Canis lupus familiaris GN=PPP1R7 PE=4 SV=2 - [H9GWB6_CANLF]	4,67	1	0	1	1
F1PLP6	SIL1 nucleotide exchange factor OS=Canis lupus familiaris GN=SIL1 PE=4 SV=2 - [F1PLP6_CANLF]	4,67	1	0	1	2
E2R0J4	Anthrax toxin receptor 2 OS=Canis lupus familiaris GN=ANTXR2 PE=4 SV=2 - [E2R0J4_CANLF]	4,23	1	1	1	2
Q28256	Platelet glycoprotein Ib alpha chain OS=Canis lupus familiaris GN=GP1BA PE=2 SV=2 - [GP1BA_CANLF]	3,84	1	1	1	1
E2RAF6	Acyl-coenzyme A oxidase OS=Canis lupus familiaris GN=ACOX1 PE=3 SV=1 - [E2RAF6_CANLF]	3,78	1	0	1	1
F1P668	Acyl-coenzyme A oxidase OS=Canis lupus familiaris GN=ACOX1 PE=3 SV=2 - [F1P668_CANLF]	3,78	1	0	1	1
E2RBT9	Pellino E3 ubiquitin protein ligase family member 3 OS=Canis lupus familiaris GN=PELI3 PE=4 SV=2 - [E2RBT9_C	3,6	1	0	1	1
J9NZ14	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NZ14_CANLF]	3,49	1	0	1	1
J9PAV0	Pellino E3 ubiquitin protein ligase family member 3 OS=Canis lupus familiaris GN=PELI3 PE=4 SV=1 - [J9PAV0_C	3,41	1	0	1	1
F7J212	p-selectin glycoprotein ligand-1 OS=Canis lupus familiaris GN=PSGL-1 PE=2 SV=1 - [F7J212_CANLF]	2,5	1	0	1	17
J9P6Q9	Selectin P ligand OS=Canis lupus familiaris GN=SELPLG PE=4 SV=1 - [J9P6Q9_CANLF]	2,47	1	0	1	17
F1Q4A3	Coagulation factor X OS=Canis lupus familiaris GN=F10 PE=3 SV=2 - [F1Q4A3_CANLF]	2,41	1	1	1	3
E2R5W1	Uncharacterized protein OS=Canis lupus familiaris GN=LOC482849 PE=4 SV=2 - [E2R5W1_CANLF]	2,23	1	1	1	1
E2RAU5	Stress-70 protein, mitochondrial OS=Canis lupus familiaris GN=HSPA9 PE=3 SV=1 - [E2RAU5_CANLF]	2,06	1	1	1	1
E2RJE0	Cartilage oligomeric matrix protein OS=Canis lupus familiaris GN=COMP PE=4 SV=2 - [E2RJE0_CANLF]	2,01	1	0	1	1
F1PXQ9	TNF receptor associated protein 1 OS=Canis lupus familiaris GN=TRAP1 PE=3 SV=2 - [F1PXQ9_CANLF]	1,99	1	0	1	1
J9NSW0	TNF receptor associated protein 1 OS=Canis lupus familiaris GN=TRAP1 PE=3 SV=1 - [J9NSW0_CANLF]	1,99	1	0	1	1
F6XYS8	RUN and FYVE domain containing 3 OS=Canis lupus familiaris GN=RUFY3 PE=4 SV=1 - [F6XYS8_CANLF]	1,45	1	0	1	1
F1PK46	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=NSD2 PE=4 SV=2 - [F1PK46_CANLF]	1,4	1	0	1	1
J9NUG7	Histone-lysine N-methyltransferase OS=Canis lupus familiaris GN=NSD2 PE=4 SV=1 - [J9NUG7_CANLF]	1,4	1	0	1	1
E2QWL4	B-TFIID TATA-box binding protein associated factor 1 OS=Canis lupus familiaris GN=BTAF1 PE=4 SV=2 - [E2QWL	1,12	1	1	1	1
J9NZT8	Protein phosphatase 4 regulatory subunit 3C, pseudogene OS=Canis lupus familiaris GN=PPP4R3CP PE=4 SV=1	0,89	1	0	1	1
E2RT85	Collagen type XIV alpha 1 chain OS=Canis lupus familiaris GN=COL14A1 PE=4 SV=2 - [E2RT85_CANLF]	0,79	1	1	1	2
F6Y2P4	Phospholipid-transporting ATPase OS=Canis lupus familiaris GN=ATP11B PE=3 SV=1 - [F6Y2P4_CANLF]	0,73	1	1	1	1
F6Y5E4	Centrosomal protein 131 OS=Canis lupus familiaris GN=CEP131 PE=4 SV=1 - [F6Y5E4_CANLF]	0,74	1	1	1	1
J9P9K1	Forkhead box D3 OS=Canis lupus familiaris GN=FOXD3 PE=4 SV=1 - [J9P9K1_CANLF]	8,11	1	0	1	5
F6USR8	Forkhead box D3 OS=Canis lupus familiaris GN=FOXD3 PE=4 SV=1 - [F6USR8_CANLF]	6,83	1	0	1	5
E2R822	USH1 protein network component harmonin binding protein 1 OS=Canis lupus familiaris GN=USHBP1 PE=4 SV=	1,56	1	1	1	1
F1PPT8	LON peptidase N-terminal domain and ring finger 2 OS=Canis lupus familiaris GN=LONRF2 PE=4 SV=2 - [F1PPT8	2,44	1	1	1	1
F1PKA7	Interferon regulatory factor 4 OS=Canis lupus familiaris GN=IRF4 PE=3 SV=2 - [F1PKA7_CANLF]	4,63	1	1	1	1
F1PHZ7	CUB and Sushi multiple domains 2 OS=Canis lupus familiaris GN=CSMD2 PE=4 SV=2 - [F1PHZ7_CANLF]	0,69	1	0	1	2
E2R911	Uncharacterized protein OS=Canis lupus familiaris GN=TAF9 PE=4 SV=2 - [E2R911_CANLF]	5,28	1	1	1	1
E2R1Y6	Secreted phosphoprotein 1 OS=Canis lupus familiaris GN=SPP1 PE=4 SV=2 - [E2R1Y6_CANLF]	7,58	1	0	1	2
Q6F3J0	Nuclear factor NF-kappa-B p105 subunit OS=Canis lupus familiaris GN=NFKB1 PE=2 SV=2 - [NFKB1_CANLF]	2,06	1	0	1	1
A0A0A0MPC3	Nuclear factor NF-kappa-B p105 subunit OS=Canis lupus familiaris GN=NFKB1 PE=4 SV=1 - [A0A0A0MPC3_CAN	2	1	0	1	1
A1XFH3	NFKB1 (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [A1XFH3_CANLF]	26,32	1	0	1	1
F1PB94	Mitochondrial ribosomal protein L4 OS=Canis lupus familiaris GN=MRPL4 PE=3 SV=2 - [F1PB94_CANLF]	10,2	1	1	1	1
J9NX42	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NX42_CANLF]	13,66	1	1	1	1
J9PBH2	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9PBH2_CANLF]	5,22	1	1	1	1
F6UMY5	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F6UMY5_CANLF]	4,87	1	1	1	1
Q95LE9	GAPDH (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q95LE9_CANLF]	31,88	1	0	1	2
Q9TV07	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [Q9TV07_CANL	20	1	0	1	2
Q0QET4	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Canis lupus familiaris GN=GAPDH PE=2 SV=1 - [Q	9,82	1	0	1	2
A0A0A0WE41	Receptor tyrosine-protein kinase erbB-2 (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [A0A0A0WE41_CAN	7,97	1	0	1	1
J9NZ39	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9NZ39_CANLF]	6,77	1	0	1	2
E2RNJ4	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris PE=3 SV=2 - [E2RNJ4_CANLF]	6,63	1	0	1	2
E2RNN4	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [E2RNN4_CANLF]	6,61	1	0	1	2
F1PFN3	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris GN=LOC106558132 PE=3 SV=2 - [F1PFN	6,61	1	0	1	2
L7N0H7	Glyceraldehyde-3-phosphate dehydrogenase OS=Canis lupus familiaris GN=LOC100683724 PE=3 SV=1 - [L7N0	6,61	1	0	1	2
J9P5S8	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Canis lupus familiaris GN=ENTPD5 PE=3 SV=1 - [J9P5S8	5,94	1	1	1	1
A0A060PY73	ERBB2 protein (Fragment) OS=Canis lupus familiaris GN=ERBB2 PE=2 SV=1 - [A0A060PY73_CANLF]	5,01	1	0	1	1
J9PBA3	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [J9PBA3_CANLF]	4,69	1	0	1	2
A0A0E3ZSG5	Lysophospholipase L2 OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_08095 PE=4 SV=1 - [A0A0	4,32	1	1	1	2
F1PPL9	Uncharacterized protein OS=Canis lupus familiaris GN=C1QTNF3 PE=4 SV=2 - [F1PPL9_CANLF]	4,08	1	1	1	3
J9P366	Ganglioside induced differentiation associated protein 2 OS=Canis lupus familiaris GN=GDAP2 PE=4 SV=1 - [J9P	4,03	1	0	1	1
E2RCF0	Ganglioside induced differentiation associated protein 2 OS=Canis lupus familiaris GN=GDAP2 PE=4 SV=1 - [E2	4,02	1	0	1	1
E2RBI4	Intermediate filament family orphan 1 OS=Canis lupus familiaris GN=IFFO1 PE=4 SV=1 - [E2RBI4_CANLF]	3,37	1	1	1	1
J9NXE8	Zinc finger protein 541 OS=Canis lupus familiaris GN=ZNF541 PE=4 SV=1 - [J9NXE8_CANLF]	2,87	1	0	1	1
E2RSC6	Semaphorin 6D OS=Canis lupus familiaris GN=SEMA6D PE=3 SV=2 - [E2RSC6_CANLF]	2,49	1	1	1	1
F1PNN3	Zinc finger protein 541 OS=Canis lupus familiaris GN=ZNF541 PE=4 SV=2 - [F1PNN3_CANLF]	2,21	1	0	1	1
J9NY16	Zinc finger protein 541 OS=Canis lupus familiaris GN=ZNF541 PE=4 SV=1 - [J9NY16_CANLF]	2,18	1	0	1	1
J9NYD8	Zinc finger protein 541 OS=Canis lupus familiaris GN=ZNF541 PE=4 SV=1 - [J9NYD8_CANLF]	2,18	1	0	1	1
E2QXL0	GRIP1 associated protein 1 OS=Canis lupus familiaris GN=GRIPAP1 PE=4 SV=2 - [E2QXL0_CANLF]	1,97	1	0	1	1
A0A0K6G4V7	Cingulin [Canis lupus familiaris] OS=Rhizoctonia solani GN=RSOLAG22IIIB_10913 PE=4 SV=1 - [A0A0K6G4V7_9	1,95	1	1	1	1
A8WED5	Receptor protein-tyrosine kinase (Fragment) OS=Canis lupus familiaris PE=2 SV=1 - [A8WED5_CANLF]	1,93	1	0	1	1
F1PIQ9	Receptor protein-tyrosine kinase OS=Canis lupus familiaris GN=ERBB2 PE=3 SV=2 - [F1PIQ9_CANLF]	1,9	1	0	1	1
E2QWT9	GRIP1 associated protein 1 OS=Canis lupus familiaris GN=GRIPAP1 PE=4 SV=2 - [E2QWT9_CANLF]	1,9	1	0	1	1
F6UPV2	Transcription initiation factor TFIID subunit OS=Canis lupus familiaris GN=TAF1 PE=3 SV=1 - [F6UPV2_CANLF]	1,69	1	0	1	1
J9NZ21	Transcription initiation factor TFIID subunit OS=Canis lupus familiaris GN=TAF1 PE=3 SV=1 - [J9NZ21_CANLF]	1,66	1	0	1	1
A0A0E3ZN11	UvrABC system protein C OS=Pasteurella multocida subsp. multocida OH4807 GN=uvrC PE=3 SV=1 - [A0A0E3Z	1,64	1	1	1	1
F1PUS7	Capping protein regulator and myosin 1 linker 1 OS=Canis lupus familiaris GN=CARMIL1 PE=4 SV=2 - [F1PUS7_	1,47	1	0	1	1
F1PUS0	Capping protein regulator and myosin 1 linker 1 OS=Canis lupus familiaris GN=CARMIL1 PE=4 SV=2 - [F1PUS0_	1,41	1	0	1	1
A0A0E3ZSB9	RNA polymerase-associated protein RapA OS=Pasteurella multocida subsp. multocida OH4807 GN=rapA PE=3	1,03	1	1	1	1
F6Y3D7	WDFY family member 4 OS=Canis lupus familiaris GN=WDFY4 PE=4 SV=1 - [F6Y3D7_CANLF]	0,77	1	0	1	1
E2QUV0	Nipped-B protein OS=Canis lupus familiaris GN=NIPBL PE=3 SV=2 - [E2QUV0_CANLF]	0,7	1	0	1	1
J9NZL2	Nipped-B protein OS=Canis lupus familiaris GN=NIPBL PE=3 SV=1 - [J9NZL2_CANLF]	0,68	1	0	1	1

J9P3A7	Nipped-B protein OS=Canis lupus familiaris GN=NIPBL PE=3 SV=1 - [J9P3A7_CANLF]	0,68	1	0	1	1
J9P6G6	Nipped-B protein OS=Canis lupus familiaris GN=NIPBL PE=3 SV=1 - [J9P6G6_CANLF]	0,68	1	0	1	1
Q3ZE66	Transducin alpha 1 (Fragment) OS=Canis lupus GN=GNAT1 PE=4 SV=1 - [Q3ZE66_CANLU]	28,05	1	0	1	1
E2RCS0	Chromosome 11 open reading frame 88 OS=Canis lupus familiaris GN=C11orf88 PE=4 SV=1 - [E2RCS0_CANLF]	19,76	1	1	1	1
J9PAR2	Exosome component 2 OS=Canis lupus familiaris GN=EXOSC2 PE=4 SV=1 - [J9PAR2_CANLF]	9,84	1	0	1	1
J9NUF5	Exosome component 2 OS=Canis lupus familiaris GN=EXOSC2 PE=4 SV=1 - [J9NUF5_CANLF]	9,73	1	0	1	1
F1PXA6	Uncharacterized protein OS=Canis lupus familiaris GN=LOC492173 PE=4 SV=2 - [F1PXA6_CANLF]	9,28	1	1	1	1
J9NT30	CDKN2A interacting protein OS=Canis lupus familiaris GN=CDKN2AIP PE=4 SV=1 - [J9NT30_CANLF]	9,01	1	0	1	1
F1PBE1	ABI family member 3 OS=Canis lupus familiaris GN=ABI3 PE=4 SV=2 - [F1PBE1_CANLF]	8,31	1	1	1	1
E2RKL1	Protein phosphatase 1 regulatory inhibitor subunit 2 pseudogene 9 OS=Canis lupus familiaris GN=PPP1R2P9 PE	8,17	1	1	1	1
J9P800	Calcium and integrin binding family member 2 OS=Canis lupus familiaris GN=CIB2 PE=4 SV=1 - [J9P800_CANLF]	8,02	1	1	1	1
E2R3Y6	Keratin 32 OS=Canis lupus familiaris GN=KRT32 PE=3 SV=1 - [E2R3Y6_CANLF]	7,09	1	1	1	1
F6Y478	Uncharacterized protein OS=Canis lupus familiaris PE=3 SV=1 - [F6Y478_CANLF]	6,67	1	1	1	1
J9P3P3	FUN14 domain containing 2 OS=Canis lupus familiaris GN=FUNDC2 PE=4 SV=1 - [J9P3P3_CANLF]	6,63	1	0	1	2
Q28300	Guanine nucleotide-binding protein G(t) subunit alpha-1 OS=Canis lupus familiaris GN=GNAT1 PE=2 SV=2 - [GN	6,57	1	0	1	1
J9P0R3	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9P0R3_CANLF]	6,36	1	0	1	1
J9NXW2	Exosome component 2 OS=Canis lupus familiaris GN=EXOSC2 PE=4 SV=1 - [J9NXW2_CANLF]	6,14	1	0	1	1
J9NT46	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [J9NT46_CANLF]	6,12	1	1	1	1
F6UY88	Exosome component 2 OS=Canis lupus familiaris GN=EXOSC2 PE=4 SV=1 - [F6UY88_CANLF]	5,96	1	0	1	1
L7N0L6	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [L7N0L6_CANLF]	5,93	1	1	1	1
F1PDH0	FUN14 domain containing 2 OS=Canis lupus familiaris GN=FUNDC2 PE=4 SV=2 - [F1PDH0_CANLF]	5,82	1	0	1	2
J9P2B1	Uncharacterized protein OS=Canis lupus familiaris GN=FYTTD1 PE=4 SV=1 - [J9P2B1_CANLF]	5,66	1	0	1	1
F1PU59	Prenylcysteine oxidase 1 like OS=Canis lupus familiaris GN=PCYOX1L PE=4 SV=2 - [F1PU59_CANLF]	5,45	1	1	1	1
A0A0E3V3Q7	Protein YgiX OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_05805 PE=4 SV=1 - [A0A0E3V3Q7_	5,38	1	1	1	1
F1PWX8	CDKN2A interacting protein OS=Canis lupus familiaris GN=CDKN2AIP PE=4 SV=2 - [F1PWX8_CANLF]	5,19	1	0	1	1
E2QYI0	Secreted frizzled related protein 4 OS=Canis lupus familiaris GN=SFRP4 PE=4 SV=1 - [E2QYI0_CANLF]	5,19	1	1	1	2
A0A0E3ZPB3	Uncharacterized protein OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_04180 PE=4 SV=1 - [A0	4,93	1	1	1	1
F1P6B8	Intraflagellar transport 57 OS=Canis lupus familiaris GN=IFT57 PE=4 SV=2 - [F1P6B8_CANLF]	4,9	1	1	1	1
A0A0E3V4L1	Alanine racemase OS=Pasteurella multocida subsp. multocida OH4807 GN=alr PE=3 SV=1 - [A0A0E3V4L1_PAS	4,75	1	1	1	1
A0A0E3V3L9	Fumarate hydratase class II OS=Pasteurella multocida subsp. multocida OH4807 GN=fumC PE=3 SV=1 - [A0A0E	4,53	1	0	1	1
F6XKG0	Uncharacterized protein OS=Canis lupus familiaris PE=4 SV=1 - [F6XKG0_CANLF]	4,35	1	1	1	1
E2QTM7	Tetratricopeptide repeat domain 26 OS=Canis lupus familiaris GN=TTC26 PE=4 SV=1 - [E2QTM7_CANLF]	3,97	1	1	1	1
E2RTM1	Neurofibromin 2 OS=Canis lupus familiaris GN=NF2 PE=4 SV=2 - [E2RTM1_CANLF]	3,89	1	0	1	3
E2QZZ2	Neurofibromin 2 OS=Canis lupus familiaris GN=NF2 PE=1 SV=1 - [E2QZZ2_CANLF]	3,86	1	0	1	3
E2RJW7	Adducin 1 OS=Canis lupus familiaris GN=ADD1 PE=4 SV=2 - [E2RJW7_CANLF]	3,77	1	0	1	1
F1PN02	Osteoclast stimulatory transmembrane protein OS=Canis lupus familiaris GN=OCSTAMP PE=4 SV=2 - [F1PN02_	3,72	1	1	1	1
E2RJW9	Adducin 1 OS=Canis lupus familiaris GN=ADD1 PE=4 SV=2 - [E2RJW9_CANLF]	3,56	1	0	1	1
F1PTE0	Serine and arginine rich splicing factor 6 OS=Canis lupus familiaris GN=SRSF6 PE=4 SV=2 - [F1PTE0_CANLF]	3,49	1	0	1	1
O77704	Desmocollin type 2 (Fragment) OS=Canis lupus familiaris GN=DSC2 PE=2 SV=1 - [O77704_CANLF]	3,44	1	1	1	1
J9NXS1	Uncharacterized protein OS=Canis lupus familiaris GN=DCAF8 PE=4 SV=1 - [J9NXS1_CANLF]	3,36	1	1	1	1
F6XIL7	Olfactory receptor OS=Canis lupus familiaris GN=OR4S1 PE=3 SV=1 - [F6XIL7_CANLF]	3,24	1	1	1	2
F1PS56	Solute carrier family 3 member 1 OS=Canis lupus familiaris GN=SLC3A1 PE=4 SV=1 - [F1PS56_CANLF]	3,14	1	0	1	1
Q9GKM3	Amino acid transporter SLC3A1 OS=Canis lupus familiaris PE=2 SV=1 - [Q9GKM3_CANLF]	3,14	1	0	1	1
F1P7Q9	Nedd4 family interacting protein 2 OS=Canis lupus familiaris GN=NDFIP2 PE=4 SV=2 - [F1P7Q9_CANLF]	3,12	1	1	1	2
E2RFR6	GATA zinc finger domain containing 2B OS=Canis lupus familiaris GN=GATAD2B PE=4 SV=1 - [E2RFR6_CANLF]	3,04	1	0	1	1
F1Q018	Sphingomyelin phosphodiesterase OS=Canis lupus familiaris GN=SMPD1 PE=3 SV=2 - [F1Q018_CANLF]	2,73	1	1	1	1
J9NU60	GATA zinc finger domain containing 2B OS=Canis lupus familiaris GN=GATAD2B PE=4 SV=1 - [J9NU60_CANLF]	2,69	1	0	1	1
F1PEZ0	Serine and arginine rich splicing factor 4 OS=Canis lupus familiaris GN=SRSF4 PE=4 SV=2 - [F1PEZ0_CANLF]	2,51	1	0	1	1
J9P6A6	RNA binding motif protein 44 OS=Canis lupus familiaris GN=RBM44 PE=4 SV=1 - [J9P6A6_CANLF]	2,19	1	0	1	1
J9NUX6	Protein phosphatase 6 regulatory subunit 2 OS=Canis lupus familiaris GN=PPP6R2 PE=4 SV=1 - [J9NUX6_CANLF	2,17	1	1	1	1
F1P657	DNA nucleotidylexotransferase OS=Canis lupus familiaris GN=DNTT PE=4 SV=2 - [F1P657_CANLF]	2,16	1	1	1	2
E2RAJ8	Transient receptor potential cation channel subfamily M member 5 OS=Canis lupus familiaris GN=TRPM5 PE=3	2,14	1	1	1	1
J9NSC8	Nibrin OS=Canis lupus familiaris GN=NBN PE=4 SV=1 - [J9NSC8_CANLF]	2,09	1	0	1	1
E2QXW0	Sprouty related EVH1 domain containing 2 OS=Canis lupus familiaris GN=SPRED2 PE=4 SV=2 - [E2QXW0_CANLF	1,93	1	0	1	1
P06625	Signal recognition particle receptor subunit alpha OS=Canis lupus familiaris GN=SRPRA PE=2 SV=2 - [SRPRA_CA	1,88	1	0	1	2
F1PLH3	Signal recognition particle receptor subunit alpha OS=Canis lupus familiaris GN=SRPRA PE=4 SV=2 - [F1PLH3_C	1,88	1	0	1	2
J9NTJ9	Signal recognition particle receptor subunit alpha OS=Canis lupus familiaris GN=SRPRA PE=4 SV=1 - [J9NTJ9_CA	1,88	1	0	1	2
J9NTJ6	Anoctamin OS=Canis lupus familiaris GN=ANO2 PE=3 SV=1 - [J9NTJ6_CANLF]	1,87	1	0	1	1
F1PST4	Nibrin OS=Canis lupus familiaris GN=NBN PE=4 SV=2 - [F1PST4_CANLF]	1,86	1	0	1	1
E2RBD2	Polyamine modulated factor 1 binding protein 1 OS=Canis lupus familiaris GN=PMFBP1 PE=4 SV=2 - [E2RBD2_	1,8	1	1	1	1
F1P6F3	Bromodomain testis associated OS=Canis lupus familiaris GN=BRDT PE=4 SV=2 - [F1P6F3_CANLF]	1,78	1	1	1	1
J9P3V0	Uncharacterized protein OS=Canis lupus familiaris GN=RAPGEF6 PE=4 SV=1 - [J9P3V0_CANLF]	1,74	1	0	1	3
F1PK77	Sperm associated antigen 9 OS=Canis lupus familiaris GN=SPAG9 PE=4 SV=2 - [F1PK77_CANLF]	1,73	1	0	1	1
J9P381	Sperm associated antigen 9 OS=Canis lupus familiaris GN=SPAG9 PE=4 SV=1 - [J9P381_CANLF]	1,73	1	0	1	1
F1PKS8	Anoctamin OS=Canis lupus familiaris GN=ANO2 PE=3 SV=2 - [F1PKS8_CANLF]	1,72	1	0	1	1
J9NSU6	Anoctamin OS=Canis lupus familiaris GN=ANO2 PE=3 SV=1 - [J9NSU6_CANLF]	1,71	1	0	1	1
J9P788	Signal recognition particle receptor subunit alpha OS=Canis lupus familiaris GN=SRPRA PE=4 SV=1 - [J9P788_C	1,55	1	0	1	2
F1PLH5	ArfGAP with FG repeats 1 OS=Canis lupus familiaris GN=AGFG1 PE=4 SV=2 - [F1PLH5_CANLF]	1,52	1	0	1	1
F1Q0T0	Golgin A3 OS=Canis lupus familiaris GN=GOLGA3 PE=4 SV=2 - [F1Q0T0_CANLF]	1,44	1	1	1	2
E2RTD7	RNA binding motif protein 44 OS=Canis lupus familiaris GN=RBM44 PE=4 SV=2 - [E2RTD7_CANLF]	1,33	1	0	1	1
J9P3Y2	RNA binding motif protein 44 OS=Canis lupus familiaris GN=RBM44 PE=4 SV=1 - [J9P3Y2_CANLF]	1,33	1	0	1	1
F1PHZ2	Triacylglycerol lipase OS=Canis lupus familiaris GN=PNLIPRP2 PE=3 SV=2 - [F1PHZ2_CANLF]	1,28	1	1	1	2
F6XGB4	Growth regulation by estrogen in breast cancer 1 OS=Canis lupus familiaris GN=GREB1 PE=4 SV=1 - [F6XGB4_C	1,23	1	0	1	1
J9P6D5	Growth regulation by estrogen in breast cancer 1 OS=Canis lupus familiaris GN=GREB1 PE=4 SV=1 - [J9P6D5_C	1,23	1	0	1	1
E2RNM4	ArfGAP with FG repeats 1 OS=Canis lupus familiaris GN=AGFG1 PE=4 SV=2 - [E2RNM4_CANLF]	1,23	1	0	1	1
E2R4E8	Ankyrin repeat domain 11 OS=Canis lupus familiaris GN=ANKRD11 PE=4 SV=2 - [E2R4E8_CANLF]	1,23	1	0	1	1
E2RHN9	Testis and ovary specific PAZ domain containing 1 OS=Canis lupus familiaris GN=TOPAZ1 PE=4 SV=2 - [E2RHN9_	1,22	1	0	1	2
F1PDY3	SH3 and PX domains 2B OS=Canis lupus familiaris GN=SH3PXD2B PE=4 SV=2 - [F1PDY3_CANLF]	1,22	1	1	1	5
J9PAS0	Ankyrin repeat domain 11 OS=Canis lupus familiaris GN=ANKRD11 PE=4 SV=1 - [J9PAS0_CANLF]	1,21	1	0	1	1
J9NX53	Testis and ovary specific PAZ domain containing 1 OS=Canis lupus familiaris GN=TOPAZ1 PE=4 SV=1 - [J9NX53_	1,16	1	0	1	2
E2RFC3	Cullin associated and neddylation dissociated 2 (putative) OS=Canis lupus familiaris GN=CAND2 PE=4 SV=2 - [E	1,16	1	1	1	1
J9P1Y0	Testis and ovary specific PAZ domain containing 1 OS=Canis lupus familiaris GN=TOPAZ1 PE=4 SV=1 - [J9P1Y0_	1,15	1	0	1	2
E2RCW0	Transferrin receptor 2 OS=Canis lupus familiaris GN=TFR2 PE=4 SV=2 - [E2RCW0_CANLF]	1,12	1	1	1	1
F1PD39	Collagen type XI alpha 1 chain OS=Canis lupus familiaris GN=COL11A1 PE=4 SV=2 - [F1PD39_CANLF]	1,09	1	0	1	1
F1PK99	ATPase copper transporting alpha OS=Canis lupus familiaris GN=ATP7A PE=3 SV=2 - [F1PK99_CANLF]	1	1	1	1	3
F1PD36	Collagen type XI alpha 1 chain OS=Canis lupus familiaris GN=COL11A1 PE=4 SV=2 - [F1PD36_CANLF]	1	1	0	1	1
J9NYK4	Collagen type XI alpha 1 chain OS=Canis lupus familiaris GN=COL11A1 PE=4 SV=1 - [J9NYK4_CANLF]	1	1	0	1	1
A0A0E3ZRD1	DNA-directed RNA polymerase subunit beta' OS=Pasteurella multocida subsp. multocida OH4807 GN=rpoC PE=	0,99	1	1	1	3
F6XRM5	Aminopeptidase OS=Canis lupus familiaris GN=ENPEP PE=3 SV=1 - [F6XRM5_CANLF]	0,94	1	1	1	1
E2RC04	Kinetochore scaffold 1 OS=Canis lupus familiaris GN=KNL1 PE=4 SV=2 - [E2RC04_CANLF]	0,88	1	1	1	1
F1Q422	Uncharacterized protein OS=Canis lupus familiaris GN=RAPGEF6 PE=4 SV=2 - [F1Q422_CANLF]	0,87	1	0	1	3
L7N051	Uncharacterized protein OS=Canis lupus familiaris GN=RAPGEF6 PE=4 SV=1 - [L7N051_CANLF]	0,87	1	0	1	3
P83509	Rho GTPase-activating protein 35 OS=Canis lupus familiaris GN=ARHGAP35 PE=2 SV=1 - [RHG35_CANLF]	0,87	1	0	1	1

E2RK70	RPGRIP1 like OS=Canis lupus familiaris GN=RPGRIP1L PE=4 SV=2 - [E2RK70_CANLF]	0,86	1	0	1	1
J9NUY1	Rho GTPase-activating protein 35 OS=Canis lupus familiaris GN=ARHGAP35 PE=4 SV=1 - [J9NUY1_CANLF]	0,86	1	0	1	1
J9P705	RPGRIP1 like OS=Canis lupus familiaris GN=RPGRIP1L PE=4 SV=1 - [J9P705_CANLF]	0,84	1	0	1	1
J9P4D0	Pericentrin OS=Canis lupus familiaris GN=PCNT PE=4 SV=1 - [J9P4D0_CANLF]	0,73	1	0	1	1
E2RJS8	Transformation/transcription domain associated protein OS=Canis lupus familiaris GN=TRRAP PE=3 SV=2 - [E2R	0,57	1	0	1	1
J9NV05	Transformation/transcription domain associated protein OS=Canis lupus familiaris GN=TRRAP PE=3 SV=1 - [J9N	0,57	1	0	1	1
E2RDZ3	Adenylate cyclase 10, soluble OS=Canis lupus familiaris GN=ADCY10 PE=4 SV=1 - [E2RDZ3_CANLF]	0,37	1	1	1	1
J9NUT9	Pericentrin OS=Canis lupus familiaris GN=PCNT PE=4 SV=1 - [J9NUT9_CANLF]	0,35	1	0	1	1
J9P3H9	MAP3K7 C-terminal like OS=Canis lupus familiaris GN=MAP3K7CL PE=4 SV=1 - [J9P3H9_CANLF]	10,95	1	1	1	1
J9NZ55	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Canis lupus familiaris GN=QPRT PE=3 SV=1 - [J9N	7,36	1	1	1	1
J9NW76	NOP2/Sun RNA methyltransferase family member 3 OS=Canis lupus familiaris GN=NSUN3 PE=3 SV=1 - [J9NW7	7,09	1	0	1	1
E2R7X5	POU domain protein OS=Canis lupus familiaris GN=POU4F2 PE=3 SV=1 - [E2R7X5_CANLF]	6,13	1	0	1	2
E2QST0	NOP2/Sun RNA methyltransferase family member 3 OS=Canis lupus familiaris GN=NSUN3 PE=3 SV=1 - [E2QST	5,39	1	0	1	1
A0A0E3V328	Carboxy-S-adenosyl-L-methionine synthase OS=Pasteurella multocida subsp. multocida OH4807 GN=cmoA PE=	5,39	1	1	1	1
J9PA83	S-(hydroxymethyl)glutathione dehydrogenase OS=Canis lupus familiaris PE=3 SV=1 - [J9PA83_CANLF]	5,35	1	0	1	1
A0A0E3ZQB8	Tyrosine--tRNA ligase OS=Pasteurella multocida subsp. multocida OH4807 GN=tyrS PE=3 SV=1 - [A0A0E3ZQB8_	5,32	1	1	1	1
F1PLM5	S-(hydroxymethyl)glutathione dehydrogenase OS=Canis lupus familiaris PE=3 SV=2 - [F1PLM5_CANLF]	5,32	1	0	1	1
A0A0E3ZSD2	Exopolyphosphatase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_07800 PE=3 SV=1 - [A0A0E	4,65	1	1	1	1
J9P151	Myocyte enhancer factor 2D OS=Canis lupus familiaris GN=MEF2D PE=4 SV=1 - [J9P151_CANLF]	4,59	1	0	1	1
F1PG05	Collagen type II alpha 1 chain OS=Canis lupus familiaris GN=COL2A1 PE=4 SV=2 - [F1PG05_CANLF]	4,44	1	0	1	1
F1PDZ9	Myocyte enhancer factor 2D OS=Canis lupus familiaris GN=MEF2D PE=4 SV=2 - [F1PDZ9_CANLF]	4,42	1	0	1	1
E2RPL0	TNF alpha induced protein 2 OS=Canis lupus familiaris GN=TNFAIP2 PE=4 SV=2 - [E2RPL0_CANLF]	4,17	1	1	1	1
E2RSB1	Kelch like family member 30 OS=Canis lupus familiaris GN=KLHL30 PE=4 SV=1 - [E2RSB1_CANLF]	3,8	1	1	1	1
F1PBW1	Septin 10 OS=Canis lupus familiaris GN=SEPT10 PE=3 SV=2 - [F1PBW1_CANLF]	3,41	1	0	1	1
J9NUL3	Septin 10 OS=Canis lupus familiaris GN=SEPT10 PE=3 SV=1 - [J9NUL3_CANLF]	3,16	1	0	1	1
A0A0E3V3F7	Long-chain-fatty-acid--CoA ligase OS=Pasteurella multocida subsp. multocida OH4807 GN=I926_01245 PE=4 SV	3,02	1	1	1	1
F1Q4I1	Pentatricopeptide repeat domain 3 OS=Canis lupus familiaris GN=PTCD3 PE=4 SV=2 - [F1Q4I1_CANLF]	2,77	1	1	1	3
E2RM17	TAO kinase 3 OS=Canis lupus familiaris GN=TAOK3 PE=4 SV=2 - [E2RM17_CANLF]	2,67	1	1	1	1
E2RJ90	Uncharacterized protein OS=Canis lupus familiaris GN=LOC100855970 PE=4 SV=2 - [E2RJ90_CANLF]	2,62	1	1	1	1
F1P6Z3	N-ethylmaleimide sensitive factor, vesicle fusing ATPase OS=Canis lupus familiaris GN=NSF PE=4 SV=1 - [F1P6Z	2,42	1	0	1	1
E2REM4	Rho GTPase activating protein 17 OS=Canis lupus familiaris GN=ARHGAP17 PE=4 SV=2 - [E2REM4_CANLF]	2,4	1	1	1	1
E2RDR5	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group) OS=Canis lupus familiaris GN=GCNT	2,23	1	1	1	1
E2RFV4	N-ethylmaleimide sensitive factor, vesicle fusing ATPase OS=Canis lupus familiaris GN=NSF PE=4 SV=2 - [E2RFV	2,22	1	0	1	1
E2RAH7	Kinesin-like protein OS=Canis lupus familiaris GN=KIF18A PE=3 SV=1 - [E2RAH7_CANLF]	2,22	1	1	1	1
F1P7R9	RNA binding motif protein 26 OS=Canis lupus familiaris GN=RBM26 PE=4 SV=2 - [F1P7R9_CANLF]	1,84	1	0	1	1
J9NRX5	RNA binding motif protein 26 OS=Canis lupus familiaris GN=RBM26 PE=4 SV=1 - [J9NRX5_CANLF]	1,79	1	0	1	1
O71024	Outer capsid protein VP2 OS=African horse sickness virus 6 GN=S2 PE=2 SV=1 - [VP2_AHSV6]	1,71	1	0	1	1
A0A189RMP8	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMP8_AHSV6]	1,71	1	0	1	1
A0A189RMP2	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMP2_AHSV6]	1,71	1	0	1	1
A0A189RMR5	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMR5_AHSV6]	1,71	1	0	1	1
A0A189RMR4	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMR4_AHSV6]	1,71	1	0	1	1
A0A189RMS5	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMS5_AHSV6]	1,71	1	0	1	1
A0A0U2DD05	VP2 OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A0U2DD05_AHSV6]	1,71	1	0	1	1
A0A189RMS0	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMS0_AHSV6]	1,71	1	0	1	1
A0A0N9LCS2	VP2 OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A0N9LCS2_AHSV6]	1,71	1	0	1	1
A0A189RMQ3	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMQ3_AHSV6]	1,71	1	0	1	1
A0A189RMT4	Major outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A189RMT4_AHSV6]	1,71	1	0	1	1
A0A0U2DGT5	VP2 OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A0U2DGT5_AHSV6]	1,71	1	0	1	1
A0A0K0P0G2	VP2 OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A0K0P0G2_AHSV6]	1,71	1	0	1	1
A0A0U1XN26	Outer capsid protein OS=African horse sickness virus 6 GN=VP2 PE=4 SV=1 - [A0A0U1XN26_AHSV6]	1,71	1	0	1	1
F1PS24	Collagen type II alpha 1 chain OS=Canis lupus familiaris GN=COL2A1 PE=4 SV=1 - [F1PS24_CANLF]	1,48	1	0	1	1
O77753	Type IIA procollagen OS=Canis lupus familiaris PE=2 SV=2 - [O77753_CANLF]	1,48	1	0	1	1
J9NYX0	DENN domain containing 4A OS=Canis lupus familiaris GN=DENND4A PE=4 SV=1 - [J9NYX0_CANLF]	1,39	1	0	1	1
E2RRL1	DENN domain containing 4A OS=Canis lupus familiaris GN=DENND4A PE=4 SV=1 - [E2RRL1_CANLF]	1,18	1	0	1	1
J9P4F8	DENN domain containing 4A OS=Canis lupus familiaris GN=DENND4A PE=4 SV=1 - [J9P4F8_CANLF]	1,15	1	0	1	1
E2R4V6	Nucleoporin 98 OS=Canis lupus familiaris GN=NUP98 PE=4 SV=2 - [E2R4V6_CANLF]	1,06	1	1	1	1

Table S4: Mass spectrometric identified biomarker candidates

Mean ratios of AM/NM and CF/NF as well as number hits that determine an altered protein as BM candidate.
Calculation of mean ratios, cf. Formula 1 in Supplementary Methods. The number of hits corresponds to protein concentration in sub-fractions included.
Here all results are given, proteins and protein clusters higher as well as lower in affected animals.
"1000" was set for an extraordinary high ratio, even when much higher, in order to apply value depending color code of Excel.
"DIV/0": division by zero, the ratio cannot calculated since there was no hit/peptide in the control sample. Figure 2 (main document) represent an excerpt from this table.

Altered proteins in dogs (7. wk)

		Males					**Females**				
		in sub-fractions				**overall trend**	**in sub-fractions**				**overall trend**
		Mean ratio (AM/NM)		**Number of hits**			**Mean ratio (CF/NF)**		**Number of hits**		
ID	**Annotation**	**higher in AM**	lower in AM	**higher in AM**	lower in AM	in AM	**higher in CF**	lower in CF	**higher in CF**	lower in CF	in CF
Plasma proteins											
F1PNV5	Kallikrein B1	1000	0,245	15	32	114,84	0	0,158	0	39	0,00
E2R886	Kininogen 1	56,2	0,043	523	609	2,08	20,3	0,227	106	361	1,35
E2QUV3	α2-HS glycoprotein	326	0,15	1056	3178	16,25	n.a.				
F1P6E1	Complement C1s	0	0,041	0	153	0,00	3,11	0	67	0	#DIV/0!
F1PNG7	Complement C1r	n.a.					115	0,105	24	29	9,99
J9P4B4	Complement C1q A chain	1000	0,133	14	53	35,13	n.f.				
J9P1G2	Complement C1q B chain	1000	0,229	60	128	107,34	4,09	0,155	22	85	0,16
E2RJC2	Complement C1q C chain	1000	0,078	90	89	78,88	3,21	0,062	17	51	0,07
E2RS79	Complement C2 (human homolog)	3,44	0,026	21	14	0,13	0	0,14	0	14	0,00
F1PIX8	Complement C3	32,2	0,086	4565	27225	0,46	34,77	0,102	2165	4973	1,54
J9PAD1	Complement C4 (human homolog)	29,6	0,057	509	3883	0,22	150	0,107	125	2148	0,93
F1PWR2	Complement C4 (human homolog)	6,09	0,077	316	759	0,20	37,3	0,094	84	615	0,48
F1P7J4	Complement C5	21,3	0,04	68	467	0,12	14,9	0,154	17	311	0,13
E2RGT6	Complement C6	1000	0,025	177	127	34,84	0	0,089	0	123	0,00
E2RG01	Complement C7	1000	0,157	56	257	34,21	0	0,225	0	82	0,00
E2R109	Complement C8 alpha chain	1000	0,143	14	45	44,49	2,26	0,011	1	10	0,00
E2R141	Complement C8 beta chain	2,41	0,197	4	76	0,02	n.a.				
J9P8Z6	Complement C9	5,79	0	8	0	#DIV/0!	n.a.				
F1PY40	Complement factor I	66,2	0,164	48	462	1,13	49,5	0,065	30	161	0,60
J9NTL7	Complementfactor H (homolog in mammals)	69,5	0,086	162	2069	0,47	47,6	0,057	87	2884	0,08
E2RS80	Complementfactor B (homolog in primates)	39	0,078	452	1516	0,91	25	0,156	57	762	0,29
F1PGM9	Complement component 4 binding protein alpha	170,4	0,17	1105	2308	13,87	20,2	0,11	279	1332	0,47
G1K2D9	Haptoglobin	114	0,07	1849	3024	4,88	0	0,127	0	5882	0,00
F6UME0	α2-macroglobulin	77,55	0,093	2383	6931	2,48	179	0,087	277	3986	1,08
F6Y713	α1-acid glycoprotein	23	0,182	816	367	9,31	13,6	0,253	29	1467	0,07
P33703	APOH, Beta-2-glycoprotein 1	42,2	0,177	293	582	3,76	15,7	0,077	112	328	0,41
T2KEN6	Pentraxin	3,53	0,006	117	41	0,06	0	0,307	0	174	0,00
A1ILJ0	Alpha-1-antitrypsin	6,2	0,076	147	52	1,33	4,08	0,186	24	175	0,10
F1PAX2	Ceruloplasmin	4,38	0,055	363	1283	0,07	6,28	0,159	49	688	0,07
F1PCE5	Serpin family A member 1	114	0,151	396	1353	5,04	53,1	0,18	378	1233	2,93
F1PH86	Serpin family A member 3	n.f.					2,4	0,298	17	107	0,11
E2RMF9	Serpin family A member 5	0	0,164	0	39	0,00	34	0,195	4	20	1,33
F1PB85	Serpin family A member 7	8,55	0,319	20	22	2,48	0	0,245	0	23	0,00
F1PYX9	Serpin family G member 1	11,3	0,064	183	944	0,14	12,9	0,13	24	499	0,08
J9P8Q8	Serpin family D member 1	2,17	0,233	12	245	0,02	2,53	0,334	29	86	0,28
J9NSS7	Leucine rich alpha-2-glycoprotein 1	22	0,275	289	133	13,15	10,6	0,208	68	348	0,43
J9NVE9	Serum amyloid A	86,4	0	70	0	#DIV/0!	0	0,148	0	275	0,00
F1PAL5	Angiotensinogen	19,4	0,289	48	75	3,59	6,4	0,186	28	40	0,83
Q7M310	Angiotensin I	2,84	0,277	69	38	1,43	n.f.				
F1PN98	Coagulation factor V	3,35	0	107	0	#DIV/0!	0	0,007	0	33	0,00
J9NSF9	Prothrombin	51	0,17	292	797	3,18	11,9	0,214	35	350	0,25
F1PZR4	Hemopexin	44,9	0,136	83	563	0,90	68,7	0,166	144	1162	1,41
F1Q421	Plasminogen	n.a.					52,6	0,251	97	403	3,18
J9P430	Transferrin	20,4	0,123	1424	6332	0,56	29,1	0,142	191	4721	0,17
F6V1W9	Transferrin	4,12	0,335	11	5	3,04	3,95	0,23	3	3	0,91
J9JHX7	Serotransferrin (homolog, several species)	9,23	0,344	355	776	1,45	20,2	0,208	102	477	0,90
E2QZQ1	Serotransferrin (homolog, several species)	6,75	0,256	17	55	0,53	1000	0,09	9	20	40,50
F1PKX3	Coagulation factor XIII A chain	2,76	0,103	6	83	0,02	41,2	0,401	8	3	44,06
F1Q041	Coagulation factor XIII B chain	1000	0,025	6	38	3,95	1000	0,068	6	19	21,47
F1PSS8	Protein S	2,98	0,125	26	170	0,06	0	0,174	0	121	0,00
F1Q4A3	Coagulation factor X	0	0,236	0	25	0,00	20,5	0,013	18	2	2,40
E2R4E7	Afamin	6,76	0,318	297	1075	0,59	14	0,268	37	604	0,23
F6Y3P9	Gelsolin	34,5	0,259	218	529	3,68	20	0,23	91	114	3,67
E2R5U8	Transthyretin	8,76	0,218	65	1143	0,11	n.a.				
A0A1K0FUG:	Globin A1	109	0,103	229	60	42,85	1000	0,01	21	32	6,56
A0A1K0GGH	Globin A2	103	0,047	118	34	16,80	0	0,157	0	42	0,00
J9NXL3	Hemoglobin subunit alpha (dog homolog)	115	0,101	155	52	34,62	2,8	0,11	2	101	0,01
E2R9B6	Fetuin B	30,4	0,221	148	212	4,69	2	0,24	16	228	0,03
F1PYM4	Insulin like growth factor binding protein acid labile subunit	31	0,258	15	147	0,82	3,15	0,24	21	10	1,59
B5U1S6	Adiponectin (fragment)	1000	0,132	22	56	51,86	1000	0,004	14	29	1,93
F1PDJ7	Alpha-2-glycoprotein 1	3,75	0,292	20	11	1,99	n.a.				
E2RPW3	Paraoxonase 1	3,55	0,018	33	28	0,08	1000	0,047	45	8	264,38
J9P8B0	Dipeptidyl peptidase 4	2,31	0	10	0	#DIV/0!	n.a.				
F1PCK2	α1-B glycoprotein	21,9	0,02	714	469	0,67	25,2	0,127	978	1688	1,85
F1Q4D9	Retinol binding protein 4	8,97	0,18	12	98	0,20	25,06	0,304	13	20	4,95
E2RPB8	C-type lectin domain family 3 member B	n.a.					2,59	0,279	11	134	0,06
E2RKQ6	Galectin 3 binding protein	2,24	0,253	18	6	1,70	3,3	0,067	24	64	0,08
Apolipoproteins											
J9P843	Apo AI	325	0,16	4231	17259	12,75	41,1	0,061	325	1356	0,60
E2RE76	Apo AIV	6,76	0,115	324	574	0,44	21,5	0,21	164	146	5,07
P56595	Apo CI	4,72	0,206	8	147	0,05	3,97	0	14	6	#DIV/0!
9NWJ6	Apo CII	15,8	0,153	58	770	0,18	50,3	0,274	33	35	12,99
D5G334	Apo E4 (fragment)	4,8	0,162	44	212	0,16	37,4	0,233	55	116	4,13
F1PJ74	Apo E	15	0,19	32	269	0,34	33	0,279	34	107	2,93
E2RQ71	Apo M	6,86	0,278	22	458	0,09	2,57	0,401	26	23	1,16
F1P8Z5	Apo B	87	0,124	470	7485	0,68	19,3	0,107	115	2837	0,08
E2RNM1	Apo D	11,7	0,16	44	111	0,74	108,2	0,124	61	27	30,31
Intracellular proteins											
F1PZK8	Dynein heavy chain domain 1	1000	0,175	24	23	182,61	3,24	0,416	3	3	1,35
E2RB62	Myosin IB	6,19	0,147	2	8	0,23					
E2R1Q3	Myosin XVIIIB	n.a.					3,02	0	5	0	#DIV/0!
J9P187	Myosin IXA	894	0,202	94	257	66,05	328	0,278	51	60	77,51
J9P007	Kinesin-like protein	3,43	0	8	0	#DIV/0!	3,46	0,146	4	2	1,01
F1PM26	CD109 molecule	17,3	0,16	20	9	6,15	n.f.				
J9P216	Formin 1	1000	0,266	10	13	204,62	4,95	0	9	0	#DIV/0!
J9P7F7	Ficolin 1	1000	0,123	7	38	22,66	4,1	0,017	23	13	0,12
F1PAQ3	Maltase-glucoamylase	6,49	0,284	70	185	0,70	2,18	0,005	11	26	0,00
J9P5V6	Talin 1	17,6	0,158	3	7	1,19	128	0,247	1	4	7,90
E2RFS6	Sacsin molecular chaperone	12	0,418	4	7	2,87	12,7	0,333	3	5	2,54

E2QV33	Mediator complex subunit 22 (RNA-Pol)	98,4	0	26	0	#DIV/0!	0	0,097	0	28	0,00
E2R926	Fukutin	29,5	0,021	12	2	3,72	n.f.				
E2RP26	Filamin C	0	0,026	0	14	0,00	n.f.				
E2RK65	Kelch like family member 8	7,84	0,04	10	4	0,78	n.f.				
F1PRY8	Dispatched RND transporter family member 2	n.a.					1000	0	5	3	#DIV/0!
F6Y1C9	DNA Polymerase	n.a.					4,14	0,232	20	4	4,80
A0A0A0MPC!	Trafficking protein particle complex subunit 2	n.f.					1000	0	9	0	#DIV/0!
J9NYC0	Microfibril associated protein 4	n.a.					0	0,181	0	12	0,00
J9P514	RB associated KRAB zinc finger	6,05	0,326	2	15	0,26	9,04	0	6	0	#DIV/0!
J9P653	Ciliogenesis-associated TTC17-interacting protein (human homolo	10,1	0	10	0	#DIV/0!	2,9	0,396	2	14	0,16
J9NYQ5	Growth arrest specific 2 like 3	6,17	0,33	4	2	4,07	11,5	0,437	7	1	35,18
E2R1C3	Proteasome subunit alpha type	0	0,186	0	35	0,00	2,27	0,08	33	6	1,00
J9NYS3	Regulating synaptic membrane exocytosis 2	2,18	0,367	5	4	1,00	0	0,276	0	5	0,00
E2RF52	Proteasome subunit alpha type	n.f.					171	0	7	0	#DIV/0!
Extracellular matrix proteins											
J9P8M2	Fibronectin	28,9	0,164	386	3982	0,46	32,6	0,157	39	1842	0,11
E2QTQ1-	Ankyrin repeat and BTB domain containing 1	0	0,346	0	4	0,00	92	0,015	29	30	1,33
J9NV47	Hyaluronan binding protein 2	31,6	0	82	0	#DIV/0!	2,18	0,116	4	5	0,20
F1Q1K9	Hyaluronan binding protein 2	31,3	0	16	0	#DIV/0!	n.a.				
F1Q3I5	Collagen α1(I) chain	2,87	0	74	0	#DIV/0!	0	0,197	0	136	0,00
E5G723	Collagen α1 (I) (Fragment)	31,05	0,096	6	12	1,49	1000	0,106	13	10	137,80
F1PHY1	Collagen α2 (I) chain	3,26	0,254	11	1	9,11	0	0,219	0	73	0,00
F1PJH3	Collagen type XIII alpha 1 chain	455	0	36	0	#DIV/0!	0	0,235	0	36	0,00
J9NRV7	Fibrinogen alpha chain	265	0,078	1394	2959	9,74	0	0,092	0	1970	0,00
F1PW65	Fibrinogen beta chain	96,9	0,095	1600	4493	3,28	37,4	0,075	483	3248	0,42
F1P8G0	Fibrinogen gamma chain	399	0,1	1683	3016	22,27	53,4	0,116	200	1983	0,62
F1Q418	Inter-alpha-trypsin inhibitor heavy chain 1	4,02	0,127	135	829	0,08	2,98	0,053	158	618	0,04
F1PG39	Inter-alpha-trypsin inhibitor heavy chain 2	3,09	0,1	142	716	0,06	42	0,094	38	554	0,27
J9P7I3	Inter-alpha-trypsin inhibitor heavy chain 3	0	0,139	0	484	0,00	25,7	0,076	81	115	1,38
H9GWY3	Inter-alpha-trypsin inhibitor heavy chain 4	59,9	0,157	423	2238	1,78	5,51	0,083	146	846	0,08
J9NUI6	Alpha-1-microglobulin/bikunin precursor	33,6	0,055	27	252	0,20	75	0,053	36	115	1,24
E2RQF8	Extracellular matrix protein 1 (human homolog)	24,1	0,191	38	93	1,88	0	0,257	0	23	0,00
J9P669	Cadherin 5	3,3	0,141	19	29	0,30	5,54	0,262	4	4	1,45
J9PAA4	Carboxypeptidase N subunit 2	5,81	0,141	97	110	0,72	177	0,038	4	142	0,19
F1PLT8	Sulfhydryl oxidase	2,92	0	20	0	#DIV/0!	0	0,343	0	30	0,00
J9P319	Osteomodulin	0	0,13	0	29	0,00	2,9	0,216	12	18	0,42
E2RJE0	Cartilage oligomeric matrix protein	0	0,155	0	47	0,00	1000	0	3	0	#DIV/0!
F1PV43	Capping actin protein of muscle Z-line alpha subunit 3	11,1	0	7	0	#DIV/0!	n.f.				
F1Q1P0	Coiled-coil domain containing 178	39,7	0,213	19	7	22,95	17,2	0,116	14	2	13,97
E2R416	Lumican	44,5	0,15	36	114	2,11	11,9	0,051	58	118	0,30
F6Y120	Serine/arginine repetitive matrix protein 3 (homolog)	20,90	0,38	14	12	9,22	3,78	0,142	10	12	0,45
Q2YF02	Vitronectin (fragment),	68,7	0,303	45	64	14,64	2,38	0,11	15	9	0,44
H2BF45	Attractin (fragment)	n.a.					4,14	0,002	7	39	0,00
F1Q117	Attractin	n.a.					2,75	0,0003	3	9	0,00

Table S4: Mass spectrometric identified biomarker candidates

Mean ratios of AM/NM and CF/NF as well as number hits that determine an altered protein as BM candidate.
Calculation of mean ratios, cf. Formula 1 in Supplementary Methods. The number of hits corresponds to protein concentration in sub-fractions included.
Here all results are given, proteins and protein clusters higher as well as lower in affected animals.
"1000" was set for an extraordinary high ratio, even when much higher, in order to apply value depending color code of Excel.
"DIV/0": division by zero, the ratio cannot calculated since there was no hit/peptide in the control sample. Figure 2 (main document) represent an excerpt from this table.

Altered proteins in dogs (7. wk)		**Males**					**Females**				
		in sub-fractions				**overall trend**	**in sub-fractions**				**overall trend**
		Mean ratio (AM/NM)		**Number of hits**			**Mean ratio (CF/NF)**		**Number of hits**		
ID	**Annotation**	**higher**	lower	**higher**	lower		**higher**	lower	**higher**	lower	
Plasma proteins		**in AM**	in AM	**in AM**	in AM	in AM	**in CF**	in CF	**in CF**	in CF	in CF
F1PNV5	Kallikrein B1	1000	0,245	15	32	114,84	0	0,158	0	39	0,00
E2R886	Kininogen 1	56,2	0,043	523	609	2,08	20,3	0,227	106	361	1,35
E2QUV3	α2-HS glycoprotein	326	0,15	1056	3178	16,25	n.a.				
F1P6E1	Complement C1s	0	0,041	0	153	0,00	3,11	0	67	0	#DIV/0!
F1PNG7	Complement C1r	n.a.					115	0,105	24	29	9,99
J9P4B4	Complement C1q A chain	1000	0,133	14	53	35,13	n.f.				
J9P1G2	Complement C1q B chain	1000	0,229	60	128	107,34	4,09	0,155	22	85	0,16
E2RJC2	Complement C1q C chain	1000	0,078	90	89	78,88	3,21	0,062	17	51	0,07
E2RS79	Complement C2 (human homolog)	3,44	0,026	21	14	0,13	0	0,14	0	14	0,00
F1PIX8	Complement C3	32,2	0,086	4565	27225	0,46	34,77	0,102	2165	4973	1,54
J9PAD1	Complement C4 (human homolog)	29,6	0,057	509	3883	0,22	150	0,107	125	2148	0,93
F1PWR2	Complement C4 (human homolog)	6,09	0,077	316	759	0,20	37,3	0,094	84	615	0,48
F1P7J4	Complement C5	21,3	0,04	68	467	0,12	14,9	0,154	17	311	0,13
E2RGT6	Complement C6	1000	0,025	177	127	34,84	0	0,089	0	123	0,00
E2RG01	Complement C7	1000	0,157	56	257	34,21	0	0,225	0	82	0,00
E2R109	Complement C8 alpha chain	1000	0,143	14	45	44,49	2,26	0,011	1	10	0,00
E2R141	Complement C8 beta chain	2,41	0,197	4	76	0,02	n.a.				
J9P8Z6	Complement C9	5,79	0	8	0	#DIV/0!	n.a.				
F1PY40	Complement factor I	66,2	0,164	48	462	1,13	49,5	0,065	30	161	0,60
J9NTL7	Complementfactor H (homolog in mammals)	69,5	0,086	162	2069	0,47	47,6	0,057	87	2884	0,08
E2RS80	Complementfactor B (homolog in primates)	39	0,078	452	1516	0,91	25	0,156	57	762	0,29
F1PGM9	Complement component 4 binding protein alpha	170,4	0,17	1105	2308	13,87	20,2	0,11	279	1332	0,47
G1K2D9	Haptoglobin	114	0,07	1849	3024	4,88	0	0,127	0	5882	0,00
F6UME0	α2-macroglobulin	77,55	0,093	2383	6931	2,48	179	0,087	277	3986	1,08
F6Y713	α1-acid glycoprotein	23	0,182	816	367	9,31	13,6	0,253	29	1467	0,07
P33703	APOH, Beta-2-glycoprotein 1	42,2	0,177	293	582	3,76	15,7	0,077	112	328	0,41
T2KEN6	Pentraxin	3,53	0,006	117	41	0,06	0	0,307	0	174	0,00
A1ILJ0	Alpha-1-antitrypsin	6,2	0,076	147	52	1,33	4,08	0,186	24	175	0,10
F1PAX2	Ceruloplasmin	4,38	0,055	363	1283	0,07	6,28	0,159	49	688	0,07
F1PCE5	Serpin family A member 1	114	0,151	396	1353	5,04	53,1	0,18	378	1233	2,93
F1PH86	Serpin family A member 3	n.f.					2,4	0,298	17	107	0,11
E2RMF9	Serpin family A member 5	0	0,164	0	39	0,00	34	0,195	4	20	1,33
F1PB85	Serpin family A member 7	8,55	0,319	20	22	2,48	0	0,245	0	23	0,00
F1PYX9	Serpin family G member 1	11,3	0,064	183	944	0,14	12,9	0,13	24	499	0,08
J9P8Q8	Serpin family D member 1	2,17	0,233	12	245	0,02	2,53	0,334	29	86	0,28
J9NSS7	Leucine rich alpha-2-glycoprotein 1	22	0,275	289	133	13,15	10,6	0,208	68	348	0,43
J9NVE9	Serum amyloid A	86,4	0	70	0	#DIV/0!	0	0,148	0	275	0,00
F1PAL5	Angiotensinogen	19,4	0,289	48	75	3,59	6,4	0,186	28	40	0,83
Q7M310	Angiotensin I	2,84	0,277	69	38	1,43	n.f.				
F1PN98	Coagulation factor V	3,35	0	107	0	#DIV/0!	0	0,007	0	33	0,00
J9NSF9	Prothrombin	51	0,17	292	797	3,18	11,9	0,214	35	350	0,25
F1PZR4	Hemopexin	44,9	0,136	83	563	0,90	68,7	0,166	144	1162	1,41
F1Q421	Plasminogen	n.a.					52,6	0,251	97	403	3,18
J9P430	Transferrin	20,4	0,123	1424	6332	0,56	29,1	0,142	191	4721	0,17
F6V1W9	Transferrin	4,12	0,335	11	5	3,04	3,95	0,23	3	3	0,91
J9JHX7	Serotransferrin (homolog, several species)	9,23	0,344	355	776	1,45	20,2	0,208	102	477	0,90
E2QZQ1	Serotransferrin (homolog, several species)	6,75	0,256	17	55	0,53	1000	0,09	9	20	40,50
F1PKX3	Coagulation factor XIII A chain	2,76	0,103	6	83	0,02	41,2	0,401	8	3	44,06
F1Q041	Coagulation factor XIII B chain	1000	0,025	6	38	3,95	1000	0,068	6	19	21,47
F1PSS8	Protein S	2,98	0,125	26	170	0,06	0	0,174	0	121	0,00
F1Q4A3	Coagulation factor X	0	0,236	0	25	0,00	20,5	0,013	18	2	2,40
E2R4E7	Afamin	6,76	0,318	297	1075	0,59	14	0,268	37	604	0,23
F6Y3P9	Gelsolin	34,5	0,259	218	529	3,68	20	0,23	91	114	3,67
E2R5U8	Transthyretin	8,76	0,218	65	1143	0,11	n.a.				
A0A1K0FUG	Globin A1	109	0,103	229	60	42,85	1000	0,01	21	32	6,56
A0A1K0GGH	Globin A2	103	0,047	118	34	16,80	0	0,157	0	42	0,00
J9NXL3	Hemoglobin subunit alpha (dog homolog)	115	0,101	155	52	34,62	2,8	0,11	2	101	0,01
E2R9B6	Fetuin B	30,4	0,221	148	212	4,69	2	0,24	16	228	0,03
F1PYM4	Insulin like growth factor binding protein acid labile subunit	31	0,258	15	147	0,82	3,15	0,24	21	10	1,59
B5U1S6	Adiponectin (fragment)	1000	0,132	22	56	51,86	1000	0,004	14	29	1,93
F1PDJ7	Alpha-2-glycoprotein 1	3,75	0,292	20	11	1,99	n.a.				
E2RPW3	Paraoxonase 1	3,55	0,018	33	28	0,08	1000	0,047	45	8	264,38
J9P8B0	Dipeptidyl peptidase 4	2,31	0	10	0	#DIV/0!	n.a.				
F1PCK2	α1-B glycoprotein	21,9	0,02	714	469	0,67	25,2	0,127	978	1688	1,85
F1Q4D9	Retinol binding protein 4	8,97	0,18	12	98	0,20	25,06	0,304	13	20	4,95
E2RPB8	C-type lectin domain family 3 member B	n.a.					2,59	0,279	11	134	0,06
E2RKQ6	Galectin 3 binding protein	2,24	0,253	18	6	1,70	3,3	0,067	24	64	0,08
Apolipoproteins											
J9P843	Apo AI	325	0,16	4231	17259	12,75	41,1	0,061	325	1356	0,60
E2RE76	Apo AIV	6,76	0,115	324	574	0,44	21,5	0,21	164	146	5,07
P56595	Apo CI	4,72	0,206	8	147	0,05	3,97	0	14	6	#DIV/0!
9NWJ6	Apo CII	15,8	0,153	58	770	0,18	50,3	0,274	33	35	12,99
D5G334	Apo E4 (fragment)	4,8	0,162	44	212	0,16	37,4	0,233	55	116	4,13
F1PJ74	Apo E	15	0,19	32	269	0,34	33	0,279	34	107	2,93
E2RQ71	Apo M	6,86	0,278	22	458	0,09	2,57	0,401	26	23	1,16
F1P8Z5	Apo B	87	0,124	470	7485	0,68	19,3	0,107	115	2837	0,08
E2RNM1	Apo D	11,7	0,16	44	111	0,74	108,2	0,124	61	27	30,31
Intracellular proteins											
F1PZK8	Dynein heavy chain domain 1	1000	0,175	24	23	182,61	3,24	0,416	3	3	1,35
E2RB62	Myosin IB	6,19	0,147	2	8	0,23					
E2R1Q3	Myosin XVIIIB	n.a.					3,02	0	5	0	#DIV/0!
J9P187	Myosin IXA	894	0,202	94	257	66,05	328	0,278	51	60	77,51
J9P007	Kinesin-like protein	3,43	0	8	0	#DIV/0!	3,46	0,146	4	2	1,01
F1PM26	CD109 molecule	17,3	0,16	20	9	6,15	n.f.				
J9P216	Formin 1	1000	0,266	10	13	204,62	4,95	0	9	0	#DIV/0!
J9P7F7	Ficolin 1	1000	0,123	7	38	22,66	4,1	0,017	23	13	0,12
F1PAQ3	Maltase-glucoamylase	6,49	0,284	70	185	0,70	2,18	0,005	11	26	0,00
J9P5V6	Talin 1	17,6	0,158	3	7	1,19	128	0,247	1	4	7,90
E2RFS6	Sacsin molecular chaperone	12	0,418	4	7	2,87	12,7	0,333	3	5	2,54

E2QV33	Mediator complex subunit 22 (RNA-Pol)	98,4	0	26	0	#DIV/0!	0	0,097	0	28	0,00
E2R926	Fukutin	29,5	0,021	12	2	3,72	n.f.				
E2RP26	Filamin C	0	0,026	0	14	0,00	n.f.				
E2RK65	Kelch like family member 8	7,84	0,04	10	4	0,78	n.f.				
F1PRY8	Dispatched RND transporter family member 2	n.a.					1000	0	5	3	#DIV/0!
F6Y1C9	DNA Polymerase	n.a.					4,14	0,232	20	4	4,80
A0A0A0MPC!	Trafficking protein particle complex subunit 2	n.f.					1000	0	9	0	#DIV/0!
J9NYC0	Microfibril associated protein 4	n.a.					0	0,181	0	12	0,00
J9P514	RB associated KRAB zinc finger	6,05	0,326	2	15	0,26	9,04	0	6	0	#DIV/0!
J9P653	Ciliogenesis-associated TTC17-interacting protein (human homolo	10,1	0	10	0	#DIV/0!	2,9	0,396	2	14	0,16
J9NYQ5	Growth arrest specific 2 like 3	6,17	0,33	4	2	4,07	11,5	0,437	7	1	35,18
E2R1C3	Proteasome subunit alpha type	0	0,186	0	35	0,00	2,27	0,08	33	6	1,00
J9NYS3	Regulating synaptic membrane exocytosis 2	2,18	0,367	5	4	1,00	0	0,276	0	5	0,00
E2RF52	Proteasome subunit alpha type	n.f.					171	0	7	0	#DIV/0!

Extracellular matrix proteins

J9P8M2	Fibronectin	28,9	0,164	386	3982	0,46	32,6	0,157	39	1842	0,11
E2QTQ1-	Ankyrin repeat and BTB domain containing 1	0	0,346	0	4	0,00	92	0,015	29	30	1,33
J9NV47	Hyaluronan binding protein 2	31,6	0	82	0	#DIV/0!	2,18	0,116	4	5	0,20
F1Q1K9	Hyaluronan binding protein 2	31,3	0	16	0	#DIV/0!	n.a.				
F1Q3I5	Collagen α1(I) chain	2,87	0	74	0	#DIV/0!	0	0,197	0	136	0,00
E5G723	Collagen α1 (I) (Fragment)	31,05	0,096	6	12	1,49	1000	0,106	13	10	137,80
F1PHY1	Collagen α2 (I) chain	3,26	0,254	11	1	9,11	0	0,219	0	73	0,00
F1PJH3	Collagen type XIII alpha 1 chain	455	0	36	0	#DIV/0!	0	0,235	0	36	0,00
J9NRV7	Fibrinogen alpha chain	265	0,078	1394	2959	9,74	0	0,092	0	1970	0,00
F1PW65	Fibrinogen beta chain	96,9	0,095	1600	4493	3,28	37,4	0,075	483	3248	0,42
F1P8G0	Fibrinogen gamma chain	399	0,1	1683	3016	22,27	53,4	0,116	200	1983	0,62
F1Q418	Inter-alpha-trypsin inhibitor heavy chain 1	4,02	0,127	135	829	0,08	2,98	0,053	158	618	0,04
F1PG39	Inter-alpha-trypsin inhibitor heavy chain 2	3,09	0,1	142	716	0,06	42	0,094	38	554	0,27
J9P7I3	Inter-alpha-trypsin inhibitor heavy chain 3	0	0,139	0	484	0,00	25,7	0,076	81	115	1,38
H9GWY3	Inter-alpha-trypsin inhibitor heavy chain 4	59,9	0,157	423	2238	1,78	5,51	0,083	146	846	0,08
J9NUI6	Alpha-1-microglobulin/bikunin precursor	33,6	0,055	27	252	0,20	75	0,053	36	115	1,24
E2RQF8	Extracellular matrix protein 1 (human homolog)	24,1	0,191	38	93	1,88	0	0,257	0	23	0,00
J9P669	Cadherin 5	3,3	0,141	19	29	0,30	5,54	0,262	4	4	1,45
J9PAA4	Carboxypeptidase N subunit 2	5,81	0,141	97	110	0,72	177	0,038	4	142	0,19
F1PLT8	Sulfhydryl oxidase	2,92	0	20	0	#DIV/0!	0	0,343	0	30	0,00
J9P319	Osteomodulin	0	0,13	0	29	0,00	2,9	0,216	12	18	0,42
E2RJE0	Cartilage oligomeric matrix protein	0	0,155	0	47	0,00	1000	0	3	0	#DIV/0!
F1PV43	Capping actin protein of muscle Z-line alpha subunit 3	11,1	0	7	0	#DIV/0!	n.f.				
F1Q1P0	Coiled-coil domain containing 178	39,7	0,213	19	7	22,95	17,2	0,116	14	2	13,97
E2R416	Lumican	44,5	0,15	36	114	2,11	11,9	0,051	58	118	0,30
F6Y120	Serine/arginine repetitive matrix protein 3 (homolog)	20,90	0,38	14	12	9,22	3,78	0,142	10	12	0,45
Q2YF02	Vitronectin (fragment),	68,7	0,303	45	64	14,64	2,38	0,11	15	9	0,44
H2BF45	Attractin (fragment)	n.a.					4,14	0,002	7	39	0,00
F1Q117	Attractin	n.a.					2,75	0,0003	3	9	0,00

Supplementary Table S5: Concentrations of some BM candidates determined by ELISA in dog samples.

BM candidate	Sample	Concentration				Unit	n	ELISA
		AM	NM	CF	NF			
LRG1	s	**26.26**	**9.70**			ng/ml	1	MBS075175
	p	27.03	28.19			ng/ml	1	
	u	***10.10***	***8.41***			µg/g c	1	
gelsolin	s	**214.1**(4)	**194.4**	**162.9**	**140.3**(2)	ng/ml[a]	1	MBS2603447
	s	**24.11**	**18.03**	16.33	19.91	µg/ml[b]	2	
	p	**28.70**	**9.48**	14.45	19.11	µg/ml[b]	2	
	u	***0.17***	***0.00***	0.68	1.41	µg/g c	2	
lumican	p	16.1	21.6	15.0	17.8	ng/ml	1	MBS2607240
PICP	p	**12.4**	**9.51**	7.31	9.68	ng/ml	1	MBS2608196
ColXIII	p	**0.338**	**0.137**	0.266	0.177	ng/ml	1	SEC138Hu
	u	***0.576***	***0***	0.172	0.115	µg/g c	1	
SAA	p	**6.67**	**1.89**	4.09	2.20	µg/ml	1	MBS740421[c]
	u	***23.08***	***9.46***	8.02	7.34	µg/g c	1	
	p	7.53	7.27	7.24	6.56	ng/ml	1	MBS1602508[d]
	u	**52.29**	**43.65**	***15.06***	***26.96***	ng/g c	1	
ADN	s	4.96	7.15(1)	5.68	5.77	µg/ml	3	RD191023100
	p	5.41	7.06(1)	**6.72**	**4.78**	µg/ml	3	
	u	***4.59***	***0.00***	0.36	1.43	µg/g c	3	
TGFβ1	p	8.27	12.30	4.62	5.18	ng/ml	1	RAF122R
	s	31.88		47.47	22.92	ng/ml	1	
	u	8.05	3.97	4.60	3.28	µg/g c	1	

ELISA (last column) have been performed by according to the supplier´s instructions each in duplicate and with different dilutions to meet the measuring range of the respective assay.
n: sample count for all of the line, in parenthesis when different from the value given in 8th column.
s: serum; p:plasma; u: urine. In urine BM concentrations are normalized by creatinine (c). Sample dilution: [a]1 to 20, [b]1 to 2500. ELISA detects: [c]intact protein, [d]c-terminal fragment.
Bold: trend in blood in accordance with proteomic data of distinct clusters, cf. Table 4; ***bold and italic***: trend in urine in accordance with the trend in blood. Empty cells: no more samples available.

Pearson	ADP	a1AGP	AGT	Col-XIII	GS	LRGP1	HABP2	PICP	TGFß	VTN	C9	C4BP	CRP	CFH	CFI	FMN	LUM	FGG	C1q	Spearman
ADP		.284** 0.000	.380** 0.000	-0.056 0.367	.365** 0.000	.271** 0.000	.172** 0.006	.417** 0.000	.210** 0.001	.326** 0.000	.398** 0.000	-0.049 0.417	-0.077 0.207	-0.042 0.497	.281** 0.000	.193** 0.002	-0.244 0.251	.213** 0.000	0.107 0.181	**ADP**
a1AGP	.318** 0.000		.410** 0.000	.280** 0.000	.511** 0.000	.149* 0.014	.320** 0.000	.387** 0.000	0.043 0.500	.248** 0.000	__.652**__ 0.000	.404** 0.000	.201** 0.001	.489** 0.000	__.703**__ 0.000	.333** 0.000	.425* 0.038	.420** 0.000	.415** 0.000	**a1AGP**
AGT	.495** 0.000	.260** 0.000		.141* 0.024	__.746**__ 0.000	.128* 0.037	.492** 0.000	__.517**__ 0.000	.353** 0.000	__.694**__ 0.000	__.570**__ 0.000	.256** 0.000	0.098 0.116	.186** 0.003	__.663**__ 0.000	.372** 0.000	__.674**__ 0.000	__.521**__ 0.000	.342** 0.000	**AGT**
Col-XIII	0.041 0.506	.256** 0.000	.327** 0.000		.250** 0.000	.185** 0.002	.380** 0.000	0.066 0.291	-.178** 0.005	-0.046 0.455	.133* 0.032	__.527**__ 0.000	.317** 0.000	__.529**__ 0.000	.313** 0.000	.299** 0.000	0.290 0.170	.363** 0.000	.290** 0.000	**Col-XIII**
GS	.493** 0.000	.221** 0.000	__.702**__ 0.000	.212** 0.001		0.117 0.062	.422** 0.000	.409** 0.000	.161* 0.014	.478** 0.000	__.603**__ 0.000	.315** 0.000	0.123 0.052	.343** 0.000	__.751**__ 0.000	.402** 0.000	.484* 0.016	.467** 0.000	.383** 0.000	**GS**
LRGP1	.251** 0.000	0.095 0.119	.258** 0.000	0.108 0.079	0.088 0.159		.154* 0.014	0.091 0.134	0.045 0.482	0.047 0.437	0.098 0.111	.330** 0.000	.243** 0.000	.228** 0.000	.177** 0.004	.354** 0.000	.431* 0.035	.336** 0.000	.350** 0.000	**LRGP1**
HABP2	0.078 0.217	.384** 0.000	.242** 0.000	.310** 0.000	.128* 0.040	0.041 0.511		.290** 0.000	-0.049 0.459	.258** 0.000	.337** 0.000	.367** 0.000	.228** 0.000	.326** 0.000	.458** 0.000	.364** 0.000	__.614**__ 0.001	.374** 0.000	.176* 0.028	**HABP2**
PICP	__.584**__ 0.000	.425** 0.000	.390** 0.000	0.081 0.193	.441** 0.000	0.078 0.199	.233** 0.000		__.511**__ 0.000	__.561**__ 0.000	.467** 0.000	0.109 0.076	-0.032 0.590	0.121 0.051	.493** 0.000	0.063 0.307	0.144 0.511	.325** 0.000	.267** 0.001	**PICP**
TGFß	0.039 0.542	.144* 0.024	0.030 0.645	0.070 0.274	0.018 0.780	-0.019 0.764	__.586**__ 0.000	.230** 0.000		.460** 0.000	.263** 0.000	-.155* 0.015	-.132* 0.039	-0.088 0.176	.167** 0.010	0.042 0.511	0.060 0.779	.162* 0.011	.232** 0.006	**TGFß**
VTN	.416** 0.000	.463** 0.000	__.575**__ 0.000	0.046 0.451	__.553**__ 0.000	.259** 0.000	.162** 0.009	.456** 0.000	0.010 0.870		__.519**__ 0.000	.127* 0.036	-0.007 0.914	-0.030 0.627	.459** 0.000	0.112 0.069	.436* 0.033	.405** 0.000	.224** 0.005	**VTN**
C9	__.560**__ 0.000	.456** 0.000	__.563**__ 0.000	0.093 0.134	__.531**__ 0.000	.271** 0.000	.229** 0.000	.398** 0.000	0.028 0.669	__.626**__ 0.000		.240** 0.000	.167** 0.007	.358** 0.000	__.704**__ 0.000	.270** 0.000	__.535**__ 0.007	.372** 0.000	__.502**__ 0.000	**C9**
C4BP	__.548**__ 0.000	.370** 0.000	.278** 0.000	.263** 0.000	.336** 0.000	.149* 0.014	.267** 0.000	.315** 0.000	0.003 0.965	.247** 0.000	.490** 0.000		.359** 0.000	__.577**__ 0.000	.492** 0.000	.342** 0.000	__.713**__ 0.000	.437** 0.000	.291** 0.000	**C4BP**
CRP	-0.041 0.496	0.034 0.585	0.024 0.701	.397** 0.000	0.039 0.536	.214** 0.00	0.066 0.298	-0.033 0.581	-0.011 0.858	-0.016 0.788	0.001 0.983	.123* 0.044		.309** 0.000	.272** 0.000	.255** 0.000	__.574**__ 0.003	.244** 0.000	.272** 0.001	**CRP**
CFH	.411** 0.000	.237** 0.000	.545** 0.000	.252** 0.000	__.747**__ 0.000	.173** 0.005	.352** 0.000	.315** 0.000	0.010 0.872	.486** 0.000	__.560**__ 0.000	.444** 0.000	0.101 0.104		.490** 0.000	.339** 0.000	.460* 0.024	.306** 0.000	.393** 0.000	**CFH**
CFI	.409** 0.000	.596** 0.00	.484** 0.000	.229** 0.000	__.686**__ 0.000	0.082 0.182	.467** 0.000	.446** 0.000	0.029 0.655	__.601**__ 0.000	.486** 0.000	.474** 0.000	0.069 0.268	__.740**__ 0.000		.367** 0.000	__.516**__ 0.010	.497** 0.000	__.545**__ 0.000	**CFI**
FMN	.122* 0.047	.383** 0.000	.371** 0.000	__.569**__ 0.000	.138* 0.030	0.096 0.116	.464** 0.000	.140* 0.022	0.011 0.867	0.094 0.129	.178** 0.004	.388** 0.000	.167** 0.006	.330** 0.000	.314** 0.000		__.772**__ 0.000	.346** 0.000	.352** 0.000	**FMN**
LUM	-0.086 0.689	0.230 0.279	.505* 0.012	0.121 0.572	0.152 0.477	0.087 0.686	0.241 0.256	-0.093 0.671	0.292 0.166	0.156 0.465	0.132 0.537	.475* 0.019	0.026 0.903	0.191 0.372	0.116 0.589	__.633**__ 0.002		__.569**__ 0.006	0.317 0.141	**LUM**
FGG	.176** 0.004	.343** 0.000	.401** 0.000	.452** 0.000	.284** 0.000	.154* 0.011	__.600**__ 0.000	.192** 0.002	0.019 0.770	.323** 0.000	.353** 0.000	.397** 0.000	.201** 0.001	__.527**__ 0.000	__.560**__ 0.000	__.730**__ 0.000	0.411 0.057		.396** 0.000	**FGG**
C1q	-0.024 0.766	0.020 0.801	-0.030 0.710	.318** 0.000	0.022 0.783	__.694**__ 0.000	0.035 0.665	0.005 0.955	0.017 0.841	0.021 0.795	0.041 0.611	.215** 0.007	__.558**__ 0.000	.456** 0.000	0.124 0.121	0.073 0.369	-0.124 0.575	0.089 0.268		**C1q**

Supplementary Table S6: Correlation of each BM with each other’s.

Analyses were performed by SPSS (v.27). Lower left halve: correlation according Pearson; upper right halve: correlation according Spearman. Each cell shows the correlation coefficient (upper figure) and a p-value (lower figure).
* and ** indicate significant and highly significant correlations proposed by SPSS. Notwithstanding that, we set a correlation coefficient >0.500 (Pearson) moderately significant and >0.600 highly significant and mark these values in blue (Pearason) and green (Spearman).

Table S7: Correlation of serum and urinary BM candidates with UACR and serum creatinine in patients with AS and similar diseases

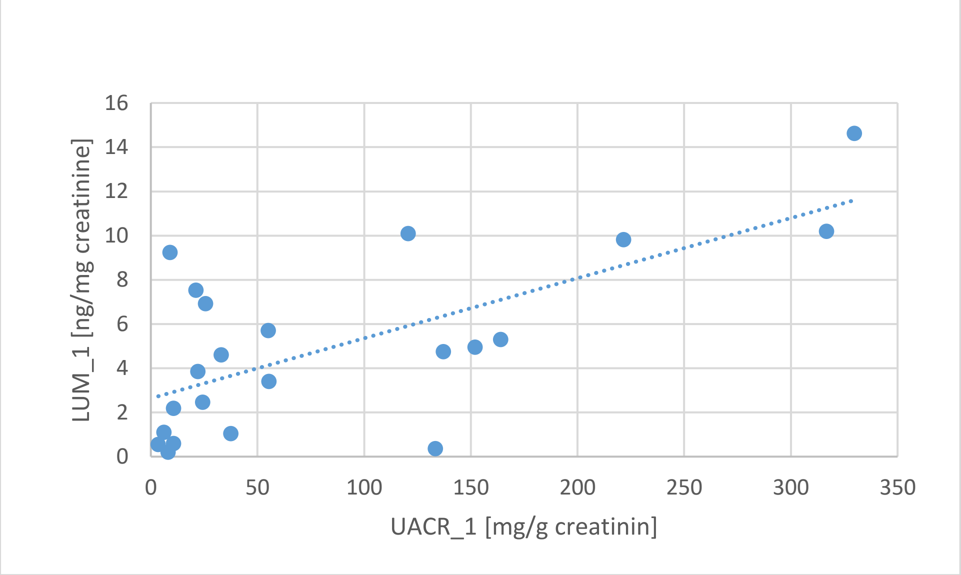
	UACR						Serum creatinine					
BM in→	**Serum**			**Urine**			**Serum**			**Urine**		
↓	**Pearson**	**Spearman**	**n**	**Pearson**	**Spearman**	**n**	**Pearson**	**Spearman**	**n**	**Pearson**	**Spearman**	**n**
ADP	0.110 0.515	.442** 0.006	37	-0.101 0.514	-0.006 0.968	44	-0.260 0.110	-0.257 0.114	39	-0.100 0.512	-0.047 0.761	45
a1AGP	-0.220 0.303	0.047 0.828	24	0.117 0.459	.628** <.001	42	-0.160 0.444	-0.129 0.538	25	-0.218 0.160	-0.200 0.199	43
AGT	.336* 0.042	0.060 0.724	37	0.139 0.382	.426** 0.005	42	.473** 0.002	.524** <.001	39	-0.169 0.278	-0.166 0.287	43
ColXIII	-0.072 0.672	0.191 0.257	37	0.242 0.122	.387* 0.011	42	.324* 0.044	0.087 0.6	39	-.328* 0.032	-.324* 0.034	43
GS	0.039 0.817	-0.030 0.858	37	.363* 0.018	.467** 0.002	42	.358* 0.025	.406* 0.010	39	-0.096 0.540	-0.078 0.619	43
LRGP1	-0.140 0.375	0.012 0.938	42	0.213 0.165	.434** 0.003	44	-0.004 0.980	-0.104 0.501	44	-0.214 0.158	-0.277 0.065	45
HABP2	0.271 0.104	0.270 0.107	37	0.166 0.293	.497** <.001	42	-0.135 0.412	-0.216 0.186	39	-.398** 0.008	-.335* 0.028	43
PICP	-0.176 0.266	0.133 0.400	42	-0.065 0.686	0.152 0.342	41	-.356* 0.019	-0.301 0.050	43	0.048 0.765	-0.152 0.343	41
TGFß	-0.166 0.305	0.262 0.103	40	-0.003 0.983	0.247 0.107	44	-.430** 0.005	-.503** <.001	41	0.030 0.847	0.078 0.613	45
VTN	-0.226 0.151	-.383* 0.012	42	0.106 0.504	0.246 0.116	42	0.227 0.138	0.222 0.147	44	-0.068 0.665	-0.065 0.680	43
C9	-0.021 0.900	0.085 0.610	38	0.145 0.358	.631** <.001	42	-0.041 0.804	-0.130 0.430	39	-0.282 0.067	-0.265 0.086	43
C4BP	0.003 0.988	0.156 0.356	37	0.295 0.057	.654** <.001	42	-0.078 0.635	-0.166 0.313	39	-0.296 0.054	-.313* 0.041	43
CRP	-0.093 0.549	0.001 0.993	44	-0.078 0.622	.375* 0.014	42	0.025 0.870	-0.077 0.617	45	0.041 0.797	-0.294 0.059	42
LUM	0.064 0.789	-0.168 0.478	20	.651** 0.002	.510* 0.022	20	0.144 0.532	0.241 0.293	21	-0.344 0.138	-0.353 0.126	20
FMN	-0.111 0.527	0.155 0.373	35	0.173 0.292	.514** <.001	39	0.044 0.797	-0.151 0.373	37	-.341* 0.033	-.365* 0.022	39
CFH	0.002 0.994	0.420 0.066	20	0.179 0.257	.605** <.001	42	0.011 0.965	0.044 0.855	20	-0.252 0.103	-.414** 0.006	43
CFI	0.298 0.157	.620** 0.001	24	0.196 0.213	.620** <.001	4	-0.322 0.125	-0.297 0.159	24	-0.280 0.069	-.359* 0.018	43
FGG	-0.603 0.282	-.900* 0.037	5	0.145 0.38	.326* 0.043	39	0.457 0.543	0.400 0.600	4	-0.306 0.055	-0.228 0.157	40
C1q	0.050 0.767	-0.029 0.865	38	-0.115 0.516	0.339 0.05	34	-0.047 0.776	0.106 0.522	39	-0.124 0.485	-.441** 0.009	34

First visit for sample set 1.

Correlation analyses were performed by SPSS (v.27). Cells contain the correlation coefficients (upper line) and the p-value (lower line). Significant correlations calculated by this software are indicated by stars and p-values below 0.05. We do not follow these proposals rather considered correlation coefficients of > 0.5 (bright grey) as moderately and > 0.6 (dark grey) as highly correlating.

Graphical visualization of correlation considered as significant:

Urinary lumican (ULUM) of first samples of sample set 1 with UACR of first and additional of the second samples



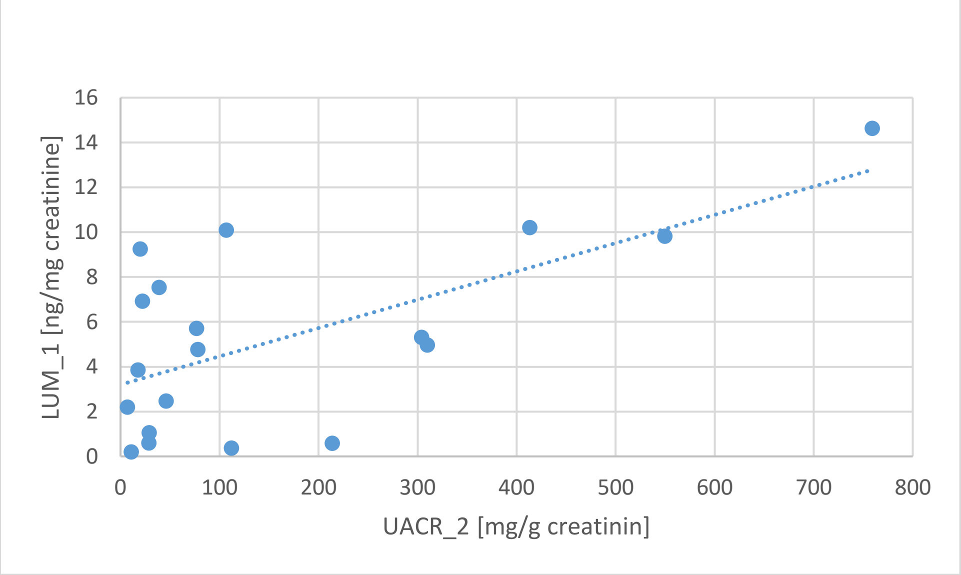
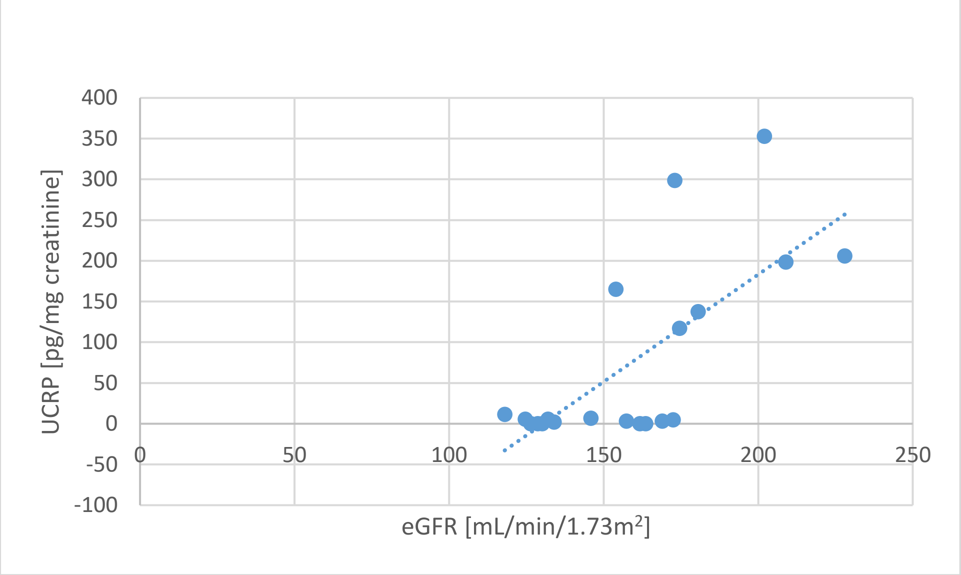


Table S8: Correlation of serum and urinary BM candidates with eGFR and cGFR in patients with AS and similar diseases.

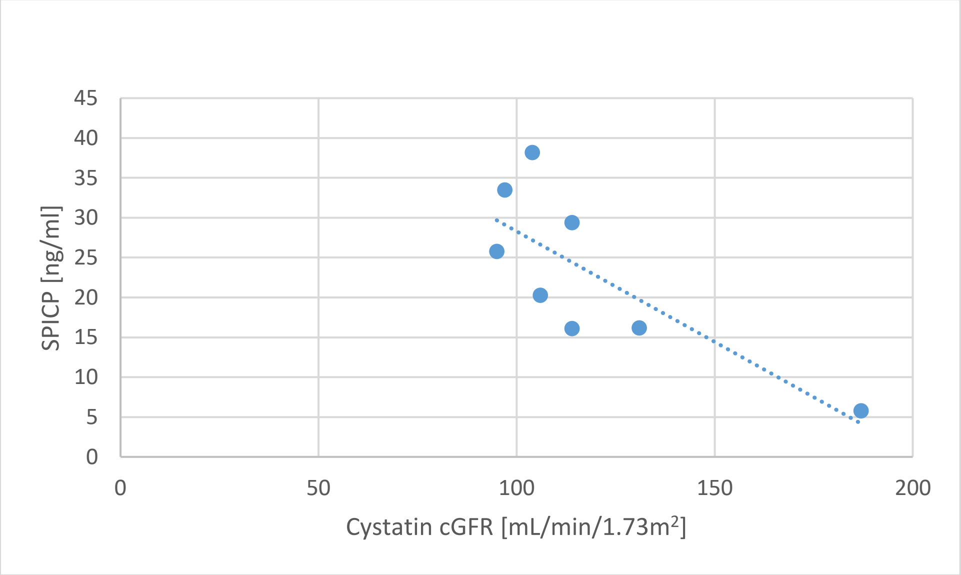
	eGFR						cGFR					
BM in→	**Serum**			**Urine**			**Serum**			**Urine**		
↓	**Pears**	**Spearm**	**n**	**Pears**	**Spearm**	**n**	**Pears**	**Spearm**	**n**	**Pears**	**Spearm**	**n**
ADP	0.360 0.188	0.100 0.723	15	0.055 0.809	-0.041 0.855	22	-0.864 0.136	-1.000**	4	-0.013 0.971	0.235 0.514	10
a1AGP	0.346 0.189	0.265 0.322	16	-0.095 0.692	-0.062 0.796	20	-0.559 0.249	-.812* 0.05	6	0.024 0.952	0.192 0.620	9
AGT	-0.478 0.071	-.557* 0.031	15	-0.165 0.487	-0.29 0.214	20	0.811 0.189	0.200 0.800	4	-0.224 0.562	-0.134 0.730	9
ColXIII	-0.276 0.319	-0.35 0.201	15	0.399 0.081	0.383 0.095	20	-0.573 0.427	-0.6 0.4	4	0.181 0.641	.684* 0.042	9
GS	-0.448 0.094	-.582* 0.023	15	0.095 0.690	0.062 0.796	20	-0.342 0.658	-0.600 0.400	4	0.214 0.581	0.494 0.177	9
LRGP1	-0.155 0.514	-0.018 0.940	20	.629** 0.002	.426* 0.048	22	-0.448 0.227	-0.527 0.145	9	-0.021 0.953	0.046 0.899	10
HABP2	-0.101 0.720	-0.021 0.940	15	0.404 0.077	0.055 0.818	20	-0.915 0.085	-0.800 0.200	4	0.45 0.225	0.492 0.179	9
PICP	0.231 0.342	0.028 0.909	19	-0.321 0.167	-0.316 0.175	20	-.783* 0.022	-.719* 0.045	8	-0.312 0.351	-0.164 0.629	11
TGFß	0.092 0.709	0.205 0.399	19	0.160 0.478	-0.026 0.908	22	0.176 0.677	0.443 0.272	8	-0.497 0.144	-0.618 0.057	10
VTN	-0.282 0.229	-0.311 0.182	20	-0.321 0.168	-0.381 0.098	20	0.583 0.100	-0.209 0.589	9	-0.553 0.123	-0.559 0.118	9
C9	-0.469 0.078	-0.129 0.648	15	-0.075 0.754	-0.272 0.246	20	0.012 0.985	-0.051 0.935	5	-0.184 0.636	-0.385 0.306	9
C4BP	-0.026 0.927	0.136 0.630	15	0.124 0.603	0.078 0.743	20	-0.403 0.597	-0.400 0.600	4	-0.193 0.619	-0.059 0.881	9
CRP	0.243 0.276	0.099 0.662	22	.711** <.001	.564** 0.01	20	0.141 0.697	0.505 0.137	10	0.064 0.851	0.587 0.058	11
LUM	0.421 0.724	0.500 0.667	3	0.827 0.380	0.5 0.667	3			0			0
FMN	0.191 0.495	0.164 0.558	15	0.132 0.590	0.087 0.724	19	-0.744 0.256	-0.800 0.200	4	0.06 0.87	0.249 0.487	10
CFH	-0.087 0.798	-0.245 0.467	11	.509* 0.022	0.367 0.112	20			1	0.188 0.629	0.418 0.262	9
CFI	0.213 0.447	0.189 0.499	15	0.089 0.708	0.189 0.425	20	0.329 0.589	0.051 0.935	5	-0.087 0.824	0.162 0.678	9
FGG	-0.772 0.228	-0.800 0.200	4	0.230 0.330	0.152 0.524	20	0.160 0.840	0.000 1.000	4	0.248 0.489	0.219 0.544	10
C1q	0.169 0.546	0.100 0.723	15	0.418 0.177	0.368 0.240	12	-0.622 0.378	-0.800 0.200	4	-0.626 0.374	-0.800 0.200	4

Graphical visualization of correlations considered as significant:

Urine CRP with eGFR



Serum PICP and HABP2 with cGFR.



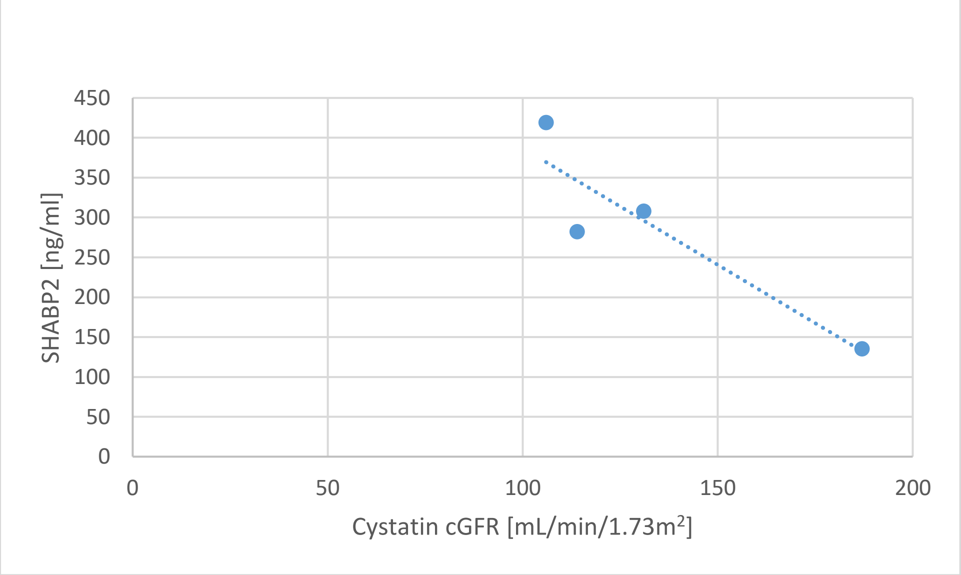
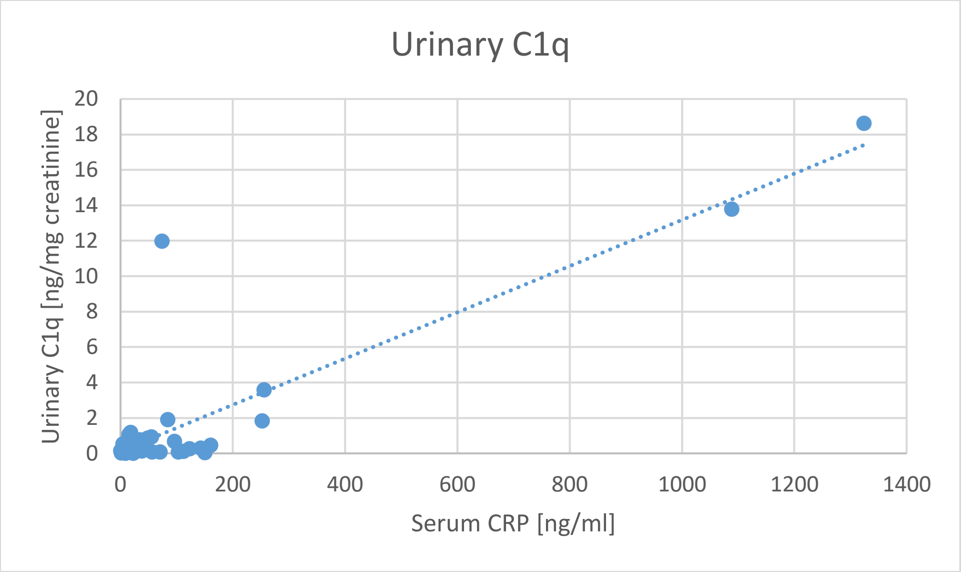


Table S9: Correlation of serum and urinary BM candidates with serum CRP in patients with AS and similar diseases.

	Serum CRP					
BM in→	**Serum**			**Urine**		
↓	**Pearson**	**Spearman**	**n**	**Pearson**	**Spearman**	**n**
ADP	-0.073 0.657	-0.116 0.483	39	-0.15 0.321	-.340* 0.021	46
a1AGP	0.221 0.277	.454* 0.020	26	-0.154 0.317	-0.153 0.321	44
AGT	-0.208 0.204	-0.028 0.864	39	-0.284 0.061	-.363* 0.015	44
ColXIII	-0.081 0.625	0.138 0.401	39	0.06 0.697	0.157 0.307	44
GS	-0.056 0.736	-0.104 0.530	39	-0.213 0.165	-0.274 0.072	44
LRGP1	0.043 0.780	.366* 0.013	45	0.237 0.112	.379** 0.009	46
HABP2	0.152 0.356	0.292 0.071	39	-0.169 0.273	-0.225 0.142	44
PICP	0.226 0.140	0.241 0.115	44	-0.137 0.392	-.370* 0.017	41
TGFß	0.113 0.475	.446** 0.003	42	-0.061 0.689	-.348* 0.018	46
VTN	-0.157 0.303	-0.068 0.657	45	-0.173 0.263	-.312* 0.039	44
C9	-0.097 0.551	0.220 0.173	40	-0.157 0.309	-0.296 0.051	44
C4BP	0.070 0.671	0.293 0.070	39	-0.073 0.638	0.164 0.287	44
CRP	1.000	1.000	47	.592** <.001	.450** 0.003	42
LUM	0.339 0.133	0.106 0.646	21	-0.282 0.228	-0.298 0.202	20
FMN	-0.154 0.363	-0.081 0.634	37	-0.158 0.329	-0.004 0.982	40
CFH	.638** 0.002	0.408 0.067	21	0.028 0.858	0.185 0.228	44
CFI	-0.070 0.738	0.192 0.359	25	-0.097 0.529	-0.068 0.662	44
FGG	-0.541 0.346	-0.500 0.391	5	-0.146 0.367	0.018 0.912	40
C1q	.381* 0.015	.386* 0.014	40	.869** <.001	0.328 0.059	34

Graphical visualization of correlation considered as significant:

Serum complement C1q with serum CRP. First samples



Supplementary Table S10:

ROC analysis, comparison of patients with AS (set1, first visit) with controls

BM	Cut-off	Sensitivity	1-specicicity	AUC	BM * BM	Cut-off	Sensitivity	1-specicicity	AUC
Serum									
ColXIII	3.55	0.800	0.167	0.821					
GS	57.80	0.857	0.333	0.783					
HABP2	343.5	0.727	0.250	0.766					
PICP	14.55	0.909	0.250	0.909					
TGFß	30.19	0.939	0.167	0.960					
C1q	20352	0.743	0.273	0.797					
Urine									
ColXIII	0.85	0.735	0.163	0.859	ColXIII * FMN	8.02	0.821	0.226	0.834
LRGP1	2.01	0.853	0.163	0.882	LRGP * C1q	0.54	0.833	0.179	0.896
HABP2	0.25	0.793	0.233	0.805	CFI * a1AGP	4.66	0.735	0.229	0.789
C4BP	8.67	0.941	0.121	0.943	C4BP * ColXIII	2.59	0.882	0.135	0.903
CFH	21.72	1.000	0.162	0.975	GS * CFH	805.9	0.824	0.214	0.896
FGG	1197	0.786	0.198	0.801	C9 * CFH	1773.3	0.794	0.153	0.889
a1AGP	4.67	0.765	0.281	0.770	CFH * FGG	46353	0.793	0.082	0.849
CRP	5.36	0.800	0.172	0.845	CFH * CFI	53.40	0.800	0.105	0.925
C1q				0.812	CRP * C1q	2.95	0.733	0.093	0.851
					C4BP * ColXIII * HABP2	0.66	0.794	0.105	0.855

ROC analysis by SPSS (cf. Methods section). Only BMs with AUC >0.700 are shown.

Concentration ranges of BMs: Serum: ColXII, HABP2, PICP, TGF-ß1 and C1q, ng/mL, GS, µg/mL.

Urine: ColXIII, HABP2, C4BP, CFH, CFI, FGG, GS, LRGP1, a1AGP, and C1q, ng/mg creatinine; CRP, C9 and FMN, pg/mg creatinine.

Section & Topic	No	Item	Reported on page #
TITLE OR ABSTRACT			
	1	Identification as a study of diagnostic accuracy using at least one measure of accuracy (such as sensitivity, specificity, predictive values, or AUC)	
ABSTRACT			
	2	Structured summary of study design, methods, results, and conclusions (for specific guidance, see STARD for Abstracts)	2
INTRODUCTION			
	3	Scientific and clinical background, including the intended use and clinical role of the index test	3, there is no index test
	4	Study objectives and hypotheses	4
METHODS			
Study design	**5**	Whether data collection was planned before the index test and reference standard were performed (prospective study) or after (retrospective study)	n/a
Participants	**6**	Eligibility criteria	
	7	On what basis potentially eligible participants were identified (such as symptoms, results from previous tests, inclusion in registry)	5, 8
	8	Where and when potentially eligible participants were identified (setting, location and dates)	4, 7, 31
	9	Whether participants formed a consecutive, random or convenience series	
Test methods	**10a**	Index test, in sufficient detail to allow replication	n/a
	10b	Reference standard, in sufficient detail to allow replication	
	11	Rationale for choosing the reference standard (if alternatives exist)	n/a
	12a	Definition of and rationale for test positivity cut-offs or result categories of the index test, distinguishing pre-specified from exploratory	
	12b	Definition of and rationale for test positivity cut-offs or result categories of the reference standard, distinguishing pre-specified from exploratory	
	13a	Whether clinical information and reference standard results were available to the performers/readers of the index test	
	13b	Whether clinical information and index test results were available to the assessors of the reference standard	
Analysis	**14**	Methods for estimating or comparing measures of diagnostic accuracy	12
	15	How indeterminate index test or reference standard results were handled	n/a
	16	How missing data on the index test and reference standard were handled	
	17	Any analyses of variability in diagnostic accuracy, distinguishing pre-specified from exploratory	
	18	Intended sample size and how it was determined	
RESULTS			
Participants	**19**	Flow of participants, using a diagram	
	20	Baseline demographic and clinical characteristics of participants	6, 9, 29-31
	21a	Distribution of severity of disease in those with the target condition	29
	21b	Distribution of alternative diagnoses in those without the target condition	30, 31
	22	Time interval and any clinical interventions between index test and reference standard	
Test results	**23**	Cross tabulation of the index test results (or their distribution) by the results of the reference standard	
	24	Estimates of diagnostic accuracy and their precision (such as 95% confidence intervals)	8, 11, 12, 37, Fig. 4, Table 6
	25	Any adverse events from performing the index test or the reference standard	
DISCUSSION			
	26	Study limitations, including sources of potential bias, statistical uncertainty, and generalisability	16
	27	Implications for practice, including the intended use and clinical role of the index test	
OTHER INFORMATION			
	28	Registration number and name of registry	
	29	Where the full study protocol can be accessed	38

	30	Sources of funding and other support; role of funders	38

AIM

STARD stands for “Standards for Reporting Diagnostic accuracy studies”. This list of items was developed to contribute to the completeness and transparency of reporting of diagnostic accuracy studies. Authors can use the list to write informative study reports. Editors and peer-reviewers can use it to evaluate whether the information has been included in manuscripts submitted for publication.

EXPLANATION

A **diagnostic accuracy study** evaluates the ability of one or more medical tests to correctly classify study participants as having a **target condition.** This can be a disease, a disease stage, response or benefit from therapy, or an event or condition in the future. A medical test can be an imaging procedure, a laboratory test, elements from history and physical examination, a combination of these, or any other method for collecting information about the current health status of a patient.

The test whose accuracy is evaluated is called **index test.** A study can evaluate the accuracy of one or more index tests. Evaluating the ability of a medical test to correctly classify patients is typically done by comparing the distribution of the index test results with those of the **reference standard**. The reference standard is the best available method for establishing the presence or absence of the target condition. An accuracy study can rely on one or more reference standards.

If test results are categorized as either positive or negative, the cross tabulation of the index test results against those of the reference standard can be used to estimate the **sensitivity** of the index test (the proportion of participants *with* the target condition who have a positive index test), and its **specificity** (the proportion *without* the target condition who have a negative index test). From this cross tabulation (sometimes referred to as the contingency or “2x2” table), several other accuracy statistics can be estimated, such as the positive and negative **predictive values** of the test. Confidence intervals around estimates of accuracy can then be calculated to quantify the statistical **precision** of the measurements.

If the index test results can take more than two values, categorization of test results as positive or negative requires a **test positivity cut-off**. When multiple such cut-offs can be defined, authors can report a receiver operating characteristic (ROC) curve which graphically represents the combination of sensitivity and specificity for each possible test positivity cut-off. The **area under the ROC curve** informs in a single numerical value about the overall diagnostic accuracy of the index test.

The **intended use** of a medical test can be diagnosis, screening, staging, monitoring, surveillance, prediction or prognosis. The **clinical role** of a test explains its position relative to existing tests in the clinical pathway. A replacement test, for example, replaces an existing test. A triage test is used before an existing test; an add-on test is used after an existing test.

Besides diagnostic accuracy, several other outcomes and statistics may be relevant in the evaluation of medical tests. Medical tests can also be used to classify patients for purposes other than diagnosis, such as staging or prognosis. The STARD list was not explicitly developed for these other outcomes, statistics, and study types, although most STARD items would still apply.

DEVELOPMENT

This STARD list was released in 2015. The 30 items were identified by an international expert group of methodologists, researchers, and editors. The guiding principle in the development of STARD was to select items that, when reported, would help readers to judge the potential for bias in the study, to appraise the applicability of the study findings and the validity of conclusions and recommendations. The list represents an update of the first version, which was published in 2003.

More information can be found on http://www.equator-network.org/reporting-guidelines/stard.